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Comparative Analysis of Stress Responses in *C. albicans* and *C. dubliniensis*

A thesis submitted to the University of Dublin in fulfilment of the requirements for the degree Doctor of Philosophy by

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April 2006

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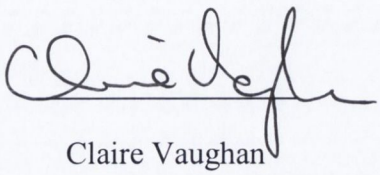

Claire Vaughan

Summary

Candida dubliniensis is apathogenic yeast that was first identified as a novel species in 1995. It is phylogenetically very closely related to *C. albicans*. However, despite the close relationship between the two species, *C. dubliniensis* is significantly less pathogenic. *Candida dubliniensis*, unlike *C. albicans*, grows poorly or not at all at temperatures greater then 42°C and when the thermoprotectant disaccharide trehalose is the only available source of carbon. In order to investigate whether the decreased ability of *C. dubliniensis* to tolerate environmental stresses might contribute to the difference in virulence between the two species the phenotypic and molecular responses of *C. albicans* and *C. dubliniensis* to thermal, osmotic and oxidative stress was compared.

Growth of representative isolates of the two species in liquid media at temperatures ranging between 30°C-44°C, and with NaCl concentrations ranging between 0.6 M-1.6 M was examined. The results confirmed that *C. albicans* strains SC5314 and 132A have a significantly shorter mean doubling time than *C. dubliniensis* strains CD36, CD539, CD514 and p7718 at temperatures >42°C ($P<0.04$). The lower survival rates of *C. dubliniensis* and heat sensitive phenotype observed on agar spot plates further confirmed this data. Similarly, *C. dubliniensis*, unlike *C. albicans*, grows relatively poorly in media containing 0.8 M-1.6 M NaCl as determined by the observed differences in doubling times, survival and spot plate assays. In addition hydrogen peroxide viability and spot plate assays confirmed the increased sensitivity of *C. dubliniensis* to hydrogen peroxide compared to *C. albicans*.

To investigate the molecular basis of the differential ability of *C. albicans* and *C. dubliniensis* to tolerate environmental stress the presence and expression of putative genes known to be instrumental in the responses of *C. albicans* to environmental stress were investigated in *C. dubliniensis* (i.e. *HSP90*, *HSP104*). Northern hybridisation analysis suggested that the faster rate of induction of *HSP90* and *HSP104* observed in *C. dubliniensis* may reflect a lower threshold of temperature tolerance of *C. dubliniensis* compared to *C. albicans*.

In order to investigate the possibility of a defect in the trehalose metabolic pathway in *C. dubliniensis*, expression of the trehalose metabolic genes (i.e. *TPS1* and *NTC1*), intracellular trehalose levels and the activity of the enzymes involved in the

trehalose metabolic pathway were investigated under conditions of environmental stress. Results demonstrated that *C. dubliniensis* has the ability to accumulate trehalose under heat and osmotic conditions and that the trehalose metabolic enzymes of *C. dubliniensis* are functional under conditions of thermal stress. It was also suggested that the accumulation of intracellular trehalose is not dependent on the transcription of the trehalose metabolic genes i.e. *TPS1* and *NTC1*

Another aim of this study was to investigate if specific *C. albicans* genes could be identified that were able to complement the low salt tolerance of *C. dubliniensis*. For this purpose a *C. albicans* genomic library was transformed into the *C. dubliniensis* strain CdMU1B, a Ura$^-$ strain that allows the selection of Ura$^-$-containing vectors, by electroporation and clones were selected on SC Ura$^-$ medium supplemented with 7% (w/v) NaCl. Analysis of the transformants led to the identification of the *C. albicans ENA21.3* gene, a P-type ATPase involved in the extrusion of cations from the cytoplasm.

Since there was no significant difference in conventionally recognised yeast stress response mechanisms transcriptional profiling was used to investigate the global expression of genes in each species in response to elevated temperature (30-42°C, osmotic (1 M NaCl) and oxidative stress (5 mM H_2O_2). The results revealed that *C. dubliniensis* is able to evoke a global transcriptional response to heat, osmotic and oxidative stress. The magnitude and nature of the transcriptional responses varied between *C. albicans* and *C. dubliniensis* reflecting the reduced tolerance of *C. dubliniensis* to high salt concentrations and its lower temperature threshold compared to *C. albicans*. Hierarchical clustering analysis suggested that *C. albicans* and *C. dubliniensis* evoke weak core stress responses compared to *S. cerevisiae* and *S. pombe*. Genes with interesting expression patterns (e.g. *IPF2839, SOD1, GRP2, GPD2, HSP10, AOX1, AOX2, MXR1, ATH1, TRR1, TRX1, SGD1*) were identified which may help explain in part, explain why *C. dubliniensis* is less tolerant of environmental stress compared to *C. albicans*. This study has provided a starting point for the investigation of numerous genes which will help to elucidate the role of stress response mechanisms in the pathogenicity of candidal disease.

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Acknowledgements

First of all I would like to thank my supervisor Dr. Derek Sullivan for his constant support and encouragement, especially when I could see no end. I wish to thank Professor David Coleman for his guidance and for providing me with the opportunity to work in his laboratory. I owe a big thank you to Dr. Gary Moran, for all his technical help, feedback and scone runs!
I am very grateful to Professor Al Brown for giving me the opportunity to work in his laboratory. Thanks to all of lab 2.50 in the Institute of Medical Sciences at the University of Aberdeen for their kindness during my stay. Thanks to Brice for all his great microarray analysis advice. I would also like to thank Professor Patrick Van Dijck for the opportunity to work in his laboratory in Leuven. His advice and expertise were greatly appreciated.

I acknowledge the financial support received from the Health Research Board and the Dublin Dental School and Hospital. I would also like to say thanks to Mary O'Donnell for making sure that the laboratory operated efficiently. I also wish to thank the staff of the Moyne prep room for supplying media and glassware.

I would especially like to thank my work colleagues from the microbiology research unit-Deirdre, Emmanuelle, Caroline, Nicole, Anna, Leanne, Tim, Martin, Rachael, Brenda, Cheryl, Francesco and Asmaa for supporting me. For the invaluable friendships, "interesting" lab nights out and of course for chocolate! In particular, thank you to Anna, for being a constant source of entertainment. But most of all for being such a good friend to me throughout the years. I will miss you all.

To Fiona, for tough love i.e. " get back into that room" and literally, for keeping me sane. I owe you so much. To Daniel for acting the eejit, keeping me smiling and of course for parting with his wireless card "I know it was tough". To my close friends and their bent ears –Michelle (for leggs!), Sinead, Annie K, Annie R, Judith, Eva, Gaffey, Toni, Kellyann, Deirdre (for all the invites!), Mary (for your landline!), Lea, Alan (for Belgium!), John, Evelyn, Michéal, Gar (for the tea bags I didn't need) Olga, Jen, Ethna, Isobel, Kate, Linda, Mary B and Jackie-thank you so much!

Finally, I would like to sincerely thank my family. Thanks to my brother Mark, who never doubted that this day would finally come. But most of all, I would like to thank my parents for their loving encouragement and constant support. I could not have come this far without the two of you.

All I can say is "that's it now!"

Abbreviations

A_{260}	absorption at 260 nm
A_{600}	absorption at 600 nm
AIDS	Aquired immunedeficiency syndrome
ATP	Adenosine5'-triphosphate
β	beta
bp	base pair
Bq	becquerel
BSA	bovine serum albumin
cDNA	Complimentary DNA
cfu	Colony forming units
CGD	*Candida* Genome Database
Ci	curie
CSR	core stress response
Δ	deletion (of part of a gene)
DEPC	diethylpyrocarbonate
DNA	deoxyribonucleic acid
DNase	deoxyribonuclease
dATP	2'-deoxyadenosine 5'-triphosphate
dCTP	2'-deoxycytodine 5'-triphosphate
dGTP	2'-deoxyguanosine 5'-triphosphate
dNTP	dideoxynucleoside
DTT	dithiothreitol
dUTP	2'-deoxyuracil 5'-triphosphate
EDTA	ethylenediamine tetraacetic acid
e.g.	for example
EMBL	European Molecular Biology Laboratory
et al.	and others
FDR	false discovery rate
g	gram
x *g*	gravity
GO	Gene ontology
h	hour(s)
HIV	human immunodeficiency virus
HSP	Heat shock protein
IPF	Individual protein file
IPTG	Isopropyl-β-thiogalactoside
i.e.	that is

kat	Katal, amount of activity that converts one mole of substrate per second
kDa	Kilodaltons
kb	kilobase pair
kg	kilogram
kV	kilovolt
l	litre(s)
L agar	Luria-Bertani agar
L broth	Luria-Bertani broth
M	molar
MAP	mitogen activated protein
MAPK	mitogen activated protein kinase kinase
MES	2-morpholinoethanesulfonic acid
mg	milligram
µg	microgram
mM	millimolar
MIC	minimum inhibitory concentration
min	minute
ml	millilitre
µl	microlitre
ng	nanogram
nm	nanometre
No.	number
ORF	open reading frame
PDA	Potato dextrose agar
PCR	polymerase chain reaction
PEG	polyethylene glycol
PFGE	pulsed-field gel electrophoresis
PMSF	Phenylmethylsulfonyl fluoride
RAPD	random amplified polymorphic DNA
RFLP	restriction fragment length polymorphism
RNA	ribonucleic acid
RNase	ribonuclease
r.p.m.	revolution per minute
RT	Reverse transcription
s	second
SAM	Significance Analysis of Microarrays
SDS	sodium dodecyl sulphate
SGD	*Saccharomyces* Genome Database
SSC	Saline-sodium citrate
STRE	Stress response element

TBE	tris-borate /EDTA
Tris	tris (hydroxymethyl)aminomethane
U	unit
UK	United Kingdom
USA	United States of America
UV	Ultra violet
v/v	% volume in volume: expresses the number of millilitres of an active constituent in 100 millilitres of solution
w/v	% weight in volume: expresses the number of grams of an active constituent in 100 millilitres of solution
X-gal	5-bromo-4-chloro-indoyl-β-D-galactoside
YPD broth	yeast extract peptone broth
YPD agar	yeast extract peptone agar
>	greater than
<	less than
≥	greater than or equal to
≤	less than or equal to

Publication

Sullivan, D. J., Moran, G. P., Pinjon, E., Al-Mosaid, A., Stokes, C., Vaughan, C. & Coleman, D. C. (2004). Comparison of the epidemiology, drug resistance mechanisms, and virulence of *Candida dubliniensis* and *Candida albicans*. *FEMS Yeast Res* **4**, 369-376.

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Chapter 1

General Introduction

1.1 Epidemiology of *Candida* species

Candida species are important human pathogens that are responsible for a wide range of diseases, ranging from superficial (e.g. oral and vaginal thrush) to systemic infections. *Candida albicans* is the species of *Candida* most frequently associated with disease, and the most pathogenic *Candida* species (Coleman *et al.*, 1997a). However, the incidence of systemic infections caused by non-*C. albicans Candida* species such as *Candida tropicalis, Candida krusei,* and *Candida glabrata* has increased dramatically during the last decade (Coleman *et al.*, 1997a and 1997b; Sullivan *et al.*, 2004). The epidemiology of the infections caused by these species differs according to geographical location. The reasons for the apparent prevalence of these species may be related to reduced tolerance to antifungal agents (Groll *et al.*, 1998), or due to lapses in cross infection procedures. A shift in the epidemiology of *Candida spp* has also been observed in cases of oral candidiasis. However, the epidemiology of *Candida* infections was further complicated by the identification in 1995 of a novel *Candida spp.* i.e *Candida dubliniensis* (Sullivan *et al.*, 1995).

1.2 Characterisation of *Candida dubliniensis*

1.2.1 *Candida dubliniensis*

During the early 1990's, epidemiological analysis of *C. albicans* isolates recovered from the oral cavities of HIV-positive individuals in Ireland revealed the presence of an unusual population of isolates, which on the basis of the ability to produce chlamydospores and germ tubes, were identified as atypical *C. albicans* isolates. When fingerprinted with the *C. albicans*-specific DNA probe 27A these were found to hybridise very poorly to this probe. Subsequent analysis revealed that the isolates also yielded unusual carbohydrate assimilation profiles. In order to investigate the precise relationship between these atypical isolates and *C. albicans*, Sullivan *et al.* (1995) carried out detailed phenotypic, genotypic and phylogenetic studies on these atypical isolates from Ireland, Australia, and the UK. When 500 bp of the variable region of the large ribosomal subunit rRNA genes from the nine atypical *C. albicans* isolates used in this study were compared with the corresponding sequences determined from *C. albicans*, *C. stellatoidea, C. tropicalis, C. parapsilosis, C. glabrata, C. kefyr and C. krusei* it was evident that the atypical isolates formed a homogeneous cluster with 100% identity that was

significantly different from the other *Candida* species, including *C. albicans*. These results led to the conclusion that these atypical isolates belong to a novel taxon, which is most closely related to *C. albicans*. For which the name *C. dubliniensis* was proposed.

1.2.2 Phenotypic properties of *Candida dubliniensis*

Since *C. dubliniensis* is phylogenetically very closely related to *C. albicans* both species share many phenotypic properties. Like *C. albicans*, *C. dubliniensis* forms germ tubes and chlamydospores, two features which were previously used to distinguish *C. albicans* from other *Candida* species. Germ tubes represent the very early stages of the growth, of hyphae. True hyphae are filamentous cells that have no visible constrictions at the site of the septa. Both *C. albicans* and *C. dubliniensis* can produce germ tubes when incubated in serum (Sullivan *et al.*, 1995), however, when incubated in medium containing N-acetyglucosamine, *C. dubliniensis* isolates tested fail to produce hyphae (Gilfillan *et al.*, 1998). *Candida dubliniensis* also produces chlamydospores, which are thick walled spherical cells of unknown function that are more rounded than yeast cells and are approximately 8-12 μm in diameter. Although both species produce chlamydospores when grown on rice Tween 80 agar (RAT), or corn meal agar, *C. albicans* chlamydospores are generally produced singly and are attached at the terminal end of hyphae or pseudohyphae via a suspensor cell, whereas *C. dubliniensis* produces chlamydospores more abundantly often in pairs, triplets or clusters attached to individual suspensor cells (Sullivan *et al.*, 1995).

Unlike *C. albicans*, *C. dubliniensis* grows poorly or not at all at temperatures ≥42°C and not at all at 45°C (Pinjon *et al.*, 1998). Growth at a temperature of 45°C was suggested as the basis of a simple test to distinguish between *C. dubliniensis* and *C. albicans* (Pinjon *et al.*, 1998), however, some isolates of *C. albicans* do not grow at this elevated temperature (Kirkpatrick *et al.*, 1998; Gales *et al.*, 1999). *Candida dubliniensis* isolates grow well at 30°C and 37°C on all media used routinely for the growth of *C. albicans* i.e., potatoe dextrose agar (PDA), Sabouraud's agar and Yeast peptone dextrose agar (YEPD). On such media it is impossible to distinguish between the two species, as both *C. abicans* and *C. dubliniensis* form spherical creamy white colonies. However, it is possible to distinguish between the two species on the commercially available

chromogenic medium CHROMagar Candida (Coleman *et al.*, 1997a, Coleman *et al.*, 1995). After 48 h of growth at 37°C *C. dubliniensis* isolates yield dark green colonies, whereas *C. albicans* isolates appear light green. CHROMagar Candida medium is only useful for presumptively identifying *C. dubliniensis* colonies following primary isolation from clinical samples, as *C. dubliniensis* isolates may lose their ability to yield dark green colonies if subcultured or stored (Schoofs *et al.* 1997a). Tintelnot *et al.* (2000) found that the use of colony colour on the CHROMagar Candida was insufficient for selecting *C. dubliniensis* as not all of the *C. dubliniensis* isolates used in this study showed a dark green colour typical for *C. dubliniensis*. Therefore, they suggested the use of CHROMagar Candida for the presumptive identification of *C. dubliniensis* and should be used alongside other phenotypic tests.

More recent studies have shown that *C. dubliniensis* can be distinguished from *C. albicans* on the basis of chlamydospore production and colony morphology when grown on other specific media such as Staib's Niger seed agar (Staib and Morschhauser, 1999). The use of Staib agar as good discriminatory medium was confirmed by Al-Mosaid *et al.* (2001), but on the basis of colony morphology only rather than colony morphology and chlamydospore production. On this agar *C. dubliniensis* isolates form rough colonies and abundant chlamydospores, whereas *C. albicans* isolates grow as smooth colonies composed entirely of yeast cells. Staib agar is a useful medium to discriminate between isolates of *C. albicans* and *C. dubliniensis*, but not absolute, as 2.3% of the *C. dubliniensis* isolates tested were indistinguishable from *C. albicans* based on colony morphology on Staib agar (Al-Mosaid *et al.*, 2003). Hence, Al-Mosaid *et al.* (2003) developed a medium with an even greater discriminatory ability i.e. Pal's agar. The formation of a hyphal fringe surrounding *C. dubliniensis* colonies on Pal's medium provides a definitive means of discrimination between this species and *C. albicans.* However, the authors stated that Pal's agar should be used only to screen isolates that are germ tube and /or chlamydospore positive. Khan *et al.* (2004) concluded that tobacco agar presents yet another simple way for differentiating between *C. albicans* and *C. dubliniensis* with 100 % accuracy. In this study all of *C. dubliniensis* isolates tested produced yellowish-brown colonies with hyphal fringes and formed abundant chlamydospores, while all the *C. albicans* isolates tested appeared as smooth, white to cream colonies with no

hyphal fringes or chlamydospores. These media provide a definitive means for the presumptive differentiation of *C. dubliniensis* and *C. albicans.*

Previous studies have also shown that Fourier transform infrared (FT-IR) spectroscopy can also successfully differentiate between *C. albicans* and *C. dubliniensis* and when used alongside hierarchical clustering it is a phenotypic method which has proved to be as reliable as genotyping (Tintelnot *et al.*, 2000). However, this method is impractical in the routine clinical laboratory.

The use of commercially available biochemical yeast identification systems such as API ID 32C and API 20C AUX revealed that *C. dubliniensis* isolates yield distinct carbohydrate assimilation profiles compared to *C. albicans* and other *Candida* species. Prior to the inclusion of *C. dubliniensis* in the databases of commercially available yeast identification systems such as bioMérieux API ID 32C and API 20C AUX systems, *C. dubliniensis* profiles did not match any profiles in the databases or they gave profiles that corresponded to poor identification of species such as *C. stellatoidea, C. sake* or *C. colliculosa* (Boerlin *et al.*, 1995; McCullough *et al.*, 1995; Sullivan *et al.*, 1995; Coleman *et al.*, 1997a; Schoofs *et al.*, 1997b; Sullivan *et al.*, 1997; Kirkpatrick *et al.*, 1998; Salkin *et al.*, 1998; Gales *et al.*, 1999; Jabra-Rizk *et al.*, 1999a; Tintelnot *et al.*, 2000). A limited number of *C. dubliniensis* profiles were introduced in the databases in 1998, however, Pincus *et al.* (1999) suggested that further modifications to these databases was necessary in order to allow for the correct identification of *C. dubliniensis* to the species level. In addition, Pincus and co workers noted that *C. dubliniensis*, unlike *C. albicans* grows very poorly on media in which the dissacharide trehalose is the only source of carbohydrate. This dissacharide is synthesised by microorganisms as a response to environmental stress. Furthermore, *C. albicans* isolates can be serotyped on the basis of agglutination reactions as either serotype A or serotype B with antisera raised against *Candida* antigenic factor number 6, which is available commercially. All *C. dubliniensis* isolates to date have been found to react with *C. albicans* serotype A antiserum as determined by agglutination reactions with antibodies raised against *Candida* antigenic factor No.6, and with serotype A-specific antisera using flow cytometry (Sullivan *et al.*, 1995; Mercure *et al.*, 1996)

These phenotypic methods provide the basis for species and strain discrimination, however, they are of limited value when used for the comparison

of *C. albicans* and *C. dubliniensis*. For this reason, much effort has been spent in the past few years, in developing more efficient methods to differentiate between *C. albicans and C. dubliniensis* using molecular techniques. This is discussed in the next section.

1.2.3 Genotypic properties of *Candida dubliniensis*

Isolates of *C. dubliniensis* have a number of genetic characteristics which establishes them as a group of organisms distinct from *C. albicans* isolates. The first of these genetic characteristics were identified from DNA fingerprinting studies where *C. dubliniensis* isolates hybridised very poorly to the *C. albicans*-specific fingerprinting probe 27A (Sullivan *et al.*, 1993) which is related to the Ca3 fingerprinting probe (Sadhu *et al.*, 1991). Both of these probes contain a repetitive DNA sequence which is dispersed throughout the *C. albicans* genome. Fingerprinting patterns comprising of 10-15 strongly hybridising bands are usually obtained when *C. albicans* genomic DNA digested with *EcoR*I, is hybridised with these probes. However, when *C. dubliniensis* genomic DNA was digested with *EcoR*I and hybridised in the same manner fingerprinting patterns containing fewer and weaker bands were obtained (Sullivan *et al.*, 1993; Sullivan *et al.*, 1995). DNA from *C. dubliniensis* isolates also yielded a distinct fingerprint pattern when digested DNA samples were hybridised to oligonucleotide probes homologous to microsatellite sequences. Microsatellites, also known as simple sequences, normally consist of mono-, di-, tri-, and tetranucleotide motifs in tandem repeats scattered at random throughout the genome [i.e., $(A)_n$, $(GT)_n$, $(GATA)_n$, $(GACA)_n$, and $(GGAT)_n$] (Sullivan *et al.*, 1995). *Candida dubliniensis* isolates can also be distinguished from other *Candida* species by a variety of other techniques ranging from restriction fragment length polymorhism (RFLP) generated using the enzymes *Hae*III and *Hinf*I (Sullivan *et al.*, 1995; Mc Cullough *et al.*, 1999) to randomly amplified polymorphic DNA (RAPD) analysis, which relies on the use of oligonucleotide primers consisting of sequences chosen at random in low stringency PCR reactions. Furthermore, karyotype analysis of *C. dubliniensis* isolates by pulse field gel electrophoresis of chromosome-sized DNA yielded 9-10 chromosome-sized DNA bands with at least one band or more less than 1 MB in size, compared to *C. albicans* isolates which usually have about seven or eight bands (Sullivan *et al.*, 1995).

Multilocus enzyme electrophoresis (MEE) is a method which examines allelic polymorphisms that results in the alteration of the electrophorectic mobility of proteins in protein gels. To date, MEE studies carried out on *C. dubliniensis* isolates have provided further data to support, *C. dubliniensis*' recognition as a separate and novel *Candida* species.

Joly *et al.* (1999) developed the Cd25 DNA fingerprinting probe cloned from *C. dubliniensis* that contained one or more *C. dubliniensis* species-specific repetitive elements, suitable for the comparison of strains. Cd25 proved to be an effective probe in broad epidemiological studies as it yielded the most stable profiles over time for populations *in vitro* and in *vivo*. Analysis of Cd25-generated profiles using the software package DENDRON divided a world-wide collection of 57 *C. dubliniensis* isolates into two distinct groups, Cd25-group I, and Cd25-group II. Gee *et al.* (2002) confirmed the results of this study using 98 isolates from 94 patients in 15 countries. In the later study 67.7% of the Cd25-group I isolates were from individuals infected with HIV, whereas, 70.4% of the Cd25-group II isolates were from patients not infected with HIV. The Cd25-group I isolates were found to consist of closely related isolates, whereas Cd25-group II isolates were found to be less closely related. Furthermore, Gee *et al.* (2002) identified four distinct genotypes, (genotypes 1-4) following nucleotide sequence analysis of the internal transcribed spacer region (ITS) of the rRNA genes. Genotype 1 contained all of the Cd25 group I isolates, while genotypes 2-4 contained isolates from Cd25 group II. The epidemiological significance of these genotypes is unknown. These studies have helped further improve our understanding of the genetic relatedness of *C. dubliniensis* isolates and their population structure. However, the majority of *C. dubliniensis* studies to date have been associated with individuals from Europe, United States, South America and Australia and until recently not much was known about the incidence of this pathogenic species in the Middle-East. Al-mosaid *et al.* (2005) investigated the genetic relatedness of *C. dubliniensis* isolates recovered from individuals in Saudia Arabia and Egypt by analysis of Cd25-generated fingerprint profiles and rRNA internal transcribed spacer region-based genotyping. The authors identified a novel flucytosine (5FC)-resistant clade of *C. dubliniensis*, called Cd25 III, (Fig. 1.1) that is predominant among isolates from Saudia Arabia, and Egypt and absent from a previously characterised collection of 98 *C. dubliniensis* isolates from 15

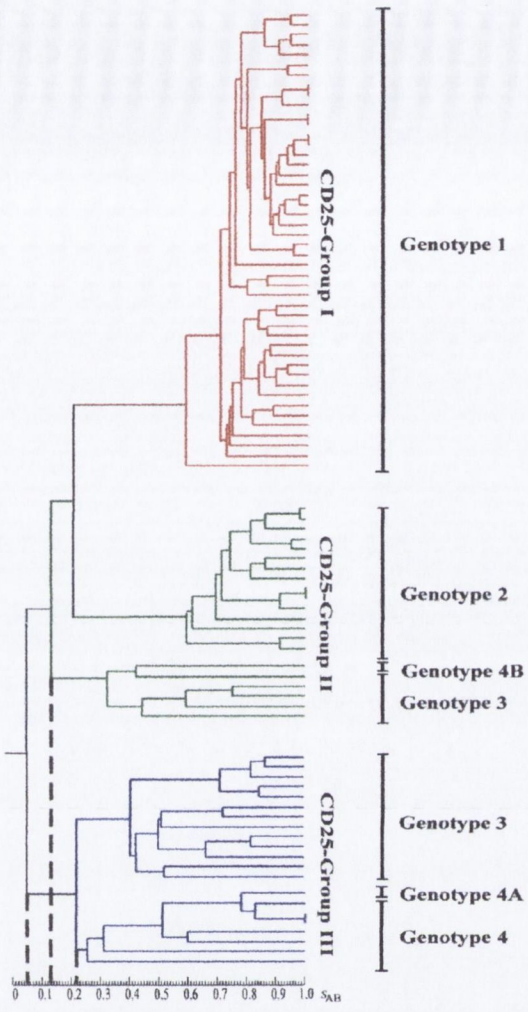


Figure 1.1. Dendogram generated from the similarity coefficient values (S_{AB}^{s}) computed for every possible pairwise combination of independent *C. dubliniensis* isolates from the study of Al- Mosaid *et al.* (2005) showing the three main clades of isolates identified to date based on Cd25 fingerprinting analysis. The ITS (internal transcribed spacer region) genotypes of the isolates within these main clades are shown to the right of the dendogram. Cd25 group III, represents a novel *C. dubliniensis* clade, predominant among Saudia Arabian and Egyptian isolates. All of the isolates, apart from a single isolate were resistant to 5-flucytosine.

countries (Gee *et al.* (2002). From these genotypic studies it is clear that *C. dubliniensis* is a species distinct from *C. albicans*, prevalent throughout the world.

1.2.4 Phylogenetic characteristics

Phylogenetic data based on the analysis of the nucleotide sequences of a variety of non-ribosomal genes including *ACT1*, *MDR1*, *CDR1*, *ERG3*, *PHR1*, *PHR2*, *SAP2* and *HWP1* indicated that *C. albicans* and *C. dubliniensis* are very closely related (Moran *et al.*, 1998, Donnelly *et al.*, 1999, Kurzai *et al.*, 1999; Yokoyama *et al.*, 2000; Moran *et al.,* 2002; Pinjon *et al.*, 2003; Moran *et al.*, 2004). The recent completion of the *C. albicans* genome sequence and the availability of *C. albicans* microarrays has allowed a gross comparison to be made of the *C. albicans* and *C. dubliniensis* genomes. In a recent study Moran *et al.* (2004) co-hybridised *C. albicans* and *C. dubliniensis* genomic DNA to *C. albicans* microarrays. This study revealed that approximately 250 (4.4%) of *C. albicans* genes are divergent (<60% homology) or absent in *C. dubliniensis*.

1.3 The epidemiology of *Candida dubliniensis*

The exact role of *C. dubliniensis* in disease has yet to be determined. Isolates of this new species have been mainly recovered from the oral cavities of HIV- infected and AIDS patients, often in association with other *Candida* species, especially *C. albicans* (Coleman *et al.*, 1997). The most extensive information on the incidence of *C. dubliniensis* in the oral cavity comes from an Irish study. In this study, *C. dubliniensis* was recovered from 32% of AIDS patients with clinical symptoms of oral candidiosis and from 25% of AIDS patients without any symptoms of the disease. A high incidence of recovery of *C. dubliniensis* was also recovered in both symptomatic (26%) and asymptomatic (18%) Irish HIV-infected patients (Coleman *et al.,* 1997b). In contrast, *C. dubliniensis* was only recovered from 3% of Irish HIV-negative healthy individuals. To date the incidence of *C. dubliniensis* amongst HIV-infected individuals appears to be higher than that of HIV-negative individuals (Ponton *et al.,* 2000). However, results from other epidemiological studies vary dramatically and disagree with these data as *C. dubliniensis* prevalence rates ranging from 1.5% to 32% in the oral cavity of HIV-positive patients have been reported (Faggi *et al.*, 2005; Milan *et al.*, 2001; Tekeli *et al.*, 2005; Meiller *et al.*, 1999; Tintelnot *et al.*, 2000 and

Ponton *et al.*, 2000). Epidemiologists are also in disagreement over the prevalence of *C. dubliniensis* in healthy non-HIV-infected individuals. Previous studies reported that *C. dubliniensis* is absent or present at low levels in the oral cavities of healthy patients (Faggi *et al.*, 2005; Ponton *et al.*, 2000; Montour *et al.*, 2003). However recent studies disclosed a high prevalence rate of *C. dubliniensis* in diabetic patients (Willis *et al.*, 2000). Furthermore a recent study from South Africa the prevalence of *C. dubliniensis* was found to be higher in the oral cavities of normal healthy individuals compared to HIV-infected individuals (Blignaut *et al.*, 2003). The reasons for the divergence in the prevalence of *C. dubliniensis* in the literature could be due to differences in methods of sampling and identification, geographical locations and differences in the cohorts of HIV-infected individuals included in theses reports (Sullivan *et al.*, 2004).

Specimens from other anatomical sites where *C. dubliniensis* has also been recovered include blood, faces, urine, sputum and vaginal cultures (Odds *et al.*, 1998; Meis *et al.,* 1999; Meis *et al.*, 2000; Polacheck *et al.*, 2000; Gee *et al.*, 2002). *Candida dubliniensis* has been reported to be a rare cause of systemic candidiasis, unlike, *C. albicans* which accounts for approximately two thirds of all cases of candidemia. Recent studies in the UK and USA reported that *C. dubliniensis* was responsible for only 2% of cases of candidemia (Sebti *et al.,* 2001; Kibbler *et al.,* 2003). Limited experimental data from animal models have shown that the survival rate of mice infected with *C. albicans* was higher than that of mice infected with *C. dubliniensis* (Gillfillan *et al.*, 1998; Vilela *et al.,* 2002). These data correlate with epidemiological data and suggest that *C. albicans* is significantly more pathogenic than *C. dubliniensis.*

Candida dubliniensis is the *Candida* species most closely related to *C. albicans*, and both species share many phenotypic properties (e.g. the ability to produce germ tubes and chlamydospores). Because of this close relationship, it is often difficult to distinguish between the two species in the routine laboratory. However, rapid and accurate methods have been developed for the reliable identification of *C. albicans* in clinical samples. The most reliable methods of identification of *C. albicans* to date are PCR tests (Donnelly *et al.,* 1999; Kurzai *et al.,* 1999; Tamura *et al.*, 2000).

1.4 Virulence of *C. dubliniensis*

The virulence attributes of *Candida* species include their ability to adhere to host epithelial cells, their ability to form hyphae, their ability to produce extracellular enzymes and their ability to exhibit phenotypic switching, which is thought to enable cells to avoid antibody recognition (Slutsky *et al.*, 1987; Odds, 1988; Monod *et al.*, 1998; Schaller *et al.*, 1999 and 2000). *Candida albicans,* which is considered the most pathogenic of the medically important *Candida* species, is known to exhibit all of these putative virulence factors.

Limited experimental data from animal models have shown that the survival rate of mice infected with *C. dubliniensis* was higher than that of mice infected with *C. albicans* (Gillfillan *et al.*, 1998; Vilela *et al.,* 2002). Gilfillan *et al.* (1998) studied the virulence of four *C. dubliniensis* isolates and demonstrated that they were less virulent than *C. albicans* isolates when an inoculum size of 2x 10^6 cells per mouse was used. When a higher inoculum was used (1 x 10^7) there was a wide variation in the mean survival times amongst the mice infected with *C. dubliniensis* (Vilela *et al.,* 2002). Histopathological analysis of infected organs revealed that *C. dubliniensis* remained in the yeast form while *C. albicans* formed hyphae. This finding, may in part explain the lower virulence of *C. dubliniensis* in the animal model (Vilela *et al.,* 2002). These animal model data reflect with epidemiological data and suggest that *C. albicans* is significantly more pathogenic than *C. albicans.* However, the reasons for this are currently unknown.

A vital trait of most pathogens, often considered to be the first step of infection is the ability to attach and invade host cells. In order for colonisation to take place yeast cells must adhere to the surface of host cells, tissues or prosthetic materials, such as catheters, or bind with other microorganisms. The adherence of *Candida* cells to host tissue is one of the first steps in the progression of candidiasis. There have been several studies to date which have compared the adherence of *C. albicans* and *C. dubliniensis* to buccal epithelial cells. McCullough *et al.* (1995) reported that *C. dubliniensis* were more adherent than *C. albicans* to buccal epithelial cells. However, few other studies are in agreement with this report (Gilfillan *et al.*, 1998; Jabra-Rizk *et al.*, 2001). Gilfillan *et al.* (1998) demonstrated that *C. dubliniensis* isolates were more adherent to buccal epithelial cells than *C. albicans* when the organisms were grown in glucose-rich medium. In contrast, depending on the conditions used, *C.*

albicans isolates were more adherent to buccal epithelial cells than *C. dubliniensis* (Gilfillan *et al.,* 1998; Borg-von Zepelin *et al.*, 2002). It is difficult to compare the results obtained from these studies as different conditions were used in each of them. However, in the presence of fluconazole *C. dubliniensis* cells were more adherent to vero cells, which might in part explain the high prevalence of *C. dubliniensis* in HIV-positive and AIDS patients receiving fluconazole therapy (Borg-Von Zepelin *et al.*, 2002).

Cell surface hydrophobicity expression varies greatly between *C. albicans* and *C. dubliniensis*. Unlike *C. albicans*, *C. dubliniensis* is hydrophobic at 25°C and 37°C, however what contribution, if any, this might have to the virulence of *C. dubliniensis* is unknown (Hazen *et al.,* 2001; Jabra-Rizk *et al.*, 2001).

Several genes with putative virulence functions have been identified in *C. albicans*, including *HWP1*, that encodes a hypha-specific substrate for host transglutaminases that mediates adhesion to epithelial cells (Staab *et al.*, 1999). Although, there is a homologue of the *HWP1* gene in the *C. dubliniensis* genome, the *C. dubliniensis HWP1* gene has several deletions in the domain containing the transglutaminase substrate activity compared to the *C. albicans HWP1* gene (Moran *et al.*, 2004). The divergence of the *HWP1* gene in *C. dubliniensis* compared to *C. albicans* may contribute to the observed differences in virulence between these two species.

The *ALS* (agglutin-like sequence) gene family is well characterised in *C. albicans* and its proteins are believed to play an important role in the pathogenesis of this species. Heterologous expression of the *ALS* genes in *S. cerevisiae* confers an adherence phenotype on the organism, suggesting that the Als proteins play a role in adhesion to host surfaces (Calderone and Braun 1991). *ALS* gene expression and cell wall protein production of *C. albicans* is regulated differently compared to *C. dubliniensis*. *ALS* Northern blots of *C. dubliniensis* total RNA contrast sharply with the appearance of *ALS* Northern blots of *C. albicans,* in two ways: a seemingly increased number of expressed genes in *C. dubliniensis* and the apparent constitutive nature of the gene expression in *C. dubliniensis* (Hoyer *et al.*, 2001).

The *SAP* (secreted aspartyl proteinase) gene family is another well characterised gene family of *C. albicans* believed to be involved in the attachment and invasion of *Candida* cells during infection (Borg and Ruchel, 1988) The *SAP*

gene family has 10 members (Monod and Borg Van Zepelin., 2002; Naglik *et al.*, 2003) and Gillfillan *et al.* (1998) identified seven of these *C. albicans SAP* gene homologues in *C. dubliniensis* by Southern analysis. McCullough *et al.* (1995) demonstrated that *C. dubliniensis* isolates produced a higher level of proteinase compared to *C. albicans* isolates, however this was contradicted in a study by Hannula *et al.* (2001) where isolates of *C. albicans* were found to exhibit higher proteolytic activity compared to *C. dubliniensis* isolates. Comparative genomic array studies carried out between *C. albicans* and *C. dubliniensis* using *C. albicans* DNA microarrays revealed that the *SAP5* was absent in *C. dubliniensis* and that this species only has one *SAP* gene that is homologous to *SAP4* and *SAP6* of *C. albicans*. The *SAP4-6* genes of *C. albicans* play an integral role in the establishment of systemic infections in mice and have been shown to be upregulated in hyphal cells. These findings may explain in part why *C. dubliniensis* is less able to establish systemic infections compared to *C. albicans* (Felk *et al.*, 2002).

In recent years, the increased use of invasive devices such as catheters has intensified the need to understand the mechanisms involved in the colonisation of these medical devices to prevent infection. In bacteria, one means of survival utilised by many oral species is the ability to form biofilms, which confers in some measure resistance to antimicrobial drugs, most likely because the drugs can not penetrate the biofilm matrix (Baillie & Douglas, 1998). In fact most manifestations of candidiasis are associated with biofilm formation. Growth competition assays carried out by Kirkpatrick *et al.* (2000) showed that *C. albicans* forms biofilms *in vitro* and that *C. albicans* exhibited a competitive advantage over *C. dubliniensis* under planktonic conditions. However, in similar experiments using a piece of PVC as a supporting structure to allow the formation of biofilm, *C. dubliniensis* was better able to withstand the competitive pressures from *C. albicans* (Kirkpatrick *et al.*, 2000). Ramage *et al.* (2001) also demonstrated *C. dubliniensis*' ability to form biofilms on the surfaces of polystyrene and acrylic materials. In the same study, susceptibility testing on *C. dubliniensis* biofilms against commonly used antifungals such as fluconazole and amphotercin B, demonstrated increased resistance of sessile *C. dubliniensis* cells compared to planktonic *C. dubliniensis* cells and also revealed that *C. dubliniensis* biofilms were intrinsically resistant to fluconazole. Thus, the formation of

biofilms by *C. dubliniensis* cells may play a significant role in the survival of this species. To date, little is known about interspecies interactions between *C. albicans* and *C. dubliniensis*, yet these species have been frequently co-isolated concomitantly from the oral cavities of immunocompromised patients (Coleman *et al.*, 1997a and 1997b).

Morphogenesis is another important virulence determinant of *C. albicans* that is associated with invasiveness of this organism. The ability to grow either in the yeast or hyphal form is called dimorphism. The clinical implications of dimorphic behaviour remain unclear as both yeast and hyphal forms of *Candida* cells have been observed in infected tissue. However, the hyphal form of *C. albicans* is thought to be more adherent than the yeast form and hyphae are more likely to be able to penetrate tissue (Cutler, 1991). *Candida albicans* and *C. dubliniensis* are the only two *Candida* species able to produce germ tubes and true hyphae. Although, Gilfillan *et al.* (1998) suggested that the kinetics of hyphal formation were slower in *C. albicans* compared to *C. dubliniensis,* under certain circumstances, like on Pal's agar, *C. dubliniensis* produces hyphae while *C. albicans* cannot (Al-mosaid *et al.*, 2003). Even though hyphal induction is differentially regulated in these two species *C. dubliniensis* may be as capable as *C. albicans* at penetrating the epithelial layers of host tissues and thus may explain the primary association of *C. albicans* with superficial infections of the oral mucosa (Coleman *et al.*, 1997a and 1997b).

Another important factor which may contribute to *C. albicans* virulence is phenotypic switching. Phenotypic switching is thought to aid survival in different microniches and to help evade the immune response. This phenomenon of phenotypic switching has been well documented in *C. albicans* (Slutsky *et al.*, 1985 and 1987; Gallagher *et al.*, 1992). Phenotypic switching has also been reported in *C. dubliniensis* and this species has also been shown to exhibit phenotypic switching more frequently than *C. albicans* which may contribute to its virulence (Hannula *et al.* 2000).

1.5 Stress responses of *Candida*

Most cells have adapted to grow and function optimally under very specific environmental conditions (for e.g. temperature, pH, osmotic and

oxidative). Alterations to these conditions can lead to the disruption of normal cell processes and ultimately affect the cells survival. In particular, fluctuations in the external environment can prevent optimal enzyme activities, disrupt metabolic pathways and destabilise cellular structures which can leave the cell in an unstable state. The ability of cells to react to sudden and dramatic changes in their environment, known as environmental stress, is critical in order for them to survive. In order to cope with the harmful effects of stress, many cell types have developed response mechanisms to repair damage and protect against further exposure to the same and other types of stress. In general, these responses involve temporary changes in the expression of genes encoding proteins that protect the cell against the stress encountered (Estruch, 2000). These proteins are called stress proteins and their synthesis is the best characterised response to stress.

The human body contains a wide range of niches with very specific environmental conditions. During the course of an infection *Candida* cells are faced with many changes in their immediate microenvironment (e.g. variation in nutrient availability, osmolarity, pH) and also have to face exposure to host immune responses. The apparent success of *C. albicans* as a pathogen relies in part on its ability to adapt to these changing and often challenging conditions. For instance, the ability of *C. albicans* to tolerate oxidative stress is very likely to play a role in its ability to escape oxidative killing by macrophages (Lo *et al.*, 1997). Although *C. albicans* has developed response mechanisms to protect itself from stresses that it encounters during disease progression, the regulation of these underlying pathways and the signal that activates them remain to be elucidated.

1.5.1 The general stress response

Our understanding of yeast stress responses is largely based on studies on the model budding yeast *Saccharomyces cerevisiae* and the model fission yeast *Schizosaccharomyces pombe*. Yeast cells exposed to a mild stress (e.g. 0.4 mM H_2O_2) for a short period can develop increased tolerance to higher, normally lethal, doses of the same stress. Stress proteins, induced already by a mild stress, are responsible for this adaptative response observed in yeast cells. The adaptative response can also lead to acquired resistance to other types of unrelated stress (Jamieson, 1992; Lee *et al.*, 1995; Moradas-Ferreira and Costa, 2000), a phenomenon known as cross-protection. Cross-protection suggests that unrelated

stresses can activate similar stress response mechanisms or that there is a general stress response system present. *Saccharomyces cerevisiae* is able to mount a general stress response, in that it induces a set of genes specific to the stress encountered, while at the same time inducing a set of genes common to a range of unrelated stresses (Ruis and Schuller, 1995). A general stress response system is a system that regulates the induction of many stress genes through a common *cis* element in their promoter. This element is known as the stress response element, STRE which has the concensus sequence "CCCCT" (Marchler *et al.*, 1993; Martinez-Pastor *et al.*, 1996; Schmitt and McEntee *et al.*, 1996). In order to investigate the global response of yeast cells to a range of environmental conditions, transcript profiling was carried out on *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001) and on the non-pathogenic model fission yeast *S. pombe* (Chen *et al.*, 2003). The data obtained from these studies revealed that a large portion of their genomes exhibit a response referred to as the Environmental Stress Response (ESR) or the Common Environmental Response (CER) in *S. cerevisiae* and the Core Environmental Stress Response (CESR) in *S. pombe*. The core stress responses of these two non-pathogenic yeasts are differentially regulated (Fig.1.2). The Styl stress activated protein kinase (SAPK) pathway is singly responsible for the regulation and the control of the CESR in *S. pombe*. In contrast, the CER/ESR in *S. cerevisiae* is not regulated by one single pathway but by a common set of genes, which are controlled by different signalling pathways and transcription factors. An example of this is the Hogl (high osmolarity glycerol) SAPK of *S. cerevisiae*, a homologue of the *S. pombe* Styl SAPK, but unlike the *S. pombe* Styl SAPK, the Hogl SAPK of *S. cerevisiae* regulates the core stress genes in response to hyperosmotic shock (Posas *et al.*, 2000; Rep *et al.*, 2000; O'Rourke *et al.*, 2002; O; Rourke and Herskowitz, 2004) but not in response to other stresses (Gasch *et al.*, 2001).

Although much less is known about the stress responses of *C. albicans*, microarrays have recently been used to investigate the global regulation of genes in response to specific environmental conditions. Transcript profiling of *C. albicans* in response to thermal, osmotic and oxidative stress conditions, similar to those conditions used to induce a core stress response in *S. cerevisiae* and *S. pombe*, revealed the absence of a general stress response (Enjalbert *et al.*, 2003). In addition, the Msn2p and Msn4p transcription factors have been shown to play a

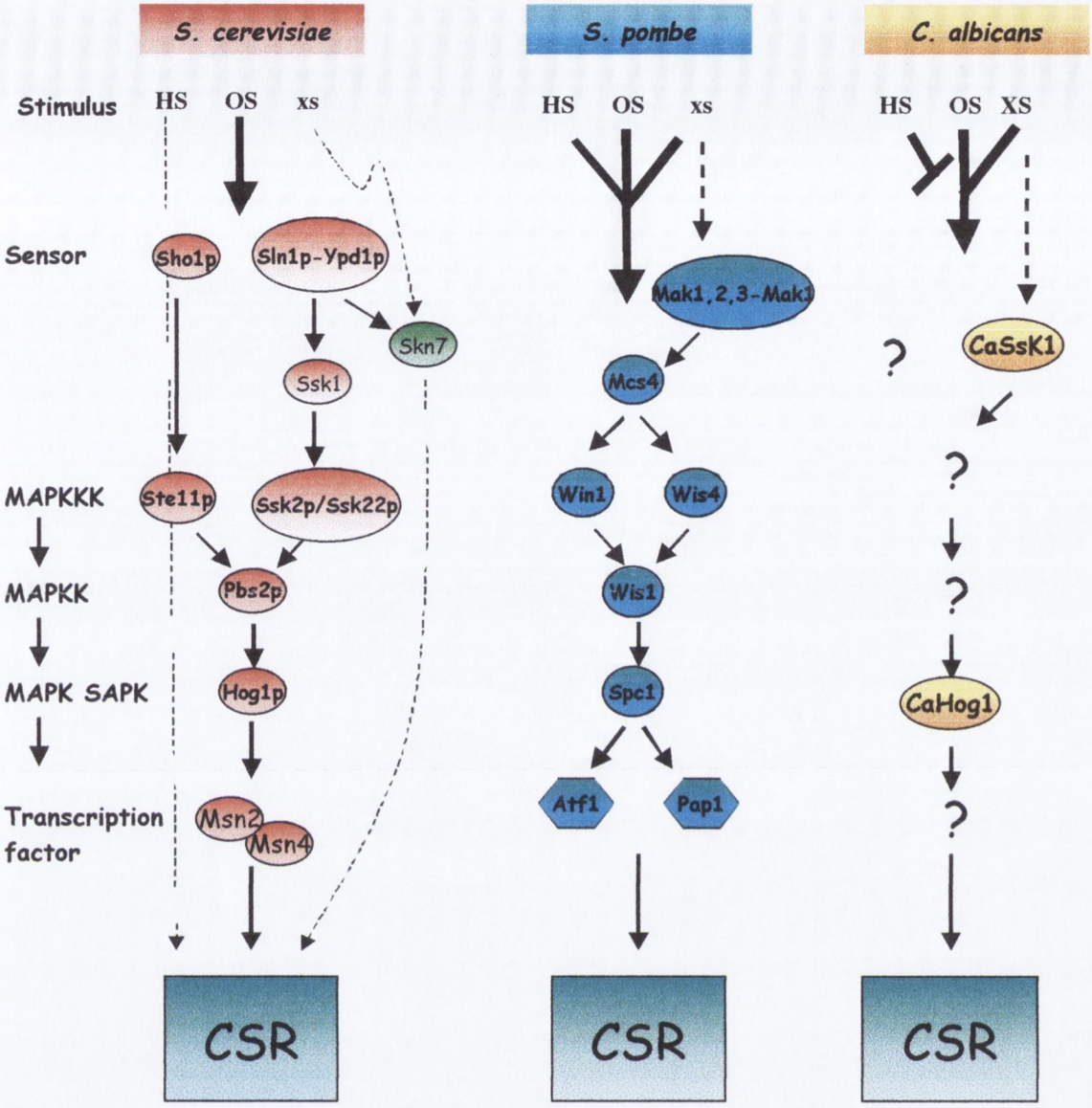


Figure 1.2. Regulation of core stress responses (CSR) in *S. cerevisiae*, *S. pombe* and *C. albicans*. In each case the stress response pathway contains a central core consisting of a serine/threonine kinase (MAPKKK); a dual specificity kinase, MAPKK; and a serine/threonine kinase, MAPK. In *S. pombe* the SAPK Spc1 cascade is activated by osmotic, heat and oxidative stress and controls the activity of transcription factors (Atf1and Pap1) to induce gene expression. Although the core stress responses in *S. cerevisiae* and *S. pombe* are activated by similar conditions, *S. cerevisiae* differs in that it regulates its core stress responses by stress specific pathways. For example, the *S. cerevisiae* Hog 1 cascade regulates core stress genes in response to osmotic stress but not other stresses. Osmostress signals are transmitted to Pbs2 MAPKK by two independent osmosensors, Slnp-Ypd1p-Ssk1p and Sho1p. Ssk2 and Ssk22 MAPKKKs (orthologs of Wis4 and Win1 in *S. pombe*) transmit signals from Ssk1 and activates the Pbs2p/Hog1p kinase cascade by phosphorylation of Pbs2p. The second pathway, Sho1p, activates the Pbs2p/Hog1p kinase cascade through Ste11p MAPKKK. The *S. cerevisiae* response regulator, Skn7 is under the regulation of Sln1p-Ypd1, but oxidative stress activates Skn7 independently of this mechanism. In *C. albicans* the Hog 1p SAPK cascade is activated in response to both heat and osmotic shock. The CaHog 1 MAPK is the only component of the SAPK cascade identified in *C. albicans*, to date. The CaSsk1response regulator is required for the activation of the CaHog1 SAPK cascade in response to oxidative stress. HS, heat stress; OS, osmotic stress; XS, strong oxidative stress; xs, low oxidative stress.

crucial role in the recognition of the STRE element in the promoters of the stress response genes of *S. cerevisiae*. However, their *C. albicans* homologues are not involved in *C. albicans* stress responses (Nicholls *et al.*, 2004). From these studies, it is evident that *C. albicans* stress response mechanisms differ from the stress response mechanisms of the model yeasts *S. cerevisiae* and *S. pombe* . However, as in *S. cerevisiae* and *S. pombe,* the Hog 1 SAPK is involved in the stress signalling network of *C. albicans*. Hog1 SAPK, the homologue of the *S. pombe* Sty1 SAPK, plays a significant role in the osmotic and oxidative stress responses of *C. albicans* (San Jose *et al.*, 1996; Alonso-Monge *et al.*, 2003; Smith *et al.*, 2004). In *S. pombe,* the Sty1 SAPK regulates the general stress response of this yeast (Chen *et al.*, 2003). In contrast, Enjalbert *et al.* (2003) demonstrated the lack of a general stress response in *C. albicans* under conditions that activate a general stress response in *S. cerevisiae* and *S. pombe*. However, Smith *et al.* (2004) suggested that a SAPK–dependent core stress response does exists in *C. albicans* and that the Hog 1 SAPK plays a key role in the regulation of this core stress response. Furthermore, it has since been suggested that Enjalbert *et al.* (2003) did not observe a general stress response in *C. albicans* because only one of the three conditions used (i.e. osmotic (0.3 M NaCl) in their transcript profiling study activates the Hog1 SAPK (Smith *et al.* 2004). Moreover, the three conditions used in the same study (i.e. oxidative (0.4 mM H_2O_2), osmotic (0.3 M NaCl) and temperature (23°C-37°C)) were previously shown to induce a strong stress response in *S. cerevisiae* but failed to do so in *C. albicans* (Gasch *et al.*, 2000; Enjalbert *et al.*, 2003). It was also noted that, unlike the Sty1 *S. pombe* SAPK, the *C. albicans* Hog1 SAPK pathway is not activated in response to a temperature shift (23°-42°C) and requires higher levels of oxidative stress for its activation (>2 mM H_2O_2) (Smith *et al.*, 2004). The same authors suggested that the core stress response observed in *C. albicans* reflects the adaptation of this species on and within the human body. *S. cerevisiae* and *S. pombe* are both non-pathogenic yeasts and thus occupy different microenvironments to the pathogen *C. albicans*. It has already been shown that *C. albicans* exhibits increased tolerance to oxidative and heat stress compared to *S. cerevisiae* and *S. pombe* (Jamieson *et al.*, 1996; Smith *et al.*, 2004). Thus, the activation of the *C. albicans* Hog1 SAPK pathway in response to strong oxidative stress and its failure to respond to temperature may allow *C. albicans* to evade phagocytic attack and

reflects on its ability to adapt to warm blooded hosts, for example in humans where temperatures are maintained consistently at 37°C. This core stress response in *C. albicans* has evolved to aid its pathogenicity, thus emphasising the importance of the link between stress responses and the virulence of *C. albicans,* and the necessity of elucidating the roles of the underlying mechanisms of the stress responses of this pathogen. The response of *C. albicans* to heat, oxidative and osmotic stress is discussed in detail in the next section.

1.5.2 Response to heat shock

The best characterised stress response displayed by yeast cells is the heat shock response (Piper, 1998). Following a heat shock, yeast cells synthesise a large set of conserved proteins which are collectively known as heat shock proteins (Hsps). Heat shock proteins play an important role as molecular chaperones (Ellis, 1987) and even play a vital part in unstressed cells by associating with new proteins and assisting in their folding (Beckmann *et al.*, 1990; Ang *et al.,* 1991; Gething and Sambrook, 1992). Molecular chaperones prevent protein aggregation by binding to exposed hydrophobic residues of non-native polpeptides. The unfolded or improperly folded protein enters the molecular chaperone where it is folded and then released. Energy from the folding comes from ATP (Fig. 1.3). In addition, under conditions of heat shock, Hsps help facilitate the disaggregation and refolding of heat denatured proteins (De Virgilio, 1994). *Saccharomyces cerevisiae* has at least 52 different proteins which are induced in response to a temperature shift from 25-38°C (Boy–Marcotte *et al.*, 1999). In *S. cerevisiae*, the induction of genes in response to heat shock is controlled by two regulatory elements called the STRE, discussed in section 1.5.1, and the heat shock element (HSE). HSEs are binding sites for the heat shock factor (Hsf), a transcriptional regulator, encoded by the *HSF1* gene (Wiederrecht *et al.*, 1988). Under normal growth conditions, Hsf1ps basal activity is enough to bind HSE and allow the expression of Hsps required for normal cellular activities. Following a temperature stress, the level of *HSF1* transcriptional activity increases and subsequently diminishes after the heat shock is removed (Bulman and Nelson, 2005).

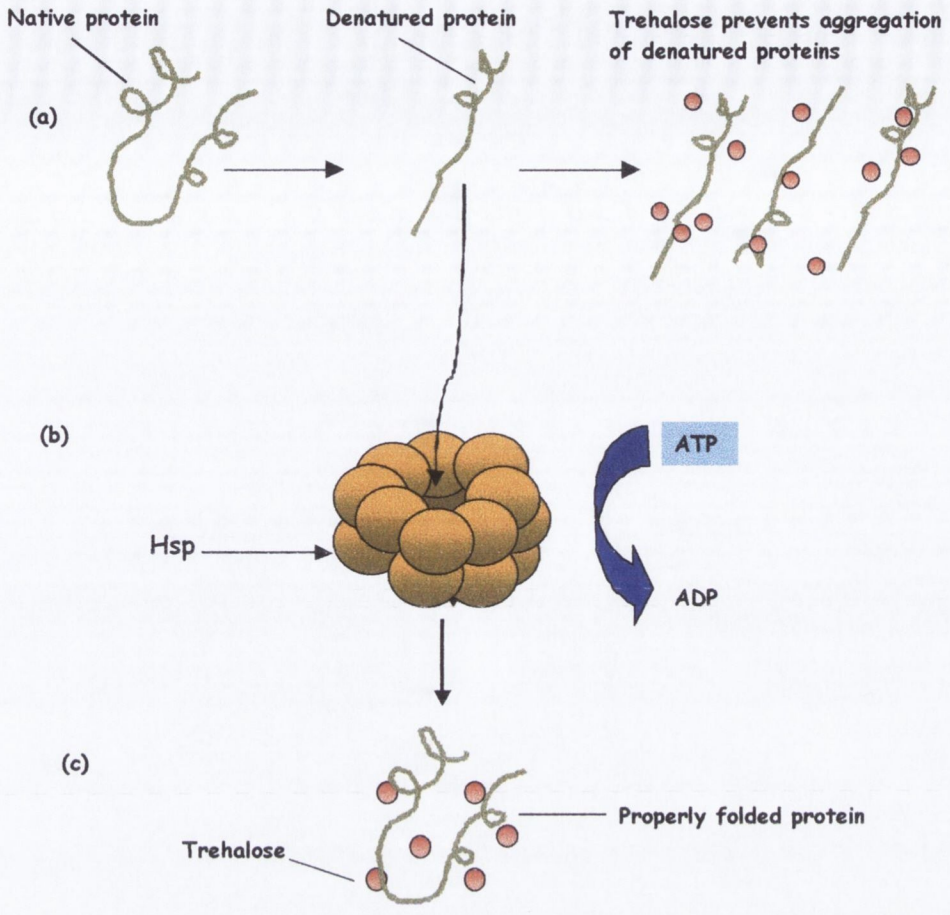


Figure 1.3. Under conditions of high temperature proteins can denature. Those proteins that do unfold are prevented from aggregating by trehalose **(a)** and are also bound by Hsps **(b)** and refolded. ATP is used to supply the energy required to fold the protein. Trehalose also helps prevent native proteins from denaturing **(c)**.

Heat shock proteins are also major targets for the immune response to several infections including candidiasis (Matthews *et al.*, 1989; Swoboda *et al.*, 1993). Several families of Hsps exist which are designated according to their average molecular mass, and genes coding for proteins belonging to the Hsp90 and Hsp70 families have been identified in *C. albicans* (Bromuro *et al.*, 1998; La Valle *et al.*, 1995; Swoboda *et al.*, 1995). In *C. albicans*, three genes related to the hsp70 protein family have been identified. In *S. cerevisiae,* there are at least 10 genes, classified into five families from *SSA* to *SSE* (La Valle *et al.*, 1995; Lopez-Ribot *et al.*, 1996; Bromuro *et al.*, 1998; Estruch, 2000). The *SSA* familiy of *S. cerevisiae* has four members (*SSA1-SSA4*) and requires high levels of at least one of these proteins for cell viability. The Hsp70s not only play a role in protein folding and heat shock protection but also in gene regulation (Estruch, 2000). Interestingly, the *C. albicans* Hsp70, although a highly immunogenic protein, located in the cell wall, enhanced *Candida* infection in a mouse model (Bromuro *et al.*, 1998).

One of the most important molecular chaperones is Hsp90. *Saccharomyces cerevisiae* contains two genes encoding Hsp90, termed *HSC82* and *HSP82* and at least one of the two isoforms has to be maintained for viability (Borkovich *et al.*, 1989). Although two genes encoding isoforms of Hsp90 have been identified in *S. cerevisiae* a single gene has been identified in *C. albicans.* Repeated attempts to construct *a C. albicans* Hsp90 homozygous mutant failed, indicating the presence of a single locus, which has been shown to be essential for viability (Swoboda *et al.*, 1995). Another important Hsp in *S. cerevisiae* is *HSP104,* a Hsp that, although dispensable for growth of *S. cerevisiae* at moderate temperatures, (Sanchez *et al.,* 1990; Lindquist *et al.,* 1996) under extreme temperatures, it is the main factor responsible for the acquisition of stress induced tolerance (Sanchez and Lindquist, 1990). *HSP104* encodes an Hsp100/Clp ATPase with two ATP- binding sites, both of which are essential for thermotolerance (Parsell *et al.,* 1991). It promotes survival of yeast cells by mediating the resolubilisation of polpeptides that have already begun to aggregate in the cytosol (Parsell *et al.*, 1994).

With the advent of DNA microarrays, global transcriptional profiling has since been used to examine the stress response of *C. albicans* to elevated temperature. Using conditions previously used to induce a classic heat shock

response in *S. cerevisiae*, Enjalbert *et al.*, (2003) demonstrated *C. albicans* ability to also induce a classic heat shock response. Hallmark heat shock genes such as *HSP12*, *HSP70*, *HSP78* and *HSP104* all showed an induction greater than or equal to twofold. In contrast to *S. cerevisiae* where *HSP30* is upregulated (12-fold), there is no induction at all of the *C. albicans HSP30* in response to heat shock (Gasch *et al.*, 2000). It was also noted that the *C. albicans HSP12* is strongly induced under conditions of high osmotic shock and poorly induced under heat shock conditions, while the homologous gene in *S. cerevisiae* is strongly induced under both of these conditions (Schuller *et al.*, 1994; Varela *et al.*, 1995). The accumulation of the dissacharide trehalose has also been implicated in the response to heat shock and this is discussed further in section 1.5.5

1.5.3 Response to oxidative stress

Approximately 1% of the 10^{12} oxygen molecules per cell that are metabolised during respiration result in the formation of reactive oxidative species (ROS), including the hyroxy radical (OH),the superoxide anion (O_2^-) and hydrogen peroxide (H_2O_2) (Jackson *et al.*, 2001). Metabolic processess such as respiration or β oxidation of fatty acids are internal sources of ROS, while phagocytes of the host are a major source of ROS. ROS are toxic in nature and react oxidatively with the nucleic acids, lipids and proteins of the cell, resulting in enzyme deactivation, membrane disruption and ultimately death (Halliwell and Gutteridge; 1990 and 1999). By understanding how *C. albicans* senses and responds to ROS, one can determine how this pathogen evades the oxidative killing mechanisms of the neutrophil-macrophage system, a system which is essential in the control and outcome of infections. Thus, in order to evade the harmful nature of these ROS, yeast cells have developed response mechanisms involving the following: (1) induction of detoxifying enzymes such as catalase, superoxide dismutase and peroxidase (2) synthesis of non-enzymic molecules (i.e glutathione and thioredoxin) and (3) accumulation of the dissacharide trehalose (Mager and Varela, 1993; Jamieson, 1998; Estruch, Moradas-Ferreira *et al.*, 2000; Benaroudj *et al.*, 2001; Alvarez-Peral *et al.*, 2002).

Catalase functions by catalysing the breakdown of toxic H_2O_2 to O_2 and H_2O. *S. cerevisiae* cells possess two different catalase enzymes, catalase A which is located in the peroxisome and encoded by the *CTA1* gene and cytoplasmic

catalase T which is encoded by the *CTT1* gene. The principal function of catalase A is to remove H_2O_2 arising from fatty acid β-oxidation, whereas the role of *CTT1* is unclear, although it has been implicated in stress response (Jamieson, 1998; Schuller *et al.*, 1994). *CTT1* expression is regulated by the transcription factors Yap1p and Skn7p. In *C. albicans,* there seems to be only one catalase present, *CTA1*, which is the homolog of the *S. cerevisiae* cytoplasmic catalase T (*CTT1*).

Another group of detoxifying enzymes produced by yeast cells to combat the harmful effects of ROS are the superoxide dismutases. Superoxide dismutase (Sod) is an antioxidant enzyme that acts by catalysing two molecules of superoxide anion to hydrogen peroxide and water. Sods are generally classified according to the metal cofactor that binds to them: there are iron (FeSod), manganese (MnSod), copper and zinc (CuZnSod), and nickel (NiSod) (Fridovich, 1995; Youn *et al.*, 1996). *S. cerevisiae* contains a copper and zinc bound Sod (*SOD1*) and also a manganese bound Sod (*SOD2*) both of which are under the control of Skn7 and Yap1 for H_2O_2 induction (Lee *et al.*, 1999). To date, six Sods have been identified in *C. albicans*: *SOD1* (CuZnSod), *SOD2* (mitochondrial MnSod), *SOD3* (cytoplasmic MnSod) and three additional CuZnSods; *SOD4*, *SOD5* and *SOD6* (Hwang *et al.*, 1999; Rhie *et al.*, 1999; Lamarre *et al.*, 2001 and Martchenko *et al.*, 2004). CuZnSod (*SOD1*) mutants of *C. albicans* display increased susceptibility to macrophage attack, delayed hyphal growth on spider medium and decreased virulence in intravenously injected immunocompetent mice compared to their wildtype strains, indicating that *SOD1* is required for *C. albicans* oxidative response (Hwang *et al.*, 2002). However, the Sod2 of *C. albicans*, although playing no apparent direct role in virulence serves to protect the cell against superoxides that have been produced intracellularly (Hwang *et al.*, 2003). As in *S. cerevisiae* and *S. pombe* (Costa *et al.*, 1993;1997; Davidson *et al.*, 1996; Pereira *et al.*, 2001 and Jeong *et al.*, 2001), inactivation of *SOD2* in *C. albicans* renders the cells more susceptible to a range of stresses such as ROS, elevated temperature, ethanol and high salt concentrations (Costa *et al.*, 1993;1997; Davidson *et al.*, 1996; Pereira *et al.*, 2001). In addition to combating these external stresses, due to its position in the *C. albicans* mitochondrial, MnSod (*SOD2*) is involved in the cyanide respiration of these species, by changing the expression of the alternate oxidase gene (*AOX*) through the control of its level in the mitochondria. This *AOX* is responsible for the mediation of

cyanide resistant respiration in *C. albicans*, which is an alternative respiratory pathway, different to the conventional, cytochrome respiratory pathway of *C. albicans* and its suggested that it may function as an antioxidant enzyme against ROS (Huh and Kang, 1999, 2001). When *C. albicans* cells are in the log phase CuZnSod (*SOD1*) and *SOD5* genes are expressed but when the cells enter the stationary phase of growth CuZnSod (*SOD1*) expression is repressed and *C. albicans* MnSod (SOD3) is upregulated and provides a protective role against ROS (Lamarre *et al.*, 2001). Martchenko *et al.* (2004) identified the three additonal superoxide dismutases, *SOD4*, *SOD5*, and *SOD6*. While *SOD4* and *SOD6* remain uncharacterised, *SOD5* is responsible for detoxification of superoxide radicals produced during the log phase and hyphal growth and is also important for the virulence of *C. albicans*. This was confirmed when a *C. albicans SOD5* mutant strain was found to have reduced virulence in a mouse infection model however, when the same strain was incubated with RAW 264.7 mouse macrophage cells the percentage survival of the *C. albicans SOD5* knockout compared to its parental strain was no different, indicating that the loss of virulence observed was not due to macrophage induced killing (Martchenko *et al.*, 2004) but suggests that Sod5p may be essential in the removal of superoxides generated by the host from other phagocytic cells such as neutrophils or dendritic cells. Furthermore, Fradin *et al.* (2005) showed that Sod5p is localised on the cell surface of C. albicans which may suggest that this enzyme is involved in external oxidative stress.

The dissacharide trehalose also plays a protective role during oxidative stress caused by hydrogen peroxide. Accumulation of intracellular trehalose in response to a strong direct oxidative shock is an essential oxidative response but is not required when cells have been previously exposed to a mild stress, as a mild stress activates some alternative pathways, providing resistance to the cells. Hence, trehalose does not play a protective role during aquired oxidative tolerance (Benaroudj *et al.*, 2001; Alvarez-Peral *et al.*, 2002).

The intracellular thiol glutathione also plays an important role in the oxidative response of yeast. Hydroxyl radicals irreversibly damage proteins and oxidised proteins cannot be broken down by the proteolytic systems. However, thiol groups in proteins are protected from hydrogen peroxide caused oxidation by S-thiolation with glutathione. S-thiolation is when the thiol group in the protein is

oxidised resulting in the formation of disulphides between cysteine residues in the protein and the thiol group of glutathione. The *GSH1* and *GSH2* genes encode the two enzymes involved in glutathione biosynthesis i.e. γ-glutamylcysteine synthetase and glutathione synthase, respectively. In *S. cerevisiae* it has been shown that *gsh1* mutants are sensitive to H_2O_2 but *gsh2* mutants are insensitive. Furthermore, only *GSH1* is induced in response to oxidative stress which is mediated by the transcription factor Yap1 (Estruch *et al.*, 2000).

Another molecule that plays a role in the oxidative response is thioredoxin. Thioredoxin (Trx) is a small detoxifying protein, along with thioredoxin reductase (Trr) both make up the thioredoxin system in *Saccharomyces cerevisiae*, which are located in the cytoplasm and the mitochondria. Mouaheb *et al.* (1998) demonstrated that *TRX1* and *TRX2* mutants displayed a H_2O_2 sensitive phenotype. Furthermore, it has been reported that both of the *S. cerevisiae TRX2* and *TRR1* genes undergo H_2O_2 induction which is controlled by Yap1p and Skn7p (Morgan *et al.*, 1997). In addition, transcript profiling experiments carried out by Enjalbert *et al.* (2003) found an induction greater than four fold for some of these detoxifying genes in *C. albicans* (*TRX1, TRR1* and *CTA1*) demonstrating *C. albicans* transcriptional capability to react to oxidative stress.

Glutaredoxins behave in a similar manner to thioredoxins. In *S. cerevisiae* there are two subfamilies. The members of the first subfamily Grx1p and Grx2p have been reported to protect the cells against superoxide anions and H_2O_2 (Luikenhuis *et al.*, 1998) while Glx5p a member of the second subfamily (i.e. Glx3p, Glx4p and Glx5p) provides protection against H_2O_2 and menadione (Rodriguez-Manzaneque *et al.*, 1999). Gene expression data obtained by Gasch *et al.* (2000) showed a strong induction of the glutaredoxin gene *TTR1* in *S. cerevisiaes'* response to oxidative stress. Enjalbert *et al.* (2003) obtained a similar result when gene profiling experiments were carried out on *C. albicans*.

Once *C. albicans* has colonised and infected its host it is subjected to ROS species generated from its own metabolism as well as from the host phagocytic cells. The production of these ROS plays a key role in pathogen killing by macrophages (Murphy,1991). The transriptional response to oxidative response in yeasts is controlled by three signalling systems: (1) the mitogen activated protein kinase (MAPK) cascade, (2) the multistep phosphorelay system and (3) the AP-1- like transcription factor.

The MAPK or stress-activated protein kinases (SAPK) cascades are signalling mechanisms which are conserved in yeast and are used to respond to a diverse range of environmental stresses (Schaeffer and Weber, 1999). A Spc/Sty 1 MAPK was identified in *S. pombe*, a Hog 1 MAPK in *S. cerevisiae* and a CaHog1 MAPK in *C. albicans* (Fig.1.2). In *S. pombe*, the Spc1 SAPK responds to a range of stresses including oxidative stress, high osmolarity, paraquat and UV irradiation and activates the transcription factor Atf1 to induce gene expression (Millar *et al.*, 1995; Shiozaki *et al.*, 1995; Degois *et al.*, 1996, 1997; Buck *et al.*, 2001). Trancriptional profiling experiments carried out by Chen *et al.* (2003) and Rodriquez-Gabriel *et al.* (2003) identified several genes induced in response to oxidative stress which were dependent on the Spc1-Atf1 pathway (e.g *CTT1, GPX1, TRR1,)* and several studies have displayed that Spc1 and Atf1 knockouts display a increased sensitivity to oxidative stress compared to their wildtype (Degois *et al.*, 1996; Nguyen *et al.*, 2000; Quinn *et al.*, 2002) emphasising their role in the oxidative response of *S. pombe* .

The Hog1 SAPK of *S. cerevisiae*, unlike *S. pombe*, responds primarily to high osmotic stress but not oxidative stress however Singh *et al.* (2000) suggest it does play a role in oxidative stress response as the Hog1 mutant displayed an oxidative sensitive phenotype when exposed to H_2O_2 and diamide (Schuller *et al.*, 1994). Induction of stress response gene expression by the *S. cerevisiae* Hog1 SAPK occurs when the bZIP -family transcriptional repressor Sko1 is inactivated. Although it has been demonstrated that the oxidative response genes, *CTT1* (cytosilic catalase), and *GLR1* (glutathione reductase), are controlled by the Hog1 and /or Sko1 pathway in *S. cerevisiae*, this cascade is not essential for these genes regulation in response to oxidative stress (Rep *et al.*, 2001).

By using *S. pombe* and *S. cerevisiae* as model systems, the *C. albicans* SAPK gene, *CaHOG1* was identified although the components of the SAPK system in *C. albicans* have not yet been reported.

Like *S. pombe*, the *C. albicans* Hog1 responds to osmotic and oxidative environmental signals (San Jose *et al.*, 1996). CaHog1 knockouts have shown to be sensitive to oxidants such as menadione and hydrogen suggesting that CaHog1 is essential for the *C. albicans* survival under oxidative stress conditions. Furthermore, the *C. albicans* Hog1 knockout strain attenuated virulence in a

mouse model, suggesting a possible role of CaHog1 in the pathogenicity of this species (Alonso-Monge *et al.*, 1999, 2003).

The second conserved signalling pathway that regulates oxidative stress and gene expression of *S. pombe*, *S. cerevisiae* and *C. albicans* is the multistep phosphorelay system. While the SAPK cascades in yeasts are primarily concerned with the protective response against stress, the multistep-phosphorelay system upstream of the SAPK cascades is responsible for the transmission of environmental signals to these SAPK cascades. This multistep-phosphorelay system is a variation of the bacterial two component system consisting of a "sensor kinase" also known as a histidine kinase and a "response regulator". In *S. cerevisiae*, the Sln1 sensor kinase is a transmembrane protein that senses osmotic signals and transmits these osmotic signals to the Hog1 cascade through a histidine containing phosphotransferase,Ypd1 and the response regulator Ssk1 (Fig. 1.2). In addition to Ssk1, *S. cerevisiae* possesses a second response regulator, Skn7 which is also under the control of the Sln1-Ypd1 pathway but appears to be activated independently of the phosphorelay system in response to oxidative stress and regulates the expression of oxidative stress response genes e.g. *CTT1* (cytosolic catalase), *SOD1* (superoxide dismutase), *TRX2* (thioredoxin), *TRR1* (thioredoxin reductase), *TSA* (thioredoxin peroxidase) and *AHP1* (alkyl hydroperoxide), (Bermingham-McDonogh *et al.*, 1988; Morgan *et al.*, 1997; Lee *et al.*, 1993, 1999; Gan, 1991; Chae *et al.*, 1994 and 1993). In addition, mutants of Skn7 are hypersensitive to oxidative stress, thus, highlighting Skn7s important role in the oxidative response in *S. cerevisiae*. Although structurally similar, in contrast to the Sln pathway of *S. cerevisiae* which is responsible for the transmission of osmostresses to the Hog1 SAPK cascade, the *S. pombe* phosphorelay system appears to be exclusive to oxidative stress. *S. pombe* transmits oxidative signals through its three sensor kinases (Mak1, Mak2 and Mak3) via Mpr1(an ortholog of Ypd1) to its response regulator Mcs4.

In *C. albicans*, three sensor kinase genes *CaSLN1*, *CANIK/COS1* and *CaHK1* have been identified although their roles in the oxidative stress response remain to be elucidated. The *C. albicans* Ssk1 response regulator which is an ortholog of the *S. cerevisiae* Ssk1 and *S. pombe* Mcs4 response regulators, is required to activate the CaHog1 SAPK cascade but whether it can transmit oxidative signals remains unclear (Calera *et al.*, 1999; Chauhan *et al.*, 2003). The

Ssk1 response regulator of *C. albicans* is one of the perhaps many signal molecules that adapts *C. albicans* cells to oxidative stress.

The AP-1(Activating Protein-1) transcription factors that bind the AP-1 site (TGACTCA) make up the third signalling module controlling transcriptional regulation in response to oxidative stress. AP-1 like factors have been identified in *S. pombe* (Pap1), *S. cerevisiae* (Yap1) and *C. albicans* (Cap1). In *S. cerevisiae*, *YAP1* mutants are hypersensitive to cadmium and H_2O_2 as the Yap1 transcription factor is required to induce oxidative stress reponse genes such as *TRX2*, *TRR1*, *GLR1* and *GSH1*. In *S. pombe* Pap1 also induces the expression of oxidative stress response genes such as *CTT1*, *TRX2*, *TRR1* and *PGR1* and the Pap1 mutant is also sensitive to oxidants.

In *C. albicans*, *CAP1* (*C. albicans* AP-1) encodes a basic region-leucine zipper (bZip) transcription factor homologous to the bZip transcription factor of Yap1 of *S. cerevisae* and the Pap1 of *S. pombe* which is required for oxidative stress tolerance in *C. albicans* (Alarco *et al.*, 1997). This has been confirmed when *CAP1* mutants were found to be hypersensitive to cadmium and hydrogen peroxide. Like Yap1 of *S. cerevisiae* and Pap1 of *S. pombe*, the glutathione reductase gene (*GLR1*) is also under Cap1 control by exposure to oxidative stress (Alarco *et al.*, 1999; Zhang *et al.*, 2000). Zhang *et al.* (2000) also demonstrated that oxidant stress induces the nuclear accumulation of Cap1 which has been previously observed for Yap1 also (Kuge *et al.*, 1997). The AP-1 factors, Yap1, Pap1 and Cap1 regulate transcription working as sensors of oxidative stress, mostly independent of the SAPK and the phosphorelay pathways.

Another protein which is essential for oxidative resistance in *C. albicans* is the recently described Tsa1p, a protein that translocates to the cell wall in hyphal cells but remains in the cytosol and nucleus when in the yeast form. The Tsa1p plays an important protective role in *C. albicans* against oxidative stress. Urban *et al.* (2005) confirmed this by demonstrating that the *C. albicans TSA1* gene confers resistance to hydrogen peroxide and is induced by hydrogen peroxide which requires *CAP1*. Transcript profiling carried out in the same study, of a *TSA1* mutant revealed that under oxidative stress conditions the mutant strain caused upregulation of other antioxidant genes compared to wildtype (e.g. the *COR33* gene encoding a newly identified oxidoreductase and *TRR1*)

Further elucidation of the underlying molecular pathways involved in the tolerance of yeasts to ROS will allow the development of novel tactics to improve the performance of macrophage-mediated clearance of these fungal pathogens in the immunocompromised patient.

1.5.4 Response to osmotic stress

In the case of *Candida spp.*, depending on the niche it inhabits in the human body (e.g. oral cavity, vagina or gastrointestinal tract), these cells are likely to be exposed to a wide variety of osmotic conditions. As well as heat and oxidative shock, *C. albicans* cells have also developed strategies to respond to changes in extracellular osmolarity i.e. osmotic shock. Salt tolerance in living cells is conditioned by the capacity to sustain intracellular ion homeostasis. In response to osmotic shock yeast cells generally shrink and accumulate harmless molecules such as glycerol which help them balance their internal environment with the changing external environment (Bloomberg and Adler, 1992). Osmotic shock, however also has a huge impact on cell physiology, cell wall dynamics, cell metabolism, ion homeostasis and also has a great affect on gene expression. High osmotic conditions have also been reported to affect different signalling pathways in yeast and several pathways are activated to help the cells adapt, protect and survive in their new hyperosmotic environment.

As previously mentioned (see p22-23) the high-osmolarity glycerol (HOG) mitogen activated protein kinase pathway (MAPK) mediates the hyperosmotic response in *S. cerevisiae* (Fig. 1.2). The MAPK pathway is regulated by two transmembrane proteins (Sln1 and Sho1) that function as omosensors. The first osmosensor, Sln1(described on p23-24) links the cell membrane and the external environment with the MAPK cascade via a multistep phosphorelay system. The second osmosensor, Sho1 transmits a signal to Pbs2p via the MAPKKK Ste1p. Activation of Hog1p results in the induction of glycerol producing, enzymes Gpd1p (glycerol-3-phosphate dehydrogenase) and Gpp2p (glycerol-3-phosphatase) and other stress induced proteins.

The MAP kinase *HOG1* has been isolated in *C. albicans* (San Jose *et al.*, 1996) and disruption of the *C. albicans HOG1* results in a osmosensitive phenotype and fails to accumulate glycerol on media supplemented with high

NaCl concentrations,thus, suggesting that glycerol synthesis is under the control of the *HOG1* gene. Furthermore, Smith *et al.* (2004) showed that the *C. albicans* Hog1 SAPK is phosphorylated and accumulates in the nucleus in response to osmotic and oxidative stresses, confirming results obtained in a previous study (Alonso-Monge *et al.*, 2003). Smith and co workers also identified some genes (*RHR2* (putative glycerol phosphate phosphatase), *HSP12*) which are under the specific control of Hog1. In addition, Fan *et al.* (2005) recently identified two *GPP* (di-glycerol 3-phosphate phophohydrolase) homologous genes, *GPP1* (glycerol 3- phosphatase) and *DOG1* (2 deoxyglucose-6-phosphate phosphatase) in *C. albicans* and demonstrated the importance of the *GPP1* gene in the osmoregulation of *C. albicans* in knock out experiments where the *GPP1* gene mutant increased susceptibility to high salt concenttrations. Microarray data obtained by Enjalbert *et al.* (2003) showed the induction of typical osmotic response genes such as *ENA1*, *ENA2*, *GPP1*, *GPD1 GPD2* and *RHR2* in *C. albicans* cell when subjected to high salt conditions.

Yeast cells have also developed extrusion systems to maintain the levels of intracellular sodium below concentrations that are toxic to the cell. In *S. cerevisiae* the *ENA1* gene encodes a P-ATPase involved in the extrusion of Na^+ ions from the cytoplasm. Active export of these toxic ions is a crucial cellular process to avoid deleterious intracellular Na^+ and Li^+ concentrations. Mutants that lack *ENA1* are hypersensitive to salt stress and cannot resume growth when exposed to moderate external NaCl concentraions (Haro *et al.,* 1991). *ENA1* is highly regulated at the transcriptional level and salt induction of *ENA1* expression depends upon two different environmental signals contributed by salt stress: osmotic concentrations (via the high-osmolarity glycerol (HOG) mitogen activated protein (MAP) kinase pathway) and sodium (via the calcineurin pathway) (Marquez and Serrano, 1996).

1.5.5 Trehalose

An additional element of the adaptive response of yeast to elevated temperature is the accumulation of the non-reducing disaccharide trehalose, which functions as a carbohydrate reserve and stress metabolite (Attfield, 1987; Hottiger *et al.,* 1987; Ribeiro *et al.,* 1994). The concentration of trehalose increases dramatically in cells exposed to high temperatures, and trehalose is required for

the acquisition of thermotolerance in exponentially growing *S. cerevisiae* and *S. pombe* cells (Wiemken, 1990; Ribeiro *et al.,* 1997).

1.5.5.1 Trehalose metabolism

Trehalose (α-D-glucopyranosyl-α-D-glucopyranoside) is synthesised by the trehalose synthase complex in two steps (Fig. 1.4). Trehalose –6-phosphate synthase (TPS), encoded by *TPS1*, catalyses the formation of trehalose-6-phosphate (Tre6P), which is dephosphorylated by trehalose-6-phosphate phosphatase (TPP), encoded by *TPS2* (Bell *et al.,* 1992; De Virgilio *et al.*, 1993). In *S. cerevisiae* disruption of the *TPS1* gene prevents growth on glucose because of the hyperaccumulation of sugar phosphates and depletion of ATP and phosphate, but is dispensable for growth on glucose in *S. pombe* (Blazquez *et al.,* 1994). Disruption of the *C. albican TPS1* gene impairs the formation of hyphae on glucose containing medium and decreases virulence in a mouse systemic infection model (Zaragoza *et al.*, 1998; Arguelles *et al.*, 1999). This decrease in virulence may be due to the lower stress resistance due to the absence of trehalose as *TPS1* mutant strains were unable to accumulate trehalose, in contrast to the wildtype (Zaragoza *et al.*, 2002)

Saccharomyces cerevisiae and *Aspergillus nidulans* strains with *TPS2* gene deletions (encoding trehalose-6-phosphate phosphatase) show a thermosensitive phenotype in comparison their parental strain (De Virgilio *et al.,* 1993; Borgia *et al.,* 1996). However, while deletion of this gene in *C. albicans* does not abolish growth even at 42°C, it does result in a decrease in the growth rate. Whereas deletion of *CaTPS1* prevents glucose induced hypha formation, deletion of *CaTPS2* does not affect hypha formation. It does however, lead to the aggregation of cells in stationary phase affecting cell intergrity and results in decreased infectivity in mice (Zaragoza *et al.*, 2002; Van Dijck *et al.,* 2002). In addition, Zaragoza *et al.* (2002) demonstrated that disruption of both copies of the *CaTPS2* gene inhibited trehalose accumulation after a heat shock of 42°C. However, in contrast, Van Dijck *et al.* (2002) showed a significant accumulation of trehalose in the *CaTPS2* mutant strains at both 30°C and 43°C. Despite these conflicting results, both reports suggest that the reduced virulence observed in both studies was, in fact, due to the hyperaccumulation of the metabolite Tre6P

which in high concentrations is toxic, as it sequestrates phosphate, resulting in the inhibition of ATP generation required for normal cellular growth (Van Dijck *et al.*, 2002; Zaragoza *et al.*, 2002).

Trehalose works in combination with the Hsps for the recovery from heat shock (Fig. 1.4). Under conditions of high temperature trehalose prevents native proteins from denaturing and those proteins that do unfold are bound by the Hsps. Trehalose suppresses the aggregation of denatured proteins and stabilises both proteins and membranes, (Crowe *et al.,* 1984, 1992). Therefore it can compensate for the lack of Hspjs when the protein-repair mechanisms are overwhelmed (Singer and Lindquist, 1998a). However, the persistance of high levels of trehalose when the thermal stress has been alleviated interferes with the refolding of denatured proteins by Hsps. Therefore, trehalose is rapidly degraded once the heat stress has been removed by the enzyme neutral trehalase which is encoded by the *NTC1* gene. This degradation of trehalose allows reactivation of proteins by Hsps and is believed to promote the refolding function of *HSP104* (Singer and Lindquist, 1998b). This neutral trehalose hydrolase, encoded by *NTC1*, is one of the two types of trehalose hydrolases present in *C. albicans*, the second is the acid trehalase which is encoded by the *ATC1* gene. Most fungi possess both trehalose hydrolases, called "acid" and "neutral" due to their pH required for optimum activity. The acid trehalase, has been identified in the filamentous fungus *Aspergillus nidulans*, *S. cerevisiae* and recently in *C. albicans* (Destruelle *et al.*, 1995; d'Enfert *et al.*, 1997; Pedreno *et al.*, 2004). The neutral trehalase, Nth1p enzyme is responsible for breakdown of intracellular trehalose whereas the acid trehalase, Ath1p has been shown to be required for growth on exogenous trehalose in *S. cerevisiae* and more recently in *C. albicans* where Atc1p is localised in the cell wall (San-Miguel *et al.*, 1994; Nwaka *et al.*, 1996; Jorge *et al.*, 1997; Pedreno *et al.*, 2004). Indeed, in *S. cerevisiae*, it has been shown that there are two independent pathways for trehalose assimiliation one of them involving the extracellular breakdown of the dissacharide by Ath1p (acid trehalase) into glucose and a second, which couples trehalose transport, mediated by a high affinity H^+ trehalose transporter, Agt1p, with trehalose hydrolysis by Nth1p (neutral trehalase). In the fission yeast *S. pombe* it has been reported that trehalose metabolic genes encoding neutral trehalase ($ntp1^+$) and trehalose-6-

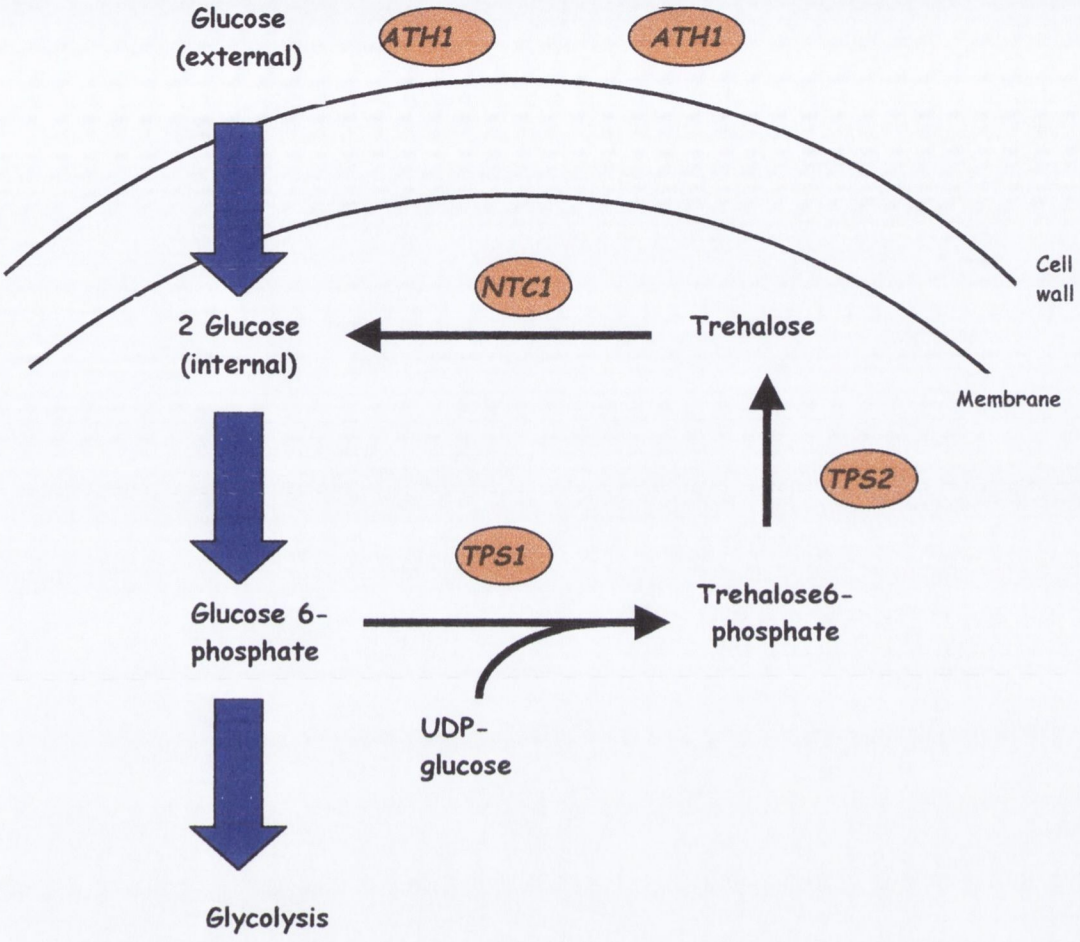


Figure 1.4. The pathway of trehalose metabolism in *C. albicans*. Trehalose is synthesised in two steps, whose substrate is glucose. Glucose is converted into glucose 6-phosphate which, together with uridine diphosphate glucose (UDPG), leads to the formation of trehalose 6-phosphate, a reaction catalysed by a trehalose-6-phosphate synthase, coded by the *TPS1* gene. Subsequent dephosphorylation by a trehalose-6-phosphate phosphatase coded by the *TPS2* gene, yields free trehalose. In turn, intracellular trehalose is split into two molecules of glucose by neutral trehalase, encoded by the *NTC1* gene. The acid trehalase, encoded by the *ACT1* gene is localised on the cell wall and appears to be required for the hydrolysis of exogenous trehalose in *C. albicans*.

phosphate synthase (*tps1*$^+$) are partially regulated by the Sty1p SAPK cascade in response to salt induced osmotic stress and oxidative stress (Paredes *et al.*, 2003).

Trehalose metabolism is of particular interest as there are no homologues of these trehalose metabolic enzymes in mammals, therefore if found to be involved in aiding the survival of *Candida* cells in vivo these could be an interesting target for antifungals. Furthermore, cell wall-linked proteins such as Atc1p, on the external surface would be a prefered antifungal drug target.

As trehalose accumulation is one of the hallmark stress responses of the general stress response in *S. cerevisiae* it is therefore not suprising that this sugar is also accumulated under both osmotic and oxidative stress conditions in yeast cells. *S. cerevisiae* has been shown to accumulate low levels of trehalose in response to oxidative and osmotic stresses (Parrou *et al.*, 1997). Moreover, trehalose also contributes to survival under severe osmotic stress conditions (Hounsa *et al.*, 1998). The low level of trehalose accumulation in *S. cerevisiae* observed by Parrou *et al.* (1997) was due to a "turnover mechanism" that involved the production and degradation of this sugar. In contrast to *S. cerevisiae*, no trehalose accumulation was observed in response to either thermal (23-37°C) or oxidative stresses (0.4 mM H_2O_2) in *C. albicans* under these conditions which was in agreement with microarray data obtained from the same study of Enjalbert *et al.* (2003), in which no induction of trehalose-related genes in response to oxidative and thermal stress was observed. This would suggest that *C. albicans* may be less efficient at accumulating trehalose in response to these weak stresses compared to *S. cerevisiae*, or perhaps, that this pathogen has adapted to its microenvironment in the human body and is more tolerant to severe stresses than *S. cerevisiae*, hence does not require trehalose under these weak stress conditions.

Benaroudj *et al.* (2001) first reported a new role for trehalose in protecting *S. cerevisiae* against ROS when it was found to reduce the oxidative damage to amino acids in cellular proteins. Trehalose also plays a role in cell-tolerance against oxidative stress in *C. albican*, and is suggested to contribute to the pathogenesis of *C. albcians*, as previously mentioned, knockouts of the *TPS1* and *TPS2* genes decreased virulence in mice (Van Dijck *et al.*, 2002; Zaragoza *et al.*, 1998, 2002). Alvarez-Peral *et al.* (2002) showed that the *tps1* mutant of *C. albicans* was hypersensitive to a severe oxidative stress of 50 mM H_2O_2 compared

to wildtype and that trehalose accumulation in response to oxidative stress is not induced by the increased expression of *TPS1* mRNA.

1.6 Aims and objectives

Candida dubliniensis is a recently defined pathogenic species which was originally identified in cases of recurrent oral candidiasis in HIV-infected and AIDS patients (Coleman *et al.*, 1997a and 1997b; Ponton *et al.*, 2000). Most of the studies on stress responses of *Candida* spp. to date have focused on the pathogenic yeast *C. albicans* or the budding model yeast *S. cerevisiae*. Although it is known that *C. dubliniensis* seems to be more sensitive to environmental stresses, such as NaCl concentration and elevated temperature (Alves *et al.*, 2002; Pinjon *et al.*, 1998) there is little or no information available on the diverse range of responses of *C. dubliniensis* to environmental stress, or on the underlying mechanisms controlling these responses. Despite, their close phylogenetic relationship it is clear that *C. albicans* is significantly more pathogenic than *C. dubliniensis* but the precise reasons for this are currently unknown.

The objectives of this study are to compare how *C. albicans* and *C. dubliniensis* react to stressful environmental conditions at the phenotypic and molecular level. The purpose of this is to determine whether an enhanced ability to survive adverse conditions may in part explain why *C. albicans* is a more successful pathogen than *C. dubliniensis*

This study aims to:

- Compare the ability of *C. albicans* and *C. dubliniensis* to grow *in vitro* under a wide range of environmental conditions (e.g. temperature, salt and oxidative concentrations).
- Identify the presence of homologues of representative *C. albicans* stress response genes in *C. dubliniensis* and to compare the expression of these genes under a range of environmental conditions i.e. heat, oxidative and osmotic stress.
- Identify genes responsible for the high salt tolerance phenotype observed in *C. albicans* and investigate if homologues are present in *C. dubliniensis*.
- Compare the global expression of genes in *C. albicans* and *C. dubliniensis* in response to specific environmental stresses i.e. heat, oxidative and osmotic stress.

Chapter 2

Materials and Methods

2.1 General Microbiological Methods

2.1.1 *Candida* strains and isolates

The *Candida* strains and isolates used in this study are listed in Table 2.1. All yeast isolates were from the culture collection of the Microbiology Research Unit, Division of Oral Biosciences, Dublin Dental school and Hospital, University of Dublin, Trinity College, Dublin 2, Ireland.

2.1.2 Culture media and growth conditions

All *Candida* clinical isolates, strains and derivatives were routinely cultured on Potato Dextrose Agar (PDA) medium (Oxoid, Basingstoke, Hampshire, UK) at pH 5.6, at 37°C. For liquid culture, isolates were routinely grown in Yeast Peptone Dextrose (YPD) broth (per litre: 10 g yeast extract [Oxoid], 20 g peptone [Difco Laboratories, Detroit, Michigan, USA], 20 g glucose, pH 5.5) at 37°C in a Gallenkamp (model G25) orbital incubator (New Brunswick Scientific Company Incorporated, Edison, New Jersey, USA) set at 200 rpm.

The *Escherichia coli* strain DH5α (*supE* Δ*lac*U169 [∅80 *lacZ*ΔM15] *hsd*R17 *recA*1 *endA*1 *gyrA*96 *thi*-1 *relA*1; Sambrook *et al.*, 1989) was routinely cultured on Luria-Bertani agar (LA), pH 7.4 (Lennox, 1955), at 37°C for 18 h in an orbital incubator (Gallenkamp) at 200 rpm. *Escherichia coli* DH5α was used as the host strain for plasmid pBluescript II KS (-) (Stratagene, La Jolla, California, USA).

2.1.3 Chemicals, enzymes, radioisotopes, antifungal drugs and oligonucleotides

Analytical-grade or molecular biology-grade chemicals were purchased from Sigma Aldrich Ireland Ltd. (Tallaght, Dublin, Ireland), BDH (Poole, Dorset, UK), or Roche Diagnostics Ltd. (Lewes, East Sussex, UK). Enzymes were purchased from the Promega Corporation (Madison, Wisconsin, USA) and from New England Biolabs (Beverly, Massachusetts, USA) and used according to manufacturer's instructions. [α-^{32}P]dATP (6,000 Ci/mmol; 222 TBq/mmol) was purchased from Amersham International Plc. (Little Chalfont, Buckinghamshire, UK). Custom-synthesised oligonucleotides were purchased from Sigma-Genosys

Table 2.1. *Candida* strains used in this study

Strain	Genotype	Country of origin	Source/notes	Year of isolation	Reference/ Source
C. albicans					
132A	NA[a]	Ireland	Oral,HIV+ve[b]	1992	Gallagher *et al.*, 1992
SC5314	NA	USA	Systemic, HIV-ve[c]	1984	Gillum *et al.*, 1984
CAI4	NA	USA	Derivative of SC5314, *ura3*Δ::imm434/*ura3*Δ::imm434	1993	Fonzi & Irwin, 1993
C. dubliniensis					
CD36	1	UK	Oral, HIV+ve	1988	Sullivan *et al.*,1995
CAN1	1	Canada	Oral, HIV+ve	1996	Pinjon *et al.*, 1998
CM1	1	Australia	Oral, HIV+ve	1991	Sullivan *et al.*,1995
CD539	2	UK	Oral, AIDS	1994	Pinjon *et al.*, 1998
CD541	2	UK	Blood, HIV-ve	1997	Pinjon *et al.*, 1998
CD514	3	Ireland	Oral, HIV-ve	1995	Gee *et al.*, 2002
p6265	3	Israel	Sputum,HIV-ve	1999	Polacheck *et al.*, 2000
p6785	3	Israel	Urine, HIV-ve	1999	Polacheck *et al.*, 2000
p7718	4	Israel	Wound, HIV-ve	1999	Gee *et al.*, 2002
Wü284	1	Ireland	Oral, AIDS	1999	Morschhäuser *et al*, 1999
CdUM1B	1	Ireland	Derivative of Wü284, *ura3*Δ1::*FRT*/ *ura3*Δ2::*FRT*	2001	Staib *et al.*, 2001

[a]NA, not applicable
[b]+ve, positive
[c]-ve, negative

Biotechnologies (Europe) Ltd. (Pampisford, Cambridgeshire, UK). DNA molecular weight markers were purchased from Gibco BRL Life Technologies (Gaithersburg, Madison, USA). Zymolase 20T (21,600 U/g) was purchased form the Seikagaku Corporation (Tokyo, Japan).

RNase solutions were prepared by dissolving pancreatic RNase (Sigma-Aldrich) at a concentration of 10 mg/ml in 10 mM Tris –Hcl (pH 7.5), 15 mM NaCl. This solution was stored in aliquots at –20°C. Proteinase K (Roche Diagnostics Ltd.) solutions were prepared in ultrapurified water from a MiliQ water purification system (Millipore SA- 67120 Molsheim, France) at a concentration of 20 mg/ml and was stored in aliquots at –20°C.

2.1.4 Buffers and solutions

Tris-EDTA (TE) buffer was routinely used in experiments and consisted of 10 mM Tris-HCl, 1 mM EDTA, pH 8.0. Phosphate buffer (CPB, 0.2M) consisted of, per 100 ml, 58 ml 0.4 M Na_2 HPO_4 and 42 ml 0.2 M citric acid.

TBE buffer was prepared at 5x concentration and consisted of 0.45 M Trizma base, 0.45 M boric acid, 0.01 M EDTA. This was diluted in ultrapurified water to a final concentration of 0.5x and was used as the buffer for agarose gel electrophoresis.

Final sample buffer was also prepared at 10x concentration and consisted of 30 %(v/v) glycerol, 0.25% (w/v) bromophenol blue and 0.1 M EDTA, pH 8.0. SSC buffer was prepared at 20x concentration and consisted of 3.0 M NaCl, 0.3 M tri-sodium citrate, pH 7.0.

Mops buffer used for RNA electrophoresis was prepared at 10x concentration and consisted of 20 mM morpholinepropanesulphonic acid, 5 mM sodium acetate, 1 mM EDTA, pH 7.5. Liquefied phenol washed in Tris-buffer was purchased from Fisher Scientific Ltd (Bishop Meadow Road, Loughborough, UK) and used in the preparation of phenol chloroform (1:1), which was prepared by mixing an equal volume of liquefied phenol and chloroform. This solution was stored at 4°C.

2.1.5 Storage of *Candida* isolates

Candida cells and derivatives were stored at -70°C in cryo-vials containing cryopreservative (Microbank™, Pro-Lab Diagnostics, Neston, Wirral, UK). Under

aseptic conditions a screw cap cryovial was opened. The cryopreservative fluid (Microbank™) was inoculated with young colonial growth (18-24 h) picked from a pure culture. The vial was then closed and inverted several times to emulsify the organism. At this point the cells binded to the porous beads contained within the cryovial. When a fresh culture was required, a single bead was removed aseptically and was used to directly streak on to PDA agar which was incubated for 48 h at 37°C.

2.2. Identification of *Candida* species

2.2.1 PCR identification of *C. dubliniensis*

PCR identification of *C. dubliniensis* was performed using the *C. dubliniensis*-specific primer pair DUBF/DUBR (Table 2.2) which amplify a portion of the *C. dubliniensis ACT1*-associated intron. Reactions were carried out in a 50 µl final volume containing 10 pmol each of the forward and reverse primers, 2.5 mM $MgCl_2$, 10 mM Tris-HCl (pH 9.0 at 25°C), 10 mM KCl, 0.1% (v/v) Triton X-100, 2.5 U *Taq* DNA polymerase (Promega) and 25 µl of template DNA containing-cell supernatant (prepared as described below) (Donnelly *et al.*, 1999). Each reaction mixture also contained 10 pmol each of the universal fungal primers RNAF/RNAR (Table 2.2) which amplify approximately 610 bp from all fungal large subunit rDNA genes and were used as an internal positive control (Fell, 1993). Cycling conditions consisted of 6 min at 95°C followed by 30 cycles of 30 s at 94°C, 30 s at 58°C, 30 s at 72°C, followed by 72°C for 10 min. Amplification products were separated by electrophoresis through 2.0% (w/v) agarose gels containing 0.5 µg ethidium bromide/ml and were visualised on a UV transilluminator (Ultra-Violet products Ltd (UVP), Upland, CA, USA)

The rapid isolation of *C. dubliniensis* template DNA for use in PCR identification experiments involved placing a single colony from a culture grown for 48 h at 37°C on CHROMagar Candida medium or PDA into 50 µl of sterile distilled water. The cell suspensions were boiled for 10 min and the lysed cells were subjected to a clearing spin for 5 min at 2,500 x *g* in an Eppendorf (model 5417C) microfuge (Eppendorf, Hamburg, Germany). A 25 µl aliquot of supernatant thus obtained was used in the PCR reactions.

2.3 Isolation of genomic DNA

2.3.1 Extraction of genomic DNA from *Candida* isolates

Genomic DNA was prepared from cells grown in 50 ml of YPD broth in a 250 ml flask at 37°C in an orbital incubator at 200 rpm for 18 h. Cultures were then decanted into 50 ml Falcon tubes (Becton Dickinson, New Jersey, USA) and centrifuged in a bench top (Sepatech Megafuge 1.0) centrifuge (Heraeus, Germany) at 2,500 x g for 5 min. The supernatant was decanted and the pellet was resuspended in 500 µl of a solution consisting of 1 M sorbitol, 20 mM phosphate buffer and transferred to a 1.5 ml microfuge tube. Cell walls were digested by the addition of 10 mg Zymolase 20T and incubated at 37°C for 30 min. The resulting protoplasts were harvested by centrifugation at 2,500 x *g* for 10 min in a bench top centrifuge (Sepatech Megafuge 1.0) and the pellet resuspended in 500 µl of 1x TE containing 1% (w/v) sodium dodecyl sulphate (SDS). Proteinase K was added to a final concentration of 2 mg/ml and the cell lysates were then incubated for 18 h at 55°C. Protein was precipitated by the addition of 250 µl of 5 M potassium acetate and incubated on ice for 15 min. The cell lysates were then centrifuged at 2,500 x *g* for 10 min. The cleared supernatant was extracted four times using an equal volume of a mixture of phenol:chloroform (1:1) and precipitated with the addition of two volumes of ice-cold iso-propanol. The resulting DNA precipitate was then transferred to a fresh tube and washed in 500 µl ice-cold 70% (v/v) ethanol, dried and resuspended in 40 µl of TE buffer.

2.3.2 Restriction endonuclease digestion of genomic DNA and agarose gel electrophoresis

Large scale restriction endonuclease digestions of genomic DNA were carried out in a 40 µl volume containing 20 U of restriction enzyme and the appropriate restriction enzyme buffer according to the manufacturer's instructions. Electrophoresis was performed in 0.65-1 % (w/v) agarose gels made with 1x TBE buffer containing 0.5 µg ethidium bromide/ml. Restriction endonuclease-generated DNA fragments in a 1x final sample buffer were applied to the gel wells. Electrophoresis was performed at 60 V. Following electrophoresis, gels were visualised on a UV transilluminator (wavelength 345_{nm}) and photographed

through a red filter with Polaroid 667 film (Polaroid (UK) Ltd., Wheathamsptead, Hertfordshire, UK).

2.3.3 Southern transfer of DNA from agarose gels

Following the separation of restriction endonuclease digested DNA fragments by agarose gel electrophoresis, DNA fragments were transferred by capillary action using the method of Southern (1975) to nylon membranes. Briefly gels were soaked in 0.02 M HCl with gentle agitation for 10 min to depurinate the DNA. Following depurination, the DNA was denatured by soaking the gel in denaturation solution (1.5 M NaCl, 0.5 M NaOH) for 45 min with gentle agitation. Following denaturation, the gels were neutralised by soaking in a solution containing 1 M Tris-HCl, pH 7.5, 1.5 M NaCl for a further 45 minutes.

DNA was transferred to MagnaGraph nylon membranes (MSI, Wesborough, Massachusetts, USA) using 20x SSC as the transfer buffer. Following transfer, the gel was rinsed in 2x SSC and baked at 80°C for 1 h to fix the DNA or the DNA was fixed using a UV crosslinker (CL-508, UVI tec, Cambridge, Cambridgeshire, UK) set at 0.120 J /cm^2.

2.3.4 Random primer labelling of DNA fragments with [α-^{32}P]dATP

DNA fragments were labelled with [α-^{32}P] dATP by random primer labelling using the Prime-a-gene kit purchased from Promega. DNA to be labelled was denatured by boiling for 2 min and then added to a reaction mixture containing 1 x labelling buffer, dNTPs (dTTP, dCTP and dGTP), bovine serum albumin, 3 µl of [α-^{32}P] dATP (6,000 Ci/mmol; 220 TBq/mmol) and 5U of Klenow DNA polymerase, and was incubated at room temperature for 2 h. Unincorporated nucleotides were removed prior to hybridisation by passing the reaction through a size exclusion matrix (SigmaSpin post reaction columns, Sigma-Aldrich) following the manufacturer's instructions.

2.3.5 Southern hybridisation

Hybridisation reactions were carried out in 25 x 3.5 cm bottles (Hybaid, Teddington, Middlesex, UK) in a rotary hybridisation oven (Hybaid) by the method of Sambrook *et al.* (1989). Nylon membranes were rinsed in 6x SSC prior to hybridisation. Membranes were then prehybridised in 15 ml of a solution

containing 1x Denhardt's solution (1% [w/v] Ficoll, 1% [w/v] polyvinylpyrrolidone, 1% [w/v] BSA), 6x SSC, 100 µg/ml denatured salmon sperm DNA and 0.5% (w/v) SDS in the oven at 65°C for 2 h.

Radiolabelled probe (~ 2 x 10^6 dpm) was denatured by boiling for 5 min followed by incubation on ice. The denatured probe was then added to the prehybridisation solution and incubated with the membrane at 65°C for 18 h. Unbound probe was removed from the membranes following hybridisation by washing the membrane in the bottle with a solution of 2x SSC, 0.1% (w/v) SDS at room temperature for 5 min, followed by a wash at room temperature in 0.1x SSC, 0.5% (w/v) SDS for 15 min and a high stringency wash at 65°C in 0.1x SSC, 0.5% (w/v) SDS for 30 min. After washing, the membranes were wrapped in Saran wrap (Dow Chemical Co., Stade, Germany) and placed in an autoradiograghy cassette with a Kodak BioMax MS-1 intensifying screen (Eastman Kodak Company, Rochester, New York, USA) and exposed to Kodak Biomax MS-1 X-ray film at –70°C. Autoradiograms were developed with Kodak GBX developer and fixed in Kodak GBX fixer.

Bound probe was removed from membrane filters by immersing the membrane in a boiling solution of sterile ultrapurified H_2O, followed by a brief rinse in 2x SSC.

2.4 Recombinant DNA techniques

2.4.1 Small scale isolation of plasmid DNA from *E. coli*

Small scale preparations of plasmid DNA from *E. coli* were prepared by the method of Sambrook *et al.* (1989). Briefly, *E. coli* cultures were grown overnight in LB medium in the presence of selective antibiotic (100 µg ampicillin/ml in the case of pBluescript II KS [-]). A 1.5 ml aliquot of this culture was pelleted at 2,500 x *g* for 30 s in a microfuge and resuspended in 100 µl ice cold solution 1 (50 mM glucose, 25 mM Tris-HCl, 10 mM EDTA, pH 8.0). Cell were lysed by the addition of 200 µl solution 2 (0.2 N NaOH, 1% [w/v] SDS) and left on ice for 5 min. Protein was then precipitated by the addition of 150 µl solution 3 (5 M potassium acetate, 11.3% (v/v) acetic acid). The mixture was vortexed and centrifuged at 2,500 x *g* for 5 min in a microfuge. The supernatant

was transferred to a fresh microfuge tube and extracted once with an equal volume of phenol:chloroform (1:1), and the DNA precipitated by the addition of 2 volumes of ice-cold ethanol. The precipitate was pelleted again at 2,500 x *g* for 5 min and resuspended in 50 µl sterile ultrapurified H_2O. RNA was removed by incubating the DNA solution with 0.1 mg RNase A for 30 min.

2.4.2 Polymerase chain reaction (PCR) and purification of PCR amplimers

Specific *C. dubliniensis* and *C. albicans* genomic DNA sequences were amplified by PCR and cloned into pBluescript. Oligonucleotide primers were designed containing specific restriction endonuclease cleavage sites (Table 2.2), to amplify the required region. PCR amplification was performed using the Expand High Fidelity PCR System (Roche Diagnostics Ltd.), or if the expected PCR product was above 3 kb the Expand Long Template PCR system (Roche Diagnostics Ltd.) was used. Amplifications were carried out in 50 µl volumes containing 2.6 U Expand High Fidelity PCR System enzyme mix (Roche Diagnostics Ltd.), 1x Expand High Fidelity buffer reaction buffer, 3 mM $MgCl_2$, 250 µM (each) dATP, dTTP, dCTP, dGTP (Promega), 10 pM of both a forward and reverse primer and 10 ng of genomic DNA template. PCR reactions were carried out in a Thermo Hybaid Multiblock System (MBS) thermal cycler (Thermo Hybaid, Ashford, Middlesex, England). Amplification products were separated by electrophoresis through 0.8 (w/v) agarose gels containing 0.5 µg/ml ethidium bromide. One kb and 100 bp DNA molecular weight markers (Promega) were loaded on each gel. Following electrophoresis at 80V with constant current for 1 h the amplification products were visualised on a UV transilluminator (Ultra Violet Products Ltd) at a wavelength of 345_{nm} and photographed using Image Store 7500 version 7.22 Gel Documentation System. Amplification conditions and specific primers will be described in the relevant sections. All PCR products were either purified using the GenElute™ PCR DNA purification kit (Sigma-Aldrich) or the Wizard Minprep PCR DNA Purification System® (Promega) according to the manufacturer's instructions. Occasionally

Table 2.2. Primers used to amplify *C. dublinensis* and *C. albicans* sequences

Primer	Nucleotide sequence (5'-3')[a]	Restriction site	Location	Amplicon size
HSP90F	CGTCTAGACTGGTATTGGTATGACC	*Xba*I	918-935	468 bp
HSP90R	CGTCTAGACAATTTTGGTTTCTTGTCG	*Xba*I	1369-1386[b]	
HSP104F	CGGAATTCAGTGCATTGGTCACTGCTGCT	*Eco*RI	1280-1300	980 bp
HSP104R	CGGAATTCAGTCAACACTTCAGGAGCAG	*Eco*RI	2241-2260[c]	
TPS1F	CGGAATTCCATGTCCTCCGGTGGAC	*Eco*RI	83-100	875 bp
TPS1R	CGGAATTCCACCTCTGGATGGAACAGC	*Eco*RI	940-958[d]	
NTC1F	CGGAATTCCTGGCCATTAGAAGGAAACC	*Eco*RI	1341-1360	1380 bp
NTC1R	CGGAATTCCATGACCAGATTCTCGAACGGC	*Eco*RI	2700-2721[e]	
ENA21.3F	CGGAATTCGTTAGGATTCTGTGGTGC	*Eco*RI	2580-2597	527 bp
ENA21.3R	CGGAATTCGTTCGGGAAATTATACGT	*Eco*RI	3090-3107[f]	
SOD1F	CGATGCTGTTCCTGATCCTGAT	-		
SOD1R	CGTTCATCAGCGAATTCG	-		
HSP10F	CGATGGTATGTTGTTTCAGA	-	1-18	351 bp
HSP10R	CGTTTGTCGGTGTACAACAAG	-	334-351[h]	
AOX1F	CGATGCTGTTCCTGATCCTGAT	-		
AOX1R	CGTTCATCAGCACGAATTCG	-	446-465 961-979[i]	533 bp
GRP2F	GCCCAGCTGTTGAAGGTAC	-	316-332	434 bp
GRP2R	CGAGCAACATCTCTAACATC	-	733-750[j]	
IPF2839F	CGGTTGAACAAGGTGAAGT	-	235-250	510 bp
IPF2839R	CGCAAGGTTCAGCTTTGGCAC	-	728-745[k]	
DUBF	GTATTTGTCGTTCCCCTTTC	-		288 bp
DUBR	GTGTTGTGTGCACTAACGTC	-		
RNAF	GCATATCAATAAGCGGAGGAAAAG	-		610 bp
RNARF	GGTCCGTGTTTCAAGACG	-		

[a] Restrtiction endonuclease recognition sites included in the primer sequences are underlined
[b] Nucleotide coordinates of *HSP90* gene from *C. albicans* accession no. X81025
[c] Nucleotide coordinates of *HSP104 from C. albicans*, accession no.AF362390
[d] Nucleotide coordinates of *TPS1* from *C. albicans*, accession no.YO7918
[e] Nucleotide coordinates of *NTC1* from *C. albicans* accession no.X95099
[f] Nucleotide coordinates of *ENA21.3* from *C. albicans* accession no. CA4425
[g] Nucleotide coordinates of *SOD1* from *C. albicans* accession no.CA4120
[h] Nucleotide coordinates of *HSP10* from *C. albicans* accession no.CA5341
[i] Nucleotide coordinates of *AOX1* from *C. albicans* accession no.CA2190
[j] Nucleotide coordinates of *GRP2* from *C. albicans* accession no.CA2644
[k] Nucleotide coordinates of *IPF2839* from *C. albicans* accession no.CA5535.
Sequence data for *C. albicans* was obtained from the Stanford Genome Technology Center website at http://www-sequence.stanford.edu/group/candida and from the CandidaDB (http://genolist.pasteur.fr/CandidaDB).

restriction endonuclease-generated DNA fragments were purified from agarose gels using NA45 DEAE membranes (Schleicher and Schuell BioScience, Inc., USA). This method is described in the next section (2.4.3).

2.4.3 Purification of restriction endonuclease-generated DNA fragments and PCR amplimers from agarose gels

Restriction endonuclease-generated DNA fragments were purified from agarose gels using NA45 DEAE membranes (Schleicher and Schuell). The NA45 DEAE membranes were pre-treated by soaking 1 cm strips in 2 M NaCl for 5 min, followed by 3 washes in sterile distilled water for 5 min each. The strips were then stored at 4°C in 1 mM EDTA, pH 8.0. Fragments were electrophoresed as described in section 2.3.2 in agarose gels and viewed on a UV transilluminator (345_{nm}). Using a clean scalpel blade, a small rectangular trough was excised from the gel immediately ahead of the fragment of interest, and a piece of NA45 DEAE paper was placed in the trough and the excised fragment of gel was replaced to hold the paper in place. The electrophoresis was allowed to continue until the fragment had run onto the paper, which could be verified by the fluorescent staining of the paper with ethidium bromide. The paper was then placed in 0.5 ml 1 M NaCl and placed in a water bath at 37°C for at least 1 h to elute the fragment. The DNA solution was then extracted twice with iso-butanol to remove the ethidium bromide, and once with phenol:chloroform (1:1). The DNA was precipitated with two volumes of ice-cold ethanol, pelleted at 10,000 x *g* in a microfuge and resuspended in 5-10 µl sterile distilled water.

2.4.4 Ligation of DNA fragments

Purified DNA fragments were ligated to pBluescript II KS (-) phagemid digested with the appropriate restriction enzyme. Ligation of PCR products to pBluescript was carried out using restriction sites that had been designed within the oligonucleotide primers used in the amplification reactions. Purified DNA fragments were ligated into the appropriate restriction enzyme generated site in

the cloning vector. Ligation reactions were carried out in a 10 µl volume, with a 3:1 ratio of insert to vector DNA in 1x ligase buffer, with 1 U of T4 DNA ligase (Promega). Reactions were carried out for 18 h at 25°C.

2.4.5 Transformation of competent *E. coli* prepared using $CaCl_2$

Transformation of *E. coli* strain DH5α with $CaCl_2$ was carried out by the method of Sambrook *et al.* (1989). *Escherchia coli* DH5α was inoculated from an overnight broth culture into 100 ml LB and grown at 200 rpm in an orbital incubator at 37°C until the OD_{600} reached ~0.5. The culture was then decanted into ice-cold 50 ml Falcon tubes (Becton Dickinson, New Jersey, USA) and chilled on ice for 10 min. Cells were then pelleted by centrifugation at 5,000 x *g* at 4°C for 10 min. Each pellet was resuspended in 10 ml of ice-cold 0.1 M $CaCl_2$, and recentrifuged as before. The pellets were then resuspended in a volume of 2 ml 0.1 M $CaCl_2$ for each 50 ml of original culture. A 200 µl aliquot of this cell-suspension was transferred to a sterile 1.5 ml microfuge tube on ice for each transformation experiment. Plasmid DNA (up to 50 ng) was added to each tube and incubated for 30 min on ice. A known amount of a standard plasmid preparation was added to a separate tube as a positive control, and a tube which contained no plasmid DNA was also included as a negative control. The cells were then heat shocked at 42°C for exactly 90 s and rapidly transferred to an ice bath. The cells were then incubated at 37°C in a water bath in the presence of 800 µl LB medium to allow the cells to recover and express the antibiotic resistance marker (ampicillin resistance in the case of pBluescript II KS [-]). A 100 µl aliquot of this suspension was then spread on to LA plates containing antibiotic (100 µg ampicillin/ml in the case of pBluescript II KS [-]), 1 mM isopropyl-β-D-thiogalactopyranoside (IPTG, Boerhringer Mannheim) and 100 µg (5-bromo-4-chloro-3-indoyl-β-D-galactopyranoside (X-gal, Roche Diagnostics Ltd.) and incubated at 37°C for 20 h. Recombinants were identified using blue-white selection as described by Sambrook *et al.* (1989).

2.5 DNA Sequencing

Commercial DNA sequencing was performed by Lark Technologies, Inc. (Saffron Walden, Essex, UK). Nucleotide sequence analysis was performed by the dideoxy chain-terminating method of Sanger *et al.* (1977) using an automated Applied Biosystems 377 DNA sequencer and dye-labelled terminators (Applied Biosystems, Foster City, California, USA). The sequencing primers used were either the M13 forward and reverse primers or in the case of direct sequencing of PCR amplimers the PCR primers were used as sequencing primers. The 373A Data Analysis program version 1.2.0 (Applied Biosystems, Foster City, California, USA) was used to analyze chromatograms and DNA Strider™ 1.3f11 software (CEA/Saclay, Gif-sur-Yvette, France) was used for sequence analysis. Searches of the EMBL and the GenBank databases for nucleotide and amino acid sequence similarities were performed using BLAST, family of computer programmes. Alignments of nucleotide and amino acid sequences were carried out using CLUSTAL W sequence alignment program (Higgins and Sharp, 1988).

2.6 Analysis of RNA

2.6.1 RNase-free conditions

All solutions used in the preparation of total RNA were rendered RNase-free by the addition of 0.1 M diethylpyrocarbonate (DEPC, Sigma-Aldrich). DEPC was dispersed in all solutions, which were then left to incubate at room temperature overnight, before autoclaving, which inactivates DEPC. Solutions containing amines (i.e. Tris-HCl and EDTA) were prepared with DEPC-pretreated water and autoclaved. Plasticware such as microfuge tubes (Eppendorf) and Falcon tubes, which were assumed to be free of RNase contamination, were handled only when wearing latex gloves. Bottles and other glassware were baked overnight at 200°C. Glass beads (Sigma) used in RNA extractions were 450-600 microns in diameter and were soaked in hydrochloric acid, washed in distilled water, and baked overnight.

2.6.2 Total RNA extraction from *Candida* isolates

Candida cells were harvested at mid-exponential phase (OD_{600}: 0.8-1.0), unless otherwise stated in specific sections) from 50 ml YPD broth cultures for RNA extractions by centrifugation at 2,500 x *g* for 5 min. Pellets were frozen immediately in liquid nitrogen or in a dry ice/ethanol bath. For each sample a 2 ml screw capped Sarstedt tube filled to the 0.25 ml marker with RNase free glass beads was prepared. The cell pellets were resuspended in 1 ml Tri-Reagent (Sigma) and quickly transferred to a Sarstedt tube. The cells were then homogenised in a Fastprep FP120 Bead Beater (Savant Instruments, Inc. Holbrook, NY) for 30 s at speed 6. The homogenate was transferred to a fresh 1.5 ml Eppendorf and incubated for 5-10 min (not longer than 40 min) at 15-30°C. After the addition of 200 µl of chloroform the sample was vortexed for 15 s and then centrifuged at 12,000 x g for 15 min at 4°C. The upper aqueous phase was carefully removed to a fresh 1.5 ml Eppendorf tube and 500 µl of isopropyl alcohol was added to the sample and left to incubate at room temperature for 10 min. The sample was then centrifuged at 12,000 x g for 10 min at 4°C. To remove DNA and polysaccharides the pellet formed was resuspended in DEPC H_2O, two volumes of 6 M LiCl was added and incubated at –20°C for 2 h. Following a centrifugation at 12,000 x g for 15 min, the resulting pellet was carefully washed in 1 ml of 70 % (v/v) ethanol. The ethanol was then removed and the pellet was air dried briefly. The pellet was resuspended in a final volume of 30 µl of DEPC H_20 and stored at –70°C.

2.6.3 RNA electrophoresis

The concentration of each RNA sample was assessed by measuring the A_{260} (1 unit of A_{260} = 42 µg RNA) and 15 µg were loaded on each gel. A test 1 % (w/v) agarose gel was prepared initially to assess the accuracy of concentration determinations and to assess the integrity of each sample. It was found that more accurate determinations of RNA loading could be made by comparison of

ethidium bromide staining of the RNA on a test gel. The integrity of each sample could then be assessed and adjustments made to ensure equal loading of the samples if necessary.

Each RNA sample to be loaded was mixed with 5x RNA loading buffer (50 % [v/v] formamide, 6 % [v/v] formaldehyde, 0.8 μg ml^{-1} ethidium bromide, 1x MOPS buffer) and made up to a uniform volume using DEPC H_2O. The samples were heated at 70°C for 15 min to denature the RNA, then placed on ice and centrifuged briefly. Samples were loaded onto 1.2 % (w/v) agarose gels containing 6 % (v/v) formaldehyde, and 1x MOPS. Electrophoresis was carried out at 60 V in 1x MOPS buffer. Fractionated RNA was transferred to MagnaGraph nylon membranes (MSI) by capillary transfer. Gels were rinsed briefly in DEPC-treated water to remove excess formaldehyde and then soaked in 0.05 N NaOH for 20 min, and then equilibrated in 10x SSC for 45 min. Capillary transfer was carried out in 10x SSC. RNA was then fixed to the membrane by baking at 80°C for 30-45 min followed by UV crosslinking of the RNA to the membrane in a crosslinker (CL-508, UVI tec, Cambridge, England) set at 365_{nm} and 0.08 J cm^2.

2.6.4 Northern hybridisation

Hybridisations were carried out in 15 ml hybridisation buffer (4x SSC, 1 % (w/v) SDS, 10 % (w/v) dextran sulphate, 50 % (v/v) formamide, 100 μg/ml denatured salmon sperm DNA). Membranes were prehybridised for 4 h at 42°C. The radiolabelled probe was then denatured by boiling for 5 min followed by incubation on ice, added to the prehybridisation solution and hybridised with the membrane overnight for 18 h at 42°C. The membrane was then washed for 15 min at 42°C with 5x SSC, 0.1 % (w/v) SDS followed by a wash in 1x SSC, 0.5 % (w/v) SDS at 42°C for 15 min also. The membrane was then exposed to BioMax Ms X-ray film (Eastman Kodak Company, Rochester, NY.) at -70°C with an intensifying screen for 24-72 h. All membranes were hybridised with a probe

homologous to either the *C. albicans* (Di Domenico *et al.*, 1992) or *C. dubliniensis TEF3* gene (Donnelly, 2000).

2.6.5 Quantification of Northern blots

Signals from Northern blot autoradiograms were quantified by scanning densitometry and normalised for loading against the *Ca/CdTEF3* expression signal using the Gelworks 1D software package, UVP Ltd). RNA gels were loaded into the Gelworks package and the following three steps in gel analysis were performed:Lane creation, background subtraction and Band detection. Once bands were detected, Intensity Calibration was carried out. Intensity Calibration matched the pixel intensity values in the gel image files measured in arbitrary units, to real-world values of optical density by using a step wedge containing areas of equal and known intensity. The step wedge was scanned alongside all gel images used. The numerical data of the analyses of the gels were viewed using the measurement table. Relative expression levels were calculated by dividing data obtained for sample gel image files by data obtained from the control gel image files (i.e. *Ca/CdTEF3*). It is important to note that in some cases (i.e. overexposed blots) signals from Northern hybridisations can exceed the linear range of intensity of the step wedges and reach a saturation point which will affect the true image intensity value of the gel file. Hence, densitometry quantification of Northern hybridisation blots can ony be deemed a semi quantitative method.

Chapter 3

Comparative phenotypic analysis of *C. albicans* and *C. dubliniensis* under heat, osmotic and oxidative stress conditions

3.1 Introduction

The activity of yeasts is greatly affected by the chemical and physical conditions of their environments. Understanding these environmental influences helps in part to explain the distribution of pathogenic species such as *Candida spp.* and has the potential to permit the development of methods for controlling and destroying these pathogens. In order to colonise and infect its host successfully, *C. albicans* has developed mechanisms to overcome the environmental stresses encountered in a wide variety of anatomic niches within the human body during the course of an infection. For example, following a sudden increase in temperature (i.e. heat shock) *C. albicans* cells express a set of conserved proteins known collectively as the heat shock proteins (Hsps), that help to stabilise and prevent denaturation of cellular proteins (Swoboda *et al.*, 1995; Enjalbert *et al.*, 2003). Following osmotic shock, *C. albicans* cells accumulate protective molecules like glycerol and trehalose express osmotic response genes encoding salt transporters to help maintain ion homeostasis (Enjalbert *et al.*, 2003; Fan *et al.*, 2005). This pathogen has also developed the ability to withstand the host immune response by escaping oxidative killing by macrophages (Lo *et al.*, 1997). These response mechanisms of *C. albicans* are potential virulence factors and it has been suggested that they may be partly responsible for its success as a pathogen.

To date, the majority of studies on *C. dubliniensis* have been concerned with the epidemiology of this species and relatively little is known about its biology. However, epidemiological and in *vivo* experimental evidence indicates clearly that *C. albicans* is more pathogenic than *C. dubliniensis* (Gilfillan *et al.*, 1998; Vilela *et al.*, 2002; Sebti *et al.*, 2001; Kibbler *et al.*, 2003; Sullivan *et al.*, 2003). Furthermore, competitive growth studies between the two species *in vitro* indicate that *C. albicans* has an advantage over *C. dubliniensis* in broth culture and in biofim producing conditions (Kirkpatrick *et al.*, 2000).

While investigating phenotypic differences between *C. dubliniensis* and *C. albicans* it was discovered that *C. dubliniensis* differs from *C. albicans* in that it grows very poorly at temperatures greater than 42°C and is less tolerant of elevated NaCl and H_2O_2 concentrations (Alves *et al.*, 2002; Pinjon *et al.*, 1998; Vilela *et al.*, 2002). These findings suggest that *C. dubliniensis* may not have the

same capacity as *C. albicans* to survive exposure to environmental stress, indicating that *C. albicans* has a competitive advantage when colonising and causing infection in the human body.

The objective of the first part of the present study was to compare for the first time how *C. albicans* and *C. dubliniensis* react to stressful conditions at the phenotypic level. In order to determine whether an enhanced ability to survive adverse conditions may in part explain why *C. albicans* is a more successful pathogen. In order to investigate this hypothesis, the growth and survival rates of representative strains of each species were compared *in vitro* when subjected to specific environmental stresses. The conditions chosen for analysis included osmotic shock, elevated temperature and exposure to oxidants such as hydrogen peroxide. These conditions were chosen specifically as the molecular basis of the stress response mechanisms induced under these conditions in *S. cerevisiae* and *C. albicans* has been previously investigated or characterised and have been proposed to be important factors for *C. albicans* pathogenesis.

3.2 Materials and Methods

3.2.1 Doubling time determination at elevated temperature and osmotic stress

Overnight broth cultures of *C. albicans* reference strains 132A and SC5314 and *C. dubliniensis* strains CD36, CD539 and CD514 (representing *C. dubliniensis* genotypes 1, 2, 3 and 4 respectively) were grown in yeast nitrogen base (0.67% (w/v) DifcoYNB, 4% (w/v) glucose) liquid medium. The cell density of each overnight culture was determined using an improved Neubauer haemocytometer (Hausser Scientific, Horsham, USA). Cells from these cultures were then added to fresh YNB at 30°C, 37°C, 40°C, 42°C and 44°C in the absence of NaCl and at 37°C with 0.6, 0.8, 1.0, 1.2, 1.4 and 1.6 M NaCl to yield a final concentration of 2 x 10^6 cfu per ml. The cultures were incubated in a shaking, temperature controlled, waterbath at 200 rpm. At specific time points, aliquots of each culture were removed and the optical densities at 600nm($O.D._{600}$) measured using a Genosys 2 spectrophotometer, ThermoSpectronic, supplied by AGB, Dublin, Ireland. These values were then used to plot a growth curve for each isolate grown under each condition. The doubling time of each strain grown under specific conditions was calculated according to the following formulas: n = log N – log N_0/ log2, where N = final cell number, N, N_0 = initial cell number, n = number of generations that have occurred during the period of exponential growth and t/n = g, where t is the hours or mins of exponential growth and g is the generation or doubling time. Experiments were performed on three separate occasions.

3.2.2 Viability assay

For each stress, cultures of the *C. albicans* reference strain SC5314 and the *C. dubliniensis* reference strain CD36 were inoculated from a fresh colony and grown overnight in YPD at 30°C (or 37°C for the osmotic experiments) at 200 rpm. These were then diluted to an OD_{600} of 0.1 in 10 ml of fresh YPD and grown at the same initial temperature until an OD_{600} of 1.0 and were diluted to 1x10^7 cells/ml in sterile ultrapurified water. The culture was divided into two

volumes of 10 ml; one sample was maintained as the control and the other subjected to the heat stress (temperature shift from 30-42°C) osmotic stress (1 M NaCl) and oxidative stress (5.0 mM H_2O_2). One hundred microlitre aliquots were removed at times 0, 30, 60, 90 and 120 min (or 0, 30 and 60 min for oxidative stress experiments) after the initiation of the stress, serial diluted with sterile ultrapurfied water and plated (100 µl) in triplicate onto YPD plates, to determine surviving cell numbers. Plates were incubated for 24 h at 30°C, and survival was expressed as a percentage of viable cells at time =0. Three independent experiments were carried out for each stress condition tested.

3.2.3 Susceptibility to hydrogen peroxide using a broth microdilution test

In order to determine the minimum inhibitory concentration of *C. albicans* and *C. dubliniensis* to hydrogen peroxide the susceptiblility of the *C. albicans* strains, SC5314 and 132A and the *C. dubliniensis* strains CD6 and CD514, (representing genotypes 1 and 3, respectively) to hydrogen peroxide was tested. Hydrogen peroxide (Sigma) was diluted with ultrapurified water to make a stock solution with a final concentration of 160 mM. The assay was carried out in sterile 96-well microtitre plates (Corning, New York, USA). Wells one and ten of each row were dispensed with 0.1 ml of YNB and were used as a sterility control and a positive growth control, respectively. Hydrogen peroxide susceptibility testing was carried out in a final volume of 200 µl in wells two to nine, ranging in concentration from 0.625 mM to 80 mM H_20_2.

The inocula were prepared from a fresh colony and grown overnight in YPD at 30°C at 200 rpm. These were then diluted to an OD_{600} of 0.1 in 10 ml of fresh YNB and grown at the same initial temperature until an OD_{600} of 1.0. The cell density of each suspension was adjusted in YNB to 2 x 10^6 cfu./ml using an Improved Neubauer haemocytometer. This suspension was then diluted in YNB and 10 µl aliquots were dispensed in wells two to nine, yielding a final cell density of 1 x 10^5 cfu/ml.

Test plates were covered with the lids supplied by the manufacturers, wrapped in tin foil and incubated for 24 h at 30°C. Prior to spectrophotometric reading of MIC (minimum inhibitory concetration) end points, the plates were agitated for 2 min using a vortex (Spinmix model, Gallenkamp). Cell densities were determined spectrophotometrically by measuring the turbidity in each well at

595_{nm} with an automated plate reader (Spectra I; SLT-Labinstruments, Salzburg, Austria). All tests were performed in triplicate on at least three separate occasions.

3.2.4 Spot plate assay

Susceptibility of the *C. dubliniensis* strains (CD36, CD539, CD514 and p7718) and *C. albicans* strains (SC5314 and 132A) to heat, osmotic and oxidative stresses was also tested qualitatively by spotting serial dilutions of yeast cultures onto YPD and YNB agar plates containing the following compounds (all compounds from Sigma Aldrich Ireland Ltd.); NaCl, sorbitiol, KCl, H_2O_2, menadione and diamide, which provided an easy visualisation of growth differences between strains. Each plate contained 25 ml of agar. *Candida* strains were grown overnight at 30°C at 200 rpm. These were then diluted to an OD_{600} of 0.1 in 10 ml of fresh YPD and grown at the same initial temperature until an OD_{600} of 1.0 (~10^7 cfu/ml). The cultures were firstly diluted to $1x10^7$ cells/ml in sterile ultrapurified water. Four serial 1:10 of this first dilution |(i.e. 10^{-6}, 10^{-5}, 10^{-4} and 10^{-3}) were made and 4 µl of each dilution was spotted on each plate and incubated for 48 h at 30°C (or 42°C for heat shock experiments).

3.2.5 Statistical analysis

Statistical analysis was carried out using EXCEL 2003 (MS Office). A student's t-test: two sample assuming unequal variances was performed. A *P*-value less than 0.05 was regarded as significant. The t-test was used to determine whether two samples are likely to have come from the same two underlying populations that have the same mean. T-Test used data from two data sets to compute a non-negative t-statistic.

3.3 Results

3.3.1 Comparison of growth of *C. albicans* and *C. dubliniensis* at elevated temperature

In order to investigate the comparative ability of *C. albicans* and *C. dubliniensis* to tolerate environmental stress, the ability of *C. albicans* strains (SC5314 and 132A) and *C. dubliniensis* strains CD36, CD539, CD514 and p7718 (representing *C. dubliniensis* genotypes 1, 2 3 and 4, respectively) to grow at elevated temperature was investigated. Representive growth curves for isolates of each species grown in YNB broth at specific temperatures ranging between 30-44°C, are presented in Fig. 3.1 and the respective doubling times are shown in Table 3.1.

All of the *C. albicans* and *C. dubliniensis* isolates examined grew well in YNB broth at both 30°C and 37°C and there was no significant difference in the doubling times of both species at these temperatures. However, when data from *C. dubliniensis* strain p7718 (genotype 4) was omitted from the analysis, the doubling times of the *C. albicans* strains grown at 37°C were found to be significantly shorter (P <0.04) than those of *C. dubliniensis*. *Candida albicans* strains SC5314 and 132A showed good growth at 40°C in YNB broth with doubling times of 121 min ± 1.73 and 125 min ± 7.8, respectively. Under the same conditions all of the *Candida dubliniensis* strains exhibited significantly longer doubling times (P <0.04) than the *C. albicans* strains. All of the four *C. dubliniensis* strains tested showed reduced growth at 42°C in YNB compared to the *C. albicans* strains. There were substantial differences between *C. dubliniensis* isolates doubling times at 42°C, with *C. dubliniensis* strains CD539 and CD514 (genotype 2 and 3, respectively) having notably longer doubling times (586 min ± 12.2 and 529 min ± 27, respectively) in YNB broth at 42°C compared to the *C. dubliniensis* genotype 1 strain, CD36 (198 min ± 10) and the genotype 4 strain, p7718 (352 min ± 19). *Candida albicans* SC5314 and 132A grew significantly faster than *C. dubliniensis* isolates at this temperature (P <0.04). At the high temperature of 44°C *C. albicans* strains SC5314 (369 min ± 10) and 132A (350 min ± 6.0) showed reduced growth, compared to growth at 42°C, whereas none of the *C. dubliniensis* isolates examined showed any appreciable growth at this temperature.

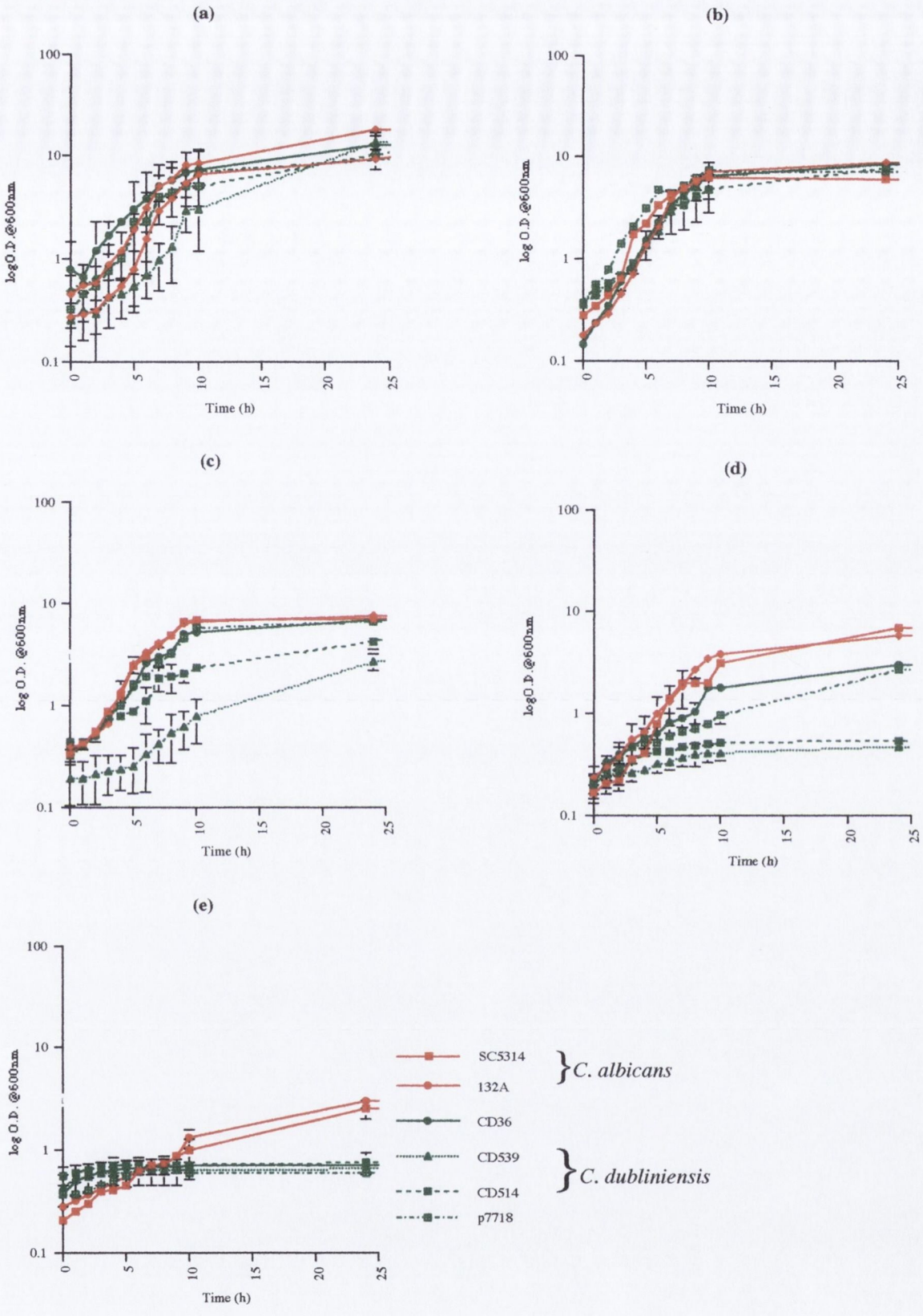


Figure 3.1. Logarithmic growth curves of *C. from thre albcians* and *C. dubliniensis* strains in YNB broth at **(a)** 30°C, **(b)** 37°C, **(c)** 40°C, **(d)** 42°C and **(e)** 44°C. The OD 600nm values shown in the graphs represent the mean values ± standard deviation from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols.

Table 3.1 Doubling times of *C. albicans* and *C. dubliniensis* strains grown at various temperatures in YNB medium

Growth Temp °C	Doubling time (min)					
	C. albicans		*C. dubliniensis*			
	SC5314	132A	CD36	CD539	CD514	p7718
30	92 ± 0.98	134 ± 7.0	157 ± 12	150 ± 3.7	206 ± 4.7	110 ± 2.3
37	87 ± 3.7	96 ± 5.5	101 ± 6.6	114 ± 7	132 ± 4	89 ± 4.0
40	121 ± 1.73	125 ± 7.8	138 ± 1.2	236 ± 10.3	217 ± 8	148 ± 5.9
42	134 ± 7.26	137 ± 2.9	198 ± 10	586 ± 12.2	529 ± 27	352 ± 19
44	369 ± 10	350 ± 6.0	NG	NG	NG	NG

NG=No growth. Data represent the mean ± standard error of 3 independent experiments

3.3.2 Comparison of growth of *C. albicans* and *C. dubliniensis* under osmotic pressure

Representative growth curves for *C. dubliniensis* strains CD36, CD539, CD514 and p7718) and *C. albicans* SC5314 and 132A grown at 37°C in YNB supplemented with 0.6, 0.8, 1.0, 1.2, 1.4 and 1.6 M NaCl were determined (Fig. 3.2) and the doubling time of each strain grown in each NaCl concentration was calculated (Table. 3.2). The doubling times for both species in YNB supplemented with NaCl at 37°C were longer than the corresponding times in YNB without NaCl at 37°C. The 2 *C. albicans* isolates, and the 4 *C. dubliniensis* strains tested grew well in YNB broth supplemented with 0.6 M NaCl and no significant difference in doubling times between the two species was observed. At a concentration of 0.8 M NaCl the doubling times of the *C. albicans* strains were significantly lower (P <0.04) than the *C. dubliniensis* strains. At the same salt concentration it was also noted that the *C. dubliniensis* strains representing genotypes 2 (CD539) and 3 (CD514) exhibited substantially longer doubling times (237 min ± 5.0 and 206 min ± 5.0, respectively) than the other *C. dubliniensis* strains tested; CD36, representing genotype 1 (160 min ± 8.5) and p7718, representing genotype 4 (130 min ± 4.0). Similarly, *C. albicans* SC5314 and 132A grew well in YNB broth supplemented with 1.0 M NaCl, whereas all of the 4 *C. dubliniensis* strains showed reduced growth at this NaCl concentration. Under the same conditions, *C. dubliniensis* isolate p7718 (genotype 4) had a substantially shorter doubling time (174 min ± 3.2) than the other *C. dubliniensis* isolates tested; CD36, representing genotype 1 (209 min ± 15.5), CD539, representing genotype 2 (316 min ± 5.5) and CD514 representing genotype 3 (226 min ± 8.0). However, both *C. albicans* isolates grew significantly faster compared to the *C. dubliniensis* strains tested (P <0.02). The doubling time of the *C. albicans* strains in YNB broth supplemented with 1.2 M NaCl was also significantly shorter than that of the *C. dubliniensis* strains (P <0.005). The doubling time of *C. dubliniensis* CD36 (236 min ± 8.2) in YNB supplemented with 1.4 M NaCl was similar to that of *C. albicans* SC5314 (245 min ± 5.0) and 132A (210 min ± 13.3), whereas *C. dubliniensis* CD539 (360 min ± 24.5), CD514 (355 min ± 5.3) and p7718 (410 min ± 5.8) showed considerably longer doubling

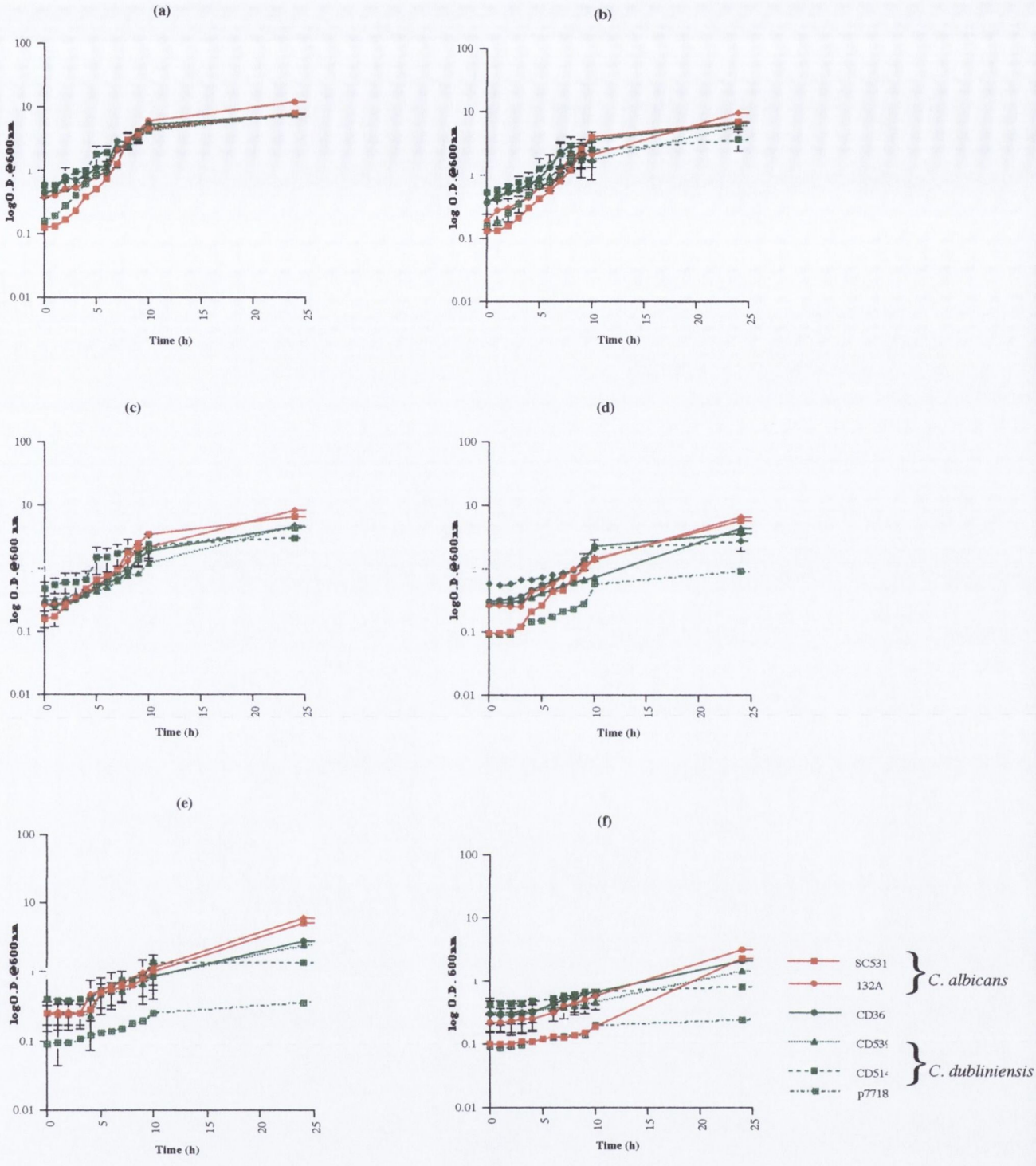


Figure. 3.2. Logarithmic growth curves of *C. albcians* and *C. dubliniensis* strains in YNB broth at 37°C supplemented with the following NaCl concentrations **(a)** 0.6, **(b)** 0.8, **(c)** 1.0, **(d)** 1.2,**(e)** 1.4 and **(f)** 1.6 M NaCl. The OD 600 values shown in the graphs represent the the mean values ± standard deviations from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols.

Table 3.2 Doubling times of *C. albicans* and *C. dubliniensis* strains grown at various NaCl concentrations in YNB medium.

[NaCl]	Doubling time (min)					
	C. albicans		*C. dubliniensis*			
(M)	SC5314	132A	CD36	CD539	CD514	p7718
0	87 ± 3.7	96 ± 5.5	101 ± 6.6	114 ± 7	132 ± 4.0	89 ± 4.0
0.6	91 ± 2.5	134 ± 7.0	157 ± 12	150 ± 3.7	206 ± 4.7	110 ± 2.3
0.8	100 ± 3.0	137 ± 5.2	160 ± 8.5	237 ± 5.0	206 ± 5.0	130 ± 4.0
1.0	127 ± 1.2	144 ± 3.0	209 ± 15.5	316 ± 5.5	226 ± 8.0	174 ± 3.2
1.2	138 ± 4.0	167 ± 8.2	224 ± 7.0	343 ± 7.4	341 ± 4.5	287 ± 8.5
1.4	245 ± 5.0	210 ± 13.3	236 ± 8.2	360 ± 24.5	355 ± 5.3	410 ± 5.8
1.6	337 ± 3.5	374 ± 9.0	433 ± 25	957 ± 29	NG	644 ± 22

NG= No growth. Data represent the mean ± standard error of 3 independent experiments.

times. On average, *C. albicans* doubling times were again significantly shorter than those of *C. dubliniensis* at this salt concentration (P <0.02). At high salt concentration (1.6 M NaCl) both species showed a large increase in their respective doubling times. *Candida albicans* SC5314 had a doubling time of 337 min ± 3.5 and 132A had a doubling time of 374 min ± 9.0. Of the 4 *C. dubliniensis* isolates tested, CD514 failed to grow, whereas isolates CD36 (433 min ± 25), CD539 (957 min ± 29) and p7718 (644 min ± 22) had extremely long doubling times.

3.3.3 Comparison of elevated temperature on *C. albicans* and *C. dubliniensis* cell viability

The degree of cell killing caused by heat shock (30°C-42°C) in both *C. albicans* and *C. dubliniensis* was analysed by placing $1x10^7$ cfu of a culture grown at 30°C in YNB medium at 42°C. Aliquots were removed at times 0, 30, 60, 90 and 120 min after heat shock, serially diluted with sterile ultrapurified water and plated (100 µl) in triplicate onto YPD plates (Fig. 3.3a). When cfu were counted for the determination of viability, the *C. albicans* strains showed higher survival rates than the *C. dubliniensis* strains. In fact, *C. albicans* cells exhibited 100% survival after being subjected for 30 min to 42°C, whereas viability of CD36 *C. dubliniensis* cells was reduced to a mean percentage of 75.6 ± 8.68 which was statistically lower than that of *C. albicans* SC5314 (P < 0.05). The mean percentage viability of *C. dubliniensis* strain CD36 was drastically reduced after 2 h at 42°C (39.9 ± 6.0), whereas, 61.3% of *C. albicans* SC5314 cells survived, which was significantly higher than that of *C. dubliniensis* CD36 strain (P <0.05). These results indicated that *C. dubliniensis* was significantly more susceptible to the heat shock than *C. albicans.*

3.3.4 Comparison of the effect of high salt concentration on *C. albicans* and *C. dubliniensis* cell viability.

The survival of both species in the presence of sodium chloride (1 M NaCl) was investigated by placing $1x10^7$ cfu of a culture grown at 37°C in YNB medium supplemented with 1 M NaCl. Aliquots were removed at times 0, 30, 60, 90 and 120 min after the initiation of the stress, serially diluted with sterile

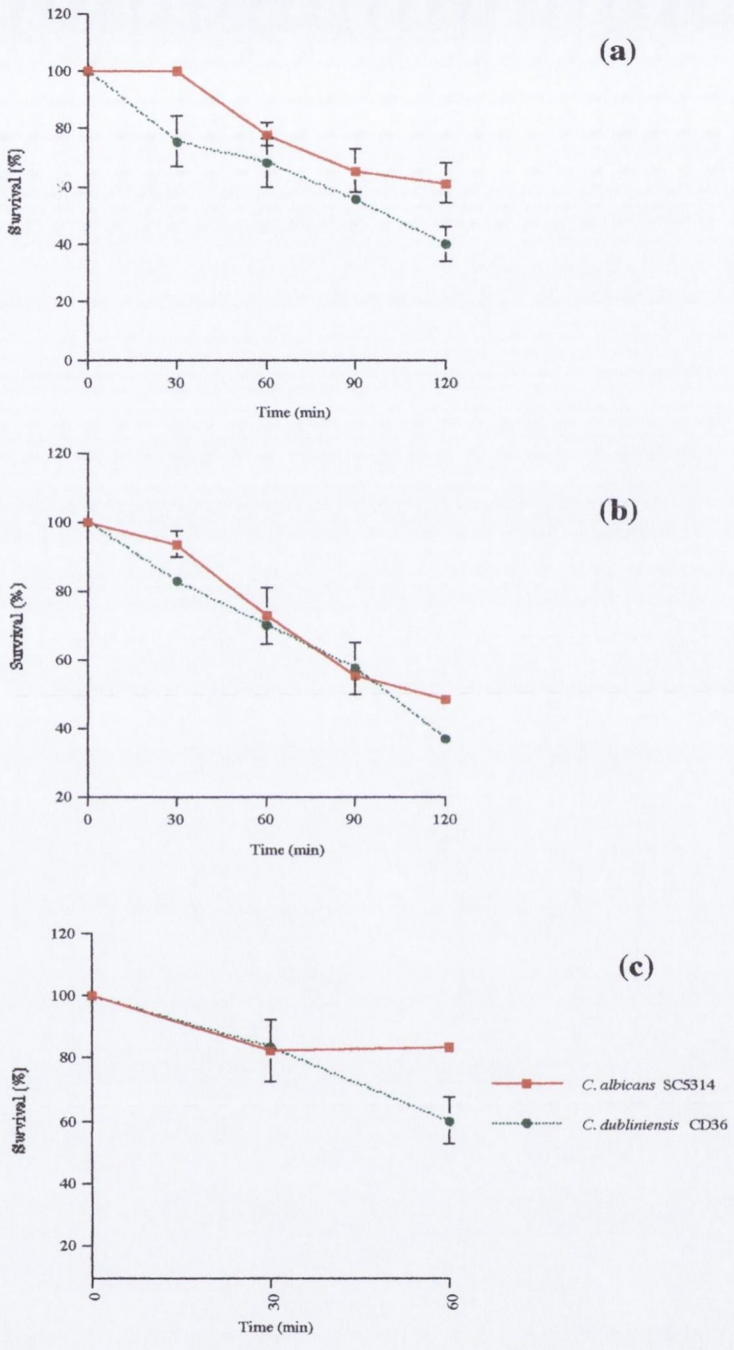


Figure 3.3. Comparison of the degree of survival of *C. albicans* strain SC5314 and *C. dubliniensis* strain CD36 to **(a)** heat shock (30°C-42°C) **(b)** osmotic stress (1 M NaCl) and **(c)** oxidative stress (5 mM H_2O_2). Cell survival was calculated after exposure to the conditions indicated. Results represent the mean values ± standard deviations from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols.

ultrapurfied water and plated (100 µl) in triplicate onto YPD plates, (Fig. 3.3b). Both species exhibited a reduction in cell viability over the duration of the experiment. However, *C. albicans* SC5314 cells displayed a higher percentage viability (93.5 ± 6.24) after 30 min exposure to osmotic treatment, compared to *C. dubliniensis* CD36 (82.6 ± 2.5). This difference was significant (P <0.02). Cell viability was drastically reduced in both species following exposure to NaCl for 2 h, however *C. albicans* (48.2 ± 3.4) mean percentage viability remained significantly higher ($P < 0.01$) than that of *C. dubliniensis* CD36 (36.8 ± 2.13).

3.3.5 Suceptibility of *C. albicans* and *C. dubliniensis* to hydrogen peroxide

MIC (minimum inhibitory concentration) is defined as the smallest amount of agent needed to inhibit the growth of an organism. Initially, the minimum inhibitory concentration of *C. albicans* and *C. dubliniensis* strains to hydrogen peroxide was investigated in order to determine a hydrogen peroxide concentration suitable for the comparison of the effect of oxidative stress on the cell viability of both these species. Exposure to hydrogen peroxide concentrations ranging from 0.625 mM to 80 mM H_2O_2 indicated that both *C. albicans* and *C. dubliniensis* are susceptible to H_2O_2 and display a MIC of ≤10.0 mM (Fig. 3.4). As both species displayed a dramatic decrease in growth at a concentration of 5.0 mM it was decided to use this condition to further investigate the effect of hydrogen peroxide on the cell viability of both these species.

3.3.6 Comparison of the effect of oxidative stress on *C. albicans* and *C. dubliniensis* cell viability

When exponential cells from both species were subjected to an oxidative stress treatment of hydrogen peroxide (5 mM H_2O_2), only *C. dubliniensis* CD36 displayed a marked loss in viability compared to *C. albicans* SC5314 over a 60 min time period (Fig. 3.3c). Both species exhibited a similar mean percentage survival following 30 min of exposure to 5 mM H_2O_2 (82.3 ± 17.11 and 83.6 ± 2.185, respectively). Overall, *C. albicans* SC5314 displayed a much greater resistance to hydrogen peroxide than *C. dubliniensis* CD36. In fact, 83.3 % of *C. albicans* SC5314 survived 5 mM hydrogen peroxide for 1 h, whereas survival of *C. dubliniensis* CD36 was reduced to 59.9 %. The higher susceptibility of *C.*

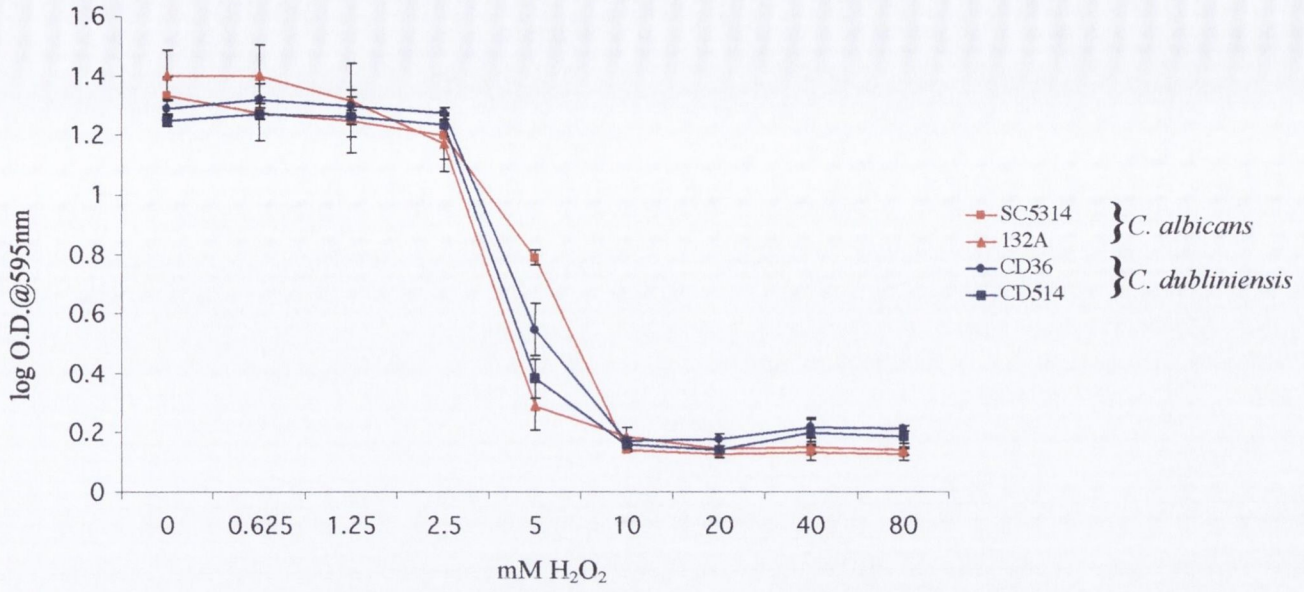


Figure 3.4. Susceptibility of *C. albicans* and *C. dubliniensis* strains to hydrogen peroxide. Approximately 10^5 cells, of exponentially growing *C. albicans* (SC5314 and 132A) and *C. dubliniensis* (CD36 and CD514, representing genotypes 1, and 3 respectively) cells were incubated with hydrogen peroxide concentrations ranging from 0.625 mM to 80 mM H_20_2 and incubated at 30°C for 24 h. Cell density at each H_20_2 concentration was determined spectrophotometrically by measuring the turbidity in each well at 595nm with an automated plate reader. All tests were performed in triplicate on at least three separate occasions.

dubliniensis CD36 to 5 mM H_2O_2 was statistically supported ($P < 0.01$).

3.3.7 Comparison of the susceptibility of *C. albicans* and *C. dubliniensis* to elevated temperature, osmotic and oxidative stresses using a spot plate assay

3.3.7.1 Effect of elevated temperature

All *C. albicans* and *C. dubliniensis* strains tested showed good growth at 30°C on YPD at 48 h. No growth was found for any of the four *C. dubliniensis* isolates at 48 h on YPD at 42°C, whereas both of the *C. albicans* strains tested showed good growth at 42°C on YPD at 48 h (Fig. 3.5).

3.3.7.2 Effect of osmotic reagents

The sensitivity of both *C. albicans* and *C. dubliniensis* cells to osmotic stress was investigated using a range of solutes including the chloride salts, NaCl and KCl and the osmolyte sorbitol. As shown in Figs. 3.6 and 3.7, significantly, all the *C. dubliniensis* isolates displayed a clear osmosensitive phenotype compared with the *C. albicans* isolates tested when challenged to increasing concentrations of the osmostressing reagents NaCl and KCl. On YPD plates supplemented with 0.6 M NaCl all of the strains tested grew, however at 0.8 M NaCl there was a decrease in growth of the *C. dubliniensis* genotype 2 strain CD539 (whose growth was also lower in the control compared to the other isolates) and the genotype 4 strain p7718. At 1.0 M NaCl, all of the *C. dubliniensis* isolates tested showed a decrease in growth compared to *C. albicans* and at a concentration of 1.4 M NaCl only *C. albicans* strains grew and this continued up to a concentration of 1.6 M NaCl. On this medium, challenged with high concentrations of NaCl (1.6 M), the growth of both the *C. albicans* strains tested appeared to be only slightly retarded. The higher susceptibility of *C. dubliniensis* isolates to osmotic reagents was also observed when cells were spotted on to YPD plates containing KCl (Fig 3.7). All of the *C. albicans* and *C. dubliniensis* strains tested grew in the presence of 0.6 M KCl. At 0.8 M KCl, the genotype 2 strain CD539 exhibited decreased growth, and at 1.0 M KCl all of the *C. dubliniensis* strains showed a significant decrease in growth compared to *C. albicans*. At 1.2 M KCl, both *C. albicans* strains tested exhibited a decrease in growth, but continued growing at 1.6 M KCl. Under the same conditions, two

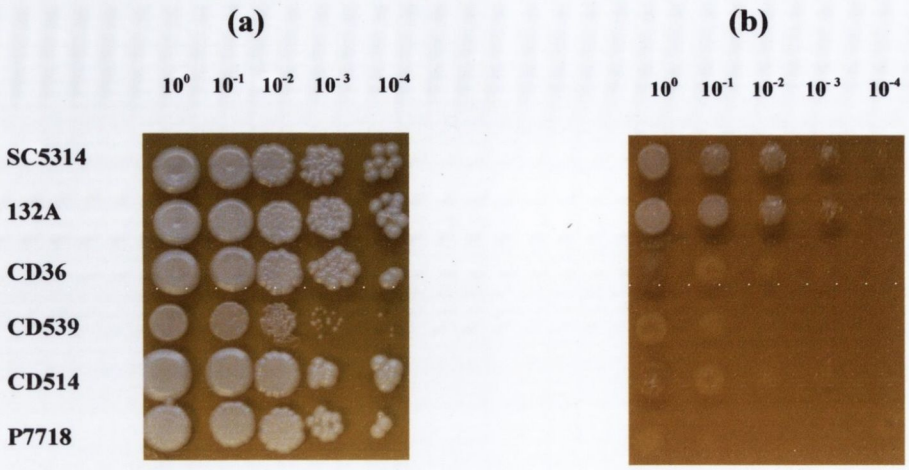


Figure 3.5. Effect of elevated temperature on *C. albicans* and *C. dubliniensis* strains. Approximately 10^7 cells, and 10-fold dilutions thereof, of exponentially growing *C. albicans* (SC5314 and 132A) and *C. dubliniensis* (CD36, CD539, CD514 and p7718, representing genotypes 1, 2, 3 and 4 respectively) cells were spotted onto YPD plates containing the indicated NaCl concentration. Plate **(a)** was incubated at 30°C and plate **(b)** was incubated at 42°C for 48 h.

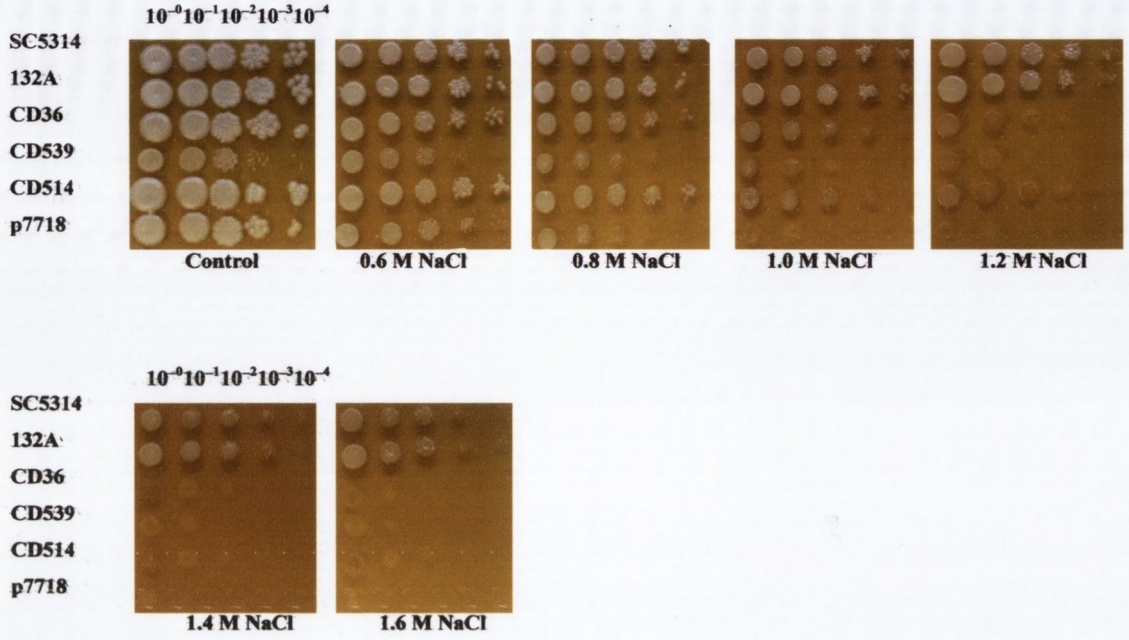


Figure 3.6. Effect of increasing concentrations of NaCl on *C. albicans* and *C. dubliniensis* strains. Approximately 10^7 cells, and 10-fold dilutions thereof, of exponentially growing *C. albicans* (SC5314 and 132A) and *C. dubliniensis* (CD36, CD539, CD514 and p7718, representing genotypes 1, 2, 3 and 4 respectively) cells were spotted onto YPD plates containing the indicated NaCl concentration. Plates were incubated at 30°C for 24 h.

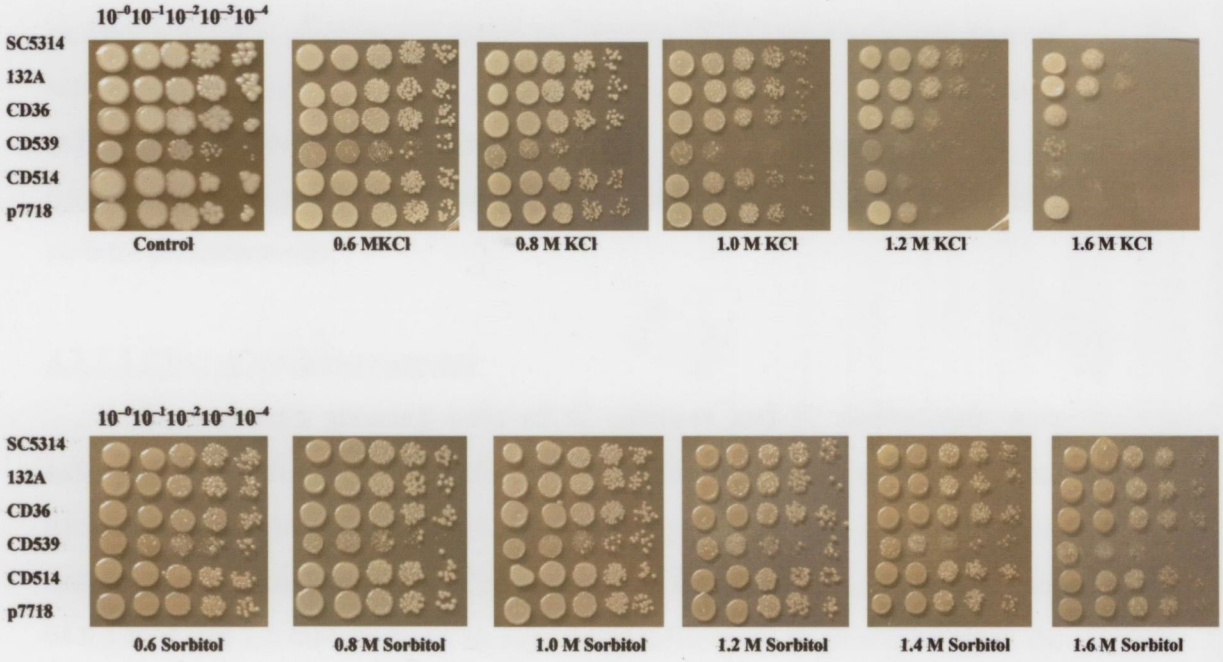


Figure 3.7. Effect of increasing concentrations of KCl on *C. albicans* and *C. dubliniensis* strains. Approximately 10^7 cells, and 10-fold dilutions thereof, of exponentially growing *C. albicans* (SC5314 and 132A) and *C. dubliniensis* (CD36, CD539, CD514 and p7718, representing genotypes 1, 2, 3 and 4 respectively) cells were spotted onto YNB plates containing the indicated NaCl concentration. Plates were incubated at 30°C for 24 h.

ofthe *C. dubliniensis* isolates, p7718 (genotype 4) and CD36 (genotype 1) displayed poor growth compared to *C. albicans*. Interestingly, it was noted that sorbitol did not inhibit growth of *C. albicans* or *C. dubliniensis* cells, with the exception of the *C. dubliniensis* genotype 2 isolate CD539 which showed a partial osmosensitive phenotype in the presence of 1.6 M (Fig. 3.7). These results indicated that both species differ in their relative susceptibilities to the osmostressing reagents, NaCl and KCl, but share a similar resistance to high sorbitol concentrations.

3.3.7.3 Effect of oxidative reagents

Exponentially growing cells of *C. albicans* and *C. dubliniensis* were subjected to increasing concentrations of oxidants, including diamide and hydrogen peroxide supplemented in YPD agar. There were substantial differences in the susceptibility of both species to these oxidants. In the presence of 0.5 mM and 1.0 mM diamide, no significant differences in growth between the two species was observed (Fig. 3.8). At a concentration of 2.0 mM diamide, *C. albicans* strain 132A was unable to grow and two of the *C. dubliniensis* strains (CD539 and p7718) showed growth similar to that of *C. albicans* strain SC5314. However, two of the remaining *C. dubliniensis* strains (CD36 and CD514) showed good growth under the same conditions. These results suggested that the resistance of these species to the oxidant diamide may be strain-specific. When the oxidative tolerance of *C. albicans* and *C. dubliniensis* was compared on YPD supplemented with hydrogen peroxide, all the *C. dubliniensis* strains tested showed a greater susceptibility to hydrogen peroxide than the *C. albicans* strains (Fig. 3.8). All strains from each species exhibited good growth in the presence of 1.0 mM H_2O_2. At 2.0 mM there was a decrease in growth observed in the *C. dubliniensis* genotype 2 strain, CD539 and at 3.0 mM this strain failed to grow. At 4.0 mM H_2O_2 the *C. dubliniensis* genotype 4 strain p7718 was unable to grow, and both of the *C. dubliniensis* strains CD36 and CD514 (genotypes 1 and 3, respectively) decreased in growth. In contrast, the two *C. albicans* strains, SC5314 and 132A showed no decrease in growth until subjected to a concentration of 5.0 mM H_2O_2. No growth was observed for any of the *C. dubliniensis* isolates at 6.0 mM H_2O_2, whereas both of the *C. albicans* isolates

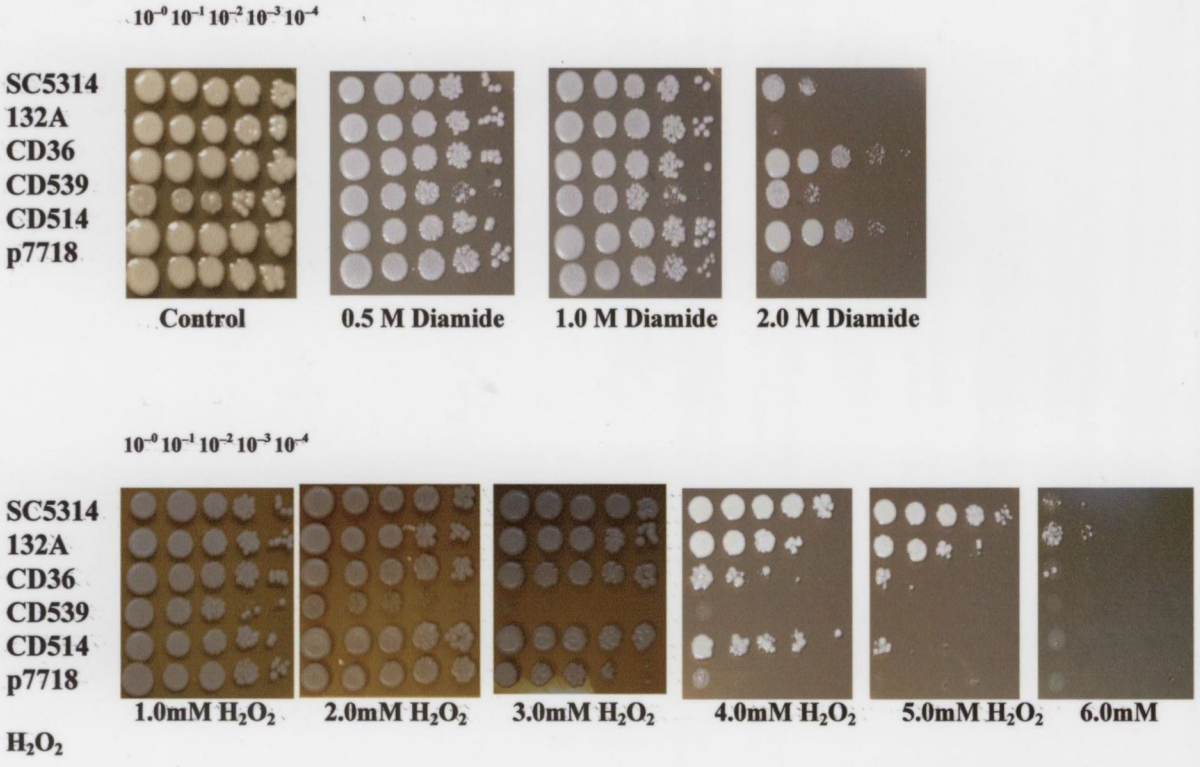


Figure 3.8. Effect of increasing concentrations of diamide and hydrogen peroxide on *C. albicans* and *C. dubliniensis* strains. Approximately 10^7 cells, and 10-fold dilutions thereof, of exponentially growing *C. albicans* (SC5314 and 132A) and *C. dubliniensis* (CD36, CD539, CD514 and p7718, representing genotypes 1, 2, 3 and 4, respectively) cells were spotted onto YPD plates containing the indicated oxidant concentration. Plates were incubated at 30°C for 24 h.

showed limited growth indicating that higher levels of H_2O_2 are required to inhibit the growth of *C. albicans*.

3.4 Discussion

When *C. dubliniensis* was first identified in 1995 it was noted that unlike *C. albicans*, this species does not grow well at 42°C. Indeed, subsequent studies have suggested that the inability of *C. dubliniensis* to grow well at 45°C is an excellent diagnostic marker for the identification of this species. More recently it has been noted that *C. dubliniensis* fails to grow on medium containing 6.5% NaCl while *C. albicans* thrives under these conditions Alves *et al.* (2001). Vilela *et al.* (2002) also demonstrated that *C. dubliniensis* was more susceptible to hydrogen peroxide than *C. albicans*. These data suggest that *C. albicans* is more tolerant of extremes of temperature, osmotic pressure and oxidative stress than *C. dubliniensis*, suggesting that *C. albicans* may have a more efficient stress response system. In order to confirm this suggestion a comprehensive comparison of both species to these stress conditions that may be encoutered in the human body was undertaken at the phenotypic level.

In the first part of this study doubling times of *C. albicans* isolates (SC5314 and 132A) and *C. dubliniensis* (CD36, CD539, CD514 and p7718 representing genotypes 1, 2, 3 and 4, respectively) were examined in liquid media at temperatures ranging between 30°C-44°C, and with NaCl concentrations ranging between 0.6 M-1.6 M. The data from these experiments and from the spot plate assay (Fig. 3.5) confirmed that *C. dubliniensis* exhibits an increased doubling time at temperatures >42°C in minimal medium. The lower survival rates of *C. dubliniensis* and heat sensitive phenotype observed on the agar spot plates further confirmed this data. The reasons for the reduced tolerance of *C. dubliniensis* to these high temperatures remains to be elucidated, however it is speculated that it may be the result of a defect in (1) the expression of genes involved in the heat shock response, or (2) the trehalose metabolic pathway. It has already been shown previously that *C. albicans* is capable of inducing a set of heat shock genes after a temperature shift of (23°C-37°C) and is also capable of accumulating trehalose at 42°C and 43°C (Van Dijck *et al.*, 2002; Zaragoza *et al.*, 1998; Arguelles *et al.*, 1997; Enjalbert *et al.*, 2003). The absence or divergence of genes encoding specific Hsps' or trehalose metabolic enzymes in the *C. dubliniensis* genome may, in part, explain the reduced thermtolerance of *C. dubliniensis* compared to *C. albicans*. In the case of osmotic stress *C.*

dubliniensis, unlike *C. albicans*, grows poorly in media containing 0.8 M-1.6 M NaCl as determined by the observed differences in doubling times (Table 3.2), survival (Fig. 3.3) and spot plate assays (Figs. 3.6). All of the *C. dubliniensis* strains tested displayed a clear osmosensitive phenotype when subjected to elevated levels of NaCl and KCl, but not sorbitol (with the exception of *C. dubliniensis* strain CD539) in the spot plate assay (Figs. 3.6 and 3.7). These results indicate that *C. dubliniensis* differs in its relative sensitivity to sorbitol and the chloride salts (NaCl and KCl). Indeed, the osmosensitive phenotype shown by *C. dubliniensis* may be due to intracellular cation toxicity (Na^+ and K^+) (Figures 3.5 and 3.6). The greater sensitivity of *C. dubliniensis* to NaCl and KCl compared to *C. albicans* suggests that these toxic cations may be accumulated to higher levels in *C. dubliniensis* cells or may be due, at least in part, to the presence of more efficient and effective cation transport systems for cation exclusion in *C. albicans*. Sodium efflux is mediated by the *ENA1* ATPase in *S. cerevisiae* which is induced upon salt stress (Haro *et al.*, 1991; Garciadeblas *et al.*, 1993). Both *C. albicans* and *C. dubliniensis* cells may possess similar pumps but with higher activity and better up- regulation by salt stress in that of *C. albicans*. Another possible reason for *C. dubliniensis*' reduced tolerance to salt stress may perhaps be explained by a reduced capability of *C. dubliniensis* for osmotic adjustment. Osmotic adjustment has been achieved in other yeast species, including *C. albicans,* through the accumulation of glycerol and the osmoregulatory solute trehalose (Fan *et al.*, 2005; Hounsa *et al.*, 1998; Garcia *et al.*, 1997; Parrou *et al.*, 1997).

The results of the hydrogen peroxide viability and spot plate assay from this study confirmed previous work by Vilela *et al.*, (2002), in which *C. dubliniensis*' greater suceptibility to hydrogen peroxide was first reported. Interestingly, the oxidant diamide did not have the same detrimental effect on *C. dubliniensis* as hydrogen peroxide, and it appears to affect both species in a strain-specific manner (Fig. 3.8). It is speculated that *C. dubliniensis'* increased sensitivity to hydrogen peroxide compared to *C. albicans* may perhaps be explained by a lack of induction of antioxidant genes or may be due to the absence of genes encoding specific transcription factors such as *C. albicans CAP1* (Alarco *et al.*, 1997) which play an essential role in the conduction of the oxidative stress response in this species.

An interesting observation in this study was the variation within species observed in both *C. albicans* and *C. dubliniensis* strains in response to different phenotypic conditions. For example in *C. albicans,* SC5314 was more tolerant than the 132A strain to the presence of H_2O_2 and diamide (Fig 3.8.) and had a shorter doubling time under the majority of the conditions tested (Tables 3.1 and 3.2). In *C. dubliniensis*, CD539 strain, (genotype 2) was consistantly less tolerant to all of the conditions tested compared to the other *C. dubliniensis* strains tested. Furthermore, *C. dubliniensis* CD514 exhibited higher doubling times (Tables 3.1 and 3.2) and also showed a reduced tolerance to KCl (Fig 3.7) compared to the CD36 (genotype 1) and p7718 (genotype 4).

The significance of *C. dubliniensis*' genotypes in relation to phenotype has not been studied extensively but the results obtained in this study suggest that under specific conditions genotypes 2 and 3 are perhaps less tolerant to environmental stress relative to genotype 1 and 4. Additional studies are required to investigate whether specific phenotypes of *C. dubliniensis* strains are associated with individual genotypes. In addition, the variation within species observed in this study highlights the importance of using multiple strains when comparing phenotypic properties between species.

The results from this part of the study strongly suggest that *C. dubliniensis* compared to *C. albicans* has a reduced capacity to tolerate a range of stress conditions at the phenotypic level.

Chapter 4

Identification of homologues of representative *C. albicans* stress response genes in *C. dubliniensis* and comparison of their expression under environmental stress conditions

4.1 Introduction

Previously described phenotypic data and data from this study have confirmed that *C. albicans* is better able to withstand and grow under a wide range of environmental conditions including elevated temperature, osmotic pressure and oxidative stress (Alves *et al.*, 2003, Pinjon *et al*, 1998; Vilela *et al.*, 2002). It is currently not known what the basis of the difference in the phenotypes observed between *C. albicans* and *C. dubliniensis* is, in response to elevated temperature, osmotic shock and oxidative stress, although one possiblity, is that *C. dubliniensis* may be defective in the expression of essential stress response genes.

Microbial heat shock proteins play a pivotal role in the heat shock response of yeasts. While *HSP90* is essential for viability in *C. albicans*, *HSP104* is the key element responsible for the acquisition of stress induced tolerance under extreme temperatures in *S. cerevisiae* (Sanchez and Lindquist, 1990). The role of *HSP104* in *C. albicans* has not yet been investigated. Based on the role of *HSP90* in *C. albicans* and *HSP104* in *S. cerevisiae*, it was postulated that the lower tolerance of *C. dubliniensis* to elevated temperature compared to *C. albicans* may be due in part to a defect in the regulation of either or both of these two important heat shock protein genes.

The dissacharide trehalose has also been implicated in the survival of yeast, not only at elevated temperature, but also under conditions of osmotic shock (Wiemken, 1990; Arguelles, 1997; Parrou *et al.*, 1997; Ribeiro *et al.,* 1997; Hounsa *et al.*, 1998; Zaragoza *et al.*, 1998; Van Dijck *et al.*, 2002; Zaragoza *et al.*, 2002). A previous study by Zaragoza *et al.* (1998) showed that deletion of the *C. albicans TPS1* gene inhibits trehalose accumulation and growth and also reduces the virulence of *C. albicans* cells. As *C. dubliniensis,* unlike *C. albicans,* grows very poorly when trehalose is the only available source of carbohydrate, the possibility exists that the enhanced ability of *C. albicans* to withstand thermal stress and perhaps osmotic stress may be due to its ability to accumulate high levels of trehalose under stress conditions. If this is the case, it could be possibly due to a fault in the genetic machinery involved in the trehalose metabolic pathway of *C. dubliniensis*.

In order to investigate the molecular basis of the differential ability of *C. albicans* and *C. dubliniensis* to tolerate environmental stress the first part of this study was designed to investigate the presence of homologues of genes known to be instrumental in the responses of *C. albicans* to environmental stress in *C. dubliniensis*. In cases where homologous pairs of genes were identified, gene fragments were cloned and sequenced to determine if there was any divergence between the two genes. In addition, in order to investigate if there were any differences in the expression of these stress response genes (i.e. *HSP90*, *HSP104*, *TPS1* and *NTC1*) between the two species Northern analyses was carried out. Since *C. dubliniensis* has been shown previously to grow very poorly when trehalose is the only available source of carbohydrate, this suggested that there may be a defect in the metabolic pathway of trehalose synthesis in *C. dubliniensis*. In order to investigate this possibility, the intracellular levels of trehalose and the activity of the enzymes involved in the trehalose metabolic pathway in *C. albicans* and *C. dubliniensis* were investigated under normal conditions and under conditions of environmental stress. By the end of this study the *C. dubliniensis* sequencing project had generated a complete sequence of the *C. dubliniensis* genome thereby providing an excellent source for the comparison of *C. albicans* and *C. dubliniensis*.

4.2 Materials and Methods

4.2.1 Amplification of *HSP90*, *HSP104*, *TPS1* and *NTC1*

Amplification of *HSP90, HSP104, TPS1* and *NTC1* gene fragments from *C. dubliniensis* CD36 and *C. albicans* 132A genomic DNA was carried out using the Expand High Fidelity PCR system. PCR primers were designed based on the *C. albicans HSP90, HSP104, TPS1* and *NTC1* sequences (Table 2.2). Amplification conditions were as follows: 30 cycles of 1 min at 94°C, 1 min at 55°C and 1 min at 72°C, followed by 72°C for 10 min.

4.2.2 Analysis of RNA

4.2.2.1 Total RNA extraction from Candida *isolates*

For each stress, cultures were inoculated from a fresh colony and grown overnight in YPD at 30°C (or 37°C for osmotic shock experiments). These were then diluted to an OD_{600} of 0.1 in fresh YPD and grown at the same initial temperature until an OD_{600} of 1. The cell density of exponentially growing cells was determined using a Neubauer haemocytometer and was adjusted to give a final cell density of 1×10^7 cfu per/ml. Total RNA was isolated from *C. albicans* and *C. dubliniensis* isolates grown to the mid-exponential phase in YPD as described in section 2.6.2.

4.2.2.2 Heat Shock

Cells growing exponentially at 30°C in YPD were shifted to 42°C or 45°C and samples were taken at 1, 5, 10 and 30 min following transfer. Total RNA was then prepared. Total RNA isolated from cells growing at 30°C prior to heat shock was used as a control.

4.2.2.3 Osmotic Shock

NaCl was added directly to exponential cells in YPD at 37°C to generate a 1.0 M final concentration. Samples were taken at 0 and 30 min after the addition of NaCl and total RNA was isolated. Total RNA isolated from cells growing at 37°C prior to osmotic shock were used as a control.

4.2.3 Preparation of trehalase from *Humicola grisea*

Trehalase was extracted from *Humicola grisea* by the method of Zimmermann *et al.* (1990).

4.2.3.1 Growth of Humicola grisea

Humicola grisea cultures were maintained on agar containing 1.8 % (w/v) bacto-agar and 4 % (w/v) ground rolled oats (Quaker, Chicago, IL). Fifty mililitres of medium was prepared in a conical flask. After sterilisation the flask was tilted at a 45°C angle (to increase the surface area for growth) and was allowed to cool. While the agar was cooling, a sterile plastic rod was used to carefully remove spores from the surface of a previously grown *H. grisea* culture. The spores were added to 1 ml of sterile ultrapurified water in a 1.5 ml Eppendorf tube, inverted several times and then spread on to the medium when it was set. The culture was allowed to grow at 40°C for approximately 15 days. After 5 to 7 days of growth the culture turns black. After an additional 15 days of growth at 40°C the flask was put in the cold room for about 5–10 days. This step increases the specific activity of trehalase. At this point the cultures are ready to be used as a source of trehalase activity.

4.2.3.2 Extraction and partial purification of conidial trehalase

Humicola grisea conidia were harvested by adding 10 ml of sterile ultrapurified water to the flask, and by gently scraping the surface of the culture with a sterile plastic rod. The conidial suspension was then poured into a beaker and filtered through glass wool through a funnel. The filtrate was centrifuged at 1,270 x *g* for 30 min at room temperature. One millilitre of 11 % (w/v) kaolin was added to 10 ml of the supernatant and was allowed to stand for 20 min at room temperature. This suspension was centrifuged at 1500 x *g* for 10 min. Supor membrane tubing, 6-8,000 (Spectra/ Por®, Spectrum laboratories, USA) for dialysis was prepared in 5 mM EDTA by boiling for 10 min, followed by rinsing several times in sterile ultrapurified H_2O. The supernatant is dialysed overnight with ultrapurified H_2O in a cold room.

4.2.3.3 Activity test

The specific activity of the trehalase was determined using the glucose oxidase/ peroxidase assay. The enzyme extract was diluted 1:10 and 1:50 with sterile ultrapurified H_2O and was incubated with a trehalose buffer (0.4 M trehalose, 300 mM N a-acetate, 30 mM $CaCl_2$ pH 5.5) for 20 min at 40°C in a waterbath. The reaction was stopped by boiling the samples for 15 min, allowing them to cool to room temperature and boiling them again for a further 15 min. Glucose standards ranging from 0.1–0.6 mM of were made from a 4mM glucose stock solution in H_2O. One mililiter of glucose oxidase and peroxidase (Sigma) and 0.1 mg of o-dianisidine (Sigma) was added to each sample and standard and was incubated at 30°C for 1h. The addition of 0.5 ml of 56 % (v/v) H_2SO_4 to each tube stopped the reaction. Absorbance was then measured at 546 nm. The amount of enzyme activity (in U/ml = nmol glucose/min/ml enzyme extract converted at 40°C) present was determined by reference to the glucose standard curve of known concentrations of glucose over the range of 0-4 mg/ml. The activity of *H. grisea* conidial trehalase is approximately 340 U/ml.

4.2.4 Determination of intracellular trehalose levels in *C. albicans* and *C. dubliniensis strains* at elevated temperature and under osmotic shock conditions

4.2.4.1 Method I for determination of trehalose

Trehalose accumulation in *C. albicans* and *C. dubliniens* cells at elevated temperature was assessed by a method previously described by Parrou and Francois, (1997) and bases its trehalose determinations on the amount of glucose equivalents produced per number of cells.

4.2.4.1.1 Sampling

Candida albicans strains SC5314 and 132A and *C. dubliniensis* strains CD36 and p7718, representing genotypes 1 and 4, respectively, were grown at 30°C in YPD broth and adjusted to give a final concentration of 10^7 cfu per/ml. To generate heat shock, the cells were transferred from a 30°C to a 42°C temperature - controlled waterbath and were harvested at 30, 60, 90 and 120 min following the transfer. Control cells were maintained at 30°C. The cells were then centrifuged quickly in a 50 ml Falcon tube (Beckton Dickinson, New Jersey, USA) at 3000 x *g* for 3 min and resuspended in 1 ml of ultrapure water in a 2 ml

Sarstedt tube (Sarstedt, Aktiengesellschaft & Co, Germany). The 2 ml Sarstedt tubes were subjected to a spin for 15 s at 20,800 x *g* in an Eppendorf (model 5417C) microfuge (Eppendorf, Hamburg, Germany) and the liquid was drained completely using a syringe to remove the culture medium.

4.2.4.1.2 Extraction and quantification

The pellet was then resuspended in 0.25 ml of 0.25 M Na_2CO_3 and incubated at 95°C for 4 h. The solution was then brought to pH 5.2 by the addition of 0.15 ml of 1 M acetic acid and 0.6 ml of 0.2 M Na-acetate, pH 5.2. This solution was then incubated overnight with 0.05 U/ml of trehalase (Sigma-Aldrich) at 37°C. The suspension was then centrifuged for 3 min at 14000 x *g*. Trehalose levels were determined using a glucose assay kit (Sigma-Aldrich) according to the manufacturer's instructions. Pre-existing glucose was determined in control reactions lacking trehalase.

4.2.4.2 Method II for determination of trehalose levels

Trehalose levels were also determined using a method by Neves *et al.* (1994). Trehalose accumulation in *C. albicans* and *C. dubliniens* cells in response to both heat and osmotic shock was assessed using this method. This assay uses the extracellular conidial trehalase extracted from *H. grisea* (described in section 4.2.3.2) instead of the commercially available trehalase (Sigma-Aldrich) for the determination of the amount of trehalose. Trehalose measurements are based on the wet weight of *Candida* cells, unlike the method described in section 4.2.4.1 which bases its measurements on cell density i.e. 1×10^7 cfu per/ml.

4.2.4.2.1 Sampling

For each stress condition, overnight cultures of *C. albicans* strains (SC5314 and 132A) and *C. dubliniensis* (CD36, CAN1, CD33, CD539, CD541, CD514 and p7718, representing genotypes 1, 2, 3 and 4 respectively) were grown in 50 ml of YPD at 30°C (or at 37°C for osmotic shock experiments). Two additional *C. dubliniensis* genotype 3 strains, p6785 and p6265 were included in the heat shock experiment. Cells from overnight cultures were harvested by centrifugation at 800 x *g* for 5 min, in preweighed 50 ml Falcon tubes (Beckton Dickinson, New Jersey, USA). The supernatant was poured off and the Falcon

tubes were reweighed. Approximately 1 g of each strain from both species was used to inoculate 150 ml of fresh YPD broth in 300 ml Erlenemeyer flasks. The flasks were then incubated at 30°C at 220 rpm for 2-3 h so that the cells were in the exponential phase. After 2-3 h incubation the cultures were removed. A 2-3 ml sample was removed before dividing the culture (T0). The culture was then divided into 3x 50 ml aliquots and the cells were further incubated at either 30°C, 37°C or 42°C. For the osmotic shock experiments, cultures were split into 2x 50 ml aliquots; one sample was maintained as the control and the other subjected to the stress. To create the hyperosmotic shock a 5 M NaCl solution was added to the medium to generate a 1.0 M final concentration. The same volume of water was added to the control cultures. Two to three millilitre aliquots of the control and stress samples were removed at times 0, 15, 30, 60, 120, 180 and 240 min after the initiation of both stresses. Cells were washed with ice-cold ultrapurified sterile H_2O to remove culture media from the cells and collected via a filter system using 0.45µm Supor® membrane filters (Pall-Life Sciences). The cells were washed again with ice-cold ultrapurified sterile H_2O, removed using an ice cold spatula to an Eppendorf tube (which has been previously tared), weighed and placed immediately (otherwise trehalose will breakdown) in Liquid nitrogen. These samples were then stored at -80°C.

4.2.4.2.2 Extraction

The cells were allowed to thaw on ice and were then resuspended in 1 ml of 0.25 M Na_2CO_3 and incubated at 95°C for 20 min. Following centrifugation at 18,000 x *g* for 1 min at, 10 µl of the supernatant was removed and transferred to an Eppendorf containing 5 µl of 1 M acetic acid. The mixture was then incubated at 95°C for 40 min. Samples can be stored at -20°C at this stage.

4.2.4.2.3 Quantification

Five microlitres of Buffer T (300 m M NaAc and 30 mM CaCl2 buffer pH 5.5) was added to the eppendorf containing the 10 µl of sample and 5 µl of 1 M acetic acid. Twenty microlitres of trehalase (~ 360 U/ml in H_2O) extracted from *H. grisea* were then added to the samples which were subsequently incubated in a waterbath for 1 h at 40°C. This suspension was then centrifuged at 18000 x *g* for

1 min at 4°C. Following centrifugation, 10 µl of the supernatant was pipetted into the wells of a 96-well plate (Corning, New York, USA) and 200 µl of glucose Trinder 100 reagent (Dialab, Aschenstedter Str.15, Dötlingen, Germany) for glucose determination was added. The plate was agitated gently and incubated for 15 min at 30°C. After incubation absorbance was measured at 505 $_{nm}$ Biomek-Beckmann (Molecular devices, Sunnyvale, CA, USA). Glucose formation was calculated from a glucose standard curve, ranging from 0-8 mM glucose and standards followed the same procedure for glucose determination.

4.2.5 Determination of trehalose-6-phosphate synthase, trehalalose-6-phosphate phosphatase activities in *C. albicans* and *C. dubliniensis* at elevated temperature

Trehalose-6-phosphate synthase (Tre6P) and Trehalose-6-phosphate phosphatase (Tre6P phosphatase) activities in *C. albicans* and *C. dubliniensis* at elevated temperature were determined according to methods described previously by Arguelles, (1994) and Bell *et al.* (1992).

4.2.5.1 Sampling

Five millilitre starter cultures of *C. albicans* isolates (SC5314 and 132A) and *C. dubliniensis* isolates (CD36 and p7718, represententing genotypes 1 and 3, respectively) , grown overnight at 30°C in YPD broth were used to inoculate 100 ml of fresh YPD broth in 300 ml Erlenemeyer flasks grown overnight at 30°C. Cells from overnight cultures were harvested using a Beckman Allegra™ 6R centrifuge at 3,000 rpm for 5 min, in preweighed Falcon tubes (Beckton Dickinson, New Jersey, USA). Approximately 2.5 g of cells, from each strain, from both species was used to inoculate 200 ml of fresh YPD broth in large Erlenemeyer flasks. The flasks were then incubated at 30°C at 220 rpm for 2-3 hours so that the cells were in the exponential phase. After 2-3 h incubation the cultures were removed. The culture was then divided into 2x 100 ml aliquots and the cells were further incubated at either 30°C or 42°C. A 2-3 ml sample was removed before dividing the culture (T0). At different time points (30 and 60 min) after the shift, 20 ml samples for Tre6P synthase and Tre6P phosphatase activity determination were taken.

4.2.5.2 Preparation of crude extract

Samples were allowed to cool quickly on ice and were washed twice with ice-cold sterile ultrapurified H_2O. The Falcon tubes were inverted to remove all the H_2O and 990 µl of extraction buffer (50 mM imidazole pH 6.3, 1 mM EDTA, 2 mM $MgCl_2$, and 1 mM PMSF in MeOH,) was added and the cells were resuspended. The cells were then transferred to 10 x 75 mm glass culture tubes (Lennox, Naas rd, Dublin, Ireland) containing the equivalent of 0.5 ml glass beads with a diameter of 0.5 mm (Sigma). Ten microlitres of PMSF was added and the mixture was vortexted for 1 min and left on ice. This was repeated twice. The supernatants were then removed and placed into eppendorfs while the Sephadex G25 (Sigma) columns were prepared. Small Sephadex G25 (Sigma) columns, made in a 1 ml pipette tip containing a 3 mm siliconised glass bead (Sigma) fitted in a glass culture tube (Lennox) were prepared by filling the pipette tip completely with pre-equilibrated G25 Sephadex. To equilibrate the Sephadex G25 (Sigma) an equal volume of sterile ultrapurified H_2O was added to Sephadex G25 (Sigma) overnight at 4°C, the H_2O was poured off and an equal volume of 50 mM Tricine buffer was added. The pipette tips containing the pre-equilibrated G25 Sephadex were then centrifuged at 100 x *g* for 1 min and placed in a new glass tube. The coloumns were then ready to use. The supernatants were then loaded onto the G25 Sephadex columns and centrifuged for 1 min at 100 x *g*. The eluate was used for both the Tre6P and Tre6P phosphatase enzyme assays and also for protein determination.

4.2.5.2.1 Measurement of Tre6P synthase activity

Thirty microlitres of the eluate collected from section 4.2.5.2 was added to 210 µl of a solution containing the following for each sample: 60 µl Tricine buffer 200 mM pH 7, 30 µl 0.1 M $MgCl_2$, 30 µl 40 mM UDPG, 30 µl 80 mM glucose-6-phosphate and 60 µl H_2O. Glucose-6-phosphate was replaced with H_2O for the control of each sample. This was repeated for all samples. Samples were incubated for 30 min at 30°C (or at 42°C for samples heat shocked at this temperature, see section 4.2.5.1). Following incubation the samples were centrifuged for 10 min at 16000 x *g*. Twenty microlitres of the extract were pipetted into a well in a 96-well microtitre plate (Corning, New York, USA) along

with 20 µl of H_2O and 200 µl of an assay solution containing 0.6 ml H_2O, 0.33 ml 200 mM Tricine pH 7.6, 0.39 mg phosphoenolpyruvate, 0.21 mg NADH and 0.9 µl LDH. Absorbance at 340 $_{nm}$ was measured using the Biomek-Beckmann. Ten micolitres of pyruvate kinase, was then added and the plate was incubated for 30 min at 37°C. Following incubation, absorbance at 340 $_{nm}$ was measured again. The enzyme activity of the control and test samples were calculated from the difference in absorbance at 340 $_{nm}$.

4.2.5.2.2 Measurement of Tre6P phosphatase activity

Thirty microlitres of the eluate collected from section 4.2.5.2 was added to 210 µl of a solution containing the following for each sample: 60 µl Tricine buffer 200 mM pH 7, 30 µl 0.1 M $MgCl_2$, 30 µl trehalose-6-P 25 mM, 90 µl H_2O. This was repeated for all samples. In control experiments trehalose-6-phosphate was replaced with H_2O. All samples were incubated for 30 min at 30°C (or at 42°C samples heat shocked at 42°C, see section 4.2.5.1). Following incubation, samples were allowed to cool until room temperature. Thirty microlitres of the extract was added to a new microcentrifuge tube and 10 µl of buffer (300 mM NaAc, 30 mM $CaCl_2$, pH 5.5 was added. Forty microlitres of *H. grisea* trehalase was added and the mixture was incubated for 45 min at 40°C. Thirty microlitres of this mixture were then pipetted into the well of a 96 well microtitre plate (Corning) and 200 µl of glucose Trinder 100 reagent (Dialab) for glucose determination was added. The plate was agitated gently and incubated for 15 min at 30° C. After incubation absorbance was measured at 505 $_{nm}$ Biomek-Beckmann (Molecular devices). Glucose formation was calculated from a glucose standard curve, ranging from 0-8 mM glucose and standards followed the same procedure for glucose determination.

4.2.5.2.3 Protein determination- Biuret method

The protein concentration of the crude extracts was measured using the Biuret method. A standard protein solution of BSA was diluted to 0-4 mg/ml. Forty microlitres of H_2O was added to BSA standards and unknown protein solutions in a 96-well UV grade microtitre plate (Greiner). This was followed by the addition of 200 µl of Biuret solution (11.5 µl of sterile ultrapurified H_2O and

8.5 ml of Biuret: 1 % $CuSO_4$ and 40 % NaOH). After mixing, the samples were left at room temperature for 7.5 min. Absorbance was measured at 290 $_{nm}$ using the Biomek-Beckmann. The amount of protein present was determined by reference to a standard curve of known concentrations of BSA over the range of 0-4 mg/ml.

4.2.6 Determination of trehalase activity in *C. albicans* and *C. dubliniensis*

Levels of trehalase activity in *C. albicans* and *C. dubliniensis* cells were determined according to the method described by Neves *et al.* (1994).

4.2.6.1 Sampling

Cultures of *C. albicans* isolate SC5314 and *C. dubliniensis* isolates CD36 and p7718, representing genotypes 1 and 4 respectively were grown overnight in 500 ml of YPD broth at 30°C in Erlenemeyer flasks. These cultures were first cooled on ice and then harvested by centrifugation at 835 x *g* at 4°C for 5 min. The pellets were chilled on ice and resuspended in Falcon tubes. Approximately 1.2 g of cells, from each strain, were resuspended in 50 ml of fresh YPD broth in 100 ml conical flasks and incubated in a temperature controlled waterbath at 30°C for 30 min. A 3 ml aliquot was removed from each culture prior to the temperature up shift, this was taken as the control at T=0. The cultures were then transferred to a waterbath at 42°C and 3 ml aliquots were removed at times 1, 5, 10 and 30 min after the initiation of the stress. After 30 min at this temperature, the cultures were shifted back to 30°C and further aliquots were removed at times 1, 5, 10 and 30 min after removal of the heat stress. At each timepoint a 1ml sample was also removed for trehalose determination.

4.2.6.2 Extraction

Samples for trehalase determination were immediately transferred to precooled Falcon tubes containing 40 ml of sterile ultrapure H_2O and were centrifuged at 800 x *g* for 3 min at 4°C. The supernatants were decanted and 500 µl of ice-cold extraction buffer (50 mM Mes/KOH pH7 and 50 µM $CaCl_2$) were added to the pellet using a precooled Pasteur pipette. Using the same Pasteur pipette (one for each individual sample) the suspensions were transferred to prechilled glass tubes (Lennox) containing 1.5 g of glass beads, 0.5 mm in

diameter (Sigma). The cell suspensions were homogenised for 1 min 30 sec using a vortex. Again using a separate chilled Pasteur pipette for each sample, the homogenates were transferred into eppendorf tubes and kept on ice. Cell extracts were subjected to a centrifugation for 3 min at 15,682 x *g* at 4°C. The supernatants were then dialysed overnight against 10 mM MES/KOH pH 7, 50 mM $CaCl_2$ in a BRL microdialysis system (Betheseda Research labs, Gaithersburg MD, USA) at 4°C.

4.2.6.3 Activity

The samples (approximately 200 µl in volume) were transferred from the microdialyser to a 96-well microtitre plate (Corning) kept on ice. Ten microlitres of each sample was pipetted into a new 96-well microtitre plate (Corning) on ice. Fifty microlitres of 250 mM trehalose contained in MES buffer pH 7 and 50 μM $CaCl_2$ was added to each sample and to glucose standards (1-6 mM glucose) which were prepared in duplicate. The plate was then incubated at 30°C for 30 min and then boiled for 3 min at 95°C to stop the reaction. For the control plate 10 µl aliquots of the samples and standards were pipetted into the wells of the 96 well plate in the same order and were boiled immediately for 3 min at 95°C to inhibit the reaction. After the addition of 50 µl of the 250 mM trehalose solution to both the samples and glucose standards the plate was immediately boiled for a further 3 min at 95°C to destroy any glucose that may be present. Both the test plate and the control plate were assayed for glucose determination using glucose Trinder 100 reagent (Dialab) as described in section 4.2.4.2.3.

4.2.6.4 Protein determination

The amount of protein in the cell extracts was determined using the Lowry method (Lowry *et al.*, 1951). A standard protein solution of BSA was suitably diluted to 0-4 mg/ml in 50 mM NaCl. An aliquot (200 µl) of a mix of Lowry A and B, along with 35 µl of sterile ultrapure H_2O was added to 5 µl of BSA standards and unknown protein solutions. After mixing the solutions, they were incubated at 25°C for 10 min. This was followed by the addition of 20 µl of Folin-Ciocalteu's reagent diluted 1:2 (v/v) with sterile ultrapure H_2O. After mixing the samples were incubated at 25°C for 30 min. The absorbance of each

sample was measured at a wavelength of 546 $_{nm}$ in the Biomek-Beckman. The amount of protein present was determined by reference to a standard curve of known concentrations of BSA over the range of 0-4 mg/ml.

4.2.7 Annotation of putative stress response genes from the *C. dubliniensis* genome sequence

The search for putative stress response gene sequences in the *C. dubliniensis* genome was completed using data from the CandidaDB World-Wide Web Server (Pasteur Institute: http:// genolist.Pasteur.fr/CandidaDB/) and the *C. dubliniensis* genome sequencing project (http://www.sanger.ac.uk/Projects/C_dubliniensis/). Sequence analysis was carried out using the DNA Strider™ 1.3f11 software package for DNA and protein analysis (CEA/Saclay, Gif-sur-Yvette, France). Nucleotide and amino acid sequence alignments were carried out using CLUSTAL W sequence alignment computer program (Higgins & Sharp, 1988).

4.3 Results

4.3.1 Identification and sequencing of homologues of the *C. albicans HSP104* and *HSP90* genes in *C. dubliniensis.*

To investigate the molecular responses of *C. albicans* and *C. dubliniensis* to the environmental stresses under study (i.e. temperature and osmotic shock) it was decided to examine the expression of genes known to be stress induced in other species such as *S. cerevisiae*, *S. pombe* and *C. albicans.* Thus, in order to investigate the presence of homologues of the *C. albicans* genes (*HSP104* and *HSP90)* in *C. dubliniensis* pairs of primers for each gene were designed based on *C. albicans* gene sequences (Table 2.2). Amplification of *HSP90* and *HSP104* gene fragments from *C. dubliniensis* CD36 and *C. albicans* 132A genomic DNA was carried out using the Expand High Fidelity PCR system (Roche, Diagnostics, Ltd) and the standard PCR conditions described in section 2.4.2. The amplimers from both species were cloned in pBluescript, sequenced and used as probes for Northern hybridisation experiments.

The *HSP104*F/R primer pair (Table 2.2) was designed to amplify a 980 bp fragment (representing 31.44% of the 2.7 kb *HSP104* gene) from the 2.7 kb *CaHSP104* gene and the putative *CdHSP104* gene. A fragment of approximately 980 bp was obtained when *C. albicans* 132A genomic DNA was used as the template, and a product of similar size was also obtained when *C. dubliniensis* CD36 genomic was used as the template. Both fragments from each species were cloned in pBluescript to yield the recombinant plasmids p*CaHSP104* and p*CdHSP104*, respectively. The cloned DNA inserts were sequenced fully in both directions. Alignment of the nucleotide sequence of the *C. albicans* 132A insert contained within the recombinant clone p*CaHSP104* revealed that this insert shared 98.7% homology with the corresponding region of the *C. albicans HSP104* gene from the Genbank database (accession no: AF362391). An alignment of the 980 bp *CdHSP104* amplimer sequence with the corresponding sequence of the 980 bp amplimer from the *C. albicans HSP104* gene (Appendix I) showed that the two nucleotide sequences share 91.2% identity. It was concluded therefore, that the cloned DNA insert contained within the recombinant plasmid p*CdHSP104* was from the putative *C. dubliniensis HSP104* gene, thus confirming the presence of this gene in *C. dubliniensis*.

Oligonucleotide primers *HSP90*F/R were designed to amplify a 469 bp (representing 22.3% of total gene length) region of the 2.1 kb *C. albicans HSP90* gene and the putative *C. dubliniensis HSP90* gene. The *HSP90*F/R primer pair generated an identically sized amplimer of approximately 470 bp in each case from *C. albicans* 132A and *C. dubliniensis* CD36 genomic DNA. The *CaHSP90* and *CdHSP90* amplimers were purified, digested with *Xba*I and cloned in pBluescript (as described in section 2.4.4) to yield the recombinant plasmids p*CaHSP90* and p*CdHSP90,* respectively. The inserts contained within the recombinant clones p*CaHSP90* and p*CdHSP90* were sequenced fully in both directions. The 469 bp insert contained within recombinant clone p*CaHSP90* shared 100% identity with the *C. albicans HSP90* sequence in the Genbank database (accession no. X81025). The overall nucleotide identity between the *CaHSP90* and *CdHSP90* amplimer sequences was 92.3% (Appendix I). These findings provided convincing evidence that the cloned DNA insert in plasmid p*CdHSP90* was from the putative *C. dubliniensis HSP90*, thus confirming the presence of this gene in *C. dubliniensis*.

4.3.2 Expression of the *CaHSP104* and *CdHSP104* heat shock protein genes in *C. albicans* and *C. dubliniensis*

In *S. cerevisiae* Hsp104p is the principal element responsible for stress induced tolerance of high temperatures (Sanchez *et al.,* 1990; Lindquist *et al.,* 1996). Therefore, in an attempt to explain the enhanced ability of *C. albicans* to grow at high temperatures compared to *C. dubliniensis*, *HSP104* expression in the two species was investigated. For analysis of *CaHSP104* and *CdHSP104* expression, the cloned PCR amplimers from *C. albicans HSP104* and *C. dubliniensis HSP104*, described in the preceding section were used as probes in Northern hybridisation experiments as described by Moran *et al.* (1998). Expression of the gene encoding translation elongation factor 3 (*TEF3*; Di Domenico *et al.,* 1992; Donnelly, 2001) was used as a normalisation control to allow comparison between gels as it is constitutively expressed under most growth conditions. The 762 bp DNA inserts contained within recombinant plasmid p*CdTEF3* and p*CaTEF3* were excised and purified and used as probes for hybridisation to RNA from two strains each of *C. albicans* (SC5314 and 132A)

and *C. dubliniensis* (CD36 and P7718). In order to induce a heat shock response, cells growing exponentially at 30°C in YPD were shifted to 42°C and samples were taken at 1, 5, 10 and 30 min following transfer. Total RNA was then prepared. A *HSP104* transcript of approximately 3.1 kb was detected in both *C. albicans* and *C. dubliniensis* strains during exponential growth at 30°C and under heat shock conditions at 42°C (Fig. 4.1). Elevated levels of *CaHSP104* expression were detected in *C. albicans* SC5314 after 10 min heatshock at 42°C (4-fold), which decreased in intensity after 30 min (2-fold). Increased levels of *CaHSP104* were also detected in *C. albicans* 132A (4-fold) after 30 min of heat shock treatment (Fig. 4.2). *Candida dubliniensis* mRNA was induced in both CD36 and p7718 after 5 min of heat shock (Fig. 4.1). However, *CdHSP104* was expressed at approximately 2-fold-higher levels in the isolate p7718 (Fig. 4.2). *CdHSP104* expression reached a peak intensity in p7718 (4-fold) and CD36 (2.5 fold) after 10 min of heat shock at 42°C, returning to lower levels after 30 min (Fig. 4.2). The constitutively expressed *CaTEF3* and *CdTEF3* genes were used as a control for RNA loading. From this data, it is evident that *HSP104* is heat-shock inducible in both species although the dynamics of induction appears to be faster in *C. dubliniensis*.

4.3.3 Expression of the *CaHSP90* and *CdHSP90* heat shock protein genes in *C. albicans* and *C. dubliniensis*

The molecular chaperone Hsp90p is a highly conserved and abundant protein which is thought to be essential for viability. In *C. albicans*, antibodies against the immunodominant 47-kDa antigen which is derived from *HSP90* are known to provide some protection against candidiasis. These antibodies are always present in humans who have survived systemic candidiasis. Hence, there has been considerable interest in the characterisation of the *C. albicans HSP90* gene. Expression of the *HSP90* gene has been previously investigated in *C. albicans* strains (Swoboda *et al.*, 1995) in an attempt to understand the importance of *HSP90* for the pathogenesis of *C. albicans*. To determine if *HSP90* is differentially expressed in *C. dubliniensis* compared with *C. albicans*, mRNA levels of *HSP90* were analysed by Northern analysis in each species at specific timepoints following heat shock. The expression of the *CdHSP90* and *CaHSP90*

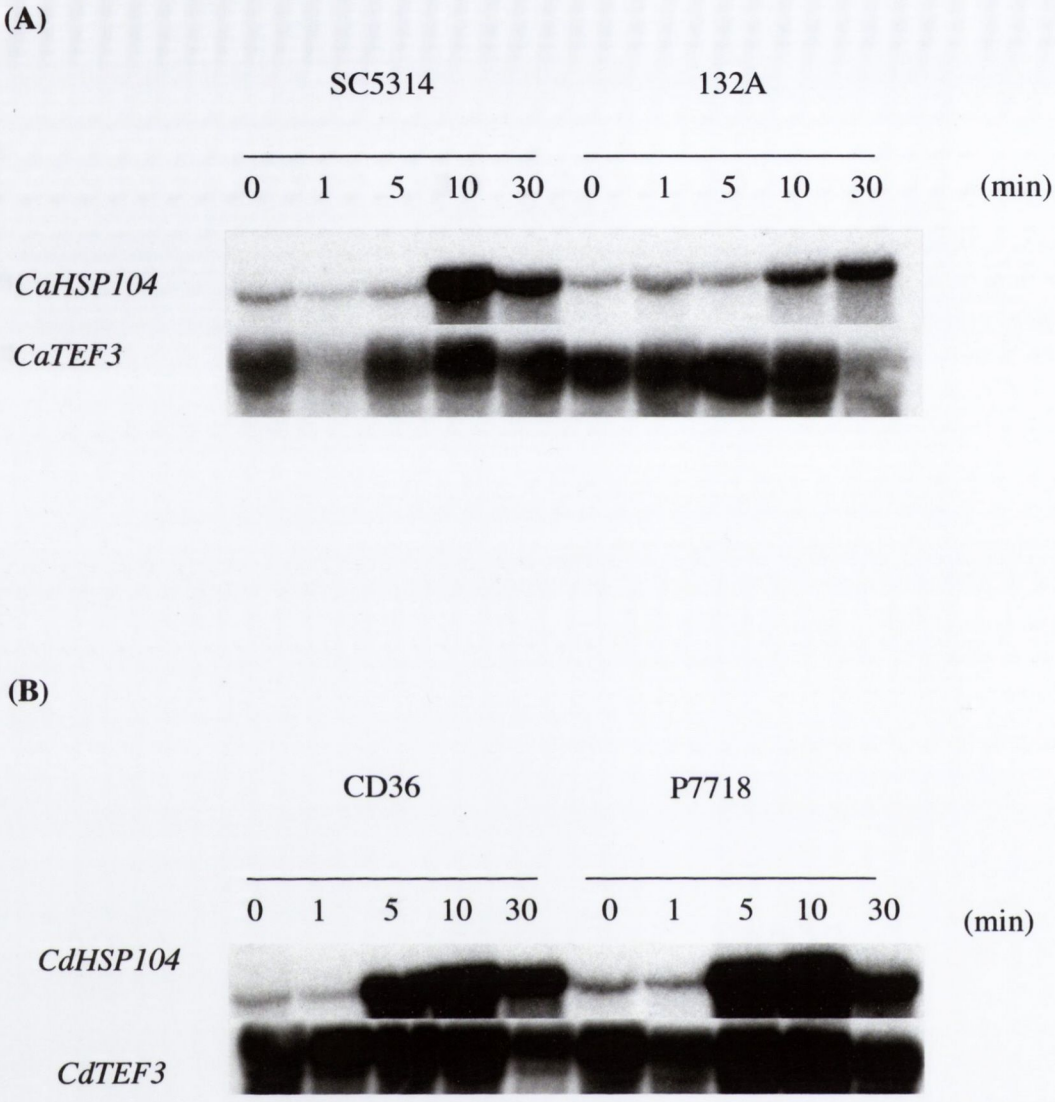


Figure 4.1. Expression of the *HSP104* gene by *C. albicans* strains SC5314 and 132A **(A)** and by *C. dubliniensis* strains CD36 and p7718 **(B)** detected by Northern hybridisation. Total RNA was extracted from cells heat shocked for 1, 5,10 and 30 mins at 42°C, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled cloned amplimers contained within the plasmid p*CaHSP104* **(A)** and p*CdHSP104* **(B).** The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

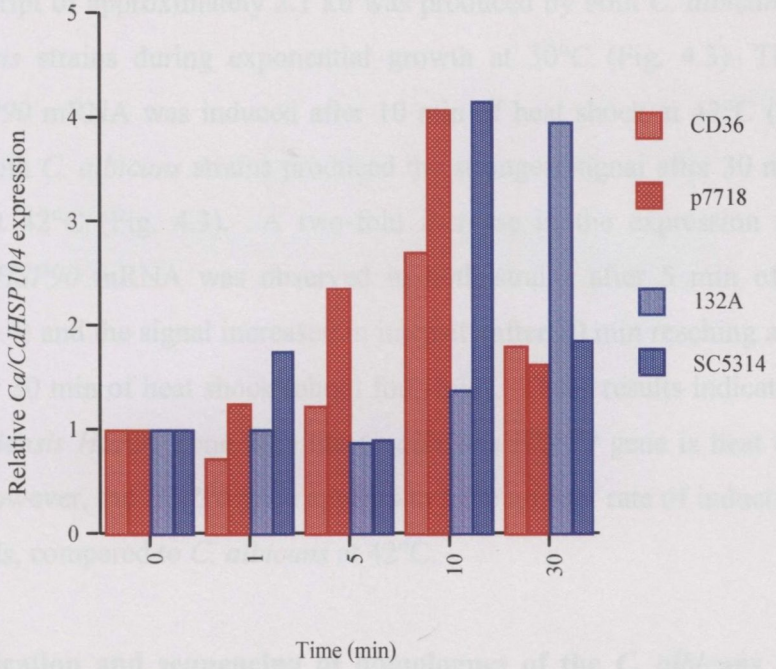


Figure 4.2. Relative increase in expression of the *HSP104* gene in *C. albicans* and *C. dubliniensis* following heat shock at 42°C. *Candida albicans* isolates 132A and SC5314 and *C. dubliniensis* isolates CD36 and p7718 cells were grown to mid exponential phase in YPD broth at 30°C. RNA was extracted from cells harvested just before heat shock, after 1, 5, 10 and 30 min incubation at 42°C. Aliquots containing 20 µg of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with the radiolabelled DNA inserts contained within the plasmids p*CdHSP104*, p*CaHSP104*. Expression *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

genes was analysed using the 469 bp DNA amplimers contained within recombinant clones p*CdHSP90* and p*CaHSP90* (both sharing a nucleotide sequence identity of 92.3%) as probes. In Northern hybridisation experiments a *HSP90* transcript of approximately 2.1 kb was produced by both *C. albicans* and *C. dubliniensis* strains during exponential growth at 30°C (Fig. 4.3). The *C. albicans HSP90* mRNA was induced after 10 min of heat shock at 42°C (about two-fold). Both *C. albicans* strains produced the strongest signal after 30 min of heat shock at 42°C (Fig. 4.3). A two-fold increase in the expression of *C. dubliniensis HSP90* mRNA was observed in both strains after 5 min of heat shock, (Fig. 4.4) and the signal increased in intensity after 10 min reaching a peak intensity after 30 min of heat shock (about four-fold). These results indicate that the *C. dubliniensis HSP90* gene, like the *C. albicans HSP90* gene is heat shock inducible. However, the *HSP90* gene appears to have a faster rate of induction in *C. dubliniensis*, compared to *C. albicans* at 42°C.

4.3.4 Identification and sequencing of homologues of the *C. albicans TPS1* and *NTC1* genes in *C. dubliniensis*.

In exponential cultures of *C. albicans* grown in nutrient rich media the intracellular trehalose content is very low, but after exposure to mild heat treatments, cells quickly accumulate a great amount of this disaccharide. *TPS1* encodes trehalose phosphate synthase the enzyme responsible for catalysing the first step in trehalose synthesis. *NTC1,* encodes neutral trehalase, another trehalose metabolic enzyme whose function involves control of intracellular trehalose concentration via the degradation of trehalose. In order to determine if homologues of these *C. albicans* trehalose metabolic enzymes are present in the *C. dubliniensis* genome, pairs of primers for each gene were designed based on *C. albicans* gene sequences (Table 2.2). Amplification of *TPS1* and *NTC1* gene fragments from *C. dubliniensis* CD36 and *C. albicans*132A genomic DNA was carried out using the Expand High Fidelity PCR system (Roche, Diagnostics, Ltd.) and the standard PCR conditions described in section 2.4.2. The amplimers from both species were cloned in pBluescript, sequenced and used as probes for Northern hybridisation experiments.

The *TPS1*F/R primer pair (Table 2.2) allowed the amplification of a fragment of approximately 875 bp (representing 62.6% of the total gene length)

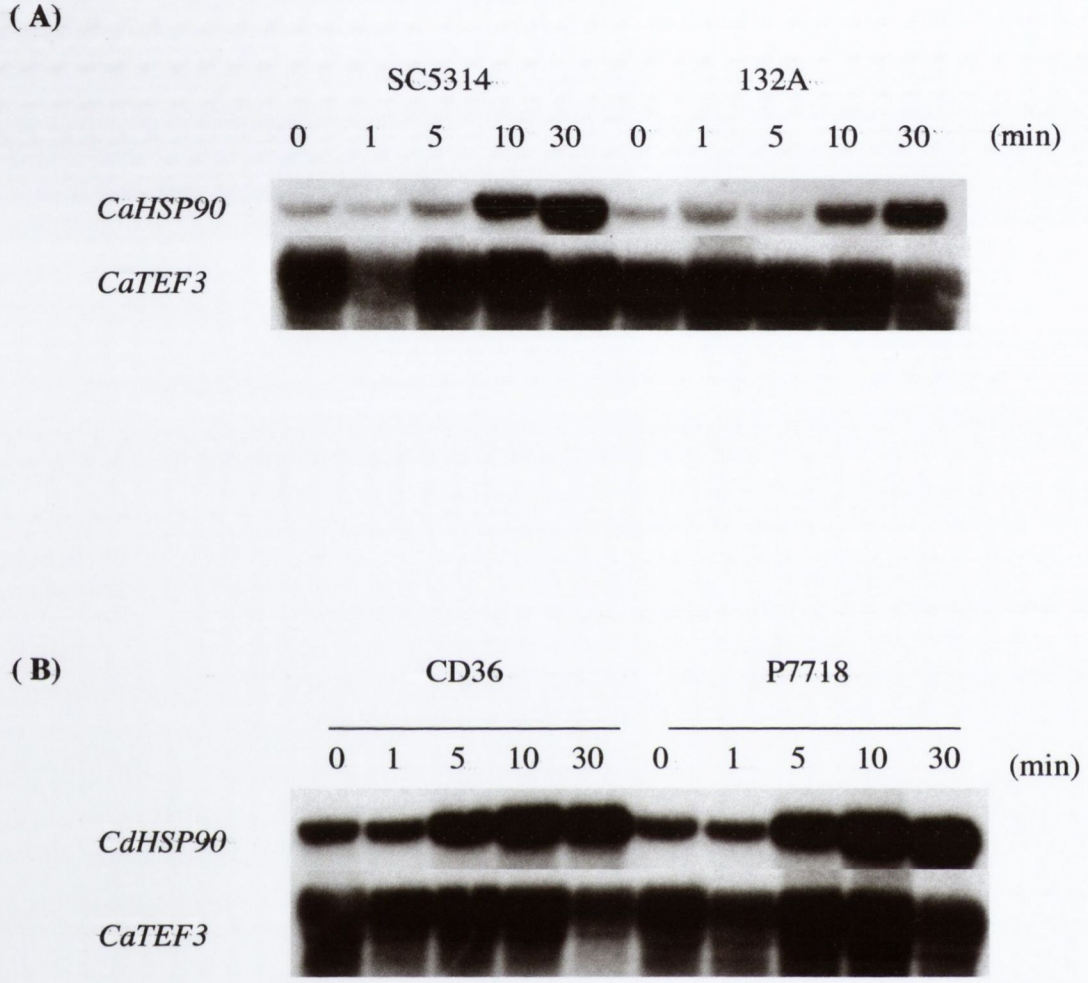


Figure 4.3. Expression of the *HSP90* gene by *C. albicans* strains SC5314 and 132A **(A)** and by *C. dubliniensis* strains CD36and P7718 **(B)** detected by Northern hybridisation. Total RNA was extracted from cells heat shocked for 1, 5,10 and 30 mins at 42°C, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled cloned amplimers*CaHSP90* **(A)**, *CdHSP90* **(B)**. The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

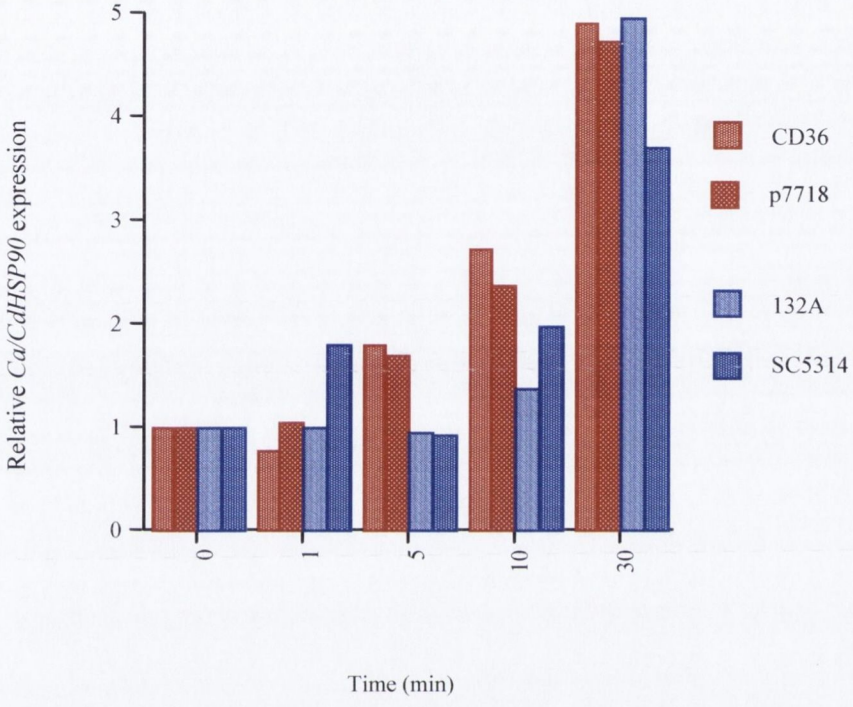


Figure 4.4. Relative increase in expression of the *HSP90* gene in *C. albicans* and *C. dubliniensis* following a heat shock at 42°C. *C. albicans* isolates 132A and SC5314 and *C. dubliniensis* isolates CD36 and P7718 cells were grown to mid exponential phase in YPD broth at 30°C. RNA was extracted from cells harvested just before heat shock, after 1, 5, 10 and 30 min incubation at 42°C. Aliquots containing 20 μg of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were sequentially probed with radiolabelled cloned amplimers *CdHSP90*, *CaHSP90*. Expression of *TEF3* was used as a positive control. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression

from *C. albicans* 132A and *C. dubliniensis* CD36 genomic DNA. This result suggested the presence of a *C. albicans TPS1* gene homologue in *C. dubliniensis*. Both fragments from each species were purified, digested with *Eco*RI cloned in pBluescript as described in section 2.4.4 and sequenced (section 2.5). DNA sequence analysis of the DNA inserts contained within the recombinant clones p*CaTPS1* and p*CdTPS1* was carried out as in section 2.5. The DNA insert contained within the recombinant plasmid p*CaTPS1* showed 99.4% identity with the *C. albicans TPS1* gene from the GeneBank database (accession no: Y07918). The 876 bp *C. dubliniensis TPS1* gene fragment showed a 92.4% identity to the *TPS1* gene of *C. albicans* (Appendix I). These results provided convincing evidence that the cloned 876 bp DNA insert was from the putative *C. dubliniensis TPS1* gene.

The oligonucleotide primers *NTC1*F/R were designed based on the *C. albicans NTC1* gene sequence to amplify approximately 1380 bp (representing 49.9% of the total gene length), of the *CaNTC1* gene and putative *CdNTC1* gene. An amplimer of approximately 1380 bp was obtained from both *C. albicans* 132A genomic DNA and from *C. dubliniensis* isolate CD36 genomic DNA when the primer pair *NTC1*F/R was used. This result confirmed the presence of a *C. albicans NTC1* gene homologue in *C. dubliniensis*. Both fragments were subsequently cloned in pBluescript by conventional methods to yield the recombinant clones p*CaNTC1* and p*CdNTC1*. Additonal primers (5' GCTAGTAGATTTGGACGTCAT 3' and 5' CCATACCACGAGCTAATTCTA 3') were designed for sequencing internal regions of the subcloned fragment contained within the recombinant plasmid p*CdNTC1*. The *C. dubliniensis NTC1* gene fragment showed a 90.6% identity to the *NTC1* gene of *C. albicans* (Appendix I). These results confirmed that the cloned DNA insert within recombinant plasmid p*CdNTC1* was from the putative *C. dubliniensis NTC1* gene.

4.3.5 Expression of the *CaTPS1* and *CdTPS1* trehalose metabolic genes in *C. albicans* and *C. dubliniensis* in response to elevated temperature

The *TPS1* gene encodes trehalose-6-phosphate synthase, the enzyme responsible for the first step in the synthesis of trehalose. Trehalose accumulation

is part of the stress response, and previous studies have shown that disruption of the *C. albicans TPSI* gene prevents the accumulation of trehalose rendering the cells less virulent in a mouse infection model (Zaragoza *et al.*, 1998). The observation that unlike *C. albicans*, *C. dubliniensis* grows very poorly on trehalose when it is the only available source of carbon (Pincus *et al.*, 1999) suggested that *C. dubliniensis* may have a defective trehalose metabolic pathway. In order to investigate the role of trehalose-6-phosphate synthase in *C. dubliniensis* cells the DNA inserts contained within the recombinant plasmids, p*CaTPS1* and p*CdTPS1* described in section 4.3.4 were used as probes in Northern hybridisation experiments to analyse the expression of the *TPS1* gene in each species under conditions of heat-shock (section 4.2.2.2). A *TPS1* transcript of approximately 1.4 kb was detected at all stages of heat shock for all *C. albicans* and *C. dubliniensis* isolates tested (Fig. 4.5). *Candida albicans* 132A, showed a decrease in *CaTPS1* expression after 1 min returning to normal levels after 30 min of heat shock (Fig. 4.6). *Candida albicans* SC5314 also showed a decrease, but after 5 min of heat-shock, returning to normal levels after 30 min (Fig. 4.5). A similar decrease in the level of *TPS1* expression was observed in *C. dubliniensis* isolate p7718 (Fig. 4.6). However, *C. dubliniensis* strain CD36, was found to express increased levels of *CdTPS1* mRNA (about 1/2 fold) compared to the *C. albicans* isolates 132A, SC5314 and *C. dubliniensis* isolate p7718, after 10 min reaching a peak level after 30 min at 42°C. These results indicate that *TPS1* expression is not heat-shock inducible in *C. albicans* cells under the conditions used but may vary from strain to strain in *C. dubliniensis.*

4.3.6 Expression of *CaNTC1* and *CdNTC1* trehalose metabolic genes in *C. albicans* and *C. dubliniensis* in response to elevated temperature

NTC1 encodes neutral trehalase, one of the trehalose metabolic enzymes. The biological function of trehalase assists in control of trehalose concentration via degradation of trehalose. After a thermal stress has been alleviated a build up of trehalose can interfere with the refolding of denatured proteins by Hsps. Therefore, trehalose is rapidly mobilised by this trehalase. Hence, to investigate if the *NTC1* gene is regulated similarly in response to heat stress in *C. albicans* and *C. dubliniensis* yeast cells, *NTC1* mRNA expression levels in both species following heat shock treatments at 30-45°C (conditions used previously by

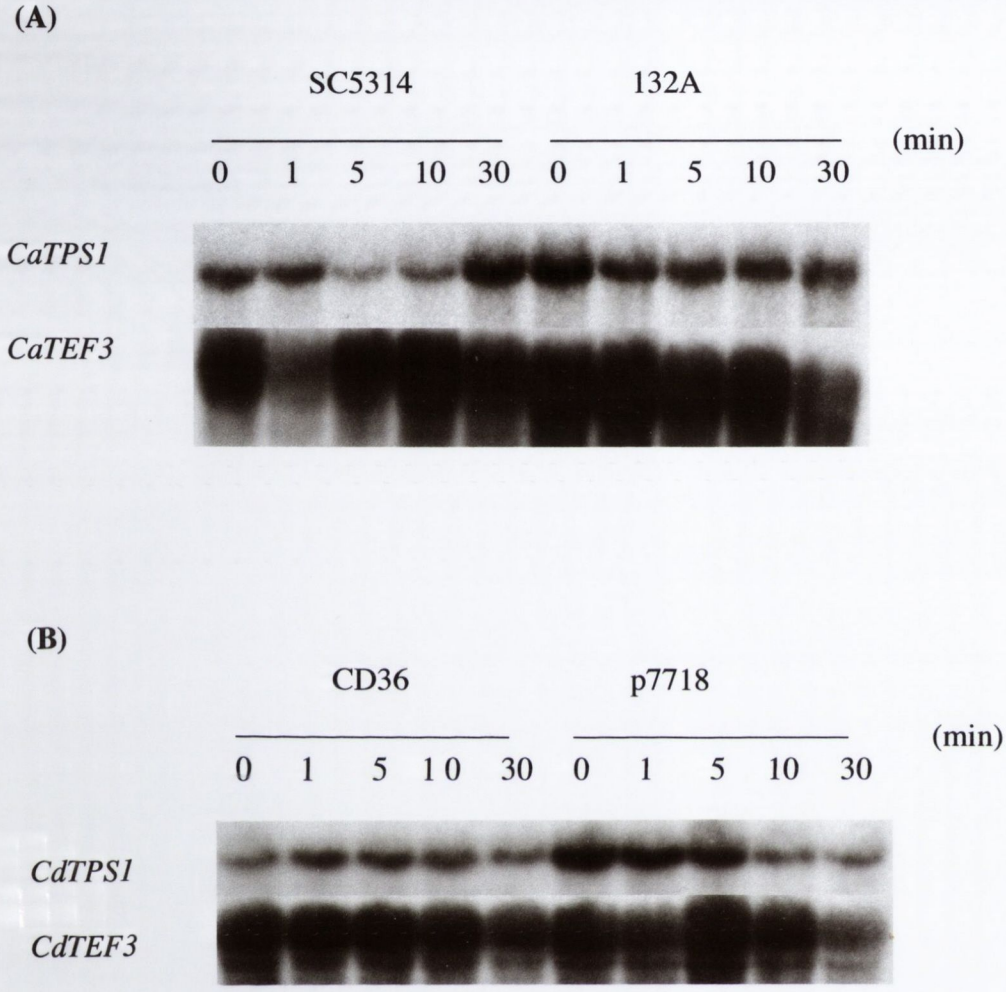


Figure 4.5. Expression of the *TPS1* gene by *C. albicans* strains SC5314 and 132A **(A)** and *C. dubliniensis* strains CD36 and p7718 **(B)** detected by Northern hybridisation. Total RNA was extracted from cells heat shocked for 1, 5,10 and 30 mins at 42°C, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were sequentially probed with radiolabelled cloned amplimers *CaTPS1* **(A)**, *CdTPS1* **(B).** The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

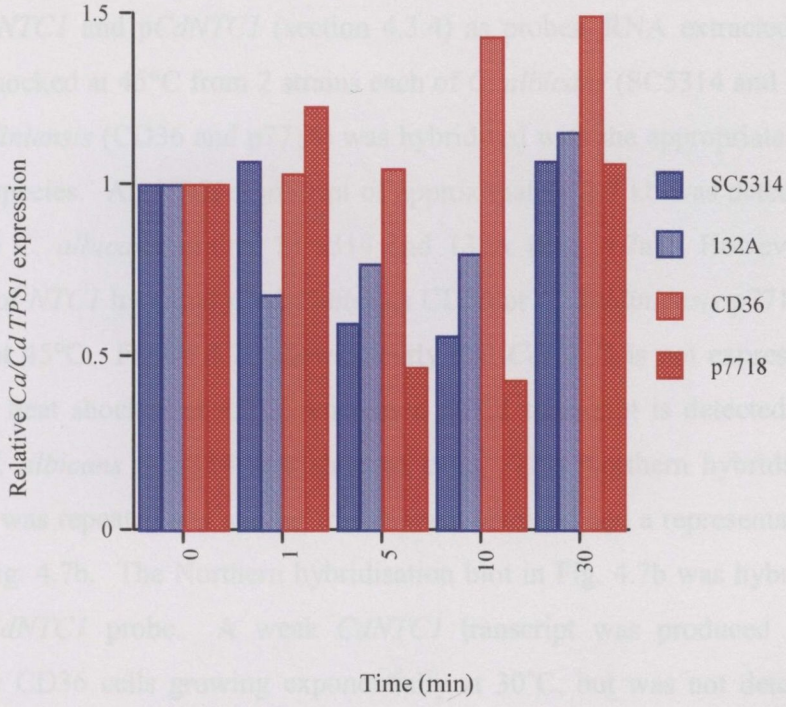


Figure 4.6. Relative increase in expression of the *TPS1* gene in *C. albicans* and *C. dubliniensis* following a heat shock 42˚C. *Candida albicans* isolates 132A and SC5314 and *C. dubliniensis* isolates CD36 and p7718 cells were grown to mid exponential phase in YPD broth at 30˚C. RNA was then extracted from cells harvested just before heat shock, after 1, 5, 10 and 30 min incubation at 42˚C. Aliquots containing 20 µg of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled cloned amplimers *CdTPS1*, *CaTPS1*. The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

Swoboda *et al.* (1995) and 30°-42°C were examined. The expression of the *CaNTC1* and *CdNTC1* genes was analysed using the DNA inserts contained within p*CaNTC1* and p*CdNTC1* (section 4.3.4) as probes. RNA extracted from cells heat shocked at 45°C from 2 strains each of *C. albicans* (SC5314 and 132A) and *C. dubliniensis* (CD36 and p7718) was hybridised with the appropriate probe from each species. An *NTC1* transcript of approximately 2.7 kb was detected in both of the *C. albicans* strains, SC5314 and 132A (Fig. 4.7a). However, no expression of *NTC1* by either *C. dubliniensis* CD36 or *C. dubliniensis* p7718 was detectable at 45°C. Figure 4.7b shows clearly that *CdNTC1* is not expressed in CD36 cells heat shocked at 45°C, whereas a *NTC1* transcript is detected at all stages in *C. albicans* SC5314 heat shocked cells. This Northern hybridisation experiment was repeated and similar results were obtained and a representative is shown in Fig. 4.7b. The Northern hybridisation blot in Fig. 4.7b was hybridised with the *CdNTC1* probe. A weak *CdNTC1* transcript was produced by *C. dubliniensis* CD36 cells growing exponentially at 30°C, but was not detectable after 1, 5 or 10 min of heat shock at 45°C. A weak signal was however detected following 30 min of incubation at 45°C (Fig. 4.7b). In contrast, *C. albicans* strain SC5314 expressed *CaNTC1* mRNA at all stages (Fig. 4.8). The constitutively expressed *TEF3* gene was used as a positive internal control for RNA loading control and was detected at all stages for all *C. albicans* strains tested (Fig. 4.7a, Fig. 4.7b). However, expression of *TEF3* in the *C. dubliniensis* strain CD36 showed a decrease following 5 min of incubation at 45°C, indicating that *C. dubliniensis* transcription was greatly reduced possibly due to the effects of this high temperature.

To verify that the *CdNTC1* probe was working, Southern analysis of *NTC1* in *Hin*dIII- digested genomic DNA from *C. dubliniensis* strains CD36, CD539, CD514 and p7718 (Fig. 4.9) using the 1380 bp DNA insert contained within the recombinant clone p*CdNTC1* (see section 4.3.4) as a probe was carried out. *Hin*dIII- digested chromosomal DNA from all *C. dubliniensis* isolates produced a hybridisation signal at 8.0 kb, when probed with the cloned amplimer *CdNTC1* (Fig. 4.9). These results indicated that the cloned amplimer *CdNTC1* was an effective hybridisation probe and that the lack of signal detected in Figure 4.7b reflects lack of *NTC1* gene expression at the high heat shock temperature of 45°C. It was decided to examine *NTC1* mRNA expression levels at the lower

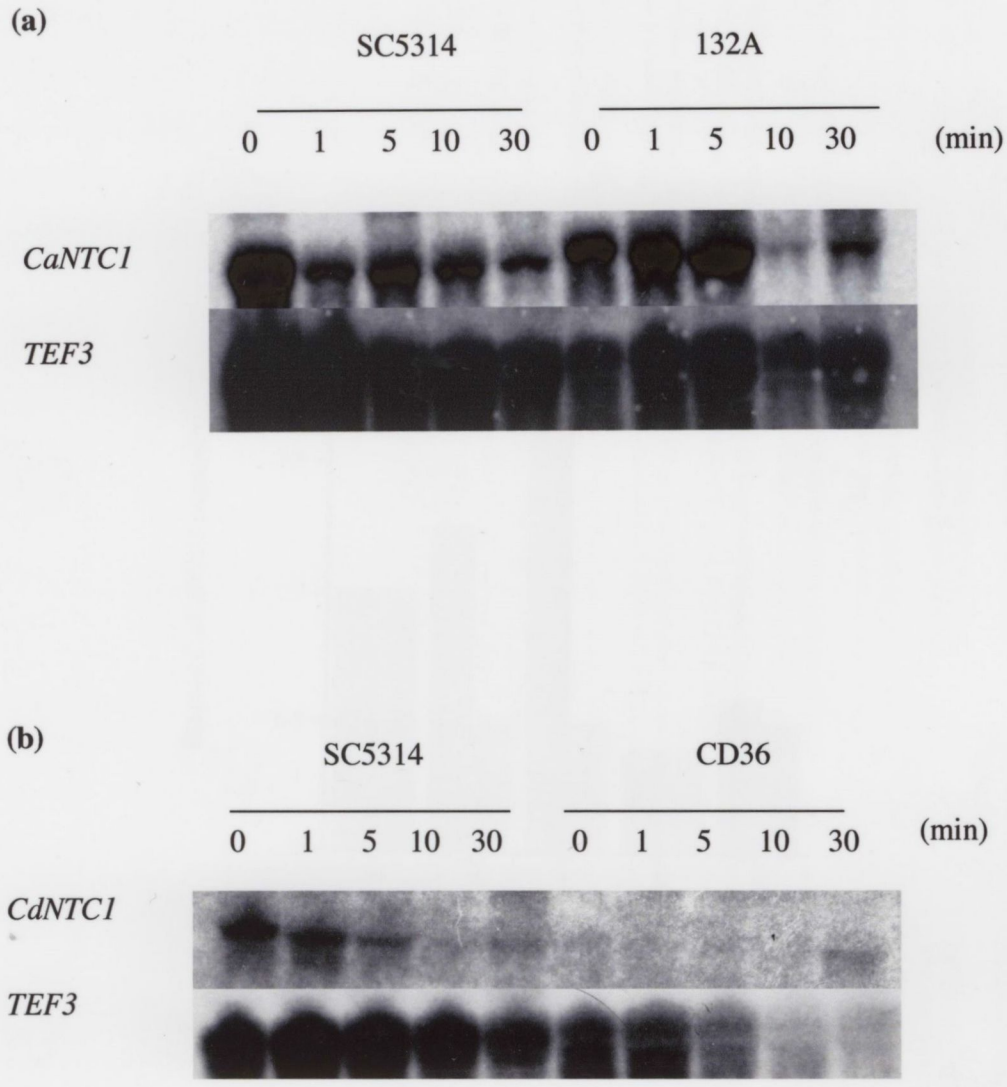


Figure 4.7. Expression of the *NTC1* gene by *C. albicans* strains SC5314 and 132A **(a)** and *C. albicans* SC5314 and *C. dubliniensis* CD36 **(b)** detected by Northern hybridisation. Total RNA was extracted from cells heat shocked for 1, 5,10 and 30 mins at 45°C, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were s probed with radiolabelled cloned amplimers *CaNTC1***(a)**, *CdNTC1***(b).** The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

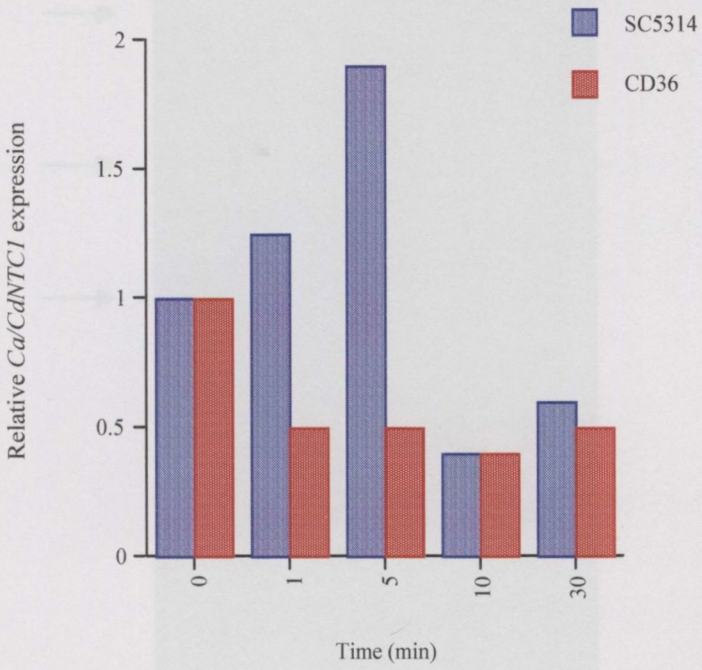


Figure 4.8. Relative increase in expression of the *NTC1* gene in *C. albicans* and *C. dubliniensis* following a heat shock at 45°C. Twenty micrograms of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the Northern blots were probed with an equal mixture of the radiolabelled cloned amplimers *CdNTC1*and *CaNTC1*. The constitutively expressed *TEF3* gene was used as a positive control. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

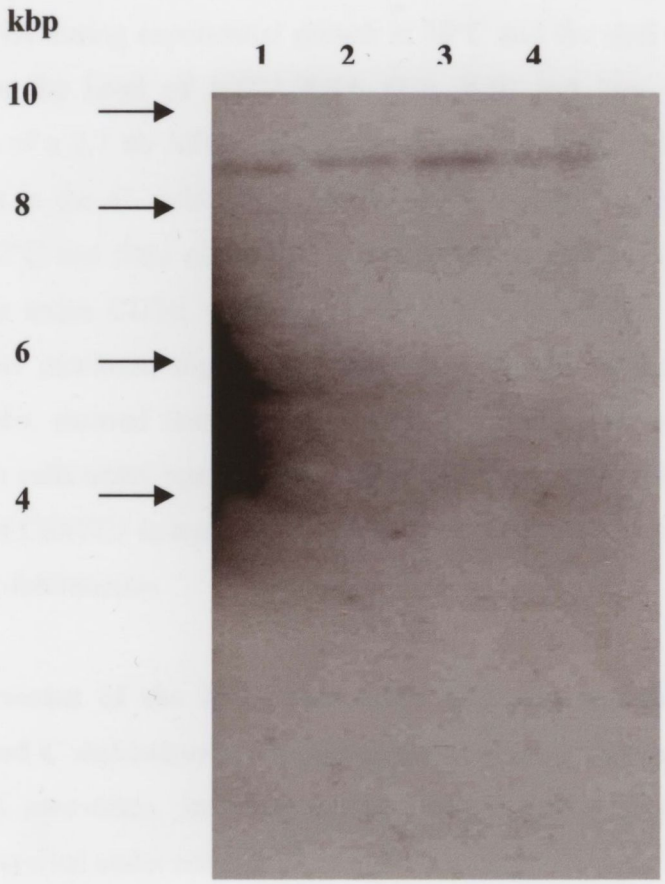


Fig. 4.9. Southern hybridisation of *Hind* III digested genomic DNA from *C. dubliniensis* isolates hybridised to 1380 bp *pCDNTC1* probe. DNA in the lanes was from C. dubliniensis isolates as follows: lane 1, CD36; lane2, CD539; lane 3, CD514; lane 4, p7718.

temperature of 42°C as *C. dubliniensis* cells are viable after 30 min of heat shock at 42°C (see section 3.3.3a). *Candida albicans* 132A and SC5314 produced *NTC1* mRNA during exponential growth at 30°C and the shift to 42°C had little effect upon the level of *NTC1* RNA (Fig. 4.10 and Fig. 4.11) expression. Expression of a 2.7 kb *NTC1* transcript was also detected at all post heat shock time points in the *C. dubliniensis* strains CD36 and p7718 (Fig. 4.10). Heat shock at 42°C had little effect on the expression of *NTC1* transcripts in the *C. dubliniensis* strain CD36, while in the *C. dubliniensis* strain p7718 the *NTC1* mRNA level increased slightly (1.5 fold) after 30 min of incubation at 42°C. These results, showed that the *NTC1* gene is present and is expressed in *C. dubliniensis* cells under heat shock conditions of 42°C but not at 45°C. However, induction of *CdNTC1* in response to a heat shock of 42°C may vary from strain to strain in *C. dubliniensis*.

4.3.7 Expression of the *TPS1* and *NTC1* trehalose metabolic genes in *C. albicans* and *C. dubliniensis* in response to osmotic shock conditions.

In *S. cerevisiae*, trehalose accumulation is known to play an important role in its survival under conditions of high osmolarity (Hounsa *et al.*, 1998). For this reason, it was postulated that the osmosensitive phenotype of *C. dubliniensis*, compared to that of *C. albicans*, may perhaps be explained by a defect in the expression of genes essential for trehalose metabolism i.e. *TPS1* and *NTC1*. Therefore, in addition to examining the expression of the *TPS1* and *NTC1* genes in response to heat shock, it was decided to investigate the response of both genes in a representative strain from *C. albicans* (SC5314) and *C. dubliniensis* (CD36) in response to an osmotic shock of 1 M NaCl. This concentration of NaCl was used as previously it has been shown that *C. dubliniensis* is has a reduced tolerance to high salt concentration compared to *C. albicans*.

The DNA inserts contained within the recombinant plasmids, p*CaTPS1*, p*CdTPS1* p*CaNTC1*, p*CdNTC1* described in section 4.3.4 were used as probes in Northern hybridisation experiments to analyse the expression of the *TPS1* and *NTC1* genes in each species grown at 37°C under osmotic shock conditions (section 4.2.2.3). A *TPS1* transcript of the expected size (i.e. approximately 1.4 kb) was detected in both species prior to osmotic shock (Fig. 4.12). *Candida albicans* SC5314, showed a decrease in *CaTPS1* (1.3-fold) expression following

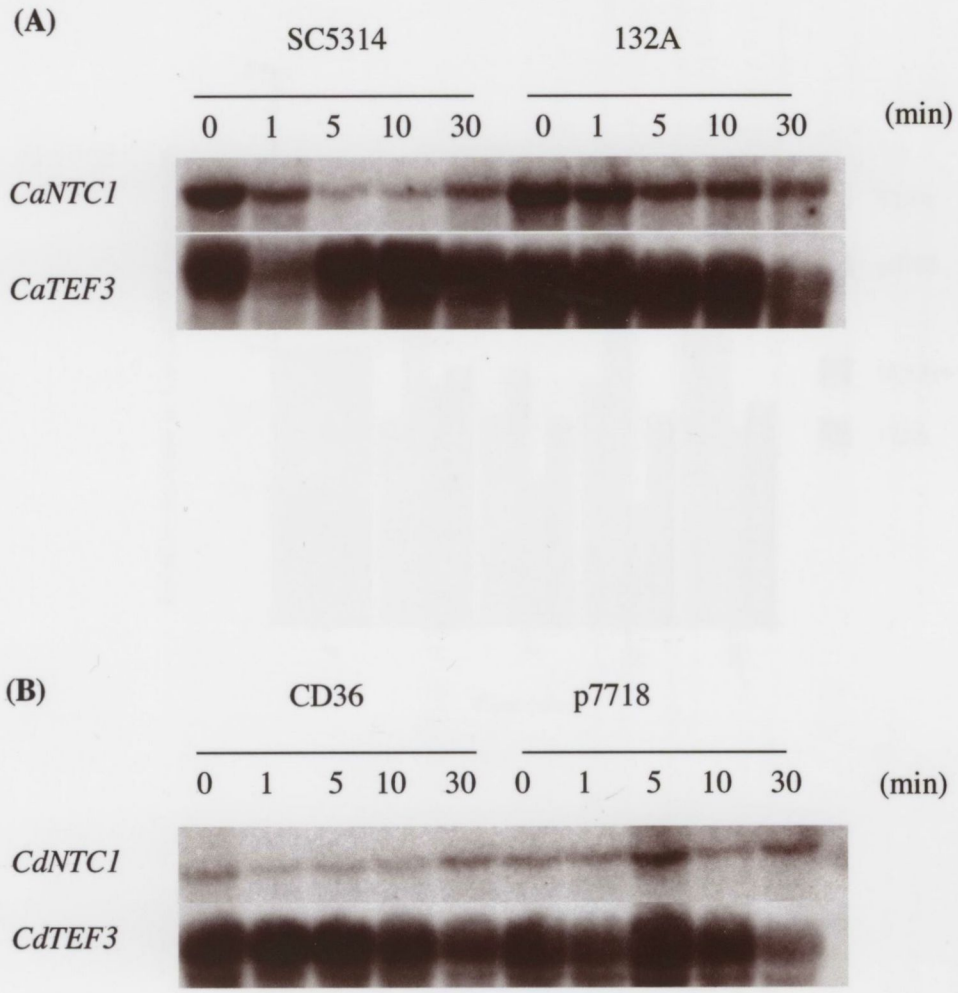


Figure 4.10. Expression of the *NTC1* gene by *C. albicans* strains SC5314 and 132A **(A)** and *C. dubliniensis* strains CD36and p7718 **(B)** detected by Northern hybridisation. Total RNA was extracted from cells heat shocked for 1,5,10 and 30 mins at 42°C, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled cloned amplimers *CaNTC1* **(A)**, *CdNTC1* **(B).** The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

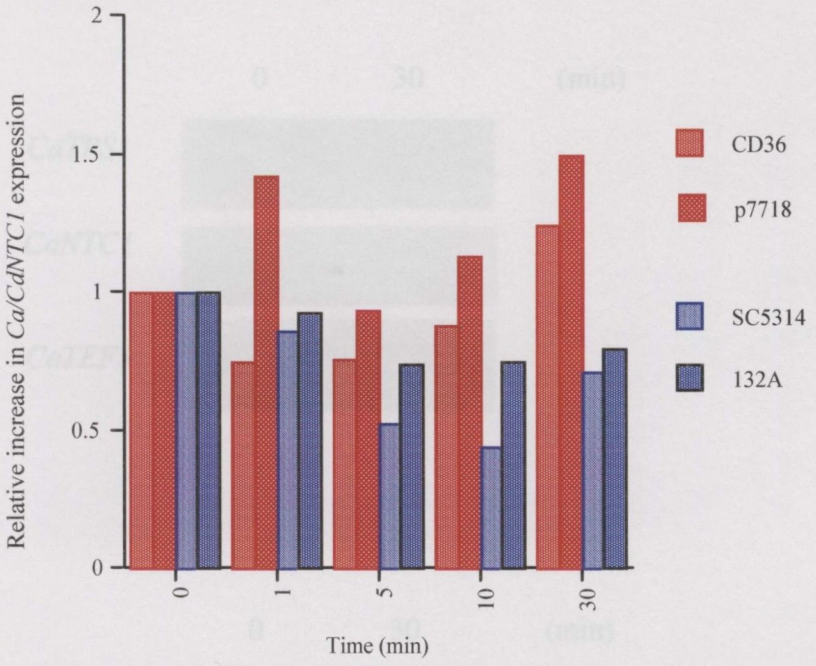


Figure 4.11. Relative increase in expression of the *NTC1* gene in *C. albicans* and *C. dubliniensis* following heat shock at 42°C. *Candida albicans* strains 132A and SC5314 and *C. dubliniensis* strains CD36 and P7718 cells were grown to mid exponential phase in YPD broth at 30°C. RNA was then extracted from cells harvested just before heat shock, after 1, 5, 10 and 30 min incubation at 42°C. Aliquots containing 20 µg of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were sequentially probed with radiolabelled cloned amplimers *CdNTC1* and *CaNTC1* The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression

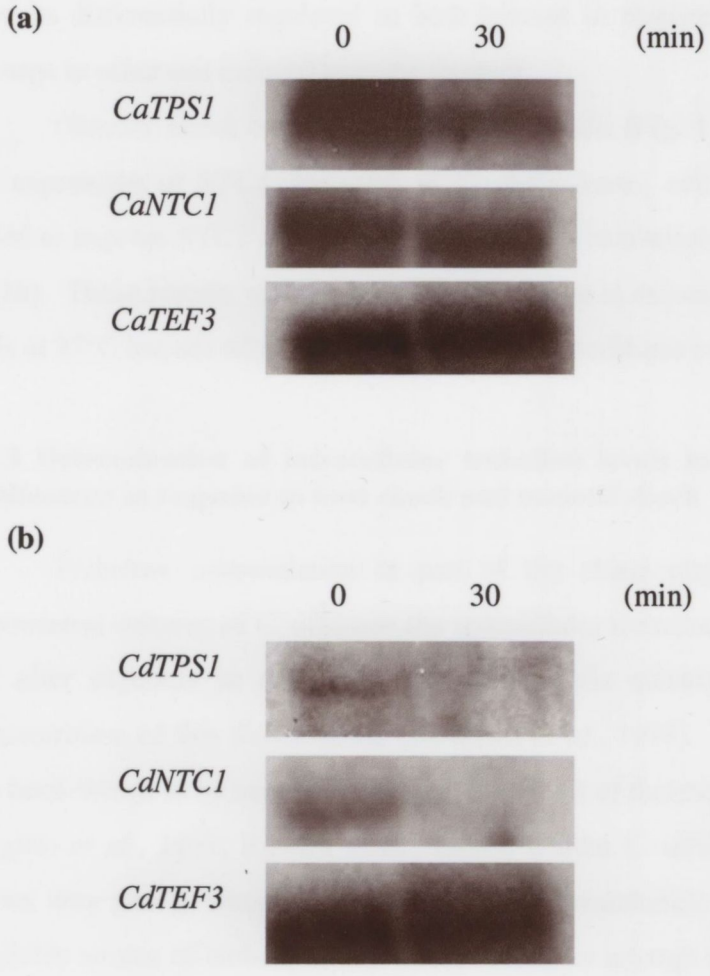


Figure 4. 12. Expression of the *TPS1* and *NTC1* genes in the *C. albicans* strain SC5314 **(a)** and the *C. dubliniensis* strain CD36 **(b)**, detected by Northern hybridisation. Total RNA was extracted from cells treated with 1 M NaCl for 0 and 30 min, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were sequentially probed with radiolabelled cloned amplimers contained within the plasmids p*CaTPS1*, p*CaNTC* **(a)** and p*CdTPS1* p*CdNTC1* **(b).** The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

30 min of treatment with 1M NaCl (Figs. 4.12a and 4.13a). However, in the *C. dubliniensis* strain CD36, no *TPS1* transcript was detected following 30 min treatment with 1M NaCl (Fig 4.12b). These results suggest that the *TPS1* gene may be differentially regulated in both species in response to 1 M NaCl, and perhaps to other salt induced osmotic stresses.

Osmotic shock treatment of *C. albicans* cells (Fig. 4.12a) had no effect on the expression of *NTC1,* however, in *C. dubliniensis,* cells of the strain CD36 failed to express *NTC1* mRNA following 30 min incubation with 1 M NaCl (Fig. 4.12b). These results, showed that the *NTC1* gene is expressed in *C. dubliniensis* cells at 37°C but not when subjected to osmotic conditions of 1 M NaCl at 37°C

4.3.8 Determination of intracellular trehalose levels in *C. albicans* and *C. dubliniensis* in response to heat shock and osmotic shock

Trehalose accumulation is part of the stress response in yeasts. In exponential cultures of *C. albicans* the intracellular trehalose content is very low, but after exposure to mild heat treatments, cells quickly accumulate a high concentration of this disaccharide (Zaragoza *et al.*, 1998). Previously, trehalose has been shown to be necessary for the acquisition of thermotolerance in yeast (de Virgilio *et al.*, 1991; Ribeiro *et al.*, 1997). Unlike *C. albicans, C. dubliniensis* grows very poorly when the thermoprotectant dissacharide trehalose is the only available source of carbohydrate. Therefore, in an attempt to investigate the role of trehalose metabolism in the heat and osmotic shock responses of *C. albicans* and *C. dubliniensis*, the production of trehalose was tested in whole cells using two different assays. The first simple assay described by Parrou and Francois (1997) based trehalose measurements on the amount of glucose equivalents produced per cell number, while the second assay (Neves *et al.*, 1994) based trehalose measurements on the wet weight of cells

4.3.8.1 Method I for measurement of trehalose

Yeast cells were grown in YPD at 30°C to mid-exponential phase and then transferred to a temperature controlled waterbath at 42°C to impose a heat shock. Cells were harvested 30, 60, 90 and 120 min after the transfer and trehalose levels were determined as described in section 2.4. At 30°C, cells of *C. albicans* isolates

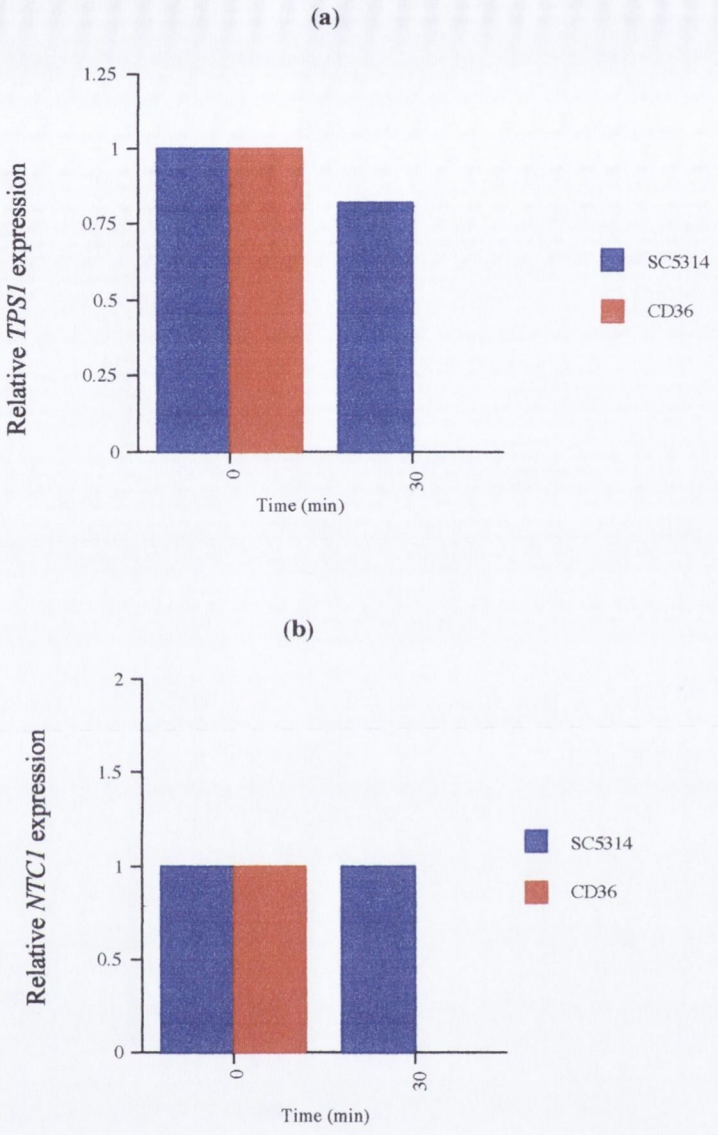


Figure 4.13. Relative expression of the *TPS1* **(a)** and *NTC1* **(b)** genes in *C. albicans* and *C. dubliniensis*. *Candida albicans* strain SC5314 and *C. dubliniensis* strain CD36 cells were grown to mid exponential phase in YPD broth at 37°C. RNA was extracted from cells just before osmotic shock and after 30 min treatment with 1 M NaCl at 37°C. Aliquots containing 20 µg of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were sequentially probed with radiolabelled cloned amplimers *CaTPS1* and *CdTPS1*. The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

132A and SC5314 growing exponentially in YPD broth contained low steady state levels of trehalose (0.83±0.18 μg-0.41±0.14 μg glucose equivalents/ 10^7 cells, respectively). However, large amounts accumulated in *C. albicans* isolates SC5314 and 132A after cells were shifted to 42°C (12-18 fold, respectively). Accumulation started immediately after cells were shifted to the higher temperature (Fig. 4.14). Furthermore, the temperature-dependent increase in the amount of trehalose is reversible in *C. albicans* strains 132A and SC5314 (Fig. 4.14). Incubation at 30°C of 132A or SC5314 for 60 min following 60 min incubation at 42°C caused a drop in the level of trehalose to about 2.43±0.24 μg glucose equivalents / 10^7 cells and 0.94±0.076 μg glucose equivalents / 10^7 cells, respectively. The trehalose content of exponentially growing *C. dubliniensis* CD36 and p7718 cells (Fig. 4.15) was very low (0.612±0.2 μg - 0.63±0.06 μg glucose equivalents / 10^7 cells and 1.0±0.2 μg - 0.61±0.46 μg glucose equivalents / 10^7 cells, respectively). Like the *C. albicans* isolates tested, transfer of exponentially growing *C. dubliniensis* CD36 and p7718 cells to 42°C caused a rapid increase in the intracellular content of trehalose. After 60 min of incubation at the elevated temperature trehalose levels increased from 1±0.2 μg to 26±6.1 μg glucose equivalents / 10^7 cells in *C. dubliniensis* isolate p7718, but to a lesser extent in *C. dubliniensis* isolate CD36 (0.6±0.06 μg -7.0±1.55 μg glucose equivalents / 10^7 cells, respectively). The temperature –dependent increase in trehalose levels was also found to be reversible in *C. dubliniensis* isolates CD36 and p7718 (Fig. 4.15). After a temperature reversion shift (from 42-30°C), the pool of trehalose in *C. dubliniensis* isolates CD36 and p7718 was rapidly mobilised after 60 min to about 0.57±0.27 μg glucose equivalents / 10^7 cells and 0.494±1.16 μg glucose equivalents / 10^7 cells, respectively. The neutral trehalase, one of the trehalose metabolic enzymes, is responsible for this rapid turnover of the disaccharide in *S. cerevisiae* (De Virgilio, 1991). The results obtained indicate that trehalose accumulation occurs in both *C. albicans* and *C. dubliniensis* cells in response to a strong heat shock (42°C).

4.3.8.2 Method II for measurement of trehalose

The second trehalose assay used was based on a method previously described by Neves *et al.* (1994). For the heat stress experiments, *C. albicans* and

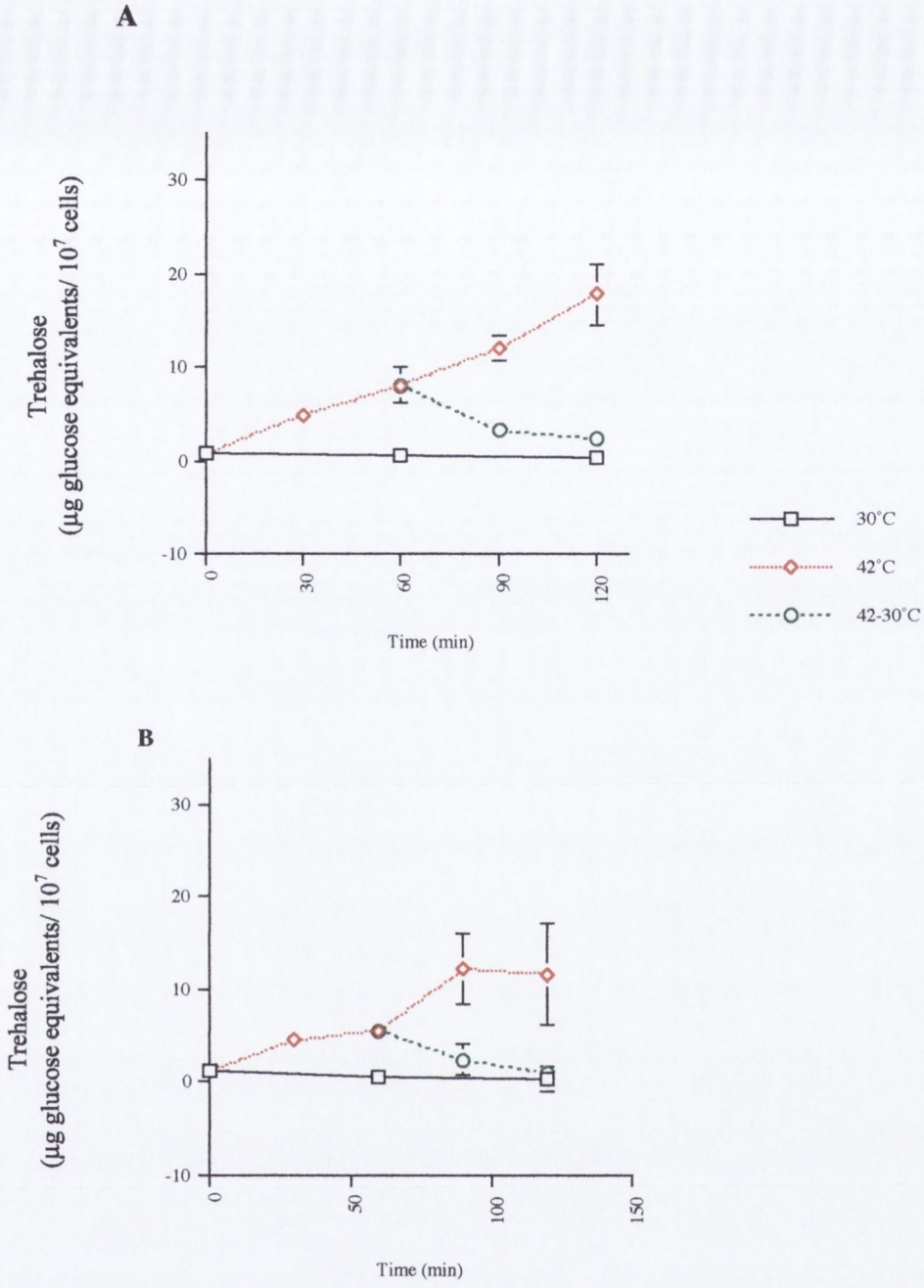


Figure 4.14. Effect of heat shock on trehalose levels in *C. albicans*. **(A)** Effect of a 30°C-42°C heat shock on the *C. albicans* isolates 132A and **(B)** SC5314. The results represent the mean values ± standard deviations from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols.

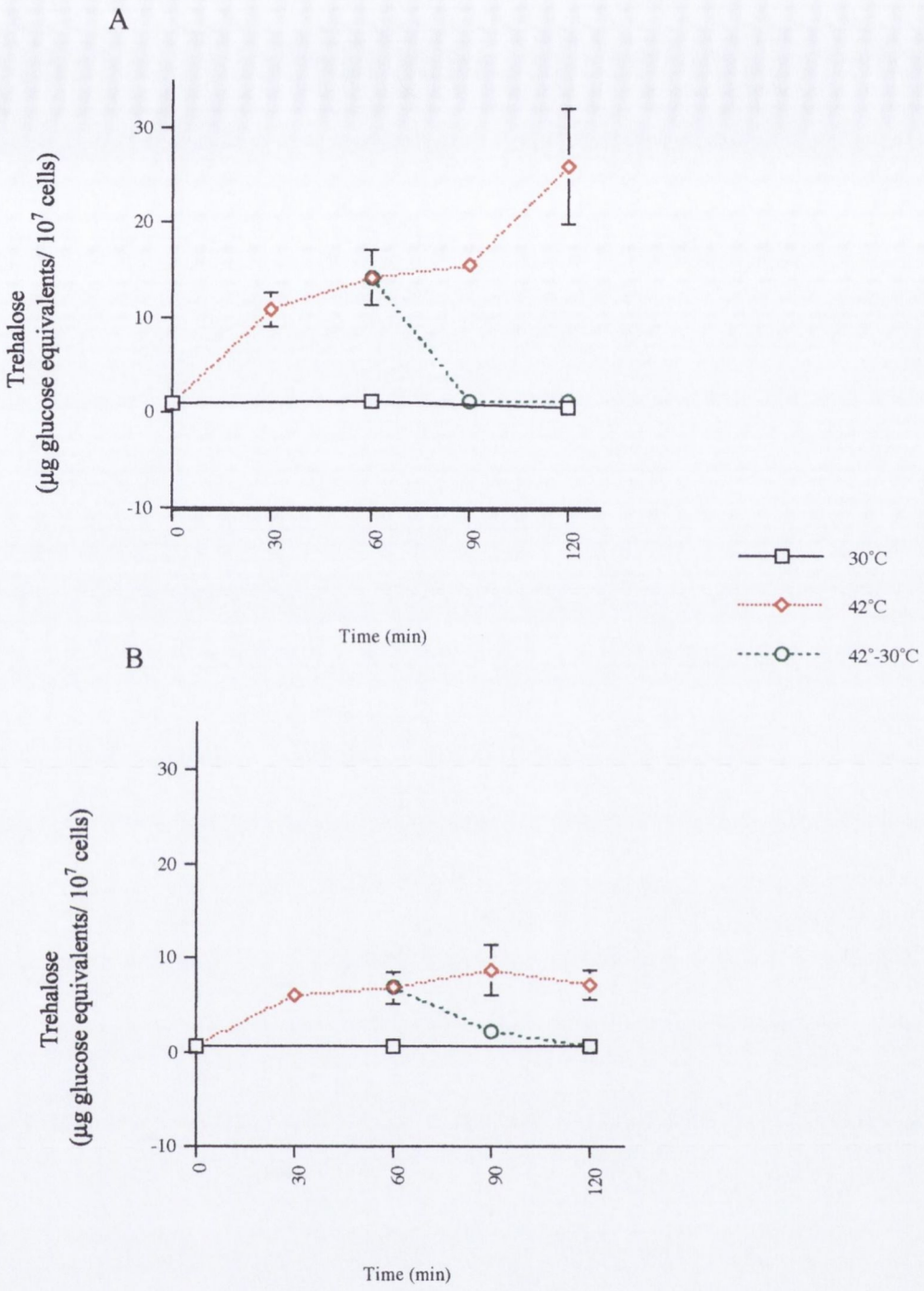
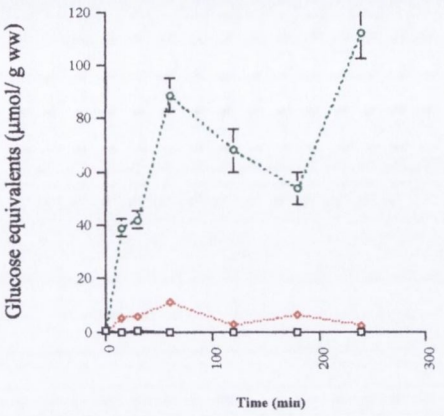


Figure 4.15. Effect of a heat shock on trehalose levels in *C. dubliniensis.***(A)** Effect of a 30°C-42°C heat shock on the *C. dubliniensis* isolates p7718 and **(B)** CD36. The results represent the mean values ± standard deviations from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols.

C. dubliniensis strains were grown in YPD medium at 30°C to exponential phase. The cultures were then divided in three and further incubated at 30, 37 and 42°C. The production of trehalose at each temperature for all strains is presented graphically in Fig. 4.16. These data showed that at 30°C and 37°C are limited or no accumulation of trehalose in the cells of *C. albicans* and *C. dubliniensis* which agree with previous reports (Enjalbert *et al.*, 2003; Van Dijck *et al.,* 2002). However, the results show that increasing the temperature to 42°C resulted in a strong accumulation of trehalose occurs in both *C. albicans* and *C. dubliniensis* isolates (Figs. 4.16). Following, 60 min incubation at 42°C the level of trehalose in the *C. albicans* strains SC5314 and 132A reached 88.6±6.3 and 76±5.0 μmol glucose equivalents / g wet weight, respectively (Fig. 4.16). However, trehalose levels in the *C. dubliniensis* isolates ranged from 21.9±2.0 μmol glucose equivalents / g wet weight to (CD539, a genotype 2) to 60±5.4 μmol glucose equivalents / g wet weight (CD36, a genotype 1 strain). Furthermore, following 120 min incubation at 42°C both of the *C. albicans* strains, SC5314 and 132A accumulated similar amounts of trehalose (68±8.0 and 61.4±8.0 μmol glucose equivalents / g wet weight, respectively), whereas the amount of trehalose accumulated at this time point varied from strain to strain in the *C. dubliniensis* isolates tested (Fig. 4.16). On the one hand the lowest level of trehalose was observed in the *C. dubliniensis* genotype 1 strain CM1 (29±2.7 μmol glucose equivalents / g wet weight) while the genotype 2 *C. dubliniensis* CD539 (93±4.3 μmol glucose equivalents / g wet weight) strain accumulated amounts of trehalose, even higher than both of the *C. albicans* strains. Before 60 min and after 120 min incubation at 42°C, there was no significant difference in the level of intracellular trehalose between the two species.

Method II (Neves *et al.*, 1994) was also used to measure the accumulation of trehalose during osmotic stress. *Candida albicans* and *C. dubliniensis* cells were grown in YPD medium at 37°C until exponential phase. The cultures were then divided in two; one sample was maintained as the control and the other was subjected to a salt induced osmotic stress of 1.0 M NaCl, both samples were further incubated at 37°C. The trehalose produced in response to osmotic stress at each time period for all strains from both species is presented graphically in Fig. 4.17. As shown in Figs 4.17c, the accumulation of trehalose is not dramatically

(a)


Glucose equivalents (µmol/ g ww)
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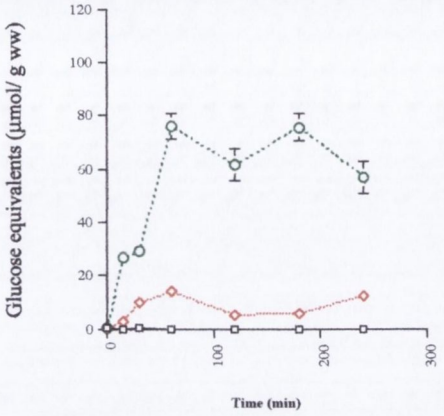
100
200
300
Time (min)

(b)


Glucose equivalents (µmol/ g ww)
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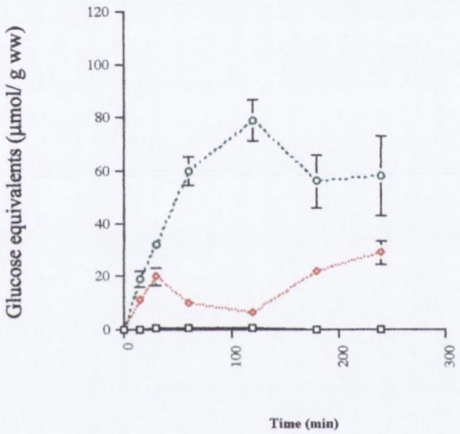
Time (min)

(c)


Glucose equivalents (µmol/ g ww)
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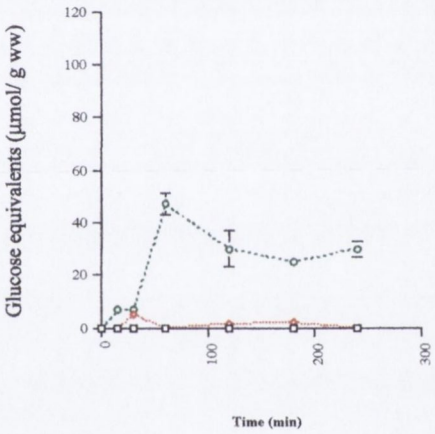
Glucose equivalents (µmol/ g ww)
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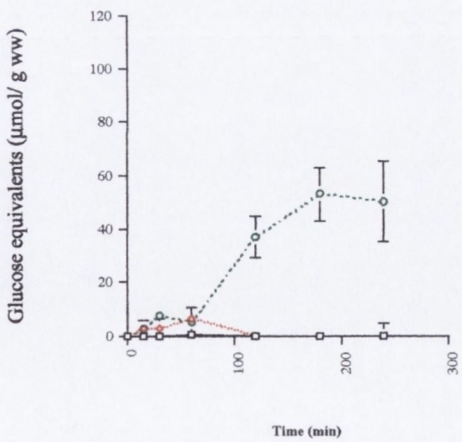
Time (min)

(e)


Glucose equivalents (µmol/ g ww)
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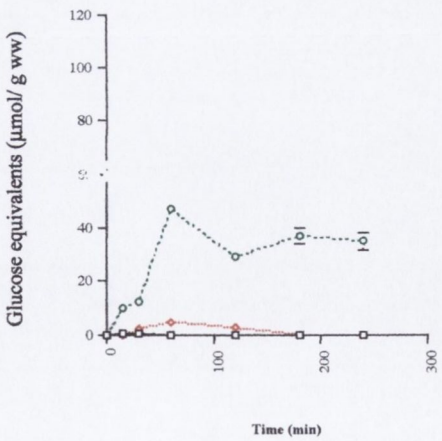
Time (min)

(f)


Glucose equivalents (µmol/ g ww)
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Time (min)

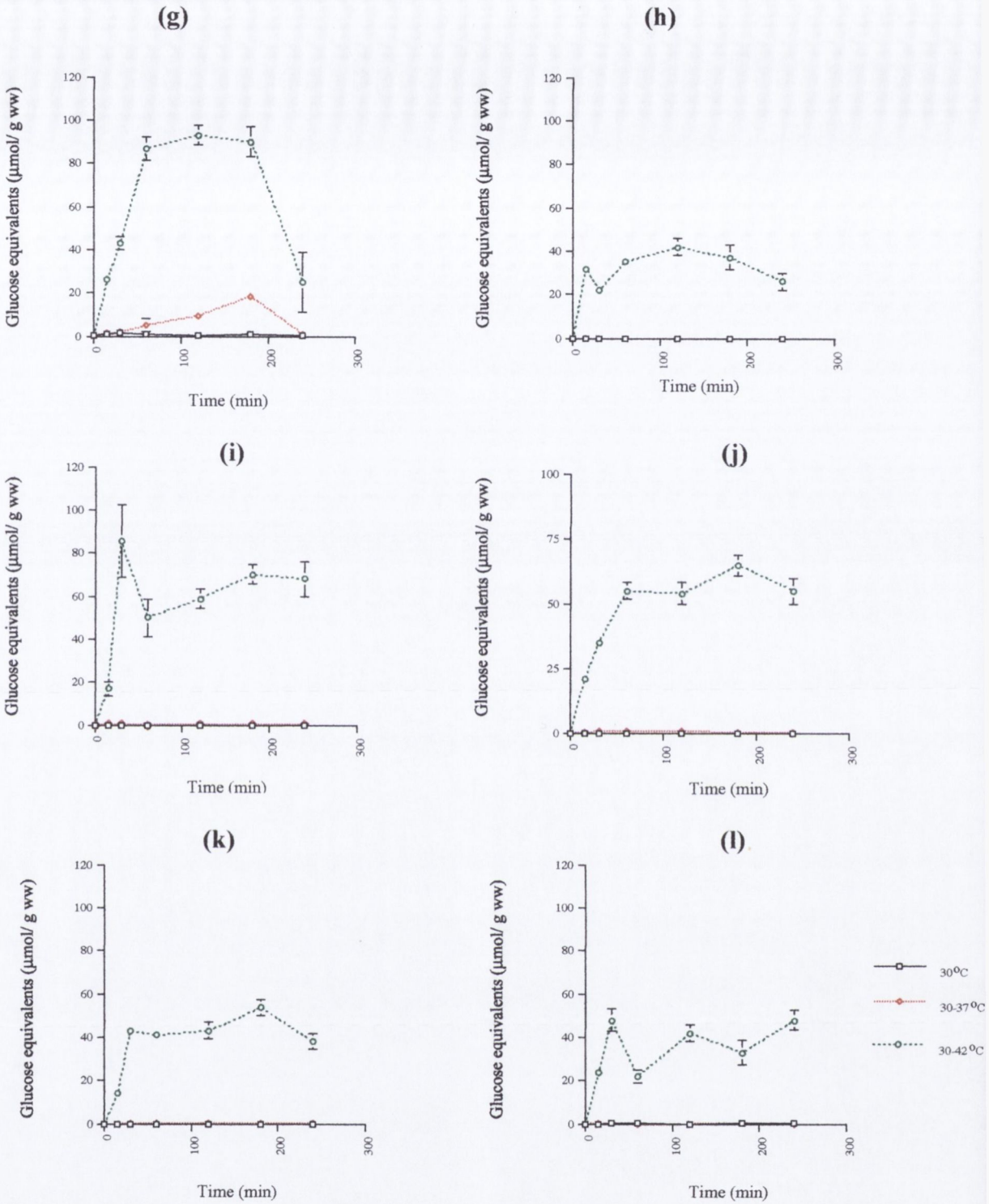
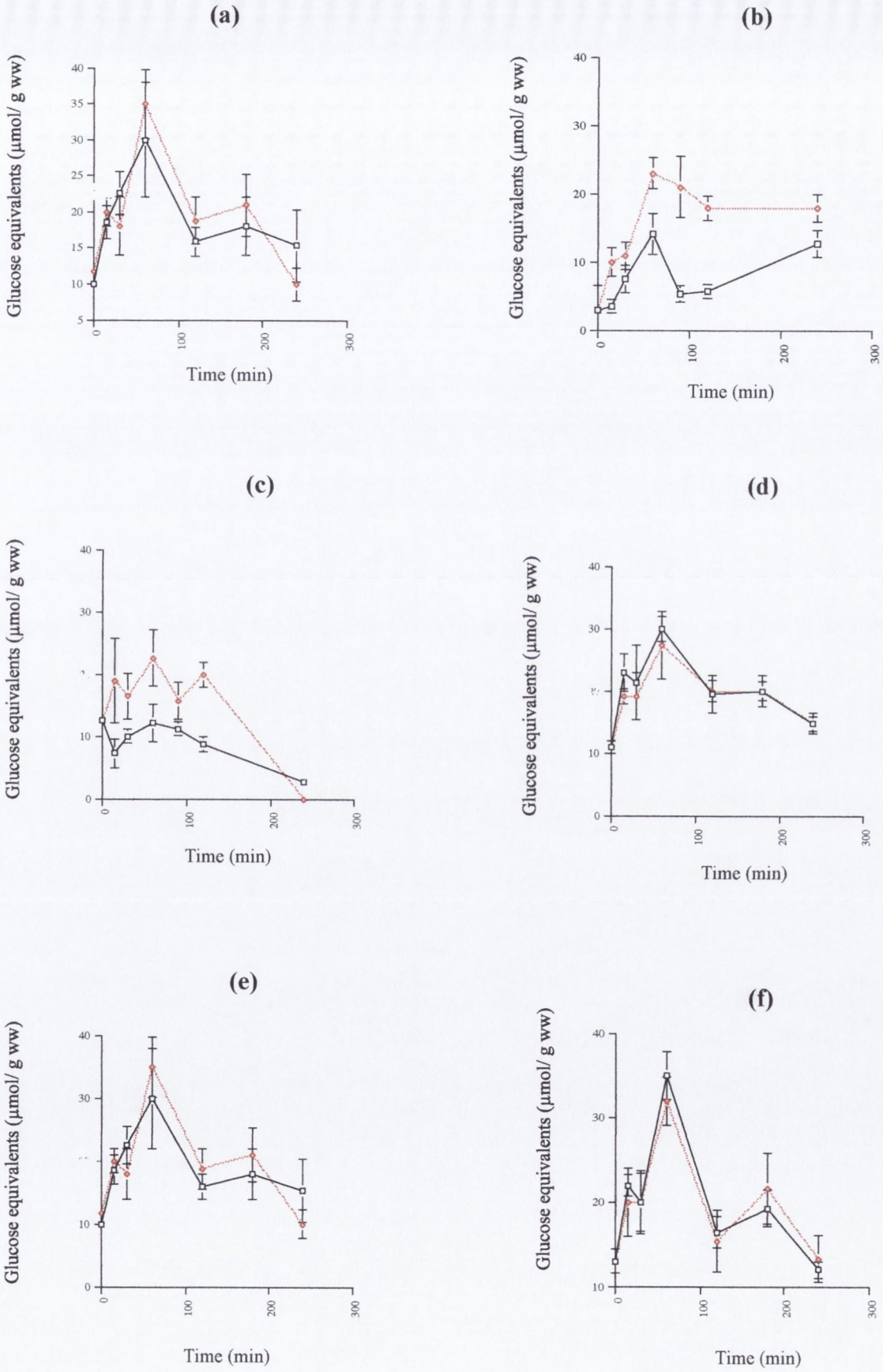


Figure 4.16. Trehalose levels during heat shock treatment. Cells of *C. albicans* strains SC5314 **(a),** 132A **(b)**, and *C. dubliniensis* strains, CD36 **(c)**, CANI **(d)**, CD33 **(e)**, CMI **(f)**, CD539 **(g)**, CD541 **(h)**, CD514 **(i)**, p6265 **(j)**, p7685 **(k)**, and p7718 **(l)**, were grown to exponential phase in YPD medium at 30°C. The cultures were then divided and incubated further at 30, 37 and 42°C. Samples for trehalose determination were taken at the indicated time points. Data represent the mean values ± standard deviations from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols. ww, wet weight.


(a)
Glucose equivalents (µmol/ g ww)
Time (min)
(b)
Glucose equivalents (µmol/ g ww)
Time (min)
(c)
Glucose equivalents (µmol/ g ww)
Time (min)
(d)
Glucose equivalents (µmol/ g ww)
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Glucose equivalents (µmol/ g ww)
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(f)
Glucose equivalents (µmol/ g ww)
Time (min)

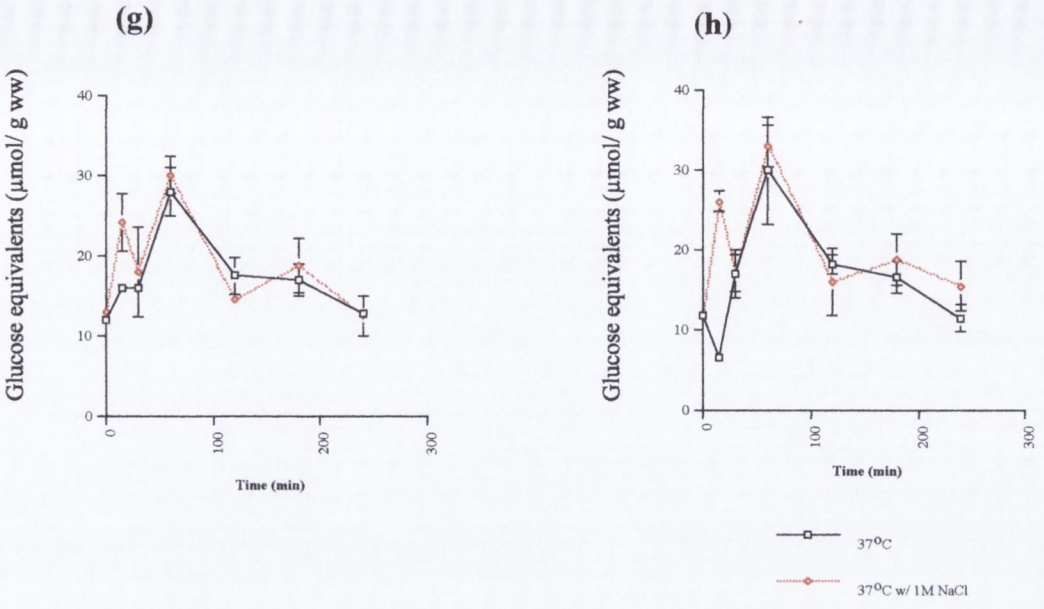


Figure 4.17. Trehalose levels during osmotic treatment. Cells of *C. albicans* strains 132A **(a)**, SC5314 **(b)**, and *C. dubliniensis* strains, CD36 **(c)**, CMI **(d)**, CD539 **(e)**, CD541 **(f)**, CD514 **(g)**, and p7718 **(h)**, were grown to exponential phase in YPD medium at 37°C. The cultures were then divided and incubated further at 37°C with 1 M NaCl. Controls were maintained at 37°C without 1 M NaCl. Samples for trehalose determination were taken at the indicated time points. Data represent the mean values ± standard deviations from three independent experiments. In some cases error bars are omitted because deviations were so small they fell within the corresponding symbols. ww, wet weight.

changed, in either species, by the application of the osmotic stress, when compared to the control. The maximum level of trehalose accumulated in both species was reached 60 min after the osmotic-shift. Interestingly, similar to the heat shock response, the level of trehalose accumulated in *C. dubliniensis* strains varied from strain to strain. Notably, the genotype 2 *C. dubliniensis* CD539 (35±11.1 μmol glucose equivalents / g wet weight) strain accumulated amounts of trehalose, even higher than both of the *C. albicans* strains following 60 min of incubation with 1 M NaCl (23 ±2.3 and 17.54 μmol glucose equivalents / g wet weight, respectively).

4.3.9 Determination of trehalose-6-phosphate synthase, trehalose-6-phosphate phosphatase and trehalase activity in *C. albicans* and *C. dubliniensis* at elevated temperature

In order to investigate the hypothesis that the thermosensitive phenotype of *C. dubliniensis* compared to *C. albicans*, may be related to a defect in the metbolic pathway of trehalose, the activities of each of the enzymes involved in the trehalose metabolic pathway i.e. trehalose-6-phosphate synthase, trehalose-6-phosphate phosphatase and trehalase were determined under conditions of heat shock in both species.

4.3.9.1 Measurement of trehalose-6-phosphate synthase activity

To determine trehalose-6-phosphate (Tre6P) synthase activity during heat stress, *C. albicans* and *C. dubliniensis* cells were grown in YPD at 30°C to exponential phase. The cultures were then divided in two and further incubated at 30 and 42°C. At different time points after the shift samples for Tre6P synthase activity were taken. As is shown in Figure 4.18, incubation at 42°C caused a rise in the Tre6P synthase activity in both of the *C. albicans* strains SC5314 and 132A. These data are in accordance to that previously reported by Arguelles *et al.*, 1997. However, a higher level of Tre6P synthase activity was observed in the *C. albicans* strain 132A. Heat induced increases of Tre6P synthase activity were also found in the *C. dubliniensis* isolate p7718, however this 3-fold increase was only observed after 60 min. Tre6P activity was induced to a much lesser extent in the *C. dubliniensis* isolate CD36 and was only observed after 60 min. Trehalose

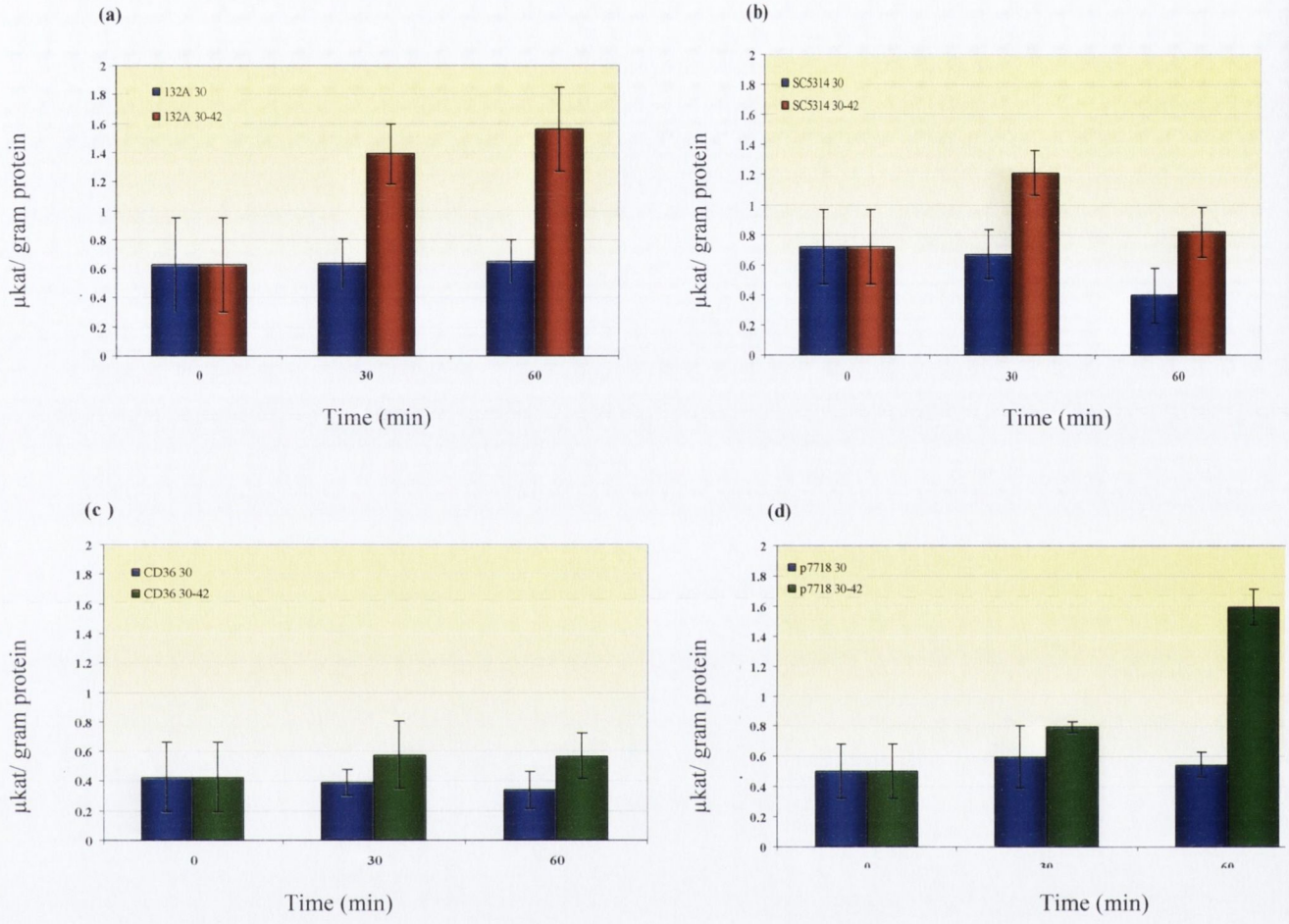


Figure 4.18. Tre6P synthase activity in C. albicans strains 132A(a), SC5314 (b) and C. dubliniensis strains CD36 (c) and p7718 (d) heatshocked at 42°C. Cells were grown at 30°C to exponential phase then heatshocked at 42°C for 60 min. Controls were maintained at 30°C. The results are the average of three independent experiments. Standard error bars are shown.

levels were also measured in parallel and heat shock at 42°C elicited a noticeable increase in intracellular trehalose levels in both species (Fig. 4.19). The increase in the level of trehalose correlated with the increase in the Tre6P synthase activites in both species.

4.3.9.2 Measurement of trehalose-6-phosphate phosphatase activity

Trehalose-6-phosphate (Tre6P) phosphatase is the second enzyme involved in the trehalose metabolic pathway and functions in hydrolysing trehalose-6-phosphate into trehalose. To determine Tre6P phosphatase activity during heat stress, *C. albicans* and *C. dubliniensis* cells were grown in YPD at 30°C to exponential phase. The cultures were then divided in two and further incubated at 30 and 42°C. At different time points after the shift samples for Tre6P phosphatase activity were taken. As shown in Figure 4.20 when exponential cells of *C. albicans* and *C. dubliniensis* were subjected to a heat stress of 42°C, Tre6P phosphatase activities increased approximately 2-fold in both species following 60 min incubation at 42°C. This heat-induced activation of Tre6P phosphatase activity has been previously reported in *S. cerevisiae* (De Virgilio *et al.*, 1991; Neves and Francois, 1992). Parallel measurements of intracellular trehalose were taken as described in section 4.2.4.2 and revealed that upon temperature upshift, both *C. dubliniensis* and *C. albicans* cells immediately accumulated a high level of trehalose (Fig. 4.19) which may be due to the increase in Tre6P phosphatase activity.

4.3.9.3 Measurement of neutral trehalase activity

The function of the trehalose degrading enzyme, neutral trehalase, involves the control of the concentration of intracellular trehalose which plays a key role in the heat shock response of yeasts. To investigate the role of neutral trehalase in *C. dubliniensis* cells, neutral trehalase activity was determined and compared in both *C. albicans* and *C. dubliniensis* cells. *Candida albicans* and *C. dubliniensis* cells were grown to exponential phase at 30°C, the cells were then shifted to 42°C for 30 min and aliquots were removed for trehalase and trehalose determination. After this time, the cells were shifted back to 30°C and further aliquots were removed over a 30 min time period. Activity of neutral trehalase in

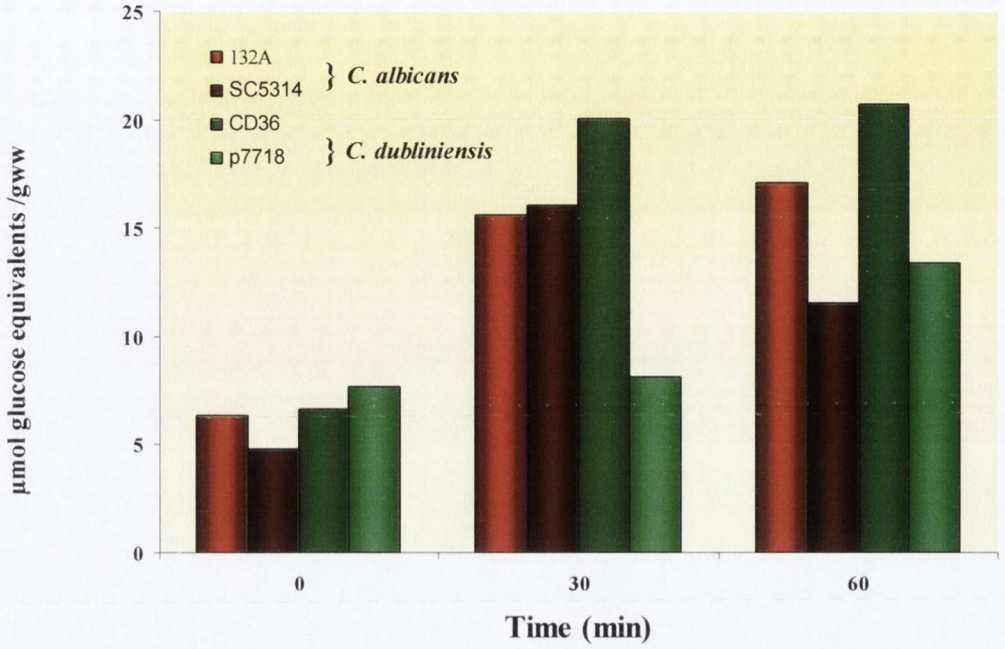


Figure 4.19. Trehalose levels during heat treatment. Cells of *C. albicans* strains 132A and SC5314 and *C. dubliniensis* strains CD36 and p7718 were grown to exponential phase in YPD medium at 30°C. The cells were then shifted to 42°C and further incubated for 60 min. Samples for trehalose determination were taken at the indicated time points. ww, wet weight.

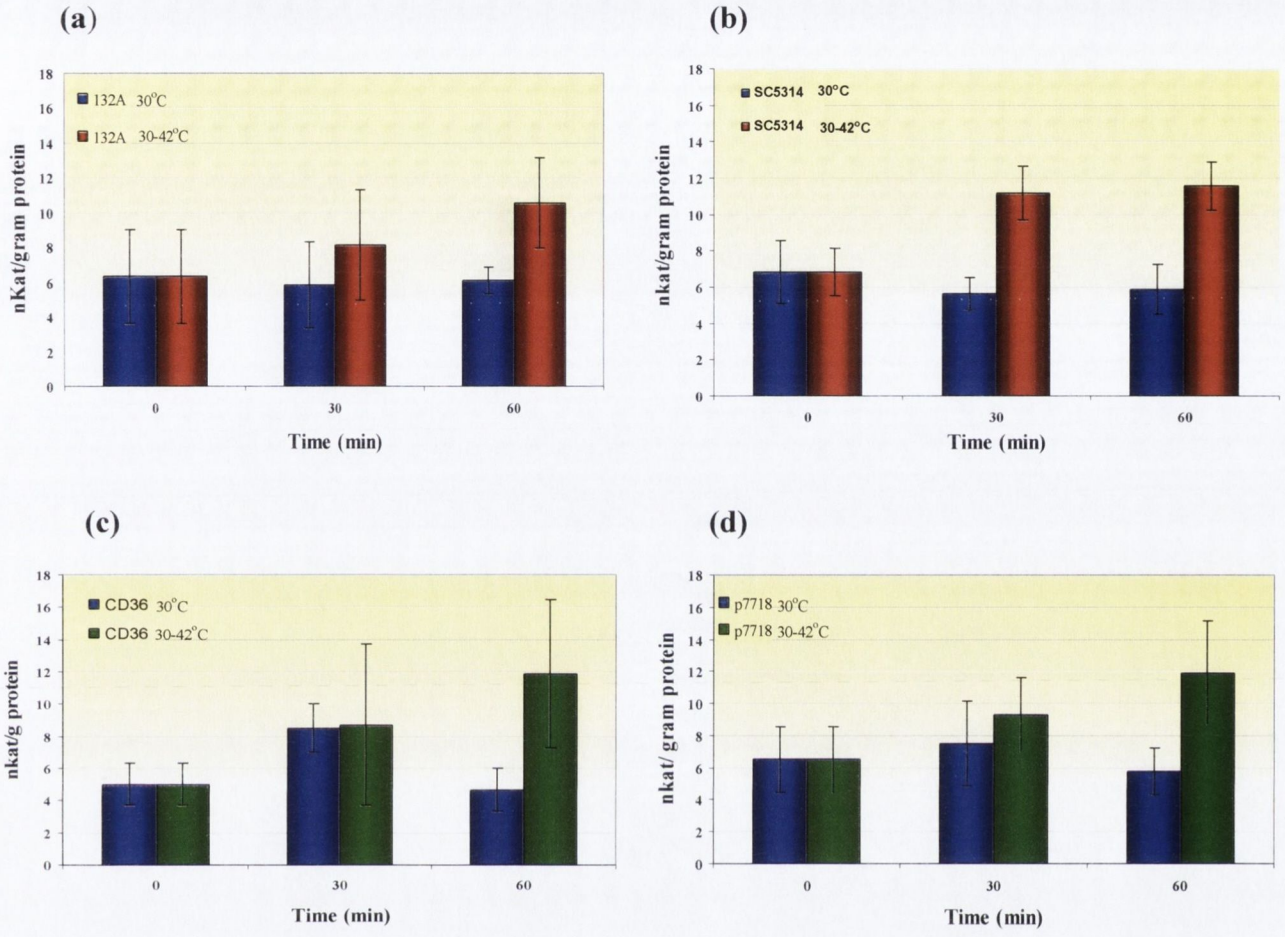


Figure 4.20. Tre6P phosphatase activity in *C. albicans* strains 132A(a), SC5314 (b) and *C. dubliniensis* strains CD36 (c) and p7718 (d) heatshocked at 42°C. Cells were grown at 30°C to exponential phase then heatshocked at 42°C for 60 min. Controls were maintained at 30°C. The results are the average of three independent experiments. Error bars are shown.

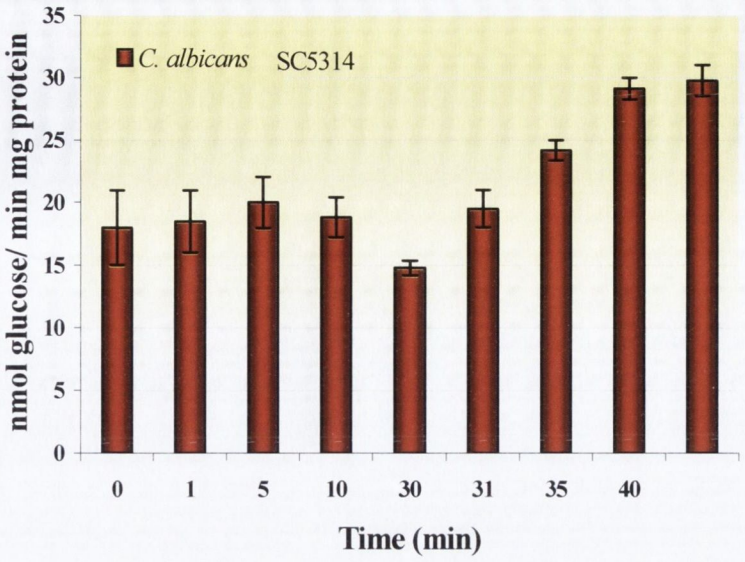
C. albicans and *C. dubliniensis* isolates are displayed graphically in Figure 4.21. In *C. albicans* SC5314, a temperature shift of 30 to 42°C did not cause any significant change in neutral trehalase activity (Fig. 4.21). However, under the same conditions intracellular trehalose levels increased in *C. albicans* SC5314 and continued to increase until the cells were transferred back to 30°C, at which temperature the elevated trehalose content of *C. albicans* cells were degraded (following 30 min at 30°C), (Fig. 4.22). Furthermore, this temperature reversion (42-30°C) caused a significant modification in the neutral trehalase activity of *C. albicans* SC5314, causing activity levels to reach 29.775±1.225 nkat /min mg protein, following 30 min incubation at 30°C (Fig. 4.21a). Similar trends were observed in both of the *C. dubliniensis* isolates; no significant changes in activity at 42°C were observed until the heat stress was removed, thereafter, activity of neutral trehalase increased in both *C. dubliniensis* CD36 and *C. dubliniensis* p7718 (Figs 4.21b and 4.21c). The rise in neutral trehalase activity appeared to coincide with the observed decrease in the amount of trehalose accumulated in both strains, 30 min after (Fig. 4.22cv).

4.3.10 Annotation of putative stress response genes from the *C. dubliniensis* genome sequence

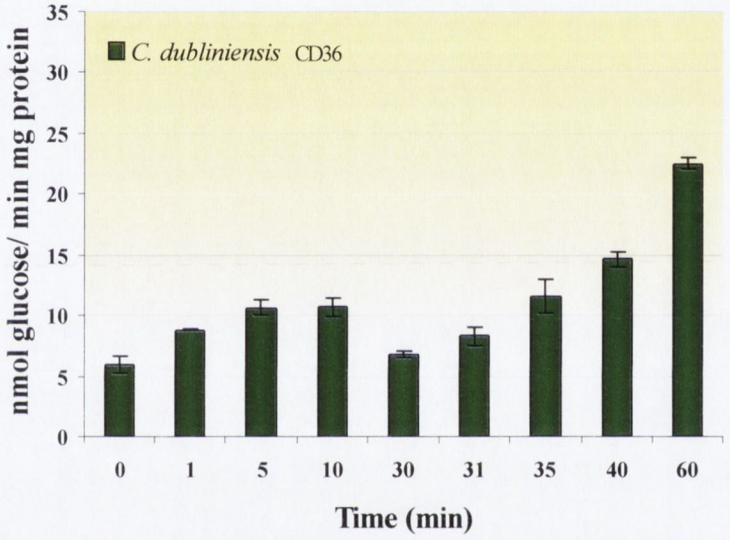
The final part of this work involved the annotation of putative stress response genes known to be involved in the stress response mechanisms of *C. albicans* from the on going *C. dubliniensis* genome sequencing (http://www.sanger.ac.uk/ Projects/C_dubliniensis/). Due to the high degree of similarity between gene sequences of *C. albicans* and *C. dubliniensis* carefully chosen primers, based on sequences of *C. albicans* genes, from the database provided by the *C. albicans* genome sequencing project (Pasteur Institute: http:// genolist.Pasteur.fr/CandidaDB/) have been shown previously to be applicable for use with *C. dubliniensis* (this study, Moran *et al.*, 2004; Moran *et al* 2002; Donnelly *et al.*, 1999; Moran *et al.*, 1998).

Therefore, in order to identify stress response genes, that may not be present, or are divergent in *C. dubliniensis*, existing CandidaDB gene sequences were used to help identify homologous regions in *C. dubliniensis* using recently available *C. dubliniensis* genome sequence data

(a)



(b)



(c)

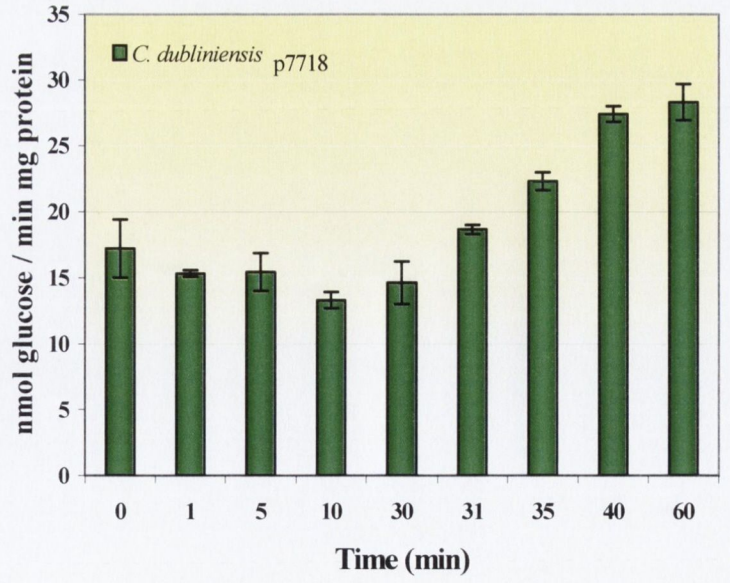


Figure 4.21. Effect of elevated temperature and temperature reversion on neutral trehalase activities in the *C. albicans* isolate SC5314 (a) and *C. dubliniensis* isolates CD36 (b) and p7718 (c). Exponential cells grown in YPD medium at 30°C, were transferred to 42°C for 30 min. At time 30, the cells were transferred back to 30°C and incubated for a further. The results are the average of three independent experiments. Error bars are shown.

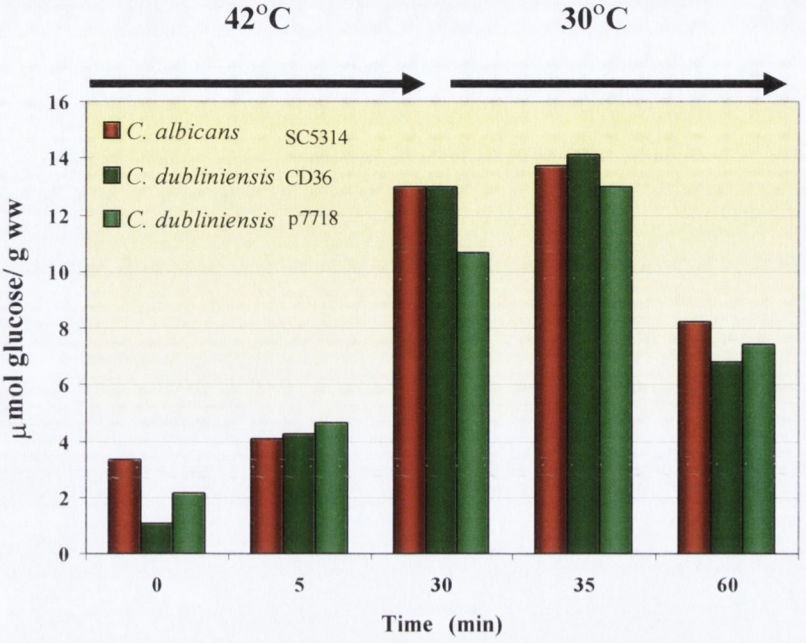


Figure. 4.22. Effect of temperature reversion on the level of trehalose in *C. albicans* strains SC5314 and 132A and *C. dubliniensis* strains CD36 and p7718. At time 0, exponential cultures growing in YPD medium were transferred from 30°C to 42°C. After 30 min at this temperature, the cultures were shifted back to 30°C. Samples for trehalose determination were taken at the indicated time points. ww, wt weight.

(http://www.sanger.ac.uk/Projects/ C_dubliniensis/). Table 4.1 contains a list of all the putative stress response genes annotated from the *C. dubliniensis* genome in this study.

The annotation process involved the use of the *C. albicans* genome database which can be searched by gene name, location or by Blast searches. When a gene of interest was entered into the search panel of the CandidaDB webserver, search results containing information about the gene name, length and size of the ORF (open reading frame) and protein and the accession number unique for the CandidaDB entry were displayed. If there was a homologue of the gene in *S. cerevisiae*, information about the homologue was provided through the SGD (*Saccharomyces* Genome Database) database link and the Stanford pages provide information regarding the ORF and the contig. For example the function of the gene was taken from the description displayed. The results from the Blast search also provided an option to view or download the nucleotide or protein sequence. Once the protein or nucleotide sequence of the gene of interest was downloaded, the sequence was copied and pasted in fasta format into the Query Data box of the *C. dubliniensis* Blast Server, (where BLASTN (DNA vs. DNA) or TBLASTN (protein vs. translated DNA) searches could be carried out). The BLASTN / TBLASTN results displayed the degree of sequence similarity with a corresponding *C. dubliniensis* sequence. The *C. dubliniensis* gene sequence was then downloaded and DNA Strider™ 1.3f11 software (CEA/Saclay, Gif-sur-Yvette, France) was used for sequence analysis to identify the ORF. Subsequent alignment of nucleotide sequences were carried out using CLUSTAL W sequence alignment program (Higgins and Sharp, 1988) to determine the percentage homology of a gene between the two species. A list of genes annotated in this study is presented in Table. 4.1. The majority of the *C. dubliniensis* genes listed were ≥ 90 % identical to the *C. albicans* gene homologues, at the nucleotide level. Thirteen of the *C. dubliniensis* genes displayed between 80-89 % sequence similarity to *C. albicans* gene homologues, while the *C. dubliniensis CdSLN1* and *CdHSP10* genes displayed the lowest sequence similiarity between the two species (78.4 and 78.5 %, respectively).

Table 4.1. List of putative stress response genes annotated from a portion of the *C. dubliniensis* genome

Gene[†]	orf	%homology[‡]	Contig[*]	SGD homologue	Function[+]
AOX1	19.12237	80.0	730	No homologue	Alternative oxidase (by homology)
AOX2.3f	19.12236	87.3	730	No homologue	Alternative oxidase by homology)
CAP1	19.1623	86.8	599.2	YML007w/*YAP1*	Transcriptional activator
CTA1	19.6229	95.0	730	YDR256c/*CTA1*	Catalase A, peroximal
SOD1	19.2770.1	95.3	11	YJR104c/*SOD1*	Cu,Zn –superoxide dismutase
SOD2	19.3340	95.3	1	YHR008c/*SOD2*	Manganese- superoxide dismutase
GPX2	19.85	90.4	593	YIR037w/*HYR1*/*GPX3*/*ORP1*	Glutathione reductase (by homology)
GRP2	19.11785	91.1	2	YOL151w/*GRE2*	Reductase (by homology)
GRP4	19.10660	86.0	13	YOL151w/*GRE2*	Putative reductase
DOG2	19.3392	89.1	593	YHR044c/*DOG1*	2-deoxyglucose-6-phosphate phosphotase
GLC3.3f	19.5622	86.6	1	YEL011w/*GLC3*/*GHA1*	1,4 glucan branching enzyme 3 prime end
GLG2	19.7434	89.9	598	YJL137c/*GLG2*	Self glucosylating initiator of glycogen synthesis (by homology)
GLR1	19.4147	90.2	2	YPL091w/*GLR1*/*LPG17*	Glutathione reductase (by homology)
GPD1	19.1756	94.1	527	YOL059w/*GPD2*/*GPD3*	Glycerol-3- phosphate dehydrogenase
GPD2	19.691	91.8	593	YDL022w/*GPD1*	Glycerol 3 –phosphate dehydrogenase
GPH1	19.702	92.3	588	YPR160w/*GPH1*	Glycogen phosphorylase
GSY1	19.3278	93.3	14	YFR015c/*GSY1*	UDP glucose starch glucosyltransferase, glycogen synthase9by homology)
ENA21	19.517	91.0	7	YDRO38c/*ENA5*	P-type ATPase
ENA22	19.6070	91.0	1	YDRO38c/*ENA5*	P-type ATPase involved in Na+ efflux
GUT1	19.558	93.3	14	YHL032c/*GUT1*	Glycerol kinase
HK1	19.896	84.3	13	YIL147c/*SLN1*/*YPD2*	Histidine kinase

Continued overleaf

Gene†	orf	%homology‡	Contig*	SGD homologue	Function+
TRX2	19.1976	92.7	2	YGR209c/*TRX2*	Thioredoxin (by homology)
TTR1	19.13480	92.8	1	YDR513w/*TTR1*	Glutaredoxin (by homology)

†Gene refers to those in the CandidaDB (http://genolist.pasteur.fr/Candida/DB/)

‡% homology refers to percentage nucleotide sequence homology between the indicated *C. albicans* and *C. dubliniensis* genes

*Contig location in the *C. dubliniensis* genome sequence (http://www.sanger.ac.uk/Projects/C_dubliniensis/)

†Function refers to those assigned in the CandidaDB

4.4 Discussion

To investigate the molecular responses of *C. albicans* and *C. dubliniensis* to the environmental stresses under study (i.e. temperature and osmotic shock) the expression of proteins known to be stress induced in other species such as *S. cerevisiae*, *S. pombe* and *C. albicans* were examined.

In the first part of this study two heat shock protein genes were examined, *HSP104* and *HSP90*. The purpose of this section of the study was to (1) investigate the presence of a *C. albicans HSP104 and HSP90* homologues in the *C. dubliniensis* genome and (2) to compare the expression of *HSP104* and *HSP90* between *C. albicans* and *C. dubliniensis*. The first heat shock protein gene investigated was *HSP104,* an important Hsp in *S. cerevisiae* which is essential for survival at extreme temperatures. The *HSP104* gene has been previously identified in the *C. albicans* genome and using PCR primers based on this sequence a homologue of this gene was identified in *C. dubliniensis*. Sequence analysis of this fragment revealed that it shared a 91.2% nucleotide sequence identity with the corresponding region of the *C. albicans HSP104* gene sequence. Furthermore, data from the recently completed *C. dubliniensis* genome sequencing project (http://www.sanger.ac.uk/Projects/C_dubliniensis/), revealed that the *C. dubliniensis HSP104* gene is 94% homologous to the *C. albicans HSP104* gene at the nucleotide level. Expression of the *C. albicans* and *C. dubliniensis HSP104* gene under conditions of heat shock was also examined for the first time in this study. All of the *C. albicans* strains (SC5314 and 132A) and *C. dubliniensis* strains (CD36 and p7718) tested were found to express the *HSP104* gene during exponential growth at 30°C and under heat shock conditions at 42°C (Fig 4.1). Elevated levels of *CaHSP104* mRNA expression were detected in *C. albicans* SC5314 and 132A strains following 10 min heatshock at 42°C (4-fold), whereas *CdHSP104* mRNA expression was induced in both CD36 and p7718 following only 5 min of heat shock (Fig. 4.1). *CaHSP104* mRNA expression levels in *C. albicans* strain SC5314 decreased in intensity following 30 min (2-fold) of heat shock, whereas, *C. albicans* strain 132A (4-fold) showed increased levels of *HSP104* expression following 30 min of heat shock treatment (Fig. 4.2). *CdHSP104* expression reached a peak intensity in both p7718 (4-fold)

and CD36 (2.5 fold) after 10 min of heat shock at 42°C, returning to lower levels after 30 min (Fig 4.2).

Another important HSP and the second heat shock protein gene investigated in this study was *HSP90.* The molecular chaperone Hsp90 is a highly conserved and abundant protein which is thought to be essential for viability in *S. cerevisiae* and in *C. albicans* (Swoboda *et al.*, 1995; Borkovich *et al.*, 1989). Sequencing of the *CdHSP90* 469 bp insert obtained in this study, using primers based on *C. albicans* gene sequences, showed that the *CdHSP90* amplimer shared a 92.3% nucleotide sequence identity with the corresponding region of the *C. albicans HSP90* gene sequence. In addition, data from the recently completed *C. dubliniensis* genome sequencing project (http://www.sanger.ac.uk/Projects/C_dubliniensis/), confirmed that the *C. dubliniensis HSP90* gene is 95% homologous to the *C. albicans HSP90* gene at the nucleotide level. These results provided evidence that *C. dubliniensis* also possesses a *HSP90* homologue.

Northern hybridisation analysis of the *CdHSP90* mRNA expression levels in *C. dubliniensis* isolates CD36 and p7718 yielded results quite similar to those obtained for the *CdHSP104* mRNA expression levels, in that both *HSP104* and *HSP90* were induced in the *C. dubliniensis* strains following 5 min of heat shock compared to the *C. albicans* strains tested. The *HSP90* gene is expressed in both *C. albicans* and *C. dubliniensis* in YPD medium at 30°C during mid-exponential growth. Previous studies have observed an induction of *HSP90* in *C. albicans* during a heat shock of 45°C (Swoboda *et al.*, 1995). In this study, following a heat shock of 42°C *HSP90* was strongly induced in both *C. albicans* and *C. dubliniensis* however the rate of induction appeared to be faster in *C. dubliniensis* compared to *C. albicans*. In *C. albicans* the *HSP90* gene was induced after 10 min of heat shock at 42°C, whereas in *C. dubliniensis* induction of the *HSP90* gene took place within 5 min of heat shock. These results suggest that the kinetics of induction of *HSP104* and *HSP90* are different in both species. The faster rate of induction of *HSP90* and *HSP104* observed in *C. dubliniensis* may reflect that heat shock is a greater stress to *C. dubliniensis* than to *C. albicans* (i.e. *C. dubliniensis* has a lower temperature threshold compared to *C. albicans*).

An additional element of the stress response of yeasts to elevated temperature is the accumulation of the non-reducing disaccharide trehalose. It has been shown previously that prevention of trehalose accumulation by deletion of the *C. albicans TPS1* gene renders the cells less virulent (Zaragoza *et al.*, 1998), impairs formation of hyphae, and prevents growth on glucose and fructose at 42°C. In other yeasts such as *S. cerevisiae* and *Kluyveromyces lactis TPS1* mutants are unable to grow at 30°C and 37°C in glucose containing media. A similar deregulation of gycolysis is found in *C. albicans TPS1* mutants but only at the higher temperature of 42°C. Some of these growth defects observed in *TPS1* mutants may be due to the unbalanced sugar metabolism that reduces the cellular content of ATP due to loss of the inhibition of hexokinase by trehalose-6-P that results in an increased glycolytic flux. In *C. dubliniensis* it has been demonstrated that when trehalose is the only available source of carbohydrate it grows very poorly unlike *C. albicans* which grows well on this dissacharide (Pincus *et al.*,1999). In order to determine the role of trehalose metabolism in thermotolerance in *C. dubliniensis* the expression of two of the trehalose metabolic genes (*TPS1* and *NTC1*) was examined. In other yeasts such as *S. pombe* and *S. cerevisiae* it has been shown previously that the mRNA level of *TPS1* rises when cells undergo thermal stresses (De Virgilio *et al.*, 1993; Blazquez *et al.*, 1994; Winderickx *et al.*, 1996). Zaragoza *et al* (1998) observed an increase in the level of *TPS1* gene expression in response to a heat shock of 42°C in *C. albicans*. However, in this study the authors did not state the level of up-regulation observed. Furthermore, data from microarray studies on *C. albicans* observed no induction of the *TPS1* or *NTC1* genes in response to a heat stress of 23-37°C, while the *TPS1* (1.6-fold) and *NTC1* (2.3-fold) genes were nearly induced twofold by a hypersomotic stress of 0.3 M NaCl (Enjalbert *et al.*, 2003)

It was decided to investigate whether a homologue of the *C. albicans* trehalose–6-phosphate synthase gene, was present in *C. dubliniensis.* Sequences were identified by PCR in *C. dubliniensis* that were homologous to the *C. albicans TPS1* gene. The 876 bp *C. dubliniensis TPS1* gene fragment obtained showed a 92.4% identity to the *TPS1* gene of *C. albicans,* representing 62.6% of the total gene length. Data from the recently completed *C. dubliniensis* genome sequencing project (http://www. sanger.ac.uk/Projects/C_dubliniensis/),

confirmed that the *C. dubliniensis TPS1* gene is 93.2% homologous to the *C. albicans TPS1* gene at the nucleotide level. These results provided convincing evidence that the cloned 876 bp DNA insert was from the putative *C. dubliniensis TPS1* gene.

Northern hybridisation analysis of *TPS1* mRNA expression levels in *C. albicans* strains 132A and SC5314 and *C. dubliniensis* strains CD36 and p7718 revealed that the *TPS1* gene is expressed during exponential growth at 30°C and under heat shock conditions at 42°C. The expression of the *TPS1* gene was not induced significantly in *C. albicans* isolates 132A and SC5314 when transferred to YPD medium at 42°C. These results are in contrast to the study of Zaragoza *et al.*, 1998 who showed an induction of the *TPS1* gene in *C. albicans* under heat shock conditions. However, as the authors did not state what level of *TPS1* gene up-regulation was observed, it is not possible to compare the data. The results found in the present study were reproducible and suggest that in *C. albicans* induction of *TPS1* expression in response to heat shock may be strain specific. *Candida dubliniensis* p7718 showed a decrease in *TPS1* expression, but after 5 min of heat-shock, returning to normal levels after 30 min. However, the *C. dubliniensis* isolate CD36 was found to express slightly increased levels of *CdTPS1* mRNA (about 1/2 fold) compared to the *C. albicans* isolates. These results indicated that *TPS1* gene expression may vary from strain to strain in *C. dubliniensis*.

The second trehalose metabolic gene investigated was the *NTC1* gene, encoding neutral trehalase, whose function consists of the control of the concentration of trehalose by degradation. Neutral trehalase genes (*NTH 1* and *NTH 2*) have been cloned from *S. cerevisisae* (Kopp *et al.*, 1993) and *K. lactis* (*NTH 1*), (Amaral *et al.*, 1997). A neutral trehalase was identified in *C. utilis* (Arguelles and Gacto, 1985) and also in *C. albicans (NTC1)*, (Eck *et al.*, 1997). It has been shown previously that mRNAs corresponding to *NTH 1* increased during a heat shock from 30°-40°C in *S. cerevisiae* (Nwaka *et al.*, 1995) and also in response to heat shock in *S. pombe* (De Virgilio *et al.*, 1990; Soto *et al.*, 1997). In this study a *C. dubliniensis NTC1* gene fragment amplified by PCR showed a 90.6% identity to the corresponding region of the *NTC1* gene of *C. albicans* (representing 49.9% of the total gene length). These results confirmed that the

cloned 1380 bp DNA insert obtained in this study was from the putative *C. dubliniensis NTC1* gene. This was further confirmed with data from the recently completed *C. dubliniensis* genome sequencing project (http://www.sanger.ac.uk Projects/C_dubliniensis/), which revealed that *NTC1* gene is 90.8% homologous to the *C. albicans NTC1* gene at the nucleotide level

The expression of the *NTC1* gene in *C. albicans* and *C. dubliniensis* under conditions of heat shock was compared for the first time within recombinant plasmids p*CaNTC1* and p*CdNTC1* obtained in section 4.3.4 as hybridisation probes. Both *C. albicans* and *C. dubliniensis* were found to express the *NTC1* gene during exponential growth at 30°C in YPD medium, although at the high temperature of 45°C the pattern of expression was different in both species. *Candida albicans NTC1* transcripts were detected in *C. albicans* isolates 132A and SC5314 at 45°C for up to 30 min. However, no expression of *NTC1* by either *C. dubliniensis* CD36 or *C. dubliniensis* p7718 was detectable at 45°C. This result may be due to the inability of *C. dubliniensis* to grow at 45°C. It was concluded that the lack of *NTC1* gene expression observed was due to the high heat shock temperature at 45°C. Therefore, it was decided to examine *NTC1* mRNA expression levels at the lower temperature of 42°C as *C. dubliniensis* cells are viable after 30 min of heat shock at 42°C (section 3.3.3). Expression of an *NTC1* transcript was detected at all time points in the *C. albicans* strains 132A and SC5314 and *C. dubliniensis* strains CD36 and p7718 at 42°C. However, the shift from 30°C to 42°C had little effect upon the level of *NTC1* mRNA expression in the *C. albicans* isolates 132A and SC5314 and in the *C. dubliniensis* strain CD36. However, in *C. dubliniensis* p7718 the *NTC1* mRNA level showed a slight increase in intensity (1.5 fold) after 30 min of incubation at 42°C. Although *NTC1* expression was not induced in both of the *C. albicans* strains tested and in the *C. dubliniensis* isolate CD36, the results obtained suggest that induction of *CdNTC1* in response to heat shock at 42°C varies from strain to strain in *C. dubliniensis* cells.

Expression of the *TPS1* and *NTC1* genes were also examined under conditions of osmotic shock (1 M NaCl). While the *C. albicans* strain SC5314 showed a slight decrease in *TPS1* expression (1.3-fold) following 30 min of osmotic shock, exposure to the osmotic stress had no affect on the level of *NTC1*

expression. In *C. dubliniensis TPS1* and *NTC1* gene expression appeared to be down-regulated in response to osmotic shock, as no transcripts were detected in the *C. dubliniensis* isolate CD36.

From these Northern analyses data it was apparent that there was no significant increase (i.e. > 1.5-fold) in expression of *TPS1* or *NTC1* in *C. albicans* or *C. dubliniensis* in response to thermal or osmotic stress. Consequently, it was decided to measure intracellular trehalose levels to see if these results correlated with trehalose accumulation in both species.

However, it is important to note that the quantification of Northern hybridisation experiments carried out in this study is semi-quantitative and should be used alongside other quantitative methods such as RT-PCR and Real time PCR

In this study trehalose accumulation in *C. dubliniensis* in response to heat and osmotic shock was analysed for the first time, to investigate whether *C. dubliniensis* is able to accumulate trehalose to the same extent as *C. albicans* under stressful conditions using two different, simple crude assays: the first, based trehalose levels on the amount glucose equivalents produced per cell number while the second, based trehalose production on the wet weight of *Candida* cells. Both methods produced similar trends, in response to heat stress, i.e. accumulation of trehalose upon initiation of heat stress was observed in both species. In the first method, the *C. albicans* strains (132A and SC5314) tested showed a 12-18 fold increase in trehalose concentration following heat shock. The transfer of exponentially growing *C. dubliniensis* CD36 and p7718 cells to the same heat stress temperature of 42°C also caused a rapid increase in the intracellular level of trehalose. After 60 min of incubation at the elevated temperature trehalose increased from a concentration of about 1±0.2 μg to 26±6.1 μg glucose equivalents / 10^7 cells in *C. dubliniensis* isolate p7718, but to a lesser extent in *C. dubliniensis* isolate CD36 (0.6±0.06 μg -7.0±1.55 μg glucose equivalents / 10^7 cells, respectively). The temperature–dependent increase in trehalose concentration was found to be reversible in *C. dubliniensis* isolates CD36 and p7718 as well as in the *C. albicans* isolates 132A and SC5314. These results indicate that like *C. albicans, C. dubliniensis* also has the ability to accumulate trehalose in response to heat stress. However, the level of accumulation seems to be strain specific in the case of *C. dubliniensis* isolates.

A similar finding was also observed using the second method, in which 10 *C. dubliniensis* isolates representing genotypes 1, 2, 3 and 4 respectively were tested. From the results obtained, it appears that the genotype of the *C. dubliniensis* isolates has no effect on the trehalose produced. For example in the case of genotype 2 isolates, while CD539 (87±5.4 μmol/ g wet weight) produced levels of trehalose similar to *C. albicans* its *C. dubliniensis* genotype 2 counterpart, isolate CD541 only reached trehalose levels of about 35±2.5 μmol/ g wet weight after 60 min incubation at 42°C. In addition, trehalose levels ranged from 47±2.0 (isolate CMI) to 60±5.4 (isolate CD36) μmol/ g wet weight among the genotype 1 strains under similar conditions.

Interestingly, similar to the heat shock response, the level of trehalose accumulated in *C. dubliniensis* strains varied from strain to strain in response to osmotic shock. Although *C. dubliniensis* did not accumulate a significant amount of trehalose in response to osmotic shock compared to the controls, it demonstrated that some *C. dubliniensis* strains are capable of producing this dissacharide to the same level as *C. albicans* under these conditions i.e. the genotype 2 *C. dubliniensis* CD539 (35±11.1 μmol glucose equivalents / g wet weight) strain accumulated levels of trehalose, even higher than both of the *C. albicans* strains following 60 min of incubation with 1 M NaCl (23 ±2.3 and 17.54 μmol glucose equivalents / g wet weight, respectively).

Taken together, these results suggested that *TPS1* and *NTC1* induction was not required for the accumulation of trehalose in response to heat and osmotic shock in both *C. albicans* and *C. dubliniensis*. This prompted the investigation of the activities of each of the individual enzymes involved in the trehalose metabolic pathway. Hence Tre6P synthase, Tre6P phosphatase and neutral trehalase activities were determined in response to heat shock.

Analysis of the average *C. albicans* and *C. dubliniensis* Tre6P synthase activities in response to heat shock showed that *C. albicans* Tre6P synthase heat induced activation was only found to be significantly higher following 30 min ($<P$ 0.02) of heat shock compared to *C. dubliniensis*, but not at 60 min. Although both species displayed heat-induced activation of Tre6P synthase, this data, suggested that perhaps the trehalose metabolic enzymes of *C. albicans* are in fact more efficient in responding to an initial thermal stress than those of *C. dubliniensis.*

However, this was not the case for Tre6P phosphatase and neutral trehalase activities, where similar trends in activities were observed between these two species. Furthermore, trehalose measurements taken under the same conditions correlated with a rise in Tre6P synthase and Tre6P phosphatase activities indicating that the Tre6P synthase and Tre6P phosphatase complex is fully functional. Strengthening, the hypothesis that a significant induction of the *TPS1* gene is not required for trehalose accumulation in response to a heat stress of 42°C, as long as there is sufficient Tps1p present.

If cells are exposed to an elevation in temperature, they have no information about how long the temperature stress will last, thus the cells must be able to accumulate trehalose immediately, and once the stress is removed, must be able to degrade it efficiently in order to provide sufficient protection. Overall it may be reasoned that no significant induction of *TPS1* was observed in *C. albicans* as there was sufficient Tps1p present to initiate trehalose synthesis. Furthermore, if the heat stress is short lived this would prevent a dentrimental build up of trehalose, as enzyme production under transcriptional control cannot be stopped easily. This might, in part, explain the slight increase in *TPS1* expression observed in the *C. dubliniensis* strain CD36 in repsonse to heat shock. A possible explanation suggested was that this *C. dubliniensis* strain did not have sufficient levels of Tre6P synthase activity to initiate trehalose synthesis and thus required the induction of the *TPS1* gene to facilitate efficient trehalose synthesis.

To investigate if there was any correlation between the level of *NTC1* mRNA expression and the level of neutral trehalase activity under heat shock conditions, the activities of neutral trehalase in the same strains under similar conditions were determined. No significant increase in neutral trehalase activity was observed in either *C. albicans* or *C. dubliniensis* strains, including the *C. dubliniensis* strain p7718 which induced *NTC1* gene expression slightly (1.5-fold) in response to a temperature up-shift of 30-42°C. Taken together, these findings suggested that *NTC1* mRNA expression and neutral trehalase activity may not be controlled in response to temperature. However, further investigation revealed that neutral trehalase activitiy does in fact, increase in both species upon removal of the heat stress i.e. 42°C. Thus, in order to confirm if there is any correlation between *NTC1* mRNA expression and neutral trehalase activity further analysis of

NTC1 mRNA expression in both species following upon removal of heat stress (i.e 42-30°C) is required. It has been proposed that a possible interaction between neutral trehalases with heat shock proteins is part of this stress response mechanism (Hottiger *et al.*, 1992). In addition, the rapid degradation of trehalose once a heat stress has been removed is an essential process in order for cells to survive. If trehalose is not degraded after the removal of a heat stress hinder the refolding of partially denatured proteins (Singer and Lindquist, 1998; Wera *et al.*, 1999).

The final aim of this section was to annotate putative stress response genes in the *C. dubliniensis* genome. *Candida dubliniensis* genes annotated in this study are listed in Table 4.1. The recent availability of the *C. dubliniensis* genome sequence has greatly facilitated global gene identification and the functional analysis of *C. dubliniensis*. It is hoped that the completion of the annotation of the *C. dubliniensis* genome will lead to the identification of genes or gene families that may explain, in part the reasons for the difference in virulence between *C. albicans* and *C. dubliniensis*.

In conclusion, this study has shown that *C. dubliniensis* has the ability to accumulate trehalose under heat and osmotic stress conditions and that the *C. dubliniensis* trehalose metabolic enzymes are functional under conditons of thermal stress. This data weakens the hypothesis that the accumulation of trehalose is one of the reasons explaining *C. albicans* enhanced ability to survive under stressful conditions compared to *C. dubliniensis*. Therefore, there must be another explanation for the inability of this species to tolerate conditions of high salt and high heat stress.

Chapter 5

Identification of the *C. albicans ENA21.3* gene by functional complementation

5.1 Introduction

Although *C. dubliniensis* and *C. albicans* are closely related, both species differ in their tolerance of high salt concentrations (this study; Alves *et al.*, 2002). While *C. albicans* grows well in Sabouraud dextrose broth supplemented with 6.5% NaCl, *C. dubliniensis* does not grow under these conditions, a phenotypic trait which has been suggested as the basis of a simple and efficient diagnostic tool that allows the differentiation between *C. albicans* and *C. dubliniensis*. Osmotic shock, stimulated by NaCl has a major impact on cell physiology, cell metabolism, ion homeostasis and gene expression, and the capacity to adjust to variations in salt concentration is likely to contribute to the ability of *C. albicans* to colonise and infect a wide range of anatomic sites. Therefore, it is also possible that the apparent lower tolerance of *C. dubliniensis* to elevated NaCl concentration may contribute to the lower virulence of *C. dubliniensis* compared with *C. albicans* (Gilfillan *et al.*, 1998; Vilela *et al.*, 2002).

The molecular basis of responses of *C. albicans* to salt-induced osmotic stress is poorly understood, therefore, the mechanisms responsible for this phenotypic difference between these two species remains to be elucidated. Studies on *S. cerevisiae* have identified extrusion systems which help keep intracellular sodium levels below concentrations that are toxic to the cell. One such ion exchange pump in *S. cerevisiae* is Ena1p, an P-ATPase involved in the extrusion of Na^+ ions from the cytoplasm. Active export of these toxic ions is a crucial cellular process to avoid deleterious intracellular Na^+ and Li^+ concentrations. Mutants lacking the P-ATPase pump, encoded by *ENA1*, are hypersensitive to salt stress and cannot resume growth when exposed to moderate external NaCl concentraions (Haro *et al.,* 1991).

In order to determine if the differential capacity of *C. albicans* and *C. dubliniensis* to tolerate high salt concentration might contribute to the differential virulence of the two species it was decided to investigate the molecular basis of the lower osmotic stress tolerance of *C. dubliniensis*. Since there was no *C. dubliniensis* genome sequence data available when this project began the strategy adapted to achieve this aim was to investigate if specific *C. albicans* genes could be identified that were able to complement the low salt tolerance of *C.*

dubliniensis. For this purpose a *C. albicans* genomic library was transformed into the *C. dubliniensis* strain CdUM1B, a Ura$^-$ strain which allows the selection of Ura$^-$ containing vectors (Staib *et al.*, 2001) by electroporation and clones were selected containing complementing genes on high salt medium (i.e. SC Ura$^-$ agar supplemented with 7% (w/v) NaCl.

5.2 Materials and Methods

5.2.1 Construction of the *C. albicans* pRMI library

The *C. albicans* genomic DNA library was kindly provided by Dr. Federico Navarro-García, Dept. Microbiología il, Fac, Farmacia, Universidad Complutense de Madrid. The *C. albicans* genomic library was constructed using the non-integrative plasmid, pRM1 (Fig. 5.1) as described by Pla *et al.* (1995). The *C. albicans* library contained cloned genomic DNA fragments with an average size of 7.5 kb, and represented greater than 99 % coverage of the 16 Mb haploid *C. albicans* genome. *Escherichia coli* strain DH5α was transformed with the *C. albicans* genomic DNA library stock by electroporation (section 5.2.2). Transformants were washed off the plates in L-amp medium, pooled and plasmid DNA was isolated using a Biorad Quantum plasmid DNA extraction kit. Isolated plasmid DNA was pooled and 1 μg used to transform the *C. dubliniensis ura3*Δ mutant CdMU1B (Table 2.1). Aliquots of the *C. albicans* genomic DNA library were stored in 15 % (v/v) glycerol at -80°C.

5.2.2 Transformation of competent *E. coli* by electroporation

Transformation of *E. coli* strain DH5α by electroporation was carried out by the method of Miller and Nickoloff (1995). Five hundred millilitres of LB was inoculated with 1/100 volume of a fresh overnight of *E. coli* strain DH5α and grown at 200 rpm in an orbital incubator at 37°C until the $OD_{600\ nm}$ reached ~0.5.-0.7. The cells were chilled on ice for 20 min, transferred to cold centrifuge bottles and centrifuged at 4000 x *g* for 15 min at 4°C. The supernatant was poured off and discarded and the remaining pellet was resuspended in 500 ml of ice-cold 10 % (v/v) glycerol. The cells were then centrifuged at 4000 x *g* for 15 min at 4°C. The supernatant was decanted and the pellet was resuspended in 250 ml of ice-cold 10 % (v/v) glycerol. The cells were then centrifuged for another 15 min at 4000 x *g* at 4°C. The remaining pellet was resuspended in 20 ml of ice-cold 10 % (v/v) glycerol and transferred to a 30 ml centrifuge tube and centrifuged at 4000 x *g* for 15 min at 4°C. The supernatant was discarded and the cell pellet was resuspended in a final volume of 1-2 ml of ice-cold 10 % (v/v) glycerol. Cell concentration at this point was ~ 1-3 x 10^{10} cells/ml. This suspension was then frozen in aliquots on dry ice and stored at -70°C. The frozen electrocompetent

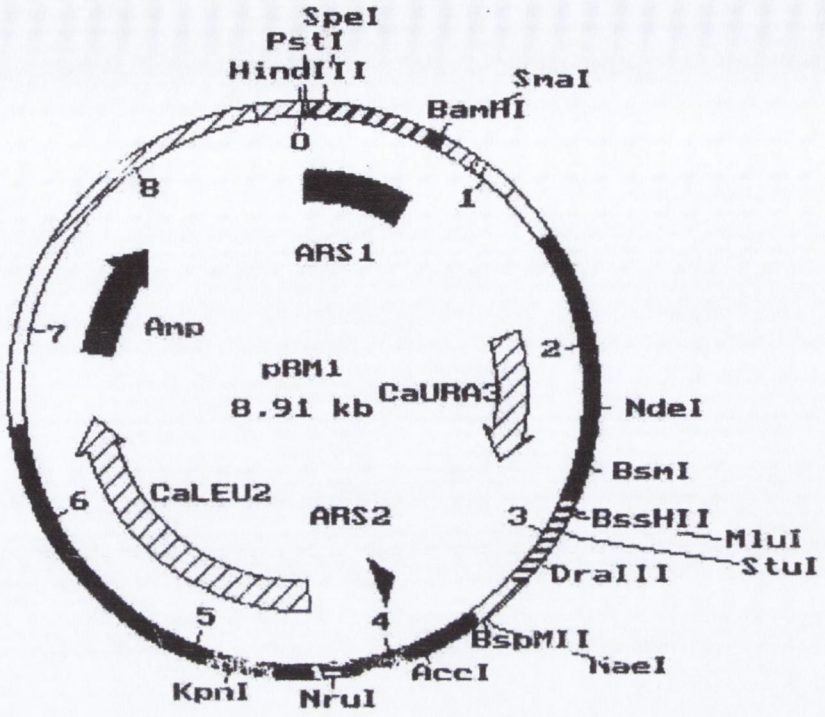


Figure 5.1. Schematic diagram showing the structure of pRM1 plasmid developed by Pla *et al.*, (1995). pRM1 contains two independent autonomously replicating sequences that allow the introduction and recovery of DNA in *C. albicans*. The vector pRM1 was used to construct the *C. albicans* genomic library used in this study.

cells were thawed on ice immediately prior to use. For each sample to be electroporated, a 1.5 ml microfuge tube and a 0.2 cm electroporation cuvette was placed on ice. In the ice-cold, 1.5 ml polypropylene microcentrifuge tubes, 40 µl of the suspension was mixed well with 1- 2 µl of DNA and incubated on ice for ~1 min. The mixture of cells and DNA was transferred to an ice-cold electroporation cuvette and the cuvette was tapped gently until the suspension was at the bottom. Electroporation was carried out in a Bio-Rad Gene Pulser (0.2 cm cuvette, 2.5 kV, 200 Ω, 25 µF). Immediately 1 ml of SOC medium was added to the cuvette and the cells were resuspended with a pasteur pipette. The cell suspension was then transferred to a 17 x 100 mm polypropylene tube and incubated at 37°C for 1 h with shaking at 225 rpm. The transformants were then plated on LA plates containing antibiotic (100 µg ampicillin/ml) and were incubated at 37°C overnight.

5.2.3 Plasmid extraction (Plasmid rescue)

The *C. albicans* DNA fragments contained in the CdUM1B transformants were identified by plasmid rescue. Transformants were grown overnight in 1 ml of SC Ura$^-$ broth at 30°C. Overnight cultures were harvested by centrifugation for 1 min at 18,188 x *g*. The cell pellets were resuspended in 200 µl of breaking buffer: 2% (v/v)Triton X 400, 1 mM EDTA, 1% (w/v) SDS, 100 mM NaCl and 10 mM Tris at pH 8. The mixture was then transferred to a Sarstedt tube cointaining 0.3 g of glass beads (Sigma) and 200 µl of phenol:chloroform 1:1. Homogenisation was carried out in a bead beater (Fast prep FP120, Savant Instruments, inc., Holbrook, NY) for 20 s at speed 4, followed by centrifugation for 5 min at 18,000 x *g*. The top layer of the homogenate was removed and was extracted using an equal volume of a mixture of phenol:chloroform (1:1) and precipitated with the addition of 400 µl of ethanol for 5 min at -20°C. Following a centrifugation of 5 min at 18000 x *g*, the resulting DNA precipitate was transferred to a fresh tube. The DNA pellet and washed in 400 µl ice-cold 70 % (v/v) ethanol, dried and resuspended in 40 µl TE. One-to-two microlitres of the plasmid DNA was used to transform *E. coli* strain DH5α by electroporation.

5.2.4 Transformation of *Candida* cells by electroporation

Candida cells were transformed by electoporation (Staib, 2001). Cells from a YPD preculture were diluted 10^{-4} in 50 ml of fresh YPD medium and grown overnight at 30°C to an optical density of $OD_{600\ nm}$ of 1.6 to 2.2. The cells were collected by centifugation and resuspended in 8 ml of water. After addition of 1 ml of 10X TE (100 mM Tris-HCl, 10 mM EDTA [pH 7.5]) and 1 ml of 1 M lithium acetate (pH 7.5), the suspension was incubated in a rotary shaker at 150 rpm for 60 min at 30°C. A 250 µl volume of 1 M dithiothreitol was then added, and the cells were incubated for a further 30 min at 30°C with shaking. After addition of 40 ml of water, the cells were centrifuged, washed sequentially in 50 ml of ice-cold water and 10 ml of ice-cold 1 M sorbitol, resuspended in 50 µl of 1 M sorbitol, and kept on ice. Five microlitres (approximately 5-100 ng) of DNA was mixed with 40 µl of electrocompetent cells and electroporation was carried out in a Bio-Rad Gene Pulser (0.2 cm cuvette, 1.6 kV, 200 Ω, 25 µF) with a Bio-Rad Pulse Controller included in the circuit. Transformants were selected on minimal agar plates without Uridine. Single colonies were picked after 5-7 days of growth at 30°C, restreaked on the same medium.

5.2.5 Spot plate assay

Susceptibility of the *C. dubliniensis* reference strains and transformants was tested qualitatively by spotting serial dilutions of yeast cultures in SC Ura^- agar plates supplemented with 5 % (w/v), 6 % (w/v) and 7 % (w/v) NaCl, which provided an easy visualisation of growth differences between strains. Each plate contained 25 ml of agar. *Candida* strains were grown overnight at 30°C with constant shaking in SC Ura^- broth. The cultures to be tested were firstly diluted to $1x10^7$ cells/ml in ultrapurified water. Four serial 1:10 dilutions of this first dilution were made and 4 µl of each dilution was spotted onto each plate surface and incubated for 48 h at 30°C.

5.2.6 Amplification of *ENA21.3*

Amplification of *ENA21.3* gene fragments from *C. dubliniensis* CD36 and *C. albicans* 132A genomic DNA was carried out using the Expand Long Template PCR System using the following cycling conditions: 1 cycle of 2 min at 92°C, followed by 10 cycles of 10 s at 92°C, 30 s at 55°C, and 9 min at 68°C

followed by 20 cycles of 15 s at 92°C, 30 s at 55°C, and 10 min at 68°C followed by 1 cycle of 7 min at 68°C. PCR primers were designed based on the *C. albicans ENA21.3* sequences (Table 2.2).

5.2.7. Osmotic Shock

A 5 M NaCl solution was added to exponential cells in YNB at 37°C to generate a 1.0 M final concentration. Samples were taken at 10, 20, 30 and 60 min after the addition of NaCl and total RNA was isolated as described in section 2.6.2. Total RNA isolated from cells growing at 37°C prior to osmotic shock were used as a control.

5.3 Results

5.3.1 Identification of *C. albicans* genes that confer enhanced tolerance of salt-induced osmotic stress in *C. dubliniensis*

In this part of the study a *C. albicans* genomic library was used in an attempt to identify *C. albicans* genes that might complement any defect in salt tolerance in *C. dubliniensis*. A *C. albicans* genomic library was constructed using the double ARS- containing plasmid vector pRM1 (Fig. 5.1). This library was used to identify *C. albicans* genes that complement the NaCl sensitive phenotype of the *C. dubliniensis* strain CdUM1B. *Candida dubliniensis* CdUM1B (Table 2.1) is a Ura$^-$ strain constructed from the *C. dubliniensis* wildtype strain Wü284 by targeted gene deletion (Staib *et al.*, 2001). While CdUM1B can grow on media supplemented with 6 % (w/v) NaCl it cannot grow on media supplemented with 7 % (w/v) NaCl. Therefore in order to identify any gene that can confer enhanced salt-induced osmotic stress tolerance transformants were selected on SC Ura$^-$ medium supplemented with 7 % (w/v) NaCl. The *C. albicans* genomic library was used to transform the *C. dubliniensis* strain CdUM1B and a pool of transformants (~50,000) was appropriately diluted and spread on SC Ura$^-$ medium supplemented with 7 % (w/v) NaCl. Plasmid DNA isolated from 4 positive clones was used to transform *E. coli* DH5α by electroporation. Analysis of these transformants led to the isolation of an insert of approximately 6 kb (pRM1-15) conferring a NaCl resistant phenotype in the strain CdUMIB. A 2.5-kb *Xba*I-*Eco*RI fragment of the clone pRM1-15 was subcloned in pBluescript and sequenced (as described in sections 2.4.3 and 2.5). A homology search using the BLAST family of computer programs was carried out and revealed that the 2.5-kb *Xba*I-EcoRI fragment was homologous with the corresponding region of the *C. albicans ENA21.3* gene. Restriction map analysis of each transformant demonstrated that all four transformants carried gene fragments from the *C. albicans ENA21.3* gene locus. Isolation of plasmid pRM1-15 was carried out by Dr G. Moran (unpublished data). The remainder of the 6–kb DNA insert contained within pRM1-15 was sequenced by primer walking. Sequence analysis of the DNA insert contained within pRM1-15 revealed that it comprised the coding region and the 5' flanking sequence of the *C. albicans ENA21.3* gene. It

also contained approximately 1.2 kb of the coding region of the *C. albicans PMT1* gene (Fig. 5.2).

To confirm that the NaCl resistant phenotype observed was due to the insertion of the 6-kb fragment (pRM1-15), the clone pRM1-15 was reintroduced into the CdUM1B strain by electroporation and plasmid DNA containing no insert was transformed into *C. dubliniensis* CdUM1B and the *C. albicans* CAI-4 strain as a control. To test the NaCl sensitivity of these transformants a spot plate assay was carried out on SC Ura^- medium containing fixed concentrations of NaCl (Fig. 5.3). At a NaCl concentration of 7%, the transformant CdUM1B-pRM1 showed severe growth inhibition compared to the transformants CAI4-pRM1 and CDMUB-pRM1-15. These results suggest that the insertion of the clone pRM1-15 is responsible for the NaCl resistant phenotype observed in CdUM1B-pRM1-15.

5.3.2 Identification and sequencing of *ENA21.3* in *C. albicans* and *C. dubliniensis*

The *ENA21.3* gene in *C. albicans* is homologous to the yeast *ENA/PMR2A* gene encodes a cation extrusion ATPase in *S. cerevisiae* which is essential for survival under salt stress conditions. Functional complementation of the NaCl sensitive phenotype of the *C. dubliniensis* strain CdUM1B using a *C. albicans* gene library identitfied a locus containing the *C. albicans ENA21.3* gene described in section 5.3.1. (Moran, unpublished). Thus, in order to determine if a homologue of the *C. albicans ENA21.3* gene is present in the *C. dubliniensis* genome the primer pair ENA21.3F/R was designed based on the *C. albicans ENA21.3* gene sequence to amplify approximately 527 bp of the gene using *C. albicans* 132A genomic DNA and *C. dubliniensis* CD36 genomic DNA as template. *Candida albicans* contains a second P-type ATPase, encoded by the *ENA22* gene, 69 % homologous to the *ENA21.3* gene at the nucleotide level, thus to ensure the specificity of the *CaENA21.3* probe, the ENA21.3F/R primer pair was designed based on the region most divergent between the *CaENA21.3* and *CaENA22* gene sequences. Sequence data for *C. albicans* was obtained from the Stanford Genome Technology Center website at http://www-sequence.stanford.edu/group/candida. In each species, fragments of the expected length (527 bp) were obtained. The 527 bp amplimers from both species were cloned in pBluescript to yield the recombinant plasmids p*CaENA21.3* and

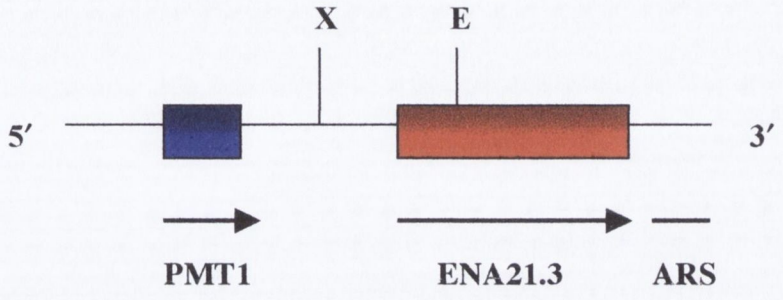


Figure 5.2. Schematic diagram of the 6 kb DNA insert, pRM1-15, containing the *C. albicans ENA21.3* gene and part of the *C. albicans PMT1* gene (1.2 kb). The letters represent restriction endonuclease cleavage sites. The abbreviations are as follows: E, *Eco*RI and X, *Xba*I.

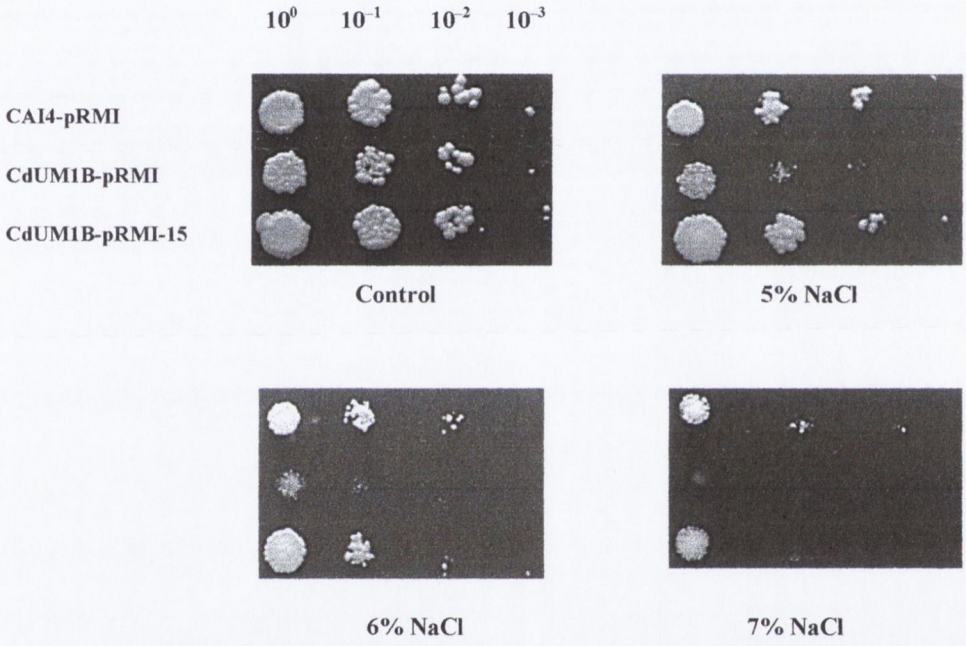


Figure 5.3. Susceptibility of *C. albicans* CAI4 transformant harbouring pRM1 plasmid (CAI4-pRM1) and *C. dubliniensis* CdUM1B harbouring pRM1 (CdUM1B-pRM1) and clone pRM1-15 (CdUM1B-pRM1-15) to increasing NaCl concentrations. Each transformant was grown overnight at 30°C in SC Ura$^-$ broth, adjusted to a cell density of $1x10^7$ cfu/ml using an Improved Neubauer Haemocytometer and 4 µl were spotted in a dilution series on SC Ura$^-$ agar plates containing fixed concentrations of NaCl as indicated. Plates were incubated for 48 h at 30°C.

p*CdENA21.3*. The DNA inserts contained within these recombinant plasmids were sequenced fully in both directions as described in section 2.5. Nucleotide sequence alignment of the *C. albicans* 132A insert contained within plasmid p*CaENA21.3* shared 100 % nucleotide sequence homology with the *C. albicans ENA21.3* gene sequence. A homology search using the family of computer programs, BLAST, was carried out which indicated that the *CdENA21.3* gene amplimer was highly homologous to the corresponding *CaENA21.3* gene amplimer. Alignment of the *CdENA21.3* amplimer and *CaENA21.3* amplimer using the CLUSTAL W sequence alignment computer program demonstrated that the gene fragments were highly similar, being 93.8% at the nucleotide level (representing 16.5 % of total gene length). These findings provided convincing evidence that the cloned DNA insert in plasmid p*CdENA21.3* was from the putative *C. dubliniensis ENA21.3* gene. Southern analysis was performed to further, determine whether *ENA21.3* homologues could be detected in *C. dubliniesis*. Southern analysis of *ENA21.3* in *Hin*dIII-digested genomic DNA from *C. albicans* strains and *C. dubliniensis* strains (Fig. 5.4) with the radiollabeled gene specific 527 bp *CdENA21.3* probe detected an expected strongly hybridising fragment of 5 kb and a second, weakly hybridising fragment of 5.5 kb. These fragments corresponded in length to the predicted sizes of *Hin*dIII fragments expected to contain the *ENA21.3* gene based on *C. albicans* genome sequences (http://genolist.pasteur.fr/CandidaDB/).

Furthermore, data from the recently completed *C. dubliniensis* genome sequencing project (http://www.sanger.ac.uk/Projects/C_dubliniensis/), revealed that the *C. dubliniensis ENA 21.3* gene is 91 % homologous to the *C. albicans ENA21.3* gene at the nucleotide level and 94.8 % homologous at the protein level (Fig. 5.5).

5.3.3 Analysis of *ENA21.3* expression in *C. albicans* and *C. dubliniensis*

In an attempt to determine if the NaCl resistant phenotype of the transformant CdUM1B-pRM1-15 was a result of increased expression of *ENA21.3,* Northern blot analysis was carried out (as described in section 2.6.4). Northern analysis on RNA extracted from CAI4-pRMI, CdUM1B-pRMI and CdUM1B-pRMI-15 cells exposed to an osmotic shock of 1 M NaCl (7% (w/v) NaCl) for 30-60 min was performed using the DNA inserts contained within the

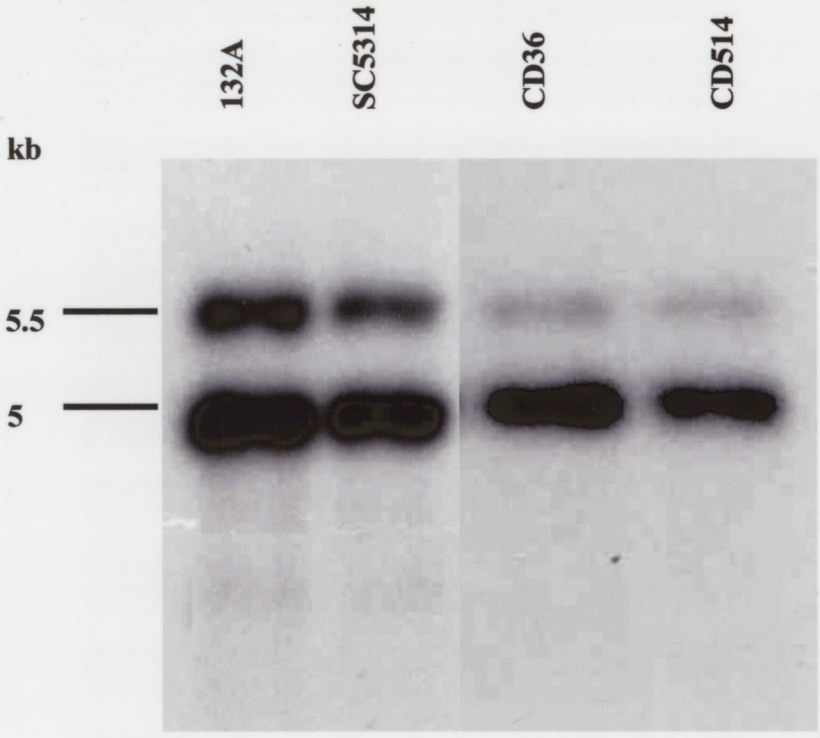


Figure 5.4. Southern hybridisation of *Hin*dIII digested genomic DNA from C. albicans SC5314 and 132A and *C. dubliniensis* CD36 and CD514 isolates hybridised with an [α-^{32}P]dATP-labelled gene specific 527 bp p*ENA21.3* probe.

```
CaEna1p     YLKINGATKINEKNGSSVSESYENESSKKSIYDNTQNIEAYRLTVENVAQEFTTNIINGL
CdEna1p     -LKINGATKINEKNGSSVSESYENESSKKSIYDNVQSIEAYRLTVENVAQEFATNIIKGL
             *********************************.*.***************:****:**

CaEna1p     STHDAAKRLQTYGPNNLGKEESISYVKILAHQVFNAMILVLIISMIIALAIKDWISGGVI
CdEna1p     STQDAAKRLQSYGPNNLGKEESISYVKILAHQVFNAMILVLIISMIIALAIKDWISGGVI
            **:*******:**************************************************

CaEna1p     AGVILINVVIGFVQELKAEKTMGSLRNLSSPTARVTRNGDDLTIPAEEVVPGDIVHVRVG
CdEna1p     AGVILINVIIGFVQELKAEKTMGSLRNLSSPTARATRNGDDLTIPAEDVVPGDIVHVKVG
            ********:************************.************:*********:**

CaEna1p     DTVPADIRLFDCMNLETDEALLTGESLPVAKNFQIVYDDFSVPIPVGDRLNLIYSSSIVS
CdEna1p     DTVPADIRLFDCMNLETDEALLTGESLPVAKNYQIVYDDYSVPIPVGDRLNLIYSSSIVS
            **********************************:******:********************

CaEna1p     KGRGSGIAIGTGLNTEIGSIAKSLQGDSGLIRKVDKSNGRQPQKREYFHAGLGSIYDIVG
CdEna1p     KGRGSGIAIGTGLNTEIGSIAKSLQSDNGLIRKVDKSNGRQPQKREYFHAGLGSIYDIVG
            *************************.*.********************************

CaEna1p     NILGVTTGTPLQKRLSWLAILLFWVAVVFAIVVMASQKFHVNKEVAIYAICVALSMIPSS
CdEna1p     NILGVTTGTPLQKRLSWLAILLFWVAVVFAIVVMASQKFHVNKEVAIYAICVALSMIPSS
            ************************************************************

CaEna1p     LIVVLTITMAVGAQVMVTKNVIVRKLDALEALGGIDNICSDKTGTLTQGKMIAKKVWLPN
CdEna1p     LIVVLTITMAVGAQVMVTKNVIVRKLDALEALGGIDNICSDKTGTLTQGKMIAKKVWLPN
            ************************************************************

CaEna1p     VGTLDVQNSNEPYNPTIGDVRYSPFSPKFIKDTDEEIDFNKPYPDPMPESMHKWLMTATL
CdEna1p     VGTLDVQNSNEPYNPTIGDIKYSPFSPKFIKDTDEEIDFNKPYPDPMPESMHNWLVTATL
            ******************:::*********************************:**:****

CaEna1p     ANIATVNETKDEETGELVWKAHGDATEIAIQVFTTRLNYGRESIAQDYEHLAEFPFDSSI
CdEna1p     ANIATVNQIKDEETGELFWKAHGDATEIAIQVFTTRLNFGRESVAQGYEHLAEFPFDSSI
            *******: ********.*********************:****:**.**************

CaEna1p     KRMSAIYKKDGETKVYTKGAVERVLELCDYWYGERTDDNFDSQTLVKLTEADIKLIEENM
CdEna1p     KRMSAIYKKGNDARVYTKGAVERVLGLCDYWYGERTEDNYDSQTLIKLTEDDINLIEENM
            *********..:::*********** ********:**:*****:**** **:******

CaEna1p     VALSSQGLRVLAFATKDLGDADISNREQVESHLIFQGLIGIYDPPREETAPSVKLCHRAG
CdEna1p     VALSSQGLRVLAFATRELGDADINDREQVESHLIFQGLIGIYDPPREETAPSVKLCHRAG
            ***************::******.:**********************************

CaEna1p     INVHMLTGDHPGTAKAIAQEVGILPRNLYHYSEDVVKAMTMTANEFDALSDEEIDKLPVL
CdEna1p     INVHMLTGDHPGTAKAIAQEVGILPRNLYHYSEDVVKAMTMTANEFDALSDEEIDKLPVL
            ************************************************************

CaEna1p     PLVIARCAPKTKVRMIDALHRRKKFAAMTGDGVNDSPSLKKADVGIAMGLNGSDVAKDAS
CdEna1p     PLVIARCAPKTKVRMIDALHRRKKFAAMTGDGVNDSPSLKKADVGIAMGLNGSDVAKDAS
            ************************************************************

CaEna1p     DIVLTDDNFASILNAIEEGRRMSSNIQKFVLQLLAENVAQALYLMIGLAFIDASGYSVFP
CdEna1p     DIVLTDDNFASILNAIEEGRRMSSNIQKFVLQLLAENVAQALYLMIGLAFIDASGYSVFP
            ************************************************************

CaEna1p     LSPVEVLFVIVITSTFPAIGLGFCGADDDILEKPPSSTIFTWEVIIDMFGYGFIMAVSCL
CdEna1p     LSPVEVLFVIVITSTFPAIGLGFCGADDDILEKPPSSTIFTWEVIIDMFGYGFIMAVSCL
            ************************************************************

CaEna1p     LCFVIIVYGAGDGDLGVNCNSIDANTDTCSLVFKGRSAAFSVMTWCALVLSLECLHPRTS
CdEna1p     LCFVIIVYGAGDGDLGVNCNSIDANTNTCSLVFKGRSAAFSVMTWCALVLSLECLHPRSS
            *************************:**********************************:*

CaEna1p     VFRFPTQDLWANQFLLWSILGGIVSVFPVIYIPVINTKVFLHKSITWEWGVAIGCTLLFL
CdEna1p     VFHFPTRDLWANQFLLWSILGGIVSVFPVIYIPVINTKVFLHKSITWEWGVAIGCTLLFL
            **:***:****************************************************

CaEna1p     LGAELWKWGKRIISRTAKASNPEYELERNDPFQKYAS----------
CdEna1p     LGAEVWKWGKRIISRTAKASNPEYELERNDPFQKYASFSKSNTMVVV
            ****:*********************************
```

Figure 5.5. Sequence alignment of the *C. albicans* and *C. dubliniensis* Ena1p proteins, taken from the *C. albicans* CandidaDB (http://genolist.pasteur.fr/CandidaDB/) and the *C. dubliniensis* genome sequence (http://www.sanger.ac.uk/Projects/C_dubliniensis/). The *C. dubliniensis* Ena1p shares 94.8 % sequence similarity with the *C.albicans* Ena1p protein.

recombinant plasmids, p*CdENA21.3* and p*CaENA21.3* as probes (section 5.3.2). An *ENA21.3* transcript of approximately 3.2 kb was produced by all of the three transformants tested (CAI-4-pRM1, CdUM1B-pRM1 and CdUM1B-pRM1-15) during growth in SC Ura$^-$ broth at 37°C (Fig. 5.6). Prior to osmotic shock, basal levels of *ENA21.3* relative to *TEF3* expression were lower in CdUM1B-pRMI compared to basal levels of CAI4-pRM1 and CdMU1B-pRMI-15. Elevated levels of *CaENA21.3* expression were detected in CAI-4-pRM1 following 30 min of osmotic shock (2-fold) and increased in intensity after 60 min (3-fold). In contrast, the *C. dubliniensis* transformants CdUM1B-pRMI and CdUMIB-pRMI-15 did not show an increase in *ENA21.3* mRNA levels in response to osmotic shock treatment (Fig. 5.6). However, CdMU1B-pRM1 expressed a lower level of *ENA21.3* compared to CdMU1B-pRM1-15 throughout the 30 min time course of osmotic shock treatment (Fig. 5.7). These results suggest that the NaCl resistant phenotype is due to increased expression of *ENA21.3* in CdUM1B-pRM1-15 compared to the low levels of expression seen in CdMU1B-pRM1, which also seems to decrease following osmotic shock.

In order to further investigate if the *in vitro* expression in YNB broth supplemented with 1 M NaCl of the *C. dubliniensis ENA21.3* gene was similar to that exhibited by the *C. albicans ENA21.3* gene, Northern blot analysis of total cellular RNA extracted from *C. dubliniensis* strain CD36 which is a representative of *C. dubliniensis* Cd25 fingerprint group I (genotype I) and *C. dubliniensis* strain CD514, a strain representative of Cd25 fingerprint group II (genotype 3) (Gee *et al.*, 2002) and *C. albicans* isolates 132A and SC5314 was performed. The expression of *CdENA21.3* and *CaENA21.3* was analysed using the purified DNA inserts contained within recombinant plasmids p*CaENA21.3* and p*CdENA21.3* as probes. An *ENA21.3* transcript of approximately 3.2 kb was expressed by both *C. albicans* and *C. dubliniensis* strains during the mid-exponential phase of growth at 37°C in YNB broth and was detected during all stages of an osmotic shock of 1M NaCl. (Fig. 5.8). *C. albicans* strains 132A and SC5314 both expressed increased levels of *CaENA21.3* mRNA following 20 min of osmotic shock (Fig. 5.9), returning to normal levels following 60 min of incubation. *CdENA21.3* mRNA levels in *C. dubliniensis* CD36 were induced by an osmotic shock of 1 M NaCl (3-fold) following 10 min of incubation, and the signal reached a peak intensity after 20 min (5.5-fold). This was in contrast to the response of the *C. dubliniensis*

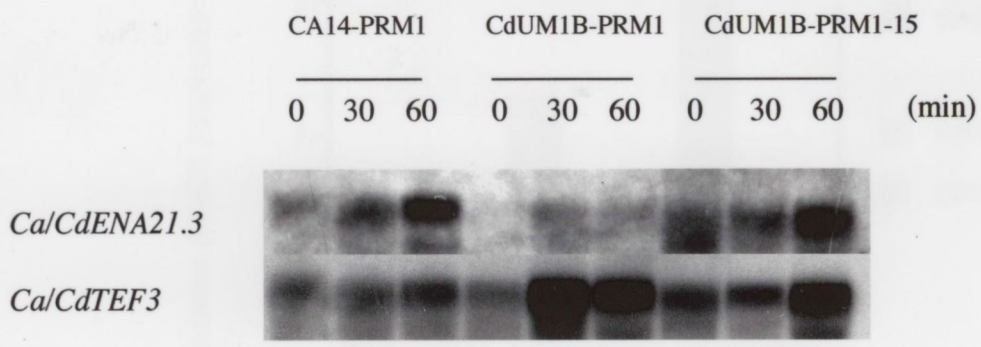


Figure 5.6. Northern hybridisation analysis of the gene *ENA21.3 in C. albicans* CAI4 transformant harbouring pRM1 plasmid (CAI4-PRM1) and *C. dubliniensis* CdUM1B harbouring pRM1(CdUM1B-pRM1) and clone pRM1-15 (CdUM1B-pRM1-15) following an osmotic shock of 1 M NaCl. Transformant cells were grown to mid-exponential phase in SC Ura^- broth at 37°C. RNA was extracted from cells harvested just before osmotic shock, after 30 and 60 min incubation at 37°C. Aliquots containing 20 µg of RNA were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blot was probed with equal volumes of the radiolabelled cloned amplimers *CdENA21.3* and *CaENA21.3*. The constitutively expressed *TEF3* gene was used as a positive control.

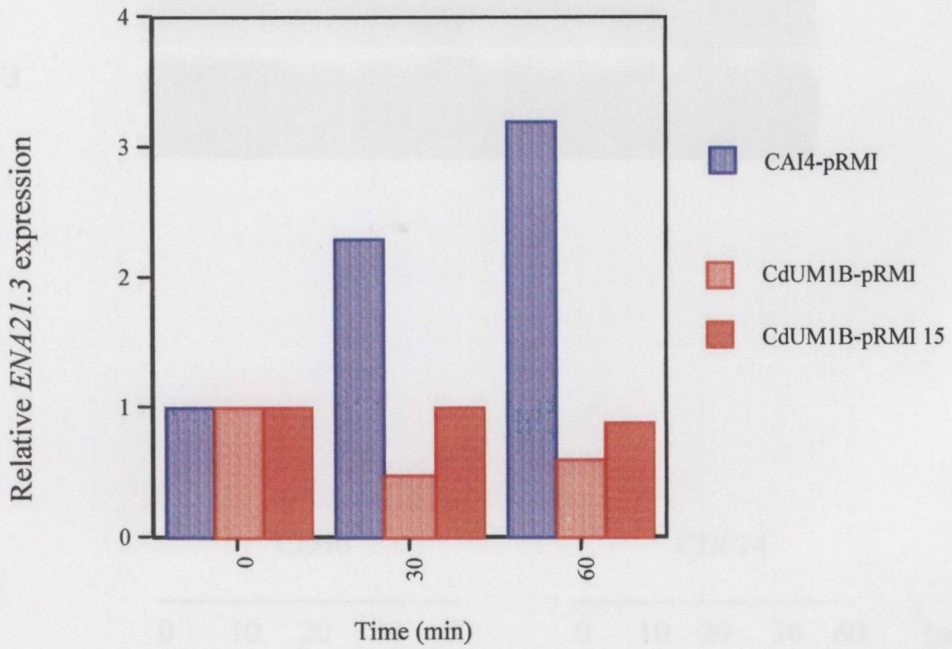


Figure 5.7. Relative increase in expression of the *ENA21.3* gene in *C. albicans* CAI4 transformant harbouring pRM1 plasmid (CAI4-pRM1) and *C. dubliniensis* CdUM1B harbouring pRM1 (CdUM1B-pRM1) and clone pRM1-15 (CdUM1B-pRM1-15) following an osmotic shock of I M NaCl. Transformant cells were grown to mid exponential phase in SC Ura-broth at 37°C. RNA was extracted from cells harvested just before osmotic shock, after 10, 20, 30 and 60 min incubation at 37°C. An aliquot containing 20 µg of RNA was electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blot was probed with equal volumes of the radiolabelled cloned amplimers *CdENA21.3* and *CaENA21.3*. The constitutively expressed *TEF3* gene was used as a positive control. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

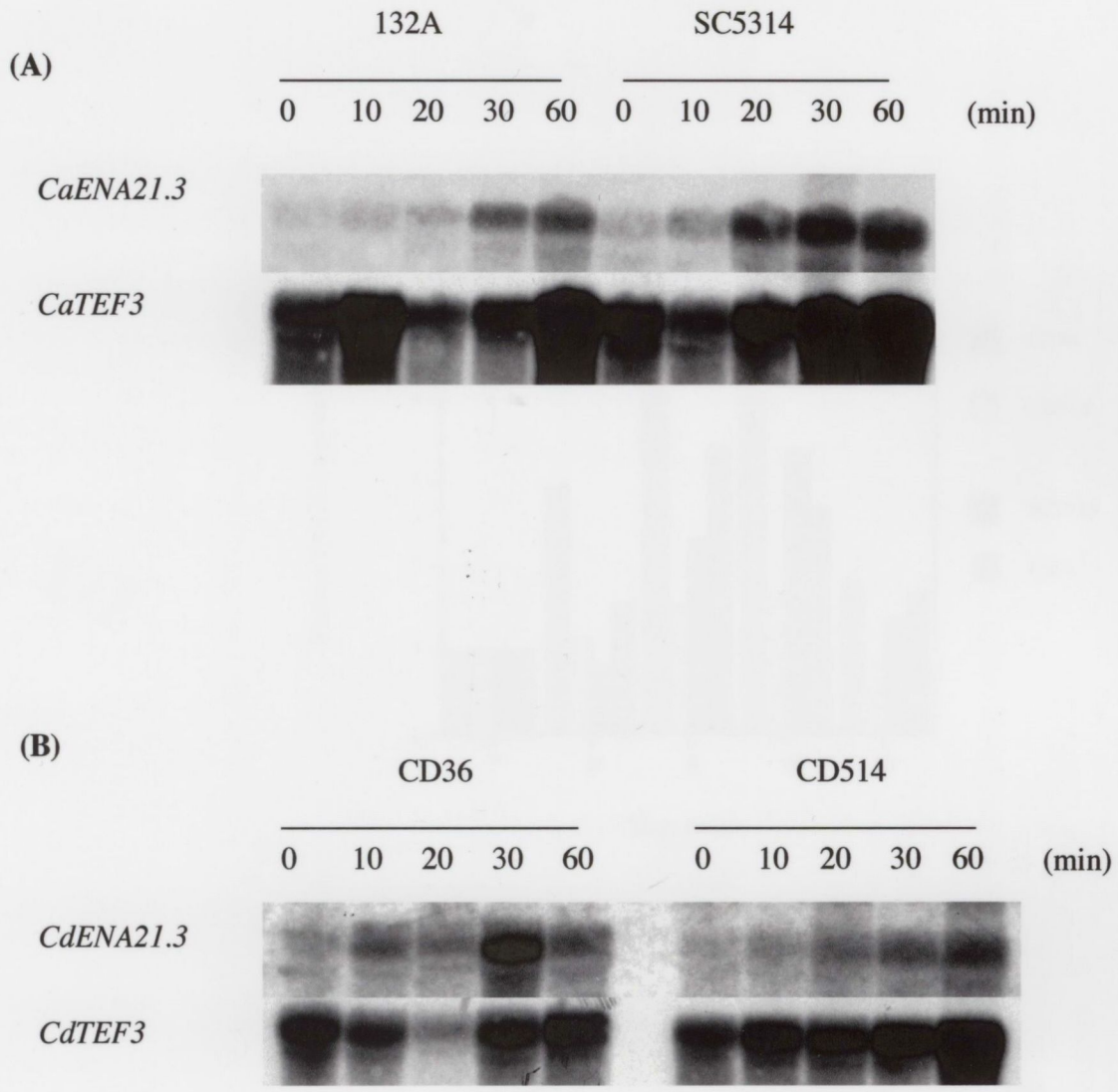


Figure 5.8. Expression of the *ENA21.3* gene by *C. albicans* strains SC5314 and 132A **(A)** and *C. dubliniensis* strains CD36 and CD514 **(B)** detected by Northern hybridisation. Total RNA was extracted from cells grown in YNB supplemented with 1 M NaCl for 10, 20, 30 and 60 mins at 37°C, and 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were sequentially probed with radiolabelled cloned amplimers *CaENA21.3* **(A)**, *CdENA21.3* **(B).** The constitutively expressed *TEF3* gene was used as an internal control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression.

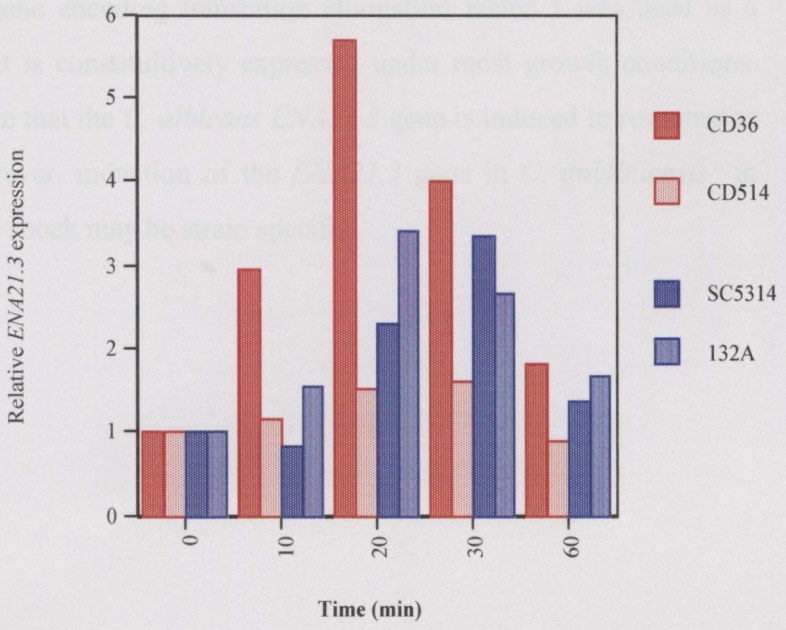


Figure 5.9. Relative increase in expression of the *ENA21.3* gene in *C. albicans* and *C. dubliniensis* following an osmotic shock of I M NaCl. *Candida albicans* isolates 132A and SC5314 and *C. dubliniensis* isolates CD36 and CD514 cells were grown to mid exponential phase in YNB broth at 37°C. RNA was extracted from cells harvested just before osmotic shock, after 10, 20, 30 and 60 min incubation at 37°C. Aliquots containing 20 µg of RNA were run on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the Northern blots were probed with an equal mixture of the radiolabelled cloned amplimers *CdENA21.3, CaENA21.3.* Expression of *TEF3* gene was used as a positive control. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression

transformants CdUM1B-pRMI and CdUMIB-pRMI-15 under similar osmotic conditions (Fig. 5.6). *C. dubliniensis strain* CD514 was found to exhibit low levels of expression of *CdENA21.3* compared to *C. dubliniensis* isolate CD36. Expression of the gene encoding translation elongation factor 3 was used as a positive control as it is constituitively expressed under most growth conditions. These results indicate that the *C. albicans ENA21.3* gene is induced in response to osmotic shock, however, induction of the *ENA21.3* gene in *C. dubliniensis* in response to osmotic shock may be strain specific.

5.4 Discussion

Yeasts have developed extrusion systems to keep levels of sodium below concentrations harmful to the cell. The best studied system is that of *S. cerevisiae*. In *S. cerevisiae* the main sodium efflux system is encoded by the *ENA* genes. The *ENA/PMR2* gene cluster of *S. cerevisiae* is comprised of four to five genes (termed *ENA1*, *ENA2* etc.) encoding nearly identical proteins. The *ENA1* gene is the most important and best studied component of this system and has been shown to be essential for salt tolerance in yeast (Haro *et al.*, 1991). It has been previously shown that in *S. cerevisiae* increased expression of the *ENA1* gene in response to salt-induced osmotic shock is a crucial cellular response (Serrano, 1996). In *S. cerevisiae* there is also an uninduced homologue of the *ENA1* gene, named *ENA2* (Garciadeblas *et al.*, 1993). A recent study using transcriptional profiling to investigate the response of *C. albicans* to various stresses found that the *ENA1* gene of *C. albicans* increased in expression in response to an osmotic shock of 0.3M NaCl (Enjalbert *et al.*, 2003). The study concluded that based on the expression profiles obtained, both of the *C. albicans ENA* genes (*ENA1* and *ENA2)* behave like the *ENA1* gene of *S. cerevisiae*.

In the present study the *C. albicans ENA21.3* gene was identified by functional complementation using a *C. albicans* genomic library. This library was used to isolate genes in *C. albicans* by complementation of the NaCl sensitive phenotype of the *C. dubliniensis* strain CdUM1B. Analysis of the transformants obtained led to the identification of a single clone. Sequence analysis of the DNA insert contained within pRM1-15 revealed that it was comprised of the coding region and the 5' flanking sequence of the *C. albicans ENA21.3* gene. The salt-tolerant phenotype observed was confirmed by a spot plate assay carried out on SC Ura^- medium containing fixed concentrations of NaCl. At a NaCl concentration of 7%, the transformant CdUM1B-pRMI showed severe growth inhibition compared to the transformants CAI4-pRMI and CDMUB-pRMI-15. It was therefore concluded that the insertion of the clone pRMI-15 was responsible for the NaCl resistant phenotype observed in CdUM1B-pRMI-15.

It has been shown previously that *C. albicans* is better able to withstand salt-induced osmotic stress than *C. dubliniensis* (Alves *et al.*, 2002). Following

identification of the *C.albicans ENA21.3* gene using functional complementation, it was reasoned that the *ENA21.3* gene may be responsible for *C. albicans* enhanced ability to survive under conditions of osmotic stress, compared to *C. dubliniensis*. Thus, in an attempt to further investigate the role of *ENA21.3* it was decided to investigate if a homologue of this gene is present and expressed in *C. dubliniensis.*

Sequence analysis of a 527 bp amplimer from the putative *C. dubliniensis ENA21.3* gene showed 93.8 % homology at the nucleotide level (representing 16.5 % of total gene length) with the corresponding region of the *C. albicans ENA21.3* gene. These findings provided convincing evidence that the cloned 527 bp DNA insert in plasmid p*CdENA21.3* was from the putative *C. dubliniensis ENA21.3* gene. The recent availability of the *C. dubliniensis* genome sequence data has since, facilitated the annotation of the *C. dubliniensis ENA21.3* gene, which shares 94.8 % sequence homology to the *C. albicans ENA21.3* at the protein level.

Northern blot analysis on the transformants CAI4-pRM1, CdUM1B-pRM1 and CdUM1B-pRM1-15 cells under osmotic shock conditions revealed that following 30 min of osmotic shock CA14-pRM1 showed an increase in the level of *CaENA21.3* expression whereas, the *C. dubliniensis* transformants CdUM1B-pRM1 and CdUM1B-pRM1-15 did not show any increase in *ENA21.3* mRNA expression, in contrast to the genotype I *C. dubliniensis* strain CD36 which showed an increase in *ENA21.3* mRNA expression after 10 min under the same conditions (Fig. 5.8). However, CdMU1B-pRM1 expressed a lower level of *ENA21.3* compared to CdMU1B-pRM1-15 following 30 min of osmotic shock treatment. This data suggests that the NaCl resistant phenotype observed was due to the increased expression of *ENA21.3* in CdUMIB-pRM1-15. Increased expression may be due to multiple copies of pRM1-15 plasmid, or perhaps additionally the *C. albicans ENA21.3* gene is transcribed more efficiently than the *C. dubliniensis ENA21.3* gene.

Examination of the expression of the *ENA21.3* gene in wildtype strains of both *C. albicans* and *C. dubliniensis* revealed that both species express this gene during exponential growth at 37°C in YNB medium. In YNB supplemented with 1 M NaCl, like CA14-pRM1 (Fig. 5.6) both of the *C. albicans* wildtype strains 132A and SC5314, showed induction of *CaENA21.3* mRNA, but following 20 min of osmotic shock and returned to normal levels following 60 min of

incubation (Fig. 5.8). Unlike the *C. dubliniensis* transformants CdUM1B-pRM1 and CdUM1B-pRM1-15, *CdENA21.3* mRNA was induced in *C. dubliniensis* CD36 by an osmotic shock of 1 M NaCl (3-fold) following 10 min of incubation, and the signal reached a peak intensity after 20 min (5.5-fold) which was higher than that observed in both of the *C. albicans* strains (2.5-3.5- fold, respectively). The *C. dubliniensis strain* CD514 was found to exhibit low levels of expression of *CdENA21.3* compared to *C. dubliniensis* isolate CD36. The expression of *ENA21.3* was induced slightly following 20 min of osmotic shock in the *C. dubliniensis* isolate CD514 (1.5-fold). These results indicate that a homologue of the *C. albicans* gene *ENA21.3* is present and expressed in *C. dubliniensis* in response to salt-induced osmotic shock, however, induction of the *ENA21.3* gene in *C. dubliniensis* in response to osmotic shock may be strain specific. It was observed that, unlike the *C. dubliniensis* wildtype strains, the *C. dubliniensis* transformants CdUM1B-pRM1 and CdUM1B-pRM1-15, did not induce *ENA21.3* mRNA levels following an osmotic shock of 1 M NaCl. A possible explanation for this could be that these strains with interupted genes (i.e. Ura^- strains) may differ in their tolerance to salt due to differences in their nutritional requirements. The existence of a homologue of the *ENA21.3* gene in *C. dubliniensis* and its ability to induce the gene in response to salt-induced osmotic stress weakens the hypothesis that the *ENA21.3* gene is responsible for *C. albicans* enhanced ability to survive in high salt environments compared to *C. dubliniensis.* However, a possible explanantion for the reduced salt tolerance of *C. dubliniensis* compared to *C. albicans*, may lie in the post-translational regulation of their P-type ATPases, which perhaps when expressed under identical conditions might display different tolerances to Na^+ ions i.e. the activities or ion affinities of these pumps may differ under specific conditions in both species.

Chapter 6

Comparative analysis of global gene expression in the response of *C. albicans* and *C. dubliniensis* to heat, osmotic and oxidative stress

6.1 Introduction

From the data previously described in this study it is clear that in comparison with *C. albicans*, *C. dubliniensis* is less able to survive, thermal, osmotic and oxidative stress (H_2O_2), thus, strengthening the hypothesis that more effective environmental stress responses in *C. albicans* may contribute to its prominent virulence compared to *C. dubliniensis*. However, when conventionally recognised yeast stress response mechanisms i.e. heat shock proteins and trehalose metabolism, were investigated there was no significant difference found between the two species. Since no major differences in the commonly studied stress response mechanisms were observed, it was decided to exploit the recently available *C. dubliniensis* genome data to investigate whether there are stress response genes that are absent or differentially expressed in *C. dubliniensis*.

During the course of this project microarrays corresponding to the entire *C. albicans* complement of 6,039 open reading frames became available. Recently, these *C. albicans* DNA microarrays, constructed by Eurogentec based on the Galar Fungail consortium's annotation of the *C. albicans* SC5314 genome sequence in the CandidaDB (http://www.pasteur.fr/Galar_Fungail/CandidaDB/) have been used in a comparative genomic hybridisation study performed between *C. albicans* and *C. dubliniensis* (Moran *et al.*, 2005). In this study *C. albicans* and *C. dubliniensis* total genomic DNA was co-hybridised to *C. albicans* DNA microarrays and the hybridisation efficiency of the *C. albicans* and *C. dubliniensis* DNA to each gene spotted on the microarray was compared. Only 4.4 % (247 genes) of C. *dubliniesis* genomic DNA was found to hybridise poorly to *C. albicans* gene-specific spots on the microarrays, whereas 95.6 % of the *C. dubliniensis* genomic DNA hybridised efficiently and reproducibly. This indicated that it was feasible to use *C. albicans* DNA microarrays, to investigate the global expression of genes in *C. dubliniensis*, under specific stress conditions using *C. dubliniensis* cDNA. Thus, with the availability of the *C. albicans* DNA microarrays and completion of the *C. dubliniensis* genome sequence more global questions can be addressed, in particular, global analysis of changes in gene expression in response to stress can be investigated.

Global transcriptional profiling has been previously used to examine the stress responses of *C. albicans* and revealed the absence of core stress response

under similar environmental conditions known to induce core stress responses in both *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001) and *S. pombe* (Chen *et al.*, 2003) However, Smith *et al.*, (2004) suggested that a SAPK–dependent core stress response adapted to aid in its pathogenicity does exists in *C. albicans*.

There is little or no information available about the stress response mechanisms of *C. dubliniensis*. Therefore the main objective of this study was to further investigate the species-specific response of *C. albicans* and *C. dubliniensis* to environmental stresses by providing a comprehensive comparative analysis of the cellular responses of both these species to specific stresses in particular heat, osmotic and oxidative stress. Hence in this study gene expression profiling was used to compare the global expression of genes in *C. albicans* and *C. dubliniensis* in response to heat, osmotic and oxidative stress conditions. It was hoped that comparing the genome-wide expression profiles of both these species would facilitate the identification of genes or gene families responsible for the species-specific response to environmental stress and perhaps explain the lower stress tolerance of *C. dubliniensis* compared to *C. albicans*, thereby possibly explaining why *C. dubliniensis* is less pathogenic.

6.2 Materials and Methods

6.2.1 Culture conditions

Cultures of *C. albicans* strain SC5314 and *C. dubliniensis* were grown in YPD.

For each stress, cultures were inoculated from a fresh colony and grown overnight in YPD at 30°C. These were then diluted to an $OD_{600\ nm}$ of 0.1 in 250 ml of YPD and grown at 30°C to an $OD_{600\ nm}$ of 1.0. The culture was divided into two aliquots one for use as a control and the other as the experimental sample. Fifty millilitre aliquots were removed at time 0 (control) and time 30 min after initiation of the heat, osmotic and oxidative shock and then harvested for 3 min at 3000 x *g*. The supernatant was removed and the pellets were resuspended in the residual supernatant (approximately 200 µl). A 50 ml Falcon tube was filled with approximately 10 ml of liquid N_2 and small drops of cell suspension were carefully and slowly released into the liquid nitrogen in the Falcon tube, to prevent the drops from merging. Once all the liquid N_2 had evaporated the frozen cell drops were stored at –80°C,

For the heat shock experiments, the cells were transferred from 30-42°C by immersing the sample in a waterbath. To create the hyperosmotic shock, NaCl was added directly to the medium to generate a 1.0 M final concentration. Hydrogen peroxide (H_2O_2) was used to create the oxidative stress and was added to the medium in order to obtain a final concentration of 5 mM. Each stress experiment was repeated four times.

6.2.2 DNA microarrays

C. albicans DNA microarrays used in this study were constructed by Eurogentec, Seraing, Belgium, based on the Galar Fungail consortium's annotation of the *C. albicans* SC5314 genome sequence in CandidaDB (http://www.Pasteur.fr/Galar_Fungail/ CandidaDB/). Each glass slide contained sequences corresponding to 6039 ORFs that were approximately 300 bp in length and printed in duplicate.

6.2.3 Isolation of RNA

The methods used for RNA isolation, cDNA preparation and hybridization were adapted from those used by the Galar Fungail Consortium. A 5 ml Teflon vessesl (Sartorious BBI Systems, Epsom, UK) and a 7 mm tungsten carbide bead (Sartorious BBI Sysytems) were soaked in RNase Away (Molecular Bioproducts, San Diego, CA, USA), dried and then pre-cooled in liquid N_2. The frozen cell drops and the carbide bead were placed in the Teflon vessel and fastened tightly. The Teflon vessel was inserted into the Mikro-Dismembrator U (B. Braun Biotech International) and shaken for 2 min at 2000 rpm. Shaking was repeated if there were any un-powdered clumps remaining. The powder was then resuspended immediately in 2 ml of TRIzol® reagent (Invitrogen). This suspension was transferred into two microcentrifuge tubes and vortexed for 15 s. The microcentrifuge tubes were then left for 5 min at room temperature to allow the dissociation of the nucleoprotein complexes and centrifuged for 10 min at 12,000 x *g*. The supernatant was tipped into new microcentrifuge tubes and 0.42 ml of chloroform was added. The samples were then shaken vigorously by hand for 15 s, left at room temperature for 5 min and centrifuged for 10 min at 12,000 x *g*. The aqueous layer (800 µl) was transferred carefully into new microcentrifuge tubes, making sure to avoid the interphase, and 0.4 ml of isopropanol was added to precipitate the RNA, for 10 min at room temperature. The supernatant was carefully removed following a 10 min centrifugation at 12000 x *g* and the resulting pellets were washed with 0.5 ml ice-cold 70 % ethanol. The samples were air dried briefly and centrifuged for a further 10 min at 12000 x g. The RNA pellets were again briefly air dried and resuspended in 500 µl of DEPC-treated H_2O using a pipette. Five hundred microlitres of LiCl buffer (4 M LiCl, 20 mM Tris-HCl pH 7.4, and 10 mM EDTA pH 8.0) was added to the samples, vortexed and left to precipitate for at least 1 h or overnight at -20°C. The samples were then centrifuged for 30 min at 14000 rpm at 4°C. The resulting pellets were washed with 1 ml of ice-cold 70 % ethanol and centrifuged for a further 10 min at 14,000 rpm. The pellets were washed again with 500 µl of ice-cold 70% ethanol and centrifuged for 10 min at 14000 rpm. Any residual ethanol was removed using a pipette. The pellets were then air-dried and duplicate samples were pooled and resuspended in a 50 µl, final volume of DEPC-treated H_2O. To calculate the concentration of the RNA, the $OD_{260\ nm}$ and $OD_{280\ nm}$ was measured

for a 1/ 1000 dilution of the RNA in a quartz cuvette. An $OD_{260\ nm}$ of 1.0 is equivalent to 40 µg/µl of RNA. Purity of the RNA was also checked by calculating the ratio of $OD_{260\ nm}$: $OD_{280\ nm}$. Pure RNA has an $OD_{260\ nm}$: $OD_{280\ nm}$ ratio of 1.9-2.1.

6.2.4 Preparation of Labelled cDNA

Each labelling reaction was carried out using 50 µg (12 µl final volume) of RNA which was added to 8 µl of oligo dT(of 0.5µg/µl; Promega) in an RNase free Eppendorf tube and was made up to a final volume of 10 µl with DEPC-treated H_20. This mixture was incubated for 10 min at 70°C and then left on ice for 1 min. Thirty microlitres of a labelling mastermix (1x RT buffer; Invitrogen, 10 µm 0.1 MDTT; Invitrogen, 500 µM each of dATP, dCTP and dGTP, 100 µM dTTP and DEPC-treated H_20 to a volume of 30 µl) was added to this mixture and 6 µl of either Cy®3-dUTP or Cy®5-dUTP (Amerscham Biosciences, Europe). The Cyanine fluorescent dyes are light sensitive and so were protected from direct light as much as possible. The reverse transcription reaction was done at 42°C for 2 h after addition of 4 µl of Superscript™ II RNase H^- Reverse Transcriptase (200 U; Invitrogen). After 2 h, an additional 2 µl of Superscript II was added to the mixture which was further incubated at 42°C for 1 h. The mixture was centrifuged briefly to collect the contents at the bottom of the Eppendorf tube. The reaction was stopped and RNA degraded by the addition of 3 µl of 20 mM EDTA pH 8.0 and 3 µl of 500 mM NaOH and incubation at 70°C for 10 min. The reaction was neutralised with the addition of 3 µl of 500 mM HCl. To purify the cDNA, a Cy3-labelled sample and 69 µl of the corresponding Cy5-labelled sample that will be co-hybridised with it, were added to 500 µl Capture Buffer in a GFX purification column (GFX gel band purification kit, Amerscham Biosciences). The column was centrifuged at 14,000 rpm for 30 s. The contents of the collection tube were discarded and 500 µl of Wash buffer was added to the column. Following centrifugation at 14,000 rpm for 30 s the column was transferred to a new microcentrifuge tube 30 µl of sterile H_2O was added to the column which was left to incubate for 1 min at room temperature. The column was then centrifuged for 1 min at 14,000 rpm and was then discarded. Labelled cDNA samples produced a tinge of blue/ red colour at this point.

6.2.5 Hybridisation of Microarrays

Microarray slides (Eurogentec) were prehybridised at 42°C for at least 1 h, with 50 µl of a prehybridisation solution containing 5x SSC, 0.1 % SDS, 1 % BSA (Sigma) and DEPC-treated H_2O. The microarray slides were covered with 22 x 50 mm glass Lifter slip (Erie Scientific Company, Portsmouth, NH, USA) during all hybridisation steps, and a high humidity level was maintained in the hybridisation chamber by placing wet pieces of paper towels in the lower part of the chamber. After prehybridisation, the prehybridisation buffer was removed by washing the DNA microarray slides three times in 50 ml of milipore H_2O. After three washes each slide was placed carefully into an empty falcon tube and centrifuged at 2000 x *g* for 5 mins to dry the slides. Hybridisation was as follows: 30 µl of Hybridisation mix containing 10x SSC, 50 % formamide and 10% SDS was added to 30 µl of the purified Cy3 and Cy5 labelled cDNA mix. This hybridisation solution was heat denatured for 3 min at 100°C, centrifuged briefly to collect the contents at the bottom, and then placed on ice for 2 min. Immediately before hybridisation the DNA microarray slides, glass Lifter slips (Erie Scientific Company) and hybridisation solution were incubated at 42°C for approximately 15 min. Fifty microlitres of hybridisation mixture was then carefully spotted onto the middle of the printed part of the microarray slide and a prewarmed 22 x 50 mm glass Lifter slip (Erie Scientific Company) was carefully placed on top. The hybridisation chamber was sealed and incubated overnight, in the dark at 42°C. Afterward, the slides were carefully removed from the hybridisation chamber using a forceps and placed in Falcon tubes containing 50 ml of wash buffer. The coverslips were carefully removed before washing at room temperature for 15 min with 2x SSC, 1 % SDS, for 8 min with 1x SSC, 0.2 % SDS, and for 5 min with 0.1x SSC, 0.2 % SDS and, finally, dipping once into a Falcon tube filled with 50 ml of Millipore H_2O. All washes were carried out in the dark with gentle agitation by inverting the Falcon tubes ~2 min per rinse. Slides were placed immediately into empty 50 ml Falcon tubes and spin-dried at 2000 x g for 5 min. The slides were stored protected from light and scanned immediately. Each of the hybrdisations performed were carried out on 4 separate occasions. Two of the four hybridisations were performed with the Cy3 and Cy5 dyes swapped.

6.2.6 Data analysis

The DNA microarray slides were scanned using a ScanArray®Lite scanner (Perkin Elmer LifeSciences, Beaconsfield, UK). An initial scan was carried out at a resolution of 50 μm and the final scan at 10 μm. The 16-bit TIFF files obtained were quantified using QuantArray software version 2.0 (Perkin Elmer LifeSciences). Quantarray (Perkin Elmer LifeSciences) was used to locate spots on the microarray and "flagged" (ignored) any spots with smears of dye or dust as such spots can interfere with subsequent analysis by artificially increasing the signal intensity of the spot. Data extracted using Quantarray (Perkin Elmer LifeSciences) were exported as text files. The text files were then imported into Genespring 6.1 (Silcon genetics, Redwood City, CA) for subsequent analysis. Dye swap, and per chip and per spot normalisations were carried out using Lowess intensity dependent normalisation. Expression ratios were calculated by comparing stressed cells with their unstressed control. To identify the statistical significance of these expression ratios, normalised data were exported from Genespring (Silicon genetics) into an Excel file and statistical analysis was performed using SAM (Significanc Analysis of Microarrays: Tusher *et al.*, 2001). This programme uses a Student's t-test, modified to cope with very large sample numbers, to create a list of genes that are significantly regulated. Data from four independent biological replicates, transformed to $\log_2$, was analysed using "one class (paired data) response analysis". The SAM False Discovery Rate (FDR) was set at < 10 %. The FDR is the percentage of genes identified by chance. These gene lists were imported back into Genespring (Silcon genetics) to carry out further analysis such as filtering on expression levels, clustering or generation of Venn diagrams. Hierarchical clustering (Eisen *et al.*, 1998) of the above genes was done in Genespring using their default conditions.

C. albicans gene annotations were obtained from CandidaDB (http://genolist pasteur.fr/CandidaDB). *C. albicans* genes with *S. cerevisiae* homologues were assigned SGD Functional Categories (http:// www.yeastgenome.org/). Gene lists and their expression profiles are located in Appendix II.

6.2.7 PCR amplification of *C. albicans* and *C. dubliniensis* genome sequences

PCR amplification from *C. albicans* SC5314 and *C. dubliniensis* CD36 genomic DNA templates were carried out as described in section 2.4.2. using the oligonuleotide primers described in Table 2.2.

6.3 Results and Discussion

In this study *C. albicans* DNA microarrays were used to compare the transcriptional profiles of *C. albicans* and *C. dubliniensis* under specific heat, osmotic and oxidative stress conditions in an attempt to identify gene(s) that may contribute to the differences in environmental stress tolerance and perhaps in turn, the differences in virulence observed between these two organisms.

The stress conditions used in this study; a heat shock of 30-42°C, an osmotic shock of 1.0 M NaCl and an oxidative shock created by the addition of H_2O_2 to a final concentration of 5 mM H_2O_2, were chosen specifically as under these conditions *C. dubliniensis* has a reduced tolerance compared to that of *C. albicans*. In addition, stressed samples were examined at the 30 min time point under each of these conditions as both *C. albicans* SC5314 and *C. dubliniensis* CD36 percentage viabilities were greater than 60 % (Fig. 3.3).

The graphical representation in Figure 6.1 reveals that the heat, osmotic and oxidative stress conditions used in this study had a significant effect upon the transcriptional responses of *C. albicans* and *C. dubliniensis*. Expression levels changed significantly in both species in response to all three stresses inferring that both species can sense and respond to these specific environmental changes. However, the magnitude of the transcriptional responses varied between both species, for each stress condition. The *C. albicans* transcriptional response to heat shock was notably weaker than its response to osmotic and oxidative stress and interestingly, the number of genes induced or repressed by heat was lower than those observed in the heat shock response of *C. dubliniensis* (Figs 6.2 and 6.3). Oxidative stress and heat stress triggered the largest expression changes in *C. dubliniensis* and the number of genes involved in both these stresses were relatively similar (Figs 6.2 and 6.3). However, the *C. dubliniensis'* transcriptional response to osmotic stress (1 M NaCl) was much weaker than the responses to the other two stresses. In addition, the proportion of genes involved in the osmotic response of *C. dubliniensis* was much lower than that of *C. albicans* (Figs 6.2 and 6.3). Moreover, while oxidative stress led to the strongest expression changes in both species, the number of genes induced or repressed in *C. albicans* oxidative response was significantly higher than that of *C. dubliniensis* (Figs 6.2 and 6.3).

(a) **(b)**

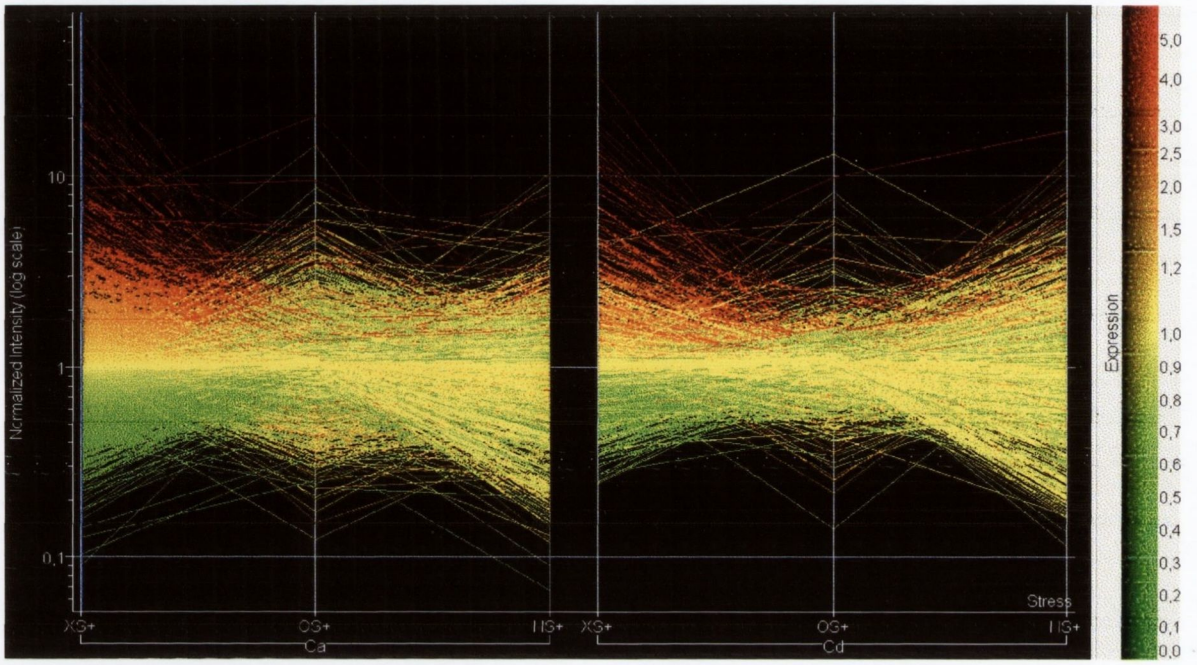


Figure 6.1. *Candida albicans* **(a)** and *Candida dubliniensis* **(b)** global transcriptional response to heat (HS), osmotic (OS) and oxidative (XS) stress. Each line represents the effect of a heat (30-42°C), osmotic (1 M NaCl) and oxidative (5 mM H_2O_2) stress upon the expression of a gene, coloured according to the expression level. Results presented represent the average of 4 independent experiments. Genes with significant changes in transcript level at a 30 min timepoint compared to control were identified using SAM with an FDR (false discovery rate) of <10%. The (X) axis represents the stress conditions.

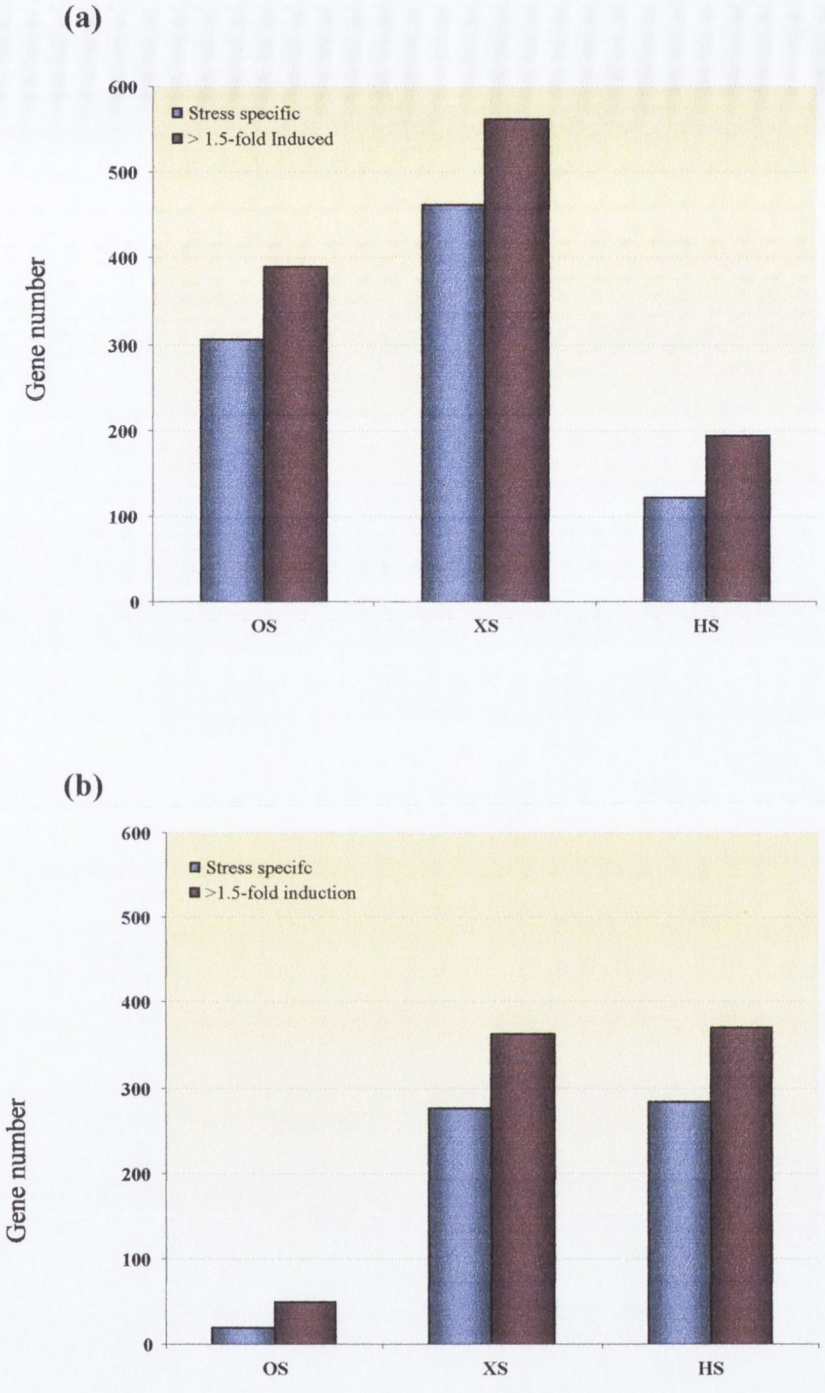
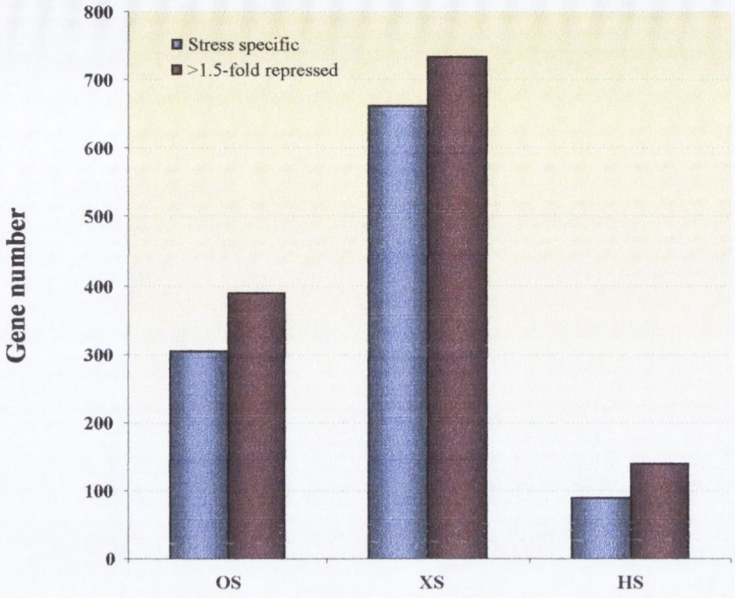


Figure 6.2. Induction of gene expression in response to stress in *C. albicans* **(a)** and in *C. dubliniensis* **(b).** The graph shows the numbers of genes that are significantly induced at least 1.5-fold, together with the number of stress-specific genes for the heat, osmotic and oxidative stress experiments.

(a)



(b)

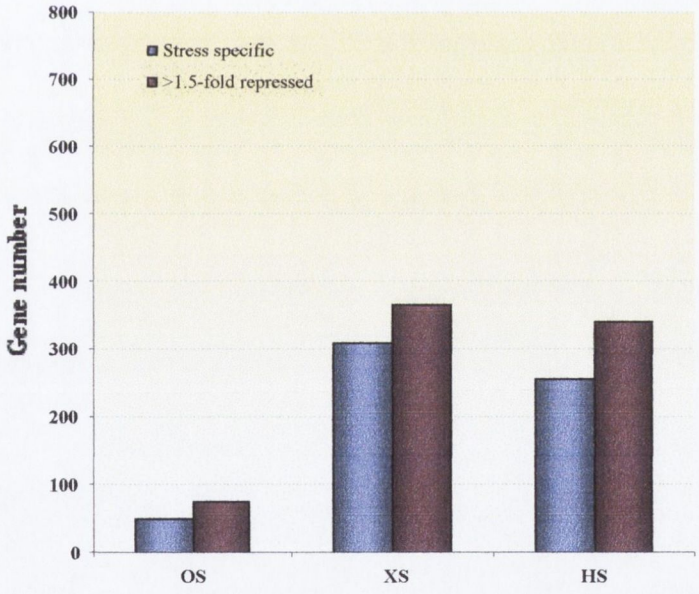


Figure 6.3. Repression of gene expression in response to stress in *C. albicans* **(a)** and in *C. dubliniensis* **(b).** The graph shows the numbers of genes that are significantly down-regulated at least 1.5-fold, together with the number of stress-specific genes for the heat, osmotic and oxidative stress experiments.

6.3.1 Stress specific responses of *C. albicans* and *C. dubliniensis*

Normalised data were analysed using SAM and genes with statistically significant changes in expression were imported back into Genespring. Filtering on expression level was then used to identify stress-specific response genes in each species. Stress-specific response genes were identified as genes whose expression was significantly induced or repressed at least 1.5-fold ($0.667 \leq$ fold change ≥ 1.5) in response to each specific stress condition. To confer specificity, genes significantly induced or repressed > 1.5 fold in response to the other environmental stresses were subtracted from these gene lists. Expression values refer to $\log_2$ scale.

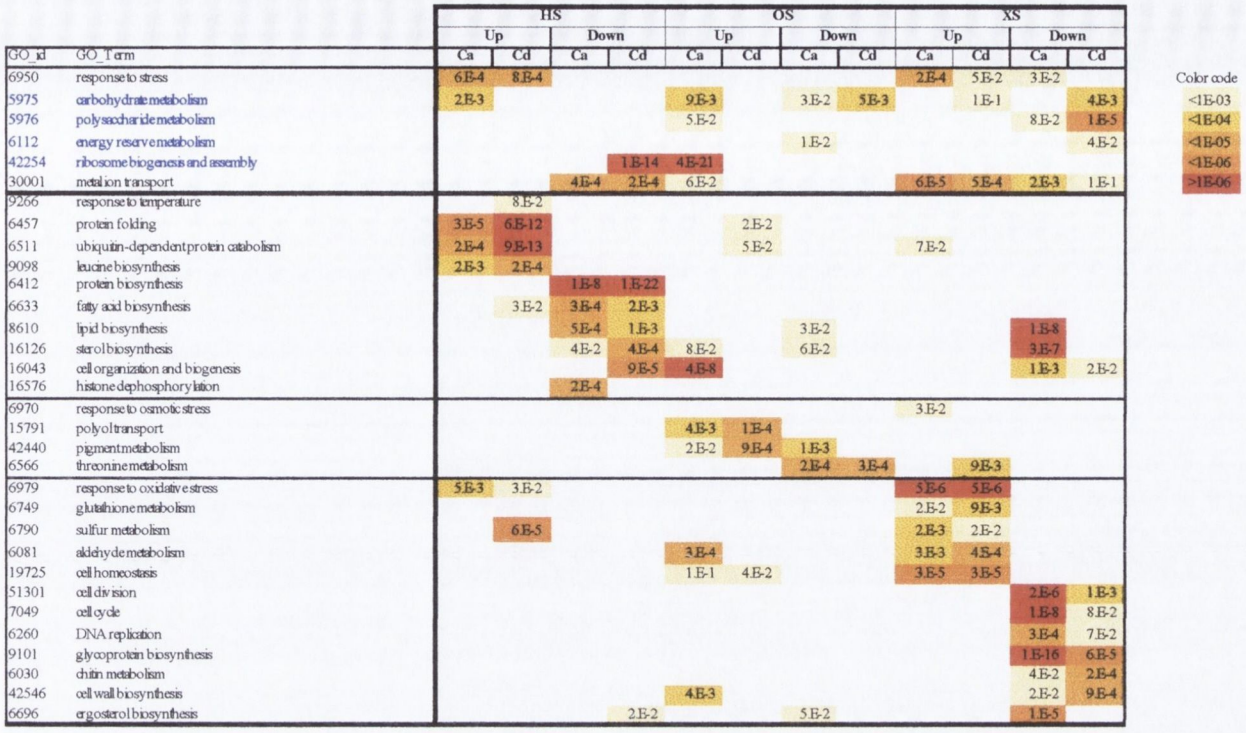
Genes displaying significant changes in expression between *C. albicans* and *C. dubliniensis* in response to each stress condition were also identified. Among the genes that were significantly induced or repressed at least 1.5-fold ($0.667 \leq$ fold change ≥ 1.5) in response to specific stress conditions in *C. albicans*, genes significantly induced or repressed at least 1.5-fold under the same stress conditions in *C. dubliniensis* were selected. Subtraction of these *C. dubliniensis* genes from the *C. albicans* gene list allowed the identification of *C. albicans*-specific differentially expressed genes. The same criterion was used to identify *C. dubliniensis*-specific differentially expressed genes.

6.3.1.1 Heat shock response

Genes whose expression was induced or repressed after a temperature shift of 30-42°C were identified in both species. In *C. albicans*, 334 genes were identified that displayed statistically significant changes in expression in response to a heat shock of 42°C for 30 min. Among these genes, 194 were significantly up-regulated and 140 genes were significantly down-regulated at least 1.5-fold. Both gene lists were filtered to remove genes significantly induced or repressed > 1.5 fold in response to the two other stress conditions used in the study i.e. osmotic and oxidative stress. Of the 194 genes significantly up-regulated at least 1.5-fold, 122 of these genes were found to be specifically up-regulated in response to a heat shock of 42°C for 30 min. Of the 140 genes significantly down-regulated at least 1.5-fold, 90 genes were identified as heat shock specific response genes. (Fig. 6.10)

Functional categories that were significantly prominent amongst genes in response to the heat stress in *C. albicans* were identified (Figure 6.4). The functional categories were based on the SGD classification of the *S. cerevisiae* homologue. Functional categories significantly prominent among *C. albicans* genes significantly up-regulated greater than 1.5-fold included "response to stress", "carbohydrate metabolism", "protein folding", "ubiquitin-dependent protein catabolism", "leucine biosynthesis" and "response to oxidative stress". Functional categories prominent among the down-regulated genes included:"metal ion transport", "protein biosynthesis", "fatty acid and lipid biosynthesis", "sterol biosynthesis" and "histone dephosphorylation". The induction of protein folding genes and protein degrading genes is consistent with the need to repair damaged proteins and degrade denatured proteins to prevent the formation of aggregates under stress conditions. In addition among the genes implicated in "oxidative stress" were genes involved in the detoxification of reactive oxidative species produced during respiration including, *TTR1*, *TRX1*, *CAP1*, *GPX2*. The enrichment of the functional category "protein synthesis" among the down-regulated genes suggests a reduction in the transcription and translation of these cells.

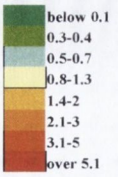
It has been previously shown that *C. albicans* is capable of responding to a rapid temperature shift from 23-37°C (Enjalbert *et al.*, 2003) which involves the induction of a set of heat shock proteins, which promote protein folding and prevent protein aggregation. Normalised data from this study for *C. albicans* cells exposed to 42°C for 30 min were compared with the normalised data obtained previously for *C. albicans* cells treated with a heat stress of 23-37°C. Expression of hallmark genes used previously by Enjalbert *et al.* (2003) as markers of the heat stress response in *C. albicans* were compared (Fig. 6.5). This revealed that *C. albicans* is capable of inducing a heat shock response at 42°C. As predicted, many of the genes up-regulated in response to a heat shock of 42°C included proteins which promote protein folding and prevent protein aggregation, including *HSP78.5f*, *HSP60*, *HSP90*, *HSP10* and *SSA4*. This set of Hsps all showed an induction greater than 2-fold in response to a heat shock of 42°C, whereas at 37°C no induction of *HSP10* was observed, *HSP78.5f*, *HSP90* and *HSP60* displayed weaker responses. However, *SSA4* showed a stronger induction (>5-fold) in response to a 37°C heat shock compared to the 42°C heat shock. Similar to the



		HS				OS				XS			
		Up		Down		Up		Down		Up		Down	
GO_id	GO_Term	Ca	Cd	Ca	Cd	Ca	Cd	Ca	Cd	Ca	Cd	Ca	Cd
6950	response to stress	6.E-4	8.E-4							2.E-4	5.E-2	3.E-2	
5975	carbohydrate metabolism	2.E-3				9.E-3		3.E-2	5.E-3		1.E-1		4.E-3
5976	polysaccharide metabolism					5.E-2						8.E-2	1.E-5
6112	energy reserve metabolism							1.E-2					4.E-2
42254	ribosome biogenesis and assembly				1.E-14	4.E-21							
30001	metal ion transport			4.E-4	2.E-4	6.E-2				6.E-5	5.E-4	2.E-3	1.E-1
9266	response to temperature		8.E-2										
6457	protein folding	3.E-5	6.E-12				2.E-2						
6511	ubiquitin-dependent protein catabolism	2.E-4	9.E-13				5.E-2			7.E-2			
9098	leucine biosynthesis	2.E-3	2.E-4										
6412	protein biosynthesis			1.E-8	1.E-22								
6633	fatty acid biosynthesis		3.E-2	3.E-4	2.E-3								
8610	lipid biosynthesis			5.E-4	1.E-3			3.E-2				1.E-8	
16126	sterol biosynthesis			4.E-2	4.E-4	8.E-2		6.E-2				3.E-7	
16043	cell organization and biogenesis				9.E-5	4.E-8						1.E-3	2.E-2
16576	histone dephosphorylation			2.E-4									
6970	response to osmotic stress									3.E-2			
15791	polyol transport					4.E-3	1.E-4						
42440	pigment metabolism					2.E-2	9.E-4	1.E-3					
6566	threonine metabolism							2.E-4	3.E-4		9.E-3		
6979	response to oxidative stress	5.E-3	3.E-2							5.E-6	5.E-6		
6749	glutathione metabolism									2.E-2	9.E-3		
6790	sulfur metabolism		6.E-5							2.E-3	2.E-2		
6081	aldehyde metabolism					3.E-4				3.E-3	4.E-4		
19725	cell homeostasis					1.E-1	4.E-2			3.E-5	3.E-5		
51301	cell division											2.E-6	1.E-3
7049	cell cycle											1.E-8	8.E-2
6260	DNA replication											3.E-4	7.E-2
9101	glycoprotein biosynthesis											1.E-16	6.E-5
6030	chitin metabolism											4.E-2	2.E-4
42546	cell wall biosynthesis					4.E-3						2.E-2	9.E-4
6696	ergosterol biosynthesis				2.E-2			5.E-2				1.E-5	

Color code
<1E-03
<1E-04
<1E-05
<1E-06
>1E-06

Figure 6.4. Functional categories significantly enchanced among up- and down-regulated *C. albicans* (Ca) and *C. dubliniensis* (Cd) genes in response to a heat shock (HS) of 30-42°C, an osmotic shock (OS) of 1 M NaCl and an oxidative shock of 5 mM H_2O_2. Functional categories were assigned based on the GO (Gene Ontology) from the SGD (*Saccharomyces cerevisiae* Genome Database). Functional categories are coloured based on their significance according to the legend.



	CA	orf19	Contig4	Cd XS+ / Cd -	Ca XS+ / Ca -	Cd OS+ / Cd -	Ca OS+ / Ca -	Cd HS+ / Cd -	Ca HS+ / Ca -	Common	Description	WT XS / WT -	WT OS / WT -	WT HS / WT -
(a)	CA3011	orf19.6229	CONTIG4-1984_0001	6.0	3.7	2.1	1.2	1.7	1.1	CTA1	catalase A, peroxisomal(by homology)	11.5	11.8	1.2
	CA4919	orf19.6059	CONTIG4-2977_0001	4.5	7.1	1.5	1.1	1.9	1.5	TTR1	Glutaredoxin (by homology)	5.5	0.9	1.4
	CA3059	orf19.4290	CONTIG4-3019_0014	4.2	6.9	1.1	1.2	1.8	1.2	TRR1	Thioredoxin reductase (by homology)	4.4	2.5	1.2
	CA6010	orf19.7611	CONTIG4-3108_0068	4.1	2.2	1.2	1.0	3.1	1.5	TRX1	thioredoxin (by homology)	4.5		1.2
	CA0183	orf19.1623	CONTIG4-2798_0003	2.2	1.4	1.1	1.5	1.9	1.5	CAP1	transcriptional acivator (by homology)	5.9	1.1	1.6
	CA2719	orf19.3340	CONTIG4-2785_0004	1.6	2.8	1.1	1.1	1.5	0.9	SOD2	Manganese-superoxide dismutase	0.8	1.1	1.2
	CA4120	orf19.2770.1	CONTIG4-3065_0005	1.5	1.2	1.1	1.0	4.8	1.4	SOD1	Cu,Zn-superoxide dismutase, 3-prime end	1.0	2.1	0.8
(b)	CA0824	orf19.691	CONTIG4-2418_0003	1.8	2.9	7.6	1.9	0.9	0.5	GPD2	Glycerol 3-phosphate dehydrogenase (by homology)	0.9	2.1	0.7
	CA0472	orf19.5753	CONTIG4-3106_0022	1.5	1.8	5.6	14.5	0.3	0.3	STL1	sugar transporter (by homology)	1.3	2.5	0.9
	CA5788	orf19.5437	CONTIG4-2896_0003	1.0	1.7	1.8	1.1	0.6	0.1	RHR2	DL-glycerol phosphatase	0.9	2.2	1.1
	CA4425	orf19.5170	CONTIG4-3092_0037	1.1	0.9	1.6	2.6	1.1	1.2	ENA21.3	P-type ATPase, 3-prime end (by homology)	1.0	1.6	1.0
	CA4929	orf19.6070	CONTIG4-2977_0027	2.3	1.1	1.3	2.8	0.7	1.1	ENA22	P-type ATPase involved in Na+ efflux (by homology)	0.7	3.0	1.2
	CA2263	orf19.1756	CONTIG4-2851_0007	1.2	2.2	0.6	0.6	0.6	0.5	GPD1	Glycerol-3-phosphate dehydrogenase (by homology)	1.0	1.7	0.6
(c)	CA4684	orf19.882	CONTIG4-2772_0010	1.5	2.2	1.0	1.1	10.5	3.0	HSP78.5f	heat shock protein of clpb family 5' end (by hom.)	1.7	1.2	1.9
	CA1239	orf19.717	CONTIG4-2196_0002	0.9	0.7	1.1	1.2	5.2	4.7	HSP60	Heat Shock Protein 60 (HSP60)	1.2	0.8	1.4
	CA4959	orf19.6515	CONTIG4-3089_0026	1.0	1.0	1.2	1.3	4.8	3.4	HSP90	heat shock protein	0.8	1.1	1.4
	CA5341	orf19.7215.3	CONTIG4-2290_0005	0.9	1.0	0.8	0.9	3.9	2.5	HSP10.3	10 kDa heat shock chaperonin, 3' end (by hom.)	1.0	0.6	1.0
	CA1507	orf19.4526	CONTIG4-2702_0009	1.1	3.6	0.9	0.9	3.8	1.0	HSP30	heat shock protein (by homology)	0.9	1.3	0.8
	CA1230	orf19.4980	CONTIG4-2251_0001	0.9	0.9	1.6	1.5	3.5	2.1	SSA4	cahsp70 mRNA for heat shock	0.9	2.9	5.1
	CA0627	orf19.3160	CONTIG4-2734_0006	1.2	0.8	1.5	1.0	1.3	1.0	HSP12	Heat shock protein (by homology)	0.6	4.5	1.7
	CA5135	orf19.6389	CONTIG4-2922_0008	1.7	1.8	1.0	1.0	1.0	1.0	HSP104	Heat shock protein (by homology)	1.6	2.2	7.5
(d)	CA5467	orf19.3278	CONTIG4-2791_0013	0.8	1.2	0.5	0.8	1.5	0.7	GSY1	glycogen synthase (by homology)	0.6	1.4	1.2
	CA5206	orf19.7021	CONTIG4-3091_0024	1.0	0.7	0.6	0.7	1.1	1.1	GPH1	Glycogen phosphorylase (by homology)	0.8	1.3	1.0
	CA2758	orf19.5622	CONTIG4-2165_0001	0.6	0.9	0.5	0.7	1.9	1.2	GLC3	1.4-glucan branching enzyme (by homology)	0.9	1.3	1.1
	CA4084	orf19.6640	CONTIG4-3035_0005	0.9	1.0	0.7	0.5	1.6	1.0	TPS1	TREHALOSE-6-PHOSPHATE SYNTHASE	0.7	1.2	1.3
	CA5066	orf19.3038	CONTIG4-3098_0048	0.7	1.5	0.7	0.5	1.2	1.0	TPS2	Threalose-6-phosphate phosphatase (by homology)	0.8	2.3	1.1
	CA5824	orf19.7479	CONTIG4-2988_0007	0.9	1.2	1.2	1.3	1.0	0.7	NTH1	Neutral trehalase	0.8	2.3	1.2
	CA2574	orf19.6214	CONTIG4-2632_0007	1.2	0.8	1.1	0.4	1.5	0.4	ATH1	acid trehalase, vacuolar	0.8	2.1	1.9

Figure 6.5. Normalised data for a selection of *C. albicans* genes taken from Enjalbert *et al.* (2003), (WT XS, WT OS, WT HS) from cells subjected to a heat shock (HS) of 23-37°C an osmotic shock (OS) of 0.3 M NaCl and an oxidative shock of 0.4mM H_2O_2 compared with normalised data obtained in this study from *C. albicans* (Ca) and *C. dubliniensis* (Cd) cells exposed to heat shock of 30-42°C, an osmotic shock of 1 M NaCl and an oxidative shock of 5 mM H_2O_2 for 30 min. Normalised data that corresponded to a set of known genes implicated in the oxidative stress response is represented in (a). A set of known osmotic response genes (b), Genes implicated in the heat shock response (c). (D) Corresponds to a panel of reserve sugar genes. Fold changes are coloured according to their value according to the legend.

37°C heat shock there was no induction at all of *HSP30* at the higher temperature of 42°C. Interestingly, *HSP104* was not induced in response to the 42°C heat shock, but showed an induction greater than 7-fold in response to the 37°C heat shock. In addition, only three of these Hsps, namely-*HSP60*, *HSP90* and *HSP10*-were among the 90 up-regulated, *C. albicans* heat shock-specific response genes. This is due to the involvement of *SSA4*, *HSP78.5f*, *HSP30*, *HSP12* and *HSP104* in the responses to the other two stress conditions examined i.e. osmotic and oxidative stress.

The accumulation of reserve sugars has also been implicated in the response to heat shock. Genes encoding enzymes involved in trehalose synthesis such as *TPS1* and *TPS2* were found not to be induced after the 42°C heat shock, similar to the response observed when cells were subjected to a 37°C heat shock (Enjalbert *et al.* 2003). Genes involved in the degradation of the stress-protectant were differentially regulated in response to 37°C or 42°C, suggesting that the regulation of these genes is temperature dependent. For example, *NTH1* and *ATH1* were down-regulated (>1.5-fold) at the higher temperature of 42°C, whereas at the lower temperature of 37°C, while *NTH1* showed no significant induction *ATH1* was induced almost 2-fold. Genes involved in carbohydrate metabolism such as *GPH1* and *GLC3* showed no significant alteration in their expression in response to heat shock at 37°C or 42°C. However, the *GSY1* gene, encoding glycogen synthase, which exhibited no significant change in expression at the lower temperature stress of 37°C was found to be down-regulated (>1.5-fold) at the higher stress temperature of 42°C. Although, these carbohydrate metabolic genes have been implicated in the heat shock response of *C. albicans*, none of these "hallmark genes" were identified as *C. albicans* heat shock-specific response genes.

Among the 334 *C. albicans* genes whose expression was altered significantly (>1.5-fold) in response to a heat shock of 42°C, 157 (107 up-regulated and 50 down-regulated) genes were identified whose expression was significantly and specifically altered in *C. albicans* but not in *C. dubliniensis*. Of the 107 up-regulated *C. albicans*-specific genes (4A, Appendix II) 47% of these genes were of "unknown function". *IPF4667* showed the highest fold difference between the two species. Interestingly two genes belonging involved in the detoxification of peroxide stress, *GPX2* encoding a glutathione peroxidase and

GRP4 encoding a putative reductase showed a greater than 3-fold significant difference in induction compared to *C. dubliniensis* in response to a heat shock of 42°C. Of the 50 down-regulated genes (1A, Appendix II) 34% of the genes were of "unknown function". Among the genes showing a significant difference in induction between the two species included *GDH3*, (encoding a NADP-glutamate dehydrogenase) belonging to the functional category "metabolism" which was down-regulated 20-fold compared to *C. dubliniensis*, *STF2*, encoding an ATP synthase regulatory factor and belonging to the functional category "energy" was significantly down-regulated greater than 6-fold compared to *C. dubliniensis*. *PGA6* encoding a putative glycosylphosphatidylinositol, belonging to the functional category "Cell wall organisation" showed a greater than 4-fold difference in regulation between the two species.

In *C. dubliniensis*, 716 genes were selected that showed statistically signifcant variation following 30 min of a thermal stress at 42°C. This was almost double the number of genes involved in the heat activated transcriptional response of *C. albicans*. Of the 716 genes selected, 370 were significantly up-regulated and 346 genes were significantly down-regulated at least 1.5-fold. Among these genes whose expression levels changed significantly by at least 1.5-fold in at least one of the three stresses, a subset was specifically induced only in response to the thermal stress at 42°C for 30 min. This subset was identified by selecting genes displaying at least a 1.5-fold change in expression in response to either the osmotic or oxidative stress and eliminating them from the list of 716 significant genes originally selected. Of the 370 up-regulated genes a subset of 285 *C. dubliniensis* genes were specifically induced only in response to the thermal stress. Among the 346 significant genes down-regulated 296 genes were down-regulated specifically in response to the thermal stress (Fig. 6.11).

The functions of *C. dubliniensis* genes whose expression was significantly altered at least 1.5-fold in response to the thermal stress were determined using the SGD functional category of their *S. cerevisiae* homologues (Fig. 6.4). Functional categories prominent among *C. dubliniensis* genes significantly up-regulated included expected categories including, "response to stress", "response to temperature", "carbohydrate metabolism", "protein folding", "ubiquitin-dependent protein metabolism", leucine biosynthesis", "fatty acid biosynthesis", "response to oxidative stress" and "sulfur metabolism". "ubiquitin-dependent

protein catabolism" and "protein folding" were the two most significant categories prominent among the up-regulated genes. This was as expected. As heat shock has been shown to favour the formation of aggregated proteins, partially denatured proteins need to be degraded resulting in the induction of genes, encoding ubiquitin such as, *UBP4*, *UBP15*, *UBC4* and *UBA3*. While at the same time genes involved in "protein folding" are induced to accomodate the refolding of heat denatured proteins for example; *HSP60*, *HSP90*, *HSP78.3f*, *HSP10*, *SSA4*. Genes involved in "sulfur metabolism" included *MET14*, *MET15* and *ECM17*, suggesting that respiration is being affected by the thermal stress. For *C. dubliniensis* genes significantly down-regulated at least 1.5-fold in response to the thermal stress, the "protein biosynthesis" and "ribosome biogenesis and assembly" categories were the most significant, indicating that the high temperature stress has a deleterious affect on the synthesis of proteins. Other categories significantly prominent among the down-regulated genes included "metal ion transport" (e.g. *CFL2*, *FRE30.53*, *CTR1*) "fatty acid biosynthesis" (*FAS2.5*, *FAS2.3F*, *OLE1*). "lipid biosynthesis" (e.g. *ERG11*, *ERG25*, *ERG251*), "sterol biosythesis" and "cell organisation and biogenesis" (e.g. *PHR1*), inferring that the high stress temperature is also having a negative affect on respiration, metabolism and normal cellular functions of the cells.

As there have been no previous studies to date, investigating the global transcriptional response of *C. dubliniensis* to environmental stress, the transcript profile obtained for *C. dubliniensis* cells heat shocked for 30 min at 42°C was compared using hallmark genes from the transcript profile obtained previously by Enjalbert *et al.* (2003) for *C. albicans* cells exposed to a heat stress of 23-37°C. In addition, the *C. albicans* and *C. dubliniensis* transcript profiles obtained in this study, from cells heat shocked at 42°C were compared (Fig. 6.5). These comparisons revealed that *C. dubliniensis* cells are not only capable of executing a transcriptional response to a heat shock of 42°C but the transcriptional response appears to be higher in *C. dubliniensis* when hallmark genes of the heat shock response are compared between both species (Fig. 6.5). Genes involved in protein folding including *HSP78.5F*, *HSP90*, *HSP60*, *HSP10.3*, *HSP30* and *SSA4* were induced in response to a thermal stress of 42°C. Each of these Hsps showed an induction greater than 3-fold and displayed higher levels of induction when compared with *C. albicans* cells at 37°C and 42°C. Interestingly, while *HSP30*

was induced in *C. dubliniensis* (>3-fold) in response to a thermal stress of 42°C there was no induction at all of *HSP30* in *C. albicans* at either 37°C or 42°C. In addition similar to *C. albicans* cells at 42°C, there was no significant induction of either *HSP12* or *HSP104* at the high thermal stress temperature of 42°C. Furthermore, *HSP78.5F*, *HSP90*, *HSP60*, *HSP10*, *HSP30* and *SSA4* were among the 285 up-regulated, *C. dubliniensis* genes identified as heat shock-specific response genes

As with *C. albicans*, genes involved in carbohydrate and trehalose metabolism, were also found to be regulated in *C. dubliniensis* in response to heat shock. This finding further established the capability of *C. dubliniensis* to sense and implement a response to a heat stress. In addition, it was revealed that among the carbohydrate metabolic genes, *GSY1*, *GLC3*, *TPS1* and *ATH1* were differentially regulated at 42°C in both species. In contrast to *C. albicans*, *GSY1*, *GLC3*, *TPS1* and *ATH1* were all induced at least 1.5-fold in *C. dubliniensis* after a heat stress of 42°C whereas in *C. albicans* cells either no induction was observed or the corresponding gene was downregulated. However, none of these reserve sugar genes were belonged to the subset of *C. dubliniensis* genes identified as heat shock-specific response genes, as they have also been implicated in the osmotic and oxidative stress responses of *C. dubliniensis* (Fig. 6.5).

Among the *C. dubliniensis* genes whose expression was altered significantly (>1.5-fold) in response to a heat shock of 42°C, 539 (283 up-regulated and 256 down-regulated) genes were identified whose expression was significantly and specifically altered in *C. dubliniensis* but not in *C. albicans*. Of the 283 up-regulated *C. dubliniensis*-specific genes (5A, Appendix II) 30% of these genes were of "unknown function". Amongst the *C. dubliniensis*-specific up-regulated genes, genes encoding detoxifying enzymes such as *SOD1.3* (encoding a Cu/Zn superoxide dismutase) and *SOD2* (encoding a Manganese-superoxide dismutase) were significantly induced (>1.5-fold) compared to *C. albicans*. Additional detoxifying genes including, *TRR1* (encoding a thioredoxin reductase) (*TRX1* (encoding thioredoxin), *IPF574* (encoding a putative thioredoxin) *CAP1* (transcriptional activator) and *CTA1* (encoding catalase A), involved also in the detoxification of peroxide were specifically induced in *C. dubliniensis* compared to *C. albicans*. Three reductases, *GRP2*, *GRP4* and *GRP5*, implicated in oxidative stress responses, were also significantly induced in

C. dubliniensis. The *MXR1* gene coding for a methione sulfoxide reductase, also implicated in oxidative stress response was induced significantly in *C. dubliniensis*. Interestingly, *AOX1* and *AOX2*, both genes encoding alternative oxidases, which have been previously shown to be involved in the mediation of an alternative respiratory pathway in *C. albicans*-cyanide resistant respiration- were found to be significantly and specifically up-regulated at least 6-fold greater in *C. dubliniensis* compared to *C. albicans*.

Of the 256 down-regulated genes identified as *C. dubliniensis*-specific response genes 21% were of unknown function (2A, Appendix II). Among these *C. dubliniensis*–specific downregulated genes as expected genes involved in ribosome synthesis were significantly downregulated. Other genes repressed specifically in *C. dubliniensis* included *FRE30.5f*, *FRE30.3f*, *CFL2*, which encode reductases involved in iron up-take, fatty acid metabolic genes (*FAS2.3f*, *FAS2.5f*), a high affinity inorganic phosphate/ H^+ symporter encoded by *PHO84*, *PET8* encoding a mitochondrial carrier protein, *GAL10* encoding a UDP-glucose4–epimerase involved in carbohydrate metabolism and *PHR1* which encodes a GPI-anchored pH responsive glycosyl transferase protein were examples of some of the genes downregulated specifically in *C. dubliniensis* in response to a thermal stress of 42°C.

6.3.1.1.1 Further analysis of heat shock response genes

Transcript profiling data of *C. dubliniensis* identified genes signifcantly up-regulated compared to *C. albicans* in response to a heat shock of 42°C (5A, Appendix II). A small subset of genes kown to be implicated in cell defense and stress response were chosen for further analysis. Among the genes selected included the gene encoding the alternative oxidase, *AOX1*, a Cu/Zn superoxide dismutase, *SOD1* and a reductase, *GRP2*. In addition, a heat shock chaperonin, *HSP10*, a gene identified in both species, specific to the heat shock response but which is up-regulated >1.5-fold in *C. dubliniensis* compared to *C. albicans*. Each of these genes were-regulated at least 2.5-fold higher in *C. dubliniensis* compared to *C. albicans* in response to the heat stress. To confirm these results Northern hybridisation experiments were carried out (Figs. 6.6 and 6.7) Amplification of *AOX1*, *HSP10*, *SOD1* and *GRP2* gene fragments from *C. dubliniensis* CD36 and *C. albicans* SC5314 were carried out using the primers in Table 6.1, as described

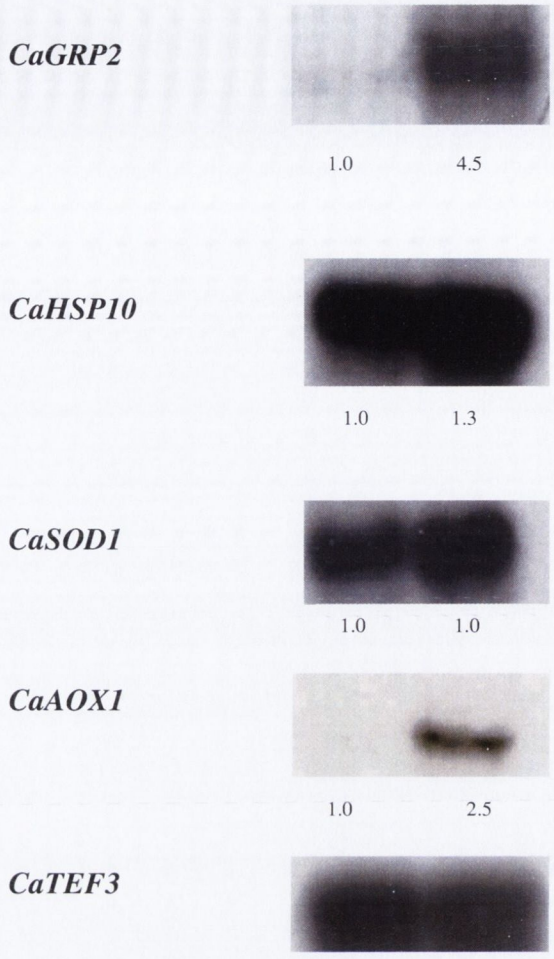


Figure 6.6. *GRP2, HSP10, AOX1* and *SOD1* expression by *C. albicans* strain SC5314 **(a)** and by *C. dubliniensis* strain CD36 **(b)** detected by Northern hybridisation. Total RNA was extracted from cells exposed a 30 - 42°C for 30 mins, and aliquots of 20 μg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled amplimers *CdGRP2, CdHSP10, CdAOX1 and CdSOD1*. The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression. Relative intensities are shown below each of the genes analysed.

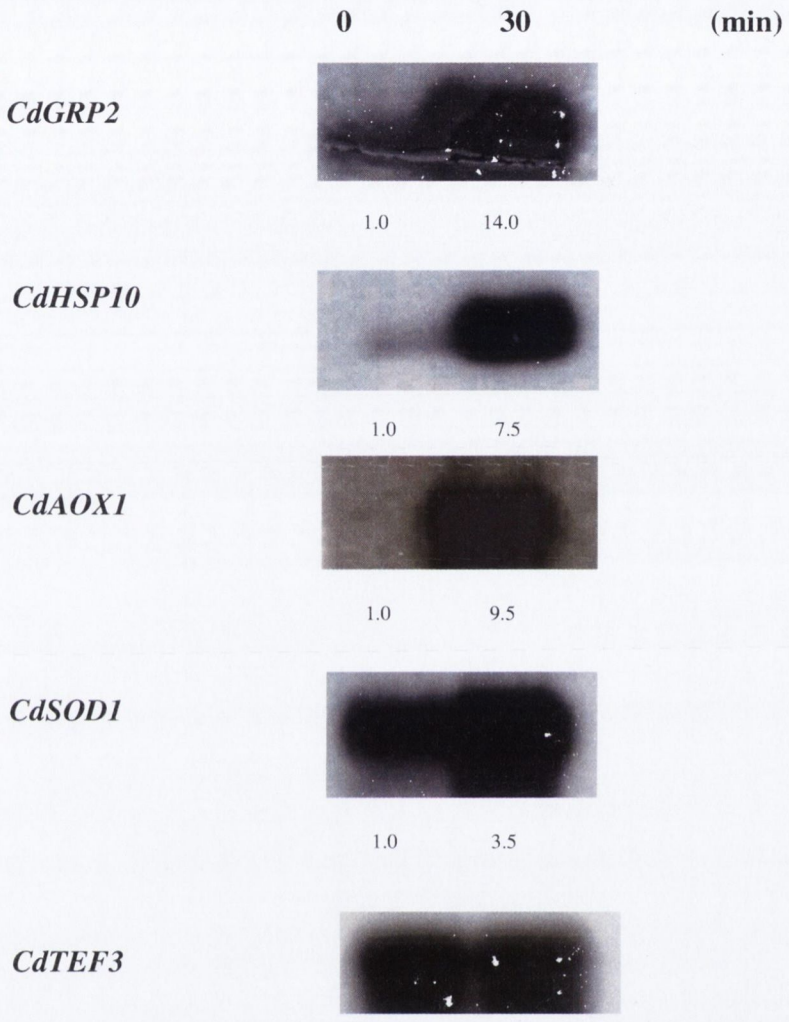


Figure 6.7. *GRP2, HSP10 AOX1* and *SOD1* and expression by *C. albicans* strain SC5314 detected by Northern hybridisation. Total RNA was extracted from cells exposed a 30-42°C for 30 mins, and aliquots of 20 μg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled amplimers *CdGRP2, CdHSP10, CdAOX1 and CdSOD1*. The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression. Relative intensities are shown below each of the genes analysed.

in section 2.4.2. The amplimers from both species were used as probes for the Northern hybridisation experiments (section 2.6.4). Northern analysis confirmed that *AOX1*, *SOD1*, *HSP10* and *GRP2* are all induced in response to a heat stress of 42°C in C. *albicans* and *C. dubliniensis*, as expected (Figs. 6.6 and 6.7). Northern analysis of *HSP10* confirmed that this transcript is induced in both species in response to a heat shock of 42°C. An interesting finding was that there was a higher level of constitutive expression of *HSP10* in untreated *C. albicans* cells (Fig. 6.6) compared to untreated *C. dubliniensis* cells (Fig. 6.7). The higher level of *HSP10* expression observed in *C. albicans* at time 0, compared to *C. dubliniensis* may confer thermotolerance on *C. albicans*. The *CdSOD1* transcript obtained confirmed that this gene is induced in response to a heat stress of 42°C in *C. dubliniensis*, whereas in *C. albicans CaSOD1* transcription appears not to be significantly affected by the heat stress. Analysis of *AOX1* gene expression in both species further confirmed that this gene is significantly up-regulated in *C. dubliniensis* compared to *C. albicans* under these specific heat shock conditions. However, it must be noted that as no expression of *AOX1* was observed in *C. albicans* and *C. dubliniensis* at time 0, the relative induction of *AOX1* should be considered infinite, making quantification of the fold increase difficult to assess. The *GRP2* mRNA was also found to show a higher level of expression in *C. dubliniensis* compared to *C. albicans* which again confirms the array data, however, *GRP2* levels were higher than one would have anticipated from the profiling data (>3-fold higher). Overall these results confirm that these heat shock response genes were induced in response to a temperature of 42°C and had a higher level of induction in *C. dubliniensis*. These data suggested that the array data are reliable.

6.3.1.2 Osmotic shock response

Genes whose expression was induced or repressed after a salt induced osmotic shock of 1 M NaCl for 30 min were identified in both species (Fig. 6.1). In *C. albicans*, 781 genes were identified that displayed statistically significant changes in expression in response to an osmotic shock of 1M NaCl. Among these genes, 391 were significantly up-regulated and 390 genes were significantly down-regulated at least 1.5-fold. Both gene lists were filtered to remove any genes significantly induced or repressed > 1.5 fold in response to heat and oxidative stress. Of the 391 genes significantly up-regulated at least 1.5-fold, 307

of these genes were found to be specifically up-regulated in response to an osmotic stress of 1 M NaCl for 30 min. Of the 390 genes significantly down-regulated at least 1.5-fold, 304 genes were identified as osmotic shock-specific response genes (Fig. 6.10).

SGD functional categories significantly prominent among the *C. albicans* genes whose expression was significantly altered at least 1.5-fold in response to osmotic shock included: "carbohydrate metabolism" "polysaccharide metabolism", for e.g. *GUT1*, *GAL7*, *GAL10*, *GAL1*, *IPF5291* "ribosome biogenesis and assembly" (*RLP7*, *RRP6*, *RRP1*, *RRP3*, *RRS1*) " metal ion transport" (*SMF*, *SMF11*) "cell organisation and biogenesis" (*SNF3*), "sterol biosynthesis", "aldehyde metabolism"(*ALD4*)", "polyol transport" "pigment metabolism" "cell homeostasis"(*CCC1*, *ENA22*, *ENA21.3*) and "cell wall biosynthesis"(*KRE6*, *SKN1.3f*, *ECM1*) (Fig. 6.4). These functional categories included genes that one might expect to be induced in response to an osmotic stress including sorbitol transporters (*SOU1*, *SOU2*), sugar transporters (*STLI*, *IPF4181*, *HGT11*, *HGT12*), P-type ATPase cation pumps (*ENA21.3*, *ENA22*) and genes involved in glycerol metabolism (*GPD2A*, *GUT1*, *RHR2*). Among the significantly down-regulated genes the functional categories that were enriched were "carbohydrate metabolism"and "energy reserve metabolism" (*ATH1*, *TPS1*, *TPS2*) "lipid biosynthesis", "sterol biosynthesis"(*IPF11815*, *ARE2*, *TGL1*), "pigment metabolism", "threonine metabolism" (*THR1*, *ILV1*, *HOM3*,*GLY1*) "cell homeostasis" (*SMF2*, *CRD1* and "ergosterol biosynthesis" (*ERG1*). "Pigment metabolism" and "Polyol metabolism" (*GPD1*) and were the two categories most significantly prominent among the down-regulated genes in response to the osmotic stress.

When the transcript profile for *C. albicans* cells exposed to high osmotic stress of 1 M NaCl for 30 min was compared with profile obtained from *C. albicans* cells treated with a lower osmotic stress (0.3 M NaCl) it showed that hallmark genes implicated in the stress response of *C. albicans* (Enjalbert *et al.*, 2003) were also regulated in response to the higher osmotic stress of 1 M NaCl (Fig. 6.5). However, it revealed that among the glycerol metabolic genes, while *GPD2* was induced similarily (>2-fold up-regulation) at both conditions, *GPD1* and *RHR2* were both differentially regulated at 0.3 M NaCl (>1.5-fold up-regulation) and at 1.0 M NaCl (>1.5-fold down-regulation). *Candida albicans*

cells treated to the higher osmotic stress of 1.0 M NaCl showed a 6-fold increase in the induction of the *STL1* gene (encoding a sugar transporter), compared to *C. albicans* cells treated to the milder osmotic stress of 0.3 M NaCl, consistent with *C. albicans* ability to cope with osmotic stress by transporting glycerol into, out of, within or between cells. The *ENA* genes, *ENA21.3* and *ENA22* (encoding P-type ATPase pumps) were also induced under both osmotic conditions, with the former displaying a 1.5-fold increase in induction at the higher Nacl concentration. Of these "hallmark" genes of osmotic stress response, both *ENA21.3* and *ENA22* genes were among a subset of *C. albicans* genes identified as osmotic shock-specific response genes, as they were not implicated in *C. albicans* response to thermal or oxidative stress (Fig. 6.5). The remainder of these "hallmark" genes were, however, involved in the later two stress responses of *C. albicans*.

Due to the role of trehalose in the osmotic stress response of yeast species (Parrou *et al.*, 1997; Hounsa *et al.*, 1998) the behaviour of the set of genes encoding the reserve sugars was also compared at 0.3 M NaCl and 1.0 M NaCl. Interestingly, it was revealed in this comparison that the transcriptional responses of the trehalose metabolic genes, including *TPS1*, *TPS2*, *ATH1* and *NTH1* are dependent on the concentration of NaCl used to induce an osmotic stress. For example at 0.3 M NaCl both *TPS2* (encoding trehalose-6-phosphate phosphatse) and *ATH1* (encoding acid trehalase) were induced greater than 2-fold, but at the higher NaCl concentration of 1.0 M NaCl, both were at least 2-fold down-regulated. In addition the gene encoding neutral trehalase, *NTH1* was induced greater than 2-fold at 0.3 M NaCl but showed no significant induction in response to the higher salt concentration of 1 M NaCl. Furthermore, the *TPS1* gene which encodes trehalose-6-phosphate synthase, expression was only altered significantly (> 2-fold down-regulation) in response to the higher NaCl concentration of 1 M NaCl. Among the set of genes involved in glycogen metabolism, *GPH1* (encoding glycogen phosphorylase) and *GLC3* (encoding 1,4-glucan branching enzyme) gene expression was also only altered (>1.5-fold down- in response to 1.0 M NaCl. While *GSY1*, which encodes glycogen synthase only showed a weak induction at the lower osmotic stress of 0.3 M NaCl. In addition, it was noted that only one (*TPS1*) of the reserve sugars genes in this comparative analysis was an osmotic-specific gene, as the expression of the other remaining "hallmark" genes

were altered either in response to the thermal and/ or oxidative stress in addition to the osmotic stress.

Candida albicans genes displaying significant changes in expression compared to *C. dubliniensis* genes in response to an osmotic stress of 1 M NaCl were identified. From the list of *C. albicans* genes (781) whose expression was altered significantly in response to 1.0 M NaCl for 30 min, *C. dubliniensis* genes (60) significantly induced or repressed at least 1.5-fold under the same stress condition were selected and eliminated from the gene list. As the *C. dubliniensis* transcriptional response to osmotic stress was much weaker than that of *C. albicans* there was little overlap between the list of significantly induced (30) and signifcantly repressed genes between both species. Hence, 92% (721 genes) of the *C. albicans* genes whose expression was altered significantly in response to osmotic shock showed significant changes (>1.5-fold) in expression in *C. albicans* but not in *C. dubliniensis*. Among the 721 *C. albicans*-specific genes 361 (10A, Appendix II) were up-regulated and 360 (7A, Appendix II) were down-regulated in response to the osmotic stress. Forty one percent of the 361 up-regulated and 40% of the 360 down-regulated *C. albicans*-specific genes were of "unknown function". Among the significantly up-regulated genes in *C. albicans*, was *1PF2839*, whose function was unknown and was induced 20-fold higher in *C. albicans* compared to *C. dubliniensis* in response to 1.0 M NaCl. Sorbitol utilisation proteins *(SOU1*, *SOU2*), sugar transporters (*HGT11*, *HGT12*) cation pumps (*ENA21.3f*, *ENA22*), genes involved in the High Osmolarity Glycerol pathway (HOG) such as *SGD1* with a possible role as a regulator of osmotic pressure (Akhtar *et al.*, 2000; Lin *et al.*, 2002) and and *SKO1.3f* a basic leucine zipper (bZIP) transcription factor, which has been shown to be involved in the control of osmotic response gene expression through the Hog1 SAPK in *S. cerevisiae* (Rep *et al.*, 2001). Among the genes significantly downregulated in *C. albicans* included the transporters *SNF31*, *SMF2* and *CRD1* and the trehalose metabolic genes *ATH1*, *TPS1* and *TPS2*. Genes associated with "energy" (*EBP4*, *EBP1*) were also found to be significantly down-regulated at least 3-fold lower in *C. albicans* compared to *C. dubliniensis*. In addition the glutamate dehydrogenase (*GDH3*) which is involved in ammonia incorporation was at least 2-fold down-regulated significantly in *C. albicans* compared to *C. dubliniensis*.

The transcriptional response of *C. dubliniensis* to an osmotic stress of 1 M NaCl was much weaker when compared with the profiles (Fig 6.1) obtained for cells treated with a heat stress of 42°C or an oxidative stress of 5 mM for 30 min. Furthermore, the *C. dubliniensis* transcriptional response to osmotic stress was strikingly weaker when compared with the transcript profile obtained with *C. albicans* under the same experimental conditions. The number of genes significantly induced or repressed (>1.5-fold) in response to 1.0 M NaCl was only 125. Among these genes, 51 were significantly up-regulated and 74 genes were significantly down-regulated at least 1.5-fold. Both gene lists were filtered to remove genes significantly induced or repressed > 1.5 fold in response to the thermal and oxidative stresses. Of the 51 genes significantly up-regulated at least 1.5-fold, 19 of these genes were found to be specifically up-regulated in response to a 1.0 M NaCl for 30 min. Of the 74 genes significantly down-regulated at least 1.5-fold, 51 genes were identified as osmotic shock-specific response genes (Fig. 6.10)

Functional categories prominent among *C. dubliniensis* genes (Fig. 6.4) whose expression was significantly altered (>1.5-fold) in response to 1 M NaCl included "protein folding", "ubiquitin-dependent protein catabolism" (*RPN4*) "polyol transport" (*IPF4181*, *AGP2*) "pigment metabolism" and "cell homeostasis" (*STL1*, *IPF8374*, *IPF11829*,) among the genes up-regulated. Among the down-regulated genes functional categories enriched were "carbohydrate metabolism" (*GSY1*, *GLC3*, *GPH1*, *PGM2*) and " threonine metabolism" e.g. *GLY1*, *HOM3*.

"Hallmark genes" of the osmotic stress response used previously by Enjalbert *et al.*, (2003) were used to compare the osmotic transcriptional response in *C. dubliniensis* which in addition, was compared with the profile obtained for *C. albicans* cells exposed to the higher salt concentration of 1.0 M NaCl in this study (Fig.6.5). Among the set of genes, previously shown to be involved in glycerol synthesis (*GPD1*, *GPD2*) (Albertyn *et al.*, 1994, Ansell *et al.*, 1997), *GPD2* (encoding glycerol 3-phosphate dehydrogenase) was significantly up-regulated greater than 7-fold in *C. dubliniensis* cells, almost 4-fold higher than *C. albicans* cells in response to 1.0 M NaCl, consistent with the cells requirement to accumulate internal osmolytes in response to osmotic stress. However, *GPD1* (encoding glycerol 3-phosphate dehydrogenase) a homologue of *GPD2* was

down-regulated in both species in response to 1.0 M NaCl. In addition, both of the ENA genes (*ENA21.3* and *ENA22*) showed no significant change in expression in response to 1.0 M NaCl, which was in contrast to *C. albicans*. The 1.6-fold increase in *ENA21.3* expression in *C. dubliniensis* cells was not statistically significant. Results from Figure 6.3 also show that while *STL1* is induced significantly in both species, the induction is higher in *C. albicans* (>14.5-fold) compared to *C. dubliniensis* (>5.6-fold) in response to 1.0 M NaCl. Furthermore, while results show that *RHR2* was up-regulated (>1.8-fold) in *C. dubliniensis* cells compared to *C. albicans* cells, this induction was not found to be statistically significant. However, the ability of *C. dubliniensis* to induce "hallmark" osmotic shock genes such as *STL1* and *GPD2* demonstrates the ability of *C. dubliniensis* to respond to an osmotic shock of 1.0 M NaCl.

When the profiles of the set of reserve sugar genes were examined, it revealed that *NTH1* (encoding neutral trehalase) expression was unaffected in both species in response to the higher salt concentration of 1.0 M NaCl, in contrast to the greater than 2-fold induction observed for *C. albicans* cells exposed to 0.3 M NaCl. The *ATH1* (acid trehalase) gene was differentially expressed in both species, while significantly repressed in *C. albicans* cells (>2.5-fold), *ATH1* expression in *C. dubliniensis* cells was unaffected. Figure 6.5 shows that both of the trehalose metabolic enzymes *TPS1* and *TPS2* were repressed in response to 1.0 M NaCl which is in accordance with *C. albicans* cells under the same condition, however the down regulation of these genes in *C. dubliniensis* cells was not found to be statistically significant. Both, *GLC3*.3f and *GSY1* genes were found to be significantly repressed (>2-fold) in *C. dubliniensis* cells but in *C. albicans* cells, while *GSY1* expression was unaffected, *GLC3*.3f gene repression was not statistically significant in response to 1.0 M NaCl. Furthermore, in contrast to *C. albicans* cells which showed no significant change in expression in response to 1.0 M NaCl the glycogen synthase gene *GSY1* was significantly down-regulated at least 1.6-fold in *C. dubliniensis* cells. Moreover, *GPH1* was the only one of these " hallmark" genes among the set of *C. dubliniensis* osmotic shock-specific genes.

Genes whose expression was altered significantly (>1.5-fold) in *C. dubliniensis* cells, but not significantly in *C. albicans* cells, in response to an osmotic shock of 1 M NaCl were identified. Of the 125 statistically significant

genes that showed a fold change of at least 1.5-fold in response to 1.0 M NaCl, 65 (21 up-regulated and 44 down-regulated) were identified as *C. dubliniensis*-specific genes. Among the 21 up-regulated genes (11A, Appendix II) KA43% were of unknown function. Among the genes identified was a family of NADPH dehydrogenases (*EBP1*, *EBP4* and *EBP6*) and *CAT1* which is responsible for catalysing the breakdown of toxic H_2O_2 to H_2O and O_2.

Among the 44 down-regulated genes (8A, Appendix II), 32% were of unknown function. This subset included genes encoding sugar transporters (*HXT5.3f*, *HXT61*) and hexokinase II (*HXK2*) which is inolved in the intracellular metabolism of glucose. Other genes identified among this subset were inolved in carbohydrate metabolism including, *GLK1*, *GSY1*, *GLC3.3f*, *GLG2* and *GPH1*).

6.3.1.2.1 C. dubliniensis Hog1 activation

When the transcript profiles of *C. albicans* and *C. dubliniensis* cells exposed to 1.0 M NaCl were compared, it was noted that Hog1-linked genes in *C. albicans* such as *ENA21.3*f, *ENA22*, *SGD1* and *SKO1.3f* were significantly up-regulated in *C. albicans*, but were not significantly up-regulated in *C. dubliniensis*. Hog1 has been previously implicated in the resistance of *C. albicans* in response to both osmotic and oxidative stress and recent studies have shown that *C. albicans* Hog1 SAPK is activated in response to several different stress conditions (San Jose *et al.*, 1996; Alonso-Monge *et al.*, 2003; Smith *et al.*, 2004). It was therefore decided to investigate the activity of Hog1 in *C. dubliniensis* to determine if a defective Hog1 pathway in *C. dubliniensis* might explain why these genes (i.e. *ENA21.3f*, *ENA22*, *SGD1*, *SKO1.3f*) are weakly or not at all expressed in this species. Hog1 phosphorylation assays were carried out by Dr Janet Quinn, University of Newcastle upon Tyne, as described by Smith *et al.* (2004). The results of these assays indicated that the *C. dubliniensis* Hog1 SAPK is activated in response to an osmotic stress of 1.0 M NaCl and thus, is not responsible for the lack of induction observed in these genes (Fig. 6.8).

6.3.1.2.2 Further analysis of IPF2839

When profiling data obtained from *C. albicans* and *C. dubliniensis* cells exposed to 1.0 M NaCl were compared, the expression ratio for the *1PF2839* gene approximated to 20-fold up-regulation in *C. albicans* cells compared to 1.4-fold

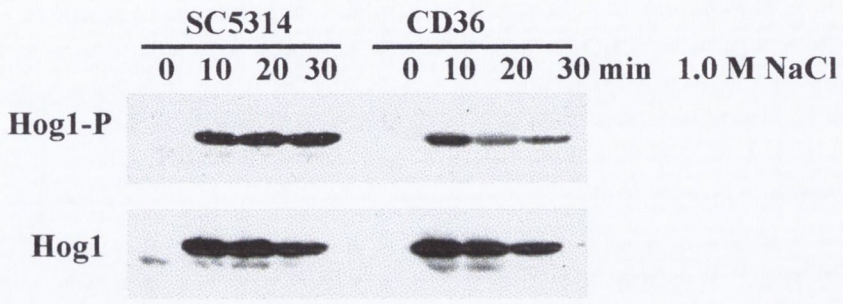


Figure 6.8. *Candida albicans* strain SC5314 and *C. dubliniensis* strain CD36 Hog1 is phosphorylated in response to 1.0 M NaCl. Western blot analysis of Ni^2-NTA agarose purified Hog1-His_6-myc from wild type *C. dubliniensis* cells after treatment with 1.0 M NaCl. Western blots were probed with an anti-phospho p38 antibody, which only recognises the phosphorylated, active form of *C. albicans* Hog1 (Hog1-P) and *C. dubliniensis* Hog1. Total levels of Hog1 protein was determined by stripping and reprobing the blot with an anti-myc antibody that recognises both phosphorylated and unphosphorylated forms of Hog1 (Hog1).

up-regulation in *C. dubliniensis* cells. This indicated that the 1.0 M NaCl stress had a significant effect upon the expression of *1PF2839* in *C. albicans* cells but not in *C. dubliniensis* cells. Based on these findings this gene was selected for further analysis. To confirm that this transcript was induced by osmotic stress in *C. albicans* and not in *C. dubliniensis* cells, Northern analysis was performed to examine the expression of this gene in response to 1.0 M NaCl. Amplification of *1PF2839* gene fragments from *C. dubliniensis* CD36 and *C. albicans* SC5314 were carried out using the primers in Table 2.2, as described in section 2.4.2. The amplimers from both species were used as probes for the Northern hybridisation experiments (section 2.6.4). The induction in *1PF2839* mRNA levels in osmotically stressed *C. albicans* cells was confirmed by Northern analysis (Fig. 6.9). Moreover, induction levels in *C. dubliniensis* were lower than that of *C. albicans*. Analysis of *IPF2839* expression also revealed that *IPF2839* is differentially expressed in both species in untreated cells at time 0. This difference is due to the presence of a higher consitutive level of *IPF2839* expression in *C. dubliniensis* compared to *C. albicans* (Fig. 6.9). These data indicated that *1PF2839* may have an important role in osmoregulation or ion homeostasis in *C. albicans*.

The *C. albicans* genome database, CandidaDB (http://genolist.Pasteur.fr/CandidaDB/) and the recently available *C. dubliniensis* genome sequence data (http:// www.sanger.ac.uk/Projects/C_dubliniensis/) were used to perform nucleotide and amino acid sequence similarities to investigate if this gene was divergent in *C. dubliniensis*. Nucleotide and protein sequence alignments revealed that *C. albicans 1PF2839* shares 89.8% homology to the *C. dubliniensis 1PF2839* homologue at the nucleotide levvel, and 95% homology at the protein level.

A BLAST search of the EMBL-EBI (European Bioinformatics Institute) database InterProScan database revealed sequence similarity to a Band 7 membrane protein or "stomatin like protein" also known as "erythrocyte membrane protein 7.2b". Described as a 32kd integral membrane protein found in the red cell membrane and was first studied as it was absent from the red cell membrane in conditions known as "hereditary stomatocytosis". "Hereditary stomatocytosis " is characterised by a "plasma membrane leak" to the cations Na+ and K+ which compromises the osmotic stability of the cell (Green *et al.*, 2004).

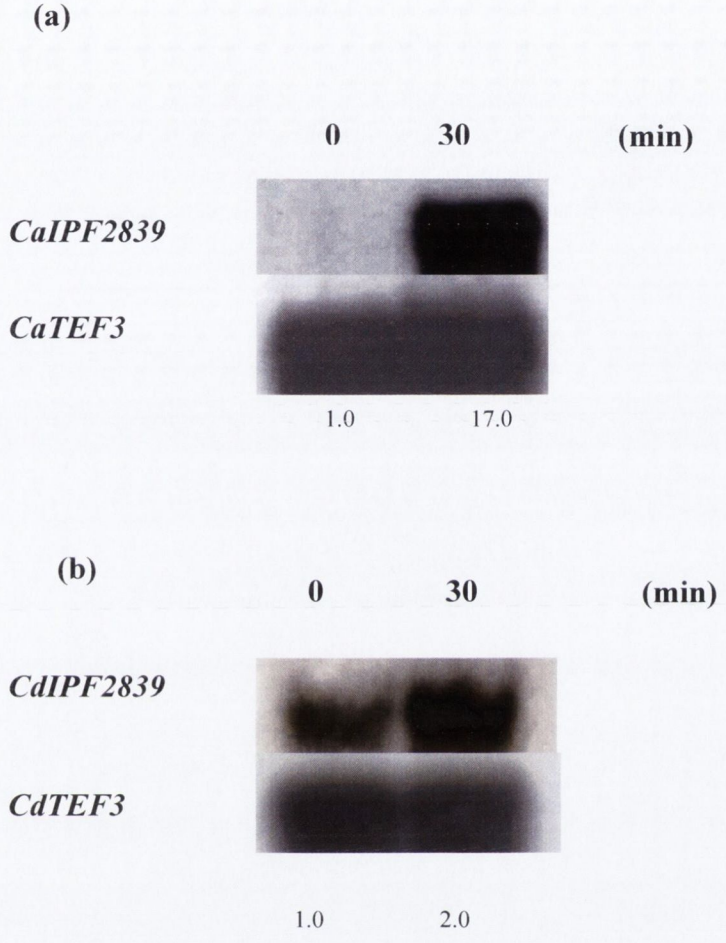


Figure 6.9. IPF2839 expression by *C. albicans* strain SC5314 **(a)** and by *C. dubliniensis* strain CD36 **(b)** detected by Northern hybridisation. Total RNA was extracted from cells exposed to 1.0 M NaCl 30 mins at 30°C, and aliquots of 20 µg were electrophoresed on a denaturing agarose gel. Following transfer to a nitrocellulose membrane, the blots were probed with radiolabelled cloned amplimers *CaIPF2839* **(a)**, *CdIPF2839* **(B).** The constitutively expressed *TEF3* gene was used as a control for RNA loading. Expression levels were analysed by scanning densitometry and normalised against levels of *TEF3* expression. Relative intensities are shown below each of the genes analysed.

Stomatin like proteins have been found in all three kingdoms of biology. Within the eukaryotes stomatin like genes have been sequenced from chordates, invertebrates, the oomycete *Phytophthora infestans*, *trypanosomatids*, *Plasmodium falciparum* and *Leishmania spp.* and the mould *Dictyostelium discoideum*. Although the function of *1PF2839* remains undetermined it is possible that it may be involved in cation transport or regulation in *Candida* cells.

6.3.1.3 Oxidative shock response

Exposure to a 5 mM H_2O_2 stress for 30 min triggered a significant change in the expression levels of genes in both *C. albicans* and *C. dubliniensis* cells (Fig 6.1). Using the same criteria as for the heat and osmotic stresses, approximatey 1300 genes whose transcript levels changed significantly by at least 1.5-fold in response to the 5 mM H_2O_2 stress condition were identified in *C. albicans*. Five hundred and sixty seven of these genes that displayed statistically significant changes in expression in response to a 5 mM H_2O_2 stress for 30 min were up-regulated and 736 genes were significantly down-regulated at least 1.5-fold. Of the 567 genes significantly up-regulated in *C. albicans* at least 1.5-fold, 462 of these genes were found to be up-regulated specifically in response to the 5 mM H_2O_2. Of the 736 significantly down-regulated genes 662 were identified as genes whose expression was altered specifically in response to 5 mM H_2O_2 (Fig. 6.10).

As expected many of the genes that showed alterations in expression were involved in the detoxification of both H_2O_2 and superoxides. Increased prominence of functional categories among *C. albicans* genes that displayed significant changes in transcript expression (>1.5-fold) in response to 5 mM H_2O_2 were identified (Fig. 6.4). This revealed the enhancement of functions involved in responding to temperature (e.g. *HSP78.5f*) osmotic (*STL1*, *GPD2*, *1PF2839*) and oxidative stress (for e.g. *TRX1*, *TTR1*, *TRR1*, *ATX1*, *CTA1*, *DOG2 AOX1*, *AOX2*, *SOD2*, *MXR1*). Other categories prominent included "Ubiquitin dependent protein catabolism"(for e.g *IPF12693*, *DOA4*, *CDC34*, RPN4) , "glutathione metabolism"(*GPX1*, *IPF2303*, *GTT1*) "sulfur metabolism"(*CYS3*) "aldehyde metabolism" (e.g.*FDH11*, *FDH2*, *FDH3.3f*, *FDH12*) and "cell homeostasis"(for e.g. *IPF9136*, *FRE30.5f*, *FRE30.32f*). The most significant category prominent was " response to oxidative" which is consistent with the stress condition used.

The significantly down-regulated gene list exhibited an enrichment of functions involved in cellular metabolism i.e. carbohydrate and polysaccharide metabolism including genes such as *UGP1*, *GCV2* metal ion transport (*FTH2*) response to stress, histone dephosphorylation. In addition functional categories such as "cell division", "cell cycle' and "DNA replication' including genes such as *CDC25*, *CDC42*, *MCM3*, *DNA2*, *SMC3.5f*, *SMC1*, *HTB1*, *HTA1*, *HEL1*, *IPF14629* were also evident among the down-regulated genes consistent with an outcome of oxidative stress which is DNA-damage. Other functional categories with increased prominence included "glycoprotein biosynthesis" (e.g *MNN11*, *MNN9*, *MNN3*, *MNN7*, *MNT1*) "chitin metabolism"(*CHS2*, *CHS8*, *CHT1*, *CHT3*). "cell wall biosynthesis"(*ROT1*, *PMTI*, *PMT4*, *PMT5*, *ECM331*, *ECM39*, *MNT1*, *ROT1*) and "lipid, sterol and ergosterol biosynthesis" (*ERG2*, *ERG3*, *ERG4*, *ERG5*, *ERG25 ERG27*). These subsequent changes in cellular activities are a result of changes in metabolism as a result of the up-regulation of antioxidant defense systems.

The transcript profile obtained for *C. albicans* cells treated with 5 mM H_2O_2 from this study was compared with results obtained in a study by Enjalbert *et al* (2003) in which, *C. albicans* cells were treated with the lower oxidative stress of 0.4 mM H_2O_2 (Fig. 6.5). This comparison indicated that genes known to be involved in the detoxification of both H_2O_2 and superoxide including *TTR1* (glutaredoxin), *TRR1* (thioredoxin reductase), *TRX1* (thioredoxin), *CTA1* (catalase A) are all induced at least 2-fold in response to 0.4 mM H_2O_2 and 5 mM H_2O_2. However, *SOD2* (manganese-superoxide dismutase) was only induced in response to the higher level of oxidative stress. In addition, the homologue of the *S. cerevisiae* YAP1 transcriptional regulator, *CAP1* showed a six-fold induction in response to 0.4 mM H_2O_2 but only showed a weak induction in response to the higher level of oxidative stress (5 mM H_2O_2). A similar lack of induction of *SOD1* (Cu, Zn-superoxide dismutase), in response to 0.4 mM H_2O_2 was observed in *C. albicans* cells exposed to the higher peroxide stress of 5 mM H_2O_2. Overall, these results indicate that *C. albicans* cells are capable of eliciting an oxidative stress response when exposed to high levels of peroxide stress.

A comparison of normalised data obtained for *C. albicans* cells treated to the higher level of oxidative stress was also made with normalised data from selected *C. albicans* reserve sugar genes previously obtained by Enjalbert *et al*

(2003) using the milder oxidative treatment i.e. 0.4 mM H_2O_2. Previously, a weak response of the reserve sugar genes in *C. albicans* cells treated with 0.4 mM was identified which was consistent with the lack of accumulation of the reserve sugars observed (Enjalbert *et al.*, 2003). With the exception of *TPS2* and *GPH1*, essentially, still no significant alteration in expression was observed among the reserve sugar genes in response to 5 mM H_2O_2. However, it has been demonstrated (Alvarez-Peral *et al* 2002) that trehalose accumulation is induced in response to a strong H_2O_2 stress, although the microarray data in this study did not indicate significant changes in expression of the trehalose metabolic genes, it suggests that the induction of the trehalose metabolic genes and trehalose accumulation are not always correlated in response to stress conditions.

Genes whose transcript levels were significantly changed in *C. albicans* cells but not significantly changed in *C. dubliniensis* cells in response to an oxidative stress of 5 mM H_2O_2 were identified. Of the 567 *C. albicans* genes significantly up-regulated, 335 of these genes were found to be specifically and significantly up-regulated in *C. albicans* (16A, Appendix II). Among the set of significant down-regulated genes (767), a subset containing 504 genes specifically down-regulated in *C. albicans* was identified (13A, Appendix II).

Almost 46% of the *C. albicans*-specific up-regulated genes were of unknown function (16A, Appendix II). Among this list of up-regulated genes included *ALS1,* the known cell adhesin of *C. albicans* which appears to be regulated by Ssk1p, a signal protein that functions in the adaptation of *C. albicans* cells to peroxide stress (Chauhan *et al.*, 2003). In addition, expression of the *ALS1* gene in *C. albicans ssk1* mutants has shown to be downregulated which correlates with the reduced adherance of *C. albicans* ssk1 mutants to human epithelial cells (Bernhardt *et al.*, 2001; Li *et al.,* 2004). The transcript profiling data in this study revealed that the *ALS1* gene is significantly up-regulated greater (>14-fold) in *C. albicans* but is not significantly up-regulated in *C. dubliniensis* under the same conditions. Hence, it may be reasoned that the functions of the *C. albicans* Ssk1p differ from those of *C. dubliniensis*. However, the profiling data revealed that other genes regulated by Ssk1p such as *STL1* were found to be significantly up-regulated in both *C. albicans* and *C. dubliniensis* in response to oxidative stress. The low homology of the *ALS1* gene between *C. albicans* and *C. dubliniensis* is a more likely explanation for the difference in *ALS1* gene

expression observed between *C. albicans* and *C. dubliniensis* (Moran *et al.*, 2004). Other genes significantly induced in *C. albicans* (but not in *C. dubliniensis*) included *GTT1* (glutathione s-transferase) which was up-regulated 4-fold compared to *C. albicans*, involved in glutathione metabolism which plays an important role in the oxidative stress response of yeasts. Heat shock proteins *HSP30*, *HSP31*, *HSP78*, also specifically up-regulated in *C. albicans*, suggesting that the oxidative stress may has resulted in the unfolding of proteins. NADH hydrogenases (*NDH2*, *NDH1*) were signifcantly up-regulated and consistent with the cells requirement to maintain sufficient NADH, as NADH is an essential reductant for the glutathione and thioredoxin reductase complexes. Due to the increased need for NADH in yeast cells exposed to peroxide, yeast cells often compromise metabolic pathways i.e glycolysis and use alternate pathways such as the pentose phosphate pathway in order to generate more NADH. Hence the induction of genes involved in the glutamate catabolic pathway, like *GAD1* (glutamate decarboylase) which was also among the genes significantly induced in *C. albicans*. *GPD1* (glycerol phosphate phosphatase) and *RHR2* (DL-glycerol phosphatase) both found to be induced significantly in *C. albicans* and both involved in the glycerol cycle. The *AOX2* gene encoding an alternative oxidase was also found to be significantly up-regulated in *C. albicans* compared to *C. dubliniensis* in response to the oxidative stress. The alternative oxidase have also been implicated in the oxidative stress response of yeast.

Of the 504 significantly down-regulated genes in *C. albicans* 40% were of unknown function (13A, Appendix II). As the oxidation of nucleic acids ultimately ends in DNA damage it was not surprising to see genes involved in DNA synthesis and maintenance being down-regulated e.g. *SMC1* (chromosomal ATPase family member), *SMC3.5f* (required for structural maintenance of chromosomes), *POL1* (DNA directed DNA polymerase), *MSH6* (DNA mismatch repair protein) *DNA2* (DNA helicase) and *MCM3* (replication initiation protein) are just some examples. *GDH3* NADP-glutamate dehydrogenase was significantly downregulated at least 2-fold compared to *C. dubliniensis*. This observed downregulation is consistent with the inhibition of glycolytic flux in response to oxidative stress so as to generate more NADPH by other routes (Missall *et al.*, 2004). *GPHI* encoding a glycogen phophorylase, is regulated by

Hog1p in cells that are osmotically stressed but appears to require the Ssk1p response regulator for adaptation to oxidative stress (Chauhan *et al.*, 2003).

The transcript profile obtained for *C. dublinienis* cells treated with 5 mM H_2O_2 for 30 min identified a total of 729 (364 up-regulated and 365 down-regulated) genes that displayed statistically significant changes (>1.5-fold) in expression. Of the 364 up-regulated genes, 132 were identified as *C. dubliniensis* oxidative-specific genes (Fig. 6.11). Consistent with a classic oxidative response *C. dubliniensis* cells induced genes known to play key roles in the defense against oxidative stresses in yeast such as glutathione peroxidases, superoxide dismutases and thioredoxins.

Significant functional categories were identified among the up-regulated genes which included; "response to stress" (e.g. *GRP1*, *BMR1* (also known as *MDR1*)) "carbohydrate metabolism" (e.g. *DLD2*, *DLD3, DOG2*, *GPD2*, *FDH2*, *FDH3.3f*, *FDH12*), "metal ion transport" (e.g. *FRE7*, *CTR2*, *CRD1* "threonine metabolism" (e.g. *GLY1*, *CHA12.3f*) "response to oxidative stress" (*SOD2*, *CAP1*, *CTA1*, *TTR1*, *TRR1*, *GPX1*, *AOX1*,*TRX1* "glutathione metabolism" (e.g. *CIS2*, *GSH1.5f*, *GSH1.3f*, *IPF12303*, *GLR1*, *GLO1*) "sulfur metabolism"(e.g. *MET1*, *MET2*, *MET16*) "aldehyde metabolism"(e.g. *FDH11*) and " cell homeostasis" (e.g. *ENA22*, *ATX1*). The most significant of these functional categories was "response to oxidative stress" (Fig. 6.4).

Functional categories enriched among *C. dubliniensis* down-regulated genes including carbohydrate, polysacharide and energy reserve metabolism, including genes such as *GLK1*, *GLG2*, *TPS2*, *PMT4*, *PMT6*, *ALG6* and *ALG8*. Other categories prominent were "metal ion transport" (*SMF2*, *SMF11*), "cell organisation and biogenesis"(e.g. *SUN41*, *GYP1*, *CWH41*, *ROT2* and *ECM3*) along with categories associated with oxidative damage such as "cell division" (*CC43*, *CDC54*, *CDC42*, *CDC47*) "cell cycle" (*CDC5*, *CCN1*, *CLN2*) "DNA replication" (e.g. *MCM2*) "glycoprotein biosynthesis", "chitin metabolism", "cell wall biosynthesis" (*OCH1*, *ECM7*, *CHT3*,*CHS4*, *CHS3.3f AMYG1* and *AMG2.5f*) and "ergosterol biosynthesis" (*ERG251*, *ERG3* and *ERG25*).

To investigate the efficacy of the transcriptional response of *C. dubliniensis* cells in response to a peroxide stress of 5 mM H_2O_2, a set of genes previously implicated in the oxidative stress response of *C. albicans* (Enjalbert *et al.*, 2003) was used to compare the profile obtained from *C. dubliniensis* cells

with the profiles obtained for *C. albicans* (Fig. 6.5). An induction of at least 1.5-fold was observed for *CTA1*, *TTR1*, *TRR1*, *TRX1*, *CAP1*, *SOD1* and *SOD2* in *C. dubliniensis* cells exposed to 5 mM H_2O_2. Interestingly, *SOD2* is induced in response to 5 mM H_2O_2, in *C. dubliniensis* but is not induced in *C. albicans* at either 0.4 mM or 5 mM H_2O_2, suggesting that *SOD2* is differentially regulated in response to oxidative stress in both species. The induction of these genes of which have known antioxidant functions, demonstrated that *C. dubliniensis* is able to respond to peroxide stress.

Candida dubliniensis genes displaying significant changes in expression compared to *C. albicans* genes in response to an oxidative stress of 5 mM were identified From the list of *C. dubliniensis* genes (729) whose expression was altered significantly in response to 5 mM for 30 min, 265 (132 up-regulated and 133 down-regulated) were identified as *C. dubliniensis*-specific genes, (i.e genes whose expression was found to be significantly altered in *C. dubliniensis* but not in *C. albicans*) in response to the oxidative stress. Of the 132 *C. dubliniensis*-specific up-regulated genes (17A, Appendix II) 46% were of unknown function. The genes induced specifically in *C. dubliniensis* was *CIS2*, encoding gamma-glutamyltransferase which is inolved in glutathione catabolism. *CIS2* was induced almost 7-fold more in *C. dubliniensis* compared to *C. albicans*. *CIS2* showed the highest significant fold difference between both species among these list of genes. Interestingly, the glutathione peroxidase (*GPX3*) and the transcriptional activator, *CAP1* were induced at least 1.5-fold higher in *C. dublinienis* compared to C albicans. Another gene known to be implicated in the oxidative stress response,which is regulated by the HOG pathway, *GRP1* (dihydroflavonol-4-reductase) was also found to be significantly up-regulated in *C. dubliniensis* compared to *C. albicans*. A significant up-regulation of sulfur metabolic genes such as *MET1*, *MET16* was observed in *C. dubliniensis*. *DLD2* and *DlD3,* both involved in aerobic respiration and carbohydrate metabolism were induced at least 2-fold greater in *C. dubliniensis* comparedto *C. albicans*. The *NRG1* transcriptional repressor of glucose metabolism and filamentation was up-regulated specifically compared to *C. albicans* in response to the peroxide stress (2.4-fold). *EBP7* (NADH dehydogenease) showed an up-regulation of at least 2.5-fold in *C. dubliniensis*, consistent with the cells added requirement to aquire NADH due to the peroxide stress.

Of the 133 genes significant down-regulated specifically in *C. dubliniensis*, 32% were of unknown function. Genes od known function, including *TPS2* which encodes trehalose-6-phosphate phosphatase, involved in trehalose metabolism showed a 2-fold down-regulation compared to *C. albicans* in response to oxidative stress. *GLC3.3f* (1,4-glucan branching enzyme, 3 prime end) and *GLG2* (self-glucosylating initiator of glycogen synthesis) both involved in glycogen synthesis are down-regulated. This is consistent with the cells reprogramming of metabolic pathways to ensure there is sufficient NADH for the reduction of antioxidant mechanisms. *GLK1* (aldohexose specific glucokinase) involved in cellular metabolism, *CWH41* (ER glucosidase), *AMGY1*, *AMYG2* (glucoamylases), *CHS3* (chitin-UDP acetyl-glucoaminyl transferase), *CHT3* (Chitinase 3 precursor), *CHS4* (chitin synthase regulatory factor), *ECM7* all involved in cell wall and chitin biosynthesis were among the *C. dubliniensis*-specifically down –regulated genes. *RGA2* (rho-GTPase activating protein) involve in the DNA damage response was significantly downregulated in *C. dubliniensis* (>1.6-fold), consistent with the effect of oxidative stress on the cells.

6.3.2 General stress response

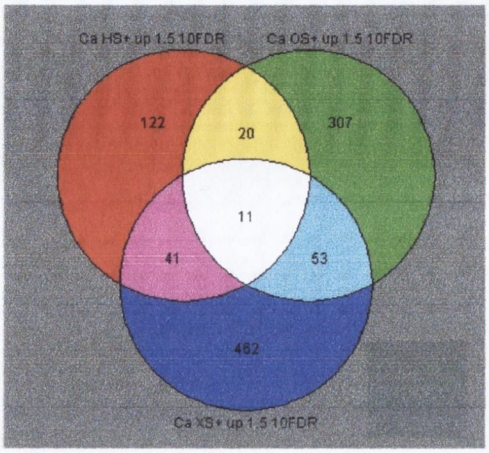
Although the core stress response genes are regulated differently in both species , *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001) and *S. pombe* (Chen *et al.*, 2003) have been shown to induce a common set of genes in response to a diverse range of stresses in what is known as the general stress response. In *C. albicans*, transcript profiling suggested that *C. albicans* does not induce a general stress response under similar conditions which induce a response in *S. cerevisiae*. However, Smith *et al.* (2004) have suggested that a core stress response is in fact activated in *C. albicans* but under conditions which activate the Hog1 SAPK i.e. oxidative stress (>2 mM H_2O_2) osmotic /saline stress (0.3 M NaCl, 0.6 KCl) and heavy metal stress (0.5 mM $CdSO_4$).

As *C. dubliniensis* was able to generate a global transcriptional response to each of the stresses used in this study (i.e. heat, osmotic and oxidative), using the normalised data obtained it was decided to investigate if *C. dubliniensis* activates a common set of genes in response to these three stresses. Core response genes

were identified as genes significantly induced or repressed (according to SAM) at least 1.5-fold in response to a heat shock of 42°C, osmotic shock of 1M NaCl and an oxidative shock of 5 mM H_2O_2. Core response genes were identified in both *C. albicans* and *C. dubliniensis* (Figs 6.10 and 6.11). The Venn diagram shows the number of genes whose expression was altered in response to a specific stress and to two or three stresses. Surprisingly, among the down-regulated genes there was less overlap between stresses compared to the up-regulated genes. However, this may be a result of the lower intensity of *C. albicans* transcriptional response to heat shock or may be a result of the stringent statistical analysis used in acquiring the data. In *C. albicans*, 19 statistically significant core response genes were identified in (Fig. 6.10), 11 of which were up-regulated and 8 of which were down-regulated. These core genes consisted of induced genes involved in transport (*IPF7530*), cell organisation and biogenesis (*KRE1*), maintaining cell ion homeostasis (CCC1), protein folding (*RPN4*), aldehyde metabolism (*IPF2897*). The function of the remainder of the genes was unclear. Among the 8 repressed genes included were *GDH3*, an NADH dehydrogenase which is involved in glutamate metabolism, *IPF7289* and *ERG1* both involved in sterol biosynthesis, *PGA4* and *PGA6* involved in cell wall organisation, *IPF19772* involved in phosphate synthesis. The function of the remaining 2 genes is yet to be elucidated. Although, the number of genes commonly induced in *C. albicans* under all three conditions was small compared with core stress genes regulated in *S. pombe* (Chen *et al.*, 2003)and *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001) it does demonstrate that *C. albicans* is capable of activating a set of genes common to all three stresses examined.

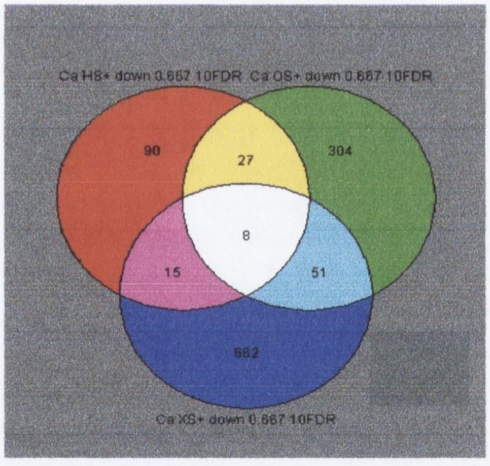
The numbers of *C. dublinienis* stress specific genes significantly regulated by each, and in response to two or more of the stresses are illustrated in the Venn diagrams in Figure 6.11. Thirteen genes in total (8 up-regulated and 5 down-regulated) were activated in response to heat, oxidative and osmotic shock. The 8 up-regulated genes included genes involved in protein folding (*RPN4*), in methionine metabolism (*MET1*) and in maintaining energy (*EBP1*, *EBP4*). The remainder of the genes included *CTA1* 2 which encodes catalase A, involved in the detoxification of superoxides, *IPF5972* (a putative cysteine doxygenase), *IFS4* (a pirin protein) and *MET1* (involved in methionine metabolism). The 5 down regulated genes included genes involved in aerobic respiration (*IPF19785*), in

(a)



HS	OS	XS	CandidaDB	orf19	Function
8.0	3.3	5.1	IPF525	orf19.7085	unknown function
5.1	3.6	2.5	IPF12897	orf19.2244	putative oxidoreductase (by homology)
3.4	1.7	5.8	IPF3264	orf19.3139	unknown function
3.2	3.6	3.7	RPN4	orf19.1069	26S proteasome subunit (by homology)
2.6	1.9	7.6	IFS1	orf19.2461	Unknown function
2.2	9.4	8.6	IPF14981	orf19.3483	unknown function
2.1	1.6	3.1	ERC1	orf19.6691	ethionine resistance protein (by homology)
2.1	2.4	1.7	CCC1	orf19.6948	Transmembrane Ca2+ transporter (by homology)
1.9	2.2	4.0	IPF9683	orf19.3644	unknown function
1.8	3.8	2.0	KRE1	orf19.4377	secretory pathway protein
1.6	2.3	4.4	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)

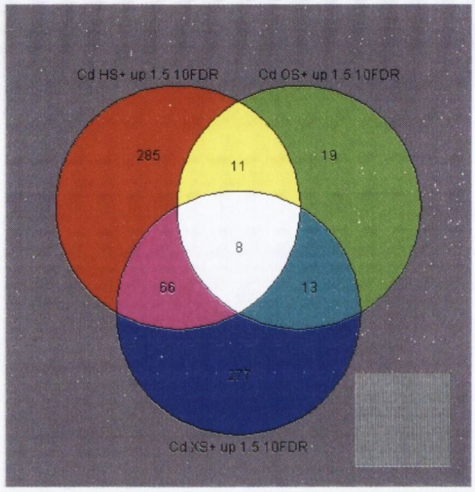
(b)



HS	OS	XS	CandidaDB	orf19	Function
0.1	0.3	0.1	IPF6518	orf19.1691	unknown function
0.1	0.6	0.5	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)
0.2	0.5	0.5	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA polymerase II transcription factor
0.2	0.4	0.7	ERG1	orf19.406	squalene epoxidase
0.2	0.6	0.5	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)
0.2	0.7	0.2	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified protein
0.4	0.7	0.5	PGA4	orf19.4035	putative GPI-anchhored protein related to Phr1, Phr2 and Phr3 (by homology)
0.4	0.4	0.6	IPF19772	orf19.5602	unknown function

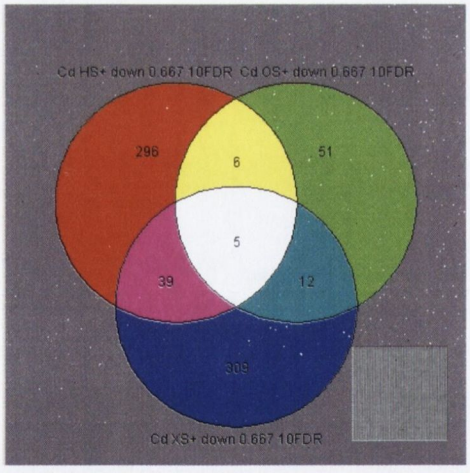
Figure 6.10 Venn diagram showing subsets of *C. albicans* genes significantly up- **(a)** and down-regulated **(b)** at least 1.5-fold in response to heat (HS), Osmotic (OS) and oxidative stress (XS). Heat shock-specific response genes are red, Osmotic shock-specific genes are green and oxidative–specific genes are blue. Genes significantly induced/repressed in response to all three stresses are in white.

(a)



HS	OS	XS	CandidaDB	Ca orf19	Ca Function
16.9	9.8	2.7	IPF525	orf19.7085	unknown function
5.0	2.1	1.5	MET1	orf19.5811	siroheme synthase (by homology)
4.1	2.0	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)
4.1	1.9	5.3	EBP1	orf19.125	NADPH dehydrogenase
3.7	2.5	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)
2.0	2.3	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)
1.8	2.4	1.9	IFS4	orf19.2467	Pirin protein (by homology)
1.7	2.1	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)

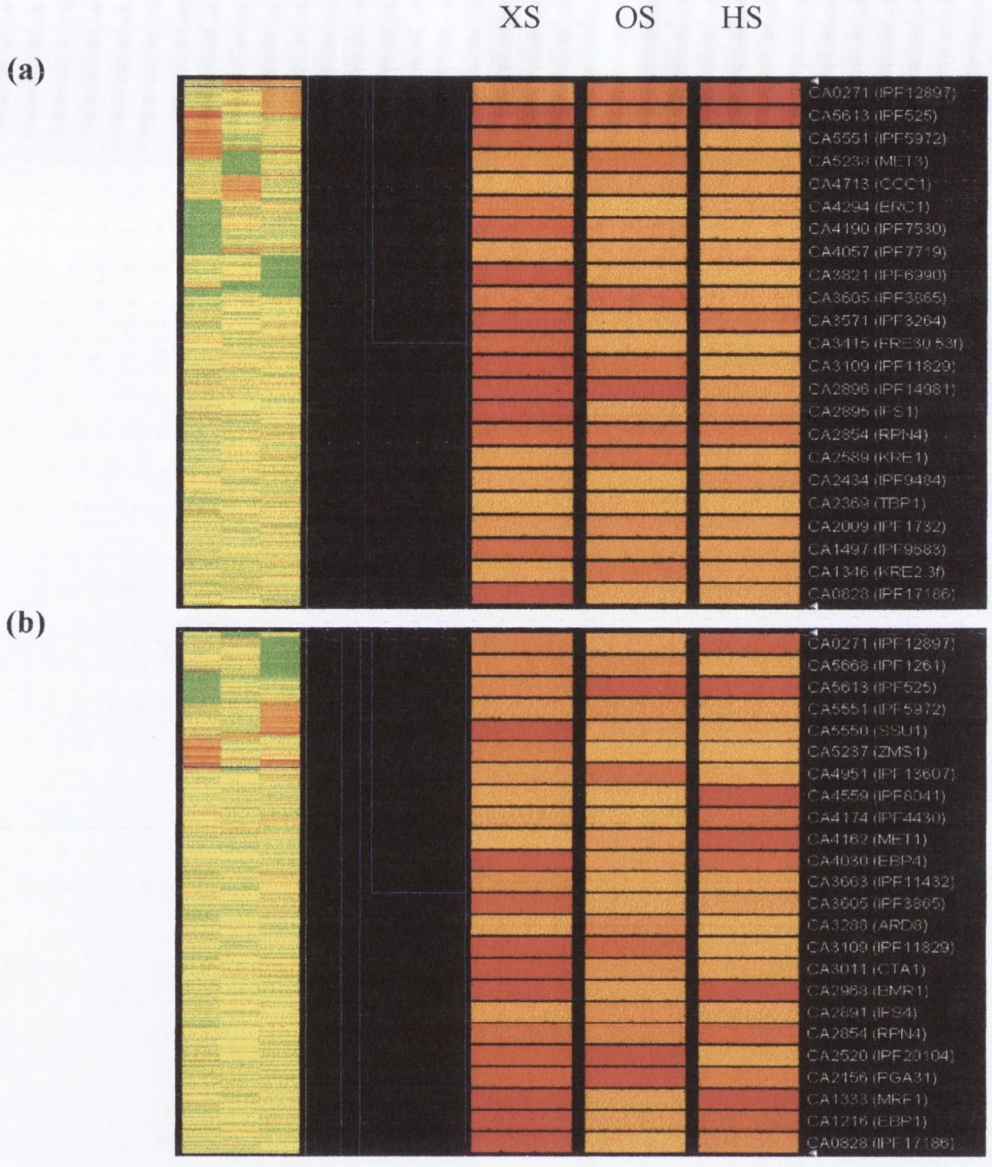
(b)



HS	OS	XS	CandidaDB	orf19	Ca Function
0.6	0.4	0.3	IPF3506	orf19.6741	unknown function
0.6	0.6	0.4	IPF19785	orf19.4929	involved in aerobic respiration
0.3	0.6	0.5	IPF7289	orf19.391	similar to S. cerevisiae Upc2p RNA polymerase II transcription factor
0.7	0.6	0.4	IPF16189.3f	orf19.5576	panthotenate kinase, 3-prime end (by homology)
0.2	0.6	0.5	IPF19772	orf19.5602	involved in phosphate metabolism

Figure 6. 11 Venn diagram showing subsets of *C. dubliniensis* genes significantly up- **(a)** and down-regulated **(b)** at least 1.5-fold in response to heat (HS), Osmotic (OS) and oxidative stress (XS). Heat shock-specific response genes are red, Osmotic shock-specific genes are green and oxidative–specific genes are blue. Genes significantly induced/repressed in response to all three stresses are in white.

sterol biosynthesis (*IPF7289*), coenzyme biosynthesis (*IPF16189*) and phosphate metabolism (*IPF19772*) and *IPF3506*, a gene of unknown function. Similar to what was observed in *C. albicans* these results demonstrate that *C. dubliniensis* is capable of stimulating a common set of genes in response to these three specific conditions used. Furthermore a comparison of the commonly responsive genes of both species revealed that only *IPF525*, *1PF19772, IPF7289* and *RPN4* were identified as being commonly regulated in both species under all three conditions. Again this could be a consequence of the weak response of *C. dubliniensis* to osmotic stress or due to the statistical analysis carried out on the dataset. It must be noted that the regulation of these genes was found to be statistically significant according to SAM. Thus, due to the stringency of this method of analysis, further analysis using less stringent criteria might identify other genes that may be involved in the core stress responses of both *C. albicans* and *C. dubliniensis*. To investigate this further, hierarchical clustering was employed to analyse the expression profiles of *C. albicans* and *C. dubliniensis* genes which are regulated in reponse to all three stresses, as this type of data analysis accounts for both significant and non-significant genes. Analysis of the expression profiles by hierarchical clustering identified an additional 34 *C. albicans* genes (12 up-regulated >1.5-fold and 23 down-regulated > 1.5-fold) and an additional 21 *C. dubliniensis* genes (16 up-regulated >1.5-fold and 5 down-regulated > 1.5-fold) with changes in transcript levels under all three conditions tested (Figs. 6.12 and 6.13). Among the *C. albicans* genes commonly induced included genes involved in protein folding and degradation (*IPF17186*, *IPF9484*, *IPF7719*), in ion homeostasis (*FRE30.53*, *IPF11829*), in sulfate (*MET3*) and ethanol (*IPF3865*) metabolism, in transcription (*TBP1*) in cell organisation and biogenesis (*KRE2.3f*), and transport (*IPF6990*). Other induced genes included a putative cysteine dioxygenase (*IPF5972*) and an intra mitochondrial sorting protein (*IPF1732*). Among the commonly down-regulated genes included genes involved in phosphate (*IPF19772*, *VTC1*) amino acid (*MAE1*), and carbohydrate metabolism (*IPF8321*, *PCK1*), transport (*ZRT2*, *QDR1*), cell wall biogenesis and assembly (*ECM331*, *ECM3*), ergosterol biosynthesis (*NCP1*), cell cycle and DNA processing (*CDC5*, *CLN2*), cell morphology (*INT1*) and differentiation (*CYB1*). Other genes repressed include *IPF18474* (involved in DNA replication), *ENG1* (involved in cytokinesis) and *MNN22* (involved in biogenesis of cellular



[Ca CSR] and [Cd CSR]

XS Ca	OS Ca	HS Ca	XS Cd	OS Cd	HS Cd		
2.5	3.6	5.1	3.0	2.0	4.9	IPF12897	putative oxidoreductase (by homology)
5.1	3.3	8.0	2.7	9.8	16.9	IPF525	unknown function
4.2	2.0	1.7	2.3	2.3	2.0	IPF5972	putative cysteine dioxygenase (by homology)
3.1	4.0	1.9	4.7	1.7	2.0	IPF3865	ethanol metabolism
7.3	3.5	1.7	6.3	4.0	1.6	IPF11829	involved in iron-ion homeostasis
3.7	3.6	3.2	3.5	2.5	3.7	RPN4	26S proteasome subunit (by homology)
11.9	1.8	1.9	18.0	1.5	2.5	IPF17186	protein degradation

Figure 6.12. Induced core stress genes in *C. albicans* **(a)** and *C. dubliniensis* **(b)** revealed by clustering. Genes displaying an induction of more than 1.5-fold in response to heat (HS), oxidative (XS) and osmotic (OS) stress were clustered. Up-regulated core stress genes in *C. albicans* and *C. dubliniensis* were compared **(c)**. The numbers of overlapping genes between the two species are shown in the Venn diagram **(c)** and the gene names and their expression profiles are provided.

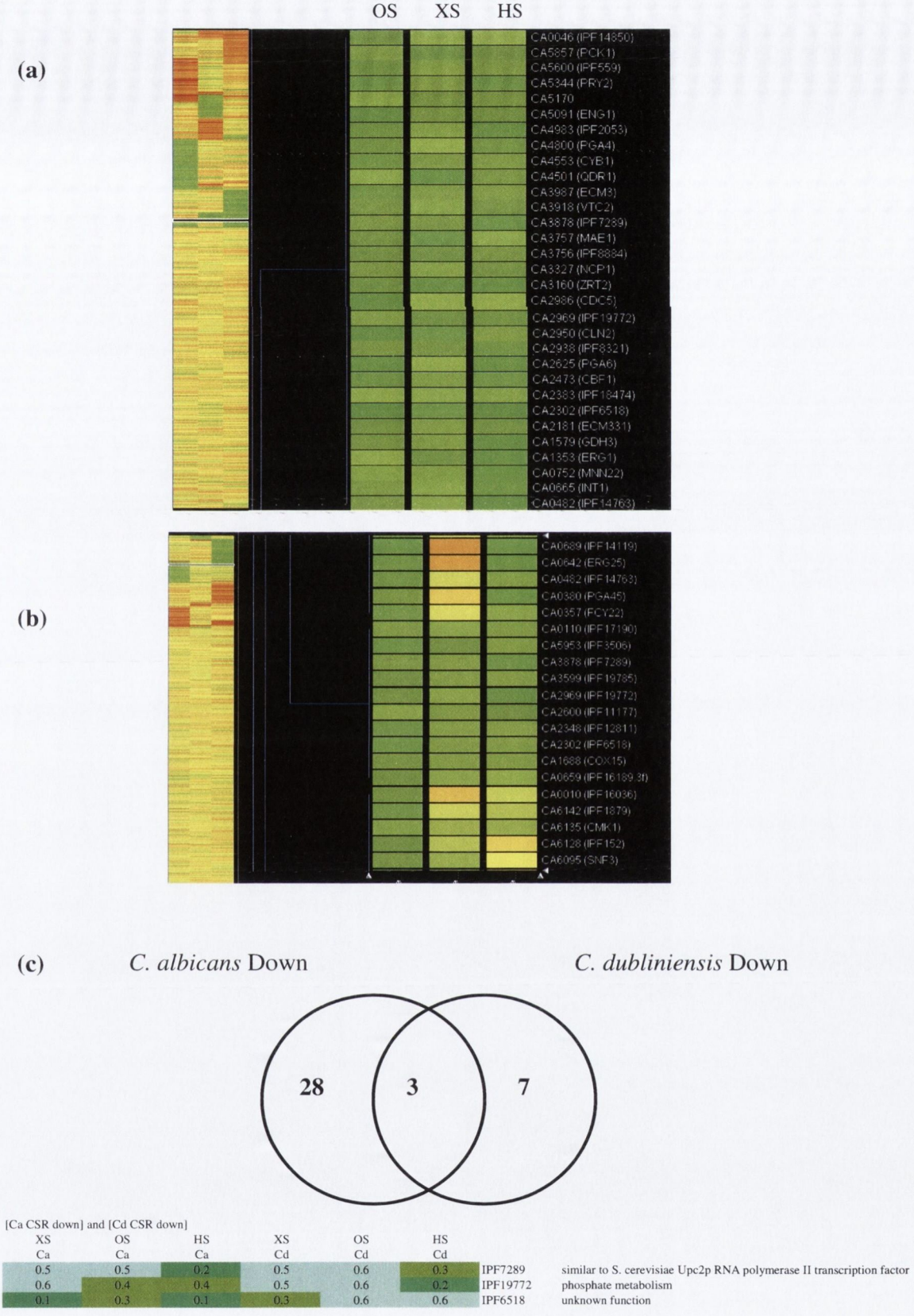


Figure 6.13. Repressed core stress genes in *C. albicans* **(a)** and *C. dubliniensis* **(b)** revealed by clustering. Genes displaying an expression ratio less than 0.667 (>1.5-fold down-regulation) in response to heat (HS), oxidative (XS) and osmotic (OS) stress were clustered. Down-regulated core stress genes in *C. albicans* and *C. dubliniensis* were compared **(c)**. The numbers of overlapping genes between the two species are shown in the Venn diagram **(c)** and the gene names and their expression profiles are provided.

components). The remainder of the genes were of unknown function. Thus, combining both methods of analysis (i.e. SAM and hierarchical clustering) identified 23 up-regulated core response genes (11 of which were significant according to SAM) and 30 down-regulated core response genes (8 of which were found to be significant by SAM) in *C. albicans*. The functional categories of the induced and repressed *C. albicans* genes mentioned above are similar to those associated with the core stress response in *S. pombe* and *S. cerevisiae* i.e. lipid or fatty acid metabolism, carbohydrate metabolism, signalling and transcriptional regulation, protein folding and degradation, transport, DNA repair, cell wall modification and metabolism

Among the commonly induced *C. dubliniensis* genes included genes involved in fatty acid (*ARD8*) ethanol (*IPF3865*) and carbohydrate metabolism (*IPF20104*), respiration (*IPF11432*, *MRF1*), protein folding (*IPF17186*), drug resistance (*BMR1/MDR1*), transport (*SSU1*, *IPF4430*), DNA damage (*IPF8041*). Of the 5 *C. dubliniensis* commonly repressed genes included *COX15* (involved in respiration), *IPF11177* (involved in mitochondrial organisation and biosynthesis), *IPF12811* (a putative serine/ threonine kinase) and *IPF17190* and *IPF6518* both of unknown function. These data taken together with the genes identified by SAM, revealed 24 up-regulated (of which 8 genes were significant according to SAM) and 10 down-regulated (of which 5 genes were significant according to SAM) *C. dubliniensis* core stress response genes. Similar to *C. albicans* the core stress response (induced and repressed) genes of *C. dubliniensis* belong to functional categories similar to those associated with the core stress response genes of *S. pombe* and *S. cerevisiae*. Interestingly, the *CTA1* gene which is involved in the detoxification of reactive oxygen species, a gene associated with the core stress response genes of *S. cerevisiae* and *S. pombe* was only found to be commonly induced in *C. dubliniensis* and not *C. albicans*.

To investigate if there was an overlap between the induced core stress genes of *C. albicans* and *C. dubliniensis*, identified by hierarchical clustering a comparison of the *C. albicans* and *C. dubliniensis* core stress genes was performed (Fig. 6.12). This comparison revealed an overlap of 7 genes (2 of which were already shown to be statistically significant by SAM, i.e. *IPF525* and *RPN4*) that were induced both species, under all three conditions tested. The 5 additional genes, identified by hierarchical clustering, overlapping between both

species under all three conditions included *IPF5972* (a putative cysteine doxygenase) *IPF12897* (involved in aldehyde metabolism), *IPF3865* (involved in ethanol metabolism), *IPF17186* (involved in protein degradation) and *IPF11829* (involved in iron ion homeostasis). A comparison of repressed genes (Fig.6.13) between the two species revealed an overlap of only 3 genes, 2 of which (*IPF19772* and *IPF7289*) were significant according to SAM).

Although the magnitude of the core stress response of both *C. albicans* and *C. dubliniensis* is much weaker when compared to *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001) and *S. pombe* (Chen *et al.*, 2003) the genes involved are belonging to functional groups which have been previously implicated in the core stress responses of *S. pombe* (Chen *et al.*, 2003) and *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001). Overall this data suggests that both *C. albicans* and *C. dubliniensis* evoke a weak core stress response under the specific conditions tested in this study i.e. heat (30-42°C), osmotic (1M NaCl) and oxidative stress (5mM H_2O_2). However, it must be noted that the data obtained from hierarchical clustering was not significant, thus to confirm the weak core stress response observed in both species further analysis using Northern hybridisation and RT-PCR would be critical.

A possible explanation for the relatively weak core stress response observed in both species may be related to the level of the three stress conditions tested in this study. For example, it has been previously suggested that a core stress response does exist in *C. albicans* (Smith *et al.*, 2004) but is dependent on conditions that activate the Hog1 SAPK. In the same study it was demonstrated that a temperature up-shift of 23-42°C does not activate Hog1 SAPK, which may explain, in part, why in this study, so few genes were commonly regulated in response to all three stress conditions when compared to the core stress responses of *S. pombe* and *S. cerevisiae*. Furthermore, the same authors suggested that *C. albicans* has evolved its environmental stress responses in order to adapt to the human body and thus has a higher threshold to adverse conditions comapared to *S. cerevisiae*. This may be the same for *C. dubliniensis*. However, as there were few core stress response genes in common between *C. albicans* and *C. dubliniensis*, it suggested that the stress responses of both these species may be divergent in these closely related species. These findings may reflect the reduced

capacity of *C. dubliniensis* to withstand environmental stress compared to *C. albicans*.

An interesting finding deduced from the cluster analysis of the expression of induced core stress response in *C. albicans* and *C. dubliniensis* was that a gene encoding a multidrug efflux pump of the major facilitator superfamily, *BMR1* (also known as *MDR1*) was induced in *C. dubliniensis* in response to heat, osmotic and oxidative stress but was only induced in *C. albicans* in response to heat and oxidative stress. The up-regulation of *MDR1* has been shown to play a key role in mediating fluconazole resistance in both clinical isolates and *in vitro*-generated fluconazole-resistant *C. dubliniensis* derivatives (Moran *et al.*, 1998; Wirsching *et al.*, 2001). In addition *MDR1* has been shown to be preferentially induced in approximately 58% of genotype I (predominant genotype recovered from HIV-infected patients) *C. dubliniensis* isolates. It has been suggested that the increase in the incidence of *C. dubliniensis* in the early 1990's might have been due to its ability to develop resistance to fluconazole. The findings in this study suggest that perhaps the ability of *C. dubliniensis* to preferentially induce *MDR1* under conditions of osmotic stress, compared to *C. albicans*, may reflect its ability to thrive in the oral cavities of patients undergoing fluconazole therapy.

The data presented in this study comprise the first examination of the global effects of a diverse range of environmental stresses i.e. osmotic (1 M NaCl), oxidative (5 mM H_2O_2) and heat stress (30-42°C) on gene expression in *C. dubliniensis*. This study provided a first step towards elucidating the role of stress responses in the lower stress tolerance of *C. dubliniensis* compared to *C. albicans*. A summary of the main findings are as follows: (1) It is feasible to use *C. albicans* DNA microarrays to examine the transcriptional responses of *C. dubliniensis*. Transcript profiles obtained from both *C. albicans* and *C. dubliniensis* cells exposed to heat and osmotic shock confirmed previous Northern hybridisation data obtained in this study; no significant increase in the induction of the trehalose metabolic genes *TPS1* and *NTC1* in response to thermal and osmotic stress and the up-regulation of *HSP90* in response to heat shock in both species was observed by both techniques.. Furthermore, the induction of the *ENA21.3* gene in the *C. dubliniensis* strain CD36 determined by Northern analysis in this study was confirmed by the transcript profiling data. Further analysis of a limited number of genes implicated in the heat shock of *C. dubliniensis* including

AOX1, *HSP10*, *SOD1* and *GRP2* also confirmed transcript profiling data. However, it was noted the transcript profiling data did not reveal an induction of *HSP104* in either *C. albicans* or *C. dubliniensis*, which was previously determined in Northern analysis data obtained in this study. An explanation for this observation is that it was likely to be due to a defect in the spotting of the arrays by Eurogentec as other researchers (Enjalbert *et al.*, 2005, unpublished data) have encountered similar problems with this gene spot. Furthermore, this observation highlights the importance of confirming transcript profiling data by using Northern hybridisation and RT-PCR.

(2) *C. dubliniensis* is able to evoke a global transcriptional response to heat, osmotic and oxidative stress. This was evident from the expression changes observed in genes whose products have been previously shown to be involved in resistance to heat (e.g *HSP90*, *HSP78*, *HSP60*, *HSP10*) osmotic (*GPD2*, *STL1*, *ENA21.3*) and oxidative shock (*TTR1*, *CTA1*,*TRR1*,*TRX1 CAP1*) in stressed cells compared with unstressed cells.

(3) The magnitude and nature of the transcriptional responses varied between *C. albicans* and *C. dubliniensis*. For example the heat shock response of *C. dubliniensis* (716 genes, >1.5-fold up/ down-regulated) was much stronger to that of *C. albicans* (334 genes, >1.5-fold up/down-regulated) suggesting that *C. albicans* has a higher temperature threshold compared to *C. dubliniensis*. In addition, the weaker response of *C. dubliniensis* to a salt induced osmotic shock (1 M NaCl) reflected its reduced tolerance to high salt concentrations, compared to *C. albicans*.

(4) Both *C. albicans* and *C. dubliniensis* evoke weak core stress responses compared to *S. cerevisiae* and *S. pombe*. Again the weaker core stress responses of *C. albicans* and *C. dubliniensis* may reflect the fact that both of these pathogens occupy different environmental niches to *S. cerevisiae* and *S. pombe* and thus have higher thresholds to adverse stress conditions. However, this needs to be confirmed with more specific expreiments i.e. RT-PCR, and Northern hybridisation analysis

(5) Genes of interest for further analysis were identified including *IPF2839, SOD1.3, SOD2, HSP10, GRP2, AOX1, AOX2, MXR1, TRR1, TRX1, GPD2, ATH1, SGD1, SKO1.3f,* which may in part explain the reduced tolerance of *C. dubliniensis* to high salt concentrations and the identification of *MDR1* as a

core stress response gene of *C. dubliniensis* may have be of clinical significance and may explain why *C. dubliniensis* is able to develop fluconazole resistance rapidly.

(6) The results have implicated a substantial set of genes of unknown function (>40%) in the response to the environmental conditions tested in this study. These genes of unknown functions may have important roles in the stress responses of both *C. albicans* and *C. dubliniensis* and thus need to be investigated further again using RT-PCR and Northern hybridisation experiments.

In conclusion, this work has provided data which with further experimental analysis will ultimately lead to an prominent understanding of the stress responses of *C. dubliniensis* and may, in part, explain the reasons for the differences in the ability of *C. albicans* and *C. dubliniensis* to cause disease.

Chapter 7

General Discussion

7.1 General Discussion

Candida albicans and *C. dubliniensis* are so closely related in phylogenetic terms that they share many phenotypic characteristics, and thus it is very difficult to differentiate between the two in clinical samples. Given this close relationship it would be expected that they would have a similar capacity to cause disease. However, the available epidemiological and infection model data indicate that *C. albicans* is a far more potent pathogen (Sebti *et al.*, 2001; Vilela *et al.*, 2002; Kibbler *et al.*, 2003; Sullivan *et al.*, 2004).

Although, the human body provides a favourable microenvironment for the growth of these two species, providing relatively constant conditions of pH and osmotic pressure, with a normal core temperature of 37°C, it should not be considered as one uniform microbial environment. Each region or organ differs both chemically and physically from other regions and thus provides a selective environment where the species that colonise the host successfully are those that have developed ways of circumventing the hosts defence mechanisms. *Candida albicans* can adapt rapidly to changes in environmental conditions and its ability to evade such defence mechanisms including, oxidative killing by macrophages has been demonstrated (Lo *et al.*, 1997). Furthermore, specific stress response mechanisms have been identified in *C. albicans*, that are essential for resistance to oxidative and osmotic stress (San José *et al.*, 1996, Alonso-Monge *et al.*, 2003). Deletion of genes encoding stress signalling proteins involved in these mechanisms has been shown to attenuate virulence in mice (Alonso-Monge *et al.*, 1999), thus highlighting the importance of stress response mechanisms and their role in the virulence of *C. albicans*.

One of the few phenotypic differences between *C. albicans* and *C. dubliniensis* is the higher tolerance of *C. albicans* to elevated temperature and NaCl concentration (Pinjon *et al.*, 1998; Alves *et al.*, 2002), thus suggesting that *C. albicans* might have a greater capacity to adapt and survive within the human body.

The purpose of the current study was to investigate the molecular basis of the differential ability of the two species to tolerate environmental stress in order

to determine if this may contribute to the greater virulence of *C. albicans* in comparison with *C. dubliniensis*.

The aim of the first section of the present study was to compare the ability of both species to grow *in vitro* under a diverse range of environmental conditions. Prior to this study, it had been shown that *C. dubliniensis* was less tolerant of environmental stresses such as heat, osmotic and oxidative stress compared to *C. albicans* (Pinjon *et al.*, 1998; Alves *et al.*, 2002; Vilela *et al.*, 2002). In order to confirm and extend these data a comprehensive analysis of the comparative growth of representative strains of *C. albicans* and *C. dubliniensis* was investigated under a wide range of environmental conditions. Doubling times of representative strains from the two species grown in liquid media at temperatures ranging from 30-44°C, and with NaCl concentrations ranging between 0.6 M-1.6 M were determined and compared. The data from these experiments confirmed that *C. dubliniensis* exhibits a longer doubling time at temperatures greater than 42°C compared to *C. albicans*. Survival rates, and spot plate assays carried out at the elevated temperature of 42°C further confirmed these data. Similarly, *C. dubliniensis*, unlike *C. albicans*, grows relatively poorly in media containing 0.8 M-1.6 M NaCl as determined by observed differences in doubling times, survival and spot plate assays. Growth on YPD medium supplemented with elevated sorbitol concentrations was also investigated. Interestingly, spot plate assays carried out using increasing concentrations of sorbitol (with the exception of *C. dubliniensis* isolate CD539) had no effect on the growth of both species. This inferred that the osmosensitive phenotype observed in *C. dubliniensis* maybe in fact due to the cation toxicity of a salt induced osmotic shock by the chloride salts NaCl and KCl. Another important result of the study was the significantly higher susceptibility of *C. dubliniensis* to H_2O_2 compared to *C. albicans*. The results for this part of the study clearly indicate that *C. dubliniensis* has a reduced capacity to tolerate a range of environmental stress conditions. As *C. dubliniensis* is less tolerant of such varied environmental stresses it was postulated that this was possibly due to a deficiency in the regulation of one or more genes known to be implicated in *C. albicans* stress response.

In order to investigate the molecular responses of each species to heat and osmotic shock, the presence and expression of putative stress response genes,

known to be stress induced in other species, i.e. the heat shock proteins and trehalose metabolic genes were compared. Using PCR primers homologous to the *C. albicans HSP90* and *HSP104* genes the presence of the closely related homologues of these genes in the *C. dubliniensis* genome was confirmed. It has been previously demonstrated that *HSP90* is induced in *C. albicans* in response to heat shock (Swoboda *et al.*, 1995; Enjalbert *et al.*, 2003). Data obtained from Northern hybridisation experiments and microarray analysis obtained in this study confirmed this finding. In addition Northern analysis of *HSP104* expession confirmed that both *C. albicans* and *C. dubliniensis* are also capable of inducing this heat shock protein gene in response to a 30-42°C temperature up-shift. Although transcript profiling data (this study), failed to show an induction of *HSP104*, this may be due to a fault in the printing of the arrays by Eurogentec as similar difficulties with the *HSP104* gene spot have been highlighted by other researchers (Enjalbert *et al.* (2005), unpublished data). An interesting finding noted from the Northern hybridisation data was that although both *HSP90* and *HSP104* were heat shock inducible in both species, the rate of induction of both these genes appeared to be faster in *C. dubliniensis* (induced following 5 min) compared to *C. albicans* (induced following 10 min) in response to the heat shock. The faster rate of induction of *HSP90* and *HSP104* observed in *C. dubliniensis* may relate to the finding that *C. dubliniensis* is less able to withstand higher temperatures compared to *C. albicans*. It also suggests that the regulatory mechanism controlling the induction of heat shock proteins in *C. dubliniensis* may have a lower temperature threshold compared to that of *C. albicans*.

One interesting phenotypic difference between *C. albicans* and *C. dubliniensis* is the increased ability of *C. albicans* to grow on trehalose. Since accumulation of this sugar is known to be an important stress response mechanism, this raised the possibility that the lowered stress tolerance of *C. dubliniensis* might be the result of a defect in trehalose metabolism. In order to investigate this possibility, the expression of the trehalose metabolic genes (i.e. *TPS1* and *NTC1*) was compared in both species. The first trehalose metabolic gene examined was *TPS1*, encoding trehalose-6-phosphate synthase the enzyme responsible for catalysing the first step in trehalose synthesis. Previous studies on yeast such as *S. pombe* and *S. cerevisiae* have shown that if the temperature rises above 37°C the mRNA level of *TPS1* increases (De Virgilio *et al.*, 1993; Parrou *et*

al., 1997). In addition, it has been shown in *S. pombe* that the level of *TPS1* increases in response to both osmotic and thermal stress (Paredes *et al.*, 2003). In *C. albicans*, according to a study by Zaragoza *et al.* (1998), (although data were not shown) it was claimed that a heat shock of 42°C increased the expression of *TPS1*. Northern hybridisation analysis of *TPS1* mRNA expression levels in *C. albicans* and *C. dubliniensis* confirmed that the *TPS1* gene is expressed during exponential growth at 30°C and under conditions of heat shock at 42°C. However, in contrast to previously published results, *TPS1* mRNA levels did not increase significantly in the two *C. albicans* strains tested (*C. albicans* 132A and *C. albicans* SC5314) which was consistent with the microarray data obtained in this study. Of the two *C. dubliniensis* isolates examined, only *C. dubliniensis* isolate CD36 was found to express slightly increased levels of *CdTPS1* mRNA (~0.5-fold) compared to *C. albicans*, again in agreement with the transcript profiling obtained in this study. These findings suggested that *TPS1* gene expression may be strain-specific in *C. dubliniensis*. These data appear to contradict the observation of Zaragoza *et al.* (1998) who observed an increase in *TPS1* gene expression in *C. albicans* when exposed to a thermal stress. In addition to heat shock, *TPS1* gene expression was examined by Northern analysis in response to an osmotic shock of 1M NaCl in both species. Northern analysis established that both *C. albicans* and *C. dubliniensis* express the *TPS1* gene at 37°C. In response to the osmotic shock, both the *CaTPS1* and *CdTPS1* transcripts were repressed, again in agreement with microarray data obtained in this study.

The second trehalose metabolic gene examined in this study was the gene encoding neutral trehalase, *NTC1*. It has been shown previously that the *S. cerevisiae* homologue of the *NTC1* gene, *NTH1*, is induced during a heat shock of 30-40°C (Nwaka *et al.*, 1995) and is also induced in *S. pombe* under both thermal and osmotic shock conditions (Paredes *et al.*, 2003). However, it has been reported that the transcription of *NTH1* expression is not induced at temperatures over 40°C (Iwahashi *et al.*, 2000). Expression of the *NTC1* gene in *C. albicans* and *C. dubliniensis* under conditions of heat shock (30-42°C) was compared by Northern analysis for the first time in this study. Northern analysis established that the *NTC1* gene was expressed in both these species in exponential cells at 30°C. In addition, Northern analysis indicated that *CaNTC1* was not induced in response to a heat shock of 30-42°C, in agreement with microarray data obtained

in this study. The transcript profiling data of Enjalbert *et al.* (2003) showed similar results with *C. albicans* cells exposed to a temperature up-shift of 23-37°C. In *C. dubliniensis*, only one of the two strains tested by Northern analysis (i.e. p7718, a genotype 4 strain), showed a weak increase (1.5-fold) in *NTC1* mRNA levels in response to a heat shock of 42°C. As no induction of the *NTC1* gene was observed in the second *C. dubliniensis* isolate tested (i.e. CD36, a genotype 1 strain), which was confirmed by transcript profiling (this study), suggesting that *NTC1* gene expression in *C. dubliniensis* may be strain specific.

Northern analysis of the *NTC1* gene under osmotic conditions (i.e. 1 M NaCl) in representative strains from both species was also examined. Northern analysis established that the *NTC1* gene was also expressed in both species at 37°C. In addition, Northern analysis showed that an osmotic shock treatment of 1 M NaCl does not induce *NTC1* gene expression in both species, which was further confirmed in the transcript profiling data (this study). Collectively, from these Northern analyses and microarray data it is apparent that there is no significant increase (i.e. > 1.5-fold) in expression of *TPS1* or *NTC1* in *C. albicans* or *C. dubliniensis* in response to thermal or osmotic stress. In order to further investigate the role of trehalose in the stress response mechanisms of these pathogens, the intracellular levels of trehalose and the activity of the enzymes involved in the trehalose metabolic pathway in *C. albicans* and *C. dubliniensis* were investigated under normal conditions and under conditions of environmental stress including osmotic and thermal stress.

Determination of intracellular trehalose levels revealed that both species were capable of accumulating intracellular trehalose in reponse to a strong heat shock of 42°C which was in agreement with a previous study carried out on *C. albicans* (Van Dijck *et al.*, 2002). In addition, an osmotic shock of 1 M NaCl had no significant effect on the accumulation of trehalose at 37°C in both species. Measurement of trehalose-6-phosphate synthase and trehalose-6-phosphate phophatase activity revealed that there was no significant diffence in the activities of these enzymes when they were induced in response to a heat shock of 30-42°C in both species. In addition measurement of neutral trehalase activities in both species showed similar trends in activation in reponse to thermal stress. In summary, these results demonstrated that *C. dubliniensis* has the ability to accumulate trehalose under heat (42°C) and osmotic conditions (1 M NaCl) and

that the trehalose metabolic enzymes of *C. dubliniensis* are functional under conditions of thermal stress. Interestingly, taken as a whole these data suggested that accumulation of intracellular trehalose upon exposure to thermal or osmotic stress is not dependent on the transcription of the trehalose metabolic genes (i.e. *TPS1* and *NTC1*). These results suggest that trehalose accumulation is a complex process and may involve post-translational regulation of the trehalose metabolic enzymes. Overall these data weakened the hypothesis that the accumulation of trehalose is a significant factor in the enhanced ability of *C. albicans* to survive under stressful conditions compared to *C. dubliniensis*.

From the previously described data it was clear to us that there were no significant differences in the conventionally recognised yeast stress response mechanisms between *C. albicans* and *C. dubliniensis*. However, during the course of this project microarrays corresponding to the entire *C. albicans* complement of 6,039 open reading frames became available. In addition, the Wellcome Trust Sanger Centre in Cambridge, began to sequence the *C. dubliniensis* genome (http://www.sanger.ac.uk/projects/ C_dubliniensis/). The availability of these two resources therefore allowed the global expression of genes under specific conditions of thermal, osmotic and oxidative shock to be investigated. Several major conclusions can be drawn from these experiments. The first main conclusion was that *C. dubliniensis* was capable of activating a global transcriptional response to heat, osmotic and oxidative stress. However, it was noted that the magnitude and the nature of the transcriptional responses varied between *C. albicans* and *C. dubliniensis;* i.e. *C. albicans* global transcriptional response to heat shock was notably lower than that of *C. dubliniensis*. For example in *C. dubliniensis* 716 (>1.5-fold up-/down-regulated genes), showed a statistically significant variation in their expression following 30 min of thermal stress whereas in *C. albicans* only 334 (> 1.5-fold up-/down-regulated genes) showed a statistically significant variation in their expression under similar conditions. This finding further strengthened the hypothesis that *C. dubliniensis* has a lower threshold to the level of heat stress required to activate a stress response, compared to *C. albicans*. Previous analysis of the heat shock proteins (*HSP90*, *HSP104*) by Northern hybridisation provided insight into the dynamics of these proteins in both species. As the threshold of these proteins appears to be shorter in *C. dubliniensis* the different time scales of production and

deactivation of these proteins may have an important dynamic consequence. Thus it would be of interest to carry out a comprehensive comparative analysis on the kinetics of these proteins in both species using both genomic and biochemical experimentation and based on a time series.

In addition, *C. dubliniensis*' response to osmotic shock (125 >1.5-fold up-/down-regulated genes) was much weaker to that of *C. albicans* (781>1.5-fold up-/down-regulated genes). Again this transcript profiling data reflected the reduced tolerance of *C. dubliniensis* to high salt concentrations. Interestingly oxidative stress led to the strongest expression changes in both species, however, the intensity of the response was still significantly higher in *C. albicans* (1300 >1.5-fold up-/down-regulated genes) compared to *C. dubliniensis* (729 >1.5-fold up-/down-regulated genes). The second main conclusion was that *C. dubliniensis* was capable of inducing or repressing "hallmark" stress response genes in response to heat (for e.g. *HSP90*, *HSP78*, *HSP60*, *HSP10* etc), osmotic (for e.g. *ENA21.3*, *STL1*, *GPD2*, *RHR2*) and oxidative stress (for e.g. *CTA1*, *TTR1*, *TRR1*, *TRX1*, *CAP1*) consistent with the dataset previously described by Enjalbert *et al.* (2003). The third main conclusion was the *C. dubliniensis* Hog1SAPK is activated under conditions of high osmotic shock (1 M NaCl) which confirmed that a defect in the Hog1 SAPK of *C. dubliniensis* is not responsible for the weak or lack of induction of the Hog1-linked genes (*ENA21.3*, *ENA22*, *SGD1*, *SKO1.3f*) in *C. dubliniensis*. Another outcome of this study was the identification of *IPF2839* which was confirmed by Northern analysis to be significantly up-regulated in *C. albicans* but not in *C. dubliniensis* in response a salt induced osmotic shock of 1 M NaCl suggesting that it may have a key role in the osmotolerance of *C. albicans* and hence, in part may explain why *C. albicans* is more resistant to high salt stress compared to *C. albicans*. Furthermore, it is possible that *IPF2839* may have a similar function to the *ENA21.3* gene (encoding a P-type ATP-ase involved in the extrusion of Na^+ ions from the cytoplasm) identified in this study in a functional genomic screen for genes involved in salt tolerance. Although *ENA21.3* was found to be present and expressed in *C. dubliniensis* in response to salt-induced osmotic shock (i.e. 1 M NaCl), confirmed by transcript profiling, it was suggested that the activities or ion affinities of this cation extrusion pump may differ between *C. albicans* and *C. dubliniensis*. In addition, transcript profiling data obtained in this study revealed that a second

gene encoding a cation extrusion pump i.e. *ENA22* was not induced in *C. dubliniensis* in reponse to salt induced osmotic shock. Taken together, these data point towards a possible defect in cation extrusion in *C. dubliniensis*, a possible explanation for the reduced salt tolerance of *C. dubliniensis*.

The final conclusion from this study was that *C. albicans* and *C. dubliniensis* both activate weak core stress responses under the three specific conditions tested in this study. Based on clustering analysis of genes up-regulated (1.5-fold) and down-regulated (>1.5-fold) in both species under all three conditions tested, it was suggested that though both *C. albicans* and *C. dubliniensis* induce/ repress a much smaller subset of genes, compared with what has been observed in the core stress responses of *S. pombe* (Chen *et al.*, 2003) and *S. cerevisiae* (Gasch *et al.*, 2000; Causton *et al.*, 2001) the genes involved were belonging to functional categories previously implicated in the general stress responses of these yeasts. However it must be taken into account that not all the core stress response genes were regulated significantly. For example of the 54 (up- and down-regulated) *C. albicans* core stress response genes identified by clustering, 19 were found to be statistically significant according to SAM. Among the 34 (up- and down-regulated) core stress response genes in *C. dubliniensis*, only 13 were found to be significant according to SAM. Hence, further analysis involving RT-PCR and Northern hybridisation would be required to confirm these data. In addition a comparison of induced and repressed core stress response genes between *C. albicans* and *C. dubliniensis* revealed an overlap of only 10 genes (7 up-regulated and 3 down-regulated) between the two species. This suggested that the stress responses of *C. albicans* and *C. dubliniensis* may be divergent and that perhaps these findings are a reflection of *C. albicans* enhanced ability to tolerate adverse stress conditions compared to *C. dubliniensis*. Furthermore, it must be taken into account that microarray analysis is merely a global screen and must be supported by further specific experiments. In this study, due to time constraints only a limited amount of Northern analyses were carried out (i.e. *AOX1*, *HSP10*, *SOD1*, *GRP2*) which confirmed the transcript profiling data. Further experiments using RT-PCR or Northern hybridisation must be carried out to confirm expression of individual genes or gene families of interest prior to functional analysis. An interesting observation from the transcript profiling data was that *C. dubliniensis* induced a sub-set of genes known to be

involved in the oxidative stress response when exposed to a heat stress including *AOX2*, *MXR1*, *TRX1*, *CAP1*, *TRR1 CTA1* and *SOD2*. The induction pattern of this set of genes which are known markers of the general stress response in *S. cerevisiae* may suggest that there is a core stress response in *C. dubliniensis*. However, this would warrant investigation into whether there are STREs (Stress Response Elements; "CCCCT") present and how many are there in the promoters of these genes. In *S. cerevisiae* activation of the general stress response involves recognition of these concensus STREs in the promoters of general stress response genes by the transcription factors Msn2p and Msn4p. By examining the effects of *MSN4* and *MNL1* (*C. albicans* homologues of the Msn2p and Msn4p transcription factors of *S. cerevisiae*) deletions would determine if these Msn2p- and Msn4p-like proteins play a role in the *C. dubliniensis* stress response. However, it must be taken into account that the Msn2p/Msn4p-STRE complex is not the only way to induce genes in reponse to a diverse range of stresses, even in *S. cerevisiae*. Overall an in depth analysis of this set of genes may lead to a better understanding of the responses involved or may lead to the identification of an alternative respiratory pathway in *C. dubliniensis*. Investigation into the phenomenon of cross protection, in which pre-treatment with one type of stress can protect the yeast from subsequent exposure to a different type of stress, in *C. dubliniensis* may also provide further insight into their reduced ability compared to *C. albicans* to respond to stressful conditions.

The work presented in this study provides for the first time a comprehensive investigation of the environmental stress responses of *C. dubliniensis* and *C. albicans*. Overall, both phenotypic and molecular data have shown that while *C. dubliniensis* is less tolerant to environmental stress it is still capable of activating classical stress response mechanisms. Whole genome expression analysis of changes in gene expression in both species has allowed more global questions to be asked and has confirmed previous Northern hybridisation data in this study (i.e. *HSP90*, *TPS1*, *NTC1*). It has also allowed the identification of genes with interesting expression patterns (e.g. *IPF2839*) which may help explain in part, explain why *C. dubliniensis* is less tolerant to environmental stress compared to *C. albicans*. In addition this study has provided a starting point for the investigation of numerous genes which may have a key role in the stress responses of these species. The wealth of unprecedented data

generated from these arrays needs to be further investigated. Analysing promoters of genes grouped by clustering may lead to the identification of regulatory motifs common to one or both of these species which could lead to a deeper understanding of their stress response machinery. By looking at metabolic pathways instead of single genes using methods such as "Pathway Processor" (http://cgr.harvard.edu/cavalieri/pp.html) which map expression data onto metabolic pathways (such as the trehalose metabolic pathway), the intricacies governing the metabolism of these species may be resolved. In addition, the implementation of powerful integrated software packages such as Cytoscape (Shannon *et al.*, 2003) a cornerstone of systems biology would help identify and elucidate regulatory pathways and their complex interconnections with other pathways in these pathogens. These extensions of microarray data analysis could be the next steps toward a deeper comprehension of the dynamics of the stress responses of *C. albicans* and *C. dubliniensis*. Looking to the future, it is hoped that completion of the annotation of the *C. dubliniensis* genome sequence (http://www.sanger.ac.uk/ Projects/C_dubliniensis/) will facilitate the design of *C. dubliniensis* microarrays for the entire genome. Further analysis of highlighted or target genes by RT-PCR, functional analysis including knockouts would ultimately lead to the use of *in vivo* models. These data will help elucidate the reasons for the differences in the capacity of these pathogens to cause disease. At the same time enhance the understanding of candidal pathogenicity and will help facilitate the identification of novel targets for future antifungal drug development.

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Appendix I

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caHSP104        AGTGCATTGGTCACTGCTGCTCAGTTGGCTTCAAGATACTTGACATACAGAGCATTACCT
cdHSP104        AGTGCATTGGTCACTGCTGCCCAGTTGGCCTCAAGATACTTGACGTACAGAGCATTGCCT
                ******************** ******** ************** *********** ***

caHSP104        GATTCAGCTGTTGATCTTGTTGATGAGAGTGCTGCTGCTGTTGCTGTGGCTAGAGACTCT
cdHSP104        GACTCTGCGGTTGATCTTGTTGACGAGAGTGCTGCTGCTGTTGCCGTTGCTAGAGATTCC
                ** ** ** ************** ******************** ** ******** **

caHSP104        AAGCCAGAAGAGTTGGACACTTTGGAAAGACAATTGCATTTGGTAGATGTCGAAATCAGT
cdHSP104        AAGCCTGAGGAGTTGGACACTTTGGAAAGACAATTGCACTTGGTGGATGTTGAAATCAAT
                ***** ** ****************************** ***** ***** ******* *

caHSP104        GCATTAGAAAGAGACAAAGATGCAGACTCTGCTTCCAAGGAACGTTTGAATTTGGCCAAA
cdHSP104        GCATTGGAAAGAGATAAAGATGCAGACTCTGCTTCTAAAGAACGTTTGAATTTGGCGAAA
                ***** ******** ******************** ** ***************** ***

caHSP104        AAGAAGAAAGCAGAATTGGAAGAAAAAATTGGACCATTGAACGAGAGATACAGACAAGAA
cdHSP104        AAGAAGAAGGCCGAATTGGAAGAAAAAATTGGTCCATTGAATGAAAGATACAAGCAGGAA
                ******** ** ******************** ******** ** *******  ** ***

caHSP104        CGAGCTAGTCATGAACAATTGACTGCTGCCAAAAGAAAATTGGATGAACTTGAGATCAAA
cdHSP104        CGTGCTAGTCATGAACAATTGACTGCAGCAAAAAGAAAATTGGACGAGCTTGAAATCAAA
                ** ********************** ** ************** ** ***** ******

caHSP104        GCTCAAGATGCTGAAAGAAGATACGATACTGCTACTGCTGCTGACTTGAGATACTTTGCT
cdHSP104        GCCCAAGATGCTGAGAGAAGATACGATACTGCCACTGCTGCTGACTTGAGATACTTTGCC
                ** ************ ***************** ***************************

caHSP104        ATCCCAGATATCCAGAAGCAAATTGAAGAGTTAGAAGTCAAAGTTGCTGAAGAGGAAGCT
cdHSP104        ATCCCAGATATCCAGAAGCAGATTGAAGAGTTGGAAGTCAAAGTTGCTGAAGAGGAGGCT
                ******************** ************ ************************ ***

caHSP104        TCTAATTTGGACAGCTTGTTGAAGAATGCAGTTGGACCAGAACAAATATGTGAAACCGCT
cdHSP104        TCTAATTTGGACAGTTTGTTGAAGAATGCAGTTGGGCCAGAACAAATATGTGAGACTGCT
                ************** ******************** ***************** ** ***

caHSP104        GCTAGATTGACTGGTATCCCTGTCACGAAATTGTCGCAAGCAGAAAACAATAAATTGATC
cdHSP104        GCTAGGTTGACCGGTATCCCTGTCACGAAATTGTCGCAAGCCGAAAATAACAAATTGATC
                ***** ***** ****************************** ***** ** *********

caHSP104        AATATGGAAGCAGAATTGTCGAAAGAAGTTGTTGGACAATCGGAAGCTGTGAAGGCAGTC
cdHSP104        AATATGGAAGCAGAATTGTCGAAAGAAGTTGTTGGACAATCGGAAGCTGTGAAGGCGGTT
                ********************************************************** **

caHSP104        TCCAATGCCATCAGATTAAGAAGATCGGGTTTGGCTAATCCTAACCAACCACCATCCTTT
cdHSP104        TCCAATGCCATCAGATTGAGAAGATCGGGTTTGGCTAATCCTAATCAACCACCATCATTT
                ***************** ************************* *********** ***

caHSP104        TTGTTTTTGGGTCTTTCTGGTTCGGGTAAGACTGAATTGGCTAAGAAGCTTGCTGGTTTT
cdHSP104        TTGTTCTTGGGTCTTTCTGGTTCAGGTAAGACTGAGTTGGCCAAAAAACTTGCTGGTTTT
                ***** ***************** *********** ***** ** ** ************
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```
caHSP104        CTCTTTGCAGACGAAAAGGCAATTATTAGAATTGACTGCTCTGAATTGGGAGACAAATGG
cdHSP104        CTTTTTGCAGATGAAAAGGCAATAATTAGAATTGACTGCTCCGAATTGGGAGACAAATGG
                ** ******** *********** ***************** ******************

caHSP104        TCTGCTTCAAAATTGTTGGGTGCTGCTCCAGGTTATGTTGGATATGAAGAAGGTGGTATC
cdHSP104        TCTGCTTCGAAATTGTTGGGTGCTGCTCCAGGTTATGTTGGATATGAAGAAGGTGGTATC
                ******** **************************************************

caHSP104        TTGACTGAGCCATTAATCAGACGGCCATACTCTGTGGTCTTGTTGGATGAAGTTGAAAAA
cdHSP104        TTAACTGAGCCATTAATCAGACGACCATATTCCGTTGTTTTATTGGATGAAGTTGAAAAA
                ** ******************** ***** ** ** ** ** ******************

caHSP104        GCTGCTCCTGAAGTGTTGACT
cdHSP104        GCTGCTCCTGAAGTGTTGACT
                *********************
```

Nucleotide sequence alignment of the 981 bp *C.dubliniensis HSP104* gene fragment obtained by PCR using the primer set HSP104F/R with part of the homologous region of *C.albicans HSP104* gene (accession no. AF362391) Asterisks denote identical nucleotides and dashes represent differences in length, introduced for alignments.

```
C.albicans      CTGGTATTGGTATGACCAAAGCTGATTTGGTCAACAATTTGGGTACTATTGCTAAATCTG
C.dubliniensis  CTGGTATTGGTATGACCAAAGCCGATTTGGTCAACAATTTGGGTACCATTGCTAAATCTG
                ********************** ********************** ************

C.albicans      GTACCAAATCCTTTATGGAAGCTTTAAGTGCTGGTGCTGACGTTTCTATGATTGGTCAAT
C.dubliniensis  GTACCAAATCCTTTATGGAAGCTTTAAGTGCTGGTGCTGACGTTTCTATGATTGGTCAAT
                ************************************************************

C.albicans      TTGGTGTTGGTTTCTACTCCTTGTTCTTGGTTGCTGATCACGTCCAAGTTATCTCCAAAC
C.dubliniensis  TTGGTGTCGGTTTCTACTCCTTGCTCTTGGTTGCTGATCACGTCCAAGTTATCTCCAAAC
                ******* *************** ************************************

C.albicans      ACAATGACGACGAACAATACGTTTGGGAATCTAACGCTGGTGGTAAGTTCACTGTTACTT
C.dubliniensis  ACAATGATGACGAACAGTACGTCTGGGAATCTAATGCCGGTGGTAAATTCACTGTTACTT
                ******* ******** ***** *********** ** ******** ************

C.albicans      TGGATGAAACTAACGAAAGATTGGGTCGTGGTACCATGTTGAGATTGTTCTTGAAGGAAG
C.dubliniensis  TGGATGAAACCAACGAAAGATTGGGACGTGGTACTATGTTGAGATTGTTCTTGAAGGAAG
                ********** ************** ******** *************************

C.albicans      ATCAATTGGAATACTTGGAAGAAAAAAGAATCAAAGAAGTTGTCAAGAAACACTCTGAAT
C.dubliniensis  ATCAATTGGAATATTTGGAAGAAAAAAGAATCAAAGAAGTTGTCAAGAAACACTCTGAAT
                ************* ************************************************

C.albicans      TCGTTGCTTATCCAATCCAATTAGTTGTCACCAAAGAAGTTGAAAAAGAAGTTCCAGAAA
C.dubliniensis  TCGTTGCTTATCCAATCCAATTAGTTGTTACCAAGGAAGTTGAAAAGGAAATTCCAGAAG
                **************************** ***** *********** *** ********

C.albicans      ------------CCGAAGAAGAAGACAAAGCTGCTGAAGAAGACGACAAGAAACCAAAAT
C.dubliniensis  ATGAAACTTTAGCTGAAGATGAAGATAAAGCCACTGAAGAAGACGACAAGAAACCAAAAT
                           * ***** ***** *****  ****************************

C.albicans      T-
C.dubliniensis  TG
                *
```

Nucleotide sequence alignment of the 469bp *C.dubliniensis* CD36 *HSP90* gene fragment obtained by PCR using the primer set HSP90F/R with part of the homologous region of *C.albicans HSP90* gene (accession no.X81025) Asterisks denote identical nucleotides and dashes represent differences in length, introduced for alignments.

```
CaTPS1          CCATGTCCTCCGGTGGACTCGTTACAGCACTTACAAGGTTTGAAAAAAACAACCGAGTTT
CdTPS1          CCATGTCCTCCGGTGGACTTGTTACGGCA-TTGCAAGGTTTGAAAAAGACAACCGAGTTC
                ******************** ***** *** ** ************** ***********

CaTPS1          CAATGGTATGGATGGCCTGGATTGGAAATTCCAGAAGATGAGCAAACTAAAGTAAATGAC
CdTPS1          CAATGGTATGGATGGCCCGGATTGGAAATTCCTGATGACGAACAAGCCAAAGTAAACGAA
                ***************** ************** ** ** ** *** * ******** **

CaTPS1          GAATTGAAATCCAAATTCAATTGTACAGCCATATTTTTAAGTGATACGATTGCTGATTTA
CdTPS1          GAATTGAAATCCAAATTTAATTGTACAGCCATATTTTTAAGTGACACAATTGCTGATTTG
                ***************** ************************** ** ***********

CaTPS1          CATTATAATGGGTTTTCAAATAGTATTTTATGGCCACTTTTCCATTATCATCCTGGGGAA
CdTPS1          CATTATAATGGGTTCTCTAATAGCATCTTATGGCCACTTTTCCATTATCATCCTGGGGAA
                ************** ** ***** ** **********************************

CaTPS1          ATGAACTTTGACGAAAATGCATGGGCAGCATATATTGAAGCCAATAAGAAATTTGCATTG
CdTPS1          ATGAATTTTGATGAAAATGCCTGGGCAGCATACATTGAAGCCAACAAGAAATTTGCGTTG
                ***** ***** ******** *********** *********** *********** ***

CaTPS1          GAAATAGTCAAACAAGTCAATGATGATGATATGATTTGGGTTCATGATTATCATTTAATG
CdTPS1          GAAATAGTCAAGCAAGTCAATGATGATGACATGATTTGGGTTCATGATTACCATTTAATG
                *********** ***************** ******************** *********

CaTPS1          CTTTTGCCAGAAATGTTAAGACAAGAAATTGGTAACAAGAAGAAAAACATTAAAATTGGA
CdTPS1          CTTTTGCCGGAAATGTTGAGACAAGAAATCGGTAACAAGAAGAAAAACATCAAAATTGGA
                ******** ******** *********** ******************** *********

CaTPS1          TTCTTCTTGCACACACCA-TTCCCATCATCAGAAATTTATCGTATTTTGCCCGTTCGTAA
CdTPS1          TTCTTCTTGCATACGCCAATTCCCATCATCGGAGATTTATCGTATTTTGCCCGTCCGTAA
                *********** ** *** *********** ** ******************** *****

CaTPS1          AGAAATTCTTGAAGGTG-TGTTGA-GTTGTGATTTAATTGGATTCCATACCTATGATTAC
CdTPS1          AGAAATTCTCAAAGGGGGTGTTGAAGTTGTGATTTGATTGGATTCCACACTTATGATTAT
                *********  **** * ****** ********** *********** ** ********

CaTPS1          GCCCGTCATTTCATCAGTTCGGTTTCAAGAATTGTGCCAAACGTCAGTACTTTACCTAAT
CdTPS1          GCCCGTCATTTTATCAGTTCTGTTTCAAGAATTGTGCCAAATGTCAGCACATTACCTAAT
                *********** ******** ******************** ***** ** *********

CaTPS1          GGTATAAAGTACCAGGGACGTTCGATCAGCATCGGGGCTTTCCCCATTGGGATTGATGTT
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CdTPS1          GGTATAAAGTACCAGGGACGTTCGATCAGCATTGGGGCTTTCCCCATTGGGATTGATGTT
                ******************************* ***************************

CaTPS1          GATAACTTTATTGACGGTTTGAAAAAAGATAGTGTTGTGGAACGTATTAAACAATTGAAA
CdTPS1          GATAACTTTATTGACGGTTTGAAAAAAGACAGTGTTGTGGAACGTATTAAACAATTGAAA
                ****************************** ********************************

CaTPS1          TCTAAATTCAAAGACGTTAAGGTTATTGTTGGTGTTGATAGATTAGACTATATCAAAGGT
CdTPS1          TCTAAATTCAAAGACGTTAAAGTTATTGTTGGTGTTGATAGATTAGACTATATCAAAGGT
                ******************* ****************************************

CaTPS1          GTTCCGCAAAAATTACATGCATTTGAAGTCTTTTTGAATGAAAATCCCGAATGGATTGGC
CdTPS1          GTTCCTCAGAAATTACATGCATTTGAAGTGTTTTTGAATGAGAATCCGGAATGGATTGGG
                ***** ** ******************** *********** ***** ***********

CaTPS1          AAAGTAGTTTTGGTCCAAGTTGCTGTTCCATCCAGAGGTG
CdTPS1          AAAGTCGTTTTGGTCCAAGTTGCTGTTCCATCCAGAGGTG
                ***** ***********************************
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Nucleotide sequence alignment of 981bp *C. dubliniensis* CD36 gene fragment obtained by PCR using the primer set TPS1F/R with part of the homologous region of *C.albicans TPS1* gene (Accession no: Y07918). Asterisks denote identical nucleotides and dashes represent differences in length, introduced for alignments.

```
CdNTC1          AGATCAATACGATTTTTTCCAATTGATTAAAAGTCACCGTACAGATGTTCAATTGGATGT
                ********* ** ***************** *  ** *** ***** *************

CaNTC1          ACAATATTTACCACAGAAAATCGATGCTGATTATATTAAATCAATCAATAAAAAACCCGG
CdNTC1          ACAATATTTACCTAAGAAAATCGATGCCGATTATATTAAATCAATTAATAAAAAACCCGG
                ************  ************* ***************** **************

CaNTC1          GTTATTATCAATTGCCACTAGACCTGATCCCCAAGCGCCTGATAGTGGAAGTTTGATTAG
CdNTC1          ATTATTATCTATTGCCACAAGACCCGATCCAGAAACTCCT------GGGAATTTAATTAG
                 ******** ******** ***** *****  ** * ***      ** * *** *****

CaNTC1          TTGGCCCTATGTTGTACCTGGTGGTAGATTTAATGAATTATATGGATGGGATTCATATAT
CdNTC1          TTGGCCTTATGTTGTCCCTGGAGGTAGATTTAATGAATTATATGGATGGGATTCATATAT
                ****** ******** ***** ****************************************

CaNTC1          GGAAACATTAGGACTATTAACTGATGTCAAAATTGATCCTTCAGGTAATCCACGTAATTT
CdNTC1          GGAAACGTTAGGATTATTAACCGATGTTAAAATTGATCCATCGGGTAATCCTTGTAATAT
                ****** ****** ******* ***** *********** ** ********  ***** *

CaNTC1          GAGACATTTAGAATTAGCTCGTGGTATGGCGGAGAATTTCATTTATGAAATTCACCATTA
CdNTC1          TAACCATTTAGAATTAGCTCGTGGTATGGCAGAAAATTTCATTTATGAAATTCATCATTA
                 *  ************************** ** ******************** *****

CaNTC1          TGGGAAAATTTTAAATGCTAATCGATCCTATTATTTAGGTCGATCTCAACCACCATTTTT
CdNTC1          TGGGAAAATATTAAATGCTAATCGATCATATTATTTAGGTCGATCTCAACCTCCATTTTT
                ********* ***************** ********************** ********

CaNTC1          AACTGATATGGCATTAAGAATTTTCAACAAGACTATAGAAGTAACCCCAGAACTCATGGA
CdNTC1          AACTGATATGGCATTAAGAATTTTTAATAAAACAATAGAAGTAGCTCCTGAATCTATGGA
                ************************ ** ** ** ********* * ** ***   *****

CaNTC1          TGAAGCTATAGATTTTTTAAAACGGGCTACATTAGCTGCCATTAAAGAATATGAAACAAT
CdNTC1          TGATGCCATAGATTTTTTGAAACGGGCTACATTAGCTGCTATTAAAGAATATGAAACAAT
                *** ** *********** ******************** ********************

CaNTC1          TTGGTGTGCCCATCCAAGATTAGATGACAAGACAGGACTTTCATGTTATCATCCAGAAGG
CdNTC1          ATGGTGTGCTCATCCAAGATTAGATGATAAAACTGGACTTTCATGTTATCATCCAGAAGG
                 ******** ***************** ** ** ***************************

CaNTC1          TAAAGGGATCCCACCAGAAACTGAACCTACTCATTTCAATGCATTATTAAAACCATATCT
CdNTC1          TAAAGGTGTCCCACCAGAAACTGAACCTACACATTTCAATGCCGTATTAAAACCATATCT
                ******  ********************** ***********  ****************
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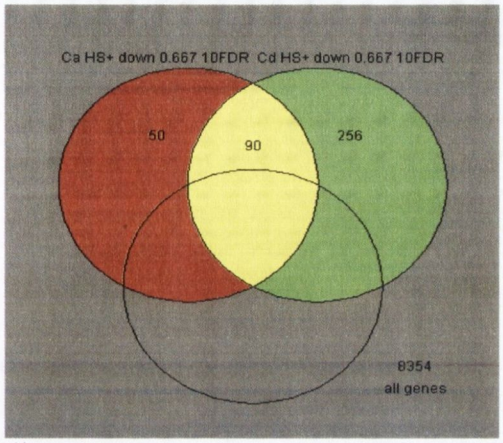
CaNTC1          TGCCAAATATAATGATATTGATCAACTTGATTTCATTGAAAAATATAATTCCGGAGAAAT
CdNTC1          TGCCAAATATGGAGGGATTGATCAACTTGATTTCATTGAAAAATATAATTCCGGGGAGAT
                **********   *  ************************************* ** **

CaNTC1          TAAAGAACCTGAATTAGATGAATATTTCTTACATGATAGAGCCGTTCGAGAATCTGGTCA
CdNTC1          TCAAGAACCTGAATTAGATGAATATTTCTTACATGACAAAACCGTTCGAGAATCTGGTCA
                * ********************************** * * ******************

CaNTC1          T-
CdNTC1          TG
                *
```

Nucleotide sequence alignment of the 1374 bp *C.dubliniensis NTC1* gene fragment obtained by PCR using the primer set NTC1F/R with part of the homologous region of *C.albicans NTC1* gene (Accession no.X95099) Asterisks denote identical nucleotides and dashes represent differences in length, introduced for alignments.

Appendix II



1A

[Ca HS+ down 0.667 10FDR],less [Cd HS+ down 0.667 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2302	0.1	0.6	0.3	0.6	0.1	0.3	IPF6518	orf19.1691	unknown function	YNR018w
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA0943	0.1	0.5	0.4	0.4	0.9	1.1	YHB1	orf19.3707	flavohemoglobin (by homology)	YGR234w
CA0482	0.2	0.6	0.6	0.9	0.5	0.4	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)	no match
CA0185	0.2	0.7	0.7	0.6	0.5	0.8	PLB4.5f	orf19.1442	Phospholipase, 5-prime end (by homology)	YOL011w
CA2625	0.2	0.9	0.7	0.9	0.2	0.3	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified protein	YLR110c
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA4516	0.3	0.5	0.3	0.5	1.3	0.8	IPF18207	orf19.489	unknown function	YPL170w
CA0273	0.3	0.9	0.3	0.5	1.0	0.6	IPF19066	orf19.1433	unknown function	YOR084w
CA2225	0.3	0.6	0.3	0.4	1.1	1.1	SUR2	orf19.5818	Hydroxylation of C-4 of the sphingoid moiety of ceramide by h	YDR297w
CA0311	0.3	0.9	0.4	1.5	0.9	1.1				
CA1902	0.3	1.1	0.4	1.1	1.0	1.0	OPT1	orf19.2602	oligopeptide transporter	YJL212c
CA4707	0.3	0.7	0.9	0.9	1.1	1.1	PTR21	orf19.6937	peptide transporter	YKR093w
CA0892	0.3	1.1	1.1	1.1	0.8	0.9	PHO8.5	orf19.4736	repressible alkaline phosphatase, 5-prime end (by homology)	YDR481c
CA5407	0.3	1.1	0.3	0.5	0.9	0.8	IPF1548	orf19.951	unknown function	no match
CA6135	0.3	0.7	0.4	0.8	1.0	0.6	CMK1	orf19.5911	Ca2+/calmodulin-dependent ser/thr protein kinase (by homol	YFR014c
CA2855	0.3	0.8	0.5	0.8	1.8	1.4	GPM2	orf19.1067	phosphoglycerate mutase (by homology)	YKL152c
CA4657	0.4	1.1	0.7	1.1	2.3	1.2	IPF3094	orf19.4444	4-nitrophenyl phosphatase (by homology)	YDL236w
CA5612	0.4	1.3	0.7	0.8	0.8	0.7	KAP114	orf19.7086	putative RAN-binding protein/importin (by homology)	YGL241w
CA5361	0.4	0.6	1.1	1.2	1.1	0.9	NPL3	orf19.7238	nucleolar shuttling protein with an RNA recognition motif (by h	YDR432w
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match
CA1625	0.4	0.9	0.6	0.7	1.5	1.0	IPF6156	orf19.1034	similar to C.elegans LIM homeobox protein	YPL170w
CA0984	0.4	0.5	0.5	0.7	0.8	0.8	IPF7400	orf19.1802	unknown function	YER049w
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membrar	YIL047c
CA5968	0.4	1.0	0.6	1.0	1.4	1.0	IPF946	orf19.7561	unknown function	no match
CA1989	0.4	0.8	0.9	0.8	0.8	0.9	IPF16596	orf19.95	unknown function	no match
CA6109	0.5	0.5	1.1	1.1	1.0	1.0	IPF89.3f	orf19.5943.1	unknown function, 3-prime end	YLR150w
CA4490	0.5	0.7	1.0	1.1	0.8	1.1	IPF4045	orf19.1872	unknown function	no match
CA1384	0.5	0.8	0.9	1.0	0.6	0.8	IPF8423	orf19.926	similar to Saccharomyces cerevisiae Dhs1p exonuclease (by	YOR033c
CA2280	0.5	1.0	0.3	1.0	0.7	0.9	DUR1,2	orf19.780	urea amidolyase (by homology)	YBR208c
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA4850	0.5	1.1	0.6	1.0	0.9	1.1	Cirt2	orf19.3820	Transposase	YJR134c
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA2898	0.5	0.6	2.0	0.9	0.6	0.8	IPF15646	orf19.3481	putative ATP-dependent RNA helicase (by homology)	YGL064c
CA5596	0.5	0.9	1.1	1.0	1.0	1.1	IPF564	orf19.7104	unknown function	no match
CA1803	0.5	0.6	1.8	1.2	1.1	1.2	IPF16748	orf19.2917	unknown function	YER006w
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA1679	0.6	0.9	1.0	1.1	0.9	1.0				
CA2733	0.6	0.7	1.2	1.1	0.9	0.8	PRP18	orf19.2112	U5 snRNA-associated protein (by homology)	YGR006w
CA2521	0.6	0.9	1.2	1.3	0.6	0.9	IPF4317	orf19.5518	unknown function	no match
CA3743	0.6	1.0	0.6	1.1	1.5	1.5	IPF19998	orf19.2175	unknown function	YNR074c
CA4926	0.6	1.1	0.6	0.9	0.8	1.0	IPF1404	orf19.6065	unknown function	YLR071c
CA2347	0.6	0.9	0.9	1.1	1.2	1.2	RAD51	orf19.3752	DNA repair protein by homology	YER095w
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA4315	0.6	0.8	0.7	1.1	1.3	0.9	PPX1	orf19.4107	Exopolyphosphatase (by homology)	YHR201c
CA5627	0.6	0.8	1.1	1.1	0.9	1.2	IPF495	orf19.7069	unknown function	YBR261c
CA5693	0.6	1.0	1.3	1.0	0.4	0.8	GDA1	orf19.7394	Golgi guanosine diphosphatase (by homology)	YEL042w
CA4708	0.7	1.0	1.8	1.1	1.2	1.1	MEU1	orf19.6938	regulator of ADH2 expression (by homology)	YLR017w
CA1982	0.7	0.6	1.0	0.8	0.9	1.1	ADK1	orf19.683	adenylate kinase, cytosolic (by homology)	YDR226w

2A

[Cd HS+ down 0.667 10FDR],less [Ca HS+ down 0.667 10FDR]

Species (Stress ()* Systemat	Ca HS+ rmali	Cd HS+ rmali	Ca OS+ rmali	Cd OS+ rmali	Ca XS+ rmali	Cd XS+ rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA0083	0.3	0.1	1.0	1.1	0.6	0.2	PHO84.5e	orf19.655	high-affinity inorganic phosphate/H+ symporter by homology	YML123c
CA3921	0.3	0.2	1.0	1.1	1.0	1.0	OLE1	orf19.5117	Stearoyl-CoA desaturase (by homology)	YGL055w
CA6105	0.4	0.2	1.1	0.7	0.9	0.9	FAS2.5f	orf19.5951	fatty-acyl-CoA synthase, alpha chain, 5-prime end	YPL231w
CA3689	0.2	0.2	1.1	1.1	0.9	1.0	RPS22A	orf19.6265	ribosomal protein S15a.e.c10 (by homology)	YJL190c
CA6107	0.5	0.2	1.1	1.0	1.0	1.0	FAS2.3f	orf19.5949	fatty-acyl-CoA synthase, alpha chain, 3-prime end	YPL231w
CA3341	0.2	0.2	1.1	1.0	1.0	1.0	RPS17	orf19.2329.1	Ribosomal protein S17 (by homology)	YDR447c
CA2817	0.2	0.2	1.1	1.1	1.0	1.0	RPS16	orf19.2994.1	ribosomal protein	YMR143w
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA1188	0.2	0.2	1.2	1.0	1.0	1.0	RPL30.3f	orf19.3788.1	RNA binding (by homology)	YGL030w
CA3739	0.4	0.2	0.9	0.9	0.9	0.9	RPS10	orf19.2179.2	ribosomal protein	YOR293w
CA3883	0.5	0.2	1.0	1.3	0.2	0.4	GCV2	orf19.385	Glycine decarboxylase P subunit	YMR189w
CA3534	0.6	0.2	1.0	0.9	1.0	1.0	SSB1	orf19.6367	heat shock protein 70	YNL209w
CA5499	0.3	0.2	1.1	1.1	1.0	1.0	RPS4A	orf19.5341	ribosomal protein S4	YJR145c
CA4571	0.4	0.2	1.0	1.1	1.0	1.1	RPL33	orf19.6882.1	ribosomal protein L35a	YPL143w
CA0763	0.3	0.2	1.1	1.1	0.9	0.9	RPL11	orf19.2232	60S ribosomal protein (by homology)	YPR102c
CA4263	0.4	0.2	1.1	0.9	0.5	0.4	IPF2277	orf19.6656	unknown function	YHL016c
CA0736	0.4	0.2	1.0	1.1	1.0	1.0	RPL20B	orf19.4632	ribosomal protein (by homology)	YOR312c
CA6123	0.2	0.2	1.0	1.0	1.0	1.0	RPS15	orf19.5927	40S ribosomal protein S15, (by homology)	YOL040c
CA2108	0.2	0.2	0.9	0.9	1.0	1.0	RPL26A.3	orf19.3690.2	ribosomal protein, 3-prime end (by homology)	YLR344w
CA5633	0.4	0.2	1.2	1.3	0.9	1.0	RPA135	orf19.7062	DNA-directed RNA polymerase I, 135 KD subunit (by homolo	YPR010c
CA2811	0.2	0.3	1.1	1.0	1.0	1.0	RPS3A	orf19.3002	Ribosomal protein 10	YML063w
CA2923	0.4	0.3	1.0	1.4	1.0	0.8	FET32	orf19.4212	cell surface ferroxidase (by homology)	YMR058w
CA3239	0.3	0.3	1.1	1.3	0.9	1.0	IPF10558	orf19.4684.2	unknown function	YKR094c
CA0472	0.3	0.3	14.5	6.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA2937	0.3	0.3	1.2	1.1	1.1	1.0	RPS21B.3	orf19.3325.3	ribosomal protein S21, 3- prime end	YJL136c
CA3226	0.3	0.3	1.2	1.1	1.0	1.0	RPS27	orf19.6286.2	ribosomal protein S27 (by homology)	YKL156w
CA1977	0.3	0.3	0.9	1.0	0.9	1.0	RPL25	orf19.687.1	ribosomal protein L23a (by homology)	YOL127w
CA2597	0.4	0.3	0.8	0.7	1.0	0.5	IFQ3	orf19.54	unknown function	no match
CA0665	0.4	0.3	0.6	0.7	0.6	0.8	INT1	orf19.4257	integrin-like protein alpha chain	YJR092w
CA3075	0.4	0.3	1.0	1.3	1.0	1.0	IPF6105	orf19.4813	similar to Saccharomyces cerevisiae Gua1p GMP synthase (	YMR217w
CA3800	0.4	0.3	1.1	0.9	1.0	1.0	RPL7A.3f	orf19.2478.1	60S Ribosomal Protein L7-A, 3-prime end	YPL198w
CA0322	0.4	0.3	1.0	1.0	1.0	1.0	RPS9B	orf19.838.1	Ribosomal protein	YBR189w
CA1298	0.4	0.3	1.0	1.1	0.9	1.0	RPL32	orf19.3415.1	ribosomal protein L32	YBL092w
CA0380	0.3	0.3	0.8	1.1	0.6	0.5	PGA45	orf19.2451	unknown function	no match
CA3864	0.4	0.3	1.0	1.0	1.0	1.0	RPL16A	orf19.6085	ribosomal protein (by homology)	YNL069c
CA6163	0.3	0.3	1.0	0.8	0.4	0.8	POL1	orf19.5873	DNA-directed DNA polymerase alpha (by homology)	YNL102w
CA0642	0.4	0.3	1.3	1.4	0.4	0.4	ERG25	orf19.3732	C-4 sterol methyl oxidase	YGR060w
CA0689	0.5	0.3	1.5	1.4	0.3	0.3	IPF14119	orf19.4688	unknown function	no match
CA2708	0.5	0.3	1.2	1.0	1.1	1.0	RPS6A	orf19.4660	ribosomal protein S6 (by homology)	YPL090c
CA3993	0.7	0.3	2.4	1.0	0.7	0.7	IPF8275	orf19.1569	unknown function	YGR090w
CA3111	0.5	0.3	1.1	1.1	1.1	1.1	RPL5	orf19.6541	ribosomal protein (by homology)	YPL131w
CA4862	0.4	0.3	1.0	1.0	1.0	1.0	EFB1	orf19.3838	translation elongation factor eEF1beta	YAL003w
CA6154	0.5	0.3	1.6	1.4	1.0	1.0	IPF1848	orf19.5885	similar to Saccharomyces cerevisiae Snu13p U4/U6.U5 snRI	YEL026w
CA1635	0.4	0.3	0.8	1.3	0.9	1.1	URA7	orf19.3941	CTP synthase 1 (by homology)	YBL039c
CA5076	0.4	0.3	0.9	0.6	0.4	0.8	IPF15301	orf19.3051	unknown function	YJR116w
CA5317	0.4	0.3	1.0	1.1	1.0	1.0	RPP1B	orf19.7188	Acidic ribosomal protein L44 (by homology)	YDL081c
CA2454	0.3	0.3	1.1	1.0	1.1	1.0	RPL23B	orf19.3504	ribosomal protein L23.e (by homology)	YER117w
CA4513	0.4	0.3	1.0	1.1	1.0	1.0	ADE17	orf19.492	5-aminoimidazole-4-carboxamide ribotide transformylase (by	YMR120c
CA5645	0.7	0.3	1.0	1.0	0.3	0.5	CYB5	orf19.7049	Cytochrome b5 (by homology)	YNL111c
CA1502	0.4	0.4	1.1	1.1	1.0	1.0	RPS7A	orf19.1700	ribosomal protein (by homology)	YOR096w
CA5354	0.3	0.4	1.0	1.2	0.6	0.7	FTR2	orf19.7231	high affinity iron permease	YER145c
CA5021	0.6	0.4	1.1	1.0	1.0	1.0				
CA2667	0.7	0.4	2.0	1.3	1.1	1.1	IPF16996	orf19.3547	unknown function	YDR496c
CA4857	1.6	0.4	0.8	1.0	0.8	0.6	PHR1	orf19.3829	GPI-anchored pH responsive glycosyl transferase	YMR307w
CA3765	1.1	0.4	0.8	1.0	0.7	0.6	IPF18298.	orf19.2904	unknown function, 5-prime end	YNL106c
CA0875	0.3	0.4	1.0	1.0	0.7	0.5	ERG251	orf19.4631	C-4 sterol methyl oxidase (by homology)	YGR060w
CA4008	0.4	0.4	0.9	1.0	1.0	1.0	DYS1	orf19.1626	deoxyhypusine synthase	YHR068w
CA0189	0.7	0.4	0.5	0.6	1.2	0.9	IPF12201	orf19.4118	Na+-nucleoside cotransporter (by homology)	no match (e-value > 0.05)
CA5990	0.9	0.4	1.5	0.8	0.8	0.8	IPF690.5f	orf19.7590	NADH dehydrogenase (ubiquinone) 78K chain precursor, 5-f	no match (e-value > 0.05)
CA4326	0.5	0.4	1.5	1.3	1.2	1.3	IPF2093	orf19.4093	nuclear protein of unknown function (by homology)	YGR103w
CA5091	0.4	0.4	0.5	0.7	0.2	0.6	ENG1	orf19.3066	endo-1,3-beta-glucanase	YNR067c
CA2250	0.6	0.4	0.8	0.7	1.0	0.9	MIS11	orf19.2364	mitochondrial C1-tetrahydrofolate synthase precursor (by hor	YBR084w
CA3602	0.3	0.4	1.0	1.0	1.0	0.9	RPL14B	orf19.4931.1	ribosomal protein L14B (by homology)	YKL006w
CA5340	0.7	0.4	1.2	1.5	0.8	0.9	IPF883	orf19.7215	unknown function	YJL109c
CA4099	0.8	0.4	2.1	1.2	0.7	1.0	IPF3986	orf19.665	unknown function	YLR186w
CA4696	0.5	0.4	0.9	0.7	0.6	0.8	HTA1	orf19.6924	Histone H2A (by homology)	YDR225w
CA2939	0.5	0.4	1.0	1.0	1.0	1.0	TIF1	orf19.3324	translation initiation factor	YKR059w
CA5638	0.6	0.4	0.9	1.1	0.9	1.0	IPF470	orf19.7057	putative glutamine-tRNA ligase (by homology)	YGL245w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA2821	0.7	0.4	0.7	0.9	0.4	0.5				
CA3112	0.6	0.4	0.8	0.6	1.1	1.0	PFK2	orf19.6540	6-phosphofructokinase, beta subunit	YMR205c
CA5975	0.7	0.4	1.1	1.1	1.2	1.2	SIK1	orf19.7569	nucleolar protein involved in pre-rRNA processing (by homol	YLR197w
CA3607	1.2	0.4	4.1	1.8	1.4	1.2	RTA2	orf19.24	Unknown function	YOR049c
CA1441	0.4	0.4	1.2	1.2	1.4	1.1	QCR8	orf19.4490.2	ubiquinol-cytochrome-c reductase chain VIII (by homology)	YJL166w
CA2493	0.5	0.4	0.9	0.8	0.9	0.8	IPF7227	orf19.4048	putative fatty acid desaturase (by homology)	YDR011w
CA2858	0.6	0.4	1.0	0.8	1.0	1.0	ACS2	orf19.1064	acetyl-coenzyme-A synthetase (by homology)	YLR153c
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)	YOR356w
CA1438	0.6	0.4	1.4	1.2	1.2	1.1	NOP58	orf19.1199	nucleolar protein required for pre-18S rRNA processing	YOR310c
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)	YLR409c
CA0874	1.3	0.4	1.5	1.3	0.8	0.8	CPA1	orf19.4630	Arginine-specific carbamoylphosphate synthase, small chain	YOR303w
CA4505	0.7	0.4	1.1	1.2	1.1	1.0	NOP2	orf19.501	nucleolar protein (by homology)	YNL061w
CA0207	0.4	0.4	1.9	1.0	1.0	0.7	IPF18002	orf19.1226	Unknown function	YKL014c
CA5568	0.8	0.4	2.0	1.0	1.2	1.0	ELF1	orf19.7332	Elongation-like factor	YPL226w
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA3003	0.7	0.4	0.6	0.9	0.5	0.5	IPF15741.	orf19.6242	similar to Saccharomyces cerevisiae Cyk3p possibly involvec	YCR088w
CA4471	1.0	0.4	1.3	1.1	0.5	0.8	MCM3	orf19.1901	replication initiation protein (by homology)	YEL032w
CA5344	0.3	0.4	0.6	2.3	0.3	0.5	PRY2	orf19.7218	putative pathogen related proteins (by homology)	YJL079c
CA6155	1.2	0.4	1.4	1.6	0.8	0.8	IPF1846	orf19.5884	unknown function	YJR041c
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)	YFL036w
CA4302	0.9	0.4	0.9	0.9	0.9	1.1	DED81	orf19.6702	Asparaginyl-tRNA synthetase (by homology)	YHR019c
CA2117	0.9	0.4	0.7	1.2	0.9	0.5	SNG3	orf19.1333	Drug transporter (by homology)	YGR197c

CA1898	0.7	0.4	0.7	0.6	0.5	1.0	PGA38	orf19.2758	unknown function	no match
CA5923	0.7	0.4	1.1	0.7	0.7	0.3	IFQ2	orf19.6782	Unknown function	no match (e-value > 0.05)
CA1387	0.3	0.4	0.7	0.7	0.8	0.9	ERG11	orf19.922	cytochrome P450 lanosterol 14a-demethylase	YHR007c
CA2303	0.6	0.5	0.9	1.2	0.8	0.7	TOS1	orf19.1690	putative Anchor subunit of a-agglutinin (by homology)	YBR162c
CA4551	0.5	0.5	1.1	1.1	1.2	1.2	APT1	orf19.1448	adenine phosphoribosyltransferase	YML022w
CA5991	0.7	0.5	1.4	1.1	1.0	1.0	IPF690.3f	orf19.7591	NADH dehydrogenase (ubiquinone) 78K chain precursor, 3-p	no match (e-value > 0.05)
CA0554	1.0	0.5	1.3	1.1	1.3	1.2	HAS1	orf19.3962	ATP-DEPENDENT RNA HELICASE (by homology)	YMR290c
CA2558	0.5	0.5	0.6	0.8	0.8	0.7	RBT5	orf19.5636	repressed by TUP1 protein 5	no match (e-value > 0.05)
CA4533	0.4	0.5	0.9	1.3	0.9	1.0	COX4	orf19.1471	cytochrome-c oxidase (by homology)	YGL187c
CA4590	0.5	0.5	1.1	1.0	0.9	0.9	IPF2218	orf19.6907	unknown function	YDL156w
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA3603	0.9	0.5	0.9	0.6	0.5	0.7	MEF1	orf19.4932	mitochondrial translation elongation factor G (by homology)	YLR069c
CA0184	0.8	0.5	1.0	0.7	1.0	0.8	IPF19142	orf19.3984	unknown function	YGR237c
CA6029	0.6	0.5	1.7	1.3	1.1	1.5	DRS1	orf19.7635	ATP dependent RNA helicase (by homology)	YLL008w
CA3918	0.5	0.5	0.6	1.1	0.5	0.7	VTC2	orf19.4381	putative polyphosphate synthetase (by homology)	YFL004w
CA4589	0.4	0.5	1.1	1.0	1.0	1.0				
CA3081	0.5	0.5	1.1	1.1	1.1	1.0	EFT3	orf19.4152	translation elongation factor 3	YNL014w
CA6122	0.4	0.5	1.2	1.1	1.1	1.0	RPP2B	orf19.5928	acidic ribosomal protein (by homology)	YDR382w
CA3066	0.8	0.5	1.1	1.0	0.6	0.8	IPF15813	orf19.4281	unknown function	YLR223c
CA0687	1.0	0.5	1.0	1.1	0.8	1.0	CPA2	orf19.3221	arginine-specific carbamoylphosphate (by homology)	YJR109c
CA1513	0.8	0.5	1.0	1.1	1.0	1.0	MIR1	orf19.4885	phosphate transport protein, mitochondrial (MCF) (by homolc	YJR077c
CA4852	0.4	0.5	0.6	0.7	0.9	0.8	SCS7	orf19.3822	Required for hydroxylation of ceramide (by homology)	YMR272c
CA1289	0.6	0.5	1.1	1.0	1.2	1.1	ZUO1	orf19.2709	Zuotin, a putative Z-DNA binding (by homology)	YGR285c
CA2848	1.0	0.5	2.5	1.4	1.2	1.1				
CA2903	1.0	0.5	0.9	0.8	0.8	0.9	IPF11725	orf19.3475	unknown function	no match
CA0615	0.8	0.5	1.0	1.1	1.0	1.0	RPL3	orf19.1601	60S large subunit ribosomal protein L3.e (by homology)	YOR063w
CA2024	0.5	0.5	0.9	1.0	0.7	0.3	PGA35	orf19.4910	unknown function	no match
CA3574	0.5	0.5	1.1	1.0	0.9	1.2	IPF19584	orf19.2266	unknown function	YFR013w
CA6079	0.5	0.5	1.1	1.0	1.0	1.0	RPL18	orf19.5981.1	Ribosomal protein L18B (large subunit), (by homology)	YOL120c
CA3461	0.9	0.5	1.2	1.1	1.4	0.9	CFL2	orf19.1264	ferric reductase (by homology)	YNR060w
CA1095	0.8	0.5	1.3	0.9	0.4	0.7	SMC1	orf19.4367	Chromosomal ATPase family member (by homology)	YFL008w
CA0829	0.7	0.5	0.8	0.6	0.7	0.7	SLC1	orf19.250	fatty acyltransferase (by homology)	YDL052c
CA0733	0.9	0.5	1.3	0.8	0.7	0.8	NIP1	orf19.4635	translation initiation factor subunit	YMR309c
CA3588	0.7	0.5	1.2	1.1	1.3	1.1	SPE3	orf19.2250	putrescine aminopropyltransferase by homology	YPR069c
CA1227	1.1	0.5	1.3	0.9	0.6	0.8	IPF16082	orf19.4160	unknown function	YDL104c
CA2986	0.7	0.5	0.7	0.9	0.2	0.3	CDC5	orf19.6010	Cell-cycle protein kinase (by homology)	YMR001c
CA1758	0.8	0.5	2.0	0.7	0.9	0.8	IPF14559.	orf19.5126	unknown function, 3-prime end	YCL037c
CA1678	0.8	0.5	1.0	1.0	0.9	0.8	PGA24	orf19.3618	putative cell wall protein (by homology)	YAR050w
CA0216	0.9	0.5	1.1	1.1	1.0	1.0	IPF11681	orf19.1682	unknown function	no match (e-value > 0.05)
CA3766	0.9	0.5	0.7	0.9	0.7	0.8	IPF18298.	orf19.2903	unknown function, 3-prime end	no match (e-value > 0.05)
CA2008	1.1	0.5	1.1	1.2	0.6	0.9				
CA5359	0.7	0.5	1.2	1.1	1.1	1.0	TIF35	orf19.7236	translation initiation factor eIF3, p33 subunit (by homology)	YDR429c
CA5101	0.7	0.5	0.9	1.0	0.7	0.7	LCB1	orf19.6438	Serine C-palmitoyltransferase subunit (by homology)	YMR296c
CA2772	1.0	0.5	3.3	1.3	0.9	1.1	IPF20112	orf19.2688	unknown function	YPL126w
CA5236	0.8	0.5	0.8	0.7	0.4	0.6	LCB2	orf19.5027	Palmitoyl transferase (by homology)	YDR062w
CA2162	0.9	0.5	1.1	1.0	1.0	0.9	PDB1	orf19.5294	pyruvate dehydrogenase (by homology)	YBR221c
CA4155	0.8	0.5	1.0	0.5	0.5	0.7	RNR21	orf19.5801	ribonucleoside-diphosphate reductase (by homology)	YJL026w
CA3376	0.5	0.5	1.0	1.3	1.0	0.9	LSC2.5eo	orf19.1857.1	succinate-CoA ligase beta subunit, 5-prime end (by homolog	YGR244c
CA0276	0.6	0.5	0.9	0.7	0.5	0.9	IPF15015	orf19.5612	unknown function	YIL091c
CA0443	0.9	0.5	2.5	1.1	1.0	1.1	SPB1	orf19.76	Putative methyltransferase by homology	YCL054w
CA5292	0.9	0.5	2.7	1.4	0.9	1.1	IPF1948	orf19.7154	unknown function	YJL069c
CA3631	0.9	0.5	0.9	1.1	0.8	1.0	TIM54	orf19.5143	Translocase for the insertion of proteins into the mitochondria	YJL054w
CA6141	0.8	0.5	1.1	1.1	1.1	1.0	RPL19A	orf19.5904	Ribosomal protein L19.e (by homology)	YBR084ca
CA2578	0.4	0.5	1.1	0.9	0.6	0.9	MMD1	orf19.6220.3	Maintenance of mitochondrial DNA (by homology)	YIL051c
CA2571	0.8	0.5	1.6	1.2	1.1	0.7	IPF13769	orf19.6209	unknown function	YKL221w
CA4147	0.7	0.5	1.0	1.0	1.0	1.2	ADE8	orf19.5789	Phosphoribosylglycinamide formyltransferase (GART)	YDR408c
CA5063	0.9	0.5	2.2	1.1	0.7	0.8	IPF8493	orf19.3034	putative member of nontransporter group of ATP-binding cas	YDR091c
CA5685	0.9	0.5	1.8	1.0	0.9	0.9	HPA1	orf19.7387	RNA polymerase II-associated Histone acetyltransferase (by	YPL086c
CA2847	0.9	0.6	4.0	1.3	1.1	1.2	NOG2	orf19.5733	unknown function Nuclear/Nucleolar GTP-binding protein, by	YNR053c
CA4089	0.8	0.6	1.5	1.2	0.9	0.8	IPF5009	orf19.6648	unknown function	YGR245c
CA3604	0.5	0.6	2.1	1.8	0.3	0.4	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)	no match (e-value > 0.05)
CA4749	0.6	0.6	1.0	0.8	0.4	0.8	IPF4481	orf19.4831	unknown function	no match (e-value > 0.05)
CA3813	0.4	0.6	2.1	1.0	1.8	0.9	FRP1	orf19.2496	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA2272	0.6	0.6	1.5	1.4	1.2	1.1	RPA43	orf19.2594	DNA-directed RNA polymerase I, 36 KD subunit(by homolog	YOR340c
CA4506	0.8	0.6	1.4	1.4	1.2	1.0	GCD10	orf19.500	translation initiation factor eIF3 RNA-binding subunit (by hom	YNL062c
CA1723	0.5	0.6	1.0	1.0	1.1	1.1	TEF4	orf19.2651	translation elongation factor eEF1 (by homology)	YPL048w
CA2764	0.7	0.6	1.1	0.8	1.0	1.0	QCR7	orf19.5629	ubiquinol--cytochrome-c reductase subunit 7 (by homology)	YDR529c
CA3599	1.1	0.6	0.7	0.6	0.4	0.4	IPF19785	orf19.4929	unknown function	YLR067c
CA5953	0.7	0.6	1.0	0.4	0.4	0.3	IPF3506	orf19.6741	unknown function	YLR414c
CA3514	0.9	0.6	1.1	0.8	0.7	0.8	IPF11245	orf19.6362	similar to Saccharomyces cerevisiae Spa2p involved in cell p	YLL021w
CA2119	1.3	0.6	2.0	0.9	0.7	0.9	MTR4	orf19.1335	RNA Helicase (by homology)	YJL050w
CA0664	0.9	0.6	1.1	1.2	1.0	1.0	LSC2.3eo	orf19.710	succinate-CoA ligase beta subunit, 3-prime end (by homolog	YGR244c
CA2326	0.6	0.6	1.1	0.9	0.8	0.8	NUBM	orf19.4495	nucleotide-binding respiratory complex I subunit (by homolog	no match
CA5425	1.4	0.6	0.8	0.7	0.9	1.0	BDF1	orf19.978	sporulation protein (by homology)	YLR399c
CA5185	0.7	0.6	1.1	1.0	1.0	1.0	NHP6A	orf19.4623.3	nonhistone chromosomal protein related to HMG1 Cell growtl	YBR089ca
CA2304	0.8	0.6	2.1	1.3	0.8	1.4	PRP43	orf19.1687	RNA-dependent ATPase (by homology)	YGL120c
CA1688	0.7	0.6	0.3	0.6	0.8	0.5	COX15	orf19.3656	cytochrome oxidase assembly factor (by homology)	YER141w
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA2368	0.6	0.6	1.2	1.2	0.9	1.0	RPA190	orf19.1839	DNA-directed RNA polymerase I (by homology)	YOR341w
CA1619	0.7	0.6	1.6	1.5	0.6	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)	YPL057c
CA5521	0.7	0.6	0.9	0.8	0.8	1.0	HEM12	orf19.5369	uroporphyrinogen decarboxylase (by homology)	YDR047w
CA4811	0.9	0.6	2.0	1.2	1.0	1.0	ECM16	orf19.2090	RNA helicase (by homology)	YMR128w
CA3491	0.9	0.6	1.5	1.1	1.3	1.4	RPC40	orf19.3564	RNA polymerase (by homology)	YPR110c
CA2587	0.4	0.6	1.1	1.1	1.0	1.0	RPS30	orf19.4375.1	40S ribosomal protein S30(by homology)	YOR182c
CA1822	1.2	0.6	2.2	1.3	0.8	0.9	IPF9525	orf19.4268	unknown function	YLR222c
CA5950	0.4	0.6	0.8	0.7	1.0	1.0	TPI1	orf19.6745	Triose phosphate isomerase	YDR050c
CA5259	1.2	0.6	0.8	0.9	0.7	1.0	OSM2	orf19.5005	Osmotic growth protein (by homology)	YJR051w
CA4536	0.6	0.6	1.1	1.1	1.0	1.0	COX13	orf19.1467	cytochrome-c oxidase chain VIa (by homology)	YGL191w
CA5829	0.7	0.6	0.9	1.1	1.0	1.0	ADE1	orf19.7484	phosphoribosyl-amidoimidazole-succinocarboxamidesynthet	YAR015w
CA5190	0.8	0.6	1.0	0.9	1.2	1.1	IPF10155	orf19.4628	unknown function	YKL059c
CA0696	0.7	0.6	1.1	1.4	1.2	1.1	HMT1	orf19.3291	hnRNP methyltransferase (by homology)	YBR034c
CA3165	0.8	0.6	1.3	1.1	0.9	1.0	FMI1	orf19.1578	processing of pre-ribosomal RNA	YMR229c
CA5788	0.1	0.6	1.1	1.8	1.7	1.0	RHR2	orf19.5437	DL-glycerol phosphatase	YIL053w
CA4418	0.5	0.6	0.8	1.0	0.7	0.8	ERG5	orf19.5178	C-22 sterol desaturase by homology	YMR015c
CA2796	0.8	0.6	1.8	1.3	1.3	1.1	IPF8405	orf19.1721	similar to Saccharomyces cerevisiae Nce103p involved in no	YNL036w
CA4435	1.1	0.6	1.3	0.9	0.7	0.7	IPF5567	orf19.5160	phosphatase associated protein by homology	YKR028w
CA2377	0.8	0.6	1.1	0.7	0.8	0.8	MRPL7	orf19.2214	Ribosomal protein of the large subunit, mitochondrial (by hon	YDR237w
CA2348	0.7	0.6	0.5	0.6	0.2	0.3	IPF12811	orf19.3751	putative serine/threonine kinase	YOR233w

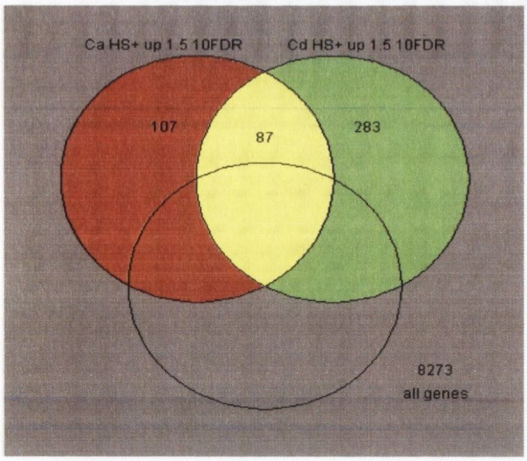
CA1417	0.9	0.6	1.9	1.2	1.2	1.4	IPF16126	orf19.172	similar to Saccharomyces cerevisiae Rpc19p DNA-directed F	YNL113w
CA3526	0.8	0.6	0.9	0.8	0.8	0.8	MRPS5.5f	orf19.989	Probable ribosomal protein S5, mitochondrial (by homology)	YBR251w
CA2861	0.4	0.6	0.8	0.9	0.7	1.0	HHT21	orf19.1061	Histone H3	YNL031c
CA0027	0.8	0.6	2.3	1.5	1.1	1.2	RCL1	orf19.1886	RNA 3 -terminal phosphate cyclase (by homology)	YOL010w
CA4077	0.8	0.6	0.9	1.0	1.0	1.0	ACO2	orf19.6632	aconitate hydratase (by homology)	YJL200c
CA5611	0.9	0.6	1.4	1.1	0.9	1.3	SUA5	orf19.7088	translation initiation protein (by homology)	YGL169w
CA1956	0.5	0.6	0.9	0.8	0.4	0.5	ERG3	orf19.767	C5,6 desaturase	YLR056w
CA6061	0.6	0.6	2.3	1.2	0.4	0.4	IPF8302	orf19.6007	unknown function	YJL196c
CA4169	1.2	0.6	1.0	0.9	0.8	0.9	RSC2	orf19.2964	Member of RSC complex, which remodels the structure of ch	YGR056w
CA3158	0.6	0.6	0.8	1.4	1.1	1.0	IPF13131.	orf19.1587	unknown function, 3-prime end	YBR241c
CA4430	1.3	0.6	1.0	1.2	0.9	0.9	IPF5577.	orf19.5165	unknown function	YNR029c
CA1560	1.0	0.6	1.0	1.0	1.1	0.9	MET18	orf19.1706	Involved in NER repair and RNA polymerase II transcription (	YIL128w
CA4116	1.1	0.6	1.3	1.0	0.6	0.9	IDI1	orf19.2775	isopentenyl-diphosphate delta-isomerase (by homology) Lipic	YPL117c
CA3619	0.7	0.6	1.1	0.9	0.4	0.6	CDC47	orf19.202	cell division control protein, ,(by homology)	YBR202w
CA4821	0.9	0.6	0.7	1.1	0.8	0.8	IPF1197	orf19.2076	unknown function	YMR130w
CA0328	0.7	0.6	1.7	1.5	1.2	1.2	IPF15217.	orf19.3778	WD-repeat protein, 3-prime end (by homology)	YCR072c
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match (e-value > 0.05)
CA4517	0.9	0.6	1.2	1.1	0.7	0.9	MEX67	orf19.488	poly(A)+RNA binding protein involved in nuclear mRNA expo	YPL169c
CA3896	0.7	0.6	1.2	1.0	0.9	1.3	IPF10339	orf19.5077	unknown function	no match (e-value > 0.05)
CA6139	0.7	0.6	1.3	1.3	1.0	1.1	ADE2	orf19.5906	phosphoribosylaminoimidazole carboxylase	YOR128c
CA1709	1.3	0.6	1.1	0.9	0.5	0.6	HOL2	orf19.4889	Multidrug-resistance protein subfamily 1 (by homology)	YNR055c
CA5348	0.7	0.6	1.3	1.1	0.8	1.2	IPF863	orf19.7223	involved in inositol biosynthesis (by homology)	YBR030w
CA1712	1.1	0.6	1.0	1.2	0.9	1.0	ABC1	orf19.3331	ubiquinol--cytochrome-c reductase(by homology)	YGL119w
CA3459	1.0	0.6	1.0	1.0	0.8	0.9	CGT1.3f	orf19.1261	mRNA capping enzyme alpha subunit, 3-prime end	YGL130w
CA4920	0.8	0.6	1.0	1.0	0.9	0.9	GCN20	orf19.6060	Positive effector of Gcn2p (by homology)	YFR009w
CA2810	0.7	0.6	1.1	1.1	1.0	1.0				
CA3977	0.7	0.6	1.2	1.0	1.2	1.2	IPF20153	orf19.1549	unknown function	no match (e-value > 0.05)
CA2181	0.5	0.6	0.6	0.9	0.5	0.9	ECM331	orf19.4255	Involved in cell wall biogenesis and architecture (by homolog	YDR055w
CA1250	1.1	0.6	0.8	1.1	0.7	0.9	IPF9626	orf19.4959	unknown function	no match (e-value > 0.05)
CA4041	1.6	0.6	1.9	1.7	1.1	0.7	GAL10	orf19.3672	UDP-glucose 4-epimerase by homology	YBR019c
CA1757	1.0	0.6	1.7	0.8	0.8	0.7	IPF14559.	orf19.5128	unknown function, 5-prime end	no match
CA2984	0.8	0.6	2.1	1.2	0.8	0.9	IPF12606.	orf19.6008.1		YNL123w
CA4225	0.6	0.6	1.1	0.9	1.0	1.0	RPL39	orf19.827.1	ribosomal protein L39	YMR194w
CA5907	0.8	0.6	1.1	1.2	0.8	0.9	SSN6	orf19.6798	transcriptional repressor (by homology)	YBR112c
CA5666	0.5	0.6	0.8	1.0	0.5	0.6	PUB1	orf19.7368	Major polyadenylated RNA-binding protein (by homology)	YNL016w
CA1770	0.7	0.6	1.8	1.3	1.3	1.4	IPF12457	orf19.2185	unknown function	YGL111w
CA5616	1.5	0.6	0.8	1.2	1.2	1.0	PET8	orf19.7082	mitochondrial carrier protein (by homology)	YNL003c
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)	YHL003c
CA3892	1.0	0.6	1.0	1.0	0.9	0.9	PSE1	orf19.5085	karyopherin-beta protein (by homology)	YMR308c
CA5702	0.7	0.6	0.9	0.8	0.5	0.7	PCH1	orf19.7402	Putative ATPase (by homology)	YDR440w
CA0357	0.4	0.6	0.5	0.9	0.8	0.4	FCY22	orf19.333	purine-cytosine permease (by homology)	YER060w
CA2801	0.9	0.6	1.0	0.9	0.9	0.9	URA3	orf19.1716	orotidine-5 -monophosphate decarboxylase [Candida albican	YEL021w
CA5396	1.0	0.6	1.1	0.8	0.7	0.8	NAM7	orf19.939	nonsense-mediated mRNA decay protein (by homology)	YMR080c
CA5149	0.7	0.6	1.1	1.1	1.3	1.1	HGH1	orf19.4587	Similar to human HMG1 and HMG2 proteins (by homology)	YGR187c
CA5401	0.9	0.6	1.0	1.1	0.5	0.7	FET35.3	orf19.943	Cell surface ferroxidase, high affinity, 3-prime end (by homolc	YMR058w
CA1525	1.1	0.6	0.9	1.0	1.4	0.8	AGP3	orf19.3795	amino acid-permease (by homology)	YFL055w
CA2176	1.2	0.6	1.3	0.8	0.2	0.3	CDC54	orf19.3761	cell division control protein (by homology)	YPR019w
CA4373	0.8	0.6	0.7	1.0	0.3	0.5	IPF5287	orf19.5664	signal transduction protein (by homology)	YMR032w
CA3854	0.5	0.6	0.8	1.0	0.9	1.2	IPF4649	orf19.6102	unknown Function	YIL036w
CA5042	0.4	0.6	0.5	0.9	2.0	5.8	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA6134	0.6	0.6	1.3	1.1	0.8	0.8	MAK21	orf19.5912	Ribosome biogenesis protein (by homology)	YDR060w
CA4102	0.5	0.6	1.1	1.1	1.1	1.0	RPL37B	orf19.667.1	Ribosomal protein	YDR500c
CA4255	0.6	0.6	1.0	1.0	1.0	0.9	FUM11	orf19.543	fumarate hydratase	YPL262w
CA2090	0.6	0.7	1.0	1.1	1.0	1.0	IPF3398.3	orf19.837.2	unknown function, 3-prime end	no match (e-value > 0.05)
CA1262	1.0	0.7	0.8	0.7	0.5	0.7	MDR1	orf19.1244	Mac1p interacting protein (by homology)	YGR100w
CA1484	0.9	0.7	1.1	1.0	1.0	1.0	ARO4	orf19.4060	3-dehydro-deoxyphosphoheptonate aldolase, tyrosine-inhibit	YBR249c
CA3799	0.9	0.7	1.1	0.9	0.7	0.9	IPF7198	orf19.2478	unknown function	YKR095w
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
CA4553	0.5	0.7	0.5	0.7	0.4	0.6	CYB1	orf19.1446	G2/Mitotic-specific cyclin	YPR119w
CA4289	1.3	0.7	2.5	1.3	0.8	1.0	IPF6665	orf19.6686	unknown function	YGR145w
CA2004	0.6	0.7	1.0	0.7	0.6	0.8	POL12	orf19.2796	DNA-directed DNA polymerase alpha (by homology)	YBL035c
CA3994	0.9	0.7	1.1	1.4	0.7	0.9	ERG7	orf19.1570	lanosterol synthase	YHR072w
CA5428	1.1	0.7	1.0	0.9	0.8	0.9	BOI2	orf19.3230	budding protein (by homology)	YER114c
CA2998	1.1	0.7	0.9	1.1	1.2	1.2	LPD1	orf19.6127	dihydrolipoamide dehydrogenase (by homology)	YFL018c
CA2388	1.1	0.7	1.3	1.1	0.7	0.9	MCM6	orf19.2611	component of MCM initiator complex involved in DNA replicat	YGL201c
CA5466	1.8	0.7	2.2	1.2	1.0	1.0	PWP2	orf19.3276	periodic tryptophan protein (by homology)	YCR057c
CA2032	1.0	0.7	1.7	0.8	0.5	0.6	IPF13112	orf19.3466	unknown function	YGL136c

3A

[Cd HS+ down 0.667 10FDR] and [Ca HS+ down 0.667 10FDR]

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	S.c. hom.
CA1051	0.1	0.3	0.7	0.9	1.0	1.0	CHT2	orf19.3895	chitinase 2 precursor	YLR286c
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA3305	0.1	0.2	1.2	1.0	1.1	0.9	RPL29	orf19.2310.1	ribosomal protein, cytosolic(by homology)	YFR032ca
CA4534	0.1	0.2	1.2	0.9	1.1	1.1	RPS26A	orf19.1470	ribosomal protein S26.e.A, cytosolic (by homology)	YGL189c
CA2920	0.1	0.2	1.0	1.1	0.9	0.7	FET5.5eo	orf19.4215	multicopy oxidase (by homology)	YFL041w
CA3084	0.1	0.2	1.0	1.1	1.0	1.1	IPF11625	orf19.4149	unknown function	no match (e-value > 0.05)
CA1637	0.2	0.2	1.0	1.1	1.0	1.0	RPL43A	orf19.3942.1	ribosomal protein (by homology)	YPR043w
CA2579	0.2	0.2	1.3	1.0	1.1	1.0				
CA3878	0.2	0.3	0.5	0.6	0.5	0.5	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA polymerase	YDR213w
CA1782	0.2	0.1	0.9	1.0	0.5	0.2	PHO84.3e	orf19.1172	Inorganic phosphate transport protein, 3-prime end (by homo	YML123c
CA4103	0.2	0.4	1.0	1.0	1.1	1.0	IPF3980	orf19.668	unknown function	YLR183c
CA2947	0.2	0.3	0.7	0.5	0.5	0.7	IPF6298	orf19.1964	unknown function	no match (e-value > 0.05)
CA5125	0.2	0.2	1.0	1.2	1.0	1.0	RPP2	orf19.6403.1	acidic ribosomal protein by homology	YOL039w
CA6068	0.2	0.2	1.2	1.2	1.0	1.0	RPS19A	orf19.5996.1	ribosomal protein S19.e (by homology)	YOL121c
CA3690	0.2	0.2	1.0	1.0	1.0	0.9	RPS14B	orf19.6265.1	ribosomal protein (by homology)	YJL191w
CA2818	0.2	0.2	1.1	1.1	1.1	1.0	RPL13	orf19.2994	Ribosomal protein	YDL082w
CA5646	0.2	0.3	1.1	1.2	1.2	1.0	RPS28B.3	orf19.7048.1	Ribosomal protein S28B (S33B) (YS27), 3-prime end (by hon	YLR264w
CA3030	0.2	0.6	1.2	0.9	0.9	1.3	IPF19968	orf19.220	putative cell wall protein of the PIR family	YKL164c
CA6092	0.2	0.3	1.2	0.9	1.1	1.0	RPL35	orf19.5964.2	Ribosomal protein L35A, (by homology)	YDL191w
CA5920	0.2	0.2	1.0	1.0	1.2	1.0	RPS12	orf19.6785	acidic ribosomal protein S12 (by homology)	YOR369c
CA4562	0.2	0.3	0.9	1.1	1.0	1.0	RPS8A	orf19.6873	ribosomal protein (by homology)	YER102w
CA3304	0.2	0.2	1.0	0.9	0.9	1.0	RPL82	orf19.2311	60S ribosomal protein L7a.e.B (by homology)	YLL045c
CA2075	0.2	0.5	0.5	0.7	1.3	1.1	IFE2	orf19.5288	Unknown function	YAL060w

CA2023	0.2	0.2	1.1	1.1	1.0	1.0	RPL42	orf19.4909.1	ribosomal protein L36a, 3- prime end (by homology)	YHR141c
CA1353	0.2	0.3	0.4	0.5	0.7	1.0	ERG1	orf19.406	squalene epoxidase	YGR175c
CA5426	0.2	0.2	1.0	0.8	1.0	1.0	FAS1	orf19.979	Fatty-acyl-CoA synthase, beta chain.	YKL182w
CA5807	0.2	0.2	1.1	1.0	0.9	1.0	RPS24	orf19.5466	ribosomal protein S24.e	YIL069c
CA2092	0.2	0.2	1.0	1.0	0.9	1.0	RPL21A	orf19.840	Ribosomal protein (by homology)	YBR191w
CA6064	0.2	0.2	1.0	0.9	0.9	1.0	RPL81	orf19.6002	60S ribosomal protein L7a.e.B (by homology)	YLL045c
CA4842	0.2	0.5	0.7	1.2	0.9	0.8	MTD1	orf19.3810	methylenetetrahydrofolate dehydrogenase	YKR080w
CA4269	0.2	0.2	0.9	1.1	0.9	1.0	RPS25B	orf19.6663	Cytosolic ribosomal protein (by homology)	YLR333c
CA6106	0.2	0.3	1.1	0.7	0.9	0.7	FAS2.53f	orf19.5948.1	fatty-acyl-CoA synthase, alpha chain, internal fragment	YPL231w
CA1972	0.2	0.3	1.3	1.1	0.9	1.0	RPL27A	orf19.5225.2	ribosomal protein L27	YHR010w
CA1189	0.2	0.2	1.0	1.0	1.0	1.0	RPL24A	orf19.3789	ribosomal protein L24 (by homology)	YGL031c
CA5203	0.2	0.2	1.0	1.2	0.9	1.0	RPS18	orf19.7018	Ribosomal protein S18 (by homology)	YML026c
CA5345	0.2	0.3	1.1	1.2	1.0	0.9	FTR1	orf19.7219	high affinity iron permease	YER145c
CA0632	0.2	0.2	1.3	1.1	1.0	1.0	RPS5	orf19.4336	ribosomal protein S5.e (by homology)	YJR123w
CA2011	0.2	0.4	1.3	1.4	1.1	1.1	RPS31	orf19.3087	Ubiquitin fusion protein	YLR167w
CA1304	0.3	0.3	1.1	1.0	1.0	1.0	RPS13.3	orf19.4193.1	ribosomal protein (by homology)	YDR064w
CA1662	0.3	0.2	0.9	1.0	1.0	1.0				
CA2862	0.3	0.5	0.8	0.9	0.2	0.6	HHF21	orf19.1059	histone H4	YNL030w
CA2734	0.3	0.5	1.2	1.1	1.0	0.9	RPL38	orf19.2111.2	ribosomal protein L38 (by homology)	YLR325c
CA5343	0.3	0.2	1.0	1.0	1.0	1.0	RPL4B	orf19.7217	Ribosomal protein L4B (by homology)	YDR012w
CA2819	0.3	0.4	1.1	1.1	1.0	1.0	RPA1	orf19.2992	60S ribosomal protein	YDL081c
CA5200	0.3	0.3	1.1	1.1	1.0	1.0	RPL10E	orf19.7015	Ribosomal protein L10, cytosolic (by homology)	YLR340w
CA4697	0.3	0.4	0.8	0.8	0.6	0.8	HTB1	orf19.6925	Histone H2B (by homology)	YDR224c
CA2031	0.3	0.2	1.0	1.1	1.0	1.0	RPL10A	orf19.3465	L10A ribosomal protein	YPL220w
CA3332	0.3	0.2	1.3	1.2	0.9	0.7	POL21.5f	orf19.2668	pol polyprotein, reverse transcripase, 5-prime end (by homol	no match
CA2805	0.3	0.4	0.7	0.8	0.7	0.8	RNR1	orf19.5779	ribonucleoside-diphosphate reductase (by homology)	YER070w
CA4882	0.3	0.3	0.7	0.9	0.5	0.8	IPF1651	orf19.6570	purine nucleoside permease (by homology)	no match
CA1062	0.3	0.2	0.6	0.4	1.0	1.2	IPF14165	orf19.4642	unknown function	no match
CA1315	0.3	0.3	0.8	0.9	1.0	0.9	URA2	orf19.2360	multifunctional pyrimidine biosynthesis protein, (by homology	YJL130c
CA5816	0.3	0.3	1.0	0.8	1.0	1.1	ACC1	orf19.7466	acetyl-coenzyme-A carboxylase (by homology)	YNR016c
CA3372	0.3	0.5	1.0	0.9	0.4	0.6	HHF22	orf19.1854	histone H4 (by homology)	YNL030w
CA4512	0.3	0.3	1.0	0.9	1.1	1.1				
CA1431	0.3	0.4	1.0	1.5	1.1	0.8	FET34.3e	orf19.1206	iron transport multicopper oxidase, 3-prime end (by homolog	YMR058w
CA3862	0.3	0.4	1.3	1.6	1.4	1.0	NSR1	orf19.6090	nuclear localization sequence binding protein (by homology)	YGR159c
CA3547	0.3	0.4	0.8	1.0	0.8	1.0	ADE13	orf19.3870	adenylosuccinate lyase (by homology)	YLR359w
CA0254	0.4	0.4	0.9	1.1	2.3	0.9	IPF14968	orf19.3461	unknown function	no match
CA3330	0.4	0.2	1.7	1.2	0.8	0.9	POL21.3f	orf19.2669	pol polyprotein, reverse transcripase, 3-prime end (by homol	YFL050c
CA3284	0.4	0.4	0.9	0.9	1.0	1.0	ADE6	orf19.6317	5 -phosphoribosylformyl glycinamidine synthetase (by homol	YGR061c
CA4800	0.4	0.6	0.7	0.9	0.5	0.6	PGA4	orf19.4035	putative GPI-anchhored protein related to Phr1, Phr2 and Ph	YOL030w
CA5065	0.4	0.3	1.0	1.0	0.8	1.0	IPF3584	orf19.3037	similar to Saccharomyces cerevisiae Pab1p mRNA polyaden	YER165w
CA2969	0.4	0.2	0.4	0.6	0.6	0.5	IPF19772	orf19.5602	unknown function	no match
CA2494	0.4	0.6	0.8	1.1	0.9	1.1	HTS1	orf19.4051	histidine tRNA synthetase (by homology)	YPR033c
CA2924	0.4	0.5	1.0	1.3	1.2	0.8	FET33	orf19.4211	cell surface ferroxidase (by homology)	YMR058w
CA4783	0.5	0.5	1.0	1.0	1.0	1.0	IPF3358	orf19.4016	ubiquinol-cytochrome-c reductase (by homology)	YBL045c
CA1503	0.5	0.4	2.0	1.6	1.0	1.1	RKI1	orf19.1701	D-ribose-5-phosphate ketol-isomerase (by homology)	YOR095c
CA5197	0.5	0.4	1.3	1.2	1.0	0.8	IPF2342	orf19.7011	unknown function	YPL012w
CA2249	0.5	0.6	0.9	0.7	0.5	0.7	POL2	orf19.2365	DNA-directed DNA polymerase epsilon, catalytic subunit A (b	YNL262w
CA4745	0.5	0.6	0.6	1.0	0.8	0.6	URA1	orf19.4836	dihydroorotate dehydrogenase	no match
CA5680	0.5	0.4	1.0	0.9	1.0	1.0				
CA2091	0.5	0.6	1.0	1.0	0.8	0.9	IPF3401	orf19.839	unknown function	YLR143w
CA5497	0.5	0.4	1.2	0.7	1.9	1.0	IPF776	orf19.5338	transcriptional activator (by homology)	YPL248c
CA5507	0.5	0.5	1.1	1.0	1.0	0.9	TIF11	orf19.5351	translation initiation factor eIF1a (by homology)	YMR260c
CA2956	0.5	0.6	0.9	1.2	1.3	1.1	EGD2	orf19.5858	Nascent polypeptide associated complex protein alpha subur	YHR193c
CA3168	0.5	0.5	1.3	1.4	1.3	1.3	PRS3	orf19.1575	ribose-phosphate pyrophosphokinase	YHL011c
CA5051	0.5	0.3	2.5	1.4	1.2	1.2	IPF3709	orf19.3015	unknown function	YDR101c
CA4270	0.5	0.3	1.0	0.9	0.6	0.7	NUP2	orf19.6665	Nuclear pore protein (by homology)	YLR335w
CA0697	0.5	0.7	0.5	0.9	0.7	0.4	VTC4	orf19.3363	putative polyphosphate synthetase (by homology)	YJL012c
CA0659	0.6	0.7	0.8	0.6	0.4	0.4	IPF16189.	orf19.5576	panthotenate kinase, 3-prime end (by homology)	YDR531w
CA5204	0.6	0.5	1.1	0.7	0.7	0.9	YML6	orf19.7019	Ribosomal protein, mitochondrial (by homology)	YML025c
CA1976	0.6	0.5	1.0	0.9	0.8	0.8	IPF9582	orf19.688	similar to Saccharomyces cerevisiae Mrps18p ribosomal prot	YNL306w
CA1927	0.6	0.6	1.0	1.1	1.0	1.0	YBN5	orf19.754	Putative purine nucleotide-binding protein (by homology)	YBR025c
CA1114	0.6	0.6	0.9	1.2	1.1	1.2	IPF9995	orf19.2286	unknown function	YJR070c
CA4498	0.6	0.4	1.4	1.4	0.9	1.0	IPF11315	orf19.512	unknown function	YNL132w
CA2682	0.6	0.6	0.9	0.9	0.9	1.1	FRS1	orf19.2573	Phenylalanyl-tRNA synthetase	YLR060w
CA4235	0.6	0.4	1.1	1.0	1.0	1.1	NCL1	orf19.518	Probable proliferating-cell nucleolar antigen (by homology)	YBL024w
CA0432	0.7	0.5	1.0	1.1	0.9	0.9	IPF7926	orf19.1341	putative protein kinase (by homology)	YDL214c
CA3240	0.7	0.6	1.4	1.1	0.6	0.8	IPF10559	orf19.4683	myosin-like protein (by homology)	YKR095w



4A

[Ca HS+up 1.5 10 FDR] less [Cd HS+ uo 1.5 10 FDR]

Species ()*S	Ca HS+	Cd HS+	Ca OS+	Cd OS+	Ca XS+	Cd XS+				
Stress ()*S	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
Systemati										
CA3367	6.5	1.0	1.1	0.9	1.1	1.1	IPF4667	orf19.1847	unknown Function	YDR380w
CA4053	4.1	0.9	0.7	1.0	1.4	1.0	IKS1	orf19.428	PROBABLE SERINE/THREONINE-PROTEIN KINASE	YJL057c
CA0821	4.1	1.0	0.5	0.9	1.3	0.9	IPF16795	orf19.2989	glycerate/formate-dehydrogenase (by homology)	YNL274c
CA2342	3.7	1.0	5.9	2.4	1.1	1.0	IPF13836	orf19.2344	probable heat shock protein (by homology)	no match
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA4676	3.6	1.1	0.7	0.9	4.8	1.1	HK1	orf19.896	Histidine kinase	YIL147c
CA2659	3.3	1.1	0.9	1.0	3.5	1.5	NDH2	orf19.5713	NADH dehydrogenase (by homology)	YMR145c
CA3211	3.1	1.1	2.2	1.2	0.7	1.0	IPF19977	orf19.6192	unknown function	YGR175c
CA2039	3.1	0.9	1.7	1.0	1.2	0.8	IPF12947	orf19.4357	unknown function	YMR115w
CA0596	3.1	1.1	0.8	1.0	0.9	1.0	IPF9706	orf19.4883	unknown function	YBR203w
CA0671	2.9	1.2	1.1	1.0	12.0	1.3	GRP4	orf19.3150	putative reductase (by homology)	YOL151w
CA4779	2.9	1.2	1.3	1.3	3.0	1.4	IPF3351	orf19.4012	unknown function	YHR071w
19812.1	2.7	0.8	0.8	1.0	0.9	0.9				
CA4987	2.7	1.0	1.1	0.9	1.2	1.0	IPF2045	orf19.5262	unknown function	no match
CA6052	2.6	1.4	1.3	1.0	0.8	1.0	IPF4942	orf19.7668	similar to Saccharomyces cerevisiae Mal32p alpha-glucosida	YBR299w
CA0929	2.6	1.4	3.8	1.1	1.0	1.1	GUT1	orf19.558	Glycerol kinase (by homology)	YHL032c
CA0457	2.5	1.2	2.2	1.8	1.2	0.8	IPF15604	orf19.2432	transcription factor (by homology)	YFL031w
CA4665	2.5	1.1	1.1	1.0	0.9	0.8	IPF6548	orf19.4451	translation elongation factor eEF4 (by homology)	YNL163c
CA0796	2.4	0.9	1.0	0.9	1.1	0.9	ALR1	orf19.1607	divalent cation transporter (by homology)	YOL130w
CA2246	2.4	1.3	2.1	1.8	1.0	0.8	IPF7405	orf19.4666	unknown function	no match
CA4016	2.4	1.2	1.0	1.0	0.9	1.0	GFA1	orf19.1618	glutamine:fructose-6-phosphateamidotransferase	YKL104c
CA2335	2.4	0.8	1.4	1.1	0.9	1.1	LYS21	orf19.4506	homocitrate synthase (by homology)	YDL131w
CA5547	2.4	1.1	1.1	2.1	0.7	0.9	IPF5981	orf19.7310	similar to Saccharomyces cerevisiae Gin3p (by homology)	YML128c
CA5864	2.3	1.2	0.9	1.1	1.1	1.1	IPF364	orf19.7522	transaminase type I (by homology)	YJL060w
CA5541	2.3	1.0	0.7	1.0	0.7	1.1	IPF2827	orf19.7303	unknown function	no match
CA4201	2.3	1.1	0.8	1.0	0.7	1.0	IPF8048	orf19.4543	probable succinate-semialdehyde dehydrogenase (by homolo	YBR006w
CA1492	2.3	1.5	1.2	1.2	0.6	1.1	IPF168	orf19.3226	unknown function	YDL046w
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA4157	2.2	1.5	0.8	1.0	0.9	1.0	HYU1	orf19.5804	hydantoin utilization protein A (hyuA) homolog	YKL215c
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homolo	YJL101c
CA5924	2.2	1.1	0.9	1.0	1.2	0.9	IPF2822	orf19.6781	unknown function	no match
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA0845	2.1	1.3	1.3	0.9	1.0	1.0	IPF16314	orf19.264	unknown function	YGL134w
CA5230	2.1	1.1	1.2	1.2	1.0	1.0	IPF10424	orf19.5034	unknown function	YBR216c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA0150	2.1	1.3	1.3	1.0	1.8	1.0	CDC123	orf19.2721	similar to Saccharomyces cerevisiae Cdc123p cell cycle regu	YLR215c
CA5142	2.1	1.3	0.7	1.0	1.0	1.0	IPF1022	orf19.4579	similar to Saccharomyces cerevisiae Erv29p ER-Golgi transp	YGR284c
CA4713	2.1	0.8	2.4	0.7	1.7	1.1	CCC1	orf19.6948	Transmembrane Ca2+ transporter (by homology)	YLR220w
CA0844	2.1	1.0	1.0	1.0	0.7	0.9	CDC3	orf19.1055	Cell division control protein	YLR314c
CA4123	2.0	1.1	1.0	1.1	1.5	1.0	AMS1	orf19.2768	alpha-mannosidase (by homology)	YGL156w
CA4199	2.0	2.1	0.6	0.9	1.4	1.4	UBC8	orf19.4540	ubiquitin-conjugating enzyme (by homology)	YEL012w
CA2874	2.0	0.8	0.3	0.7	0.1	0.5	IPF4999	orf19.5843	unknown function	no match
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA3218	2.0	1.0	1.0	1.0	1.2	1.0	IPF10005	orf19.6196	unknown function	no match
CA1308	2.0	1.0	1.1	1.0	1.0	1.0				
CA2129	1.9	1.1	1.3	1.1	0.5	1.3	IPF4899	orf19.414	unknown function	YKL155c
CA1497	1.9	1.1	2.2	1.5	4.0	1.2	IPF9683	orf19.3644	unknown function	YHR006w
CA4889	1.9	1.1	1.0	0.9	0.8	1.0	IPF1629	orf19.6581	unknown function	YOL003c
CA2539	1.9	1.4	1.3	0.9	0.9	0.9	IPF9188	orf19.3187	unknown function	YOL089c
CA1891	1.9	1.2	1.5	1.2	0.8	0.9	IPF10196	orf19.2752	unknown function	YDR216w
CA1896	1.9	1.1	1.1	1.4	1.0	0.8	ERD2	orf19.2756	ER lumen protein retaining receptor (by homology)	YBL040c
CA1267	1.9	1.2	0.9	1.0	0.7	0.5	YSY6	orf19.242.2	protein involved in the secretory pathway, by homology	YBR162wa
CA3842	1.8	1.1	1.3	1.0	0.8	1.1	YKE2.3f	orf19.6601.1	Gim complex component, 3-prime end (by homology)	YLR200w
CA5459	1.8	1.2	1.3	1.1	0.9	0.7	IPF276	orf19.3267	unknown function	YDR126w
CA0374	1.8	1.0	0.8	1.0	1.0	1.0				
CA5983	1.8	1.2	0.8	1.3	0.9	1.1	IPF913	orf19.7579	unknown function	no match
CA0494	1.8	1.3	0.9	1.0	1.3	1.1	RAD7	orf19.1493	nucleotide excision repair protein (by homology)	YJR052w
CA5773	1.8	1.4	0.9	1.0	2.5	1.4	DOT5	orf19.5417	Derepression of telomeric silencing (by homology)	YIL010w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match
CA5649	1.7	0.8	1.8	1.0	0.9	0.6	CHS4	orf19.7349	Chitin synthase regulatory factor	YBL061c
CA6127	1.7	0.9	1.4	1.4	1.0	1.0	IPF149	orf19.5921	peroxisomal membrane protein (by homology)	YEL006w

[Ca HS+up 1.5 10 FDR] less [Cd HS+ uo 1.5 10 FDR]

HS+ OS+									
Species ()*:	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+			
Systemati	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
CA2109	1.7	1.1	1.4	1.2	0.9	0.8	IPF13749.	orf19.3690	unknown function, 5-prime end	YLR345w
CA3750	1.7	1.2	1.9	1.4	0.8	0.9	IPF7377	orf19.3428	unknown function	YMR044w
CA0010	1.7	0.9	0.9	1.1	1.0	0.5	IPF16036	orf19.150	similar to Saccharomyces cerevisiae Tim17p mitochondrial in	YJL143w
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match
CA3453	1.7	1.3	0.9	1.0	1.0	0.9	SEC23	orf19.1254	Component of COPII coat (by homology)	YPR181c
CA3627	1.7	1.3	1.1	0.9	0.8	0.9	IPF18318	orf19.5147	unknown function	YLL007c
CA0792	1.7	1.1	0.9	0.9	1.1	0.8	DIT2.3eoc	orf19.554	putative cytochrome P450, 3-prime end	YDR402c
CA1585	1.7	1.2	1.0	0.9	1.1	0.9	VPS27	orf19.6031	Vacuolar protein sorting (by homology)	YNR006w
CA4581	1.7	1.0	1.4	1.1	18.7	1.2	IPF2232	orf19.6899	unknown function	YMR315w
CA1616	1.7	0.8	1.1	0.6	0.6	0.6	IPF14538	orf19.3219	unknown function	YOR137c
CA2424	1.7	0.8	1.0	0.8	0.9	0.7	IPF18468	orf19.4467	unknown function	no match
CA0639	1.6	1.8	1.0	1.0	9.0	10.6				
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA1248	1.6	1.5	1.3	1.0	1.6	1.4	IPF3866	orf19.21	unknown function	YLR251w
CA2207	1.6	1.0	0.8	1.1	1.0	1.1	IPF12169	orf19.697	unknown function	YHR017w
CA2853	1.6	1.0	1.0	1.1	0.9	1.0	IPF17057	orf19.1070	unknown function	YMR010w
CA5349	1.6	1.2	1.0	0.9	1.1	1.1	IPF861	orf19.7224	unknown function	YKR017c
CA2964	1.6	0.9	1.0	0.8	1.1	1.0	IPF13176.	orf19.5610	ornithine carbamoyltransferase, 3-prime end (by homology)	YJL088w
CA5326	1.6	1.0	0.9	1.0	0.5	1.0	IPF2137	orf19.7200	unknown function	no match
CA2295	1.6	1.4	1.1	1.0	0.7	0.8	HOS2	orf19.5377	putative histone deacetylase (by homology)	YGL194c
CA0720	1.6	1.4	1.2	1.0	0.9	1.1	IPF17932	orf19.3457	unknown function	YBR175w
CA2990	1.6	1.5	0.8	0.9	0.5	0.8	IPF5092	orf19.6012	unknown function	YOR296w
CA1018	1.6	1.2	0.6	0.7	1.0	1.1	IPF13479.	orf19.3768	unknown function, 3-prime end	YCR081w
CA5676	1.6	1.0	1.0	1.0	1.1	1.0	FAA22	orf19.7379	Long-chain-fatty-acid--CoA ligase (by homology)	YER015w
CA4042	1.6	1.6	1.2	1.1	0.8	1.0	TRS23	orf19.3673	targeting and fusion of ER to golgi transport vesicles by homc	YDR246w
CA3026	1.6	1.0	1.0	1.0	0.9	1.0	IFZ1	orf19.3901		no match
CA3818	1.6	1.4	0.8	0.6	0.9	1.1	IPF6695	orf19.5773	unknown function	YOL057w
CA0843	1.6	1.3	1.1	1.2	0.5	0.7	IPF18853	orf19.1054	unknown function	YLL023c
CA2887	1.6	1.1	1.0	1.1	1.1	0.9	IPF13631	orf19.2472	unknown function	no match
CA3151	1.6	1.4	0.9	1.1	0.5	1.1	IPF4033	orf19.6167	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihydroxyac	YIL124w
CA2906	1.6	1.0	0.9	0.8	0.8	0.8	IPF15523	orf19.4521	unknown function	YOR246c
CA5976	1.6	1.0	0.8	0.9	1.6	0.9	IPF928	orf19.7570	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear c	YDL170w
CA4594	1.5	1.1	1.2	1.1	0.7	0.9	IPF2212	orf19.6912	unknown function	YLR133w
CA0881	1.5	0.8	0.7	1.0	0.8	1.1	IPF16965	orf19.374	unknown function	YOR256c
CA3875	1.5	1.1	0.5	1.0	1.2	1.0	IPF14430	orf19.394	putative kynureninase (by homology)	YLR231c
CA6011	1.5	1.0	0.6	1.0	1.5	1.1	CTM1	orf19.7612	cytochrome c methyltransferase (by homology)	YHR109w
CA1700	1.5	1.3	1.3	0.9	1.1	1.2	RAM1.5f	orf19.5046	protein farnesyltransferase, beta subunit, 5-prime end (by hor	YDL090c
CA3134	1.5	1.2	0.8	1.0	1.2	1.1	IFZ2	orf19.1365	unknown function	no match
CA4804	1.5	1.1	0.8	1.4	1.4	1.1	ARO8	orf19.2098	aromatic amino acid aminotransferase I (by homology)	YGL202w
CA1980	1.5	1.1	1.4	0.9	0.5	0.6	YHM1	orf19.685	member of the mitochondrial carrier family (MCF) (by homolo	YDL198c
CA3958	1.5	1.1	0.7	0.9	0.7	1.0	COX11	orf19.1416	cytochrome-c oxidase assembly protein by homology to S. ce	YPL132w
CA0739	1.5	1.1	0.9	1.0	0.6	0.7				
CA5560	1.5	1.2	1.3	0.9	1.1	1.0	THI13	orf19.7324	Pyrimidine precursor biosynthesis enzyme (by homology)	YDL244w
CA0280	1.5	1.0	1.4	1.1	0.8	0.7	IPF10566	orf19.1439	unknown function	YDR315c
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c

5A

[Cd HS+ up 1.5 10FDR], less [Ca HS+ up 1.5 10FDR]

HS+ OS+ XS+									
Species ()*:	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+			
Systemati	rmali:	rmali:	rmali:	rmali:	rmali:	rmali:	Common	Ca orf19	Ca Function	S.c. hom.
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA4684	3.0	10.5	1.1	1.0	2.2	1.5	HSP78.5f	orf19.882	heat shock protein of clpb family of ATP-dependent protease:	YDR258c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)	no match
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homolo	YMR152w
CA1075	1.5	7.0	0.8	0.8	0.8	0.7	IPF4991	orf19.2531	putative membrane protein	YDL058w
CA0785	2.2	5.9	0.9	1.1	1.2	1.1	IPF14603	orf19.3929	unknown function	YJR100c
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)	YLR216c
CA2513	1.0	5.2	1.6	1.5	0.7	1.1	SNG1	orf19.308	Involved in nitroguanidine resistance (by homology)	YGR197c
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match
CA4120	1.4	4.8	1.0	1.1	1.2	1.5	SOD1	orf19.2770.1	Cu,Zn-superoxide dismutase	YJR104c
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA0551	2.5	4.0	1.4	1.3	1.3	1.0	CDC37	orf19.5531	Cell division control protein (by homology)	YDR168w
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w
CA4021	1.5	3.8	0.7	1.6	1.1	1.1	EBP2	orf19.3442	NADPH dehydrogenase (by homology)	YHR179w
CA5558	1.5	3.8	1.1	1.4	1.3	1.2	IPF1969	orf19.7322	unknown function	YPL225w
CA1180	1.7	3.7	1.1	0.9	0.8	1.4	UGA12.3f	orf19.803	4-aminobutyrate aminotransferase (GABA transaminase), 3-p	YGR019w
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA2130	1.4	3.6	1.2	1.0	1.2	1.1	RPS27A	orf19.413.1	ribosomal protein S27.e (by homology)	YKL156w
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function	YNL111c
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease	YHL036w
CA4609	0.9	3.6	1.2	1.3	1.5	1.2	ZPR1	orf19.3300	Zinc finger protein (by homology)	YGR211w
CA1230	2.1	3.5	1.5	1.6	0.9	0.9	SSA4	orf19.4980	cahsp70 mRNA for heat shock	YER103w
CA1181	1.9	3.5	0.9	0.8	0.8	1.4	UGA12.5f	orf19.802	4-aminobutyrate aminotransferase (GABA transaminase), 5-p	YGR019w
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inn	YMR152w
CA0706	1.7	3.4	1.1	1.5	0.9	1.0	IPF7715.3	orf19.682	unknown function	YJL078c
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase	YER042w
CA1330	1.0	3.4	1.0	1.6	1.0	1.0	IPF11713.	orf19.1151	unknown function, 3-prime end	no match
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w

[Ca HS+up 1.5 10 FDR] less [Cd HS+ uo 1.5 10 FDR]

HS+ OS+										
Species ()*	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase	YNL277w
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA2729	0.9	3.2	1.0	1.1	0.9	0.7	NAT2	orf19.2116	N-acetyltransferase for N-terminal methionine (by homology)	YGR147c
CA3099	2.2	3.2	1.0	1.4	1.4	1.3	LST8	orf19.3862	required for transport of permeases from the golgi to the plas	YNL006w
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA0117	1.5	3.1	1.1	1.1	0.9	1.1	IPF19231	orf19.916	unknown function	YNL305c
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)	YLR043c
CA1287	1.8	3.1	1.1	1.2	1.2	1.2	IPF5545	orf19.4430	unknown function	YDR330w
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function	YNL229c
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology	YDR032c
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholester	YNR008w
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function	YHR067w
CA4380	0.7	2.9	0.8	1.1	1.1	2.1	IPF12736	orf19.5673	unknown function	YPR194c
CA0219	1.6	2.9	1.1	1.2	1.2	0.9	YAP3	orf19.3193	transcription factor of a fungal-specific family of bzip proteins	YHL009c
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function	YBR042c
CA0740	1.2	2.8	1.0	1.0	1.3	1.5	UMP1	orf19.3140.1	proteasome maturtion factor (by homology)	YBR173c
CA2258	1.1	2.8	0.9	0.9	7.4	15.1	IFR1	orf19.1763	Unknown function	YNL134c
CA0915	3.0	2.8	1.1	1.0	1.0	0.7	KAR2	orf19.2013	dnaK-type molecular chaperone (by homology)	YJL034w
CA5060	1.5	2.8	0.9	1.0	1.2	1.2	IPF3690	orf19.3029	unknown function	YDR036c
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)	YDR069c
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA2131	1.4	2.6	0.9	1.0	1.0	1.1	IDP1	orf19.5211	isocitrate dehydrogenase, cytosolic (by homology)	YDL066w
CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA1759	1.5	2.6	1.3	0.9	1.0	1.0	IPF14744	orf19.5125	unknown function	YLR149c
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA5049	1.5	2.5	1.0	1.1	0.9	0.9	CDC12	orf19.3013	septin (by homology)	YHR107c
CA4319	1.9	2.5	1.1	1.2	1.1	0.9	RPN10	orf19.4102	Protein degradation (by homology)	YHR200w
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA0155	1.9	2.5	1.2	1.0	1.4	1.2	RPT6	orf19.3593	26S proteasome regulatory subunit (by homology)	YGL048c
CA5040	1.4	2.5	0.8	0.8	0.9	0.9	BAT22	orf19.6994	branched chain amino acid aminotransferase (by homology)	YJR148w
CA4924	2.0	2.5	1.2	1.2	1.4	1.0	UBP6.3f	orf19.6063	Ubiquitin-specific protease, 3-prime end (by homology)	YFR010w
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-bind	YGL091c
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)	YNL270c
CA6091	1.6	2.5	0.8	0.7	0.8	0.8	UFD2	orf19.5965	Ubiquitin fusion degradation protein 2 (by homology)	YDL190c
CA2698	1.2	2.5	1.1	0.8	0.9	1.0	SUL1	orf19.2738	High-affinity sulfate transport protein (by homology)	YLR092w
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function	YNL134c
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA2296	1.3	2.5	0.8	1.0	1.1	1.0	SCL1	orf19.5378	Proteasome subunit YC7alpha (by homology)	YGL011c
CA4525	1.2	2.5	1.0	1.1	1.1	1.2	SEC22	orf19.479.2	synaptobrevin-type protein transport protein (by homology)	YLR268w
CA4168	1.8	2.4	1.1	1.2	1.0	1.1	IPF7781	orf19.2965	putative pump-driving ATPase	YDL100c
CA1285	1.0	2.4	1.1	1.3	1.1	1.0	SKP1	orf19.4427	kinetochore protein complex CBF3 by homology	YDR328c
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA0265	1.6	2.4	1.3	1.0	1.0	1.0	STI1.3f	orf19.3191	stress-induced protein (by homology)	YOR027w
CA5087	1.0	2.4	1.1	0.9	0.7	0.9	IPF20025	orf19.3062	unknown function	YKL033w
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA5435	1.6	2.4	0.7	0.7	0.9	0.9	UFD4	orf19.3237	ubiquitin fusion degradation protein (by homology)	YKL010c
CA1569	1.8	2.4	1.5	1.2	1.1	2.4	IPF7616	orf19.1159	putative homoserine O-acetyltransferase (by homology)	YNL277w
CA1882	1.1	2.4	0.8	1.0	0.8	1.9	IPF19934	orf19.2210	unknown function	no match
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end	YKR076w
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match
CA2857	2.1	2.3	1.2	1.2	1.0	1.0	SSA1	orf19.1065	Heat shock protein of HSP70 family	YER103w
CA5173	0.9	2.3	0.8	1.1	0.8	1.0	CPS2.3f	orf19.4610.1	Carboxypeptidase YSCS precursor, 3-prime end (by homolog	YJL172w
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)	YHR137w
CA5791	1.5	2.3	1.2	1.0	1.4	1.2	RPT2	orf19.5440	26S proteasome regulatory subunit (by homology)	YDL007w
CA4772	1.8	2.3	1.3	1.1	1.1	1.1	CCT3	orf19.4004	Chaperonin (by homology)	YJL014w
CA1653	2.8	2.3	1.3	1.4	1.0	0.7	STE23	orf19.5561	protease involved in a-factor processing by homology	YLR389c
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)	YOL151w
CA2121	1.3	2.3	0.9	0.9	1.1	1.2	IPF7930	orf19.1338	unknown function	YJL123c
CA1846	1.5	2.2	0.8	0.9	12.5	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)	YOR388c
CA5618	1.4	2.2	1.0	1.0	1.0	1.1	LEU2	orf19.7080	isopropyl malate dehydrogenase	YCL018w
CA5303	1.2	2.2	1.1	1.2	1.5	0.8	IPF2180	orf19.7170	unknown function	no match
CA4257	1.2	2.2	1.0	0.9	1.3	1.1	PRE6	orf19.544.1	20S proteasome subunit	YOL038w
CA3706	0.9	2.2	0.7	0.8	1.1	1.0	PSA2	orf19.4943	mannose-1-phosphate guanyltransferase by homology	YDL055c
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA2565	1.6	2.2	1.1	1.0	0.9	1.3	MET15	orf19.5645	O-acetylhomoserine O-acetylserine sulphydrylase	YLR303w
6100.2	1.5	2.2	2.0	1.2	1.1	1.0				
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA5308	1.5	2.2	1.0	0.9	1.3	1.1	PRE5	orf19.7178	20S proteasome subunit alpha6 (by homology)	YMR314w
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA1508	2.1	2.2	0.7	1.0	0.7	0.9	IPF9977	orf19.4525	unknown function	YLR064w
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA1629	0.6	2.2	1.2	1.5	1.4	1.3	NPI46	orf19.1030	proline cis-trans isomerase (by homology)	YLR449w
CA2951	1.3	2.1	0.8	1.0	0.9	1.0	SBP1	orf19.5854	RNA binding protein-like (by homology)	YHL034c
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase	YKR070w
CA4865	1.5	2.1	1.0	1.0	1.1	1.2	IPF4085	orf19.3841	similar to Saccharomyces cerevisiae Apg1p essential for aut	YGL180w
CA4604	1.2	2.1	1.3	1.3	1.2	0.9	MBF1	orf19.3294	Multiprotein bridging factor mediates GCN4-dependent trans	YOR298ca
CA1116	1.3	2.1	1.1	1.3	0.9	1.0	CCT5	orf19.2288	T-complex protein 1, epsilon subunit (by homology)	YJR064w
CA0914	1.6	2.1	0.9	1.0	1.2	1.1	SRA1	orf19.2015	cAMP dependent protein kinase, regulatory subunit (by homo	YIL033c
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)	YPR086w
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA4167	0.6	2.1	0.8	1.0	0.9	1.1	IPF7778	orf19.2966	putative carboxymethylenebutenolidase (dienelactone hydrol	YDL086w

[Ca HS+up 1.5 10 FDR] less [Cd HS+ uo 1.5 10 FDR]

HS+ OS+									
Species ()	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+			
Systemati	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5717	1.0	2.1	0.9	1.1	0.8	1.1	CYP51	orf19.7421	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by	YDR304c
CA1256	2.2	2.0	1.0	1.1	0.7	1.1	UBP15	orf19.1777	ubiquitin-specific protease (by homology)	YMR304w
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA1911	1.1	2.0	1.1	0.9	1.0	1.0	SSE1	orf19.2435	heat shock protein of HSP70 family (by homology)	YPL106c
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable monoc	no match
CA5977	1.2	2.0	1.2	1.0	1.3	1.2	UBC4	orf19.7571	E2 ubiquitin-conjugating enzyme (by homology)	YBR082c
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in regu	YIL046w
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA0663	2.1	1.9	0.9	0.9	1.0	1.1	PUP2	orf19.709	20S proteasome subunit(alpha5) (by homology)	YGR253c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA4988	1.4	1.9	1.0	0.9	0.9	0.8	RPN2	orf19.5260	Proteasome regulatory subunit (by homology)	YIL075c
CA1880	1.7	1.9	1.2	1.3	1.4	1.0	IPF13316	orf19.2269	unknown function	YNL010w
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)	YNL040w
CA5862	1.0	1.9	1.2	1.3	1.1	1.1	POT11	orf19.7520	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)	YIL160c
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA4522	1.2	1.9	1.0	0.9	1.1	1.0	RPT4	orf19.482	26S proteasome regulatory subunit (by homology)	YOR259c
CA4389	1.6	1.9	1.2	1.0	1.2	1.2	RPT5	orf19.3123	26S proteasome regulatory subunit (by homology)	YOR117w
CA5268	1.8	1.9	1.1	1.1	0.7	0.9	SEC18.3f	orf19.4994	vesicular fusion protein, 3-prime end (by homology)	YBR080c
CA3868	1.3	1.9	1.1	1.1	0.8	1.0	CCT1	orf19.401	component of chaperonin-containing T-complex (by homolog	YDR212w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA0183	1.5	1.9	1.5	1.1	1.4	2.2	CAP1	orf19.1623	transcriptional acivator (by homology)	YML007w
CA0394	1.6	1.9	1.0	1.3	1.4	1.4	IPF12758.	orf19.334	unknown function, 5-prime end	no match
CA3247	1.2	1.9	1.1	1.0	0.7	0.8	IPF15832	orf19.4676	unknown function	YKL053ca
CA4695	1.2	1.9	0.9	1.4	1.3	1.0	IPF4229	orf19.6923	unknown function	YML015c
CA3898	1.3	1.9	1.1	0.9	0.8	1.0	UBA2	orf19.5074	ubiquitin-activating -like enzyme by homology	YDR390c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA0661	1.9	1.9	0.7	0.9	1.0	1.0	APG7	orf19.707	component of the autophagic system (by homology)	YHR171w
CA2120	1.6	1.9	0.9	1.0	1.2	1.2	PUP3	orf19.1336	PRCT yeast proteasome component (by homology)	YER094c
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA5554	1.0	1.9	0.7	1.0	0.9	1.0	IPF1960.5	orf19.7318	putative transcriptional activator, 5-prime end	YCR106w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA1395	1.1	1.9	1.0	0.9	11.5	11.7				
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA3422	1.6	1.9	0.9	0.8	0.7	0.9	IPF17289	orf19.6134	unknown function	YLR440c
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA1755	1.6	1.8	1.1	0.9	0.8	1.1	PDI1	orf19.5130	protein disulfide-isomerase precursor (by homology)	YCL043c
CA0408	1.9	1.8	0.9	1.0	0.9	1.0	SAC6.5f	orf19.5544	actin filament bundling protein, fimbrin, 5-prime end (by homc	YDR129c
CA1389	1.5	1.8	1.4	1.3	0.8	1.1	PLP2	orf19.1769	Might regulate Ste4p in pheromone response (by homology)	YOR281c
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA3191	1.5	1.8	0.7	1.0	0.7	0.8	IPF11601	orf19.2151	unknown function	YOR165w
CA1693	1.6	1.8	1.0	1.0	1.0	1.1	IPF17054	orf19.5037	unknown function	no match
CA2286	0.9	1.8	0.8	1.1	1.4	1.4	IPF5369	orf19.5553	unknown function	YKL069w
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match
CA0164	1.0	1.8	1.0	1.0	0.9	1.0	IPF11694	orf19.4335	similar to Saccharomyces cerevisiae Tna1p high affinity nicot	YGR260w
CA2278	1.8	1.8	1.2	1.0	1.2	1.2	IPF10806	orf19.782	unknown function	YBR204c
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)	YIR035c
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA5836	1.1	1.8	0.8	1.1	1.2	0.7	IPF428	orf19.7490	transport protein (by homology)	YOL137w
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function	YIR017c
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA3059	1.2	1.8	1.2	1.1	6.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)	YDR353w
CA3435	1.0	1.8	0.9	1.4	1.3	1.2	IPF6391	orf19.583	indoleamine 2,3-dioxygenase (by homology)	YJR078w
CA2669	1.2	1.8	0.8	0.9	1.0	1.0				
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA1269	1.6	1.7	1.1	1.1	1.1	1.4	IPF19726	orf19.3158	unknown function	YDL001w
CA4798	1.4	1.7	0.9	1.0	0.9	0.9	RPN5.3f	orf19.4032	subunit of the regulatory particle of the proteasome, 3-prime	YDL147w
CA0345	1.2	1.7	1.0	1.0	1.0	0.9	ACH1	orf19.3171	acetyl-coenzyme-A hydrolase (by homology)	YBL015w
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA5146	1.2	1.7	0.9	1.0	1.0	1.0	YMC2	orf19.4583	Carnitine/acylcarnitine translocase (by homology)	YBR104w
CA2785	0.6	1.7	0.6	0.9	0.9	1.0	MET13	orf19.288	Methylene tetrahydrofolate reductase (by homology)	YGL125w
CA0840	1.1	1.7	1.4	1.0	1.3	1.0				
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA3086	1.0	1.7	1.1	1.2	2.3	3.9	GLR1	orf19.4147	by similarity to S. cerev. and C. albicans:glutathione reductas	YPL091w
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function	YLR256w
CA4480	0.9	1.7	0.7	1.1	1.5	1.4	IPF6464	orf19.1887	putative triacylglycerol lipase (by homology)	YLL012w
CA4219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein phc	YKL193c
CA5555	0.9	1.7	1.0	1.0	1.3	1.1	SUC1	orf19.7319	Putative zinc finger protein Suc1	YFL052w
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)	YOR388c
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA5695	1.3	1.7	0.9	0.8	0.7	1.1	IPF3310	orf19.7397	unknown function	YPR022c
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w

[Ca HS+up 1.5 10 FDR] less [Cd HS+ uo 1.5 10 FDR]

Species ()*	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
CA5283	0.9	1.7	0.8	1.0	0.8	1.2	IPF1912	orf19.7140	putative catechol o-methyltransferase	no match
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c
CA2508	1.9	1.7	1.4	1.1	0.9	1.0	BET5	orf19.302	targeting and fusion of ER to Golgi transport vesicles (by hon	YML077w
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA4165	1.0	1.7	1.0	1.1	1.0	1.0	IPF7774	orf19.2968	unknown function	no match
CA4890	1.5	1.7	1.0	0.9	1.0	1.1	PRE10	orf19.6582	20S proteasome subunit C1 (by homology)	YOR362c
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by hor	YDL168w
CA5941	1.5	1.7	1.0	1.3	1.4	0.9	IPF3486	orf19.6756	unknown function	YGL198w
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA4142	1.5	1.7	1.0	1.0	1.5	1.2	PRE4	orf19.4230	20S proteasome subunit(beta7) (by homology)	YFR050c
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA5559	1.0	1.7	1.2	1.1	0.8	1.1	CBP1	orf19.7323	Corticosteroid binding protein	YMR020w
CA3870	1.0	1.7	0.6	0.9	1.3	1.0	YPK1	orf19.399	ser/thr-specific protein kinase (by homology)	YMR104c
CA5306	1.2	1.7	1.0	1.0	1.1	1.1	NPT1	orf19.7176	Nicotinate phosphoribosyltransferase (by homology)	YOR209c
CA2548	1.6	1.7	1.0	0.9	0.9	0.9	PGA34	orf19.2833	unknown function	no match
CA0972	1.1	1.6	1.1	1.2	1.0	1.0	CYP1	orf19.6472	cyclophilin (peptidylprolyl isomerase), mitochondrial (by hom	YDR155c
CA1252	1.9	1.6	0.9	0.9	0.9	0.9	RPN1	orf19.4956	26S proteasome regulatory subunit (by homology)	YHR027c
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA4333	1.2	1.6	1.2	1.1	1.4	1.2	IPF2083	orf19.4086	unknown function	YNL056w
CA1942	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eo	orf19.4191.1	Ubiquitin--protein ligase, 3-prime end (by homology) FALSOF	YGL141w
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function	no match
CA3956	1.2	1.6	1.0	1.0	1.0	1.2	IPF6712.3	orf19.1414.2	unknown function, 3-prime end | Unknown function	no match
CA4127	0.9	1.6	0.7	0.9	0.9	0.9	IPF6629	orf19.2762	unknown function	YLR109w
CA3310	1.4	1.6	1.1	1.2	0.7	1.0	PFS2	orf19.2307	Polyadenylation Factor I subunit (by homology)	YNL317w
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA3746	1.2	1.6	1.6	1.0	0.8	1.1	ARA1	orf19.2172	D-arabinose dehydrogenase (by homology)	YBR149w
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA2888	1.6	1.6	1.0	1.1	1.2	1.2	GIM5	orf19.2471	Gim complex component (by homology)	YML094w
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function	YMR226c
CA3569	1.3	1.6	1.0	1.1	1.0	1.1	IPF3268	orf19.3136	unknown function	YDR325w
CA0670	0.6	1.6	0.5	0.7	6.4	6.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA2157	2.2	1.6	1.5	1.1	0.8	0.8	IPF8537	orf19.5300	similar to Saccharomyces cerevisiae Cne1p calnexin, involve	YAL058w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match
CA4320	1.1	1.6	1.2	1.1	0.8	1.1	ECM17	orf19.4099	Putative sulfite reductase (by homology)	YJR137c
CA2561	1.0	1.6	1.2	1.5	0.8	0.9	CAR2	orf19.5641	ornithine aminotransferase (by homology)	YLR438w
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA5564	1.2	1.6	0.7	0.9	1.0	0.9	IPF1980	orf19.7328	unknown function	no match
CA1452	1.6	1.6	0.8	0.8	1.3	1.0	REV1	orf19.4412	DNA repair protein (by homology)	YOR346w
CA1756	1.0	1.6	1.1	1.2	1.5	1.0	IPF14562	orf19.5129	unknown function	no match
CA1913	1.4	1.6	0.9	0.9	1.2	1.2	ARC35	orf19.2437	subunit of the Arp2/3 complex involved in the control of actin	YNR035c
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA2863	1.3	1.6	1.0	1.0	1.3	1.1	IPF20117	orf19.1058	unknown function	YLR421c
CA0593	1.3	1.6	1.0	0.8	1.2	1.2	ARP6	orf19.4904	actin-related protein (by homology)	YLR085c
CA1838	1.3	1.6	1.1	1.1	1.4	1.3	IPF5777	orf19.3963	unknown function	YER182w
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA2926	1.1	1.6	0.8	1.1	1.3	1.3	UBA3	orf19.4209	Ubiquitin-like protein activating enzyme	YPR066w
CA5595	1.1	1.6	0.9	1.0	0.9	1.4	IPF568	orf19.7105	similar to Saccharomyces cerevisiae Far1p cyclin-dependent	YJL157c
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c
CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal asse	YKL197c
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA2867	1.2	1.5	0.9	0.8	0.8	0.8	IPF11688	orf19.2844	similar to Saccharomyces cerevisiae Apl4p AP-1 complex sut	YPR029c
CA3336	1.0	1.5	0.8	0.8	1.1	1.3	IPF19983	orf19.2335	unknown function	YHR113w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA2133	1.2	1.5	1.0	1.0	1.0	0.8	IPF5866	orf19.5213	unknown function	YDR228c
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA3907	1.2	1.5	0.7	1.0	1.0	0.9	IPF3304	orf19.4395	similar to Saccharomyces cerevisiae Aip1p actin cytoskeletor	YMR092c
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase	YHR008c
CA3683	1.2	1.5	1.1	1.0	1.1	1.2	PPZ1	orf19.726	ser/thr phosphatase required for normal osmoregulation (by h	YML016c
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase	YFR015c
CA4625	1.1	1.5	0.8	0.9	0.9	1.2	IPF5742	orf19.3319	thioredoxin-like protein (by homology)	YGR209c
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w
CA4720	1.2	1.5	1.0	1.0	1.3	1.0	ECM18	orf19.6958	Involved in cell wall biogenesis and architecture (by homolog	YDR125c
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA3057	1.3	1.5	1.0	1.2	1.5	1.2	IPF2954	orf19.4293	unknown function	YDR267c
CA3589	0.8	1.5	0.8	1.2	1.4	1.1	IPF10113	orf19.2249	unknown function	YNR020c

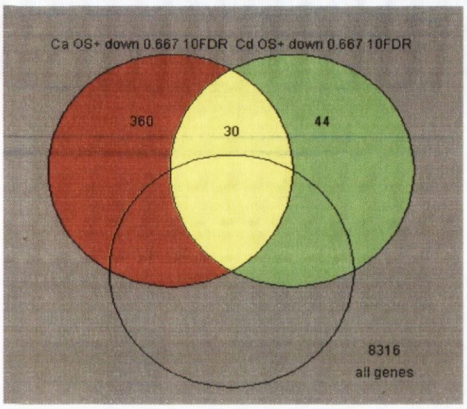
6A

[Cd HS+ up 1.5 10FDR] and [Ca HS+ up 1.5 10FDR]

Species ()*	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	rmali:	rmali:	rmali:	rmali:	rmali:	rmali:	Common	Ca orf19	Ca Function	S.c. hom.
CA4683	10.3	6.7	1.1	1.1	2.3	1.5	HSP78.3f	orf19.884	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function	no match
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA1239	4.7	5.2	1.2	1.1	0.7	0.9	HSP60	orf19.717	Heat Shock Protein 60 (HSP60)	YLR259c
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function	YMR002w

[Ca HS+up 1.5 10 FDR] less [Cd HS+ uo 1.5 10 FDR]

HS+ OS+									
Species ()	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemati	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homolog	YPL171c
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA4959	3.4	4.8	1.3	1.2	1.0	1.0	HSP90	orf19.6515	heat shock protein	YMR186w
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function	YGR101w
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function	YGL145w
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA4856	3.1	3.2	0.9	1.1	1.1	0.9	IPF15950	orf19.3827	unknown function	YKR087c
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)	YKR039w
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA4030	2.9	4.1	0.7	2.0	19.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)	YGR234w
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by ho	YML130c
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)	YCR098c
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function	YML041c
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA2146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function	no match
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA4437	2.5	7.3	0.7	1.3	1.2	1.2	IPF13867	orf19.5158	unknown function	YGL145w
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)	YPL088w
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function	YBR101c
CA5341	2.5	3.9	0.9	0.8	1.0	0.9	HSP10	orf19.7215.3	10 kDa mitochondrial heat shock chaperonin (by homology)	YOR020c
CA3078	2.5	5.4	0.8	1.3	1.2	1.1	IPF19970	orf19.4816	unknown function	YMR209c
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)	YKL188c
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function	YKL094w
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)	YER021w
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)	YJR107w
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function	YDR430c
CA0417	2.3	2.7	0.9	1.0	1.4	1.2	UBC13	orf19.933	E2 ubiquitin-conjugating enzyme (by homology)	YDR092w
CA3034	2.3	2.7	0.8	0.9	1.4	1.3	RPN12	orf19.213	26S proteasome regulatory subunit (by homology)	YFR052w
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)	YGL009c
CA5930	2.3	1.8	1.1	0.9	1.1	1.0	ECM29.3f	orf19.6773	Involved in cell wall biogenesis and architecture, 3-prime end	YHL030w
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function	YPL110c
CA4643	2.2	2.7	1.1	1.2	1.3	1.0	PRE9	orf19.350	20S proteasome subunit Y13 (alpha3) (by homology)	YGR135w
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase	YLR377c
CA0636	2.2	2.5	0.9	0.9	10.8	15.0				
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)	YBR058c
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA2773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase	YOR211c
CA1894	2.2	2.0	1.0	1.1	1.2	1.0	PRE7.5f	orf19.2755	putative subunit of 20S proteasome, exon 1 (by homology)	YBL041w
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)	YHR104w
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)	YIR037w
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homology)	YMR302c
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in acetic	YCR032w
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)	YJL001w
CA5536	2.0	4.4	0.9	1.0	1.1	1.2	IPF2837	orf19.7297	putative cystathionine gamma-synthase (by homology)	YHR112c
CA5196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function	YIL001w
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)	YOR157c
CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)	YIL095w
CA5528	1.9	2.4	1.2	1.3	1.2	1.1	RPN7	orf19.7286	Subunit of the regulatory particle of the proteasome (by homc	YPR108w
CA3796	1.9	3.5	1.2	1.2	0.9	0.9	SGT2	orf19.5823	small glutamine-rich tetratricopeptide repeat containing prote	YOR007c
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)	YMR234w
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase	no match
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex	YDL143w
CA3697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific	YJR099w
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homol	YPR183w
CA4799	1.6	1.6	1.1	1.0	0.8	1.0	RPN5.5f	orf19.4034	subunit of the regulatory particle of the proteasome, 5-prime	YDL147w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltra	YMR149w
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle	YLR178c
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function	YDL012c
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c



7A

[Ca OS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]

HS+ OS+ XS

Species	Ca	Cd	Ca	Cd	Ca	Cd				
Stress (	HS+	HS+	OS+	OS+	XS+	XS+				
System	Non	Non	Non	Non	Norm	Non	Common	Ca orf19	Ca Function	S.c. hom.
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
11759	0.6	1.2	0.2	0.3	1.4	1.5				
CA0368	0.6	0.9	0.2	0.9	1.0	0.9	IPF11646	orf19.1353	unknown function	no match
CA4492	0.3	0.9	0.2	0.7	1.3	1.1	RNR22	orf19.1868	ribonucleoside-diphosphate reductase (by homolo	YJL026w
CA3160	0.2	1.0	0.2	0.7	0.4	0.6	ZRT2	orf19.1585	zinc transport protein (by homology)	YLR130c
CA2874	2.0	0.8	0.3	0.7	0.1	0.5	IPF4999	orf19.5843	unknown function	no match
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel	YPR192w
CA0526	0.7	1.4	0.3	0.7	1.0	1.0	BUB3	orf19.2655	cell cycle arrest protein (by homology)	YOR026w
CA1688	0.7	0.6	0.3	0.6	0.8	0.5	COX15	orf19.3656	cytochrome oxidase assembly factor (by homology	YER141w
CA2280	0.5	1.0	0.3	1.0	0.7	0.9	DUR1,2	orf19.780	urea amidolyase (by homology)	YBR208c
CA2214	0.6	0.8	0.3	0.6	1.2	0.8	IPF9939	orf19.4752	similar to Saccharomyces cerevisiae Msn4p transc	YKL062w
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA0684	0.7	1.0	0.3	0.9	1.1	1.1				
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA0616	0.8	1.0	0.3	0.9	2.5	1.0	PHO11	orf19.2619	Secreted acid phosphatase	YBR092c
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA3880	0.5	1.0	0.3	0.7	1.9	1.0	CAF16	orf19.388	ABC ATPase (by homology)	YFL028c
CA0109	0.6	0.8	0.3	0.6	1.0	1.0	IPF13723	orf19.260	unknown function	no match
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function	YHR067w
CA2950	0.6	0.7	0.3	0.8	0.1	0.4	CLN2	orf19.1960	G1/S-SPECIFIC CYCLIN CLN2	YAL040c
CA2302	0.1	0.6	0.3	0.6	0.1	0.3	IPF6518	orf19.1691	unknown function	YNR018w
CA5705	0.7	1.1	0.4	1.0	3.3	1.1	IPF2645	orf19.7405	unknown function	no match
CA5605	0.7	1.0	0.4	0.9	1.1	1.0	SNF31	orf19.7094	high-affinity glucose transporter (by homology)	YDL194w
CA4827	0.7	1.2	0.4	0.8	0.8	0.8	SMF2	orf19.2069	Manganese transporter (by homology)	YLR034c
CA2490	1.0	1.4	0.4	0.8	1.5	0.9	MUM2	orf19.4044	ubiquitin C-terminal hydrolase (by homology)	YBR057c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA5468	1.1	1.1	0.4	0.8	1.0	0.9	IFF7	orf19.3279	unknown function	YOL155c
CA2314	0.5	0.8	0.4	0.8	1.9	1.0	IPF14545	orf19.1381	unknown function	YCL034w
CA5857	0.4	1.2	0.4	0.6	0.6	0.7	PCK1	orf19.7514	phosphoenolpyruvate carboxykinase	YKR097w
CA0045	0.8	0.7	0.4	0.9	0.7	1.0	IPF8985	orf19.1368	unknown function	no match
CA4780	0.7	0.9	0.4	0.9	0.8	0.9	IPF3352	orf19.4013	unknown function	YHR045w
CA0884	1.3	0.9	0.4	0.9	1.7	1.1	CAN5	orf19.3641	basic amino acid permease (by homology)	YEL063c
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA5766	0.7	0.7	0.4	0.7	1.5	1.0	IPF1097	orf19.5408	serine/threonine protein kinase (by homology)	YOR267c
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5	YDR487c
CA6135	0.3	0.7	0.4	0.8	1.0	0.6	CMK1	orf19.5911	Ca2+/calmodulin-dependent ser/thr protein kinase	YFR014c
CA0691	1.0	1.1	0.4	1.0	1.3	1.1				
2566.2	0.9	1.0	0.4	0.9	1.1	1.1				
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involv	YCR032w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match
CA1902	0.3	1.1	0.4	1.1	1.0	1.0	OPT1	orf19.2602	oligopeptide transporter	YJL212c
CA2391	0.4	1.3	0.4	0.8	0.8	1.0	ADH5	orf19.2608	probable alcohol dehydrogenase (by homology)	YMR303c
CA2266	0.8	0.6	0.4	0.6	1.4	1.0	HEM1	orf19.2601	5-aminolevulinic acid synthase	YDR232w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA1791	0.7	1.2	0.4	1.1	1.0	1.1	IPF13967	orf19.5205	unknown function	YLR108c
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA0576	0.9	1.8	0.4	0.8	1.4	1.0	NPR1	orf19.6232	nitrogen permease reactivator protein (by homolog	YNL183c
CA1944	0.8	1.0	0.4	0.9	1.2	0.6	IPF10645	orf19.4738	unknown function	YOR154w
CA5144	0.9	0.9	0.4	0.9	1.1	0.9	IPF1019	orf19.4581	unknown function	YJR013w
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w
CA5157	0.8	1.0	0.4	1.0	1.4	1.0	IPF993	orf19.4595	unknown function	no match
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA4206	0.6	0.8	0.4	0.8	1.2	0.6	IPF9079	orf19.4550	Membrane transporter (by homology)	YCR023c
CA3756	0.5	0.8	0.4	0.6	0.4	0.7	IPF8884	orf19.3422	unknown function	YLR454w

[Ca OS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]
HS+ OS+ XS

Species	Ca	Cd	Ca	Cd	Ca	Cd			
Stress (	HS+	HS+	OS+	OS+	XS+	XS+			
System	Non	Non	Non	Non	Norm	Non	Common	Ca orf19	Ca Function	S.c. hom.
CA1426	1.0	1.1	0.4	1.0	2.2	1.1	ALS9.3f	orf19.5745	agglutinin-like protein, 3-prime end	YAL063c
CA3353	0.8	0.8	0.4	0.7	1.5	1.4	AUR1	orf19.1945	aureobasidin-resistance protein	YKL004w
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA4081	0.6	1.1	0.4	0.9	0.9	1.0	IPF2523	orf19.6637	unknown function	no match
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homolog	YMR275c
CA4529	1.0	1.3	0.4	0.7	1.0	1.1	IPF4395	orf19.1477	unknown function	YGL010w
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA4022	0.7	0.8	0.4	0.9	0.8	1.4	FRP6	orf19.3441	member of the FRP family of proteins related to Ya	YNR002c
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA1951	0.9	0.9	0.4	0.8	1.0	0.7	HEM14	orf19.4747	Mitochondrial protoporphyrinogen oxidase (by hom	YER014w
CA1411	1.2	1.0	0.4	0.9	0.8	1.0	IPF11858	orf19.1277	unknown function	no match
CA0367	0.6	0.9	0.4	1.0	1.4	0.9	TIM22	orf19.1352	Mitochondrial import inner membrane translocase :	YDL217c
CA5603	0.9	1.0	0.4	0.7	0.8	0.7	IPF553	orf19.7096	unknown function	YLR001c
CA3338	0.4	0.7	0.4	0.9	1.4	1.5	IPF13582	orf19.2333	unknown function	YHR009c
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homo	YOR356w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (b	YER053c
CA1410	0.8	1.1	0.4	1.0	1.0	1.1	GAT1	orf19.1275	nitrogen regulation (by homology)	YFL021w
CA0357	0.4	0.6	0.5	0.9	0.8	0.4	FCY22	orf19.333	purine-cytosine permease (by homology)	YER060w
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA0202	1.0	0.8	0.5	0.9	0.9	1.0	IPF19126	orf19.1210	putative aminoacid transporter (by homology)	YER119c
CA1377	0.9	0.9	0.5	0.8	1.0	1.0	IPF18690.5e	orf19.461	unknown function	no match
CA0984	0.4	0.5	0.5	0.7	0.8	0.8	IPF7400	orf19.1802	unknown function	YER049w
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA4189	0.6	1.1	0.5	1.0	1.0	1.0	IPF7527	orf19.4530.1	unknown function	YHR146w
CA2348	0.7	0.6	0.5	0.6	0.2	0.3	IPF12811	orf19.3751	putative serine/threonine kinase	YOR233w
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA0005	3.8	###	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA0697	0.5	0.7	0.5	0.9	0.7	0.4	VTC4	orf19.3363	putative polyphosphate synthetase (by homology)	YJL012c
CA0998	1.3	1.3	0.5	1.0	0.8	0.9	IPF12369	orf19.4368	Putative dipeptidase (by homology)	YLL029w
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA2855	0.3	0.8	0.5	0.8	1.8	1.4	GPM2	orf19.1067	phosphoglycerate mutase (by homology)	YKL152c
CA0821	4.1	1.0	0.5	0.9	1.3	0.9	IPF16795	orf19.2989	glycerate/formate-dehydrogenase (by homology)	YNL274c
CA4250	0.7	1.0	0.5	0.9	0.6	1.5	IPF4292	orf19.539	bleomycin Hydrolase	YNL239w
CA0189	0.7	0.4	0.5	0.6	1.2	0.9	IPF12201	orf19.4118	Na+-nucleoside cotransporter (by homology)	no match
CA1676	1.0	0.6	0.5	0.8	1.0	1.0	ERG9	orf19.3616	farnesyl-diphosphate farnesyltransferase	YHR190w
CA4564	1.0	0.9	0.5	0.5	0.6	0.8	IPF6572	orf19.6874	unknown function	YMR213w
CA0890	0.5	1.0	0.5	1.0	1.2	1.3	IPF11766	orf19.4734	unknown function	YOR132w
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA6057	0.8	2.0	0.5	0.9	1.3	1.2	IPF4959	orf19.7676	D-xylulose reductase (by homology)	YDL246c
5124.1	1.1	1.2	0.5	1.0	1.0	0.6				
CA5704	0.6	1.7	0.5	0.9	1.2	1.2	CHA11	orf19.7404	L-serine/L-threonine deaminase (by homology)	YCL064c
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA5072	1.2	1.0	0.5	0.8	0.9	0.6	IPF3598	orf19.3047	similar to Saccharomyces cerevisiae Sip3p protein	YNL257c
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homol	YGL257c
CA2392	0.8	1.2	0.5	1.1	2.1	1.2	IPF15672	orf19.2607	unknown function	YKL128c
CA2017	0.9	0.9	0.5	0.7	0.7	0.6	IPF3414	orf19.846	putative serine/threonine protein kinase	YKL171w
CA6131	0.6	0.9	0.5	0.8	0.7	0.9	IPF4369	orf19.5917	similar to Saccharomyces cerevisiae Stp2p involve	YHR006w
CA3258	1.1	1.0	0.5	0.9	1.1	2.7				
CA2938	0.4	0.8	0.5	0.7	0.6	0.4	IPF8321	orf19.3325	similar to Saccharomyces cerevisiae Glg2p self-glu	YJL137c
CA4381	0.5	0.8	0.5	0.7	0.8	0.6	PGA10	orf19.5674	unknown function	no match
CA4764	1.0	1.1	0.5	0.7	0.7	0.9	GPI10	orf19.3996	required for Glycosyl Phosphatdyl Inositol synthesi	YGL142c
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida	YOR319w
CA4261	0.3	1.1	0.5	0.8	1.0	0.8	PDX3	orf19.550	pyridoxamine-phosphate oxidase (by homology)	YBR035c
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA3141	1.0	1.3	0.5	0.5	1.0	0.6	IPF9211.3f	orf19.3712	unknown function, 3-prime end	no match
CA1344	1.0	1.0	0.5	1.0	0.8	1.0	IPF14623	orf19.4342	unknown function	YPR009w
CA0383	1.0	1.0	0.5	0.8	1.1	0.9	IPF16028	orf19.1841	unknown function	YJR066w
CA1104	1.3	2.1	0.5	0.9	0.7	0.8	IPF18761	orf19.4947	unknown function	YPR098c
CA5170	0.5	1.0	0.5	0.9	0.6	0.9				
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA5337	1.1	1.1	0.5	0.9	1.4	0.9	APL1	orf19.7212	AP-2 complex subunit, beta2-adaptin (by homolog	YJR005w
CA1548	0.6	1.1	0.5	0.9	1.5	1.0	IPF8746	orf19.4279	putative alpha-1,3-mannosyltransferase (by homol	YER001w
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA3122	0.8	1.2	0.5	1.0	1.3	1.2	IPF5356	orf19.3004	unknown function	YDR262w
CA0775	1.5	1.2	0.5	0.8	1.2	0.9	IFK2	orf19.856	probable monoxygenase (by homology)	no match
CA5091	0.4	0.4	0.5	0.7	0.2	0.6	ENG1	orf19.3066	endo-1,3-beta-glucanase	YNR067c
CA3875	1.5	1.1	0.5	1.0	1.2	1.0	IPF14430	orf19.394	putative kynureninase (by homology)	YLR231c
CA5066	1.0	1.2	0.5	0.7	1.5	0.7	TPS2	orf19.3038	Threalose-6-phosphate phosphatase (by homolog	YDR074w
CA3319	1.1	0.7	0.5	0.8	0.6	0.5	DRS25	orf19.2680	Probable ATPase, Potential phospholipid-transport	YMR162c
CA3797	1.0	1.0	0.5	0.8	0.7	0.7	IPF5633	orf19.5821	unknown function	YML002w
CA5877	0.7	0.9	0.5	0.9	0.6	0.5	IPF12082.3f	orf19.6832	bumetanide-sensitive Na-K-Cl cotransport protein,	YBR235w
CA4082	0.9	1.3	0.5	0.8	1.3	0.7	PTC4	orf19.6638	ser/thr protein phosphatase PP2C(by homology)	YBR125c
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homol	YMR302c
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w

[Ca OS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]
HS+ OS+ XS

Species	Ca	Cd	Ca	Cd	Ca	Cd			
Stress (	HS+	HS+	OS+	OS+	XS+	XS+			
System:	Non	Non	Non	Non	Norm	Non	Common	Ca orf19	Ca Function	S.c. hom.
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function	YBR042c
CA4655	0.9	1.5	0.5	0.9	0.6	0.8	IPF3098	orf19.4442	Putative mannosyltransferase (by homology)	YNL219c
CA4949	0.8	0.7	0.5	1.0	2.1	0.9	CDC34	orf19.6529	Ubiquitin-conjugating enzyme (by homology)	YDR054c
CA2595	1.1	1.0	0.5	0.9	1.9	1.0	ARG2	orf19.56	acetylglutamate synthase (by homology)	YJL071w
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by hon	YPR194c
CA0609	1.4	1.3	0.5	1.0	1.8	1.0	CDR11.3f	orf19.919	multidrug resistance protein, 3-prime end (by homc	YOR153w
CA5353	1.1	1.2	0.5	0.9	1.7	0.9	IML2	orf19.7229	unknown function	YKR018c
CA4939	0.9	0.6	0.5	0.8	0.4	0.7	IQG1	orf19.6536	RAS GTPase-activating-like protein by homology	YPL242c
CA5024	1.0	1.2	0.5	0.8	0.5	0.6	IPF3009	orf19.6977	similar to Saccharomyces cerevisiae Gpi1p require	YGR216c
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by I	YIL124w
CA1386	0.9	0.8	0.5	1.0	1.0	1.1	THR1	orf19.923	homoserine kinase	YHR025w
CA5694	0.6	1.0	0.5	0.9	1.1	0.8	IPF3311	orf19.7396	unknown function	no match
CA0600	1.2	0.8	0.5	0.7	1.4	0.9	MSN5.5f	orf19.2666	Importin-beta family member required for nuclear e	YDR335w
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA3724	0.9	0.9	0.5	1.1	1.7	0.7	IPF6181	orf19.4174	similar to Saccharomyces cerevisiae Fun 26p nucl	YAL022c
CA1436	0.9	0.9	0.5	1.0	1.2	1.0	IPF7165	orf19.1201	similar to Saccharomyces cerevisiae Dia4p seryl-tF	YHR011w
CA4751	1.0	0.8	0.5	0.9	1.3	0.9	IPF11473	orf19.4828	unknown function	no match
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA1687	1.0	0.9	0.5	0.8	0.7	0.7	IPF12275	orf19.3658	unknown function	YER140w
CA1509	1.2	1.0	0.5	0.9	0.9	0.9	IPF19920	orf19.4524	unknown function	YKL015w
CA3931	0.7	0.9	0.5	1.0	1.1	1.1	IPF12719	orf19.5103	unknown function	YKL128c
CA2913	1.7	1.2	0.5	0.8	1.1	0.7	IPF11205	orf19.4513	unknown function	YLR305c
CA0214	0.9	0.9	0.5	0.7	0.7	0.7	SCT11	orf19.1289	Suppresses a choline-transport mutant	YBL011w
CA5263	0.8	1.2	0.5	1.0	1.0	0.9	CYB3	orf19.5000	Lactate dehydrogenase cytochrome b2 (by homolo	YML054c
CA3656	1.2	1.2	0.5	1.0	1.9	0.9	IPF7456	orf19.2047	unknown function	YOR289w
CA5483	0.8	0.9	0.5	0.9	0.5	0.7	IPF817	orf19.5316	unknown function	YOR088w
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA6011	1.5	1.0	0.6	1.0	1.5	1.1	CTM1	orf19.7612	cytochrome c methyltransferase (by homology)	YHR109w
CA3987	0.5	0.9	0.6	1.0	0.4	0.7	ECM3	orf19.1563	Involved in cell wall biogenesis and architecture (b	YOR092w
CA3755	0.8	1.1	0.6	0.7	1.0	1.0	IPF17743	orf19.3421.1	Unknown function	YBL093c
CA1359	1.1	1.0	0.6	0.9	1.1	0.9	IPF11842	orf19.4405	unknown function	YBR276c
CA5794	0.6	0.8	0.6	1.0	0.7	0.7	IPF4191	orf19.5443	unknown function	YBL098w
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA4617	1.4	1.3	0.6	1.0	1.6	1.0	STB5	orf19.3308	SIN3 binding protein (by homology)	YHR178w
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA5561	0.9	1.1	0.6	0.7	0.8	1.0	SCO1	orf19.7325	Inner mitochondrial membrane protein (by homolo	YBR037c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA6150	1.4	1.0	0.6	1.0	1.5	1.1	IPF1857	orf19.5892	similar to Saccharomyces cerevisiae Hul4p hect dc	YJR036c
CA2822	0.6	1.0	0.6	0.9	1.4	0.9	IPF14550	orf19.1314	unknown function	YMR031c
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c
CA5186	0.7	0.9	0.6	0.7	1.2	0.9	HRT2	orf19.4624	Similar to ScHRT2 (by homology)	YMR027w
CA3142	1.1	1.0	0.6	0.9	0.9	0.7	IPF9211.5f	orf19.3713	unknown function, 3-prime end	no match
CA1625	0.4	0.9	0.6	0.7	1.5	1.0	IPF6156	orf19.1034	similar to C.elegans LIM homeobox protein	YPL170w
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA0548	0.7	0.9	0.6	0.7	1.2	0.4	PHO87	orf19.2454	Member of the phosphate permease family (by hor	YCR037c
CA4745	0.5	0.6	0.6	1.0	0.8	0.6	URA1	orf19.4836	dihydroorotate dehydrogenase	no match
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match
CA1434	1.6	1.3	0.6	0.9	0.9	1.3	SNI2	orf19.1203	Sec9 interacting protein (by homology)	YBL106c
CA3249	1.2	1.1	0.6	0.9	0.8	1.0	GEF2.3f	orf19.3734	Putative voltage-gated chloride channel protein (by	YJR040w
CA0921	1.0	1.0	0.6	0.9	1.0	1.0	IPF12992	orf19.1043	unknown function	YPR139c
CA4850	0.5	1.1	0.6	1.0	0.9	1.1	Cirt2	orf19.3820	Transposase	YJR134c
CA1018	1.6	1.2	0.6	0.7	1.0	1.1	IPF13479.3e	orf19.3768	unknown function, 3-prime end	YCR081w
CA2181	0.5	0.6	0.6	0.9	0.5	0.9	ECM331	orf19.4255	Involved in cell wall biogenesis and architecture (b	YDR055w
CA2473	0.4	0.8	0.6	0.8	0.4	0.4	CBF1	orf19.2876	putative centromere binding factor 1	YJR060w
CA1519	1.1	1.2	0.6	0.9	1.1	1.2	RIM20	orf19.4800	Rim101 activating protein	YOR275c
CA2554	0.9	1.0	0.6	1.2	1.1	1.1	Cirt4	orf19.2839	probable transposase (by homology)	YMR167w
CA5469	0.9	1.1	0.6	0.9	1.1	1.0	IPF298	orf19.3281	unknown function	YER051w
CA3517	1.0	1.0	0.6	1.0	0.9	1.0	IFA22	orf19.1002	Unknown function	YJL005w
CA3346	0.6	1.4	0.6	1.1	1.8	1.2	IPF13356	orf19.2324	molybdopterin biosynthesis (by homology)	YHR111w
CA5754	0.9	0.9	0.6	0.9	1.3	0.8				
CA3029	0.9	1.0	0.6	0.9	1.7	1.1	IPF13825	orf19.223	serine/threonine protein kinases (by homology)	YNR047w
CA3743	0.6	1.0	0.6	1.1	1.5	1.5	IPF19998	orf19.2175	unknown function	YNR074c
CA3912	0.7	1.0	0.6	0.8	0.2	0.7	IPF3288	orf19.4390	unknown function	no match
CA2558	0.5	0.5	0.6	0.8	0.8	0.7	RBT5	orf19.5636	repressed by TUP1 protein 5	no match
CA1364	1.1	1.4	0.6	0.9	0.9	0.7	IPF5561	orf19.4423	unknown function	YDR326c
CA5484	1.2	1.1	0.6	0.8	0.8	0.8	RAD1.3f	orf19.5318	UV endonuclease, component of the nucleotide ex	YPL022w
CA5344	0.3	0.4	0.6	2.3	0.3	0.5	PRY2	orf19.7218	putative pathogen related proteins (by homology)	YJL079c
CA5068	0.7	1.0	0.6	1.1	0.9	1.5	IPF3592	orf19.3041	unknown function	YGR068c
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA2807	1.0	1.2	0.6	0.8	1.2	1.1	IPF11965	orf19.5782	unknown function	YOR022c
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA3877	0.6	0.9	0.6	0.7	0.9	0.8	CBP4	orf19.392	Ubiquinol--cytochrome-c reductase assembly facto	YGR174c
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA4926	0.6	1.1	0.6	0.9	0.8	1.0	IPF1404	orf19.6065	unknown function	YLR071c
CA4900	0.9	1.1	0.6	0.9	1.4	0.9	IFP2	orf19.6037	unknown function	no match

[Ca OS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]

HS+ OS+ XS

Species	Ca	Cd	Ca	Cd	Ca	Cd				
Stress (	HS+	HS+	OS+	OS+	XS+	XS+				
System	Non	Non	Non	Non	Norm	Non	Common	Ca orf19	Ca Function	S.c. hom.
CA1470	0.8	0.9	0.6	0.8	1.2	1.0	IPF17942	orf19.796	unknown function	YKL189w
CA3327	0.5	0.7	0.6	0.7	0.5	0.7	NCP1	orf19.2672	NADPH-cytochrome P450 reductase	YHR042w
CA5968	0.4	1.0	0.6	1.0	1.4	1.0	IPF946	orf19.7561	unknown function	no match
CA4647	1.0	0.9	0.6	1.1	0.7	0.7	IPF1493	orf19.354	X-Pro aminopeptidase II (by homology)	YER078c
CA2318	1.0	0.7	0.6	1.1	1.1	1.0	ILV1	orf19.5480	Threonine dehydratase (by homology)	YER086w
CA4484	1.4	1.1	0.6	1.1	1.1	1.3	HEM15	orf19.1880	ferrochelatase precursor (by homology)	YOR176w
CA3003	0.7	0.4	0.6	0.9	0.5	0.5	IPF15741.5f	orf19.6242	similar to Saccharomyces cerevisiae Cyk3p possib	YCR088w
CA2299	1.6	1.2	0.6	0.7	0.5	0.6	IPF8222	orf19.5381	unknown function	YGL014w
CA2364	1.0	1.1	0.6	0.7	0.5	0.7	MEC1	orf19.1283	cell cycle checkpoint protein (by homology)	YBR136w
CA1797	0.9	0.6	0.6	0.8	0.6	0.9	NUM12	orf19.2924	nuclear migration protein (by homology)	YDR150w
CA4983	0.2	0.7	0.6	1.2	0.4	0.5	IPF2053	orf19.5267	unknown function	no match
CA2859	1.1	0.9	0.6	1.0	0.9	0.7	IPF7056	orf19.1063	unknown function	YBR004c
CA5506	0.7	1.0	0.6	1.0	0.9	1.0	IPF748	orf19.5350	unknown function	YML112w
CA0953	1.0	1.2	0.6	0.8	0.6	0.8	IPF13166	orf19.1144	unknown function	YDL203c
CA2650	1.3	1.9	0.6	0.8	1.0	1.0	STV1	orf19.1190	H+-ATPase V0 domain (by homology)	YOR270c
CA3658	0.8	1.1	0.6	1.1	1.5	1.0	TGL1	orf19.2050	Triacylglycerol lipase (by homology)	YKL140w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match
CA3918	0.5	0.5	0.6	1.1	0.5	0.7	VTC2	orf19.4381	putative polyphosphate synthetase (by homology)	YFL004w
CA5699	1.1	1.0	0.6	1.0	1.3	1.0	ALS7	orf19.7400	agglutinin-like protein	YAR050w
CA1357	0.7	0.9	0.6	0.8	1.5	1.0	ARH1	orf19.410	adrenodoxin reductase and ferredoxin-NADP+ redu	YDR376w
CA5973	1.4	1.0	0.6	1.0	1.7	1.1	IPF931	orf19.7567	unknown function	YDR124w
CA1015	1.0	1.0	0.6	0.9	1.3	1.2	IPF15547	orf19.3956	putative glutamyl-tRNA amidotransferase subunit A	YMR293c
CA2745	0.8	0.9	0.6	1.2	0.8	0.7	HIR1.3f	orf19.2099	Histone transcription regulator (by homology)	YBL008w
CA3365	1.0	0.9	0.6	0.7	0.5	0.5	ALG6	orf19.1843	glucosyltransferase (by homology)	YOR002w
CA0476	1.7	1.1	0.6	0.9	0.9	1.0	UBP2	orf19.457	Ubiquitin-specific proteinase (by homology)	YOR124c
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA1942	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eoc	orf19.4191.1	Ubiquitin--protein ligase, 3-prime end (by homolog	YGL141w
CA0267	1.0	1.0	0.6	1.0	1.0	1.0	PGA40	orf19.1616	extracellular alpha-1,4-glucan (by homology)	no match
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA4678	1.3	1.1	0.6	0.9	0.8	1.0	IPF3670	orf19.894	unknown function	YDR137w
CA4907	0.8	0.9	0.6	1.1	0.9	0.9	PSD1	orf19.6045	Phosphatidylserine decarboxylase 1 (by homology)	YNL169c
6532.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA2215	1.2	1.3	0.6	0.8	1.2	0.9	PFK26	orf19.4753	6-phosphofructose-2-kinase (by homology)	YIL107c
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match
CA4899	1.3	0.9	0.6	0.7	0.8	0.9	IPF1460	orf19.6036	unknown function	YLR039c
CA2872	1.1	1.0	0.6	1.0	0.8	0.9	APG13	orf19.2848	probable component of the autophagic system (by	YPR185w
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the	YML130c
CA4243	0.9	1.1	0.6	0.9	0.8	0.9	IPF16491	orf19.529	unknown function	YIR019c
CA5753	1.1	0.9	0.6	0.9	1.2	0.8	FKH2	orf19.5390	Fork head protein type transcription factor	YNL068c
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match
CA3843	0.8	1.0	0.6	0.8	0.9	1.0	IPF7947	orf19.6602	unknown function	YLR201c
CA4215	0.7	0.8	0.6	0.9	1.1	1.4	SSY1	orf19.814	Regulator of transporters (by homology)	YDR160w
CA2844	0.9	1.1	0.6	1.0	1.2	1.1	IPF13158	orf19.5729	unknown function	YLR098c
CA3403	1.5	1.2	0.6	0.7	0.8	1.2	IPF8650	orf19.3980	RNA helicase (by homology)	YGR271w
CA4469	1.1	1.3	0.6	0.8	0.8	1.0	TOR2.3f	orf19.1903	phosphatidylinositol 3-kinase, 3-prime end (by hom	YKL203c
CA6151	1.2	1.0	0.6	1.0	1.3	1.0	IPF1853	orf19.5890	unknown function	no match
CA4183	1.2	0.8	0.6	1.0	1.0	1.1	SNO1	orf19.2948	hisH-like protein (by homology)	YMR095c
CA1643	1.0	1.1	0.6	0.8	1.5	0.9	IPF9347	orf19.1729	unknown function	no match
CA1798	1.1	1.1	0.6	0.9	0.4	0.6	IPF11448	orf19.2923	unknown function	YMR155w
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA2116	1.0	0.7	0.6	1.0	0.6	0.7	SNG4	orf19.1332	Drug transporter (by homology)	YJR015w
CA3635	0.7	1.1	0.6	1.0	0.6	1.0	IFA20	orf19.5139	unknown function	YJL005w
CA6031	0.9	0.9	0.6	1.1	1.4	1.0	PRO1	orf19.7638	glutamate 5-kinase (by homology)	YDR300c
CA3625	1.2	1.3	0.6	0.8	0.5	0.6	CYR1.3f	orf19.5151	adenylate cyclase, 3-prime end	YJL005w
CA4372	0.9	0.8	0.6	0.9	0.8	1.0	IPF5282	orf19.5663	unknown function	YMR034c
CA3468	1.1	1.0	0.6	1.0	1.3	0.9	IPF6318	orf19.1664	beta-glucosidase (by homology)	no match
CA1935	0.8	1.2	0.6	1.0	1.0	1.0	IPF19936	orf19.4185	unknown function	YGR203w
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA2263	0.5	0.6	0.6	0.6	2.2	1.2	GPD1	orf19.1756	Glycerol-3-phosphate dehydrogenase (by homolog	YOL059w
CA5955	0.9	1.1	0.6	0.8	0.8	0.8	IPF3510	orf19.6739	unknown function	YMR278w
CA2803	0.8	1.2	0.6	0.9	0.9	1.0	IPF11711	orf19.5776	ubiquitin-protein ligase (by homology)	YDR457w
CA2285	1.1	1.4	0.6	0.9	1.0	0.7	IPF12629	orf19.5552	unknown function	YOL063c
CA2383	0.6	1.3	0.6	1.0	0.7	1.2	IPF18474	orf19.2222.2	unknown function	no match
CA4527	0.8	1.1	0.6	1.0	0.7	0.9	IPF4398	orf19.1479	unknown function	YGL023c
CA0702	0.9	1.2	0.6	0.8	1.0	0.8	IPF11812.3f	orf19.2913	unknown function	no match
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA0482	0.2	0.6	0.6	0.9	0.5	0.4	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)	no match)
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA4382	0.9	0.9	0.6	0.9	0.9	0.5	IPF8576	orf19.5675	similar to Saccharomyces cerevisiae Ris1p DNA h	YOR191w
CA2037	0.9	1.0	0.6	1.0	0.9	0.8	IFF3	orf19.4361	unknown function	YOL155c
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w
CA3681	1.1	1.1	0.6	0.9	0.8	0.8	IPF19787	orf19.728	unknown function	YER093c
CA4341	0.9	1.0	0.6	0.9	1.0	0.8	IPF3624	orf19.6713	unknown function	no match
CA0665	0.4	0.3	0.6	0.7	0.6	0.8	INT1	orf19.4257	integrin-like protein alpha chain	YJR092w
CA5358	0.8	1.2	0.6	0.9	2.1	1.4	IPF846	orf19.7235	WD-repeat protein, beta-transducin (by homology)	YMR102c
CA2871	1.1	1.0	0.6	0.9	1.0	1.3	OPT2.3f	orf19.2847.2	Oligopeptide transporter, 3-prime end (by homolog	YPR194c
CA2384	0.9	1.1	0.6	0.8	1.0	0.8	MDL1	orf19.2615	ATP-DEPENDENT PERMEASE	YLR188w

[Ca OS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]
HS+ OS+ XS

Species	Ca	Cd	Ca	Cd	Ca	Cd			
Stress (	HS+	HS+	OS+	OS+	XS+	XS+			
System	Non	Non	Non	Non	Norm	Non	Common	Ca orf19	Ca Function	S.c. hom.
CA2007	1.0	1.4	0.6	0.8	1.0	1.3	GPI8	orf19.2799	essential for GPI anchor attachment (by homology)	YDR331w
CA4199	2.0	2.1	0.6	0.9	1.4	1.4	UBC8	orf19.4540	ubiquitin-conjugating enzyme (by homology)	YEL012w
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA1197	1.2	1.0	0.6	0.9	3.6	1.1				
CA4681	1.1	0.9	0.6	1.0	1.1	0.9	IPF3679	orf19.889	similar to Saccharomyces cerevisiae Thi20p hydro:	YOL055c
CA5762	1.3	0.9	0.6	1.0	0.9	0.9	IFF10.3f	orf19.5401	unknown function, 3-prime end	YJR151c
CA4852	0.4	0.5	0.6	0.7	0.9	0.8	SCS7	orf19.3822	Required for hydroxylation of ceramide (by homolo	YMR272c
CA5257	1.0	1.4	0.6	1.0	0.9	1.1				
CA3834	0.6	0.8	0.6	0.9	1.0	0.7	PLB3	orf19.6594	phospholipase B (by homology)	YMR008c
CA2995	1.0	1.0	0.6	0.7	1.0	0.9	IPF9113	orf19.6121	unknown function	YER130c
CA1737	0.5	0.8	0.6	1.1	1.0	0.9	LYS12	orf19.2525	homo-isocitrate dehydrogenase (by homology)	YIL094c
CA5159	0.9	1.4	0.6	0.9	1.2	1.0	CAP2	orf19.4597	F-actin capping protein, beta subunit (by homology	YIL034c
CA4622	1.6	0.7	0.6	0.9	0.6	0.6	IPF5751	orf19.3314	TRAPP subunit of 20 kDa involved in targeting and	YBR254c
CA1494	0.4	0.8	0.6	0.8	0.9	0.7	IPF171	orf19.3228	unknown function	YER113c
CA3027	1.0	1.0	0.6	0.9	1.0	0.8	IPF20126	orf19.3900	putative chromosome segregation protein (by hom	YDR470c
CA5735	0.5	1.0	0.6	0.8	1.6	0.9	IPF2878	orf19.7445	unknown function	YBR105c
CA6157	0.9	1.1	0.6	0.8	1.1	0.8	GEF1.5f	orf19.5880	Voltage-gated chloride channel protein, 5-prime en	YJR040w
CA5713	1.1	1.0	0.6	1.0	1.0	1.3	ALS6	orf19.7414	agglutinin-like protein	YJR004c
CA0317	1.4	1.3	0.6	0.9	0.8	0.8	SSD1	orf19.3959	Protein phosphatase (by homology)	YDR293c
CA3358	0.6	0.9	0.6	1.0	1.0	1.2	IPF19984	orf19.1940	similar to Saccharomyces cerevisiae Cat5p involve	YOR125c
CA2852	1.2	1.0	0.6	1.0	1.1	1.2	ALS5	orf19.5736	agglutinin-like protein	YJR004c
CA4410	1.2	0.7	0.6	1.1	1.5	1.1	TRP4	orf19.3099	Anthranilate phosphoribosyltransferase	YDR354w
CA0855	1.0	1.0	0.6	0.8	0.9	0.4	AMYG1	orf19.4899	glucoamylase	YBR229c
CA2553	1.1	1.2	0.6	0.9	0.9	1.0	IPF9096	orf19.2838	probable mannosidase (by homology)	no match
CA2994	0.7	0.9	0.6	0.9	0.6	0.5	IPF9116	orf19.6119	unknown function	no match
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA2103	0.9	0.8	0.6	0.7	0.6	0.6	ISM1	orf19.2382	isoleucyl-tRNA synthetase (by homology)	YPL040c
CA2795	0.6	1.1	0.6	0.9	0.9	1.1	IPF8407	orf19.1723	unknown function	YJL055w
CA4085	0.9	1.1	0.6	0.9	1.3	1.0	IPF5015	orf19.6641	unknown function	no match
CA4874	0.6	0.6	0.6	0.5	1.8	1.4	IPF1674	orf19.6559	putative transcription initiation factor (by homology)	YNL108c
CA2185	1.1	1.1	0.7	1.1	0.9	0.9	IPF6880	orf19.4247	unknown function	no match
CA0601	1.0	0.9	0.7	0.7	0.9	1.0	MSN5.3f	orf19.2665	Importin-beta family member required for nuclear e	YDR335w
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA4800	0.4	0.6	0.7	0.9	0.5	0.6	PGA4	orf19.4035	putative GPI-anchhored protein related to Phr1, Ph	YOL030w
CA1469	1.0	1.2	0.7	0.9	1.4	1.0	IPF5078	orf19.795	unknown function	YLR417w
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA1165	1.2	0.9	0.7	1.1	3.0	1.3	IPF19902	orf19.3360	unknown function	no match
CA4828	0.6	1.4	0.7	0.9	0.9	1.0	IPF1209	orf19.2068	unknown function	YJL010c
CA2339	0.8	0.8	0.7	1.6	2.3	1.4	IPF13377	orf19.2350	unknown function	YOR378w
CA4315	0.6	0.8	0.7	1.1	1.3	0.9	PPX1	orf19.4107	Exopolyphosphatase (by homology)	YHR201c
CA4053	4.1	0.9	0.7	1.0	1.4	1.0	IKS1	orf19.428	PROBABLE SERINE/THREONINE-PROTEIN KINA	YJL057c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3f	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by ho	YDL174c
CA4842	0.2	0.5	0.7	1.2	0.9	0.8	MTD1	orf19.3810	methylenetetrahydrofolate dehydrogenase	YKR080w
CA4657	0.4	1.1	0.7	1.1	2.3	1.2	IPF3094	orf19.4444	4-nitrophenyl phosphatase (by homology)	YDL236w
CA2288	0.9	0.8	0.7	0.9	1.0	0.9	IPF5376	orf19.5557	unknown function	YKL201c
CA1491	1.2	0.9	0.7	0.7	0.5	0.5	IPF166	orf19.3225	unknown function	YCR017c
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA2547	1.2	1.0	0.7	0.7	0.9	0.6	IPF14911	orf19.2832	unknown function	YNL152w
CA3866	0.7	0.7	0.7	1.3	0.9	0.8	IPF4606	orf19.6082	unknown Function	YML048w
CA2179	1.2	1.4	0.7	0.9	0.6	0.9	FAB1	orf19.1513	phosphatidylinositol 3-phosphate 5-kinase (by hom	YFR019w
CA5750	1.1	1.5	0.7	1.4	0.5	0.7	CHS8	orf19.5384	Chitin synthase (by homology)	YNL192w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA1754	1.0	1.3	0.7	0.7	1.3	1.1	IPF16320	orf19.5131	Unknown function	YCL039w
CA5843	0.5	0.9	0.7	0.7	0.8	1.0	IPF416	orf19.7499	unknown function	YLR328w
CA0103	1.3	1.0	0.7	0.9	1.3	0.9	IPF17515	orf19.749	unknown function	YAL002w
CA2625	0.2	0.9	0.7	0.9	0.2	0.3	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified prot	YLR110c
CA4433	1.0	1.1	0.7	0.9	0.6	0.8	BCK1	orf19.5162	serine/threonine protein kinase of the MEKK family	YJL095w
CA3206	0.8	1.1	0.7	1.1	0.9	1.0	IPF3454	orf19.6187	unknown function	no match
CA5784	1.5	0.9	0.7	1.0	0.6	1.4	IPF1129	orf19.5431	unknown function	no match (
CA0046	0.7	0.9	0.7	0.7	0.4	0.3	IPF14850	orf19.2452	Hypothetical protein	no match
CA4621	1.6	0.9	0.7	0.9	0.8	0.8	IPF5753	orf19.3312	unknown function	YER080w
CA1967	0.9	0.9	0.7	1.1	1.0	0.8	IPF10866	orf19.5219	GTPase-activator protein (by homology)	YOL081w
CA5225	0.9	1.0	0.7	1.0	1.6	0.9	ACB1.3f	orf19.7043.1	acyl-coenzyme-A-binding protein, 3-prime nd (by h	YGR037c
CA3321	1.1	1.2	0.7	0.7	0.6	0.7	IPF6896.5f	orf19.2677	unknown function, 5-prime end	YHR188c
CA4314	1.1	1.1	0.7	0.9	0.5	0.5	PMT4	orf19.4109	Mannosyltransferase (by homology)	YJR143c

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[Cd OS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]
HS+ OS+ XS

Species	Ca	Cd	Ca	Cd	Ca	Cd			
Stress (	HS+	HS+	OS+	OS+	XS+	XS+			
System	Non	Non	Non	Non	Norm	Non	Common	Ca orf19	Ca Function	S.c. hom.
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA0127	0.6	0.9	0.8	0.4	1.0	1.0	HXK2	orf19.542	hexokinase II (by homology)	YGL253w
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA1070	0.4	0.6	0.7	0.4	1.0	0.9	HXT61	orf19.2020	sugar transporter	YDR343c

[Ca OS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]
HS+ OS+ XS

Species Stress (System	Ca HS+ Non	Cd HS+ Non	Ca OS+ Non	Cd OS+ Non	Ca XS+ Norm	Cd XS+ Non	Common	Ca orf19	Ca Function	S.c. hom.
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA5953	0.7	0.6	1.0	0.4	0.4	0.3	IPF3506	orf19.6741	unknown function	YLR414c
CA5897	0.9	0.6	0.6	0.5	1.5	0.9	IPF2384	orf19.6809	unknown function	YKL128c
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA4155	0.8	0.5	1.0	0.5	0.5	0.7	RNR21	orf19.5801	ribonucleoside-diphosphate reductase (by homolo	YJL026w
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycoger	YFR015c
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match (e-value
CA3707	1.0	1.0	0.7	0.5	0.9	1.0	TYE7	orf19.4941	Basic helix-loop-helix transcription factor by homol	YOR344c
CA0471	0.8	0.8	0.6	0.5	4.1	1.4	ECM22	orf19.2623	putative protein involved in cell wall biogenesis (by	YDR213w
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by hor	YEL011w
CA1069	0.9	0.9	1.0	0.6	1.1	1.0	HXT5.3f	orf19.2021	sugar transporter, 3-prime end	YHR096c
CA3603	0.9	0.5	0.9	0.6	0.5	0.7	MEF1	orf19.4932	mitochondrial translation elongation factor G (by hc	YLR069c
CA1898	0.7	0.4	0.7	0.6	0.5	1.0	PGA38	orf19.2758	unknown function	no match
CA3599	1.1	0.6	0.7	0.6	0.4	0.4	IPF19785	orf19.4929	unknown function	YLR067c
CA4203	0.5	0.7	0.7	0.6	0.6	0.8	SWI4.3f	orf19.4545	transcription factor (by homology)	YDL056w
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA2600	1.1	0.4	0.9	0.6	0.8	0.6	IPF11177	orf19.51	similar to Saccharomyces cerevisiae Clu1p transla	YMR012w
CA2787	1.0	0.8	0.8	0.6	0.5	0.7	EFG1	orf19.610	Enhanced filamentous growth factor	YMR016c
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA0509	1.2	1.1	0.7	0.6	0.5	0.6	CDC42	orf19.3174	GTP/GDP exchange factor for Cdc42p (by homolo	YAL041w
CA5206	1.1	1.1	0.7	0.6	0.7	1.0	GPH1	orf19.7021	Glycogen phosphorylase (by homology)	YPR160w
CA4668	1.1	1.1	0.7	0.6	1.0	1.0	ROM2	orf19.906	GDP/GTP exchange factor for Rho1p (by homolog	YLR371w
CA2661	1.4	1.2	0.8	0.6	0.9	0.9	AAT1	orf19.3554	aspartate aminotransferase (by homology)	YLR027c
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA0660	0.6	0.8	0.7	0.6	0.5	0.4	IPF16189.5f	orf19.5577	panthotenate kinase, 5-prime end (by homology)	YDR531w
CA4059	0.7	0.9	0.7	0.6	0.8	1.2	PRD1	orf19.434	Proteinase (by homology)	YCL057w
CA3112	0.6	0.4	0.8	0.6	1.1	1.0	PFK2	orf19.6540	6-phosphofructokinase, beta subunit	YMR205c
CA3818	1.6	1.4	0.8	0.6	0.9	1.1	IPF6695	orf19.5773	unknown function	YOL057w
CA0659	0.6	0.7	0.8	0.6	0.4	0.4	IPF16189.3f	orf19.5576	panthotenate kinase, 3-prime end (by homology)	YDR531w
CA3518	1.1	1.0	0.9	0.6	0.9	0.6	AMYG2.5f	orf19.999	glucoamylase, 5-prime end	YBR229c
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA2945	0.9	0.8	1.0	0.6	0.7	0.9	IMG1	orf19.1967	Ribosomal protein, mitochondrial (by homology)	YCR046c
CA1616	1.7	0.8	1.1	0.6	0.6	0.6	IPF14538	orf19.3219	unknown function	YOR137c
CA5725	1.2	1.2	1.0	0.6	1.0	0.3	GLG2	orf19.7434	Self-glucosylating initiator of glycogen synthesis (b	YJL137c
CA0688	1.0	0.8	0.8	0.7	0.9	0.5				
CA2150	0.7	1.0	0.8	0.7	0.3	0.7	IPF19940	orf19.6022	unknown function	no match
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA2415	1.5	1.3	0.8	0.7	0.8	0.9	MSD1	orf19.4478	Aspartyl-tRNA synthetase, mitochondrial.	YPL104w
CA3456	1.0	0.8	0.9	0.7	0.7	0.8	IPF19986	orf19.1259	unknown function	YGL131c

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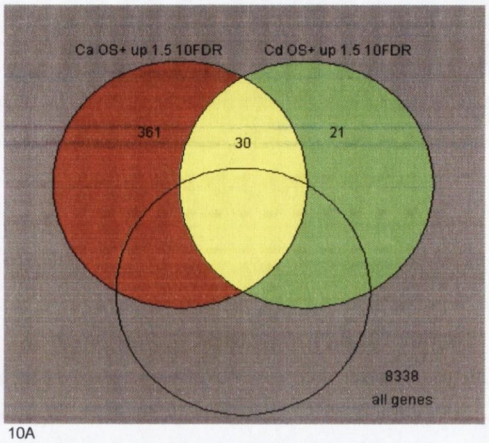
[Cd OS+ down 0.667 10FDR] and [Ca OS+ down 0.667 10FDR
HS+ OS+ XS

Species Stress (System	Ca HS+ Non	Cd HS+ Non	Ca OS+ Non	Cd OS+ Non	Ca XS+ Norm	Cd XS+ Non	Common	Ca orf19	Ca Function	S.c. hom.
CA4501	0.5	1.3	0.1	0.1	0.6	0.9	QDR1	orf19.508	putative antibiotic resistance proteins (by homolog	YIL120w
CA0495	0.8	1.0	0.2	0.5	1.1	1.0	IPF20056	orf19.2659	unknown function	YER067w
CA3757	0.6	0.8	0.2	0.3	0.5	0.5	MAE1	orf19.3419	mitochondrial malic enzyme (by homology)	YKL029c
CA3637	0.3	0.9	0.2	0.5	1.8	1.3	IPF9255	orf19.5136	unknown function	YGR017w
CA2225	0.3	0.6	0.3	0.4	1.1	1.1	SUR2	orf19.5818	Hydroxylation of C-4 of the sphingoid moiety of cer	YDR297w
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA0273	0.3	0.9	0.3	0.5	1.0	0.6	IPF19066	orf19.1433	unknown function	YOR084w
CA4516	0.3	0.5	0.3	0.5	1.3	0.8	IPF18207	orf19.489	unknown function	YPL170w
CA5407	0.3	1.1	0.3	0.5	0.9	0.8	IPF1548	orf19.951	unknown function	no match
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasm	YIL047c
CA2977	1.3	0.9	0.4	0.5	1.4	0.8	HOM3	orf19.1235	Aspartokinase (by homology)	YER052c
CA5749	0.9	0.7	0.4	0.4	0.8	1.0	IPF2908	orf19.7459	unknown function	YBR238c
CA0943	0.1	0.5	0.4	0.4	0.9	1.1	YHB1	orf19.3707	flavohemoglobin (by homology)	YGR234w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA1353	0.2	0.3	0.4	0.5	0.7	1.0	ERG1	orf19.406	squalene epoxidase	YGR175c
CA2969	0.4	0.2	0.4	0.6	0.6	0.5	IPF19772	orf19.5602	unknown function	no match
CA4039	0.9	1.1	0.4	0.3	1.0	1.0	SKS1	orf19.3669	serine/threonine kinase by homology	YPL026c
CA2075	0.2	0.5	0.5	0.7	1.3	1.1	IFE2	orf19.5288	Unknown function	YAL060w
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA5494	0.5	0.7	0.5	0.6	0.9	0.9	IPF85	orf19.5334	similar to Saccharomyces cerevisiae Tis11p tRNA-	YLR136c
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA3878	0.2	0.3	0.5	0.6	0.5	0.5	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA p	YDR213w
CA0578	0.9	0.9	0.6	0.7	1.2	0.6	IPF9605	orf19.3071	similar to Saccharomyces cerevisiae Mih1p M-pha	YMR036c
CA4629	1.7	1.4	0.6	0.6	1.2	0.9	IPF13709	orf19.335	unknown function	YKL193c
CA0752	0.3	1.4	0.6	0.5	0.6	1.3	MNN22	orf19.3803	Golgi alpha-1,2-mannosyltransferase (by homolog	YBR015c
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA4608	1.0	0.9	0.6	0.7	0.8	0.9	CCH1	orf19.3298	Calcium channel protein (by homology)	YGR217w
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA1232	1.0	1.1	0.6	0.6	1.0	1.3	IPF11815	orf19.4982	similar to Saccharomyces cerevisiae Lys14 triacyg	YKL140w
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match



10A

[Ca OS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5535	1.1	1.1	20.4	1.4	6.5	1.0	IPF2839	orf19.7296	unknown function	no match
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA2342	3.7	1.0	5.9	2.4	1.1	1.0	IPF13836	orf19.2344	probable heat shock protein (by homology)	no match
CA1812	1.4	0.9	5.6	1.3	0.9	1.0	IPF13879	orf19.1120	unknown function	no match
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match
CA5526	0.8	1.2	4.8	1.9	1.1	1.0	IPF2857	orf19.7284	unknown function	YFR016c
CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA5191	1.1	0.7	4.7	1.0	1.1	1.2	IPF19538.3f	orf19.6957.3	partially similar to Isocitrate dehydrogenase (NAD+) subunit 1	YNL037c
CA1779	1.2	1.1	4.5	1.5	0.5	0.8	IPF14510	orf19.1826	unknown function	YGL219c
CA3607	1.2	0.4	4.1	1.8	1.4	1.2	RTA2	orf19.24	Unknown function	YOR049c
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA1296	1.1	1.0	4.0	1.9	0.9	0.9				
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA2847	0.9	0.6	4.0	1.3	1.1	1.2	NOG2	orf19.5733	unknown function Nuclear/Nucleolar GTP-binding protein, by	YNR053c
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)	YLR409c
CA0929	2.6	1.4	3.8	1.1	1.0	1.1	GUT1	orf19.558	Glycerol kinase (by homology)	YHL032c
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match
CA4641	1.0	1.1	3.8	1.4	0.8	1.0	IPF1505	orf19.348	similar to saccharomyces cerevisiae Kre6p glucan synthase s	YPR159w
CA5650	1.5	2.8	3.7	1.2	1.1	1.0	IPF7109	orf19.7350	unknown function	YNL208w
CA0271	6.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA4004	0.7	0.7	3.4	1.5	1.1	0.7	IPF4256	orf19.1632	unknown function	YKL046c
CA3927	1.0	0.7	3.4	1.3	0.7	0.8	DIP2	orf19.5106	beta transducin	YLR129w
CA1988	2.2	1.7	3.4	1.2	0.9	0.9	IPF19749	orf19.94	unknown function	no match
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w
CA2772	1.0	0.5	3.3	1.3	0.9	1.1	IPF20112	orf19.2688	unknown function	YPL126w
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match
CA6022	0.8	0.9	3.3	1.2	0.4	0.4	PGA1	orf19.7625	GPI-anchored cell surface protein (by homology)	no match
CA2240	1.3	0.9	3.3	1.2	0.7	0.9				
CA3939	1.0	0.9	3.2	1.1	0.4	0.8	HNM1	orf19.2003	Choline permease (by homology)	YGL077c
CA1506	1.1	1.0	3.2	1.1	1.4	1.0	HGT11	orf19.4527	hexose transporter	YFL040w
CA1558	0.7	1.1	3.2	2.1	0.8	1.0	IPF15679	orf19.1709	lipid transfer protein (by homology)	no match
CA0098	1.0	0.5	3.1	1.4	1.0	1.1	IPF16479	orf19.2319	unknown function	YDR365c
CA3560	1.1	1.0	3.1	1.0	1.6	1.2	CZF1	orf19.3127	canal zinc finger protein	no match
CA5114	0.7	0.7	3.1	1.5	0.7	1.0	IPF1334	orf19.6417	Conserved hypothetical protein	YDL060w
CA6062	1.5	1.3	3.0	1.5	0.6	0.8	IPF8307	orf19.6005	putative permease (by homology)	YDR536w
CA5192	1.4	1.0	2.9	1.4	1.1	1.0	HOK	orf19.7004	unknown function	no match
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA2697	1.2	1.5	2.9	2.6	0.9	0.8	IPF9167	orf19.2737	unknown function	YDR109c
CA4929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA1293	1.7	0.7	2.8	1.3	0.9	1.0	HCA4	orf19.2712	Can suppress the U14 snoRNA rRNA processing function	YJL033w
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function	YNL111c
CA5292	0.9	0.5	2.7	1.4	0.9	1.1	IPF1948	orf19.7154	unknown function	YJL069c
CA5856	1.0	1.1	2.7	1.1	0.7	1.0	ALK2	orf19.7513	n-alkane inducible cytochrome P-450 (by homology)	YDR402c
CA2040	0.9	1.3	2.7	1.5	0.9	0.6	IPF12946	orf19.4356	unknown function	YDL199c
CA0003	2.0	0.9	2.7	0.7	0.8	0.8				
CA0204	1.5	0.5	2.7	1.1	0.7	0.9	IKI3	orf19.1222	killer toxin insensitive protein 3 (by homology)	YLR384c
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA4038	1.1	0.9	2.7	1.2	1.4	0.9	HGT12	orf19.3668	hexose transporter	YFL040w
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha	YIL099w
CA4467	1.0	1.0	2.6	1.1	0.9	0.9	IPF9833	orf19.6864	unknown function	no match
CA0823	1.0	1.0	2.6	1.9	1.5	1.4	IPF11987.3(	orf19.692	unknown function, 3-prime end	no match
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in regu	YIL046w
CA1666	0.8	0.6	2.6	1.7	1.0	1.0	SRP40	orf19.2859	RNA I and II supressor (by homology)	YKR092c
CA5652	1.1	0.9	2.6	0.8	0.5	0.6	IPF19815	orf19.7354	longevity-assurance protein (by homology)	YKL008c
CA4425	1.2	1.1	2.6	1.6	0.9	1.1	ENA21.3f	orf19.5170	P-type ATPase, 3-prime end (by homology)	YDR038c
CA4003	0.9	0.7	2.6	1.5	0.9	0.9	IPF4257	orf19.1633	unknown function	YDR324c
CA1694	0.9	0.8	2.6	1.1	0.5	0.9	TRM3	orf19.5038	2 -O-ribose methyltransferase (by homology)	YDL112w
CA1984	0.9	1.3	2.5	1.1	0.8	0.7	IPF9592	orf19.90	unknown function	YFL042c
CA1879	1.0	1.0	2.5	1.0	1.0	0.6	SMF12	orf19.2270	manganese transporter (by homology)	YOL122c
CA6072	0.9	0.9	2.5	1.1	1.0	1.2	DBP10	orf19.5991	Putative ATP-dependent RNA helicase (by homology)	YDL031w
CA2848	1.0	0.5	2.5	1.4	1.2	1.1				
CA3770	0.9	1.1	2.5	1.4	0.9	1.1	SOU2	orf19.2897	Sorbitol utilization protein Sou2p [Candida albicans]	YNL202w

[Ca OS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]
HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress (+	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
CA0715	1.1	0.9	2.5	1.3	1.4	1.4	DBP9	orf19.3393	dead box helicase	YLR276c
CA0251	1.0	1.0	2.5	1.0	2.1	1.0	IPF9146	orf19.6244	unknown function	no match
CA5998	1.2	1.0	2.5	1.0	2.1	1.1	IPF670	orf19.7598	unknown function	YOR023c
CA3340	0.9	1.0	2.5	1.0	0.7	1.0	ADA2	orf19.2331	general transcriptional adaptor or co-activator (by homology)	YDR448w
CA5323	0.9	0.7	2.5	1.2	0.7	1.1	IPF2142	orf19.7197	unknown function	YLR002c
CA4289	1.3	0.7	2.5	1.3	0.8	1.0	IPF6665	orf19.6686	unknown function	YGR145w
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA0443	0.9	0.5	2.5	1.1	1.0	1.1	SPB1	orf19.76	Putative methyltransferase by homology	YCL054w
CA4718	1.0	0.7	2.5	1.4	1.2	1.0	IPF8661	orf19.6955	unknown function	YOR056c
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA5051	0.5	0.3	2.5	1.4	1.2	1.2	IPF3709	orf19.3015	unknown function	YDR101c
CA5787	0.8	0.8	2.4	1.3	1.1	0.9	IPF1136	orf19.5436	unknown function	YGR128c
CA4044	1.8	0.8	2.4	3.3	0.7	0.9	GAL7	orf19.3675	UDP-glucose-hexose-1-phosphate uridylyltransferase (by hor	YBR018c
CA3993	0.7	0.3	2.4	1.0	0.7	0.7	IPF8275	orf19.1569	unknown function	YGR090w
CA3710	1.5	1.0	2.4	0.9	0.7	0.4	CHS3.5f	orf19.4938	chitin-UDP acetyl-glucosaminyl transferase 3, 3-prime end	YBR023c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA4713	2.1	0.8	2.4	0.7	1.7	1.1	CCC1	orf19.6948	Transmembrane Ca2+ transporter (by homology)	YLR220w
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA6061	0.6	0.6	2.3	1.2	0.4	0.4	IPF8302	orf19.6007	unknown function	YJL196c
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA1590	1.1	1.0	2.3	1.0	0.9	1.0	IPF14665	orf19.4315	unknown function	YFL027c
CA0027	0.8	0.6	2.3	1.5	1.1	1.2	RCL1	orf19.1886	RNA 3 -terminal phosphate cyclase (by homology)	YOL010w
CA0854	1.0	0.7	2.3	1.1	1.1	0.8	IPF8854	orf19.4900	similar to Saccharomyces cerevisiae Mnn1p alpha-1,3-mannc	YER001w
CA5529	1.1	1.1	2.3	1.1	1.0	0.9	IPF2852	orf19.7288	putative acetyl-coenzyme-A dehydrogenase	no match
CA2459	0.9	0.9	2.2	1.3	1.2	1.1	IPF12234.5(	orf19.3509	unknown function, 5- prime end	no match
CA1660	0.8	0.8	2.2	1.2	0.8	0.5	DAP2	orf19.4322	dipeptidyl aminopeptidase B (by homology)	YHR028c
CA1822	1.2	0.6	2.2	1.3	0.8	0.9	IPF9525	orf19.4268	unknown function	YLR222c
CA1640	0.8	0.7	2.2	0.9	0.7	0.9	IPF18641.3f	orf19.1732	unknown function, 3-prime end	YBL004w
CA1497	1.9	1.1	2.2	1.5	4.0	1.2	IPF9683	orf19.3644	unknown function	YHR006w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match
CA5466	1.8	0.7	2.2	1.2	1.0	1.0	PWP2	orf19.3276	periodic tryptophan protein (by homology)	YCR057c
CA1793	1.2	1.2	2.2	1.1	0.9	1.0	IPF18608.5f	orf19.5207	unknown function, 5-prime end	YIL103w
CA2204	0.6	0.5	2.2	1.0	0.5	0.9	DIP51.5f	orf19.2943	dicarboxylic amino acid permease, 5-prime end (by homology	YPL265w
CA3211	3.1	1.1	2.2	1.2	0.7	1.0	IPF19977	orf19.6192	unknown function	YGR175c
CA5457	1.2	1.0	2.2	1.2	0.9	1.0	TRM1	orf19.3265	N2,N2-dimethylguanine tRNA methyltransferase (by homolog	YDR120c
CA5063	0.9	0.5	2.2	1.1	0.7	0.8	IPF8493	orf19.3034	putative member of nontransporter group of ATP-binding cas	YDR091c
CA3308	0.6	0.8	2.2	1.0	0.6	1.0	PET127.5f	orf19.2309	component of mitochondrial translation (by homology)	YOR017w
CA3925	1.2	1.0	2.2	1.2	0.8	1.0	IPF13257	orf19.5110	unknown function	no match
CA3131	1.3	0.9	2.2	1.1	1.3	1.4	IPF8910	orf19.1362	unknown function	YNR015w
CA1631	1.4	1.0	2.2	1.0	1.2	1.1	IPF19582	orf19.1028	unknown function	YNL230c
CA0457	2.5	1.2	2.2	1.8	1.2	0.8	IPF15604	orf19.2432	transcription factor (by homology)	YFL031w
CA5367	1.1	1.1	2.2	1.2	1.0	1.0	RIM101	orf19.7247	Zn finger transcription factor homolog; regulator of pH respon	YHL027w
CA0973	1.0	1.5	2.1	1.6	1.3	1.3	IPF12662	orf19.6474	unknown function	no match
CA4227	0.8	1.0	2.1	1.1	0.8	1.2	SCH9	orf19.829	protein kinase (by homology)	YHR205w
CA1407	0.9	0.9	2.1	1.4	0.9	0.7	UAPC	orf19.2882	purine permease (by homology)	no match
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)	YPL088w
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA1300	0.9	1.0	2.1	1.4	3.9	1.2	SLY41	orf19.4199	vesicular transport (by homology)	YOR307c
CA5023	0.7	0.7	2.1	1.0	0.4	0.6	IPF7547	orf19.6976	unknown function	YJL163c
CA1155	1.1	0.8	2.1	1.2	0.7	0.8	JA2	orf19.107	ATP-dependent RNA helicases-like (by homology)	YKL078w
CA4470	1.0	0.8	2.1	1.5	1.1	1.1	IPF9717	orf19.1902	unknown function	YPR144c
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA4099	0.8	0.4	2.1	1.2	0.7	1.0	IPF3986	orf19.665	unknown function	YLR186w
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA2246	2.4	1.3	2.1	1.8	1.0	0.8	IPF7405	orf19.4666	unknown function	no match
CA2984	0.8	0.6	2.1	1.2	0.8	0.9	IPF12606.3(	orf19.6008.1		YNL123w
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA5957	1.2	0.7	2.1	1.0	1.2	1.0	RRP3.3eoc	orf19.7546	RNA-dependent ATPase, helicase,required for maturation of	YHR065c
CA2304	0.8	0.6	2.1	1.3	0.8	1.4	PRP43	orf19.1687	RNA-dependent ATPase (by homology)	YGL120c
CA4840	1.0	1.0	2.1	1.1	0.6	1.0	IPF1235	orf19.2054	unknown function	YDL020c
CA3604	0.5	0.6	2.1	1.8	0.3	0.4	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)	no match
CA5644	0.8	0.8	2.1	1.2	1.1	1.1	IPF447	orf19.7050	unknown function	YNL110c
CA2593	0.9	0.8	2.1	1.1	1.1	1.1	RRP6	orf19.58	involved in 5.8S rRNA processing (by homology)	YOR001w
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA2731	0.7	1.0	2.0	1.3	1.0	1.0	URIC	orf19.2114	uricase (urate oxidase) (by homology)	no match
CA1706	1.0	0.7	2.0	1.3	1.5	1.4	NMD3	orf19.706	RNA binding (by homology)	YHR170w
CA2035	0.9	1.4	2.0	1.0	0.7	0.9	SGD1	orf19.4363	involved in the HOG pathway (by homology)	YLR336c
6100.2	1.5	2.2	2.0	1.2	1.1	1.0				
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA4811	0.9	0.6	2.0	1.2	1.0	1.0	ECM16	orf19.2090	RNA helicase (by homology)	YMR128w
CA0693	1.0	0.8	2.0	1.2	0.8	1.0	IPF12606.5(	orf19.3288	unknown function, 5-prime end	YNL123w
CA5568	0.8	0.4	2.0	1.0	1.2	1.0	ELF1	orf19.7332	Elongation-like factor	YPL226w
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)	YFL036w
CA3272	0.8	1.1	2.0	1.0	0.7	1.1	ALD4	orf19.6306	aldehyde dehydrogenase, mitochondrial (by homology)	YOR374w
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA1503	0.5	0.4	2.0	1.6	1.0	1.1	RKI1	orf19.1701	D-ribose-5-phosphate ketol-isomerase (by homology)	YOR095c
CA2119	1.3	0.6	2.0	0.9	0.7	0.9	MTR4	orf19.1335	RNA Helicase (by homology)	YJL050w
CA0651	1.0	0.9	2.0	1.0	1.0	1.1	ALK8	orf19.10	n-alkane inducible cytochrome P-450 (by homology)	YDR402c
CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA2670	1.0	0.8	2.0	1.3	0.8	1.1	MAK16	orf19.5500	nuclear viral propagation protein (by homology)	YAL025c
CA2898	0.5	0.6	2.0	0.9	0.6	0.8	IPF15646	orf19.3481	putative ATP-dependent RNA helicase (by homology)	YGL064c
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA2667	0.7	0.4	2.0	1.3	1.1	1.1	IPF16996	orf19.3547	unknown function	YDR496c
CA4575	0.8	0.8	2.0	1.2	0.9	1.4	IPF9428	orf19.6886	unknown function	YPL146c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA5718	1.2	1.0	1.9	1.4	1.1	1.5	LCP5	orf19.7422	Ngg1p interacting protein (by homology)	YER127w

[Ca OS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]

HS+ OS+ XS+ Species (Stress ()* Systemat	Ca HS+ Norn	Cd HS+ Norn	Ca OS+ Norn	Cd OS+ Norn	Ca XS+ Norn	Cd XS+ Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4339	0.8	0.7	1.9	1.3	1.1	0.9	IPF3618	orf19.6710	Unknown function	YHR196w
CA3750	1.7	1.2	1.9	1.4	0.8	0.9	IPF7377	orf19.3428	unknown function	YMR044w
CA1929	1.0	1.0	1.9	1.6	0.9	0.7	SAP7	orf19.756	secreted aspartyl proteinase 7	YLR121c
CA1784	1.2	1.1	1.9	1.2	0.7	0.9	ARO7	orf19.1170	chorismate mutase (by homology)	YPR060c
CA0782	1.9	1.8	1.9	1.4	1.2	1.3	IPF16253	orf19.3932	unknown function	no match
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match
CA2044	1.2	0.7	1.9	1.1	0.9	0.9	IPF10668	orf19.2930	unknown function	YGR054w
CA0011	1.2	1.0	1.9	0.7	0.8	0.7	IPF17430.5	orf19.73	possible zinc protease, 5-prime end (by homology)	YIL137c
CA2449	1.0	0.6	1.9	1.1	0.9	1.1	ENP1	orf19.5507	Essential nuclear protein (by homology)	YBR247c
CA4041	1.6	0.6	1.9	1.7	1.1	0.7	GAL10	orf19.3672	UDP-glucose 4-epimerase by homology	YBR019c
CA2812	1.2	0.7	1.9	1.2	0.9	1.0	TEM1	orf19.3001	GTP-binding protein of the RAS superfamily	YML064c
CA2100	0.8	0.8	1.9	1.2	1.1	1.1	KTI12	orf19.2385	involved in resistance to K.lactis killer toxin (by homology)	YKL110c
CA3995	0.9	0.7	1.9	1.3	1.0	1.2				
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function	YMR002w
CA0207	0.4	0.4	1.9	1.0	1.0	0.7	IPF18002	orf19.1226	Unknown function	YKL014c
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA0087	0.9	1.2	1.9	0.9	1.0	0.6	SMF11	orf19.4690	manganese transporter (by homology)	YOL122c
CA0327	0.7	0.7	1.9	1.4	1.1	1.1	IPF15217.5	orf19.3779	WD-repeat protein, 5-prime end (by homology)	YCR072c
CA1999	1.2	0.9	1.9	1.0	0.8	1.0	IPF19513	orf19.6476	unknown function	YLR114c
CA0813	0.7	0.7	1.9	1.3	1.3	0.8	MPP10	orf19.1915	component of the U3 small nucleolar ribonucleoprotein (by hc	YJR002w
CA1100	1.2	0.8	1.9	1.3	1.3	0.9	IPF5681	orf19.4952	unknown function	no match
CA5067	0.5	0.9	1.9	1.6	1.5	1.2	IPF3589	orf19.3040	putative alcohol acyl transferase (by homology)	YBR177c
CA5113	1.0	0.8	1.9	1.4	1.0	1.0	IPF20026	orf19.6418	unknown function	YDL063c
CA4912	1.3	0.9	1.9	1.1	0.8	1.2	CNS1	orf19.6052	Cyclophilin Seven Suppressor (by homology)	YBR155w
CA1639	1.3	0.7	1.9	0.9	0.8	0.7	IPF18641.5	orf19.1733	unknown function, 5-prime end	YBL004w
CA3069	0.8	0.7	1.9	2.1	0.6	0.7	IPF6117	orf19.4805	unknown function	YMR266w
CA6098	1.0	0.7	1.9	1.4	0.8	0.9	IPF61	orf19.5959	unknown function	YDL148c
CA6128	0.9	1.0	1.9	0.8	0.3	0.5	IPF152	orf19.5919	unknown function	YOR129c
CA4768	0.8	1.0	1.9	0.9	1.7	0.8	IPF9385	orf19.4000	similar to Saccharomyces cerevisiae Pho2p homeobox-doma	YDL106c
CA2414	1.6	1.2	1.9	1.1	0.9	1.1	IPF13756.3	orf19.4479	unknown function, 3-prime end	YJL010c
CA1417	0.9	0.6	1.9	1.2	1.2	1.4	IPF16126	orf19.172	similar to Saccharomyces cerevisiae Rpc19p DNA-directed R	YNL113w
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match
CA1627	0.9	0.8	1.8	1.0	1.3	1.4	SKO1.3f	orf19.1032	Cre-binding bzip protein, 3-prime end (by homology)	YNL167c
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rR	YDR087c
CA5685	0.9	0.5	1.8	1.0	0.9	0.9	HPA1	orf19.7387	RNA polymerase II-associated Histone acetyltransferase (by	YPL086c
CA2244	0.9	0.8	1.8	0.9	1.0	1.0	AAT22	orf19.4669	aspartate aminotransferase (by homology)	YLR027c
CA2869	0.9	0.9	1.8	1.0	0.8	0.8	RPC82	orf19.2847	DNA-directed RNA polymerase III, 82 KD subunit (by homolo	YPR190c
CA3175	1.1	0.7	1.8	1.3	1.1	0.8	IPF11587	orf19.1403	unknown function	YNL083w
CA3159	1.7	1.4	1.8	1.2	1.4	1.2	PLC3	orf19.1586	phosphatidylinositol phospholipase C	YLR197w
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA4043	1.3	0.9	1.8	2.0	0.7	1.0	IPF5291	orf19.3674	UDP-glucose 4-epimerase (by homology)	YBR019c
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match
CA2629	0.8	1.1	1.8	1.1	1.2	1.1	IPF10911	orf19.4760	unknown function	YIL110w
CA3007	0.9	0.8	1.8	1.4	1.1	1.4	IPF12148	orf19.6234	Unknown function	YNL182c
CA4113	1.2	1.0	1.8	1.5	0.4	0.7	CHO1	orf19.677	Phosphatidylserine synthase	YER026c
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA4387	0.8	0.7	1.8	1.0	1.4	1.2	MAP1	orf19.3124	methionine aminopeptidase, isoform 1 (by homology)	YLR244c
CA2399	1.0	0.7	1.8	1.2	1.0	1.3	MAK5	orf19.3540	ATP-dependent RNA helicase (by homology)	YBR142w
CA2461	1.3	0.8	1.8	1.2	1.2	1.3	MAK11	orf19.1791	involved in cell growth and replication of M1 dsRNA virus (by	YKL021c
CA3608	1.0	0.9	1.8	1.3	1.5	1.4	IPF3857	orf19.25	unknown function	YOL093w
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA6039	1.2	1.0	1.8	1.3	1.0	1.1	CKA1	orf19.7652	casein kinase II, catalytic alpha chain (by homology)	YIL035c
CA2796	0.8	0.6	1.8	1.3	1.3	1.1	IPF8405	orf19.1721	similar to Saccharomyces cerevisiae Nce103p involved in no	YNL036w
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eoc	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA1561	1.5	1.3	1.8	1.5	0.9	1.0	POT12	orf19.1704	peroxysomal 3-ketoacyl-CoA thiolase B (by homology)	YIL160c
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function	YML041c
CA5649	1.7	0.8	1.8	1.0	0.9	0.6	CHS4	orf19.7349	Chitin synthase regulatory factor	YBL061c
CA1770	0.7	0.6	1.8	1.3	1.3	1.4	IPF12457	orf19.2185	unknown function	YGL111w
CA1786	0.8	1.1	1.8	1.1	1.0	1.0	IPF7629	orf19.1168	unknown function	no match
CA1370	1.5	0.9	1.8	1.0	0.8	0.8	TCI1	orf19.4963	protein phosphatase Two C-Interacting protein (by homology)	YDR161w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4708	0.7	1.0	1.8	1.1	1.2	1.1	MEU1	orf19.6938	regulator of ADH2 expression (by homology)	YLR017w
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homolo	YOR049c
CA1938	1.2	0.7	1.8	1.1	0.8	0.8	NMD5	orf19.4188	putative Nam7p/Upf1p-interacting protein (by homolgy)	YJR132w
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA4336	0.9	1.1	1.8	1.5	0.6	0.9	DDR48	orf19.4082	stress protein (by homology)	YMR173w
CA3242	0.5	0.6	1.8	1.2	0.7	0.9	RAT1	orf19.4681	5 -3 Exoribonuclease (by homology)	YOR048c
CA2099	0.8	0.8	1.8	1.1	1.1	1.1	IPF11484	orf19.2386	unknown function	YKL099c
CA6074	1.0	0.7	1.8	1.3	1.1	1.0	IPF11	orf19.5987	unknown function	YOL124c
CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA1000	1.2	1.0	1.8	0.9	1.0	0.9	IPF6011	orf19.1486	unknown function	no match
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA4458	1.1	1.0	1.7	1.1	0.7	0.8	IPF8464	orf19.6855	unknown function	no match
CA1047	1.1	0.9	1.7	1.2	0.9	1.1	IPF11615	orf19.1646	RNA-binding proteins (by homology)	YPR112c
CA0743	1.3	1.0	1.7	1.0	1.1	1.0	RNA14	orf19.1531	component of pre-mRNA 3 -end processing factor CF I (by hc	YMR061w
CA3688	0.9	0.9	1.7	1.2	0.4	0.7	YIP3	orf19.6264.3	protein of unknown function, (by homology)	YNL044w
CA6029	0.6	0.5	1.7	1.3	1.1	1.5	DRS1	orf19.7635	ATP dependent RNA helicase (by homology)	YLL008w
CA2034	0.9	1.1	1.7	1.1	0.8	1.0				
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w
CA1318	1.4	0.7	1.7	1.2	0.8	1.1	IPF3147	orf19.4219	Nuclear valosin-containing protein-like (by homology)	YLL034c
CA4933	1.6	1.2	1.7	1.2	1.1	1.3	IPF8372	orf19.6074	unknown function	YDL166c
CA2881	0.6	0.5	1.7	1.1	1.1	1.1	RAD4	orf19.5850	Excision repair protein (by homology)	YOR206w

[Ca OS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]

Species (	Ca HS+	Cd HS+	Ca OS+	Cd OS+	Ca XS+	Cd XS+				
Stress ()*										
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0923	0.9	0.8	1.7	1.4	0.9	1.1	IPF12987	orf19.1047	unknown function	YMR049c
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA0939	1.2	0.9	1.7	1.2	1.1	1.4	DBP6	orf19.3704	RNA helicase required for 60S ribosomal subunit assembly (t	YNR038w
CA2695	1.3	0.9	1.7	1.0	0.8	1.2	SEN2	0	tRNA splicing endonuclease beta subunit(by homology)	YLR105c
CA6054	2.1	0.8	1.7	1.2	0.6	0.6	IPF4952	orf19.7672	unknown function	YDR411c
CA3236	1.2	0.8	1.7	1.3	0.7	0.9	DEG1	orf19.6297	pseudouridine synthase (by homology)	YFL001w
CA3330	0.4	0.2	1.7	1.2	0.8	0.9	POL21.3f	orf19.2669	pol polyprotein, reverse transcripase, 3-prime end (by homol	YFL050c
CA5999	1.0	1.1	1.7	1.2	1.1	1.1	IPF668	orf19.7599	unknown function	YDR398w
CA1714	1.1	1.0	1.7	1.2	1.1	0.9	NAB2	orf19.3333	Nuclear poly(A)-RNA-binding protein (by homology)	YGL122c
CA2045	2.1	1.0	1.7	1.1	1.0	1.2	IPF8107	orf19.2933	unknown function	YFL044c
CA3342	0.8	0.7	1.7	1.4	0.7	1.1	IPF13361	orf19.2330	unknown function	YDR449c
CA2442	1.0	0.7	1.7	1.3	1.2	1.5	PRS5	orf19.2193	Phosphoribosylpyrophosphate synthetase (ribose-phosphate	YOL061w
CA2935	0.9	0.8	1.7	1.0	0.5	0.5	IPF11521	orf19.3328	unknown function	YMR172w
CA1094	1.6	1.1	1.7	1.3	0.6	0.7	YIP1	orf19.3951	golgi membrane protein (by homology)	YGR172c
CA5902	1.1	0.8	1.7	0.8	0.9	0.9	SRP68	orf19.6804	SIGNAL RECOGNITION PARTICLE 68 (by homology)	YPL243w
CA0260	1.2	0.7	1.7	0.9	0.4	0.7	IPF13683	orf19.2547	unknown function	no match
CA1110	1.3	1.2	1.7	0.9	0.9	1.3	DIS3	orf19.5229	3 --5 exoribonuclease required for 3 end formation of 5.8S rR	YOL021c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA0206	0.9	1.0	1.7	1.1	1.0	1.0	IPF14089	orf19.2781	putative serine/threonine protein kinase	YLR248w
CA4803	1.0	1.0	1.7	1.0	1.4	1.0	PEX4	orf19.4041	E2 ubiquitin-conjugating enzyme -peroxin (by homology)	YGR133w
CA0328	0.7	0.6	1.7	1.5	1.2	1.2	IPF15217.3f	orf19.3778	WD-repeat protein, 3-prime end (by homology)	YCR072c
CA2032	1.0	0.7	1.7	0.8	0.5	0.6	IPF13112	orf19.3466	unknown function	YGL136c
CA2039	3.1	0.9	1.7	1.0	1.2	0.8	IPF12947	orf19.4357	unknown function	YMR115w
CA2359	0.7	0.6	1.7	1.2	0.8	1.0	IPF8952	orf19.4896	similar to Saccharomyces cerevisiae Rpa34p nonessential cc	YJL148w
CA3828	0.9	1.2	1.7	1.1	1.6	1.2	SNQ2	orf19.5759	multidrug resistance protein (by homology)	YDR011w
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA2842	1.1	1.0	1.7	1.0	0.9	0.8	ALK5.3f	orf19.5727.1	n-alkane-inducible cytochrome P-450, 3-prime end	YDR402c
CA1039	0.8	0.8	1.7	0.9	0.5	0.5	IPF4012	orf19.2501	Unknown Function	YPL221w
CA5097	0.9	0.8	1.7	1.1	0.9	1.1	IPF1382	orf19.6444	unknown function	YHL023c
CA5252	1.0	0.8	1.7	1.4	0.9	1.2	DIM1	orf19.5010	rRNA (adenine-N6,N6-)-dimethyltransferase (by homology)	YPL266w
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA2645	0.8	1.1	1.7	1.2	1.0	1.1	YNK1	orf19.4311	Nucleoside diphosphate kinase (by homology)	YKL067w
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA1619	0.7	0.6	1.6	1.5	0.6	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)	YPL057c
CA2014	1.5	0.9	1.6	0.9	0.8	0.9	IPF1717.3f	orf19.3080	similar to Saccharomyces cerevisiae Scc2p involved in sister	YDR180w
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)	YKL188c
CA1291	0.9	0.7	1.6	1.2	0.9	1.1	IPF16752	orf19.2711	unknown function	YGR200c
CA5584	0.9	1.1	1.6	1.0	0.7	0.8	SAC7	orf19.7115	GAP for RHO1 by homology	YDR389w
CA3691	1.0	1.0	1.6	1.0	0.4	0.8	IPF4880	orf19.6266	unknown function	YCR093w
CA5880	1.1	1.0	1.6	1.2	0.8	0.9	IPF12074	orf19.6829	unknown function	YMR282c
CA5670	1.1	1.1	1.6	1.0	0.5	1.1	IPF1266	orf19.7372	Probable transcription factor	YAL051w
CA5450	1.0	1.1	1.6	1.0	0.8	0.9	IPF243	orf19.3254	unknown function	no match
CA3268	1.2	1.0	1.6	1.6	2.2	1.1	RPS620b	orf19.6301	unknown function	no match
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA1350	0.8	0.8	1.6	1.2	0.3	0.6	MCM2	orf19.4354	replication licensing factor (by homology)	YBL023c
CA4443	1.4	0.9	1.6	1.0	1.0	1.0	IPF3535	orf19.6840	unknown function	no match
CA2515	0.8	1.0	1.6	0.9	0.6	0.8	IPF19759	orf19.5510	Unknown Function	YGL133w
CA1695	1.0	0.9	1.6	1.1	1.0	1.4	RRP42	orf19.5039	rRNA processing protein (by homology)	YDL111c
CA0228	0.8	1.0	1.6	1.1	0.5	0.7	IPT1.5f	orf19.4769	Mannosyl diphosphorylinositol ceramide, 5-prime end (by hor	YDR072c
CA4040	1.0	0.9	1.6	1.5	1.2	1.0	GAL1	orf19.3670	galactokinase	YDR009w
CA2369	1.5	1.4	1.6	1.4	1.6	1.1	TBP1	orf19.1837	TATA-binding protein (by homology)	YER148w
CA5667	1.0	1.0	1.6	1.2	1.5	1.4	IPF1259	orf19.7369	Conserved hypothetical protein	YML005w
CA1626	0.8	1.3	1.6	1.4	1.3	1.1	STR2	orf19.1033	O-succinylhomoserine (thiol)-lyase (by homology)	YJR130c
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c
CA3010	1.1	0.7	1.6	1.0	1.6	1.0	IPF14568	orf19.6230	unknown function	YGL246c
CA4246	0.9	1.0	1.6	1.6	1.3	1.1	PGA20	orf19.535	unknown function	no match
CA4096	1.3	1.0	1.6	1.0	1.1	1.3	KRR1	orf19.661	involved in cell division and spore germination	YCL059c
CA3267	1.3	1.0	1.6	1.4	2.3	1.0	RPS620a	orf19.6300	unknown function	no match
CA6021	1.0	0.8	1.6	1.2	1.1	1.3	BFR2	orf19.7624	involved in protein transport steps at the Brefeldin A block (b	YDR299w
CA1702	1.4	0.7	1.6	1.0	0.7	0.9	HEL1	orf19.702	DNA helicase I (by homology)	YER176w
CA3315	0.9	1.1	1.6	1.5	1.0	1.0	IPF8814	orf19.2302	unknown function	no match
CA5811	1.6	1.0	1.6	1.0	0.8	1.0	IPF1699	orf19.6614	unknown function	YDR021w
CA6095	1.1	1.0	1.6	0.7	0.4	0.5	SNF3	orf19.5962	High affinity glucose transport protein (by homology)	YDL194w
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)	YLR216c
CA0504	0.9	1.0	1.6	1.0	0.9	0.9	IPF16466.5	orf19.2778	unknown function	YKL014c
CA4524	1.6	1.3	1.6	1.3	0.9	1.1	IPF7097	orf19.480	unknown function	YJR056c
CA5121	0.7	0.8	1.6	1.2	1.0	0.9	IPF1310	orf19.6407	unknown function	YLR387c
CA2367	1.7	1.5	1.6	1.1	0.8	1.0	SUI1	orf19.1280	translation initiation factor 3 (eIF3) (by homology)	YNL244c
CA5251	1.2	0.9	1.6	1.3	0.7	0.8	IPF1824	orf19.5011	unknown function	YPL269w
CA1422	1.0	0.7	1.6	1.3	1.0	1.1	IPF14248	orf19.3798	putative methyltransferase (by homology)	YDL201w
CA3006	1.1	0.7	1.6	1.3	1.1	1.2	IPF12152	orf19.6236	unknown function	YDL213c
CA4584	0.9	1.0	1.6	1.0	1.2	1.0	IPF2228	orf19.6902	similar to Saccharomyces cerevisiae Dbp7p RNA helicase re	YKR024c
CA5765	0.9	0.9	1.6	1.1	1.2	1.5	SOF1	orf19.5407	Involved in 18S pre-rRNA production (by homology)	YLL011w
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA6140	0.7	0.7	1.6	1.2	0.6	1.2	IPF1882	orf19.5905	unknown function Unknown function	YBL028c
CA1125	1.1	0.9	1.6	1.2	1.1	1.4	RRP43	orf19.6259	rRNA processing protein (by homology)	YCR035c
CA4585	0.8	0.9	1.6	1.2	1.2	1.3	IPF2227	orf19.6903	unknown function	YKR025w
CA5660	1.6	1.0	1.6	1.3	0.8	0.9	SKN1.3f	orf19.7362	Glucan synthase subunit, 3-prime end	YPR159w
CA4663	1.6	1.4	1.6	1.1	0.7	0.8	IPF6554	orf19.4450	unknown function	YJL103c
CA2283	1.3	0.7	1.6	1.7	1.3	1.2	MRT4	orf19.5550	required for mRNA decay (by homology)	YKL009w
CA5661	1.4	1.5	1.6	1.5	0.8	0.9	KRE6	orf19.7363	Glucan synthase subunit	YPR159w
CA5943	0.9	1.0	1.6	1.0	0.9	1.2	IPF3490	orf19.6754	unknown function	no match
CA3196	1.0	1.0	1.6	1.4	1.1	1.2	IPF3428	orf19.6175	unknown function	YLR051c
CA4972	1.3	1.2	1.5	1.0	1.2	0.9	MUP1	orf19.5280	High affinity methionine permease (by homology)	YGR055w

[Ca OS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]
HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)	YHL003c
CA0734	1.2	0.9	1.5	1.5	0.8	1.0	IPF8996	orf19.4634	unknown function	YGL211w
CA3527	1.4	2.1	1.5	1.6	1.0	1.4	IPF9934	orf19.988	unknown function	YGR149w
CA0142	1.0	1.4	1.5	1.0	1.4	1.3	CSL4	orf19.1026	Involved in kinetochore-related function (by homology)	YNL232w
CA0874	1.3	0.4	1.5	1.3	0.8	0.8	CPA1	orf19.4630	Arginine-specific carbamoylphosphate synthase, small chain	YOR303w
CA3225	0.8	1.0	1.5	0.9	1.2	1.0	IPF9329	orf19.6286	unknown function	YER128w
CA3243	1.0	1.0	1.5	1.1	1.1	1.0	IPF7489	orf19.4680	unknown function	no match
CA3909	1.1	0.9	1.5	1.1	1.1	1.1	CIT1	orf19.4393	Citrate synthase	YNR001c
CA5719	1.0	1.0	1.5	1.2	1.2	1.4	IPF2441	orf19.7424	unknown function	YER126c
CA1596	1.4	1.0	1.5	1.0	1.0	1.0	FAA21	orf19.272	long-chain-fatty-acid-CoA ligase (by homology)	YER015w
CA1406	1.1	0.9	1.5	1.1	0.5	0.6	DOT4	orf19.3370	derepression of telomeric silencing (by homology)	YNL186w
CA3234	1.5	0.9	1.5	0.8	0.7	0.8	MAS2	orf19.6295	processing peptidase, catalytic 53kDa (alpha) subunit, mitoch	YHR024c
CA4036	1.3	0.9	1.5	1.0	0.8	0.9	IPF12042	orf19.3666	unknown function	YGR093w
CA2856	1.0	1.1	1.5	1.4	1.4	1.2	IPF7062	orf19.1066	unknown function	YPL067c
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)	YJR107w
CA1655	0.9	1.0	1.5	0.9	1.5	0.8	CCC2	orf19.4328	putative copper-transporting ATPase (by homology)	YDR270w
CA1891	1.9	1.2	1.5	1.2	0.8	0.9	IPF10196	orf19.2752	unknown function	YDR216w
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA1064	0.8	0.9	1.5	1.1	1.0	1.0	PWP1	orf19.4640	beta-transducin superfamily (by homology)	YLR196w
CA2434	2.4	2.5	1.5	1.1	1.7	1.4	IPF9484	orf19.3396	unknown function	YNL281w
CA3130	1.0	0.9	1.5	1.0	0.7	0.8	TIM23	orf19.1361	mitochondrial inner membrane import translocase subunit (by	YNR017w
CA6063	0.8	1.1	1.5	1.0	1.0	1.0	IPF8311	orf19.6003	unknown function	YLR094c
CA2272	0.6	0.6	1.5	1.4	1.2	1.1	RPA43	orf19.2594	DNA-directed RNA polymerase I, 36 KD subunit(by homology	YOR340c
CA3491	0.9	0.6	1.5	1.1	1.3	1.4	RPC40	orf19.3564	RNA polymerase (by homology)	YPR110c
CA0599	0.7	0.9	1.5	1.2	1.1	1.1	IPF12428	orf19.2667	unknown function	YHR088w
CA5901	1.2	0.9	1.5	1.0	0.5	0.4	IPF2374	orf19.6805	unknown function	YDR089w
CA4332	1.0	1.2	1.5	1.4	1.5	1.2	GLO2	orf19.4088	Glyoxalase II (hydroxyacylglutathione hydrolase) (by homolo	YDR272w
CA6014	1.2	1.0	1.5	1.1	0.6	1.1	TRS31	orf19.7615	targeting complex (TRAPP) component involved in ER to Gol	YDR472w
CA1275	1.7	0.8	1.5	1.4	1.2	1.0	RPC53	orf19.2715	DNA-directed RNA polymerase III (by homology)	YDL150w
CA1023	1.0	1.3	1.5	1.4	1.1	1.2	IPF4817.3f	orf19.3351.1	unknown Function	YOR246c
CA4089	0.8	0.6	1.5	1.2	0.9	0.8	IPF5009	orf19.6648	unknown function	YGR245c

11A
[Cd OS+ up 1.5 10FDR] less [Ca OS+ up 1.5 10FDR]
HS+ OS+ XS+

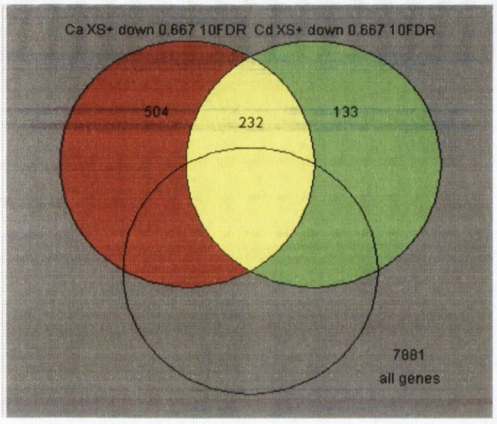
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase	YKR070w
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA0721	1.5	0.9	1.3	2.3	0.8	0.8	IPF10429	orf19.2887	unknown function	YMR295c
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA5840	1.2	1.0	1.3	1.9	1.0	1.2	EBP6	orf19.7495	NADPH dehydrogenase (by homology)	YPL171c
CA0948	0.6	1.1	0.9	1.9	1.1	1.0	IPF10270	orf19.1272	unknown function	YGR111w
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function	YMR226c
CA0677	1.4	1.3	1.2	1.8	1.0	0.8	IPF13095	orf19.1182	unknown function	YGL212w
CA4870	1.5	1.1	1.3	1.7	1.2	1.3	IPF19568	orf19.6556	unknown function	no match
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA1187	0.7	0.9	1.2	1.5	1.1	1.0	QRI7	orf19.3787	putative glycoprotease (by homology)	YKR038c
CA2161	1.1	1.1	1.1	1.5	1.0	1.1	IPF11876	orf19.5295	unknown function	no match
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w

12A
[Cd OS+ up 1.5 10FDR] and [Ca OS+ up 1.5 10FDR]
HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA5797	1.2	0.9	8.7	8.2	0.7	1.0	IPF4182	orf19.5446	unknown function	no match
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)	YDR497c
CA5120	4.6	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA4162	4.3	5.0	6.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function	no match
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function	YLR205c
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function	no match
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match

[Ca OS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]
HS+ OS+ XS+

Species (Stress ()* Systemat	Ca HS+ Norn	Cd HS+ Norn	Ca OS+ Norn	Cd OS+ Norn	Ca XS+ Norn	Cd XS+ Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5f	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function	no match
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c



13A

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA3912	0.7	1.0	0.6	0.8	0.2	0.7	IPF3288	orf19.4390	unknown function	no match
CA3452	0.7	1.0	0.9	1.0	0.2	0.9	IPF10541	orf19.1253	unknown function	YFR034c
CA0056	1.0	1.1	1.0	1.0	0.3	0.7	IPF15839	orf19.556	unknown function	no match
CA1583	1.2	1.1	1.1	1.2	0.3	0.8	ROT1	orf19.6029	Suppressor of TOR2 mutations (by homology)	YMR200w
CA1776	1.2	1.0	0.7	0.8	0.3	0.8	IPF14704	orf19.1823	unknown function	YLR241w
CA1749	0.9	1.0	0.7	0.9	0.3	0.7	IPF8257.3f	orf19.1518.3	unknown function, 3-prime end	no match
CA6028	0.7	0.9	1.0	0.8	0.3	0.8	IPF607	orf19.7634	unknown function	YDL003w
CA2150	0.7	1.0	0.8	0.7	0.3	0.7	IPF19940	orf19.6022	unknown function	no match
CA2885	0.5	0.6	0.9	0.9	0.3	0.8	PGA26	orf19.2475	unknown function	no match
CA1778	0.8	1.0	1.7	1.0	0.3	1.0	IPF13810	orf19.1825	unknown function	no match
CA1493	1.4	0.8	1.3	1.0	0.3	0.7	FTH2	orf19.3227	iron transporter (by homology)	YBR207w
CA3613	1.1	0.9	1.0	0.8	0.3	0.7	SPF1	orf19.30	P-type ATPase	YEL031w
CA2405	1.2	1.1	0.9	0.9	0.3	0.7	PGA18	orf19.301	unknown function	no match
CA3705	0.5	0.9	1.1	1.0	0.3	0.7	MSH6	orf19.4945	DNA mismatch repair protein by homology	YDR097c
CA2674	1.4	1.0	1.3	0.9	0.3	0.7	IPF5846	orf19.5495	unknown function	YML117w
CA5406	0.8	0.9	1.0	1.1	0.3	0.9	IPF1547	orf19.949	unknown function	YLR309c
CA1710	0.9	1.2	0.9	0.9	0.3	0.8	CLA4	orf19.4890	protein kinase homolog (by homology)	YNL298w
CA4554	1.0	1.0	0.9	0.9	0.3	0.8	IPF7874	orf19.1445	similar to Saccharomyces cerevisiae Esc4p involved in chron	YHR154w
CA1748	0.8	0.9	0.6	0.9	0.3	0.7	IPF8257.5f	orf19.1522	unknown function, 5-prime end	no match
CA1072	1.0	1.1	1.0	1.1	0.3	0.8	SBH1	orf19.2533.1	involved in translocation into the ER (by homology)	YER087cb
CA0156	0.9	1.0	1.0	1.1	0.3	0.9	SCW1.3f	orf19.1779	glucanase (by homology)	YGR279c
CA0104	0.6	0.8	0.7	1.1	0.3	0.8	RBT4	orf19.6202	repressed by TUP1 protein	YJL079c
CA0435	1.1	1.4	0.9	0.7	0.3	0.8	UGP1	orf19.1738	UTP--glucose-1-phosphate uridylyltransferase (by homology)	YKL035w
CA0846	0.7	0.8	1.2	0.8	0.4	0.7	SMC3.5f	orf19.262	required for structural maintenance of chromosomes, 5-prime	YJL074c
CA5454	0.5	1.1	1.3	0.9	0.4	1.0	IPF257.3f	orf19.3261	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA2154	0.4	1.3	1.2	1.1	0.4	0.7	ERG2	orf19.6026	C-8 sterol isomerase	YMR202w
CA3939	1.0	0.9	3.2	1.1	0.4	0.8	HNM1	orf19.2003	Choline permease (by homology)	YGL077c
CA3688	0.9	0.9	1.7	1.2	0.4	0.7	YIP3	orf19.6264.3	protein of unknown function, (by homology)	YNL044w
CA1095	0.8	0.5	1.3	0.9	0.4	0.7	SMC1	orf19.4367	Chromosomal ATPase family member (by homology)	YFL008w
CA5076	0.4	0.3	0.9	0.6	0.4	0.8	IPF15301	orf19.3051	unknown function	YJR116w
CA4887	1.1	1.0	1.2	1.3	0.4	0.7	IPF1632	orf19.6579	unknown function	no match
CA0358	1.0	1.0	1.0	1.0	0.4	1.0	IPF17488.5f	orf19.1818	unknown function, 5-prime end	no match
CA3072	0.8	1.2	0.9	1.0	0.4	0.8	ERG12	orf19.4809	Mevalonate kinase (by homology)	YMR208w
CA0260	1.2	0.7	1.7	0.9	0.4	0.7	IPF13683	orf19.2547	unknown function	no match
CA4528	1.4	1.3	0.9	0.9	0.4	0.7	STT3	orf19.1478	oligosaccharyl transferase (by homology)	YGL022w
CA2637	0.7	0.8	1.1	1.0	0.4	0.9	IPF19954	orf19.4301	unknown function	no match
CA4749	0.6	0.6	1.0	0.8	0.4	0.8	IPF4481	orf19.4831	unknown function	no match
CA0411	0.8	1.0	1.4	1.0	0.4	0.8	IPF17676	orf19.1507	similar to Saccharomyces cerevisiae Cst13p involved in chroi	YBR158w
CA1819	1.1	1.0	1.2	1.0	0.4	0.9	IPF16549	orf19.4273	Unknown function	YLR139c
CA3093	0.7	0.9	1.1	0.8	0.4	0.8	TOF1.5f	orf19.4136	Topoisomerase I interacting factor 1, 5-prime end (by homolo	YNL273w
CA5844	1.3	1.1	1.3	1.2	0.4	0.7	PXA1	orf19.7500	long chain fatty acid ABC transporter (by homology)	YPL147w
CA0852	1.1	0.9	0.8	0.9	0.4	0.8	KIP2	orf19.1747	Kinesin-related protein required for nuclear migration (by hon	YPL155c
CA1076	1.0	0.9	0.7	0.8	0.4	0.7	IPF19721	orf19.2239	similar to Saccharomyces cerevisiae Lte1p GDP/GTP exchan	YAL024c
CA4094	0.6	0.7	1.2	0.9	0.4	0.8	IPF4004	orf19.658	unknown function	YCL061c
CA1140	0.7	1.0	1.3	0.9	0.4	1.0	IPF17322.3f	orf19.4068	unknown function, 3-prime end	YNR052c
CA1226	0.9	1.1	1.1	0.9	0.4	0.7	IPF15660	orf19.4159	putative mitochondrial carrier (by homology)	YMR166c
CA4233	0.8	0.9	1.0	1.1	0.4	0.7	RFT1	orf19.516	nuclear division protein (by homology)	YBL020w
CA4295	1.0	1.0	0.9	1.0	0.4	0.8	MNN7	orf19.6692	putative Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA6163	0.3	0.3	1.0	0.8	0.4	0.8	POL1	orf19.5873	DNA-directed DNA polymerase alpha (by homology)	YNL102w
CA2591	0.8	1.2	0.8	0.9	0.4	0.7	IPF18448.3e	orf19.60	unknown function, 3-prime end	YJL062w
CA3548	0.9	1.0	1.0	1.1	0.4	0.8	IPF12179	orf19.3872	unknown function	YGR026w
CA5858	1.0	0.9	1.0	1.0	0.4	0.8	IPF380	orf19.7516	unknown function	no match
CA4113	1.2	1.0	1.8	1.5	0.4	0.7	CHO1	orf19.677	Phosphatidylserine synthase	YER026c
CA2509	1.2	0.9	1.5	1.4	0.4	0.7	IPF1471	orf19.304	aminotriazole resistance protein (by homology)	YOR378w
CA5736	1.0	1.6	0.7	1.1	0.4	0.9	OPI3	orf19.7446	Methylene-fatty-acyl-phospholipid synthase (by homology)	YJR073c
CA5859	1.0	0.9	0.9	1.0	0.4	0.8	CHT1	orf19.7517	endochitinase 1 precursor	YLR286c
CA1476	1.0	0.9	1.0	0.9	0.4	0.8	IPF10214	orf19.1093	unknown function	no match
CA3197	1.2	1.1	1.0	1.2	0.4	0.7	SEC61	orf19.6176	ER protein-translocation complex subunit	YLR378c
CA1365	1.6	1.0	0.9	0.9	0.4	1.3	IPF11849	orf19.4459	unknown function	YNL234w
CA4939	0.9	0.6	0.5	0.8	0.4	0.7	IQG1	orf19.6536	RAS GTPase-activating-like protein by homology	YPL242c
CA4514	1.2	0.9	1.2	0.8	0.4	0.8	IPF20016	orf19.491	similar to Saccharomyces cerevisiae Sec63p ER protein-tran	YOR254c
CA5232	1.0	1.0	1.0	1.1	0.4	1.0	SUN42	orf19.5032	Putative cell wall beta-glucosidase (by homology)	YIL123w
CA5693	0.6	1.0	1.3	1.0	0.4	0.8	GDA1	orf19.7394	Golgi guanosine diphosphatase (by homology)	YEL042w
CA3462	1.2	1.1	1.0	0.8	0.4	0.8	IPF14959	orf19.1265	similar to Saccharomyces cerevisiae Trs130p TRAPP subunit	YMR218c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR] HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA3282	0.9	1.0	1.0	1.0	0.4	0.9	IPF6272	orf19.6315	unknown function	no match
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA4194	1.2	1.0	1.0	1.0	0.4	0.7	PTR3	orf19.4535	transcriptional regulator (by homology)	YFR029w
CA0049	1.3	1.4	1.2	1.0	0.4	0.8	IPF3908	orf19.757	unknown function	YPR090w
CA3756	0.5	0.8	0.4	0.6	0.4	0.7	IPF8884	orf19.3422	unknown function	YLR454w
CA1223	1.1	1.2	0.9	0.8	0.4	0.7	IPF14870	orf19.4131	unknown function	YCL045c
CA3965	0.8	1.0	1.0	1.0	0.4	0.8	IPF9375	orf19.1426	unknown function	YHR149c
CA3320	0.8	0.8	0.7	0.8	0.4	0.7	IPF6898	orf19.2678	similar to Saccharomyces cerevisiae Bub1p serine/threonine	YGR188c
CA4360	0.7	1.1	0.9	1.0	0.4	0.8	IPF6050	orf19.6737	unknown function	no match
CA5397	1.5	1.2	0.7	0.8	0.4	0.8	IPF9663	orf19.940	similar to Saccharomyces cerevisiae Bud2p GTPase-activatir	YKL092c
CA2267	1.4	1.1	0.9	0.8	0.4	0.7	IFU1.5f	orf19.2600	Unknown function, 5-prime end	YNL126w
CA2020	1.6	1.5	1.0	0.9	0.4	1.0	IPF16901	orf19.842	unknown function	no match
CA3691	1.0	1.0	1.6	1.0	0.4	0.8	IPF4880	orf19.6266	unknown function	YCR093w
CA0089	1.4	0.8	1.4	0.9	0.4	0.8	MRPL3	orf19.5064	ribosomal protein of the large subunit, mitochondrial (by hom	YMR024w
CA3716	0.8	1.0	1.1	1.1	0.4	0.9	IPF6203	orf19.4166	unknown function	YLR228c
CA2948	0.4	0.9	1.6	0.9	0.5	0.8	GDS1	orf19.1963	nam9-1 suppressor (by homology)	YOR355w
CA5483	0.8	0.9	0.5	0.9	0.5	0.7	IPF817	orf19.5316	unknown function	YOR088w
CA1728	1.2	1.1	0.8	0.9	0.5	0.8	WHI3	orf19.6494	Putative RNA binding protein (by homology)	YNL197c
CA2379	0.5	0.8	1.3	1.0	0.5	0.7	IPF4073	orf19.2216	similar to Saccharomyces cerevisiae CaPds5p regulation of c	YMR076c
CA4424	1.1	1.1	0.8	0.9	0.5	0.9	PMT1	orf19.5171	mannosyltransferase	YDL095w
CA5774	1.2	1.0	0.9	1.0	0.5	0.7	IPF1113	orf19.5418	unknown function	YIL039w
CA5315	0.6	0.8	0.7	1.2	0.5	0.7	CYB2	orf19.7186	B-type cyclin	YLR210w
CA5702	0.7	0.6	0.9	0.8	0.5	0.7	PCH1	orf19.7402	Putative ATPase (by homology)	YDR440w
CA1501	1.0	0.9	0.8	0.9	0.5	0.9	IPF13217	orf19.1698	unknown function	YNL094w
CA0882	1.1	0.9	0.8	1.0	0.5	0.9	PHR3	orf19.377	surface glycoprotein (by homology)	YOL132w
CA4159	0.9	1.0	1.5	1.1	0.5	1.1	ALD5	orf19.5806	aldehyde dehydrogenase (NAD+) (by homology)	YER073w
CA4743	0.9	1.0	1.1	1.1	0.5	0.8	IPF4491	orf19.4839	unknown function	YER083c
CA3233	0.7	1.0	1.0	0.7	0.5	0.8	MYO1	orf19.6294	myosin-1 isoform (type II myosin) heavy chain (by homology)	YHR023w
CA3966	1.3	1.0	0.8	1.0	0.5	0.9	IPF9376	orf19.1427	unknown function	YLR004c
CA0878	0.8	0.7	1.1	1.0	0.5	0.7				
CA5751	1.2	1.3	0.9	0.9	0.5	0.7	VPS8	orf19.5387	Vacuolar sorting protein (by homology)	YAL002w
CA5243	0.9	1.1	1.5	1.1	0.5	0.7	IPF3040	orf19.5020	unknown function	no match
CA0581	1.0	0.7	1.0	0.9	0.5	0.8	IPF3181	orf19.3558	similar to Saccharomyces cerevisiae Erp3p p24 protein involv	YDL018c
CA0877	1.0	1.0	1.0	1.1	0.5	0.7	CNH1	orf19.367	Na+/H+ antiporter	YLR138w
CA2181	0.5	0.6	0.6	0.9	0.5	0.9	ECM331	orf19.4255	Involved in cell wall biogenesis and architecture (by homolog	YDR055w
CA5401	0.9	0.6	1.0	1.1	0.5	0.7	FET35.3	orf19.943	Cell surface ferroxidase, high affinity, 3-prime end (by homol	YMR058w
CA2268	1.0	1.0	1.0	0.9	0.5	0.8	IFU1.3f	orf19.2599.3	Unknown function, 3-prime end	no match
CA1010	1.0	0.9	0.8	0.9	0.5	1.0	GLT1	orf19.6257	glutamate synthase (NAPDPH), (by homology)	YDL171c
CA2990	1.6	1.5	0.8	0.9	0.5	0.8	IPF5092	orf19.6012	unknown function	YOR296w
CA1262	1.0	0.7	0.8	0.7	0.5	0.7	MDR1	orf19.1244	Mac1p interacting protein (by homology)	YGR100w
CA1037	1.0	1.1	0.8	0.9	0.5	0.7	MNS1	orf19.1036	Alpha1,2-mannosidase (by homology)	YJR131w
CA2118	1.0	1.0	0.7	0.9	0.5	0.7	IPF8024	orf19.1334	unknown function	no match
CA2196	1.1	0.8	1.0	0.9	0.5	0.7				
CA2249	0.5	0.6	0.9	0.7	0.5	0.7	POL2	orf19.2365	DNA-directed DNA polymerase epsilon, catalytic subunit A (b	YNL262w
CA1605	0.9	1.0	1.5	1.1	0.5	0.9	SWI6	orf19.4725	Transcription factor (by homology)	YLR182w
CA1779	1.2	1.1	4.5	1.5	0.5	0.8	IPF14510	orf19.1826	unknown function	YGL219c
CA1060	1.3	0.9	0.9	0.9	0.5	0.8	IPF11460	orf19.267	unknown function	YJL076w
CA5881	1.1	1.0	1.1	1.1	0.5	0.8	SSS1	orf19.6828.1	ER protein-translocase complex subunit (by homology)	YDR086c
CA0662	1.2	1.0	0.8	1.0	0.5	0.7	SPC97	orf19.708	spindle pole body component (by homology)	YHR172w
CA3151	1.6	1.4	0.9	1.1	0.5	1.1	IPF4033	orf19.6167	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihydroxyac	YIL124w
CA5274	1.1	1.0	0.9	0.9	0.5	0.7	IPF1764	orf19.4985	similar to Saccharomyces cerevisiae Gup1p glycerol transpor	YGL084c
CA5721	0.8	1.0	1.1	1.1	0.5	0.8	IPF2443	orf19.7426	similar to Saccharomyces cerevisiae Ost6p N-oligosaccharylt	YML019w
CA2787	1.0	0.8	0.8	0.6	0.5	0.7	EFG1	orf19.610	Enhanced filamentous growth factor	YMR016c
CA5701	0.9	0.7	1.2	0.8	0.5	0.7	ISW2	orf19.7401	Chromatin remodeling complex (by homology)	YOR304w
CA5750	1.1	1.5	0.7	1.4	0.5	0.7	CHS8	orf19.5384	Chitin synthase (by homology)	YNL192w
CA5202	0.7	1.0	1.2	0.9	0.5	0.8	YOX1	orf19.7017	Similar to homoeodomain protein (by homology)	YML027w
CA1694	0.9	0.8	2.6	1.1	0.5	0.9	TRM3	orf19.5038	2 -O-ribose methyltransferase (by homology)	YDL112w
CA5802	0.6	0.9	1.0	1.4	0.5	0.9	IPF4164	orf19.5455	similar to Saccharomyces cerevisiae Vtc1p negative regulato	YER072w
CA3351	1.0	1.0	1.0	1.0	0.5	0.7				
CA4882	0.3	0.3	0.7	0.9	0.5	0.8	IPF1651	orf19.6570	purine nucleoside permease (by homology)	no match
CA0614	0.8	0.8	0.8	0.9	0.5	0.7	IPF19700	orf19.1600	unknown function	no match
CA2287	0.8	1.0	0.8	1.0	0.5	0.9	IPF5373	orf19.5555	unknown function	YIR019c
CA2633	1.8	1.2	1.3	0.9	0.5	0.7	KEX2	orf19.4755	Kexin precursor (KEX2 protease)	YNL238w
CA4602	1.6	2.0	1.2	1.2	0.5	0.7	IPF6231	orf19.3292	unknown function Unknown function	YCL033c
CA3092	1.0	1.0	1.2	0.8	0.5	0.8	IPF9821.3f	orf19.4141	unknown function, 3-prime end	YEL064c
CA3617	1.5	1.1	1.3	0.8	0.5	0.8	IPF9069	orf19.199	unknown function	YKL039w
CA5412	0.8	1.3	0.7	0.9	0.5	0.8	IPF1566	orf19.956	unknown function	YLR087c
CA5711	1.8	1.2	1.3	0.9	0.5	0.7	MUB1	orf19.7412	Regulation of bud site selection (by homology)	YMR100w
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA1127	0.8	0.9	1.2	0.8	0.5	1.1	MSH3	orf19.3608	DNA mismatch repair by homology	YCR092c
CA2947	0.2	0.3	0.7	0.5	0.5	0.7	IPF6298	orf19.1964	unknown function	no match
CA2243	1.3	0.9	1.1	0.9	0.5	0.9	IPF7414	orf19.4670	putative transcription factor (by homology)	YGL209w
CA3469	0.6	0.7	0.8	1.0	0.5	0.9	MNT1	orf19.1665	Mannosyltransferase involved in n-linked and o-linked glycos	YOR099w
CA0960	1.0	1.1	0.8	1.1	0.5	0.8	DPP1	orf19.656	Diacylglycerol Pyrophosphate Phosphatase by homology	YDR284c
CA5495	0.6	0.9	0.9	0.9	0.5	1.1	SGS1	orf19.5335	ATP-dependent DNA helicase (by homology)	YMR190c
CA4348	1.3	1.0	1.1	0.8	0.5	0.8	IPF3638	orf19.6723	unknown function	YGL036w
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA4095	1.0	1.0	1.2	1.0	0.5	0.8	IPF4002	orf19.660	unknown function	no match
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)	YHL003c
CA1312	0.8	1.1	0.8	0.7	0.5	0.7	IPF14241	orf19.3635	unknown function	no match
CA3603	0.9	0.5	0.9	0.6	0.5	0.7	MEF1	orf19.4932	mitochondrial translation elongation factor G (by homology)	YLR069c
CA5326	1.6	1.0	0.9	1.0	0.5	1.0	IPF2137	orf19.7200	unknown function	no match
CA4432	0.9	1.0	0.9	0.8	0.5	0.8	IPF5574	orf19.5163	unknown function	YLL003w
CA4471	1.0	0.4	1.3	1.1	0.5	0.8	MCM3	orf19.1901	replication initiation protein (by homology)	YEL032w
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.5f	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholester	YNR008w
CA2652	1.0	1.0	1.2	0.9	0.5	0.9	DNA2	orf19.1192	DNA helicase (by homology)	YHR164c
CA5670	1.1	1.1	1.6	1.0	0.5	1.1	IPF1266	orf19.7372	Probable transcription factor	YAL051w
CA4182	1.0	0.9	0.9	0.8	0.5	0.9	IPF19797	orf19.2949	unknown	YJR138w

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]
HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA3785	0.9	0.7	1.1	0.9	0.5	0.8	IPF19788	orf19.5834	similar to Saccharomyces cerevisiae Sxm1p putative beta-kai	YDR395w
CA2949	0.6	0.9	1.3	1.0	0.5	0.8	IPF14506	orf19.1961	unknown function	no match
CA1657	1.0	1.0	1.3	1.0	0.5	0.7	IPF16022	orf19.4325	unknown function	YPL183c
CA0276	0.6	0.5	0.9	0.7	0.5	0.9	IPF15015	orf19.5612	unknown function	YIL091c
CA3918	0.5	0.5	0.6	1.1	0.5	0.7	VTC2	orf19.4381	putative polyphosphate synthetase (by homology)	YFL004w
CA2277	1.3	1.4	0.9	1.1	0.5	0.7	DRS21.5eoc	orf19.783	Membrane-spanning Ca-ATPase (by homology)	YIL048w
CA4155	0.8	0.5	1.0	0.5	0.5	0.7	RNR21	orf19.5801	ribonucleoside-diphosphate reductase (by homology)	YJL026w
CA0843	1.6	1.3	1.1	1.2	0.5	0.7	IPF18853	orf19.1054	unknown function	YLL023c
CA4648	1.2	0.9	1.1	0.9	0.5	0.8	IPF9864	orf19.4435	similar to Saccharomyces cerevisiae Stu1p mitotic spindle pr	YBL034c
CA6137	1.0	1.0	1.4	0.9	0.5	0.8	IPF4356	orf19.5910	unknown function	YPR031w
CA2204	0.6	0.5	2.2	1.0	0.5	0.9	DIP51.5f	orf19.2943	dicarboxylic amino acid permease, 5-prime end (by homology	YPL265w
CA0525	1.1	0.9	0.8	0.9	0.5	1.0	MSB1.5eoc	orf19.1133	Morphogenesis-related protein (by homology)	YOR188w
CA2144	1.2	1.1	1.1	1.0	0.5	0.8	IPF12802	orf19.2513	unknown function	YDR495c
CA1818	0.9	1.0	1.3	0.9	0.5	1.0	IPF7023.3f	orf19.134	unknown function, 3-prime end	no match
CA1219	1.0	1.0	1.0	1.0	0.5	0.9	PRC2	orf19.4135	carboxypeptidase y precursor , serine-type protease (by hom	YMR297w
CA6153	1.0	1.0	1.0	1.1	0.5	0.7	CUP5	orf19.5886	Vacuolar H+-ATPase (by homology)	YEL027w
CA2336	0.8	1.0	1.1	1.1	0.5	0.7	IPF13383.5e	orf19.2353	unknown function, 5 prime end	YOR086c
CA5355	0.6	1.1	1.4	1.2	0.5	0.8	IRR1.3f	orf19.7232	cohesin complex subunit, 3-prime end (by homology)	YIL026c
CA0185	0.2	0.7	0.7	0.6	0.5	0.8	PLB4.5f	orf19.1442	Phospholipase, 5-prime end (by homology)	YOL011w
CA0100	1.0	1.0	0.9	1.2	0.5	0.7	IPF11569	orf19.9	unknown function	no match
CA3221	1.1	1.0	0.9	0.9	0.5	0.9	IPF10000.5e	orf19.6193	unknown function, 5-prime end	YGR274c
CA1362	1.0	1.0	1.1	1.1	0.5	0.8	PEX3	orf19.4426	PEROXISOMAL MEMBRANE PROTEIN by homology	YDR329c
CA3331	0.5	1.0	1.4	1.0	0.5	1.0	POL21.53f	orf19.2668.1	pol polyprotein, reverse transcripase, internal fragment (by h	no match
CA5470	0.9	1.0	1.2	1.0	0.5	0.9	IPF300	orf19.3282	unknown function	YMR266w
CA3327	0.5	0.7	0.6	0.7	0.5	0.7	NCP1	orf19.2672	NADPH-cytochrome P450 reductase	YHR042w
CA0474	1.1	1.0	0.9	1.1	0.5	0.7	IPF12887	orf19.4780	Putative multidrug protein (by homology)	YJR124c
CA2465	1.5	1.1	0.9	0.9	0.5	0.7	IPF8726	orf19.1795	unknown function	YLL013c
CA3774	1.1	1.0	0.8	1.0	0.5	0.7	IPF10437	orf19.2892	budding protein-like (by homology)	YHR103w
9601.2	1.1	1.0	0.8	1.0	0.5	1.1				
CA1167	1.0	1.2	0.8	1.1	0.5	0.8	IPF16646	orf19.1782	unknown function	YEL001c
CA4552	1.0	1.0	0.9	1.0	0.5	0.9	IPF7869	orf19.1447	unknown function	YLR086w
CA2931	0.8	0.9	0.7	0.9	0.5	0.9	IPF7841	orf19.4203	similar to Saccharomyces cerevisiae Ndc1p nuclear envelope	YML031w
CA2001	1.0	1.0	1.0	0.8	0.5	0.7	IPF17074	orf19.2792	unknown function	YBR086c
CA1731	1.5	0.9	1.0	1.0	0.5	0.7	IPF8437	orf19.6499	putative DNA-directed RNA polymerase (by homology)	YFL036w
CA1898	0.7	0.4	0.7	0.6	0.5	1.0	PGA38	orf19.2758	unknown function	no match
CA3967	1.3	1.0	1.0	1.0	0.5	0.9	IPF9377	orf19.1428	unknown function	no match
CA2364	1.0	1.1	0.6	0.7	0.5	0.7	MEC1	orf19.1283	cell cycle checkpoint protein (by homology)	YBR136w
CA1709	1.3	0.6	1.1	0.9	0.5	0.6	HOL2	orf19.4889	Multidrug-resistance protein subfamily 1 (by homology)	YNR055c
CA2129	1.9	1.1	1.3	1.1	0.5	1.3	IPF4899	orf19.414	unknown function	YKL155c
CA2166	0.9	0.8	0.8	1.1	0.5	0.8	FEN12	orf19.908	Probable subunit of 1,3-beta-glucan synthase (by homology)	YCR034w
CA1228	1.0	1.0	1.1	0.9	0.5	0.8	IPF16081	orf19.4161	unknown function	YDL105w
CA3212	1.1	0.9	1.1	0.9	0.5	0.8	MEF2	orf19.6208	translation elongation factor (by homology)	YJL102w
CA3950	1.1	1.1	0.8	0.9	0.5	0.7	PTM1	orf19.1991	Possibly involved in the TCA cycle (by homology)	YKL039w
CA2221	0.8	0.8	1.0	0.9	0.5	0.7	IPF9670	orf19.5100	membrane transporter of the ATP-binding cassette (ABC) sup	YLL015w
CA4409	0.6	0.7	0.8	0.8	0.5	0.7	IPF13151	orf19.3100	unknown function	YDL058w
CA4126	1.0	1.0	0.9	0.8	0.5	0.7	IPF6631	orf19.2763	unknown function	YJL019w
CA0228	0.8	1.0	1.6	1.1	0.5	0.7	IPT1.5f	orf19.4769	Mannosyl diphosphorylinositol ceramide, 5-prime end (by hor	YDR072c
CA4595	1.6	1.0	0.8	0.9	0.5	0.9	GCN2	orf19.6913	Ser/thr protein kinase (by homology)	YDR283c
CA3349	0.7	0.8	1.0	1.3	0.5	0.8	IPF19588	orf19.2318.1	unknown function	YDR367w
CA4461	1.2	1.2	1.5	1.0	0.5	1.0	IPF8470	orf19.6858	unknown function	YEL015w
CA4052	1.2	1.0	1.3	1.2	0.5	1.1	IPF10231.3f	orf19.427	unkown function, 3-prime end	YBR275c
CA4560	0.7	0.8	1.2	0.8	0.5	0.9	IPF8038	orf19.6871	unknown function	YMR124w
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA4627	0.6	0.6	1.0	1.0	0.5	1.1	DUT1	orf19.3322	dUTP pyrophosphatase	YBR252w
CA1147	1.0	1.0	1.2	0.9	0.5	0.8	KAP95	orf19.3681	karyopherin-beta protein (by homology)	YLR347c
CA3229	0.6	0.9	1.8	1.1	0.5	0.9	FUN30	orf19.6291	helicases of the Snf2/Rad54 family(by homology)	YAL019w
CA0838	1.0	1.1	1.0	1.1	0.5	0.8	TFP1.5f	orf19.1680	vacuolar ATPase subunit (by homology)	YDL185w
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA2203	0.5	0.5	1.3	1.1	0.5	1.0	DIP51.3f	orf19.2942	dicarboxylic amino acid permease, 3-prime end (by homology	YPL265w
CA0862	0.8	0.9	1.0	0.8	0.5	0.6	CRK1.5f	orf19.3524	Protein kinase, 5-prime end	YPR161c
CA2774	1.0	1.0	1.0	1.0	0.5	1.4	TFC4	orf19.274	transcription factor IIIC chain TFC4- like by homology	YGR047c
CA2114	1.0	1.1	1.0	1.0	0.5	0.9	IPF13744	orf19.3685	protein involved in regulation of carbon metabolism (by homo	YNL201c
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)	YFL036w
CA4897	1.1	1.0	1.0	1.1	0.5	0.7	TUB2	orf19.6034	Beta-tubulin	YFL037w
CA4363	1.0	0.8	0.8	1.0	0.5	0.8				
CA1126	1.1	1.3	1.0	0.9	0.5	0.9	IPF5203	orf19.3607	unknown function	YGR110w
CA0284	0.9	0.9	1.2	1.0	0.5	0.9	IPF14657	orf19.1441	unknown function	no match
CA4603	1.3	1.5	1.1	1.4	0.5	0.7	IPF6230	orf19.3293	unknown function	YDL015c
CA4878	1.2	0.8	0.8	0.8	0.5	0.8	OXA1	orf19.6565	Cytochrome oxidase biogenesis protein (by homology)	YER154w
CA5006	1.2	1.2	1.1	0.7	0.5	0.8	IPF12584	orf19.5241	unknown function	YCR033w
CA2453	1.3	1.0	1.3	0.9	0.6	0.7	IPF9950	orf19.3501	unknown function	YKR090w
CA2004	0.6	0.7	1.0	0.7	0.6	0.8	POL12	orf19.2796	DNA-directed DNA polymerase alpha (by homology)	YBL035c
CA4463	1.3	1.1	1.0	1.0	0.6	0.8	PIS1	orf19.6860	CDP diacylglycerol--inositol 3-phosphatidyltransferase (by ho	YPR113w
CA1495	1.3	0.9	1.0	0.8	0.6	0.8	IPF9686	orf19.3647	similar to Saccharomyces cerevisiae Sec8p Golgi - plasma m	YPR055w
CA5545	1.5	1.3	1.3	1.0	0.6	0.8	IPF5986	orf19.7307	similar to cytochrome-b5- and nitrate reductases	YML125c
CA2793	1.3	0.8	1.0	1.1	0.6	1.1	TRK1.5f	orf19.600	Potassium transporter, 5-prime end	YKR050w
CA4203	0.5	0.7	0.7	0.6	0.6	0.8	SWI4.3f	orf19.4545	transcription factor (by homology)	YDL056w
CA5981	1.1	0.7	0.7	0.8	0.6	0.8	MSS51	orf19.7577	involved in maturation of COX1 and COB mRNA (by homolog	YLR203c
CA2481	1.1	1.0	1.0	0.9	0.6	0.9	MRPL36	orf19.3205	ribosomal protein YmL36 precursor, mitochondrial (by homol	YBR122c
CA2770	0.9	1.1	0.7	1.2	0.6	0.8	CPS1	orf19.2686	Carboxypeptidase YSCS precursor, second fragment (by hon	YJL172w
CA0953	1.0	1.2	0.6	0.8	0.6	0.8	IPF13166	orf19.1144	unknown function	YDL203c
CA3497	1.0	0.7	1.0	1.2	0.6	0.7	FEN11	orf19.6343	Fatty acid elongase required for sphingolipid formation (by ho	YCR034w
CA1990	0.9	0.9	1.4	1.0	0.6	0.9	TOP1	orf19.96	CANAL DNA TOPOISOMERASE I	YOL006c
CA5048	1.0	1.0	1.1	1.0	0.6	1.1	IPF20024	orf19.3012	unknown function	YDR421w
CA3678	0.9	0.9	0.9	1.1	0.6	0.7	IPF8392	orf19.731	unknown function	YLR080w
CA0176	1.4	1.3	1.0	1.0	0.6	0.8	IPF11388	orf19.652	unknown function	YER041w
CA5437	1.0	1.2	0.8	1.0	0.6	1.1	ERG27	orf19.3240	3-keto sterol reductase (by homology)	YLR100w
CA5894	1.5	1.5	0.9	1.0	0.6	0.8	PMT2	orf19.6812	O-D-mannosyltransferase (by homology)	YAL023c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]
HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2191	1.4	1.1	1.3	1.1	0.6	1.1	IPF9417	orf19.4775	similar to Saccharomyces cerevisiae Hsf1p heat shock transc	YGL073w
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w
CA4149	1.1	0.7	1.0	1.0	0.6	0.8	SMP3	orf19.5792	Protein kinase C pathway protein	YOR149c
CA3047	1.2	1.1	0.8	0.8	0.6	0.8				
CA3065	0.9	0.7	1.1	0.9	0.6	0.8	IPF19775	orf19.4282	unknown function	no match
CA1384	0.5	0.8	0.9	1.0	0.6	0.8	IPF8423	orf19.926	similar to Saccharomyces cerevisiae Dhs1p exonuclease (by	YOR033c
CA0717	1.3	1.1	0.9	0.8	0.6	0.7	IPF9785	orf19.3453	unknown function	YFL047w
CA2436	0.9	1.1	0.9	1.0	0.6	0.7	IPF5500	orf19.2200	unknown function	YKR044w
CA4696	0.5	0.4	0.9	0.7	0.6	0.8	HTA1	orf19.6924	Histone H2A (by homology)	YDR225w
CA3322	0.8	1.0	0.8	0.9	0.6	0.8	IPF6895.3f	orf19.2676.1	unknown function, 3-prime end | FALSORF=SMALLORF	YHR188c
CA0913	0.9	1.1	0.8	1.1	0.6	0.8	IPF14810	orf19.2016	unknown function	YER044c
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA4655	0.9	1.5	0.5	0.9	0.6	0.8	IPF3098	orf19.4442	Putative mannosyltransferase (by homology)	YNL219c
CA2008	1.1	0.5	1.1	1.2	0.6	0.9				
CA2393	1.1	0.8	0.8	1.0	0.6	0.8	RHO3	orf19.3534	GTP-binding protein of the rho family	YIL118w
CA4860	1.0	0.9	1.2	1.0	0.6	0.9	IPF19804	orf19.3835	unknown Function	YAL001c
CA0665	0.4	0.3	0.6	0.7	0.6	0.8	INT1	orf19.4257	integrin-like protein alpha chain	YJR092w
CA5700	1.1	0.9	1.0	0.9	0.6	1.1	IPF2630	orf19.7399.3	unknown function	no match
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA5889	0.7	0.7	1.5	1.1	0.6	0.8	IPF2409	orf19.6818	RNA-dependent ATPase (by homology)	YLR419w
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA4429	1.2	1.0	1.2	1.2	0.6	0.9	DBF4	orf19.5166	regulatory subunit for Cdc7 by homology	YDR052c
CA4767	1.2	1.1	1.0	1.0	0.6	0.9	IPF13054	orf19.3999	unknown function	YML020w
CA1061	1.4	1.1	1.1	1.0	0.6	1.1	IPF19720	orf19.4643	unknown function	no match
CA5784	1.5	0.9	0.7	1.0	0.6	1.4	IPF1129	orf19.5431	unknown function	no match
CA0550	1.5	1.1	1.2	1.8	0.6	0.9	IPF14030	orf19.851	unknown function	YJR061w
CA4623	0.9	1.0	0.7	1.0	0.6	0.8	CTA9	orf19.3315	Putative transcriptional regulator	no match
CA4086	1.2	1.3	0.9	1.1	0.6	0.8	IPF5014	orf19.6642	unknown function	YNL263c
CA1094	1.6	1.1	1.7	1.3	0.6	0.7	YIP1	orf19.3951	golgi membrane protein (by homology)	YGR172c
CA0319	1.1	1.1	1.3	1.0	0.6	0.8				
CA3789	2.0	1.5	0.9	0.9	0.6	0.6	IPF11217	orf19.5830	similar to Saccharomyces cerevisiae Lhs1p chaperone of the	YKL073w
CA3776	0.8	1.2	0.9	1.1	0.6	0.9	IPF10435	orf19.2890	unknown function	YML038c
CA0418	1.1	0.9	0.9	0.9	0.6	0.8	IPF9051.5eo	orf19.2227	unknown function, 5-prime end	YHR166c
CA5857	0.4	1.2	0.4	0.6	0.6	0.7	PCK1	orf19.7514	phosphoenolpyruvate carboxykinase	YKR097w
CA2678	0.9	1.1	1.2	1.0	0.6	0.9	IPF5834	orf19.5491	unknown function	YDR356w
CA3321	1.1	1.2	0.7	0.7	0.6	0.7	IPF6896.5f	orf19.2677	unknown function, 5-prime end	YHR188c
CA2576	1.0	0.8	1.0	1.0	0.6	0.9	IPF7432	orf19.6219	unknown function	no match
CA2223	0.8	1.0	0.7	0.8	0.6	0.8	PLB5	orf19.5102	putative phospholipase B precursor	YOL011w
CA0739	1.5	1.1	0.9	1.0	0.6	0.7				
CA0723	0.7	0.8	1.1	0.9	0.6	0.8	PRI2	orf19.2885	DNA-directed DNA polymerase alpha , 58 KD subunit (DNA p	YKL045w
CA1345	1.0	1.4	0.8	1.1	0.6	0.8	IPF6003	orf19.1490	similar to Saccharomyces cerevisiae Msb2p multicopy suppre	YGR014w
CA0952	0.9	0.9	0.9	1.1	0.6	0.7				
CA3263	1.1	1.1	1.3	0.9	0.6	0.7	UBR12	orf19.2697	ubiquitin-protein ligase by homology	YLR024c
CA2307	1.0	1.1	0.8	0.8	0.6	0.9	IPF18488	orf19.1684	unknown function	no match
CA1220	1.0	1.0	1.0	1.0	0.6	1.0	IPF14985	orf19.4134	unknown function	YDR459c
CA4433	1.0	1.1	0.7	0.9	0.6	0.8	BCK1	orf19.5162	serine/threonine protein kinase of the MEKK family (by homol	YJL095w
CA5162	1.1	1.0	1.0	0.9	0.6	0.9	IPF982	orf19.4600.1	Weakly similar to human dolichol-phosphate-mannose synthe	no match
CA5970	0.8	0.7	1.1	0.8	0.6	0.8	DPB2	orf19.7564	DNA-directed DNA polymerase epsilon, subunit B (by homolc	YPR175w
CA6060	0.9	0.8	1.3	0.9	0.6	0.7	IPF8301	orf19.6008	unknown function	YLL032c
CA4605	1.0	1.0	1.0	1.3	0.6	0.7	IPF6226	orf19.3295	unknown function	YIR010w
CA5019	1.1	0.9	1.3	0.9	0.6	0.7	IPF7557	orf19.6972	similar to Saccharomyces cerevisiae Smi1p involved in beta-'	YGR229c
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5eo	orf19.6654	unknown function	YMR221c
CA2425	1.2	1.0	0.7	1.0	0.6	0.9	IPF9907	orf19.3409	similar to Saccharomyces cerevisiae Sed4 protein of the end	YCR067c
CA1488	1.1	1.2	0.9	0.8	0.6	0.7	IPF17402.5e	orf19.4064	unknown function	YJL062w
CA3779	1.0	1.0	1.1	1.0	0.6	0.8	IPF11221	orf19.5841	unknown function	no match
CA5291	1.3	0.7	1.2	0.8	0.6	0.8	LOS1	orf19.7153	pre-tRNA splicing protein (by homology)	YKL205w
CA2262	1.3	1.0	1.2	1.1	0.6	1.0	IPF6857	orf19.1757	putative transcriptional regulator (unknown function)	YDR253c
CA3002	0.8	0.9	1.1	0.9	0.6	0.7	PIF1	orf19.6133	mitochondrial DNA helicase (by homology)	YML061c
CA1652	0.8	1.0	0.7	1.0	0.6	1.0	RNH11	orf19.5563	Ribonuclease H (by homology)	YMR234w
CA1797	0.9	0.6	0.6	0.8	0.6	0.9	NUM12	orf19.2924	nuclear migration protein (by homology)	YDR150w
CA2936	0.8	0.8	1.4	1.2	0.6	0.7	IPF8326	orf19.3327	similar to Saccharomyces cerevisiae Rnc1p endo-exonucleas	YKR056w
CA2521	0.6	0.9	1.2	1.3	0.6	0.9	IPF4317	orf19.5518	unknown function	no match
CA5919	0.8	0.9	1.4	0.9	0.6	0.9	IPF8926.3	orf19.6786	unknown function, 3-prime end	no match
CA3017	1.6	1.3	1.2	1.0	0.6	0.8	IPF10021	orf19.3912	unknown function	YER040w
CA3714	1.3	0.9	0.9	0.9	0.6	0.7	IPF16223	orf19.4163	unknown function	YGR198w
CA5960	0.9	0.8	0.8	0.8	0.6	0.7	PMT5	orf19.7549	protein mannosyltransferase (by homology)	YDL095w
CA2362	1.3	1.0	1.1	1.1	0.6	0.7	IPF10595	orf19.1287	unknown function	no match
CA4697	0.3	0.4	0.8	0.8	0.6	0.8	HTB1	orf19.6925	Histone H2B (by homology)	YDR224c
CA4250	0.7	1.0	0.5	0.9	0.6	1.5	IPF4292	orf19.539	bleomycin Hydrolase	YNL239w
CA5938	0.7	0.9	0.9	1.1	0.6	0.7	IPF3481	orf19.6759	unknown function	YGL197w
CA6062	1.5	1.3	3.0	1.5	0.6	0.8	IPF8307	orf19.6005	putative permease (by homology)	YDR536w
CA5356	0.8	1.0	1.3	1.1	0.6	0.8	IRR1.5f	orf19.7233	cohesin complex subunit, 5-prime end (by homology)	YIL026c
CA1097	1.2	0.8	1.1	0.9	0.6	1.1	IPF7575	orf19.4365	putative endo-exonuclease (by homology)	YKR056w
CA2179	1.2	1.4	0.7	0.9	0.6	0.9	FAB1	orf19.1513	phosphatidylinositol 3-phosphate 5-kinase (by homology)	YFR019w
CA4879	1.0	1.0	1.0	1.0	0.6	0.7	IPF1660	orf19.6566	unknown function	YOR365c
CA0186	0.2	0.7	0.7	0.7	0.6	0.7	PLB4.3f	orf19.1443	phospholipase, 3-prime end (by homology)	YOL011w
CA0861	0.7	0.9	0.9	1.0	0.6	0.8	CRK1.3f	orf19.3523	Protein kinase, 3-prime end	no match
CA4107	1.0	1.1	1.3	0.9	0.6	0.8	IPF3970	orf19.671	unknown function	YLR177w
CA2228	1.1	1.3	0.8	0.8	0.6	0.9	SCT12	orf19.5815	Suppresses a choline-transport mutant	YBL011w
CA5363	0.7	1.4	0.9	1.2	0.6	0.7	NCR1	orf19.7242	Polytopic membrane protein involved in sterol homeostasis a	YPL006w
CA2505	0.6	0.7	1.2	1.0	0.6	0.7	IPF6796	orf19.5595	unknown function	YBR130c
CA0178	1.1	0.9	1.0	1.0	0.6	0.8				
CA0151	1.1	1.0	0.9	1.0	0.6	1.0	IPF15923.5e	orf19.177	unknown function, 5-prime end	YBR200w
CA3687	1.1	1.1	1.2	1.0	0.6	0.9	IPF4889	orf19.6264	unknown function	YLR071c
CA6088	1.1	1.1	0.9	1.0	0.6	0.8	HPR5	orf19.5970	ATP-dependent DNA Helicase (by homology)	YJL092w
CA4336	0.9	1.1	1.8	1.5	0.6	0.9	DDR48	orf19.4082	stress protein (by homology)	YMR173w
CA4564	1.0	0.9	0.5	0.5	0.6	0.8	IPF6572	orf19.6874	unknown function	YMR213w
CA5594	0.5	1.3	0.8	1.1	0.6	1.1	IPF19814	orf19.7106	folate hydrolase (by homology)	YJR126c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]

Species (Stress ()* Systemat	Ca HS+ Norn	Cd HS+ Norn	Ca OS+ Norn	Cd OS+ Norn	Ca XS+ Norn	Cd XS+ Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5461	1.0	1.3	1.0	0.9	0.6	0.9	GSL23.5f	orf19.3269	1,3-beta-D-glucan synthase subunit, 5-prime end	YLR342w
CA4439	1.3	0.7	0.9	1.1	0.6	0.8	IPF13865	orf19.5156	unknown function	YJL097w
CA3529	1.0	0.9	1.0	0.8	0.6	0.8	IPF9929	orf19.985	unknown function	YEL043w
CA1578	1.0	0.7	0.8	1.0	0.6	0.8	NUM11.5eoc	orf19.4715	nuclear migration protein (by homology)	YDR150w
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA0329	1.0	0.8	0.9	1.0	0.6	0.8	IMG2	orf19.3777	Required for Integrity of Mitochondrial Genome (by homology	YCR071c
CA2883	1.3	0.9	0.7	0.8	0.6	0.9	IPF3790	orf19.5852	unknown function	YML103c
CA3431	1.5	1.3	0.8	1.0	0.6	0.7	FUN9	orf19.586	Protein involved in vesicular transport between the endoplasr	YAL042w
CA1872	1.2	1.0	0.7	0.9	0.6	0.8	IPF6700	orf19.2459	unknown function	no match
CA5686	0.9	0.7	1.2	1.1	0.6	0.8	IPF3329	orf19.7388	similar to Saccharomyces cerevisiae Pbs2p tyrosine protein k	YJL128c
CA2786	1.1	0.9	0.8	0.9	0.6	0.7	KRE5	orf19.290	UDP-glucose:glycoprotein glucosyltransferase,(by homology)	YOR336w
CA4722	1.2	1.1	0.7	1.0	0.6	0.8	SAC1	orf19.4865	integral membrane protein localizing to the ER and Golgi (by	YKL212w
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA0619	1.3	0.9	0.8	0.9	0.6	0.9	IPF18924	orf19.3146	unknown function	no match
CA1182	1.0	0.9	1.1	1.0	0.6	1.0	IPF19724	orf19.801	similar to Saccharomyces cerevisiae Tbf1ptelomere repeat-bi	YPL128c
CA4985	1.6	1.0	0.9	0.9	0.6	0.8	IPF2050	orf19.5265	similar to Saccharomyces cerevisiae Kip1p kinesin-related pr	YBL063w
CA1492	2.3	1.5	1.2	1.2	0.6	1.1	IPF168	orf19.3226	unknown function	YDL046w
CA2511	1.0	1.1	0.9	0.9	0.6	0.8	IPF1474	orf19.306	myosin-like protein	YDL058w
CA3069	0.8	0.7	1.9	2.1	0.6	0.7	IPF6117	orf19.4805	unknown function	YMR266w
CA5900	1.0	1.0	0.9	1.0	0.6	1.0	IPF2379	orf19.6806	unknown function	no match
CA0765	0.9	0.8	0.8	0.9	0.6	0.9	IPF9040	orf19.2236	similar to Saccharomyces cerevisiae Fhl1p transcriptional act	YPR104c
CA3414	1.1	0.8	1.2	1.1	0.6	1.0	IPF9240	orf19.6141	probable permease	YHR094c
CA3635	0.7	1.1	0.6	1.0	0.6	1.0	IFA20	orf19.5139	unknown function	YJL005w
CA4877	1.2	1.6	1.0	0.8	0.6	0.7	IPF1667	orf19.6563	unknown function	YJR054w
CA0789	1.2	1.0	1.1	0.9	0.6	0.7	ESP1	orf19.3356	Required for sister chromatid separation (by homology)	YGR098c
CA1284	0.9	1.1	1.0	1.0	0.6	1.0	IPF10168	orf19.643	unknown function	YJR089w
CA5986	1.0	0.9	0.6	1.0	0.6	0.7	INO1	orf19.7585	myo-inositol-1-phosphate synthase	YJL153c
CA4415	0.9	1.0	1.1	1.1	0.6	0.8				
CA2194	1.8	1.3	0.8	0.8	0.6	0.7	RGR1	orf19.4348	DNA-directed RNA polymerase II (by homology)	YLR071c
CA4698	1.1	1.4	0.7	0.9	0.6	0.7	CDC25	orf19.6926	cell division cycle protein	YLR310c
CA0928	0.5	0.8	0.8	1.0	0.6	0.9	IPF19891	orf19.557	unknown function	no match
CA3066	0.8	0.5	1.1	1.0	0.6	0.8	IPF15813	orf19.4281	unknown function	YLR223c
CA6112	1.0	1.1	0.8	1.2	0.6	0.8	IPF97	orf19.5941	unknown function	YML067c
CA6164	0.9	0.9	0.9	0.9	0.6	0.8	SNF5.5f	orf19.5872	Component of SWI/SNF transcription activator complex, 5-pri	no match
CA1533	1.1	1.1	1.2	0.9	0.6	1.0	IPF9510	orf19.1215	unknown function	no match
CA2365	1.3	0.8	1.4	1.1	0.6	0.9	CKS1	orf19.1282	cyclin-dependent kinases regulatory subunit (by homology)	YBR135w
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA2792	1.1	1.0	0.9	1.0	0.6	1.2	TRK1.3f	orf19.602	Potassium transporter, 3-prime end	YKR050w
CA5436	1.0	1.0	1.0	0.9	0.6	0.8	CTF18	orf19.3239	chromosome transmission in mitosis and maintenance of telo	YMR078c
CA2116	1.0	0.7	0.6	1.0	0.6	0.7	SNG4	orf19.1332	Drug transporter (by homology)	YJR015w
CA2797	1.1	1.0	1.2	0.9	0.6	0.8	IPF8404	orf19.1720	putative helicase (by homology)	YFR038w
CA5346	0.8	0.9	1.1	0.8	0.6	0.9	IPF867	orf19.7221	unknown function	YKR029c
CA5508	0.7	0.8	0.8	0.9	0.6	0.7	IPF745	orf19.5352	unknown function	YDR438w
CA0255	1.0	1.2	0.9	0.9	0.6	0.8	IPF16558.3e	orf19.735	putative transcription initiation factor, 3-prime end (by homolc	YGR274c
CA1227	1.1	0.5	1.3	0.9	0.6	0.8	IPF16082	orf19.4160	unknown function	YDL104c
CA2500	1.1	1.0	0.8	0.9	0.6	1.0	FIG4	orf19.5586	suppressor of sac1 mutation (by homology)	YNL325c
CA5415	1.1	1.0	1.0	0.9	0.6	0.8	SMC4	orf19.964	Stable Maintenance of Chromosomes (by homology)	YLR086w
CA2136	1.2	1.1	0.9	0.9	0.6	0.8	VPS33	orf19.5214	VACUOLAR PROTEIN SORTING (by homology)	YLR396c
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4840	1.0	1.0	2.1	1.1	0.6	1.0	IPF1235	orf19.2054	unknown function	YDL020c
CA0304	1.1	1.0	1.4	1.1	0.6	1.2	IPF12829	orf19.721	unknown function	YLL035w
CA3487	0.7	0.9	0.8	0.9	0.6	0.9	IPF3203	orf19.3569	unknown function	YLR407w
CA1205	1.0	0.6	1.0	0.9	0.6	0.7	SSK2.3f	orf19.3776	MAP kinase kinase kinase of the high osmolarity signal transi	YNR031c
CA5817	1.1	1.0	1.6	1.0	0.6	0.9	IPF2511	orf19.7468	unknown function	YER064c
CA0077	1.2	0.9	1.3	1.0	0.6	0.8				
CA1444	0.8	0.8	1.4	1.1	0.6	0.7	KTR2	orf19.4494	mannosyltransferase (by homology)	YKR061w
CA2723	0.9	1.0	0.7	1.0	0.6	0.9	IPF4805	orf19.3345	unknown Function	YDR409w
CA2297	1.1	0.9	1.0	0.9	0.6	0.8	ERG4	orf19.5379	sterol C-24 reductase (by homology)	YGL012w
CA4440	1.1	0.8	0.7	0.8	0.6	0.7	IPF13864	orf19.5155	similar to Saccharomyces cerevisiae Chs6p chitin biosynthes	YJL099w
CA5354	0.3	0.4	1.0	1.2	0.6	0.7	FTR2	orf19.7231	high affinity iron permease	YER145c
CA0752	0.3	1.4	0.6	0.5	0.6	1.3	MNN22	orf19.3803	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA2989	0.6	1.0	0.7	0.9	0.6	1.0				
CA3124	0.9	0.9	1.1	1.0	0.6	0.8	IPF5353	orf19.3003	unknown function,	YML072c
CA5293	1.5	1.1	0.9	0.9	0.6	1.0	FAA24	orf19.7156	Long-chain-fatty-acid--CoA ligase (by homology)	YER015w
CA4296	1.1	0.9	1.2	0.9	0.6	0.8	IPF2605	orf19.6693	unknown function	YOL098c
CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal asse	YKL197c
CA0450	0.7	0.9	0.8	1.1	0.6	0.9	IPF9353	orf19.2378	unknown function	YMR123w
CA2882	1.3	0.9	1.2	0.8	0.6	0.8	STE13	orf19.5851	type IV dipeptidyl aminopeptidase (by homology)	YOR219c
CA4650	0.7	0.7	0.9	0.8	0.6	0.7	ISW1	orf19.4437	ATPase component of a four subunit chromatin remodeling c	YBR245c
CA6140	0.7	0.7	1.6	1.2	0.6	1.2	IPF1882	orf19.5905	unknown function Unknown function	YBL028c
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA3308	0.6	0.8	2.2	1.0	0.6	1.0	PET127.5f	orf19.2309	component of mitochondrial translation (by homology)	YOR017w
CA3675	1.2	1.0	1.0	0.9	0.6	0.9	IPF19529.3f	orf19.6453	unknown function, 3-prime end	no match
CA5571	1.0	1.0	0.9	0.9	0.6	1.1	IPF2001	orf19.7337	unknown function	no match
CA2137	1.0	0.9	0.8	0.8	0.6	0.9	ARP9	orf19.2507	actin-related protein (by homology)	YMR033w
CA2898	0.5	0.6	2.0	0.9	0.6	0.8	IPF15646	orf19.3481	putative ATP-dependent RNA helicase (by homology)	YGL064c
CA4501	0.5	1.3	0.1	0.1	0.6	0.9	QDR1	orf19.508	putative antibiotic resistance proteins (by homology)	YIL120w
CA2033	1.1	0.9	1.1	1.0	0.6	0.8	SEC27	orf19.3467	coatomer complex beta chain (beta -cop) of secretory pathwa	YGL137w
CA4116	1.1	0.6	1.3	1.0	0.6	0.9	IDI1	orf19.2775	isopentenyl-diphosphate delta-isomerase (by homology) Lipic	YPL117c
CA1423	1.0	1.2	1.0	0.9	0.6	0.8	IPF14247	orf19.3799	unknown function	YDR233c
CA4367	0.7	0.8	0.8	1.1	0.6	0.7	MNN10	orf19.5658	galactosyltransferase (by homology)	YDR245w
CA0634	1.1	1.0	1.2	1.0	0.6	0.9	IPF16267	orf19.1772	unknown function	YER077c
CA5228	0.8	0.9	1.7	1.0	0.6	0.8	RTF1.3f	orf19.7047	Regulates DNA binding properties of TBP, 3-prime end (by h	YGL244w
CA2269	1.2	1.2	1.2	1.3	0.6	0.7	YOR100	orf19.2599	Putative mitochondrial carrier protein	YOR100c
CA4170	1.0	1.2	1.0	1.0	0.6	0.7	IPF7784	orf19.2963	unknown function	YDL042c
CA2643	0.8	0.9	1.0	0.9	0.6	0.8	HSL1	orf19.4308	Ser/thr protein kinase that interacts genetically with histone m	YKL101w
CA2988	1.0	0.9	0.9	1.0	0.6	0.8	SIN3	orf19.6010.3	Histone deacetylase by homology	YOL004w
CA5665	0.9	0.7	1.4	0.9	0.6	0.8	UBP1	orf19.7367	Ubiquitin-specific protease (by homology)	YDL122w

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA1795	1.3	1.1	1.0	0.9	0.6	0.9	IPF11261	orf19.5209	unknown function	YNL041c
CA4521	0.9	0.9	1.2	0.8	0.6	0.9	MRPL40	orf19.484	Putative mitochondrial ribosomal protein (by homology)	YPL173w
CA4859	1.0	0.8	1.0	1.0	0.6	0.8	IPF15927.5f	orf19.3833	similar to Saccharomyces cerevisiae Tfc3p transcription initia	YAL001c
CA4322	1.5	1.1	1.1	1.0	0.6	0.7	IPF2097	orf19.4097	unknown function	YML081w
CA3362	1.4	1.2	0.8	0.8	0.6	0.8	IPF9789	orf19.1933	unknown function	YDR479c
CA4680	1.4	1.3	1.1	1.3	0.6	0.9	AMD1	orf19.891	AMP deaminase (by homology)	YML035c
CA2105	0.8	1.0	1.0	1.0	0.6	0.8	IPF10711	orf19.3694	unknown function	YOR191w
CA2515	0.8	1.0	1.6	0.9	0.6	0.8	IPF19759	orf19.5510	Unknown Function	YGL133w
CA2578	0.4	0.5	1.1	0.9	0.6	0.9	MMD1	orf19.6220.3	Maintenance of mitochondrial DNA (by homology)	YIL051c
CA2545	1.0	0.8	1.7	1.3	0.6	1.1	RRP9	orf19.2830	U3 small nucleolar ribonucleoprotein-associated protein invol	YPR137w
CA2884	1.3	0.8	0.7	0.9	0.6	0.8	IPF7201	orf19.2476	similar to Saccharomyces cerevisiae Ecm5p involved in cell v	YMR176w
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)	YLR409c
CA2510	1.2	1.0	0.8	0.9	0.6	0.8	IPF1472	orf19.305	unknown function	YHL035c
CA2636	1.0	1.0	0.8	0.9	0.6	0.8	MSW1	orf19.4299	Mitochondrial tryptophanyl-tRNA synthetase (by homology)	YDR268w
CA0983	1.0	1.2	1.0	0.9	0.6	0.9	CBR1	orf19.1801	Cytochrome-b5 reductase (by homology)	YIL043c
CA2394	1.4	1.0	1.3	1.0	0.6	0.8	IPF6424	orf19.3535	unknown function	YIL117c
CA1632	1.2	0.8	1.0	0.8	0.6	0.8	IPF10181	orf19.3938	similar to Saccharomyces cerevisiae Rsm26p protein of the s	YJR101w
CA6014	1.2	1.0	1.5	1.1	0.6	1.1	TRS31	orf19.7615	targeting complex (TRAPP) component involved in ER to Gol	YDR472w
CA5473	1.1	1.1	1.1	0.9	0.6	0.8	IPF16947	orf19.3286	unknown function	YDR221w
CA0645	1.0	1.0	0.9	1.0	0.6	0.8				
CA3951	0.9	1.1	1.2	1.1	0.6	0.9	VAC7.3	orf19.1409	Vacuolar protein, 3-prime end (by homology)	YNL054w
CA3240	0.7	0.6	1.4	1.1	0.6	0.8	IPF10559	orf19.4683	myosin-like protein (by homology)	YKR095w
CA3654	1.1	0.8	1.3	1.3	0.6	0.8	IPF7452	orf19.2045	unknown function	YOR311c
CA4971	1.1	1.1	0.8	0.9	0.6	0.9	IPF4697	orf19.5281	similar to Saccharomyces cerevisiae Scp160p required for m	YJL080c
CA1200	0.7	0.9	0.7	0.8	0.6	0.8	IPF10223	orf19.4867	putative serine/threonine kinase	YJL187c
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA4815	1.0	1.0	0.8	1.1	0.6	0.7	CDH1	orf19.2084	Substrate-specific activator of APC-dependent proteolysis (b	YGL003c
CA2689	1.0	1.1	1.0	0.9	0.6	1.0	IFU2	orf19.2582	Unknown function	YPL009c
CA2835	1.3	1.0	0.8	0.7	0.6	1.0	IPF12091	orf19.4787	Unknown function	YNL064c
CA3600	0.9	1.0	0.8	0.8	0.6	0.7	SPC3	orf19.4930	signal peptidase subunit (by homology)	YLR066w
CA1832	0.9	1.0	0.8	1.0	0.6	1.1	IPF17727	orf19.5190	unknown function	YHR023w
CA3256	1.5	1.4	1.2	1.1	0.6	0.9	IPF4730	orf19.3744	unknown Function	YOR112w
CA4270	0.5	0.3	1.0	0.9	0.6	0.7	NUP2	orf19.6665	Nuclear pore protein (by homology)	YLR335w
CA3418	1.3	0.9	1.1	1.2	0.6	0.9	IPF12777	orf19.6137	unknown function	YGL078c
CA3188	0.9	1.0	1.1	1.0	0.6	0.7	IPF11610	orf19.2146	similar to Saccharomyces cerevisiae Hat2 subunit of the majc	YEL056w
CA4136	1.5	1.0	0.9	0.9	0.7	0.9	RET2	orf19.4236	Coatomer complex delta chain (by homology)	YFR051c
CA2728	0.9	1.2	1.3	1.4	0.7	0.9	IPF10322	orf19.2117	putative mitochondrial carrier protein (by homology)	YHR002w
CA5206	1.1	1.1	0.7	0.6	0.7	1.0	GPH1	orf19.7021	Glycogen phosphorylase (by homology)	YPR160w
CA1809	1.0	1.0	0.9	1.0	0.7	1.1	IPF6325	orf19.1116	unknown function	no match
CA5090	0.7	0.8	1.2	1.2	0.7	0.7	IFG4	orf19.3065	probable d-amino acid oxidase (by homology)	no match
CA4321	1.3	1.0	1.2	1.1	0.7	0.8	KAR3.3	orf19.4100	Kinesin-related protein, 3-prime end	YPR141c
CA1883	0.8	1.5	0.9	1.0	0.7	0.7	IPF5479	orf19.2209	unknown function	YOR088w
CA3283	0.9	0.9	0.8	1.1	0.7	0.9	IPF6274	orf19.6316	unknown function	YMR221c
CA2647	1.0	0.8	1.0	1.2	0.7	0.7	IPF13088	orf19.1186	unknown function	YHR088w
CA4226	0.6	0.6	1.3	0.7	0.7	0.8	IPF8752	orf19.828	similar to Saccharomyces cerevisiae Mrpl24p ribosomal prote	YMR193w
CA5101	0.7	0.5	0.9	1.0	0.7	0.7	LCB1	orf19.6438	Serine C-palmitoyltransferase subunit (by homology)	YMR296c
CA0108	1.1	0.8	1.2	1.1	0.7	0.8	HIK1	orf19.5181	histidine kinase	YIL147c
CA3008	1.2	1.1	1.3	1.1	0.7	0.9	IPF12147	orf19.6233	oxidoreductase, acting on CH2 groups, NAD or NADP as acc	YNL181w
CA3211	3.1	1.1	2.2	1.2	0.7	1.0	IPF19977	orf19.6192	unknown function	YGR175c
CA2216	0.7	0.9	1.0	1.0	0.7	1.3	IPF6235	orf19.5372	Candida albicans Tca2 retrotransposon	no match
CA2098	1.3	0.8	0.8	1.0	0.7	0.9	IPF11487	orf19.2387	unknown function	YMR098c
CA4770	0.8	0.9	0.9	1.0	0.7	0.8	IPF9382.3	orf19.4002	similar to Saccharomyces cerevisiae Dun1p protein kinase (b	YDL101c
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA1538	1.0	0.9	1.3	1.0	0.7	0.9				
CA1260	1.7	1.0	0.7	0.9	0.7	0.8	IPF3170	orf19.3166	unknown function	YDR141c
CA5823	0.8	0.9	1.1	0.8	0.7	0.8	COQ1	orf19.7478	Hexaprenyl pyrophosphate synthetase (by homology)	YBR003w
CA3223	1.0	1.0	1.2	0.9	0.7	0.8	SRP102	orf19.6284	Signal recognition particle receptor (by homology)	YKL154w
CA3927	1.0	0.7	3.4	1.3	0.7	0.8	DIP2	orf19.5106	beta transducin	YLR129w
CA3509	1.0	1.2	1.0	1.0	0.7	1.1	PRP6	orf19.6356	snRNP(U4/U6)-associated splicing factor (by homology)	YBR055c
CA1702	1.4	0.7	1.6	1.0	0.7	0.9	HEL1	orf19.702	DNA helicase I (by homology)	YER176w
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA4051	1.0	0.9	0.8	1.0	0.7	1.0	IPF10231.5f	orf19.426	unkown function, 5-prime end	YPL122c
CA5117	1.0	1.0	1.1	0.9	0.7	0.8	IPF1323	orf19.6414	unknown function	no match
CA2562	1.0	1.5	0.8	1.3	0.7	0.8	IPF19953	orf19.5642	unknown function	no match
CA4418	0.5	0.6	0.8	1.0	0.7	0.8	ERG5	orf19.5178	C-22 sterol desaturase by homology	YMR015c
CA1851	0.8	1.0	0.9	1.0	0.7	0.9	IPF14629	orf19.642	Cell cycle protein, interacts with Sit4 (by homology)	YFR040w
CA2006	1.1	1.0	0.7	0.8	0.7	0.7	IPF11801	orf19.2798	unknown function	YDR332w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA0579	1.1	0.9	0.9	0.9	0.7	0.9	IPF3184	orf19.3559	unknown function	YGR165w
CA3488	0.8	1.1	0.9	1.0	0.7	0.7	IPF3198	orf19.3568	unknown function	YDL076c
CA4663	1.6	1.4	1.6	1.1	0.7	0.8	IPF6554	orf19.4450	unknown function	YJL103c
CA4435	1.1	0.6	1.3	0.9	0.7	0.7	IPF5567	orf19.5160	phosphatase associated protein by homology	YKR028w
CA4495	0.6	1.1	0.9	0.8	0.7	0.7	IPF4059	orf19.1865	aldehyde dehydrogenase (by homology)	YHR039c
CA4131	1.4	1.0	1.1	1.0	0.7	1.0	IPF6886.3f	orf19.4243	unknown function, 3-prime end	YKL090w
CA2383	0.6	1.3	0.6	1.0	0.7	1.2	IPF18474	orf19.2222.2	unknown function	no match
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA3775	1.1	0.7	1.1	0.9	0.7	0.9	AFG1	orf19.2891	ATPase family gene (by homology)	YEL052w
CA4499	1.1	1.1	1.0	1.0	0.7	1.0	IPF11316	orf19.511	unknown function	YNL129w
CA2991	1.0	0.9	1.0	0.9	0.7	0.9	IPF5088	orf19.6013	unknown function	YMR233w
CA0898	1.0	0.7	0.9	1.0	0.7	0.9	SSH1.3f	orf19.412	involved in co-translational pathway of protein transport, 3-pri	YBR283c
CA4043	1.3	0.9	1.8	2.0	0.7	1.0	IPF5291	orf19.3674	UDP-glucose 4-epimerase (by homology)	YBR019c
CA1353	0.2	0.3	0.4	0.5	0.7	1.0	ERG1	orf19.406	squalene epoxidase	YGR175c
CA0851	1.4	0.9	0.9	1.1	0.7	1.0	IPF16670	orf19.1746	unknown function	YOR242c
CA2388	1.1	0.7	1.3	1.1	0.7	0.9	MCM6	orf19.2611	component of MCM initiator complex involved in DNA replicat	YGL201c
CA4729	1.1	1.1	1.2	1.1	0.7	0.7	VPS41.5f	orf19.4858	required for the vacuolar assembly, 5-prime end (by homolog	YDR080w
CA0041	1.1	0.9	1.0	1.1	0.7	0.9	IPF10360	orf19.3804	unknown function	YMR134w
CA2407	0.8	0.8	0.8	1.2	0.7	0.7	ECM14	orf19.299	carboxypeptidase involved in cell wall biogenesis and archite	YHR132c
CA5792	1.1	1.0	1.3	1.0	0.7	0.9	IPF4195	orf19.5441	similar to Saccharomyces cerevisiae Ulp2p involved in ubiqui	YIL031w

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]
HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.

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[Cd XS+ down 0.667 10FDR] less [Ca XS+ down 0.667 10FDR]
HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
CA5923	0.7	0.4	1.1	0.7	0.7	0.3	IFQ2	orf19.6782	Unknown function	no match
CA5725	1.2	1.2	1.0	0.6	1.0	0.3	GLG2	orf19.7434	Self-glucosylating initiator of glycogen synthesis (by homolog	YJL137c
CA0855	1.0	1.0	0.6	0.8	0.9	0.4	AMYG1	orf19.4899	glucoamylase	YBR229c
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA0697	0.5	0.7	0.5	0.9	0.7	0.4	VTC4	orf19.3363	putative polyphosphate synthetase (by homology)	YJL012c
CA3710	1.5	1.0	2.4	0.9	0.7	0.4	CHS3.5f	orf19.4938	chitin-UDP acetyl-glucosaminyl transferase 3, 3-prime end	YBR023c
CA0357	0.4	0.6	0.5	0.9	0.8	0.4	FCY22	orf19.333	purine-cytosine permease (by homology)	YER060w
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA3005	1.2	1.0	1.4	1.1	0.7	0.4	CC43	orf19.6237	Cell Division Control -like (by homology)	YLR229c
CA2291	0.8	0.8	0.8	0.7	0.8	0.4	IPF9740	orf19.744	oligo-1,4 -1,4-glucantransferase / amylo-1,6-glucosidase (by	YPR184w
CA1572	1.0	0.9	1.0	1.0	0.7	0.4	POX4	orf19.1652	peroxisomal fatty acyl-CoA oxidase (by homology)	YGL205w
CA0548	0.7	0.9	0.6	0.7	1.2	0.4	PHO87	orf19.2454	Member of the phosphate permease family (by homology)	YCR037c
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA0875	0.3	0.4	1.0	1.0	0.7	0.5	ERG251	orf19.4631	C-4 sterol methyl oxidase (by homology)	YGR060w
CA0010	1.7	0.9	0.9	1.1	1.0	0.5	IPF16036	orf19.150	similar to Saccharomyces cerevisiae Tim17p mitochondrial in	YJL143w
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA5987	0.4	0.7	0.6	0.7	0.7	0.5	CHT3	orf19.7586	chitinase 3 precursor	YLR286c
CA1267	1.9	1.2	0.9	1.0	0.7	0.5	YSY6	orf19.242.2	protein involved in the secretory pathway, by homology	YBR162wa
CA2597	0.4	0.3	0.8	0.7	1.0	0.5	IFQ3	orf19.54	unknown function	no match
CA1926	1.0	1.1	0.8	0.9	1.0	0.5	IPF13407	orf19.753	Unknown function	YNR059w
CA2117	0.9	0.4	0.7	1.2	0.9	0.5	SNG3	orf19.1333	Drug transporter (by homology)	YGR197c
CA5691	0.5	0.5	1.4	1.2	0.7	0.5	DED1	orf19.7392	RNA helicase (by homology)	YOR204w
CA0532	1.0	0.9	0.7	0.7	0.7	0.5	IRE1	orf19.5068	protein kinase (by homology)	YHR079c
CA1688	0.7	0.6	0.3	0.6	0.8	0.5	COX15	orf19.3656	cytochrome oxidase assembly factor (by homology)	YER141w
CA0198	1.1	1.2	1.1	1.0	1.4	0.5	IPF19685	orf19.1658	unknown function	YHR097c
CA0688	1.0	0.8	0.8	0.7	0.9	0.5				
CA0274	1.0	1.4	1.0	0.9	0.9	0.5	IPF15153	orf19.5867	unknown function	YOL105c
CA3296	1.0	0.6	1.1	1.2	0.9	0.5				
CA4382	0.9	0.9	0.6	0.9	0.9	0.5	IPF8576	orf19.5675	similar to Saccharomyces cerevisiae Ris1p DNA helicase (by	YOR191w
CA1259	1.1	1.0	1.0	1.0	0.8	0.5	IPF3174	orf19.3167	Farnesyl transferase (by homology)	YPL172c
CA1930	1.1	0.9	1.3	0.9	0.9	0.5	IPF3906.3f	orf19.758	unknown function, 3-prime end	YPR079w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3f	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA5703	1.1	0.9	0.9	1.0	0.7	0.5	IPF2463	orf19.7403	unknown function	YML020w
CA1660	0.8	0.8	2.2	1.2	0.8	0.5	DAP2	orf19.4322	dipeptidyl aminopeptidase B (by homology)	YHR028c
CA5922	1.3	0.8	1.0	0.8	0.8	0.5	MRS6	orf19.6783	geranylgeranyltransferase regulatory subunit	YOR370c
CA4420	1.3	1.5	1.2	0.9	0.8	0.5	SSM4	orf19.5175	involved in mRNA turnover by homology	YIL030c
CA2018	1.2	1.1	0.9	0.9	0.8	0.6	STE11	orf19.844	ser/thr protein kinase of the MEKK family (by homology)	YLR362w
CA5026	1.2	1.0	1.1	0.8	0.8	0.6	IPF3001	orf19.6980	serine/threonine protein kinase (by homology)	YDL025c
CA2163	0.8	1.2	0.8	1.0	1.0	0.6	IPF11879	orf19.5293	unknown function	no match
CA5873	1.1	1.0	1.0	1.0	0.9	0.6	PGA25	orf19.7542	GPI-anchored cell surface protein (by homology)	no match
CA4857	1.6	0.4	0.8	1.0	0.8	0.6	PHR1	orf19.3829	GPI-anchored pH responsive glycosyl transferase	YMR307w
CA0233	1.4	1.1	1.0	0.9	1.1	0.6	URE2	orf19.155	Nitrogen catabolite repression regulator (by homology)	YNL229c
CA1854	1.0	0.9	0.8	0.9	0.8	0.6	IPF12611	orf19.649	unknown function	YGL228w
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5f	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA2484	1.3	1.0	0.9	0.8	0.7	0.6	IPF9846	orf19.3202	unknown function	YMR247c
CA4721	1.3	0.9	0.8	0.9	0.7	0.6	CPP1	orf19.4866	probable protein-tyrosine phosphatase	YNL053w
CA2261	1.2	0.8	0.9	0.9	1.1	0.6	RAS1	orf19.1760	GTP-binding protein (by homology)	YNL098c
CA4245	1.2	0.7	1.1	1.3	0.7	0.6	PGA21	orf19.532	unknown function	no match
CA4781	0.9	1.1	0.7	0.8	0.7	0.6	IPF3355	orf19.4014	similar to Saccharomyces cerevisiae Cdc1 cell cycle protein i	YDR182w
CA2941	0.6	0.9	1.3	1.1	0.7	0.6	CVB1	orf19.1970	vacuole biogenesis component	no match
CA4876	0.6	1.0	1.0	1.1	1.0	0.6	RNH35	orf19.6562	RNase H (by homology)	YNL072w
CA3141	1.0	1.3	0.5	0.5	1.0	0.6	IPF9211.3f	orf19.3712	unknown function, 3-prime end	no match
CA0213	1.3	0.9	1.2	1.0	0.7	0.6	CDS1	orf19.1279	CDP-diacylglycerol synthase (by homology)	YBR029c
CA4206	0.6	0.8	0.4	0.8	1.2	0.6	IPF9079	orf19.4550	Membrane transporter (by homology)	YCR023c
5124.1	1.1	1.2	0.5	1.0	1.0	0.6				
CA1324	1.1	0.6	1.7	0.9	0.8	0.6	IPF6676	orf19.1308	polytopic membrane protein involved in drug transport (by ho	YBR293w
CA1878	1.0	0.7	1.0	0.9	0.8	0.6	IPF10298	orf19.2272	unknown function	YPL202c
CA2470	1.0	0.8	0.9	1.0	0.7	0.6	SDH12	orf19.2871	Succinate dehydrogenase (by homology)	YKL148c
CA5215	1.1	0.9	1.0	0.8	0.7	0.6	PPS1	orf19.7033	protein tyrosine phosphatase (by homology)	YBR276c
CA2827	1.3	0.8	0.9	0.8	0.7	0.6	RAD2	orf19.1324	structure-specific nuclease of the nucleotide excision repair	YGR258c
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA1265	0.8	0.8	1.3	1.0	1.0	0.6	IPF10510	orf19.240	unknown function	YKR065c
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match
CA0302	0.5	0.9	1.2	1.4	0.7	0.6	MEP3	orf19.1614	low affinity high capacity ammonium permease (by homology	YPR138c
CA0553	1.1	1.1	1.1	1.5	0.7	0.6	IPF16653	orf19.5534	unknown function	YKR088c
CA2530	1.0	1.1	0.9	1.0	0.8	0.6	IPF12782	orf19.3176	unknown function	YNL294c
CA2017	0.9	0.9	0.5	0.7	0.7	0.6	IPF3414	orf19.846	putative serine/threonine protein kinase	YKL171w
CA0273	0.3	0.9	0.3	0.5	1.0	0.6	IPF19066	orf19.1433	unknown function	YOR084w
CA5936	1.5	1.4	0.9	1.1	0.7	0.6	IPF2795	orf19.6763	unknown function	YOR195w
CA1465	1.0	0.7	0.7	0.7	0.8	0.6	RIM11	orf19.791	Ser/thr protein kinase (by homology)	YMR139w
CA4204	1.0	0.8	0.7	1.1	1.8	0.6	HOL4	orf19.4546	member of major facilitator superfamily multidrug-resistance p	YNR055c
CA4717	1.2	1.0	1.4	1.0	0.8	0.6	IPF8663	orf19.6953	Unknown function	YJL083w
CA2199	1.4	1.4	1.0	1.0	0.7	0.6	IPF8113	orf19.2938	unknown function	YLR077w
CA3765	1.1	0.4	0.8	1.0	0.7	0.6	IPF18298.5f	orf19.2904	unknown function, 5-prime end	YNL106c
CA3711	1.0	1.2	1.3	1.1	0.9	0.6	CHS3.3f	orf19.4937	chitin-UDP acetyl-glucosaminyl transferase 3, 5-prime end	YBR023c
CA0578	0.9	0.9	0.6	0.7	1.2	0.6	IPF9605	orf19.3071	similar to Saccharomyces cerevisiae Mih1p M-phase inducing	YMR036c
CA1268	1.2	0.8	1.6	1.0	0.6	0.6	IPF14693	orf19.3159	unknown function	YBL004w
CA5649	1.7	0.8	1.8	1.0	0.9	0.6	CHS4	orf19.7349	Chitin synthase regulatory factor	YBL061c
CA6135	0.3	0.7	0.4	0.8	1.0	0.6	CMK1	orf19.5911	Ca2+/calmodulin-dependent ser/thr protein kinase (by homol	YFR014c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]
HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5154	1.8	1.4	0.8	0.8	0.8	0.6	RGA2	orf19.4593	rho-GTPase activating protein 2 (by homology)	YOR127w
CA2164	0.9	0.9	0.9	0.8	0.7	0.6	AXL2	orf19.5292	similar to saccharomyces cerevisiae Axl2p required for axial p	YIL140w
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA5205	1.3	1.2	0.9	0.9	1.4	0.6	KEX1	orf19.7020	Carboxypeptidase-alpha (by homology)	YGL203c
CA5072	1.2	1.0	0.5	0.8	0.9	0.6	IPF3598	orf19.3047	similar to Saccharomyces cerevisiae Sip3p protein which inte	YNL257c
CA0173	0.8	1.0	1.0	0.9	0.7	0.6	IPF6913	orf19.3793	unknown function	no match
CA1944	0.8	1.0	0.4	0.9	1.2	0.6	IPF10645	orf19.4738	unknown function	YOR154w
CA2040	0.9	1.3	2.7	1.5	0.9	0.6	IPF12946	orf19.4356	unknown function	YDL199c
CA2308	1.2	1.1	0.8	0.9	0.7	0.6	IPF9874.3	orf19.1373	similar to Saccharomyces cerevisiae Inp51p phosphatidylinos	YIL002c
CA5119	0.9	1.0	0.8	1.0	0.8	0.6	IPF1320	orf19.6411	unknown function	YLR386w
CA4843	1.0	1.2	0.7	0.9	0.7	0.6	GYP1	orf19.3811	GTPase activating protein (by homology)	YOR070c
CA4381	0.5	0.8	0.5	0.7	0.8	0.6	PGA10	orf19.5674	unknown function	no match
CA4921	0.8	1.1	1.1	1.1	1.2	0.6	IPF1416	orf19.6061	unknown function	YPL103c
CA5362	0.6	0.8	1.3	1.0	0.9	0.6	IPF836.3	orf19.7239	regulation of G-protein function, (by homology)	YHR146w
CA3518	1.1	1.0	0.9	0.6	0.9	0.6	AMYG2.5f	orf19.999	glucoamylase, 5-prime end	YBR229c
CA2600	1.1	0.4	0.9	0.6	0.8	0.6	IPF11177	orf19.51	similar to Saccharomyces cerevisiae Clu1p translation initiati	YMR012w
CA2563	1.3	1.0	1.0	1.1	1.0	0.6	ECM7	orf19.5643	cell wall biogenesis and architecture (by homology)	YLR443w
CA1615	1.0	1.1	0.9	1.0	0.8	0.6	IPF14540	orf19.3218	putative multidrug protein (by homology)	YJR124c
CA1879	1.0	1.0	2.5	1.0	1.0	0.6	SMF12	orf19.2270	manganese transporter (by homology)	YOL122c
CA0722	2.2	0.8	0.9	0.8	0.7	0.6	ERK1	orf19.2886	mitogen-activated protein kinase (FUS3 homolog)	YGR040w
CA1030	0.7	0.9	1.1	0.9	0.8	0.6	ZRC1.3f	orf19.1537	Zinc and cadmium resistance protein (by homology)	YMR243c
CA2547	1.2	1.0	0.7	0.7	0.9	0.6	IPF14911	orf19.2832	unknown function	YNL152w
CA2653	1.0	1.0	1.0	1.0	0.8	0.6	IPF8472.3eo	orf19.5701	unknown function, 3-prime end	YLR381w
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA5382	0.8	0.6	0.9	0.9	0.9	0.6	IPF5217	orf19.7270	unknown function	no match
CA4702	0.9	1.2	1.2	1.3	0.7	0.6	IPF4213	orf19.6930	unknown function	no match
CA2350	1.3	0.9	0.8	0.9	1.0	0.6	CWH41.5eoc	orf19.4421	ER glucosidase I, 5-prime end (by homology)	YGL027c
CA0481	0.9	1.0	0.8	1.0	0.7	0.6	STE14.3f	orf19.119	farnesyl cystein carboxyl-methyltransferase, 3-prime end (by	YDR410c
CA0087	0.9	1.2	1.9	0.9	1.0	0.6	SMF11	orf19.4690	manganese transporter (by homology)	YOL122c
CA4739	1.2	1.1	0.7	1.1	0.8	0.6	IPF4498	orf19.4845	unknown function	YMR071c
CA0587	0.8	0.9	0.8	0.9	0.9	0.6	PLD1	orf19.1161	phospholipase D	YKR031c
CA2051	1.2	1.0	0.7	1.0	1.0	0.6	PXP5	orf19.5723	acyl-coenzyme A oxidase I precursor by homology to Candida	YGL205w
CA4745	0.5	0.6	0.6	1.0	0.8	0.6	URA1	orf19.4836	dihydroorotate dehydrogenase	no match
CA2424	1.7	0.8	1.0	0.8	0.9	0.7	IPF18468	orf19.4467	unknown function	no match
CA3709	1.8	1.2	0.7	0.8	0.7	0.7	IPF7880	orf19.4939	unknown function	YNL297c
CA5424	1.2	0.7	1.4	1.0	0.7	0.7	IPF1598	orf19.976	unknown function	YDL074c
CA4088	0.8	1.1	0.7	1.0	0.9	0.7	HMO1	orf19.6645	High-mobility protein 1 by homology	YDR174w
CA5794	0.6	0.8	0.6	1.0	0.7	0.7	IPF4191	orf19.5443	unknown function	YBL098w
CA3384	1.1	0.6	0.9	0.8	0.7	0.7	IPF8362	orf19.325	similar to Saccharomyces cerevisiae Cft2p involved in cleava	YLR115w
CA0491	0.9	0.8	1.0	1.1	1.0	0.7				
CA5066	1.0	1.2	0.5	0.7	1.5	0.7	TPS2	orf19.3038	Threalose-6-phosphate phosphatase (by homology)	YDR074w
CA3615	0.9	1.0	1.0	1.1	1.1	0.7	GIT1	orf19.34	glycerophosphoinositol transporter (by homology)	YCR098c
CA5906	0.8	0.8	0.7	0.8	0.8	0.7	IPF5949	orf19.6800	unknown function	YPL188w
CA4068	1.7	1.2	1.2	0.9	0.7	0.7	IPF5922	orf19.446	unknown function	no match
CA2171	1.1	1.0	0.8	1.0	0.7	0.7	PEP1.3eoc	orf19.3767	Vacuolar protein sorting/targeting protein, 3-prime end (by ho	YBL017c
CA3016	1.1	0.7	1.0	0.8	0.7	0.7	IPF10027	orf19.3914	unknown function	YOL139c
CA3147	1.2	1.2	1.3	1.2	0.8	0.7	IPF9803	orf19.6160	unknown function	YMR031c
CA0991	1.3	1.0	1.0	1.1	1.1	0.7	IPF11065	orf19.1393	unknown function	YIL006w
CA3867	0.5	0.8	0.9	1.5	0.9	0.7	PHR2	orf19.6081	pH-regulated protein 2	YMR307w
CA2518	1.1	1.0	0.9	1.0	0.9	0.7	CBP3	orf19.5515	involved in cytochrome-c reductase assembly (by homology)	YPL215w
CA6087	1.3	1.1	0.9	0.8	0.8	0.7	YHV1	orf19.5971	unknown function	YHR151c
CA3023	1.0	1.0	1.0	1.1	1.0	0.7	IPF11508	orf19.3904	unknown function	YLR046c

15A

[Cd XS+ down 0.667 10FDR] and [Ca XS+ down 0.667 10FDR]
HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0375	0.7	1.1	1.3	1.1	0.1	0.5	CRH11	orf19.2706	Probable membrane protein (by homology)	YGR189c
CA5903	0.6	0.7	0.3	0.8	0.1	0.4	IPF5942	orf19.6803	transmembrane sugar transporter (by homology)	YPL244c
CA1570	2.0	0.8	0.3	0.7	0.1	0.5	IPF7617	orf19.1160	unknown function	YHR181w
CA4906	0.1	0.6	0.3	0.6	0.1	0.3	MOB2	orf19.6044	Required for maintenance in ploidy	YFL034cb
CA2024	0.6	1.0	0.8	0.9	0.2	0.6	PGA35	orf19.4910	unknown function	no match
CA1409	1.0	0.9	0.9	0.8	0.2	0.3	SPT16	orf19.2884	general chromatin factor (by homology)	YGL207w
CA4359	0.5	0.2	1.0	1.3	0.2	0.4	IPF6054	orf19.6736	unnown function	YOR205c
CA6054	0.4	0.4	0.5	0.7	0.2	0.6	IPF4952	orf19.7672	unknown function	YDR411c
CA2552	0.5	0.6	1.1	1.1	0.2	0.5	ALG5	orf19.2837	dolichol-P-glucose synthetase (by homology)	YPL227c
CA3879	0.7	0.5	0.7	0.9	0.2	0.3	CDC42	orf19.390	Cell Division Control	YLR229c
CA1207	0.7	0.8	1.3	0.9	0.2	0.5	PPG1	orf19.3774	Phosphoprotein phosphatase PPG catalytic chain (by homolo	YNR032w
CA0380	0.7	0.6	0.5	0.6	0.2	0.3	PGA45	orf19.2451	unknown function	no match
CA5690	0.2	0.9	0.7	0.9	0.2	0.3	OCH1	orf19.7391	Alpha-1,6-mannosyltransferase (by homology)	YGL038c
CA3438	0.8	1.0	1.5	0.7	0.2	0.6	IPF11330	orf19.2987	unknown function	YHR194w
CA2083	1.2	0.6	1.3	0.8	0.2	0.3	IPF3384.5f	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA1211	0.3	0.5	0.8	0.9	0.2	0.6	IPF7031.3f	orf19.131.2	unknown function, 3-prime end	YPR063c
CA0083	0.6	0.9	1.1	0.9	0.2	0.6	PHO84.5eoc	orf19.655	high-affinity inorganic phosphate/H+ symporter by homology	YML123c
CA2866	1.2	1.3	0.9	1.1	0.2	0.4	RHO1	orf19.2843	GTP-binding protein of the rho subfamily of ras-like proteins (	YPR165w
CA4132	1.2	2.4	0.9	1.1	0.3	0.7	STE20	orf19.4242	serine/threonine-specific protein kinase	YHL007c
CA1616	0.9	1.0	1.9	0.8	0.3	0.5	IPF14538	orf19.3219	unknown function	YOR137c
CA0425	0.5	0.3	1.5	1.4	0.3	0.3	PPH21	orf19.1683	protein ser/thr phosphatase PP2A-1 (by homology)	YDL188c
CA0990	0.9	1.0	1.2	0.9	0.3	0.6	IPF11068	orf19.1392	unknown function	YIL005w
CA4025	1.0	0.7	1.8	0.9	0.3	0.3	SCJ1	orf19.3438	Mitochondrial and ER import protein (by homology)	YMR214w
CA5937	1.5	0.8	1.2	1.0	0.3	0.3	IPF2784	orf19.6760	unknown function	YER132c
CA5502	0.9	1.0	0.9	1.0	0.3	0.6	IPF763	orf19.5343	putative transcription factor with a Cys4- zinc finger (by homo	YKL185w
CA6077	0.8	0.6	0.7	1.0	0.3	0.5	IPF16	orf19.5984	unknown function	YOL073c
CA4667	1.0	0.7	1.3	1.3	0.3	0.6	GAP5	orf19.4456	General amino acid permease (by homology)	YKR039w
CA2198	1.2	0.6	1.4	0.8	0.3	0.4	PMM1	orf19.2937	phosphomannomutase	YFL045c
CA2027	1.4	2.0	1.4	2.5	0.3	0.4	MCK1	orf19.3459	ser/thr/tyr protein kinase (by homology)	YNL307c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]
HS+ OS+

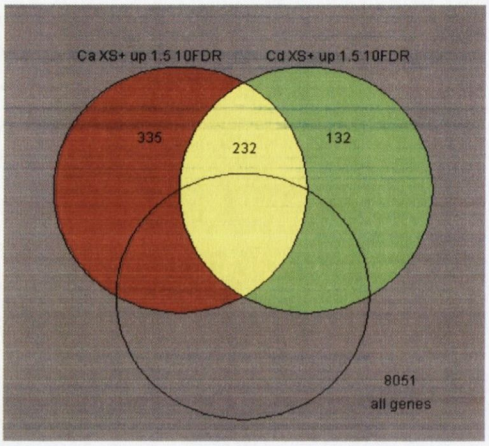
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA1619	1.0	0.6	1.0	1.2	0.3	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)	YPL057c
CA4573	0.3	0.4	0.6	2.3	0.3	0.5	IPF9431	orf19.6884	unknown function	YJL091c
CA2103	0.7	0.9	0.8	0.8	0.3	0.5	ISM1	orf19.2382	isoleucyl-tRNA synthetase (by homology)	YPL040c
CA1645	0.9	1.0	0.9	0.7	0.3	0.5	PMC1	orf19.1727	Ca2+-transporting P-type ATPase (by homology)	YGL006w
CA0704	1.1	0.8	0.9	0.8	0.3	0.5	IPF11806	orf19.2915	similar to Saccharomyces cerevisiae Ynd1p nucleoside diphc	YER005w
CA2969	0.9	0.8	0.8	0.9	0.3	0.6	IPF19772	orf19.5602	unknown function	no match
CA0535	1.0	0.8	0.8	0.9	0.3	0.5	IPF15606	orf19.5065	similar to Saccharomyces cerevisiae Erd1p required for reten	YDR414c
CA2019	0.5	0.6	2.1	1.8	0.3	0.4	IPF3409	orf19.843	unknown function	YLR361c
CA3494	1.2	0.7	0.7	1.1	0.3	0.5	RPB5	orf19.6340	DNA-directed RNA polymerase I, II, III (by homology)	YBR154c
CA1421	0.7	0.3	1.0	1.0	0.3	0.5	MRPL11	orf19.3797	Mitochondrial ribosomal protein (by komology)	YDL202w
CA5265	0.8	0.8	1.6	1.2	0.3	0.6	IPF1792	orf19.4997	unknown function	YER027c
CA5896	0.9	0.7	0.8	0.7	0.3	0.5	TPD3	orf19.6810	Ser/thr protein phosphatase (by homology)	YAL016w
CA3319	0.8	0.7	0.7	0.7	0.3	0.4	DRS25	orf19.2680	Probable ATPase, Potential phospholipid-transporting ATPas	YMR162c
CA2656	1.1	0.9	1.4	1.1	0.3	0.6	NAM2	orf19.5705	mitochondrial leucine--tRNA ligase (by homology)	YLR382c
CA4733	1.1	1.0	0.9	0.9	0.3	0.6	IPF7732	orf19.4853	similar to Saccharomyces cerevisiae Hcm1p transcription fac	YCR065w
CA5927	1.1	0.7	1.2	1.2	0.4	0.5	DRS22	orf19.6778	Membrane-spanning Ca-ATPase (by homology)	YAL026c
CA6053	1.2	1.0	1.0	0.9	0.4	0.5	IPF4949	orf19.7670	unknown function	YNL321w
CA4622	1.1	0.8	1.1	1.0	0.4	0.6	IPF5751	orf19.3314	TRAPP subunit of 20 kDa involved in targeting and fusion of I	YBR254c
CA2994	0.9	0.8	1.0	1.1	0.4	0.5	IPF9116	orf19.6119	unknown function	no match
CA0488	0.3	0.5	1.0	0.9	0.4	0.6	SEC59	orf19.261	Dolichol kinase (by homology)	YMR013c
CA0453	0.9	0.9	1.1	1.0	0.4	0.7	IPF13552	orf19.1300	putative methyltransferase (by homology)	YDR316w
CA0951	0.7	0.9	0.6	0.9	0.4	0.6	MNN6	orf19.1011	putative golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA1530	0.8	0.9	3.3	1.2	0.4	0.4	ALG2.5	orf19.1221	mannosyltransferase, 5-prime end (by homology)	YGL065c
CA5877	0.7	0.4	0.7	0.9	0.4	0.5	IPF12082.3f	orf19.6832	bumetanide-sensitive Na-K-Cl cotransport protein, 3-prime er	YBR235w
CA2438	0.9	0.5	0.7	0.8	0.4	0.5	IPF5505	orf19.2198	unknown function	YAL053w
CA4067	0.7	0.9	2.3	2.0	0.4	0.6	IPF5924	orf19.445	unknown function	YNR040w
CA4872	0.9	0.7	0.7	1.1	0.4	0.5	SEC231	orf19.6558	Component of COPII coat (by homology)	YPR181c
CA5876	0.8	1.0	0.8	0.9	0.4	0.5	IPF12082.5f	orf19.6833	bumetanide-sensitive Na-K-Cl cotransport protein, 5-prime er	YBR235w
CA1504	0.4	0.8	0.6	0.8	0.4	0.4	ARF3	orf19.1702	GTP-binding protein of the ARF family (by homology)	YOR094w
CA2340	1.1	1.1	1.0	1.0	0.4	0.6	MNN5	orf19.2347	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA2820	1.0	1.1	1.0	1.0	0.4	0.5	HOL1	orf19.2991	member of major facilitator superfamily multidrug-resistance p	YNR055c
CA1183	0.8	0.5	0.8	0.7	0.4	0.6	IPF14805	orf19.3782	acetyl-coenzyme A transporter(by homology)	YBR220c
CA2938	0.7	0.7	2.1	1.0	0.4	0.6	IPF8321	orf19.3325	similar to Saccharomyces cerevisiae Glg2p self-glucosylating	YJL137c
CA4119	0.5	0.6	0.9	0.8	0.4	0.5	BEM3	orf19.2771	GTPase-activating protein for Cdc42p and Rho1p (by homolo	YPL115c
CA1406	0.8	1.1	1.0	1.0	0.4	0.6	DOT4	orf19.3370	derepression of telomeric silencing (by homology)	YNL186w
CA4112	0.9	0.9	0.7	1.0	0.4	0.5	BIM1	orf19.676	microtubule-binding protein (by homology)	YER016w
CA5034	0.5	0.9	0.6	1.0	0.4	0.7	OST1	orf19.6988	oligosaccharyltransferase	YJL002c
CA2985	0.5	0.7	0.6	1.0	0.4	0.5	SET1	orf19.6009	Chromatin regulatory protein (by homology)	YHR119w
CA0308	0.9	1.0	0.7	1.0	0.4	0.5	RHK1	orf19.1092	Mannosyltransferase (by homology)	YBL082c
CA1980	0.9	1.0	0.9	1.3	0.4	0.5	YHM1	orf19.685	member of the mitochondrial carrier family (MCF) (by homolo	YDL198c
CA5666	0.2	0.7	0.6	1.2	0.4	0.5	PUB1	orf19.7368	Major polyadenylated RNA-binding protein (by homology)	YNL016w
CA1713	0.2	1.0	0.2	0.7	0.4	0.6	IPF19743	orf19.3332	unknown function	YDL231c
CA0482	0.5	0.7	0.5	0.7	0.4	0.6	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)	no match
CA1039	0.7	0.8	0.8	1.0	0.4	0.7	IPF4012	orf19.2501	Unknown Function	YPL221w
CA4936	0.7	0.6	1.1	0.9	0.4	0.6	IPF8369	orf19.6077	unknown function	YOR161c
CA0503	0.9	0.9	1.0	0.8	0.4	0.6	PMT6	orf19.3802	protein mannosyltransferase	YGR199w
CA4263	1.4	1.0	1.6	1.1	0.4	0.6	IPF2277	orf19.6656	unknown function	YHL016c
CA3878	1.0	0.7	1.3	1.0	0.4	0.6	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA polymerase	YDR213w
CA5024	0.7	0.8	0.8	0.8	0.4	0.6	IPF3009	orf19.6977	similar to Saccharomyces cerevisiae Gpi1p required for N-ac	YGR216c
CA4817	0.7	0.6	1.0	0.4	0.4	0.3	POM152	orf19.2081	Nuclear pore membrane glycoprotein (by homology)	YMR129w
CA5637	0.7	0.7	0.9	1.0	0.4	0.6	IPF472	orf19.7058	unknown Function	YFR048w
CA4314	0.9	0.9	1.4	1.2	0.4	0.6	PMT4	orf19.4109	Mannosyltransferase (by homology)	YJR143c
CA4762	1.4	0.9	1.3	0.9	0.4	0.6	IPF9647	orf19.3994	similar to Saccharomyces cerevisiae Ost3p oligosaccharyltrai	YOR085w
CA1517	0.4	0.6	0.8	0.9	0.4	0.6	IPF11045	orf19.4798	unknown function	YMR212c
CA0605	1.1	0.6	0.7	0.6	0.4	0.4	UTR2	orf19.1671	1,3-1,4-beta-glucanase (by homology)	YEL040w
CA1414	1.1	0.6	0.8	0.6	0.4	0.6	CHO2	orf19.169	phosphatidylethanolamine N-methyltransferase (by homology	YGR157w
CA5083	1.1	1.1	0.6	0.9	0.4	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltra	YMR149w
CA0205	0.9	0.9	0.9	0.8	0.4	0.7	DBF2	orf19.1223	putative ser/thr protein kinase by homology	YGR092w
CA2934	1.0	0.8	0.9	0.8	0.4	0.5	IPF11515	orf19.3329	similar to Saccharomyces cerevisiae Lcb3p sphingoid base-p	YJL134w
CA0832	1.1	1.0	1.6	0.7	0.4	0.5	IPF14225	orf19.1675	unknown function	YDL133w
CA5016	0.9	1.0	1.0	1.1	0.4	0.5	IPF7561	orf19.6968	unknown function	no match
CA0660	1.0	0.8	1.0	1.2	0.4	0.4	IPF16189.5f	orf19.5577	panthotenate kinase, 5-prime end (by homology)	YDR531w
CA5322	0.7	0.8	0.7	1.0	0.4	0.5	PRB1	orf19.7196	Protease B, vacuolar (by homology)	YEL060c
CA0403	0.9	0.9	1.2	0.8	0.4	0.6	PGA51	orf19.1989	unknown function	YKL046c
CA3470	1.2	1.1	1.0	1.1	0.4	0.6	IPF6310	orf19.1666	unknown function	no match
CA2324	0.4	0.3	1.3	1.4	0.4	0.4	CDC46	orf19.5487	cell division control protein (by homology)	YLR274w
CA2032	1.0	1.0	0.7	1.0	0.4	0.3	IPF13112	orf19.3466	unknown function	YGL136c
CA0658	0.7	0.9	0.7	0.7	0.4	0.3	IPF16505	orf19.5575	Unknown function	YPL112c
CA2732	0.6	0.6	2.3	1.2	0.4	0.4	IPF10327	orf19.2113	unknown function	YLR324w
CA1073	1.1	1.0	0.9	0.8	0.4	0.3	PRORS.3f	orf19.2533	prolyl-tRNA synthetase, 3-prime end	YER087w
CA3365	0.9	0.9	1.2	0.8	0.4	0.6	ALG6	orf19.1843	glucosyltransferase (by homology)	YOR002w
CA3318	0.6	0.7	0.8	0.6	0.4	0.4	WBP1	orf19.2298	Oligosaccharyl transferase beta subunit (by homology)	YEL002c
CA1074	1.0	0.9	0.9	0.9	0.4	0.6	PRORS.5f	orf19.2532	prolyl-tRNA synthetase, 5-prime end	YER087w
CA1526	1.0	0.7	0.8	0.8	0.4	0.5	IPF13815	orf19.4553	unknown function	no match
CA3757	1.5	1.0	0.9	1.1	0.4	0.6	MAE1	orf19.3419	mitochondrial malic enzyme (by homology)	YKL029c
CA4728	0.7	0.7	0.9	0.9	0.4	0.5	VPS41.3f	orf19.4859	required for the vacuolar assembly, 3-prime end (by homolog	YDR080w
CA2996	0.7	1.0	1.0	0.9	0.4	0.6	IPF9108	orf19.6124	similar to Saccharomyces cerevisiae Ace2p transcription fact	YLR131c
CA0509	1.1	0.9	2.6	0.8	0.5	0.6	CDC24	orf19.3174	GTP/GDP exchange factor for Cdc42p (by homology)	YAL041w
CA5901	1.5	1.1	1.1	1.1	0.5	0.7	IPF2374	orf19.6805	unknown function	YDR089w
CA3003	1.6	1.2	0.6	0.7	0.5	0.6	IPF15741.5f	orf19.6242	similar to Saccharomyces cerevisiae Cyk3p possibly involved	YCR088w
CA4431	0.8	0.9	1.2	0.9	0.5	0.4	ECM39	orf19.5164	cell wall biogenesis by homology	YNR030w
CA6142	0.8	1.2	0.9	0.9	0.5	0.6	IPF1879	orf19.5903	unknown function	YOR301w
CA2935	0.8	0.9	1.0	1.1	0.5	0.6	IPF11521	orf19.3328	unknown function	YMR172w
CA4428	1.2	1.3	0.6	0.8	0.5	0.6	IFM1	orf19.5167	translation initiation factor 2 by homology	YOL023w
CA1782	1.1	1.1	0.9	1.0	0.5	0.6	PHO84.3eoc	orf19.1172	Inorganic phosphate transport protein, 3-prime end (by homo	YML123c
CA2374	0.4	0.6	0.7	0.9	0.5	0.6	FCY23	orf19.1832	Putative purine-cytosine transport protein	YGL186c
CA1491	0.9	1.1	1.0	1.1	0.5	0.4	IPF166	orf19.3225	unknown function	YCR017c
CA5488	1.2	0.9	0.7	0.7	0.5	0.5	IPF810	orf19.5322	unknown function	YJL178c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]

Species (Ca HS+ OS+ Stress ()*	Ca HS+	Cd HS+	Ca OS+	Cd OS+	Ca XS+	Cd XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4800	1.0	0.8	1.2	1.0	0.5	0.4	PGA4	orf19.4035	putative GPI-anchhored protein related to Phr1, Phr2 and Phi	YOL030w
CA3463	0.2	0.1	0.9	1.0	0.5	0.2	ALG8	orf19.1659	glucosyltransferase (by homology)	YOR067c
CA3625	1.2	0.9	1.1	0.9	0.5	0.6	CYR1.3f	orf19.5151	adenylate cyclase, 3-prime end	YJL005w
CA3467	0.9	0.8	1.7	1.0	0.5	0.5	MNT2	orf19.1663	Alpha-1,2-mannosyltransferase (by homology)	YDR483w
CA4510	1.0	0.8	0.9	0.9	0.5	0.4	IPF8970	orf19.496	similar to Saccharomyces cerevisiae Msh1p DNA mismatch r	YHR120w
CA4574	0.9	1.1	0.8	0.9	0.5	0.6	IPF9430	orf19.6885	similar to Saccharomyces cerevisiae Spo7p meiotic protein (t	YAL009w
CA2299	0.7	0.4	0.6	0.9	0.5	0.5	IPF8222	orf19.5381	unknown function	YGL014w
CA5062	1.2	0.9	1.5	1.0	0.5	0.4	SEC62	orf19.3031	subunit of ER protein-translocation complex (by homology)	YPL094c
CA5652	1.2	1.1	0.7	0.6	0.5	0.6	IPF19815	orf19.7354	longevity-assurance protein (by homology)	YKL008c
CA5029	1.1	0.9	0.7	0.8	0.5	0.6	IPF2997	orf19.6983	unknown function	YDR028c
CA5956	1.1	1.0	1.3	1.1	0.5	0.5	VAN1	orf19.6738	Vanadate resistance protein	YML115c
CA3626	0.6	0.8	0.2	0.3	0.5	0.5				
CA5834	1.0	0.9	1.3	1.0	0.5	0.5	LRG1	orf19.7489	GTPase-activating protein of the rho/rac family (by homology	YDL240w
CA4134	0.9	1.1	1.1	0.8	0.5	0.6	COS162	orf19.4240	involved in manganese homeostasis (by homology)	YCR044c
CA0659	1.3	1.1	0.8	0.8	0.5	0.6	IPF16189.3f	orf19.5576	panthotenate kinase, 3-prime end (by homology)	YDR531w
CA0528	1.0	0.9	0.6	0.7	0.5	0.5	ANP1	orf19.3622	Golgi mannosyltransferase (by homology)	YEL036c
CA1146	1.1	1.0	1.1	0.8	0.5	0.7	CWH8	orf19.3682	putative required protein for full levels of dolichol-linked oligo	YGR036c
CA6061	0.8	0.7	0.9	0.8	0.5	0.6	IPF8302	orf19.6007	unknown function	YJL196c
CA0046	1.4	1.0	1.2	0.8	0.5	0.7	IPF14850	orf19.2452	Hypothetical protein	no match
CA5241	1.0	0.7	1.7	0.8	0.5	0.6	SMF3	orf19.5022	Probable manganese transporter (by homology)	YOL122c
CA0642	0.9	0.9	1.3	0.9	0.5	0.4	ERG25	orf19.3732	C-4 sterol methyl oxidase	YGR060w
CA2188	1.1	1.0	0.9	0.9	0.5	0.6	SSU81	orf19.4772	protein involved in the HOG1 high-osmolarity signal transduc	YER118c
CA3046	0.6	0.9	0.8	1.1	0.5	0.6	IPF7295	orf19.2417	unknown function	YOL034w
CA2724	0.9	1.7	0.8	1.5	0.5	0.4	RPB7	orf19.3347	DNA-directed RNA polymerase II, 19 KD subunit (by homolog	YDR404c
CA2418	0.6	0.8	0.7	0.6	0.5	0.4	MNT4	orf19.4475	putative mannosyltransferase	YBR199w
CA5153	0.7	1.2	1.3	0.9	0.5	0.6	IPF1003	orf19.4592	unknown function	no match
CA6095	0.7	0.8	1.3	1.4	0.5	0.4	SNF3	orf19.5962	High affinity glucose transport protein (by homology)	YDL194w
CA2769	0.9	1.1	1.0	1.1	0.5	0.6	PGA54	orf19.2685	unknown function	no match
CA1499	0.9	1.0	1.0	1.0	0.5	0.6				
CA1798	1.6	1.5	0.8	1.1	0.5	0.6	IPF11448	orf19.2923	unknown function	YMR155w
CA0110	0.9	0.6	1.2	0.9	0.5	0.5	IPF17190	orf19.3869	unknown function	no match
CA3599	1.5	1.3	0.8	0.8	0.5	0.4	IPF19785	orf19.4929	unknown function	YLR067c
CA0964	1.4	1.1	0.8	0.9	0.5	0.6	IPF9141	orf19.6247	similar to Saccharomyces cerevisiae Ctf4p DNA-directed DN/	YPR135w
CA0563	1.3	1.0	1.0	1.0	0.5	0.6	MNN11	orf19.2927	Mannosyltransferase complex component (by homology)	YJL183w
CA5209	1.1	1.1	0.7	0.9	0.5	0.5	MCM1	orf19.7025	Transcription factor of the MADS box (by homology)	YMR043w
CA0300	0.8	0.9	0.9	1.1	0.5	0.7	ERG24	orf19.1598	C-14 sterol reductase (by homology)	YNL280c
CA5953	0.8	0.8	0.9	0.8	0.5	0.6	IPF3506	orf19.6741	unknown function	YLR414c
CA2193	1.0	1.2	0.5	0.8	0.5	0.6	IPF14273	orf19.4347	Probable ser/thr protein kinase (by homology)	YKL116c
CA0199	0.2	0.3	0.5	0.6	0.5	0.5	KAP104	orf19.3556	karyopherin-beta protein (by homology)	YBR017c
CA3397	0.4	0.2	1.1	0.9	0.5	0.4	IPF13618	orf19.3972	unknown function	YMR292w
CA1945	1.0	0.9	0.8	1.3	0.5	0.6	MSS116	orf19.4739	RNA helicase of the DEAD box family (by homology)	YDR194c
CA3619	1.3	1.1	1.3	3.1	0.5	0.6	CDC47	orf19.202	cell division control protein, ,(by homology)	YBR202w
CA3040	0.8	0.8	1.7	0.9	0.5	0.5	IPF7306	orf19.2425	putative permease (by homology)	YBR241c
CA4553	0.2	0.6	0.6	0.9	0.5	0.4	CYB1	orf19.1446	G2/Mitotic-specific cyclin	YPR119w
CA3160	0.8	1.0	1.0	1.3	0.5	0.3	ZRT2	orf19.1585	zinc transport protein (by homology)	YLR130c
CA4983	0.5	0.6	0.8	1.0	0.5	0.6	IPF2053	orf19.5267	unknown function	no match
CA1352	1.5	1.1	1.4	0.9	0.5	0.6	VCX1	orf19.405	Ca2+-transport by homology	YDL128w
CA5423	1.1	1.0	0.8	0.8	0.5	0.6	ROT2	orf19.974	Glucosidase II, catalytic subunit (by homology)	YBR229c
CA5600	1.3	0.8	1.0	0.9	0.5	0.7	IPF559	orf19.7100	unknown function	YJR001w
CA3987	1.4	1.2	0.9	0.7	0.5	0.6	ECM3	orf19.1563	Involved in cell wall biogenesis and architecture (by homolog	YOR092w
CA0349	1.0	0.7	1.1	1.1	0.5	0.6	IPF19026	orf19.1813	unknown function	YAL053w
CA5681	1.1	0.9	1.5	1.1	0.5	0.6	MNN9	orf19.7383	Required for complex N-glycosylation	YPL050c
CA1956	1.3	1.2	0.9	0.8	0.6	0.6	ERG3	orf19.767	C5,6 desaturase	YLR056w
CA5023	0.4	0.8	0.5	0.7	0.6	0.4	IPF7547	orf19.6976	unknown function	YJL163c
CA5236	1.6	1.6	1.2	1.2	0.6	0.6	LCB2	orf19.5027	Palmitoyl transferase (by homology)	YDR062w
CA1628	0.9	0.8	1.2	1.2	0.6	0.5	HMG1	orf19.1031	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (by hom	YLR450w
CA5533	0.8	0.7	0.7	1.1	0.6	0.6	IPF2846	orf19.7293	similar to Saccharomyces cerevisiae Mps1p serine/threonine	YDL028c
CA2473	0.9	0.9	0.9	1.2	0.6	0.5	CBF1	orf19.2876	putative centromere binding factor 1	YJR060w
CA1772	0.9	0.8	0.6	0.7	0.6	0.5	ALG7	orf19.2187	UDP-N-acetylglucosamine-1-phosphate transferase (by homo	YBR243c
CA1831	1.2	0.8	1.1	1.0	0.6	0.7	CHS1	orf19.5188	Chitin synthase (by homology)	YBR038w
CA0197	0.8	0.8	1.3	0.9	0.6	0.5	IPF9787	orf19.1934	similar to Saccharomyces cerevisiae Hst3p silencing protein	YOR025w
CA2079	1.0	1.0	0.9	0.9	0.6	0.5	MNN3	orf19.4874	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA2821	0.7	0.9	0.5	0.9	0.6	0.5				
CA6022	1.0	0.9	1.0	1.0	0.6	0.6	PGA1	orf19.7625	GPI-anchored cell surface protein (by homology)	no match
CA5674	0.8	1.1	1.0	1.0	0.6	0.6	IPF1274	orf19.7377	similar to Saccharomyces cerevisiae Ase1p component of the	YOR058c
CA1351	1.0	1.2	1.3	0.8	0.6	0.7	PCL2	orf19.403	G1/S specific cyclin	YDL127w
CA3372	1.1	1.1	0.8	0.8	0.6	0.6	HHF22	orf19.1854	histone H4 (by homology)	YNL030w
CA1306	0.7	0.9	0.6	0.9	0.6	0.5	CDC14	orf19.4192	protein phosphatase	YFR028c
CA2980	1.6	0.7	0.6	0.9	0.6	0.6	GOG5	orf19.1232	GDP-mannose transporter (by homology)	YGL225w
CA5003	1.1	0.9	1.0	1.0	0.6	0.5	MCD4	orf19.5244	Sporulation protein (by homology)	YKL165c
CA0932	1.3	0.9	0.8	0.8	0.6	0.6	EPT1	orf19.3695	alcohol phosphatidyl transferase (by homology)	YHR123w
CA5839	0.7	0.9	1.0	0.9	0.6	0.6	IPF423	orf19.7494	unknown function	YLR320w
CA5563	1.6	0.8	0.7	0.8	0.6	0.6	PHO88	orf19.7327	Involved in phosphate transport (by homology)	YBR106w
CA1218	1.1	0.7	0.5	0.8	0.6	0.5	CDC20	orf19.122	anaphase promoting complex subunit (by homology)	YGL116w
CA1053	1.8	1.1	0.8	1.0	0.6	0.7	SCW11.3eoc	orf19.3893	glucanase gene family member, 3-prime end (by homology)	YGL028c
CA1350	0.9	0.8	0.8	1.1	0.6	0.5	MCM2	orf19.4354	replication licensing factor (by homology)	YBL023c
CA5645	1.1	0.7	1.2	0.8	0.6	0.6	CYB5	orf19.7049	Cytochrome b5 (by homology)	YNL111c
CA2172	1.5	1.5	1.0	0.9	0.6	0.6	IPF15377	orf19.3765	probable membrane protein involved in bipolar budding (by h	YLR084c
CA3604	0.8	1.0	1.0	1.0	0.6	0.6	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)	no match
CA5482	0.8	0.9	1.4	1.0	0.6	0.6	IFV4.3f	orf19.5315	unknown function	no match
CA2195	0.4	0.2	0.4	0.6	0.6	0.5	IPF18517	orf19.4349	unknown function	YOL070c
CA1077	1.0	1.1	0.8	0.9	0.6	0.6	IPF13694	orf19.2238	unknown function	YAL024c
CA0686	0.9	0.8	1.0	0.9	0.6	0.6	IPF162	orf19.3222	sulphate transporter (by homology)	YGR125w
CA2042	0.9	0.8	0.6	0.7	0.6	0.6				
CA5344	1.1	0.7	0.8	1.0	0.6	0.6	PRY2	orf19.7218	putative pathogen related proteins (by homology)	YJL079c
CA0883	0.7	0.6	1.6	1.5	0.6	0.6	SUN41	orf19.3642	Putative cell wall beta-glucosidase (by homology)	YIL123w
CA1921	0.9	1.0	0.8	0.9	0.6	0.5	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA0969	0.9	1.5	0.9	0.9	0.6	0.7	IPF9132	orf19.5541	unknown function	YPL184c

[Ca XS+ down 0.667 10FDR] less [Cd XS+ down 0.667 10FDR]

Species (Stress ()*	Ca HS+	Cd HS+	Ca OS+	Cd OS+	Ca XS+	Cd XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5918	1.1	0.7	0.9	1.4	0.6	0.3	ERV14	orf19.6787	membrane protein	YGL054c
CA4373	1.1	0.9	2.2	1.6	0.6	0.7	IPF5287	orf19.5664	signal transduction protein (by homology)	YMR032w
CA1745	0.6	0.6	1.0	0.9	0.6	0.6	IPF10888	orf19.5051	unknown function	no match
CA0822	1.0	0.7	1.1	1.0	0.6	0.6	EXG1	orf19.2990	glucan 1,3-beta-glucosidase	YLR300w
CA0415	1.6	1.4	1.0	0.9	0.6	0.7	FRP3	orf19.1224	member of the FRP family of proteins related to Yarrowia lipo	YCR010c
CA4880	1.0	0.9	0.8	0.8	0.6	0.6	RHC18	orf19.6568	Recombination repair protein (by homology)	YLR383w
CA0689	1.2	1.2	0.9	1.2	0.6	0.5	IPF14119	orf19.4688	unknown function	no match
CA6128	1.7	0.8	1.1	0.6	0.6	0.6	IPF152	orf19.5919	unknown function	YOR129c
CA5537	1.1	1.0	0.9	1.0	0.6	0.6	CHS2	orf19.7298	Chitin synthase	YNL192w
CA1614	1.1	1.0	1.0	1.1	0.6	0.5	IPF18645	orf19.3216	unknown function	YAL018c
CA5201	0.3	0.1	1.0	1.1	0.6	0.2	IPF2349	orf19.7016	similar to human sphingomyelin	YDR452w
CA2862	0.6	1.1	0.7	0.8	0.6	0.5	HHF21	orf19.1059	histone H4	YNL030w
CA2176	1.5	1.9	0.9	0.8	0.6	0.6	CDC54	orf19.3761	cell division control protein (by homology)	YPR019w
CA0095	1.3	1.3	1.0	1.0	0.6	0.6	ALG11	orf19.3468	required for asparagine-linked oligosaccharide assembly (by	YNL048w
CA2625	1.1	0.9	0.8	0.9	0.6	0.4	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified protein	YLR110c
CA2348	0.3	0.3	0.8	1.1	0.6	0.5	IPF12811	orf19.3751	putative serine/threonine kinase	YOR233w
CA4097	0.9	0.9	0.9	0.9	0.6	0.6	GIN4	orf19.663	ser/thr protein kinase (by homology)	YDR507c
CA2986	1.1	0.7	0.9	1.0	0.6	0.5	CDC5	orf19.6010	Cell-cycle protein kinase (by homology)	YMR001c
CA4005	0.9	0.9	1.2	0.9	0.6	0.4	ERG6	orf19.1631	sterol transmethylase	YML008c
CA5091	2.1	0.8	1.7	1.2	0.6	0.6	ENG1	orf19.3066	endo-1,3-beta-glucanase	YNR067c
CA3883	1.0	0.9	0.9	0.9	0.6	0.7	GCV2	orf19.385	Glycine decarboxylase P subunit	YMR189w
CA5152	1.2	0.8	1.2	1.0	0.6	0.6	CAT2	orf19.4591	carnitine O-acetyltransferase (by homology)	YML042w
CA5073	0.5	0.5	0.9	1.0	0.7	0.3	IPF3603	orf19.3048	unknown function	no match
CA2302	1.4	1.2	1.0	1.3	0.7	0.6	IPF6518	orf19.1691	unknown function	YNR018w
CA2874	0.9	0.9	0.7	1.1	0.7	0.6	IPF4999	orf19.5843	unknown function	no match
CA2950	1.2	1.0	1.2	1.1	0.7	0.4	CLN2	orf19.1960	G1/S-SPECIFIC CYCLIN CLN2	YAL040c
CA2479	0.4	1.1	1.1	0.8	0.7	0.6	CCN1	orf19.3207	G1 cyclin	YAL040c



16A

[Ca XS+ up 1.5 10FDR] less [Cd XS+ up 1.5 10FDR] HS+ OS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0966	1.7	0.9	1.0	0.9	25.2	1.2	IPF9136	orf19.6249	potassium transporter, (by homology)	YMR088c
CA4581	1.7	1.0	1.4	1.1	18.7	1.2	IPF2232	orf19.6899	unknown function	YMR315w
CA0316	0.9	1.0	1.2	0.9	14.1	2.0	ALS1	orf19.5741	agglutinin-like protein	YJR004c
CA0671	2.9	1.2	1.1	1.0	12.0	1.3	GRP4	orf19.3150	putative reductase (by homology)	YOL151w
CA4293	1.3	1.0	0.7	1.0	9.1	1.0	IFA8	orf19.6690	Unknown function	YOR353c
CA5961	1.1	1.0	0.9	1.0	8.1	1.0	IFA14	orf19.7550	unknown function	no match
CA4990	1.5	1.0	0.8	1.0	8.0	1.2	IPF2039	orf19.5258	unknown function	no match
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA0644	1.4	0.9	0.9	1.0	7.0	1.0	IPF17131	orf19.69	unknown function	no match
CA5535	1.1	1.1	20.4	1.4	6.5	1.0	IPF2839	orf19.7296	unknown function	no match
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function	no match
CA0869	1.2	1.0	1.0	1.0	5.7	1.2	IPF14772	orf19.3589	unknown function	YHL022c
CA5224	0.8	1.6	0.7	1.0	5.4	0.7	IPF3081	orf19.7043	unknown function	YLR050c
CA4759	1.3	1.0	0.9	1.0	5.4	1.0	IPF9655	orf19.3988	unknown function	no match
CA3104	1.4	1.4	1.1	1.1	4.9	1.3	IPF12084	orf19.6554	unknown function	YOR220w
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA4676	3.6	1.1	0.7	0.9	4.8	1.1	HK1	orf19.896	Histidine kinase	YIL147c
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA0471	0.8	0.8	0.6	0.5	4.1	1.4	ECM22	orf19.2623	putative protein involved in cell wall biogenesis (by homology)	YDR213w
CA1497	1.9	1.1	2.2	1.5	4.0	1.2	IPF9683	orf19.3644	unknown function	YHR006w
CA4712	0.9	1.1	1.0	1.1	4.0	1.1	GTT1	orf19.6947	glutathione S-transferase (by homology)	YIR038c
CA1300	0.9	1.0	2.1	1.4	3.9	1.2	SLY41	orf19.4199	vesicular transport (by homology)	YOR307c
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)	YDR069c
CA1664	1.2	1.2	0.8	1.0	3.8	1.0	ERV1.3f	orf19.2863.1	Mitochondrial biogenesis and regulation of cell cycle, 3-prime end (by homo	YGR029w
CA2450	1.2	1.0	0.7	1.0	3.8	1.0	IPF2589	orf19.5508	unknown function	YOR353c
CA4034	1.0	1.3	0.8	0.9	3.8	1.1	HSP31	orf19.3664	heat shock protein (by homology)	YCR021c
CA0935	1.0	1.0	1.0	1.0	3.7	1.0	IPF14203.5f	orf19.1079	similarity to several transaminases, 5-prime end (by homology)	YFL030w
CA0963	1.0	1.0	0.9	1.0	3.6	1.4	IPF9143	orf19.6246	similar to Saccharomyces cerevisiae Nat3p N-acetyltransferase (by homolo	YPR131c
CA1507	1.0	3.8	0.9	0.9	3.6	1.1	HSP30	orf19.4526	heat shock protein (by homology)	YCR021c
CA3587	0.6	1.2	0.8	1.5	3.6	1.0	AAH1	orf19.2251	adenosine deaminase (by homology)	YNL141w
CA3103	1.1	1.0	0.9	1.0	3.6	1.0				
CA1197	1.2	1.0	0.6	0.9	3.6	1.1				
CA1787	0.9	1.0	0.9	1.1	3.6	1.0	IFH3	orf19.1167	Dioxygenase (by homology)	YLL057c
CA2659	3.3	1.1	0.9	1.0	3.5	1.5	NDH2	orf19.5713	NADH dehydrogenase (by homology)	YMR145c
CA2721	1.3	1.0	0.7	1.0	3.5	1.2	IPF4799	orf19.3342	unknown Function	YOR138c
CA4304	1.4	1.0	0.7	0.9	3.4	1.1	IPF6649	orf19.6704	unknown function	YFR031c
CA2583	1.4	1.0	0.6	1.0	3.4	1.4	IPF9445	orf19.4372	unknown function	YDL206w
CA2747	1.3	1.0	1.1	1.0	3.4	1.1	IPF11467	orf19.2367	unknown function	YNL260c
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease	YHL036w
CA5895	1.0	1.0	0.9	1.0	3.3	1.4	ISA2	orf19.6811	Mitochondrial protein required for iron metabolism (by homology)	YPR067w
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA5705	0.7	1.1	0.4	1.0	3.3	1.1	IPF2645	orf19.7405	unknown function	no match
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA4444	1.0	1.1	0.8	1.0	3.1	1.1	IPF3533	orf19.6842	putative GDP/GTP exchange factor (by homology)	YLR425w
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA0934	1.2	1.3	0.9	1.1	3.1	1.0	IPF14203.3f	orf19.1078	similarity to several transaminases, 3-prime end (by homology)	YFL030w
CA0654	1.1	1.4	0.8	0.9	3.1	1.0	IPF11550.3f	orf19.2552	Ca2+-transporting P-type ATPase, 3-prime end (by homology)	YGL167c
CA5041	1.0	1.0	0.8	1.0	3.1	1.0	FRP7	orf19.6995	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylat	YCR010c
CA1947	1.2	1.2	0.9	0.9	3.1	0.9	IPF10637	orf19.4742	starvation protein -like (by homology)	YDR388w
CA0112	1.5	0.9	1.2	0.9	3.1	1.3	IPF17358	orf19.5754	unknown function	YLR023c
CA2868	1.2	1.4	0.8	1.0	3.0	1.0	IPF20118	orf19.2846	unknown function	no match
CA0724	0.8	1.0	1.4	1.0	3.0	1.4	IPF13398	orf19.35	protein kinase (by homology)	YMR216c
CA0850	1.2	1.0	0.8	1.0	3.0	1.0	IPF16671	orf19.1745	unknown function	no match
CA4779	2.9	1.2	1.3	1.3	3.0	1.4	IPF3351	orf19.4012	unknown function	YHR071w
CA6158	1.5	1.0	0.8	1.0	3.0	1.0	IPF1839	orf19.5879	putative 1-Acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)	no match
CA3025	1.1	1.0	0.8	1.1	3.0	1.0	IPF11503	orf19.3902	unknown function	YGR131w
CA1165	1.2	0.9	0.7	1.1	3.0	1.3	IPF19902	orf19.3360	unknown function	no match
CA0965	0.9	0.9	1.0	0.9	2.9	1.0	IPF9139	orf19.6248	unknown function	no match
CA1332	1.5	1.0	1.3	1.4	2.9	1.1	IPF11716	orf19.1150	unknown function	YER040w
CA2893	0.9	0.9	1.0	1.0	2.8	1.2	IFS3	orf19.2463	Unknown function	YDR014w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match
CA3178	2.4	1.2	1.2	1.1	2.8	1.0	IPF19974	orf19.1406	unknown function	YJL030w

CA4637	1.0	1.0	1.2	1.0	2.8	1.5	IPF1514	orf19.344	unknown function	no match
CA4675	1.0	1.0	0.9	1.0	2.8	1.2	IPF3664	orf19.897	unknown function	YMR077c
CA1965	1.2	1.2	1.0	1.0	2.8	1.2	IPF14035	orf19.2395	Similar to serine/threonine protein kinase (by homology)	YJL106w
CA0026	1.0	1.1	0.8	0.9	2.7	1.5	IPF16843	orf19.2397.3	unknown function	YGR127w
CA3662	1.1	0.9	1.1	1.1	2.6	0.8	IPF17021	orf19.6464	unknown function	YLR420w
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA4656	0.8	1.1	1.5	1.1	2.5	1.5	IPF3095	orf19.4443	unknown function	YDL235c
CA5773	1.8	1.4	0.9	1.0	2.5	1.4	DOT5	orf19.5417	Derepression of telomeric silencing (by homology)	YIL010w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c
CA0616	0.8	1.0	0.3	0.9	2.5	1.0	PHO11	orf19.2619	Secreted acid phosphatase	YBR092c
CA3110	1.0	1.0	1.1	1.2	2.4	1.3	LPI9	orf19.6544	Microtubule-associated protein (by homology)	YOR227w
CA0355	2.5	1.1	0.6	1.0	2.4	1.0				
CA6160	2.1	1.4	0.8	0.9	2.4	1.2	IPF1835	orf19.5876	unknown function	no match
CA1129	1.2	1.0	1.1	0.9	2.4	1.1	IPF5197	orf19.3610	unknown function	no match
CA3445	1.2	1.1	1.1	1.0	2.4	1.4	IPF7325	orf19.2978	unknown function	no match
CA2954	1.0	1.3	1.0	0.8	2.4	1.5	IPF10685	orf19.5856	unknown function	YBL034c
CA5002	1.2	1.1	0.9	1.0	2.4	1.2	IPF2021	orf19.5245	unknown function	YML111w
CA4683	10.3	6.7	1.1	1.1	2.3	1.5	HSP78.3f	orf19.884	heat shock protein of clpb family of ATP-dependent proteases, mitochondria	YDR258c
CA1101	1.5	0.9	1.1	0.9	2.3	1.0	IPF5678	orf19.4951	unknown function	no match
CA2339	0.8	0.8	0.7	1.6	2.3	1.4	IPF13377	orf19.2350	unknown function	YOR378w
CA4479	1.0	1.0	1.0	1.0	2.3	1.4	URH1	orf19.1888	Uridine ribohydrolase (by homology)	YDR400w
CA0756	1.4	1.0	0.9	1.1	2.3	1.1	IPF14859	orf19.3488	acyl-coenzyme-A dehydrogenase (by homology)	no match
CA2778	1.2	1.5	0.9	1.1	2.3	1.3	MTR	orf19.278	neutral amino acid permease-like by homology	YNL101w
CA2876	1.2	0.9	1.0	0.8	2.3	1.3	RNR2	orf19.5845	Ribonucleotide reductase (by homology)	YER070w
CA3655	1.2	1.1	1.0	1.1	2.3	1.1	POT13	orf19.2046	Acetyl-CoA C-acyltransferase, peroxisomal (by homology)	YIL160c
CA3267	1.3	1.0	1.6	1.4	2.3	1.0	RPS620a	orf19.6300	unknown function	no match
CA2741	1.0	0.9	1.0	1.3	2.3	1.2	IPF10632	orf19.2105	unknown function	YLR323c
CA0817	1.5	1.0	0.9	0.9	2.3	1.0	IPF6339	orf19.2724	unknown function	no match
CA0254	0.4	0.4	0.9	1.1	2.3	0.9	IPF14968	orf19.3461	unknown function	no match
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match
CA3558	1.0	1.0	1.0	1.0	2.3	1.1	IPF7760	orf19.3887	unknown function	no match
CA4657	0.4	1.1	0.7	1.1	2.3	1.2	IPF3094	orf19.4444	4-nitrophenyl phosphatase (by homology)	YDL236w
CA5442	1.2	1.3	0.9	0.7	2.3	1.1	IPF18105.3f	orf19.3245	unknown function, 3-prime end	no match
CA4219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein phosphatase (by h	YKL193c
CA0424	1.0	1.0	1.1	0.8	2.2	1.0	IPF10795	orf19.2356	putative transcription factor (by homology)	YNL027w
CA4833	1.4	1.0	0.7	1.0	2.2	1.1	IPF1216	orf19.2064	unknown function	YKL165c
CA3657	1.8	1.0	1.1	1.0	2.2	1.0	IPF7459	orf19.2049	unknown function	no match
CA2963	1.1	1.1	1.0	1.0	2.2	1.0	GRP3	orf19.5611	dihydroflavonol-4-reductases (by homology)	YOL151w
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA4252	1.0	0.9	0.8	1.0	2.2	1.3	IPF4290	orf19.541	unknown function	no match
CA2263	0.5	0.6	0.6	0.6	2.2	1.2	GPD1	orf19.1756	Glycerol-3-phosphate dehydrogenase (by homology)	YOL059w
CA0961	1.4	1.6	0.7	0.9	2.2	1.2	IPF18822	orf19.3720	unknown function	YJR090c
CA5734	1.0	1.1	1.0	0.9	2.2	1.0	IPF20029	orf19.7444	unknown function	YOR352w
CA3268	1.2	1.0	1.6	1.6	2.2	1.1	RPS620b	orf19.6301	unknown function	no match
CA1426	1.0	1.1	0.4	1.0	2.2	1.1	ALS9.3f	orf19.5745	agglutinin-like protein, 3-prime end	YAL063c
CA2355	0.9	1.2	0.9	0.8	2.2	1.4	TPK1	orf19.4892	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA4684	3.0	10.5	1.1	1.0	2.2	1.5	HSP78.5f	orf19.882	heat shock protein of clpb family of ATP-dependent proteases, mitochondria	YDR258c
CA1136	1.5	3.0	0.8	0.9	2.1	1.2	IFN2	orf19.1980	glycerophosphoinositol transporter (by homology)	YCR098c
CA1686	0.9	1.2	0.7	0.8	2.1	1.5	IPF12272	orf19.3659	unknown function	YER139c
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA4949	0.8	0.7	0.5	1.0	2.1	0.9	CDC34	orf19.6529	Ubiquitin-conjugating enzyme (by homology)	YDR054c
CA2392	0.8	1.2	0.5	1.1	2.1	1.2	IPF15672	orf19.2607	unknown function	YKL128c
CA0251	1.0	1.0	2.5	1.0	2.1	1.0	IPF9146	orf19.6244	unknown function	no match
CA2025	0.8	1.0	0.8	1.0	2.1	1.3	IPF9618	orf19.4911	unknown function	no match
CA5358	0.8	1.2	0.6	0.9	2.1	1.4	IPF846	orf19.7235	WD-repeat protein, beta-transducin (by homology)	YMR102c
CA4110	1.0	1.0	1.3	1.1	2.1	1.4	IPF3965	orf19.674	unknown function	YDL209c
CA4396	1.0	1.0	0.7	1.0	2.1	1.1	IPF12294	orf19.3115	unknown function	YBL034c
CA3100	1.4	1.0	1.1	0.9	2.1	1.1	IPF6594	orf19.3863	unknown function	YLR266c
CA4587	1.3	1.4	1.4	0.9	2.1	1.1	IPF2223	orf19.6905	unknown function	YNL011c
CA5330	1.2	1.0	1.0	1.0	2.1	1.1	IPF2130	orf19.7204	similar to 2-nitropropane dioxygenases	YJR149w
CA5998	1.2	1.0	2.5	1.0	2.1	1.1	IPF670	orf19.7598	unknown function	YOR023c
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA5966	1.5	1.5	1.0	1.1	2.1	1.0	IPF959	orf19.7556	unknown function	no match
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end (by homology)	YKR076w
CA4886	1.1	0.7	1.5	1.0	2.0	1.4	IPF1634	orf19.6578	unknown function	YML123c
CA0194	1.1	1.3	0.8	1.0	2.0	1.1	IPF16228	orf19.3922	unknown function	YGL224c
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)	YCR098c
CA1257	1.0	1.1	0.9	1.0	2.0	1.2	IPF18725	orf19.3169	unknown function	YOR262w
CA4693	1.0	1.0	1.2	1.1	2.0	1.0	IPF3952	orf19.872	unknown function	no match
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA4855	1.1	1.0	1.2	1.3	2.0	0.7	IPF5830	orf19.3826	unknown function	YKR100c
CA3359	1.2	1.0	0.9	1.0	2.0	1.1	IPF9566	orf19.1939	unknown function	YDR374c
ATP6	0.6	0.8	1.0	1.4	2.0	1.1				
CA4837	0.9	1.1	0.9	1.0	2.0	1.1	IPF1228	orf19.2059	unknown function	no match
CA4239	1.0	1.0	0.8	1.1	2.0	1.3	IPF8174	orf19.524	unknown function	no match
CA5726	0.9	0.9	1.0	1.0	2.0	1.1	AAF1	orf19.7436	Adhesion and aggregation mediating surface antigen	no match
CA5939	1.0	1.2	1.1	1.1	2.0	1.0	IPF3484	orf19.6758	aldo/keto reductase (by homology)	YOR120w
CA2877	1.1	1.0	0.8	1.0	2.0	1.3	TFB2	orf19.5846	Transcription/repair factor (by homology)	YPL122c
CA0054	0.7	1.4	1.3	1.0	2.0	1.1	RIB4	orf19.410.3	6,7-dimethyl-8-ribityllumazine synthase (by homology)	YOL143c
CA2420	1.0	1.1	1.1	1.0	1.9	0.8	SPC19	orf19.4473	spindle pole body protein (by homology)	YDR201w
CA2740	0.9	1.1	1.0	1.2	1.9	1.2	IPF10633	orf19.2106	unknown function	YLR326w
CA2957	1.1	1.0	1.0	1.0	1.9	1.0	DAL53	orf19.5859	allantoate permease (by homology)	YJR152w
CA1865	0.7	1.2	0.7	1.1	1.9	1.2	IPF7646	orf19.861	putative transcription factor (by homology)	YDR259c
CA1026	1.1	1.1	0.9	1.0	1.9	1.2	TIP41.5f	orf19.3937	unknown function, 5-prime end	YPR040w
CA2077	1.1	1.0	0.9	1.0	1.9	1.1	IPF13353	orf19.4872	unknown function	no match
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA3742	1.0	1.0	0.8	1.0	1.9	1.0	IFM3	orf19.2176	2-hydroxyacid dehydrogenase by homology, Glycerate-formate-dehydrogen	YNL274c
CA0410	1.2	1.1	0.9	1.0	1.9	1.2	IPF15065	orf19.5757	unknown function	YMR178w
CA3656	1.2	1.2	0.5	1.0	1.9	0.9	IPF7456	orf19.2047	unknown function	YOR289w
CA4847	1.5	1.6	0.7	0.9	1.9	1.5	IPF6951	orf19.3815	similar to Saccharomyces cerevisiae Ubp11p ubiquitin C-terminal hydrolase	YKR098c
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA5443	1.3	1.4	1.2	0.8	1.9	0.9	IPF18105.5f	orf19.3246	unknown function, 3-prime end	no match

CA3880	0.5	1.0	0.3	0.7	1.9	1.0	CAF16	orf19.388	ABC ATPase (by homology)	YFL028c
CA2595	1.1	1.0	0.5	0.9	1.9	1.0	ARG2	orf19.56	acetylglutamate synthase (by homology)	YJL071w
CA5497	0.5	0.4	1.2	0.7	1.9	1.0	IPF776	orf19.5338	transcriptional activator (by homology)	YPL248c
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA2314	0.5	0.8	0.4	0.8	1.9	1.0	IPF14545	orf19.1381	unknown function	YCL034w
CA3062	1.0	1.0	0.9	1.1	1.9	1.2	IPF2968	orf19.4286	unknown function	no match
CA0981	0.8	0.7	0.6	1.0	1.9	1.3	GAP4	orf19.1799	general amino acid permease (by homology)	YKR039w
CA0917	1.1	1.2	0.8	1.3	1.9	1.1	RAD16	orf19.2969	nucleotide excision repair protein (by homology)	YBR114w
CA5985	1.7	1.1	0.9	0.9	1.9	1.0	IPF907	orf19.7583	unknown function	YAL051w
CA0656	1.0	1.0	0.8	0.9	1.9	1.3	IPF12470	orf19.5573	unknown function	no match
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)	YGL009c
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA1997	1.4	1.3	1.0	1.1	1.8	1.3	YCF1	orf19.6478	Glutathione S-conjugate transporter (by homology)	YDR135c
CA4874	0.6	0.6	0.6	0.5	1.8	1.4	IPF1674	orf19.6559	putative transcription initiation factor (by homology)	YNL108c
CA0150	2.1	1.3	1.3	1.0	1.8	1.0	CDC123	orf19.2721	similar to Saccharomyces cerevisiae Cdc123p cell cycle regulator (by homo	YLR215c
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA3182	1.1	1.0	0.9	1.0	1.8	1.0	LIP4	orf19.2133	secretory lipase	no match
CA3637	0.3	0.9	0.2	0.5	1.8	1.3	IPF9255	orf19.5136	unknown function	YGR017w
CA4204	1.0	0.8	0.7	1.1	1.8	0.6	HOL4	orf19.4546	member of major facilitator superfamily multidrug-resistance protein subfami	YNR055c
CA3036	1.0	1.0	0.9	1.1	1.8	0.8	IPF13443	orf19.211	unknown function	no match
CA1258	1.3	2.2	0.9	0.9	1.8	1.2	RPN8	orf19.3168	26S proteasome regulatory subunit (by homology)	YOR261c
CA1020	0.8	1.1	0.7	1.1	1.8	1.0	IPF4824	orf19.3355	unknown function	YOR155c
CA0609	1.4	1.3	0.5	1.0	1.8	1.0	CDR11.3f	orf19.919	multidrug resistance protein, 3-prime end (by homology)	YOR153w
CA2321	0.9	1.2	0.9	1.0	1.8	1.0	MEC3	orf19.5485	G2-specific checkpoint protein (by homology)	YLR288c
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)	YOR356w
CA3963	1.2	1.0	0.8	0.8	1.8	0.8	IPF11233	orf19.1422	similar to Saccharomyces cerevisiae Fzo1p required for biogenesis of mitoc	YBR179c
CA2467	1.1	1.0	1.3	1.0	1.8	1.1	IPF8724	orf19.1796	unknown function	YPL113c
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA3952	1.1	1.0	1.0	1.0	1.8	1.1	IPF6716	orf19.1411	Phenylacetate 2-hydroxylase (by homology)	YMR015c
CA5949	0.9	1.1	0.8	1.2	1.8	1.4	IPF3498	orf19.6747	unknown function	YDR051c
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA2440	1.2	1.0	1.1	1.2	1.8	1.0	IPF7513	orf19.2196	unknown function	YGL110c
CA3035	1.0	1.2	0.8	0.9	1.8	1.4	VPS28	orf19.212	involved in vacuolar traffic (by homology)	YPL065w
CA2855	0.3	0.8	0.5	0.8	1.8	1.4	GPM2	orf19.1067	phosphoglycerate mutase (by homology)	YKL152c
CA2915	1.3	1.0	0.8	1.0	1.8	1.0	IFA17.3f	orf19.4511	unknown function, 3-prime end	YJL005w
CA3346	0.6	1.4	0.6	1.1	1.8	1.2	IPF13356	orf19.2324	molybdopterin biosynthesis (by homology)	YHR111w
CA1460	1.0	0.9	1.2	1.2	1.8	1.3	HAM1	orf19.1108	Controls 6-N-hydroxylaminopurine sensitivity and mutagenesis (by homolog	YJR069c
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase	no match
CA6099	0.9	1.0	1.3	1.3	1.8	0.9	CDR2	orf19.5958	Candida albicans drug resistance protein 2	YOR153w
CA4794	1.0	0.8	1.5	1.2	1.8	1.3	SQT1	orf19.4029	suppresses dominant-negative mutants of the ribosomal protein QSR1 (by h	YIR012w
CA1027	1.0	1.4	0.8	0.8	1.8	1.4	TIP41.3f	orf19.3937.2	unknown function, 3-prime end	YPR040w
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c
CA1576	1.0	0.9	0.9	1.0	1.8	1.1	HYR1	orf19.4975	hyphally regulated protein	no match
CA2775	1.1	1.0	1.1	1.0	1.8	1.2	POP5	orf19.275	subunit of RNase P- like by homology	YAL033w
CA5788	0.1	0.6	1.1	1.8	1.7	1.0	RHR2	orf19.5437	DL-glycerol phosphatase	YIL053w
CA5365	0.9	0.9	0.9	1.1	1.7	1.5	IPF824	orf19.7244	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (by homology)	YNL168c
CA2434	2.4	2.5	1.5	1.1	1.7	1.4	IPF9484	orf19.3396	unknown function	YNL281w
CA4950	0.9	1.0	0.9	1.0	1.7	1.2	IPF5143	orf19.6528	Unknown function	no match
CA6166	0.8	0.9	0.6	1.1	1.7	0.9	CTP1.3f	orf19.5870	Citrate transport protein (by homology)	YBR291c
CA5150	1.0	0.8	0.7	1.0	1.7	1.1	FMS1	orf19.4589	Similar to corticosteroid-binding protein CBP1 (by homology)	YMR020w
CA0335	0.9	1.0	1.0	1.0	1.7	1.0	IFA2	orf19.195	unknown function	YJL005w
CA5973	1.4	1.0	0.6	1.0	1.7	1.1	IPF931	orf19.7567	unknown function	YDR124w
CA1781	0.9	1.0	1.5	1.0	1.7	0.8	IPF14508	orf19.1828	unknown function	YEL029c
CA0655	1.2	1.0	0.9	0.9	1.7	1.0	IPF11560.5f	orf19.2553	Ca2+-transporting P-type ATPase, 5-prime end (by homology)	YGL167c
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA6104	0.8	0.9	1.1	1.1	1.7	1.1	IPF65	orf19.5952	unknown function	YDL231c
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA2389	0.9	1.0	1.1	1.0	1.7	1.0	IPF8500	orf19.2610	unknown function	YGL105w
CA3552	1.2	1.0	0.8	1.0	1.7	1.0	IPF13231	orf19.3877	unknown function	no match
CA2755	1.4	1.0	0.7	1.0	1.7	1.1	IFA12	orf19.5619	unknown function	no match
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA2897	0.9	0.9	1.1	1.1	1.7	1.1	IPF14979	orf19.3482	similar to Saccharomyces cerevisiae Npy1p NADH pyrophosphatase (by hor	YGL067w
CA3724	0.9	0.9	0.5	1.1	1.7	0.7	IPF6181	orf19.4174	similar to Saccharomyces cerevisiae Fun 26p nucleoside transporter (by hor	YAL022c
CA5208	0.8	1.0	1.0	1.0	1.7	1.0	IPF2361	orf19.7023	unknown function	YLR455w
CA2679	1.0	1.0	1.0	1.0	1.7	1.2	IFU5	orf19.2568	Unknown function	YFL010c
CA3802	1.4	2.2	1.0	1.1	1.7	0.7	AUT7	orf19.2480.1	microtubule-associated protein essential for autophagy (by homology)	YBL078c
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function	YBR101c
CA3058	1.0	1.3	0.9	0.9	1.7	1.3	IPF2955	orf19.4292	unknown function	YOR036w
CA5352	1.1	1.4	0.7	1.2	1.7	0.8	IPF856	orf19.7228	unknown function	YKR030w
CA0827	0.7	0.8	0.7	1.0	1.7	1.3				
CA0413	1.0	0.8	0.6	1.1	1.7	1.3	ALS12.3f	orf19.2122	agglutinin-like protein, 3-prime end	no match
CA1996	1.2	1.1	1.0	1.0	1.7	0.9	SEC1	orf19.6479	transport protein	YDR164c
CA3390	1.2	1.1	0.9	1.0	1.7	1.1	CAF17	orf19.318	Component of CCR4 transcriptional complex	YJR122w
CA4164	1.7	2.0	1.0	1.1	1.7	1.1	IPF9302	orf19.5813	unknown function	YOR052c
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA0610	1.5	0.6	0.9	1.0	1.7	0.9	CDR11.5f	orf19.918	multidrug resistance protein, 5-prime end (by homology)	YOR153w
CA3029	0.9	1.0	0.6	0.9	1.7	1.1	IPF13825	orf19.223	serine/threonine protein kinases (by homology)	YNR047w
CA2475	0.9	1.0	1.0	1.0	1.7	1.0	PGA15	orf19.2878	unknown function	no match
CA1764	0.6	1.2	1.0	1.1	1.7	1.2	IPF7596	orf19.5196	similar to Saccharomyces cerevisiae Ess1p peptidyl-prolyl cis/trans isomera	YJR017c
CA6096	1.3	1.8	1.0	1.2	1.7	1.2	IPF56	orf19.5961	similar to Saccharomyces cerevisiae Nas6p subunit of 26S proteasome (by	YGR232w
CA4768	0.8	1.0	1.9	0.9	1.7	0.8	IPF9385	orf19.4000	similar to Saccharomyces cerevisiae Pho2p homeobox-domain containing tr	YDL106c
CA2560	1.3	1.1	0.8	1.2	1.7	1.2	PEX5	orf19.5640	peroxisomal targeting signal receptor	YDR244w
CA4713	2.1	0.8	2.4	0.7	1.7	1.1	CCC1	orf19.6948	Transmembrane Ca2+ transporter (by homology)	YLR220w
CA3614	1.2	1.1	0.8	1.0	1.7	1.1	IPF8878	orf19.31	unknown function	YJL158c
CA4719	1.0	1.0	0.8	1.0	1.7	1.0	DAL51	orf19.6956	allantoate permease (by homology)	YJR152w
CA0093	1.0	1.0	1.1	0.9	1.7	1.1	IPF29954	orf19.100	putative lipase (by homology)	YJR107w
CA2742	1.1	1.1	1.1	1.3	1.7	1.2	JAC1	orf19.2104	molecular chaperone (by homology)	YGL018c
CA2777	1.0	0.8	1.0	0.9	1.6	0.9	THI6	orf19.277	thiamin-phosphate pyrophosphorylase and hydroxyethylthiazole kinase-like	YPL214c
CA2096	1.2	1.0	0.9	1.0	1.6	1.1	IPF11491	orf19.2391	unknown function	YKR023w
CA4205	1.6	1.0	0.9	1.0	1.6	1.3	IFA10	orf19.4549	unknown function	YJL005w
CA0307	1.1	0.8	1.1	0.8	1.6	1.3	IPF4719	orf19.3736	similar to Saccharomyces cerevisiae Kar4p regulatory protein required for p	YCL055w
CA5045	1.0	1.0	0.9	1.0	1.6	1.3	IPF4510	orf19.6999	unknown function	YLL057c
CA2124	1.0	1.1	0.9	1.0	1.6	1.1	IPF10490	orf19.419	unknown function	no match

CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA3828	0.9	1.2	1.7	1.1	1.6	1.2	SNQ2	orf19.5759	multidrug resistance protein (by homology)	YDR011w
CA0414	0.6	1.1	0.9	0.8	1.6	1.2	IPF4068	orf19.2164	reverse transcriptase	no match
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA0221	1.2	1.2	1.5	1.2	1.6	1.3	PUS4	orf19.1954	pseudouridine synthase (by homology)	YNL292w
CA2284	0.8	1.0	0.8	1.1	1.6	1.0	MIF2	orf19.5551	required for normal chromosome segregation and spindle integrity (by homo	YKL089w
CA3553	1.0	1.0	0.7	1.0	1.6	1.0	IFA27.5	orf19.3878	unknown function, 5-prime end	no match
CA1871	0.8	0.9	0.9	0.7	1.6	0.9	IPF16981	orf19.2458	unknown function	YMR140w
CA5332	1.0	1.1	0.9	1.0	1.6	1.2	IPF900.3f	orf19.7206	unknown function, , 3-prime end	YDR067c
CA2369	1.5	1.4	1.6	1.4	1.6	1.1	TBP1	orf19.1837	TATA-binding protein (by homology)	YER148w
CA3316	1.3	1.1	1.0	1.0	1.6	1.4	IPF8817	orf19.2301	putative proteasome subunit (by homology)	YIL007c
CA4812	1.2	0.9	0.7	0.9	1.6	1.3	IPF1171.3f	orf19.2089	Putative synaptobrevin (by homology)	YLR093c
CA1528	1.0	0.7	0.6	1.1	1.6	1.2	ALS4.3f	orf19.4556	agglutinin-like protein, 3-prime end	YIR019c
CA0069	0.7	1.0	1.4	1.0	1.6	1.0	IPF19295.5f	orf19.6468	unknown function, 5-prime end	no match
CA2912	1.2	1.1	0.9	0.9	1.6	0.9	IPF11206	orf19.4515	unknown function	YJL158c
CA3177	1.2	1.1	1.0	1.3	1.6	1.4	IPF11589	orf19.1405	similar to Saccharomyces cerevisiae Pho13p 4-nitrophenylphosphatase	YDL236w
CA3010	1.1	0.7	1.6	1.0	1.6	1.0	IPF14568	orf19.6230	unknown function	YGL246c
CA4138	1.4	1.0	1.1	1.0	1.6	1.5	IPF11954	orf19.4234	unknown function	YCR054c
CA5735	0.5	1.0	0.6	0.8	1.6	0.9	IPF2878	orf19.7445	unknown function	YBR105c
CA3620	1.0	1.0	0.8	0.9	1.6	0.8	IPF9063	orf19.203	similar to Saccharomyces cerevisiae Stb3p protein binding Sin3p (by homol	YDR169c
CA2914	1.4	1.0	0.8	1.0	1.6	1.1	IFA17.5f	orf19.4512	unknown function, 5-prime end	no match
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)	YJL001w
CA0306	0.9	0.8	1.1	1.0	1.6	0.9	HEM3	orf19.1742	porphobilinogen deaminase	YDL205c
CA2718	1.0	0.9	1.0	1.1	1.6	1.3	IPF7374.3f	orf19.3338	unknown function	no match
CA0483	1.2	1.5	1.1	0.6	1.6	1.3	SEC9	orf19.117	transport protein (by homology)	YGR009c
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA0020	1.0	1.0	1.0	1.0	1.6	1.5	IPF7046	orf19.124	unknown function	YHR052w
CA2749	1.2	1.0	1.0	1.0	1.6	1.4	IPF11465	orf19.2369	unknown function	YNL261w
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA4020	1.2	1.0	0.9	1.0	1.6	1.1	IPF5324	orf19.3444	putative transporter (by homology)	YGR224w
CA0992	1.2	1.1	0.9	1.0	1.6	1.1	IPF11063	orf19.1394	unknown function	YCR090c
CA1537	1.0	1.0	0.9	1.0	1.6	1.0	IPF17483	orf19.450	unknown function	no match
CA5593	0.9	1.1	1.1	1.1	1.6	1.2	IPF5615	orf19.7107	unknown function	YJL122w
CA1459	1.1	1.1	1.2	0.9	1.6	1.4	IPF6340	orf19.1107	unknown function	YDL173w
CA3815	1.3	1.0	0.9	1.0	1.6	1.4	CYP7	orf19.2499	peptidyl-prolyl cis-trans isomerase cyp7 (ppiase)	YJR032w
CA1762	1.1	1.2	0.9	1.0	1.6	1.1	IPF20014	orf19.5194.1	oxidoreductase by homology	YIR035c
CA4277	1.1	1.4	1.1	1.1	1.6	1.2	BTS1	orf19.6674	Geranylgeranyl diphosphate synthase (by homology)	YPL069c
CA1357	0.7	0.9	0.6	0.8	1.5	1.0	ARH1	orf19.410	adrenodoxin reductase and ferredoxin-NADP+ reductase (by homology)	YDR376w
CA6150	1.4	1.0	0.6	1.0	1.5	1.1	IPF1857	orf19.5892	similar to Saccharomyces cerevisiae Hul4p hect domain E3 ubiquitin-protein	YJR036c
CA5297	0.9	0.9	1.3	1.2	1.5	1.2	YAR1	orf19.7160	Ankyrin repeat-containing protein (by homology)	YPL239w
CA4601	1.0	0.9	1.0	1.1	1.5	1.0	IPF2195	orf19.6920	unknown function	no match
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)	YOR157c
CA3658	0.8	1.1	0.6	1.1	1.5	1.0	TGL1	orf19.2050	Triacylglycerol lipase (by homology)	YKL140w
CA1625	0.4	0.9	0.6	0.7	1.5	1.0	IPF6156	orf19.1034	similar to C.elegans LIM homeobox protein	YPL170w
CA3353	0.8	0.8	0.4	0.7	1.5	1.4	AUR1	orf19.1945	aureobasidin-resistance protein	YKL004w
CA1859	1.1	1.0	1.0	1.0	1.5	0.8	IPF19614.3f	orf19.1496	putative transcription factor similar to positive activator of the proline utilisati	YKL015w
CA5408	1.0	1.0	1.2	1.0	1.5	1.3	IPF1551	orf19.952	unknown function	no match
CA5538	1.6	1.1	1.2	1.1	1.5	1.4	IPF2830	orf19.7300	unknown function	no match
CA0122	1.1	1.5	0.9	1.1	1.5	1.2	SNF4.5f	orf19.5768	Nuclear regulatory protein, 5-prime end (by homology)	YGL115w
CA1643	1.0	1.1	0.6	0.8	1.5	0.9	IPF9347	orf19.1729	unknown function	no match
CA4618	1.7	1.1	0.9	1.0	1.5	1.1	IPF5757	orf19.3309	unknown function	no match
CA4405	1.1	1.0	1.1	1.0	1.5	1.0	IPF8773	orf19.3105	putative cytochrome P450 (by homology)	YDR402c
CA2276	1.0	1.1	0.8	1.0	1.5	1.1	HNM3	orf19.2587	Choline permease (by homology)	YGL077c
CA2094	1.3	1.1	0.7	0.8	1.5	1.4	IPF11493	orf19.2393	unknown function	YPR107c
CA3391	1.1	1.2	0.8	1.0	1.5	1.2	PNP1	orf19.317	Purine Nucleoside Phosphorylase (by homology)	YLR209c
CA4996	1.2	1.1	1.0	1.0	1.5	1.0	IPF2029	orf19.5251	unknown function	YBL005w
CA4282	1.1	1.3	0.9	1.1	1.5	1.0	IPF2319	orf19.6680	unknown function	YIL130w
CA4332	1.0	1.2	1.5	1.4	1.5	1.2	GLO2	orf19.4088	Glyoxalase II (hydroxyacylglutathione hydrolase) (by homology)	YDR272w
CA2927	1.1	1.1	0.9	1.1	1.5	1.0	RAD52	orf19.4208	Nuclear ribonucleoprotein E	YML032c
CA2397	1.1	1.0	1.1	1.0	1.5	1.0	CFL12	orf19.3538	Strong similarity to ferric reductase Fre2p (by homology)	YOR381w
CA4416	1.2	1.1	1.3	1.0	1.5	1.3	IPF11888	orf19.5180	unknown function	YBL064c
CA1655	0.9	1.0	1.5	0.9	1.5	0.8	CCC2	orf19.4328	putative copper-transporting ATPase (by homology)	YDR270w
CA0957	1.0	0.9	0.8	0.9	1.5	1.0	IPF14322	orf19.4731	unknown function	YNL051w
CA2837	1.2	1.1	1.0	1.0	1.5	0.9	IPF8340	orf19.4789	unknown function	no match
CA4123	2.0	1.1	1.0	1.1	1.5	1.0	AMS1	orf19.2768	alpha-mannosidase (by homology)	YGL156w
CA1827	1.1	1.0	1.1	1.1	1.5	1.2	IPF9520	orf19.4264	unknown function	no match
CA2756	1.5	0.9	0.7	1.0	1.5	1.0	IPF18418	orf19.5620	unknown function	YHR029c
CA4863	0.9	1.2	1.1	1.1	1.5	1.4	SAP10	orf19.3839	secretory aspartyl proteinase	YDR144c
CA4390	1.2	1.2	1.0	1.0	1.5	1.2	HOD1	orf19.3122.2	regulator of G2/M progression (by homology)	no match
CA3641	1.2	1.0	1.0	1.0	1.5	1.2	IPF4122	orf19.2032	unknown function	no match
CA1654	1.2	1.3	1.3	0.9	1.5	1.2	IPF19660	orf19.5559	unknown function	YDR202c
CA1302	0.5	0.9	0.9	1.1	1.5	1.5	FCA1	orf19.4195.1	cytosine deaminase	YPR062w
CA3079	1.3	1.1	0.9	1.0	1.5	1.2	RAM2	orf19.4817	geranylgeranyltransferase type I alpha subunit	YKL019w
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5078	0.6	1.1	0.8	0.8	1.5	1.3	IPF15297	orf19.3053	unknown function	no match
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA1498	1.1	1.0	1.0	1.0	1.5	1.0	IPF12371	orf19.3643	extracellular alpha-1,4-glucan glucosidase (by homology)	YHR006w
CA0075	1.0	1.1	0.7	1.0	1.5	1.0				
CA1870	1.0	1.1	0.9	0.8	1.5	1.0				
CA0076	0.9	1.2	1.2	1.1	1.5	1.1	IPF8866	orf19.4906	unknown function	no match
CA1548	0.6	1.1	0.5	0.9	1.5	1.0	IPF8746	orf19.4279	putative alpha-1,3-mannosyltransferase (by homology)	YER001w
CA5567	0.9	0.9	0.8	1.0	1.5	1.0	FCY24	orf19.7331	Putative purine-cytosine transport protein	YGL186c
CA3185	1.1	1.0	0.8	1.3	1.5	1.3	IPF13637	orf19.2137	unknown function	no match
CA4633	0.9	0.8	0.7	0.8	1.5	1.2	NDH1	orf19.339	Mitochondrial NADH dehydrogenase	YMR145c
CA5897	0.9	0.6	0.6	0.5	1.5	0.9	IPF2384	orf19.6809	unknown function	YKL128c
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c

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[Cd XS+ up 1.5 10FDR] less [Ca XS+ up 1.5 10FDR]

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress (|	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**

CA4913	1.1	1.0	1.3	1.0	1.2	6.8	CIS2	orf19.6053	Gamma-glutamyltransferase (by homology)	YLR299w
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match
CA4399	1.4	1.7	1.2	1.3	1.1	3.8	PRA1	orf19.3111	pH-regulated antigen	YOL154w
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA1157	1.2	1.0	1.4	1.1	0.8	2.8	PZF1	orf19.4125	TFIIIA (transcription initiation factor) (by homology)	YPR186c
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA3258	1.1	1.0	0.5	0.9	1.1	2.7				
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)	YPR194c
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA4885	1.2	1.3	1.2	1.1	1.1	2.6	IPF1636	orf19.6577	similar to Saccharomyces cerevisiae Tpo1p multidrug resistance protein	YLL028w
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by homology)	YML130c
CA3919	1.1	1.0	0.8	0.8	1.0	2.5	IFC5	orf19.5121	unknown function	YPR194c
CA2227	1.5	1.2	1.0	0.9	1.4	2.5	EBP7	orf19.5816	NADPH DEHYDROGENASE by homology	YHR179w
CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA5289	0.7	0.9	0.9	0.9	1.4	2.4	NRG1	orf19.7150	similar to transcriptional repressor Nrg1p/Nrg2p	YBR066c
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA1372	0.9	1.0	1.2	1.0	1.1	2.4	IPF15844	orf19.4961	similar to Saccharomyces cerevisiae Stp2p involved in pre-tRNA splicing	YHR006w
CA1569	1.8	2.4	1.5	1.2	1.1	2.4	IPF7616	orf19.1159	putative homoserine O-acetyltransferase (by homology)	YNL277w
CA4929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA1108	1.1	1.1	1.0	1.0	1.0	2.3	IPF11273	orf19.5231	unknown function	no match
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA1536	1.6	1.6	1.1	1.3	1.3	2.2	SOK1	orf19.451	high copy suppressor of a cyclic AMP-dependent protein kinase mutan (by h	YDR006c
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA0129	1.1	0.9	1.0	1.0	1.2	2.2	IPF10495	orf19.246	unknown function	YIL108w
CA0183	1.5	1.9	1.5	1.1	1.4	2.2	CAP1	orf19.1623	transcriptional acivator (by homology)	YML007w
CA3354	1.1	1.1	0.7	0.7	1.2	2.2	GPR1	orf19.1944	similar to Saccharomyces cerevisiae Gpr1p G-protein coupled receptor (by l	YDL035c
CA0560	1.2	1.0	0.9	1.0	1.2	2.1	GPX3	orf19.87	glutathione peroxidase (by homology)	YIR037w
CA3094	1.1	1.1	1.1	0.7	1.3	2.1	IPF11548	orf19.3854	serine/threonine protein kinase (by homology)	YCR008w
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c
CA0500	0.9	1.0	1.4	1.2	0.9	2.0	IPF20058	orf19.4793	unknown function	YOR252w
CA5008	1.0	0.8	1.1	1.3	1.2	2.0	IPF12577	orf19.5238	unknown function	no match
CA5678	0.8	1.0	1.0	0.8	0.9	2.0	IPF1292	orf19.7381	unknown function Hypothetical zinc-finger protein	YML099c
CA1002	1.0	1.0	1.9	1.2	0.9	1.9	ROK1.3f	orf19.3756	RNA helicase, 3-prime end	YGL171w
CA4023	1.0	1.0	0.9	1.0	0.9	1.9	FRP5	orf19.3440	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylat	YNR002c
CA1882	1.1	2.4	0.8	1.0	0.8	1.9	IPF19934	orf19.2210	unknown function	no match
CA4778	1.0	1.1	0.9	1.0	1.2	1.8	IFJ1	orf19.4011	Unknown function	YGR263c
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA4174	1.2	3.6	1.3	1.6	1.6	1.8	IPF4430	orf19.2959.1	unknown function	YDR276c
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match
CA0052	1.0	1.1	1.4	1.0	1.3	1.8	IPF19567	orf19.475	Unknown function	YHR085w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)	YMR275c
CA3187	1.0	0.8	1.5	1.2	0.8	1.8	IPF17094	orf19.2143	unknown function	YPL183c
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4960	0.7	0.8	0.7	0.7	1.2	1.8	IPF3912	orf19.6514	unknown function	YPL177c
CA1277	1.3	1.0	1.4	1.0	1.2	1.8	IPF10837	orf19.3630	unknown function	YDR083w
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA4477	0.9	1.2	1.2	1.1	1.2	1.8	IPF6459	orf19.1890	unknown function	YMR210w
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5eo	orf19.6654	unknown function	YMR221c
CA4612	1.1	0.9	1.4	1.0	1.5	1.7	PPM2	orf19.3303	carboxy methyl transferase; homolog of PPM1 (by homology)	YOL141w
CA0629	1.1	1.3	0.7	0.8	1.0	1.7	IPF3876	orf19.775	unknown function	YJR126c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA5287	0.8	1.0	1.0	0.9	1.0	1.7	IPF1922	orf19.7148	similar to multidrug resistance proteins	YLL028w
CA5696	0.9	1.0	1.6	1.3	1.4	1.7	IPF3309.3eo	orf19.7398	unknown function, 3-prime end	YER126c
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA4614	1.1	1.3	1.4	0.8	1.0	1.7	IPF7952	orf19.3305	unknown function	YDR213w
CA6009	0.8	1.0	1.3	1.0	1.2	1.7	IPF643	orf19.7610	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine phosphatase (b	YER075c
CA0626	1.1	0.9	1.3	1.1	1.4	1.7	IPF3161	orf19.3161	Unknown function	YNR054c
CA3157	0.9	1.4	1.0	1.3	1.5	1.7	IPF14456	orf19.1588	unknown function Unknown function	YBR269c
CA4563	1.0	1.0	1.0	1.1	0.8	1.7	IPF6566	orf19.6873.1	unknown function	YBL071wa
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homology)	YMR152w
CA5580	1.2	1.4	0.9	1.0	1.3	1.6	RVS161	orf19.7124	cytoskeletal binding protein (by homology)	YCR009c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA6038	0.8	1.2	1.8	1.2	1.1	1.6	LTV1	orf19.7650	low-temperature viability protein (by homology)	YKL143w
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homology)	YOR049c
CA5739	1.0	1.1	0.9	1.0	1.4	1.6	IPF2884	orf19.7449	unknown function	YMR211w
CA0941	0.9	1.0	0.8	1.0	1.3	1.6	IPF8617	orf19.3705	unknown function	YCR079w
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA5474	1.3	0.9	1.8	1.1	1.0	1.6	IPF16944.3e	orf19.3287	unknown function, 3-prime end	YMR014w
CA1958	1.0	1.0	0.9	0.9	1.2	1.6	IFE1	orf19.769	Unknown function	YAL061w
CA0393	1.4	1.1	1.0	1.1	1.7	1.6	IPF12758.3f	orf19.333.2	unknown function, 3-prime end	no match
CA2395	1.1	1.1	1.1	1.0	1.0	1.6	IPF6425	orf19.3536	unknown function	YOR320c

CA1540	0.9	0.9	1.2	1.5	0.9	1.6	IPF1047	orf19.4563	unknown function	YMR310c
CA2460	1.5	1.1	1.0	1.0	1.1	1.6				
CA2233	1.0	1.0	1.0	1.0	1.1	1.6	IFJ3	orf19.3924	unknown function	YGR263c
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w
CA6016	0.9	0.8	1.4	1.4	1.4	1.6	IPF630	orf19.7618	unknown function	YOR145c
CA1703	0.9	1.2	0.8	1.0	1.4	1.6	IPF7987	orf19.703	unknown function	YGR247w
CA3808	0.8	1.1	1.5	1.2	1.1	1.6	FAL1	orf19.2488	ATP-dependent RNA helicase	YDR021w
CA5875	1.2	1.1	0.9	1.0	0.8	1.6	IPF324.3f	orf19.7545	unknown function, , 3-prime end	no match
CA3741	0.9	0.9	0.9	1.0	0.7	1.6	MRS4	orf19.2178	RNA splicing protein and member of the mitochondrial carrier family (MCF) I	YKR052c
CA1080	1.0	0.9	1.3	0.9	1.4	1.6	IPF14710	orf19.4820	unknown function	YKL162c
CA4158	0.9	0.9	0.9	0.9	0.7	1.6	DLD3	orf19.5805	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA3080	0.9	1.1	1.0	0.8	1.0	1.6	IPF14634	orf19.4153	APP-binding protein 1 (by homology)	YPL003w
CA5833	0.9	0.9	1.2	1.1	1.2	1.5	IMP3	orf19.7488	U3 small nucleolar ribonucleoprotein (by homology)	YHR148w
CA4818	0.7	0.9	0.8	0.7	1.2	1.5	IPF1193	orf19.2079	unknown function Unknown function	YHL018w
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membrane protein of the	YIL047c
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA2592	1.2	0.9	1.4	1.1	1.6	1.5	IPF18447	orf19.59	putative zinc-finger protein (by homology)	YBR267w
CA0473	1.0	1.0	1.0	1.0	1.3	1.5	GRP1	orf19.4781	dihydroflavonol-4-reductases (by homology)	YOL151w
CA3722	1.3	1.2	0.9	1.0	1.5	1.5	PHO13	orf19.4172	4-nitrophenylphosphatase (by homology)	YDL236w
CA4507	1.0	1.1	1.1	1.3	1.0	1.5	IPF20015	orf19.499	unknown function	YNL063w
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rRNAs (by homolo	YDR087c
CA2398	1.1	1.0	1.0	1.0	1.1	1.5	IPF6431	orf19.3539	unknown function	YBR141c
CA0343	1.6	1.2	1.1	1.0	0.9	1.5	LYS1	orf19.1789.1	saccharopine dehydrogenase (by homology)	YIR034c
CA1689	1.0	1.0	0.9	1.1	1.1	1.5	IPF13030	orf19.3655	unknown function	no match
CA2428	1.0	1.1	0.9	0.9	1.3	1.5	IPF9894	orf19.3405	possible zinc-finger protein	no match
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha-glucosidase (I	YIL099w
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA4754	0.7	1.0	1.0	1.0	1.2	1.5	IPF11479	orf19.4825	unknown function	YIL098c
CA1630	1.4	1.2	1.5	1.1	1.1	1.5	RPP1	orf19.1029	required for processing of tRNA and 35S rRNA (by homology)	YHR062c
CA5626	0.9	1.1	0.9	1.0	1.1	1.5	IPF498	orf19.7071	unknown function	YML123c
CA4613	1.0	1.0	1.3	1.1	1.3	1.5	IPF7950	orf19.3304	similar to Saccharomyces cerevisiae Rrp40p involved in ribosomal RNA pro	YOL142w
CA4404	1.0	1.3	1.4	1.1	1.2	1.5	MET16	orf19.3106	3 -phosphoadenylylsulfate reductase (by homology)	YPR167c
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by homology)	YPL211w
	11759.2	0.6	1.2	0.2	0.3	1.4	1.5			
CA0730	0.9	0.7	1.2	1.1	1.6	1.5	IPF7334	orf19.3724	unknown function	YOR004w
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c

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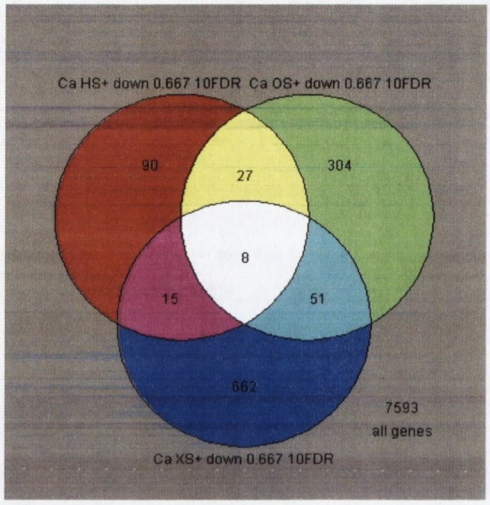
[Cd XS+ up 1.5 10FDR] and [Ca XS+ up 1.5 10FDR] HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function	YDR371w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase	YBR046c
CA2894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function	no match
CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homology)	YPL171c
CA4392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)	YNL229c
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function	YKL086w
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function	no match
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match
CA2435	1.1	1.7	1.2	1.1	17.7	13.6	IPF9483	orf19.3395	probable permease (by homology)	YHR048w
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function	no match
CA0595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5f	orf19.4901	unknown function, 5-prime end	YER175c
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)	YOR388c
CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA1846	1.5	2.2	0.8	0.9	12.5	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)	YOR388c
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function	YPL092w
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA1395	1.1	1.9	1.0	0.9	11.5	11.7				
CA0636	2.2	2.5	0.9	0.9	10.8	15.0				
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function	YNL229c
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function	no match
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inner membrane p	YMR152w
CA0639	1.6	1.8	1.0	1.0	9.0	10.5				
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function	no match
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function	no match
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function	YKR071c
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-binding protein	YGL091c
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)	YBR293w
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)	YHR137w
CA2258	1.1	2.8	0.9	0.9	7.4	15.1	IFR1	orf19.1763	Unknown function	YNL134c
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)	YDR513w
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA3059	1.2	1.8	1.2	1.1	6.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)	YDR353w
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA	YAL049c

CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function	no match
CA4829	1.0	1.1	1.3	1.0	6.3	5.5	IPF1210	orf19.2067	similar to Saccharomyces cerevisiae Nfu1p involved in homeostasis (by hon	YKL040c
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)	YDR338c
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function	no match
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)	YIR037w
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA0933	1.3	1.1	0.8	1.0	5.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)	YMR301c
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function	no match
CA4662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by homology)	YMR038c
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function	YMR136w
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homology)	YJL101c
CA2750	1.1	1.0	1.1	1.0	4.6	1.7	ATX1	orf19.2369.1	antioxidant protein and metal homeostasis factor (by homology to S. cerevis	YNL259c
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)	YPL171c
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53f	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.5f	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable monocarboxylate per	no match
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function	YGL136c
CA1016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function	YOR273c
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)	YOR101w
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)	YNL270c
CA1775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology)	YDL215c
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function	no match
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match
CA0583	1.2	2.5	1.3	1.3	3.9	3.2	GSH1.3f	orf19.5059	gamma-glutamylcysteine synthetase, 3 prime end (by homology)	YJL101c
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA5697	1.3	1.0	0.8	1.1	3.8	3.0				
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA0995	1.0	1.0	0.9	0.9	3.8	1.9				
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)	YNL240c
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)	YHR044c
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA0385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function	YNL250w
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA2711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)	YDR460w
CA1005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)	YPL101w
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)	YKR039w
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function	YHR087w
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function	YGR110w
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (aquaporin-like) (	YPR192w
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function	YOL119c
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology	YAL012w
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA0996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)	no match
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA0942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function	YER101c
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase	YHR008c
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase	YER042w
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function	YDR336w
CA5868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function	YMR090w
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)	YIL120w
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function	YPL122c
CA4836	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)	YJR104c
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)	YNL229c
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function	YLR256w
CA1600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)	YHR175w
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c

CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in regulation of sulfur	YIL046w
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase	YOR202w
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match
CA4630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by homology)	YDL168w
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)	YLR120c
6532.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA3086	1.0	1.7	1.1	1.2	2.3	3.9	GLR1	orf19.4147	by similarity to S. cerev. and C. albicans:glutathione reductase	YPL091w
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (by homology)	YOL119c
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)	YLR043c
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)	YOR171c
3692.2	1.2	1.2	0.8	0.9	2.2	2.1				
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match
CA0757	1.0	0.7	0.6	0.8	2.2	2.0				
CA0160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease	YKR039w
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]	YOR005c
CA2177	1.1	1.1	1.3	1.0	2.2	2.2	ROD1	orf19.1509	O-dinitrobenzene,calcium and zinc resistance protein (by homology)	YFR022w
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function	YNL144c
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA3087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)	YLR147c
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function	YNL166c
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA1170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function	YDR132c
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function	YLR021w
CA2584	0.8	1.2	1.0	1.1	2.1	2.0	IPF9440	orf19.4373	similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase (by homology)	YDR236c
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase	YAL039c
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase	YNL277w
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3f	orf19.4266.1	septin, 3-prime end (by homology)	YDR218c
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)	YIR035c
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function	no match
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function	YNL134c
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function	YCL044c
CA4917	0.7	0.8	0.8	1.4	2.0	2.1	ECM31	orf19.6057	Involved in cell wall biogenesis and architecture (by homology)	YBR176w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA5009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)	YKL119c
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)	YEL060c
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function	YNL191w
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)	YNL040w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homology)	YER053c
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)	YGR234w
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)	YOL151w
CA5135	1.0	1.0	1.0	1.0	1.8	1.7	HSP104.5f	orf19.6389	Heat shock protein, 5-prime end (by homology)	YLL026w
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function	no match
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)	YPL140c
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA3446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function	YKL195w
CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function	YDR219c
CA5010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function	YMR101c
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function	YHR101c
CA5011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function	YMR101c
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function	no match
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eoc	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)	YML004c
CA4580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function	no match
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function	YOR292c
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)	YPR086w
CA5934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function	YHL029c
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function	YJL092w
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function	no match
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function	no match
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)	YPR016c
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)	YGR234w
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime end (by homology	YDR487c
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology	YDR032c
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function	YIR017c
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function	no match
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA2477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)	YJR061w



19A

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA1051	0.1	0.3	0.7	0.9	1.0	1.0	CHT2	orf19.3895	chitinase 2 precursor	YLR286c
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA3305	0.1	0.2	1.2	1.0	1.1	0.9	RPL29	orf19.2310.1	ribosomal protein, cytosolic(by homology)	YFR032ca
CA4534	0.1	0.2	1.2	0.9	1.1	1.1	RPS26A	orf19.1470	ribosomal protein S26.e.A, cytosolic (by homology)	YGL189c
CA2920	0.1	0.2	1.0	1.1	0.9	0.7	FET5.5eoc	orf19.4215	multicopy oxidase (by homology)	YFL041w
CA3084	0.1	0.2	1.0	1.1	1.0	1.1	IPF11625	orf19.4149	unknown function	no match
CA1637	0.2	0.2	1.0	1.1	1.0	1.0	RPL43A	orf19.3942.1	ribosomal protein (by homology)	YPR043w
CA2579	0.2	0.2	1.3	1.0	1.1	1.0				
CA4103	0.2	0.4	1.0	1.0	1.1	1.0	IPF3980	orf19.668	unknown function	YLR183c
CA5125	0.2	0.2	1.0	1.2	1.0	1.0	RPP2	orf19.6403.1	acidic ribosomal protein by homology	YOL039w
CA6068	0.2	0.2	1.2	1.2	1.0	1.0	RPS19A	orf19.5996.1	ribosomal protein S19.e (by homology)	YOL121c
CA3690	0.2	0.2	1.0	1.0	1.0	0.9	RPS14B	orf19.6265.1	ribosomal protein (by homology)	YJL191w
CA2818	0.2	0.2	1.1	1.1	1.1	1.0	RPL13	orf19.2994	Ribosomal protein	YDL082w
CA5646	0.2	0.3	1.1	1.2	1.2	1.0	RPS28B.3f	orf19.7048.1	Ribosomal protein S28B (S33B) (YS27), 3-prime end (by hon	YLR264w
CA3030	0.2	0.6	1.2	0.9	0.9	1.3	IPF19968	orf19.220	putative cell wall protein of the PIR family	YKL164c
CA6092	0.2	0.3	1.2	0.9	1.1	1.0	RPL35	orf19.5964.2	Ribosomal protein L35A, (by homology)	YDL191w
CA5920	0.2	0.2	1.0	1.0	1.2	1.0	RPS12	orf19.6785	acidic ribosomal protein S12 (by homology)	YOR369c
CA4562	0.2	0.3	0.9	1.1	1.0	1.0	RPS8A	orf19.6873	ribosomal protein (by homology)	YER102w
CA3304	0.2	0.2	1.0	0.9	0.9	1.0	RPL82	orf19.2311	60S ribosomal protein L7a.e.B (by homology)	YLL045c
CA2023	0.2	0.2	1.1	1.1	1.0	1.0	RPL42	orf19.4909.1	ribosomal protein L36a, 3- prime end (by homology)	YHR141c
CA5426	0.2	0.2	1.0	0.8	1.0	1.0	FAS1	orf19.979	Fatty-acyl-CoA synthase, beta chain.	YKL182w
CA5807	0.2	0.2	1.1	1.0	0.9	1.0	RPS24	orf19.5466	ribosomal protein S24.e	YIL069c
CA2092	0.2	0.2	1.0	1.0	0.9	1.0	RPL21A	orf19.840	Ribosomal protein (by homology)	YBR191w
CA6064	0.2	0.2	1.0	0.9	0.9	1.0	RPL81	orf19.6002	60S ribosomal protein L7a.e.B (by homology)	YLL045c
CA4269	0.2	0.2	0.9	1.1	0.9	1.0	RPS25B	orf19.6663	Cytosolic ribosomal protein (by homology)	YLR333c
CA6106	0.2	0.3	1.1	0.7	0.9	0.7	FAS2.53f	orf19.5948.1	fatty-acyl-CoA synthase, alpha chain, internal fragment	YPL231w
CA1972	0.2	0.3	1.3	1.1	0.9	1.0	RPL27A	orf19.5225.2	ribosomal protein L27	YHR010w
CA1189	0.2	0.2	1.0	1.0	1.0	1.0	RPL24A	orf19.3789	ribosomal protein L24 (by homology)	YGL031c
CA5203	0.2	0.2	1.0	1.2	0.9	1.0	RPS18	orf19.7018	Ribosomal protein S18 (by homology)	YML026c
CA5345	0.2	0.3	1.1	1.2	1.0	0.9	FTR1	orf19.7219	high affinity iron permease	YER145c
CA0632	0.2	0.2	1.3	1.1	1.0	1.0	RPS5	orf19.4336	ribosomal protein S5.e (by homology)	YJR123w
CA2011	0.2	0.4	1.3	1.4	1.1	1.1	RPS31	orf19.3087	Ubiquitin fusion protein	YLR167w
CA1304	0.3	0.3	1.1	1.0	1.0	1.0	RPS13.3	orf19.4193.1	ribosomal protein (by homology)	YDR064w
CA1662	0.3	0.2	0.9	1.0	1.0	1.0				
CA2734	0.3	0.5	1.2	1.1	1.0	0.9	RPL38	orf19.2111.2	ribosomal protein L38 (by homology)	YLR325c
CA0311	0.3	0.9	0.4	1.5	0.9	1.1				
CA5343	0.3	0.2	1.0	1.0	1.0	1.0	RPL4B	orf19.7217	Ribosomal protein L4B (by homology)	YDR012w
CA2819	0.3	0.4	1.1	1.1	1.0	1.0	RPA1	orf19.2992	60S ribosomal protein	YDL081c
CA5200	0.3	0.3	1.1	1.1	1.0	1.0	RPL10E	orf19.7015	Ribosomal protein L10, cytosolic (by homology)	YLR340w
CA2031	0.3	0.2	1.0	1.1	1.0	1.0	RPL10A	orf19.3465	L10A ribosomal protein	YPL220w
CA3332	0.3	0.2	1.3	1.2	0.9	0.7	POL21.5f	orf19.2668	pol polyprotein, reverse transcripase, 5-prime end (by homol	no match
CA2805	0.3	0.4	0.7	0.8	0.7	0.8	RNR1	orf19.5779	ribonucleoside-diphosphate reductase (by homology)	YER070w
CA1062	0.3	0.2	0.6	0.4	1.0	1.2	IPF14165	orf19.4642	unknown function	no match
CA1315	0.3	0.3	0.8	0.9	1.0	0.9	URA2	orf19.2360	multifunctional pyrimidine biosynthesis protein, (by homolog	YJL130c
CA4707	0.3	0.7	0.9	0.9	1.1	1.1	PTR21	orf19.6937	peptide transporter	YKR093w
CA5816	0.3	0.3	1.0	0.8	1.0	1.1	ACC1	orf19.7466	acetyl-coenzyme-A carboxylase (by homology)	YNR016c
CA0892	0.3	1.1	1.1	1.1	0.8	0.9	PHO8.5	orf19.4736	repressible alkaline phosphatase, 5-prime end (by homology)	YDR481c
CA4512	0.3	0.3	1.0	0.9	1.1	1.1				
CA1431	0.3	0.4	1.0	1.5	1.1	0.8	FET34.3eoc	orf19.1206	iron transport multicopper oxidase, 3-prime end (by homolog	YMR058w
CA3862	0.3	0.4	1.3	1.6	1.4	1.0	NSR1	orf19.6090	nuclear localization sequence binding protein (by homology)	YGR159c
CA3547	0.3	0.4	0.8	1.0	0.8	1.0	ADE13	orf19.3870	adenylosuccinate lyase (by homology)	YLR359w
CA0254	0.4	0.4	0.9	1.1	2.3	0.9	IPF14968	orf19.3461	unknown function	no match
CA3330	0.4	0.2	1.7	1.2	0.8	0.9	POL21.3f	orf19.2669	pol polyprotein, reverse transcripase, 3-prime end (by homol	YFL050c
CA3284	0.4	0.4	0.9	0.9	1.0	1.0	ADE6	orf19.6317	5 -phosphoribosylformyl glycinamidine synthetase (by homol	YGR061c
CA5612	0.4	1.3	0.7	0.8	0.8	0.7	KAP114	orf19.7086	putative RAN-binding protein/importin (by homology)	YGL241w
CA5361	0.4	0.6	1.1	1.2	1.1	0.9	NPL3	orf19.7238	nucleolar shuttling protein with an RNA recognition motif (by I	YDR432w
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5065	0.4	0.3	1.0	1.0	0.8	1.0	IPF3584	orf19.3037	similar to Saccharomyces cerevisiae Pab1p mRNA polyaden	YER165w
CA2494	0.4	0.6	0.8	1.1	0.9	1.1	HTS1	orf19.4051	histidine tRNA synthetase (by homology)	YPR033c
CA2924	0.4	0.5	1.0	1.3	1.2	0.8	FET33	orf19.4211	cell surface ferroxidase (by homology)	YMR058w
CA1989	0.4	0.8	0.9	0.8	0.8	0.9	IPF16596	orf19.95	unknown function	no match

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

Species (Ca HS+ OS+ XS+									
Stress ()*	HS+	Cd HS+	OS+	Cd OS+	XS+	Cd XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA6109	0.5	0.5	1.1	1.1	1.0	1.0	IPF89.3f	orf19.5943.1	unknown function, 3-prime end	YLR150w
CA4490	0.5	0.7	1.0	1.1	0.8	1.1	IPF4045	orf19.1872	unknown function	no match
CA4783	0.5	0.5	1.0	1.0	1.0	1.0	IPF3358	orf19.4016	ubiquinol-cytochrome-c reductase (by homology)	YBL045c
CA1503	0.5	0.4	2.0	1.6	1.0	1.1	RKI1	orf19.1701	D-ribose-5-phosphate ketol-isomerase (by homology)	YOR095c
CA5197	0.5	0.4	1.3	1.2	1.0	0.8	IPF2342	orf19.7011	unknown function	YPL012w
CA5680	0.5	0.4	1.0	0.9	1.0	1.0				
CA2091	0.5	0.6	1.0	1.0	0.8	0.9	IPF3401	orf19.839	unknown function	YLR143w
CA5497	0.5	0.4	1.2	0.7	1.9	1.0	IPF776	orf19.5338	transcriptional activator (by homology)	YPL248c
CA5507	0.5	0.5	1.1	1.0	1.0	0.9	TIF11	orf19.5351	translation initiation factor eIF1a (by homology)	YMR260c
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA2956	0.5	0.6	0.9	1.2	1.3	1.1	EGD2	orf19.5858	Nascent polypeptide associated complex protein alpha subur	YHR193c
CA3168	0.5	0.5	1.3	1.4	1.3	1.3	PRS3	orf19.1575	ribose-phosphate pyrophosphokinase	YHL011c
CA5051	0.5	0.3	2.5	1.4	1.2	1.2	IPF3709	orf19.3015	unknown function	YDR101c
CA5596	0.5	0.9	1.1	1.0	1.0	1.1	IPF564	orf19.7104	unknown function	no match
CA1803	0.5	0.6	1.8	1.2	1.1	1.2	IPF16748	orf19.2917	unknown function	YER006w
CA1679	0.6	0.9	1.0	1.1	0.9	1.0				
CA2733	0.6	0.7	1.2	1.1	0.9	0.8	PRP18	orf19.2112	U5 snRNA-associated protein (by homology)	YGR006w
CA5204	0.6	0.5	1.1	0.7	0.7	0.9	YML6	orf19.7019	Ribosomal protein, mitochondrial (by homology)	YML025c
CA2347	0.6	0.9	0.9	1.1	1.2	1.2	RAD51	orf19.3752	DNA repair protein by homology	YER095w
CA1976	0.6	0.5	1.0	0.9	0.8	0.8	IPF9582	orf19.688	similar to Saccharomyces cerevisiae Mrps18p ribosomal prot	YNL306w
CA5627	0.6	0.8	1.1	1.1	0.9	1.2	IPF495	orf19.7069	unknown function	YBR261c
CA1927	0.6	0.6	1.0	1.1	1.0	1.0	YBN5	orf19.754	Putative purine nucleotide-binding protein (by homology)	YBR025c
CA1114	0.6	0.6	0.9	1.2	1.1	1.2	IPF9995	orf19.2286	unknown function	YJR070c
CA4498	0.6	0.4	1.4	1.4	0.9	1.0	IPF11315	orf19.512	unknown function	YNL132w
CA2682	0.6	0.6	0.9	0.9	0.9	1.1	FRS1	orf19.2573	Phenylalanyl-tRNA synthetase	YLR060w
CA4235	0.6	0.4	1.1	1.0	1.0	1.1	NCL1	orf19.518	Probable proliferating-cell nucleolar antigen (by homology)	YBL024w
CA0432	0.7	0.5	1.0	1.1	0.9	0.9	IPF7926	orf19.1341	putative protein kinase (by homology)	YDL214c
CA4708	0.7	1.0	1.8	1.1	1.2	1.1	MEU1	orf19.6938	regulator of ADH2 expression (by homology)	YLR017w
CA1982	0.7	0.6	1.0	0.8	0.9	1.1	ADK1	orf19.683	adenylate kinase, cytosolic (by homology)	YDR226w

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[[Ca OS+ down 0.667 10FDR] less [Ca HS+ down 0.667 10FDR]] less [Ca XS+ d...

Species (Ca HS+ OS+ XS+									
Stress ()*	HS+	Cd HS+	OS+	Cd OS+	XS+	Cd XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA0495	0.8	1.0	0.2	0.5	1.1	1.0	IPF20056	orf19.2659	unknown function	YER067w
11759.2	0.6	1.2	0.2	0.3	1.4	1.5				
CA0368	0.6	0.9	0.2	0.9	1.0	0.9	IPF11646	orf19.1353	unknown function	no match
CA4492	0.3	0.9	0.2	0.7	1.3	1.1	RNR22	orf19.1868	ribonucleoside-diphosphate reductase (by homology)	YJL026w
CA3637	0.3	0.9	0.2	0.5	1.8	1.3	IPF9255	orf19.5136	unknown function	YGR017w
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (a	YPR192w
CA0526	0.7	1.4	0.3	0.7	1.0	1.0	BUB3	orf19.2655	cell cycle arrest protein (by homology)	YOR026w
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA1688	0.7	0.6	0.3	0.6	0.8	0.5	COX15	orf19.3656	cytochrome oxidase assembly factor (by homology)	YER141w
CA2214	0.6	0.8	0.3	0.6	1.2	0.8	IPF9939	orf19.4752	similar to Saccharomyces cerevisiae Msn4p transcriptional ac	YKL062w
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA0684	0.7	1.0	0.3	0.9	1.1	1.1				
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA0616	0.8	1.0	0.3	0.9	2.5	1.0	PHO11	orf19.2619	Secreted acid phosphatase	YBR092c
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA3880	0.5	1.0	0.3	0.7	1.9	1.0	CAF16	orf19.388	ABC ATPase (by homology)	YFL028c
CA0109	0.6	0.8	0.3	0.6	1.0	1.0	IPF13723	orf19.260	unknown function	no match
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function	YHR067w
CA5705	0.7	1.1	0.4	1.0	3.3	1.1	IPF2645	orf19.7405	unknown function	no match
CA5605	0.7	1.0	0.4	0.9	1.1	1.0	SNF31	orf19.7094	high-affinity glucose transporter (by homology)	YDL194w
CA2977	1.3	0.9	0.4	0.5	1.4	0.8	HOM3	orf19.1235	Aspartokinase (by homology)	YER052c
CA4827	0.7	1.2	0.4	0.8	0.8	0.8	SMF2	orf19.2069	Manganese transporter (by homology)	YLR034c
CA2490	1.0	1.4	0.4	0.8	1.5	0.9	MUM2	orf19.4044	ubiquitin C-terminal hydrolase (by homology)	YBR057c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA5468	1.1	1.1	0.4	0.8	1.0	0.9	IFF7	orf19.3279	unknown function	YOL155c
CA2314	0.5	0.8	0.4	0.8	1.9	1.0	IPF14545	orf19.1381	unknown function	YCL034w
CA5749	0.9	0.7	0.4	0.4	0.8	1.0	IPF2908	orf19.7459	unknown function	YBR238c
CA0045	0.8	0.7	0.4	0.9	0.7	1.0	IPF8985	orf19.1368	unknown function	no match
CA4780	0.7	0.9	0.4	0.9	0.8	0.9	IPF3352	orf19.4013	unknown function	YHR045w
CA0884	1.3	0.9	0.4	0.9	1.7	1.1	CAN5	orf19.3641	basic amino acid permease (by homology)	YEL063c
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA5766	0.7	0.7	0.4	0.7	1.5	1.0	IPF1097	orf19.5408	serine/threonine protein kinase (by homology)	YOR267c
CA0691	1.0	1.1	0.4	1.0	1.3	1.1				
2566.2	0.9	1.0	0.4	0.9	1.1	1.1				
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in aceti	YCR032w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match
CA2391	0.4	1.3	0.4	0.8	0.8	1.0	ADH5	orf19.2608	probable alcohol dehydrogenase (by homology)	YMR303c
CA2266	0.8	0.6	0.4	0.6	1.4	1.0	HEM1	orf19.2601	5-aminolevulinic acid synthase	YDR232w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA1791	0.7	1.2	0.4	1.1	1.0	1.1	IPF13967	orf19.5205	unknown function	YLR108c
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA0576	0.9	1.8	0.4	0.8	1.4	1.0	NPR1	orf19.6232	nitrogen permease reactivator protein (by homology)	YNL183c
CA1944	0.8	1.0	0.4	0.9	1.2	0.6	IPF10645	orf19.4738	unknown function	YOR154w
CA5144	0.9	0.9	0.4	0.9	1.1	0.9	IPF1019	orf19.4581	unknown function	YJR013w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w
CA5157	0.8	1.0	0.4	1.0	1.4	1.0	IPF993	orf19.4595	unknown function	no match
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA4206	0.6	0.8	0.4	0.8	1.2	0.6	IPF9079	orf19.4550	Membrane transporter (by homology)	YCR023c
CA1426	1.0	1.1	0.4	1.0	2.2	1.1	ALS9.3f	orf19.5745	agglutinin-like protein, 3-prime end	YAL063c
CA3353	0.8	0.8	0.4	0.7	1.5	1.4	AUR1	orf19.1945	aureobasidin-resistance protein	YKL004w

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+ Species (Stress ()* Systemat	Ca HS+ Norn	Cd HS+ Norn	Ca OS+ Norn	Cd OS+ Norn	Ca XS+ Norn	Cd XS+ Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4266	1.1	1.2	0.4	0.6	5.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA4081	0.6	1.1	0.4	0.9	0.9	1.0	IPF2523	orf19.6637	unknown function	no match
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)	YMR275c
CA4529	1.0	1.3	0.4	0.7	1.0	1.1	IPF4395	orf19.1477	unknown function	YGL010w
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA4022	0.7	0.8	0.4	0.9	0.8	1.4	FRP6	orf19.3441	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA1951	0.9	0.9	0.4	0.8	1.0	0.7	HEM14	orf19.4747	Mitochondrial protoporphyrinogen oxidase (by homology)	YER014w
CA1411	1.2	1.0	0.4	0.9	0.8	1.0	IPF11858	orf19.1277	unknown function	no match
CA0367	0.6	0.9	0.4	1.0	1.4	0.9	TIM22	orf19.1352	Mitochondrial import inner membrane translocase subunit (by	YDL217c
CA5603	0.9	1.0	0.4	0.7	0.8	0.7	IPF553	orf19.7096	unknown function	YLR001c
CA3338	0.4	0.7	0.4	0.9	1.4	1.5	IPF13582	orf19.2333	unknown function	YHR009c
CA4039	0.9	1.1	0.4	0.3	1.0	1.0	SKS1	orf19.3669	serine/threonine kinase by homology	YPL026c
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)	YOR356w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homolog	YER053c
CA1410	0.8	1.1	0.4	1.0	1.0	1.1	GAT1	orf19.1275	nitrogen regulation (by homology)	YFL021w
CA0357	0.4	0.6	0.5	0.9	0.8	0.4	FCY22	orf19.333	purine-cytosine permease (by homology)	YER060w
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA0202	1.0	0.8	0.5	0.9	0.9	1.0	IPF19126	orf19.1210	putative aminoacid transporter (by homology)	YER119c
CA1377	0.9	0.9	0.5	0.8	1.0	1.0	IPF18690.5eo	orf19.461	unknown function	no match
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA4189	0.6	1.1	0.5	1.0	1.0	1.0	IPF7527	orf19.4530.1	unknown function	YHR146w
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA0998	1.3	1.3	0.5	1.0	0.8	0.9	IPF12369	orf19.4368	Putative dipeptidase (by homology)	YLL029w
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA0821	4.1	1.0	0.5	0.9	1.3	0.9	IPF16795	orf19.2989	glycerate/formate-dehydrogenase (by homology)	YNL274c
CA0189	0.7	0.4	0.5	0.6	1.2	0.9	IPF12201	orf19.4118	Na+-nucleoside cotransporter (by homology)	no match
CA1676	1.0	0.6	0.5	0.8	1.0	1.0	ERG9	orf19.3616	farnesyl-diphosphate farnesyltransferase	YHR190w
CA0890	0.5	1.0	0.5	1.0	1.2	1.3	IPF11766	orf19.4734	unknown function	YOR132w
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA6057	0.8	2.0	0.5	0.9	1.3	1.2	IPF4959	orf19.7676	D-xylulose reductase (by homology)	YDL246c
5124.1	1.1	1.2	0.5	1.0	1.0	0.6				
CA5704	0.6	1.7	0.5	0.9	1.2	1.2	CHA11	orf19.7404	L-serine/L-threonine deaminase (by homology)	YCL064c
CA5072	1.2	1.0	0.5	0.8	0.9	0.6	IPF3598	orf19.3047	similar to Saccharomyces cerevisiae Sip3p protein which inte	YNL257c
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA2392	0.8	1.2	0.5	1.1	2.1	1.2	IPF15672	orf19.2607	unknown function	YKL128c
CA2017	0.9	0.9	0.5	0.7	0.7	0.6	IPF3414	orf19.846	putative serine/threonine protein kinase	YKL171w
CA6131	0.6	0.9	0.5	0.8	0.7	0.9	IPF4369	orf19.5917	similar to Saccharomyces cerevisiae Stp2p involved in pre-tR	YHR006w
CA3258	1.1	1.0	0.5	0.9	1.1	2.7				
CA4381	0.5	0.8	0.5	0.7	0.8	0.6	PGA10	orf19.5674	unknown function	no match
CA5494	0.5	0.7	0.5	0.6	0.9	0.9	IPF85	orf19.5334	similar to Saccharomyces cerevisiae Tis11p tRNA-specific ac	YLR136c
CA4764	1.0	1.1	0.5	0.7	0.7	0.9	GPI10	orf19.3996	required for Glycosyl Phosphatdyl Inositol synthesis (by hom	YGL142c
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA4261	0.3	1.1	0.5	0.8	1.0	0.8	PDX3	orf19.550	pyridoxamine-phosphate oxidase (by homology)	YBR035c
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA3141	1.0	1.3	0.5	0.5	1.0	0.6	IPF9211.3f	orf19.3712	unknown function, 3-prime end	no match
CA1344	1.0	1.0	0.5	1.0	0.8	1.0	IPF14623	orf19.4342	unknown function	YPR009w
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA0383	1.0	1.0	0.5	0.8	1.1	0.9	IPF16028	orf19.1841	unknown function	YJR066w
CA1104	1.3	2.1	0.5	0.9	0.7	0.8	IPF18761	orf19.4947	unknown function	YPR098c
CA5170	0.5	1.0	0.5	0.9	0.6	0.9				
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA5337	1.1	1.1	0.5	0.9	1.4	0.9	APL1	orf19.7212	AP-2 complex subunit, beta2-adaptin (by homology)	YJR005w
CA1548	0.6	1.1	0.5	0.9	1.5	1.0	IPF8746	orf19.4279	putative alpha-1,3-mannosyltransferase (by homology)	YER001w
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA3122	0.8	1.2	0.5	1.0	1.3	1.2	IPF5356	orf19.3004	unknown function	YDR262w
CA0775	1.5	1.2	0.5	0.8	1.2	0.9	IFK2	orf19.856	probable monoxygenase (by homology)	no match
CA3875	1.5	1.1	0.5	1.0	1.2	1.0	IPF14430	orf19.394	putative kynureninase (by homology)	YLR231c
CA5066	1.0	1.2	0.5	0.7	1.5	0.7	TPS2	orf19.3038	Threalose-6-phosphate phosphatase (by homology)	YDR074w
CA3797	1.0	1.0	0.5	0.8	0.7	0.7	IPF5633	orf19.5821	unknown function	YML002w
CA4082	0.9	1.3	0.5	0.8	1.3	0.7	PTC4	orf19.6638	ser/thr protein phosphatase PP2C(by homology)	YBR125c
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homology)	YMR302c
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function	YBR042c
CA4949	0.8	0.7	0.5	1.0	2.1	0.9	CDC34	orf19.6529	Ubiquitin-conjugating enzyme (by homology)	YDR054c
CA2595	1.1	1.0	0.5	0.9	1.9	1.0	ARG2	orf19.56	acetylglutamate synthase (by homology)	YJL071w
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)	YPR194c
CA0609	1.4	1.3	0.5	1.0	1.8	1.0	CDR11.3f	orf19.919	multidrug resistance protein, 3-prime end (by homology)	YOR153w
CA5353	1.1	1.2	0.5	0.9	1.7	0.9	IML2	orf19.7229	unknown function	YKR018c
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA1386	0.9	0.8	0.5	1.0	1.0	1.1	THR1	orf19.923	homoserine kinase	YHR025w
CA5694	0.6	1.0	0.5	0.9	1.1	0.8	IPF3311	orf19.7396	unknown function	no match
CA0600	1.2	0.8	0.5	0.7	1.4	0.9	MSN5.5f	orf19.2666	Importin-beta family member required for nuclear export of Pl	YDR335w
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA3724	0.9	0.9	0.5	1.1	1.7	0.7	IPF6181	orf19.4174	similar to Saccharomyces cerevisiae Fun 26p nucleoside trar	YAL022c
CA1436	0.9	0.9	0.5	1.0	1.2	1.0	IPF7165	orf19.1201	similar to Saccharomyces cerevisiae Dia4p seryl-tRNA synth	YHR011w
CA4751	1.0	0.8	0.5	0.9	1.3	0.9	IPF11473	orf19.4828	unknown function	no match
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA1687	1.0	0.9	0.5	0.8	0.7	0.7	IPF12275	orf19.3658	unknown function	YER140w
CA1509	1.2	1.0	0.5	0.9	0.9	0.9	IPF19920	orf19.4524	unknown function	YKL015w
CA3931	0.7	0.9	0.5	1.0	1.1	1.1	IPF12719	orf19.5103	unknown function	YKL128c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+ Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2913	1.7	1.2	0.5	0.8	1.1	0.7	IPF11205	orf19.4513	unknown function	YLR305c
CA0214	0.9	0.9	0.5	0.7	0.7	0.7	SCT11	orf19.1289	Suppresses a choline-transport mutant	YBL011w
CA5263	0.8	1.2	0.5	1.0	1.0	0.9	CYB3	orf19.5000	Lactate dehydrogenase cytochrome b2 (by homology)	YML054c
CA3656	1.2	1.2	0.5	1.0	1.9	0.9	IPF7456	orf19.2047	unknown function	YOR289w
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA6011	1.5	1.0	0.6	1.0	1.5	1.1	CTM1	orf19.7612	cytochrome c methyltransferase (by homology)	YHR109w
CA3755	0.8	1.1	0.6	0.7	1.0	1.0	IPF17743	orf19.3421.1	Unknown function	YBL093c
CA1359	1.1	1.0	0.6	0.9	1.1	0.9	IPF11842	orf19.4405	unknown function	YBR276c
CA5794	0.6	0.8	0.6	1.0	0.7	0.7	IPF4191	orf19.5443	unknown function	YBL098w
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA4617	1.4	1.3	0.6	1.0	1.6	1.0	STB5	orf19.3308	SIN3 binding protein (by homology)	YHR178w
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA5561	0.9	1.1	0.6	0.7	0.8	1.0	SCO1	orf19.7325	Inner mitochondrial membrane protein (by homology)	YBR037c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA0578	0.9	0.9	0.6	0.7	1.2	0.6	IPF9605	orf19.3071	similar to Saccharomyces cerevisiae Mih1p M-phase inducing	YMR036c
CA6150	1.4	1.0	0.6	1.0	1.5	1.1	IPF1857	orf19.5892	similar to Saccharomyces cerevisiae Hul4p hect domain E3 u	YJR036c
CA2822	0.6	1.0	0.6	0.9	1.4	0.9	IPF14550	orf19.1314	unknown function	YMR031c
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c
CA5186	0.7	0.9	0.6	0.7	1.2	0.9	HRT2	orf19.4624	Similar to ScHRT2 (by homology)	YMR027w
CA3142	1.1	1.0	0.6	0.9	0.9	0.7	IPF9211.5f	orf19.3713	unknown function, 3-prime end	no match
CA0548	0.7	0.9	0.6	0.7	1.2	0.4	PHO87	orf19.2454	Member of the phosphate permease family (by homology)	YCR037c
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match
CA1434	1.6	1.3	0.6	0.9	0.9	1.3	SNI2	orf19.1203	Sec9 interacting protein (by homology)	YBL106c
CA3249	1.2	1.1	0.6	0.9	0.8	1.0	GEF2.3f	orf19.3734	Putative voltage-gated chloride channel protein (by homology	YJR040w
CA0921	1.0	1.0	0.6	0.9	1.0	1.0	IPF12992	orf19.1043	unknown function	YPR139c
CA1018	1.6	1.2	0.6	0.7	1.0	1.1	IPF13479.3eo	orf19.3768	unknown function, 3-prime end	YCR081w
CA1519	1.1	1.2	0.6	0.9	1.1	1.2	RIM20	orf19.4800	Rim101 activating protein	YOR275c
CA2554	0.9	1.0	0.6	1.2	1.1	1.1	Cirt4	orf19.2839	probable transposase (by homology)	YMR167w
CA5469	0.9	1.1	0.6	0.9	1.1	1.0	IPF298	orf19.3281	unknown function	YER051w
CA3517	1.0	1.0	0.6	1.0	0.9	1.0	IFA22	orf19.1002	Unknown function	YJL005w
CA3346	0.6	1.4	0.6	1.1	1.8	1.2	IPF13356	orf19.2324	molybdopterin biosynthesis (by homology)	YHR111w
CA5754	0.9	0.9	0.6	0.9	1.3	0.8				
CA3029	0.9	1.0	0.6	0.9	1.7	1.1	IPF13825	orf19.223	serine/threonine protein kinases (by homology)	YNR047w
CA2558	0.5	0.5	0.6	0.8	0.8	0.7	RBT5	orf19.5636	repressed by TUP1 protein 5	no match
CA1364	1.1	1.4	0.6	0.9	0.9	0.7	IPF5561	orf19.4423	unknown function	YDR326c
CA5484	1.2	1.1	0.6	0.8	0.8	0.8	RAD1.3f	orf19.5318	UV endonuclease, component of the nucleotide excision repa	YPL022w
CA5068	0.7	1.0	0.6	1.1	0.9	1.5	IPF3592	orf19.3041	unknown function	YGR068c
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA2807	1.0	1.2	0.6	0.8	1.2	1.1	IPF11965	orf19.5782	unknown function	YOR022c
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA3877	0.6	0.9	0.6	0.7	0.9	0.8	CBP4	orf19.392	Ubiquinol--cytochrome-c reductase assembly factor (by homc	YGR174c
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA4900	0.9	1.1	0.6	0.9	1.4	0.9	IFP2	orf19.6037	unknown function	no match
CA4629	1.7	1.4	0.6	0.6	1.2	0.9	IPF13709	orf19.335	unknown function	YKL193c
CA1470	0.8	0.9	0.6	0.8	1.2	1.0	IPF17942	orf19.796	unknown function	YKL189w
CA4647	1.0	0.9	0.6	1.1	0.7	0.7	IPF1493	orf19.354	X-Pro aminopeptidase II (by homology)	YER078c
CA2318	1.0	0.7	0.6	1.1	1.1	1.0	ILV1	orf19.5480	Threonine dehydratase (by homology)	YER086w
CA4484	1.4	1.1	0.6	1.1	1.1	1.3	HEM15	orf19.1880	ferrochelatase precursor (by homology)	YOR176w
CA2859	1.1	0.9	0.6	1.0	0.9	0.7	IPF7056	orf19.1063	unknown function	YBR004c
CA5506	0.7	1.0	0.6	1.0	0.9	1.0	IPF748	orf19.5350	unknown function	YML112w
CA2650	1.3	1.9	0.6	0.8	1.0	1.0	STV1	orf19.1190	H+-ATPase V0 domain (by homology)	YOR270c
CA3658	0.8	1.1	0.6	1.1	1.5	1.0	TGL1	orf19.2050	Triacylglycerol lipase (by homology)	YKL140w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match
CA5699	1.1	1.0	0.6	1.0	1.3	1.0	ALS7	orf19.7400	agglutinin-like protein	YAR050w
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA1357	0.7	0.9	0.6	0.8	1.5	1.0	ARH1	orf19.410	adrenodoxin reductase and ferredoxin-NADP+ reductase (by	YDR376w
CA5973	1.4	1.0	0.6	1.0	1.7	1.1	IPF931	orf19.7567	unknown function	YDR124w
CA1015	1.0	1.0	0.6	0.9	1.3	1.2	IPF15547	orf19.3956	putative glutamyl-tRNA amidotransferase subunit A (by homo	YMR293c
CA2745	0.8	0.9	0.6	1.2	0.8	0.7	HIR1.3f	orf19.2099	Histone transcription regulator (by homology)	YBL008w
CA0476	1.7	1.1	0.6	0.9	0.9	1.0	UBP2	orf19.457	Ubiquitin-specific proteinase (by homology)	YOR124c
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA1942	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eoc	orf19.4191.1	Ubiquitin--protein ligase, 3-prime end (by homology) FALSOF	YGL141w
CA4608	1.0	0.9	0.6	0.7	0.8	0.9	CCH1	orf19.3298	Calcium channel protein (by homology)	YGR217w
CA0267	1.0	1.0	0.6	1.0	1.0	1.0	PGA40	orf19.1616	extracellular alpha-1,4-glucan (by homology)	no match
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA4678	1.3	1.1	0.6	0.9	0.8	1.0	IPF3670	orf19.894	unknown function	YDR137w
CA4907	0.8	0.9	0.6	1.1	0.9	0.9	PSD1	orf19.6045	Phosphatidylserine decarboxylase 1 (by homology)	YNL169c
6832.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA2215	1.2	1.3	0.6	0.8	1.2	0.9	PFK26	orf19.4753	6-phosphofructose-2-kinase (by homology)	YIL107c
CA4899	1.3	0.9	0.6	0.7	0.8	0.9	IPF1460	orf19.6036	unknown function	YLR039c
CA2872	1.1	1.0	0.6	1.0	0.8	0.9	APG13	orf19.2848	probable component of the autophagic system (by homology)	YPR185w
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by ho	YML130c
CA4243	0.9	1.1	0.6	0.9	0.8	0.9	IPF16491	orf19.529	unknown function	YIR019c
CA5753	1.1	0.9	0.6	0.9	1.2	0.8	FKH2	orf19.5390	Fork head protein type transcription factor	YNL068c
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match
CA3843	0.8	1.0	0.6	0.8	0.9	1.0	IPF7947	orf19.6602	unknown function	YLR201c
CA4215	0.7	0.8	0.6	0.9	1.1	1.4	SSY1	orf19.814	Regulator of transporters (by homology)	YDR160w
CA2844	0.9	1.1	0.6	1.0	1.2	1.1	IPF13158	orf19.5729	unknown function	YLR098c
CA3403	1.5	1.2	0.6	0.7	0.8	1.2	IPF8650	orf19.3980	RNA helicase (by homology)	YGR271w
CA4469	1.1	1.3	0.6	0.8	0.8	1.0	TOR2.3f	orf19.1903	phosphatidylinositol 3-kinase, 3-prime end (by homology)	YKL203c
CA6151	1.2	1.0	0.6	1.0	1.3	1.0	IPF1853	orf19.5890	unknown function	no match
CA4183	1.2	0.8	0.6	1.0	1.0	1.1	SNO1	orf19.2948	hisH-like protein (by homology)	YMR095c
CA1643	1.0	1.1	0.6	0.8	1.5	0.9	IPF9347	orf19.1729	unknown function	no match
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA6031	0.9	0.9	0.6	1.1	1.4	1.0	PRO1	orf19.7638	glutamate 5-kinase (by homology)	YDR300c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA1232	1.0	1.1	0.6	0.6	1.0	1.3	IPF11815	orf19.4982	similar to Saccharomyces cerevisiae Lys14 triacyglycerol lipa	YKL140w
CA4372	0.9	0.8	0.6	0.9	0.8	1.0	IPF5282	orf19.5663	unknown function	YMR034c
CA3468	1.1	1.0	0.6	1.0	1.3	0.9	IPF6318	orf19.1664	beta-glucosidase (by homology)	no match
CA1935	0.8	1.2	0.6	1.0	1.0	1.0	IPF19936	orf19.4185	unknown function	YGR203w
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA2263	0.5	0.6	0.6	0.6	2.2	1.2	GPD1	orf19.1756	Glycerol-3-phosphate dehydrogenase (by homology)	YOL059w
CA5955	0.9	1.1	0.6	0.8	0.8	0.8	IPF3510	orf19.6739	unknown function	YMR278w
CA2803	0.8	1.2	0.6	0.9	0.9	1.0	IPF11711	orf19.5776	ubiquitin-protein ligase (by homology)	YDR457w
CA2285	1.1	1.4	0.6	0.9	1.0	0.7	IPF12629	orf19.5552	unknown function	YOL063c
CA4527	0.8	1.1	0.6	1.0	0.7	0.9	IPF4398	orf19.1479	unknown function	YGL023c
CA0702	0.9	1.2	0.6	0.8	1.0	0.8	IPF11812.3f	orf19.2913	unknown function	no match
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA4382	0.9	0.9	0.6	0.9	0.9	0.5	IPF8576	orf19.5675	similar to Saccharomyces cerevisiae Ris1p DNA helicase (by	YOR191w
CA2037	0.9	1.0	0.6	1.0	0.9	0.8	IFF3	orf19.4361	unknown function	YOL155c
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w
CA3681	1.1	1.1	0.6	0.9	0.8	0.8	IPF19787	orf19.728	unknown function	YER093c
CA4341	0.9	1.0	0.6	0.9	1.0	0.8	IPF3624	orf19.6713	unknown function	no match
CA5358	0.8	1.2	0.6	0.9	2.1	1.4	IPF846	orf19.7235	WD-repeat protein, beta-transducin (by homology)	YMR102c
CA2871	1.1	1.0	0.6	0.9	1.0	1.3	OPT2.3f	orf19.2847.2	Oligopeptide transporter, 3-prime end (by homology)	YPR194c
CA2384	0.9	1.1	0.6	0.8	1.0	0.8	MDL1	orf19.2615	ATP-DEPENDENT PERMEASE	YLR188w
CA2007	1.0	1.4	0.6	0.8	1.0	1.3	GPI8	orf19.2799	essential for GPI anchor attachment (by homology)	YDR331w
CA4199	2.0	2.1	0.6	0.9	1.4	1.4	UBC8	orf19.4540	ubiquitin-conjugating enzyme (by homology)	YEL012w
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA1197	1.2	1.0	0.6	0.9	3.6	1.1				
CA4681	1.1	0.9	0.6	1.0	1.1	0.9	IPF3679	orf19.889	similar to Saccharomyces cerevisiae Thi20p hydroxymethylpy	YOL055c
CA5762	1.3	0.9	0.6	1.0	0.9	0.9	IFF10.3f	orf19.5401	unknown function, 3-prime end	YJR151c
CA4852	0.4	0.5	0.6	0.7	0.9	0.8	SCS7	orf19.3822	Required for hydroxylation of ceramide (by homology)	YMR272c
CA5257	1.0	1.4	0.6	1.0	0.9	1.1				
CA3834	0.6	0.8	0.6	0.9	1.0	0.7	PLB3	orf19.6594	phospholipase B (by homology)	YMR008c
CA2995	1.0	1.0	0.6	0.7	1.0	0.9	IPF9113	orf19.6121	unknown function	YER130c
CA1737	0.5	0.8	0.6	1.1	1.0	0.9	LYS12	orf19.2525	homo-isocitrate dehydrogenase (by homology)	YIL094c
CA5159	0.9	1.4	0.6	0.9	1.2	1.0	CAP2	orf19.4597	F-actin capping protein, beta subunit (by homology)	YIL034c
CA1494	0.4	0.8	0.6	0.8	0.9	0.7	IPF171	orf19.3228	unknown function	YER113c
CA3027	1.0	1.0	0.6	0.9	1.0	0.8	IPF20126	orf19.3900	putative chromosome segregation protein (by homology)	YDR470c
CA5735	0.5	1.0	0.6	0.8	1.6	0.9	IPF2878	orf19.7445	unknown function	YBR105c
CA6157	0.9	1.1	0.6	0.8	1.1	0.8	GEF1.5f	orf19.5880	Voltage-gated chloride channel protein, 5-prime end (by hom	YJR040w
CA5713	1.1	1.0	0.6	1.0	1.0	1.3	ALS6	orf19.7414	agglutinin-like protein	YJR004c
CA0317	1.4	1.3	0.6	0.9	0.8	0.8	SSD1	orf19.3959	Protein phosphatase (by homology)	YDR293c
CA3358	0.6	0.9	0.6	1.0	1.0	1.2	IPF19984	orf19.1940	similar to Saccharomyces cerevisiae Cat5p involved in coenz	YOR125c
CA2852	1.2	1.0	0.6	1.0	1.1	1.2	ALS5	orf19.5736	agglutinin-like protein	YJR004c
CA4410	1.2	0.7	0.6	1.1	1.5	1.1	TRP4	orf19.3099	Anthranilate phosphoribosyltransferase	YDR354w
CA0855	1.0	1.0	0.6	0.8	0.9	0.4	AMYG1	orf19.4899	glucoamylase	YBR229c
CA2553	1.1	1.2	0.6	0.9	0.9	1.0	IPF9096	orf19.2838	probable mannosidase (by homology)	no match
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA2795	0.6	1.1	0.6	0.9	0.9	1.1	IPF8407	orf19.1723	unknown function	YJL055w
CA4085	0.9	1.1	0.6	0.9	1.3	1.0	IPF5015	orf19.6641	unknown function	no match
CA4874	0.6	0.6	0.6	0.5	1.8	1.4	IPF1674	orf19.6559	putative transcription initiation factor (by homology)	YNL108c
CA2185	1.1	1.1	0.7	1.1	0.9	0.9	IPF6880	orf19.4247	unknown function	no match
CA0601	1.0	0.9	0.7	0.7	0.9	1.0	MSN5.3f	orf19.2665	Importin-beta family member required for nuclear export of Pt	YDR335w
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA1469	1.0	1.2	0.7	0.9	1.4	1.0	IPF5078	orf19.795	unknown function	YLR417w
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA1165	1.2	0.9	0.7	1.1	3.0	1.3	IPF19902	orf19.3360	unknown function	no match
CA4828	0.6	1.4	0.7	0.9	0.9	1.0	IPF1209	orf19.2068	unknown function	YJL010c
CA2339	0.8	0.8	0.7	1.6	2.3	1.4	IPF13377	orf19.2350	unknown function	YOR378w
CA4053	4.1	0.9	0.7	1.0	1.4	1.0	IKS1	orf19.428	PROBABLE SERINE/THREONINE-PROTEIN KINASE	YJL057c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3f	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA2288	0.9	0.8	0.7	0.9	1.0	0.9	IPF5376	orf19.5557	unknown function	YKL201c
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA2547	1.2	1.0	0.7	0.7	0.9	0.6	IPF14911	orf19.2832	unknown function	YNL152w
CA3866	0.7	0.7	0.7	1.3	0.9	0.8	IPF4606	orf19.6082	unknown Function	YML048w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA1754	1.0	1.3	0.7	0.7	1.3	1.1	IPF16320	orf19.5131	Unknown function	YCL039w
CA5843	0.5	0.9	0.7	0.7	0.8	1.0	IPF416	orf19.7499	unknown function	YLR328w
CA0103	1.3	1.0	0.7	0.9	1.3	0.9	IPF17515	orf19.749	unknown function	YAL002w
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match
CA3206	0.8	1.1	0.7	1.1	0.9	1.0	IPF3454	orf19.6187	unknown function	no match
CA4621	1.6	0.9	0.7	0.9	0.8	0.8	IPF5753	orf19.3312	unknown function	YER080w
CA1967	0.9	0.9	0.7	1.1	1.0	0.8	IPF10866	orf19.5219	GTPase-activator protein (by homology)	YOL081w
CA5225	0.9	1.0	0.7	1.0	1.6	0.9	ACB1.3f	orf19.7043.1	acyl-coenzyme-A-binding protein, 3-prime nd (by homology)	YGR037c

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[[Ca XS+ down 0.667 10FDR] less [Ca HS+ down 0.667 10FDR]] less [Ca OS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2479	0.7	1.1	1.3	1.1	0.1	0.5	CCN1	orf19.3207	G1 cyclin	YAL040c
CA5073	0.6	1.0	0.8	0.9	0.2	0.6	IPF3603	orf19.3048	unknown function	no match
CA5152	1.0	0.9	0.9	0.8	0.2	0.3	CAT2	orf19.4591	carnitine O-acetyltransferase (by homology)	YML042w
CA3883	0.5	0.2	1.0	1.3	0.2	0.4	GCV2	orf19.385	Glycine decarboxylase P subunit	YMR189w
CA4005	0.5	0.6	1.1	1.1	0.2	0.5	ERG6	orf19.1631	sterol transmethylase	YML008c
CA2986	0.7	0.5	0.7	0.9	0.2	0.3	CDC5	orf19.6010	Cell-cycle protein kinase (by homology)	YMR001c
CA4097	0.7	0.8	1.3	0.9	0.2	0.5	GIN4	orf19.663	ser/thr protein kinase (by homology)	YDR507c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0095	0.8	1.0	1.5	0.7	0.2	0.6	ALG11	orf19.3468	required for asparagine-linked oligosaccharide assembly (by	YNL048w
CA2176	1.2	0.6	1.3	0.8	0.2	0.3	CDC54	orf19.3761	cell division control protein (by homology)	YPR019w
CA5201	0.6	0.9	1.1	0.9	0.2	0.6	IPF2349	orf19.7016	similar to human sphingomyelin	YDR452w
CA1614	1.2	1.3	0.9	1.1	0.2	0.4	IPF18645	orf19.3216	unknown function	YAL018c
CA3452	0.7	1.0	0.9	1.0	0.2	0.9	IPF10541	orf19.1253	unknown function	YFR034c
CA0056	1.0	1.1	1.0	1.0	0.3	0.7	IPF15839	orf19.556	unknown function	no match
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA1583	1.2	1.1	1.1	1.2	0.3	0.8	ROT1	orf19.6029	Suppressor of TOR2 mutations (by homology)	YMR200w
CA1776	1.2	1.0	0.7	0.8	0.3	0.8	IPF14704	orf19.1823	unknown function	YLR241w
CA6128	0.9	1.0	1.9	0.8	0.3	0.5	IPF152	orf19.5919	unknown function	YOR129c
CA0689	0.5	0.3	1.5	1.4	0.3	0.3	IPF14119	orf19.4688	unknown function	no match
CA4880	0.9	1.0	1.2	0.9	0.3	0.6	RHC18	orf19.6568	Recombination repair protein (by homology)	YLR383w
CA1749	0.9	1.0	0.7	0.9	0.3	0.7	IPF8257.3f	orf19.1518.3	unknown function, 3-prime end	no match
CA0415	1.0	0.7	1.8	0.9	0.3	0.3	FRP3	orf19.1224	member of the FRP family of proteins related to Yarrowia lipo	YCR010c
CA6028	0.7	0.9	1.0	0.8	0.3	0.8	IPF607	orf19.7634	unknown function	YDL003w
CA0822	1.5	0.8	1.2	1.0	0.3	0.3	EXG1	orf19.2990	glucan 1,3-beta-glucosidase	YLR300w
CA2150	0.7	1.0	0.8	0.7	0.3	0.7	IPF19940	orf19.6022	unknown function	no match
CA1745	0.9	1.0	0.9	1.0	0.3	0.6	IPF10888	orf19.5051	unknown function	no match
CA2885	0.5	0.6	0.9	0.9	0.3	0.8	PGA26	orf19.2475	unknown function	no match
CA4373	0.8	0.6	0.7	1.0	0.3	0.5	IPF5287	orf19.5664	signal transduction protein (by homology)	YMR032w
CA5918	1.0	0.7	1.3	1.3	0.3	0.6	ERV14	orf19.6787	membrane protein	YGL054c
CA0969	1.2	0.6	1.4	0.8	0.3	0.4	IPF9132	orf19.5541	unknown function	YPL184c
CA1778	0.8	1.0	1.7	1.0	0.3	1.0	IPF13810	orf19.1825	unknown function	no match
CA1493	1.4	0.8	1.3	1.0	0.3	0.7	FTH2	orf19.3227	iron transporter (by homology)	YBR207w
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA0883	1.0	0.6	1.0	1.2	0.3	0.6	SUN41	orf19.3642	Putative cell wall beta-glucosidase (by homology)	YIL123w
CA3613	1.1	0.9	1.0	0.8	0.3	0.7	SPF1	orf19.30	P-type ATPase	YEL031w
CA2042	0.7	0.9	0.8	0.8	0.3	0.5				
CA0686	0.9	1.0	0.9	0.7	0.3	0.5	IPF162	orf19.3222	sulphate transporter (by homology)	YGR125w
CA2405	1.2	1.1	0.9	0.9	0.3	0.7	PGA18	orf19.301	unknown function	no match
CA1077	1.1	0.8	0.9	0.8	0.3	0.5	IPF13694	orf19.2238	unknown function	YAL024c
CA2195	0.9	0.8	0.8	0.9	0.3	0.6	IPF18517	orf19.4349	unknown function	YOL070c
CA5482	1.0	0.8	0.8	0.9	0.3	0.5	IFV4.3f	orf19.5315	unknown function	no match
CA3604	0.5	0.6	2.1	1.8	0.3	0.4	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)	no match
CA2172	1.2	0.7	0.7	1.1	0.3	0.5	IPF15377	orf19.3765	probable membrane protein involved in bipolar budding (by h	YLR084c
CA3705	0.5	0.9	1.1	1.0	0.3	0.7	MSH6	orf19.4945	DNA mismatch repair protein by homology	YDR097c
CA2674	1.4	1.0	1.3	0.9	0.3	0.7	IPF5846	orf19.5495	unknown function	YML117w
CA5406	0.8	0.9	1.0	1.1	0.3	0.9	IPF1547	orf19.949	unknown function	YLR309c
CA1710	0.9	1.2	0.9	0.9	0.3	0.8	CLA4	orf19.4890	protein kinase homolog (by homology)	YNL298w
CA4554	1.0	1.0	0.9	0.9	0.3	0.8	IPF7874	orf19.1445	similar to Saccharomyces cerevisiae Esc4p involved in chrom	YHR154w
CA1748	0.8	0.9	0.6	0.9	0.3	0.7	IPF8257.5f	orf19.1522	unknown function, 5-prime end	no match
CA5645	0.7	0.3	1.0	1.0	0.3	0.5	CYB5	orf19.7049	Cytochrome b5 (by homology)	YNL111c
CA1350	0.8	0.8	1.6	1.2	0.3	0.6	MCM2	orf19.4354	replication licensing factor (by homology)	YBL023c
CA1072	1.0	1.1	1.0	1.1	0.3	0.8	SBH1	orf19.2533.1	involved in translocation into the ER (by homology)	YER087cb
CA0156	0.9	1.0	1.0	1.1	0.3	0.9	SCW1.3f	orf19.1779	glucanase (by homology)	YGR279c
CA0104	0.6	0.8	0.7	1.1	0.3	0.8	RBT4	orf19.6202	repressed by TUP1 protein	YJL079c
CA0435	1.1	1.4	0.9	0.7	0.3	0.8	UGP1	orf19.1738	UTP--glucose-1-phosphate uridylyltransferase (by homology)	YKL035w
CA1053	0.9	0.7	0.8	0.7	0.3	0.5	SCW11.3eoc	orf19.3893	glucanase gene family member, 3-prime end (by homology)	YGL028c
CA1218	0.8	0.7	0.7	0.7	0.3	0.4	CDC20	orf19.122	anaphase promoting complex subunit (by homology)	YGL116w
CA5563	1.1	0.9	1.4	1.1	0.3	0.6	PHO88	orf19.7327	Involved in phosphate transport (by homology)	YBR106w
CA5839	1.1	1.0	0.9	0.9	0.3	0.6	IPF423	orf19.7494	unknown function	YLR320w
CA0932	1.1	0.7	1.2	1.2	0.4	0.5	EPT1	orf19.3695	alcohol phosphatidyl transferase (by homology)	YHR123w
CA5003	1.2	1.0	1.0	0.9	0.4	0.5	MCD4	orf19.5244	Sporulation protein (by homology)	YKL165c
CA2980	1.1	0.8	1.1	1.0	0.4	0.6	GOG5	orf19.1232	GDP-mannose transporter (by homology)	YGL225w
CA0846	0.7	0.8	1.2	0.8	0.4	0.7	SMC3.5f	orf19.262	required for structural maintenance of chromosomes, 5-prime	YJL074c
CA5454	0.5	1.1	1.3	0.9	0.4	1.0	IPF257.3f	orf19.3261	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA1306	0.9	0.8	1.0	1.1	0.4	0.5	CDC14	orf19.4192	protein phosphatase	YFR028c
CA2154	0.4	1.3	1.2	1.1	0.4	0.7	ERG2	orf19.6026	C-8 sterol isomerase	YMR202w
CA1351	0.9	0.9	1.1	1.0	0.4	0.7	PCL2	orf19.403	G1/S specific cyclin	YDL127w
CA5674	0.7	0.9	0.6	0.9	0.4	0.6	IPF1274	orf19.7377	similar to Saccharomyces cerevisiae Ase1p component of the	YOR058c
CA6022	0.8	0.9	3.3	1.2	0.4	0.4	PGA1	orf19.7625	GPI-anchored cell surface protein (by homology)	no match
CA3939	1.0	0.9	3.2	1.1	0.4	0.8	HNM1	orf19.2003	Choline permease (by homology)	YGL077c
CA3688	0.9	0.9	1.7	1.2	0.4	0.7	YIP3	orf19.6264.3	protein of unknown function, (by homology)	YNL044w
CA2821	0.7	0.4	0.7	0.9	0.4	0.5				
CA1095	0.8	0.5	1.3	0.9	0.4	0.7	SMC1	orf19.4367	Chromosomal ATPase family member (by homology)	YFL008w
CA5076	0.4	0.3	0.9	0.6	0.4	0.8	IPF15301	orf19.3051	unknown function	YJR116w
CA4887	1.1	1.0	1.2	1.3	0.4	0.7	IPF1632	orf19.6579	unknown function	no match
CA0358	1.0	1.0	1.0	1.0	0.4	1.0	IPF17488.5f	orf19.1818	unknown function, 5-prime end	no match
CA2079	0.9	0.5	0.7	0.8	0.4	0.5	MNN3	orf19.4874	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA0197	0.7	0.9	2.3	2.0	0.4	0.6	IPF9787	orf19.1934	similar to Saccharomyces cerevisiae Hst3p silencing protein i	YOR025w
CA1831	0.9	0.7	0.7	1.1	0.4	0.5	CHS1	orf19.5188	Chitin synthase (by homology)	YBR038w
CA1772	0.8	1.0	0.8	0.9	0.4	0.5	ALG7	orf19.2187	UDP-N-acetylglucosamine-1-phosphate transferase (by hom	YBR243c
CA3072	0.8	1.2	0.9	1.0	0.4	0.8	ERG12	orf19.4809	Mevalonate kinase (by homology)	YMR208w
CA0260	1.2	0.7	1.7	0.9	0.4	0.7	IPF13683	orf19.2547	unknown function	no match
CA5533	1.1	1.1	1.0	1.0	0.4	0.6	IPF2846	orf19.7293	similar to Saccharomyces cerevisiae Mps1p serine/threonine	YDL028c
CA1628	1.0	1.1	1.0	1.0	0.4	0.5	HMG1	orf19.1031	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (by hom	YLR450w
CA4528	1.4	1.3	0.9	0.9	0.4	0.7	STT3	orf19.1478	oligosaccharyl transferase (by homology)	YGL022w
CA5236	0.8	0.5	0.8	0.7	0.4	0.6	LCB2	orf19.5027	Palmitoyl transferase (by homology)	YDR062w
CA2637	0.7	0.8	1.1	1.0	0.4	0.9	IPF19954	orf19.4301	unknown function	no match
CA5023	0.7	0.7	2.1	1.0	0.4	0.6	IPF7547	orf19.6976	unknown function	YJL163c
CA4749	0.6	0.6	1.0	0.8	0.4	0.8	IPF4481	orf19.4831	unknown function	no match
CA0411	0.8	1.0	1.4	1.0	0.4	0.8	IPF17676	orf19.1507	similar to Saccharomyces cerevisiae Cst13p involved in chro	YBR158w
CA1819	1.1	1.0	1.2	1.0	0.4	0.9	IPF16549	orf19.4273	Unknown function	YLR139c
CA3093	0.7	0.9	1.1	0.8	0.4	0.8	TOF1.5f	orf19.4136	Topoisomerase I interacting factor 1, 5-prime end (by homolo	YNL273w
CA5844	1.3	1.1	1.3	1.2	0.4	0.7	PXA1	orf19.7500	long chain fatty acid ABC transporter (by homology)	YPL147w
CA1956	0.5	0.6	0.9	0.8	0.4	0.5	ERG3	orf19.767	C5,6 desaturase	YLR056w
CA0852	1.1	0.9	0.8	0.9	0.4	0.8	KIP2	orf19.1747	Kinesin-related protein required for nuclear migration (by hon	YPL155c
CA1076	1.0	0.9	0.7	0.8	0.4	0.7	IPF19721	orf19.2239	similar to Saccharomyces cerevisiae Lte1p GDP/GTP exchan	YAL024c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+ Species (Stress ()* Systemat	Ca HS+ Norn	Cd HS+ Norn	Ca OS+ Norn	Cd OS+ Norn	Ca XS+ Norn	Cd XS+ Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5681	0.8	1.1	1.0	1.0	0.4	0.6	MNN9	orf19.7383	Required for complex N-glycosylation	YPL050c
CA4094	0.6	0.7	1.2	0.9	0.4	0.8	IPF4004	orf19.658	unknown function	YCL061c
CA1140	0.7	1.0	1.3	0.9	0.4	1.0	IPF17322.3f	orf19.4068	unknown function, 3-prime end	YNR052c
CA0349	0.9	0.9	0.7	1.0	0.4	0.5	IPF19026	orf19.1813	unknown function	YAL053w
CA1226	0.9	1.1	1.1	0.9	0.4	0.7	IPF15660	orf19.4159	putative mitochondrial carrier (by homology)	YMR166c
CA5600	0.5	0.7	0.6	1.0	0.4	0.5	IPF559	orf19.7100	unknown function	YJR001w
CA4233	0.8	0.9	1.0	1.1	0.4	0.7	RFT1	orf19.516	nuclear division protein (by homology)	YBL020w
CA5423	0.9	1.0	0.7	1.0	0.4	0.5	ROT2	orf19.974	Glucosidase II, catalytic subunit (by homology)	YBR229c
CA4295	1.0	1.0	0.9	1.0	0.4	0.8	MNN7	orf19.6692	putative Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA1352	0.9	1.0	0.9	1.3	0.4	0.5	VCX1	orf19.405	Ca2+-transport by homology	YDL128w
CA4553	0.5	0.7	0.5	0.7	0.4	0.6	CYB1	orf19.1446	G2/Mitotic-specific cyclin	YPR119w
CA6163	0.3	0.3	1.0	0.8	0.4	0.8	POL1	orf19.5873	DNA-directed DNA polymerase alpha (by homology)	YNL102w
CA3040	0.7	0.8	0.8	1.0	0.4	0.7	IPF7306	orf19.2425	putative permease (by homology)	YBR241c
CA3619	0.7	0.6	1.1	0.9	0.4	0.6	CDC47	orf19.202	cell division control protein, ,(by homology)	YBR202w
CA1945	0.9	0.9	1.0	0.8	0.4	0.6	MSS116	orf19.4739	RNA helicase of the DEAD box family (by homology)	YDR194c
CA2591	0.8	1.2	0.8	0.9	0.4	0.7	IPF18448.3eo	orf19.60	unknown function, 3-prime end	YJL062w
CA3548	0.9	1.0	1.0	1.1	0.4	0.8	IPF12179	orf19.3872	unknown function	YGR026w
CA3397	1.4	1.0	1.6	1.1	0.4	0.6	IPF13618	orf19.3972	unknown function	YMR292w
CA5858	1.0	0.9	1.0	1.0	0.4	0.8	IPF380	orf19.7516	unknown function	no match
CA4113	1.2	1.0	1.8	1.5	0.4	0.7	CHO1	orf19.677	Phosphatidylserine synthase	YER026c
CA0199	1.0	0.7	1.3	1.0	0.4	0.6	KAP104	orf19.3556	karyopherin-beta protein (by homology)	YBR017c
CA2509	1.2	0.9	1.5	1.4	0.4	0.7	IPF1471	orf19.304	aminotriazole resistance protein (by homology)	YOR378w
CA2193	0.7	0.8	0.8	0.8	0.4	0.6	IPF14273	orf19.4347	Probable ser/thr protein kinase (by homology)	YKL116c
CA5953	0.7	0.6	1.0	0.4	0.4	0.3	IPF3506	orf19.6741	unknown function	YLR414c
CA0300	0.7	0.7	0.9	1.0	0.4	0.6	ERG24	orf19.1598	C-14 sterol reductase (by homology)	YNL280c
CA5736	1.0	1.6	0.7	1.1	0.4	0.9	OPI3	orf19.7446	Methylene-fatty-acyl-phospholipid synthase (by homology)	YJR073c
CA5209	0.9	0.9	1.4	1.2	0.4	0.6	MCM1	orf19.7025	Transcription factor of the MADS box (by homology)	YMR043w
CA5859	1.0	0.9	0.9	1.0	0.4	0.8	CHT1	orf19.7517	endochitinase 1 precursor	YLR286c
CA0563	1.4	0.9	1.3	0.9	0.4	0.6	MNN11	orf19.2927	Mannosyltransferase complex component (by homology)	YJL183w
CA1476	1.0	0.9	1.0	0.9	0.4	0.8	IPF10214	orf19.1093	unknown function	no match
CA3197	1.2	1.1	1.0	1.2	0.4	0.7	SEC61	orf19.6176	ER protein-translocation complex subunit	YLR378c
CA0964	0.4	0.6	0.8	0.9	0.4	0.6	IPF9141	orf19.6247	similar to Saccharomyces cerevisiae Ctf4p DNA-directed DN/	YPR135w
CA3599	1.1	0.6	0.7	0.6	0.4	0.4	IPF19785	orf19.4929	unknown function	YLR067c
CA1365	1.6	1.0	0.9	0.9	0.4	1.3	IPF11849	orf19.4459	unknown function	YNL234w
CA4514	1.2	0.9	1.2	0.8	0.4	0.8	IPF20016	orf19.491	similar to Saccharomyces cerevisiae Sec63p ER protein-tran:	YOR254c
CA5232	1.0	1.0	1.0	1.1	0.4	1.0	SUN42	orf19.5032	Putative cell wall beta-glucosidase (by homology)	YIL123w
CA0110	1.1	0.6	0.8	0.6	0.4	0.6	IPF17190	orf19.3869	unknown function	no match
CA1499	0.9	0.9	0.9	0.8	0.4	0.7				
CA2769	1.0	0.8	0.9	0.8	0.4	0.5	PGA54	orf19.2685	unknown function	no match
CA6095	1.1	1.0	1.6	0.7	0.4	0.5	SNF3	orf19.5962	High affinity glucose transport protein (by homology)	YDL194w
CA5153	0.9	1.0	1.0	1.1	0.4	0.5	IPF1003	orf19.4592	unknown function	no match
CA2418	1.0	0.8	1.0	1.2	0.4	0.4	MNT4	orf19.4475	putative mannosyltransferase	YBR199w
CA3462	1.2	1.1	1.0	0.8	0.4	0.8	IPF14959	orf19.1265	similar to Saccharomyces cerevisiae Trs130p TRAPP subunit	YMR218c
CA3282	0.9	1.0	1.0	1.0	0.4	0.9	IPF6272	orf19.6315	unknown function	no match
CA2724	0.7	0.8	0.7	1.0	0.4	0.5	RPB7	orf19.3347	DNA-directed RNA polymerase II, 19 KD subunit (by homolog	YDR404c
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA4194	1.2	1.0	1.0	1.0	0.4	0.7	PTR3	orf19.4535	transcriptional regulator (by homology)	YFR029w
CA3046	0.9	0.9	1.2	0.8	0.4	0.6	IPF7295	orf19.2417	unknown function	YOL034w
CA0049	1.3	1.4	1.2	1.0	0.4	0.8	IPF3908	orf19.757	unknown function	YPR090w
CA2188	1.2	1.1	1.0	1.1	0.4	0.6	SSU81	orf19.4772	protein involved in the HOG1 high-osmolarity signal transduc	YER118c
CA0642	0.4	0.3	1.3	1.4	0.4	0.4	ERG25	orf19.3732	C-4 sterol methyl oxidase	YGR060w
CA5241	1.0	1.0	0.7	1.0	0.4	0.3	SMF3	orf19.5022	Probable manganese transporter (by homology)	YOL122c
CA1223	1.1	1.2	0.9	0.8	0.4	0.7	IPF14870	orf19.4131	unknown function	YCL045c
CA3965	0.8	1.0	1.0	1.0	0.4	0.8	IPF9375	orf19.1426	unknown function	YHR149c
CA3320	0.8	0.8	0.7	0.8	0.4	0.7	IPF6898	orf19.2678	similar to Saccharomyces cerevisiae Bub1p serine/threonine	YGR188c
CA6061	0.6	0.6	2.3	1.2	0.4	0.4	IPF8302	orf19.6007	unknown function	YJL196c
CA4360	0.7	1.1	0.9	1.0	0.4	0.8	IPF6050	orf19.6737	unknown function	no match
CA1146	1.1	1.0	0.9	0.8	0.4	0.3	CWH8	orf19.3682	putative required protein for full levels of dolichol-linked oligo	YGR036c
CA5397	1.5	1.2	0.7	0.8	0.4	0.8	IPF9663	orf19.940	similar to Saccharomyces cerevisiae Bud2p GTPase-activatir	YKL092c
CA0528	0.9	0.9	1.2	0.8	0.4	0.6	ANP1	orf19.3622	Golgi mannosyltransferase (by homology)	YEL036c
CA4134	1.0	0.9	0.9	0.9	0.4	0.6	COS162	orf19.4240	involved in manganese homeostasis (by homology)	YCR044c
CA5834	1.0	0.7	0.8	0.8	0.4	0.5	LRG1	orf19.7489	GTPase-activating protein of the rho/rac family (by homology	YDL240w
CA3626	1.5	1.0	0.9	1.1	0.4	0.6				
CA5956	0.7	0.7	0.9	0.9	0.4	0.5	VAN1	orf19.6738	Vanadate resistance protein	YML115c
CA2267	1.4	1.1	0.9	0.8	0.4	0.7	IFU1.5f	orf19.2600	Unknown function, 5-prime end	YNL126w
CA2020	1.6	1.5	1.0	0.9	0.4	1.0	IPF16901	orf19.842	unknown function	no match
CA3691	1.0	1.0	1.6	1.0	0.4	0.8	IPF4880	orf19.6266	unknown function	YCR093w
CA5029	0.7	1.0	1.0	0.9	0.4	0.6	IPF2997	orf19.6983	unknown function	YDR028c
CA0089	1.4	0.8	1.4	0.9	0.4	0.8	MRPL3	orf19.5064	ribosomal protein of the large subunit, mitochondrial (by hom	YMR024w
CA3716	0.8	1.0	1.1	1.1	0.4	0.9	IPF6203	orf19.4166	unknown function	YLR228c
CA2948	0.4	0.9	1.6	0.9	0.5	0.8	GDS1	orf19.1963	nam9-1 suppressor (by homology)	YOR355w
CA5652	1.1	0.9	2.6	0.8	0.5	0.6	IPF19815	orf19.7354	longevity-assurance protein (by homology)	YKL008c
CA1728	1.2	1.1	0.8	0.9	0.5	0.8	WHI3	orf19.6494	Putative RNA binding protein (by homology)	YNL197c
CA2379	0.5	0.8	1.3	1.0	0.5	0.7	IPF4073	orf19.2216	similar to Saccharomyces cerevisiae CaPds5p regulation of c	YMR076c
CA4424	1.1	1.1	0.8	0.9	0.5	0.9	PMT1	orf19.5171	mannosyltransferase	YDL095w
CA5062	1.5	1.1	1.1	1.1	0.5	0.7	SEC62	orf19.3031	subunit of ER protein-translocation complex (by homology)	YPL094c
CA5774	1.2	1.0	0.9	1.0	0.5	0.7	IPF1113	orf19.5418	unknown function	YIL039w
CA4574	0.8	0.9	1.2	0.9	0.5	0.4	IPF9430	orf19.6885	similar to Saccharomyces cerevisiae Spo7p meiotic protein (t	YAL009w
CA5315	0.6	0.8	0.7	1.2	0.5	0.7	CYB2	orf19.7186	B-type cyclin	YLR210w
CA5702	0.7	0.6	0.9	0.8	0.5	0.7	PCH1	orf19.7402	Putative ATPase (by homology)	YDR440w
CA4510	0.8	1.2	0.9	0.9	0.5	0.6	IPF8970	orf19.496	similar to Saccharomyces cerevisiae Msh1p DNA mismatch r	YHR120w
CA1501	1.0	0.9	0.8	0.9	0.5	0.9	IPF13217	orf19.1698	unknown function	YNL094w
CA3467	0.8	0.9	1.0	1.1	0.5	0.6	MNT2	orf19.1663	Alpha-1,2-mannosyltransferase (by homology)	YDR483w
CA3463	1.1	1.1	0.9	1.0	0.5	0.6	ALG8	orf19.1659	glucosyltransferase (by homology)	YOR067c
CA0882	1.1	0.9	0.8	1.0	0.5	0.9	PHR3	orf19.377	surface glycoprotein (by homology)	YOL132w
CA4159	0.9	1.0	1.5	1.1	0.5	1.1	ALD5	orf19.5806	aldehyde dehydrogenase (NAD+) (by homology)	YER073w
CA4743	0.9	1.0	1.1	1.1	0.5	0.8	IPF4491	orf19.4839	unknown function	YER083c
CA3233	0.7	1.0	1.0	0.7	0.5	0.8	MYO1	orf19.6294	myosin-1 isoform (type II myosin) heavy chain (by homology)	YHR023w

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA3966	1.3	1.0	0.8	1.0	0.5	0.9	IPF9376	orf19.1427	unknown function	YLR004c
CA5488	0.9	1.1	1.0	1.1	0.5	0.4	IPF810	orf19.5322	unknown function	YJL178c
CA0878	0.8	0.7	1.1	1.0	0.5	0.7				
CA5751	1.2	1.3	0.9	0.9	0.5	0.7	VPS8	orf19.5387	Vacuolar sorting protein (by homology)	YAL002w
CA5243	0.9	1.1	1.5	1.1	0.5	0.7	IPF3040	orf19.5020	unknown function	no match
CA2374	1.0	0.8	1.2	1.0	0.5	0.4	FCY23	orf19.1832	Putative purine-cytosine transport protein	YGL186c
CA0581	1.0	0.7	1.0	0.9	0.5	0.8	IPF3181	orf19.3558	similar to Saccharomyces cerevisiae Erp3p p24 protein involv	YDL018c
CA0877	1.0	1.0	1.0	1.1	0.5	0.7	CNH1	orf19.367	Na+/H+ antiporter	YLR138w
CA5401	0.9	0.6	1.0	1.1	0.5	0.7	FET35.3	orf19.943	Cell surface ferroxidase, high affinity, 3-prime end (by homolc	YMR058w
CA2268	1.0	1.0	1.0	0.9	0.5	0.8	IFU1.3f	orf19.2599.3	Unknown function, 3-prime end	no match
CA1010	1.0	0.9	0.8	0.9	0.5	1.0	GLT1	orf19.6257	glutamate synthase (NAPDPH), (by homology)	YDL171c
CA2990	1.6	1.5	0.8	0.9	0.5	0.8	IPF5092	orf19.6012	unknown function	YOR296w
CA4428	1.2	0.9	1.1	0.9	0.5	0.6	IFM1	orf19.5167	translation initiation factor 2 by homology	YOL023w
CA1262	1.0	0.7	0.8	0.7	0.5	0.7	MDR1	orf19.1244	Mac1p interacting protein (by homology)	YGR100w
CA1037	1.0	1.1	0.8	0.9	0.5	0.7	MNS1	orf19.1036	Alpha1,2-mannosidase (by homology)	YJR131w
CA2118	1.0	1.0	0.7	0.9	0.5	0.7	IPF8024	orf19.1334	unknown function	no match
CA2196	1.1	0.8	1.0	0.9	0.5	0.7				
CA2935	0.9	0.8	1.7	1.0	0.5	0.5	IPF11521	orf19.3328	unknown function	YMR172w
CA6142	1.0	0.8	0.9	0.9	0.5	0.4	IPF1879	orf19.5903	unknown function	YOR301w
CA4431	0.9	1.1	0.8	0.9	0.5	0.6	ECM39	orf19.5164	cell wall biogenesis by homology	YNR030w
CA1605	0.9	1.0	1.5	1.1	0.5	0.9	SWI6	orf19.4725	Transcription factor (by homology)	YLR182w
CA1779	1.2	1.1	4.5	1.5	0.5	0.8	IPF14510	orf19.1826	unknown function	YGL219c
CA1060	1.3	0.9	0.9	0.9	0.5	0.8	IPF11460	orf19.267	unknown function	YJL076w
CA5881	1.1	1.0	1.1	1.1	0.5	0.8	SSS1	orf19.6828.1	ER protein-translocase complex subunit (by homology)	YDR086c
CA0662	1.2	1.0	0.8	1.0	0.5	0.7	SPC97	orf19.708	spindle pole body component (by homology)	YHR172w
CA3151	1.6	1.4	0.9	1.1	0.5	1.1	IPF4033	orf19.6167	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihydroxyac	YIL124w
CA5274	1.1	1.0	0.9	0.9	0.5	0.7	IPF1764	orf19.4985	similar to Saccharomyces cerevisiae Gup1p glycerol transpor	YGL084c
CA5901	1.2	0.9	1.5	1.0	0.5	0.4	IPF2374	orf19.6805	unknown function	YDR089w
CA5721	0.8	1.0	1.1	1.1	0.5	0.8	IPF2443	orf19.7426	similar to Saccharomyces cerevisiae Ost6p N-oligosaccharylt	YML019w
CA2787	1.0	0.8	0.8	0.6	0.5	0.7	EFG1	orf19.610	Enhanced filamentous growth factor	YMR016c
CA0509	1.2	1.1	0.7	0.6	0.5	0.6	CDC24	orf19.3174	GTP/GDP exchange factor for Cdc42p (by homology)	YAL041w
CA5701	0.9	0.7	1.2	0.8	0.5	0.7	ISW2	orf19.7401	Chromatin remodeling complex (by homology)	YOR304w
CA2996	1.1	0.9	0.7	0.8	0.5	0.6	IPF9108	orf19.6124	similar to Saccharomyces cerevisiae Ace2p transcription fact	YLR131c
CA5202	0.7	1.0	1.2	0.9	0.5	0.8	YOX1	orf19.7017	Similar to homoeodomain protein (by homology)	YML027w
CA4728	1.1	1.0	1.3	1.1	0.5	0.5	VPS41.3f	orf19.4859	required for the vacuolar assembly, 3-prime end (by homolog	YDR080w
CA1694	0.9	0.8	2.6	1.1	0.5	0.9	TRM3	orf19.5038	2 -O-ribose methyltransferase (by homology)	YDL112w
CA5802	0.6	0.9	1.0	1.4	0.5	0.9	IPF4164	orf19.5455	similar to Saccharomyces cerevisiae Vtc1p negative regulato	YER072w
CA1526	1.0	0.9	1.3	1.0	0.5	0.5	IPF13815	orf19.4553	unknown function	no match
CA3351	1.0	1.0	1.0	1.0	0.5	0.7				
CA1074	0.9	1.1	1.1	0.8	0.5	0.6	PRORS.5f	orf19.2532	prolyl-tRNA synthetase, 5-prime end	YER087w
CA3318	1.3	1.1	0.8	0.8	0.5	0.6	WBP1	orf19.2298	Oligosaccharyl transferase beta subunit (by homology)	YEL002c
CA1073	1.1	1.0	1.1	0.8	0.5	0.7	PRORS.3f	orf19.2533	prolyl-tRNA synthetase, 3-prime end	YER087w
CA2732	0.8	0.7	0.9	0.8	0.5	0.6	IPF10327	orf19.2113	unknown function	YLR324w
CA0658	1.4	1.0	1.2	0.8	0.5	0.7	IPF16505	orf19.5575	Unknown function	YPL112c
CA0614	0.8	0.8	0.8	0.9	0.5	0.7	IPF19700	orf19.1600	unknown function	no match
CA2032	1.0	0.7	1.7	0.8	0.5	0.6	IPF13112	orf19.3466	unknown function	YGL136c
CA2287	0.8	1.0	0.8	1.0	0.5	0.9	IPF5373	orf19.5555	unknown function	YIR019c
CA2633	1.8	1.2	1.3	0.9	0.5	0.7	KEX2	orf19.4755	Kexin precursor (KEX2 protease)	YNL238w
CA2324	0.9	0.9	1.3	0.9	0.5	0.4	CDC46	orf19.5487	cell division control protein (by homology)	YLR274w
CA4602	1.6	2.0	1.2	1.2	0.5	0.7	IPF6231	orf19.3292	unknown function Unknown function	YCL033c
CA3092	1.0	1.0	1.2	0.8	0.5	0.8	IPF9821.3f	orf19.4141	unknown function, 3-prime end	YEL064c
CA3617	1.5	1.1	1.3	0.8	0.5	0.8	IPF9069	orf19.199	unknown function	YKL039w
CA5412	0.8	1.3	0.7	0.9	0.5	0.8	IPF1566	orf19.956	unknown function	YLR087c
CA5711	1.8	1.2	1.3	0.9	0.5	0.7	MUB1	orf19.7412	Regulation of bud site selection (by homology)	YMR100w
CA1127	0.8	0.9	1.2	0.8	0.5	1.1	MSH3	orf19.3608	DNA mismatch repair by homology	YCR092c
CA3470	1.1	1.0	0.9	0.9	0.5	0.6	IPF6310	orf19.1666	unknown function	no match
CA0403	0.6	0.9	0.8	1.1	0.5	0.6	PGA51	orf19.1989	unknown function	YKL046c
CA2243	1.3	0.9	1.1	0.9	0.5	0.9	IPF7414	orf19.4670	putative transcription factor (by homology)	YGL209w
CA5322	0.9	1.7	0.8	1.5	0.5	0.4	PRB1	orf19.7196	Protease B, vacuolar (by homology)	YEL060c
CA3469	0.6	0.7	0.8	1.0	0.5	0.9	MNT1	orf19.1665	Mannosyltransferase involved in n-linked and o-linked glycos	YOR099w
CA0960	1.0	1.1	0.8	1.1	0.5	0.8	DPP1	orf19.656	Diacylglycerol Pyrophosphate Phosphatase by homology	YDR284c
CA5495	0.6	0.9	0.9	0.9	0.5	1.1	SGS1	orf19.5335	ATP-dependent DNA helicase (by homology)	YMR190c
CA4348	1.3	1.0	1.1	0.8	0.5	0.8	IPF3638	orf19.6723	unknown function	YGL036w
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA4095	1.0	1.0	1.2	1.0	0.5	0.8	IPF4002	orf19.660	unknown function	no match
CA0660	0.6	0.8	0.7	0.6	0.5	0.4	IPF16189.5f	orf19.5577	panthotenate kinase, 5-prime end (by homology)	YDR531w
CA5016	0.7	1.2	1.3	0.9	0.5	0.6	IPF7561	orf19.6968	unknown function	no match
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)	YHL003c
CA0832	0.7	0.8	1.3	1.4	0.5	0.4	IPF14225	orf19.1675	unknown function	YDL133w
CA2934	0.9	1.1	1.0	1.1	0.5	0.6	IPF11515	orf19.3329	similar to Saccharomyces cerevisiae Lcb3p sphingoid base-p	YJL134w
CA1312	0.8	1.1	0.8	0.7	0.5	0.7	IPF14241	orf19.3635	unknown function	no match
CA3603	0.9	0.5	0.9	0.6	0.5	0.7	MEF1	orf19.4932	mitochondrial translation elongation factor G (by homology)	YLR069c
CA5326	1.6	1.0	0.9	1.0	0.5	1.0	IPF2137	orf19.7200	unknown function	no match
CA4432	0.9	1.0	0.9	0.8	0.5	0.8	IPF5574	orf19.5163	unknown function	YLL003w
CA4471	1.0	0.4	1.3	1.1	0.5	0.8	MCM3	orf19.1901	replication initiation protein (by homology)	YEL032w
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.5f	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholester	YNR008w
CA2652	1.0	1.0	1.2	0.9	0.5	0.9	DNA2	orf19.1192	DNA helicase (by homology)	YHR164c
CA5670	1.1	1.1	1.6	1.0	0.5	1.1	IPF1266	orf19.7372	Probable transcription factor	YAL051w
CA4182	1.0	0.9	0.9	0.8	0.5	0.9	IPF19797	orf19.2949	unknown	YJR138w
CA3785	0.9	0.7	1.1	0.9	0.5	0.8	IPF19788	orf19.5834	similar to Saccharomyces cerevisiae Sxm1p putative beta-kai	YDR395w
CA2949	0.6	0.9	1.3	1.0	0.5	0.8	IPF14506	orf19.1961	unknown function	no match
CA0205	0.9	1.0	1.0	1.0	0.5	0.6	DBF2	orf19.1223	putative ser/thr protein kinase by homology	YGR092w
CA1657	1.0	1.0	1.3	1.0	0.5	0.7	IPF16022	orf19.4325	unknown function	YPL183c
CA0276	0.6	0.5	0.9	0.7	0.5	0.9	IPF15015	orf19.5612	unknown function	YIL091c
CA2277	1.3	1.4	0.9	1.1	0.5	0.7	DRS21.5eoc	orf19.783	Membrane-spanning Ca-ATPase (by homology)	YIL048w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltra	YMR149w
CA4155	0.8	0.5	1.0	0.5	0.5	0.7	RNR21	orf19.5801	ribonucleoside-diphosphate reductase (by homology)	YJL026w
CA0843	1.6	1.3	1.1	1.2	0.5	0.7	IPF18853	orf19.1054	unknown function	YLL023c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4648	1.2	0.9	1.1	0.9	0.5	0.8	IPF9864	orf19.4435	similar to Saccharomyces cerevisiae Stu1p mitotic spindle pr	YBL034c
CA6137	1.0	1.0	1.4	0.9	0.5	0.8	IPF4356	orf19.5910	unknown function	YPR031w
CA2204	0.6	0.5	2.2	1.0	0.5	0.9	DIP51.5f	orf19.2943	dicarboxylic amino acid permease, 5-prime end (by homology	YPL265w
CA1414	0.9	0.6	1.2	0.9	0.5	0.5	CHO2	orf19.169	phosphatidylethanolamine N-methyltransferase (by homology	YGR157w
CA0525	1.1	0.9	0.8	0.9	0.5	1.0	MSB1.5eoc	orf19.1133	Morphogenesis-related protein (by homology)	YOR188w
CA0605	1.5	1.3	0.8	0.8	0.5	0.4	UTR2	orf19.1671	1,3-1,4-beta-glucanase (by homology)	YEL040w
CA2144	1.2	1.1	1.1	1.0	0.5	0.8	IPF12802	orf19.2513	unknown function	YDR495c
CA1818	0.9	1.0	1.3	0.9	0.5	1.0	IPF7023.3f	orf19.134	unknown function, 3-prime end	no match
CA1517	1.4	1.1	0.8	0.9	0.5	0.6	IPF11045	orf19.4798	unknown function	YMR212c
CA1219	1.0	1.0	1.0	1.0	0.5	0.9	PRC2	orf19.4135	carboxypeptidase y precursor , serine-type protease (by hom	YMR297w
CA4762	1.3	1.0	1.0	1.0	0.5	0.6	IPF9647	orf19.3994	similar to Saccharomyces cerevisiae Ost3p oligosaccharyltra	YOR085w
CA6153	1.0	1.0	1.0	1.1	0.5	0.7	CUP5	orf19.5886	Vacuolar H+-ATPase (by homology)	YEL027w
CA2336	0.8	1.0	1.1	1.1	0.5	0.7	IPF13383.5eo	orf19.2353	unknown function, 5 prime end	YOR086c
CA5355	0.6	1.1	1.4	1.2	0.5	0.8	IRR1.3f	orf19.7232	cohesin complex subunit, 3-prime end (by homology)	YIL026c
CA0100	1.0	1.0	0.9	1.2	0.5	0.7	IPF11569	orf19.9	unknown function	no match
CA3221	1.1	1.0	0.9	0.9	0.5	0.9	IPF10000.5eo	orf19.6193	unknown function, 5-prime end	YGR274c
CA1362	1.0	1.0	1.1	1.1	0.5	0.8	PEX3	orf19.4426	PEROXISOMAL MEMBRANE PROTEIN by homology	YDR329c
CA3331	0.5	1.0	1.4	1.0	0.5	1.0	POL21.53f	orf19.2668.1	pol polyprotein, reverse transcripase, internal fragment (by h	no match
CA5470	0.9	1.0	1.2	1.0	0.5	0.9	IPF300	orf19.3282	unknown function	YMR266w
CA0474	1.1	1.0	0.9	1.1	0.5	0.7	IPF12887	orf19.4780	Putative multidrug protein (by homology)	YJR124c
CA2465	1.5	1.1	0.9	0.9	0.5	0.7	IPF8726	orf19.1795	unknown function	YLL013c
CA3774	1.1	1.0	0.8	1.0	0.5	0.7	IPF10437	orf19.2892	budding protein-like (by homology)	YHR103w
9601.2	1.1	1.0	0.8	1.0	0.5	1.1				
CA1167	1.0	1.2	0.8	1.1	0.5	0.8	IPF16646	orf19.1782	unknown function	YEL001c
CA5637	0.8	0.9	0.9	1.1	0.5	0.7	IPF472	orf19.7058	unknown Function	YFR048w
CA4817	0.8	0.8	0.9	0.8	0.5	0.6	POM152	orf19.2081	Nuclear pore membrane glycoprotein (by homology)	YMR129w
CA4552	1.0	1.0	0.9	1.0	0.5	0.9	IPF7869	orf19.1447	unknown function	YLR086w
CA2931	0.8	0.9	0.7	0.9	0.5	0.9	IPF7841	orf19.4203	similar to Saccharomyces cerevisiae Ndc1p nuclear envelope	YML031w
CA2001	1.0	1.0	1.0	0.8	0.5	0.7	IPF17074	orf19.2792	unknown function	YBR086c
CA1731	1.5	0.9	1.0	1.0	0.5	0.7	IPF8437	orf19.6499	putative DNA-directed RNA polymerase (by homology)	YFL036w
CA1898	0.7	0.4	0.7	0.6	0.5	1.0	PGA38	orf19.2758	unknown function	no match
CA3967	1.3	1.0	1.0	1.0	0.5	0.9	IPF9377	orf19.1428	unknown function	no match
CA1709	1.3	0.6	1.1	0.9	0.5	0.6	HOL2	orf19.4889	Multidrug-resistance protein subfamily 1 (by homology)	YNR055c
CA2129	1.9	1.1	1.3	1.1	0.5	1.3	IPF4899	orf19.414	unknown function	YKL155c
CA2166	0.9	0.8	0.8	1.1	0.5	0.8	FEN12	orf19.908	Probable subunit of 1,3-beta-glucan synthase (by homology)	YCR034w
CA1228	1.0	1.0	1.1	0.9	0.5	0.8	IPF16081	orf19.4161	unknown function	YDL105w
CA3212	1.1	0.9	1.1	0.9	0.5	0.8	MEF2	orf19.6208	translation elongation factor (by homology)	YJL102w
CA3950	1.1	1.1	0.8	0.9	0.5	0.7	PTM1	orf19.1991	Possibly involved in the TCA cycle (by homology)	YKL039w
CA2221	0.8	0.8	1.0	0.9	0.5	0.7	IPF9670	orf19.5100	membrane transporter of the ATP-binding cassette (ABC) sup	YLL015w
CA4409	0.6	0.7	0.8	0.8	0.5	0.7	IPF13151	orf19.3100	unknown function	YDL058w
CA4126	1.0	1.0	0.9	0.8	0.5	0.7	IPF6631	orf19.2763	unknown function	YJL019w
CA0228	0.8	1.0	1.6	1.1	0.5	0.7	IPT1.5f	orf19.4769	Mannosyl diphosphorylinositol ceramide, 5-prime end (by hor	YDR072c
CA4595	1.6	1.0	0.8	0.9	0.5	0.9	GCN2	orf19.6913	Ser/thr protein kinase (by homology)	YDR283c
CA3349	0.7	0.8	1.0	1.3	0.5	0.8	IPF19588	orf19.2318.1	unknown function	YDR367w
CA4263	0.4	0.2	1.1	0.9	0.5	0.4	IPF2277	orf19.6656	unknown function	YHL016c
CA0503	1.0	0.9	0.8	1.3	0.5	0.6	PMT6	orf19.3802	protein mannosyltransferase	YGR199w
CA4461	1.2	1.2	1.5	1.0	0.5	1.0	IPF8470	orf19.6858	unknown function	YEL015w
CA4936	1.3	1.1	1.3	3.1	0.5	0.6	IPF8369	orf19.6077	unknown function	YOR161c
CA4052	1.2	1.0	1.3	1.2	0.5	1.1	IPF10231.3f	orf19.427	unkown function, 3-prime end	YBR275c
CA1039	0.8	0.8	1.7	0.9	0.5	0.5	IPF4012	orf19.2501	Unknown Function	YPL221w
CA1713	0.8	1.0	1.0	1.3	0.5	0.3	IPF19743	orf19.3332	unknown function	YDL231c
CA4560	0.7	0.8	1.2	0.8	0.5	0.9	IPF8038	orf19.6871	unknown function	YMR124w
CA5666	0.5	0.6	0.8	1.0	0.5	0.6	PUB1	orf19.7368	Major polyadenylated RNA-binding protein (by homology)	YNL016w
CA1980	1.5	1.1	1.4	0.9	0.5	0.6	YHM1	orf19.685	member of the mitochondrial carrier family (MCF) (by homolo	YDL198c
CA0308	1.1	1.0	0.8	0.8	0.5	0.6	RHK1	orf19.1092	Mannosyltransferase (by homology)	YBL082c
CA4627	0.6	0.6	1.0	1.0	0.5	1.1	DUT1	orf19.3322	dUTP pyrophosphatase	YBR252w
CA1147	1.0	1.0	1.2	0.9	0.5	0.8	KAP95	orf19.3681	karyopherin-beta protein (by homology)	YLR347c
CA3229	0.6	0.9	1.8	1.1	0.5	0.9	FUN30	orf19.6291	helicases of the Snf2/Rad54 family(by homology)	YAL019w
CA2985	1.3	0.8	1.0	0.9	0.5	0.7	SET1	orf19.6009	Chromatin regulatory protein (by homology)	YHR119w
CA0838	1.0	1.1	1.0	1.1	0.5	0.8	TFP1.5f	orf19.1680	vacuolar ATPase subunit (by homology)	YDL185w
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA2203	0.5	0.5	1.3	1.1	0.5	1.0	DIP51.3f	orf19.2942	dicarboxylic amino acid permease, 3-prime end (by homology	YPL265w
CA0862	0.8	0.9	1.0	0.8	0.5	0.6	CRK1.5f	orf19.3524	Protein kinase, 5-prime end	YPR161c
CA5034	1.4	1.2	0.9	0.7	0.5	0.6	OST1	orf19.6988	oligosaccharyltransferase	YJL002c
CA2774	1.0	1.0	1.0	1.0	0.5	1.4	TFC4	orf19.274	transcription factor IIIC chain TFC4- like by homology	YGR047c
CA2114	1.0	1.1	1.0	1.0	0.5	0.9	IPF13744	orf19.3685	protein involved in regulation of carbon metabolism (by homo	YNL201c
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)	YFL036w
CA4112	1.0	0.7	1.1	1.1	0.5	0.6	BIM1	orf19.676	microtubule-binding protein (by homology)	YER016w
CA4897	1.1	1.0	1.0	1.1	0.5	0.7	TUB2	orf19.6034	Beta-tubulin	YFL037w
CA4363	1.0	0.8	0.8	1.0	0.5	0.8				
CA1126	1.1	1.3	1.0	0.9	0.5	0.9	IPF5203	orf19.3607	unknown function	YGR110w
CA0284	0.9	0.9	1.2	1.0	0.5	0.9	IPF14657	orf19.1441	unknown function	no match
CA4603	1.3	1.5	1.1	1.4	0.5	0.7	IPF6230	orf19.3293	unknown function	YDL015c
CA1406	1.1	0.9	1.5	1.1	0.5	0.6	DOT4	orf19.3370	derepression of telomeric silencing (by homology)	YNL186w
CA4878	1.2	0.8	0.8	0.8	0.5	0.8	OXA1	orf19.6565	Cytochrome oxidase biogenesis protein (by homology)	YER154w
CA5006	1.2	1.2	1.1	0.7	0.5	0.8	IPF12584	orf19.5241	unknown function	YCR033w
CA2453	1.3	1.0	1.3	0.9	0.6	0.7	IPF9950	orf19.3501	unknown function	YKR090w
CA2004	0.6	0.7	1.0	0.7	0.6	0.8	POL12	orf19.2796	DNA-directed DNA polymerase alpha (by homology)	YBL035c
CA4119	1.3	1.2	0.9	0.8	0.6	0.6	BEM3	orf19.2771	GTPase-activating protein for Cdc42p and Rho1p (by homolo	YPL115c
CA4463	1.3	1.1	1.0	1.0	0.6	0.8	PIS1	orf19.6860	CDP diacylglycerol--inositol 3-phosphatidyltransferase (by ho	YPR113w
CA1495	1.3	0.9	1.0	0.8	0.6	0.8	IPF9686	orf19.3647	similar to Saccharomyces cerevisiae Sec8p Golgi - plasma m	YPR055w
CA5545	1.5	1.3	1.3	1.0	0.6	0.8	IPF5986	orf19.7307	similar to cytochrome-b5- and nitrate reductases	YML125c
CA2793	1.3	0.8	1.0	1.1	0.6	1.1	TRK1.5f	orf19.600	Potassium transporter, 5-prime end	YKR050w
CA4203	0.5	0.7	0.7	0.6	0.6	0.8	SWI4.3f	orf19.4545	transcription factor (by homology)	YDL056w
CA5981	1.1	0.7	0.7	0.8	0.6	0.8	MSS51	orf19.7577	involved in maturation of COX1 and COB mRNA (by homolog	YLR203c
CA1183	1.6	1.6	1.2	1.2	0.6	0.6	IPF14805	orf19.3782	acetyl-coenzyme A transporter(by homology)	YBR220c
CA2820	0.9	0.8	1.2	1.2	0.6	0.5	HOL1	orf19.2991	member of major facilitator superfamily multidrug-resistance p	YNR055c
CA2481	1.1	1.0	1.0	0.9	0.6	0.9	MRPL36	orf19.3205	ribosomal protein YmL36 precursor, mitochondrial (by homol	YBR122c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+									
Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2770	0.9	1.1	0.7	1.2	0.6	0.8	CPS1	orf19.2686	Carboxypeptidase YSCS precursor, second fragment (by hon	YJL172w
CA3497	1.0	0.7	1.0	1.2	0.6	0.7	FEN11	orf19.6343	Fatty acid elongase required for sphingolipid formation (by hc	YCR034w
CA1990	0.9	0.9	1.4	1.0	0.6	0.9	TOP1	orf19.96	CANAL DNA TOPOISOMERASE I	YOL006c
CA2340	0.8	0.7	0.7	1.1	0.6	0.6	MNN5	orf19.2347	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA5048	1.0	1.0	1.1	1.0	0.6	1.1	IPF20024	orf19.3012	unknown function	YDR421w
CA1504	0.9	0.9	0.9	1.2	0.6	0.5	ARF3	orf19.1702	GTP-binding protein of the ARF family (by homology)	YOR094w
CA3678	0.9	0.9	0.9	1.1	0.6	0.7	IPF8392	orf19.731	unknown function	YLR080w
CA5876	0.9	0.8	0.6	0.7	0.6	0.5	IPF12082.5f	orf19.6833	bumetanide-sensitive Na-K-Cl cotransport protein, 5-prime er	YBR235w
CA4872	1.2	0.8	1.1	1.0	0.6	0.7	SEC231	orf19.6558	Component of COPII coat (by homology)	YPR181c
CA4067	0.8	0.8	1.3	0.9	0.6	0.5	IPF5924	orf19.445	unknown function	YNR040w
CA0176	1.4	1.3	1.0	1.0	0.6	0.8	IPF11388	orf19.652	unknown function	YER041w
CA5437	1.0	1.2	0.8	1.0	0.6	1.1	ERG27	orf19.3240	3-keto sterol reductase (by homology)	YLR100w
CA5894	1.5	1.5	0.9	1.0	0.6	0.8	PMT2	orf19.6812	O-D-mannosyltransferase (by homology)	YAL023c
CA2438	1.0	1.0	0.9	0.9	0.6	0.5	IPF5505	orf19.2198	unknown function	YAL053w
CA2191	1.4	1.1	1.3	1.1	0.6	1.1	IPF9417	orf19.4775	similar to Saccharomyces cerevisiae Hsf1p heat shock transc	YGL073w
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w
CA4149	1.1	0.7	1.0	1.0	0.6	0.8	SMP3	orf19.5792	Protein kinase C pathway protein	YOR149c
CA3047	1.2	1.1	0.8	0.8	0.6	0.8				
CA3065	0.9	0.7	1.1	0.9	0.6	0.8	IPF19775	orf19.4282	unknown function	no match
CA0717	1.3	1.1	0.9	0.8	0.6	0.7	IPF9785	orf19.3453	unknown function	YFL047w
CA1530	1.0	0.9	1.0	1.0	0.6	0.6	ALG2.5	orf19.1221	mannosyltransferase, 5-prime end (by homology)	YGL065c
CA2436	0.9	1.1	0.9	1.0	0.6	0.7	IPF5500	orf19.2200	unknown function	YKR044w
CA4696	0.5	0.4	0.9	0.7	0.6	0.8	HTA1	orf19.6924	Histone H2A (by homology)	YDR225w
CA3322	0.8	1.0	0.8	0.9	0.6	0.8	IPF6895.3f	orf19.2676.1	unknown function, 3-prime end | FALSORF=SMALLORF	YHR188c
CA0913	0.9	1.1	0.8	1.1	0.6	0.8	IPF14810	orf19.2016	unknown function	YER044c
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA2008	1.1	0.5	1.1	1.2	0.6	0.9				
CA2393	1.1	0.8	0.8	1.0	0.6	0.8	RHO3	orf19.3534	GTP-binding protein of the rho family	YIL118w
CA4860	1.0	0.9	1.2	1.0	0.6	0.9	IPF19804	orf19.3835	unknown Function	YAL001c
CA5700	1.1	0.9	1.0	0.9	0.6	1.1	IPF2630	orf19.7399.3	unknown function	no match
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA5889	0.7	0.7	1.5	1.1	0.6	0.8	IPF2409	orf19.6818	RNA-dependent ATPase (by homology)	YLR419w
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA0951	0.8	1.1	1.0	1.0	0.6	0.6	MNN6	orf19.1011	putative golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA4429	1.2	1.0	1.2	1.2	0.6	0.9	DBF4	orf19.5166	regulatory subunit for Cdc7 by homology	YDR052c
CA0453	1.0	1.2	1.3	0.8	0.6	0.7	IPF13552	orf19.1300	putative methyltransferase (by homology)	YDR316w
CA4767	1.2	1.1	1.0	1.0	0.6	0.9	IPF13054	orf19.3999	unknown function	YML020w
CA1061	1.4	1.1	1.1	1.0	0.6	1.1	IPF19720	orf19.4643	unknown function	no match
CA0550	1.5	1.1	1.2	1.8	0.6	0.9	IPF14030	orf19.851	unknown function	YJR061w
CA4623	0.9	1.0	0.7	1.0	0.6	0.8	CTA9	orf19.3315	Putative transcriptional regulator	no match
CA4086	1.2	1.3	0.9	1.1	0.6	0.8	IPF5014	orf19.6642	unknown function	YNL263c
CA1094	1.6	1.1	1.7	1.3	0.6	0.7	YIP1	orf19.3951	golgi membrane protein (by homology)	YGR172c
CA0319	1.1	1.1	1.3	1.0	0.6	0.8				
CA3789	2.0	1.5	0.9	0.9	0.6	0.6	IPF11217	orf19.5830	similar to Saccharomyces cerevisiae Lhs1p chaperone of the	YKL073w
CA3776	0.8	1.2	0.9	1.1	0.6	0.9	IPF10435	orf19.2890	unknown function	YML038c
CA0488	1.1	1.1	0.8	0.8	0.6	0.6	SEC59	orf19.261	Dolichol kinase (by homology)	YMR013c
CA0418	1.1	0.9	0.9	0.9	0.6	0.8	IPF9051.5eoc	orf19.2227	unknown function, 5-prime end	YHR166c
CA2678	0.9	1.1	1.2	1.0	0.6	0.9	IPF5834	orf19.5491	unknown function	YDR356w
CA6053	1.1	0.9	1.0	1.0	0.6	0.5	IPF4949	orf19.7670	unknown function	YNL321w
CA2576	1.0	0.8	1.0	1.0	0.6	0.9	IPF7432	orf19.6219	unknown function	no match
CA2223	0.8	1.0	0.7	0.8	0.6	0.8	PLB5	orf19.5102	putative phospholipase B precursor	YOL011w
CA0739	1.5	1.1	0.9	1.0	0.6	0.7				
CA0723	0.7	0.8	1.1	0.9	0.6	0.8	PRI2	orf19.2885	DNA-directed DNA polymerase alpha , 58 KD subunit (DNA p	YKL045w
CA1345	1.0	1.4	0.8	1.1	0.6	0.8	IPF6003	orf19.1490	similar to Saccharomyces cerevisiae Msb2p multicopy suppre	YGR014w
CA0952	0.9	0.9	0.9	1.1	0.6	0.7				
CA3263	1.1	1.1	1.3	0.9	0.6	0.7	UBR12	orf19.2697	ubiquitin-protein ligase by homology	YLR024c
CA5927	1.3	0.9	0.8	0.8	0.6	0.6	DRS22	orf19.6778	Membrane-spanning Ca-ATPase (by homology)	YAL026c
CA2307	1.0	1.1	0.8	0.8	0.6	0.9	IPF18488	orf19.1684	unknown function	no match
CA1220	1.0	1.0	1.0	1.0	0.6	1.0	IPF14985	orf19.4134	unknown function	YDR459c
CA4733	0.7	0.9	1.0	0.9	0.6	0.6	IPF7732	orf19.4853	similar to Saccharomyces cerevisiae Hcm1p transcription fac	YCR065w
CA2656	1.6	0.8	0.7	0.8	0.6	0.6	NAM2	orf19.5705	mitochondrial leucine--tRNA ligase (by homology)	YLR382c
CA5162	1.1	1.0	1.0	0.9	0.6	0.9	IPF982	orf19.4600.1	Weakly similar to human dolichol-phosphate-mannose synth	no match
CA5970	0.8	0.7	1.1	0.8	0.6	0.8	DPB2	orf19.7564	DNA-directed DNA polymerase epsilon, subunit B (by homolc	YPR175w
CA6060	0.9	0.8	1.3	0.9	0.6	0.7	IPF8301	orf19.6008	unknown function	YLL032c
CA4605	1.0	1.0	1.0	1.3	0.6	0.7	IPF6226	orf19.3295	unknown function	YIR010w
CA5019	1.1	0.9	1.3	0.9	0.6	0.7	IPF7557	orf19.6972	similar to Saccharomyces cerevisiae Smi1p involved in beta-'	YGR229c
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5eoc	orf19.6654	unknown function	YMR221c
CA2425	1.2	1.0	0.7	1.0	0.6	0.9	IPF9907	orf19.3409	similar to Saccharomyces cerevisiae Sed4 protein of the end	YCR067c
CA1488	1.1	1.2	0.9	0.8	0.6	0.7	IPF17402.5eo	orf19.4064	unknown function	YJL062w
CA5896	1.8	1.1	0.8	1.0	0.6	0.7	TPD3	orf19.6810	Ser/thr protein phosphatase (by homology)	YAL016w
CA3779	1.0	1.0	1.1	1.0	0.6	0.8	IPF11221	orf19.5841	unknown function	no match
CA5291	1.3	0.7	1.2	0.8	0.6	0.8	LOS1	orf19.7153	pre-tRNA splicing protein (by homology)	YKL205w
CA2262	1.3	1.0	1.2	1.1	0.6	1.0	IPF6857	orf19.1757	putative transcriptional regulator (unknown function)	YDR253c
CA3002	0.8	0.9	1.1	0.9	0.6	0.7	PIF1	orf19.6133	mitochondrial DNA helicase (by homology)	YML061c
CA1652	0.8	1.0	0.7	1.0	0.6	1.0	RNH11	orf19.5563	Ribonuclease H (by homology)	YMR234w
CA2936	0.8	0.8	1.4	1.2	0.6	0.7	IPF8326	orf19.3327	similar to Saccharomyces cerevisiae Rnc1p endo-exonucleas	YKR056w
CA5919	0.8	0.9	1.4	0.9	0.6	0.9	IPF8926.3	orf19.6786	unknown function, 3-prime end	no match
CA5265	0.9	0.8	0.8	1.1	0.6	0.5	IPF1792	orf19.4997	unknown function	YER027c
CA3017	1.6	1.3	1.2	1.0	0.6	0.8	IPF10021	orf19.3912	unknown function	YER040w
CA3714	1.3	0.9	0.9	0.9	0.6	0.7	IPF16223	orf19.4163	unknown function	YGR198w
CA5960	0.9	0.8	0.8	0.8	0.6	0.7	PMT5	orf19.7549	protein mannosyltransferase (by homology)	YDL095w
CA2362	1.3	1.0	1.1	1.1	0.6	0.7	IPF10595	orf19.1287	unknown function	no match
CA1421	1.1	0.7	1.2	0.8	0.6	0.6	MRPL11	orf19.3797	Mitochondrial ribosomal protein (by komology)	YDL202w
CA5938	0.7	0.9	0.9	1.1	0.6	0.7	IPF3481	orf19.6759	unknown function	YGL197w
CA6062	1.5	1.3	3.0	1.5	0.6	0.8	IPF8307	orf19.6005	putative permease (by homology)	YDR536w
CA5356	0.8	1.0	1.3	1.1	0.6	0.8	IRR1.5f	orf19.7233	cohesin complex subunit, 5-prime end (by homology)	YIL026c
CA1097	1.2	0.8	1.1	0.9	0.6	1.1	IPF7575	orf19.4365	putative endo-exonuclease (by homology)	YKR056w
CA3494	1.5	1.5	1.0	0.9	0.6	0.6	RPB5	orf19.6340	DNA-directed RNA polymerase I, II, III (by homology)	YBR154c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4879	1.0	1.0	1.0	1.0	0.6	0.7	IPF1660	orf19.6566	unknown function	YOR365c
CA0186	0.2	0.7	0.7	0.7	0.6	0.7	PLB4.3f	orf19.1443	phospholipase, 3-prime end (by homology)	YOL011w
CA0861	0.7	0.9	0.9	1.0	0.6	0.8	CRK1.3f	orf19.3523	Protein kinase, 3-prime end	no match
CA4107	1.0	1.1	1.3	0.9	0.6	0.8	IPF3970	orf19.671	unknown function	YLR177w
CA2019	0.8	1.0	1.0	1.0	0.6	0.6	IPF3409	orf19.843	unknown function	YLR361c
CA2228	1.1	1.3	0.8	0.8	0.6	0.9	SCT12	orf19.5815	Suppresses a choline-transport mutant	YBL011w
CA5363	0.7	1.4	0.9	1.2	0.6	0.7	NCR1	orf19.7242	Polytopic membrane protein involved in sterol homeostasis ar	YPL006w
CA0535	0.8	0.9	1.4	1.0	0.6	0.6	IPF15606	orf19.5065	similar to Saccharomyces cerevisiae Erd1p required for reten	YDR414c
CA2505	0.6	0.7	1.2	1.0	0.6	0.7	IPF6796	orf19.5595	unknown function	YBR130c
CA0178	1.1	0.9	1.0	1.0	0.6	0.8				
CA0151	1.1	1.0	0.9	1.0	0.6	1.0	IPF15923.5eo	orf19.177	unknown function, 5-prime end	YBR200w
CA3687	1.1	1.1	1.2	1.0	0.6	0.9	IPF4889	orf19.6264	unknown function	YLR071c
CA6088	1.1	1.1	0.9	1.0	0.6	0.8	HPR5	orf19.5970	ATP-dependent DNA Helicase (by homology)	YJL092w
CA4336	0.9	1.1	1.8	1.5	0.6	0.9	DDR48	orf19.4082	stress protein (by homology)	YMR173w
CA5594	0.5	1.3	0.8	1.1	0.6	1.1	IPF19814	orf19.7106	folate hydrolase (by homology)	YJR126c
CA5461	1.0	1.3	1.0	0.9	0.6	0.9	GSL23.5f	orf19.3269	1,3-beta-D-glucan synthase subunit, 5-prime end	YLR342w
CA4439	1.3	0.7	0.9	1.1	0.6	0.8	IPF13865	orf19.5156	unknown function	YJL097w
CA0704	1.0	1.1	0.8	0.9	0.6	0.6	IPF11806	orf19.2915	similar to Saccharomyces cerevisiae Ynd1p nucleoside diphc	YER005w
CA3529	1.0	0.9	1.0	0.8	0.6	0.8	IPF9929	orf19.985	unknown function	YEL043w
CA1578	1.0	0.7	0.8	1.0	0.6	0.8	NUM11.5eoc	orf19.4715	nuclear migration protein (by homology)	YDR150w
CA1645	0.9	0.8	1.0	0.9	0.6	0.6	PMC1	orf19.1727	Ca2+-transporting P-type ATPase (by homology)	YGL006w
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4573	1.1	0.7	0.8	1.0	0.6	0.6	IPF9431	orf19.6884	unknown function	YJL091c
CA0329	1.0	0.8	0.9	1.0	0.6	0.8	IMG2	orf19.3777	Required for Integrity of Mitochondrial Genome (by homology	YCR071c
CA1619	0.7	0.6	1.6	1.5	0.6	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)	YPL057c
CA2883	1.3	0.9	0.7	0.8	0.6	0.9	IPF3790	orf19.5852	unknown function	YML103c
CA2027	0.9	1.0	0.8	0.9	0.6	0.5	MCK1	orf19.3459	ser/thr/tyr protein kinase (by homology)	YNL307c
CA3431	1.5	1.3	0.8	1.0	0.6	0.7	FUN9	orf19.586	Protein involved in vesicular transport between the endoplasr	YAL042w
CA1872	1.2	1.0	0.7	0.9	0.6	0.8	IPF6700	orf19.2459	unknown function	no match
CA5686	0.9	0.7	1.2	1.1	0.6	0.8	IPF3329	orf19.7388	similar to Saccharomyces cerevisiae Pbs2p tyrosine protein k	YJL128c
CA2786	1.1	0.9	0.8	0.9	0.6	0.7	KRE5	orf19.290	UDP-glucose:glycoprotein glucosyltransferase,(by homology)	YOR336w
CA4722	1.2	1.1	0.7	1.0	0.6	0.8	SAC1	orf19.4865	integral membrane protein localizing to the ER and Golgi (by	YKL212w
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA0619	1.3	0.9	0.8	0.9	0.6	0.9	IPF18924	orf19.3146	unknown function	no match
CA1182	1.0	0.9	1.1	1.0	0.6	1.0	IPF19724	orf19.801	similar to Saccharomyces cerevisiae Tbf1ptelomere repeat-bi	YPL128c
CA2198	0.9	1.5	0.9	0.9	0.6	0.7	PMM1	orf19.2937	phosphomannomutase	YFL045c
CA4985	1.6	1.0	0.9	0.9	0.6	0.8	IPF2050	orf19.5265	similar to Saccharomyces cerevisiae Kip1p kinesin-related pr	YBL063w
CA4667	1.1	0.7	0.9	1.4	0.6	0.3	GAP5	orf19.4456	General amino acid permease (by homology)	YKR039w
CA1492	2.3	1.5	1.2	1.2	0.6	1.1	IPF168	orf19.3226	unknown function	YDL046w
CA2511	1.0	1.1	0.9	0.9	0.6	0.8	IPF1474	orf19.306	myosin-like protein	YDL058w
CA3069	0.8	0.7	1.9	2.1	0.6	0.7	IPF6117	orf19.4805	unknown function	YMR266w
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA5502	0.6	0.6	1.0	0.9	0.6	0.6	IPF763	orf19.5343	putative transcription factor with a Cys4- zinc finger (by homo	YKL185w
CA5937	1.0	0.7	1.1	1.0	0.6	0.6	IPF2784	orf19.6760	unknown function	YER132c
CA5900	1.0	1.0	0.9	1.0	0.6	1.0	IPF2379	orf19.6806	unknown function	no match
CA0765	0.9	0.8	0.8	0.9	0.6	0.9	IPF9040	orf19.2236	similar to Saccharomyces cerevisiae Fhl1p transcriptional act	YPR104c
CA3414	1.1	0.8	1.2	1.1	0.6	1.0	IPF9240	orf19.6141	probable permease	YHR094c
CA4877	1.2	1.6	1.0	0.8	0.6	0.7	IPF1667	orf19.6563	unknown function	YJR054w
CA0789	1.2	1.0	1.1	0.9	0.6	0.7	ESP1	orf19.3356	Required for sister chromatid separation (by homology)	YGR098c
CA1284	0.9	1.1	1.0	1.0	0.6	1.0	IPF10168	orf19.643	unknown function	YJR089w
CA4025	1.6	1.4	1.0	0.9	0.6	0.7	SCJ1	orf19.3438	Mitochondrial and ER import protein (by homology)	YMR214w
CA5986	1.0	0.9	0.6	1.0	0.6	0.7	INO1	orf19.7585	myo-inositol-1-phosphate synthase	YJL153c
CA0990	1.0	0.9	0.8	0.8	0.6	0.6	IPF11068	orf19.1392	unknown function	YIL005w
CA4415	0.9	1.0	1.1	1.1	0.6	0.8				
CA2194	1.8	1.3	0.8	0.8	0.6	0.7	RGR1	orf19.4348	DNA-directed RNA polymerase II (by homology)	YLR071c
CA4698	1.1	1.4	0.7	0.9	0.6	0.7	CDC25	orf19.6926	cell division cycle protein	YLR310c
CA0928	0.5	0.8	0.8	1.0	0.6	0.9	IPF19891	orf19.557	unknown function	no match
CA3066	0.8	0.5	1.1	1.0	0.6	0.8	IPF15813	orf19.4281	unknown function	YLR223c
CA6112	1.0	1.1	0.8	1.2	0.6	0.8	IPF97	orf19.5941	unknown function	YML067c
CA6164	0.9	0.9	0.9	0.9	0.6	0.8	SNF5.5f	orf19.5872	Component of SWI/SNF transcription activator complex, 5-pri	no match
CA1533	1.1	1.1	1.2	0.9	0.6	1.0	IPF9510	orf19.1215	unknown function	no match
CA2365	1.3	0.8	1.4	1.1	0.6	0.9	CKS1	orf19.1282	cyclin-dependent kinases regulatory subunit (by homology)	YBR135w
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA0425	1.2	1.2	0.9	1.2	0.6	0.5	PPH21	orf19.1683	protein ser/thr phosphatase PP2A-1 (by homology)	YDL188c
CA2792	1.1	1.0	0.9	1.0	0.6	1.2	TRK1.3f	orf19.602	Potassium transporter, 3-prime end	YKR050w
CA5436	1.0	1.0	1.0	0.9	0.6	0.8	CTF18	orf19.3239	chromosome transmission in mitosis and maintenance of telo	YMR078c
CA2797	1.1	1.0	1.2	0.9	0.6	0.8	IPF8404	orf19.1720	putative helicase (by homology)	YFR038w
CA5346	0.8	0.9	1.1	0.8	0.6	0.9	IPF867	orf19.7221	unknown function	YKR029c
CA1616	1.7	0.8	1.1	0.6	0.6	0.6	IPF14538	orf19.3219	unknown function	YOR137c
CA5508	0.7	0.8	0.8	0.9	0.6	0.7	IPF745	orf19.5352	unknown function	YDR438w
CA0255	1.0	1.2	0.9	0.9	0.6	0.8	IPF16558.3eo	orf19.735	putative transcription initiation factor, 3-prime end (by homolc	YGR274c
CA1227	1.1	0.5	1.3	0.9	0.6	0.8	IPF16082	orf19.4160	unknown function	YDL104c
CA2500	1.1	1.0	0.8	0.9	0.6	1.0	FIG4	orf19.5586	suppressor of sac1 mutation (by homology)	YNL325c
CA5415	1.1	1.0	1.0	0.9	0.6	0.8	SMC4	orf19.964	Stable Maintenance of Chromosomes (by homology)	YLR086w
CA2136	1.2	1.1	0.9	0.9	0.6	0.8	VPS33	orf19.5214	VACUOLAR PROTEIN SORTING (by homology)	YLR396c
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4132	1.1	1.0	0.9	1.0	0.6	0.6	STE20	orf19.4242	serine/threonine-specific protein kinase	YHL007c
CA2866	1.1	1.0	1.0	1.1	0.6	0.5	RHO1	orf19.2843	GTP-binding protein of the rho subfamily of ras-like proteins (	YPR165w
CA4840	1.0	1.0	2.1	1.1	0.6	1.0	IPF1235	orf19.2054	unknown function	YDL020c
CA0304	1.1	1.0	1.4	1.1	0.6	1.2	IPF12829	orf19.721	unknown function	YLL035w
CA0083	0.3	0.1	1.0	1.1	0.6	0.2	PHO84.5eoc	orf19.655	high-affinity inorganic phosphate/H+ symporter by homology	YML123c
CA3487	0.7	0.9	0.8	0.9	0.6	0.9	IPF3203	orf19.3569	unknown function	YLR407w
CA1211	0.6	1.1	0.7	0.8	0.6	0.5	IPF7031.3f	orf19.131.2	unknown function, 3-prime end	YPR063c
CA1205	1.0	0.6	1.0	0.9	0.6	0.7	SSK2.3f	orf19.3776	MAP kinase kinase kinase of the high osmolarity signal trans	YNR031c
CA5817	1.1	1.0	1.6	1.0	0.6	0.9	IPF2511	orf19.7468	unknown function	YER064c
CA0077	1.2	0.9	1.3	1.0	0.6	0.8				
CA1444	0.8	0.8	1.4	1.1	0.6	0.7	KTR2	orf19.4494	mannosyltransferase (by homology)	YKR061w
CA2723	0.9	1.0	0.7	1.0	0.6	0.9	IPF4805	orf19.3345	unknown Function	YDR409w

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+ Species (Stress ()* Systemat	Ca HS+ Norn	Cd HS+ Norn	Ca OS+ Norn	Cd OS+ Norn	Ca XS+ Norn	Cd XS+ Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2297	1.1	0.9	1.0	0.9	0.6	0.8	ERG4	orf19.5379	sterol C-24 reductase (by homology)	YGL012w
CA4440	1.1	0.8	0.7	0.8	0.6	0.7	IPF13864	orf19.5155	similar to Saccharomyces cerevisiae Chs6p chitin biosynthes	YJL099w
CA5354	0.3	0.4	1.0	1.2	0.6	0.7	FTR2	orf19.7231	high affinity iron permease	YER145c
CA2989	0.6	1.0	0.7	0.9	0.6	1.0				
CA3124	0.9	0.9	1.1	1.0	0.6	0.8	IPF5353	orf19.3003	unknown function,	YML072c
CA5293	1.5	1.1	0.9	0.9	0.6	1.0	FAA24	orf19.7156	Long-chain-fatty-acid--CoA ligase (by homology)	YER015w
CA4296	1.1	0.9	1.2	0.9	0.6	0.8	IPF2605	orf19.6693	unknown function	YOL098c
CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal asse	YKL197c
CA0450	0.7	0.9	0.8	1.1	0.6	0.9	IPF9353	orf19.2378	unknown function	YMR123w
CA2882	1.3	0.9	1.2	0.8	0.6	0.8	STE13	orf19.5851	type IV dipeptidyl aminopeptidase (by homology)	YOR219c
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5f	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA4650	0.7	0.7	0.9	0.8	0.6	0.7	ISW1	orf19.4437	ATPase component of a four subunit chromatin remodeling c	YBR245c
CA6140	0.7	0.7	1.6	1.2	0.6	1.2	IPF1882	orf19.5905	unknown function Unknown function	YBL028c
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA3308	0.6	0.8	2.2	1.0	0.6	1.0	PET127.5f	orf19.2309	component of mitochondrial translation (by homology)	YOR017w
CA3675	1.2	1.0	1.0	0.9	0.6	0.9	IPF19529.3f	orf19.6453	unknown function, 3-prime end	no match
CA3438	1.3	1.3	1.0	1.0	0.6	0.6	IPF11330	orf19.2987	unknown function	YHR194w
CA5571	1.0	1.0	0.9	0.9	0.6	1.1	IPF2001	orf19.7337	unknown function	no match
CA2137	1.0	0.9	0.8	0.8	0.6	0.9	ARP9	orf19.2507	actin-related protein (by homology)	YMR033w
CA5690	1.1	0.9	0.8	0.9	0.6	0.4	OCH1	orf19.7391	Alpha-1,6-mannosyltransferase (by homology)	YGL038c
CA2033	1.1	0.9	1.1	1.0	0.6	0.8	SEC27	orf19.3467	coatomer complex beta chain (beta -cop) of secretory pathwa	YGL137w
CA4116	1.1	0.6	1.3	1.0	0.6	0.9	IDI1	orf19.2775	isopentenyl-diphosphate delta-isomerase (by homology) Lipic	YPL117c
CA1423	1.0	1.2	1.0	0.9	0.6	0.8	IPF14247	orf19.3799	unknown function	YDR233c
CA0380	0.3	0.3	0.8	1.1	0.6	0.5	PGA45	orf19.2451	unknown function	no match
CA4367	0.7	0.8	0.8	1.1	0.6	0.7	MNN10	orf19.5658	galactosyltransferase (by homology)	YDR245w
CA0634	1.1	1.0	1.2	1.0	0.6	0.9	IPF16267	orf19.1772	unknown function	YER077c
CA5228	0.8	0.9	1.7	1.0	0.6	0.8	RTF1.3f	orf19.7047	Regulates DNA binding properties of TBP, 3-prime end (by h	YGL244w
CA2269	1.2	1.2	1.2	1.3	0.6	0.7	YOR100	orf19.2599	Putative mitochondrial carrier protein	YOR100c
CA4170	1.0	1.2	1.0	1.0	0.6	0.7	IPF7784	orf19.2963	unknown function	YDL042c
CA1207	0.9	0.9	0.9	0.9	0.6	0.6	PPG1	orf19.3774	Phosphoprotein phosphatase PPG catalytic chain (by homolc	YNR032w
CA2643	0.8	0.9	1.0	0.9	0.6	0.8	HSL1	orf19.4308	Ser/thr protein kinase that interacts genetically with histone r	YKL101w
CA2988	1.0	0.9	0.9	1.0	0.6	0.8	SIN3	orf19.6010.3	Histone deacetylase by homology	YOL004w
CA5665	0.9	0.7	1.4	0.9	0.6	0.8	UBP1	orf19.7367	Ubiquitin-specific protease (by homology)	YDL122w
CA1795	1.3	1.1	1.0	0.9	0.6	0.9	IPF11261	orf19.5209	unknown function	YNL041c
CA4521	0.9	0.9	1.2	0.8	0.6	0.9	MRPL40	orf19.484	Putative mitochondrial ribosomal protein (by homology)	YPL173w
CA4859	1.0	0.8	1.0	1.0	0.6	0.8	IPF15927.5f	orf19.3833	similar to Saccharomyces cerevisiae Tfc3p transcription initia	YAL001c
CA4322	1.5	1.1	1.1	1.0	0.6	0.7	IPF2097	orf19.4097	unknown function	YML081w
CA3362	1.4	1.2	0.8	0.8	0.6	0.8	IPF9789	orf19.1933	unknown function	YDR479c
CA4680	1.4	1.3	1.1	1.3	0.6	0.9	AMD1	orf19.891	AMP deaminase (by homology)	YML035c
CA2105	0.8	1.0	1.0	1.0	0.6	0.8	IPF10711	orf19.3694	unknown function	YOR191w
CA3879	1.1	0.7	0.9	1.0	0.6	0.5	CDC42	orf19.390	Cell Division Control	YLR229c
CA2515	0.8	1.0	1.6	0.9	0.6	0.8	IPF19759	orf19.5510	Unknown Function	YGL133w
CA2578	0.4	0.5	1.1	0.9	0.6	0.9	MMD1	orf19.6220.3	Maintenance of mitochondrial DNA (by homology)	YIL051c
CA2545	1.0	0.8	1.7	1.3	0.6	1.1	RRP9	orf19.2830	U3 small nucleolar ribonucleoprotein-associated protein invol	YPR137w
CA2884	1.3	0.8	0.7	0.9	0.6	0.8	IPF7201	orf19.2476	similar to Saccharomyces cerevisiae Ecm5p involved in cell v	YMR176w
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)	YLR409c
CA2510	1.2	1.0	0.8	0.9	0.6	0.8	IPF1472	orf19.305	unknown function	YHL035c
CA2636	1.0	1.0	0.8	0.9	0.6	0.8	MSW1	orf19.4299	Mitochondrial tryptophanyl-tRNA synthetase (by homology)	YDR268w
CA0983	1.0	1.2	1.0	0.9	0.6	0.9	CBR1	orf19.1801	Cytochrome-b5 reductase (by homology)	YIL043c
CA2552	0.9	0.9	1.2	0.9	0.6	0.4	ALG5	orf19.2837	dolichol-P-glucose synthetase (by homology)	YPL227c
CA2394	1.4	1.0	1.3	1.0	0.6	0.8	IPF6424	orf19.3535	unknown function	YIL117c
CA1632	1.2	0.8	1.0	0.8	0.6	0.8	IPF10181	orf19.3938	similar to Saccharomyces cerevisiae Rsm26p protein of the s	YJR101w
CA6014	1.2	1.0	1.5	1.1	0.6	1.1	TRS31	orf19.7615	targeting complex (TRAPP) component involved in ER to Gol	YDR472w
CA5473	1.1	1.1	1.1	0.9	0.6	0.8	IPF16947	orf19.3286	unknown function	YDR221w
CA0645	1.0	1.0	0.9	1.0	0.6	0.8				
CA3951	0.9	1.1	1.2	1.1	0.6	0.9	VAC7.3	orf19.1409	Vacuolar protein, 3-prime end (by homology)	YNL054w
CA3654	1.1	0.8	1.3	1.3	0.6	0.8	IPF7452	orf19.2045	unknown function	YOR311c
CA6054	2.1	0.8	1.7	1.2	0.6	0.6	IPF4952	orf19.7672	unknown function	YDR411c
CA4971	1.1	1.1	0.8	0.9	0.6	0.9	IPF4697	orf19.5281	similar to Saccharomyces cerevisiae Scp160p required for ma	YJL080c
CA4359	1.0	0.9	0.9	0.9	0.6	0.7	IPF6054	orf19.6736	unnown function	YOR205c
CA1200	0.7	0.9	0.7	0.8	0.6	0.8	IPF10223	orf19.4867	putative serine/threonine kinase	YJL187c
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA4815	1.0	1.0	0.8	1.1	0.6	0.7	CDH1	orf19.2084	Substrate-specific activator of APC-dependent proteolysis (b	YGL003c
CA2689	1.0	1.1	1.0	0.9	0.6	1.0	IFU2	orf19.2582	Unknown function	YPL009c
CA2835	1.3	1.0	0.8	0.7	0.6	1.0	IPF12091	orf19.4787	Unknown function	YNL064c
CA3600	0.9	1.0	0.8	0.8	0.6	0.7	SPC3	orf19.4930	signal peptidase subunit (by homology)	YLR066w
CA1409	1.2	0.8	1.2	1.0	0.6	0.6	SPT16	orf19.2884	general chromatin factor (by homology)	YGL207w
CA1832	0.9	1.0	0.8	1.0	0.6	1.1	IPF17727	orf19.5190	unknown function	YHR023w
CA3256	1.5	1.4	1.2	1.1	0.6	0.9	IPF4730	orf19.3744	unknown Function	YOR112w
CA3418	1.3	0.9	1.1	1.2	0.6	0.9	IPF12777	orf19.6137	unknown function	YGL078c
CA3188	0.9	1.0	1.1	1.0	0.6	0.7	IPF11610	orf19.2146	similar to Saccharomyces cerevisiae Hat2 subunit of the majc	YEL056w
CA4136	1.5	1.0	0.9	0.9	0.7	0.9	RET2	orf19.4236	Coatomer complex delta chain (by homology)	YFR051c
CA2728	0.9	1.2	1.3	1.4	0.7	0.9	IPF10322	orf19.2117	putative mitochondrial carrier protein (by homology)	YHR002w
CA2024	0.5	0.5	0.9	1.0	0.7	0.3	PGA35	orf19.4910	unknown function	no match
CA5206	1.1	1.1	0.7	0.6	0.7	1.0	GPH1	orf19.7021	Glycogen phosphorylase (by homology)	YPR160w
CA1809	1.0	1.0	0.9	1.0	0.7	1.1	IPF6325	orf19.1116	unknown function	no match
CA5090	0.7	0.8	1.2	1.2	0.7	0.7	IFG4	orf19.3065	probable d-amino acid oxidase (by homology)	no match
CA4906	1.4	1.2	1.0	1.3	0.7	0.6	MOB2	orf19.6044	Required for maintenance in ploidy	YFL034cb
CA4321	1.3	1.0	1.2	1.1	0.7	0.8	KAR3.3	orf19.4100	Kinesin-related protein, 3-prime end	YPR141c
CA1883	0.8	1.5	0.9	1.0	0.7	0.7	IPF5479	orf19.2209	unknown function	YOR088w
CA3283	0.9	0.9	0.8	1.1	0.7	0.9	IPF6274	orf19.6316	unknown function	YMR221c
CA2647	1.0	0.8	1.0	1.2	0.7	0.7	IPF13088	orf19.1186	unknown function	YHR088w
CA4226	0.6	0.6	1.3	0.7	0.7	0.8	IPF8752	orf19.828	similar to Saccharomyces cerevisiae Mrpl24p ribosomal prote	YMR193w
CA5101	0.7	0.5	0.9	1.0	0.7	0.7	LCB1	orf19.6438	Serine C-palmitoyltransferase subunit (by homology)	YMR296c
CA0108	1.1	0.8	1.2	1.1	0.7	0.8	HIK1	orf19.5181	histidine kinase	YIL147c
CA3008	1.2	1.1	1.3	1.1	0.7	0.9	IPF12147	orf19.6233	oxidoreductase, acting on CH2 groups, NAD or NADP as acc	YNL181w
CA3211	3.1	1.1	2.2	1.2	0.7	1.0	IPF19977	orf19.6192	unknown function	YGR175c
CA1570	0.9	0.9	0.7	1.1	0.7	0.6	IPF7617	orf19.1160	unknown function	YHR181w

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2216	0.7	0.9	1.0	1.0	0.7	1.3	IPF6235	orf19.5372	Candida albicans Tca2 retrotransposon	no match
CA2098	1.3	0.8	0.8	1.0	0.7	0.9	IPF11487	orf19.2387	unknown function	YMR098c
CA5903	1.2	1.0	1.2	1.1	0.7	0.4	IPF5942	orf19.6803	transmembrane sugar transporter (by homology)	YPL244c
CA4770	0.8	0.9	0.9	1.0	0.7	0.8	IPF9382.3	orf19.4002	similar to Saccharomyces cerevisiae Dun1p protein kinase (b	YDL101c
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA1538	1.0	0.9	1.3	1.0	0.7	0.9				
CA1260	1.7	1.0	0.7	0.9	0.7	0.8	IPF3170	orf19.3166	unknown function	YDR141c
CA5823	0.8	0.9	1.1	0.8	0.7	0.8	COQ1	orf19.7478	Hexaprenyl pyrophosphate synthetase (by homology)	YBR003w
CA3223	1.0	1.0	1.2	0.9	0.7	0.8	SRP102	orf19.6284	Signal recognition particle receptor (by homology)	YKL154w
CA3927	1.0	0.7	3.4	1.3	0.7	0.8	DIP2	orf19.5106	beta transducin	YLR129w
CA3509	1.0	1.2	1.0	1.0	0.7	1.1	PRP6	orf19.6356	snRNP(U4/U6)-associated splicing factor (by homology)	YBR055c
CA1702	1.4	0.7	1.6	1.0	0.7	0.9	HEL1	orf19.702	DNA helicase I (by homology)	YER176w
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA4051	1.0	0.9	0.8	1.0	0.7	1.0	IPF10231.5f	orf19.426	unkown function, 5-prime end	YPL122c
CA5117	1.0	1.0	1.1	0.9	0.7	0.8	IPF1323	orf19.6414	unknown function	no match
CA2562	1.0	1.5	0.8	1.3	0.7	0.8	IPF19953	orf19.5642	unknown function	no match
CA4418	0.5	0.6	0.8	1.0	0.7	0.8	ERG5	orf19.5178	C-22 sterol desaturase by homology	YMR015c
CA1851	0.8	1.0	0.9	1.0	0.7	0.9	IPF14629	orf19.642	Cell cycle protein, interacts with Sit4 (by homology)	YFR040w
CA2006	1.1	1.0	0.7	0.8	0.7	0.7	IPF11801	orf19.2798	unknown function	YDR332w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA0579	1.1	0.9	0.9	0.9	0.7	0.9	IPF3184	orf19.3559	unknown function	YGR165w
CA3488	0.8	1.1	0.9	1.0	0.7	0.7	IPF3198	orf19.3568	unknown function	YDL076c
CA4663	1.6	1.4	1.6	1.1	0.7	0.8	IPF6554	orf19.4450	unknown function	YJL103c
CA4435	1.1	0.6	1.3	0.9	0.7	0.7	IPF5567	orf19.5160	phosphatase associated protein by homology	YKR028w
CA4495	0.6	1.1	0.9	0.8	0.7	0.7	IPF4059	orf19.1865	aldehyde dehydrogenase (by homology)	YHR039c
CA4131	1.4	1.0	1.1	1.0	0.7	1.0	IPF6886.3f	orf19.4243	unknown function, 3-prime end	YKL090w
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA3775	1.1	0.7	1.1	0.9	0.7	0.9	AFG1	orf19.2891	ATPase family gene (by homology)	YEL052w
CA4499	1.1	1.1	1.0	1.0	0.7	1.0	IPF11316	orf19.511	unknown function	YNL129w
CA0375	0.4	1.1	1.1	0.8	0.7	0.6	CRH11	orf19.2706	Probable membrane protein (by homology)	YGR189c
CA2991	1.0	0.9	1.0	0.9	0.7	0.9	IPF5088	orf19.6013	unknown function	YMR233w
CA0898	1.0	0.7	0.9	1.0	0.7	0.9	SSH1.3f	orf19.412	involved in co-translational pathway of protein transport, 3-pri	YBR283c
CA4043	1.3	0.9	1.8	2.0	0.7	1.0	IPF5291	orf19.3674	UDP-glucose 4-epimerase (by homology)	YBR019c
CA0851	1.4	0.9	0.9	1.1	0.7	1.0	IPF16670	orf19.1746	unknown function	YOR242c
CA2388	1.1	0.7	1.3	1.1	0.7	0.9	MCM6	orf19.2611	component of MCM initiator complex involved in DNA replicat	YGL201c
CA4729	1.1	1.1	1.2	1.1	0.7	0.7	VPS41.5f	orf19.4858	required for the vacuolar assembly, 5-prime end (by homolog	YDR080w
CA0041	1.1	0.9	1.0	1.1	0.7	0.9	IPF10360	orf19.3804	unknown function	YMR134w
CA2407	0.8	0.8	0.8	1.2	0.7	0.7	ECM14	orf19.299	carboxypeptidase involved in cell wall biogenesis and archite	YHR132c
CA5792	1.1	1.0	1.3	1.0	0.7	0.9	IPF4195	orf19.5441	similar to Saccharomyces cerevisiae Ulp2p involved in ubiqui	YIL031w

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[[Ca OS+ down 0.667 10FDR] and [Ca HS+ down 0.667 10FDR]] less [Ca XS+ do...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2225	0.3	0.6	0.3	0.4	1.1	1.1	SUR2	orf19.5818	Hydroxylation of C-4 of the sphingoid moiety of ceramide by h	YDR297w
CA2280	0.5	1.0	0.3	1.0	0.7	0.9	DUR1,2	orf19.780	urea amidolyase (by homology)	YBR208c
CA0273	0.3	0.9	0.3	0.5	1.0	0.6	IPF19066	orf19.1433	unknown function	YOR084w
CA4516	0.3	0.5	0.3	0.5	1.3	0.8	IPF18207	orf19.489	unknown function	YPL170w
CA5407	0.3	1.1	0.3	0.5	0.9	0.8	IPF1548	orf19.951	unknown function	no match
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membran	YIL047c
CA0943	0.1	0.5	0.4	0.4	0.9	1.1	YHB1	orf19.3707	flavohemoglobin (by homology)	YGR234w
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA6135	0.3	0.7	0.4	0.8	1.0	0.6	CMK1	orf19.5911	Ca2+/calmodulin-dependent ser/thr protein kinase (by homol	YFR014c
CA1902	0.3	1.1	0.4	1.1	1.0	1.0	OPT1	orf19.2602	oligopeptide transporter	YJL212c
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA0984	0.4	0.5	0.5	0.7	0.8	0.8	IPF7400	orf19.1802	unknown function	YER049w
CA2075	0.2	0.5	0.5	0.7	1.3	1.1	IFE2	orf19.5288	Unknown function	YAL060w
CA0697	0.5	0.7	0.5	0.9	0.7	0.4	VTC4	orf19.3363	putative polyphosphate synthetase (by homology)	YJL012c
CA2855	0.3	0.8	0.5	0.8	1.8	1.4	GPM2	orf19.1067	phosphoglycerate mutase (by homology)	YKL152c
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA1625	0.4	0.9	0.6	0.7	1.5	1.0	IPF6156	orf19.1034	similar to C.elegans LIM homeobox protein	YPL170w
CA4745	0.5	0.6	0.6	1.0	0.8	0.6	URA1	orf19.4836	dihydroorotate dehydrogenase	no match
CA4850	0.5	1.1	0.6	1.0	0.9	1.1	Cirt2	orf19.3820	Transposase	YJR134c
CA3743	0.6	1.0	0.6	1.1	1.5	1.5	IPF19998	orf19.2175	unknown function	YNR074c
CA4926	0.6	1.1	0.6	0.9	0.8	1.0	IPF1404	orf19.6065	unknown function	YLR071c
CA5968	0.4	1.0	0.6	1.0	1.4	1.0	IPF946	orf19.7561	unknown function	no match
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match
CA4315	0.6	0.8	0.7	1.1	1.3	0.9	PPX1	orf19.4107	Exopolyphosphatase (by homology)	YHR201c
CA4842	0.2	0.5	0.7	1.2	0.9	0.8	MTD1	orf19.3810	methylenetetrahydrofolate dehydrogenase	YKR080w
CA4657	0.4	1.1	0.7	1.1	2.3	1.2	IPF3094	orf19.4444	4-nitrophenyl phosphatase (by homology)	YDL236w

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[[Ca XS+ down 0.667 10FDR] and [Ca OS+ down 0.667 10FDR]] less [Ca HS+ do...

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2950	0.6	0.7	0.3	0.8	0.1	0.4	CLN2	orf19.1960	G1/S-SPECIFIC CYCLIN CLN2	YAL040c
CA2874	2.0	0.8	0.3	0.7	0.1	0.5	IPF4999	orf19.5843	unknown function	no match
CA5091	0.4	0.4	0.5	0.7	0.2	0.6	ENG1	orf19.3066	endo-1,3-beta-glucanase	YNR067c
CA2348	0.7	0.6	0.5	0.6	0.2	0.3	IPF12811	orf19.3751	putative serine/threonine kinase	YOR233w
CA3912	0.7	1.0	0.6	0.8	0.2	0.7	IPF3288	orf19.4390	unknown function	no match
CA5344	0.3	0.4	0.6	2.3	0.3	0.5	PRY2	orf19.7218	putative pathogen related proteins (by homology)	YJL079c
CA2473	0.4	0.8	0.6	0.8	0.4	0.4	CBF1	orf19.2876	putative centromere binding factor 1	YJR060w
CA3987	0.5	0.9	0.6	1.0	0.4	0.7	ECM3	orf19.1563	Involved in cell wall biogenesis and architecture (by homolog	YOR092w
CA4983	0.2	0.7	0.6	1.2	0.4	0.5	IPF2053	orf19.5267	unknown function	no match
CA3160	0.2	1.0	0.2	0.7	0.4	0.6	ZRT2	orf19.1585	zinc transport protein (by homology)	YLR130c

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...

HS+ OS+ XS+									
Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4939	0.9	0.6	0.5	0.8	0.4	0.7	IQG1	orf19.6536	RAS GTPase-activating-like protein by homology	YPL242c
CA1798	1.1	1.1	0.6	0.9	0.4	0.6	IPF11448	orf19.2923	unknown function	YMR155w
CA3756	0.5	0.8	0.4	0.6	0.4	0.7	IPF8884	orf19.3422	unknown function	YLR454w
CA0046	0.7	0.9	0.7	0.7	0.4	0.3	IPF14850	orf19.2452	Hypothetical protein	no match
CA5483	0.8	0.9	0.5	0.9	0.5	0.7	IPF817	orf19.5316	unknown function	YOR088w
CA2299	1.6	1.2	0.6	0.7	0.5	0.6	IPF8222	orf19.5381	unknown function	YGL014w
CA3625	1.2	1.3	0.6	0.8	0.5	0.6	CYR1.3f	orf19.5151	adenylate cyclase, 3-prime end	YJL005w
CA1491	1.2	0.9	0.7	0.7	0.5	0.5	IPF166	orf19.3225	unknown function	YCR017c
CA2181	0.5	0.6	0.6	0.9	0.5	0.9	ECM331	orf19.4255	Involved in cell wall biogenesis and architecture (by homolog	YDR055w
CA3003	0.7	0.4	0.6	0.9	0.5	0.5	IPF15741.5f	orf19.6242	similar to Saccharomyces cerevisiae Cyk3p possibly involved	YCR088w
CA5750	1.1	1.5	0.7	1.4	0.5	0.7	CHS8	orf19.5384	Chitin synthase (by homology)	YNL192w
CA3757	0.6	0.8	0.2	0.3	0.5	0.5	MAE1	orf19.3419	mitochondrial malic enzyme (by homology)	YKL029c
CA3365	1.0	0.9	0.6	0.7	0.5	0.5	ALG6	orf19.1843	glucosyltransferase (by homology)	YOR002w
CA3918	0.5	0.5	0.6	1.1	0.5	0.7	VTC2	orf19.4381	putative polyphosphate synthetase (by homology)	YFL004w
CA4314	1.1	1.1	0.7	0.9	0.5	0.5	PMT4	orf19.4109	Mannosyltransferase (by homology)	YJR143c
CA3327	0.5	0.7	0.6	0.7	0.5	0.7	NCP1	orf19.2672	NADPH-cytochrome P450 reductase	YHR042w
CA2364	1.0	1.1	0.6	0.7	0.5	0.7	MEC1	orf19.1283	cell cycle checkpoint protein (by homology)	YBR136w
CA5024	1.0	1.2	0.5	0.8	0.5	0.6	IPF3009	orf19.6977	similar to Saccharomyces cerevisiae Gpi1p required for N-ac	YGR216c
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA2938	0.4	0.8	0.5	0.7	0.6	0.4	IPF8321	orf19.3325	similar to Saccharomyces cerevisiae Glg2p self-glucosylating	YJL137c
CA0953	1.0	1.2	0.6	0.8	0.6	0.8	IPF13166	orf19.1144	unknown function	YDL203c
CA5877	0.7	0.9	0.5	0.9	0.6	0.5	IPF12082.3f	orf19.6832	bumetanide-sensitive Na-K-Cl cotransport protein, 3-prime er	YBR235w
CA4655	0.9	1.5	0.5	0.9	0.6	0.8	IPF3098	orf19.4442	Putative mannosyltransferase (by homology)	YNL219c
CA0665	0.4	0.3	0.6	0.7	0.6	0.8	INT1	orf19.4257	integrin-like protein alpha chain	YJR092w
CA5784	1.5	0.9	0.7	1.0	0.6	1.4	IPF1129	orf19.5431	unknown function	no match
CA2994	0.7	0.9	0.6	0.9	0.6	0.5	IPF9116	orf19.6119	unknown function	no match
CA5857	0.4	1.2	0.4	0.6	0.6	0.7	PCK1	orf19.7514	phosphoenolpyruvate carboxykinase	YKR097w
CA4622	1.6	0.7	0.6	0.9	0.6	0.6	IPF5751	orf19.3314	TRAPP subunit of 20 kDa involved in targeting and fusion of I	YBR254c
CA3321	1.1	1.2	0.7	0.7	0.6	0.7	IPF6896.5f	orf19.2677	unknown function, 5-prime end	YHR188c
CA4433	1.0	1.1	0.7	0.9	0.6	0.8	BCK1	orf19.5162	serine/threonine protein kinase of the MEKK family (by homol	YJL095w
CA3319	1.1	0.7	0.5	0.8	0.6	0.5	DRS25	orf19.2680	Probable ATPase, Potential phospholipid-transporting ATPas	YMR162c
CA1797	0.9	0.6	0.6	0.8	0.6	0.9	NUM12	orf19.2924	nuclear migration protein (by homology)	YDR150w
CA4250	0.7	1.0	0.5	0.9	0.6	1.5	IPF4292	orf19.539	bleomycin Hydrolase	YNL239w
CA2179	1.2	1.4	0.7	0.9	0.6	0.9	FAB1	orf19.1513	phosphatidylinositol 3-phosphate 5-kinase (by homology)	YFR019w
CA4564	1.0	0.9	0.5	0.5	0.6	0.8	IPF6572	orf19.6874	unknown function	YMR213w
CA2103	0.9	0.8	0.6	0.7	0.6	0.6	ISM1	orf19.2382	isoleucyl-tRNA synthetase (by homology)	YPL040c
CA3635	0.7	1.1	0.6	1.0	0.6	1.0	IFA20	orf19.5139	unknown function	YJL005w
CA2116	1.0	0.7	0.6	1.0	0.6	0.7	SNG4	orf19.1332	Drug transporter (by homology)	YJR015w
CA0752	0.3	1.4	0.6	0.5	0.6	1.3	MNN22	orf19.3803	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA4501	0.5	1.3	0.1	0.1	0.6	0.9	QDR1	orf19.508	putative antibiotic resistance proteins (by homology)	YIL120w
CA2383	0.6	1.3	0.6	1.0	0.7	1.2	IPF18474	orf19.2222.2	unknown function	no match

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[[Ca XS+ down 0.667 10FDR] and [Ca HS+ down 0.667 10FDR]] less [Ca OS+ do...

HS+ OS+ XS+									
Species (	Ca	Cd	Ca	Cd	Ca	Cd			
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+			
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2862	0.3	0.5	0.8	0.9	0.2	0.6	HHF21	orf19.1059	histone H4	YNL030w
CA3372	0.3	0.5	1.0	0.9	0.4	0.6	HHF22	orf19.1854	histone H4 (by homology)	YNL030w
CA5693	0.6	1.0	1.3	1.0	0.4	0.8	GDA1	orf19.7394	Golgi guanosine diphosphatase (by homology)	YEL042w
CA0659	0.6	0.7	0.8	0.6	0.4	0.4	IPF16189.3f	orf19.5576	panthotenate kinase, 3-prime end (by homology)	YDR531w
CA1782	0.2	0.1	0.9	1.0	0.5	0.2	PHO84.3eoc	orf19.1172	Inorganic phosphate transport protein, 3-prime end (by homo	YML123c
CA2249	0.5	0.6	0.9	0.7	0.5	0.7	POL2	orf19.2365	DNA-directed DNA polymerase epsilon, catalytic subunit A (b	YNL262w
CA4882	0.3	0.3	0.7	0.9	0.5	0.8	IPF1651	orf19.6570	purine nucleoside permease (by homology)	no match
CA2947	0.2	0.3	0.7	0.5	0.5	0.7	IPF6298	orf19.1964	unknown function	no match
CA0185	0.2	0.7	0.7	0.6	0.5	0.8	PLB4.5f	orf19.1442	Phospholipase, 5-prime end (by homology)	YOL011w
CA1384	0.5	0.8	0.9	1.0	0.6	0.8	IPF8423	orf19.926	similar to Saccharomyces cerevisiae Dhs1p exonuclease (by	YOR033c
CA2521	0.6	0.9	1.2	1.3	0.6	0.9	IPF4317	orf19.5518	unknown function	no match
CA4697	0.3	0.4	0.8	0.8	0.6	0.8	HTB1	orf19.6925	Histone H2B (by homology)	YDR224c
CA2898	0.5	0.6	2.0	0.9	0.6	0.8	IPF15646	orf19.3481	putative ATP-dependent RNA helicase (by homology)	YGL064c
CA3240	0.7	0.6	1.4	1.1	0.6	0.8	IPF10559	orf19.4683	myosin-like protein (by homology)	YKR095w
CA4270	0.5	0.3	1.0	0.9	0.6	0.7	NUP2	orf19.6665	Nuclear pore protein (by homology)	YLR335w

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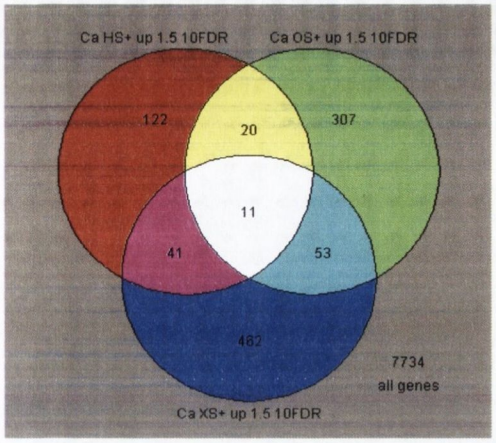
[[Ca OS+ down 0.667 10FDR] and [Ca XS+ down 0.667 10FDR]] and [Ca HS+ dow...

HS+ OS+ XS+						
Species (	Ca	Cd	Ca	Cd	Ca	Cd
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+

[[Ca HS+ down 0.667 10FDR] less [Ca OS+ down 0.667 10FDR]] less [Ca XS+ d...
HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA2302	0.1	0.6	0.3	0.6	0.1	0.3	IPF6518	orf19.1691	unknown function	YNR018w
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA3878	0.2	0.3	0.5	0.6	0.5	0.5	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA polymerase	YDR213w
CA1353	0.2	0.3	0.4	0.5	0.7	1.0	ERG1	orf19.406	squalene epoxidase	YGR175c
CA0482	0.2	0.6	0.6	0.9	0.5	0.4	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)	no match
CA2625	0.2	0.9	0.7	0.9	0.2	0.3	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified protein	YLR110c
CA4800	0.4	0.6	0.7	0.9	0.5	0.6	PGA4	orf19.4035	putative GPI-anchhored protein related to Phr1, Phr2 and Phı	YOL030w
CA2969	0.4	0.2	0.4	0.6	0.6	0.5	IPF19772	orf19.5602	unknown function	no match



26A

[Ca HS+ up 1.5 10FDR] less [Ca OS+ up 1.5 10FDR]] less [Ca XS+ up 1.5 10...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA3367	6.5	1.0	1.1	0.9	1.1	1.1	IPF4667	orf19.1847	unknown Function	YDR380w
CA1239	4.7	5.2	1.2	1.1	0.7	0.9	HSP60	orf19.717	Heat Shock Protein 60 (HSP60)	YLR259c
CA4053	4.1	0.9	0.7	1.0	1.4	1.0	IKS1	orf19.428	PROBABLE SERINE/THREONINE-PROTEIN KINASE	YJL057c
CA0821	4.1	1.0	0.5	0.9	1.3	0.9	IPF16795	orf19.2989	glycerate/formate-dehydrogenase (by homology)	YNL274c
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA4959	3.4	4.8	1.3	1.2	1.0	1.0	HSP90	orf19.6515	heat shock protein	YMR186w
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function	YGR101w
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function	YGL145w
CA4856	3.1	3.2	0.9	1.1	1.1	0.9	IPF15950	orf19.3827	unknown function	YKR087c
CA0596	3.1	1.1	0.8	1.0	0.9	1.0	IPF9706	orf19.4883	unknown function	YBR203w
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by hc	YML130c
19812.1	2.7	0.8	0.8	1.0	0.9	0.9				
CA4987	2.7	1.0	1.1	0.9	1.2	1.0	IPF2045	orf19.5262	unknown function	no match
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA6052	2.6	1.4	1.3	1.0	0.8	1.0	IPF4942	orf19.7668	similar to Saccharomyces cerevisiae Mal32p alpha-glucosida	YBR299w
CA2146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function	no match
CA4437	2.5	7.3	0.7	1.3	1.2	1.2	IPF13867	orf19.5158	unknown function	YGL145w
CA5341	2.5	3.9	0.9	0.8	1.0	0.9	HSP10	orf19.7215.3	10 kDa mitochondrial heat shock chaperonin (by homology)	YOR020c
CA3078	2.5	5.4	0.8	1.3	1.2	1.1	IPF19970	orf19.4816	unknown function	YMR209c
CA4665	2.5	1.1	1.1	1.0	0.9	0.8	IPF6548	orf19.4451	translation elongation factor eEF4 (by homology)	YNL163c
CA0796	2.4	0.9	1.0	0.9	1.1	0.9	ALR1	orf19.1607	divalent cation transporter (by homology)	YOL130w
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function	YKL094w
CA4016	2.4	1.2	1.0	1.0	0.9	1.0	GFA1	orf19.1618	glutamine:fructose-6-phosphateamidotransferase	YKL104c
CA2335	2.4	0.8	1.4	1.1	0.9	1.1	LYS21	orf19.4506	homocitrate synthase (by homology)	YDL131w
CA5547	2.4	1.1	1.1	2.1	0.7	0.9	IPF5981	orf19.7310	similar to Saccharomyces cerevisiae Gin3p (by homology)	YML128c
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)	YER021w
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function	YDR430c
CA0417	2.3	2.7	0.9	1.0	1.4	1.2	UBC13	orf19.933	E2 ubiquitin-conjugating enzyme (by homology)	YDR092w
CA5864	2.3	1.2	0.9	1.1	1.1	1.1	IPF364	orf19.7522	transaminase type I (by homology)	YJL060w
CA5541	2.3	1.0	0.7	1.0	0.7	1.1	IPF2827	orf19.7303	unknown function	no match
CA4201	2.3	1.1	0.8	1.0	0.7	1.0	IPF8048	orf19.4543	probable succinate-semialdehyde dehydrogenase (by homolc	YBR006w
CA1492	2.3	1.5	1.2	1.2	0.6	1.1	IPF168	orf19.3226	unknown function	YDL046w
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA3034	2.3	2.7	0.8	0.9	1.4	1.3	RPN12	orf19.213	26S proteasome regulatory subunit (by homology)	YFR052w
CA5930	2.3	1.8	1.1	0.9	1.1	1.0	ECM29.3f	orf19.6773	Involved in cell wall biogenesis and architecture, 3-prime end	YHL030w
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function	YPL110c
CA4157	2.2	1.5	0.8	1.0	0.9	1.0	HYU1	orf19.5804	hydantoin utilization protein A (hyuA) homolog	YKL215c
CA4643	2.2	2.7	1.1	1.2	1.3	1.0	PRE9	orf19.350	20S proteasome subunit Y13 (alpha3) (by homology)	YGR135w
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase	YLR377c
CA5924	2.2	1.1	0.9	1.0	1.2	0.9	IPF2822	orf19.6781	unknown function	no match
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)	YBR058c
CA2773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase	YOR211c
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA1894	2.2	2.0	1.0	1.1	1.2	1.0	PRE7.5f	orf19.2755	putative subunit of 20S proteasome, exon 1 (by homology)	YBL041w
CA0845	2.1	1.3	1.3	0.9	1.0	1.0	IPF16314	orf19.264	unknown function	YGL134w
CA5230	2.1	1.1	1.2	1.2	1.0	1.0	IPF10424	orf19.5034	unknown function	YBR216c
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)	YHR104w
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA5142	2.1	1.3	0.7	1.0	1.0	1.0	IPF1022	orf19.4579	similar to Saccharomyces cerevisiae Erv29p ER-Golgi transp	YGR284c
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homology)	YMR302c
CA0844	2.1	1.0	1.0	1.0	0.7	0.9	CDC3	orf19.1055	Cell division control protein	YLR314c
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in aceti	YCR032w
CA4199	2.0	2.1	0.6	0.9	1.4	1.4	UBC8	orf19.4540	ubiquitin-conjugating enzyme (by homology)	YEL012w
CA2874	2.0	0.8	0.3	0.7	0.1	0.5	IPF4999	orf19.5843	unknown function	no match
CA5536	2.0	4.4	0.9	1.0	1.1	1.2	IPF2837	orf19.7297	putative cystathionine gamma-synthase (by homology)	YHR112c
CA3218	2.0	1.0	1.0	1.0	1.2	1.0	IPF10005	orf19.6196	unknown function	no match
CA5196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function	YIL001w
CA1308	2.0	1.0	1.1	1.0	1.0	1.0				
CA2129	1.9	1.1	1.3	1.1	0.5	1.3	IPF4899	orf19.414	unknown function	YKL155c
CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)	YIL095w
CA4889	1.9	1.1	1.0	0.9	0.8	1.0	IPF1629	orf19.6581	unknown function	YOL003c
CA2539	1.9	1.4	1.3	0.9	0.9	0.9	IPF9188	orf19.3187	unknown function	YOL089c

CA5528	1.9	2.4	1.2	1.3	1.2	1.1	RPN7	orf19.7286	Subunit of the regulatory particle of the proteasome (by homc	YPR108w
CA3796	1.9	3.5	1.2	1.2	0.9	0.9	SGT2	orf19.5823	small glutamine-rich tetratricopeptide repeat containing prote	YOR007c
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)	YMR234w
CA1896	1.9	1.1	1.1	1.4	1.0	0.8	ERD2	orf19.2756	ER lumen protein retaining receptor (by homology)	YBL040c
CA1267	1.9	1.2	0.9	1.0	0.7	0.5	YSY6	orf19.242.2	protein involved in the secretory pathway, by homology	YBR162wa
CA3842	1.8	1.1	1.3	1.0	0.8	1.1	YKE2.3f	orf19.6601.1	Gim complex component, 3-prime end (by homology)	YLR200w
CA5459	1.8	1.2	1.3	1.1	0.9	0.7	IPF276	orf19.3267	unknown function	YDR126w
CA0374	1.8	1.0	0.8	1.0	1.0	1.0				
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA5983	1.8	1.2	0.8	1.3	0.9	1.1	IPF913	orf19.7579	unknown function	no match
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex	YDL143w
CA0494	1.8	1.3	0.9	1.0	1.3	1.1	RAD7	orf19.1493	nucleotide excision repair protein (by homology)	YJR052w
CA6127	1.7	0.9	1.4	1.4	1.0	1.0	IPF149	orf19.5921	peroxisomal membrane protein (by homology)	YEL006w
CA2109	1.7	1.1	1.4	1.2	0.9	0.8	IPF13749.	orf19.3690	unknown function, 5-prime end	YLR345w
CA0010	1.7	0.9	0.9	1.1	1.0	0.5	IPF16036	orf19.150	similar to Saccharomyces cerevisiae Tim17p mitochondrial in	YJL143w
CA3697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific	YJR099w
CA3453	1.7	1.3	0.9	1.0	1.0	0.9	SEC23	orf19.1254	Component of COPII coat (by homology)	YPR181c
CA3627	1.7	1.3	1.1	0.9	0.8	0.9	IPF18318	orf19.5147	unknown function	YLL007c
CA0792	1.7	1.1	0.9	0.9	1.1	0.8	DIT2.3eoc	orf19.554	putative cytochrome P450, 3-prime end	YDR402c
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA1585	1.7	1.2	1.0	0.9	1.1	0.9	VPS27	orf19.6031	Vacuolar protein sorting (by homology)	YNR006w
CA1616	1.7	0.8	1.1	0.6	0.6	0.6	IPF14538	orf19.3219	unknown function	YOR137c
CA2424	1.7	0.8	1.0	0.8	0.9	0.7	IPF18468	orf19.4467	unknown function	no match
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homol	YPR183w
CA1248	1.6	1.5	1.3	1.0	1.6	1.4	IPF3866	orf19.21	unknown function	YLR251w
CA4799	1.6	1.6	1.1	1.0	0.8	1.0	RPN5.5f	orf19.4034	subunit of the regulatory particle of the proteasome, 5-prime (	YDL147w
CA2207	1.6	1.0	0.8	1.1	1.0	1.1	IPF12169	orf19.697	unknown function	YHR017w
CA2853	1.6	1.0	1.0	1.1	0.9	1.0	IPF17057	orf19.1070	unknown function	YMR010w
CA5349	1.6	1.2	1.0	0.9	1.1	1.1	IPF861	orf19.7224	unknown function	YKR017c
CA2964	1.6	0.9	1.0	0.8	1.1	1.0	IPF13176.	orf19.5610	ornithine carbamoyltransferase, 3-prime end (by homology)	YJL088w
CA5326	1.6	1.0	0.9	1.0	0.5	1.0	IPF2137	orf19.7200	unknown function	no match
CA2295	1.6	1.4	1.1	1.0	0.7	0.8	HOS2	orf19.5377	putative histone deacetylase (by homology)	YGL194c
CA0720	1.6	1.4	1.2	1.0	0.9	1.1	IPF17932	orf19.3457	unknown function	YBR175w
CA2990	1.6	1.5	0.8	0.9	0.5	0.8	IPF5092	orf19.6012	unknown function	YOR296w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltra	YMR149w
CA1018	1.6	1.2	0.6	0.7	1.0	1.1	IPF13479.	orf19.3768	unknown function, 3-prime end	YCR081w
CA5676	1.6	1.0	1.0	1.0	1.1	1.0	FAA22	orf19.7379	Long-chain-fatty-acid--CoA ligase (by homology)	YER015w
CA4042	1.6	1.6	1.2	1.1	0.8	1.0	TRS23	orf19.3673	targeting and fusion of ER to golgi transport vesicles by homc	YDR246w
CA3026	1.6	1.0	1.0	1.0	0.9	1.0	IFZ1	orf19.3901		no match
CA3818	1.6	1.4	0.8	0.6	0.9	1.1	IPF6695	orf19.5773	unknown function	YOL057w
CA0843	1.6	1.3	1.1	1.2	0.5	0.7	IPF18853	orf19.1054	unknown function	YLL023c
CA2887	1.6	1.1	1.0	1.1	1.1	0.9	IPF13631	orf19.2472	unknown function	no match
CA3151	1.6	1.4	0.9	1.1	0.5	1.1	IPF4033	orf19.6167	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihydroxyac	YIL124w
CA2906	1.6	1.0	0.9	0.8	0.8	0.8	IPF15523	orf19.4521	unknown function	YOR246c
CA5976	1.6	1.0	0.8	0.9	1.6	0.9	IPF928	orf19.7570	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear c	YDL170w
CA4594	1.5	1.1	1.2	1.1	0.7	0.9	IPF2212	orf19.6912	unknown function	YLR133w
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle	YLR178c
CA0881	1.5	0.8	0.7	1.0	0.8	1.1	IPF16965	orf19.374	unknown function	YOR256c
CA3875	1.5	1.1	0.5	1.0	1.2	1.0	IPF14430	orf19.394	putative kynureninase (by homology)	YLR231c
CA6011	1.5	1.0	0.6	1.0	1.5	1.1	CTM1	orf19.7612	cytochrome c methyltransferase (by homology)	YHR109w
CA1700	1.5	1.3	1.3	0.9	1.1	1.2	RAM1.5f	orf19.5046	protein farnesyltransferase, beta subunit, 5-prime end (by hor	YDL090c
CA3134	1.5	1.2	0.8	1.0	1.2	1.1	IFZ2	orf19.1365	unknown function	no match
CA4804	1.5	1.1	0.8	1.4	1.4	1.1	ARO8	orf19.2098	aromatic amino acid aminotransferase I (by homology)	YGL202w
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function	YDL012c
CA1980	1.5	1.1	1.4	0.9	0.5	0.6	YHM1	orf19.685	member of the mitochondrial carrier family (MCF) (by homolo	YDL198c
CA3958	1.5	1.1	0.7	0.9	0.7	1.0	COX11	orf19.1416	cytochrome-c oxidase assembly protein by homology to S. ce	YPL132w
CA0739	1.5	1.1	0.9	1.0	0.6	0.7				
CA5560	1.5	1.2	1.3	0.9	1.1	1.0	THI13	orf19.7324	Pyrimidine precursor biosynthesis enzyme (by homology)	YDL244w
CA0280	1.5	1.0	1.4	1.1	0.8	0.7	IPF10566	orf19.1439	unknown function	YDR315c

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[Ca OS+ up 1.5 10FDR] less [Ca HS+ up 1.5 10FDR]] less [Ca XS+ up 1.5 10...

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA5797	1.2	0.9	8.7	8.2	0.7	1.0	IPF4182	orf19.5446	unknown function	no match
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)	YDR497c
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function	no match
CA1812	1.4	0.9	5.5	1.3	0.9	1.0	IPF13879	orf19.1120	unknown function	no match
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function	YLR205c
CA5526	0.8	1.2	4.8	1.9	1.1	1.0	IPF2857	orf19.7284	unknown function	YFR016c
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA5191	1.1	0.7	4.7	1.0	1.1	1.2	IPF19538.	orf19.6957.3	partially similar to Isocitrate dehydrogenase (NAD+) subunit 1	YNL037c
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c
CA1779	1.2	1.1	4.5	1.5	0.5	0.8	IPF14510	orf19.1826	unknown function	YGL219c
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA3607	1.2	0.4	4.1	1.8	1.4	1.2	RTA2	orf19.24	Unknown function	YOR049c
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA1296	1.1	1.0	4.0	1.9	0.9	0.9				
CA2847	0.9	0.6	4.0	1.3	1.1	1.2	NOG2	orf19.5733	unknown function Nuclear/Nucleolar GTP-binding protein, by	YNR053c
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)	YLR409c
CA4641	1.0	1.1	3.8	1.4	0.8	1.0	IPF1505	orf19.348	similar to saccharomyces cerevisiae Kre6p glucan synthase s	YPR159w
CA5650	1.5	2.8	3.7	1.2	1.1	1.0	IPF7109	orf19.7350	unknown function	YNL208w
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match
CA4004	0.7	0.7	3.4	1.5	1.1	0.7	IPF4256	orf19.1632	unknown function	YKL046c
CA3927	1.0	0.7	3.4	1.3	0.7	0.8	DIP2	orf19.5106	beta transducin	YLR129w
CA1988	2.2	1.7	3.4	1.2	0.9	0.9	IPF19749	orf19.94	unknown function	no match
CA2772	1.0	0.5	3.3	1.3	0.9	1.1	IPF20112	orf19.2688	unknown function	YPL126w
CA6022	0.8	0.9	3.3	1.2	0.4	0.4	PGA1	orf19.7625	GPI-anchored cell surface protein (by homology)	no match
CA2240	1.3	0.9	3.3	1.2	0.7	0.9				
CA3939	1.0	0.9	3.2	1.1	0.4	0.8	HNM1	orf19.2003	Choline permease (by homology)	YGL077c
CA1506	1.1	1.0	3.2	1.1	1.4	1.0	HGT11	orf19.4527	hexose transporter	YFL040w

CA1558	0.7	1.1	3.2	2.1	0.8	1.0	IPF15679	orf19.1709	lipid transfer protein (by homology)	no match
CA0098	1.0	0.5	3.1	1.4	1.0	1.1	IPF16479	orf19.2319	unknown function	YDR365c
CA3560	1.1	1.0	3.1	1.0	1.6	1.2	CZF1	orf19.3127	canal zinc finger protein	no match
CA5114	0.7	0.7	3.1	1.5	0.7	1.0	IPF1334	orf19.6417	Conserved hypothetical protein	YDL060w
CA6062	1.5	1.3	3.0	1.5	0.6	0.8	IPF8307	orf19.6005	putative permease (by homology)	YDR536w
CA5192	1.4	1.0	2.9	1.4	1.1	1.0	HOK	orf19.7004	unknown function	no match
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA2697	1.2	1.5	2.9	2.6	0.9	0.8	IPF9167	orf19.2737	unknown function	YDR109c
CA4929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA1293	1.7	0.7	2.8	1.3	0.9	1.0	HCA4	orf19.2712	Can suppress the U14 snoRNA rRNA processing function	YJL033w
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function	YNL111c
CA5292	0.9	0.5	2.7	1.4	0.9	1.1	IPF1948	orf19.7154	unknown function	YJL069c
CA5856	1.0	1.1	2.7	1.1	0.7	1.0	ALK2	orf19.7513	n-alkane inducible cytochrome P-450 (by homology)	YDR402c
CA2040	0.9	1.3	2.7	1.5	0.9	0.6	IPF12946	orf19.4356	unknown function	YDL199c
CA0003	2.0	0.9	2.7	0.7	0.8	0.8				
CA0204	1.5	0.5	2.7	1.1	0.7	0.9	IKI3	orf19.1222	killer toxin insensitive protein 3 (by homology)	YLR384c
CA4038	1.1	0.9	2.7	1.2	1.4	0.9	HGT12	orf19.3668	hexose transporter	YFL040w
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha	YIL099w
CA4467	1.0	1.0	2.6	1.1	0.9	0.9	IPF9833	orf19.6864	unknown function	no match
CA0823	1.0	1.0	2.6	1.9	1.5	1.4	IPF11987.	orf19.692	unknown function, 3-prime end	no match
CA1666	0.8	0.6	2.6	1.7	1.0	1.0	SRP40	orf19.2859	RNA I and II supressor (by homology)	YKR092c
CA5652	1.1	0.9	2.6	0.8	0.5	0.6	IPF19815	orf19.7354	longevity-assurance protein (by homology)	YKL008c
CA4425	1.2	1.1	2.6	1.6	0.9	1.1	ENA21.3f	orf19.5170	P-type ATPase, 3-prime end (by homology)	YDR038c
CA4003	0.9	0.7	2.6	1.5	0.9	0.9	IPF4257	orf19.1633	unknown function	YDR324c
CA1694	0.9	0.8	2.6	1.1	0.5	0.9	TRM3	orf19.5038	2 -O-ribose methyltransferase (by homology)	YDL112w
CA1984	0.9	1.3	2.5	1.1	0.8	0.7	IPF9592	orf19.90	unknown function	YFL042c
CA1879	1.0	1.0	2.5	1.0	1.0	0.6	SMF12	orf19.2270	manganese transporter (by homology)	YOL122c
CA6072	0.9	0.9	2.5	1.1	1.0	1.2	DBP10	orf19.5991	Putative ATP-dependent RNA helicase (by homology)	YDL031w
CA2848	1.0	0.5	2.5	1.4	1.2	1.1				
CA3770	0.9	1.1	2.5	1.4	0.9	1.1	SOU2	orf19.2897	Sorbitol utilization protein Sou2p [Candida albicans]	YNL202w
CA0715	1.1	0.9	2.5	1.3	1.4	1.4	DBP9	orf19.3393	dead box helicase	YLR276c
CA3340	0.9	1.0	2.5	1.0	0.7	1.0	ADA2	orf19.2331	general transcriptional adaptor or co-activator (by homology)	YDR448w
CA5323	0.9	0.7	2.5	1.2	0.7	1.1	IPF2142	orf19.7197	unknown function	YLR002c
CA4289	1.3	0.7	2.5	1.3	0.8	1.0	IPF6665	orf19.6686	unknown function	YGR145w
CA0443	0.9	0.5	2.5	1.1	1.0	1.1	SPB1	orf19.76	Putative methyltransferase by homology	YCL054w
CA4718	1.0	0.7	2.5	1.4	1.2	1.0	IPF8661	orf19.6955	unknown function	YOR056c
CA5051	0.5	0.3	2.5	1.4	1.2	1.2	IPF3709	orf19.3015	unknown function	YDR101c
CA5787	0.8	0.8	2.4	1.3	1.1	0.9	IPF1136	orf19.5436	unknown function	YGR128c
CA4044	1.8	0.8	2.4	3.3	0.7	0.9	GAL7	orf19.3675	UDP-glucose-hexose-1-phosphate uridylyltransferase (by hor	YBR018c
CA3993	0.7	0.3	2.4	1.0	0.7	0.7	IPF8275	orf19.1569	unknown function	YGR090w
CA3710	1.5	1.0	2.4	0.9	0.7	0.4	CHS3.5f	orf19.4938	chitin-UDP acetyl-glucosaminyl transferase 3, 3-prime end	YBR023c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA6061	0.6	0.6	2.3	1.2	0.4	0.4	IPF8302	orf19.6007	unknown function	YJL196c
CA1590	1.1	1.0	2.3	1.0	0.9	1.0	IPF14665	orf19.4315	unknown function	YFL027c
CA0027	0.8	0.6	2.3	1.5	1.1	1.2	RCL1	orf19.1886	RNA 3 -terminal phosphate cyclase (by homology)	YOL010w
CA0854	1.0	0.7	2.3	1.1	1.1	0.8	IPF8854	orf19.4900	similar to Saccharomyces cerevisiae Mnn1p alpha-1,3-mannc	YER001w
CA5529	1.1	1.1	2.3	1.1	1.0	0.9	IPF2852	orf19.7288	putative acetyl-coenzyme-A dehydrogenase	no match
CA2459	0.9	0.9	2.2	1.3	1.2	1.1	IPF12234.	orf19.3509	unknown function, 5- prime end	no match
CA1660	0.8	0.8	2.2	1.2	0.8	0.5	DAP2	orf19.4322	dipeptidyl aminopeptidase B (by homology)	YHR028c
CA1822	1.2	0.6	2.2	1.3	0.8	0.9	IPF9525	orf19.4268	unknown function	YLR222c
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA1640	0.8	0.7	2.2	0.9	0.7	0.9	IPF18641.	orf19.1732	unknown function, 3-prime end	YBL004w
CA5466	1.8	0.7	2.2	1.2	1.0	1.0	PWP2	orf19.3276	periodic tryptophan protein (by homology)	YCR057c
CA1793	1.2	1.2	2.2	1.1	0.9	1.0	IPF18608.	orf19.5207	unknown function, 5-prime end	YIL103w
CA2204	0.6	0.5	2.2	1.0	0.5	0.9	DIP51.5f	orf19.2943	dicarboxylic amino acid permease, 5-prime end (by homology	YPL265w
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match
CA5457	1.2	1.0	2.2	1.2	0.9	1.0	TRM1	orf19.3265	N2,N2-dimethylguanine tRNA methyltransferase (by homolog	YDR120c
CA5063	0.9	0.5	2.2	1.1	0.7	0.8	IPF8493	orf19.3034	putative member of nontransporter group of ATP-binding cas	YDR091c
CA3308	0.6	0.8	2.2	1.0	0.6	1.0	PET127.5f	orf19.2309	component of mitochondrial translation (by homology)	YOR017w
CA3925	1.2	1.0	2.2	1.2	0.8	1.0	IPF13257	orf19.5110	unknown function	no match
CA3131	1.3	0.9	2.2	1.1	1.3	1.4	IPF8910	orf19.1362	unknown function	YNR015w
CA1631	1.4	1.0	2.2	1.0	1.2	1.1	IPF19582	orf19.1028	unknown function	YNL230c
CA5367	1.1	1.1	2.2	1.2	1.0	1.0	RIM101	orf19.7247	Zn finger transcription factor homolog; regulator of pH respon	YHL027w
CA0973	1.0	1.5	2.1	1.6	1.3	1.3	IPF12662	orf19.6474	unknown function	no match
CA4227	0.8	1.0	2.1	1.1	0.8	1.2	SCH9	orf19.829	protein kinase (by homology)	YHR205w
CA1407	0.9	0.9	2.1	1.4	0.9	0.7	UAPC	orf19.2882	purine permease (by homology)	no match
CA5023	0.7	0.7	2.1	1.0	0.4	0.6	IPF7547	orf19.6976	unknown function	YJL163c
CA1155	1.1	0.8	2.1	1.2	0.7	0.8	JA2	orf19.107	ATP-dependent RNA helicases-like (by homology)	YKL078w
CA4470	1.0	0.8	2.1	1.5	1.1	1.1	IPF9717	orf19.1902	unknown function	YPR144c
CA4099	0.8	0.4	2.1	1.2	0.7	1.0	IPF3986	orf19.665	unknown function	YLR186w
CA2984	0.8	0.6	2.1	1.2	0.8	0.9	IPF12606.	orf19.6008.1		YNL123w
CA5957	1.2	0.7	2.1	1.0	1.2	1.0	RRP3.3eo	orf19.7546	RNA-dependent ATPase, helicase,required for maturation of	YHR065c
CA2304	0.8	0.6	2.1	1.3	0.8	1.4	PRP43	orf19.1687	RNA-dependent ATPase (by homology)	YGL120c
CA4840	1.0	1.0	2.1	1.1	0.6	1.0	IPF1235	orf19.2054	unknown function	YDL020c
CA3604	0.5	0.6	2.1	1.8	0.3	0.4	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)	no match
CA5644	0.8	0.8	2.1	1.2	1.1	1.1	IPF447	orf19.7050	unknown function	YNL110c
CA2593	0.9	0.8	2.1	1.1	1.1	1.1	RRP6	orf19.58	involved in 5.8S rRNA processing (by homology)	YOR001w
CA2731	0.7	1.0	2.0	1.3	1.0	1.0	URIC	orf19.2114	uricase (urate oxidase) (by homology)	no match
CA1706	1.0	0.7	2.0	1.3	1.5	1.4	NMD3	orf19.706	RNA binding (by homology)	YHR170w
CA2035	0.9	1.4	2.0	1.0	0.7	0.9	SGD1	orf19.4363	involved in the HOG pathway (by homology)	YLR336c
6100.2	1.5	2.2	2.0	1.2	1.1	1.0				
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA4811	0.9	0.6	2.0	1.2	1.0	1.0	ECM16	orf19.2090	RNA helicase (by homology)	YMR128w
CA0693	1.0	0.8	2.0	1.2	0.8	1.0	IPF12606.	orf19.3288	unknown function, 5-prime end	YNL123w
CA5568	0.8	0.4	2.0	1.0	1.2	1.0	ELF1	orf19.7332	Elongation-like factor	YPL226w
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)	YFL036w
CA3272	0.8	1.1	2.0	1.0	0.7	1.1	ALD4	orf19.6306	aldehyde dehydrogenase, mitochondrial (by homology)	YOR374w
CA1503	0.5	0.4	2.0	1.6	1.0	1.1	RKI1	orf19.1701	D-ribose-5-phosphate ketol-isomerase (by homology)	YOR095c
CA2119	1.3	0.6	2.0	0.9	0.7	0.9	MTR4	orf19.1335	RNA Helicase (by homology)	YJL050w
CA0651	1.0	0.9	2.0	1.0	1.0	1.1	ALK8	orf19.10	n-alkane inducible cytochrome P-450 (by homology)	YDR402c

CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA2670	1.0	0.8	2.0	1.3	0.8	1.1	MAK16	orf19.5500	nuclear viral propagation protein (by homology)	YAL025c
CA2898	0.5	0.6	2.0	0.9	0.6	0.8	IPF15646	orf19.3481	putative ATP-dependent RNA helicase (by homology)	YGL064c
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA2667	0.7	0.4	2.0	1.3	1.1	1.1	IPF16996	orf19.3547	unknown function	YDR496c
CA4575	0.8	0.8	2.0	1.2	0.9	1.4	IPF9428	orf19.6886	unknown function	YPL146c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA5718	1.2	1.0	1.9	1.4	1.1	1.5	LCP5	orf19.7422	Ngg1p interacting protein (by homology)	YER127w
CA4339	0.8	0.7	1.9	1.3	1.1	0.9	IPF3618	orf19.6710	Unknown function	YHR196w
CA1929	1.0	1.0	1.9	1.6	0.9	0.7	SAP7	orf19.756	secreted aspartyl proteinase 7	YLR121c
CA1784	1.2	1.1	1.9	1.2	0.7	0.9	ARO7	orf19.1170	chorismate mutase (by homology)	YPR060c
CA0782	1.9	1.8	1.9	1.4	1.2	1.3	IPF16253	orf19.3932	unknown function	no match
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match
CA2044	1.2	0.7	1.9	1.1	0.9	0.9	IPF10668	orf19.2930	unknown function	YGR054w
CA0011	1.2	1.0	1.9	0.7	0.8	0.7	IPF17430.	orf19.73	possible zinc protease, 5-prime end (by homology)	YIL137c
CA2449	1.0	0.6	1.9	1.1	0.9	1.1	ENP1	orf19.5507	Essential nuclear protein (by homology)	YBR247c
CA4041	1.6	0.6	1.9	1.7	1.1	0.7	GAL10	orf19.3672	UDP-glucose 4-epimerase by homology	YBR019c
CA2812	1.2	0.7	1.9	1.2	0.9	1.0	TEM1	orf19.3001	GTP-binding protein of the RAS superfamily	YML064c
CA2100	0.8	0.8	1.9	1.2	1.1	1.1	KTI12	orf19.2385	involved in resistance to K.lactis killer toxin (by homology)	YKL110c
CA3995	0.9	0.7	1.9	1.3	1.0	1.2				
CA0207	0.4	0.4	1.9	1.0	1.0	0.7	IPF18002	orf19.1226	Unknown function	YKL014c
CA0087	0.9	1.2	1.9	0.9	1.0	0.6	SMF11	orf19.4690	manganese transporter (by homology)	YOL122c
CA0327	0.7	0.7	1.9	1.4	1.1	1.1	IPF15217.	orf19.3779	WD-repeat protein, 5-prime end (by homology)	YCR072c
CA1999	1.2	0.9	1.9	1.0	0.8	1.0	IPF19513	orf19.6476	unknown function	YLR114c
CA0813	0.7	0.7	1.9	1.3	1.3	0.8	MPP10	orf19.1915	component of the U3 small nucleolar ribonucleoprotein (by hc	YJR002w
CA1100	1.2	0.8	1.9	1.3	1.3	0.9	IPF5681	orf19.4952	unknown function	no match
CA5067	0.5	0.9	1.9	1.6	1.5	1.2	IPF3589	orf19.3040	putative alcohol acyl transferase (by homology)	YBR177c
CA5113	1.0	0.8	1.9	1.4	1.0	1.0	IPF20026	orf19.6418	unknown function	YDL063c
CA4912	1.3	0.9	1.9	1.1	0.8	1.2	CNS1	orf19.6052	Cyclophilin Seven Suppressor (by homology)	YBR155w
CA1639	1.3	0.7	1.9	0.9	0.8	0.7	IPF18641.	orf19.1733	unknown function, 5-prime end	YBL004w
CA3069	0.8	0.7	1.9	2.1	0.6	0.7	IPF6117	orf19.4805	unknown function	YMR266w
CA6098	1.0	0.7	1.9	1.4	0.8	0.9	IPF61	orf19.5959	unknown function	YDL148c
CA6128	0.9	1.0	1.9	0.8	0.3	0.5	IPF152	orf19.5919	unknown function	YOR129c
CA2414	1.6	1.2	1.9	1.1	0.9	1.1	IPF13756.	orf19.4479	unknown function, 3-prime end	YJL010c
CA1417	0.9	0.6	1.9	1.2	1.2	1.4	IPF16126	orf19.172	similar to Saccharomyces cerevisiae Rpc19p DNA-directed R	YNL113w
CA1627	0.9	0.8	1.8	1.0	1.3	1.4	SKO1.3f	orf19.1032	Cre-binding bzip protein, 3-prime end (by homology)	YNL167c
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rRN	YDR087c
CA5685	0.9	0.5	1.8	1.0	0.9	0.9	HPA1	orf19.7387	RNA polymerase II-associated Histone acetyltransferase (by	YPL086c
CA2244	0.9	0.8	1.8	0.9	1.0	1.0	AAT22	orf19.4669	aspartate aminotransferase (by homology)	YLR027c
CA2869	0.9	0.9	1.8	1.0	0.8	0.8	RPC82	orf19.2847	DNA-directed RNA polymerase III, 82 KD subunit (by homolo	YPR190c
CA3175	1.1	0.7	1.8	1.3	1.1	0.8	IPF11587	orf19.1403	unknown function	YNL083w
CA3159	1.7	1.4	1.8	1.2	1.4	1.2	PLC3	orf19.1586	phosphatidylinositol phospholipase C	YLR197w
CA4043	1.3	0.9	1.8	2.0	0.7	1.0	IPF5291	orf19.3674	UDP-glucose 4-epimerase (by homology)	YBR019c
CA2629	0.8	1.1	1.8	1.1	1.2	1.1	IPF10911	orf19.4760	unknown function	YIL110w
CA3007	0.9	0.8	1.8	1.4	1.1	1.4	IPF12148	orf19.6234	Unknown function	YNL182c
CA4113	1.2	1.0	1.8	1.5	0.4	0.7	CHO1	orf19.677	Phosphatidylserine synthase	YER026c
CA4387	0.8	0.7	1.8	1.0	1.4	1.2	MAP1	orf19.3124	methionine aminopeptidase, isoform 1 (by homology)	YLR244c
CA2399	1.0	0.7	1.8	1.2	1.0	1.3	MAK5	orf19.3540	ATP-dependent RNA helicase (by homology)	YBR142w
CA2461	1.3	0.8	1.8	1.2	1.2	1.3	MAK11	orf19.1791	involved in cell growth and replication of M1 dsRNA virus (by	YKL021c
CA3608	1.0	0.9	1.8	1.3	1.5	1.4	IPF3857	orf19.25	unknown function	YOL093w
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA6039	1.2	1.0	1.8	1.3	1.0	1.1	CKA1	orf19.7652	casein kinase II, catalytic alpha chain (by homology)	YIL035c
CA2796	0.8	0.6	1.8	1.3	1.3	1.1	IPF8405	orf19.1721	similar to Saccharomyces cerevisiae Nce103p involved in nor	YNL036w
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA1561	1.5	1.3	1.8	1.5	0.9	1.0	POT12	orf19.1704	peroxysomal 3-ketoacyl-CoA thiolase B (by homology)	YIL160c
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA1770	0.7	0.6	1.8	1.3	1.3	1.4	IPF12457	orf19.2185	unknown function	YGL111w
CA1786	0.8	1.1	1.8	1.1	1.0	1.0	IPF7629	orf19.1168	unknown function	no match
CA1370	1.5	0.9	1.8	1.0	0.8	0.8	TCI1	orf19.4963	protein phosphatase Two C-Interacting protein (by homology)	YDR161w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4708	0.7	1.0	1.8	1.1	1.2	1.1	MEU1	orf19.6938	regulator of ADH2 expression (by homology)	YLR017w
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homolo	YOR049c
CA1938	1.2	0.7	1.8	1.1	0.8	0.8	NMD5	orf19.4188	putative Nam7p/Upf1p-interacting protein (by homolgy)	YJR132w
CA4336	0.9	1.1	1.8	1.5	0.6	0.9	DDR48	orf19.4082	stress protein (by homology)	YMR173w
CA3242	0.5	0.6	1.8	1.2	0.7	0.9	RAT1	orf19.4681	5 -3 Exoribonuclease (by homology)	YOR048c
CA2099	0.8	0.8	1.8	1.1	1.1	1.1	IPF11484	orf19.2386	unknown function	YKL099c
CA6074	1.0	0.7	1.8	1.3	1.1	1.0	IPF11	orf19.5987	unknown function	YOL124c
CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA1000	1.2	1.0	1.8	0.9	1.0	0.9	IPF6011	orf19.1486	unknown function	no match
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA4458	1.1	1.0	1.7	1.1	0.7	0.8	IPF8464	orf19.6855	unknown function	no match
CA1047	1.1	0.9	1.7	1.2	0.9	1.1	IPF11615	orf19.1646	RNA-binding proteins (by homology)	YPR112c
CA0743	1.3	1.0	1.7	1.0	1.1	1.0	RNA14	orf19.1531	component of pre-mRNA 3 -end processing factor CF I (by hc	YMR061w
CA3688	0.9	0.9	1.7	1.2	0.4	0.7	YIP3	orf19.6264.3	protein of unknown function, (by homology)	YNL044w
CA6029	0.6	0.5	1.7	1.3	1.1	1.5	DRS1	orf19.7635	ATP dependent RNA helicase (by homology)	YLL008w
CA2034	0.9	1.1	1.7	1.1	0.8	1.0				
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w
CA1318	1.4	0.7	1.7	1.2	0.8	1.1	IPF3147	orf19.4219	Nuclear valosin-containing protein-like (by homology)	YLL034c
CA4933	1.6	1.2	1.7	1.2	1.1	1.3	IPF8372	orf19.6074	unknown function	YDL166c
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match
CA2881	0.6	0.5	1.7	1.1	1.1	1.1	RAD4	orf19.5850	Excision repair protein (by homology)	YOR206w
CA0923	0.9	0.8	1.7	1.4	0.9	1.1	IPF12987	orf19.1047	unknown function	YMR049c
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA0939	1.2	0.9	1.7	1.2	1.1	1.4	DBP6	orf19.3704	RNA helicase required for 60S ribosomal subunit assembly (t	YNR038w
CA2695	1.3	0.9	1.7	1.0	0.8	1.2	SEN2	0	tRNA splicing endonuclease beta subunit(by homology)	YLR105c
CA6054	2.1	0.8	1.7	1.2	0.6	0.6	IPF4952	orf19.7672	unknown function	YDR411c
CA3236	1.2	0.8	1.7	1.3	0.7	0.9	DEG1	orf19.6297	pseudouridine synthase (by homology)	YFL001w
CA3330	0.4	0.2	1.7	1.2	0.8	0.9	POL21.3f	orf19.2669	pol polyprotein, reverse transcripase, 3-prime end (by homolc	YFL050c
CA5999	1.0	1.1	1.7	1.2	1.1	1.1	IPF668	orf19.7599	unknown function	YDR398w
CA1714	1.1	1.0	1.7	1.2	1.1	0.9	NAB2	orf19.3333	Nuclear poly(A)-RNA-binding protein (by homology)	YGL122c
CA2045	2.1	1.0	1.7	1.1	1.0	1.2	IPF8107	orf19.2933	unknown function	YFL044c

CA3342	0.8	0.7	1.7	1.4	0.7	1.1	IPF13361	orf19.2330	unknown function	YDR449c
CA2442	1.0	0.7	1.7	1.3	1.2	1.5	PRS5	orf19.2193	Phosphoribosylpyrophosphate synthetase (ribose-phosphate	YOL061w
CA2935	0.9	0.8	1.7	1.0	0.5	0.5	IPF11521	orf19.3328	unknown function	YMR172w
CA1094	1.6	1.1	1.7	1.3	0.6	0.7	YIP1	orf19.3951	golgi membrane protein (by homology)	YGR172c
CA5902	1.1	0.8	1.7	0.8	0.9	0.9	SRP68	orf19.6804	SIGNAL RECOGNITION PARTICLE 68 (by homology)	YPL243w
CA0260	1.2	0.7	1.7	0.9	0.4	0.7	IPF13683	orf19.2547	unknown function	no match
CA1110	1.3	1.2	1.7	0.9	0.9	1.3	DIS3	orf19.5229	3 –5 exoribonuclease required for 3 end formation of 5.8S rR	YOL021c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA0206	0.9	1.0	1.7	1.1	1.0	1.0	IPF14089	orf19.2781	putative serine/threonine protein kinase	YLR248w
CA4803	1.0	1.0	1.7	1.0	1.4	1.0	PEX4	orf19.4041	E2 ubiquitin-conjugating enzyme -peroxin (by homology)	YGR133w
CA0328	0.7	0.6	1.7	1.5	1.2	1.2	IPF15217.	orf19.3778	WD-repeat protein, 3-prime end (by homology)	YCR072c
CA2032	1.0	0.7	1.7	0.8	0.5	0.6	IPF13112	orf19.3466	unknown function	YGL136c
CA2359	0.7	0.6	1.7	1.2	0.8	1.0	IPF8952	orf19.4896	similar to Saccharomyces cerevisiae Rpa34p nonessential cc	YJL148w
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA2842	1.1	1.0	1.7	1.0	0.9	0.8	ALK5.3f	orf19.5727.1	n-alkane-inducible cytochrome P-450, 3-prime end	YDR402c
CA1039	0.8	0.8	1.7	0.9	0.5	0.5	IPF4012	orf19.2501	Unknown Function	YPL221w
CA5097	0.9	0.8	1.7	1.1	0.9	1.1	IPF1382	orf19.6444	unknown function	YHL023c
CA5252	1.0	0.8	1.7	1.4	0.9	1.2	DIM1	orf19.5010	rRNA (adenine-N6,N6-)-dimethyltransferase (by homology)	YPL266w
CA2645	0.8	1.1	1.7	1.2	1.0	1.1	YNK1	orf19.4311	Nucleoside diphosphate kinase (by homology)	YKL067w
CA1619	0.7	0.6	1.6	1.5	0.6	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)	YPL057c
CA2014	1.5	0.9	1.6	0.9	0.8	0.9	IPF1717.3	orf19.3080	similar to Saccharomyces cerevisiae Scc2p involved in sister	YDR180w
CA1291	0.9	0.7	1.6	1.2	0.9	1.1	IPF16752	orf19.2711	unknown function	YGR200c
CA5584	0.9	1.1	1.6	1.0	0.7	0.8	SAC7	orf19.7115	GAP for RHO1 by homology	YDR389w
CA3691	1.0	1.0	1.6	1.0	0.4	0.8	IPF4880	orf19.6266	unknown function	YCR093w
CA5880	1.1	1.0	1.6	1.2	0.8	0.9	IPF12074	orf19.6829	unknown function	YMR282c
CA5670	1.1	1.1	1.6	1.0	0.5	1.1	IPF1266	orf19.7372	Probable transcription factor	YAL051w
CA5450	1.0	1.1	1.6	1.0	0.8	0.9	IPF243	orf19.3254	unknown function	no match
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA1350	0.8	0.8	1.6	1.2	0.3	0.6	MCM2	orf19.4354	replication licensing factor (by homology)	YBL023c
CA4443	1.4	0.9	1.6	1.0	1.0	1.0	IPF3535	orf19.6840	unknown function	no match
CA2515	0.8	1.0	1.6	0.9	0.6	0.8	IPF19759	orf19.5510	Unknown Function	YGL133w
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function	no match
CA1695	1.0	0.9	1.6	1.1	1.0	1.4	RRP42	orf19.5039	rRNA processing protein (by homology)	YDL111c
CA0228	0.8	1.0	1.6	1.1	0.5	0.7	IPT1.5f	orf19.4769	Mannosyl diphosphorylinositol ceramide, 5-prime end (by hor	YDR072c
CA4040	1.0	0.9	1.6	1.5	1.2	1.0	GAL1	orf19.3670	galactokinase	YDR009w
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA5667	1.0	1.0	1.6	1.2	1.5	1.4	IPF1259	orf19.7369	Conserved hypothetical protein	YML005w
CA1626	0.8	1.3	1.6	1.4	1.3	1.1	STR2	orf19.1033	O-succinylhomoserine (thiol)-lyase (by homology)	YJR130c
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c
CA4246	0.9	1.0	1.6	1.6	1.3	1.1	PGA20	orf19.535	unknown function	no match
CA4096	1.3	1.0	1.6	1.0	1.1	1.3	KRR1	orf19.661	involved in cell division and spore germination	YCL059c
CA6021	1.0	0.8	1.6	1.2	1.1	1.3	BFR2	orf19.7624	involved in protein transport steps at the Brefeldin A block (b	YDR299w
CA1702	1.4	0.7	1.6	1.0	0.7	0.9	HEL1	orf19.702	DNA helicase I (by homology)	YER176w
CA3315	0.9	1.1	1.6	1.5	1.0	1.0	IPF8814	orf19.2302	unknown function	no match
CA5811	1.6	1.0	1.6	1.0	0.8	1.0	IPF1699	orf19.6614	unknown function	YDR021w
CA6095	1.1	1.0	1.6	0.7	0.4	0.5	SNF3	orf19.5962	High affinity glucose transport protein (by homology)	YDL194w
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)	YLR216c
CA0504	0.9	1.0	1.6	1.0	0.9	0.9	IPF16466.	orf19.2778	unknown function	YKL014c
CA4524	1.6	1.3	1.6	1.3	0.9	1.1	IPF7097	orf19.480	unknown function	YJR056c
CA5121	0.7	0.8	1.6	1.2	1.0	0.9	IPF1310	orf19.6407	unknown function	YLR387c
CA2367	1.7	1.5	1.6	1.1	0.8	1.0	SUI1	orf19.1280	translation initiation factor 3 (eIF3) (by homology)	YNL244c
CA5251	1.2	0.9	1.6	1.3	0.7	0.8	IPF1824	orf19.5011	unknown function	YPL269w
CA1422	1.0	0.7	1.6	1.3	1.0	1.1	IPF14248	orf19.3798	putative methyltransferase (by homology)	YDL201w
CA3006	1.1	0.7	1.6	1.3	1.1	1.2	IPF12152	orf19.6236	unknown function	YDL213c
CA4584	0.9	1.0	1.6	1.0	1.2	1.0	IPF2228	orf19.6902	similar to Saccharomyces cerevisiae Dbp7p RNA helicase re	YKR024c
CA5765	0.9	0.9	1.6	1.1	1.2	1.5	SOF1	orf19.5407	Involved in 18S pre-rRNA production (by homology)	YLL011w
CA6140	0.7	0.7	1.6	1.2	0.6	1.2	IPF1882	orf19.5905	unknown function Unknown function	YBL028c
CA1125	1.1	0.9	1.6	1.2	1.1	1.4	RRP43	orf19.6259	rRNA processing protein (by homology)	YCR035c
CA4585	0.8	0.9	1.6	1.2	1.2	1.3	IPF2227	orf19.6903	unknown function	YKR025w
CA5660	1.6	1.0	1.6	1.3	0.8	0.9	SKN1.3f	orf19.7362	Glucan synthase subunit, 3-prime end	YPR159w
CA4663	1.6	1.4	1.6	1.1	0.7	0.8	IPF6554	orf19.4450	unknown function	YJL103c
CA2283	1.3	0.7	1.6	1.7	1.3	1.2	MRT4	orf19.5550	required for mRNA decay (by homology)	YKL009w
CA5661	1.4	1.5	1.6	1.5	0.8	0.9	KRE6	orf19.7363	Glucan synthase subunit	YPR159w
CA5943	0.9	1.0	1.6	1.0	0.9	1.2	IPF3490	orf19.6754	unknown function	no match
CA3196	1.0	1.0	1.6	1.4	1.1	1.2	IPF3428	orf19.6175	unknown function	YLR051c
CA4972	1.3	1.2	1.5	1.0	1.2	0.9	MUP1	orf19.5280	High affinity methionine permease (by homology)	YGR055w
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)	YHL003c
CA0734	1.2	0.9	1.5	1.5	0.8	1.0	IPF8996	orf19.4634	unknown function	YGL211w
CA3527	1.4	2.1	1.5	1.6	1.0	1.4	IPF9934	orf19.988	unknown function	YGR149w
CA0142	1.0	1.4	1.5	1.0	1.4	1.3	CSL4	orf19.1026	Involved in kinetochore-related function (by homology)	YNL232w
CA0874	1.3	0.4	1.5	1.3	0.8	0.8	CPA1	orf19.4630	Arginine-specific carbamoylphosphate synthase, small chain	YOR303w
CA3225	0.8	1.0	1.5	0.9	1.2	1.0	IPF9329	orf19.6286	unknown function	YER128w
CA3243	1.0	1.0	1.5	1.1	1.1	1.0	IPF7489	orf19.4680	unknown function	no match
CA3909	1.1	0.9	1.5	1.1	1.1	1.1	CIT1	orf19.4393	Citrate synthase	YNR001c
CA5719	1.0	1.0	1.5	1.2	1.2	1.4	IPF2441	orf19.7424	unknown function	YER126c
CA1596	1.4	1.0	1.5	1.0	1.0	1.0	FAA21	orf19.272	long-chain-fatty-acid-CoA ligase (by homology)	YER015w
CA1406	1.1	0.9	1.5	1.1	0.5	0.6	DOT4	orf19.3370	derepression of telomeric silencing (by homology)	YNL186w
CA3234	1.5	0.9	1.5	0.8	0.7	0.8	MAS2	orf19.6295	processing peptidase, catalytic 53kDa (alpha) subunit, mitoch	YHR024c
CA4036	1.3	0.9	1.5	1.0	0.8	0.9	IPF12042	orf19.3666	unknown function	YGR093w
CA2856	1.0	1.1	1.5	1.4	1.4	1.2	IPF7062	orf19.1066	unknown function	YPL067c
CA1064	0.8	0.9	1.5	1.1	1.0	1.0	PWP1	orf19.4640	beta-transducin superfamily (by homology)	YLR196w
CA3130	1.0	0.9	1.5	1.0	0.7	0.8	TIM23	orf19.1361	mitochondrial inner membrane import translocase subunit (by	YNR017w
CA6063	0.8	1.1	1.5	1.0	1.0	1.0	IPF8311	orf19.6003	unknown function	YLR094c
CA2272	0.6	0.6	1.5	1.4	1.2	1.1	RPA43	orf19.2594	DNA-directed RNA polymerase I, 36 KD subunit(by homology	YOR340c
CA3491	0.9	0.6	1.5	1.1	1.3	1.4	RPC40	orf19.3564	RNA polymerase (by homology)	YPR110c
CA0599	0.7	0.9	1.5	1.2	1.1	1.1	IPF12428	orf19.2667	unknown function	YHR088w
CA5901	1.2	0.9	1.5	1.0	0.5	0.4	IPF2374	orf19.6805	unknown function	YDR089w
CA6014	1.2	1.0	1.5	1.1	0.6	1.1	TRS31	orf19.7615	targeting complex (TRAPP) component involved in ER to Gol	YDR472w
CA1275	1.7	0.8	1.5	1.4	1.2	1.0	RPC53	orf19.2715	DNA-directed RNA polymerase III (by homology)	YDL150w
CA1023	1.0	1.3	1.5	1.4	1.1	1.2	IPF4817.3	orf19.3351.1	unknown Function	YOR246c
CA4089	0.8	0.6	1.5	1.2	0.9	0.8	IPF5009	orf19.6648	unknown function	YGR245c

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[Ca XS+ up 1.5 10FDR] less [Ca HS+ up 1.5 10FDR]] less [Ca OS+ up 1.5 10...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function	YDR371w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase	YBR046c
CA2894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function	no match
CA0966	1.7	0.9	1.0	0.9	25.2	1.2	IPF9136	orf19.6249	potassium transporter, (by homology)	YMR088c
CA4392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)	YNL229c
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function	YKL086w
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match
CA2435	1.1	1.7	1.2	1.1	17.7	13.6	IPF9483	orf19.3395	probable permease (by homology)	YHR048w
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function	no match
CA0316	0.9	1.0	1.2	0.9	14.1	2.0	ALS1	orf19.5741	agglutinin-like protein	YJR004c
CA0595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5	orf19.4901	unknown function, 5-prime end	YER175c
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)	YOR388c
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA1846	1.5	2.2	0.8	0.9	12.5	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)	YOR388c
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function	YPL092w
CA1395	1.1	1.9	1.0	0.9	11.5	11.7				
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function	YNL229c
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function	no match
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inn	YMR152w
CA4293	1.3	1.0	0.7	1.0	9.1	1.0	IFA8	orf19.6690	Unknown function	YOR353c
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function	no match
CA5961	1.1	1.0	0.9	1.0	8.1	1.0	IFA14	orf19.7550	unknown function	no match
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function	no match
CA4990	1.5	1.0	0.8	1.0	8.0	1.2	IPF2039	orf19.5258	unknown function	no match
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function	YKR071c
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-bind	YGL091c
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)	YBR293w
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)	YHR137w
CA2258	1.1	2.8	0.9	0.9	7.4	16.1	IFR1	orf19.1763	Unknown function	YNL134c
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)	YDR513w
CA0644	1.4	0.9	0.9	1.0	7.0	1.0	IPF17131	orf19.69	unknown function	no match
CA3059	1.2	1.8	1.2	1.1	6.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)	YDR353w
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA	YAL049c
CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function	no match
CA4829	1.0	1.1	1.3	1.0	6.3	5.5	IPF1210	orf19.2067	similar to Saccharomyces cerevisiae Nfu1p involved in home	YKL040c
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)	YDR338c
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function	no match
CA0869	1.2	1.0	1.0	1.0	5.7	1.2	IPF14772	orf19.3589	unknown function	YHL022c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA5224	0.8	1.6	0.7	1.0	5.4	0.7	IPF3081	orf19.7043	unknown function	YLR050c
CA4759	1.3	1.0	0.9	1.0	5.4	1.0	IPF9655	orf19.3988	unknown function	no match
CA0933	1.3	1.1	0.8	1.0	5.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)	YMR301c
CA3104	1.4	1.4	1.1	1.1	4.9	1.3	IPF12084	orf19.6554	unknown function	YOR220w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function	no match
CA4662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by hom	YMR038c
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function	YMR136w
CA2750	1.1	1.0	1.1	1.0	4.6	1.7	ATX1	orf19.2369.1	antioxidant protein and metal homeostasis factor (by homolo	YNL259c
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)	YPL171c
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable monoc	no match
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function	YGL136c
CA1016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function	YOR273c
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)	YOR101w
CA0471	0.8	0.8	0.6	0.5	4.1	1.4	ECM22	orf19.2623	putative protein involved in cell wall biogenesis (by homology	YDR213w
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)	YNL270c
CA1775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology	YDL215c
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function	no match
CA4712	0.9	1.1	1.0	1.1	4.0	1.1	GTT1	orf19.6947	glutathione S-transferase (by homology)	YIR038c
CA0583	1.2	2.5	1.3	1.3	3.9	3.2	GSH1.3f	orf19.5059	gamma-glutamylcysteine synthetase, 3 prime end (by homolo	YJL101c
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)	YDR069c
CA1664	1.2	1.2	0.8	1.0	3.8	1.0	ERV1.3f	orf19.2863.1	Mitochondrial biogenesis and regulation of cell cycle, 3-prime	YGR029w
CA5697	1.3	1.0	0.8	1.1	3.8	3.0				
CA2450	1.2	1.0	0.7	1.0	3.8	1.0	IPF2589	orf19.5508	unknown function	YOR353c
CA0995	1.0	1.0	0.9	0.9	3.8	1.9				
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match
CA4034	1.0	1.3	0.8	0.9	3.8	1.1	HSP31	orf19.3664	heat shock protein (by homology)	YCR021c
CA0935	1.0	1.0	1.0	1.0	3.7	1.0	IPF14203.	orf19.1079	similarity to several transaminases, 5-prime end (by homolog	YFL030w
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)	YNL240c
CA0963	1.0	1.0	0.9	1.0	3.6	1.4	IPF9143	orf19.6246	similar to Saccharomyces cerevisiae Nat3p N-acetyltransfera	YPR131c
CA1507	1.0	3.8	0.9	0.9	3.6	1.1	HSP30	orf19.4526	heat shock protein (by homology)	YCR021c
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)	YHR044c
CA3587	0.6	1.2	0.8	1.5	3.6	1.0	AAH1	orf19.2251	adenosine deaminase (by homology)	YNL141w
CA3103	1.1	1.0	0.9	1.0	3.6	1.0				

CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA1197	1.2	1.0	0.6	0.9	3.6	1.1				
CA0385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function	YNL250w
CA1787	0.9	1.0	0.9	1.1	3.6	1.0	IFH3	orf19.1167	Dioxygenase (by homology)	YLL057c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA2711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)	YDR460w
CA2721	1.3	1.0	0.7	1.0	3.5	1.2	IPF4799	orf19.3342	unknown Function	YOR138c
CA1005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)	YPL101w
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA4304	1.4	1.0	0.7	0.9	3.4	1.1	IPF6649	orf19.6704	unknown function	YFR031c
CA2583	1.4	1.0	0.6	1.0	3.4	1.4	IPF9445	orf19.4372	unknown function	YDL206w
CA2747	1.3	1.0	1.1	1.0	3.4	1.1	IPF11467	orf19.2367	unknown function	YNL260c
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease	YHL036w
CA5895	1.0	1.0	0.9	1.0	3.3	1.4	ISA2	orf19.6811	Mitochondrial protein required for iron metabolism (by homol	YPR067w
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA5705	0.7	1.1	0.4	1.0	3.3	1.1	IPF2645	orf19.7405	unknown function	no match
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function	YHR087w
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function	YGR110w
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (a	YPR192w
CA4444	1.0	1.1	0.8	1.0	3.1	1.1	IPF3533	orf19.6842	putative GDP/GTP exchange factor (by homology)	YLR425w
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function	YOL119c
CA0934	1.2	1.3	0.9	1.1	3.1	1.0	IPF14203.	orf19.1078	similarity to several transaminases, 3-prime end (by homolog	YFL030w
CA0654	1.1	1.4	0.8	0.9	3.1	1.0	IPF11550.	orf19.2552	Ca2+-transporting P-type ATPase, 3-prime end (by homology	YGL167c
CA5041	1.0	1.0	0.8	1.0	3.1	1.0	FRP7	orf19.6995	member of the FRP family of proteins related to Yarrowia lipo	YCR010c
CA1947	1.2	1.2	0.9	0.9	3.1	0.9	IPF10637	orf19.4742	starvation protein -like (by homology)	YDR388w
CA0112	1.5	0.9	1.2	0.9	3.1	1.3	IPF17358	orf19.5754	unknown function	YLR023c
CA2868	1.2	1.4	0.8	1.0	3.0	1.0	IPF20118	orf19.2846	unknown function	no match
CA0724	0.8	1.0	1.4	1.0	3.0	1.4	IPF13398	orf19.35	protein kinase (by homology)	YMR216c
CA0850	1.2	1.0	0.8	1.0	3.0	1.0	IPF16671	orf19.1745	unknown function	no match
CA6158	1.5	1.0	0.8	1.0	3.0	1.0	IPF1839	orf19.5879	putative 1-Acyl dihydroxyacetone phosphate reductase (by h	YIL124w
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology	YAL012w
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA0996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)	no match
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)	no match
CA3025	1.1	1.0	0.8	1.1	3.0	1.0	IPF11503	orf19.3902	unknown function	YGR131w
CA1165	1.2	0.9	0.7	1.1	3.0	1.3	IPF19902	orf19.3360	unknown function	no match
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA0965	0.9	0.9	1.0	0.9	2.9	1.0	IPF9139	orf19.6248	unknown function	no match
CA1332	1.5	1.0	1.3	1.4	2.9	1.1	IPF11716	orf19.1150	unknown function	YER040w
CA0942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function	YER101c
CA2893	0.9	0.9	1.0	1.0	2.8	1.2	IFS3	orf19.2463	Unknown function	YDR014w
CA3178	2.4	1.2	1.2	1.1	2.8	1.0	IPF19974	orf19.1406	unknown function	YJL030w
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase	YHR008c
CA4637	1.0	1.0	1.2	1.0	2.8	1.5	IPF1514	orf19.344	unknown function	no match
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA4675	1.0	1.0	0.9	1.0	2.8	1.2	IPF3664	orf19.897	unknown function	YMR077c
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase	YER042w
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function	YDR336w
CA1965	1.2	1.2	1.0	1.0	2.8	1.2	IPF14035	orf19.2395	Similar to serine/threonine protein kinase (by homology)	YJL106w
CA0026	1.0	1.1	0.8	0.9	2.7	1.5	IPF16843	orf19.2397.3	unknown function	YGR127w
CA5868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function	YMR090w
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)	YIL120w
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function	YPL122c
CA4836	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)	YJR104c
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)	YNL229c
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function	YLR256w
CA3662	1.1	0.9	1.1	1.1	2.6	0.8	IPF17021	orf19.6464	unknown function	YLR420w
CA1600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)	YHR175w
CA4656	0.8	1.1	1.5	1.1	2.5	1.5	IPF3095	orf19.4443	unknown function	YDL235c
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c
CA0616	0.8	1.0	0.3	0.9	2.5	1.0	PHO11	orf19.2619	Secreted acid phosphatase	YBR092c
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase	YOR202w
CA3110	1.0	1.0	1.1	1.2	2.4	1.3	LPI9	orf19.6544	Microtubule-associated protein (by homology)	YOR227w
CA0355	2.5	1.1	0.6	1.0	2.4	1.0				
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA6160	2.1	1.4	0.8	0.9	2.4	1.2	IPF1835	orf19.5876	unknown function	no match
CA1129	1.2	1.0	1.1	0.9	2.4	1.1	IPF5197	orf19.3610	unknown function	no match
CA3445	1.2	1.1	1.1	1.0	2.4	1.4	IPF7325	orf19.2978	unknown function	no match
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match
CA2954	1.0	1.3	1.0	0.8	2.4	1.5	IPF10685	orf19.5856	unknown function	YBL034c
CA5002	1.2	1.1	0.9	1.0	2.4	1.2	IPF2021	orf19.5245	unknown function	YML111w
CA4630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA1101	1.5	0.9	1.1	0.9	2.3	1.0	IPF5678	orf19.4951	unknown function	no match
CA2339	0.8	0.8	0.7	1.6	2.3	1.4	IPF13377	orf19.2350	unknown function	YOR378w
CA4479	1.0	1.0	1.0	1.0	2.3	1.4	URH1	orf19.1888	Uridine ribohydrolase (by homology)	YDR400w
CA0756	1.4	1.0	0.9	1.1	2.3	1.1	IPF14859	orf19.3488	acyl-coenzyme-A dehydrogenase (by homology)	no match
CA2778	1.2	1.5	0.9	1.1	2.3	1.3	MTR	orf19.278	neutral amino acid permease-like by homology	YNL101w
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA2876	1.2	0.9	1.0	0.8	2.3	1.3	RNR2	orf19.5845	Ribonucleotide reductase (by homology)	YER070w
CA3655	1.2	1.1	1.0	1.1	2.3	1.1	POT13	orf19.2046	Acetyl-CoA C-acyltransferase, peroxisomal (by homology)	YIL160c
CA2741	1.0	0.9	1.0	1.3	2.3	1.2	IPF10632	orf19.2105	unknown function	YLR323c
CA0817	1.5	1.0	0.9	0.9	2.3	1.0	IPF6339	orf19.2724	unknown function	no match
CA0254	0.4	0.4	0.9	1.1	2.3	0.9	IPF14968	orf19.3461	unknown function	no match
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by ho	YDL168w

CA3558	1.0	1.0	1.0	1.0	2.3	1.1	IPF7760	orf19.3887	unknown function	no match
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)	YLR120c
CA4657	0.4	1.1	0.7	1.1	2.3	1.2	IPF3094	orf19.4444	4-nitrophenyl phosphatase (by homology)	YDL236w
6532.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA3086	1.0	1.7	1.1	1.2	2.3	3.9	GLR1	orf19.4147	by similarity to S. cerev. and C. albicans:glutathione reductas	YPL091w
CA5442	1.2	1.3	0.9	0.7	2.3	1.1	IPF18105.	orf19.3245	unknown function, 3-prime end	no match
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (t	YOL119c
CA4219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein phc	YKL193c
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)	YLR043c
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)	YOR171c
3692.2	1.2	1.2	0.8	0.9	2.2	2.1				
CA0424	1.0	1.0	1.1	0.8	2.2	1.0	IPF10795	orf19.2356	putative transcription factor (by homology)	YNL027w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match
CA4833	1.4	1.0	0.7	1.0	2.2	1.1	IPF1216	orf19.2064	unknown function	YKL165c
CA3657	1.8	1.0	1.1	1.0	2.2	1.0	IPF7459	orf19.2049	unknown function	no match
CA0757	1.0	0.7	0.6	0.8	2.2	2.0				
CA2963	1.1	1.1	1.0	1.0	2.2	1.0	GRP3	orf19.5611	dihydroflavonol-4-reductases (by homology)	YOL151w
CA0160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease	YKR039w
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYI	YOR005c
CA4252	1.0	0.9	0.8	1.0	2.2	1.3	IPF4290	orf19.541	unknown function	no match
CA2177	1.1	1.1	1.3	1.0	2.2	2.2	ROD1	orf19.1509	O-dinitrobenzene,calcium and zinc resistance protein (by hon	YFR022w
CA2263	0.5	0.6	0.6	0.6	2.2	1.2	GPD1	orf19.1756	Glycerol-3-phosphate dehydrogenase (by homology)	YOL059w
CA0961	1.4	1.6	0.7	0.9	2.2	1.2	IPF18822	orf19.3720	unknown function	YJR090c
CA5734	1.0	1.1	1.0	0.9	2.2	1.0	IPF20029	orf19.7444	unknown function	YOR352w
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function	YNL144c
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA1426	1.0	1.1	0.4	1.0	2.2	1.1	ALS9.3f	orf19.5745	agglutinin-like protein, 3-prime end	YAL063c
CA3087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)	YLR147c
CA2355	0.9	1.2	0.9	0.8	2.2	1.4	TPK1	orf19.4892	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA4684	3.0	10.5	1.1	1.0	2.2	1.5	HSP78.5f	orf19.882	heat shock protein of clpb family of ATP-dependent protease:	YDR258c
CA1136	1.5	3.0	0.8	0.9	2.1	1.2	IFN2	orf19.1980	glycerophosphoinositol transporter (by homology)	YCR098c
CA1686	0.9	1.2	0.7	0.8	2.1	1.5	IPF12272	orf19.3659	unknown function	YER139c
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function	YNL166c
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA4949	0.8	0.7	0.5	1.0	2.1	0.9	CDC34	orf19.6529	Ubiquitin-conjugating enzyme (by homology)	YDR054c
CA2392	0.8	1.2	0.5	1.1	2.1	1.2	IPF15672	orf19.2607	unknown function	YKL128c
CA2025	0.8	1.0	0.8	1.0	2.1	1.3	IPF9618	orf19.4911	unknown function	no match
CA5358	0.8	1.2	0.6	0.9	2.1	1.4	IPF846	orf19.7235	WD-repeat protein, beta-transducin (by homology)	YMR102c
CA4110	1.0	1.0	1.3	1.1	2.1	1.4	IPF3965	orf19.674	unknown function	YDL209c
CA4396	1.0	1.0	0.7	1.0	2.1	1.1	IPF12294	orf19.3115	unknown function	YBL034c
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA1170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function	YDR132c
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function	YLR021w
CA3100	1.4	1.0	1.1	0.9	2.1	1.1	IPF6594	orf19.3863	unknown function	YLR266c
CA4587	1.3	1.4	1.4	0.9	2.1	1.1	IPF2223	orf19.6905	unknown function	YNL011c
CA2584	0.8	1.2	1.0	1.1	2.1	2.0	IPF9440	orf19.4373	similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase	YDR236c
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA5330	1.2	1.0	1.0	1.0	2.1	1.1	IPF2130	orf19.7204	similar to 2-nitropropane dioxygenases	YJR149w
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase	YAL039c
CA5966	1.5	1.5	1.0	1.1	2.1	1.0	IPF959	orf19.7556	unknown function	no match
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end	YKR076w
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase	YNL277w
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3	orf19.4266.1	septin, 3-prime end (by homology)	YDR218c
CA5042	0.4	0.6	0.5	0.9	2.0	6.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA4886	1.1	0.7	1.5	1.0	2.0	1.4	IPF1634	orf19.6578	unknown function	YML123c
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)	YIR035c
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function	no match
CA0194	1.1	1.3	0.8	1.0	2.0	1.1	IPF16228	orf19.3922	unknown function	YGL224c
CA1257	1.0	1.1	0.9	1.0	2.0	1.2	IPF18725	orf19.3169	unknown function	YOR262w
CA4693	1.0	1.0	1.2	1.1	2.0	1.0	IPF3952	orf19.872	unknown function	no match
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function	YNL134c
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA4855	1.1	1.0	1.2	1.3	2.0	0.7	IPF5830	orf19.3826	unknown function	YKR100c
CA3359	1.2	1.0	0.9	1.0	2.0	1.1	IPF9566	orf19.1939	unknown function	YDR374c
ATP6	0.6	0.8	1.0	1.4	2.0	1.1				
CA4837	0.9	1.1	0.9	1.0	2.0	1.1	IPF1228	orf19.2059	unknown function	no match
CA4239	1.0	1.0	0.8	1.1	2.0	1.3	IPF8174	orf19.524	unknown function	no match
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function	YCL044c
CA4917	0.7	0.8	0.8	1.4	2.0	2.1	ECM31	orf19.6057	Involved in cell wall biogenesis and architecture (by homolog	YBR176w
CA5726	0.9	0.9	1.0	1.0	2.0	1.1	AAF1	orf19.7436	Adhesion and aggregation mediating surface antigen	no match
CA5939	1.0	1.2	1.1	1.1	2.0	1.0	IPF3484	orf19.6758	aldo/keto reductase (by homology)	YOR120w
CA2877	1.1	1.0	0.8	1.0	2.0	1.3	TFB2	orf19.5846	Transcription/repair factor (by homology)	YPL122c
CA0054	0.7	1.4	1.3	1.0	2.0	1.1	RIB4	orf19.410.3	6,7-dimethyl-8-ribityllumazine synthase (by homology)	YOL143c
CA2420	1.0	1.1	1.1	1.0	1.9	0.8	SPC19	orf19.4473	spindle pole body protein (by homology)	YDR201w
CA2740	0.9	1.1	1.0	1.2	1.9	1.2	IPF10633	orf19.2106	unknown function	YLR326w
CA5009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)	YKL119c
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)	YEL060c
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA2957	1.1	1.0	1.0	1.0	1.9	1.0	DAL53	orf19.5859	allantoate permease (by homology)	YJR152w
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function	YNL191w
CA1865	0.7	1.2	0.7	1.1	1.9	1.2	IPF7646	orf19.861	putative transcription factor (by homology)	YDR259c
CA1026	1.1	1.1	0.9	1.0	1.9	1.2	TIP41.5f	orf19.3937	unknown function, 5-prime end	YPR040w
CA2077	1.1	1.0	0.9	1.0	1.9	1.1	IPF13353	orf19.4872	unknown function	no match
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA3742	1.0	1.0	0.8	1.0	1.9	1.0	IFM3	orf19.2176	2-hydroxyacid dehydrogenase by homology, Glycerate-forma	YNL274c
CA0410	1.2	1.1	0.9	1.0	1.9	1.2	IPF15065	orf19.5757	unknown function	YMR178w
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)	YNL040w
CA3656	1.2	1.2	0.5	1.0	1.9	0.9	IPF7456	orf19.2047	unknown function	YOR289w
CA4847	1.5	1.6	0.7	0.9	1.9	1.5	IPF6951	orf19.3815	similar to Saccharomyces cerevisiae Ubp11p ubiquitin C-terr	YKR098c
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA5443	1.3	1.4	1.2	0.8	1.9	0.9	IPF18105.	orf19.3246	unknown function, 3-prime end	no match
CA3880	0.5	1.0	0.3	0.7	1.9	1.0	CAF16	orf19.388	ABC ATPase (by homology)	YFL028c

CA2595	1.1	1.0	0.5	0.9	1.9	1.0	ARG2	orf19.56	acetylglutamate synthase (by homology)	YJL071w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homolog	YER053c
CA5497	0.5	0.4	1.2	0.7	1.9	1.0	IPF776	orf19.5338	transcriptional activator (by homology)	YPL248c
CA2314	0.5	0.8	0.4	0.8	1.9	1.0	IPF14545	orf19.1381	unknown function	YCL034w
CA3062	1.0	1.0	0.9	1.1	1.9	1.2	IPF2968	orf19.4286	unknown function	no match
CA0981	0.8	0.7	0.6	1.0	1.9	1.3	GAP4	orf19.1799	general amino acid permease (by homology)	YKR039w
CA0917	1.1	1.2	0.8	1.3	1.9	1.1	RAD16	orf19.2969	nucleotide excision repair protein (by homology)	YBR114w
CA5985	1.7	1.1	0.9	0.9	1.9	1.0	IPF907	orf19.7583	unknown function	YAL051w
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)	YGR234w
CA0656	1.0	1.0	0.8	0.9	1.9	1.3	IPF12470	orf19.5573	unknown function	no match
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)	YOL151w
CA5135	1.0	1.0	1.0	1.0	1.8	1.7	HSP104.5	orf19.6389	Heat shock protein, 5-prime end (by homology)	YLL026w
CA1997	1.4	1.3	1.0	1.1	1.8	1.3	YCF1	orf19.6478	Glutathione S-conjugate transporter (by homology)	YDR135c
CA4874	0.6	0.6	0.6	0.5	1.8	1.4	IPF1674	orf19.6559	putative transcription initiation factor (by homology)	YNL108c
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA3182	1.1	1.0	0.9	1.0	1.8	1.0	LIP4	orf19.2133	secretory lipase	no match
CA3637	0.3	0.9	0.2	0.5	1.8	1.3	IPF9255	orf19.5136	unknown function	YGR017w
CA4204	1.0	0.8	0.7	1.1	1.8	0.6	HOL4	orf19.4546	member of major facilitator superfamily multidrug-resistance p	YNR055c
CA3036	1.0	1.0	0.9	1.1	1.8	0.8	IPF13443	orf19.211	unknown function	no match
CA1258	1.3	2.2	0.9	0.9	1.8	1.2	RPN8	orf19.3168	26S proteasome regulatory subunit (by homology)	YOR261c
CA1020	0.8	1.1	0.7	1.1	1.8	1.0	IPF4824	orf19.3355	unknown function	YOR155c
CA0609	1.4	1.3	0.5	1.0	1.8	1.0	CDR11.3f	orf19.919	multidrug resistance protein, 3-prime end (by homology)	YOR153w
CA2321	0.9	1.2	0.9	1.0	1.8	1.0	MEC3	orf19.5485	G2-specific checkpoint protein (by homology)	YLR288c
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)	YOR356w
CA3963	1.2	1.0	0.8	0.8	1.8	0.8	IPF11233	orf19.1422	similar to Saccharomyces cerevisiae Fzo1p required for biog	YBR179c
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function	no match
CA2467	1.1	1.0	1.3	1.0	1.8	1.1	IPF8724	orf19.1796	unknown function	YPL113c
CA3952	1.1	1.0	1.0	1.0	1.8	1.1	IPF6716	orf19.1411	Phenylacetate 2-hydroxylase (by homology)	YMR015c
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA5949	0.9	1.1	0.8	1.2	1.8	1.4	IPF3498	orf19.6747	unknown function	YDR051c
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA2440	1.2	1.0	1.1	1.2	1.8	1.0	IPF7513	orf19.2196	unknown function	YGL110c
CA3035	1.0	1.2	0.8	0.9	1.8	1.4	VPS28	orf19.212	involved in vacuolar traffic (by homology)	YPL065w
CA2855	0.3	0.8	0.5	0.8	1.8	1.4	GPM2	orf19.1067	phosphoglycerate mutase (by homology)	YKL152c
CA2915	1.3	1.0	0.8	1.0	1.8	1.0	IFA17.3f	orf19.4511	unknown function, 3-prime end	YJL005w
CA3346	0.6	1.4	0.6	1.1	1.8	1.2	IPF13356	orf19.2324	molybdopterin biosynthesis (by homology)	YHR111w
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)	YPL140c
CA1460	1.0	0.9	1.2	1.2	1.8	1.3	HAM1	orf19.1108	Controls 6-N-hydroxylaminopurine sensitivity and mutagenes	YJR069c
CA3446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function	YKL195w
CA6099	0.9	1.0	1.3	1.3	1.8	0.9	CDR2	orf19.5958	Candida albicans drug resistance protein 2	YOR153w
CA4794	1.0	0.8	1.5	1.2	1.8	1.3	SQT1	orf19.4029	suppresses dominant-negative mutants of the ribosomal prot	YIR012w
CA1027	1.0	1.4	0.8	0.8	1.8	1.4	TIP41.3f	orf19.3937.2	unknown function, 3-prime end	YPR040w
CA1576	1.0	0.9	0.9	1.0	1.8	1.1	HYR1	orf19.4975	hyphally regulated protein	no match
CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function	YDR219c
CA2775	1.1	1.0	1.1	1.0	1.8	1.2	POP5	orf19.275	subunit of RNase P- like by homology	YAL033w
CA5010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function	YMR101c
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function	YHR101c
CA5788	0.1	0.6	1.1	1.8	1.7	1.0	RHR2	orf19.5437	DL-glycerol phosphatase	YIL053w
CA5011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function	YMR101c
CA5365	0.9	0.9	0.9	1.1	1.7	1.5	IPF824	orf19.7244	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (by homolog	YNL168c
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function	no match
CA4950	0.9	1.0	0.9	1.0	1.7	1.2	IPF5143	orf19.6528	Unknown function	no match
CA6166	0.8	0.9	0.6	1.1	1.7	0.9	CTP1.3f	orf19.5870	Citrate transport protein (by homology)	YBR291c
CA5150	1.0	0.8	0.7	1.0	1.7	1.1	FMS1	orf19.4589	Similar to corticosteroid-binding protein CBP1 (by homology)	YMR020w
CA0335	0.9	1.0	1.0	1.0	1.7	1.0	IFA2	orf19.195	unknown function	YJL005w
CA5973	1.4	1.0	0.6	1.0	1.7	1.1	IPF931	orf19.7567	unknown function	YDR124w
CA1781	0.9	1.0	1.5	1.0	1.7	0.8	IPF14508	orf19.1828	unknown function	YEL029c
CA0655	1.2	1.0	0.9	0.9	1.7	1.0	IPF11560.	orf19.2553	Ca2+-transporting P-type ATPase, 5-prime end (by homolog	YGL167c
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA6104	0.8	0.9	1.1	1.1	1.7	1.1	IPF65	orf19.5952	unknown function	YDL231c
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA2389	0.9	1.0	1.1	1.0	1.7	1.0	IPF8500	orf19.2610	unknown function	YGL105w
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)	YML004c
CA3552	1.2	1.0	0.8	1.0	1.7	1.0	IPF13231	orf19.3877	unknown function	no match
CA2755	1.4	1.0	0.7	1.0	1.7	1.1	IFA12	orf19.5619	unknown function	no match
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA4580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function	no match
CA2897	0.9	0.9	1.1	1.1	1.7	1.1	IPF14979	orf19.3482	similar to Saccharomyces cerevisiae Npy1p NADH pyrophos	YGL067w
CA3724	0.9	0.9	0.5	1.1	1.7	0.7	IPF6181	orf19.4174	similar to Saccharomyces cerevisiae Fun 26p nucleoside trar	YAL022c
CA5208	0.8	1.0	1.0	1.0	1.7	1.0	IPF2361	orf19.7023	unknown function	YLR455w
CA2679	1.0	1.0	1.0	1.0	1.7	1.2	IFU5	orf19.2568	Unknown function	YFL010c
CA3802	1.4	2.2	1.0	1.1	1.7	0.7	AUT7	orf19.2480.1	microtubule-associated protein essential for autophagy (by h	YBL078c
CA3058	1.0	1.3	0.9	0.9	1.7	1.3	IPF2955	orf19.4292	unknown function	YOR036w
CA5352	1.1	1.4	0.7	1.2	1.7	0.8	IPF856	orf19.7228	unknown function	YKR030w
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function	YOR292c
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)	YPR086w
CA0827	0.7	0.8	0.7	1.0	1.7	1.3				
CA0413	1.0	0.8	0.6	1.1	1.7	1.3	ALS12.3f	orf19.2122	agglutinin-like protein, 3-prime end	no match
CA1996	1.2	1.1	1.0	1.0	1.7	0.9	SEC1	orf19.6479	transport protein	YDR164c
CA3390	1.2	1.1	0.9	1.0	1.7	1.1	CAF17	orf19.318	Component of CCR4 transcriptional complex	YJR122w
CA4164	1.7	2.0	1.0	1.1	1.7	1.1	IPF9302	orf19.5813	unknown function	YOR052c
CA5934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function	YHL029c
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA0610	1.5	0.6	0.9	1.0	1.7	0.9	CDR11.5f	orf19.918	multidrug resistance protein, 5-prime end (by homology)	YOR153w
CA3029	0.9	1.0	0.6	0.9	1.7	1.1	IPF13825	orf19.223	serine/threonine protein kinases (by homology)	YNR047w
CA2475	0.9	1.0	1.0	1.0	1.7	1.0	PGA15	orf19.2878	unknown function	no match
CA1764	0.6	1.2	1.0	1.1	1.7	1.2	IPF7596	orf19.5196	similar to Saccharomyces cerevisiae Ess1p peptidyl-prolyl cis	YJR017c
CA6096	1.3	1.8	1.0	1.2	1.7	1.2	IPF56	orf19.5961	similar to Saccharomyces cerevisiae Nas6p subunit of 26S pr	YGR232w
CA2560	1.3	1.1	0.8	1.2	1.7	1.2	PEX5	orf19.5640	peroxisomal targeting signal receptor	YDR244w
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function	YJL092w
CA3614	1.2	1.1	0.8	1.0	1.7	1.1	IPF8878	orf19.31	unknown function	YJL158c
CA4719	1.0	1.0	0.8	1.0	1.7	1.0	DAL51	orf19.6956	allantoate permease (by homology)	YJR152w
CA0093	1.0	1.0	1.1	0.9	1.7	1.1	IPF29954	orf19.100	putative lipase (by homology)	YJR107w

CA2742	1.1	1.1	1.1	1.3	1.7	1.2	JAC1	orf19.2104	molecular chaperone (by homology)	YGL018c
CA2777	1.0	0.8	1.0	0.9	1.6	0.9	THI6	orf19.277	thiamin-phosphate pyrophosphorylase and hydroxyethylthiaz	YPL214c
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA2096	1.2	1.0	0.9	1.0	1.6	1.1	IPF11491	orf19.2391	unknown function	YKR023w
CA4205	1.6	1.0	0.9	1.0	1.6	1.3	IFA10	orf19.4549	unknown function	YJL005w
CA0307	1.1	0.8	1.1	0.8	1.6	1.3	IPF4719	orf19.3736	similar to Saccharomyces cerevisiae Kar4p regulatory protein	YCL055w
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function	no match
CA5045	1.0	1.0	0.9	1.0	1.6	1.3	IPF4510	orf19.6999	unknown function	YLL057c
CA2124	1.0	1.1	0.9	1.0	1.6	1.1	IPF10490	orf19.419	unknown function	no match
CA0414	0.6	1.1	0.9	0.8	1.6	1.2	IPF4068	orf19.2164	reverse transcriptase	no match
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function	no match
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA0221	1.2	1.2	1.5	1.2	1.6	1.3	PUS4	orf19.1954	pseudouridine synthase (by homology)	YNL292w
CA2284	0.8	1.0	0.8	1.1	1.6	1.0	MIF2	orf19.5551	required for normal chromosome segregation and spindle int	YKL089w
CA3553	1.0	1.0	0.7	1.0	1.6	1.0	IFA27.5	orf19.3878	unknown function, 5-prime end	no match
CA1871	0.8	0.9	0.9	0.7	1.6	0.9	IPF16981	orf19.2458	unknown function	YMR140w
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match
CA5332	1.0	1.1	0.9	1.0	1.6	1.2	IPF900.3f	orf19.7206	unknown function, , 3-prime end	YDR067c
CA3316	1.3	1.1	1.0	1.0	1.6	1.4	IPF8817	orf19.2301	putative proteasome subunit (by homology)	YIL007c
CA4812	1.2	0.9	0.7	0.9	1.6	1.3	IPF1171.3	orf19.2089	Putative synaptobrevin (by homology)	YLR093c
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)	YPR016c
CA1528	1.0	0.7	0.6	1.1	1.6	1.2	ALS4.3f	orf19.4556	agglutinin-like protein, 3-prime end	YIR019c
CA0069	0.7	1.0	1.4	1.0	1.6	1.0	IPF19295.	orf19.6468	unknown function, 5-prime end	no match
CA2912	1.2	1.1	0.9	0.9	1.6	0.9	IPF11206	orf19.4515	unknown function	YJL158c
CA3177	1.2	1.1	1.0	1.3	1.6	1.4	IPF11589	orf19.1405	similar to Saccharomyces cerevisiae Pho13p 4-nitrophenylph	YDL236w
CA4138	1.4	1.0	1.1	1.0	1.6	1.5	IPF11954	orf19.4234	unknown function	YCR054c
CA5735	0.5	1.0	0.6	0.8	1.6	0.9	IPF2878	orf19.7445	unknown function	YBR105c
CA3620	1.0	1.0	0.8	0.9	1.6	0.8	IPF9063	orf19.203	similar to Saccharomyces cerevisiae Stb3p protein binding Si	YDR169c
CA2914	1.4	1.0	0.8	1.0	1.6	1.1	IFA17.5f	orf19.4512	unknown function, 5-prime end	no match
CA0306	0.9	0.8	1.1	1.0	1.6	0.9	HEM3	orf19.1742	porphobilinogen deaminase	YDL205c
CA2718	1.0	0.9	1.0	1.1	1.6	1.3	IPF7374.3	orf19.3338	unknown function	no match
CA0483	1.2	1.5	1.1	0.6	1.6	1.3	SEC9	orf19.117	transport protein (by homology)	YGR009c
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA0020	1.0	1.0	1.0	1.0	1.6	1.5	IPF7046	orf19.124	unknown function	YHR052w
CA2749	1.2	1.0	1.0	1.0	1.6	1.4	IPF11465	orf19.2369	unknown function	YNL261w
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA4020	1.2	1.0	0.9	1.0	1.6	1.1	IPF5324	orf19.3444	putative transporter (by homology)	YGR224w
CA0992	1.2	1.1	0.9	1.0	1.6	1.1	IPF11063	orf19.1394	unknown function	YCR090c
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology	YDR032c
CA1537	1.0	1.0	0.9	1.0	1.6	1.0	IPF17483	orf19.450	unknown function	no match
CA5593	0.9	1.1	1.1	1.1	1.6	1.2	IPF5615	orf19.7107	unknown function	YJL122w
CA1459	1.1	1.1	1.2	0.9	1.6	1.4	IPF6340	orf19.1107	unknown function	YDL173w
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function	YIR017c
CA3815	1.3	1.0	0.9	1.0	1.6	1.4	CYP7	orf19.2499	peptidyl-prolyl cis-trans isomerase cyp7 (ppiase)	YJR032w
CA1762	1.1	1.2	0.9	1.0	1.6	1.1	IPF20014	orf19.5194.1	oxidoreductase by homology	YIR035c
CA4277	1.1	1.4	1.1	1.1	1.6	1.2	BTS1	orf19.6674	Geranylgeranyl diphosphate synthase (by homology)	YPL069c
CA1357	0.7	0.9	0.6	0.8	1.5	1.0	ARH1	orf19.410	adrenodoxin reductase and ferredoxin-NADP+ reductase (by	YDR376w
CA6150	1.4	1.0	0.6	1.0	1.5	1.1	IPF1857	orf19.5892	similar to Saccharomyces cerevisiae Hul4p hect domain E3 u	YJR036c
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5297	0.9	0.9	1.3	1.2	1.5	1.2	YAR1	orf19.7160	Ankyrin repeat-containing protein (by homology)	YPL239w
CA4601	1.0	0.9	1.0	1.1	1.5	1.0	IPF2195	orf19.6920	unknown function	no match
CA3658	0.8	1.1	0.6	1.1	1.5	1.0	TGL1	orf19.2050	Triacylglycerol lipase (by homology)	YKL140w
CA1625	0.4	0.9	0.6	0.7	1.5	1.0	IPF6156	orf19.1034	similar to C.elegans LIM homeobox protein	YPL170w
CA3353	0.8	0.8	0.4	0.7	1.5	1.4	AUR1	orf19.1945	aureobasidin-resistance protein	YKL004w
CA1859	1.1	1.0	1.0	1.0	1.5	0.8	IPF19614.	orf19.1496	putative transcription factor similar to positive activator of the	YKL015w
CA5408	1.0	1.0	1.2	1.0	1.5	1.3	IPF1551	orf19.952	unknown function	no match
CA5538	1.6	1.1	1.2	1.1	1.5	1.4	IPF2830	orf19.7300	unknown function	no match
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA0122	1.1	1.5	0.9	1.1	1.5	1.2	SNF4.5f	orf19.5768	Nuclear regulatory protein, 5-prime end (by homology)	YGL115w
CA1643	1.0	1.1	0.6	0.8	1.5	0.9	IPF9347	orf19.1729	unknown function	no match
CA4618	1.7	1.1	0.9	1.0	1.5	1.1	IPF5757	orf19.3309	unknown function	no match
CA4405	1.1	1.0	1.1	1.0	1.5	1.0	IPF8773	orf19.3105	putative cytochrome P450 (by homology)	YDR402c
CA2276	1.0	1.1	0.8	1.0	1.5	1.1	HNM3	orf19.2587	Choline permease (by homology)	YGL077c
CA2094	1.3	1.1	0.7	0.8	1.5	1.4	IPF11493	orf19.2393	unknown function	YPR107c
CA3391	1.1	1.2	0.8	1.0	1.5	1.2	PNP1	orf19.317	Purine Nucleoside Phosphorylase (by homology)	YLR209c
CA4996	1.2	1.1	1.0	1.0	1.5	1.0	IPF2029	orf19.5251	unknown function	YBL005w
CA4282	1.1	1.3	0.9	1.1	1.5	1.0	IPF2319	orf19.6680	unknown function	YIL130w
CA2927	1.1	1.1	0.9	1.1	1.5	1.0	RAD52	orf19.4208	Nuclear ribonucleoprotein E	YML032c
CA2397	1.1	1.0	1.1	1.0	1.5	1.0	CFL12	orf19.3538	Strong similarity to ferric reductase Fre2p (by homology)	YOR381w
CA4416	1.2	1.1	1.3	1.0	1.5	1.3	IPF11888	orf19.5180	unknown function	YBL064c
CA0957	1.0	0.9	0.8	0.9	1.5	1.0	IPF14322	orf19.4731	unknown function	YNL051w
CA2837	1.2	1.1	1.0	1.0	1.5	0.9	IPF8340	orf19.4789	unknown function	no match
CA1827	1.1	1.0	1.1	1.1	1.5	1.2	IPF9520	orf19.4264	unknown function	no match
CA2756	1.5	0.9	0.7	1.0	1.5	1.0	IPF18418	orf19.5620	unknown function	YHR029c
CA4863	0.9	1.2	1.1	1.1	1.5	1.4	SAP10	orf19.3839	secretory aspartyl proteinase	YDR144c
CA4390	1.2	1.2	1.0	1.0	1.5	1.2	HOD1	orf19.3122.2	regulator of G2/M progression (by homology)	no match
CA3641	1.2	1.0	1.0	1.0	1.5	1.2	IPF4122	orf19.2032	unknown function	no match
CA1654	1.2	1.3	1.3	0.9	1.5	1.2	IPF19660	orf19.5559	unknown function	YDR202c
CA1302	0.5	0.9	0.9	1.1	1.5	1.5	FCA1	orf19.4195.1	cytosine deaminase	YPR062w
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function	no match
CA3079	1.3	1.1	0.9	1.0	1.5	1.2	RAM2	orf19.4817	geranylgeranyltransferase type I alpha subunit	YKL019w
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5078	0.6	1.1	0.8	0.8	1.5	1.3	IPF15297	orf19.3053	unknown function	no match
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA1498	1.1	1.0	1.0	1.0	1.5	1.0	IPF12371	orf19.3643	extracellular alpha-1,4-glucan glucosidase (by homology)	YHR006w
CA0075	1.0	1.1	0.7	1.0	1.5	1.0				
CA1870	1.0	1.1	0.9	0.8	1.5	1.0				
CA0076	0.9	1.2	1.2	1.1	1.5	1.1	IPF8866	orf19.4906	unknown function	no match
CA1548	0.6	1.1	0.5	0.9	1.5	1.0	IPF8746	orf19.4279	putative alpha-1,3-mannosyltransferase (by homology)	YER001w
CA5567	0.9	0.9	0.8	1.0	1.5	1.0	FCY24	orf19.7331	Putative purine-cytosine transport protein	YGL186c
CA3185	1.1	1.0	0.8	1.3	1.5	1.3	IPF13637	orf19.2137	unknown function	no match
CA4633	0.9	0.8	0.7	0.8	1.5	1.2	NDH1	orf19.339	Mitochondrial NADH dehydrogenase	YMR145c

CA5897	0.9	0.6	0.6	0.5	1.5	0.9	IPF2384	orf19.6809	unknown function	YKL128c
CA2477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)	YJR061w
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c

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[[Ca OS+ up 1.5 10FDR] and [Ca HS+ up 1.5 10FDR]] less [Ca XS+ up 1.5 10FDR]

HS+ OS+ XS+

Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function	YMR002w
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA2342	3.7	1.0	5.9	2.4	1.1	1.0	IPF13836	orf19.2344	probable heat shock protein (by homology)	no match
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA3211	3.1	1.1	2.2	1.2	0.7	1.0	IPF19977	orf19.6192	unknown function	YGR175c
CA2039	3.1	0.9	1.7	1.0	1.2	0.8	IPF12947	orf19.4357	unknown function	YMR115w
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function	YML041c
CA0929	2.6	1.4	3.8	1.1	1.0	1.1	GUT1	orf19.558	Glycerol kinase (by homology)	YHL032c
CA0457	2.5	1.2	2.2	1.8	1.2	0.8	IPF15604	orf19.2432	transcription factor (by homology)	YFL031w
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)	YPL088w
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)	YKL188c
CA2246	2.4	1.3	2.1	1.8	1.0	0.8	IPF7405	orf19.4666	unknown function	no match
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)	YJR107w
CA1891	1.9	1.2	1.5	1.2	0.8	0.9	IPF10196	orf19.2752	unknown function	YDR216w
CA5649	1.7	0.8	1.8	1.0	0.9	0.6	CHS4	orf19.7349	Chitin synthase regulatory factor	YBL061c
CA3750	1.7	1.2	1.9	1.4	0.8	0.9	IPF7377	orf19.3428	unknown function	YMR044w

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[Ca XS+ up 1.5 10FDR] and [Ca OS+ up 1.5 10FDR]] less [Ca HS+ up 1.5 10FDR]

HS+ OS+ XS+

Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA5535	1.1	1.1	20.4	1.4	6.5	1.0	IPF2839	orf19.7296	unknown function	no match
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA2581	1.4	1.2	3.6	2.8	19.0	11.8	IPF9450	orf19.4370	unknown function	no match
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in regu	YIL046w
CA0251	1.0	1.0	2.5	1.0	2.1	1.0	IPF9146	orf19.6244	unknown function	no match
CA5998	1.2	1.0	2.5	1.0	2.1	1.1	IPF670	orf19.7598	unknown function	YOR023c
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA1300	0.9	1.0	2.1	1.4	3.9	1.2	SLY41	orf19.4199	vesicular transport (by homology)	YOR307c
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA4768	0.8	1.0	1.9	0.9	1.7	0.8	IPF9385	orf19.4000	similar to Saccharomyces cerevisiae Pho2p homeobox-doma	YDL106c
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eo	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA3828	0.9	1.2	1.7	1.1	1.6	1.2	SNQ2	orf19.5759	multidrug resistance protein (by homology)	YDR011w
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA3268	1.2	1.0	1.6	1.6	2.2	1.1	RPS620b	orf19.6301	unknown function	no match
CA2369	1.5	1.4	1.6	1.4	1.6	1.1	TBP1	orf19.1837	TATA-binding protein (by homology)	YER148w
CA3010	1.1	0.7	1.6	1.0	1.6	1.0	IPF14568	orf19.6230	unknown function	YGL246c
CA3267	1.3	1.0	1.6	1.4	2.3	1.0	RPS620a	orf19.6300	unknown function	no match
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA1655	0.9	1.0	1.5	0.9	1.5	0.8	CCC2	orf19.4328	putative copper-transporting ATPase (by homology)	YDR270w
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA2434	2.4	2.5	1.5	1.1	1.7	1.4	IPF9484	orf19.3396	unknown function	YNL281w
CA4332	1.0	1.2	1.5	1.4	1.5	1.2	GLO2	orf19.4088	Glyoxalase II (hydroxyacylglutathione hydrolase) (by homolo	YDR272w

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[[Ca XS+ up 1.5 10FDR] and [Ca HS+ up 1.5 10FDR]] less [Ca OS+ up 1.5 10FDR]

HS+ OS+ XS+

Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**

Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA4683	10.3	6.7	1.1	1.1	2.3	1.5	HSP78.3f	orf19.884	heat shock protein of clpb family of ATP-dependent protease:	YDR258c
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function	no match
CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homolog	YPL171c
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA4676	3.6	1.1	0.7	0.9	4.8	1.1	HK1	orf19.896	Histidine kinase	YIL147c
CA2659	3.3	1.1	0.9	1.0	3.5	1.5	NDH2	orf19.5713	NADH dehydrogenase (by homology)	YMR145c
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)	YKR039w
CA0671	2.9	1.2	1.1	1.0	12.0	1.3	GRP4	orf19.3150	putative reductase (by homology)	YOL151w
CA4779	2.9	1.2	1.3	1.3	3.0	1.4	IPF3351	orf19.4012	unknown function	YHR071w
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)	YGR234w
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)	YCR098c
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function	YBR101c
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)	YGL009c
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homolo	YJL101c
CA0636	2.2	2.5	0.9	0.9	10.8	15.0				
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA0150	2.1	1.3	1.3	1.0	1.8	1.0	CDC123	orf19.2721	similar to Saccharomyces cerevisiae Cdc123p cell cycle regu	YLR215c
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)	YIR037w
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA4123	2.0	1.1	1.0	1.1	1.5	1.0	AMS1	orf19.2768	alpha-mannosidase (by homology)	YGL156w
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)	YJL001w
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)	YOR157c
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase	no match
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA5773	1.8	1.4	0.9	1.0	2.5	1.4	DOT5	orf19.5417	Derepression of telomeric silencing (by homology)	YIL010w
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match
CA4581	1.7	1.0	1.4	1.1	18.7	1.2	IPF2232	orf19.6899	unknown function	YMR315w
CA0639	1.6	1.8	1.0	1.0	9.0	10.5				
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c

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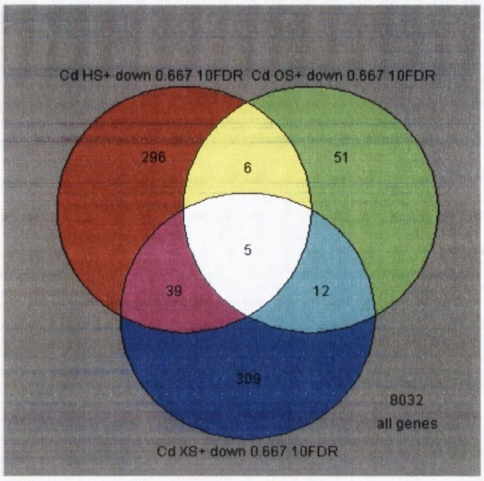
[[Ca OS+ up 1.5 10FDR] and [Ca XS+ up 1.5 10FDR]] and [Ca HS+ up 1.5 10FDR]

HS+ OS+ XS+										
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA4713	2.1	0.8	2.4	0.7	1.7	1.1	CCC1	orf19.6948	Transmembrane Ca2+ transporter (by homology)	YLR220w
CA1497	1.9	1.1	2.2	1.5	4.0	1.2	IPF9683	orf19.3644	unknown function	YHR006w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c



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[[Cd HS+ down 0.667 10FDR] less [Cd OS+ down 0.667 10FDR]] less [Cd XS+ d...

HS+ OS+

Species ():	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ():*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
CA5426	0.2	0.2	1.0	0.8	1.0	1.0	FAS1	orf19.979	Fatty-acyl-CoA synthase, beta chain.	YKL182w
CA3690	0.2	0.2	1.0	1.0	1.0	0.9	RPS14B	orf19.6265.1	ribosomal protein (by homology)	YJL191w
CA1062	0.3	0.2	0.6	0.4	1.0	1.2	IPF14165	orf19.4642	unknown function	no match
CA2920	0.1	0.2	1.0	1.1	0.9	0.7	FET5.5eo	orf19.4215	multicopy oxidase (by homology)	YFL041w
CA3921	0.3	0.2	1.0	1.1	1.0	1.0	OLE1	orf19.5117	Stearoyl-CoA desaturase (by homology)	YGL055w
CA4534	0.1	0.2	1.2	0.9	1.1	1.1	RPS26A	orf19.1470	ribosomal protein S26.e.A, cytosolic (by homology)	YGL189c
CA4269	0.2	0.2	0.9	1.1	0.9	1.0	RPS25B	orf19.6663	Cytosolic ribosomal protein (by homology)	YLR333c
CA2818	0.2	0.2	1.1	1.1	1.1	1.0	RPL13	orf19.2994	Ribosomal protein	YDL082w
CA6105	0.4	0.2	1.1	0.7	0.9	0.9	FAS2.5f	orf19.5951	fatty-acyl-CoA synthase, alpha chain, 5-prime end	YPL231w
CA3689	0.2	0.2	1.1	1.1	0.9	1.0	RPS22A	orf19.6265	ribosomal protein S15a.e.c10 (by homology)	YJL190c
CA6107	0.5	0.2	1.1	1.0	1.0	1.0	FAS2.3f	orf19.5949	fatty-acyl-CoA synthase, alpha chain, 3-prime end	YPL231w
CA1637	0.2	0.2	1.0	1.1	1.0	1.0	RPL43A	orf19.3942.1	ribosomal protein (by homology)	YPR043w
CA5343	0.3	0.2	1.0	1.0	1.0	1.0	RPL4B	orf19.7217	Ribosomal protein L4B (by homology)	YDR012w
CA6064	0.2	0.2	1.0	0.9	0.9	1.0	RPL81	orf19.6002	60S ribosomal protein L7a.e.B (by homology)	YLL045c
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA1662	0.3	0.2	0.9	1.0	1.0	1.0				
CA3305	0.1	0.2	1.2	1.0	1.1	0.9	RPL29	orf19.2310.1	ribosomal protein, cytosolic(by homology)	YFR032ca
CA3341	0.2	0.2	1.1	1.0	1.0	1.0	RPS17	orf19.2329.1	Ribosomal protein S17 (by homology)	YDR447c
CA2817	0.2	0.2	1.1	1.1	1.0	1.0	RPS16	orf19.2994.1	ribosomal protein	YMR143w
CA6068	0.2	0.2	1.2	1.2	1.0	1.0	RPS19A	orf19.5996.1	ribosomal protein S19.e (by homology)	YOL121c
CA3084	0.1	0.2	1.0	1.1	1.0	1.1	IPF11625	orf19.4149	unknown function	no match
CA1189	0.2	0.2	1.0	1.0	1.0	1.0	RPL24A	orf19.3789	ribosomal protein L24 (by homology)	YGL031c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA2023	0.2	0.2	1.1	1.1	1.0	1.0	RPL42	orf19.4909.1	ribosomal protein L36a, 3- prime end (by homology)	YHR141c
CA0632	0.2	0.2	1.3	1.1	1.0	1.0	RPS5	orf19.4336	ribosomal protein S5.e (by homology)	YJR123w
CA3304	0.2	0.2	1.0	0.9	0.9	1.0	RPL82	orf19.2311	60S ribosomal protein L7a.e.B (by homology)	YLL045c
CA5807	0.2	0.2	1.1	1.0	0.9	1.0	RPS24	orf19.5466	ribosomal protein S24.e	YIL069c
CA1188	0.2	0.2	1.2	1.0	1.0	1.0	RPL30.3f	orf19.3788.1	RNA binding (by homology)	YGL030w
CA2031	0.3	0.2	1.0	1.1	1.0	1.0	RPL10A	orf19.3465	L10A ribosomal protein	YPL220w
CA3739	0.4	0.2	0.9	0.9	0.9	0.9	RPS10	orf19.2179.2	ribosomal protein	YOR293w
CA5920	0.2	0.2	1.0	1.0	1.2	1.0	RPS12	orf19.6785	acidic ribosomal protein S12 (by homology)	YOR369c
CA3534	0.6	0.2	1.0	0.9	1.0	1.0	SSB1	orf19.6367	heat shock protein 70	YNL209w
CA5499	0.3	0.2	1.1	1.1	1.0	1.0	RPS4A	orf19.5341	ribosomal protein S4	YJR145c
CA3332	0.3	0.2	1.3	1.2	0.9	0.7	POL21.5f	orf19.2668	pol polyprotein, reverse transcripase, 5-prime end (by homolo	no match
CA4571	0.4	0.2	1.0	1.1	1.0	1.1	RPL33	orf19.6882.1	ribosomal protein L35a	YPL143w
CA2579	0.2	0.2	1.3	1.0	1.1	1.0				
CA0763	0.3	0.2	1.1	1.1	0.9	0.9	RPL11	orf19.2232	60S ribosomal protein (by homology)	YPR102c
CA2092	0.2	0.2	1.0	1.0	0.9	1.0	RPL21A	orf19.840	Ribosomal protein (by homology)	YBR191w
CA0736	0.4	0.2	1.0	1.1	1.0	1.0	RPL20B	orf19.4632	ribosomal protein (by homology)	YOR312c
CA6123	0.2	0.2	1.0	1.0	1.0	1.0	RPS15	orf19.5927	40S ribosomal protein S15, (by homology)	YOL040c
CA3330	0.4	0.2	1.7	1.2	0.8	0.9	POL21.3f	orf19.2669	pol polyprotein, reverse transcripase, 3-prime end (by homolo	YFL050c
CA5203	0.2	0.2	1.0	1.2	0.9	1.0	RPS18	orf19.7018	Ribosomal protein S18 (by homology)	YML026c
CA5125	0.2	0.2	1.0	1.2	1.0	1.0	RPP2	orf19.6403.1	acidic ribosomal protein by homology	YOL039w
CA2108	0.2	0.2	0.9	0.9	1.0	1.0	RPL26A.3	orf19.3690.2	ribosomal protein, 3-prime end (by homology)	YLR344w
CA5633	0.4	0.2	1.2	1.3	0.9	1.0	RPA135	orf19.7062	DNA-directed RNA polymerase I, 135 KD subunit (by homolo	YPR010c
CA2811	0.2	0.3	1.1	1.0	1.0	1.0	RPS3A	orf19.3002	Ribosomal protein 10	YML063w
CA5345	0.2	0.3	1.1	1.2	1.0	0.9	FTR1	orf19.7219	high affinity iron permease	YER145c
CA2923	0.4	0.3	1.0	1.4	1.0	0.8	FET32	orf19.4212	cell surface ferroxidase (by homology)	YMR058w
CA4562	0.2	0.3	0.9	1.1	1.0	1.0	RPS8A	orf19.6873	ribosomal protein (by homology)	YER102w
CA6092	0.2	0.3	1.2	0.9	1.1	1.0	RPL35	orf19.5964.2	Ribosomal protein L35A, (by homology)	YDL191w
CA5816	0.3	0.3	1.0	0.8	1.0	1.1	ACC1	orf19.7466	acetyl-coenzyme-A carboxylase (by homology)	YNR016c
CA1051	0.1	0.3	0.7	0.9	1.0	1.0	CHT2	orf19.3895	chitinase 2 precursor	YLR286c
CA6106	0.2	0.3	1.1	0.7	0.9	0.7	FAS2.53f	orf19.5948.1	fatty-acyl-CoA synthase, alpha chain, internal fragment	YPL231w
CA1304	0.3	0.3	1.1	1.0	1.0	1.0	RPS13.3	orf19.4193.1	ribosomal protein (by homology)	YDR064w
CA3239	0.3	0.3	1.1	1.3	0.9	1.0	IPF10558	orf19.4684.2	unknown function	YKR094c
CA4512	0.3	0.3	1.0	0.9	1.1	1.1				
CA1972	0.2	0.3	1.3	1.1	0.9	1.0	RPL27A	orf19.5225.2	ribosomal protein L27	YHR010w
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA2937	0.3	0.3	1.2	1.1	1.1	1.0	RPS21B.3	orf19.3325.3	ribosomal protein S21, 3- prime end	YJL136c
CA3226	0.3	0.3	1.2	1.1	1.0	1.0	RPS27	orf19.6286.2	ribosomal protein S27 (by homology)	YKL156w
CA1977	0.3	0.3	0.9	1.0	0.9	1.0	RPL25	orf19.687.1	ribosomal protein L23a (by homology)	YOL127w
CA0665	0.4	0.3	0.6	0.7	0.6	0.8	INT1	orf19.4257	integrin-like protein alpha chain	YJR092w
CA5200	0.3	0.3	1.1	1.1	1.0	1.0	RPL10E	orf19.7015	Ribosomal protein L10, cytosolic (by homology)	YLR340w

CA3075	0.4	0.3	1.0	1.3	1.0	1.0	IPF6105	orf19.4813	similar to Saccharomyces cerevisiae Gua1p GMP synthase ((	YMR217w
CA3800	0.4	0.3	1.1	0.9	1.0	1.0	RPL7A.3f	orf19.2478.1	60S Ribosomal Protein L7-A, 3-prime end	YPL198w
CA0322	0.4	0.3	1.0	1.0	1.0	1.0	RPS9B	orf19.838.1	Ribosomal protein	YBR189w
CA1298	0.4	0.3	1.0	1.1	0.9	1.0	RPL32	orf19.3415.1	ribosomal protein L32	YBL092w
CA4882	0.3	0.3	0.7	0.9	0.5	0.8	IPF1651	orf19.6570	purine nucleoside permease (by homology)	no match
CA3864	0.4	0.3	1.0	1.0	1.0	1.0	RPL16A	orf19.6085	ribosomal protein (by homology)	YNL069c
CA5646	0.2	0.3	1.1	1.2	1.2	1.0	RPS28B.3	orf19.7048.1	Ribosomal protein S28B (S33B) (YS27), 3-prime end (by hon	YLR264w
CA6163	0.3	0.3	1.0	0.8	0.4	0.8	POL1	orf19.5873	DNA-directed DNA polymerase alpha (by homology)	YNL102w
CA4270	0.5	0.3	1.0	0.9	0.6	0.7	NUP2	orf19.6665	Nuclear pore protein (by homology)	YLR335w
CA2947	0.2	0.3	0.7	0.5	0.5	0.7	IPF6298	orf19.1964	unknown function	no match
CA2708	0.5	0.3	1.2	1.0	1.1	1.0	RPS6A	orf19.4660	ribosomal protein S6 (by homology)	YPL090c
CA1315	0.3	0.3	0.8	0.9	1.0	0.9	URA2	orf19.2360	multifunctional pyrimidine biosynthesis protein, (by homolog	YJL130c
CA3993	0.7	0.3	2.4	1.0	0.7	0.7	IPF8275	orf19.1569	unknown function	YGR090w
CA3111	0.5	0.3	1.1	1.1	1.1	1.1	RPL5	orf19.6541	ribosomal protein (by homology)	YPL131w
CA4862	0.4	0.3	1.0	1.0	1.0	1.0	EFB1	orf19.3838	translation elongation factor eEF1beta	YAL003w
CA6154	0.5	0.3	1.6	1.4	1.0	1.0	IPF1848	orf19.5885	similar to Saccharomyces cerevisiae Snu13p U4/U6.U5 snRN	YEL026w
CA5051	0.5	0.3	2.5	1.4	1.2	1.2	IPF3709	orf19.3015	unknown function	YDR101c
CA1635	0.4	0.3	0.8	1.3	0.9	1.1	URA7	orf19.3941	CTP synthase 1 (by homology)	YBL039c
CA5076	0.4	0.3	0.9	0.6	0.4	0.8	IPF15301	orf19.3051	unknown function	YJR116w
CA5317	0.4	0.3	1.0	1.1	1.0	1.0	RPP1B	orf19.7188	Acidic ribosomal protein L44 (by homology)	YDL081c
CA5065	0.4	0.3	1.0	1.0	0.8	1.0	IPF3584	orf19.3037	similar to Saccharomyces cerevisiae Pab1p mRNA polyaden	YER165w
CA2454	0.3	0.3	1.1	1.0	1.1	1.0	RPL23B	orf19.3504	ribosomal protein L23.e (by homology)	YER117w
CA4513	0.4	0.3	1.0	1.1	1.0	1.0	ADE17	orf19.492	5-aminoimidazole-4-carboxamide ribotide transformylase (by	YMR120c
CA1502	0.4	0.4	1.1	1.1	1.0	1.0	RPS7A	orf19.1700	ribosomal protein (by homology)	YOR096w
CA5354	0.3	0.4	1.0	1.2	0.6	0.7	FTR2	orf19.7231	high affinity iron permease	YER145c
CA4103	0.2	0.4	1.0	1.0	1.1	1.0	IPF3980	orf19.668	unknown function	YLR183c
CA1431	0.3	0.4	1.0	1.5	1.1	0.8	FET34.3e	orf19.1206	iron transport multicopper oxidase, 3-prime end (by homolog	YMR058w
CA2011	0.2	0.4	1.3	1.4	1.1	1.1	RPS31	orf19.3087	Ubiquitin fusion protein	YLR167w
CA5021	0.6	0.4	1.1	1.0	1.0	1.0				
CA2667	0.7	0.4	2.0	1.3	1.1	1.1	IPF16996	orf19.3547	unknown function	YDR496c
CA2819	0.3	0.4	1.1	1.1	1.0	1.0	RPA1	orf19.2992	60S ribosomal protein	YDL081c
CA4498	0.6	0.4	1.4	1.4	0.9	1.0	IPF11315	orf19.512	unknown function	YNL132w
CA4008	0.4	0.4	0.9	1.0	1.0	1.0	DYS1	orf19.1626	deoxyhypusine synthase	YHR068w
CA3284	0.4	0.4	0.9	0.9	1.0	1.0	ADE6	orf19.6317	5 -phosphoribosylformyl glycinamidine synthetase (by homol	YGR061c
CA0189	0.7	0.4	0.5	0.6	1.2	0.9	IPF12201	orf19.4118	Na+-nucleoside cotransporter (by homology)	no match
CA5990	0.9	0.4	1.5	0.8	0.8	0.8	IPF690.5f	orf19.7590	NADH dehydrogenase (ubiquinone) 78K chain precursor, 5-p	no match
CA3547	0.3	0.4	0.8	1.0	0.8	1.0	ADE13	orf19.3870	adenylosuccinate lyase (by homology)	YLR359w
CA4326	0.5	0.4	1.5	1.3	1.2	1.3	IPF2093	orf19.4093	nuclear protein of unknown function (by homology)	YGR103w
CA1503	0.5	0.4	2.0	1.6	1.0	1.1	RKI1	orf19.1701	D-ribose-5-phosphate ketol-isomerase (by homology)	YOR095c
CA2250	0.6	0.4	0.8	0.7	1.0	0.9	MIS11	orf19.2364	mitochondrial C1-tetrahydrofolate synthase precursor (by hor	YBR084w
CA4235	0.6	0.4	1.1	1.0	1.0	1.1	NCL1	orf19.518	Probable proliferating-cell nucleolar antigen (by homology)	YBL024w
CA3602	0.3	0.4	1.0	1.0	1.0	0.9	RPL14B	orf19.4931.1	ribosomal protein L14B (by homology)	YKL006w
CA5340	0.7	0.4	1.2	1.5	0.8	0.9	IPF883	orf19.7215	unknown function	YJL109c
CA4099	0.8	0.4	2.1	1.2	0.7	1.0	IPF3986	orf19.665	unknown function	YLR186w
CA5680	0.5	0.4	1.0	0.9	1.0	1.0				
CA4696	0.5	0.4	0.9	0.7	0.6	0.8	HTA1	orf19.6924	Histone H2A (by homology)	YDR225w
CA2939	0.5	0.4	1.0	1.0	1.0	1.0	TIF1	orf19.3324	translation initiation factor	YKR059w
CA5638	0.6	0.4	0.9	1.1	0.9	1.0	IPF470	orf19.7057	putative glutamine-tRNA ligase (by homology)	YGL245w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA5197	0.5	0.4	1.3	1.2	1.0	0.8	IPF2342	orf19.7011	unknown function	YPL012w
CA5975	0.7	0.4	1.1	1.1	1.2	1.2	SIK1	orf19.7569	nucleolar protein involved in pre-rRNA processing (by homol	YLR197w
CA3607	1.2	0.4	4.1	1.8	1.4	1.2	RTA2	orf19.24	Unknown function	YOR049c
CA4697	0.3	0.4	0.8	0.8	0.6	0.8	HTB1	orf19.6925	Histone H2B (by homology)	YDR224c
CA1441	0.4	0.4	1.2	1.2	1.4	1.1	QCR8	orf19.4490.2	ubiquinol-cytochrome-c reductase chain VIII (by homology)	YJL166w
CA2493	0.5	0.4	0.9	0.8	0.9	0.8	IPF7227	orf19.4048	putative fatty acid desaturase (by homology)	YDR011w
CA2858	0.6	0.4	1.0	0.8	1.0	1.0	ACS2	orf19.1064	acetyl-coenzyme-A synthetase (by homology)	YLR153c
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)	YOR356w
CA1438	0.6	0.4	1.4	1.2	1.2	1.1	NOP58	orf19.1199	nucleolar protein required for pre-18S rRNA processing	YOR310c
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)	YLR409c
CA0874	1.3	0.4	1.5	1.3	0.8	0.8	CPA1	orf19.4630	Arginine-specific carbamoylphosphate synthase, small chain	YOR303w
CA2805	0.3	0.4	0.7	0.8	0.7	0.8	RNR1	orf19.5779	ribonucleoside-diphosphate reductase (by homology)	YER070w
CA3862	0.3	0.4	1.3	1.6	1.4	1.0	NSR1	orf19.6090	nuclear localization sequence binding protein (by homology)	YGR159c
CA4505	0.7	0.4	1.1	1.2	1.1	1.0	NOP2	orf19.501	nucleolar protein (by homology)	YNL061w
CA0207	0.4	0.4	1.9	1.0	1.0	0.7	IPF18002	orf19.1226	Unknown function	YKL014c
CA5568	0.8	0.4	2.0	1.0	1.2	1.0	ELF1	orf19.7332	Elongation-like factor	YPL226w
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA5497	0.5	0.4	1.2	0.7	1.9	1.0	IPF776	orf19.5338	transcriptional activator (by homology)	YPL248c
CA4471	1.0	0.4	1.3	1.1	0.5	0.8	MCM3	orf19.1901	replication initiation protein (by homology)	YEL032w
CA0254	0.4	0.4	0.9	1.1	2.3	0.9	IPF14968	orf19.3461	unknown function	no match
CA6155	1.2	0.4	1.4	1.6	0.8	0.8	IPF1846	orf19.5884	unknown function	YJR041c
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)	YFL036w
CA4302	0.9	0.4	0.9	0.9	0.9	1.1	DED81	orf19.6702	Asparaginyl-tRNA synthetase (by homology)	YHR019c
CA1387	0.3	0.4	0.7	0.7	0.8	0.9	ERG11	orf19.922	cytochrome P450 lanosterol 14a-demethylase	YHR007c
CA2303	0.6	0.5	0.9	1.2	0.8	0.7	TOS1	orf19.1690	putative Anchor subunit of a-agglutinin (by homology)	YBR162c
CA4551	0.5	0.5	1.1	1.1	1.2	1.2	APT1	orf19.1448	adenine phosphoribosyltransferase	YML022w
CA5991	0.7	0.5	1.4	1.1	1.0	1.0	IPF690.3f	orf19.7591	NADH dehydrogenase (ubiquinone) 78K chain precursor, 3-p	no match
CA2924	0.4	0.5	1.0	1.3	1.2	0.8	FET33	orf19.4211	cell surface ferroxidase (by homology)	YMR058w
CA0554	1.0	0.5	1.3	1.1	1.3	1.2	HAS1	orf19.3962	ATP-DEPENDENT RNA HELICASE (by homology)	YMR290c
CA2558	0.5	0.5	0.6	0.8	0.8	0.7	RBT5	orf19.5636	repressed by TUP1 protein 5	no match
CA4533	0.4	0.5	0.9	1.3	0.9	1.0	COX4	orf19.1471	cytochrome-c oxidase (by homology)	YGL187c
CA4590	0.5	0.5	1.1	1.0	0.9	0.9	IPF2218	orf19.6907	unknown function	YDL156w
CA2734	0.3	0.5	1.2	1.1	1.0	0.9	RPL38	orf19.2111.2	ribosomal protein L38 (by homology)	YLR325c
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA0184	0.8	0.5	1.0	0.7	1.0	0.8	IPF19142	orf19.3984	unknown function	YGR237c
CA6029	0.6	0.5	1.7	1.3	1.1	1.5	DRS1	orf19.7635	ATP dependent RNA helicase (by homology)	YLL008w
CA5204	0.6	0.5	1.1	0.7	0.7	0.9	YML6	orf19.7019	Ribosomal protein, mitochondrial (by homology)	YML025c
CA3918	0.5	0.5	0.6	1.1	0.5	0.7	VTC2	orf19.4381	putative polyphosphate synthetase (by homology)	YFL004w
CA4589	0.4	0.5	1.1	1.0	1.0	1.0				
CA3081	0.5	0.5	1.1	1.1	1.1	1.0	EFT3	orf19.4152	translation elongation factor 3	YNL014w
CA6122	0.4	0.5	1.2	1.1	1.1	1.0	RPP2B	orf19.5928	acidic ribosomal protein (by homology)	YDR382w
CA3066	0.8	0.5	1.1	1.0	0.6	0.8	IPF15813	orf19.4281	unknown function	YLR223c
CA0687	1.0	0.5	1.0	1.1	0.8	1.0	CPA2	orf19.3221	arginine-specific carbamoylphosphate (by homology)	YJR109c
CA1513	0.8	0.5	1.0	1.1	1.0	1.0	MIR1	orf19.4885	phosphate transport protein, mitochondrial (MCF) (by homolo	YJR077c

CA4852	0.4	0.5	0.6	0.7	0.9	0.8	SCS7	orf19.3822	Required for hydroxylation of ceramide (by homology)	YMR272c
CA1289	0.6	0.5	1.1	1.0	1.2	1.1	ZUO1	orf19.2709	Zuotin, a putative Z-DNA binding (by homology)	YGR285c
CA2848	1.0	0.5	2.5	1.4	1.2	1.1				
CA2903	1.0	0.5	0.9	0.8	0.8	0.9	IPF11725	orf19.3475	unknown function	no match
CA0615	0.8	0.5	1.0	1.1	1.0	1.0	RPL3	orf19.1601	60S large subunit ribosomal protein L3.e (by homology)	YOR063w
CA3574	0.5	0.5	1.1	1.0	0.9	1.2	IPF19584	orf19.2266	unknown function	YFR013w
CA6079	0.5	0.5	1.1	1.0	1.0	1.0	RPL18	orf19.5981.1	Ribosomal protein L18B (large subunit), (by homology)	YOL120c
CA3168	0.5	0.5	1.3	1.4	1.3	1.3	PRS3	orf19.1575	ribose-phosphate pyrophosphokinase	YHL011c
CA4783	0.5	0.5	1.0	1.0	1.0	1.0	IPF3358	orf19.4016	ubiquinol-cytochrome-c reductase (by homology)	YBL045c
CA3461	0.9	0.5	1.2	1.1	1.4	0.9	CFL2	orf19.1264	ferric reductase (by homology)	YNR060w
CA1095	0.8	0.5	1.3	0.9	0.4	0.7	SMC1	orf19.4367	Chromosomal ATPase family member (by homology)	YFL008w
CA0829	0.7	0.5	0.8	0.6	0.7	0.7	SLC1	orf19.250	fatty acyltransferase (by homology)	YDL052c
CA0733	0.9	0.5	1.3	0.8	0.7	0.8	NIP1	orf19.4635	translation initiation factor subunit	YMR309c
CA3588	0.7	0.5	1.2	1.1	1.3	1.1	SPE3	orf19.2250	putrescine aminopropyltransferase by homology	YPR069c
CA1227	1.1	0.5	1.3	0.9	0.6	0.8	IPF16082	orf19.4160	unknown function	YDL104c
CA1976	0.6	0.5	1.0	0.9	0.8	0.8	IPF9582	orf19.688	similar to Saccharomyces cerevisiae Mrps18p ribosomal prot	YNL306w
CA1758	0.8	0.5	2.0	0.7	0.9	0.8	IPF14559.	orf19.5126	unknown function, 3-prime end	YCL037c
CA1678	0.8	0.5	1.0	1.0	0.9	0.8	PGA24	orf19.3618	putative cell wall protein (by homology)	YAR050w
CA0216	0.9	0.5	1.1	1.1	1.0	1.0	IPF11681	orf19.1682	unknown function	no match
CA3766	0.9	0.5	0.7	0.9	0.7	0.8	IPF18298.	orf19.2903	unknown function, 3-prime end	no match
CA2008	1.1	0.5	1.1	1.2	0.6	0.9				
CA5359	0.7	0.5	1.2	1.1	1.1	1.0	TIF35	orf19.7236	translation initiation factor eIF3, p33 subunit (by homology)	YDR429c
CA5101	0.7	0.5	0.9	1.0	0.7	0.7	LCB1	orf19.6438	Serine C-palmitoyltransferase subunit (by homology)	YMR296c
CA2772	1.0	0.5	3.3	1.3	0.9	1.1	IPF20112	orf19.2688	unknown function	YPL126w
CA0432	0.7	0.5	1.0	1.1	0.9	0.9	IPF7926	orf19.1341	putative protein kinase (by homology)	YDL214c
CA2162	0.9	0.5	1.1	1.0	1.0	0.9	PDB1	orf19.5294	pyruvate dehydrogenase (by homology)	YBR221c
CA3376	0.5	0.5	1.0	1.3	1.0	0.9	LSC2.5eo	orf19.1857.1	succinate-CoA ligase beta subunit, 5-prime end (by homolog	YGR244c
CA5507	0.5	0.5	1.1	1.0	1.0	0.9	TIF11	orf19.5351	translation initiation factor eIF1a (by homology)	YMR260c
CA4842	0.2	0.5	0.7	1.2	0.9	0.8	MTD1	orf19.3810	methylenetetrahydrofolate dehydrogenase	YKR080w
CA0276	0.6	0.5	0.9	0.7	0.5	0.9	IPF15015	orf19.5612	unknown function	YIL091c
CA0443	0.9	0.5	2.5	1.1	1.0	1.1	SPB1	orf19.76	Putative methyltransferase by homology	YCL054w
CA5292	0.9	0.5	2.7	1.4	0.9	1.1	IPF1948	orf19.7154	unknown function	YJL069c
CA3631	0.9	0.5	0.9	1.1	0.8	1.0	TIM54	orf19.5143	Translocase for the insertion of proteins into the mitochondria	YJL054w
CA6141	0.8	0.5	1.1	1.1	1.1	1.0	RPL19A	orf19.5904	Ribosomal protein L19.e (by homology)	YBR084ca
CA2578	0.4	0.5	1.1	0.9	0.6	0.9	MMD1	orf19.6220.3	Maintenance of mitochondrial DNA (by homology)	YIL051c
CA2571	0.8	0.5	1.6	1.2	1.1	0.7	IPF13769	orf19.6209	unknown function	YKL221w
CA4147	0.7	0.5	1.0	1.0	1.0	1.2	ADE8	orf19.5789	Phosphoribosylglycinamide formyltransferase (GART)	YDR408c
CA5063	0.9	0.5	2.2	1.1	0.7	0.8	IPF8493	orf19.3034	putative member of nontransporter group of ATP-binding cas	YDR091c
CA5685	0.9	0.5	1.8	1.0	0.9	0.9	HPA1	orf19.7387	RNA polymerase II-associated Histone acetyltransferase (by	YPL086c
CA2847	0.9	0.6	4.0	1.3	1.1	1.2	NOG2	orf19.5733	unknown function Nuclear/Nucleolar GTP-binding protein, by	YNR053c
CA4089	0.8	0.6	1.5	1.2	0.9	0.8	IPF5009	orf19.6648	unknown function	YGR245c
CA4749	0.6	0.6	1.0	0.8	0.4	0.8	IPF4481	orf19.4831	unknown function	no match
CA3813	0.4	0.6	2.1	1.0	1.8	0.9	FRP1	orf19.2496	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA2272	0.6	0.6	1.5	1.4	1.2	1.1	RPA43	orf19.2594	DNA-directed RNA polymerase I, 36 KD subunit(by homology	YOR340c
CA4506	0.8	0.6	1.4	1.4	1.2	1.0	GCD10	orf19.500	translation initiation factor eIF3 RNA-binding subunit (by hom	YNL062c
CA1723	0.5	0.6	1.0	1.0	1.1	1.1	TEF4	orf19.2651	translation elongation factor eEF1 (by homology)	YPL048w
CA2764	0.7	0.6	1.1	0.8	1.0	1.0	QCR7	orf19.5629	ubiquinol--cytochrome-c reductase subunit 7 (by homology)	YDR529c
CA3514	0.9	0.6	1.1	0.8	0.7	0.8	IPF11245	orf19.6362	similar to Saccharomyces cerevisiae Spa2p involved in cell p	YLL021w
CA2119	1.3	0.6	2.0	0.9	0.7	0.9	MTR4	orf19.1335	RNA Helicase (by homology)	YJL050w
CA0664	0.9	0.6	1.1	1.2	1.0	1.0	LSC2.3eo	orf19.710	succinate-CoA ligase beta subunit, 3-prime end (by homolog	YGR244c
CA2249	0.5	0.6	0.9	0.7	0.5	0.7	POL2	orf19.2365	DNA-directed DNA polymerase epsilon, catalytic subunit A (b	YNL262w
CA2326	0.6	0.6	1.1	0.9	0.8	0.8	NUBM	orf19.4495	nucleotide-binding respiratory complex I subunit (by homolog	no match
CA3240	0.7	0.6	1.4	1.1	0.6	0.8	IPF10559	orf19.4683	myosin-like protein (by homology)	YKR095w
CA5425	1.4	0.6	0.8	0.7	0.9	1.0	BDF1	orf19.978	sporulation protein (by homology)	YLR399c
CA5185	0.7	0.6	1.1	1.0	1.0	1.0	NHP6A	orf19.4623.3	nonhistone chromosomal protein related to HMG1 Cell growth	YBR089ca
CA2494	0.4	0.6	0.8	1.1	0.9	1.1	HTS1	orf19.4051	histidine tRNA synthetase (by homology)	YPR033c
CA2304	0.8	0.6	2.1	1.3	0.8	1.4	PRP43	orf19.1687	RNA-dependent ATPase (by homology)	YGL120c
CA2956	0.5	0.6	0.9	1.2	1.3	1.1	EGD2	orf19.5858	Nascent polypeptide associated complex protein alpha subur	YHR193c
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA2368	0.6	0.6	1.2	1.2	0.9	1.0	RPA190	orf19.1839	DNA-directed RNA polymerase I (by homology)	YOR341w
CA5521	0.7	0.6	0.9	0.8	0.8	1.0	HEM12	orf19.5369	uroporphyrinogen decarboxylase (by homology)	YDR047w
CA2682	0.6	0.6	0.9	0.9	0.9	1.1	FRS1	orf19.2573	Phenylalanyl-tRNA synthetase	YLR060w
CA4811	0.9	0.6	2.0	1.2	1.0	1.0	ECM16	orf19.2090	RNA helicase (by homology)	YMR128w
CA3491	0.9	0.6	1.5	1.1	1.3	1.4	RPC40	orf19.3564	RNA polymerase (by homology)	YPR110c
CA2587	0.4	0.6	1.1	1.1	1.0	1.0	RPS30	orf19.4375.1	40S ribosomal protein S30(by homology)	YOR182c
CA1822	1.2	0.6	2.2	1.3	0.8	0.9	IPF9525	orf19.4268	unknown function	YLR222c
CA5950	0.4	0.6	0.8	0.7	1.0	1.0	TPI1	orf19.6745	Triose phosphate isomerase	YDR050c
CA5259	1.2	0.6	0.8	0.9	0.7	1.0	OSM2	orf19.5005	Osmotic growth protein (by homology)	YJR051w
CA4536	0.6	0.6	1.1	1.1	1.0	1.0	COX13	orf19.1467	cytochrome-c oxidase chain VIa (by homology)	YGL191w
CA5829	0.7	0.6	0.9	1.1	1.0	1.0	ADE1	orf19.7484	phosphoribosyl-amidoimidazole-succinocarboxamidesynthet	YAR015w
CA5190	0.8	0.6	1.0	0.9	1.2	1.1	IPF10155	orf19.4628	unknown function	YKL059c
CA0696	0.7	0.6	1.1	1.4	1.2	1.1	HMT1	orf19.3291	hnRNP methyltransferase (by homology)	YBR034c
CA3165	0.8	0.6	1.3	1.1	0.9	1.0	FMI1	orf19.1578	processing of pre-ribosomal RNA	YMR229c
CA1927	0.6	0.6	1.0	1.1	1.0	1.0	YBN5	orf19.754	Putative purine nucleotide-binding protein (by homology)	YBR025c
CA5788	0.1	0.6	1.1	1.8	1.7	1.0	RHR2	orf19.5437	DL-glycerol phosphatase	YIL053w
CA4418	0.5	0.6	0.8	1.0	0.7	0.8	ERG5	orf19.5178	C-22 sterol desaturase by homology	YMR015c
CA2796	0.8	0.6	1.8	1.3	1.3	1.1	IPF8405	orf19.1721	similar to Saccharomyces cerevisiae Nce103p involved in no	YNL036w
CA4435	1.1	0.6	1.3	0.9	0.7	0.7	IPF5567	orf19.5160	phosphatase associated protein by homology	YKR028w
CA2377	0.8	0.6	1.1	0.7	0.8	0.8	MRPL7	orf19.2214	Ribosomal protein of the large subunit, mitochondrial (by hom	YDR237w
CA1417	0.9	0.6	1.9	1.2	1.2	1.4	IPF16126	orf19.172	similar to Saccharomyces cerevisiae Rpc19p DNA-directed R	YNL113w
CA3526	0.8	0.6	0.9	0.8	0.8	0.8	MRPS5.5f	orf19.989	Probable ribosomal protein S5, mitochondrial (by homology)	YBR251w
CA2861	0.4	0.6	0.8	0.9	0.7	1.0	HHT21	orf19.1061	Histone H3	YNL031c
CA0027	0.8	0.6	2.3	1.5	1.1	1.2	RCL1	orf19.1886	RNA 3 -terminal phosphate cyclase (by homology)	YOL010w
CA4077	0.8	0.6	0.9	1.0	1.0	1.0	ACO2	orf19.6632	aconitate hydratase (by homology)	YJL200c
CA5611	0.9	0.6	1.4	1.1	0.9	1.3	SUA5	orf19.7088	translation initiation protein (by homology)	YGL169w
CA4169	1.2	0.6	1.0	0.9	0.8	0.9	RSC2	orf19.2964	Member of RSC complex, which remodels the structure of chr	YGR056w
CA3158	0.6	0.6	0.8	1.4	1.1	1.0	IPF13131.	orf19.1587	unknown function, 3-prime end	YBR241c
CA4430	1.3	0.6	1.0	1.2	0.9	0.9	IPF5577	orf19.5165	unknown function	YNR029c
CA1560	1.0	0.6	1.0	1.0	1.1	0.9	MET18	orf19.1706	Involved in NER repair and RNA polymerase II transcription (	YIL128w
CA4116	1.1	0.6	1.3	1.0	0.6	0.9	IDI1	orf19.2775	isopentenyl-diphosphate delta-isomerase (by homology) Lipic	YPL117c
CA4821	0.9	0.6	0.7	1.1	0.8	0.8	IPF1197	orf19.2076	unknown function	YMR130w
CA0328	0.7	0.6	1.7	1.5	1.2	1.2	IPF15217.	orf19.3778	WD-repeat protein, 3-prime end (by homology)	YCR072c
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match

CA4517	0.9	0.6	1.2	1.1	0.7	0.9	MEX67	orf19.488	poly(A)+RNA binding protein involved in nuclear mRNA expo	YPL169c
CA3896	0.7	0.6	1.2	1.0	0.9	1.3	IPF10339	orf19.5077	unknown function	no match
CA6139	0.7	0.6	1.3	1.3	1.0	1.1	ADE2	orf19.5906	phosphoribosylaminoimidazole carboxylase	YOR128c
CA1709	1.3	0.6	1.1	0.9	0.5	0.6	HOL2	orf19.4889	Multidrug-resistance protein subfamily 1 (by homology)	YNR055c
CA5348	0.7	0.6	1.3	1.1	0.8	1.2	IPF863	orf19.7223	involved in inositol biosynthesis (by homology)	YBR030w
CA1712	1.1	0.6	1.0	1.2	0.9	1.0	ABC1	orf19.3331	ubiquinol--cytochrome-c reductase(by homology)	YGL119w
CA3459	1.0	0.6	1.0	1.0	0.8	0.9	CGT1.3f	orf19.1261	mRNA capping enzyme alpha subunit, 3-prime end	YGL130w
CA4920	0.8	0.6	1.0	1.0	0.9	0.9	GCN20	orf19.6060	Positive effector of Gcn2p (by homology)	YFR009w
CA2810	0.7	0.6	1.1	1.1	1.0	1.0				
CA3977	0.7	0.6	1.2	1.0	1.2	1.2	IPF20153	orf19.1549	unknown function	no match
CA2181	0.5	0.6	0.6	0.9	0.5	0.9	ECM331	orf19.4255	Involved in cell wall biogenesis and architecture (by homolog	YDR055w
CA1250	1.1	0.6	0.8	1.1	0.7	0.9	IPF9626	orf19.4959	unknown function	no match
CA4041	1.6	0.6	1.9	1.7	1.1	0.7	GAL10	orf19.3672	UDP-glucose 4-epimerase by homology	YBR019c
CA1757	1.0	0.6	1.7	0.8	0.8	0.7	IPF14559.	orf19.5128	unknown function, 5-prime end	no match
CA2984	0.8	0.6	2.1	1.2	0.8	0.9	IPF12606.	orf19.6008.1		YNL123w
CA4225	0.6	0.6	1.1	0.9	1.0	1.0	RPL39	orf19.827.1	ribosomal protein L39	YMR194w
CA5907	0.8	0.6	1.1	1.2	0.8	0.9	SSN6	orf19.6798	transcriptional repressor (by homology)	YBR112c
CA1770	0.7	0.6	1.8	1.3	1.3	1.4	IPF12457	orf19.2185	unknown function	YGL111w
CA5616	1.5	0.6	0.8	1.2	1.2	1.0	PET8	orf19.7082	mitochondrial carrier protein (by homology)	YNL003c
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)	YHL003c
CA2091	0.5	0.6	1.0	1.0	0.8	0.9	IPF3401	orf19.839	unknown function	YLR143w
CA3892	1.0	0.6	1.0	1.0	0.9	0.9	PSE1	orf19.5085	karyopherin-beta protein (by homology)	YMR308c
CA3030	0.2	0.6	1.2	0.9	0.9	1.3	IPF19968	orf19.220	putative cell wall protein of the PIR family	YKL164c
CA5702	0.7	0.6	0.9	0.8	0.5	0.7	PCH1	orf19.7402	Putative ATPase (by homology)	YDR440w
CA1114	0.6	0.6	0.9	1.2	1.1	1.2	IPF9995	orf19.2286	unknown function	YJR070c
CA2801	0.9	0.6	1.0	0.9	0.9	0.9	URA3	orf19.1716	orotidine-5 -monophosphate decarboxylase [Candida albican	YEL021w
CA5396	1.0	0.6	1.1	0.8	0.7	0.8	NAM7	orf19.939	nonsense-mediated mRNA decay protein (by homology)	YMR080c
CA5149	0.7	0.6	1.1	1.1	1.3	1.1	HGH1	orf19.4587	Similar to human HMG1 and HMG2 proteins (by homology)	YGR187c
CA5401	0.9	0.6	1.0	1.1	0.5	0.7	FET35.3	orf19.943	Cell surface ferroxidase, high affinity, 3-prime end (by homol	YMR058w
CA1525	1.1	0.6	0.9	1.0	1.4	0.8	AGP3	orf19.3795	amino acid-permease (by homology)	YFL055w
CA3854	0.5	0.6	0.8	1.0	0.9	1.2	IPF4649	orf19.6102	unknown Function	YIL036w
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA6134	0.6	0.6	1.3	1.1	0.8	0.8	MAK21	orf19.5912	Ribosome biogenesis protein (by homology)	YDR060w
CA4102	0.5	0.6	1.1	1.1	1.1	1.0	RPL37B	orf19.667.1	Ribosomal protein	YDR500c
CA4255	0.6	0.6	1.0	1.0	1.0	0.9	FUM11	orf19.543	fumarate hydratase	YPL262w
CA2090	0.6	0.7	1.0	1.1	1.0	1.0	IPF3398.3	orf19.837.2	unknown function, 3-prime end	no match
CA1262	1.0	0.7	0.8	0.7	0.5	0.7	MDR1	orf19.1244	Mac1p interacting protein (by homology)	YGR100w
CA1484	0.9	0.7	1.1	1.0	1.0	1.0	ARO4	orf19.4060	3-dehydro-deoxyphosphoheptonate aldolase, tyrosine-inhibit	YBR249c
CA3799	0.9	0.7	1.1	0.9	0.7	0.9	IPF7198	orf19.2478	unknown function	YKR095w
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
CA4289	1.3	0.7	2.5	1.3	0.8	1.0	IPF6665	orf19.6686	unknown function	YGR145w
CA2004	0.6	0.7	1.0	0.7	0.6	0.8	POL12	orf19.2796	DNA-directed DNA polymerase alpha (by homology)	YBL035c
CA3994	0.9	0.7	1.1	1.4	0.7	0.9	ERG7	orf19.1570	lanosterol synthase	YHR072w
CA5428	1.1	0.7	1.0	0.9	0.8	0.9	BOI2	orf19.3230	budding protein (by homology)	YER114c
CA2998	1.1	0.7	0.9	1.1	1.2	1.2	LPD1	orf19.6127	dihydrolipoamide dehydrogenase (by homology)	YFL018c
CA2388	1.1	0.7	1.3	1.1	0.7	0.9	MCM6	orf19.2611	component of MCM initiator complex involved in DNA replicat	YGL201c
CA5466	1.8	0.7	2.2	1.2	1.0	1.0	PWP2	orf19.3276	periodic tryptophan protein (by homology)	YCR057c

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[[Cd OS+ down 0.667 10FDR] less [Cd HS+ down 0.667 10FDR]] less [Cd XS+ d...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4501	0.5	1.3	0.1	0.1	0.6	0.9	QDR1	orf19.508	putative antibiotic resistance proteins (by homology)	YIL120w
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membran	YIL047c
CA4039	0.9	1.1	0.4	0.3	1.0	1.0	SKS1	orf19.3669	serine/threonine kinase by homology	YPL026c
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA0127	0.6	0.9	0.8	0.4	1.0	1.0	HXK2	orf19.542	hexokinase II (by homology)	YGL253w
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA1070	0.4	0.6	0.7	0.4	1.0	0.9	HXT61	orf19.2020	sugar transporter	YDR343c
CA2225	0.3	0.6	0.3	0.4	1.1	1.1	SUR2	orf19.5818	Hydroxylation of C-4 of the sphingoid moiety of ceramide by h	YDR297w
CA5749	0.9	0.7	0.4	0.4	0.8	1.0	IPF2908	orf19.7459	unknown function	YBR238c
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA0943	0.1	0.5	0.4	0.4	0.9	1.1	YHB1	orf19.3707	flavohemoglobin (by homology)	YGR234w
CA5897	0.9	0.6	0.6	0.5	1.5	0.9	IPF2384	orf19.6809	unknown function	YKL128c
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA0495	0.8	1.0	0.2	0.5	1.1	1.0	IPF20056	orf19.2659	unknown function	YER067w
CA0752	0.3	1.4	0.6	0.5	0.6	1.3	MNN22	orf19.3803	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA2977	1.3	0.9	0.4	0.5	1.4	0.8	HOM3	orf19.1235	Aspartokinase (by homology)	YER052c
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase	YFR015c
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match
CA3707	1.0	1.0	0.7	0.5	0.9	1.0	TYE7	orf19.4941	Basic helix-loop-helix transcription factor by homology	YOR344c
CA3637	0.3	0.9	0.2	0.5	1.8	1.3	IPF9255	orf19.5136	unknown function	YGR017w
CA4516	0.3	0.5	0.3	0.5	1.3	0.8	IPF18207	orf19.489	unknown function	YPL170w
CA5407	0.3	1.1	0.3	0.5	0.9	0.8	IPF1548	orf19.951	unknown function	no match
CA0471	0.8	0.8	0.6	0.5	4.1	1.4	ECM22	orf19.2623	putative protein involved in cell wall biogenesis (by homology	YDR213w
CA1069	0.9	0.9	1.0	0.6	1.1	1.0	HXT5.3f	orf19.2021	sugar transporter, 3-prime end	YHR096c
CA4203	0.5	0.7	0.7	0.6	0.6	0.8	SWI4.3f	orf19.4545	transcription factor (by homology)	YDL056w
CA5494	0.5	0.7	0.5	0.6	0.9	0.9	IPF85	orf19.5334	similar to Saccharomyces cerevisiae Tis11p tRNA-specific ac	YLR136c
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA2787	1.0	0.8	0.8	0.6	0.5	0.7	EFG1	orf19.610	Enhanced filamentous growth factor	YMR016c
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA4629	1.7	1.4	0.6	0.6	1.2	0.9	IPF13709	orf19.335	unknown function	YKL193c
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA5206	1.1	1.1	0.7	0.6	0.7	1.0	GPH1	orf19.7021	Glycogen phosphorylase (by homology)	YPR160w
CA4668	1.1	1.1	0.7	0.6	1.0	1.0	ROM2	orf19.906	GDP/GTP exchange factor for Rho1p (by homology)	YLR371w
CA1232	1.0	1.1	0.6	0.6	1.0	1.3	IPF11815	orf19.4982	similar to Saccharomyces cerevisiae Lys14 triacyglycerol lipa	YKL140w

CA2661	1.4	1.2	0.8	0.6	0.9	0.9	AAT1	orf19.3554	aspartate aminotransferase (by homology)	YLR027c
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA4059	0.7	0.9	0.7	0.6	0.8	1.2	PRD1	orf19.434	Proteinase (by homology)	YCL057w
CA3818	1.6	1.4	0.8	0.6	0.9	1.1	IPF6695	orf19.5773	unknown function	YOL057w
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA2945	0.9	0.8	1.0	0.6	0.7	0.9	IMG1	orf19.1967	Ribosomal protein, mitochondrial (by homology)	YCR046c
CA2150	0.7	1.0	0.8	0.7	0.3	0.7	IPF19940	orf19.6022	unknown function	no match
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4608	1.0	0.9	0.6	0.7	0.8	0.9	CCH1	orf19.3298	Calcium channel protein (by homology)	YGR217w
CA2415	1.5	1.3	0.8	0.7	0.8	0.9	MSD1	orf19.4478	Aspartyl-tRNA synthetase, mitochondrial.	YPL104w
CA3456	1.0	0.8	0.9	0.7	0.7	0.8	IPF19986	orf19.1259	unknown function	YGL131c

35A

[[Cd XS+ down 0.667 10FDR] less [Cd HS+ down 0.667 10FDR]] less [Cd OS+ d...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4667	1.1	0.7	0.9	1.4	0.6	0.3	GAP5	orf19.4456	General amino acid permease (by homology)	YKR039w
CA2625	0.2	0.9	0.7	0.9	0.2	0.3	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified protein	YLR110c
CA5152	1.0	0.9	0.9	0.8	0.2	0.3	CAT2	orf19.4591	carnitine O-acetyltransferase (by homology)	YML042w
CA0046	0.7	0.9	0.7	0.7	0.4	0.3	IPF14850	orf19.2452	Hypothetical protein	no match
CA2302	0.1	0.6	0.3	0.6	0.1	0.3	IPF6518	orf19.1691	unknown function	YNR018w
CA0415	1.0	0.7	1.8	0.9	0.3	0.3	FRP3	orf19.1224	member of the FRP family of proteins related to Yarrowia lipo	YCR010c
CA0822	1.5	0.8	1.2	1.0	0.3	0.3	EXG1	orf19.2990	glucan 1,3-beta-glucosidase	YLR300w
CA1713	0.8	1.0	1.0	1.3	0.5	0.3	IPF19743	orf19.3332	unknown function	YDL231c
CA1146	1.1	1.0	0.9	0.8	0.4	0.3	CWH8	orf19.3682	putative required protein for full levels of dolichol-linked oligo	YGR036c
CA5241	1.0	1.0	0.7	1.0	0.4	0.3	SMF3	orf19.5022	Probable manganese transporter (by homology)	YOL122c
CA0855	1.0	1.0	0.6	0.8	0.9	0.4	AMYG1	orf19.4899	glucoamylase	YBR229c
CA0605	1.5	1.3	0.8	0.8	0.5	0.4	UTR2	orf19.1671	1,3-1,4-beta-glucanase (by homology)	YEL040w
CA0482	0.2	0.6	0.6	0.9	0.5	0.4	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)	no match
CA1614	1.2	1.3	0.9	1.1	0.2	0.4	IPF18645	orf19.3216	unknown function	YAL018c
CA6142	1.0	0.8	0.9	0.9	0.5	0.4	IPF1879	orf19.5903	unknown function	YOR301w
CA6022	0.8	0.9	3.3	1.2	0.4	0.4	PGA1	orf19.7625	GPI-anchored cell surface protein (by homology)	no match
CA3710	1.5	1.0	2.4	0.9	0.7	0.4	CHS3.5f	orf19.4938	chitin-UDP acetyl-glucosaminyl transferase 3, 3-prime end	YBR023c
CA5322	0.9	1.7	0.8	1.5	0.5	0.4	PRB1	orf19.7196	Protease B, vacuolar (by homology)	YEL060c
CA2950	0.6	0.7	0.3	0.8	0.1	0.4	CLN2	orf19.1960	G1/S-SPECIFIC CYCLIN CLN2	YAL040c
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA1218	0.8	0.7	0.7	0.7	0.3	0.4	CDC20	orf19.122	anaphase promoting complex subunit (by homology)	YGL116w
CA2374	1.0	0.8	1.2	1.0	0.5	0.4	FCY23	orf19.1832	Putative purine-cytosine transport protein	YGL186c
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA3005	1.2	1.0	1.4	1.1	0.7	0.4	CC43	orf19.6237	Cell Division Control -like (by homology)	YLR229c
CA5903	1.2	1.0	1.2	1.1	0.7	0.4	IPF5942	orf19.6803	transmembrane sugar transporter (by homology)	YPL244c
CA2291	0.8	0.8	0.8	0.7	0.8	0.4	IPF9740	orf19.744	oligo-1,4 -1,4-glucantransferase / amylo-1,6-glucosidase (by	YPR184w
CA1572	1.0	0.9	1.0	1.0	0.7	0.4	POX4	orf19.1652	peroxisomal fatty acyl-CoA oxidase (by homology)	YGL205w
CA2552	0.9	0.9	1.2	0.9	0.6	0.4	ALG5	orf19.2837	dolichol-P-glucose synthetase (by homology)	YPL227c
CA5488	0.9	1.1	1.0	1.1	0.5	0.4	IPF810	orf19.5322	unknown function	YJL178c
CA0548	0.7	0.9	0.6	0.7	1.2	0.4	PHO87	orf19.2454	Member of the phosphate permease family (by homology)	YCR037c
CA2473	0.4	0.8	0.6	0.8	0.4	0.4	CBF1	orf19.2876	putative centromere binding factor 1	YJR060w
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA2938	0.4	0.8	0.5	0.7	0.6	0.4	IPF8321	orf19.3325	similar to Saccharomyces cerevisiae Glg2p self-glucosylating	YJL137c
CA5690	1.1	0.9	0.8	0.9	0.6	0.4	OCH1	orf19.7391	Alpha-1,6-mannosyltransferase (by homology)	YGL038c
CA5901	1.2	0.9	1.5	1.0	0.5	0.4	IPF2374	orf19.6805	unknown function	YDR089w
CA0832	0.7	0.8	1.3	1.4	0.5	0.4	IPF14225	orf19.1675	unknown function	YDL133w
CA4574	0.8	0.9	1.2	0.9	0.5	0.4	IPF9430	orf19.6885	similar to Saccharomyces cerevisiae Spo7p meiotic protein (t	YAL009w
CA2324	0.9	0.9	1.3	0.9	0.5	0.4	CDC46	orf19.5487	cell division control protein (by homology)	YLR274w
CA0969	1.2	0.6	1.4	0.8	0.3	0.4	IPF9132	orf19.5541	unknown function	YPL184c
CA2418	1.0	0.8	1.0	1.2	0.4	0.4	MNT4	orf19.4475	putative mannosyltransferase	YBR199w
CA2820	0.9	0.8	1.2	1.2	0.6	0.5	HOL1	orf19.2991	member of major facilitator superfamily multidrug-resistance p	YNR055c
CA1526	1.0	0.9	1.3	1.0	0.5	0.5	IPF13815	orf19.4553	unknown function	no match
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA1504	0.9	0.9	0.9	1.2	0.6	0.5	ARF3	orf19.1702	GTP-binding protein of the ARF family (by homology)	YOR094w
CA6128	0.9	1.0	1.9	0.8	0.3	0.5	IPF152	orf19.5919	unknown function	YOR129c
CA1831	0.9	0.7	0.7	1.1	0.4	0.5	CHS1	orf19.5188	Chitin synthase (by homology)	YBR038w
CA2479	0.7	1.1	1.3	1.1	0.1	0.5	CCN1	orf19.3207	G1 cyclin	YAL040c
CA0010	1.7	0.9	0.9	1.1	1.0	0.5	IPF16036	orf19.150	similar to Saccharomyces cerevisiae Tim17p mitochondrial in	YJL143w
CA1772	0.8	1.0	0.8	0.9	0.4	0.5	ALG7	orf19.2187	UDP-N-acetylglucosamine-1-phosphate transferase (by homc	YBR243c
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA6095	1.1	1.0	1.6	0.7	0.4	0.5	SNF3	orf19.5962	High affinity glucose transport protein (by homology)	YDL194w
CA3879	1.1	0.7	0.9	1.0	0.6	0.5	CDC42	orf19.390	Cell Division Control	YLR229c
CA5153	0.9	1.0	1.0	1.1	0.4	0.5	IPF1003	orf19.4592	unknown function	no match
CA2874	2.0	0.8	0.3	0.7	0.1	0.5	IPF4999	orf19.5843	unknown function	no match
CA5987	0.4	0.7	0.6	0.7	0.7	0.5	CHT3	orf19.7586	chitinase 3 precursor	YLR286c
CA2027	0.9	1.0	0.8	0.9	0.6	0.5	MCK1	orf19.3459	ser/thr/tyr protein kinase (by homology)	YNL307c
CA5876	0.9	0.8	0.6	0.7	0.6	0.5	IPF12082.	orf19.6833	bumetanide-sensitive Na-K-Cl cotransport protein, 5-prime er	YBR235w
CA2724	0.7	0.8	0.7	1.0	0.4	0.5	RPB7	orf19.3347	DNA-directed RNA polymerase II, 19 KD subunit (by homolo	YDR404c
CA1267	1.9	1.2	0.9	1.0	0.7	0.5	YSY6	orf19.242.2	protein involved in the secretory pathway, by homology	YBR162wa
CA5877	0.7	0.9	0.5	0.9	0.6	0.5	IPF12082.	orf19.6832	bumetanide-sensitive Na-K-Cl cotransport protein, 3-prime er	YBR235w
CA1926	1.0	1.1	0.8	0.9	1.0	0.5	IPF13407	orf19.753	Unknown function	YNR059w
CA5423	0.9	1.0	0.7	1.0	0.4	0.5	ROT2	orf19.974	Glucosidase II, catalytic subunit (by homology)	YBR229c
CA0932	1.1	0.7	1.2	1.2	0.4	0.5	EPT1	orf19.3695	alcohol phosphatidyl transferase (by homology)	YHR123w
CA5691	0.5	0.5	1.4	1.2	0.7	0.5	DED1	orf19.7392	RNA helicase (by homology)	YOR204w
CA0532	1.0	0.9	0.7	0.7	0.7	0.5	IRE1	orf19.5068	protein kinase (by homology)	YHR079c
CA1306	0.9	0.8	1.0	1.1	0.4	0.5	CDC14	orf19.4192	protein phosphatase	YFR028c
CA1077	1.1	0.8	0.9	0.8	0.3	0.5	IPF13694	orf19.2238	unknown function	YAL024c
CA4097	0.7	0.8	1.3	0.9	0.2	0.5	GIN4	orf19.663	ser/thr protein kinase (by homology)	YDR507c
CA5003	1.2	1.0	1.0	0.9	0.4	0.5	MCD4	orf19.5244	Sporulation protein (by homology)	YKL165c
CA0198	1.1	1.2	1.1	1.0	1.4	0.5	IPF19685	orf19.1658	unknown function	YHR097c
CA5600	0.5	0.7	0.6	1.0	0.4	0.5	IPF559	orf19.7100	unknown function	YJR001w
CA4005	0.5	0.6	1.1	1.1	0.2	0.5	ERG6	orf19.1631	sterol transmethylase	YML008c
CA2042	0.7	0.9	0.8	0.8	0.3	0.5				
CA5834	1.0	0.7	0.8	0.8	0.4	0.5	LRG1	orf19.7489	GTPase-activating protein of the rho/rac family (by homology	YDL240w

CA5265	0.9	0.8	0.8	1.1	0.6	0.5	IPF1792	orf19.4997	unknown function	YER027c
CA3319	1.1	0.7	0.5	0.8	0.6	0.5	DRS25	orf19.2680	Probable ATPase, Potential phospholipid-transporting ATPas	YMR162c
CA1211	0.6	1.1	0.7	0.8	0.6	0.5	IPF7031.3	orf19.131.2	unknown function, 3-prime end	YPR063c
CA5956	0.7	0.7	0.9	0.9	0.4	0.5	VAN1	orf19.6738	Vanadate resistance protein	YML115c
CA1414	0.9	0.6	1.2	0.9	0.5	0.5	CHO2	orf19.169	phosphatidylethanolamine N-methyltransferase (by homology	YGR157w
CA5482	1.0	0.8	0.8	0.9	0.3	0.5	IFV4.3f	orf19.5315	unknown function	no match
CA1039	0.8	0.8	1.7	0.9	0.5	0.5	IPF4012	orf19.2501	Unknown Function	YPL221w
CA1053	0.9	0.7	0.8	0.7	0.3	0.5	SCW11.3c	orf19.3893	glucanase gene family member, 3-prime end (by homology)	YGL028c
CA0425	1.2	1.2	0.9	1.2	0.6	0.5	PPH21	orf19.1683	protein ser/thr phosphatase PP2A-1 (by homology)	YDL188c
CA1628	1.0	1.1	1.0	1.0	0.4	0.5	HMG1	orf19.1031	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 (by hom	YLR450w
CA2438	1.0	1.0	0.9	0.9	0.6	0.5	IPF5505	orf19.2198	unknown function	YAL053w
CA0274	1.0	1.4	1.0	0.9	0.9	0.5	IPF15153	orf19.5867	unknown function	YOL105c
CA0349	0.9	0.9	0.7	1.0	0.4	0.5	IPF19026	orf19.1813	unknown function	YAL053w
CA3296	1.0	0.6	1.1	1.2	0.9	0.5				
CA1352	0.9	1.0	0.9	1.3	0.4	0.5	VCX1	orf19.405	Ca2+-transport by homology	YDL128w
CA2769	1.0	0.8	0.9	0.8	0.4	0.5	PGA54	orf19.2685	unknown function	no match
CA4382	0.9	0.9	0.6	0.9	0.9	0.5	IPF8576	orf19.5675	similar to Saccharomyces cerevisiae Ris1p DNA helicase (by	YOR191w
CA3365	1.0	0.9	0.6	0.7	0.5	0.5	ALG6	orf19.1843	glucosyltransferase (by homology)	YOR002w
CA1259	1.1	1.0	1.0	1.0	0.8	0.5	IPF3174	orf19.3167	Farnesyl transferase (by homology)	YPL172c
CA2172	1.2	0.7	0.7	1.1	0.3	0.5	IPF15377	orf19.3765	probable membrane protein involved in bipolar budding (by h	YLR084c
CA4728	1.1	1.0	1.3	1.1	0.5	0.5	VPS41.3f	orf19.4859	required for the vacuolar assembly, 3-prime end (by homolog	YDR080w
CA2866	1.1	1.0	1.0	1.1	0.6	0.5	RHO1	orf19.2843	GTP-binding protein of the rho subfamily of ras-like proteins (	YPR165w
CA1930	1.1	0.9	1.3	0.9	0.9	0.5	IPF3906.3	orf19.758	unknown function, 3-prime end	YPR079w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA5703	1.1	0.9	0.9	1.0	0.7	0.5	IPF2463	orf19.7403	unknown function	YML020w
CA4314	1.1	1.1	0.7	0.9	0.5	0.5	PMT4	orf19.4109	Mannosyltransferase (by homology)	YJR143c
CA1660	0.8	0.8	2.2	1.2	0.8	0.5	DAP2	orf19.4322	dipeptidyl aminopeptidase B (by homology)	YHR028c
CA4983	0.2	0.7	0.6	1.2	0.4	0.5	IPF2053	orf19.5267	unknown function	no match
CA5922	1.3	0.8	1.0	0.8	0.8	0.5	MRS6	orf19.6783	geranylgeranyltransferase regulatory subunit	YOR370c
CA2079	0.9	0.5	0.7	0.8	0.4	0.5	MNN3	orf19.4874	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA2994	0.7	0.9	0.6	0.9	0.6	0.5	IPF9116	orf19.6119	unknown function	no match
CA4067	0.8	0.8	1.3	0.9	0.6	0.5	IPF5924	orf19.445	unknown function	YNR040w
CA0686	0.9	1.0	0.9	0.7	0.3	0.5	IPF162	orf19.3222	sulphate transporter (by homology)	YGR125w
CA2935	0.9	0.8	1.7	1.0	0.5	0.5	IPF11521	orf19.3328	unknown function	YMR172w
CA4420	1.3	1.5	1.2	0.9	0.8	0.5	SSM4	orf19.5175	involved in mRNA turnover by homology	YIL030c
CA6053	1.1	0.9	1.0	1.0	0.6	0.5	IPF4949	orf19.7670	unknown function	YNL321w
CA1491	1.2	0.9	0.7	0.7	0.5	0.5	IPF166	orf19.3225	unknown function	YCR017c
CA2980	1.1	0.8	1.1	1.0	0.4	0.6	GOG5	orf19.1232	GDP-mannose transporter (by homology)	YGL225w
CA2018	1.2	1.1	0.9	0.9	0.8	0.6	STE11	orf19.844	ser/thr protein kinase of the MEKK family (by homology)	YLR362w
CA5026	1.2	1.0	1.1	0.8	0.8	0.6	IPF3001	orf19.6980	serine/threonine protein kinase (by homology)	YDL025c
CA2163	0.8	1.2	0.8	1.0	1.0	0.6	IPF11879	orf19.5293	unknown function	no match
CA4428	1.2	0.9	1.1	0.9	0.5	0.6	IFM1	orf19.5167	translation initiation factor 2 by homology	YOL023w
CA5873	1.1	1.0	1.0	1.0	0.9	0.6	PGA25	orf19.7542	GPI-anchored cell surface protein (by homology)	no match
CA5016	0.7	1.2	1.3	0.9	0.5	0.6	IPF7561	orf19.6968	unknown function	no match
CA4119	1.3	1.2	0.9	0.8	0.6	0.6	BEM3	orf19.2771	GTPase-activating protein for Cdc42p and Rho1p (by homolo	YPL115c
CA0535	0.8	0.9	1.4	1.0	0.6	0.6	IPF15606	orf19.5065	similar to Saccharomyces cerevisiae Erd1p required for reten	YDR414c
CA0095	0.8	1.0	1.5	0.7	0.2	0.6	ALG11	orf19.3468	required for asparagine-linked oligosaccharide assembly (by	YNL048w
CA0503	1.0	0.9	0.8	1.3	0.5	0.6	PMT6	orf19.3802	protein mannosyltransferase	YGR199w
CA4112	1.0	0.7	1.1	1.1	0.5	0.6	BIM1	orf19.676	microtubule-binding protein (by homology)	YER016w
CA0233	1.4	1.1	1.0	0.9	1.1	0.6	URE2	orf19.155	Nitrogen catabolite repression regulator (by homology)	YNL229c
CA1945	0.9	0.9	1.0	0.8	0.4	0.6	MSS116	orf19.4739	RNA helicase of the DEAD box family (by homology)	YDR194c
CA2340	0.8	0.7	0.7	1.1	0.6	0.6	MNN5	orf19.2347	Golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA5533	1.1	1.1	1.0	1.0	0.4	0.6	IPF2846	orf19.7293	similar to Saccharomyces cerevisiae Mps1p serine/threonine	YDL028c
CA5918	1.0	0.7	1.3	1.3	0.3	0.6	ERV14	orf19.6787	membrane protein	YGL054c
CA4762	1.3	1.0	1.0	1.0	0.5	0.6	IPF9647	orf19.3994	similar to Saccharomyces cerevisiae Ost3p oligosaccharyltra	YOR085w
CA1854	1.0	0.9	0.8	0.9	0.8	0.6	IPF12611	orf19.649	unknown function	YGL228w
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA0528	0.9	0.9	1.2	0.8	0.4	0.6	ANP1	orf19.3622	Golgi mannosyltransferase (by homology)	YEL036c
CA0110	1.1	0.6	0.8	0.6	0.4	0.6	IPF17190	orf19.3869	unknown function	no match
CA2484	1.3	1.0	0.9	0.8	0.7	0.6	IPF9846	orf19.3202	unknown function	YMR247c
CA4721	1.3	0.9	0.8	0.9	0.7	0.6	CPP1	orf19.4866	probable protein-tyrosine phosphatase	YNL053w
CA2261	1.2	0.8	0.9	0.9	1.1	0.6	RAS1	orf19.1760	GTP-binding protein (by homology)	YNL098c
CA0375	0.4	1.1	1.1	0.8	0.7	0.6	CRH11	orf19.2706	Probable membrane protein (by homology)	YGR189c
CA4245	1.2	0.7	1.1	1.3	0.7	0.6	PGA21	orf19.532	unknown function	no match
CA5201	0.6	0.9	1.1	0.9	0.2	0.6	IPF2349	orf19.7016	similar to human sphingomyelin	YDR452w
CA4781	0.9	1.1	0.7	0.8	0.7	0.6	IPF3355	orf19.4014	similar to Saccharomyces cerevisiae Cdc1 cell cycle protein i	YDR182w
CA1745	0.9	1.0	0.9	1.0	0.3	0.6	IPF10888	orf19.5051	unknown function	no match
CA2941	0.6	0.9	1.3	1.1	0.7	0.6	CVB1	orf19.1970	vacuole biogenesis component	no match
CA2656	1.6	0.8	0.7	0.8	0.6	0.6	NAM2	orf19.5705	mitochondrial leucine--tRNA ligase (by homology)	YLR382c
CA2299	1.6	1.2	0.6	0.7	0.5	0.6	IPF8222	orf19.5381	unknown function	YGL014w
CA5023	0.7	0.7	2.1	1.0	0.4	0.6	IPF7547	orf19.6976	unknown function	YJL163c
CA5927	1.3	0.9	0.8	0.8	0.6	0.6	DRS22	orf19.6778	Membrane-spanning Ca-ATPase (by homology)	YAL026c
CA3438	1.3	1.3	1.0	1.0	0.6	0.6	IPF11330	orf19.2987	unknown function	YHR194w
CA1406	1.1	0.9	1.5	1.1	0.5	0.6	DOT4	orf19.3370	derepression of telomeric silencing (by homology)	YNL186w
CA4876	0.6	1.0	1.0	1.1	1.0	0.6	RNH35	orf19.6562	RNase H (by homology)	YNL072w
CA2732	0.8	0.7	0.9	0.8	0.5	0.6	IPF10327	orf19.2113	unknown function	YLR324w
CA3141	1.0	1.3	0.5	0.5	1.0	0.6	IPF9211.3	orf19.3712	unknown function, 3-prime end	no match
CA1570	0.9	0.9	0.7	1.1	0.7	0.6	IPF7617	orf19.1160	unknown function	YHR181w
CA5937	1.0	0.7	1.1	1.0	0.6	0.6	IPF2784	orf19.6760	unknown function	YER132c
CA0990	1.0	0.9	0.8	0.8	0.6	0.6	IPF11068	orf19.1392	unknown function	YIL005w
CA0213	1.3	0.9	1.2	1.0	0.7	0.6	CDS1	orf19.1279	CDP-diacylglycerol synthase (by homology)	YBR029c
CA4206	0.6	0.8	0.4	0.8	1.2	0.6	IPF9079	orf19.4550	Membrane transporter (by homology)	YCR023c
CA3467	0.8	0.9	1.0	1.1	0.5	0.6	MNT2	orf19.1663	Alpha-1,2-mannosyltransferase (by homology)	YDR483w
CA2019	0.8	1.0	1.0	1.0	0.6	0.6	IPF3409	orf19.843	unknown function	YLR361c
CA3625	1.2	1.3	0.6	0.8	0.5	0.6	CYR1.3f	orf19.5151	adenylate cyclase, 3-prime end	YJL005w
5124.1	1.1	1.2	0.5	1.0	1.0	0.6				
CA3463	1.1	1.1	0.9	1.0	0.5	0.6	ALG8	orf19.1659	glucosyltransferase (by homology)	YOR067c
CA1350	0.8	0.8	1.6	1.2	0.3	0.6	MCM2	orf19.4354	replication licensing factor (by homology)	YBL023c
CA1324	1.1	0.6	1.7	0.9	0.8	0.6	IPF6676	orf19.1308	polytopic membrane protein involved in drug transport (by ho	YBR293w
CA1530	1.0	0.9	1.0	1.0	0.6	0.6	ALG2.5	orf19.1221	mannosyltransferase, 5-prime end (by homology)	YGL065c
CA3160	0.2	1.0	0.2	0.7	0.4	0.6	ZRT2	orf19.1585	zinc transport protein (by homology)	YLR130c
CA2996	1.1	0.9	0.7	0.8	0.5	0.6	IPF9108	orf19.6124	similar to Saccharomyces cerevisiae Ace2p transcription fact	YLR131c

CA1878	1.0	0.7	1.0	0.9	0.8	0.6	IPF10298	orf19.2272	unknown function	YPL202c
CA4906	1.4	1.2	1.0	1.3	0.7	0.6	MOB2	orf19.6044	Required for maintenance in ploidy	YFL034cb
CA3494	1.5	1.5	1.0	0.9	0.6	0.6	RPB5	orf19.6340	DNA-directed RNA polymerase I, II, III (by homology)	YBR154c
CA2470	1.0	0.8	0.9	1.0	0.7	0.6	SDH12	orf19.2871	Succinate dehydrogenase (by homology)	YKL148c
CA5652	1.1	0.9	2.6	0.8	0.5	0.6	IPF19815	orf19.7354	longevity-assurance protein (by homology)	YKL008c
CA5215	1.1	0.9	1.0	0.8	0.7	0.6	PPS1	orf19.7033	protein tyrosine phosphatase (by homology)	YBR276c
CA0704	1.0	1.1	0.8	0.9	0.6	0.6	IPF11806	orf19.2915	similar to Saccharomyces cerevisiae Ynd1p nucleoside diphc	YER005w
CA2827	1.3	0.8	0.9	0.8	0.7	0.6	RAD2	orf19.1324	structure-specific nuclease of the nucleotide excision repairs	YGR258c
CA0197	0.7	0.9	2.3	2.0	0.4	0.6	IPF9787	orf19.1934	similar to Saccharomyces cerevisiae Hst3p silencing protein (	YOR025w
CA1517	1.4	1.1	0.8	0.9	0.5	0.6	IPF11045	orf19.4798	unknown function	YMR212c
CA1265	0.8	0.8	1.3	1.0	1.0	0.6	IPF10510	orf19.240	unknown function	YKR065c
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match
CA0302	0.5	0.9	1.2	1.4	0.7	0.6	MEP3	orf19.1614	low affinity high capacity ammonium permease (by homology	YPR138c
CA1207	0.9	0.9	0.9	0.9	0.6	0.6	PPG1	orf19.3774	Phosphoprotein phosphatase PPG catalytic chain (by homolc	YNR032w
CA0300	0.7	0.7	0.9	1.0	0.4	0.6	ERG24	orf19.1598	C-14 sterol reductase (by homology)	YNL280c
CA4936	1.3	1.1	1.3	3.1	0.5	0.6	IPF8369	orf19.6077	unknown function	YOR161c
CA0553	1.1	1.1	1.1	1.5	0.7	0.6	IPF16653	orf19.5534	unknown function	YKR088c
CA2530	1.0	1.1	0.9	1.0	0.8	0.6	IPF12782	orf19.3176	unknown function	YNL294c
CA2017	0.9	0.9	0.5	0.7	0.7	0.6	IPF3414	orf19.846	putative serine/threonine protein kinase	YKL171w
CA5936	1.5	1.4	0.9	1.1	0.7	0.6	IPF2795	orf19.6763	unknown function	YOR195w
CA5563	1.1	0.9	1.4	1.1	0.3	0.6	PHO88	orf19.7327	Involved in phosphate transport (by homology)	YBR106w
CA1465	1.0	0.7	0.7	0.7	0.8	0.6	RIM11	orf19.791	Ser/thr protein kinase (by homology)	YMR139w
CA0964	0.4	0.6	0.8	0.9	0.4	0.6	IPF9141	orf19.6247	similar to Saccharomyces cerevisiae Ctf4p DNA-directed DN/	YPR135w
CA2103	0.9	0.8	0.6	0.7	0.6	0.6	ISM1	orf19.2382	isoleucyl-tRNA synthetase (by homology)	YPL040c
CA6054	2.1	0.8	1.7	1.2	0.6	0.6	IPF4952	orf19.7672	unknown function	YDR411c
CA2195	0.9	0.8	0.8	0.9	0.3	0.6	IPF18517	orf19.4349	unknown function	YOL070c
CA4204	1.0	0.8	0.7	1.1	1.8	0.6	HOL4	orf19.4546	member of major facilitator superfamily multidrug-resistance p	YNR055c
CA4717	1.2	1.0	1.4	1.0	0.8	0.6	IPF8663	orf19.6953	Unknown function	YJL083w
CA2199	1.4	1.4	1.0	1.0	0.7	0.6	IPF8113	orf19.2938	unknown function	YLR077w
CA5073	0.6	1.0	0.8	0.9	0.2	0.6	IPF3603	orf19.3048	unknown function	no match
CA3711	1.0	1.2	1.3	1.1	0.9	0.6	CHS3.3f	orf19.4937	chitin-UDP acetyl-glucosaminyl transferase 3, 5-prime end	YBR023c
CA1980	1.5	1.1	1.4	0.9	0.5	0.6	YHM1	orf19.685	member of the mitochondrial carrier family (MCF) (by homolo	YDL198c
CA0883	1.0	0.6	1.0	1.2	0.3	0.6	SUN41	orf19.3642	Putative cell wall beta-glucosidase (by homology)	YIL123w
CA4431	0.9	1.1	0.8	0.9	0.5	0.6	ECM39	orf19.5164	cell wall biogenesis by homology	YNR030w
CA5502	0.6	0.6	1.0	0.9	0.6	0.6	IPF763	orf19.5343	putative transcription factor with a Cys4- zinc finger (by homo	YKL185w
CA1268	1.2	0.8	1.6	1.0	0.6	0.6	IPF14693	orf19.3159	unknown function	YBL004w
CA5649	1.7	0.8	1.8	1.0	0.9	0.6	CHS4	orf19.7349	Chitin synthase regulatory factor	YBL061c
CA6135	0.3	0.7	0.4	0.8	1.0	0.6	CMK1	orf19.5911	Ca2+/calmodulin-dependent ser/thr protein kinase (by homol	YFR014c
CA5154	1.8	1.4	0.8	0.8	0.8	0.6	RGA2	orf19.4593	rho-GTPase activating protein 2 (by homology)	YOR127w
CA2164	0.9	0.9	0.9	0.8	0.7	0.6	AXL2	orf19.5292	similar to saccharomyces cerevisiae Axl2p required for axial p	YIL140w
CA0199	1.0	0.7	1.3	1.0	0.4	0.6	KAP104	orf19.3556	karyopherin-beta protein (by homology)	YBR017c
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA3046	0.9	0.9	1.2	0.8	0.4	0.6	IPF7295	orf19.2417	unknown function	YOL034w
CA2188	1.2	1.1	1.0	1.1	0.4	0.6	SSU81	orf19.4772	protein involved in the HOG1 high-osmolarity signal transduc	YER118c
CA0308	1.1	1.0	0.8	0.8	0.5	0.6	RHK1	orf19.1092	Mannosyltransferase (by homology)	YBL082c
CA0488	1.1	1.1	0.8	0.8	0.6	0.6	SEC59	orf19.261	Dolichol kinase (by homology)	YMR013c
CA1074	0.9	1.1	1.1	0.8	0.5	0.6	PRORS.5f	orf19.2532	prolyl-tRNA synthetase, 5-prime end	YER087w
CA0951	0.8	1.1	1.0	1.0	0.6	0.6	MNN6	orf19.1011	putative golgi alpha-1,2-mannosyltransferase (by homology)	YBR015c
CA5205	1.3	1.2	0.9	0.9	1.4	0.6	KEX1	orf19.7020	Carboxypeptidase-alpha (by homology)	YGL203c
CA5072	1.2	1.0	0.5	0.8	0.9	0.6	IPF3598	orf19.3047	similar to Saccharomyces cerevisiae Sip3p protein which inte	YNL257c
CA0173	0.8	1.0	1.0	0.9	0.7	0.6	IPF6913	orf19.3793	unknown function	no match
CA1944	0.8	1.0	0.4	0.9	1.2	0.6	IPF10645	orf19.4738	unknown function	YOR154w
CA4132	1.1	1.0	0.9	1.0	0.6	0.6	STE20	orf19.4242	serine/threonine-specific protein kinase	YHL007c
CA0403	0.6	0.9	0.8	1.1	0.5	0.6	PGA51	orf19.1989	unknown function	YKL046c
CA1183	1.6	1.6	1.2	1.2	0.6	0.6	IPF14805	orf19.3782	acetyl-coenzyme A transporter(by homology)	YBR220c
CA3397	1.4	1.0	1.6	1.1	0.4	0.6	IPF13618	orf19.3972	unknown function	YMR292w
CA2040	0.9	1.3	2.7	1.5	0.9	0.6	IPF12946	orf19.4356	unknown function	YDL199c
CA2308	1.2	1.1	0.8	0.9	0.7	0.6	IPF9874.3	orf19.1373	similar to Saccharomyces cerevisiae Inp51p phosphatidylinos	YIL002c
CA1421	1.1	0.7	1.2	0.8	0.6	0.6	MRPL11	orf19.3797	Mitochondrial ribosomal protein (by komology)	YDL202w
CA5119	0.9	1.0	0.8	1.0	0.8	0.6	IPF1320	orf19.6411	unknown function	YLR386w
CA3318	1.3	1.1	0.8	0.8	0.5	0.6	WBP1	orf19.2298	Oligosaccharyl transferase beta subunit (by homology)	YEL002c
CA4843	1.0	1.2	0.7	0.9	0.7	0.6	GYP1	orf19.3811	GTPase activating protein (by homology)	YOR070c
CA4381	0.5	0.8	0.5	0.7	0.8	0.6	PGA10	orf19.5674	unknown function	no match
CA4880	0.9	1.0	1.2	0.9	0.3	0.6	RHC18	orf19.6568	Recombination repair protein (by homology)	YLR383w
CA4921	0.8	1.1	1.1	1.1	1.2	0.6	IPF1416	orf19.6061	unknown function	YPL103c
CA5362	0.6	0.8	1.3	1.0	0.9	0.6	IPF836.3	orf19.7239	regulation of G-protein function, (by homology)	YHR146w
CA4817	0.8	0.8	0.9	0.8	0.5	0.6	POM152	orf19.2081	Nuclear pore membrane glycoprotein (by homology)	YMR129w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltra	YMR149w
CA5034	1.4	1.2	0.9	0.7	0.5	0.6	OST1	orf19.6988	oligosaccharyltransferase	YJL002c
CA1409	1.2	0.8	1.2	1.0	0.6	0.6	SPT16	orf19.2884	general chromatin factor (by homology)	YGL207w
CA4134	1.0	0.9	0.9	0.9	0.4	0.6	COS162	orf19.4240	involved in manganese homeostasis (by homology)	YCR044c
CA5839	1.1	1.0	0.9	0.9	0.3	0.6	IPF423	orf19.7494	unknown function	YLR320w
CA3470	1.1	1.0	0.9	0.9	0.5	0.6	IPF6310	orf19.1666	unknown function	no match
CA2563	1.3	1.0	1.0	1.1	1.0	0.6	ECM7	orf19.5643	cell wall biogenesis and architecture (by homology)	YLR443w
CA5681	0.8	1.1	1.0	1.0	0.4	0.6	MNN9	orf19.7383	Required for complex N-glycosylation	YPL050c
CA1615	1.0	1.1	0.9	1.0	0.8	0.6	IPF14540	orf19.3218	putative multidrug protein (by homology)	YJR124c
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA1879	1.0	1.0	2.5	1.0	1.0	0.6	SMF12	orf19.2270	manganese transporter (by homology)	YOL122c
CA4573	1.1	0.7	0.8	1.0	0.6	0.6	IPF9431	orf19.6884	unknown function	YJL091c
CA3626	1.5	1.0	0.9	1.1	0.4	0.6				
CA4622	1.6	0.7	0.6	0.9	0.6	0.6	IPF5751	orf19.3314	TRAPP subunit of 20 kDa involved in targeting and fusion of I	YBR254c
CA0722	2.2	0.8	0.9	0.8	0.7	0.6	ERK1	orf19.2886	mitogen-activated protein kinase (FUS3 homolog)	YGR040w
CA1030	0.7	0.9	1.1	0.9	0.8	0.6	ZRC1.3f	orf19.1537	Zinc and cadmium resistance protein (by homology)	YMR243c
CA2547	1.2	1.0	0.7	0.7	0.9	0.6	IPF14911	orf19.2832	unknown function	YNL152w
CA5029	0.7	1.0	1.0	0.9	0.4	0.6	IPF2997	orf19.6983	unknown function	YDR028c
CA2653	1.0	1.0	1.0	1.0	0.8	0.6	IPF8472.3	orf19.5701	unknown function, 3-prime end	YLR381w
CA1645	0.9	0.8	1.0	0.9	0.6	0.6	PMC1	orf19.1727	Ca2+-transporting P-type ATPase (by homology)	YGL006w
CA0563	1.4	0.9	1.3	0.9	0.4	0.6	MNN11	orf19.2927	Mannosyltransferase complex component (by homology)	YJL183w
CA5674	0.7	0.9	0.6	0.9	0.4	0.6	IPF1274	orf19.7377	similar to Saccharomyces cerevisiae Ase1p component of the	YOR058c
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA5382	0.8	0.6	0.9	0.9	0.9	0.6	IPF5217	orf19.7270	unknown function	no match
CA4510	0.8	1.2	0.9	0.9	0.5	0.6	IPF8970	orf19.496	similar to Saccharomyces cerevisiae Msh1p DNA mismatch r	YHR120w
CA4702	0.9	1.2	1.2	1.3	0.7	0.6	IPF4213	orf19.6930	unknown function	no match

CA2934	0.9	1.1	1.0	1.1	0.5	0.6	IPF11515	orf19.3329	similar to Saccharomyces cerevisiae Lcb3p sphingoid base-p	YJL134w
CA2350	1.3	0.9	0.8	0.9	1.0	0.6	CWH41.5(	orf19.4421	ER glucosidase I, 5-prime end (by homology)	YGL027c
CA0481	0.9	1.0	0.8	1.0	0.7	0.6	STE14.3f	orf19.119	farnesyl cystein carboxyl-methyltransferase, 3-prime end (by	YDR410c
CA5024	1.0	1.2	0.5	0.8	0.5	0.6	IPF3009	orf19.6977	similar to Saccharomyces cerevisiae Gpi1p required for N-ac	YGR216c
CA5209	0.9	0.9	1.4	1.2	0.4	0.6	MCM1	orf19.7025	Transcription factor of the MADS box (by homology)	YMR043w
CA0087	0.9	1.2	1.9	0.9	1.0	0.6	SMF11	orf19.4690	manganese transporter (by homology)	YOL122c
CA4739	1.2	1.1	0.7	1.1	0.8	0.6	IPF4498	orf19.4845	unknown function	YMR071c
CA0205	0.9	1.0	1.0	1.0	0.5	0.6	DBF2	orf19.1223	putative ser/thr protein kinase by homology	YGR092w
CA0587	0.8	0.9	0.8	0.9	0.9	0.6	PLD1	orf19.1161	phospholipase D	YKR031c
CA2051	1.2	1.0	0.7	1.0	1.0	0.6	PXP5	orf19.5723	acyl-coenzyme A oxidase I precursor by homology to Candid	YGL205w
CA2193	0.7	0.8	0.8	0.8	0.4	0.6	IPF14273	orf19.4347	Probable ser/thr protein kinase (by homology)	YKL116c
CA1798	1.1	1.1	0.6	0.9	0.4	0.6	IPF11448	orf19.2923	unknown function	YMR155w
CA4733	0.7	0.9	1.0	0.9	0.6	0.6	IPF7732	orf19.4853	similar to Saccharomyces cerevisiae Hcm1p transcription fac	YCR065w
CA2424	1.7	0.8	1.0	0.8	0.9	0.7	IPF18468	orf19.4467	unknown function	no match
CA3709	1.8	1.2	0.7	0.8	0.7	0.7	IPF7880	orf19.4939	unknown function	YNL297c
CA3040	0.7	0.8	0.8	1.0	0.4	0.7	IPF7306	orf19.2425	putative permease (by homology)	YBR241c
CA5424	1.2	0.7	1.4	1.0	0.7	0.7	IPF1598	orf19.976	unknown function	YDL074c
CA4088	0.8	1.1	0.7	1.0	0.9	0.7	HMO1	orf19.6645	High-mobility protein 1 by homology	YDR174w
CA5637	0.8	0.9	0.9	1.1	0.5	0.7	IPF472	orf19.7058	unknown Function	YFR048w
CA5794	0.6	0.8	0.6	1.0	0.7	0.7	IPF4191	orf19.5443	unknown function	YBL098w
CA1351	0.9	0.9	1.1	1.0	0.4	0.7	PCL2	orf19.403	G1/S specific cyclin	YDL127w
CA3384	1.1	0.6	0.9	0.8	0.7	0.7	IPF8362	orf19.325	similar to Saccharomyces cerevisiae Cft2p involved in cleava	YLR115w
CA1499	0.9	0.9	0.9	0.8	0.4	0.7				
CA2985	1.3	0.8	1.0	0.9	0.5	0.7	SET1	orf19.6009	Chromatin regulatory protein (by homology)	YHR119w
CA4872	1.2	0.8	1.1	1.0	0.6	0.7	SEC231	orf19.6558	Component of COPII coat (by homology)	YPR181c
CA0491	0.9	0.8	1.0	1.1	1.0	0.7				
CA5066	1.0	1.2	0.5	0.7	1.5	0.7	TPS2	orf19.3038	Threalose-6-phosphate phosphatase (by homology)	YDR074w
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA5896	1.8	1.1	0.8	1.0	0.6	0.7	TPD3	orf19.6810	Ser/thr protein phosphatase (by homology)	YAL016w
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA0453	1.0	1.2	1.3	0.8	0.6	0.7	IPF13552	orf19.1300	putative methyltransferase (by homology)	YDR316w
CA3615	0.9	1.0	1.0	1.1	1.1	0.7	GIT1	orf19.34	glycerophosphoinositol transporter (by homology)	YCR098c
CA0658	1.4	1.0	1.2	0.8	0.5	0.7	IPF16505	orf19.5575	Unknown function	YPL112c
CA5906	0.8	0.8	0.7	0.8	0.8	0.7	IPF5949	orf19.6800	unknown function	YPL188w
CA4068	1.7	1.2	1.2	0.9	0.7	0.7	IPF5922	orf19.446	unknown function	no match
CA1073	1.1	1.0	1.1	0.8	0.5	0.7	PRORS.3f	orf19.2533	prolyl-tRNA synthetase, 3-prime end	YER087w
CA2171	1.1	1.0	0.8	1.0	0.7	0.7	PEP1.3eo	orf19.3767	Vacuolar protein sorting/targeting protein, 3-prime end (by ho	YBL017c
CA3016	1.1	0.7	1.0	0.8	0.7	0.7	IPF10027	orf19.3914	unknown function	YOL139c
CA3147	1.2	1.2	1.3	1.2	0.8	0.7	IPF9803	orf19.6160	unknown function	YMR031c
CA3987	0.5	0.9	0.6	1.0	0.4	0.7	ECM3	orf19.1563	Involved in cell wall biogenesis and architecture (by homolog	YOR092w
CA5062	1.5	1.1	1.1	1.1	0.5	0.7	SEC62	orf19.3031	subunit of ER protein-translocation complex (by homology)	YPL094c
CA0991	1.3	1.0	1.0	1.1	1.1	0.7	IPF11065	orf19.1393	unknown function	YIL006w
CA4025	1.6	1.4	1.0	0.9	0.6	0.7	SCJ1	orf19.3438	Mitochondrial and ER import protein (by homology)	YMR214w
CA3867	0.5	0.8	0.9	1.5	0.9	0.7	PHR2	orf19.6081	pH-regulated protein 2	YMR307w
CA2198	0.9	1.5	0.9	0.9	0.6	0.7	PMM1	orf19.2937	phosphomannomutase	YFL045c
CA2518	1.1	1.0	0.9	1.0	0.9	0.7	CBP3	orf19.5515	involved in cytochrome-c reductase assembly (by homology)	YPL215w
CA6087	1.3	1.1	0.9	0.8	0.8	0.7	YHV1	orf19.5971	unknown function	YHR151c
CA4359	1.0	0.9	0.9	0.9	0.6	0.7	IPF6054	orf19.6736	unnown function	YOR205c
CA3023	1.0	1.0	1.0	1.1	1.0	0.7	IPF11508	orf19.3904	unknown function	YLR046c

36A

[[Cd OS+ down 0.667 10FDR] and [Cd HS+ down 0.667 10FDR]] less [Cd XS+ do...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA4155	0.8	0.5	1.0	0.5	0.5	0.7	RNR21	orf19.5801	ribonucleoside-diphosphate reductase (by homology)	YJL026w
CA1353	0.2	0.3	0.4	0.5	0.7	1.0	ERG1	orf19.406	squalene epoxidase	YGR175c
CA3603	0.9	0.5	0.9	0.6	0.5	0.7	MEF1	orf19.4932	mitochondrial translation elongation factor G (by homology)	YLR069c
CA1898	0.7	0.4	0.7	0.6	0.5	1.0	PGA38	orf19.2758	unknown function	no match
CA3112	0.6	0.4	0.8	0.6	1.1	1.0	PFK2	orf19.6540	6-phosphofructokinase, beta subunit	YMR205c
CA2075	0.2	0.5	0.5	0.7	1.3	1.1	IFE2	orf19.5288	Unknown function	YAL060w

37A

[[Cd XS+ down 0.667 10FDR] and [Cd OS+ down 0.667 10FDR]] less [Cd HS+ do...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA5725	1.2	1.2	1.0	0.6	1.0	0.3	GLG2	orf19.7434	Self-glucosylating initiator of glycogen synthesis (by homolog	YJL137c
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA0660	0.6	0.8	0.7	0.6	0.5	0.4	IPF16189.	orf19.5577	panthotenate kinase, 5-prime end (by homology)	YDR531w
CA3757	0.6	0.8	0.2	0.3	0.5	0.5	MAE1	orf19.3419	mitochondrial malic enzyme (by homology)	YKL029c
CA0688	1.0	0.8	0.8	0.7	0.9	0.5				
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA0273	0.3	0.9	0.3	0.5	1.0	0.6	IPF19066	orf19.1433	unknown function	YOR084w
CA1616	1.7	0.8	1.1	0.6	0.6	0.6	IPF14538	orf19.3219	unknown function	YOR137c
CA0509	1.2	1.1	0.7	0.6	0.5	0.6	CDC24	orf19.3174	GTP/GDP exchange factor for Cdc42p (by homology)	YAL041w
CA0578	0.9	0.9	0.6	0.7	1.2	0.6	IPF9605	orf19.3071	similar to Saccharomyces cerevisiae Mih1p M-phase inducin	YMR036c
CA3518	1.1	1.0	0.9	0.6	0.9	0.6	AMYG2.5f	orf19.999	glucoamylase, 5-prime end	YBR229c
CA2600	1.1	0.4	0.9	0.6	0.8	0.6	IPF11177	orf19.51	similar to Saccharomyces cerevisiae Clu1p translation initiati	YMR012w

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[[Cd XS+ down 0.667 10FDR] and [Cd HS+ down 0.667 10FDR]] less [Cd OS+ do...

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
CA1782	0.2	0.1	0.9	1.0	0.5	0.2	PHO84.3e	orf19.1172	Inorganic phosphate transport protein, 3-prime end (by homo	YML123c

CA0083	0.3	0.1	1.0	1.1	0.6	0.2	PHO84.5e	orf19.655	high-affinity inorganic phosphate/H+ symporter by homology	YML123c
CA2986	0.7	0.5	0.7	0.9	0.2	0.3	CDC5	orf19.6010	Cell-cycle protein kinase (by homology)	YMR001c
CA0689	0.5	0.3	1.5	1.4	0.3	0.3	IPF14119	orf19.4688	unknown function	no match
CA2024	0.5	0.5	0.9	1.0	0.7	0.3	PGA35	orf19.4910	unknown function	no match
CA2348	0.7	0.6	0.5	0.6	0.2	0.3	IPF12811	orf19.3751	putative serine/threonine kinase	YOR233w
CA2176	1.2	0.6	1.3	0.8	0.2	0.3	CDC54	orf19.3761	cell division control protein (by homology)	YPR019w
CA5923	0.7	0.4	1.1	0.7	0.7	0.3	IFQ2	orf19.6782	Unknown function	no match
CA6061	0.6	0.6	2.3	1.2	0.4	0.4	IPF8302	orf19.6007	unknown function	YJL196c
CA3883	0.5	0.2	1.0	1.3	0.2	0.4	GCV2	orf19.385	Glycine decarboxylase P subunit	YMR189w
CA0697	0.5	0.7	0.5	0.9	0.7	0.4	VTC4	orf19.3363	putative polyphosphate synthetase (by homology)	YJL012c
CA3604	0.5	0.6	2.1	1.8	0.3	0.4	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)	no match
CA0357	0.4	0.6	0.5	0.9	0.8	0.4	FCY22	orf19.333	purine-cytosine permease (by homology)	YER060w
CA0642	0.4	0.3	1.3	1.4	0.4	0.4	ERG25	orf19.3732	C-4 sterol methyl oxidase	YGR060w
CA4263	0.4	0.2	1.1	0.9	0.5	0.4	IPF2277	orf19.6656	unknown function	YHL016c
CA0875	0.3	0.4	1.0	1.0	0.7	0.5	ERG251	orf19.4631	C-4 sterol methyl oxidase (by homology)	YGR060w
CA4373	0.8	0.6	0.7	1.0	0.3	0.5	IPF5287	orf19.5664	signal transduction protein (by homology)	YMR032w
CA2597	0.4	0.3	0.8	0.7	1.0	0.5	IFQ3	orf19.54	unknown function	no match
CA2117	0.9	0.4	0.7	1.2	0.9	0.5	SNG3	orf19.1333	Drug transporter (by homology)	YGR197c
CA1688	0.7	0.6	0.3	0.6	0.8	0.5	COX15	orf19.3656	cytochrome oxidase assembly factor (by homology)	YER141w
CA5645	0.7	0.3	1.0	1.0	0.3	0.5	CYB5	orf19.7049	Cytochrome b5 (by homology)	YNL111c
CA0380	0.3	0.3	0.8	1.1	0.6	0.5	PGA45	orf19.2451	unknown function	no match
CA3003	0.7	0.4	0.6	0.9	0.5	0.5	IPF15741.	orf19.6242	similar to Saccharomyces cerevisiae Cyk3p possibly involved	YCR088w
CA2821	0.7	0.4	0.7	0.9	0.4	0.5				
CA5344	0.3	0.4	0.6	2.3	0.3	0.5	PRY2	orf19.7218	putative pathogen related proteins (by homology)	YJL079c
CA1956	0.5	0.6	0.9	0.8	0.4	0.5	ERG3	orf19.767	C5,6 desaturase	YLR056w
CA4553	0.5	0.7	0.5	0.7	0.4	0.6	CYB1	orf19.1446	G2/Mitotic-specific cyclin	YPR119w
CA4857	1.6	0.4	0.8	1.0	0.8	0.6	PHR1	orf19.3829	GPI-anchored pH responsive glycosyl transferase	YMR307w
CA5091	0.4	0.4	0.5	0.7	0.2	0.6	ENG1	orf19.3066	endo-1,3-beta-glucanase	YNR067c
CA5666	0.5	0.6	0.8	1.0	0.5	0.6	PUB1	orf19.7368	Major polyadenylated RNA-binding protein (by homology)	YNL016w
CA5236	0.8	0.5	0.8	0.7	0.4	0.6	LCB2	orf19.5027	Palmitoyl transferase (by homology)	YDR062w
CA3619	0.7	0.6	1.1	0.9	0.4	0.6	CDC47	orf19.202	cell division control protein, ,(by homology)	YBR202w
CA2032	1.0	0.7	1.7	0.8	0.5	0.6	IPF13112	orf19.3466	unknown function	YGL136c
CA1619	0.7	0.6	1.6	1.5	0.6	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)	YPL057c
CA3765	1.1	0.4	0.8	1.0	0.7	0.6	IPF18298.	orf19.2904	unknown function, 5-prime end	YNL106c
CA2862	0.3	0.5	0.8	0.9	0.2	0.6	HHF21	orf19.1059	histone H4	YNL030w
CA3372	0.3	0.5	1.0	0.9	0.4	0.6	HHF22	orf19.1854	histone H4 (by homology)	YNL030w
CA4800	0.4	0.6	0.7	0.9	0.5	0.6	PGA4	orf19.4035	putative GPI-anchhored protein related to Phr1, Phr2 and Phi	YOL030w
CA4745	0.5	0.6	0.6	1.0	0.8	0.6	URA1	orf19.4836	dihydroorotate dehydrogenase	no match

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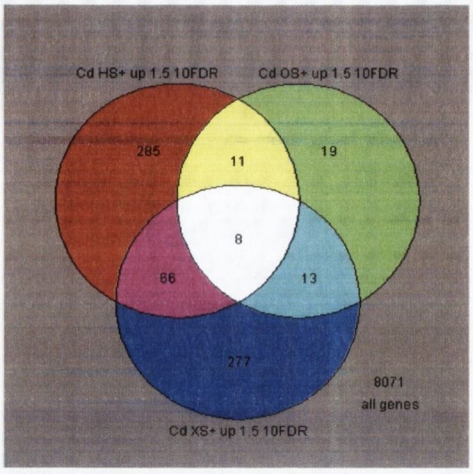
[[Cd OS+ down 0.667 10FDR] and [Cd XS+ down 0.667 10FDR]] and [Cd HS+ dow...

HS+ OS+ XS+										
Species (Stress ()* Systemat	**Ca HS+ Norn**	**Cd HS+ Norn**	**Ca OS+ Norn**	**Cd OS+ Norn**	**Ca XS+ Norn**	**Cd XS+ Norn**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA5953	0.7	0.6	1.0	0.4	0.4	0.3	IPF3506	orf19.6741	unknown function	YLR414c
CA3599	1.1	0.6	0.7	0.6	0.4	0.4	IPF19785	orf19.4929	unknown function	YLR067c
CA3878	0.2	0.3	0.5	0.6	0.5	0.5	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA polymerase	YDR213w
CA0659	0.6	0.7	0.8	0.6	0.4	0.4	IPF16189.	orf19.5576	panthotenate kinase, 3-prime end (by homology)	YDR531w
CA2969	0.4	0.2	0.4	0.6	0.6	0.5	IPF19772	orf19.5602	unknown function	no match



40A

[Cd HS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA4684	3.0	10.5	1.1	1.0	2.2	1.5	HSP78.5f	orf19.882	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)	no match (e-value > 0.05)
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function	no match (e-value > 0.05)
CA4437	2.5	7.3	0.7	1.3	1.2	1.2	IPF13867	orf19.5158	unknown function	YGL145w
CA1075	1.5	7.0	0.8	0.8	0.8	0.7	IPF4991	orf19.2531	putative membrane protein	YDL058w
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA4683	10.3	6.7	1.1	1.1	2.3	1.5	HSP78.3f	orf19.884	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)	YCR098c
CA0785	2.2	5.9	0.9	1.1	1.2	1.1	IPF14603	orf19.3929	unknown function	YJR100c
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)	YGL009c
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)	YLR216c
CA3078	2.5	5.4	0.8	1.3	1.2	1.1	IPF19970	orf19.4816	unknown function	YMR209c
CA1239	4.7	5.2	1.2	1.1	0.7	0.9	HSP60	orf19.717	Heat Shock Protein 60 (HSP60)	YLR259c
CA2513	1.0	5.2	1.6	1.5	0.7	1.1	SNG1	orf19.308	Involved in nitroguanidine resistance (by homology)	YGR197c
CA4120	1.4	4.8	1.0	1.1	1.2	1.5	SOD1	orf19.2770.1	Cu,Zn-superoxide dismutase	YJR104c
CA4959	3.4	4.8	1.3	1.2	1.0	1.0	HSP90	orf19.6515	heat shock protein	YMR186w
CA5536	2.0	4.4	0.9	1.0	1.1	1.2	IPF2837	orf19.7297	putative cystathionine gamma-synthase (by homology)	YHR112c
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)	YJR107w
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function	YMR002w
CA0551	2.5	4.0	1.4	1.3	1.3	1.0	CDC37	orf19.5531	Cell division control protein (by homology)	YDR168w
CA5341	2.5	3.9	0.9	0.8	1.0	0.9	HSP10	orf19.7215.3	10 kDa mitochondrial heat shock chaperonin (by homology)	YOR020c
CA4021	1.5	3.8	0.7	1.6	1.1	1.1	EBP2	orf19.3442	NADPH dehydrogenase (by homology)	YHR179w
CA5558	1.5	3.8	1.1	1.4	1.3	1.2	IPF1969	orf19.7322	unknown function	YPL225w
CA1180	1.7	3.7	1.1	0.9	0.8	1.4	UGA12.3f	orf19.803	4-aminobutyrate aminotransferase (GABA transaminase), 3-p	YGR019w
CA2130	1.4	3.6	1.2	1.0	1.2	1.1	RPS27A	orf19.413.1	ribosomal protein S27.e (by homology)	YKL156w
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function	YNL111c
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)	YPL088w
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease	YHL036w
CA4609	0.9	3.6	1.2	1.3	1.5	1.2	ZPR1	orf19.3300	Zinc finger protein (by homology)	YGR211w
CA3796	1.9	3.5	1.2	1.2	0.9	0.9	SGT2	orf19.5823	small glutamine-rich tetratricopeptide repeat containing prote	YOR007c
CA1230	2.1	3.5	1.5	1.6	0.9	0.9	SSA4	orf19.4980	cahsp70 mRNA for heat shock	YER103w
CA1181	1.9	3.5	0.9	0.8	0.8	1.4	UGA12.5f	orf19.802	4-aminobutyrate aminotransferase (GABA transaminase), 5-p	YGR019w
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homology)	YMR302c
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function	YML041c
CA0706	1.7	3.4	1.1	1.5	0.9	1.0	IPF7715.3	orf19.682	unknown function	YJL078c
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA1330	1.0	3.4	1.0	1.6	1.0	1.0	IPF11713.	orf19.1151	unknown function, 3-prime end	no match (e-value > 0.05)
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA2729	0.9	3.2	1.0	1.1	0.9	0.7	NAT2	orf19.2116	N-acetyltransferase for N-terminal methionine (by homology)	YGR147c
CA4856	3.1	3.2	0.9	1.1	1.1	0.9	IPF15950	orf19.3827	unknown function	YKR087c
CA3099	2.2	3.2	1.0	1.4	1.4	1.3	LST8	orf19.3862	required for transport of permeases from the golgi to the plas	YNL006w
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function	YBR101c
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)	YKL188c
CA0117	1.5	3.1	1.1	1.1	0.9	1.1	IPF19231	orf19.916	unknown function	YNL305c
CA1287	1.8	3.1	1.1	1.2	1.2	1.2	IPF5545	orf19.4430	unknown function	YDR330w
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholesterc	YNR008w
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function	YHR067w
CA4380	0.7	2.9	0.8	1.1	1.1	2.1	IPF12736	orf19.5673	unknown function	YPR194c
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase	no match (e-value > 0.05)
CA0219	1.6	2.9	1.1	1.2	1.2	0.9	YAP3	orf19.3193	transcription factor of a fungal-specific family of bzip proteins	YHL009c
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function	YBR042c
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)	YOR157c
CA0740	1.2	2.8	1.0	1.0	1.3	1.5	UMP1	orf19.3140.1	proteasome maturtion factor (by homology)	YBR173c
CA0915	3.0	2.8	1.1	1.0	1.0	0.7	KAR2	orf19.2013	dnaK-type molecular chaperone (by homology)	YJL034w
CA5060	1.5	2.8	0.9	1.0	1.2	1.2	IPF3690	orf19.3029	unknown function	YDR036c
CA4643	2.2	2.7	1.1	1.2	1.3	1.0	PRE9	orf19.350	20S proteasome subunit Y13 (alpha3) (by homology)	YGR135w
CA3034	2.3	2.7	0.8	0.9	1.4	1.3	RPN12	orf19.213	26S proteasome regulatory subunit (by homology)	YFR052w
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA0417	2.3	2.7	0.9	1.0	1.4	1.2	UBC13	orf19.933	E2 ubiquitin-conjugating enzyme (by homology)	YDR092w
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)	YDR069c
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)	YJL001w
CA2131	1.4	2.6	0.9	1.0	1.0	1.1	IDP1	orf19.5211	isocitrate dehydrogenase, cytosolic (by homology)	YDL066w

CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA1759	1.5	2.6	1.3	0.9	1.0	1.0	IPF14744	orf19.5125	unknown function	YLR149c
CA5049	1.5	2.5	1.0	1.1	0.9	0.9	CDC12	orf19.3013	septin (by homology)	YHR107c
CA4319	1.9	2.5	1.1	1.2	1.1	0.9	RPN10	orf19.4102	Protein degradation (by homology)	YHR200w
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA0155	1.9	2.5	1.2	1.0	1.4	1.2	RPT6	orf19.3593	26S proteasome regulatory subunit (by homology)	YGL048c
CA5040	1.4	2.5	0.8	0.8	0.9	0.9	BAT22	orf19.6994	branched chain amino acid aminotransferase (by homology)	YJR148w
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex	YDL143w
CA4924	2.0	2.5	1.2	1.2	1.4	1.0	UBP6.3f	orf19.6063	Ubiquitin-specific protease, 3-prime end (by homology)	YFR010w
CA6091	1.6	2.5	0.8	0.7	0.8	0.8	UFD2	orf19.5965	Ubiquitin fusion degradation protein 2 (by homology)	YDL190c
CA2698	1.2	2.5	1.1	0.8	0.9	1.0	SUL1	orf19.2738	High-affinity sulfate transport protein (by homology)	YLR092w
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA2296	1.3	2.5	0.8	1.0	1.1	1.0	SCL1	orf19.5378	Proteasome subunit YC7alpha (by homology)	YGL011c
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA4525	1.2	2.5	1.0	1.1	1.1	1.2	SEC22	orf19.479.2	synaptobrevin-type protein transport protein (by homology)	YLR268w
CA4168	1.8	2.4	1.1	1.2	1.0	1.1	IPF7781	orf19.2965	putative pump-driving ATPase	YDL100c
CA1285	1.0	2.4	1.1	1.3	1.1	1.0	SKP1	orf19.4427	kinetochore protein complex CBF3 by homology	YDR328c
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA0265	1.6	2.4	1.3	1.0	1.0	1.0	STI1.3f	orf19.3191	stress-induced protein (by homology)	YOR027w
CA5087	1.0	2.4	1.1	0.9	0.7	0.9	IPF20025	orf19.3062	unknown function	YKL033w
CA5528	1.9	2.4	1.2	1.3	1.2	1.1	RPN7	orf19.7286	Subunit of the regulatory particle of the proteasome (by homc	YPR108w
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA5435	1.6	2.4	0.7	0.7	0.9	0.9	UFD4	orf19.3237	ubiquitin fusion degradation protein (by homology)	YKL010c
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end	YKR076w
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase	YLR377c
CA2857	2.1	2.3	1.2	1.2	1.0	1.0	SSA1	orf19.1065	Heat shock protein of HSP70 family	YER103w
CA5173	0.9	2.3	0.8	1.1	0.8	1.0	CPS2.3f	orf19.4610.1	Carboxypeptidase YSCS precursor, 3-prime end (by homolo	YJL172w
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function	YDR430c
CA5791	1.5	2.3	1.2	1.0	1.4	1.2	RPT2	orf19.5440	26S proteasome regulatory subunit (by homology)	YDL007w
CA4772	1.8	2.3	1.3	1.1	1.1	1.1	CCT3	orf19.4004	Chaperonin (by homology)	YJL014w
CA1653	2.8	2.3	1.3	1.4	1.0	0.7	STE23	orf19.5561	protease involved in a-factor processing by homology	YLR389c
CA2121	1.3	2.3	0.9	0.9	1.1	1.2	IPF7930	orf19.1338	unknown function	YJL123c
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)	YER021w
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function	YGL145w
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)	YBR058c
CA5618	1.4	2.2	1.0	1.0	1.0	1.1	LEU2	orf19.7080	isopropyl malate dehydrogenase	YCL018w
CA5303	1.2	2.2	1.1	1.2	1.5	0.8	IPF2180	orf19.7170	unknown function	no match
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function	YPL110c
CA4257	1.2	2.2	1.0	0.9	1.3	1.1	PRE6	orf19.544.1	20S proteasome subunit	YOL038w
CA3706	0.9	2.2	0.7	0.8	1.1	1.0	PSA2	orf19.4943	mannose-1-phosphate guanyltransferase by homology	YDL055c
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA2565	1.6	2.2	1.1	1.0	0.9	1.3	MET15	orf19.5645	O-acetylhomoserine O-acetylserine sulphydrylase	YLR303w
B10012	1.5	2.2	2.0	1.2	1.1	1.0				
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA5308	1.5	2.2	1.0	0.9	1.3	1.1	PRE5	orf19.7178	20S proteasome subunit alpha6 (by homology)	YMR314w
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA1508	2.1	2.2	0.7	1.0	0.7	0.9	IPF9977	orf19.4525	unknown function	YLR064w
CA1629	0.6	2.2	1.2	1.5	1.4	1.3	NPI46	orf19.1030	proline cis-trans isomerase (by homology)	YLR449w
CA2951	1.3	2.1	0.8	1.0	0.9	1.0	SBP1	orf19.5854	RNA binding protein-like (by homology)	YHL034c
CA4865	1.5	2.1	1.0	1.0	1.1	1.2	IPF4085	orf19.3841	similar to Saccharomyces cerevisiae Apg1p essential for aut	YGL180w
CA4604	1.2	2.1	1.3	1.3	1.2	0.9	MBF1	orf19.3294	Multiprotein bridging factor mediates GCN4-dependent trans	YOR298ca
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function	YGR101w
CA1116	1.3	2.1	1.1	1.3	0.9	1.0	CCT5	orf19.2288	T-complex protein 1, epsilon subunit (by homology)	YJR064w
CA0914	1.6	2.1	0.9	1.0	1.2	1.1	SRA1	orf19.2015	cAMP dependent protein kinase, regulatory subunit (by homc	YIL033c
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA4167	0.6	2.1	0.8	1.0	0.9	1.1	IPF7778	orf19.2966	putative carboxymethylenebutenolidase (dienelactone hydrol	YDL086w
CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)	YIL095w
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5717	1.0	2.1	0.9	1.1	0.8	1.1	CYP51	orf19.7421	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by	YDR304c
CA1256	2.2	2.0	1.0	1.1	0.7	1.1	UBP15	orf19.1777	ubiquitin-specific protease (by homology)	YMR304w
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA1894	2.2	2.0	1.0	1.1	1.2	1.0	PRE7.5f	orf19.2755	putative subunit of 20S proteasome, exon 1 (by homology)	YBL041w
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA1911	1.1	2.0	1.1	0.9	1.0	1.0	SSE1	orf19.2435	heat shock protein of HSP70 family (by homology)	YPL106c
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA5977	1.2	2.0	1.2	1.0	1.3	1.2	UBC4	orf19.7571	E2 ubiquitin-conjugating enzyme (by homology)	YBR082c
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)	YMR234w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)	YHR104w
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle	YLR178c
CA0663	2.1	1.9	0.9	0.9	1.0	1.1	PUP2	orf19.709	20S proteasome subunit(alpha5) (by homology)	YGR253c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA4988	1.4	1.9	1.0	0.9	0.9	0.8	RPN2	orf19.5260	Proteasome regulatory subunit (by homology)	YIL075c
CA1880	1.7	1.9	1.2	1.3	1.4	1.0	IPF13316	orf19.2269	unknown function	YNL010w
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homo	YPR183w
CA5862	1.0	1.9	1.2	1.3	1.1	1.1	POT11	orf19.7520	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)	YIL160c
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function	YKL094w
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA4522	1.2	1.9	1.0	0.9	1.1	1.0	RPT4	orf19.482	26S proteasome regulatory subunit (by homology)	YOR259c
CA4389	1.6	1.9	1.2	1.0	1.2	1.2	RPT5	orf19.3123	26S proteasome regulatory subunit (by homology)	YOR117w
CA5268	1.8	1.9	1.1	1.1	0.7	0.9	SEC18.3f	orf19.4994	vesicular fusion protein, 3-prime end (by homology)	YBR080c
CA3868	1.3	1.9	1.1	1.1	0.8	1.0	CCT1	orf19.401	component of chaperonin-containing T-complex (by homolog	YDR212w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA0394	1.6	1.9	1.0	1.3	1.4	1.4	IPF12758.	orf19.334	unknown function, 5-prime end	no match (e-value > 0.05)
CA3247	1.2	1.9	1.1	1.0	0.7	0.8	IPF15832	orf19.4676	unknown function	YKL053ca
CA4695	1.2	1.9	0.9	1.4	1.3	1.0	IPF4229	orf19.6923	unknown function	YML015c
CA3898	1.3	1.9	1.1	0.9	0.8	1.0	UBA2	orf19.5074	ubiquitin-activating -like enzyme by homology	YDR390c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function	YDL012c

CA0661	1.9	1.9	0.7	0.9	1.0	1.0	APG7	orf19.707	component of the autophagic system (by homology)	YHR171w
CA2120	1.6	1.9	0.9	1.0	1.2	1.2	PUP3	orf19.1336	PRCT yeast proteasome component (by homology)	YER094c
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA5554	1.0	1.9	0.7	1.0	0.9	1.0	IPF1960.5	orf19.7318	putative transcriptional activator, 5-prime end	YCR106w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match (e-value > 0.05)
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA3422	1.6	1.9	0.9	0.8	0.7	0.9	IPF17289	orf19.6134	unknown function	YLR440c
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match (e-value > 0.05)
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA1755	1.6	1.8	1.1	0.9	0.8	1.1	PDI1	orf19.5130	protein disulfide-isomerase precursor (by homology)	YCL043c
CA0408	1.9	1.8	0.9	1.0	0.9	1.0	SAC6.5f	orf19.5544	actin filament bundling protein, fimbrin, 5-prime end (by homc	YDR129c
CA1389	1.5	1.8	1.4	1.3	0.8	1.1	PLP2	orf19.1769	Might regulate Ste4p in pheromone response (by homology)	YOR281c
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA3191	1.5	1.8	0.7	1.0	0.7	0.8	IPF11601	orf19.2151	unknown function	YOR165w
CA5930	2.3	1.8	1.1	0.9	1.1	1.0	ECM29.3f	orf19.6773	Involved in cell wall biogenesis and architecture, 3-prime end	YHL030w
CA1693	1.6	1.8	1.0	1.0	1.0	1.1	IPF17054	orf19.5037	unknown function	no match (e-value > 0.05)
CA2286	0.9	1.8	0.8	1.1	1.4	1.4	IPF5369	orf19.5553	unknown function	YKL069w
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA0164	1.0	1.8	1.0	1.0	0.9	1.0	IPF11694	orf19.4335	similar to Saccharomyces cerevisiae Tna1p high affinity nicot	YGR260w
CA2278	1.8	1.8	1.2	1.0	1.2	1.2	IPF10806	orf19.782	unknown function	YBR204c
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA5836	1.1	1.8	0.8	1.1	1.2	0.7	IPF428	orf19.7490	transport protein (by homology)	YOL137w
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA3435	1.0	1.8	0.9	1.4	1.3	1.2	IPF6391	orf19.583	indoleamine 2,3-dioxygenase (by homology)	YJR078w
CA2669	1.2	1.8	0.8	0.9	1.0	1.0				
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA1269	1.6	1.7	1.1	1.1	1.1	1.4	IPF19726	orf19.3158	unknown function	YDL001w
CA4798	1.4	1.7	0.9	1.0	0.9	0.9	RPN5.3f	orf19.4032	subunit of the regulatory particle of the proteasome, 3-prime (	YDL147w
CA2146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function	no match (e-value > 0.05)
CA0345	1.2	1.7	1.0	1.0	1.0	0.9	ACH1	orf19.3171	acetyl-coenzyme-A hydrolase (by homology)	YBL015w
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA5146	1.2	1.7	0.9	1.0	1.0	1.0	YMC2	orf19.4583	Carnitine/acylcarnitine translocase (by homology)	YBR104w
CA2785	0.6	1.7	0.6	0.9	0.9	1.0	MET13	orf19.288	Methylene tetrahydrofolate reductase (by homology)	YGL125w
CA0840	1.1	1.7	1.4	1.0	1.3	1.0				
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in aceti	YCR032w
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA3697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific	YJR099w
CA4480	0.9	1.7	0.7	1.1	1.5	1.4	IPF6464	orf19.1887	putative triacylglycerol lipase (by homology)	YLL012w
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA4219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein pho	YKL193c
CA5555	0.9	1.7	1.0	1.0	1.3	1.1	SUC1	orf19.7319	Putative zinc finger protein Suc1	YFL052w
CA5196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function	YIL001w
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA5695	1.3	1.7	0.9	0.8	0.7	1.1	IPF3310	orf19.7397	unknown function	YPR022c
CA5283	0.9	1.7	0.8	1.0	0.8	1.2	IPF1912	orf19.7140	putative catechol o-methyltransferase	no match (e-value > 0.05)
CA2508	1.9	1.7	1.4	1.1	0.9	1.0	BET5	orf19.302	targeting and fusion of ER to Golgi transport vesicles (by hon	YML077w
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA4165	1.0	1.7	1.0	1.1	1.0	1.0	IPF7774	orf19.2968	unknown function	no match (e-value > 0.05)
CA4890	1.5	1.7	1.0	0.9	1.0	1.1	PRE10	orf19.6582	20S proteasome subunit C1 (by homology)	YOR362c
CA5941	1.5	1.7	1.0	1.3	1.4	0.9	IPF3486	orf19.6756	unknown function	YGL198w
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA4142	1.5	1.7	1.0	1.0	1.5	1.2	PRE4	orf19.4230	20S proteasome subunit(beta7) (by homology)	YFR050c
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA5559	1.0	1.7	1.2	1.1	0.8	1.1	CBP1	orf19.7323	Corticosteroid binding protein	YMR020w
CA3870	1.0	1.7	0.6	0.9	1.3	1.0	YPK1	orf19.399	ser/thr-specific protein kinase (by homology)	YMR104c
CA5306	1.2	1.7	1.0	1.0	1.1	1.1	NPT1	orf19.7176	Nicotinate phosphoribosyltransferase (by homology)	YOR209c
CA2548	1.6	1.7	1.0	0.9	0.9	0.9	PGA34	orf19.2833	unknown function	no match
CA0972	1.1	1.6	1.1	1.2	1.0	1.0	CYP1	orf19.6472	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homc	YDR155c
CA1252	1.9	1.6	0.9	0.9	0.9	0.9	RPN1	orf19.4956	26S proteasome regulatory subunit (by homology)	YHR027c
CA4333	1.2	1.6	1.2	1.1	1.4	1.2	IPF2083	orf19.4086	unknown function	YNL056w
CA1942	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eo	orf19.4191.1	Ubiquitin--protein ligase, 3-prime end (by homology) FALSOF	YGL141w
CA4799	1.6	1.6	1.1	1.0	0.8	1.0	RPN5.5f	orf19.4034	subunit of the regulatory particle of the proteasome, 5-prime (	YDL147w
CA3956	1.2	1.6	1.0	1.0	1.0	1.2	IPF6712.3	orf19.1414.2	unknown function, 3-prime end | Unknown function	no match
CA4127	0.9	1.6	0.7	0.9	0.9	0.9	IPF6629	orf19.2762	unknown function	YLR109w
CA3310	1.4	1.6	1.1	1.2	0.7	1.0	PFS2	orf19.2307	Polyadenylation Factor I subunit (by homology)	YNL317w
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA3746	1.2	1.6	1.6	1.0	0.8	1.1	ARA1	orf19.2172	D-arabinose dehydrogenase (by homology)	YBR149w
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA2888	1.6	1.6	1.0	1.1	1.2	1.2	GIM5	orf19.2471	Gim complex component (by homology)	YML094w
CA2773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase	YOR211c
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c
CA3569	1.3	1.6	1.0	1.1	1.0	1.1	IPF3268	orf19.3136	unknown function	YDR325w
CA2157	2.2	1.6	1.5	1.1	0.8	0.8	IPF8537	orf19.5300	similar to Saccharomyces cerevisiae Cne1p calnexin, involve	YAL058w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match (e-value > 0.05)
CA4320	1.1	1.6	1.2	1.1	0.8	1.1	ECM17	orf19.4099	Putative sulfite reductase (by homology)	YJR137c
CA2561	1.0	1.6	1.2	1.5	0.8	0.9	CAR2	orf19.5641	ornithine aminotransferase (by homology)	YLR438w
CA5564	1.2	1.6	0.7	0.9	1.0	0.9	IPF1980	orf19.7328	unknown function	no match (e-value > 0.05)
CA1452	1.6	1.6	0.8	0.8	1.3	1.0	REV1	orf19.4412	DNA repair protein (by homology)	YOR346w
CA1756	1.0	1.6	1.1	1.2	1.5	1.0	IPF14562	orf19.5129	unknown function	no match (e-value > 0.05)
CA1913	1.4	1.6	0.9	0.9	1.2	1.2	ARC35	orf19.2437	subunit of the Arp2/3 complex involved in the control of actin	YNR035c
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match (e-value > 0.05)
CA2863	1.3	1.6	1.0	1.0	1.3	1.1	IPF20117	orf19.1058	unknown function	YLR421c
CA0593	1.3	1.6	1.0	0.8	1.2	1.2	ARP6	orf19.4904	actin-related protein (by homology)	YLR085c
CA1838	1.3	1.6	1.1	1.1	1.4	1.3	IPF5777	orf19.3963	unknown function	YER182w
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA2926	1.1	1.6	0.8	1.1	1.3	1.3	UBA3	orf19.4209	Ubiquitin-like protein activating enzyme	YPR066w
CA5595	1.1	1.6	0.9	1.0	0.9	1.4	IPF568	orf19.7105	similar to Saccharomyces cerevisiae Far1p cyclin-dependent	YJL157c
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c

CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal ass	YKL197c
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA2867	1.2	1.5	0.9	0.8	0.8	0.8	IPF11688	orf19.2844	similar to Saccharomyces cerevisiae Apl4p AP-1 complex su	YPR029c
CA3336	1.0	1.5	0.8	0.8	1.1	1.3	IPF19983	orf19.2335	unknown function	YHR113w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltr	YMR149w
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA2133	1.2	1.5	1.0	1.0	1.0	0.8	IPF5866	orf19.5213	unknown function	YDR228c
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA3907	1.2	1.5	0.7	1.0	1.0	0.9	IPF3304	orf19.4395	similar to Saccharomyces cerevisiae Aip1p actin cytoskeletor	YMR092c
CA3683	1.2	1.5	1.1	1.0	1.1	1.2	PPZ1	orf19.726	ser/thr phosphatase required for normal osmoregulation (by I	YML016c
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase	YFR015c
CA4625	1.1	1.5	0.8	0.9	0.9	1.2	IPF5742	orf19.3319	thioredoxin-like protein (by homology)	YGR209c
CA4720	1.2	1.5	1.0	1.0	1.3	1.0	ECM18	orf19.6958	Involved in cell wall biogenesis and architecture (by homolog	YDR125c
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA3057	1.3	1.5	1.0	1.2	1.5	1.2	IPF2954	orf19.4293	unknown function	YDR267c
CA3589	0.8	1.5	0.8	1.2	1.4	1.1	IPF10113	orf19.2249	unknown function	YNR020c

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[[Cd OS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10...

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA5797	1.2	0.9	2.7	3.2	0.7	1.0	IPF4182	orf19.5446	unknown function	no match (e-value > 0.05)
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)	YDR497c
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function	no match
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function	YLR205c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match (e-value > 0.05)
CA0721	1.5	0.9	1.3	2.3	0.8	0.8	IPF10429	orf19.2887	unknown function	YMR295c
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function	no match (e-value > 0.05)
CA5840	1.2	1.0	1.3	1.9	1.0	1.2	EBP6	orf19.7495	NADPH dehydrogenase (by homology)	YPL171c
CA0948	0.6	1.1	0.9	1.9	1.1	1.0	IPF10270	orf19.1272	unknown function	YGR111w
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match (e-value > 0.05)
CA0677	1.4	1.3	1.2	1.8	1.0	0.8	IPF13095	orf19.1182	unknown function	YGL212w
CA4870	1.5	1.1	1.3	1.7	1.2	1.3	IPF19568	orf19.6556	unknown function	no match (e-value > 0.05)
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA1187	0.7	0.9	1.2	1.5	1.1	1.0	QRI7	orf19.3787	putative glycoprotease (by homology)	YKR038c
CA2161	1.1	1.1	1.1	1.5	1.0	1.1	IPF11876	orf19.5295	unknown function	no match (e-value > 0.05)

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[[Cd XS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10...

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function	YDR371w
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function	no match (e-value > 0.05)
CA2435	1.1	1.7	1.2	1.1	17.7	13.8	IPF9483	orf19.3395	probable permease (by homology)	YHR048w
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function	YKL086w
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function	no match (e-value > 0.05)
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase	YBR046c
CA0639	1.6	1.8	1.0	1.0	9.0	10.5				
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match (e-value > 0.05)
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function	no match (e-value > 0.05)
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA4913	1.1	1.0	1.3	1.0	1.2	6.8	CIS2	orf19.6053	Gamma-glutamyltransferase (by homology)	YLR299w
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)	YBR293w
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function	YKR071c
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA4829	1.0	1.1	1.3	1.0	6.3	5.5	IPF1210	orf19.2067	similar to Saccharomyces cerevisiae Nfu1p involved in home	YKL040c
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)	YHR044c
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function	no match (e-value > 0.05)
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)	YPL171c
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)	YDR338c
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function	YOR292c
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)	YOR101w
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function	no match (e-value > 0.05)
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)	YDR513w
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match (e-value > 0.05)
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function	YOL119c
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)	YIL120w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homolog	YER053c
CA4399	1.4	1.7	1.2	1.3	1.1	3.8	PRA1	orf19.3111	pH-regulated antigen	YOL154w
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function	YGL136c
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match (e-value > 0.05)
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function	YNL144c
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function	YDR336w
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)	YNL229c
CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function	no match (e-value > 0.05)

CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match (e-value > 0.05)
CA1005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)	YPL101w
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match (e-value > 0.05)
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homolc	YJL101c
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA0583	1.2	2.5	1.3	1.3	3.9	3.2	GSH1.3f	orf19.5059	gamma-glutamylcysteine synthetase, 3 prime end (by homolc	YJL101c
CA0996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)	no match (e-value > 0.05)
CA0933	1.3	1.1	0.8	1.0	5.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)	YMR301c
CA1775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology	YDL215c
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA0385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function	YNL250w
CA5697	1.3	1.0	0.8	1.1	3.8	3.0				
CA1170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function	YDR132c
CA4392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)	YNL229c
CA1016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function	YOR273c
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA5868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function	YMR090w
CA0595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5	orf19.4901	unknown function, 5-prime end	YER175c
CA1157	1.2	1.0	1.4	1.1	0.8	2.8	PZF1	orf19.4125	TFIIIA (transcription initiation factor) (by homology)	YPR186c
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA3258	1.1	1.0	0.5	0.9	1.1	2.7				
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)	YPR194c
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA4885	1.2	1.3	1.2	1.1	1.1	2.6	IPF1636	orf19.6577	similar to Saccharomyces cerevisiae Tpo1p multidrug resista	YLL028w
CA4662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by hom	YMR038c
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA3919	1.1	1.0	0.8	0.8	1.0	2.5	IFC5	orf19.5121	unknown function	YPR194c
CA2227	1.5	1.2	1.0	0.9	1.4	2.5	EBP7	orf19.5816	NADPH DEHYDROGENASE by homology	YHR179w
CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA2894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function	no match (e-value > 0.05)
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA5289	0.7	0.9	0.9	0.9	1.4	2.4	NRG1	orf19.7150	similar to transcriptional repressor Nrg1p/Nrg2p	YBR066c
CA0942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function	YER101c
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA1372	0.9	1.0	1.2	1.0	1.1	2.4	IPF15844	orf19.4961	similar to Saccharomyces cerevisiae Stp2p involved in pre-tF	YHR006w
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA4929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA1108	1.1	1.1	1.0	1.0	1.0	2.3	IPF11273	orf19.5231	unknown function	no match (e-value > 0.05)
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match (e-value > 0.05)
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (a	YPR192w
CA1536	1.6	1.6	1.1	1.3	1.3	2.2	SOK1	orf19.451	high copy suppressor of a cyclic AMP-dependent protein kina	YDR006c
CA2177	1.1	1.1	1.3	1.0	2.2	2.2	ROD1	orf19.1509	O-dinitrobenzene,calcium and zinc resistance protein (by hor	YFR022w
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA0129	1.1	0.9	1.0	1.0	1.2	2.2	IPF10495	orf19.246	unknown function	YIL108w
CA2711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)	YDR460w
CA5011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function	YMR101c
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA3354	1.1	1.1	0.7	0.7	1.2	2.2	GPR1	orf19.1944	similar to Saccharomyces cerevisiae Gpr1p G-protein couple	YDL035c
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA0560	1.2	1.0	0.9	1.0	1.2	2.1	GPX3	orf19.87	glutathione peroxidase (by homology)	YIR037w
CA4630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c
3692.2	1.2	1.2	0.8	0.9	2.2	2.1				
6532.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA5009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)	YKL119c
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA4917	0.7	0.8	0.8	1.4	2.0	2.1	ECM31	orf19.6057	Involved in cell wall biogenesis and architecture (by homolog	YBR176w
CA2477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)	YJR061w
CA3094	1.1	1.1	1.1	0.7	1.3	2.1	IPF11548	orf19.3854	serine/threonine protein kinase (by homology)	YCR008w
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA5934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function	YHL029c
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA3087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)	YLR147c
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA0160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease	YKR039w
CA3446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function	YKL195w
CA4580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function	no match (e-value > 0.05)
CA4836	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)	YJR104c
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA0757	1.0	0.7	0.6	0.8	2.2	2.0				
CA1600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)	YHR175w
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA0500	0.9	1.0	1.4	1.2	0.9	2.0	IPF20058	orf19.4793	unknown function	YOR252w
CA2584	0.8	1.2	1.0	1.1	2.1	2.0	IPF9440	orf19.4373	similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase	YDR236c
CA5008	1.0	0.8	1.1	1.3	1.2	2.0	IPF12577	orf19.5238	unknown function	no match (e-value > 0.05)
CA5678	0.8	1.0	1.0	0.8	0.9	2.0	IPF1292	orf19.7381	unknown function Hypothetical zinc-finger protein	YML099c
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA5010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function	YMR101c

CA1002	1.0	1.0	1.9	1.2	0.9	1.9	ROK1.3f	orf19.3756	RNA helicase, 3-prime end	YGL171w
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (	YOL119c
CA4023	1.0	1.0	0.9	1.0	0.9	1.9	FRP5	orf19.3440	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function	YGR110w
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function	no match (e-value > 0.05)
CA0995	1.0	1.0	0.9	0.9	3.8	1.9				
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)	YGR234w
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function	no match (e-value > 0.05)
CA4778	1.0	1.1	0.9	1.0	1.2	1.8	IFJ1	orf19.4011	Unknown function	YGR263c
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA4174	1.2	3.6	1.3	1.6	1.6	1.8	IPF4430	orf19.2959.1	unknown function	YDR276c
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match (e-value > 0.05)
CA0052	1.0	1.1	1.4	1.0	1.3	1.8	IPF19567	orf19.475	Unknown function	YHR085w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)	YML004c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase	YOR202w
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)	YMR275c
CA3187	1.0	0.8	1.5	1.2	0.8	1.8	IPF17094	orf19.2143	unknown function	YPL183c
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4960	0.7	0.8	0.7	0.7	1.2	1.8	IPF3912	orf19.6514	unknown function	YPL177c
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function	YCL044c
CA1277	1.3	1.0	1.4	1.0	1.2	1.8	IPF10837	orf19.3630	unknown function	YDR083w
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA4477	0.9	1.2	1.2	1.1	1.2	1.8	IPF6459	orf19.1890	unknown function	YMR210w
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function	no match (e-value > 0.05)
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology	YAL012w
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match (e-value > 0.05)
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5	orf19.6654	unknown function	YMR221c
CA4612	1.1	0.9	1.4	1.0	1.5	1.7	PPM2	orf19.3303	carboxy methyl transferase; homolog of PPM1 (by homology)	YOL141w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match (e-value > 0.05)
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eo	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA5135	1.0	1.0	1.0	1.0	1.8	1.7	HSP104.5	orf19.6389	Heat shock protein, 5-prime end (by homology)	YLL026w
CA0629	1.1	1.3	0.7	0.8	1.0	1.7	IPF3876	orf19.775	unknown function	YJR126c
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)	YNL240c
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)	YPL140c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA2750	1.1	1.0	1.1	1.0	4.6	1.7	ATX1	orf19.2369.1	antioxidant protein and metal homeostasis factor (by homolo	YNL259c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA	YAL049c
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function	YNL166c
CA5287	0.8	1.0	1.0	0.9	1.0	1.7	IPF1922	orf19.7148	similar to multidrug resistance proteins	YLL028w
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function	YPL092w
CA5696	0.9	1.0	1.6	1.3	1.4	1.7	IPF3309.3	orf19.7398	unknown function, 3-prime end	YER126c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA4614	1.1	1.3	1.4	0.8	1.0	1.7	IPF7952	orf19.3305	unknown function	YDR213w
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA6009	0.8	1.0	1.3	1.0	1.2	1.7	IPF643	orf19.7610	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine p	YER075c
CA0626	1.1	0.9	1.3	1.1	1.4	1.7	IPF3161	orf19.3161	Unknown function	YNR054c
CA3157	0.9	1.4	1.0	1.3	1.5	1.7	IPF14456	orf19.1588	unknown function Unknown function	YBR269c
CA4563	1.0	1.0	1.0	1.1	0.8	1.7	IPF6566	orf19.6873.1	unknown function	YBL071wa
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase	YAL039c
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match (e-value > 0.05)
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function	YMR136w
CA5580	1.2	1.4	0.9	1.0	1.3	1.6	RVS161	orf19.7124	cytoskeletal binding protein (by homology)	YCR009c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA6038	0.8	1.2	1.8	1.2	1.1	1.6	LTV1	orf19.7650	low-temperature viability protein (by homology)	YKL143w
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)	YLR120c
CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function	YDR219c
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homolo	YOR049c
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function	no match
CA5739	1.0	1.1	0.9	1.0	1.4	1.6	IPF2884	orf19.7449	unknown function	YMR211w
CA0941	0.9	1.0	0.8	1.0	1.3	1.6	IPF8617	orf19.3705	unknown function	YCR079w
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match (e-value > 0.05)
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA5474	1.3	0.9	1.8	1.1	1.0	1.6	IPF16944.	orf19.3287	unknown function, 3-prime end	YMR014w
CA1958	1.0	1.0	0.9	0.9	1.2	1.6	IFE1	orf19.769	Unknown function	YAL061w
CA0393	1.4	1.1	1.0	1.1	1.7	1.6	IPF12758.	orf19.333.2	unknown function, 3-prime end	no match
CA2395	1.1	1.1	1.1	1.0	1.0	1.6	IPF6425	orf19.3536	unknown function	YOR320c
CA1540	0.9	0.9	1.2	1.5	0.9	1.6	IPF1047	orf19.4563	unknown function	YMR310c
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function	YHR087w
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA2460	1.5	1.1	1.0	1.0	1.1	1.6				
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA2233	1.0	1.0	1.0	1.0	1.1	1.6	IFJ3	orf19.3924	unknown function	YGR263c
CA6016	0.9	0.8	1.4	1.4	1.4	1.6	IPF630	orf19.7618	unknown function	YOR145c
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function	YLR021w
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3	orf19.4266.1	septin, 3-prime end (by homology)	YDR218c
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function	YHR101c
CA1703	0.9	1.2	0.8	1.0	1.4	1.6	IPF7987	orf19.703	unknown function	YGR247w
CA3808	0.8	1.1	1.5	1.2	1.1	1.6	FAL1	orf19.2488	ATP-dependent RNA helicase	YDR021w
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function	YJL092w

CA5875	1.2	1.1	0.9	1.0	0.8	1.6	IPF324.3f	orf19.7545	unknown function, , 3-prime end	no match (e-value > 0.05)
CA3741	0.9	0.9	0.9	1.0	0.7	1.6	MRS4	orf19.2178	RNA splicing protein and member of the mitochondrial carrier	YKR052c
CA1080	1.0	0.9	1.3	0.9	1.4	1.6	IPF14710	orf19.4820	unknown function	YKL162c
CA4158	0.9	0.9	0.9	0.9	0.7	1.6	DLD3	orf19.5805	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA3080	0.9	1.1	1.0	0.8	1.0	1.6	IPF14634	orf19.4153	APP-binding protein 1 (by homology)	YPL003w
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)	YOR171c
CA5833	0.9	0.9	1.2	1.1	1.2	1.5	IMP3	orf19.7488	U3 small nucleolar ribonucleoprotein (by homology)	YHR148w
CA4818	0.7	0.9	0.8	0.7	1.2	1.5	IPF1193	orf19.2079	unknown function Unknown function	YHL018w
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membra	YIL047c
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA2592	1.2	0.9	1.4	1.1	1.6	1.5	IPF18447	orf19.59	putative zinc-finger protein (by homology)	YBR267w
CA0473	1.0	1.0	1.0	1.0	1.3	1.5	GRP1	orf19.4781	dihydroflavonol-4-reductases (by homology)	YOL151w
CA3722	1.3	1.2	0.9	1.0	1.5	1.5	PHO13	orf19.4172	4-nitrophenylphosphatase (by homology)	YDL236w
CA4507	1.0	1.1	1.1	1.3	1.0	1.5	IPF20015	orf19.499	unknown function	YNL063w
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)	YPR016c
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rR	YDR087c
CA2398	1.1	1.0	1.0	1.0	1.1	1.5	IPF6431	orf19.3539	unknown function	YBR141c
CA0343	1.6	1.2	1.1	1.0	0.9	1.5	LYS1	orf19.1789.1	saccharopine dehydrogenase (by homology)	YIR034c
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function	no match (e-value > 0.05)
CA1689	1.0	1.0	0.9	1.1	1.1	1.5	IPF13030	orf19.3655	unknown function	no match (e-value > 0.05)
CA2428	1.0	1.1	0.9	0.9	1.3	1.5	IPF9894	orf19.3405	possible zinc-finger protein	no match (e-value > 0.05)
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function	no match (e-value > 0.05)
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha	YIL099w
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA4754	0.7	1.0	1.0	1.0	1.2	1.5	IPF11479	orf19.4825	unknown function	YIL098c
CA1630	1.4	1.2	1.5	1.1	1.1	1.5	RPP1	orf19.1029	required for processing of tRNA and 35S rRNA (by homology	YHR062c
CA5626	0.9	1.1	0.9	1.0	1.1	1.5	IPF498	orf19.7071	unknown function	YML123c
CA4613	1.0	1.0	1.3	1.1	1.3	1.5	IPF7950	orf19.3304	similar to Saccharomyces cerevisiae Rrp40p involved in ribos	YOL142w
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function	no match (e-value > 0.05)
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)	YEL060c
CA4404	1.0	1.3	1.4	1.1	1.2	1.5	MET16	orf19.3106	3 -phosphoadenylylsulfate reductase (by homology)	YPR167c
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
11759.2	0.6	1.2	0.2	0.3	1.4	1.5				
CA0730	0.9	0.7	1.2	1.1	1.6	1.5	IPF7334	orf19.3724	unknown function	YOR004w
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function	YPL122c
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SY	YOR005c
CA1314	1.5	1.5	0.8	1.0	6.6	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function	YNL191w

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[[Cd OS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase	YKR070w
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function	YMR226c
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w

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[Cd XS+ up 1.5 10FDR] and [Cd OS+ up 1.5 10FDR]] less [Cd HS+ up 1.5 10FDR]

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match (e-value > 0.05)
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA0472	0.3	0.3	14.5	5.3	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match (e-value > 0.05)
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function	no match (e-value > 0.05)
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c

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[Cd XS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10FDR]

HS+ OS+ XS+										
Species (	**Ca**	**Cd**	**Ca**	**Cd**	**Ca**	**Cd**				
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match (e-value > 0.05)
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homolo	YMR152w
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match (e-value > 0.05)
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match (e-value > 0.05)
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by h	YML130c
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match (e-value > 0.05)
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w

CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA1759	1.5	2.6	1.3	0.9	1.0	1.0	IPF14744	orf19.5125	unknown function	YLR149c
CA5049	1.5	2.5	1.0	1.1	0.9	0.9	CDC12	orf19.3013	septin (by homology)	YHR107c
CA4319	1.9	2.5	1.1	1.2	1.1	0.9	RPN10	orf19.4102	Protein degradation (by homology)	YHR200w
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA0155	1.9	2.5	1.2	1.0	1.4	1.2	RPT6	orf19.3593	26S proteasome regulatory subunit (by homology)	YGL048c
CA5040	1.4	2.5	0.8	0.8	0.9	0.9	BAT22	orf19.6994	branched chain amino acid aminotransferase (by homology)	YJR148w
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex	YDL143w
CA4924	2.0	2.5	1.2	1.2	1.4	1.0	UBP6.3f	orf19.6063	Ubiquitin-specific protease, 3-prime end (by homology)	YFR010w
CA6091	1.6	2.5	0.8	0.7	0.8	0.8	UFD2	orf19.5965	Ubiquitin fusion degradation protein 2 (by homology)	YDL190c
CA2698	1.2	2.5	1.1	0.8	0.9	1.0	SUL1	orf19.2738	High-affinity sulfate transport protein (by homology)	YLR092w
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA2296	1.3	2.5	0.8	1.0	1.1	1.0	SCL1	orf19.5378	Proteasome subunit YC7alpha (by homology)	YGL011c
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA4525	1.2	2.5	1.0	1.1	1.1	1.2	SEC22	orf19.479.2	synaptobrevin-type protein transport protein (by homology)	YLR268w
CA4168	1.8	2.4	1.1	1.2	1.0	1.1	IPF7781	orf19.2965	putative pump-driving ATPase	YDL100c
CA1285	1.0	2.4	1.1	1.3	1.1	1.0	SKP1	orf19.4427	kinetochore protein complex CBF3 by homology	YDR328c
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA0265	1.6	2.4	1.3	1.0	1.0	1.0	STI1.3f	orf19.3191	stress-induced protein (by homology)	YOR027w
CA5087	1.0	2.4	1.1	0.9	0.7	0.9	IPF20025	orf19.3062	unknown function	YKL033w
CA5528	1.9	2.4	1.2	1.3	1.2	1.1	RPN7	orf19.7286	Subunit of the regulatory particle of the proteasome (by homc	YPR108w
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA5435	1.6	2.4	0.7	0.7	0.9	0.9	UFD4	orf19.3237	ubiquitin fusion degradation protein (by homology)	YKL010c
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end	YKR076w
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase	YLR377c
CA2857	2.1	2.3	1.2	1.2	1.0	1.0	SSA1	orf19.1065	Heat shock protein of HSP70 family	YER103w
CA5173	0.9	2.3	0.8	1.1	0.8	1.0	CPS2.3f	orf19.4610.1	Carboxypeptidase YSCS precursor, 3-prime end (by homolo	YJL172w
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function	YDR430c
CA5791	1.5	2.3	1.2	1.0	1.4	1.2	RPT2	orf19.5440	26S proteasome regulatory subunit (by homology)	YDL007w
CA4772	1.8	2.3	1.3	1.1	1.1	1.1	CCT3	orf19.4004	Chaperonin (by homology)	YJL014w
CA1653	2.8	2.3	1.3	1.4	1.0	0.7	STE23	orf19.5561	protease involved in a-factor processing by homology	YLR389c
CA2121	1.3	2.3	0.9	0.9	1.1	1.2	IPF7930	orf19.1338	unknown function	YJL123c
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)	YER021w
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function	YGL145w
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)	YBR058c
CA5618	1.4	2.2	1.0	1.0	1.0	1.1	LEU2	orf19.7080	isopropyl malate dehydrogenase	YCL018w
CA5303	1.2	2.2	1.1	1.2	1.5	0.8	IPF2180	orf19.7170	unknown function	no match
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function	YPL110c
CA4257	1.2	2.2	1.0	0.9	1.3	1.1	PRE6	orf19.544.1	20S proteasome subunit	YOL038w
CA3706	0.9	2.2	0.7	0.8	1.1	1.0	PSA2	orf19.4943	mannose-1-phosphate guanyltransferase by homology	YDL055c
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA2565	1.6	2.2	1.1	1.0	0.9	1.3	MET15	orf19.5645	O-acetylhomoserine O-acetylserine sulphydrylase	YLR303w
6100.2	1.5	2.2	2.0	1.2	1.1	1.0				
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA5308	1.5	2.2	1.0	0.9	1.3	1.1	PRE5	orf19.7178	20S proteasome subunit alpha6 (by homology)	YMR314w
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA1508	2.1	2.2	0.7	1.0	0.7	0.9	IPF9977	orf19.4525	unknown function	YLR064w
CA1629	0.6	2.2	1.2	1.5	1.4	1.3	NPI46	orf19.1030	proline cis-trans isomerase (by homology)	YLR449w
CA2951	1.3	2.1	0.8	1.0	0.9	1.0	SBP1	orf19.5854	RNA binding protein-like (by homology)	YHL034c
CA4865	1.5	2.1	1.0	1.0	1.1	1.2	IPF4085	orf19.3841	similar to Saccharomyces cerevisiae Apg1p essential for aut	YGL180w
CA4604	1.2	2.1	1.3	1.3	1.2	0.9	MBF1	orf19.3294	Multiprotein bridging factor mediates GCN4-dependent trans	YOR298ca
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function	YGR101w
CA1116	1.3	2.1	1.1	1.3	0.9	1.0	CCT5	orf19.2288	T-complex protein 1, epsilon subunit (by homology)	YJR064w
CA0914	1.6	2.1	0.9	1.0	1.2	1.1	SRA1	orf19.2015	cAMP dependent protein kinase, regulatory subunit (by homc	YIL033c
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA4167	0.6	2.1	0.8	1.0	0.9	1.1	IPF7778	orf19.2966	putative carboxymethylenebutenolidase (dienelactone hydrol	YDL086w
CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)	YIL095w
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5717	1.0	2.1	0.9	1.1	0.8	1.1	CYP51	orf19.7421	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by	YDR304c
CA1256	2.2	2.0	1.0	1.1	0.7	1.1	UBP15	orf19.1777	ubiquitin-specific protease (by homology)	YMR304w
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA1894	2.2	2.0	1.0	1.1	1.2	1.0	PRE7.5f	orf19.2755	putative subunit of 20S proteasome, exon 1 (by homology)	YBL041w
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA1911	1.1	2.0	1.1	0.9	1.0	1.0	SSE1	orf19.2435	heat shock protein of HSP70 family (by homology)	YPL106c
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA5977	1.2	2.0	1.2	1.0	1.3	1.2	UBC4	orf19.7571	E2 ubiquitin-conjugating enzyme (by homology)	YBR082c
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)	YMR234w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)	YHR104w
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle	YLR178c
CA0663	2.1	1.9	0.9	0.9	1.0	1.1	PUP2	orf19.709	20S proteasome subunit(alpha5) (by homology)	YGR253c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA4988	1.4	1.9	1.0	0.9	0.9	0.8	RPN2	orf19.5260	Proteasome regulatory subunit (by homology)	YIL075c
CA1880	1.7	1.9	1.2	1.3	1.4	1.0	IPF13316	orf19.2269	unknown function	YNL010w
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homo	YPR183w
CA5862	1.0	1.9	1.2	1.3	1.1	1.1	POT11	orf19.7520	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)	YIL160c
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function	YKL094w
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA4522	1.2	1.9	1.0	0.9	1.1	1.0	RPT4	orf19.482	26S proteasome regulatory subunit (by homology)	YOR259c
CA4389	1.6	1.9	1.2	1.0	1.2	1.2	RPT5	orf19.3123	26S proteasome regulatory subunit (by homology)	YOR117w
CA5268	1.8	1.9	1.1	1.1	0.7	0.9	SEC18.3f	orf19.4994	vesicular fusion protein, 3-prime end (by homology)	YBR080c
CA3868	1.3	1.9	1.1	1.1	0.8	1.0	CCT1	orf19.401	component of chaperonin-containing T-complex (by homolog	YDR212w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA0394	1.6	1.9	1.0	1.3	1.4	1.4	IPF12758.	orf19.334	unknown function, 5-prime end	no match (e-value > 0.05)
CA3247	1.2	1.9	1.1	1.0	0.7	0.8	IPF15832	orf19.4676	unknown function	YKL053ca
CA4695	1.2	1.9	0.9	1.4	1.3	1.0	IPF4229	orf19.6923	unknown function	YML015c
CA3898	1.3	1.9	1.1	0.9	0.8	1.0	UBA2	orf19.5074	ubiquitin-activating -like enzyme by homology	YDR390c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function	YDL012c

CA00661	1.9	1.9	0.7	0.9	1.0	1.0	APG7	orf19.707	component of the autophagic system (by homology)	YHR171w
CA22120	1.6	1.9	0.9	1.0	1.2	1.2	PUP3	orf19.1336	PRCT yeast proteasome component (by homology)	YER094c
CA33290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA55554	1.0	1.9	0.7	1.0	0.9	1.0	IPF1960.5	orf19.7318	putative transcriptional activator, 5-prime end	YCR106w
CA00081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match (e-value > 0.05)
CA44161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA22758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA33049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA44624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA33422	1.6	1.9	0.9	0.8	0.7	0.9	IPF17289	orf19.6134	unknown function	YLR440c
CA44566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match (e-value > 0.05)
CA33385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA11755	1.6	1.8	1.1	0.9	0.8	1.1	PDI1	orf19.5130	protein disulfide-isomerase precursor (by homology)	YCL043c
CA00408	1.9	1.8	0.9	1.0	0.9	1.0	SAC6.5f	orf19.5544	actin filament bundling protein, fimbrin, 5-prime end (by homc	YDR129c
CA11389	1.5	1.8	1.4	1.3	0.8	1.1	PLP2	orf19.1769	Might regulate Ste4p in pheromone response (by homology)	YOR281c
CA00341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA33191	1.5	1.8	0.7	1.0	0.7	0.8	IPF11601	orf19.2151	unknown function	YOR165w
CA55930	2.3	1.8	1.1	0.9	1.1	1.0	ECM29.3f	orf19.6773	Involved in cell wall biogenesis and architecture, 3-prime end	YHL030w
CA11693	1.6	1.8	1.0	1.0	1.0	1.1	IPF17054	orf19.5037	unknown function	no match (e-value > 0.05)
CA22286	0.9	1.8	0.8	1.1	1.4	1.4	IPF5369	orf19.5553	unknown function	YKL069w
CA11261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA00164	1.0	1.8	1.0	1.0	0.9	1.0	IPF11694	orf19.4335	similar to Saccharomyces cerevisiae Tna1p high affinity nicot	YGR260w
CA22278	1.8	1.8	1.2	1.0	1.2	1.2	IPF10806	orf19.782	unknown function	YBR204c
CA00163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA55836	1.1	1.8	0.8	1.1	1.2	0.7	IPF428	orf19.7490	transport protein (by homology)	YOL137w
CA55891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA00262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA11983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA34435	1.0	1.8	0.9	1.4	1.3	1.2	IPF6391	orf19.583	indoleamine 2,3-dioxygenase (by homology)	YJR078w
CA22669	1.2	1.8	0.8	0.9	1.0	1.0				
CA15595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA12269	1.6	1.7	1.1	1.1	1.1	1.4	IPF19726	orf19.3158	unknown function	YDL001w
CA47798	1.4	1.7	0.9	1.0	0.9	0.9	RPN5.3f	orf19.4032	subunit of the regulatory particle of the proteasome, 3-prime e	YDL147w
CA22146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function	no match (e-value > 0.05)
CA03345	1.2	1.7	1.0	1.0	1.0	0.9	ACH1	orf19.3171	acetyl-coenzyme-A hydrolase (by homology)	YBL015w
CA39936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA51146	1.2	1.7	0.9	1.0	1.0	1.0	YMC2	orf19.4583	Carnitine/acylcarnitine translocase (by homology)	YBR104w
CA27785	0.6	1.7	0.6	0.9	0.9	1.0	MET13	orf19.288	Methylene tetrahydrofolate reductase (by homology)	YGL125w
CA08840	1.1	1.7	1.4	1.0	1.3	1.0				
CA04441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA11123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in aceti	YCR032w
CA52296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA36697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific	YJR099w
CA44480	0.9	1.7	0.7	1.1	1.5	1.4	IPF6464	orf19.1887	putative triacylglycerol lipase (by homology)	YLL012w
CA61159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA42219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein pho	YKL193c
CA55555	0.9	1.7	1.0	1.0	1.3	1.1	SUC1	orf19.7319	Putative zinc finger protein Suc1	YFL052w
CA51196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function	YIL001w
CA46616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA56695	1.3	1.7	0.9	0.8	0.7	1.1	IPF3310	orf19.7397	unknown function	YPR022c
CA52283	0.9	1.7	0.8	1.0	0.8	1.2	IPF1912	orf19.7140	putative catechol o-methyltransferase	no match (e-value > 0.05)
CA25508	1.9	1.7	1.4	1.1	0.9	1.0	BET5	orf19.302	targeting and fusion of ER to Golgi transport vesicles (by hon	YML077w
CA58326	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA41165	1.0	1.7	1.0	1.1	1.0	1.0	IPF7774	orf19.2968	unknown function	no match (e-value > 0.05)
CA48890	1.5	1.7	1.0	0.9	1.0	1.1	PRE10	orf19.6582	20S proteasome subunit C1 (by homology)	YOR362c
CA59941	1.5	1.7	1.0	1.3	1.4	0.9	IPF3486	orf19.6756	unknown function	YGL198w
CA30961	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA41442	1.5	1.7	1.0	1.0	1.5	1.2	PRE4	orf19.4230	20S proteasome subunit(beta7) (by homology)	YFR050c
CA34228	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c
CA13374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA55559	1.0	1.7	1.2	1.1	0.8	1.1	CBP1	orf19.7323	Corticosteroid binding protein	YMR020w
CA38770	1.0	1.7	0.6	0.9	1.3	1.0	YPK1	orf19.399	ser/thr-specific protein kinase (by homology)	YMR104c
CA53006	1.2	1.7	1.0	1.0	1.1	1.1	NPT1	orf19.7176	Nicotinate phosphoribosyltransferase (by homology)	YOR209c
CA25648	1.6	1.7	1.0	0.9	0.9	0.9	PGA34	orf19.2833	unknown function	no match
CA09772	1.1	1.6	1.1	1.2	1.0	1.0	CYP1	orf19.6472	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homc	YDR155c
CA12252	1.9	1.6	0.9	0.9	0.9	0.9	RPN1	orf19.4956	26S proteasome regulatory subunit (by homology)	YHR027c
CA43333	1.2	1.6	1.2	1.1	1.4	1.2	IPF2083	orf19.4086	unknown function	YNL056w
CA19442	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eo	orf19.4191.1	Ubiquitin--protein ligase, 3-prime end (by homology) FALSOF	YGL141w
CA47999	1.6	1.6	1.1	1.0	0.8	1.0	RPN5.5f	orf19.4034	subunit of the regulatory particle of the proteasome, 5-prime e	YDL147w
CA39556	1.2	1.6	1.0	1.0	1.0	1.2	IPF6712.3	orf19.1414.2	unknown function, 3-prime end | Unknown function	no match
CA41227	0.9	1.6	0.7	0.9	0.9	0.9	IPF6629	orf19.2762	unknown function	YLR109w
CA33110	1.4	1.6	1.1	1.2	0.7	1.0	PFS2	orf19.2307	Polyadenylation Factor I subunit (by homology)	YNL317w
CA40884	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA38336	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA37446	1.2	1.6	1.6	1.0	0.8	1.1	ARA1	orf19.2172	D-arabinose dehydrogenase (by homology)	YBR149w
CA37337	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA18774	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA28888	1.6	1.6	1.0	1.1	1.2	1.2	GIM5	orf19.2471	Gim complex component (by homology)	YML094w
CA27773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase	YOR211c
CA09226	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c
CA35669	1.3	1.6	1.0	1.1	1.0	1.1	IPF3268	orf19.3136	unknown function	YDR325w
CA21557	2.2	1.6	1.5	1.1	0.8	0.8	IPF8537	orf19.5300	similar to Saccharomyces cerevisiae Cne1p calnexin, involve	YAL058w
CA09652	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match (e-value > 0.05)
CA43220	1.1	1.6	1.2	1.1	0.8	1.1	ECM17	orf19.4099	Putative sulfite reductase (by homology)	YJR137c
CA25651	1.0	1.6	1.2	1.5	0.8	0.9	CAR2	orf19.5641	ornithine aminotransferase (by homology)	YLR438w
CA55684	1.2	1.6	0.7	0.9	1.0	0.9	IPF1980	orf19.7328	unknown function	no match (e-value > 0.05)
CA14552	1.6	1.6	0.8	0.8	1.3	1.0	REV1	orf19.4412	DNA repair protein (by homology)	YOR346w
CA17566	1.0	1.6	1.1	1.2	1.5	1.0	IPF14562	orf19.5129	unknown function	no match (e-value > 0.05)
CA19113	1.4	1.6	0.9	0.9	1.2	1.2	ARC35	orf19.2437	subunit of the Arp2/3 complex involved in the control of actin	YNR035c
CA53336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA42684	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match (e-value > 0.05)
CA28653	1.3	1.6	1.0	1.0	1.3	1.1	IPF20117	orf19.1058	unknown function	YLR421c
CA05993	1.3	1.6	1.0	0.8	1.2	1.2	ARP6	orf19.4904	actin-related protein (by homology)	YLR085c
CA18388	1.3	1.6	1.1	1.1	1.4	1.3	IPF5777	orf19.3963	unknown function	YER182w
CA05300	1.4	1.6	0.7	0.6	0.7	0.9				
CA29266	1.1	1.6	0.8	1.1	1.3	1.3	UBA3	orf19.4209	Ubiquitin-like protein activating enzyme	YPR066w
CA55995	1.1	1.6	0.9	1.0	0.9	1.4	IPF568	orf19.7105	similar to Saccharomyces cerevisiae Far1p cyclin-dependent	YJL157c
CA23388	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c

CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal ass	YKL197c
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA2867	1.2	1.5	0.9	0.8	0.8	0.8	IPF11688	orf19.2844	similar to Saccharomyces cerevisiae Apl4p AP-1 complex su	YPR029c
CA3336	1.0	1.5	0.8	0.8	1.1	1.3	IPF19983	orf19.2335	unknown function	YHR113w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltr	YMR149w
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA2133	1.2	1.5	1.0	1.0	1.0	0.8	IPF5866	orf19.5213	unknown function	YDR228c
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA3907	1.2	1.5	0.7	1.0	1.0	0.9	IPF3304	orf19.4395	similar to Saccharomyces cerevisiae Aip1p actin cytoskeleto	YMR092c
CA3683	1.2	1.5	1.1	1.0	1.1	1.2	PPZ1	orf19.726	ser/thr phosphatase required for normal osmoregulation (by	YML016c
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase	YFR015c
CA4625	1.1	1.5	0.8	0.9	0.9	1.2	IPF5742	orf19.3319	thioredoxin-like protein (by homology)	YGR209c
CA4720	1.2	1.5	1.0	1.0	1.3	1.0	ECM18	orf19.6958	Involved in cell wall biogenesis and architecture (by homolog	YDR125c
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA3057	1.3	1.5	1.0	1.2	1.5	1.2	IPF2954	orf19.4293	unknown function	YDR267c
CA3589	0.8	1.5	0.8	1.2	1.4	1.1	IPF10113	orf19.2249	unknown function	YNR020c

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[[Cd OS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
HS+ OS+ XS+										
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA5797	1.2	0.9	8.7	8.2	0.7	1.0	IPF4182	orf19.5446	unknown function	no match (e-value > 0.05)
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)	YDR497c
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function	no match
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function	YLR205c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match (e-value > 0.05)
CA0721	1.5	0.9	1.3	2.3	0.8	0.8	IPF10429	orf19.2887	unknown function	YMR295c
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function	no match (e-value > 0.05)
CA5840	1.2	1.0	1.3	1.9	1.0	1.2	EBP6	orf19.7495	NADPH dehydrogenase (by homology)	YPL171c
CA0948	0.6	1.1	0.9	1.9	1.1	1.0	IPF10270	orf19.1272	unknown function	YGR111w
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match (e-value > 0.05)
CA0677	1.4	1.3	1.2	1.8	1.0	0.8	IPF13095	orf19.1182	unknown function	YGL212w
CA4870	1.5	1.1	1.3	1.7	1.2	1.3	IPF19568	orf19.6556	unknown function	no match (e-value > 0.05)
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA1187	0.7	0.9	1.2	1.5	1.1	1.0	QRI7	orf19.3787	putative glycoprotease (by homology)	YKR038c
CA2161	1.1	1.1	1.1	1.5	1.0	1.1	IPF11876	orf19.5295	unknown function	no match (e-value > 0.05)

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[[Cd XS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
HS+ OS+ XS+										
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function	YDR371w
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function	no match (e-value > 0.05)
CA2435	1.1	1.7	1.2	1.1	17.7	13.6	IPF9483	orf19.3395	probable permease (by homology)	YHR048w
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function	YKL086w
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function	no match (e-value > 0.05)
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase	YBR046c
CA0639	1.6	1.8	1.0	1.0	9.0	10.5				
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match (e-value > 0.05)
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function	no match (e-value > 0.05)
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA4913	1.1	1.0	1.3	1.0	1.2	6.8	CIS2	orf19.6053	Gamma-glutamyltransferase (by homology)	YLR299w
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)	YBR293w
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function	YKR071c
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA4829	1.0	1.1	1.3	1.0	6.3	5.5	IPF1210	orf19.2067	similar to Saccharomyces cerevisiae Nfu1p involved in home	YKL040c
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)	YHR044c
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function	no match (e-value > 0.05)
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)	YPL171c
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)	YDR338c
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function	YOR292c
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)	YOR101w
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function	no match (e-value > 0.05)
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)	YDR513w
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match (e-value > 0.05)
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function	YOL119c
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)	YIL120w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homolog	YER053c
CA4399	1.4	1.7	1.2	1.3	1.1	3.8	PRA1	orf19.3111	pH-regulated antigen	YOL154w
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function	YGL136c
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match (e-value > 0.05)
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function	YNL144c
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function	YDR336w
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)	YNL229c
CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function	no match (e-value > 0.05)

CA11098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match (e-value > 0.05)
CA11005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)	YPL101w
CA22468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match (e-value > 0.05)
CA00584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homolc	YJL101c
CA22638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA00583	1.2	2.5	1.3	1.3	3.9	3.2	GSH1.3f	orf19.5059	gamma-glutamylcysteine synthetase, 3 prime end (by homolc	YJL101c
CA00996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)	no match (e-value > 0.05)
CA00933	1.3	1.1	0.8	1.0	3.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)	YMR301c
CA11775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology	YDL215c
CA33814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA00385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function	YNL250w
CA55697	1.3	1.0	0.8	1.1	3.8	3.0				
CA11170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function	YDR132c
CA44392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)	YNL229c
CA11016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function	YOR273c
CA55237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA55933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA11111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA55942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA55868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function	YMR090w
CA00595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5	orf19.4901	unknown function, 5-prime end	YER175c
CA11157	1.2	1.0	1.4	1.1	0.8	2.8	PZF1	orf19.4125	TFIIIA (transcription initiation factor) (by homology)	YPR186c
CA44670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA44446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA00778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA33895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA33258	1.1	1.0	0.5	0.9	1.1	2.7				
CA44873	1.0	0.8	0.7	0.7	3.0	2.7				
CA22870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)	YPR194c
CA22349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA00442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA44885	1.2	1.3	1.2	1.1	1.1	2.6	IPF1636	orf19.6577	similar to Saccharomyces cerevisiae Tpo1p multidrug resista	YLL028w
CA44662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by hom	YMR038c
CA11496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA33919	1.1	1.0	0.8	0.8	1.0	2.5	IFC5	orf19.5121	unknown function	YPR194c
CA22227	1.5	1.2	1.0	0.9	1.4	2.5	EBP7	orf19.5816	NADPH DEHYDROGENASE by homology	YHR179w
CA33708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA33277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA22894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function	no match (e-value > 0.05)
CA22967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA22403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA55289	0.7	0.9	0.9	0.9	1.4	2.4	NRG1	orf19.7150	similar to transcriptional repressor Nrg1p/Nrg2p	YBR066c
CA00942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function	YER101c
CA33257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA33528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA00993	1.0	1.0	0.6	0.9	2.2	2.4				
CA36663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA13372	0.9	1.0	1.2	1.0	1.1	2.4	IPF15844	orf19.4961	similar to Saccharomyces cerevisiae Stp2p involved in pre-tF	YHR006w
CA33309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA36639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA49929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA11108	1.1	1.1	1.0	1.0	1.0	2.3	IPF11273	orf19.5231	unknown function	no match (e-value > 0.05)
CA45569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA28839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match (e-value > 0.05)
CA49914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA28873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (a	YPR192w
CA15536	1.6	1.6	1.1	1.3	1.3	2.2	SOK1	orf19.451	high copy suppressor of a cyclic AMP-dependent protein kina	YDR006c
CA21177	1.1	1.1	1.3	1.0	2.2	2.2	ROD1	orf19.1509	O-dinitrobenzene,calcium and zinc resistance protein (by hor	YFR022w
CA24427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA01129	1.1	0.9	1.0	1.0	1.2	2.2	IPF10495	orf19.246	unknown function	YIL108w
CA27711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)	YDR460w
CA50011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function	YMR101c
CA24458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA33354	1.1	1.1	0.7	0.7	1.2	2.2	GPR1	orf19.1944	similar to Saccharomyces cerevisiae Gpr1p G-protein couple	YDL035c
CA56669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA05560	1.2	1.0	0.9	1.0	1.2	2.1	GPX3	orf19.87	glutathione peroxidase (by homology)	YIR037w
CA46630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c
36692.2	1.2	1.2	0.8	0.9	2.2	2.1				
65332.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA50009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)	YKL119c
CA05558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA28896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA04431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA49917	0.7	0.8	0.8	1.4	2.0	2.1	ECM31	orf19.6057	Involved in cell wall biogenesis and architecture (by homolog	YBR176w
CA24477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)	YJR061w
CA30094	1.1	1.1	1.1	0.7	1.3	2.1	IPF11548	orf19.3854	serine/threonine protein kinase (by homology)	YCR008w
CA53351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA09927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA59934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function	YHL029c
CA26649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA30087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)	YLR147c
CA20021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA41190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA01160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease	YKR039w
CA34446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function	YKL195w
CA45580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function	no match (e-value > 0.05)
CA48336	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)	YJR104c
CA48319	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA07757	1.0	0.7	0.6	0.8	2.2	2.0				
CA16600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)	YHR175w
CA57789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA05500	0.9	1.0	1.4	1.2	0.9	2.0	IPF20058	orf19.4793	unknown function	YOR252w
CA25584	0.8	1.2	1.0	1.1	2.1	2.0	IPF9440	orf19.4373	similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase	YDR236c
CA50008	1.0	0.8	1.1	1.3	1.2	2.0	IPF12577	orf19.5238	unknown function	no match (e-value > 0.05)
CA56378	0.8	1.0	1.0	0.8	0.9	2.0	IPF1292	orf19.7381	unknown function Hypothetical zinc-finger protein	YML099c
CA13556	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA46551	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA50010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function	YMR101c

CA1002	1.0	1.0	1.9	1.2	0.9	1.9	ROK1.3f	orf19.3756	RNA helicase, 3-prime end	YGL171w
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (	YOL119c
CA4023	1.0	1.0	0.9	1.0	0.9	1.9	FRP5	orf19.3440	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function	YGR110w
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function	no match (e-value > 0.05)
CA0995	1.0	1.0	0.9	0.9	3.8	1.9				
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)	YGR234w
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function	no match (e-value > 0.05)
CA4778	1.0	1.1	0.9	1.0	1.2	1.8	IFJ1	orf19.4011	Unknown function	YGR263c
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA4174	1.2	3.6	1.3	1.6	1.6	1.8	IPF4430	orf19.2959.1	unknown function	YDR276c
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match (e-value > 0.05)
CA0052	1.0	1.1	1.4	1.0	1.3	1.8	IPF19567	orf19.475	Unknown function	YHR085w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)	YML004c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase	YOR202w
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)	YMR275c
CA3187	1.0	0.8	1.5	1.2	0.8	1.8	IPF17094	orf19.2143	unknown function	YPL183c
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4960	0.7	0.8	0.7	0.7	1.2	1.8	IPF3912	orf19.6514	unknown function	YPL177c
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function	YCL044c
CA1277	1.3	1.0	1.4	1.0	1.2	1.8	IPF10837	orf19.3630	unknown function	YDR083w
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA4477	0.9	1.2	1.2	1.1	1.2	1.8	IPF6459	orf19.1890	unknown function	YMR210w
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function	no match (e-value > 0.05)
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology	YAL012w
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match (e-value > 0.05)
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5	orf19.6654	unknown function	YMR221c
CA4612	1.1	0.9	1.4	1.0	1.5	1.7	PPM2	orf19.3303	carboxy methyl transferase; homolog of PPM1 (by homology)	YOL141w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match (e-value > 0.05)
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eo	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA5135	1.0	1.0	1.0	1.0	1.8	1.7	HSP104.5	orf19.6389	Heat shock protein, 5-prime end (by homology)	YLL026w
CA0629	1.1	1.3	0.7	0.8	1.0	1.7	IPF3876	orf19.775	unknown function	YJR126c
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)	YNL240c
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)	YPL140c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA2750	1.1	1.0	1.1	1.0	4.6	1.7	ATX1	orf19.2369.1	antioxidant protein and metal homeostasis factor (by homolo	YNL259c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.5f	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA	YAL049c
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function	YNL166c
CA5287	0.8	1.0	1.0	0.9	1.0	1.7	IPF1922	orf19.7148	similar to multidrug resistance proteins	YLL028w
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function	YPL092w
CA5696	0.9	1.0	1.6	1.3	1.4	1.7	IPF3309.3	orf19.7398	unknown function, 3-prime end	YER126c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA4614	1.1	1.3	1.4	0.8	1.0	1.7	IPF7952	orf19.3305	unknown function	YDR213w
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA6009	0.8	1.0	1.3	1.0	1.2	1.7	IPF643	orf19.7610	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine p	YER075c
CA0626	1.1	0.9	1.3	1.1	1.4	1.7	IPF3161	orf19.3161	Unknown function	YNR054c
CA3157	0.9	1.4	1.0	1.3	1.5	1.7	IPF14456	orf19.1588	unknown function Unknown function	YBR269c
CA4563	1.0	1.0	1.0	1.1	0.8	1.7	IPF6566	orf19.6873.1	unknown function	YBL071wa
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase	YAL039c
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match (e-value > 0.05)
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function	YMR136w
CA5580	1.2	1.4	0.9	1.0	1.3	1.6	RVS161	orf19.7124	cytoskeletal binding protein (by homology)	YCR009c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA6038	0.8	1.2	1.8	1.2	1.1	1.6	LTV1	orf19.7650	low-temperature viability protein (by homology)	YKL143w
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)	YLR120c
CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function	YDR219c
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homolo	YOR049c
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function	no match
CA5739	1.0	1.1	0.9	1.0	1.4	1.6	IPF2884	orf19.7449	unknown function	YMR211w
CA0941	0.9	1.0	0.8	1.0	1.3	1.6	IPF8617	orf19.3705	unknown function	YCR079w
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match (e-value > 0.05)
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA5474	1.3	0.9	1.8	1.1	1.0	1.6	IPF16944.	orf19.3287	unknown function, 3-prime end	YMR014w
CA1958	1.0	1.0	0.9	0.9	1.2	1.6	IFE1	orf19.769	Unknown function	YAL061w
CA0393	1.4	1.1	1.0	1.1	1.7	1.6	IPF12758.	orf19.333.2	unknown function, 3-prime end	no match
CA2395	1.1	1.1	1.1	1.0	1.0	1.6	IPF6425	orf19.3536	unknown function	YOR320c
CA1540	0.9	0.9	1.2	1.5	0.9	1.6	IPF1047	orf19.4563	unknown function	YMR310c
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function	YHR087w
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA2460	1.5	1.1	1.0	1.0	1.1	1.6				
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA2233	1.0	1.0	1.0	1.0	1.1	1.6	IFJ3	orf19.3924	unknown function	YGR263c
CA6016	0.9	0.8	1.4	1.4	1.4	1.6	IPF630	orf19.7618	unknown function	YOR145c
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function	YLR021w
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3	orf19.4266.1	septin, 3-prime end (by homology)	YDR218c
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function	YHR101c
CA1703	0.9	1.2	0.8	1.0	1.4	1.6	IPF7987	orf19.703	unknown function	YGR247w
CA3808	0.8	1.1	1.5	1.2	1.1	1.6	FAL1	orf19.2488	ATP-dependent RNA helicase	YDR021w
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function	YJL092w

CA5875	1.2	1.1	0.9	1.0	0.8	1.6	IPF324.3f	orf19.7545	unknown function, , 3-prime end	no match (e-value > 0.05)
CA3741	0.9	0.9	0.9	1.0	0.7	1.6	MRS4	orf19.2178	RNA splicing protein and member of the mitochondrial carrie	YKR052c
CA1080	1.0	0.9	1.3	0.9	1.4	1.6	IPF14710	orf19.4820	unknown function	YKL162c
CA4158	0.9	0.9	0.9	0.9	0.7	1.6	DLD3	orf19.5805	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA3080	0.9	1.1	1.0	0.8	1.0	1.6	IPF14634	orf19.4153	APP-binding protein 1 (by homology)	YPL003w
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)	YOR171c
CA5833	0.9	0.9	1.2	1.1	1.2	1.5	IMP3	orf19.7488	U3 small nucleolar ribonucleoprotein (by homology)	YHR148w
CA4818	0.7	0.9	0.8	0.7	1.2	1.5	IPF1193	orf19.2079	unknown function Unknown function	YHL018w
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membra	YIL047c
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA2592	1.2	0.9	1.4	1.1	1.6	1.5	IPF18447	orf19.59	putative zinc-finger protein (by homology)	YBR267w
CA0473	1.0	1.0	1.0	1.0	1.3	1.5	GRP1	orf19.4781	dihydroflavonol-4-reductases (by homology)	YOL151w
CA3722	1.3	1.2	0.9	1.0	1.5	1.5	PHO13	orf19.4172	4-nitrophenylphosphatase (by homology)	YDL236w
CA4507	1.0	1.1	1.1	1.3	1.0	1.5	IPF20015	orf19.499	unknown function	YNL063w
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)	YPR016c
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rR	YDR087c
CA2398	1.1	1.0	1.0	1.0	1.1	1.5	IPF6431	orf19.3539	unknown function	YBR141c
CA0343	1.6	1.2	1.1	1.0	0.9	1.5	LYS1	orf19.1789.1	saccharopine dehydrogenase (by homology)	YIR034c
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function	no match (e-value > 0.05)
CA1689	1.0	1.0	0.9	1.1	1.1	1.5	IPF13030	orf19.3655	unknown function	no match (e-value > 0.05)
CA2428	1.0	1.1	0.9	0.9	1.3	1.5	IPF9894	orf19.3405	possible zinc-finger protein	no match (e-value > 0.05)
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function	no match (e-value > 0.05)
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha	YIL099w
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA4754	0.7	1.0	1.0	1.0	1.2	1.5	IPF11479	orf19.4825	unknown function	YIL098c
CA1630	1.4	1.2	1.5	1.1	1.1	1.5	RPP1	orf19.1029	required for processing of tRNA and 35S rRNA (by homology	YHR062c
CA5626	0.9	1.1	0.9	1.0	1.1	1.5	IPF498	orf19.7071	unknown function	YML123c
CA4613	1.0	1.0	1.3	1.1	1.3	1.5	IPF7950	orf19.3304	similar to Saccharomyces cerevisiae Rrp40p involved in ribo	YOL142w
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function	no match (e-value > 0.05)
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)	YEL060c
CA4404	1.0	1.3	1.4	1.1	1.2	1.5	MET16	orf19.3106	3 -phosphoadenylylsulfate reductase (by homology)	YPR167c
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
11759.2	0.6	1.2	0.2	0.3	1.4	1.5				
CA0730	0.9	0.7	1.2	1.1	1.6	1.5	IPF7334	orf19.3724	unknown function	YOR004w
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function	YPL122c
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SY	YOR005c
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function	YNL191w

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[[Cd OS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

Species (Stress ()* Systemat	Ca HS+ rmali	Cd HS+ rmali	Ca OS+ rmali	Cd OS+ rmali	Ca XS+ rmali	Cd XS+ rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase	YKR070w
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function	YMR226c
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w

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[Cd XS+ up 1.5 10FDR] and [Cd OS+ up 1.5 10FDR]] less [Cd HS+ up 1.5 10FDR]

Species (Stress ()* Systemat	Ca HS+ rmali	Cd HS+ rmali	Ca OS+ rmali	Cd OS+ rmali	Ca XS+ rmali	Cd XS+ rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match (e-value > 0.05)
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match (e-value > 0.05)
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function	no match (e-value > 0.05)
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c

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[Cd XS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10FDR]

Species (Stress ()* Systemat	Ca HS+ rmali	Cd HS+ rmali	Ca OS+ rmali	Cd OS+ rmali	Ca XS+ rmali	Cd XS+ rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match (e-value > 0.05)
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homolo	YMR152w
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match (e-value > 0.05)
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match (e-value > 0.05)
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by h	YML130c
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match (e-value > 0.05)
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w

CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homolo	YPL171c
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)	YKR039w
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inn	YMR152w
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase	YER042w
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase	YNL277w
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)	YLR043c
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function	YNL229c
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology	YDR032c
CA2258	1.1	2.8	0.9	0.9	7.4	15.1	IFR1	orf19.1763	Unknown function	YNL134c
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-bind	YGL091c
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)	YNL270c
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function	YNL134c
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA0636	2.2	2.5	0.9	0.9	10.8	15.0				
CA1569	1.8	2.4	1.5	1.2	1.1	2.4	IPF7616	orf19.1159	putative homoserine O-acetyltransferase (by homology)	YNL277w
CA1882	1.1	2.4	0.8	1.0	0.8	1.9	IPF19934	orf19.2210	unknown function	no match (e-value > 0.05)
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match (e-value > 0.05)
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)	YGR234w
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)	YHR137w
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)	YOL151w
CA1846	1.5	2.2	0.8	0.9	12.8	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)	YOR388c
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)	YPR086w
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable mono	no match
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in reg	YIL046w
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)	YIR037w
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)	YNL040w
CA0183	1.5	1.9	1.5	1.1	1.4	2.2	CAP1	orf19.1623	transcriptional acivator (by homology)	YML007w
CA1395	1.1	1.9	1.0	0.9	11.5	11.7				
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)	YIR035c
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function	YIR017c
CA3059	1.2	1.8	1.2	1.1	6.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)	YDR353w
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA3086	1.0	1.7	1.1	1.2	2.3	3.9	GLR1	orf19.4147	by similarity to S. cerev. and C. albicans:glutathione reductas	YPL091w
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function	YLR256w
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)	YOR388c
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by ho	YDL168w
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function	no match (e-value > 0.05)
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase	YHR008c
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w

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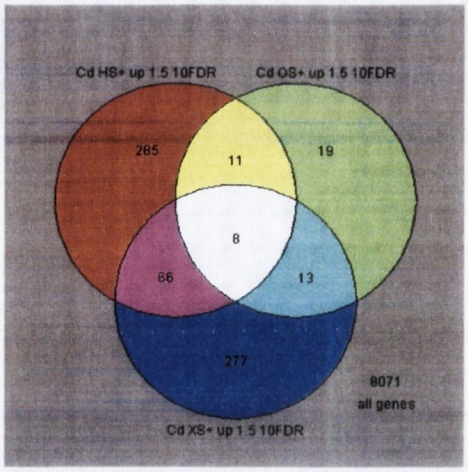
[[Cd OS+ up 1.5 10FDR] and [Cd XS+ up 1.5 10FDR]] and [Cd HS+ up 1.5 10FDR]

HS+ OS+										
Species ():	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*:	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	rmali:	rmali:	rmali:	rmali:	rmali:	rmali:	Common	Ca orf19	Ca Function	S.c. hom.
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match (e-value > 0.05)
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match (e-value > 0.05)
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c



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[Cd HS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

Systemat	Norn	Norn	Norn	Norn	Norn	Norn	Common	Ca orf19	Ca Function	S.c. hom.
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA4684	3.0	10.5	1.1	1.0	2.2	1.5	HSP78.5f	orf19.882	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)	no match (e-value > 0.05)
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function	no match (e-value > 0.05)
CA4437	2.5	7.3	0.7	1.3	1.2	1.2	IPF13867	orf19.5158	unknown function	YGL145w
CA1075	1.5	7.0	0.8	0.8	0.8	0.7	IPF4991	orf19.2531	putative membrane protein	YDL058w
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA4683	10.3	6.7	1.1	1.1	2.3	1.5	HSP78.3f	orf19.884	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)	YCR098c
CA0785	2.2	5.9	0.9	1.1	1.2	1.1	IPF14603	orf19.3929	unknown function	YJR100c
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)	YGL009c
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)	YLR216c
CA3078	2.5	5.4	0.8	1.3	1.2	1.1	IPF19970	orf19.4816	unknown function	YMR209c
CA1239	4.7	5.2	1.2	1.1	0.7	0.9	HSP60	orf19.717	Heat Shock Protein 60 (HSP60)	YLR259c
CA2513	1.0	5.2	1.6	1.5	0.7	1.1	SNG1	orf19.308	Involved in nitroguanidine resistance (by homology)	YGR197c
CA4120	1.4	4.8	1.0	1.1	1.2	1.5	SOD1	orf19.2770.1	Cu,Zn-superoxide dismutase	YJR104c
CA4959	3.4	4.8	1.3	1.2	1.0	1.0	HSP90	orf19.6515	heat shock protein	YMR186w
CA5536	2.0	4.4	0.9	1.0	1.1	1.2	IPF2837	orf19.7297	putative cystathionine gamma-synthase (by homology)	YHR112c
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)	YJR107w
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function	YMR002w
CA0551	2.5	4.0	1.4	1.3	1.3	1.0	CDC37	orf19.5531	Cell division control protein (by homology)	YDR168w
CA5341	2.5	3.9	0.9	0.8	1.0	0.9	HSP10	orf19.7215.3	10 kDa mitochondrial heat shock chaperonin (by homology)	YOR020c
CA4021	1.5	3.8	0.7	1.6	1.1	1.1	EBP2	orf19.3442	NADPH dehydrogenase (by homology)	YHR179w
CA5558	1.5	3.8	1.1	1.4	1.3	1.2	IPF1969	orf19.7322	unknown function	YPL225w
CA1180	1.7	3.7	1.1	0.9	0.8	1.4	UGA12.3f	orf19.803	4-aminobutyrate aminotransferase (GABA transaminase), 3-I	YGR019w
CA2130	1.4	3.6	1.2	1.0	1.2	1.1	RPS27A	orf19.413.1	ribosomal protein S27.e (by homology)	YKL156w
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function	YNL111c
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)	YPL088w
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease	YHL036w
CA4609	0.9	3.6	1.2	1.3	1.5	1.2	ZPR1	orf19.3300	Zinc finger protein (by homology)	YGR211w
CA3796	1.9	3.5	1.2	1.2	0.9	0.9	SGT2	orf19.5823	small glutamine-rich tetratricopeptide repeat containing protei	YOR007c
CA1230	2.1	3.5	1.5	1.6	0.9	0.9	SSA4	orf19.4980	cahsp70 mRNA for heat shock	YER103w
CA1181	1.9	3.5	0.9	0.8	0.8	1.4	UGA12.5f	orf19.802	4-aminobutyrate aminotransferase (GABA transaminase), 5-I	YGR019w
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homology)	YMR302c
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function	YML041c
CA0706	1.7	3.4	1.1	1.5	0.9	1.0	IPF7715.3	orf19.682	unknown function	YJL078c
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA1330	1.0	3.4	1.0	1.6	1.0	1.0	IPF11713.	orf19.1151	unknown function, 3-prime end	no match (e-value > 0.05)
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA2729	0.9	3.2	1.0	1.1	0.9	0.7	NAT2	orf19.2116	N-acetyltransferase for N-terminal methionine (by homology)	YGR147c
CA4856	3.1	3.2	0.9	1.1	1.1	0.9	IPF15950	orf19.3827	unknown function	YKR087c
CA3099	2.2	3.2	1.0	1.4	1.4	1.3	LST8	orf19.3862	required for transport of permeases from the golgi to the plas	YNL006w
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function	YBR101c
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)	YKL188c
CA0117	1.5	3.1	1.1	1.1	0.9	1.1	IPF19231	orf19.916	unknown function	YNL305c
CA1287	1.8	3.1	1.1	1.2	1.2	1.2	IPF5545	orf19.4430	unknown function	YDR330w
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholester	YNR008w
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function	YHR067w
CA4380	0.7	2.9	0.8	1.1	1.1	2.1	IPF12736	orf19.5673	unknown function	YPR194c
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase	no match (e-value > 0.05)
CA0219	1.6	2.9	1.1	1.2	1.2	0.9	YAP3	orf19.3193	transcription factor of a fungal-specific family of bzip proteins	YHL009c
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function	YBR042c
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)	YOR157c
CA0740	1.2	2.8	1.0	1.0	1.3	1.5	UMP1	orf19.3140.1	proteasome maturtion factor (by homology)	YBR173c
CA0915	3.0	2.8	1.1	1.0	1.0	0.7	KAR2	orf19.2013	dnaK-type molecular chaperone (by homology)	YJL034w
CA5060	1.5	2.8	0.9	1.0	1.2	1.2	IPF3690	orf19.3029	unknown function	YDR036c
CA4643	2.2	2.7	1.1	1.2	1.3	1.0	PRE9	orf19.350	20S proteasome subunit Y13 (alpha3) (by homology)	YGR135w
CA3034	2.3	2.7	0.8	0.9	1.4	1.3	RPN12	orf19.213	26S proteasome regulatory subunit (by homology)	YFR052w
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA0417	2.3	2.7	0.9	1.0	1.4	1.2	UBC13	orf19.933	E2 ubiquitin-conjugating enzyme (by homology)	YDR092w
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)	YDR069c
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)	YJL001w
CA2131	1.4	2.6	0.9	1.0	1.0	1.1	IDP1	orf19.5211	isocitrate dehydrogenase, cytosolic (by homology)	YDL066w

CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA1759	1.5	2.6	1.3	0.9	1.0	1.0	IPF14744	orf19.5125	unknown function	YLR149c
CA5049	1.5	2.5	1.0	1.1	0.9	0.9	CDC12	orf19.3013	septin (by homology)	YHR107c
CA4319	1.9	2.5	1.1	1.2	1.1	0.9	RPN10	orf19.4102	Protein degradation (by homology)	YHR200w
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA0155	1.9	2.5	1.2	1.0	1.4	1.2	RPT6	orf19.3593	26S proteasome regulatory subunit (by homology)	YGL048c
CA5040	1.4	2.5	0.8	0.8	0.9	0.9	BAT22	orf19.6994	branched chain amino acid aminotransferase (by homology)	YJR148w
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex	YDL143w
CA4924	2.0	2.5	1.2	1.2	1.4	1.0	UBP6.3f	orf19.6063	Ubiquitin-specific protease, 3-prime end (by homology)	YFR010w
CA6091	1.6	2.5	0.8	0.7	0.8	0.8	UFD2	orf19.5965	Ubiquitin fusion degradation protein 2 (by homology)	YDL190c
CA2698	1.2	2.5	1.1	0.8	0.9	1.0	SUL1	orf19.2738	High-affinity sulfate transport protein (by homology)	YLR092w
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA2296	1.3	2.5	0.8	1.0	1.1	1.0	SCL1	orf19.5378	Proteasome subunit YC7alpha (by homology)	YGL011c
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA4525	1.2	2.5	1.0	1.1	1.1	1.2	SEC22	orf19.479.2	synaptobrevin-type protein transport protein (by homology)	YLR268w
CA4168	1.8	2.4	1.1	1.2	1.0	1.1	IPF7781	orf19.2965	putative pump-driving ATPase	YDL100c
CA1285	1.0	2.4	1.1	1.3	1.1	1.0	SKP1	orf19.4427	kinetochore protein complex CBF3 by homology	YDR328c
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA0265	1.6	2.4	1.3	1.0	1.0	1.0	STI1.3f	orf19.3191	stress-induced protein (by homology)	YOR027w
CA5087	1.0	2.4	1.1	0.9	0.7	0.9	IPF20025	orf19.3062	unknown function	YKL033w
CA5528	1.9	2.4	1.2	1.3	1.2	1.1	RPN7	orf19.7286	Subunit of the regulatory particle of the proteasome (by homc	YPR108w
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA5435	1.6	2.4	0.7	0.7	0.9	0.9	UFD4	orf19.3237	ubiquitin fusion degradation protein (by homology)	YKL010c
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end	YKR076w
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase	YLR377c
CA2857	2.1	2.3	1.2	1.2	1.0	1.0	SSA1	orf19.1065	Heat shock protein of HSP70 family	YER103w
CA5173	0.9	2.3	0.8	1.1	0.8	1.0	CPS2.3f	orf19.4610.1	Carboxypeptidase YSCS precursor, 3-prime end (by homolo	YJL172w
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function	YDR430c
CA5791	1.5	2.3	1.2	1.0	1.4	1.2	RPT2	orf19.5440	26S proteasome regulatory subunit (by homology)	YDL007w
CA4772	1.8	2.3	1.3	1.1	1.1	1.1	CCT3	orf19.4004	Chaperonin (by homology)	YJL014w
CA1653	2.8	2.3	1.3	1.4	1.0	0.7	STE23	orf19.5561	protease involved in a-factor processing by homology	YLR389c
CA2121	1.3	2.3	0.9	0.9	1.1	1.2	IPF7930	orf19.1338	unknown function	YJL123c
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)	YER021w
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function	YGL145w
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)	YBR058c
CA5618	1.4	2.2	1.0	1.0	1.0	1.1	LEU2	orf19.7080	isopropyl malate dehydrogenase	YCL018w
CA5303	1.2	2.2	1.1	1.2	1.5	0.8	IPF2180	orf19.7170	unknown function	no match
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function	YPL110c
CA4257	1.2	2.2	1.0	0.9	1.3	1.1	PRE6	orf19.544.1	20S proteasome subunit	YOL038w
CA3706	0.9	2.2	0.7	0.8	1.1	1.0	PSA2	orf19.4943	mannose-1-phosphate guanyltransferase by homology	YDL055c
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA2565	1.6	2.2	1.1	1.0	0.9	1.3	MET15	orf19.5645	O-acetylhomoserine O-acetylserine sulphydrylase	YLR303w
6100.2	1.5	2.2	2.0	1.2	1.1	1.0				
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA5308	1.5	2.2	1.0	0.9	1.3	1.1	PRE5	orf19.7178	20S proteasome subunit alpha6 (by homology)	YMR314w
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA1508	2.1	2.2	0.7	1.0	0.7	0.9	IPF9977	orf19.4525	unknown function	YLR064w
CA1629	0.6	2.2	1.2	1.5	1.4	1.3	NPI46	orf19.1030	proline cis-trans isomerase (by homology)	YLR449w
CA2951	1.3	2.1	0.8	1.0	0.9	1.0	SBP1	orf19.5854	RNA binding protein-like (by homology)	YHL034c
CA4865	1.5	2.1	1.0	1.0	1.1	1.2	IPF4085	orf19.3841	similar to Saccharomyces cerevisiae Apg1p essential for aut	YGL180w
CA4604	1.2	2.1	1.3	1.3	1.2	0.9	MBF1	orf19.3294	Multiprotein bridging factor mediates GCN4-dependent trans	YOR298ca
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function	YGR101w
CA1116	1.3	2.1	1.1	1.3	0.9	1.0	CCT5	orf19.2288	T-complex protein 1, epsilon subunit (by homology)	YJR064w
CA0914	1.6	2.1	0.9	1.0	1.2	1.1	SRA1	orf19.2015	cAMP dependent protein kinase, regulatory subunit (by homc	YIL033c
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA4167	0.6	2.1	0.8	1.0	0.9	1.1	IPF7778	orf19.2966	putative carboxymethylenebutenolidase (dienelactone hydrol	YDL086w
CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)	YIL095w
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5717	1.0	2.1	0.9	1.1	0.8	1.1	CYP51	orf19.7421	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by	YDR304c
CA1256	2.2	2.0	1.0	1.1	0.7	1.1	UBP15	orf19.1777	ubiquitin-specific protease (by homology)	YMR304w
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA1894	2.2	2.0	1.0	1.1	1.2	1.0	PRE7.5f	orf19.2755	putative subunit of 20S proteasome, exon 1 (by homology)	YBL041w
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA1911	1.1	2.0	1.1	0.9	1.0	1.0	SSE1	orf19.2435	heat shock protein of HSP70 family (by homology)	YPL106c
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA5977	1.2	2.0	1.2	1.0	1.3	1.2	UBC4	orf19.7571	E2 ubiquitin-conjugating enzyme (by homology)	YBR082c
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)	YMR234w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)	YHR104w
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle	YLR178c
CA0663	2.1	1.9	0.9	0.9	1.0	1.1	PUP2	orf19.709	20S proteasome subunit(alpha5) (by homology)	YGR253c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA4988	1.4	1.9	1.0	0.9	0.9	0.8	RPN2	orf19.5260	Proteasome regulatory subunit (by homology)	YIL075c
CA1880	1.7	1.9	1.2	1.3	1.4	1.0	IPF13316	orf19.2269	unknown function	YNL010w
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homo	YPR183w
CA5862	1.0	1.9	1.2	1.3	1.1	1.1	POT11	orf19.7520	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)	YIL160c
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function	YKL094w
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA4522	1.2	1.9	1.0	0.9	1.1	1.0	RPT4	orf19.482	26S proteasome regulatory subunit (by homology)	YOR259c
CA4389	1.6	1.9	1.2	1.0	1.2	1.2	RPT5	orf19.3123	26S proteasome regulatory subunit (by homology)	YOR117w
CA5268	1.8	1.9	1.1	1.1	0.7	0.9	SEC18.3f	orf19.4994	vesicular fusion protein, 3-prime end (by homology)	YBR080c
CA3868	1.3	1.9	1.1	1.1	0.8	1.0	CCT1	orf19.401	component of chaperonin-containing T-complex (by homolog	YDR212w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA0394	1.6	1.9	1.0	1.3	1.4	1.4	IPF12758.	orf19.334	unknown function, 5-prime end	no match (e-value > 0.05)
CA3247	1.2	1.9	1.1	1.0	0.7	0.8	IPF15832	orf19.4676	unknown function	YKL053ca
CA4695	1.2	1.9	0.9	1.4	1.3	1.0	IPF4229	orf19.6923	unknown function	YML015c
CA3898	1.3	1.9	1.1	0.9	0.8	1.0	UBA2	orf19.5074	ubiquitin-activating -like enzyme by homology	YDR390c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function	YDL012c

CA0661	1.9	1.9	0.7	0.9	1.0	1.0	APG7	orf19.707	component of the autophagic system (by homology)	YHR171w
CA2120	1.6	1.9	0.9	1.0	1.2	1.2	PUP3	orf19.1336	PRCT yeast proteasome component (by homology)	YER094c
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA5554	1.0	1.9	0.7	1.0	0.9	1.0	IPF1960.5	orf19.7318	putative transcriptional activator, 5-prime end	YCR106w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match (e-value > 0.05)
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA3422	1.6	1.9	0.9	0.8	0.7	0.9	IPF17289	orf19.6134	unknown function	YLR440c
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match (e-value > 0.05)
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA1755	1.6	1.8	1.1	0.9	0.8	1.1	PDI1	orf19.5130	protein disulfide-isomerase precursor (by homology)	YCL043c
CA0408	1.9	1.8	0.9	1.0	0.9	1.0	SAC6.5f	orf19.5544	actin filament bundling protein, fimbrin, 5-prime end (by homc	YDR129c
CA1389	1.5	1.8	1.4	1.3	0.8	1.1	PLP2	orf19.1769	Might regulate Ste4p in pheromone response (by homology)	YOR281c
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA3191	1.5	1.8	0.7	1.0	0.7	0.8	IPF11601	orf19.2151	unknown function	YOR165w
CA5930	2.3	1.8	1.1	0.9	1.1	1.0	ECM29.3f	orf19.6773	Involved in cell wall biogenesis and architecture, 3-prime end	YHL030w
CA1693	1.6	1.8	1.0	1.0	1.0	1.1	IPF17054	orf19.5037	unknown function	no match (e-value > 0.05)
CA2286	0.9	1.8	0.8	1.1	1.4	1.4	IPF5369	orf19.5553	unknown function	YKL069w
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA0164	1.0	1.8	1.0	1.0	0.9	1.0	IPF11694	orf19.4335	similar to Saccharomyces cerevisiae Tna1p high affinity nicot	YGR260w
CA2278	1.8	1.8	1.2	1.0	1.2	1.2	IPF10806	orf19.782	unknown function	YBR204c
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA5836	1.1	1.8	0.8	1.1	1.2	0.7	IPF428	orf19.7490	transport protein (by homology)	YOL137w
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA3435	1.0	1.8	0.9	1.4	1.3	1.2	IPF6391	orf19.583	indoleamine 2,3-dioxygenase (by homology)	YJR078w
CA2669	1.2	1.8	0.8	0.9	1.0	1.0				
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA1269	1.6	1.7	1.1	1.1	1.1	1.4	IPF19726	orf19.3158	unknown function	YDL001w
CA4798	1.4	1.7	0.9	1.0	0.9	0.9	RPN5.3f	orf19.4032	subunit of the regulatory particle of the proteasome, 3-prime (	YDL147w
CA2146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function	no match (e-value > 0.05)
CA0345	1.2	1.7	1.0	1.0	1.0	0.9	ACH1	orf19.3171	acetyl-coenzyme-A hydrolase (by homology)	YBL015w
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA5146	1.2	1.7	0.9	1.0	1.0	1.0	YMC2	orf19.4583	Carnitine/acylcarnitine translocase (by homology)	YBR104w
CA2785	0.6	1.7	0.6	0.9	0.9	1.0	MET13	orf19.288	Methylene tetrahydrofolate reductase (by homology)	YGL125w
CA0840	1.1	1.7	1.4	1.0	1.3	1.0				
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in acetic	YCR032w
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA3697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific	YJR099w
CA4480	0.9	1.7	0.7	1.1	1.5	1.4	IPF6464	orf19.1887	putative triacylglycerol lipase (by homology)	YLL012w
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA4219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein pho	YKL193c
CA5555	0.9	1.7	1.0	1.0	1.3	1.1	SUC1	orf19.7319	Putative zinc finger protein Suc1	YFL052w
CA5196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function	YIL001w
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA5695	1.3	1.7	0.9	0.8	0.7	1.1	IPF3310	orf19.7397	unknown function	YPR022c
CA5283	0.9	1.7	0.8	1.0	0.8	1.2	IPF1912	orf19.7140	putative catechol o-methyltransferase	no match (e-value > 0.05)
CA2508	1.9	1.7	1.4	1.1	0.9	1.0	BET5	orf19.302	targeting and fusion of ER to Golgi transport vesicles (by hon	YML077w
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA4165	1.0	1.7	1.0	1.1	1.0	1.0	IPF7774	orf19.2968	unknown function	no match (e-value > 0.05)
CA4890	1.5	1.7	1.0	0.9	1.0	1.1	PRE10	orf19.6582	20S proteasome subunit C1 (by homology)	YOR362c
CA5941	1.5	1.7	1.0	1.3	1.4	0.9	IPF3486	orf19.6756	unknown function	YGL198w
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA4142	1.5	1.7	1.0	1.0	1.5	1.2	PRE4	orf19.4230	20S proteasome subunit(beta7) (by homology)	YFR050c
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA5559	1.0	1.7	1.2	1.1	0.8	1.1	CBP1	orf19.7323	Corticosteroid binding protein	YMR020w
CA3870	1.0	1.7	0.6	0.9	1.3	1.0	YPK1	orf19.399	ser/thr-specific protein kinase (by homology)	YMR104c
CA5306	1.2	1.7	1.0	1.0	1.1	1.1	NPT1	orf19.7176	Nicotinate phosphoribosyltransferase (by homology)	YOR209c
CA2548	1.6	1.7	1.0	0.9	0.9	0.9	PGA34	orf19.2833	unknown function	no match
CA0972	1.1	1.6	1.1	1.2	1.0	1.0	CYP1	orf19.6472	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homc	YDR155c
CA1252	1.9	1.6	0.9	0.9	0.9	0.9	RPN1	orf19.4956	26S proteasome regulatory subunit (by homology)	YHR027c
CA4333	1.2	1.6	1.2	1.1	1.4	1.2	IPF2083	orf19.4086	unknown function	YNL056w
CA1942	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eo	orf19.4191.1	Ubiquitin--protein ligase, 3-prime end (by homology) FALSOF	YGL141w
CA4799	1.6	1.6	1.1	1.0	0.8	1.0	RPN5.5f	orf19.4034	subunit of the regulatory particle of the proteasome, 5-prime (	YDL147w
CA3956	1.2	1.6	1.0	1.0	1.0	1.2	IPF6712.3	orf19.1414.2	unknown function, 3-prime end | Unknown function	no match
CA4127	0.9	1.6	0.7	0.9	0.9	0.9	IPF6629	orf19.2762	unknown function	YLR109w
CA3310	1.4	1.6	1.1	1.2	0.7	1.0	PFS2	orf19.2307	Polyadenylation Factor I subunit (by homology)	YNL317w
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA3746	1.2	1.6	1.6	1.0	0.8	1.1	ARA1	orf19.2172	D-arabinose dehydrogenase (by homology)	YBR149w
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA2888	1.6	1.6	1.0	1.1	1.2	1.2	GIM5	orf19.2471	Gim complex component (by homology)	YML094w
CA2773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase	YOR211c
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c
CA3569	1.3	1.6	1.0	1.1	1.0	1.1	IPF3268	orf19.3136	unknown function	YDR325w
CA2157	2.2	1.6	1.5	1.1	0.8	0.8	IPF8537	orf19.5300	similar to Saccharomyces cerevisiae Cne1p calnexin, involve	YAL058w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match (e-value > 0.05)
CA4320	1.1	1.6	1.2	1.1	0.8	1.1	ECM17	orf19.4099	Putative sulfite reductase (by homology)	YJR137c
CA2561	1.0	1.6	1.2	1.5	0.8	0.9	CAR2	orf19.5641	ornithine aminotransferase (by homology)	YLR438w
CA5564	1.2	1.6	0.7	0.9	1.0	0.9	IPF1980	orf19.7328	unknown function	no match (e-value > 0.05)
CA1452	1.6	1.6	0.8	0.8	1.3	1.0	REV1	orf19.4412	DNA repair protein (by homology)	YOR346w
CA1756	1.0	1.6	1.1	1.2	1.5	1.0	IPF14562	orf19.5129	unknown function	no match (e-value > 0.05)
CA1913	1.4	1.6	0.9	0.9	1.2	1.2	ARC35	orf19.2437	subunit of the Arp2/3 complex involved in the control of actin	YNR035c
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match (e-value > 0.05)
CA2863	1.3	1.6	1.0	1.0	1.3	1.1	IPF20117	orf19.1058	unknown function	YLR421c
CA0593	1.3	1.6	1.0	0.8	1.2	1.2	ARP6	orf19.4904	actin-related protein (by homology)	YLR085c
CA1838	1.3	1.6	1.1	1.1	1.4	1.3	IPF5777	orf19.3963	unknown function	YER182w
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA2926	1.1	1.6	0.8	1.1	1.3	1.3	UBA3	orf19.4209	Ubiquitin-like protein activating enzyme	YPR066w
CA5595	1.1	1.6	0.9	1.0	0.9	1.4	IPF568	orf19.7105	similar to Saccharomyces cerevisiae Far1p cyclin-dependent	YJL157c
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c

CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal ass	YKL197c
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA2867	1.2	1.5	0.9	0.8	0.8	0.8	IPF11688	orf19.2844	similar to Saccharomyces cerevisiae Apl4p AP-1 complex su	YPR029c
CA3336	1.0	1.5	0.8	0.8	1.1	1.3	IPF19983	orf19.2335	unknown function	YHR113w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltra	YMR149w
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA2133	1.2	1.5	1.0	1.0	1.0	0.8	IPF5866	orf19.5213	unknown function	YDR228c
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA3907	1.2	1.5	0.7	1.0	1.0	0.9	IPF3304	orf19.4395	similar to Saccharomyces cerevisiae Aip1p actin cytoskeletor	YMR092c
CA3683	1.2	1.5	1.1	1.0	1.1	1.2	PPZ1	orf19.726	ser/thr phosphatase required for normal osmoregulation (by h	YML016c
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase	YFR015c
CA4625	1.1	1.5	0.8	0.9	0.9	1.2	IPF5742	orf19.3319	thioredoxin-like protein (by homology)	YGR209c
CA4720	1.2	1.5	1.0	1.0	1.3	1.0	ECM18	orf19.6958	Involved in cell wall biogenesis and architecture (by homolog	YDR125c
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA3057	1.3	1.5	1.0	1.2	1.5	1.2	IPF2954	orf19.4293	unknown function	YDR267c
CA3589	0.8	1.5	0.8	1.2	1.4	1.1	IPF10113	orf19.2249	unknown function	YNR020c

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[[Cd OS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
HS+ OS+ XS+										
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA5797	1.2	0.9	8.7	8.2	0.7	1.0	IPF4182	orf19.5446	unknown function	no match (e-value > 0.05)
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)	YDR497c
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function	no match
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function	YLR205c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match (e-value > 0.05)
CA0721	1.5	0.9	1.3	2.3	0.8	0.8	IPF10429	orf19.2887	unknown function	YMR295c
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function	no match (e-value > 0.05)
CA5840	1.2	1.0	1.3	1.9	1.0	1.2	EBP6	orf19.7495	NADPH dehydrogenase (by homology)	YPL171c
CA0948	0.6	1.1	0.9	1.9	1.1	1.0	IPF10270	orf19.1272	unknown function	YGR111w
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match (e-value > 0.05)
CA0677	1.4	1.3	1.2	1.8	1.0	0.8	IPF13095	orf19.1182	unknown function	YGL212w
CA4870	1.5	1.1	1.3	1.7	1.2	1.3	IPF19568	orf19.6556	unknown function	no match (e-value > 0.05)
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA1187	0.7	0.9	1.2	1.5	1.1	1.0	QRI7	orf19.3787	putative glycoprotease (by homology)	YKR038c
CA2161	1.1	1.1	1.1	1.5	1.0	1.1	IPF11876	orf19.5295	unknown function	no match (e-value > 0.05)

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[[Cd XS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
HS+ OS+ XS+										
Stress ()*	**HS+**	**HS+**	**OS+**	**OS+**	**XS+**	**XS+**				
Systemat	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**rmali**	**Common**	**Ca orf19**	**Ca Function**	**S.c. hom.**
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function	YDR371w
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function	no match (e-value > 0.05)
CA2435	1.1	1.7	1.2	1.1	17.7	13.6	IPF9483	orf19.3395	probable permease (by homology)	YHR048w
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function	YKL086w
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function	no match (e-value > 0.05)
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase	YBR046c
CA0639	1.6	1.8	1.0	1.0	9.0	10.5				
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match (e-value > 0.05)
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function	no match (e-value > 0.05)
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA4913	1.1	1.0	1.3	1.0	1.2	6.8	CIS2	orf19.6053	Gamma-glutamyltransferase (by homology)	YLR299w
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)	YBR293w
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function	YKR071c
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA4829	1.0	1.1	1.3	1.0	6.3	5.5	IPF1210	orf19.2067	similar to Saccharomyces cerevisiae Nfu1p involved in home	YKL040c
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)	YHR044c
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function	no match (e-value > 0.05)
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)	YPL171c
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)	YDR338c
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function	YOR292c
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)	YOR101w
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function	no match (e-value > 0.05)
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)	YDR513w
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match (e-value > 0.05)
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function	YOL119c
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)	YIL120w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homolog	YER053c
CA4399	1.4	1.7	1.2	1.3	1.1	3.8	PRA1	orf19.3111	pH-regulated antigen	YOL154w
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function	YGL136c
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match (e-value > 0.05)
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function	YNL144c
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function	YDR336w
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)	YNL229c
CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function	no match (e-value > 0.05)

CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match (e-value > 0.05)
CA1005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)	YPL101w
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match (e-value > 0.05)
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homolc	YJL101c
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA0583	1.2	2.5	1.3	1.3	3.9	3.2	GSH1.3f	orf19.5059	gamma-glutamylcysteine synthetase, 3 prime end (by homolc	YJL101c
CA0996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)	no match (e-value > 0.05)
CA0933	1.3	1.1	0.8	1.0	5.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)	YMR301c
CA1775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology	YDL215c
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA0385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function	YNL250w
CA5697	1.3	1.0	0.8	1.1	3.8	3.0				
CA1170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function	YDR132c
CA4392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)	YNL229c
CA1016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function	YOR273c
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA5868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function	YMR090w
CA0595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5	orf19.4901	unknown function, 5-prime end	YER175c
CA1157	1.2	1.0	1.4	1.1	0.8	2.8	PZF1	orf19.4125	TFIIIA (transcription initiation factor) (by homology)	YPR186c
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA3258	1.1	1.0	0.5	0.9	1.1	2.7				
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)	YPR194c
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA4885	1.2	1.3	1.2	1.1	1.1	2.6	IPF1636	orf19.6577	similar to Saccharomyces cerevisiae Tpo1p multidrug resista	YLL028w
CA4662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by hom	YMR038c
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA3919	1.1	1.0	0.8	0.8	1.0	2.5	IFC5	orf19.5121	unknown function	YPR194c
CA2227	1.5	1.2	1.0	0.9	1.4	2.5	EBP7	orf19.5816	NADPH DEHYDROGENASE by homology	YHR179w
CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA2894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function	no match (e-value > 0.05)
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA5289	0.7	0.9	0.9	0.9	1.4	2.4	NRG1	orf19.7150	similar to transcriptional repressor Nrg1p/Nrg2p	YBR066c
CA0942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function	YER101c
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA1372	0.9	1.0	1.2	1.0	1.1	2.4	IPF15844	orf19.4961	similar to Saccharomyces cerevisiae Stp2p involved in pre-tF	YHR006w
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA4929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA1108	1.1	1.1	1.0	1.0	1.0	2.3	IPF11273	orf19.5231	unknown function	no match (e-value > 0.05)
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match (e-value > 0.05)
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (a	YPR192w
CA1536	1.6	1.6	1.1	1.3	1.3	2.2	SOK1	orf19.451	high copy suppressor of a cyclic AMP-dependent protein kina	YDR006c
CA2177	1.1	1.1	1.3	1.0	2.2	2.2	ROD1	orf19.1509	O-dinitrobenzene,calcium and zinc resistance protein (by hor	YFR022w
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA0129	1.1	0.9	1.0	1.0	1.2	2.2	IPF10495	orf19.246	unknown function	YIL108w
CA2711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)	YDR460w
CA5011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function	YMR101c
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA3354	1.1	1.1	0.7	0.7	1.2	2.2	GPR1	orf19.1944	similar to Saccharomyces cerevisiae Gpr1p G-protein couple	YDL035c
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA0560	1.2	1.0	0.9	1.0	1.2	2.1	GPX3	orf19.87	glutathione peroxidase (by homology)	YIR037w
CA4630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c
3692.2	1.2	1.2	0.8	0.9	2.2	2.1				
6532.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA5009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)	YKL119c
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA4917	0.7	0.8	0.8	1.4	2.0	2.1	ECM31	orf19.6057	Involved in cell wall biogenesis and architecture (by homolog	YBR176w
CA2477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)	YJR061w
CA3094	1.1	1.1	1.1	0.7	1.3	2.1	IPF11548	orf19.3854	serine/threonine protein kinase (by homology)	YCR008w
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA5934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function	YHL029c
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA3087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)	YLR147c
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA0160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease	YKR039w
CA3446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function	YKL195w
CA4580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function	no match (e-value > 0.05)
CA4836	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)	YJR104c
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA0757	1.0	0.7	0.6	0.8	2.2	2.0				
CA1600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)	YHR175w
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA0500	0.9	1.0	1.4	1.2	0.9	2.0	IPF20058	orf19.4793	unknown function	YOR252w
CA2584	0.8	1.2	1.0	1.1	2.1	2.0	IPF9440	orf19.4373	similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase	YDR236c
CA5008	1.0	0.8	1.1	1.3	1.2	2.0	IPF12577	orf19.5238	unknown function	no match (e-value > 0.05)
CA5678	0.8	1.0	1.0	0.8	0.9	2.0	IPF1292	orf19.7381	unknown function Hypothetical zinc-finger protein	YML099c
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA5010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function	YMR101c

CA1002	1.0	1.0	1.9	1.2	0.9	1.9	ROK1.3f	orf19.3756	RNA helicase, 3-prime end	YGL171w
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (	YOL119c
CA4023	1.0	1.0	0.9	1.0	0.9	1.9	FRP5	orf19.3440	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function	YGR110w
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function	no match (e-value > 0.05)
CA0995	1.0	1.0	0.9	0.9	3.8	1.9				
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)	YGR234w
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function	no match (e-value > 0.05)
CA4778	1.0	1.1	0.9	1.0	1.2	1.8	IFJ1	orf19.4011	Unknown function	YGR263c
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA4174	1.2	3.6	1.3	1.6	1.6	1.8	IPF4430	orf19.2959.1	unknown function	YDR276c
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match (e-value > 0.05)
CA0052	1.0	1.1	1.4	1.0	1.3	1.8	IPF19567	orf19.475	Unknown function	YHR085w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)	YML004c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase	YOR202w
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)	YMR275c
CA3187	1.0	0.8	1.5	1.2	0.8	1.8	IPF17094	orf19.2143	unknown function	YPL183c
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4960	0.7	0.8	0.7	0.7	1.2	1.8	IPF3912	orf19.6514	unknown function	YPL177c
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function	YCL044c
CA1277	1.3	1.0	1.4	1.0	1.2	1.8	IPF10837	orf19.3630	unknown function	YDR083w
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA4477	0.9	1.2	1.2	1.1	1.2	1.8	IPF6459	orf19.1890	unknown function	YMR210w
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function	no match (e-value > 0.05)
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology	YAL012w
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match (e-value > 0.05)
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5	orf19.6654	unknown function	YMR221c
CA4612	1.1	0.9	1.4	1.0	1.5	1.7	PPM2	orf19.3303	carboxy methyl transferase; homolog of PPM1 (by homology)	YOL141w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match (e-value > 0.05)
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eo	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA5135	1.0	1.0	1.0	1.0	1.8	1.7	HSP104.5	orf19.6389	Heat shock protein, 5-prime end (by homology)	YLL026w
CA0629	1.1	1.3	0.7	0.8	1.0	1.7	IPF3876	orf19.775	unknown function	YJR126c
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)	YNL240c
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)	YPL140c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA2750	1.1	1.0	1.1	1.0	4.6	1.7	ATX1	orf19.2369.1	antioxidant protein and metal homeostasis factor (by homolo	YNL259c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.5f	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA	YAL049c
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function	YNL166c
CA5287	0.8	1.0	1.0	0.9	1.0	1.7	IPF1922	orf19.7148	similar to multidrug resistance proteins	YLL028w
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function	YPL092w
CA5696	0.9	1.0	1.6	1.3	1.4	1.7	IPF3309.3	orf19.7398	unknown function, 3-prime end	YER126c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA4614	1.1	1.3	1.4	0.8	1.0	1.7	IPF7952	orf19.3305	unknown function	YDR213w
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA6009	0.8	1.0	1.3	1.0	1.2	1.7	IPF643	orf19.7610	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine p	YER075c
CA0626	1.1	0.9	1.3	1.1	1.4	1.7	IPF3161	orf19.3161	Unknown function	YNR054c
CA3157	0.9	1.4	1.0	1.3	1.5	1.7	IPF14456	orf19.1588	unknown function Unknown function	YBR269c
CA4563	1.0	1.0	1.0	1.1	0.8	1.7	IPF6566	orf19.6873.1	unknown function	YBL071wa
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase	YAL039c
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match (e-value > 0.05)
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function	YMR136w
CA5580	1.2	1.4	0.9	1.0	1.3	1.6	RVS161	orf19.7124	cytoskeletal binding protein (by homology)	YCR009c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA6038	0.8	1.2	1.8	1.2	1.1	1.6	LTV1	orf19.7650	low-temperature viability protein (by homology)	YKL143w
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)	YLR120c
CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function	YDR219c
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homolo	YOR049c
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function	no match
CA5739	1.0	1.1	0.9	1.0	1.4	1.6	IPF2884	orf19.7449	unknown function	YMR211w
CA0941	0.9	1.0	0.8	1.0	1.3	1.6	IPF8617	orf19.3705	unknown function	YCR079w
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match (e-value > 0.05)
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA5474	1.3	0.9	1.8	1.1	1.0	1.6	IPF16944.	orf19.3287	unknown function, 3-prime end	YMR014w
CA1958	1.0	1.0	0.9	0.9	1.2	1.6	IFE1	orf19.769	Unknown function	YAL061w
CA0393	1.4	1.1	1.0	1.1	1.7	1.6	IPF12758.	orf19.333.2	unknown function, 3-prime end	no match
CA2395	1.1	1.1	1.1	1.0	1.0	1.6	IPF6425	orf19.3536	unknown function	YOR320c
CA1540	0.9	0.9	1.2	1.5	0.9	1.6	IPF1047	orf19.4563	unknown function	YMR310c
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function	YHR087w
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA2460	1.5	1.1	1.0	1.0	1.1	1.6				
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA2233	1.0	1.0	1.0	1.0	1.1	1.6	IFJ3	orf19.3924	unknown function	YGR263c
CA6016	0.9	0.8	1.4	1.4	1.4	1.6	IPF630	orf19.7618	unknown function	YOR145c
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function	YLR021w
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3	orf19.4266.1	septin, 3-prime end (by homology)	YDR218c
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function	YHR101c
CA1703	0.9	1.2	0.8	1.0	1.4	1.6	IPF7987	orf19.703	unknown function	YGR247w
CA3808	0.8	1.1	1.5	1.2	1.1	1.6	FAL1	orf19.2488	ATP-dependent RNA helicase	YDR021w
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function	YJL092w

CA5875	1.2	1.1	0.9	1.0	0.8	1.6	IPF324.3f	orf19.7545	unknown function, , 3-prime end	no match (e-value > 0.05)
CA3741	0.9	0.9	0.9	1.0	0.7	1.6	MRS4	orf19.2178	RNA splicing protein and member of the mitochondrial carrier	YKR052c
CA1080	1.0	0.9	1.3	0.9	1.4	1.6	IPF14710	orf19.4820	unknown function	YKL162c
CA4158	0.9	0.9	0.9	0.9	0.7	1.6	DLD3	orf19.5805	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA3080	0.9	1.1	1.0	0.8	1.0	1.6	IPF14634	orf19.4153	APP-binding protein 1 (by homology)	YPL003w
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)	YOR171c
CA5833	0.9	0.9	1.2	1.1	1.2	1.5	IMP3	orf19.7488	U3 small nucleolar ribonucleoprotein (by homology)	YHR148w
CA4818	0.7	0.9	0.8	0.7	1.2	1.5	IPF1193	orf19.2079	unknown function Unknown function	YHL018w
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membrar	YIL047c
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA2592	1.2	0.9	1.4	1.1	1.6	1.5	IPF18447	orf19.59	putative zinc-finger protein (by homology)	YBR267w
CA0473	1.0	1.0	1.0	1.0	1.3	1.5	GRP1	orf19.4781	dihydroflavonol-4-reductases (by homology)	YOL151w
CA3722	1.3	1.2	0.9	1.0	1.5	1.5	PHO13	orf19.4172	4-nitrophenylphosphatase (by homology)	YDL236w
CA4507	1.0	1.1	1.1	1.3	1.0	1.5	IPF20015	orf19.499	unknown function	YNL063w
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)	YPR016c
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rRI	YDR087c
CA2398	1.1	1.0	1.0	1.0	1.1	1.5	IPF6431	orf19.3539	unknown function	YBR141c
CA0343	1.6	1.2	1.1	1.0	0.9	1.5	LYS1	orf19.1789.1	saccharopine dehydrogenase (by homology)	YIR034c
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function	no match (e-value > 0.05)
CA1689	1.0	1.0	0.9	1.1	1.1	1.5	IPF13030	orf19.3655	unknown function	no match (e-value > 0.05)
CA2428	1.0	1.1	0.9	0.9	1.3	1.5	IPF9894	orf19.3405	possible zinc-finger protein	no match (e-value > 0.05)
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function	no match (e-value > 0.05)
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha	YIL099w
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA4754	0.7	1.0	1.0	1.0	1.2	1.5	IPF11479	orf19.4825	unknown function	YIL098c
CA1630	1.4	1.2	1.5	1.1	1.1	1.5	RPP1	orf19.1029	required for processing of tRNA and 35S rRNA (by homology	YHR062c
CA5626	0.9	1.1	0.9	1.0	1.1	1.5	IPF498	orf19.7071	unknown function	YML123c
CA4613	1.0	1.0	1.3	1.1	1.3	1.5	IPF7950	orf19.3304	similar to Saccharomyces cerevisiae Rrp40p involved in ribos	YOL142w
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function	no match (e-value > 0.05)
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)	YEL060c
CA4404	1.0	1.3	1.4	1.1	1.2	1.5	MET16	orf19.3106	3 -phosphoadenylylsulfate reductase (by homology)	YPR167c
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
11759.2	0.6	1.2	0.2	0.3	1.4	1.5				
CA0730	0.9	0.7	1.2	1.1	1.6	1.5	IPF7334	orf19.3724	unknown function	YOR004w
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function	YPL122c
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYI	YOR005c
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function	YNL191w

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[[Cd OS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase	YKR070w
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function	YMR226c
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w

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[Cd XS+ up 1.5 10FDR] and [Cd OS+ up 1.5 10FDR]] less [Cd HS+ up 1.5 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match (e-value > 0.05)
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match (e-value > 0.05)
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function	no match (e-value > 0.05)
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c

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[Cd XS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10FDR]

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match (e-value > 0.05)
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homolo	YMR152w
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match (e-value > 0.05)
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match (e-value > 0.05)
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by ho	YML130c
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match (e-value > 0.05)
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w

CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homolo	YPL171c
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)	YKR039w
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inn	YMR152w
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase	YER042w
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase	YNL277w
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)	YLR043c
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function	YNL229c
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology	YDR032c
CA2258	1.1	2.8	0.9	0.9	7.4	15.1	IFR1	orf19.1763	Unknown function	YNL134c
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-bind	YGL091c
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)	YNL270c
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function	YNL134c
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA0636	2.2	2.5	0.9	0.9	10.8	15.0				
CA1569	1.8	2.4	1.5	1.2	1.1	2.4	IPF7616	orf19.1159	putative homoserine O-acetyltransferase (by homology)	YNL277w
CA1882	1.1	2.4	0.8	1.0	0.8	1.9	IPF19934	orf19.2210	unknown function	no match (e-value > 0.05)
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match (e-value > 0.05)
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)	YGR234w
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)	YHR137w
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)	YOL151w
CA1846	1.5	2.2	0.8	0.9	12.5	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)	YOR388c
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)	YPR086w
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable mono	no match
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in regu	YIL046w
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)	YIR037w
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)	YNL040w
CA0183	1.5	1.9	1.5	1.1	1.4	2.2	CAP1	orf19.1623	transcriptional acivator (by homology)	YML007w
CA1395	1.1	1.9	1.0	0.9	11.5	11.7				
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)	YIR035c
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function	YIR017c
CA3059	1.2	1.8	1.2	1.1	6.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)	YDR353w
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA3086	1.0	1.7	1.1	1.2	2.3	3.9	GLR1	orf19.4147	by similarity to S. cerev. and C. albicans:glutathione reductas	YPL091w
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function	YLR256w
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)	YOR388c
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by ho	YDL168w
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function	no match (e-value > 0.05)
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase	YHR008c
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w

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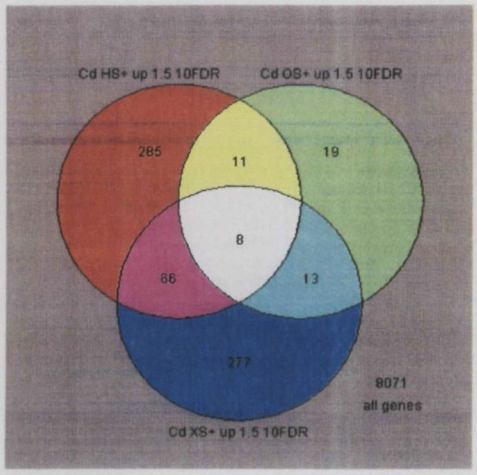
[[Cd OS+ up 1.5 10FDR] and [Cd XS+ up 1.5 10FDR]] and [Cd HS+ up 1.5 10FDR]

	HS+ OS+									
Species ()	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	rmali:	rmali:	rmali:	rmali:	rmali:	rmali:	Common	Ca orf19	Ca Function	S.c. hom.
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match (e-value > 0.05)
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match (e-value > 0.05)
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c



40A

[Cd HS+ up 1.5 10FDR] less [Cd OS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

Systemat	Norm	Norm	Norm	Norm	Norm	Norm	Common	Ca orf19	Ca Function	S.c. hom.
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Species (	Ca	Cd	Ca	Cd	Ca	Cd				
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function	YJL066c
CA4684	3.0	10.5	1.1	1.0	2.2	1.5	HSP78.5f	orf19.882	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)	no match (e-value > 0.05)
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function	no match (e-value > 0.05)
CA4437	2.5	7.3	0.7	1.3	1.2	1.2	IPF13867	orf19.5158	unknown function	YGL145w
CA1075	1.5	7.0	0.8	0.8	0.8	0.7	IPF4991	orf19.2531	putative membrane protein	YDL058w
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)	YOL103w
CA4683	10.3	6.7	1.1	1.1	2.3	1.5	HSP78.3f	orf19.884	heat shock protein of clpb family of ATP-dependent protease	YDR258c
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)	YCR098c
CA0785	2.2	5.9	0.9	1.1	1.2	1.1	IPF14603	orf19.3929	unknown function	YJR100c
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)	YGL009c
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)	YLR216c
CA3078	2.5	5.4	0.8	1.3	1.2	1.1	IPF19970	orf19.4816	unknown function	YMR209c
CA1239	4.7	5.2	1.2	1.1	0.7	0.9	HSP60	orf19.717	Heat Shock Protein 60 (HSP60)	YLR259c
CA2513	1.0	5.2	1.6	1.5	0.7	1.1	SNG1	orf19.308	Involved in nitroguanidine resistance (by homology)	YGR197c
CA4120	1.4	4.8	1.0	1.1	1.2	1.5	SOD1	orf19.2770.1	Cu,Zn-superoxide dismutase	YJR104c
CA4959	3.4	4.8	1.3	1.2	1.0	1.0	HSP90	orf19.6515	heat shock protein	YMR186w
CA5536	2.0	4.4	0.9	1.0	1.1	1.2	IPF2837	orf19.7297	putative cystathionine gamma-synthase (by homology)	YHR112c
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)	YJR107w
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function	YMR002w
CA0551	2.5	4.0	1.4	1.3	1.3	1.0	CDC37	orf19.5531	Cell division control protein (by homology)	YDR168w
CA5341	2.5	3.9	0.9	0.8	1.0	0.9	HSP10	orf19.7215.3	10 kDa mitochondrial heat shock chaperonin (by homology)	YOR020c
CA4021	1.5	3.8	0.7	1.6	1.1	1.1	EBP2	orf19.3442	NADPH dehydrogenase (by homology)	YHR179w
CA5558	1.5	3.8	1.1	1.4	1.3	1.2	IPF1969	orf19.7322	unknown function	YPL225w
CA1180	1.7	3.7	1.1	0.9	0.8	1.4	UGA12.3f	orf19.803	4-aminobutyrate aminotransferase (GABA transaminase), 3-p	YGR019w
CA2130	1.4	3.6	1.2	1.0	1.2	1.1	RPS27A	orf19.413.1	ribosomal protein S27.e (by homology)	YKL156w
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function	YNL111c
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)	YPL088w
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease	YHL036w
CA4609	0.9	3.6	1.2	1.3	1.5	1.2	ZPR1	orf19.3300	Zinc finger protein (by homology)	YGR211w
CA3796	1.9	3.5	1.2	1.2	0.9	0.9	SGT2	orf19.5823	small glutamine-rich tetratricopeptide repeat containing protei	YOR007c
CA1230	2.1	3.5	1.5	1.6	0.9	0.9	SSA4	orf19.4980	cahsp70 mRNA for heat shock	YER103w
CA1181	1.9	3.5	0.9	0.8	0.8	1.4	UGA12.5f	orf19.802	4-aminobutyrate aminotransferase (GABA transaminase), 5-p	YGR019w
CA1349	2.1	3.5	0.5	0.9	0.7	0.9	PRP12	orf19.4351	involved in early maturation of pre-rRNA (by homology)	YMR302c
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function	YML041c
CA0706	1.7	3.4	1.1	1.5	0.9	1.0	IPF7715.3	orf19.682	unknown function	YJL078c
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown	YDL157c
CA1330	1.0	3.4	1.0	1.6	1.0	1.0	IPF11713.	orf19.1151	unknown function, 3-prime end	no match (e-value > 0.05)
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function	YDR090c
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase	YJL218w
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)	YLR168c
CA2729	0.9	3.2	1.0	1.1	0.9	0.7	NAT2	orf19.2116	N-acetyltransferase for N-terminal methionine (by homology)	YGR147c
CA4856	3.1	3.2	0.9	1.1	1.1	0.9	IPF15950	orf19.3827	unknown function	YKR087c
CA3099	2.2	3.2	1.0	1.4	1.4	1.3	LST8	orf19.3862	required for transport of permeases from the golgi to the plas	YNL006w
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function	YBR101c
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)	YLL028w
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)	YKL188c
CA0117	1.5	3.1	1.1	1.1	0.9	1.1	IPF19231	orf19.916	unknown function	YNL305c
CA1287	1.8	3.1	1.1	1.2	1.2	1.2	IPF5545	orf19.4430	unknown function	YDR330w
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)	YCL040w
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholester	YNR008w
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function	YHR067w
CA4380	0.7	2.9	0.8	1.1	1.1	2.1	IPF12736	orf19.5673	unknown function	YPR194c
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase	no match (e-value > 0.05)
CA0219	1.6	2.9	1.1	1.2	1.2	0.9	YAP3	orf19.3193	transcription factor of a fungal-specific family of bzip proteins	YHL009c
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function	YBR042c
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)	YOR157c
CA0740	1.2	2.8	1.0	1.0	1.3	1.5	UMP1	orf19.3140.1	proteasome maturtion factor (by homology)	YBR173c
CA0915	3.0	2.8	1.1	1.0	1.0	0.7	KAR2	orf19.2013	dnaK-type molecular chaperone (by homology)	YJL034w
CA5060	1.5	2.8	0.9	1.0	1.2	1.2	IPF3690	orf19.3029	unknown function	YDR036c
CA4643	2.2	2.7	1.1	1.2	1.3	1.0	PRE9	orf19.350	20S proteasome subunit Y13 (alpha3) (by homology)	YGR135w
CA3034	2.3	2.7	0.8	0.9	1.4	1.3	RPN12	orf19.213	26S proteasome regulatory subunit (by homology)	YFR052w
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)	YNL104c
CA0417	2.3	2.7	0.9	1.0	1.4	1.2	UBC13	orf19.933	E2 ubiquitin-conjugating enzyme (by homology)	YDR092w
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)	YDR069c
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function	YBR272c
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)	YJL001w
CA2131	1.4	2.6	0.9	1.0	1.0	1.1	IDP1	orf19.5211	isocitrate dehydrogenase, cytosolic (by homology)	YDL066w

CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)	YKL117w
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)	YGL184c
CA1759	1.5	2.6	1.3	0.9	1.0	1.0	IPF14744	orf19.5125	unknown function	YLR149c
CA5049	1.5	2.5	1.0	1.1	0.9	0.9	CDC12	orf19.3013	septin (by homology)	YHR107c
CA4319	1.9	2.5	1.1	1.2	1.1	0.9	RPN10	orf19.4102	Protein degradation (by homology)	YHR200w
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins	YNL064c
CA0155	1.9	2.5	1.2	1.0	1.4	1.2	RPT6	orf19.3593	26S proteasome regulatory subunit (by homology)	YGL048c
CA5040	1.4	2.5	0.8	0.8	0.9	0.9	BAT22	orf19.6994	branched chain amino acid aminotransferase (by homology)	YJR148w
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function	YDR014w
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex	YDL143w
CA4924	2.0	2.5	1.2	1.2	1.4	1.0	UBP6.3f	orf19.6063	Ubiquitin-specific protease, 3-prime end (by homology)	YFR010w
CA6091	1.6	2.5	0.8	0.7	0.8	0.8	UFD2	orf19.5965	Ubiquitin fusion degradation protein 2 (by homology)	YDL190c
CA2698	1.2	2.5	1.1	0.8	0.9	1.0	SUL1	orf19.2738	High-affinity sulfate transport protein (by homology)	YLR092w
CA5270	2.3	2.5	1.1	0.9	0.6	0.8	SEC18.5f	orf19.4993	vesicular fusion protein by homology, 5-prime end	YBR080c
CA2296	1.3	2.5	0.8	1.0	1.1	1.0	SCL1	orf19.5378	Proteasome subunit YC7alpha (by homology)	YGL011c
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function	YGR161c
CA4525	1.2	2.5	1.0	1.1	1.1	1.2	SEC22	orf19.479.2	synaptobrevin-type protein transport protein (by homology)	YLR268w
CA4168	1.8	2.4	1.1	1.2	1.0	1.1	IPF7781	orf19.2965	putative pump-driving ATPase	YDL100c
CA1285	1.0	2.4	1.1	1.3	1.1	1.0	SKP1	orf19.4427	kinetochore protein complex CBF3 by homology	YDR328c
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases	YPR024w
CA0265	1.6	2.4	1.3	1.0	1.0	1.0	STI1.3f	orf19.3191	stress-induced protein (by homology)	YOR027w
CA5087	1.0	2.4	1.1	0.9	0.7	0.9	IPF20025	orf19.3062	unknown function	YKL033w
CA5528	1.9	2.4	1.2	1.3	1.2	1.1	RPN7	orf19.7286	Subunit of the regulatory particle of the proteasome (by homc	YPR108w
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase	YNL192w
CA5435	1.6	2.4	0.7	0.7	0.9	0.9	UFD4	orf19.3237	ubiquitin fusion degradation protein (by homology)	YKL010c
CA2386	1.6	2.4	1.0	1.2	2.1	1.3	ECM41.3f	orf19.2613	involved in cell wall biogenesis and architecture, 3-prime end	YKR076w
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase	YLR377c
CA2857	2.1	2.3	1.2	1.2	1.0	1.0	SSA1	orf19.1065	Heat shock protein of HSP70 family	YER103w
CA5173	0.9	2.3	0.8	1.1	0.8	1.0	CPS2.3f	orf19.4610.1	Carboxypeptidase YSCS precursor, 3-prime end (by homolo	YJL172w
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function	YDR430c
CA5791	1.5	2.3	1.2	1.0	1.4	1.2	RPT2	orf19.5440	26S proteasome regulatory subunit (by homology)	YDL007w
CA4772	1.8	2.3	1.3	1.1	1.1	1.1	CCT3	orf19.4004	Chaperonin (by homology)	YJL014w
CA1653	2.8	2.3	1.3	1.4	1.0	0.7	STE23	orf19.5561	protease involved in a-factor processing by homology	YLR389c
CA2121	1.3	2.3	0.9	0.9	1.1	1.2	IPF7930	orf19.1338	unknown function	YJL123c
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)	YER021w
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function	YGL145w
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)	YBR058c
CA5618	1.4	2.2	1.0	1.0	1.0	1.1	LEU2	orf19.7080	isopropyl malate dehydrogenase	YCL018w
CA5303	1.2	2.2	1.1	1.2	1.5	0.8	IPF2180	orf19.7170	unknown function	no match
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function	YPL110c
CA4257	1.2	2.2	1.0	0.9	1.3	1.1	PRE6	orf19.544.1	20S proteasome subunit	YOL038w
CA3706	0.9	2.2	0.7	0.8	1.1	1.0	PSA2	orf19.4943	mannose-1-phosphate guanyltransferase by homology	YDL055c
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function	YBR280c
CA2565	1.6	2.2	1.1	1.0	0.9	1.3	MET15	orf19.5645	O-acetylhomoserine O-acetylserine sulphydrylase	YLR303w
6100.2	1.5	2.2	2.0	1.2	1.1	1.0				
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)	YOR232w
CA5308	1.5	2.2	1.0	0.9	1.3	1.1	PRE5	orf19.7178	20S proteasome subunit alpha6 (by homology)	YMR314w
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]	YNL202w
CA1508	2.1	2.2	0.7	1.0	0.7	0.9	IPF9977	orf19.4525	unknown function	YLR064w
CA1629	0.6	2.2	1.2	1.5	1.4	1.3	NPI46	orf19.1030	proline cis-trans isomerase (by homology)	YLR449w
CA2951	1.3	2.1	0.8	1.0	0.9	1.0	SBP1	orf19.5854	RNA binding protein-like (by homology)	YHL034c
CA4865	1.5	2.1	1.0	1.0	1.1	1.2	IPF4085	orf19.3841	similar to Saccharomyces cerevisiae Apg1p essential for aut	YGL180w
CA4604	1.2	2.1	1.3	1.3	1.2	0.9	MBF1	orf19.3294	Multiprotein bridging factor mediates GCN4-dependent trans	YOR298ca
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function	YGR101w
CA1116	1.3	2.1	1.1	1.3	0.9	1.0	CCT5	orf19.2288	T-complex protein 1, epsilon subunit (by homology)	YJR064w
CA0914	1.6	2.1	0.9	1.0	1.2	1.1	SRA1	orf19.2015	cAMP dependent protein kinase, regulatory subunit (by homc	YIL033c
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)	YAL048c
CA4167	0.6	2.1	0.8	1.0	0.9	1.1	IPF7778	orf19.2966	putative carboxymethylenebutenolidase (dienelactone hydrol	YDL086w
CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)	YIL095w
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)	YMR250w
CA5717	1.0	2.1	0.9	1.1	0.8	1.1	CYP51	orf19.7421	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by	YDR304c
CA1256	2.2	2.0	1.0	1.1	0.7	1.1	UBP15	orf19.1777	ubiquitin-specific protease (by homology)	YMR304w
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function	YDL057w
CA1894	2.2	2.0	1.0	1.1	1.2	1.0	PRE7.5f	orf19.2755	putative subunit of 20S proteasome, exon 1 (by homology)	YBL041w
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)	YMR105c
CA1911	1.1	2.0	1.1	0.9	1.0	1.0	SSE1	orf19.2435	heat shock protein of HSP70 family (by homology)	YPL106c
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)	YOR375c
CA5977	1.2	2.0	1.2	1.0	1.3	1.2	UBC4	orf19.7571	E2 ubiquitin-conjugating enzyme (by homology)	YBR082c
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)	YMR275c
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)	YMR234w
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function	YLR380w
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function	YKL034w
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)	YHR104w
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function	YHR132wa
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation comp	YBR170c
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle	YLR178c
CA0663	2.1	1.9	0.9	0.9	1.0	1.1	PUP2	orf19.709	20S proteasome subunit(alpha5) (by homology)	YGR253c
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function	YHR172w
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA4988	1.4	1.9	1.0	0.9	0.9	0.8	RPN2	orf19.5260	Proteasome regulatory subunit (by homology)	YIL075c
CA1880	1.7	1.9	1.2	1.3	1.4	1.0	IPF13316	orf19.2269	unknown function	YNL010w
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)	YJL155c
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homo	YPR183w
CA5862	1.0	1.9	1.2	1.3	1.1	1.1	POT11	orf19.7520	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)	YIL160c
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function	YKL094w
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P.	YPL109c
CA4522	1.2	1.9	1.0	0.9	1.1	1.0	RPT4	orf19.482	26S proteasome regulatory subunit (by homology)	YOR259c
CA4389	1.6	1.9	1.2	1.0	1.2	1.2	RPT5	orf19.3123	26S proteasome regulatory subunit (by homology)	YOR117w
CA5268	1.8	1.9	1.1	1.1	0.7	0.9	SEC18.3f	orf19.4994	vesicular fusion protein, 3-prime end (by homology)	YBR080c
CA3868	1.3	1.9	1.1	1.1	0.8	1.0	CCT1	orf19.401	component of chaperonin-containing T-complex (by homolog	YDR212w
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltrans	YLL031c
CA0394	1.6	1.9	1.0	1.3	1.4	1.4	IPF12758.	orf19.334	unknown function, 5-prime end	no match (e-value > 0.05)
CA3247	1.2	1.9	1.1	1.0	0.7	0.8	IPF15832	orf19.4676	unknown function	YKL053ca
CA4695	1.2	1.9	0.9	1.4	1.3	1.0	IPF4229	orf19.6923	unknown function	YML015c
CA3898	1.3	1.9	1.1	0.9	0.8	1.0	UBA2	orf19.5074	ubiquitin-activating -like enzyme by homology	YDR390c
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3	orf19.7317	putative transcriptional activator, 3-prime end	YDL170w
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)	YDL141w
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function	YDL012c

CA0661	1.9	1.9	0.7	0.9	1.0	1.0	APG7	orf19.707	component of the autophagic system (by homology)	YHR171w
CA2120	1.6	1.9	0.9	1.0	1.2	1.2	PUP3	orf19.1336	PRCT yeast proteasome component (by homology)	YER094c
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function	YNL212w
CA5554	1.0	1.9	0.7	1.0	0.9	1.0	IPF1960.5	orf19.7318	putative transcriptional activator, 5-prime end	YCR106w
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function	no match (e-value > 0.05)
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)	YJL060w
CA2758	1.2	1.9	0.7	0.5	0.9	0.6	GLC3.3f	orf19.5622	1,4-glucan branching enzyme , 3 prime end (by homology)	YEL011w
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function	YAL014c
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function	YBR255w
CA3422	1.6	1.9	0.9	0.8	0.7	0.9	IPF17289	orf19.6134	unknown function	YLR440c
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function	no match (e-value > 0.05)
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)	YDR093w
CA1755	1.6	1.8	1.1	0.9	0.8	1.1	PDI1	orf19.5130	protein disulfide-isomerase precursor (by homology)	YCL043c
CA0408	1.9	1.8	0.9	1.0	0.9	1.0	SAC6.5f	orf19.5544	actin filament bundling protein, fimbrin, 5-prime end (by homc	YDR129c
CA1389	1.5	1.8	1.4	1.3	0.8	1.1	PLP2	orf19.1769	Might regulate Ste4p in pheromone response (by homology)	YOR281c
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)	YGR194c
CA3191	1.5	1.8	0.7	1.0	0.7	0.8	IPF11601	orf19.2151	unknown function	YOR165w
CA5930	2.3	1.8	1.1	0.9	1.1	1.0	ECM29.3f	orf19.6773	Involved in cell wall biogenesis and architecture, 3-prime end	YHL030w
CA1693	1.6	1.8	1.0	1.0	1.0	1.1	IPF17054	orf19.5037	unknown function	no match (e-value > 0.05)
CA2286	0.9	1.8	0.8	1.1	1.4	1.4	IPF5369	orf19.5553	unknown function	YKL069w
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function	YPR117w
CA0164	1.0	1.8	1.0	1.0	0.9	1.0	IPF11694	orf19.4335	similar to Saccharomyces cerevisiae Tna1p high affinity nicot	YGR260w
CA2278	1.8	1.8	1.2	1.0	1.2	1.2	IPF10806	orf19.782	unknown function	YBR204c
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)	YIL124w
CA5836	1.1	1.8	0.8	1.1	1.2	0.7	IPF428	orf19.7490	transport protein (by homology)	YOL137w
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)	YJR096w
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117		YBR287w
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)	YLR355c
CA3435	1.0	1.8	0.9	1.4	1.3	1.2	IPF6391	orf19.583	indoleamine 2,3-dioxygenase (by homology)	YJR078w
CA2669	1.2	1.8	0.8	0.9	1.0	1.0				
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function	YNL156c
CA1269	1.6	1.7	1.1	1.1	1.1	1.4	IPF19726	orf19.3158	unknown function	YDL001w
CA4798	1.4	1.7	0.9	1.0	0.9	0.9	RPN5.3f	orf19.4032	subunit of the regulatory particle of the proteasome, 3-prime (	YDL147w
CA2146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function	no match (e-value > 0.05)
CA0345	1.2	1.7	1.0	1.0	1.0	0.9	ACH1	orf19.3171	acetyl-coenzyme-A hydrolase (by homology)	YBL015w
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)	YLL009c
CA5146	1.2	1.7	0.9	1.0	1.0	1.0	YMC2	orf19.4583	Carnitine/acylcarnitine translocase (by homology)	YBR104w
CA2785	0.6	1.7	0.6	0.9	0.9	1.0	MET13	orf19.288	Methylene tetrahydrofolate reductase (by homology)	YGL125w
CA0840	1.1	1.7	1.4	1.0	1.3	1.0				
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function	YPL050c
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in aceti	YCR032w
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function	YMR185w
CA3697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific	YJR099w
CA4480	0.9	1.7	0.7	1.1	1.5	1.4	IPF6464	orf19.1887	putative triacylglycerol lipase (by homology)	YLL012w
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function	YOR377w
CA4219	1.3	1.7	0.8	1.1	2.2	1.3	SDS22	orf19.820	regulatory subunit for the mitotic function of type I protein pho	YKL193c
CA5555	0.9	1.7	1.0	1.0	1.3	1.1	SUC1	orf19.7319	Putative zinc finger protein Suc1	YFL052w
CA5196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function	YIL001w
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)	YHR176w
CA5695	1.3	1.7	0.9	0.8	0.7	1.1	IPF3310	orf19.7397	unknown function	YPR022c
CA5283	0.9	1.7	0.8	1.0	0.8	1.2	IPF1912	orf19.7140	putative catechol o-methyltransferase	no match (e-value > 0.05)
CA2508	1.9	1.7	1.4	1.1	0.9	1.0	BET5	orf19.302	targeting and fusion of ER to Golgi transport vesicles (by hon	YML077w
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)	YKL085w
CA4165	1.0	1.7	1.0	1.1	1.0	1.0	IPF7774	orf19.2968	unknown function	no match (e-value > 0.05)
CA4890	1.5	1.7	1.0	0.9	1.0	1.1	PRE10	orf19.6582	20S proteasome subunit C1 (by homology)	YOR362c
CA5941	1.5	1.7	1.0	1.3	1.4	0.9	IPF3486	orf19.6756	unknown function	YGL198w
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function	YAL060w
CA4142	1.5	1.7	1.0	1.0	1.5	1.2	PRE4	orf19.4230	20S proteasome subunit(beta7) (by homology)	YFR050c
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)	YOR089c
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)	YKL134c
CA5559	1.0	1.7	1.2	1.1	0.8	1.1	CBP1	orf19.7323	Corticosteroid binding protein	YMR020w
CA3870	1.0	1.7	0.6	0.9	1.3	1.0	YPK1	orf19.399	ser/thr-specific protein kinase (by homology)	YMR104c
CA5306	1.2	1.7	1.0	1.0	1.1	1.1	NPT1	orf19.7176	Nicotinate phosphoribosyltransferase (by homology)	YOR209c
CA2548	1.6	1.7	1.0	0.9	0.9	0.9	PGA34	orf19.2833	unknown function	no match
CA0972	1.1	1.6	1.1	1.2	1.0	1.0	CYP1	orf19.6472	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homc	YDR155c
CA1252	1.9	1.6	0.9	0.9	0.9	0.9	RPN1	orf19.4956	26S proteasome regulatory subunit (by homology)	YHR027c
CA4333	1.2	1.6	1.2	1.1	1.4	1.2	IPF2083	orf19.4086	unknown function	YNL056w
CA1942	1.3	1.6	0.6	0.9	1.0	1.1	HCT5.3eo	orf19.4191.1	Ubiquitin–protein ligase, 3-prime end (by homology) FALSOF	YGL141w
CA4799	1.6	1.6	1.1	1.0	0.8	1.0	RPN5.5f	orf19.4034	subunit of the regulatory particle of the proteasome, 5-prime (	YDL147w
CA3956	1.2	1.6	1.0	1.0	1.0	1.2	IPF6712.3	orf19.1414.2	unknown function, 3-prime end | Unknown function	no match
CA4127	0.9	1.6	0.7	0.9	0.9	0.9	IPF6629	orf19.2762	unknown function	YLR109w
CA3310	1.4	1.6	1.1	1.2	0.7	1.0	PFS2	orf19.2307	Polyadenylation Factor I subunit (by homology)	YNL317w
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE	YBR126c
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)	YJL068c
CA3746	1.2	1.6	1.6	1.0	0.8	1.1	ARA1	orf19.2172	D-arabinose dehydrogenase (by homology)	YBR149w
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)	YFL007w
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)	YPL203w
CA2888	1.6	1.6	1.0	1.1	1.2	1.2	GIM5	orf19.2471	Gim complex component (by homology)	YML094w
CA2773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase	YOR211c
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)	YNR013c
CA3569	1.3	1.6	1.0	1.1	1.0	1.1	IPF3268	orf19.3136	unknown function	YDR325w
CA2157	2.2	1.6	1.5	1.1	0.8	0.8	IPF8537	orf19.5300	similar to Saccharomyces cerevisiae Cne1p calnexin, involve	YAL058w
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function	no match (e-value > 0.05)
CA4320	1.1	1.6	1.2	1.1	0.8	1.1	ECM17	orf19.4099	Putative sulfite reductase (by homology)	YJR137c
CA2561	1.0	1.6	1.2	1.5	0.8	0.9	CAR2	orf19.5641	ornithine aminotransferase (by homology)	YLR438w
CA5564	1.2	1.6	0.7	0.9	1.0	0.9	IPF1980	orf19.7328	unknown function	no match (e-value > 0.05)
CA1452	1.6	1.6	0.8	0.8	1.3	1.0	REV1	orf19.4412	DNA repair protein (by homology)	YOR346w
CA1756	1.0	1.6	1.1	1.2	1.5	1.0	IPF14562	orf19.5129	unknown function	no match (e-value > 0.05)
CA1913	1.4	1.6	0.9	0.9	1.2	1.2	ARC35	orf19.2437	subunit of the Arp2/3 complex involved in the control of actin	YNR035c
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function	YJR008w
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function	no match (e-value > 0.05)
CA2863	1.3	1.6	1.0	1.0	1.3	1.1	IPF20117	orf19.1058	unknown function	YLR421c
CA0593	1.3	1.6	1.0	0.8	1.2	1.2	ARP6	orf19.4904	actin-related protein (by homology)	YLR085c
CA1838	1.3	1.6	1.1	1.1	1.4	1.3	IPF5777	orf19.3963	unknown function	YER182w
CA0530	1.4	1.6	0.7	0.6	0.7	0.9				
CA2926	1.1	1.6	0.8	1.1	1.3	1.3	UBA3	orf19.4209	Ubiquitin-like protein activating enzyme	YPR066w
CA5595	1.1	1.6	0.9	1.0	0.9	1.4	IPF568	orf19.7105	similar to Saccharomyces cerevisiae Far1p cyclin-dependent	YJL157c
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)	YLR351c

CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal ass	YKL197c
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function	YNL155w
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)	YOL151w
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function	YPR154w
CA2867	1.2	1.5	0.9	0.8	0.8	0.8	IPF11688	orf19.2844	similar to Saccharomyces cerevisiae Apl4p AP-1 complex su	YPR029c
CA3336	1.0	1.5	0.8	0.8	1.1	1.3	IPF19983	orf19.2335	unknown function	YHR113w
CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar	YPR026w
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltr	YMR149w
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function	YNL008c
CA2133	1.2	1.5	1.0	1.0	1.0	0.8	IPF5866	orf19.5213	unknown function	YDR228c
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)	YOR120w
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function	no match
CA3907	1.2	1.5	0.7	1.0	1.0	0.9	IPF3304	orf19.4395	similar to Saccharomyces cerevisiae Aip1p actin cytoskeletor	YMR092c
CA3683	1.2	1.5	1.1	1.0	1.1	1.2	PPZ1	orf19.726	ser/thr phosphatase required for normal osmoregulation (by I	YML016c
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase	YFR015c
CA4625	1.1	1.5	0.8	0.9	0.9	1.2	IPF5742	orf19.3319	thioredoxin-like protein (by homology)	YGR209c
CA4720	1.2	1.5	1.0	1.0	1.3	1.0	ECM18	orf19.6958	Involved in cell wall biogenesis and architecture (by homolog	YDR125c
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)	YNR019w
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function	YML018c
CA3057	1.3	1.5	1.0	1.2	1.5	1.2	IPF2954	orf19.4293	unknown function	YDR267c
CA3589	0.8	1.5	0.8	1.2	1.4	1.1	IPF10113	orf19.2249	unknown function	YNR020c

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[[Cd OS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
HS+ OS+ XS+										
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA5797	1.2	0.9	8.7	8.2	0.7	1.0	IPF4182	orf19.5446	unknown function	no match (e-value > 0.05)
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)	YDR497c
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function	no match
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function	YLR205c
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)	YHR032w
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function	no match (e-value > 0.05)
CA0721	1.5	0.9	1.3	2.3	0.8	0.8	IPF10429	orf19.2887	unknown function	YMR295c
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)	YPR058w
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function	no match (e-value > 0.05)
CA5840	1.2	1.0	1.3	1.9	1.0	1.2	EBP6	orf19.7495	NADPH dehydrogenase (by homology)	YPL171c
CA0948	0.6	1.1	0.9	1.9	1.1	1.0	IPF10270	orf19.1272	unknown function	YGR111w
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by	no match (e-value > 0.05)
CA0677	1.4	1.3	1.2	1.8	1.0	0.8	IPF13095	orf19.1182	unknown function	YGL212w
CA4870	1.5	1.1	1.3	1.7	1.2	1.3	IPF19568	orf19.6556	unknown function	no match (e-value > 0.05)
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)	YBR132c
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function	YOL073c
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function	YPL246c
CA1187	0.7	0.9	1.2	1.5	1.1	1.0	QRI7	orf19.3787	putative glycoprotease (by homology)	YKR038c
CA2161	1.1	1.1	1.1	1.5	1.0	1.1	IPF11876	orf19.5295	unknown function	no match (e-value > 0.05)

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[[Cd XS+ up 1.5 10FDR] less [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10...

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
HS+ OS+ XS+										
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function	YDR371w
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function	no match (e-value > 0.05)
CA2435	1.1	1.7	1.2	1.1	17.7	13.6	IPF9483	orf19.3395	probable permease (by homology)	YHR048w
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function	YKL086w
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function	no match (e-value > 0.05)
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase	YBR046c
CA0639	1.6	1.8	1.0	1.0	9.0	10.5				
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)	no match (e-value > 0.05)
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function	no match (e-value > 0.05)
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)	YPL092w
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)	YOL152w
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)	YPR201w
CA4913	1.1	1.0	1.3	1.0	1.2	6.8	CIS2	orf19.6053	Gamma-glutamyltransferase (by homology)	YLR299w
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)	YBR293w
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function	YKR071c
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function	YGL114w
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)	YGL257c
CA4829	1.0	1.1	1.3	1.0	6.3	5.5	IPF1210	orf19.2067	similar to Saccharomyces cerevisiae Nfu1p involved in home	YKL040c
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)	YHR044c
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae	YBL033c
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function	no match (e-value > 0.05)
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)	YPL171c
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)	YDR338c
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function	YLR251w
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function	YOR292c
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)	YOR101w
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function	no match (e-value > 0.05)
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase	YNL117w
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)	YDR513w
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function	no match (e-value > 0.05)
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function	YOL119c
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)	YIL120w
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homolog	YER053c
CA4399	1.4	1.7	1.2	1.3	1.1	3.8	PRA1	orf19.3111	pH-regulated antigen	YOL154w
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function	YGL136c
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function	no match (e-value > 0.05)
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function	YHR131c
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function	YNL144c
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function	YDR336w
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)	YNL229c
CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function	no match (e-value > 0.05)

CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function	no match (e-value > 0.05)
CA1005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)	YPL101w
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function	no match (e-value > 0.05)
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homolc	YJL101c
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)	YKR039w
CA0583	1.2	2.5	1.3	1.3	3.9	3.2	GSH1.3f	orf19.5059	gamma-glutamylcysteine synthetase, 3 prime end (by homolc	YJL101c
CA0996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)	no match (e-value > 0.05)
CA0933	1.3	1.1	0.8	1.0	5.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)	YMR301c
CA1775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology	YDL215c
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function	YDR143c
CA0385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function	YNL250w
CA5697	1.3	1.0	0.8	1.1	3.8	3.0				
CA1170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function	YDR132c
CA4392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)	YNL229c
CA1016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function	YOR273c
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)	YML081w
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function	YLL038c
CA1111	0.6	0.8	0.4	0.8	1.6	2.9	RIB3.5f	orf19.5228	3,4-dihydroxy-2-butanone 4-phosphate synthase, 5-prime en	YDR487c
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA5868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function	YMR090w
CA0595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5	orf19.4901	unknown function, 5-prime end	YER175c
CA1157	1.2	1.0	1.4	1.1	0.8	2.8	PZF1	orf19.4125	TFIIIA (transcription initiation factor) (by homology)	YPR186c
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function	YDR019c
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase	YER065c
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function	YKR105c
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein	YOR153w
CA3258	1.1	1.0	0.5	0.9	1.1	2.7				
CA4873	1.0	0.8	0.7	0.7	3.0	2.7				
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)	YPR194c
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function	YPR194c
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function	YPR194c
CA4885	1.2	1.3	1.2	1.1	1.1	2.6	IPF1636	orf19.6577	similar to Saccharomyces cerevisiae Tpo1p multidrug resista	YLL028w
CA4662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by hom	YMR038c
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein	YPR124w
CA3919	1.1	1.0	0.8	0.8	1.0	2.5	IFC5	orf19.5121	unknown function	YPR194c
CA2227	1.5	1.2	1.0	0.9	1.4	2.5	EBP7	orf19.5816	NADPH DEHYDROGENASE by homology	YHR179w
CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)	YGR191w
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function	no match
CA2894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function	no match (e-value > 0.05)
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function	YJL084c
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function	YML131w
CA5289	0.7	0.9	0.9	0.9	1.4	2.4	NRG1	orf19.7150	similar to transcriptional repressor Nrg1p/Nrg2p	YBR066c
CA0942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function	YER101c
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function	YPR194c
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase	YEL046c
CA0993	1.0	1.0	0.6	0.9	2.2	2.4				
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function	YJR072c
CA1372	0.9	1.0	1.2	1.0	1.1	2.4	IPF15844	orf19.4961	similar to Saccharomyces cerevisiae Stp2p involved in pre-tR	YHR006w
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)	YIL107c
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function	YOR363c
CA4929	1.1	0.7	2.8	1.3	1.1	2.3	ENA22	orf19.6070	P-type ATPase involved in Na+ efflux (by homology)	YDR038c
CA1108	1.1	1.1	1.0	1.0	1.0	2.3	IPF11273	orf19.5231	unknown function	no match (e-value > 0.05)
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function	YPR107c
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function	no match (e-value > 0.05)
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)	YML111w
CA2873	0.5	0.8	0.3	0.8	3.2	2.3	AQY1	orf19.2849	similarity to plasma membrane and water channel proteins (a	YPR192w
CA1536	1.6	1.6	1.1	1.3	1.3	2.2	SOK1	orf19.451	high copy suppressor of a cyclic AMP-dependent protein kina	YDR006c
CA2177	1.1	1.1	1.3	1.0	2.2	2.2	ROD1	orf19.1509	O-dinitrobenzene,calcium and zinc resistance protein (by hor	YFR022w
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)	YHL008c
CA0129	1.1	0.9	1.0	1.0	1.2	2.2	IPF10495	orf19.246	unknown function	YIL108w
CA2711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)	YDR460w
CA5011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function	YMR101c
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function	YKL151c
CA3354	1.1	1.1	0.7	0.7	1.2	2.2	GPR1	orf19.1944	similar to Saccharomyces cerevisiae Gpr1p G-protein couple	YDL035c
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich	YCR106w
CA0560	1.2	1.0	0.9	1.0	1.2	2.1	GPX3	orf19.87	glutathione peroxidase (by homology)	YIR037w
CA4630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)	YPL252c
3692.2	1.2	1.2	0.8	0.9	2.2	2.1				
6532.2	0.9	0.9	0.6	0.8	2.3	2.1				
CA5009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)	YKL119c
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)	YIR037w
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function	YPL206c
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)	YDL124w
CA4917	0.7	0.8	0.8	1.4	2.0	2.1	ECM31	orf19.6057	Involved in cell wall biogenesis and architecture (by homolog	YBR176w
CA2477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)	YJR061w
CA3094	1.1	1.1	1.1	0.7	1.3	2.1	IPF11548	orf19.3854	serine/threonine protein kinase (by homology)	YCR008w
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function	YFR003c
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function	YPL072w
CA5934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function	YHL029c
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function	YGR140w
CA3087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)	YLR147c
CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function	YCR061w
CA4190	1.6	1.2	2.3	1.4	4.4	2.1	IPF7530	orf19.4531	ATP-binding-cassette protein (by homology to A.gambiae)	YOL075c
CA0160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease	YKR039w
CA3446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function	YKL195w
CA4580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function	no match (e-value > 0.05)
CA4836	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)	YJR104c
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins	YHL019c
CA0757	1.0	0.7	0.6	0.8	2.2	2.0				
CA1600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)	YHR175w
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function	YER116c
CA0500	0.9	1.0	1.4	1.2	0.9	2.0	IPF20058	orf19.4793	unknown function	YOR252w
CA2584	0.8	1.2	1.0	1.1	2.1	2.0	IPF9440	orf19.4373	similar to Saccharomyces cerevisiae Fmn1p riboflavin kinase	YDR236c
CA5008	1.0	0.8	1.1	1.3	1.2	2.0	IPF12577	orf19.5238	unknown function	no match (e-value > 0.05)
CA5678	0.8	1.0	1.0	0.8	0.9	2.0	IPF1292	orf19.7381	unknown function Hypothetical zinc-finger protein	YML099c
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function	YNR018w
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function	YGR044c
CA5010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function	YMR101c

CA1002	1.0	1.0	1.9	1.2	0.9	1.9	ROK1.3f	orf19.3756	RNA helicase, 3-prime end	YGL171w
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (	YOL119c
CA4023	1.0	1.0	0.9	1.0	0.9	1.9	FRP5	orf19.3440	member of the FRP family of proteins related to Yarrowia lipo	YNR002c
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor	YIL130w
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function	YGR110w
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function	YOR338w
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function	no match (e-value > 0.05)
CA0995	1.0	1.0	0.9	0.9	3.8	1.9				
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)	YGR234w
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function	no match (e-value > 0.05)
CA4778	1.0	1.1	0.9	1.0	1.2	1.8	IFJ1	orf19.4011	Unknown function	YGR263c
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function	YDR034c
CA4174	1.2	3.6	1.3	1.6	1.6	1.8	IPF4430	orf19.2959.1	unknown function	YDR276c
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function	no match (e-value > 0.05)
CA0052	1.0	1.1	1.4	1.0	1.3	1.8	IPF19567	orf19.475	Unknown function	YHR085w
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)	YAL059w
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)	YML004c
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor	YAL051w
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase	YOR202w
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)	YMR275c
CA3187	1.0	0.8	1.5	1.2	0.8	1.8	IPF17094	orf19.2143	unknown function	YPL183c
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function	YKL077w
CA4960	0.7	0.8	0.7	0.7	1.2	1.8	IPF3912	orf19.6514	unknown function	YPL177c
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function	YCL044c
CA1277	1.3	1.0	1.4	1.0	1.2	1.8	IPF10837	orf19.3630	unknown function	YDR083w
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function	YKL175w
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function	YGR141w
CA4477	0.9	1.2	1.2	1.1	1.2	1.8	IPF6459	orf19.1890	unknown function	YMR210w
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function	no match (e-value > 0.05)
CA3416	1.6	0.4	1.5	1.0	4.4	1.7	FRE30.3f	orf19.6139	ferric reductase, 5 prime end fragment (by homology)	YOR381w
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology	YAL012w
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function	no match (e-value > 0.05)
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5	orf19.6654	unknown function	YMR221c
CA4612	1.1	0.9	1.4	1.0	1.5	1.7	PPM2	orf19.3303	carboxy methyl transferase; homolog of PPM1 (by homology)	YOL141w
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein	no match (e-value > 0.05)
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eo	orf19.920	N-delta-arginine methyltransferase (by homology)	YDR465c
CA5135	1.0	1.0	1.0	1.0	1.8	1.7	HSP104.5	orf19.6389	Heat shock protein, 5-prime end (by homology)	YLL026w
CA0629	1.1	1.3	0.7	0.8	1.0	1.7	IPF3876	orf19.775	unknown function	YJR126c
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)	YNL240c
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)	YPL140c
CA0019	1.0	0.9	1.7	0.8	0.9	1.7				
CA2750	1.1	1.0	1.1	1.0	4.6	1.7	ATX1	orf19.2369.1	antioxidant protein and metal homeostasis factor (by homolo	YNL259c
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53	orf19.6140	ferric reductase, internal fragment (by homology)	YOR381w
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA	YAL049c
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function	YNL166c
CA5287	0.8	1.0	1.0	0.9	1.0	1.7	IPF1922	orf19.7148	similar to multidrug resistance proteins	YLL028w
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function	YPL092w
CA5696	0.9	1.0	1.6	1.3	1.4	1.7	IPF3309.3	orf19.7398	unknown function, 3-prime end	YER126c
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)	YOR294w
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function	YOR178c
CA4614	1.1	1.3	1.4	0.8	1.0	1.7	IPF7952	orf19.3305	unknown function	YDR213w
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function	YOR084w
CA6009	0.8	1.0	1.3	1.0	1.2	1.7	IPF643	orf19.7610	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine p	YER075c
CA0626	1.1	0.9	1.3	1.1	1.4	1.7	IPF3161	orf19.3161	Unknown function	YNR054c
CA3157	0.9	1.4	1.0	1.3	1.5	1.7	IPF14456	orf19.1588	unknown function Unknown function	YBR269c
CA4563	1.0	1.0	1.0	1.1	0.8	1.7	IPF6566	orf19.6873.1	unknown function	YBL071wa
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726	unknown function	YKL051w
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase	YAL039c
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function	YIL003w
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function	YMR093w
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function	no match (e-value > 0.05)
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function	YMR136w
CA5580	1.2	1.4	0.9	1.0	1.3	1.6	RVS161	orf19.7124	cytoskeletal binding protein (by homology)	YCR009c
CA0057	0.9	0.8	1.6	1.3	1.4	1.6				
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function	YGL099w
CA6038	0.8	1.2	1.8	1.2	1.1	1.6	LTV1	orf19.7650	low-temperature viability protein (by homology)	YKL143w
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)	YLR120c
CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function	YDR219c
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homolo	YOR049c
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function	no match
CA5739	1.0	1.1	0.9	1.0	1.4	1.6	IPF2884	orf19.7449	unknown function	YMR211w
CA0941	0.9	1.0	0.8	1.0	1.3	1.6	IPF8617	orf19.3705	unknown function	YCR079w
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end	no match (e-value > 0.05)
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function	YKL165c
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function	YJR061w
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)	YLR327c
CA1515	0.8	1.0	0.4	0.8	2.4	1.6				
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins	YNL002c
CA5474	1.3	0.9	1.8	1.1	1.0	1.6	IPF16944.	orf19.3287	unknown function, 3-prime end	YMR014w
CA1958	1.0	1.0	0.9	0.9	1.2	1.6	IFE1	orf19.769	Unknown function	YAL061w
CA0393	1.4	1.1	1.0	1.1	1.7	1.6	IPF12758.	orf19.333.2	unknown function, 3-prime end	no match
CA2395	1.1	1.1	1.1	1.0	1.0	1.6	IPF6425	orf19.3536	unknown function	YOR320c
CA1540	0.9	0.9	1.2	1.5	0.9	1.6	IPF1047	orf19.4563	unknown function	YMR310c
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function	YHR087w
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)	YPR051w
CA2460	1.5	1.1	1.0	1.0	1.1	1.6				
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function	no match
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)	YDL234c
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)	YGR007w
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function	YEL064c
CA2233	1.0	1.0	1.0	1.0	1.1	1.6	IFJ3	orf19.3924	unknown function	YGR263c
CA6016	0.9	0.8	1.4	1.4	1.4	1.6	IPF630	orf19.7618	unknown function	YOR145c
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function	YLR021w
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3	orf19.4266.1	septin, 3-prime end (by homology)	YDR218c
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function	YHR101c
CA1703	0.9	1.2	0.8	1.0	1.4	1.6	IPF7987	orf19.703	unknown function	YGR247w
CA3808	0.8	1.1	1.5	1.2	1.1	1.6	FAL1	orf19.2488	ATP-dependent RNA helicase	YDR021w
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function	YJL092w

CA5875	1.2	1.1	0.9	1.0	0.8	1.6	IPF324.3f	orf19.7545	unknown function, , 3-prime end	no match (e-value > 0.05)
CA3741	0.9	0.9	0.9	1.0	0.7	1.6	MRS4	orf19.2178	RNA splicing protein and member of the mitochondrial carrier	YKR052c
CA1080	1.0	0.9	1.3	0.9	1.4	1.6	IPF14710	orf19.4820	unknown function	YKL162c
CA4158	0.9	0.9	0.9	0.9	0.7	1.6	DLD3	orf19.5805	D-lactate ferrycytochrome C oxidoreductase (by homology)	YDL174c
CA3080	0.9	1.1	1.0	0.8	1.0	1.6	IPF14634	orf19.4153	APP-binding protein 1 (by homology)	YPL003w
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)	YOR171c
CA5833	0.9	0.9	1.2	1.1	1.2	1.5	IMP3	orf19.7488	U3 small nucleolar ribonucleoprotein (by homology)	YHR148w
CA4818	0.7	0.9	0.8	0.7	1.2	1.5	IPF1193	orf19.2079	unknown function Unknown function	YHL018w
CA1957	0.4	0.8	0.4	0.3	0.9	1.5	IPF3887	orf19.768	similar to Saccharomyces cerevisiae Syg1p plasma membra	YIL047c
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]	YOR319w
CA2592	1.2	0.9	1.4	1.1	1.6	1.5	IPF18447	orf19.59	putative zinc-finger protein (by homology)	YBR267w
CA0473	1.0	1.0	1.0	1.0	1.3	1.5	GRP1	orf19.4781	dihydroflavonol-4-reductases (by homology)	YOL151w
CA3722	1.3	1.2	0.9	1.0	1.5	1.5	PHO13	orf19.4172	4-nitrophenylphosphatase (by homology)	YDL236w
CA4507	1.0	1.1	1.1	1.3	1.0	1.5	IPF20015	orf19.499	unknown function	YNL063w
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)	YPR016c
CA5882	1.1	0.7	1.8	1.8	1.3	1.5	RRP1	orf19.6828	Involved in processing rRNA precursor species to mature rRI	YDR087c
CA2398	1.1	1.0	1.0	1.0	1.1	1.5	IPF6431	orf19.3539	unknown function	YBR141c
CA0343	1.6	1.2	1.1	1.0	0.9	1.5	LYS1	orf19.1789.1	saccharopine dehydrogenase (by homology)	YIR034c
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function	no match (e-value > 0.05)
CA1689	1.0	1.0	0.9	1.1	1.1	1.5	IPF13030	orf19.3655	unknown function	no match (e-value > 0.05)
CA2428	1.0	1.1	0.9	0.9	1.3	1.5	IPF9894	orf19.3405	possible zinc-finger protein	no match (e-value > 0.05)
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function	no match (e-value > 0.05)
CA2798	1.5	1.1	2.7	1.3	1.5	1.5	IPF8402	orf19.1719	similar to Saccharomyces cerevisiae Sga1p glucan 1,4-alpha	YIL099w
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function	YNL313c
CA4754	0.7	1.0	1.0	1.0	1.2	1.5	IPF11479	orf19.4825	unknown function	YIL098c
CA1630	1.4	1.2	1.5	1.1	1.1	1.5	RPP1	orf19.1029	required for processing of tRNA and 35S rRNA (by homology	YHR062c
CA5626	0.9	1.1	0.9	1.0	1.1	1.5	IPF498	orf19.7071	unknown function	YML123c
CA4613	1.0	1.0	1.3	1.1	1.3	1.5	IPF7950	orf19.3304	similar to Saccharomyces cerevisiae Rrp40p involved in ribo	YOL142w
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function	no match (e-value > 0.05)
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)	YEL060c
CA4404	1.0	1.3	1.4	1.1	1.2	1.5	MET16	orf19.3106	3 -phosphoadenylylsulfate reductase (by homology)	YPR167c
CA2900	1.3	0.7	1.7	1.2	1.1	1.5	NIP7	orf19.3478	required for efficient 60S ribosome subunit biogenesis (by ho	YPL211w
11759.2	0.6	1.2	0.2	0.3	1.4	1.5				
CA0730	0.9	0.7	1.2	1.1	1.6	1.5	IPF7334	orf19.3724	unknown function	YOR004w
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function	YPL122c
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYI	YOR005c
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)	YER142c
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function	YOL077c
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)	YOL052c
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function	YNL191w

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[[Cd OS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd XS+ up 1.5 10FDR]

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)	YNL007c
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function	YLR109w
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)	YNL064c
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)	YNL104c
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)	YHR037w
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function	YDL072c
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase	YKR070w
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in contr	YHR142w
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)	YJR019c
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function	YMR226c
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function	YLR326w

44A

[Cd XS+ up 1.5 10FDR] and [Cd OS+ up 1.5 10FDR]] less [Cd HS+ up 1.5 10FDR]

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function	no match (e-value > 0.05)
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)	YDL022w
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)	YMR318c
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)	YDR536w
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function	YPL135w
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function	YJL108c
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function	no match (e-value > 0.05)
CA1991	1.1	1.0	4.2	3.2	1.2	1.7				
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function	no match (e-value > 0.05)
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function	YOL092w
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase	YNL202w
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function	YLL027w
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function	YOR049c

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[Cd XS+ up 1.5 10FDR] and [Cd HS+ up 1.5 10FDR]] less [Cd OS+ up 1.5 10FDR]

HS+ OS+ XS+

Species (	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*	HS+	HS+	OS+	OS+	XS+	XS+				
Systemat	rmali	rmali	rmali	rmali	rmali	rmali	Common	Ca orf19	Ca Function	S.c. hom.
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)	YBR026c
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function	YNL134c
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)	no match (e-value > 0.05)
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)	YOL151w
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function	YML131w
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homolo	YMR152w
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function	YDR214w
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)	YBR008c
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)	no match (e-value > 0.05)
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function	YER004w
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)	YJR096w
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function	no match (e-value > 0.05)
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)	YOR388c
CA2076	2.7	4.5	0.6	1.1	1.0	2.5	ERO1	orf19.4871	Required for protein disulfide bond formation in the ER (by ho	YML130c
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function	no match (e-value > 0.05)
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase	YJR010w

CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homolo	YPL171c
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)	YKR039w
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inn	YMR152w
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase	YER042w
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function	YBL049w
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase	YDR270w
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase	YNL277w
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)	YLR043c
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function	YNL229c
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology	YDR032c
CA2258	1.1	2.8	0.9	0.9	7.4	15.1	IFR1	orf19.1763	Unknown function	YNL134c
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)	YKL001c
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology	YPL111w
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function	YLR243w
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-bind	YGL091c
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)	YNL270c
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function	YNL134c
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function	YDR533c
CA0636	2.2	2.5	0.9	0.9	10.8	15.0				
CA1569	1.8	2.4	1.5	1.2	1.1	2.4	IPF7616	orf19.1159	putative homoserine O-acetyltransferase (by homology)	YNL277w
CA1882	1.1	2.4	0.8	1.0	0.8	1.9	IPF19934	orf19.2210	unknown function	no match (e-value > 0.05)
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function	no match (e-value > 0.05)
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)	YGR234w
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)	YHR137w
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)	YOL151w
CA1846	1.5	2.2	0.8	0.9	12.5	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)	YOR388c
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function	YDL048c
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function	YDR306c
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)	YPR086w
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable mono	no match
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p involved in regu	YIL046w
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)	YIR037w
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)	YNL040w
CA0183	1.5	1.9	1.5	1.1	1.4	2.2	CAP1	orf19.1623	transcriptional acivator (by homology)	YML007w
CA1395	1.1	1.9	1.0	0.9	11.5	11.7				
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)	YIR035c
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function	YIR017c
CA3059	1.2	1.8	1.2	1.1	8.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)	YDR353w
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)	YCL064c
CA3086	1.0	1.7	1.1	1.2	2.3	3.9	GLR1	orf19.4147	by similarity to S. cerev. and C. albicans:glutathione reductas	YPL091w
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function	YLR256w
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)	YOR388c
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function	YNL278w
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by ho	YDL168w
CA0781	0.9	1.6	1.8	1.2	1.6	1.9				
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function	no match (e-value > 0.05)
CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)	YKR070w
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function	YHR016c
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase	YHR008c
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function	YLR422w

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[[Cd OS+ up 1.5 10FDR] and [Cd XS+ up 1.5 10FDR]] and [Cd HS+ up 1.5 10FDR]

HS+ OS+										
Species ()	Ca	Cd	Ca	Cd	Ca	Cd				
Stress ()*(	HS+	HS+	OS+	OS+	XS+	XS+				
Systemati	rmali:	rmali:	rmali:	rmali:	rmali:	rmali:	Common	Ca orf19	Ca Function	S.c. hom.
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function	no match (e-value > 0.05)
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)	YKR069w
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)	YHR179w
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase	YHR179w
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)	YDL020c
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)	no match
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)	no match (e-value > 0.05)
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)	YDR256c