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Genome-wide gene expression profiling and a forward genetic screen show that differential expression of the sodium ion transporter Ena21 contributes to the differential tolerance of *Candida albicans* and *Candida dubliniensis* to osmotic stress

Brice Enjalbert,[1**] Gary P. Moran,[2**] Claire Vaughan,[2**] Tim Yeomans,[2] Donna M. MacCallum,[1] Janet Quinn,[3] David C. Coleman,[2] Al J.P. Brown[1] and Derek J. Sullivan[2*]

[1]*Aberdeen Fungal Group, School of Medical Sciences, Institute of Medical Sciences, University of Aberdeen, Aberdeen AB25 2ZD, UK.*
[2]*Microbiology Research Unit, Division of Oral Biosciences, Dublin Dental School and Hospital, Trinity College Dublin, Dublin 2, Ireland.*
[3]*Institute for Cell and Molecular Biosciences, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne NE2 4HH, UK.*

** These authors contributed equally to this work

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* Address for correspondence: Derek J. Sullivan, Microbiology Research Unit, Division of Oral Biosciences, Dublin Dental School & Hospital, Trinity College Dublin, Dublin 2, Republic of Ireland. Phone: +353 1 6127276. Fax: +353 1 6127295. E-mail: Derek.Sullivan@dental.tcd.ie

ABSTRACT

Candida albicans is more pathogenic than *Candida dubliniensis.* However, this disparity in virulence is surprising given the high level of sequence conservation and the wide range of phenotypic traits shared by these two species. Increased sensitivity to environmental stresses has been suggested to be a possible contributory factor to the lower virulence of *C. dubliniensis*. In this study, we investigated, in the first comparison of *C. albicans* and *C. dubliniensis* by transcriptional profiling, global gene expression in each species when grown under conditions in which the two species exhibit differential stress tolerance. The profiles revealed similar core responses to stresses in both species, but differences in the amplitude of the general transcriptional responses to thermal, salt and oxidative stress. Differences in the regulation of specific stress genes were observed between the two species. In particular, *ENA21* encoding a sodium ion transporter, was strongly induced in *C. albicans* but not in *C. dubliniensis*. In addition, *ENA21* was identified in a forward genetic screen for *C. albicans* genomic sequences that increase salt tolerance in *C. dubliniensis*. Introduction of a single copy of *CaENA21* was subsequently shown to be sufficient to confer salt tolerance upon *C. dubliniensis.*

INTRODUCTION

Candida albicans is the most pathogenic yeast species. It is a common cause of superficial infections (e.g. vaginitis, diaper rash and oral thrush) and in certain groups of immunocompromised patients it can cause systemic infections with high levels of mortality (Odds, 1988). A number of factors contribute to the virulence of *C. albicans*, including the ability to form filaments, cell-cell and cell-surface adhesion, the production of extracellular proteinases and stress adaptation. *Candida dubliniensis* is closely related to *C. albicans* in evolutionary terms, sharing its properties of commensalism and opportunistic infection (Sullivan *et al.*, 1995). In a recent study it was shown that 95.6% of genes are ≥60% homologous in the two species, with vast majority of genes being approximately 90% homologous (Moran *et al.*, 2004). Given the similarity of the genomes of these two species it is not surprising that they share many phenotypic traits, including the ability to produce hyphae and chlamydospores. This can present difficulties in accurately discriminating between them in clinical samples. However, despite their phylogenetic relatedness, epidemiological data suggest that *C. albicans* is significantly more pathogenic than *C. dubliniensis* which is rarely identified in cases of systemic disease (i.e. 2% of cases of candidemia) while *C. albicans* is usually responsible for approximately 50-65% of cases. (Kibbler *et al.*, 2003; Sullivan *et al.*, 2004; Odds *et al.*, 2007). This observation has been confirmed using a range of infection models, including the mouse model of systemic infection and the neonatal mouse gastric infection model (Gilfillan *et al.*, 1998; Vilela *et al.*, 2002; Stokes *et al.*, 2007). The molecular basis for the differential virulence of *C. dubliniensis* and *C. albicans* has yet to be established. However, it has recently been shown that *C. dubliniensis* has a lower filamentation rate than *C. albicans,* resulting in a decreased capacity to invade tissues in a reconstituted human epithelial infection model (Stokes *et al.*, 2007). This suggests that a lower capacity to produce hyphae *in vivo* might contribute to the relatively low virulence of *C. dubliniensis*. However, other factors might also contribute, at least in part, to the reduced virulence of *C. dubliniensis* in comparison with *C. albicans.*

Candida albicans can colonize diverse niches within its human host (e.g. the oral cavity, the gastrointestinal tract and the vagina (Odds, 1988)) and has the capacity to respond rapidly to changes in environmental conditions (Enjalbert *et al.*, 2003; Lorenz *et al.*, 2004; Fradin *et al.*, 2005; Tournu *et al.*, 2005). This species is also able to tolerate a wide range of environmental stresses (Smith *et al.*, 2004). The inactivation of key stress-protective enzymes or stress-signaling proteins attenuates the virulence of *C. albicans*, indicating that stress responses contribute to the virulence of this pathogen (Wysong *et al.*, 1998; Alonso-Monge *et al.*, 1999; Hwang *et al.*, 1999; Fradin *et al.*, 2005). Genome-wide analyses of *C. albicans* have revealed major transcriptional reprogramming following exposure to specific stresses. This has provided insights into the mechanisms of stress adaptation in this fungus, and highlighted differences in these stress adaptation mechanisms compared with those found in model yeast species (Gasch *et al.*, 2000; Chen *et al.*, 2003; Enjalbert *et al.*, 2003; Enjalbert *et al.*, 2006). For example, it was shown that *C. albicans* does not mount a core transcriptional response under environmental conditions that stimulate a common stress response in *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. Instead, *C. albicans* mounts a more specific core stress response, involving the activation of a relatively small set of genes under stress conditions that activate the stress activated protein kinase, Hog1 (Enjalbert *et al.*, 2006). Also, while Msn2-like transcription factors play a key role in the core stress response in *S. cerevisiae,* their role in *C. albicans* has diverged significantly (Nicholls *et al.*, 2004; Ramsdale *et al.*, 2008) suggesting that stress responses have diverged in pathogenic yeasts in comparison with benign model yeasts.

Several studies have reported that *C. dubliniensis* is less resistant than *C. albicans* to elevated temperatures, high salt concentrations and oxidative stress (Pinjon *et al.*, 1998;

Alves *et al.*, 2002; Vilela *et al.*, 2002). Given the importance of stress responses for the virulence of *C. albicans,* we reasoned that the lower stress tolerance of *C. dubliniensis* might help to explain the disparity in the virulence of these two species. Therefore, in this study we have compared the genome-wide transcriptional responses of *C. dubliniensis* and *C. albicans* under environmental conditions that emphasize their differential stress tolerances. In addition we have performed a genome-wide screen for *C. albicans* sequences that confer increased salt tolerance upon *C. dubliniensis.* Both approaches indicate that differential regulation of the *ENA21* gene, encoding a sodium ion transporter, can account for the different salt tolerance of *C. dubliniensis* and *C. albicans.* However, ectopic expression on *ENA21* in *C. dubliniensis* was insufficient to increase the virulence of this pathogen.

RESULTS

Sensitivity of *C. dubliniensis* and *C. albicans* to environmental stresses.

Previous studies have suggested that *C. dubliniensis* is less tolerant of environmental stress than *C. albicans* (Pinjon *et al.*, 1998; Alves *et al.*, 2002; Vilela *et al.*, 2002). Given the importance of stress responses in microbial pathogenesis we reasoned that this reduced tolerance to stress might (partially) account for the reduced virulence of *C. dubliniensis* relative to *C. albicans*. Therefore, before embarking upon a genomic comparison of stress responses in these species, we first confirmed their differential tolerance of the specific stresses used in the expression profiling experiments.

The comparative ability of *C. albicans* SC5314 and *C. dubliniensis* CD36 to tolerate specific stresses was tested (Fig. 1). The data obtained using these strains (whose genomes have been sequenced) were representative of those obtained for a range of strains belonging to both species (data not shown). Both *C. albicans* and *C. dubliniensis* displayed similar tolerance of mild stress conditions (e.g. on media supplemented with 0.6 M NaCl or 1m M H_2O_2). However, the growth of *C. dubliniensis* was inhibited to a significantly greater extent, compared with the inhibition of *C. albicans* growth, when cells were exposed to more acute stresses (e.g. temperatures $\geq$ 42 °C; osmotic stresses $\geq$1 M NaCl; oxidative stresses $\geq$ 5 mM H_2O_2) (Fig.1). These data indicate that while *C. dubliniensis* is able to adapt to mild stresses it does not have the same capacity as *C. albicans* to adapt to more extreme osmotic, oxidative and temperature stresses.

Expression profiling of *C. dubliniensis* and *C. albicans* following exposure to acute stresses.

Establishing the molecular basis of the differential stress phenotypes of *C. albicans* and *C. dubliniensis* is likely to contribute to our understanding of the role of stress responses in the virulence of *Candida* species. Therefore, we used genome-wide expression profiling to perform an unbiased exploration of the molecular differences between the stress responses of *C. albicans* and *C. dubliniensis.* Exponentially growing *C. dubliniensis* CD36 and *C. albicans* SC5314 cells were exposed to the following stress conditions and transcript profiling performed 30 minutes later: a shift from 30 °C to 42 °C; 1.0 M NaCl; and 5 mM H_2O_2. These conditions were chosen because the two *Candida* species displayed differential sensitivities to these relatively acute stresses (Fig. 1). A thirty-minute timepoint was used because previous studies have shown that most *C. albicans* stress genes are induced at this point (Enjalbert *et al.*, 2003). Four independent biological replicates (with dye swap) were analysed for each condition, statistically robust changes in expression were identified using SAM software, and a cut-off of $\geq$ 1.5-fold changes was used to identify stress-regulated genes.

A previous microarray analysis in *C. albicans* examined the effects of mild stress conditions (i.e. a shift from 25 °C to 37 °C; 0.3 M NaCl; and 0.4 mM H_2O_2) upon global gene expression (Enjalbert *et al.*, 2003). These conditions had previously been demonstrated to stimulate broad-ranging core transcriptional responses to stress in model yeasts (Gasch *et al.*, 2000; Chen *et al.*, 2003). However, of the 445 *C. albicans* genes that were induced in response to at least one of these conditions, only one gene was commonly induced by all three conditions (Enjalbert *et al.*, 2003). In the current study, where we have examined more extreme levels of the same stresses, there was a significant increase in the number of stress-induced genes in *C. albicans.* A total of 1,016 *C. albicans* genes were induced in response to at least one of these conditions (Fig. 2A). Despite this 2.5-fold increase in the number of stress-induced genes, the number of genes that were commonly induced by all three stress conditions remained low. Eleven genes (1.1% of the stress genes) were induced by all three stresses, of which seven have no known function. This finding is consistent with our previous report indicating that *C. albicans* expresses a relatively small core stress response, compared with benign model yeasts (Enjalbert *et al.*, 2006).

A similar observation was made in *C. dubliniensis.* A total of 679 *C. dubliniensis* genes were induced in response to at least one of the three stress conditions examined. Eight (1.2%) of these genes were induced by all three stresses. Of these eight genes, two are in common with the eleven core stress genes from *C. albicans*: *orf19.7085* (unknown function) and *RPN4*/*orf19.1069* (a putative regulator of proteasome genes). Both of these belong to the previously defined core stress genes of *C. albicans* (Enjalbert *et al.*, 2006). Therefore, like *C. albicans*, *C. dubliniensis* exhibits a relatively small core transcriptional stress in terms of the numbers of genes involved, compared with model yeasts.

General impact of acute stresses upon the *C. dubliniensis* and *C. albicans* transcriptomes

The transcriptional responses of *C. albicans* and *C. dubliniensis* to the acute heat, osmotic and oxidative stresses displayed a relatively high degree of similarity (Fig. 2B). About 45% of the *C. albicans* genes that were induced in response to the heat shock were also induced in *C. dubliniensis* (Fig. 2B). Approximately 59% of the *C. dubliniensis* genes that were induced by the salt stress were also induced in *C. albicans.* Similarly, about 64% of the *C. dubliniensis* genes that were induced by the oxidative stress were also induced in *C. albicans.* Our comparison of the genes that are regulated in each species suggests that, while there is significant overlap between the transcriptional responses of *C. dubliniensis* and *C. albicans* to each of these stresses, the corresponding stress signalling pathways have some different outputs in each species.

However, the number of genes that were induced in each species differed significantly from one condition to another. For example, about twice as many genes were induced in response to heat shock in *C. dubliniensis* (370 genes) than in *C. albicans* (194 genes). In contrast, approximately twice as many genes were induced in response to oxidative stress in *C. albicans* (567 genes) compared with *C. dubliniensis* (364 genes). In the case of the osmotic stress, the response mounted by *C. dubliniensis* to salt osmotic stress was relatively weak, with only 51 genes induced, compared to the 391 genes that were up-regulated in *C. albicans*. These differences do not simply reflect the differential stress sensitivities of these pathogens because in all cases *C. dubliniensis* was more sensitive to these stresses (Fig. 1). Instead the data suggest that the stress signalling pathways might exhibit different levels of responsiveness to these environmental changes as well as some differences in their downstream targets.

Impact of the stresses upon cellular functions in *C. dubliniensis* and *C. albicans*

We examined the behaviour of "hallmark genes" in the microarray experiments to facilitate the comparison of the two species with regard to the impact of stresses upon relevant cellular functions. Hallmark genes were defined as genes of known function in *S. cerevisiae* that display regulatory responses characteristic of the relevant functional category in that yeast. Having selected these hallmark genes we then examined their fold-regulation in both *C. dubliniensis* and *C. albicans* under each of the three stress conditions analysed (Fig. 3). In general these hallmark genes behaved similarly in both species, although there were some notable differences.

Heat shock genes: Most of the heat shock hallmark genes, many of which encode molecular chaperones, were strongly induced in response to heat shock in both *C. dubliniensis* and *C. albicans* (Fig. 3). Of the eight heat shock hallmark genes examined, five were induced in both species, two were induced in neither species, and *HSP30* was induced only in *C. dubliniensis*. Our previous studies have indicated that *HSP12* expression is induced in *C. albicans* in response to heat, oxidative and osmotic stresses (Enjalbert *et al.*, 2003;

Smith *et al.*, 2004). However, *HSP12* up-regulation was not observed in this study, possibly because of the different stress conditions examined. In general the heat shock hallmark genes were not induced in response to the other stresses examined, but several were up-regulated in response to the oxidative stress in *C. albicans* (*HSP30, HSP78, HSP104*).

Osmotic stress genes: The majority of the osmotic stress hallmark genes were up-regulated in both *C. dubliniensis* and *C. albicans* following exposure to 1.0 M NaCl. The *ENA21* and *ENA22* genes were up-regulated in *C. albicans,* as reported previously in other microarray studies of the osmotic stress response in this pathogen (Enjalbert *et al.*, 2003; Enjalbert *et al.*, 2006). However, the *C. dubliniensis ENA* genes displayed minimal levels of activation. The *C. albicans ENA21* gene and its paralogue *ENA22* are orthologues of the *S. cerevisiae ENA2* gene that encodes a P-type ATPase sodium pump. *ScENA2* confers salt tolerance upon *S. cerevisiae* through sodium ion efflux (Garciadeblas *et al.*, 1993). The *C. dubliniensis* genome (http://www.sanger.ac.uk/sequencing/Candida/dubliniensis/) contains two genes with over 90% nucleotide sequence identity to *CaENA21* and *CaENA22* (Cd36_72570/*CdENA21* and Cd36_00320/*CdENA22*). Therefore, the lack of induction of *CdENA21* and *CdENA22* in response to salt stress was surprising. We reasoned that this lack of induction might partially account for the relative sensitivity of *C. dubliniensis* to salt stress (Fig. 1).

Oxidative stress genes: The oxidative stress hallmarks, which include catalase, superoxide dismutase, glutaredoxin and thioredoxin genes, were generally strongly induced in both *C. dubliniensis* and *C. albicans* in response to 5 mM H_2O_2. As described previously for mild stress conditions (0.4 M H_2O_2), the oxidative stress hallmark genes were also up-regulated slightly in response to a mild heat-shock (Enjalbert *et al.*, 2003), a phenomenon that seems more pronounced in *C. dubliniensis*.

Other cellular functions: We have established that, with some notable exceptions, most of the stress hallmark genes displayed similar expression patterns in *C. dubliniensis* and *C. albicans*. Using the gene ontology tool we then screened our transcript profiling datasets for functional categories that displayed statistically significant differences in their regulation between these two species. For most functional categories no significant differences were observed. However, a small number of processes did display significant differences between *C. dubliniensis* and *C. albicans* ($P<10^{-3}$). These were nitrogen utilization, peptide transport, glucose transport and manganese ion transport (Fig. 3). The oligopeptide transporter genes (*OPT*) and the nitrogen utilization genes, which include the regulators *GAT1* and *NPR1* (Boeckstaens *et al.*, 2007; Dabas and Morschhauser, 2007), were repressed in response to the acute osmotic stress in *C. albicans,* but only to a minor extent in *C. dubliniensis*. Also most *OPT* genes were induced in response to the oxidative stress in *C. dubliniensis,* but not in *C. albicans*. Some genes involved in glucose and manganese ion transport were more strongly induced by osmotic stress in *C. albicans* than in *C. dubliniensis*.

To summarise, our genome-wide expression profiling indicated that *C. albicans* and *C. dubliniensis* generally display similar transcriptional responses to the relatively acute heat, salt and oxidative stresses examined here. However, some differences were observed between these species with respect to the regulation of genes encoding various transporters, and in particular, the lack of induction of *ENA21/22* sodium ion efflux pumps in *C. dubliniensis* provided a possible explanation for the relative sensitivity of this pathogen to salt stress.

A genetic screen for *C. albicans* genes that suppress the osmotic sensitivity of *C. dubliniensis*.

Our transcript profiling provided a powerful screen for genes whose stress regulation differs between *C. dubliniensis* and *C. albicans.* In parallel we performed forward genetic screens for *C. albicans* sequences capable of suppressing the relative sensitivity of *C. dubliniensis* to heat or salt stress. We reasoned that these two screens – one based on stress gene regulation, and the other upon stress phenotype – would provide complementary insights into the mechanistic basis for the differential stress sensitivities of these two pathogens.

The genetic screens were performed by transforming *C. dubliniensis* CdUM4B (*ura3/ura3*) with a *C. albicans* genomic library constructed in the plasmid pRMI (*URA3*), and selecting for transformants capable of growth at 42˚C or on medium supplemented with 1 M NaCl. Several saturating screens yielded no *C. dubliniensis* transformants capable of growth at 42˚C. This was consistent with the idea that the ability to grow at relatively high temperatures is a polygenic trait. However, eleven transformants capable of growth on 1 M NaCl were identified. Of these, four exhibited a stable and reproducible salt-resistant phenotype, tolerating up to 1.2 M NaCl. Sequence analysis revealed that all four *C. dubliniensis* transformants carried plasmids containing the entire coding sequence of the *C. albicans ENA21* gene. This strongly suggested that the transformation of *C. dubliniensis* with *CaENA21* was sufficient to increase the salt tolerance of this species, despite the presence of an orthologous gene in *C. dubliniensis* (*CdENA21*) that shares 91% identity.

To test this further, we integrated a single copy of the *CaENA21* gene at the *CDR1* locus in *C. dubliniensis* strain CD36. This had no effect upon the growth of *C. dubliniensis* on YPD medium. However, a single copy of *CaENA21* was sufficient to confer resistance to 1.2 M NaCl (Fig. 4). Similar results were obtained with another reference *C. dubliniensis* strain, Wü284 (Fig. 4). Therefore the introduction of *CaENA21* was sufficient to confer salt tolerance upon *C. dubliniensis*.

To determine whether the native *C. dubliniensis ENA21* gene is capable of conferring a similar phenotype, we then integrated the *CdENA21* gene at the *CDR1* locus in *C.*

dubliniensis strains CD36 and Wü284. The introduction of one additional single copy of *CdENA21* did enhance the growth of *C. dubliniensis* at 1 M NaCl, but unlike the *C. albicans* *ENA21* gene, *CdENA21* did not support significant growth at 1.2 M NaCl. These data suggested that either differential expression of the *CaENA21* and *CdENA21* genes, or perhaps functional differences in the activity of the encoded protein, might account for the relatively high salt resistance of *C. albicans* compared to *C. dubliniensis*.

Differential expression of *ENA21* in *C. albicans* and *C. dubliniensis*

Our microarray experiments suggested that the *ENA21* gene is differentially expressed in *C. dubliniensis* and *C. albicans* in response to 1.0 M NaCl. To test this further we performed RT-PCR on the *ENA21* transcript and its paralogue *ENA22* in both species, measuring their expression levels relative to the *TEF1* internal control (Fig. 5A). The basal levels of *ENA21* mRNA were approximately 10-fold higher in *C. albicans* compared with *C. dubliniensis*. By 1 h post exposure to 1 M NaCl *CaENA21* mRNA levels were induced 5-fold in *C. albicans*, whereas *CdENA21* expression levels did not increase in *C. dubliniensis*. These data were consistent with our transcript profiling data, confirming that while *ENA21* responds to salt stress in *C. albicans,* it does not do so in *C. dubliniensis.*

When *ENA22* mRNA levels were examined it was observed that the basal levels of expression were low in both species (Fig. 5A). *ENA22* expression was induced in both species following exposure to 1 M NaCl, but the levels of *ENA22* induction were lower than the basal levels of *ENA21* mRNA in *C. albicans*. These data reinforced the idea that differential *ENA21* expression levels in *C. dubliniensis* and *C. albicans* contribute to the different salt tolerances of these pathogens.

If differential *ENA21* expression levels do account for the different salt tolerances of *C. dubliniensis* and *C. albicans* one would expect this to be reflected in relatively high *ENA21* mRNA levels in salt tolerant *C. dubliniensis* transformants. Therefore, we measured *ENA21* mRNA levels in the *C. dubliniensis* CD36 and Wü284 transformants carrying *CaENA21* and *CdENA21* in the presence or absence of 1 M NaCl (Fig. 5B). Once again, *ENA21* mRNA levels were measured by RT-PCR relative to the *TEF1* internal control. *CaENA21* mRNA levels were strongly induced by NaCl in both *C. dubliniensis* CD36 and Wü284. Some induction of the cloned *CdENA21* gene was observed in *C. dubliniensis* CD36 in the presence of NaCl. However, no induction of chromosomal *CdENA1* sequences was observed in *C. dubliniensis* transformants carrying the empty pCDRI vector, and no *CdENA1* induction in *C. dubliniensis* Wü284 cells carrying pCdENA21. These data reinforce the view that elevated *ENA21* expression levels increase the salt tolerance of *C. dubliniensis*.

Hog1 activation in *C. dubliniensis*

ENA21 is a target of the stress-activated protein kinase Hog1 in *C. albicans*. To investigate whether the minimal induction of *ENA21* and *ENA22* in *C. dubliniensis* in response to salt stress was due to a lack of Hog1p activation, we examined the phosphorylation status of this protein by western blot analysis. Following exposure to NaCl, Hog1p was expressed and phosphorylated at similar levels in *C. dubliniensis* and *C. albicans* (Fig. 6). Therefore the absence of *ENA21* and *ENA22* induction in *C. dubliniensis* is not due to a lack of Hog1 signalling. This view is reinforced by the observation that other Hog1-dependent genes such as *GPD2* and *SLT1* were strongly induced by NaCl (Fig. 3).

Effect of *CaENA21* upon the virulence of *C. dubliniensis.*

Our data indicated strongly that *CaENA21* confers increased salt stress tolerance upon *C. dubliniensis.* To test whether this influenced the virulence of *C. dubliniensis,* we compared the virulence of *C. dubliniensis* cells containing pCaENA21, pCdENA21 and the control pCDRI plasmid using the classical mouse model of disseminated candidiasis (MacCallum and Odds, 2005). No significant difference in the survival of mice infected with these isogenic strains was observed (not shown). Furthermore, these strains displayed no significant differences with respect to their fungal burdens in the kidney, brain and liver (Fig. 7). Therefore, the increased salt tolerance of *C. dubliniensis* cells carrying the *CaENA21* gene was not sufficient to increase their virulence. This indicates that increasing the osmotic stress resistance of *C. dubliniensis* is not sufficient to increase the virulence of this species to the virulence levels of *C. albicans*, for example. Therefore, other traits of *C. dubliniensis* cells such as their thermal sensitivity, oxidative stress sensitivity and reduced rates of hyphal development might contribute to their relatively low virulence. Our data are consistent with the idea that the basis of this low virulence phenotype is multifactorial.

DISCUSSION

Epidemiological observations and virulence data from animal models both indicate that, despite the close phylogenetic relationship between *C. albicans* and *C. dubliniensis*, the latter species is less capable of colonizing and infecting humans. Recent studies have confirmed that the genomes of both species are closely related, with only 4.4% of *C. albicans* genes being absent or significantly divergent in the *C. dubliniensis* genome (Moran *et al.*, 2004). Comparison of the *C. albicans* and *C. dubliniensis* genome sequences indicates that the vast majority of gene orthologues in these species are ≥90% identical and both species share a high degree of synteny. This close genetic relatedness of the two species results in their sharing many phenotypic traits, to the point where it can be difficult to discriminate between them using phenotypic tests.

One phenotypic difference identified soon after the discovery of *C. dubliniensis* is the reduced capacity of this species to grow at temperatures ≥42°C, conditions under which the majority of *C. albicans* strains grow (Sullivan *et al.*, 1995). Indeed, comparative growth at 45°C has been recommended as a simple phenotypic test to discriminate between the two species (Pinjon *et al.*, 1998). These findings suggest that *C. albicans* is better able to tolerate thermal stress than *C. dubliniensis*.

Data presented here (Fig. 1) and in other studies (Sullivan *et al.*, 1995; Pinjon *et al.*, 1998; Alves *et al.*, 2002; Vilela *et al.*, 2002) show that *C. dubliniensis* is also less tolerant than *C. albicans* to heat shock, NaCl and H_2O_2, indicating that *C. dubliniensis* is relatively susceptible to a range of environmental stresses compared with *C. albicans*. Therefore *C. dubliniensis* appears less well equipped than *C. albicans* to adapt to the stresses experienced by these pathogens in the diverse environmental niches they occupy in the human body. This might, in part, contribute to the lower virulence of *C. dubliniensis* compared to *C. albicans*.

It was conceivable that a general lack of activation of stress responses in *C. dubliniensis* might have accounted for the relatively low tolerance of this pathogen to environmental stress. Therefore, in the first transcript profiling comparison of the two species, we used genome-wide expression profiling to compare the transcriptional responses of *C. dubliniensis* and *C. albicans* to stresses, focusing on experimental conditions under which *C. dubliniensis* grows relatively poorly (a 30-42°C heat shock, 1.0 M NaCl and 5 mM H_2O_2). These experiments revealed that, in general, *C. dubliniensis* mounts a similar transcriptional response to *C. albicans* following exposure to these heat, salt and oxidative stresses (Figs. 2 and 3). In both *C. dubliniensis* and *C. albicans* a relatively small subset of genes was commonly induced by all three of the stresses examined (about 1% of the set of stress induced genes). This strengthens the view that *C. albicans* (and now *C. dubliniensis*) exhibits a relatively narrow core stress response compared with the benign model yeasts *S. cerevisiae* and *S. pombe* (Enjalbert *et al.*, 2006). The expression of hallmark stress genes was remarkably similar in both species. There were differences between the species with respect to the expression of a variety of transporters involved in peptide and manganese uptake. However, with one notable exception, the transcript profiling data revealed no obvious explanations for the relatively low stress tolerance of *C. dubliniensis* compared with *C. albicans*.

One notable exception was the minimal induction of *ENA21* and *ENA22* in *C. dubliniensis* following exposure to salt stress. This suggested that insufficient expression of the Ena21/22 sodium ion efflux pumps might contribute to the salt sensitivity of this species. This view was strongly reinforced by the repeated isolation of the *CaENA21* gene in an unbiased genetic screen for *C. albicans* genes that can suppress the salt sensitivity of *C. dubliniensis.* All four of the *C. albicans* genomic clones that were capable of suppressing the salt sensitivity of *C. dubliniensis* carried the *CaENA21* gene. The significance of the

CaENA21 gene in conferring salt resistance upon *C. dubliniensis* was further confirmed by the subsequent integration of this gene into the *C. dubliniensis* genome. Once again, this increased the resistance of *C. dubliniensis* cells to salt stress (Fig. 4). Furthermore, increased *CaENA21* expression in *C. dubliniensis* gene correlated with elevated salt resistance (Fig. 5).

Our data strongly suggest that the relatively low levels of *CdENA21* expression in *C. dubliniensis* contribute to the salt sensitivity of this species, compared with *C. albicans.* These relatively low *CdENA21* expression levels are not due to a lack of Hog1 signaling as the Hog1 stress-activated protein kinase was phosphorylated in response to salt stress in *C. dubliniensis* (Fig. 6). Other osmotic stress genes were also induced in response to the NaCl treatment (Fig. 3). Therefore differences in the *ENA21* promoters might account for the differential responsiveness of this gene in *C. dubliniensis* and *C. albicans*. Experiments are currently underway to compare the two promoters.

We tested whether increasing the salt tolerance of *C. dubliniensis* has an impact upon the virulence of this pathogen. This was done by comparing the survival rates and tissue burdens for mice infected with *CaENA1* transformants and control strains (Fig. 7). *CaENA1* expression did not increase the virulence of *C. dubliniensis.* This suggests that traits in addition to salt sensitivity contribute to the relatively low virulence of this species compared with *C. albicans.* These additional traits might include the thermal and oxidative stress sensitivity of *C. dubliniensis* (Fig. 1) and/or the relatively low rates of hyphal development observed for this species (Gilfillan *et al.*, 1998; Stokes *et al.*, 2007).

In summary, our data indicate that the lack of induction of *ENA21* in response to NaCl stress accounts for the relative salt sensitivity of *C. dubliniensis* compared with *C. albicans*. This suggests that there may be differences in the transcriptional regulatory pathways responsible for *ENA21* expression in *C. albicans* and *C. dubliniensis* and that there may be other differences in the transcriptional wiring of the two species which might account for other phenotypic differences between them. Our work shows how a combination of expression profiling and forward genetic screens can provide a powerful experimental approach towards the elucidation of the mechanistic basis for important phenotypic differences between these closely related *Candida* species.

EXPERIMENTAL PROCEDURES

Strain and growth conditions

Candida dubliniensis strains CD36 (Sullivan *et al.*, 1995), Wü284 (Morschhauser *et al.*, 1999) and CdUM4B (*ura3/ura3*: (Staib *et al.*, 2001)) and *C. albicans* SC5314 (Gillum *et al.*, 1984) were used in this study. Strains were routinely grown at 30°C in YPD containing 0.02% adenine and 0.008% uridine or in SD minimal medium (Sherman, 1991).

Stress sensitivity tests

To test the sensitivity of strains to specific stresses, they were grown in YPD broth at 30 °C to mid-exponential phase and 10-fold serial dilutions of these cells spotted onto YPD plates and YPD plates supplemented with the appropriate concentration of NaCl or H_2O_2. Growth was monitored after 24h at 30 °C (42 ºC for the heat-shock assay).

Transcript profiling

Transcript profiling was performed on *C. albicans* SC5314 and *C. dubliniensis* CD36 as described previously (Enjalbert *et al.*, 2006). The strains were cultured to OD_{600} = 1 in YPD supplemented with uridine at 30 ºC (200 rpm), and then divided into two parts: one was exposed to a stress condition whereas the other was the control. For the heat shock experiments, cells were transferred from 30 to 42 °C by immersing the sample in a water bath at t = 0. To impose the hyperosmotic shock, NaCl was added to a final concentration of 1.0 M. To apply the oxidative shock, hydrogen peroxide (H_2O_2) was added to a final concentration of 5 mM. After 30 minutes, cells were collected by centrifugation, snap frozen in liquid N_2, disrupted using a microdismembrator (Braun, Melsungen, Germany) and RNA prepared as described previously (Hauser *et al.*, 1998). Cy3- and Cy5-labeled cDNAs were prepared from total RNA, and the probes were hybridized with whole genome microarrays containing ca. 6000 *C. albicans* genes (Eurogentec, Seraing, Belgium). Slides were scanned using a ScanArray Lite scanner (PerkinElmer Life Sciences, Beaconsfield, United Kingdom) and quantified using QuantArray software (version 2.0). Data normalization and analysis were performed using GeneSpring (Silicon Genetics, Redwood City, CA), and statistical analysis was performed using SAM (Significance Analysis of Microarrays; (Tusher *et al.*, 2001)). Expression ratios were calculated by comparing stressed cells with their unstressed control. Data from four independent biological replicates, two of them obtained with a dye swap, were used for each strain and each condition. These datasets are available at ArrayExpress (http://www.ebi.ac.uk/microarray/ with the experiment code: E-MEXP-1650).

Forward genetic screen in *C. dubliniensis*

A *C. albicans* genomic DNA library constructed in the plasmid pRM1 (Pla *et al.*, 1995) was kindly provided by Dr. Federico Navarro-García (Universidad Complutense de Madrid). *C. dubliniensis* CdUM4B cells were transformed with this library by electroporation (Staib *et al.*, 2001) to yield about 40,000 independent transformants. To identify *C. albicans* genes that suppress the inability of *C. dubliniensis* to grow under stressful conditions, 40 pools of transformants were generated and 5×10^5 cells from each pool were spread onto SD plates containing 1.2 M NaCl and grown at 30˚C, or onto SD medium alone and incubated at 42˚C. Positive clones were subcultured and the stability of their salt or temperature tolerant phenotypes was assessed, and the plasmids rescued from stable *C. dubliniensis* transformants. To ascertain the identity of *C. albicans* ORFs isolated in this screen, the inserts were sequenced and homology searches performed using the *C. albicans* WU-BLAST2 Search facility at the *Candida* genome database (CGD; http://www.candidagenome.org/).

Gene manipulations in *C. dubliniensis*

The *C. albicans ENA21* (*CaENA21*) and *C. dubliniensis ENA21* (*CdENA21*) genes were integrated into the *C. dubliniensis* genome in single copy. This was accomplished by PCR amplification of these genes from chromosomal DNA using the Expand Long Template PCR System (Roche Applied Science) using template DNA from *C. albicans* SC5314 and *C. dubliniensis* CD36. The entire *CaENA21* open reading frame was amplified, including 1385 bp of upstream sequences and 588 bp of downstream sequences. The *CdENA21* gene was PCR amplified including 2,414 bp of upstream sequences and 223 bp of downstream sequences. These PCR products were cloned in pGEM-T (Promega) and sequenced to confirm that no mutations had been introduced. The products were then subcloned into pCDRI (Moran *et al.*, 2007) using the *Not*I and *Sac*II restriction endonuclease sites in pGEM-T, to create the plasmids pCaENA21 and pCdENA21. Targeted integration of these pCDRI-based plasmids at the *CDR1* locus of *C. dubliniensis* strains CD36 and Wü284 was carried out as described by Moran *et al.* (Moran *et al.*, 2007). The *ENA21* copy number in these strains was assayed by real-time PCR (RT-PCR) using the primers ENA21F/R (see next section). Strains carrying pCaENA21 or pCdENA21 were shown to harbour three copies of *ENA21* gene relative to *TEF1*.

Real-time PCR analysis of gene expression

For RNA preparation, cells were harvested from YPD cultures and frozen in liquid nitrogen. RNA was prepared using TRI-reagent (Sigma) as described (Stokes *et al.*, 2007). RNA samples were rendered DNA free by incubation with Turbo-RNAfree reagent (Ambion, Austin, TX) and RNA concentrations determined using the Ribo-green kit (Molecular Probes). Reverse transcription was carried out with 1 μg of total RNA with an oligo-dT primer (Promega) and Superscript II reverse transcriptase (Invitrogen, Carlsbad, CA).

Amplification was carried out using the following primers pairs: QRTEF1F/R (Green *et al.*, 2005); ENA21F/R (ENA21F: 5′-GGGCCAACCAATTTTTACTTTG-3′; ENA21R: 5′-AATAAAGTACAACCAATTGCAACACC-3′); and ENA22F/R (ENA22F: 5′-GATCCACTGCATTTGCCTCA-3′; ENA22R: 5′-AAATTGGTTAGCCCAAAGTTCACT-3′). Primer sets ENA21F/R and ENA22 F/R were designed using Primer Express software v1.5 (Applied Bisosytems, Foster City, CA) and were homologous to *C. albicans* and *C. dubliniensis ENA21* and *ENA22* ORFs, respectively. These primers yielded single, specific amplimers from genomic DNA and cDNA templates from both *C. albicans* and *C. dubliniensis*. Real-time detection of *TEF1* and *ENA* amplimers was carried out using the QuantiTect Sybr green PCR kit (Qiagen, West Sussex, U.K.) and the ABI 7700 sequence detector. *ENA* gene expression levels were normalised against the expression levels of the constitutively expressed *TEF1* gene in the same cDNA sample.

Hog1 phosphorylation assays

Hog1 phosphorylation was examined by western blotting (New England Biolabs) as described previously (Smith *et al.*, 2004). Western blots were probed with an anti-phospho p38 antibody, which only recognises the phosphorylated, active form of *C. albicans* and *C. dubliniensis* Hog1 (Hog1-P). Total levels of Hog1 protein were determined by stripping and reprobing the blot with an anti-Hog1 antibody (santa Cruz Biotechnology, Sanata Cruz, Ca) that recognises both phosphorylated and unphosphorylated forms of Hog1.

Virulence assays

Immunocompetent 6-8 week-old female BALB/c mice (Harlan Sera-lab, Loughborough, UK) were challenged intravenously with *C. dubliniensis* cells grown with shaking for 18-24 h at 30°C in NGY medium (0.1% (w/v) Neopeptone, 0.4% (w/v) glucose and 0.1% (w/v) Yeast

Extract). Cells were harvested, washed twice, and then resuspended in physiological saline. Groups of 5 or 6 mice were inoculated via the lateral tail vein with 1.7 x 10^5 CFU/g body weight (MacCallum and Odds, 2005). Mice were monitored over 28 days and animals showing signs of distress or illness were humanely terminated and deaths recorded as occurring the following day. Kidneys, liver and brain were removed aseptically post mortem, homogenized in 0.5 ml of water, and *C. dubliniensis* tissue burdens determined by viable counting. Organ burdens were compared by Mann-Whitney *U* test. All experimentation was carried out under the terms of the UK Home Office licenses for research on animals.

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FIGURE LEGENDS

FIG. 1. Comparative growth of *C. albicans* SC5314 (C. a) and *C. dubliniensis* CD36 (C. d) under conditions of heat shock, osmotic stress (NaCl) and oxidative stress (H_2O_2). Ten-fold dilutions of mid-exponential phase cultures were spotted onto YPD plates supplemented with the compounds indicated on the left of the figure, with the exception of the spots incubated at 42ºC; all other spots were incubated at 30ºC.

FIG. 2. Global analysis of *C. albicans* and *C. dubliniensis* gene expression exposed to heat shock, osmotic stress and oxidative stress. (A) Venn diagrams indicating the numbers of genes induced in *C. albicans* (C. a) and *C. dubliniensis* (C. d) subjected to the three stress conditions (HS+; heat shock from 30°C to 42°C; OS+: osmotic stress with 1 M NaCl; XS+: oxidative stress with 5 mM H_2O_2. (B) Venn diagrams indicating the numbers of overlapping induced genes in *C. albicans* and *C. dubliniensis* submitted to the same stress condition. The gene lists were obtained using the SAM software to define the statistically significant genes and by refining the list with a cut-off of 1.5.

FIG. 3. Comparison of expression of specific genes in specific functional categories. These include the three stress hallmark groups as well as other gene groups selected for their specificity to one of the species. For the latter, genes that were induced or repressed ≥2 fold in either species were entered to the GO Term Finder tool (http://www.candidagenome.org/cgi-bin/GO/goTermFinder). Four processes (nitrogen utilization, peptide transport, glucose transport and manganese transport) were found to be significant in only one species ($P<10^{-2}$).

FIG 4. Growth of derivatives of *C. dubliniensis* strains CD36 and Wü284 harboring the integrative plasmid pCDRI on YPD agar supplemented with NaCl. Strains were transformed with empty plasmid (pCDRI) or derivatives containing the *C. albicans* (pCaENA21) or *C. dubliniensis* (pCdENA21) genes. Spot plates were prepared as described in the materials and methods.

FIG. 5. Real-time PCR analysis of *ENA21* and *ENA22* expression. (A) Expression of *ENA21* (left) and *ENA22* (right) was analysed in *C. albicans* (dark grey bars) and *C. dubliniensis* (light grey bars) relative to the expression of *TEF1*. Cells were grown to OD600nm 1.0 (0 min) before the addition of 1 M NaCl. RNA was isolated 30 min and 60 min after the addition of NaCl. (B) Expression of *ENA21* in derivatives of *C. dubliniensis* strain CD36 (left) and Wü284 (right) harbouring the integrative plasmid pCDRI or derivatives of the plasmid containing the cloned *C. albicans ENA21* gene (pCaENA21) or the cloned *C. dubliniensis ENA21* gene (pCdENA21).

FIG 6. Phosphorylation of Hog1 in *C. albicans* and *C. dubliniensis* exposed to 1.0 M NaCl. Western blot analysis of Hog1 from *C. albicans* SC5314 (C.a) and *C. dubliniensis* CD36 (C.d) cells after treatment with 1.0 M NaCl for the times indicated. Western blots were probed with an anti-phospho p38 antibody, which only recognises the phosphorylated, active form of *C. albicans* and *C. dubliniensis* Hog1 (Hog1-P). 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.

FIG. 7. Effect of heterologous expression of *CaENA21* on virulence. Organ burdens determined for groups of six BALB/c mice infected with the CD36 strains. Black bars

represent *C. dubliniensis* CD36 containing pCDRI; grey bars, CD36 containing pCdENA21; white bars, and CD36 containing pCaENA21.

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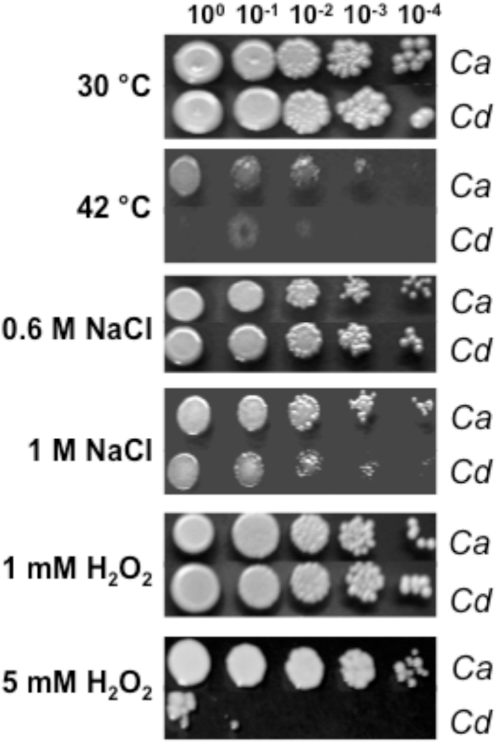
Fig. 1



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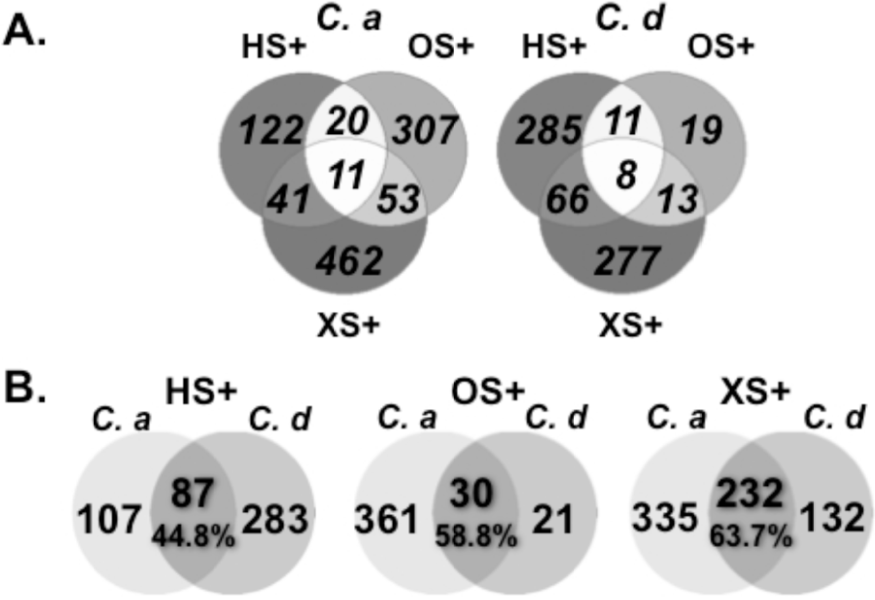
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277
B.
HS+
C. a
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87
44.8%
283
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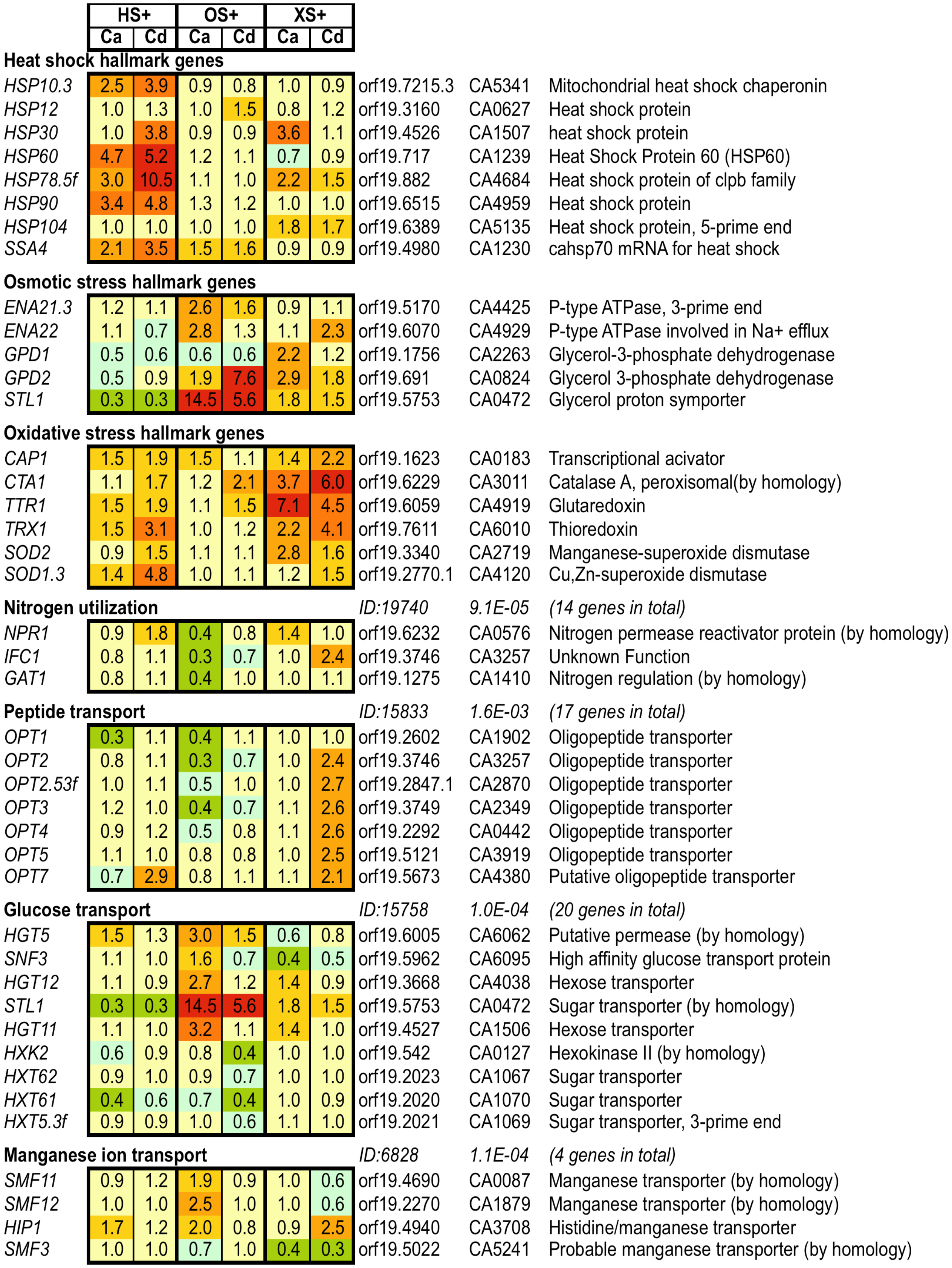
Fig. 3



	HS+		OS+		XS+				
	Ca	Cd	Ca	Cd	Ca	Cd			
Heat shock hallmark genes									
HSP10.3	2.5	3.9	0.9	0.8	1.0	0.9	orf19.7215.3	CA5341	Mitochondrial heat shock chaperonin
HSP12	1.0	1.3	1.0	1.5	0.8	1.2	orf19.3160	CA0627	Heat shock protein
HSP30	1.0	3.8	0.9	0.9	3.6	1.1	orf19.4526	CA1507	heat shock protein
HSP60	4.7	5.2	1.2	1.1	0.7	0.9	orf19.717	CA1239	Heat Shock Protein 60 (HSP60)
HSP78.5f	3.0	10.5	1.1	1.0	2.2	1.5	orf19.882	CA4684	Heat shock protein of clpb family
HSP90	3.4	4.8	1.3	1.2	1.0	1.0	orf19.6515	CA4959	Heat shock protein
HSP104	1.0	1.0	1.0	1.0	1.8	1.7	orf19.6389	CA5135	Heat shock protein, 5-prime end
SSA4	2.1	3.5	1.5	1.6	0.9	0.9	orf19.4980	CA1230	cahsp70 mRNA for heat shock
Osmotic stress hallmark genes									
ENA21.3	1.2	1.1	2.6	1.6	0.9	1.1	orf19.5170	CA4425	P-type ATPase, 3-prime end
ENA22	1.1	0.7	2.8	1.3	1.1	2.3	orf19.6070	CA4929	P-type ATPase involved in Na+ efflux
GPD1	0.5	0.6	0.6	0.6	2.2	1.2	orf19.1756	CA2263	Glycerol-3-phosphate dehydrogenase
GPD2	0.5	0.9	1.9	7.6	2.9	1.8	orf19.691	CA0824	Glycerol 3-phosphate dehydrogenase
STL1	0.3	0.3	14.5	5.6	1.8	1.5	orf19.5753	CA0472	Glycerol proton symporter
Oxidative stress hallmark genes									
CAP1	1.5	1.9	1.5	1.1	1.4	2.2	orf19.1623	CA0183	Transcriptional acivator
CTA1	1.1	1.7	1.2	2.1	3.7	6.0	orf19.6229	CA3011	Catalase A, peroxisomal(by homology)
TTR1	1.5	1.9	1.1	1.5	7.1	4.5	orf19.6059	CA4919	Glutaredoxin
TRX1	1.5	3.1	1.0	1.2	2.2	4.1	orf19.7611	CA6010	Thioredoxin
SOD2	0.9	1.5	1.1	1.1	2.8	1.6	orf19.3340	CA2719	Manganese-superoxide dismutase
SOD1.3	1.4	4.8	1.0	1.1	1.2	1.5	orf19.2770.1	CA4120	Cu,Zn-superoxide dismutase
Nitrogen utilization							*ID:19740*	*9.1E-05*	*(14 genes in total)*
NPR1	0.9	1.8	0.4	0.8	1.4	1.0	orf19.6232	CA0576	Nitrogen permease reactivator protein (by homology)
IFC1	0.8	1.1	0.3	0.7	1.0	2.4	orf19.3746	CA3257	Unknown Function
GAT1	0.8	1.1	0.4	1.0	1.0	1.1	orf19.1275	CA1410	Nitrogen regulation (by homology)
Peptide transport							*ID:15833*	*1.6E-03*	*(17 genes in total)*
OPT1	0.3	1.1	0.4	1.1	1.0	1.0	orf19.2602	CA1902	Oligopeptide transporter
OPT2	0.8	1.1	0.3	0.7	1.0	2.4	orf19.3746	CA3257	Oligopeptide transporter
OPT2.53f	1.0	1.1	0.5	1.0	1.0	2.7	orf19.2847.1	CA2870	Oligopeptide transporter
OPT3	1.2	1.0	0.4	0.7	1.1	2.6	orf19.3749	CA2349	Oligopeptide transporter
OPT4	0.9	1.2	0.5	0.8	1.1	2.6	orf19.2292	CA0442	Oligopeptide transporter
OPT5	1.1	1.0	0.8	0.8	1.0	2.5	orf19.5121	CA3919	Oligopeptide transporter
OPT7	0.7	2.9	0.8	1.1	1.1	2.1	orf19.5673	CA4380	Putative oligopeptide transporter
Glucose transport							*ID:15758*	*1.0E-04*	*(20 genes in total)*
HGT5	1.5	1.3	3.0	1.5	0.6	0.8	orf19.6005	CA6062	Putative permease (by homology)
SNF3	1.1	1.0	1.6	0.7	0.4	0.5	orf19.5962	CA6095	High affinity glucose transport protein
HGT12	1.1	0.9	2.7	1.2	1.4	0.9	orf19.3668	CA4038	Hexose transporter
STL1	0.3	0.3	14.5	5.6	1.8	1.5	orf19.5753	CA0472	Sugar transporter (by homology)
HGT11	1.1	1.0	3.2	1.1	1.4	1.0	orf19.4527	CA1506	Hexose transporter
HXK2	0.6	0.9	0.8	0.4	1.0	1.0	orf19.542	CA0127	Hexokinase II (by homology)
HXT62	0.9	1.0	0.9	0.7	1.0	1.0	orf19.2023	CA1067	Sugar transporter
HXT61	0.4	0.6	0.7	0.4	1.0	0.9	orf19.2020	CA1070	Sugar transporter
HXT5.3f	0.9	0.9	1.0	0.6	1.1	1.0	orf19.2021	CA1069	Sugar transporter, 3-prime end
Manganese ion transport							*ID:6828*	*1.1E-04*	*(4 genes in total)*
SMF11	0.9	1.2	1.9	0.9	1.0	0.6	orf19.4690	CA0087	Manganese transporter (by homology)
SMF12	1.0	1.0	2.5	1.0	1.0	0.6	orf19.2270	CA1879	Manganese transporter (by homology)
HIP1	1.7	1.2	2.0	0.8	0.9	2.5	orf19.4940	CA3708	Histidine/manganese transporter
SMF3	1.0	1.0	0.7	1.0	0.4	0.3	orf19.5022	CA5241	Probable manganese transporter (by homology)

Fig. 4

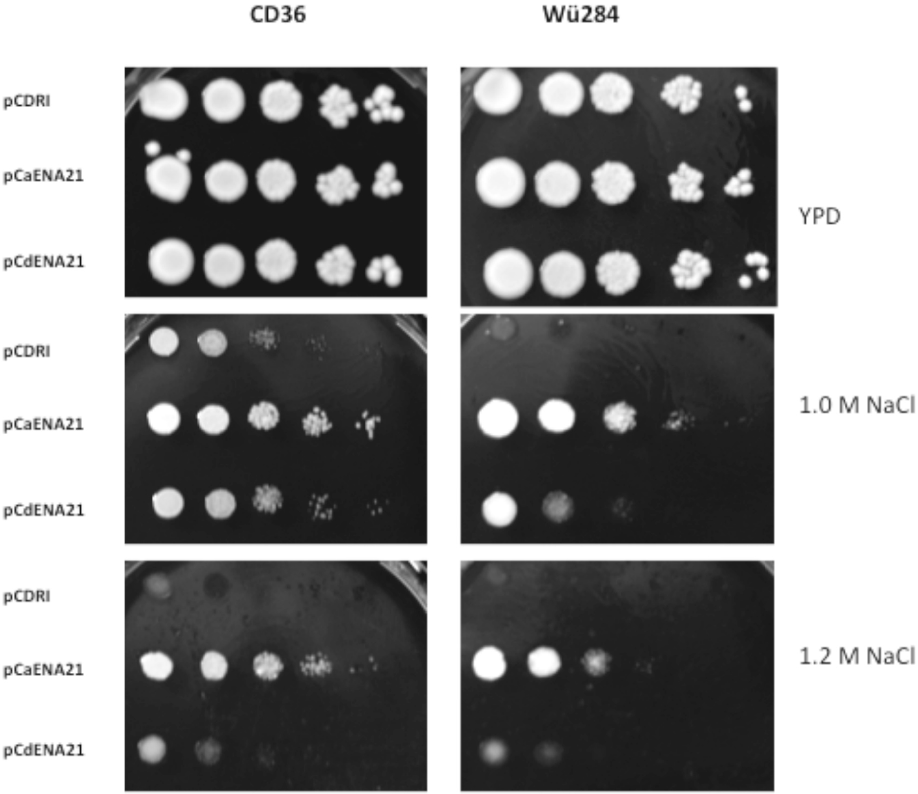

CD36
Wü284
pCDRI
pCaENA21
pCdENA21
YPD
pCDRI
pCaENA21
pCdENA21
1.0 M NaCl
pCDRI
pCaENA21
pCdENA21
1.2 M NaCl

Fig. 5

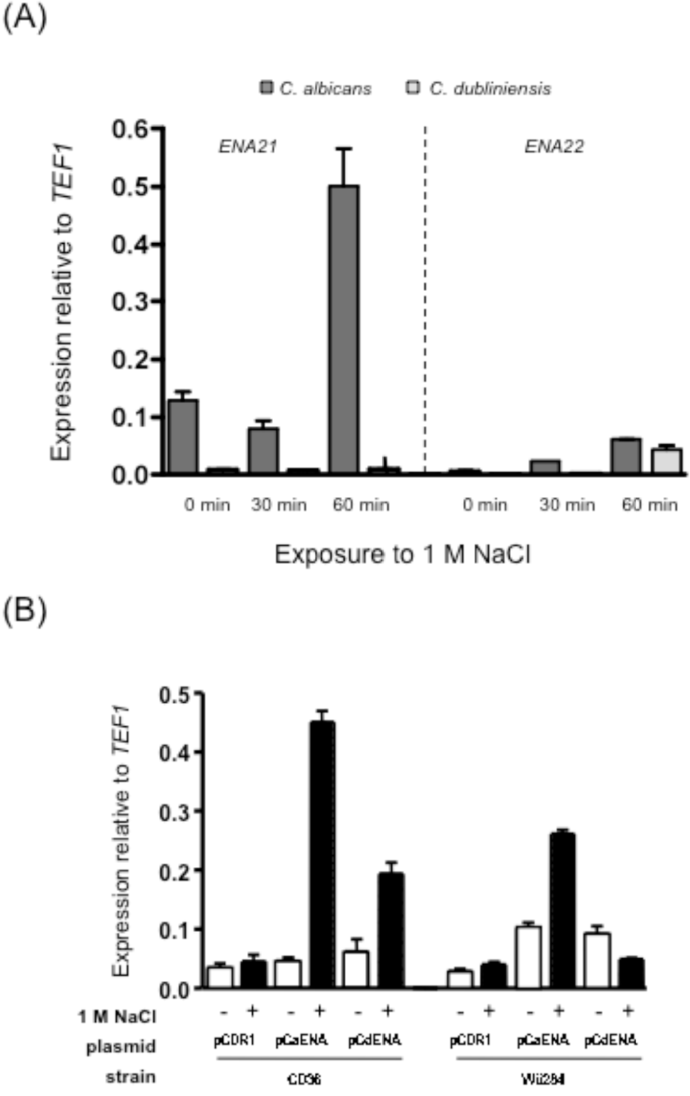

(A)
C. albicans
C. dubliniensis
Expression relative to TEF1
0.6
0.5
0.4
0.3
0.2
0.1
0.0
ENA21
ENA22
0 min
30 min
60 min
0 min
30 min
60 min
Exposure to 1 M NaCl
(B)
Expression relative to TEF1
0.5
0.4
0.3
0.2
0.1
0.0
1 M NaCl
- + - + - + - + - + - +
plasmid
pCDR1
pCaENA
pCdENA
pCDR1
pCaENA
pCdENA
strain
CD36
Wü284

Fig. 6.

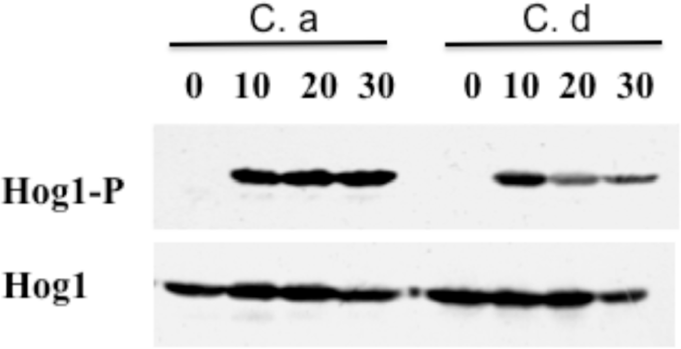
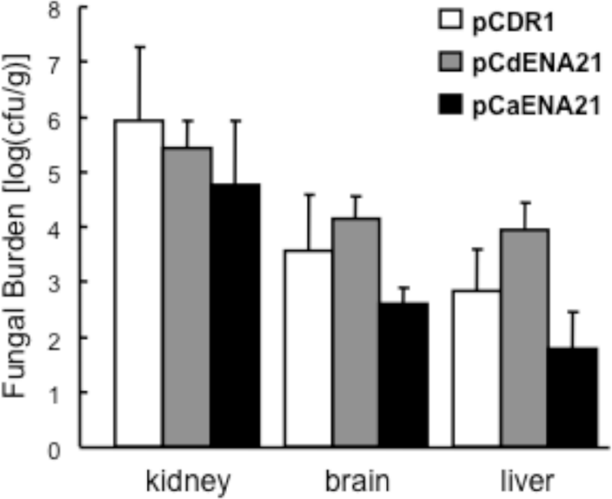


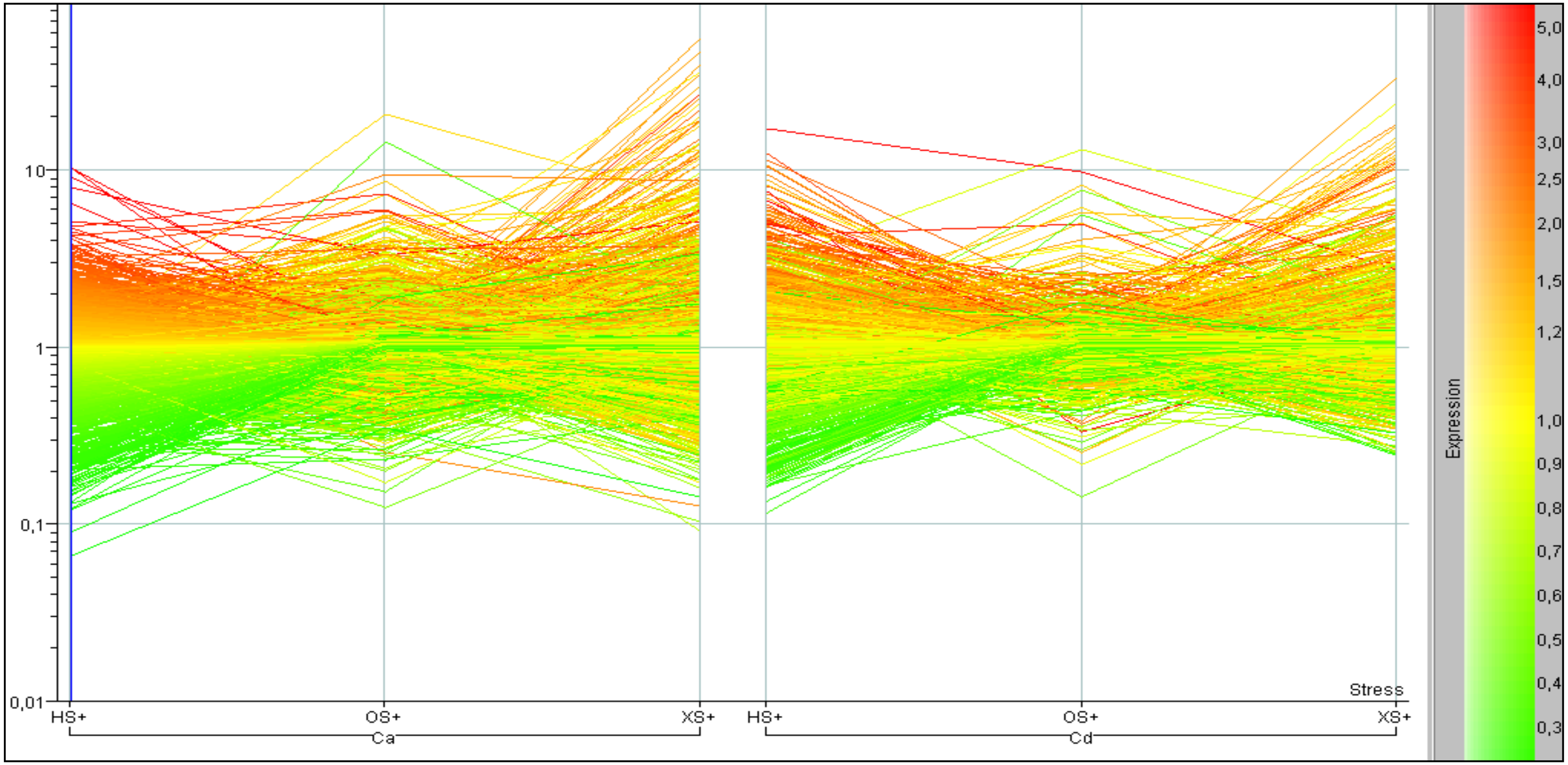
Fig. 7



pCDR1
pCdENA21
pCaENA21
Fungal Burden [log(cfu/g)]
8
7
6
5
4
3
2
1
0
kidney
brain
liver

Supplementary Figure 1: Whole genome expression data

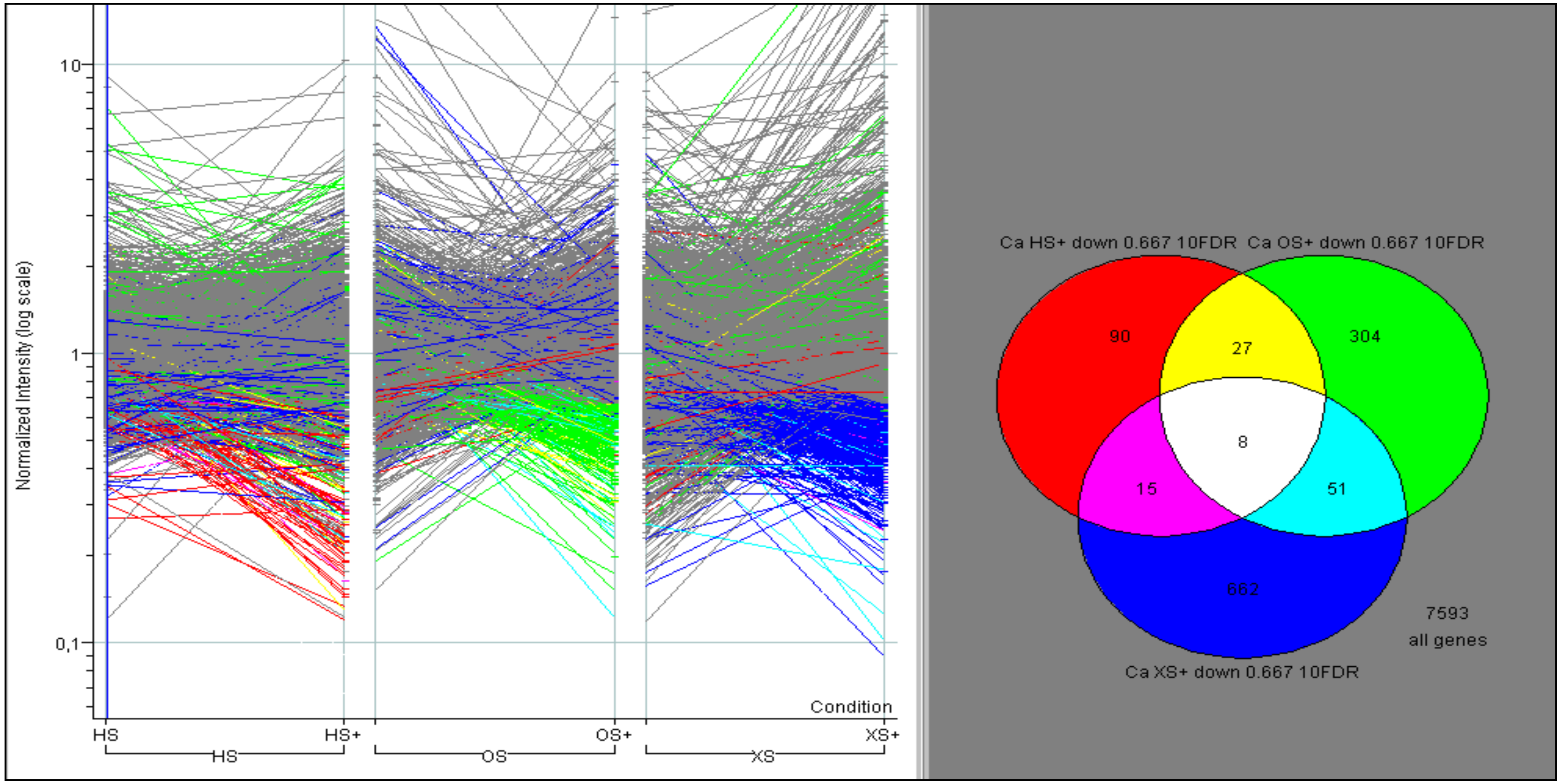
Candida albicans (Ca) and Candida dubliniensis (Cd) transcriptional response to strong heat shock (HS+), strong osmotic (OS+) and strong oxidative (XS+) stresses. The (X) axis represents the time course and type of stress, the logarithmic (Y) axis corresponds to the mean normalized ratio of the change in transcript abundance. Each gene is represented by a single line that is colored according to the value in the C. albicans strong heat shock experiment (left).



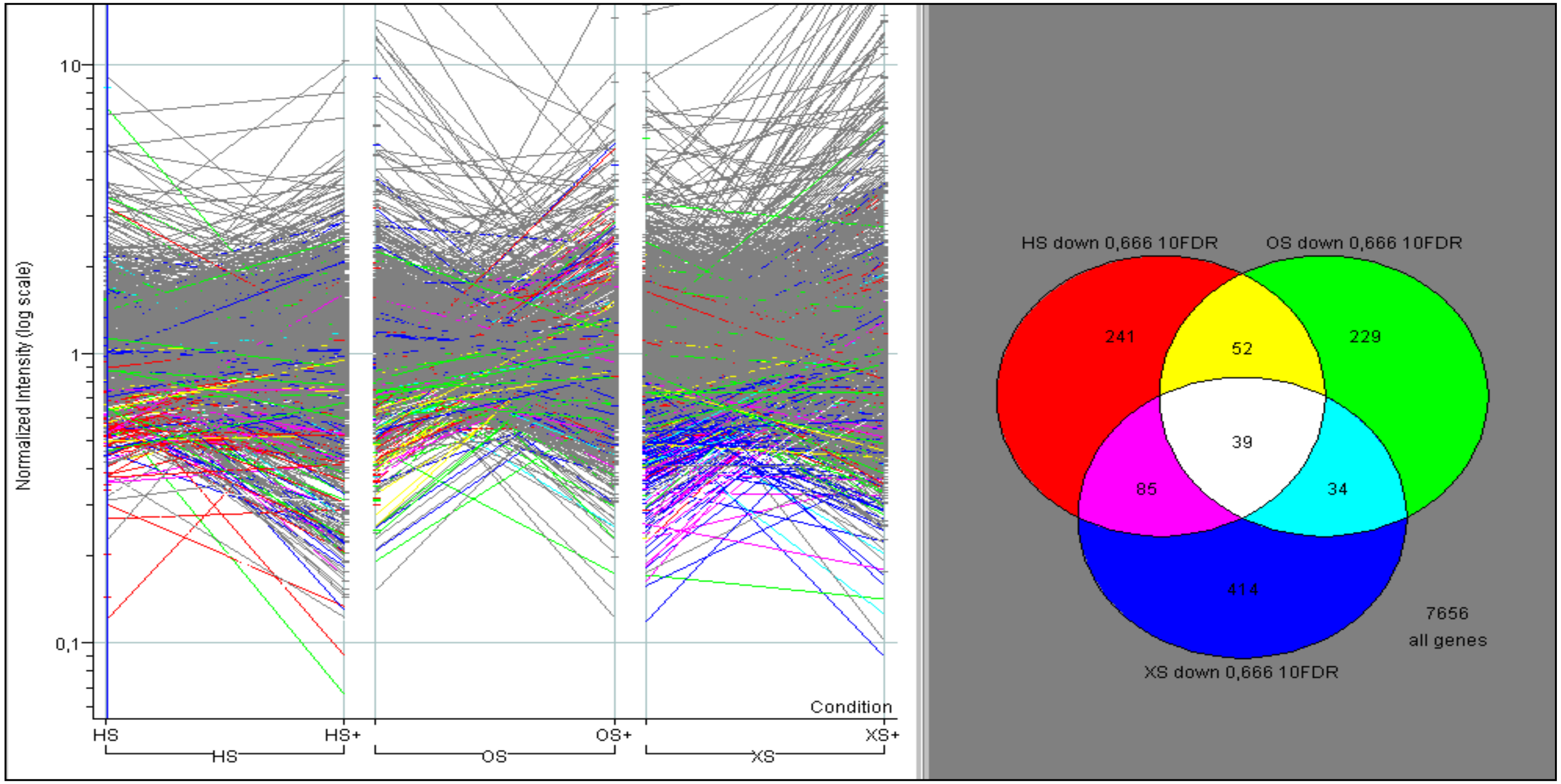
Supplementary Figure 2: Strong stresses versus mild stresses and Venn Diagrams

Candida albicans transcriptional response to strong and mild heat shock (HS+ ; HS), strong and mild osmotic (OS+ ; OS) and strong oxidative (XS+ ; XS) stresses. The (X) axis represents the time course and type of stress, the logarithmic (Y) axis corresponds to the mean normalized ratio of the change in transcript abundance. Each gene is represented by a single line that is colored according to the venn diagram on the right. "Down 0.667" means list of genes with expression ratio lower than 0.667. "Up 1.5" means list of genes with expression ratio greater than 1.5. 10FDR means list of genes whose expression ratio reproducibility satisfied the SAM software with a False Discovery Rate lower than 10%.
2A: down regulated genes in response to the three strong stresses.
2B: down regulated genes in response to the three mild stresses (data set from Enjalbert *et al*., 2003).
2C: up regulated genes in response to a mild heat stress (data set from Enjalbert et al., 2003) versus a strong heat stress (this work).
2D: up regulated genes in response to a mild osmotic stress (data set from Enjalbert et al., 2003) versus a strong osmotic stress (this work).
2E: up regulated genes in response to a mild oxidative stress (data set from Enjalbert et al., 2003) versus a strong oxidative stress (this work).

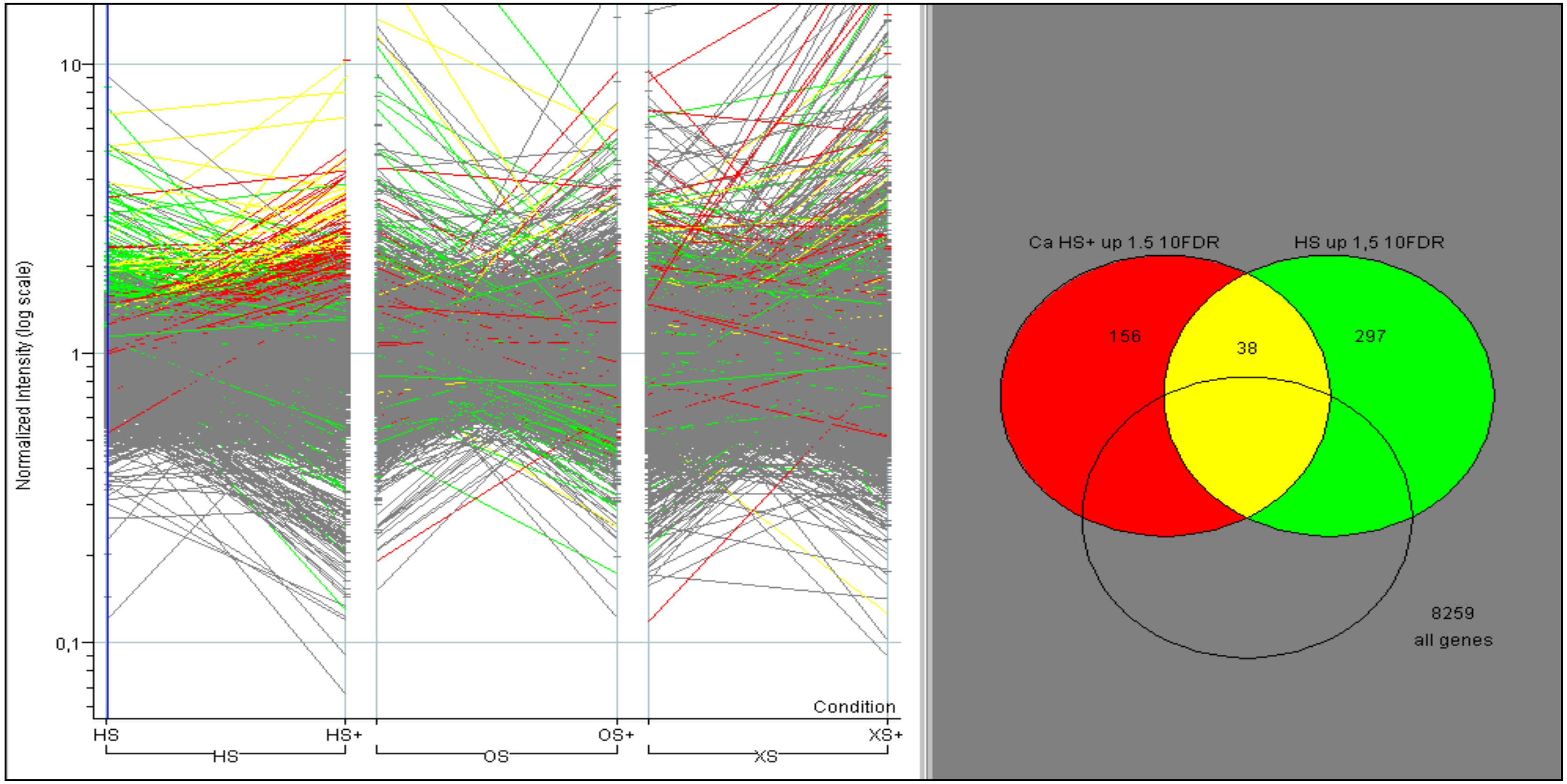
2A.



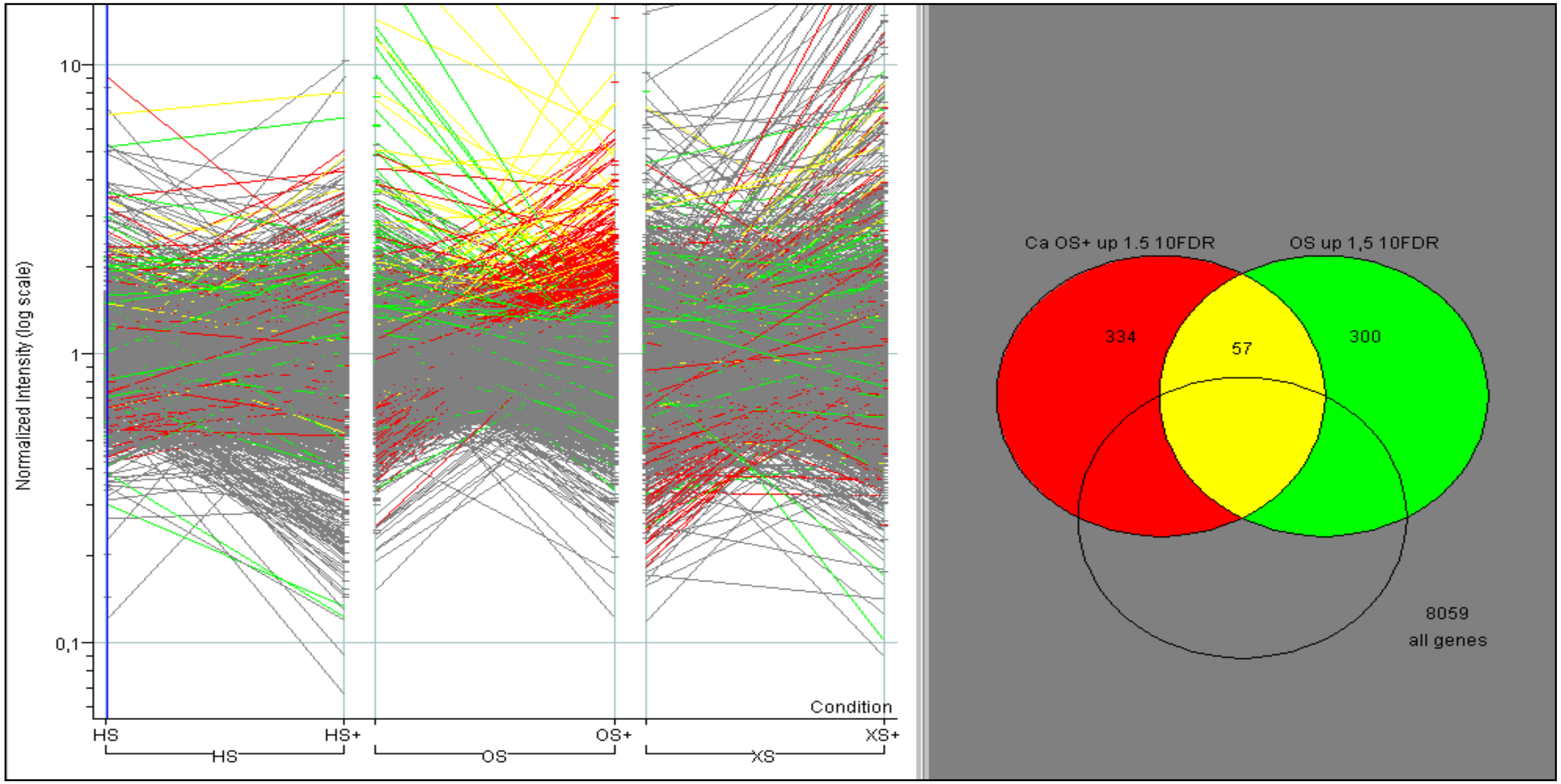
2B.


Normalized Intensity (log scale)
10
1
0,1
Condition
HS
HS+
OS+
XS+
HS
OS
XS
HS down 0,666 10FDR
OS down 0,666 10FDR
XS down 0,666 10FDR
241
52
229
39
85
34
414
7656
all genes

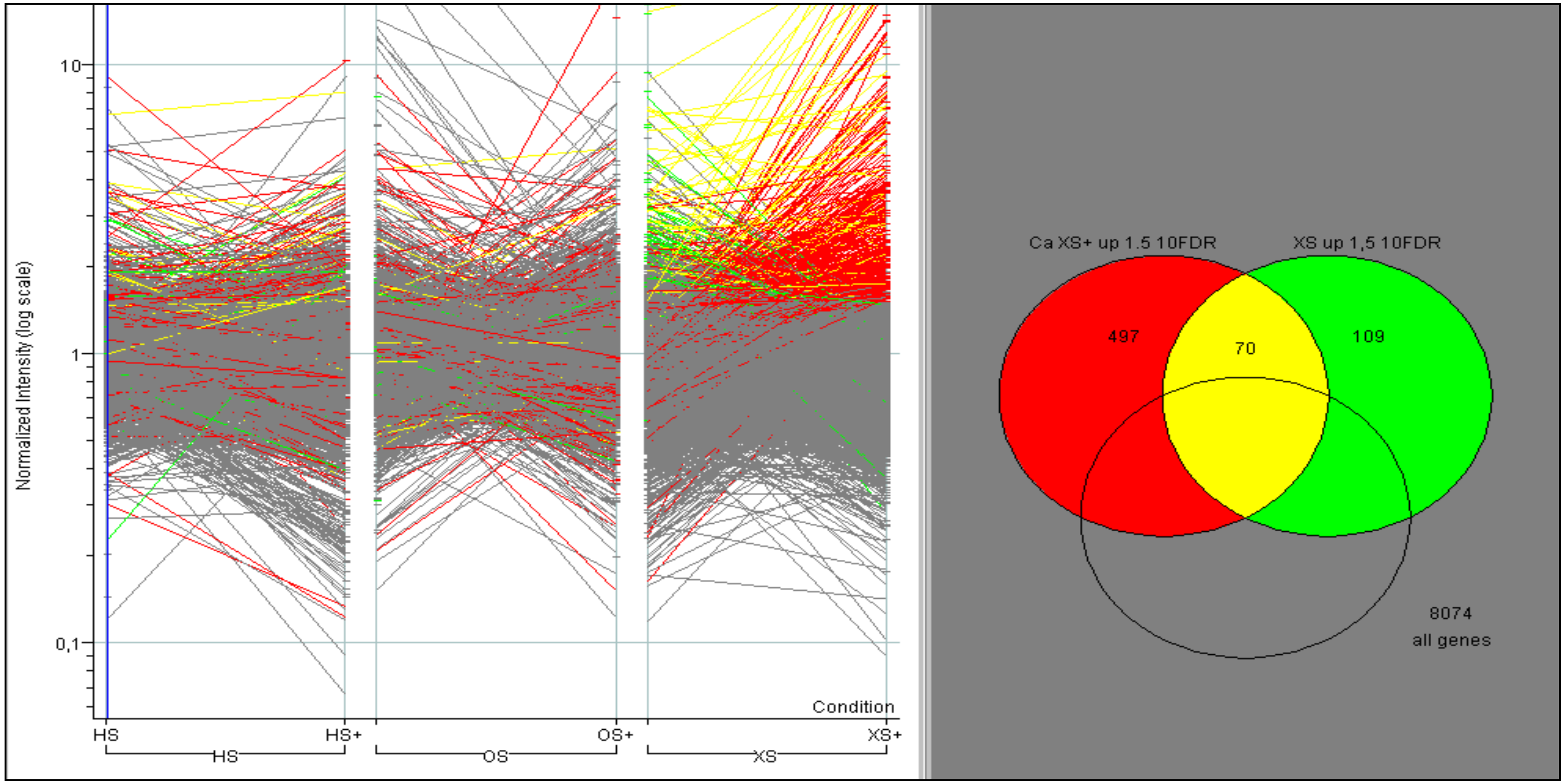
2C.


Normalized Intensity (log scale)
10
1
0,1
Condition
HS
HS+
OS+
XS+
HS
OS
XS
Ca HS+ up 1.5 10FDR
HS up 1,5 10FDR
156
38
297
8259
all genes

2D.


Normalized Intensity (log scale)
10
1
0,1
Condition
HS
HS+
OS+
XS+
HS
OS
XS
Ca OS+ up 1.5 10FDR
OS up 1,5 10FDR
334
57
300
8059
all genes

2E.

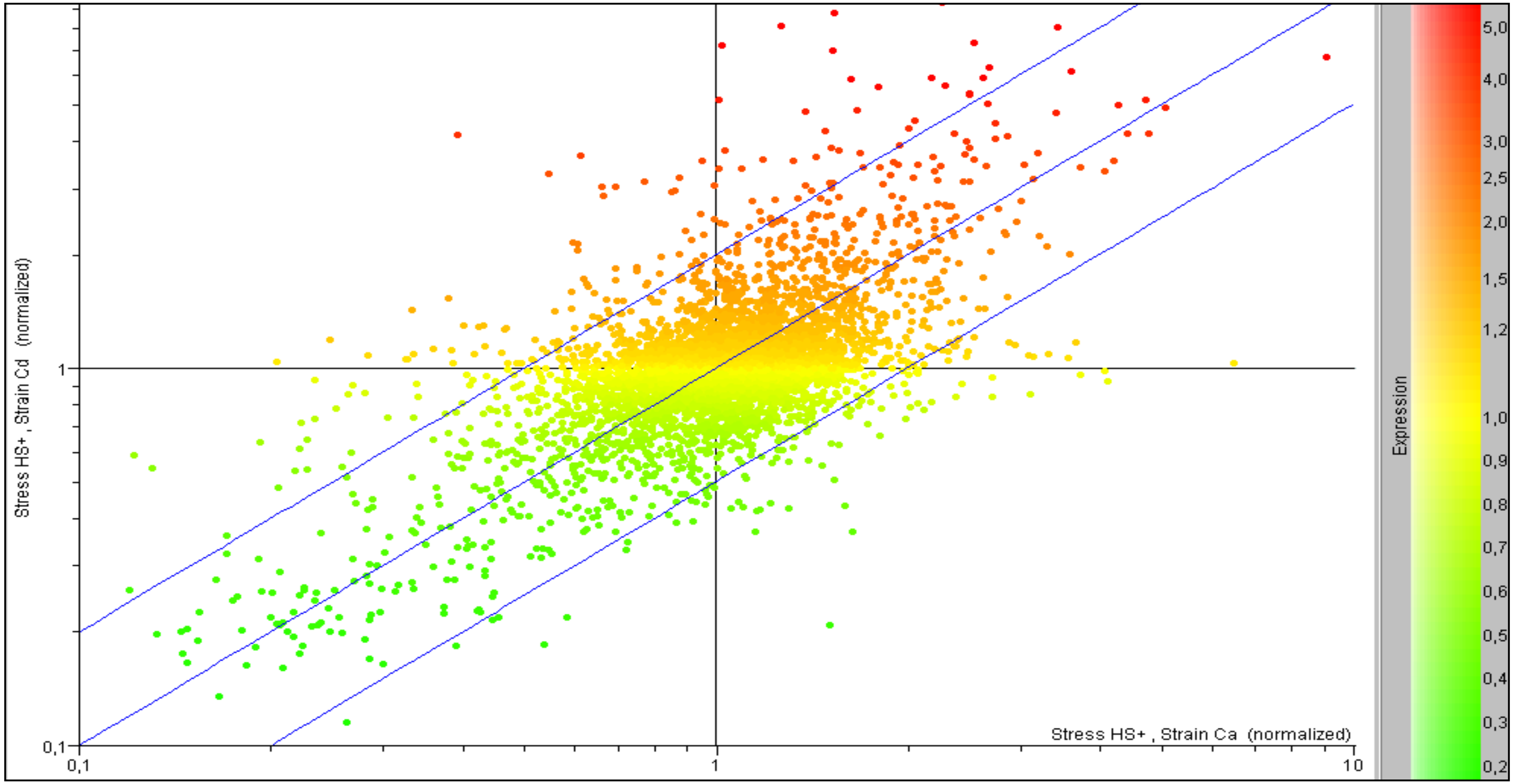

10
1
0,1
Normalized Intensity (log scale)
Condition
HS
HS+
OS+
XS+
HS
OS
XS
Ca XS+ up 1.5 10FDR
XS up 1,5 10FDR
497
70
109
8074
all genes

Supplementary Figure 3: Scatter plots of C. albicans versus C. dubliniensis strong stress responses

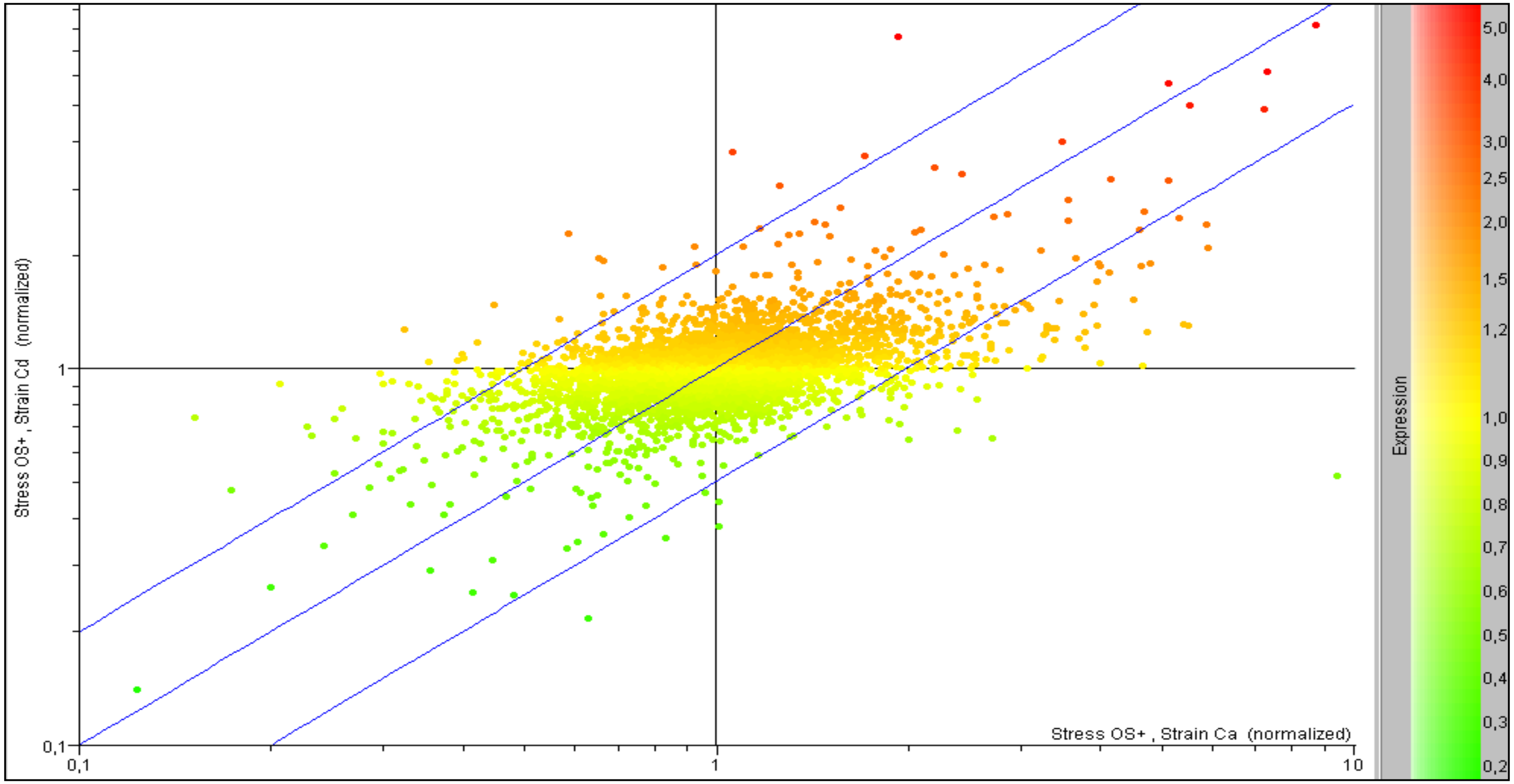
Candida albicans (Ca ; X axis) and Candida dubliniensis (Cd ; Y axis) transcriptional response to strong and mild heat shock (HS+ ; HS), strong and mild osmotic (OS+ ; OS) and strong oxidative (XS+ ; XS) stresses. Each gene is represented by a single dot that is colored according to expression and trust scale displayed on the right.

3A: strong heat stress.
3B: strong osmotic stress.
3C: strong oxidative stress.

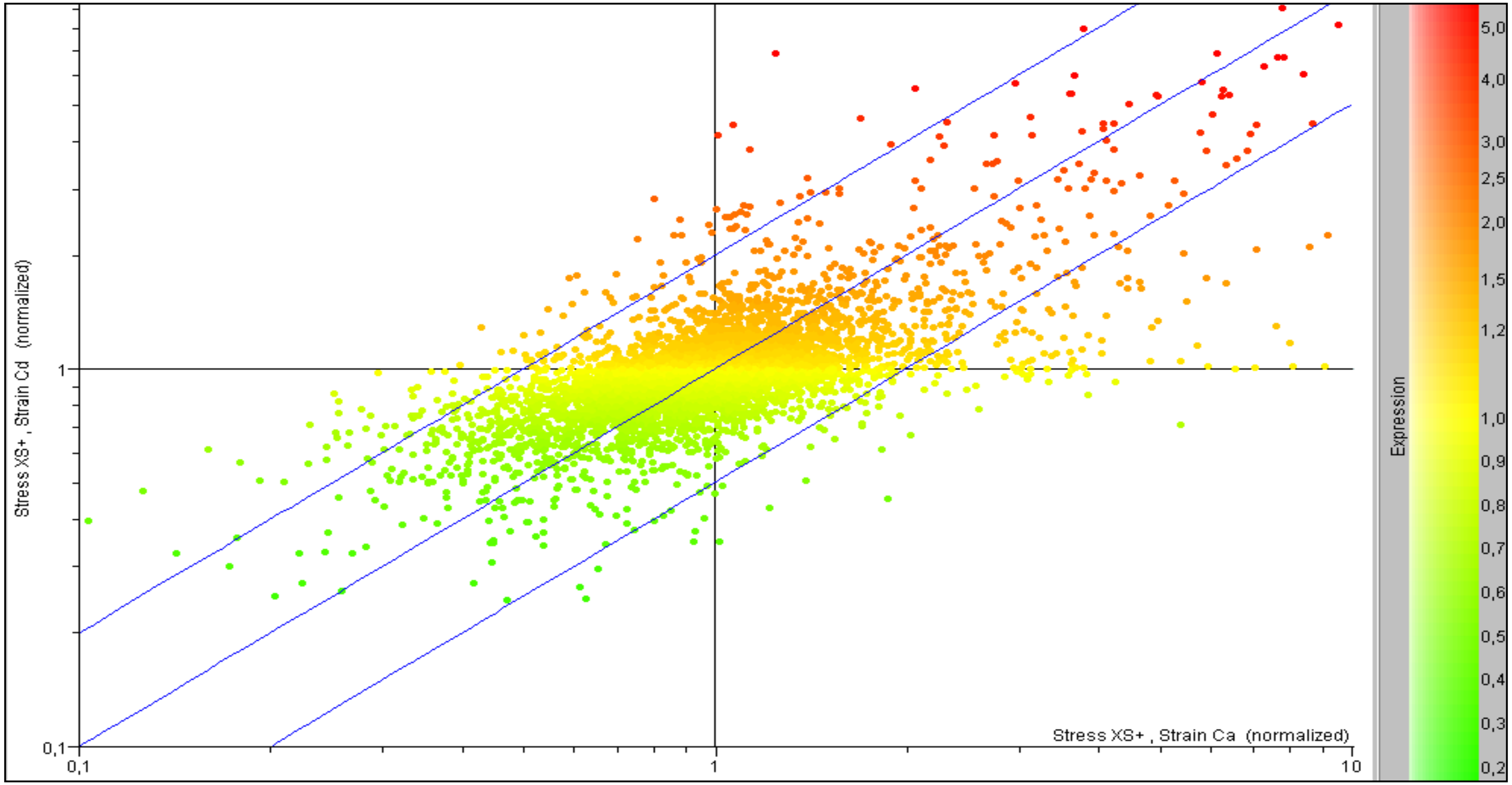
3A.



3B.


Stress OS+ , Strain Cd (normalized)
Stress OS+ , Strain Ca (normalized)
0,1
1
10
0,1
1
Expression
5,0
4,0
3,0
2,5
2,0
1,5
1,2
1,0
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2

3C.


Stress XS+ , Strain Cd (normalized)
Stress XS+ , Strain Ca (normalized)
0,1
1
10
0,1
1
Expression
5,0
4,0
3,0
2,5
2,0
1,5
1,2
1,0
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2

Supplementary Table 1: Whole genome expression data

Stress	HS+		OS+		XS+				
Strain	Ca	Cd	Ca	Cd	Ca	Cd	Common	Ca orf19	Ca Function
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, mitochondrial, 3-prime end (by homology)
CA4220	10.2	7.6	0.6	0.3	5.9	1.0	IPF8762	orf19.822	unknown function
CA0863	9.1	6.7	1.4	0.9	1.0	0.6	ITR2	orf19.3526	Myo-inositol transporter (by homology)
CA5613	8.0	16.9	3.3	9.8	5.1	2.7	IPF525	orf19.7085	unknown function
CA3367	6.5	1.0	1.1	0.9	1.1	1.1	IPF4667	orf19.1847	unknown Function
CA0271	5.1	4.9	3.6	2.0	2.5	3.0	IPF12897	orf19.2244	putative oxidoreductase (by homology)
CA5120	4.8	4.2	7.2	4.9	1.4	1.1	YDJ1	orf19.6408	Mitochondrial and ER import protein (by homology)
CA1239	4.7	5.2	1.2	1.1	0.7	0.9	HSP60	orf19.717	Heat Shock Protein 60 (HSP60)
CA1987	4.4	4.2	1.9	1.3	1.4	1.2	IPF14895	orf19.93	unknown function
CA4162	4.3	5.0	5.9	2.1	1.3	1.5	MET1	orf19.5811	siroheme synthase (by homology)
CA3564	4.2	3.6	1.0	1.1	26.3	11.0	IPF7817	orf19.3131	putative NADH-dependent flavin oxidoreductase (by homology)
CA4053	4.1	0.9	0.7	1.0	1.4	1.0	IKS1	orf19.428	PROBABLE SERINE/THREONINE-PROTEIN KINASE
CA1199	4.1	3.3	0.5	1.0	1.9	1.9	IPF10404	orf19.3369	unknown function
CA0821	4.1	1.0	0.5	0.9	1.3	0.9	IPF16795	orf19.2989	glycerate/formate-dehydrogenase (by homology)
CA0005	3.8	12.2	0.5	0.8	2.0	1.2	IPF14994	orf19.2414	unknown function
CA2038	3.7	3.4	0.6	0.8	1.0	1.0	IPF17510	orf19.4358	unknown
CA2342	3.7	1.0	5.9	2.4	1.1	1.0	IPF13836	orf19.2344	probable heat shock protein (by homology)
CA0558	3.7	1.2	0.6	0.7	1.8	2.1	GPX2	orf19.85	glutathione peroxidase (by homology)
CA6002	3.6	6.1	1.8	1.2	1.3	1.5	IPF661	orf19.7602	unknown function
CA3886	3.6	2.0	0.7	0.7	1.6	1.0	IPF12963	orf19.5094	ubiquitin-mediated protein degradation (by homology)
CA4676	3.6	1.1	0.7	0.9	4.8	1.1	HK1	orf19.896	Histidine kinase
CA3571	3.4	8.0	1.7	1.5	5.8	5.8	IPF3264	orf19.3139	unknown function
CA4959	3.4	4.8	1.3	1.2	1.0	1.0	HSP90	orf19.6515	heat shock protein
CA2659	3.3	1.1	0.9	1.0	3.5	1.5	NDH2	orf19.5713	NADH dehydrogenase (by homology)
CA3996	3.3	2.1	1.3	1.0	0.8	0.8	IPF10440	orf19.1643	unknown function
CA4771	3.2	2.2	1.2	1.1	1.0	1.2	IPF3336	orf19.4003	unknown function
CA2854	3.2	3.7	3.6	2.5	3.7	3.5	RPN4	orf19.1069	26S proteasome subunit (by homology)
CA4856	3.1	3.2	0.9	1.1	1.1	0.9	IPF15950	orf19.3827	unknown function
CA3211	3.1	1.1	2.2	1.2	0.7	1.0	IPF19977	orf19.6192	unknown function
CA2039	3.1	0.9	1.7	1.0	1.2	0.8	IPF12947	orf19.4357	unknown function
CA0596	3.1	1.1	0.8	1.0	0.9	1.0	IPF9706	orf19.4883	unknown function
CA4265	3.0	3.5	1.4	1.2	3.4	3.2	GAP6	orf19.6659	General amino acid permease (by homology)
CA0915	3.0	2.8	1.1	1.0	1.0	0.7	KAR2	orf19.2013	dnaK-type molecular chaperone (by homology)
CA5848	3.0	2.5	1.7	1.7	1.0	1.0	IPF407	orf19.7504	unknown function
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, mitochondrial, 5-prime end (by homology)
CA0671	2.9	1.2	1.1	1.0	12.0	1.3	GRP4	orf19.3150	putative reductase (by homology)
CA4779	2.9	1.2	1.3	1.3	3.0	1.4	IPF3351	orf19.4012	unknown function
CA3686	2.9	1.5	0.8	1.4	0.9	0.7	IPF4890	orf19.6263	unknown function
CA4030	2.9	4.1	0.7	2.0	18.8	8.7	EBP4	orf19.3433	NADPH dehydrogenase (by homology)
CA1653	2.8	2.3	1.3	1.4	1.0	0.7	STE23	orf19.5561	protease involved in a-factor processing by homology
CA3139	2.8	2.3	1.2	1.5	1.6	1.6	YHB3	orf19.3710	flavohemoglobin (by homology)
CA2115	2.8	2.7	0.4	0.9	1.8	1.1	IPF8030	orf19.1331	unknown function

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)
CA1216	2.7	4.1	0.7	1.9	4.9	5.3	EBP1	orf19.125	NADPH dehydrogenase
CA1333	2.7	11.4	1.0	1.8	21.5	5.9	MRF1	orf19.1149	mitochondrial respiratory function protein (by homology)
19812.10	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
CA2716	2.7	2.0	0.6	1.0	0.9	1.0	IPF7353	orf19.577	unknown function
CA1137	2.7	6.3	0.6	0.7	2.0	1.2	IFN1	orf19.1979	glycerophosphoinositol transporter (by homology)
CA3098	2.7	5.1	1.8	2.1	1.3	1.0	SIS1	orf19.3861	heat shock protein (by homology)
CA3246	2.6	3.4	1.8	1.4	1.1	1.2	IPF15830	orf19.4677	unknown function
CA6052	2.6	1.4	1.3	1.0	0.8	1.0	IPF4942	orf19.7668	similar to Saccharomyces cerevisiae Mal32p alpha-glucosidase (by homology)
CA2968	2.6	5.9	1.1	1.8	14.8	10.0	BMR1	orf19.5604	benomyl/methothrexate resistance protein (by homology)
CA2146	2.6	1.7	0.9	1.1	1.1	1.0	IPF12799	orf19.2515	unknown function
CA2895	2.6	2.5	1.9	1.1	7.6	1.3	IFS1	orf19.2461	Unknown function
CA0929	2.6	1.4	3.8	1.1	1.0	1.1	GUT1	orf19.558	Glycerol kinase (by homology)
CA4437	2.5	7.3	0.7	1.3	1.2	1.2	IPF13867	orf19.5158	unknown function
CA0457	2.5	1.2	2.2	1.8	1.2	0.8	IPF15604	orf19.2432	transcription factor (by homology)
CA2416	2.5	3.6	2.1	0.9	1.1	1.0	IFD4	orf19.4477	Putative aryl-alcohol dehydrogenase (by homology)
CA2361	2.5	5.3	0.7	1.0	3.1	1.9	IPF8950	orf19.4898	unknown function
CA0147	2.5	3.1	1.3	1.8	1.7	1.4	IPF9690	orf19.3649	unknown function
CA4111	2.5	2.3	0.7	0.4	2.4	1.8	IPF3964	orf19.675	unknown function
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)
CA3078	2.5	5.4	0.8	1.3	1.2	1.1	IPF19970	orf19.4816	unknown function
CA4665	2.5	1.1	1.1	1.0	0.9	0.8	IPF6548	orf19.4451	translation elongation factor eEF4 (by homology)
CA0551	2.5	4.0	1.4	1.3	1.3	1.0	CDC37	orf19.5531	Cell division control protein (by homology)
CA0355	2.5	1.1	0.6	1.0	2.4	1.0			
CA3863	2.5	3.7	1.5	2.2	0.8	1.1	LEU41	orf19.6086	2-isopropylmalalate synthase (by homology)
CA4894	2.4	1.5	0.9	0.5	4.4	1.6	IPF1617	orf19.6586	unknown function
CA4993	2.4	3.1	1.6	1.3	0.8	0.9	PXA2	orf19.5255	ABC transporter, peroxisomal (by homology)
CA0796	2.4	0.9	1.0	0.9	1.1	0.9	ALR1	orf19.1607	divalent cation transporter (by homology)
CA2246	2.4	1.3	2.1	1.8	1.0	0.8	IPF7405	orf19.4666	unknown function
CA4723	2.4	1.9	0.9	0.9	1.1	1.1	IPF18177	orf19.4864	Unknown function
CA4016	2.4	1.2	1.0	1.0	0.9	1.0	GFA1	orf19.1618	glutamine:fructose-6-phosphateamidotransferase
CA3178	2.4	1.2	1.2	1.1	2.8	1.0	IPF19974	orf19.1406	unknown function
CA2335	2.4	0.8	1.4	1.1	0.9	1.1	LYS21	orf19.4506	homocitrate synthase (by homology)
CA2434	2.4	2.5	1.5	1.1	1.7	1.4	IPF9484	orf19.3396	unknown function
CA5979	2.4	1.1	0.8	0.9	1.2	0.9	IPF921	orf19.7574	BTB domain and Ankaryin repeat containing protein (by homology)
CA5547	2.4	1.1	1.1	2.1	0.7	0.9	IPF5981	orf19.7310	similar to Saccharomyces cerevisiae Gin3p (by homology)
CA5079	2.4	2.2	1.0	1.1	1.4	1.1	RPN3	orf19.3054	26S proteasome regulatory subunit (by homology)
CA3245	2.4	4.2	1.5	1.4	0.9	1.0	IPF19980	orf19.4678	putative lipase (by homology)
CA5709	2.3	2.3	0.9	0.7	1.0	0.8	IPF2653	orf19.7410	unknown function
CA0256	2.3	1.3	0.9	1.0	1.0	1.1	IPF10309	orf19.2278	unknown function
CA0417	2.3	2.7	0.9	1.0	1.4	1.2	UBC13	orf19.933	E2 ubiquitin-conjugating enzyme (by homology)
CA5864	2.3	1.2	0.9	1.1	1.1	1.1	IPF364	orf19.7522	transaminase type I (by homology)
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
CA5541	2.3	1.0	0.7	1.0	0.7	1.1	IPF2827	orf19.7303	unknown function
CA4201	2.3	1.1	0.8	1.0	0.7	1.0	IPF8048	orf19.4543	probable succinate-semialdehyde dehydrogenase (by homology)

CA1492	2.3	1.5	1.2	1.2	0.6	1.1	IPF168	orf19.3226	unknown function
CA0175	2.3	2.0	1.6	0.9	1.1	1.0	NPL4	orf19.2434	nuclear protein localization factor and ER translocation component (by homology)
CA2403	2.3	2.7	1.0	1.2	1.3	2.5	IPF6438	orf19.3544	unknown function
CA3034	2.3	2.7	0.8	0.9	1.4	1.3	RPN12	orf19.213	26S proteasome regulatory subunit (by homology)
CA5842	2.3	5.7	1.1	1.3	1.8	1.3	LEU1	orf19.7498	3-isopropylmalate dehydratase (by homology)
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 (by homology)
CA2190	2.3	9.3	0.8	1.0	5.4	2.9	AOX1	orf19.4774	alternative oxidase (by homology)
CA1168	2.3	1.1	1.0	1.0	1.0	1.0	IPF13017	orf19.1785	unknown function
CA4750	2.2	1.6	0.8	0.9	1.1	1.0	IPF4477	orf19.4829	similar to Saccharomyces cerevisiae Doa1p involved in ubiquitin-dependent proteolysis (by homology)
CA1025	2.2	2.2	1.0	1.1	0.9	1.0	IPF10184	orf19.3936	unknown function
CA0893	2.2	2.2	1.2	1.1	1.5	0.8	IPF13517	orf19.5752	unknown function
CA2016	2.2	3.5	1.1	1.5	9.1	2.3	IPF3415	orf19.847	similar to Saccharomyces cerevisiae Yim1p mitochondrial inner membrane protease (by homology)
CA4157	2.2	1.5	0.8	1.0	0.9	1.0	HYU1	orf19.5804	hydantoin utilization protein A (hyuA) homolog
CA1256	2.2	2.0	1.0	1.1	0.7	1.1	UBP15	orf19.1777	ubiquitin-specific protease (by homology)
CA4643	2.2	2.7	1.1	1.2	1.3	1.0	PRE9	orf19.350	20S proteasome subunit Y13 (alpha3) (by homology)
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 plasma membrane (by homoloy)
CA2896	2.2	1.7	9.4	0.5	8.6	2.1	IPF14981	orf19.3483	unknown function
CA0584	2.2	1.7	1.3	1.0	4.6	3.3	GSH1.5f	orf19.5060	Gamma-glutamylcysteine synthetase, 5prime end (by homology)
CA2157	2.2	1.6	1.5	1.1	0.8	0.8	IPF8537	orf19.5300	similar to Saccharomyces cerevisiae Cne1p calnexin, involved in regulation of secretion (by homology)
CA3199	2.2	2.4	1.4	1.5	1.1	0.9	FBP1	orf19.6178	Fructose-1,6-bisphosphatase
CA0636	2.2	2.5	0.9	0.9	10.8	15.0			
CA5924	2.2	1.1	0.9	1.0	1.2	0.9	IPF2822	orf19.6781	unknown function
CA1752	2.2	2.2	1.0	0.9	1.0	1.1	UBP14	orf19.1516	Ubiquitin-specific protease (by homology)
CA5728	2.2	3.3	0.6	0.9	1.8	1.3	IPF2471	orf19.7437	maltose acetyltransferase
CA3171	2.2	3.6	2.8	1.8	0.7	0.9	IPF7681	orf19.1397	unknown function
CA0785	2.2	5.9	0.9	1.1	1.2	1.1	IPF14603	orf19.3929	unknown function
CA2773	2.2	1.6	0.8	1.0	1.1	1.0	MGM1	orf19.2690	GTPase
CA0889	2.2	1.5	1.3	2.3	0.8	0.7	IPF11767	orf19.4733	mitochondrial carrier protein (by homology)
CA0722	2.2	0.8	0.9	0.8	0.7	0.6	ERK1	orf19.2886	mitogen-activated protein kinase (FUS3 homolog)
CA1988	2.2	1.7	3.4	1.2	0.9	0.9	IPF19749	orf19.94	unknown function
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)
CA1554	2.2	1.5	1.2	0.9	0.9	0.7	GEA2.3f	orf19.1713	GTP/GDP exchange factor, 3-prime end (by homology)
CA0845	2.1	1.3	1.3	0.9	1.0	1.0	IPF16314	orf19.264	unknown function
CA6003	2.1	1.7	1.1	1.0	1.1	1.0	IPF660	orf19.7603	unknown function
CA5230	2.1	1.1	1.2	1.2	1.0	1.0	IPF10424	orf19.5034	unknown function
CA6160	2.1	1.4	0.8	0.9	2.4	1.2	IPF1835	orf19.5876	unknown function
CA2310	2.1	2.7	0.4	1.2	3.2	1.2	LEU42	orf19.1375	2-isopropylmalalate synthase (by homology)
CA1592	2.1	2.0	0.8	0.9	1.0	1.0	IPF14662	orf19.4317	D-xylose reductase (by homology)
CA4294	2.1	1.0	1.6	2.7	3.1	1.3	ERC1	orf19.6691	ethionine resistance protein (by homology)
CA6054	2.1	0.8	1.7	1.2	0.6	0.6	IPF4952	orf19.7672	unknown function
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 homology)
CA0559	2.1	1.9	0.9	1.0	5.8	4.2	GPX1	orf19.86	glutathione peroxidase (by homology)
CA3254	2.1	1.9	2.4	1.6	1.4	1.1	IPF4728	orf19.3742	unknown Function
CA2419	2.1	1.6	1.3	1.1	4.9	1.3	IPF14379	orf19.4474	unknown function
CA3180	2.1	2.0	0.6	1.0	1.4	1.0	IPF12244	orf19.2131	unknown function
CA5142	2.1	1.3	0.7	1.0	1.0	1.0	IPF1022	orf19.4579	similar to Saccharomyces cerevisiae Erv29p ER-Golgi transport vesicle protein (by homology)

CA2564	2.1	1.1	0.9	0.9	1.4	1.0	IPF12127	orf19.5644	unknown function
CA1508	2.1	2.2	0.7	1.0	0.7	0.9	IPF9977	orf19.4525	unknown function
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)
CA4713	2.1	0.8	2.4	0.7	1.7	1.1	CCC1	orf19.6948	Transmembrane Ca2+ transporter (by homology)
CA0844	2.1	1.0	1.0	1.0	0.7	0.9	CDC3	orf19.1055	Cell division control protein
CA2045	2.1	1.0	1.7	1.1	1.0	1.2	IPF8107	orf19.2933	unknown function
CA2857	2.1	2.3	1.2	1.2	1.0	1.0	SSA1	orf19.1065	Heat shock protein of HSP70 family
CA1230	2.1	3.5	1.5	1.6	0.9	0.9	SSA4	orf19.4980	cahsp70 mRNA for heat shock
CA0663	2.1	1.9	0.9	0.9	1.0	1.1	PUP2	orf19.709	20S proteasome subunit(alpha5) (by homology)
CA2712	2.1	1.0	1.6	1.1	1.4	1.5	SPE2	orf19.568	adenosylmethionine decarboxylase precurser(by homology)
CA4057	2.0	2.1	2.0	1.3	2.1	1.8	IPF7719	orf19.432	unknown function
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)
CA1253	2.0	4.6	0.8	0.9	12.7	12.8	FDH3.3f	orf19.1774	formate dehydrogenase, 3-prime end (by homology)
CA2009	2.0	3.2	2.5	1.4	2.2	0.9	IPF1732	orf19.3089	intramitochondrial protein sorting (by homology)
CA1123	2.0	1.7	0.4	0.8	0.9	1.0	IPF19723	orf19.6261	similar to Saccharomyces cerevisiae Bph1p involved in acetic acid export
CA4123	2.0	1.1	1.0	1.1	1.5	1.0	AMS1	orf19.2768	alpha-mannosidase (by homology)
CA3844	2.0	1.0	1.0	1.0	1.0	1.0	IPF7945	orf19.6604	unknown function
CA5037	2.0	2.6	0.9	0.9	1.6	1.3	PRE3	orf19.6991	20S proteasome subunit (beta1)(by homology)
CA0446	2.0	1.6	1.4	1.3	0.7	0.9	IPF14282.5	orf19.2296	Similar to mucin proteins (by homology)
CA0896	2.0	2.6	1.8	1.3	1.2	1.1	SBA1	orf19.5749	Hsp90 (Ninety) Associated Co-chaperone (by homology)
CA4927	2.0	1.3	1.6	1.1	0.7	1.0	IPF1401	orf19.6066	similarity to aldehyde dehydrogenase (by homology)
CA2344	2.0	1.4	1.0	1.0	1.2	0.9	SFT2	orf19.2342	similar to Saccharomyces cerevisiae Sft2p suppressor of SED5 thermosensitive mutations (by homology)
CA5391	2.0	1.3	0.9	1.0	1.2	1.1	IPF18109	orf19.934	unknown function Unknown function
CA4199	2.0	2.1	0.6	0.9	1.4	1.4	UBC8	orf19.4540	ubiquitin-conjugating enzyme (by homology)
CA2874	2.0	0.8	0.3	0.7	0.1	0.5	IPF4999	orf19.5843	unknown function
CA5536	2.0	4.4	0.9	1.0	1.1	1.2	IPF2837	orf19.7297	putative cystathionine gamma-synthase (by homology)
CA1477	2.0	2.4	0.7	0.8	1.6	1.3	YME1	orf19.1252	family of ATPases
CA4184	2.0	1.0	0.7	0.9	1.0	1.1	SNZ1	orf19.2947	stationary phase protein by homology
CA5669	2.0	1.0	1.5	1.0	2.6	2.1	IPF1264	orf19.7371	unknown function, Asn rich
CA0003	2.0	0.9	2.7	0.7	0.8	0.8			
CA4064	2.0	1.2	1.1	1.0	1.1	1.1	RPT1	orf19.441	26S PROTEASE REGULATORY SUBUNIT 7 (by homology)
CA4838	2.0	1.0	0.9	0.8	0.8	0.8	YTA12	orf19.2057	Protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) (by homology)
CA3789	2.0	1.5	0.9	0.9	0.6	0.6	IPF11217	orf19.5830	similar to Saccharomyces cerevisiae Lhs1p chaperone of the ER lumen (by homology)
CA5316	2.0	0.7	1.1	0.7	0.7	0.7	MAM33	orf19.7187	Mitochondrial acidic matrix protein (by homology)
CA2577	2.0	1.2	1.6	1.1	0.9	0.8	IPF7430	orf19.6220	unknown function
CA3218	2.0	1.0	1.0	1.0	1.2	1.0	IPF10005	orf19.6196	unknown function
CA5196	2.0	1.7	1.3	1.1	0.9	1.2	IPF2338	orf19.7010	unknown function
CA2059	2.0	0.9	0.8	0.9	0.9	0.8	CDC4	orf19.2559	CANAL CELL DIVISION CONTROL PROTEIN 4
CA6005	2.0	2.8	1.0	1.0	1.5	1.4	PUP1	orf19.7605	20S proteasom ebeta2 subunit (by homology)
CA1308	2.0	1.0	1.1	1.0	1.0	1.0			
CA0155	1.9	2.5	1.2	1.0	1.4	1.2	RPT6	orf19.3593	26S proteasome regulatory subunit (by homology)
CA4319	1.9	2.5	1.1	1.2	1.1	0.9	RPN10	orf19.4102	Protein degradation (by homology)
CA2129	1.9	1.1	1.3	1.1	0.5	1.3	IPF4899	orf19.414	unknown function
CA1497	1.9	1.1	2.2	1.5	4.0	1.2	IPF9683	orf19.3644	unknown function
CA3605	1.9	2.0	4.0	1.7	3.1	4.7	IPF3865	orf19.22	unknown function
CA5238	1.9	3.9	3.4	1.3	2.2	1.9	MET3	orf19.5025	ATP sulfurylase

CA5511	1.9	2.1	1.0	0.9	1.1	0.8	AKL1	orf19.5357	serine/threonine protein kinase (by homology)
CA4889	1.9	1.1	1.0	0.9	0.8	1.0	IPF1629	orf19.6581	unknown function
CA5336	1.9	1.6	0.6	0.8	1.5	1.0	IPF893	orf19.7210	unknown function
CA5333	1.9	2.7	0.7	0.8	3.8	0.9	DOA4	orf19.7207	ubiquitin-specific isopeptidase (by homology)
CA1181	1.9	3.5	0.9	0.8	0.8	1.4	UGA12.5f	orf19.802	4-aminobutyrate aminotransferase (GABA transaminase), 5-prime end (by homology)
CA3265	1.9	1.4	1.1	1.1	1.1	1.0	ABP1	orf19.2699	actin-binding protein (by homology)
CA2539	1.9	1.4	1.3	0.9	0.9	0.9	IPF9188	orf19.3187	unknown function
CA0828	1.9	2.5	1.8	1.5	11.9	18.0	IPF17186	orf19.251	unknown function
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 homology)
CA0661	1.9	1.9	0.7	0.9	1.0	1.0	APG7	orf19.707	component of the autophagic system (by homology)
CA2167	1.9	2.2	1.0	0.4	2.9	5.7	IPF4553	orf19.909	unknown function
CA0382	1.9	0.8	1.3	0.9	0.8	0.8	IPF16030	orf19.1842	similar to Saccharomyces cerevisiae Bud5p GDP/GTP exchange factor for Rsr1P/Bud1p involved in bud site selection
CA3796	1.9	3.5	1.2	1.2	0.9	0.9	SGT2	orf19.5823	small glutamine-rich tetratricopeptide repeat containing protein by homology
CA0782	1.9	1.8	1.9	1.4	1.2	1.3	IPF16253	orf19.3932	unknown function
CA0277	1.9	2.0	0.7	1.0	0.9	0.8	RNH1	orf19.5614	ribonuclease H (by homology)
CA1131	1.9	2.9	0.6	0.9	1.8	1.2	NAG2	orf19.2157	N-acetyl-glucosamine-6-phosphate deacetylase
CA1346	1.9	1.0	3.3	1.3	1.6	1.6	KRE2.3f	orf19.4349.5	secretory pathway protein, 3-prime end
CA6159	1.9	1.7	0.5	1.0	2.1	1.1	IPF1837	orf19.5877	unknown function
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 homology)
CA0617	1.9	3.3	0.8	1.0	2.1	3.2	MET2	orf19.2618	Homoserine O-acetyltransferase
CA4050	1.9	0.9	1.0	1.1	1.1	0.9	IPF20007	orf19.425	unknown function
CA2219	1.9	1.1	0.6	1.0	1.2	1.0	CAT8	orf19.5097	transcription factor involved in gluconeogenesis (by homology)
CA1891	1.9	1.2	1.5	1.2	0.8	0.9	IPF10196	orf19.2752	unknown function
CA1896	1.9	1.1	1.1	1.4	1.0	0.8	ERD2	orf19.2756	ER lumen protein retaining receptor (by homology)
CA1252	1.9	1.6	0.9	0.9	0.9	0.9	RPN1	orf19.4956	26S proteasome regulatory subunit (by homology)
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
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 homology)
CA3639	1.8	1.4	0.5	0.7	2.1	2.3	IPF9251	orf19.5133	unknown function
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)
CA1964	1.8	10.5	1.3	1.0	2.7	3.5	IFR2	orf19.2396	unknown function
CA5896	1.8	1.1	0.8	1.0	0.6	0.7	TPD3	orf19.6810	Ser/thr protein phosphatase (by homology)
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)
CA0262	1.8	1.8	0.5	0.8	2.6	0.9	IPF20054	orf19.6117	
CA2278	1.8	1.8	1.2	1.0	1.2	1.2	IPF10806	orf19.782	unknown function
CA3657	1.8	1.0	1.1	1.0	2.2	1.0	IPF7459	orf19.2049	unknown function
CA5459	1.8	1.2	1.3	1.1	0.9	0.7	IPF276	orf19.3267	unknown function
CA1746	1.8	1.0	1.1	0.9	0.7	0.8	IPF10886	orf19.5050	unknown function
CA0872	1.8	1.3	1.0	0.9	0.8	0.7	IPF13100	orf19.3592	unknown function
CA1569	1.8	2.4	1.5	1.2	1.1	2.4	IPF7616	orf19.1159	putative homoserine O-acetyltransferase (by homology)
CA1287	1.8	3.1	1.1	1.2	1.2	1.2	IPF5545	orf19.4430	unknown function
CA0374	1.8	1.0	0.8	1.0	1.0	1.0			
CA5296	1.8	1.7	1.8	1.1	1.4	1.1	IPF1956	orf19.7159	unknown function
CA5154	1.8	1.4	0.8	0.8	0.8	0.6	RGA2	orf19.4593	rho-GTPase activating protein 2 (by homology)
CA2085	1.8	1.0	0.8	1.0	0.9	0.7	IPF3388	orf19.834	unknown function
CA3737	1.8	1.6	0.8	0.8	0.7	0.8	BLM3	orf19.2182	bleomycin resistance (by homology)
CA4168	1.8	2.4	1.1	1.2	1.0	1.1	IPF7781	orf19.2965	putative pump-driving ATPase

CA4044	1.8	0.8	2.4	3.3	0.7	0.9	GAL7	orf19.3675	UDP-glucose-hexose-1-phosphate uridylyltransferase (by homology)
CA5055	1.8	1.0	0.9	1.1	1.4	1.0	IPF3701	orf19.3021	unknown function
CA5983	1.8	1.2	0.8	1.3	0.9	1.1	IPF913	orf19.7579	unknown function
CA4502	1.8	2.5	2.0	1.3	1.0	1.1	IPF10391	orf19.506	Similar to dnaJ proteins
CA5466	1.8	0.7	2.2	1.2	1.0	1.0	PWP2	orf19.3276	periodic tryptophan protein (by homology)
CA1273	1.8	2.5	1.2	1.2	0.9	0.9	CCT4	orf19.2720	Component of chaperonin-containing T-complex
CA0494	1.8	1.3	0.9	1.0	1.3	1.1	RAD7	orf19.1493	nucleotide excision repair protein (by homology)
CA2633	1.8	1.2	1.3	0.9	0.5	0.7	KEX2	orf19.4755	Kexin precursor (KEX2 protease)
CA0123	1.8	3.4	1.2	1.1	2.8	2.1	MXR1	orf19.2028	methionine sulfoxide reductase
CA5773	1.8	1.4	0.9	1.0	2.5	1.4	DOT5	orf19.5417	Derepression of telomeric silencing (by homology)
CA2194	1.8	1.3	0.8	0.8	0.6	0.7	RGR1	orf19.4348	DNA-directed RNA polymerase II (by homology)
CA5826	1.8	1.7	1.0	0.9	1.0	0.6	MDH11	orf19.7481	Malate dehydrogenase (by homology)
CA6040	1.8	5.6	1.6	1.3	1.1	1.1	CPR6	orf19.7654	cyclophylin (by homology)
CA5926	1.8	1.3	1.1	0.9	1.1	1.1	PRO2	orf19.6779	Proline biosynthetic enzyme (by homology)
CA4772	1.8	2.3	1.3	1.1	1.1	1.1	CCT3	orf19.4004	Chaperonin (by homology)
CA5007	1.8	1.9	0.8	0.9	1.9	1.5	IPF12579	orf19.5239	putative phospholipase A2 (by homology)
CA1738	1.8	2.2	0.6	0.8	1.1	1.1	MGE1	orf19.2524	heat shock protein (by homology)
CA3709	1.8	1.2	0.7	0.8	0.7	0.7	IPF7880	orf19.4939	unknown function
CA4577	1.8	1.2	0.8	1.1	1.8	1.7	MKK2	orf19.6889	Protein kinase of MEK (by homology)
CA1404	1.8	1.4	0.7	0.8	1.0	1.0	IPF19554.5f	orf19.3372	unknown function, 5-prime end
CA5020	1.8	1.1	1.1	1.3	1.5	1.0	IPF7556	orf19.6973	similar to Saccharomyces cerevisiae Pim1p mitochondrial ATP-dependent protease (by homology)
CA5711	1.8	1.2	1.3	0.9	0.5	0.7	MUB1	orf19.7412	Regulation of bud site selection (by homology)
CA5931	1.8	1.1	1.1	1.0	1.0	0.9	ECM29.5f	orf19.6772	Involved in cell wall biogenesis and architecture, 5-prime end (by homology)
CA2589	1.8	1.4	3.8	1.2	2.0	1.7	KRE1	orf19.4377	secretory pathway protein
CA4658	1.7	1.0	1.3	1.0	8.7	4.5	IPF3092	orf19.4445	unknown function
CA5649	1.7	0.8	1.8	1.0	0.9	0.6	CHS4	orf19.7349	Chitin synthase regulatory factor
CA6127	1.7	0.9	1.4	1.4	1.0	1.0	IPF149	orf19.5921	peroxisomal membrane protein (by homology)
CA4704	1.7	1.4	1.2	1.2	1.3	1.3	RRD2	orf19.6933	hosphotyrosyl phosphatase activator
CA2109	1.7	1.1	1.4	1.2	0.9	0.8	IPF13749.5f	orf19.3690	unknown function, 5-prime end
CA3750	1.7	1.2	1.9	1.4	0.8	0.9	IPF7377	orf19.3428	unknown function
CA0894	1.7	1.4	1.4	1.6	1.0	0.8	ORM1	orf19.5751	unknown function
CA1293	1.7	0.7	2.8	1.3	0.9	1.0	HCA4	orf19.2712	Can suppress the U14 snoRNA rRNA processing function
CA0010	1.7	0.9	0.9	1.1	1.0	0.5	IPF16036	orf19.150	similar to Saccharomyces cerevisiae Tim17p mitochondrial inner membrane import translocase subunit (by homology)
CA3101	1.7	1.2	1.3	1.0	0.7	0.8	IPF6593	orf19.3865	similar to Saccharomyces cerevisiae Rfx1p DNA-binding protein (by homology)
CA5985	1.7	1.1	0.9	0.9	1.9	1.0	IPF907	orf19.7583	unknown function
CA1880	1.7	1.9	1.2	1.3	1.4	1.0	IPF13316	orf19.2269	unknown function
CA3697	1.7	1.7	1.0	1.0	1.3	1.2	IPF4866	orf19.6272	similar to Saccharomyces cerevisiae Yuh1p ubiquitin-specific protease
CA4934	1.7	1.2	0.9	1.2	1.0	0.9	CDC36	orf19.6075	transcription factor (by homology)
CA0476	1.7	1.1	0.6	0.9	0.9	1.0	UBP2	orf19.457	Ubiquitin-specific proteinase (by homology)
CA3109	1.7	1.6	3.5	4.0	7.3	6.3	IPF11829	orf19.6548	unknown function
CA3708	1.7	1.2	2.0	0.8	0.9	2.5	HIP1	orf19.4940	Histidine permease (by homology)
CA5223	1.7	1.1	1.1	1.2	34.4	9.0	IPF3080	orf19.7042	unknown function (by homology)
CA4161	1.7	1.9	1.0	1.1	1.8	1.2	IPF20164	orf19.5809	putative kynurenine aminotransferase (by homology)
CA4164	1.7	2.0	1.0	1.1	1.7	1.1	IPF9302	orf19.5813	unknown function
CA3453	1.7	1.3	0.9	1.0	1.0	0.9	SEC23	orf19.1254	Component of COPII coat (by homology)
CA5687	1.7	1.0	0.9	0.9	1.0	0.8	REV3.5f	orf19.7389	DNA-directed DNA polymerase zeta subunit, 5-prime end (by homology)

CA0068	1.7	1.5	0.9	0.7	1.1	1.2	ARC18	orf19.121	subunit of the Arp2/3 complex involved in the control of actin polymerization (by homology)
CA3627	1.7	1.3	1.1	0.9	0.8	0.9	IPF18318	orf19.5147	unknown function
CA0706	1.7	3.4	1.1	1.5	0.9	1.0	IPF7715.3e	orf19.682	unknown function
CA0792	1.7	1.1	0.9	0.9	1.1	0.8	DIT2.3eoc	orf19.554	putative cytochrome P450, 3-prime end
CA4391	1.7	0.9	0.5	1.1	38.8	6.9	ARR3	orf19.3122	involved in arsenite transport (by homology)
CA3174	1.7	2.6	1.3	1.1	1.0	0.9	CCT2	orf19.1402	chaperonin of the TCP1 ring complex,cytosolic (by homology to S. cerev.)
CA1261	1.7	1.8	0.5	0.6	1.1	1.1	IPF9887	orf19.1240	unknown function
CA6086	1.7	1.2	0.8	1.0	1.1	1.0	PHB2	orf19.5973	Mitochondrial protein, prohibitin homolog (by homology)
CA1275	1.7	0.8	1.5	1.4	1.2	1.0	RPC53	orf19.2715	DNA-directed RNA polymerase III (by homology)
CA1113	1.7	1.4	1.3	1.0	46.6	33.0	IPF9996	orf19.2285	unknown function
CA1585	1.7	1.2	1.0	0.9	1.1	0.9	VPS27	orf19.6031	Vacuolar protein sorting (by homology)
CA3159	1.7	1.4	1.8	1.2	1.4	1.2	PLC3	orf19.1586	phosphatidylinositol phospholipase C
CA4989	1.7	1.1	1.0	1.0	5.9	1.8	IPF2041	orf19.5259	unknown function
CA1180	1.7	3.7	1.1	0.9	0.8	1.4	UGA12.3f	orf19.803	4-aminobutyrate aminotransferase (GABA transaminase), 3-prime end (by homology)
CA4809	1.7	2.6	1.1	1.3	1.9	1.2	IPF1162	orf19.2092	Cystathionine beta-lyase (by homology)
CA1237	1.7	1.1	1.2	1.0	0.9	1.1	IPF15784	orf19.715	unknown function
CA2367	1.7	1.5	1.6	1.1	0.8	1.0	SUI1	orf19.1280	translation initiation factor 3 (eIF3) (by homology)
CA4581	1.7	1.0	1.4	1.1	18.7	1.2	IPF2232	orf19.6899	unknown function
CA4629	1.7	1.4	0.6	0.6	1.2	0.9	IPF13709	orf19.335	unknown function
CA4068	1.7	1.2	1.2	0.9	0.7	0.7	IPF5922	orf19.446	unknown function
CA5551	1.7	2.0	2.0	2.3	4.2	2.3	IPF5972	orf19.7314	putative cysteine dioxygenase (by homology)
CA1616	1.7	0.8	1.1	0.6	0.6	0.6	IPF14538	orf19.3219	unknown function
CA0997	1.7	1.1	0.6	0.9	3.8	4.3	IPF9998	orf19.2284	unknown function
CA2424	1.7	0.8	1.0	0.8	0.9	0.7	IPF18468	orf19.4467	unknown function
CA2913	1.7	1.2	0.5	0.8	1.1	0.7	IPF11205	orf19.4513	unknown function
CA1260	1.7	1.0	0.7	0.9	0.7	0.8	IPF3170	orf19.3166	unknown function
CA1339	1.7	4.9	0.4	0.6	2.2	2.3	IPF5330	orf19.3448	unknown function
CA4618	1.7	1.1	0.9	1.0	1.5	1.1	IPF5757	orf19.3309	unknown function
CA1805	1.7	1.1	1.0	0.9	0.9	0.7	IPF6332	orf19.1112	similar to Saccharomyces cerevisiae Bud7p chitin biosynthesis protein involved in bud site selection (by homology)
CA0966	1.7	0.9	1.0	0.9	25.2	1.2	IPF9136	orf19.6249	potassium transporter, (by homology)
CA0639	1.6	1.8	1.0	1.0	9.0	10.5			
CA2236	1.6	1.1	0.7	0.9	1.2	0.9	IFA23	orf19.3919	unknown function
CA5660	1.6	1.0	1.6	1.3	0.8	0.9	SKN1.3f	orf19.7362	Glucan synthase subunit, 3-prime end
CA3899	1.6	1.9	0.9	0.9	0.9	1.1	DPM1	orf19.5073	dolichol-phosphate (beta-D) mannosyltransferase 1 by homology
CA1183	1.6	1.6	1.2	1.2	0.6	0.6	IPF14805	orf19.3782	acetyl-coenzyme A transporter(by homology)
CA0378	1.6	1.5	1.4	1.0	0.9	1.1	IPF3178	orf19.3170	Unknown function
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)
CA4205	1.6	1.0	0.9	1.0	1.6	1.3	IFA10	orf19.4549	unknown function
CA5138	1.6	1.9	0.9	0.8	0.7	0.8	IPF1031	orf19.4575	Similar to aminoglycoside acetyltransferase regulator from P. stuartii
CA3412	1.6	1.0	0.9	1.0	0.8	1.0	IPF9238	orf19.6143	long chain fatty alcohol oxidase (by homology)
CA1248	1.6	1.5	1.3	1.0	1.6	1.4	IPF3866	orf19.21	unknown function
CA2120	1.6	1.9	0.9	1.0	1.2	1.2	PUP3	orf19.1336	PRCT yeast proteasome component (by homology)
CA1193	1.6	1.1	0.7	0.9	1.1	1.0	MSY1	orf19.109	tyrosyl-tRNA synthetase 8by homology
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 end (by homology)
CA4025	1.6	1.4	1.0	0.9	0.6	0.7	SCJ1	orf19.3438	Mitochondrial and ER import protein (by homology)
CA2565	1.6	2.2	1.1	1.0	0.9	1.3	MET15	orf19.5645	O-acetylhomoserine O-acetylserine sulphydrylase

CA2299	1.6	1.2	0.6	0.7	0.5	0.6	IPF8222	orf19.5381	unknown function
CA4857	1.6	0.4	0.8	1.0	0.8	0.6	PHR1	orf19.3829	GPI-anchored pH responsive glycosyl transferase
CA1452	1.6	1.6	0.8	0.8	1.3	1.0	REV1	orf19.4412	DNA repair protein (by homology)
CA1986	1.6	1.5	0.9	1.0	0.8	1.7	IPF14899	orf19.92	unknown function
CA2207	1.6	1.0	0.8	1.1	1.0	1.1	IPF12169	orf19.697	unknown function
CA1238	1.6	1.2	1.5	2.4	0.9	0.6	IPF15781	orf19.716	unknown function
CA2414	1.6	1.2	1.9	1.1	0.9	1.1	IPF13756.3f	orf19.4479	unknown function, 3-prime end
CA2853	1.6	1.0	1.0	1.1	0.9	1.0	IPF17057	orf19.1070	unknown function
CA5032	1.6	1.2	0.9	1.0	0.9	0.9	IPF2982	orf19.6986	unknown function
CA5349	1.6	1.2	1.0	0.9	1.1	1.1	IPF861	orf19.7224	unknown function
CA2751	1.6	1.3	0.9	0.9	1.1	1.0	IPF19558	orf19.2370	unknown function
CA5435	1.6	2.4	0.7	0.7	0.9	0.9	UFD4	orf19.3237	ubiquitin fusion degradation protein (by homology)
CA1434	1.6	1.3	0.6	0.9	0.9	1.3	SNI2	orf19.1203	Sec9 interacting protein (by homology)
CA2656	1.6	0.8	0.7	0.8	0.6	0.6	NAM2	orf19.5705	mitochondrial leucine--tRNA ligase (by homology)
CA0914	1.6	2.1	0.9	1.0	1.2	1.1	SRA1	orf19.2015	cAMP dependent protein kinase, regulatory subunit (by homology)
CA4985	1.6	1.0	0.9	0.9	0.6	0.8	IPF2050	orf19.5265	similar to Saccharomyces cerevisiae Kip1p kinesin-related protein (by homology)
CA2964	1.6	0.9	1.0	0.8	1.1	1.0	IPF13176.3	orf19.5610	ornithine carbamoyltransferase, 3-prime end (by homology)
CA5326	1.6	1.0	0.9	1.0	0.5	1.0	IPF2137	orf19.7200	unknown function
CA5134	1.6	1.0	1.0	1.1	1.2	1.1	IPF5131	orf19.6391	unknown function
CA1190	1.6	5.9	1.0	1.2	55.2	2.5	CIP1	orf19.113	Cadmium induced protein (by homology)
CA2295	1.6	1.4	1.1	1.0	0.7	0.8	HOS2	orf19.5377	putative histone deacetylase (by homology)
CA2541	1.6	1.4	1.2	0.8	0.7	0.8	IPF9191.3f	orf19.3188	unknown function, 3-prime end
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 homology)
CA2026	1.6	1.3	0.9	1.3	0.8	0.7	IPF9777	orf19.3458	unknown function
14432.20	1.6	1.6	1.0	1.1	0.9	1.0			
CA3836	1.6	1.6	0.6	0.8	1.4	0.9	IPF8179	orf19.6596	putative esterase (by homology)
CA1580	1.6	1.0	1.0	1.2	1.1	0.8	TRP5	orf19.4718	tryptophan synthase (by homology)
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 ER to golgi transport vesicles (by homology)
CA5747	1.6	1.0	0.8	1.0	0.9	1.0	IPF2903	orf19.7456	unknown function
CA0720	1.6	1.4	1.2	1.0	0.9	1.1	IPF17932	orf19.3457	unknown function
CA4933	1.6	1.2	1.7	1.2	1.1	1.3	IPF8372	orf19.6074	unknown function
CA2990	1.6	1.5	0.8	0.9	0.5	0.8	IPF5092	orf19.6012	unknown function
CA5083	1.6	1.5	0.8	1.1	0.5	0.6	IPF9278	orf19.3060	similar to Saccharomyces cerevisiae Swp1p oligosaccharyltransferase delta subunit (by homology)
CA5811	1.6	1.0	1.6	1.0	0.8	1.0	IPF1699	orf19.6614	unknown function
CA0394	1.6	1.9	1.0	1.3	1.4	1.4	IPF12758.5f	orf19.334	unknown function, 5-prime end
CA1018	1.6	1.2	0.6	0.7	1.0	1.1	IPF13479.3	orf19.3768	unknown function, 3-prime end
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)
CA5657	1.6	0.9	1.2	0.9	1.1	1.0	IPF14682	orf19.7359	putative transcription factor (by homology)
CA5676	1.6	1.0	1.0	1.0	1.1	1.0	FAA22	orf19.7379	Long-chain-fatty-acid--CoA ligase (by homology)
CA4602	1.6	2.0	1.2	1.2	0.5	0.7	IPF6231	orf19.3292	unknown function Unknown function
CA3525	1.6	1.3	1.2	1.0	1.0	1.1	DJP1	orf19.991	DnaJ-like protein involved in peroxisome biogenesis (by homology)
CA2888	1.6	1.6	1.0	1.1	1.2	1.2	GIM5	orf19.2471	Gim complex component (by homology)
CA0323	1.6	0.8	1.1	1.1	1.6	1.5	CDC95	orf19.1815	translation initiation factor 6 (eIF6) (by homology)
CA4389	1.6	1.9	1.2	1.0	1.2	1.2	RPT5	orf19.3123	26S proteasome regulatory subunit (by homology)
CA4524	1.6	1.3	1.6	1.3	0.9	1.1	IPF7097	orf19.480	unknown function
CA4595	1.6	1.0	0.8	0.9	0.5	0.9	GCN2	orf19.6913	Ser/thr protein kinase (by homology)

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 homology
CA3550	1.6	0.8	1.5	1.2	0.7	1.5	IPF13228	orf19.3874	unknown function
CA6091	1.6	2.5	0.8	0.7	0.8	0.8	UFD2	orf19.5965	Ubiquitin fusion degradation protein 2 (by homology)
CA4621	1.6	0.9	0.7	0.9	0.8	0.8	IPF5753	orf19.3312	unknown function
CA1365	1.6	1.0	0.9	0.9	0.4	1.3	IPF11849	orf19.4459	unknown function
CA1755	1.6	1.8	1.1	0.9	0.8	1.1	PDI1	orf19.5130	protein disulfide-isomerase precursor (by homology)
CA5127	1.6	1.5	1.4	1.1	3.0	1.7	CYS3	orf19.6402	cystathionine gamma-lyase by homology
CA1693	1.6	1.8	1.0	1.0	1.0	1.1	IPF17054	orf19.5037	unknown function
CA6069	1.6	1.3	1.3	1.0	1.0	1.0	IPF4847	orf19.5995	unknown function
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)
CA0805	1.6	1.5	1.3	1.2	1.2	1.2	IPF12568	orf19.3516	unknown function
CA0265	1.6	2.4	1.3	1.0	1.0	1.0	STI1.3f	orf19.3191	stress-induced protein (by homology)
CA1753	1.6	1.8	0.9	1.0	1.1	1.1	IPF8245	orf19.1515	putative chitinase
CA4663	1.6	1.4	1.6	1.1	0.7	0.8	IPF6554	orf19.4450	unknown function
CA2967	1.6	1.5	0.7	1.0	2.8	2.5	IPF12513	orf19.5605	unknown function
CA5689	1.6	0.9	0.8	1.0	1.0	0.9	REV3.3f	orf19.7390	DNA-directed DNA polymerase zeta subunit, 3-prime end (by homology)
CA2020	1.6	1.5	1.0	0.9	0.4	1.0	IPF16901	orf19.842	unknown function
CA5714	1.6	1.1	1.0	1.1	1.1	1.1	IPF2431	orf19.7417	similar to Saccharomyces cerevisiae Tsa1p thiol-specific antioxidant-like protein (by homology)
CA0511	1.6	1.4	1.0	1.3	1.3	1.1	IPF13975	orf19.4953	unknown function
CA1094	1.6	1.1	1.7	1.3	0.6	0.7	YIP1	orf19.3951	golgi membrane protein (by homology)
CA1004	1.6	1.2	0.9	0.8	1.7	1.4	IPF8901	orf19.3758	unknown function
CA3026	1.6	1.0	1.0	1.0	0.9	1.0	IFZ1	orf19.3901	
CA3818	1.6	1.4	0.8	0.6	0.9	1.1	IPF6695	orf19.5773	unknown function
CA2981	1.6	1.1	1.5	0.9	0.8	0.7	CSE1.5f	orf19.1231	Importin-beta-like protein, 5-prime end (by homology)
CA0343	1.6	1.2	1.1	1.0	0.9	1.5	LYS1	orf19.1789.1	saccharopine dehydrogenase (by homology)
CA3422	1.6	1.9	0.9	0.8	0.7	0.9	IPF17289	orf19.6134	unknown function
CA5538	1.6	1.1	1.2	1.1	1.5	1.4	IPF2830	orf19.7300	unknown function
CA0843	1.6	1.3	1.1	1.2	0.5	0.7	IPF18853	orf19.1054	unknown function
CA1577	1.6	1.1	1.0	1.1	1.1	0.9	KNS1	orf19.4979	Ser/thr protein kinase (by homology)
CA2887	1.6	1.1	1.0	1.1	1.1	0.9	IPF13631	orf19.2472	unknown function
CA1467	1.6	1.0	0.8	1.1	0.8	1.0	IPF5082	orf19.793	similar to Saccharomyces cerevisiae Cak1p cdk-activating protein kinase (by homology)
CA6111	1.6	1.1	1.0	0.9	0.8	1.0	IPF96	orf19.5942	C3HC4 type zinc finger protein (by homology)
CA2548	1.6	1.7	1.0	0.9	0.9	0.9	PGA34	orf19.2833	unknown function
CA3151	1.6	1.4	0.9	1.1	0.5	1.1	IPF4033	orf19.6167	similar to Saccharomyces cerevisiae Ayr1p 1-acyldihydroxyacetone-phosphate reductase (by homology)
CA5878	1.6	1.0	1.3	1.1	1.2	1.3	PRP5	orf19.6831	pre-mRNA processing RNA-helicase (by homology)
CA1608	1.6	2.0	1.6	1.7	1.2	1.4	TES12	orf19.4122	Thiosterase (by homology)
CA1269	1.6	1.7	1.1	1.1	1.1	1.4	IPF19726	orf19.3158	unknown function
CA2906	1.6	1.0	0.9	0.8	0.8	0.8	IPF15523	orf19.4521	unknown function
CA3474	1.6	1.2	1.0	0.8	0.8	0.7	AFG3	orf19.1669	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family of ATPases (by homology)
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 cluster domain type (by homology)
CA2537	1.6	1.8	1.0	1.1	1.0	1.0	IPF20108	orf19.3184	similar to Saccharomyces cerevisiae Sft2p suppressor of SED5 thermosensitive mutations (by homology)
CA5107	1.6	1.1	1.2	1.1	1.3	1.0	IPF1358	orf19.6431	unknown function
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 (by homology)
CA3017	1.6	1.3	1.2	1.0	0.6	0.8	IPF10021	orf19.3912	unknown function
CA4041	1.6	0.6	1.9	1.7	1.1	0.7	GAL10	orf19.3672	UDP-glucose 4-epimerase by homology
CA3443	1.5	1.2	1.2	1.0	1.1	1.0	IPF11324	orf19.2982	unknown function

CA4662	1.5	1.3	0.9	1.0	4.8	2.5	LYS7	orf19.4449	Copper chaperone for superoxide dismutase Sod1p (by homology)
CA5305	1.5	1.6	1.1	1.1	0.7	0.9	IPF2175	orf19.7175	similar to Saccharomyces cerevisiae Hlj1p dnaJ-type protein (by homology)
CA4594	1.5	1.1	1.2	1.1	0.7	0.9	IPF2212	orf19.6912	unknown function
CA5558	1.5	3.8	1.1	1.4	1.3	1.2	IPF1969	orf19.7322	unknown function
CA0748	1.5	2.0	0.8	1.2	1.0	1.0	TFS1	orf19.1974	cdc25-dependent nutrient- and ammonia-response cell-cycle regulator (by homology)
CA0881	1.5	0.8	0.7	1.0	0.8	1.1	IPF16965	orf19.374	unknown function
CA2415	1.5	1.3	0.8	0.7	0.8	0.9	MSD1	orf19.4478	Aspartyl-tRNA synthetase, mitochondrial.
CA5033	1.5	1.4	1.0	0.8	0.7	0.7	DNM1	orf19.6987	Dynamin-related protein (by homology)
CA3875	1.5	1.1	0.5	1.0	1.2	1.0	IPF14430	orf19.394	putative kynureninase (by homology)
CA1849	1.5	1.0	1.2	0.9	0.9	0.7	IPF19932	orf19.640	unknown function
CA0911	1.5	1.0	1.4	1.3	0.9	1.1	IPF14814	orf19.2018	unknown function
CA6011	1.5	1.0	0.6	1.0	1.5	1.1	CTM1	orf19.7612	cytochrome c methyltransferase (by homology)
CA2369	1.5	1.4	1.6	1.4	1.6	1.1	TBP1	orf19.1837	TATA-binding protein (by homology)
CA4264	1.5	1.6	0.9	1.1	2.3	1.4	IPF2280	orf19.6658	unknown function
CA0721	1.5	0.9	1.3	2.3	0.8	0.8	IPF10429	orf19.2887	unknown function
CA2341	1.5	1.5	1.0	1.1	1.3	1.1	IPF13838	orf19.2346	unknown function
CA4136	1.5	1.0	0.9	0.9	0.7	0.9	RET2	orf19.4236	Coatomer complex delta chain (by homology)
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 homology)
CA1389	1.5	1.8	1.4	1.3	0.8	1.1	PLP2	orf19.1769	Might regulate Ste4p in pheromone response (by homology)
CA3134	1.5	1.2	0.8	1.0	1.2	1.1	IFZ2	orf19.1365	unknown function
CA1561	1.5	1.3	1.8	1.5	0.9	1.0	POT12	orf19.1704	peroxysomal 3-ketoacyl-CoA thiolase B (by homology)
CA5397	1.5	1.2	0.7	0.8	0.4	0.8	IPF9663	orf19.940	similar to Saccharomyces cerevisiae Bud2p GTPase-activating protein for Bud1p/Rsr1p (by homology)
CA4919	1.5	1.9	1.1	1.5	7.1	4.5	TTR1	orf19.6059	Glutaredoxin (by homology)
CA4804	1.5	1.1	0.8	1.4	1.4	1.1	ARO8	orf19.2098	aromatic amino acid aminotransferase I (by homology)
CA3152	1.5	1.0	0.9	1.0	0.9	1.0	IPF4032	orf19.6168	unknown function
CA4870	1.5	1.1	1.3	1.7	1.2	1.3	IPF19568	orf19.6556	unknown function
CA2084	1.5	1.9	0.8	0.8	0.7	0.5	IPF3384.3f	orf19.833	similar to Saccharomyces cerevisiae Gpi13p phosphoryltransferase
CA2465	1.5	1.1	0.9	0.9	0.5	0.7	IPF8726	orf19.1795	unknown function
CA2480	1.5	2.1	1.2	1.0	0.9	0.9	CCT7	orf19.3206	component of chaperonin-containing T-complex (by homology)
CA4447	1.5	1.0	1.4	1.2	1.3	1.4	IPF3523	orf19.6845	unknown function
CA5062	1.5	1.1	1.1	1.1	0.5	0.7	SEC62	orf19.3031	subunit of ER protein-translocation complex (by homology)
CA1846	1.5	2.2	0.8	0.9	12.5	11.2	FDH12	orf19.638	Formate dehydrogenase (by homology)
CA2402	1.5	0.9	1.2	1.0	1.0	1.0	IPF6437	orf19.3543	unknown function
CA4504	1.5	0.9	1.7	1.4	0.9	1.0	ARP5	orf19.504	actin-related protein (by homology)
CA1613	1.5	1.9	1.0	1.3	1.0	1.0	IPF19735	orf19.3215	unknown function
CA3685	1.5	1.0	0.9	0.9	0.7	1.1	IPF19540	orf19.723	unknown function
CA1081	1.5	1.2	1.5	1.1	0.8	1.4	IPF14797.3f	orf19.4818.3	unknown function, 3-prime end
CA5791	1.5	2.3	1.2	1.0	1.4	1.2	RPT2	orf19.5440	26S proteasome regulatory subunit (by homology)
CA3288	1.5	1.5	5.3	2.5	1.2	1.7	ARD8	orf19.6322	D-arabinitol dehydrogenase
CA0204	1.5	0.5	2.7	1.1	0.7	0.9	IKI3	orf19.1222	killer toxin insensitive protein 3 (by homology)
CA2189	1.5	8.8	0.8	1.0	3.0	1.3	AOX2.3f	orf19.4773	alternative oxidase (by homology)
CA5894	1.5	1.5	0.9	1.0	0.6	0.8	PMT2	orf19.6812	O-D-mannosyltransferase (by homology)
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
CA4406	1.5	2.2	0.7	1.4	1.1	1.0	YDC1	orf19.3104	alkaline dihydroceramidase (by homology)
CA5309	1.5	1.3	1.1	0.8	0.9	0.9	IPF2170	orf19.7179	similar to saccharomyces cerevisiae Ssc1pmitochondrial hsp70-type heat shock protein (by homology)
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 chromatid cohesion (by homology)

CA5879	1.5	1.0	1.1	1.0	1.1	1.1	IPF12076	orf19.6830	enoyl CoA hydratase (by homology)
CA5738	1.5	1.1	1.1	1.2	1.0	1.1	LYS9	orf19.7448	Lysine biosynthesis (by homology)
CA0808	1.5	1.3	0.9	0.9	1.1	1.2	SUA71	orf19.3519	TFIIB subunit (transcription initiation factor E)(by homology)
CA5966	1.5	1.5	1.0	1.1	2.1	1.0	IPF959	orf19.7556	unknown function
CA3428	1.5	1.7	0.9	1.2	1.8	1.2	VPS21	orf19.589	GTP-binding protein (by homology)
CA4736	1.5	1.2	1.0	1.0	1.2	1.1	IPF4503	orf19.4849	unknown function
CA4354	1.5	1.2	1.0	1.0	0.9	0.8	IPF3647	orf19.6729	unknown function
CA0297	1.5	0.9	1.1	1.1	0.9	0.7	CDC53	orf19.1674	Cell division control protein (by homology)
CA0775	1.5	1.2	0.5	0.8	1.2	0.9	IFK2	orf19.856	probable monoxygenase (by homology)
CA1075	1.5	7.0	0.8	0.8	0.8	0.7	IPF4991	orf19.2531	putative membrane protein
CA0236	1.5	0.9	1.0	0.8	1.3	1.0	MDM10	orf19.184	Involved in mitochondrial morphology and inheritance (by homology)
CA1731	1.5	0.9	1.0	1.0	0.5	0.7	IPF8437	orf19.6499	putative DNA-directed RNA polymerase (by homology)
CA4669	1.5	1.0	0.6	1.1	0.7	0.8	IPF4537	orf19.905	putative permease (by homology)
CA4305	1.5	0.8	0.9	0.8	0.8	1.1	IPF6654	orf19.6705	unknown function
CA6158	1.5	1.0	0.8	1.0	3.0	1.0	IPF1839	orf19.5879	putative 1-Acyl dihydroxyacetone phosphate reductase (by homology)
CA5374	1.5	2.0	1.3	1.1	1.4	1.2	DDI1	orf19.7258	Response to DNA alkylation by homology
CA0117	1.5	3.1	1.1	1.1	0.9	1.1	IPF19231	orf19.916	unknown function
CA3446	1.5	1.5	0.7	0.9	1.8	2.0	IPF7324	orf19.2977	unknown function
CA3256	1.5	1.4	1.2	1.1	0.6	0.9	IPF4730	orf19.3744	unknown Function
CA4990	1.5	1.0	0.8	1.0	8.0	1.2	IPF2039	orf19.5258	unknown function
CA2338	1.5	1.6	0.6	1.0	2.5	1.4	NIT3	orf19.2351	nitrilase (by homology)
CA1980	1.5	1.1	1.4	0.9	0.5	0.6	YHM1	orf19.685	member of the mitochondrial carrier family (MCF) (by homology)
CA5616	1.5	0.6	0.8	1.2	1.2	1.0	PET8	orf19.7082	mitochondrial carrier protein (by homology)
CA2447	1.5	1.1	0.9	1.0	1.1	0.9	HIS7	orf19.5505	Histidine biosynthesis
CA5557	1.5	1.6	0.8	1.1	0.9	0.9	IPF1968	orf19.7321	unknown function
CA3821	1.5	1.2	1.8	1.6	8.4	6.1	IPF6990	orf19.5770	unknown function
CA1136	1.5	3.0	0.8	0.9	2.1	1.2	IFN2	orf19.1980	glycerophosphoinositol transporter (by homology)
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. cerevisiae
CA4021	1.5	3.8	0.7	1.6	1.1	1.1	EBP2	orf19.3442	NADPH dehydrogenase (by homology)
CA0739	1.5	1.1	0.9	1.0	0.6	0.7			
CA1759	1.5	2.6	1.3	0.9	1.0	1.0	IPF14744	orf19.5125	unknown function
CA3415	1.5	0.2	1.7	1.0	4.3	1.7	FRE30.53f	orf19.6140	ferric reductase, internal fragment (by homology)
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 (by homology)
CA1162	1.5	1.3	1.2	1.0	0.7	0.9	IPF10258	orf19.2728	cell cycle checkpoint protein (by homology)
CA5560	1.5	1.2	1.3	0.9	1.1	1.0	THI13	orf19.7324	Pyrimidine precursor biosynthesis enzyme (by homology)
CA2460	1.5	1.1	1.0	1.0	1.1	1.6			
CA0280	1.5	1.0	1.4	1.1	0.8	0.7	IPF10566	orf19.1439	unknown function
CA6062	1.5	1.3	3.0	1.5	0.6	0.8	IPF8307	orf19.6005	putative permease (by homology)
CA3617	1.5	1.1	1.3	0.8	0.5	0.8	IPF9069	orf19.199	unknown function
CA1314	1.5	1.5	0.8	1.0	5.5	1.5	MAG1	orf19.3639	3-methyladenine DNA glycosylase (by homology)
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)
CA1019	1.5	1.2	1.2	0.9	0.9	0.7	IPF13485	orf19.3769	unknown function
CA0595	1.5	1.0	1.0	1.0	14.0	2.8	IPF8856.5f	orf19.4901	unknown function, 5-prime end
CA6010	1.5	3.1	1.0	1.2	2.2	4.1	TRX1	orf19.7611	thioredoxin (by homology)
CA1044	1.5	1.0	0.9	1.0	1.0	1.2	RNA1	orf19.1649	GTPase activating protein (by homology)
CA3402	1.5	0.8	1.0	1.0	1.6	1.5	IPF8651	orf19.3978	unknown function

CA3984	1.5	1.3	0.9	1.0	1.2	1.0	HOM2	orf19.1559	Aspartate-semialdehyde dehydrogenase (by homology)
CA5060	1.5	2.8	0.9	1.0	1.2	1.2	IPF3690	orf19.3029	unknown function
CA4890	1.5	1.7	1.0	0.9	1.0	1.1	PRE10	orf19.6582	20S proteasome subunit C1 (by homology)
CA5545	1.5	1.3	1.3	1.0	0.6	0.8	IPF5986	orf19.7307	similar to cytochrome-b5- and nitrate reductases
CA4323	1.5	1.0	1.4	1.0	0.7	0.9	IPF2096	orf19.4096	putative acyltransferase (by homology)
CA3167	1.5	1.0	1.0	0.8	1.1	0.9	IPF9632	orf19.1576	unknown function
CA4691	1.5	1.1	1.0	1.0	2.0	1.8	IPF3958	orf19.874	unknown function
CA5812	1.5	1.0	1.4	1.0	0.8	1.0			
CA3511	1.5	1.3	0.8	1.0	1.1	1.0	MMS2	orf19.6358	ubiquitin-conjugating enzyme (by homology)
CA4793	1.5	1.1	1.3	1.1	1.1	1.1	IPF3375	orf19.4028	similar to Saccharomyces cerevisiae Rer2p cis-prenyltransferase, a key enzyme in dolichol synthesis (by homology)
CA0817	1.5	1.0	0.9	0.9	2.3	1.0	IPF6339	orf19.2724	unknown function
CA1544	1.5	0.9	1.0	1.1	1.1	1.1	IPF1040	orf19.4568	Similar to transcriptional activators
CA3191	1.5	1.8	0.7	1.0	0.7	0.8	IPF11601	orf19.2151	unknown function
CA2469	1.5	0.8	1.0	0.8	1.1	0.7	IPF7393	orf19.1798	unknown function
CA5941	1.5	1.7	1.0	1.3	1.4	0.9	IPF3486	orf19.6756	unknown function
CA4065	1.5	0.9	1.2	1.2	1.0	1.1	RPC25	orf19.443	DNA-direcred RNA polymerase III (by homology)
CA4322	1.5	1.1	1.1	1.0	0.6	0.7	IPF2097	orf19.4097	unknown function
CA3626	1.5	1.0	0.9	1.1	0.4	0.6			
CA5313	1.5	1.1	1.0	1.1	1.4	0.9	IPF2163	orf19.7184	unknown function
CA5049	1.5	2.5	1.0	1.1	0.9	0.9	CDC12	orf19.3013	septin (by homology)
CA1215	1.5	1.5	0.7	0.9	1.0	0.9	VPS15.3f	orf19.127	serine/threonine protein kinase, 3-prime end
CA2483	1.5	1.1	0.9	0.8	0.7	0.8	IPF19758	orf19.3203	unknown function
CA0261	1.5	0.9	1.2	1.2	0.9	1.1	LYS22	orf19.772	Homocitrate synthase (by homology)
CA6126	1.5	0.9	1.0	0.9	1.1	1.0	IPF143	orf19.5924	unknown function
CA3234	1.5	0.9	1.5	0.8	0.7	0.8	MAS2	orf19.6295	processing peptidase, catalytic 53kDa (alpha) subunit, mitochondrial (by homology)
CA4142	1.5	1.7	1.0	1.0	1.5	1.2	PRE4	orf19.4230	20S proteasome subunit(beta7) (by homology)
CA0971	1.5	4.3	2.0	1.8	1.1	1.1	IPF11428	orf19.6470	unknown function
CA0448	1.5	1.1	0.7	1.0	1.4	1.3	ALS10	orf19.2355	agglutinin like protein
CA0819	1.5	1.5	1.1	0.9	0.8	1.0	VPS1	orf19.1949	member of the dynamin family of GTPases (by homology)
CA4865	1.5	2.1	1.0	1.0	1.1	1.2	IPF4085	orf19.3841	similar to Saccharomyces cerevisiae Apg1p essential for autophagocytosis (by homology)
CA3427	1.5	1.3	0.8	1.0	1.3	1.2	IPF11865	orf19.590	unknown function
6100.20	1.5	2.2	2.0	1.2	1.1	1.0			
CA3217	1.5	1.1	0.9	0.6	0.9	0.8	DHH1	orf19.6197	RNA helicase by homology
CA0988	1.5	1.1	0.9	1.1	0.9	0.8	PMI40	orf19.1390	mannose-6-phosphate isomerase (PHOSPHOMANNOSE ISOMERASE) (PMI)(PHOSPHOHEXOMUTASE)
CA1272	1.5	1.0	0.9	0.8	1.3	0.9	CGR1	orf19.2722	Cell growth protein (by homology)
CA5936	1.5	1.4	0.9	1.1	0.7	0.6	IPF2795	orf19.6763	unknown function
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 (by homology)
CA3725	1.5	1.0	0.9	1.1	1.4	0.8	TOK1.3f	orf19.4175	Outward-rectifier potassium channel, 3-prime end (by homology)
CA0822	1.5	0.8	1.2	1.0	0.3	0.3	EXG1	orf19.2990	glucan 1,3-beta-glucosidase
CA1370	1.5	0.9	1.8	1.0	0.8	0.8	TCI1	orf19.4963	protein phosphatase Two C-Interacting protein (by homology)
CA3431	1.5	1.3	0.8	1.0	0.6	0.7	FUN9	orf19.586	Protein involved in vesicular transport between the endoplasmic reticulum and Golgi apparatus (by homology)
CA1995	1.5	1.0	0.8	1.0	0.9	0.8	IPF6612	orf19.6480	unknown function
CA3814	1.5	1.2	0.6	1.0	4.3	3.1	IPF4023	orf19.2498	unknown function
CA4026	1.5	1.3	0.9	0.9	1.0	0.9	IPF7175	orf19.3437	unknown function
CA1235	1.5	1.2	1.0	1.0	1.1	1.0	IPF20079	orf19.713	unknown function
CA5464	1.5	1.1	0.8	1.0	1.4	1.4	IPF285.5f	orf19.3273	unknown function, 5-prime end

CA3251	1.5	1.1	1.0	1.0	0.7	0.8	IPF4721	orf19.3737	unknown Function
CA2083	1.5	1.9	0.9	0.8	0.6	0.6	IPF3384.5f	orf19.832	similar to Saccharomyces cerevisiae Gpi13p phosphoryltransferase
CA3464	1.5	1.1	1.0	0.9	0.9	1.0	DBP5	orf19.1661	RNA helicase (by homology)
CA0802	1.5	1.2	1.3	1.2	0.8	0.8	IPF14060	orf19.3498	unknown function
CA2654	1.5	1.0	0.7	0.7	1.0	0.7	IPF8474	orf19.5702	unknown function
CA2756	1.5	0.9	0.7	1.0	1.5	1.0	IPF18418	orf19.5620	unknown function
CA0183	1.5	1.9	1.5	1.1	1.4	2.2	CAP1	orf19.1623	transcriptional acivator (by homology)
CA3219	1.5	0.8	1.1	1.0	0.9	0.7	IPF10003	orf19.6195	similar to Saccharomyces cerevisiae Rnh70p ribonuclease H (by homology)
CA0550	1.5	1.1	1.2	1.8	0.6	0.9	IPF14030	orf19.851	unknown function
CA0226	1.5	1.1	1.0	1.1	0.9	1.1	IPF16024	orf19.1297	unknown function
CA5176	1.5	1.4	0.7	0.8	1.2	0.9	IPF6045	orf19.4614	unknown function
CA1101	1.5	0.9	1.1	0.9	2.3	1.0	IPF5678	orf19.4951	unknown function
CA2227	1.5	1.2	1.0	0.9	1.4	2.5	EBP7	orf19.5816	NADPH DEHYDROGENASE by homology
CA4977	1.5	1.0	1.0	0.9	1.3	1.0	IPF4710	orf19.5275	unknown Function
CA3403	1.5	1.2	0.6	0.7	0.8	1.2	IPF8650	orf19.3980	RNA helicase (by homology)
CA5509	1.5	0.8	2.1	1.3	1.5	1.6	IPF743	orf19.5353	unknown function
CA0605	1.5	1.3	0.8	0.8	0.5	0.4	UTR2	orf19.1671	1,3-1,4-beta-glucanase (by homology)
CA3290	1.5	1.9	1.3	1.5	0.9	0.5	IPF5734	orf19.6324	unknown function
CA5569	1.5	1.6	1.1	0.9	1.2	0.9	PRE8	orf19.7335	20S proteasome subunit Y7 (by homology)
CA1690	1.5	1.5	1.1	1.4	1.0	1.4	FAT1	orf19.3653	very long-chain fatty acyl-CoA synthetase (by homology)
CA5784	1.5	0.9	0.7	1.0	0.6	1.4	IPF1129	orf19.5431	unknown function
CA0537	1.5	0.8	1.0	0.9	0.8	0.9	PRP16	orf19.2818	RNA-dependent ATPase (by homology)
CA5818	1.5	1.0	1.4	1.3	0.9	1.1	ARG1	orf19.7469	argininosuccinate synthetase (by homology)
CA3936	1.5	1.7	1.0	0.9	1.7	1.4	COX17	orf19.2006.1	cysteine-rich cytoplasmic protein(by homology)
CA1708	1.5	1.0	1.2	1.1	1.0	1.0	IPF7543	orf19.4888	unknown function
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)
CA0454	1.5	1.7	1.2	0.9	1.0	1.0	RPN6	orf19.1299	subunit of the regulatory particle of the proteasome (by homology)
CA0112	1.5	0.9	1.2	0.9	3.1	1.3	IPF17358	orf19.5754	unknown function
CA1332	1.5	1.0	1.3	1.4	2.9	1.1	IPF11716	orf19.1150	unknown function
CA5293	1.5	1.1	0.9	0.9	0.6	1.0	FAA24	orf19.7156	Long-chain-fatty-acid--CoA ligase (by homology)
CA1222	1.5	1.1	0.9	0.9	0.9	1.0	SNA2	orf19.4132	unknown function
CA2546	1.5	1.0	1.0	1.0	1.1	1.0	RPC31	orf19.2831	DNA-directed RNA polymerase III (by homology)
CA5308	1.5	2.2	1.0	0.9	1.3	1.1	PRE5	orf19.7178	20S proteasome subunit alpha6 (by homology)
CA5650	1.5	2.8	3.7	1.2	1.1	1.0	IPF7109	orf19.7350	unknown function
CA3401	1.5	1.3	1.1	1.0	1.5	1.3	IPF8652	orf19.3977	putative GTP-binding protein (by homology)
CA1997	1.4	1.3	1.0	1.1	1.8	1.3	YCF1	orf19.6478	Glutathione S-conjugate transporter (by homology)
CA1169	1.4	1.2	1.0	0.9	2.3	1.9	Mch4p	orf19.2751	probable monocarboxylate permease Yeast Mch4p protein (by homology)
CA5758	1.4	1.2	0.7	0.9	0.8	1.1	IPF1069	orf19.5395	similar to Saccharomyces cerevisiae Rav1p involved in regulation of (H+)-ATPase in vacuolar membrane
CA1921	1.4	2.0	1.4	2.5	0.3	0.4	IPF7475	orf19.2444	similar to Saccharomyces cerevisiae Chs7p involved in control of protein export from the ER (by homology)
CA4997	1.4	1.2	1.1	1.4	1.0	1.4	IPF2027	orf19.5250	unknown function
CA0677	1.4	1.3	1.2	1.8	1.0	0.8	IPF13095	orf19.1182	unknown function
CA5692	1.4	1.3	0.9	1.0	1.2	1.3	UTR1	orf19.7393	Associated with ferric reductase activity (by homology)
CA1392	1.4	1.1	1.0	0.9	1.1	0.9	IPF6149	orf19.1767	similar to Saccharomyces cerevisiae Ubp8p deubiquinating enzyme (by homology)
CA0618	1.4	1.1	0.7	1.0	1.3	1.0	UGT51	orf19.2616	UDP-glucose:sterol glucosyltransferase
CA4988	1.4	1.9	1.0	0.9	0.9	0.8	RPN2	orf19.5260	Proteasome regulatory subunit (by homology)
CA5510	1.4	0.9	2.8	1.5	1.5	1.5	IPF741	orf19.5356	unknown function

CA0310	1.4	1.0	0.9	0.9	0.9	1.0	PEX11	orf19.1089	peroxisomal membrane protein - peroxin by homology
CA0592	1.4	1.2	0.8	1.0	1.4	1.0	IPF8862	orf19.4905	unknown function
CA2634	1.4	1.9	1.1	1.0	1.1	1.3	ZWF1	orf19.4754	glucose-6-phosphate dehydrogenase (by homology)
CA3104	1.4	1.4	1.1	1.1	4.9	1.3	IPF12084	orf19.6554	unknown function
CA5659	1.4	1.0	1.2	0.9	1.0	0.9	SEN54	orf19.7361	tRNA splicing endonuclease alpha subunit(by homology)
CA2748	1.4	1.1	1.0	0.9	1.2	1.1	IPF11466	orf19.2368	unknown function
CA4597	1.4	1.0	1.1	1.1	1.0	1.3	ATP11	orf19.6916	F1F0-ATPase complex assembly protein (by homology)
CA5668	1.4	1.6	2.7	2.5	2.0	2.7	IPF1261	orf19.7370	unknown function
CA0930	1.4	1.2	1.0	0.8	0.9	0.9	Zorro1a	orf19.559	Putative reverse transcriptase
CA4680	1.4	1.3	1.1	1.3	0.6	0.9	AMD1	orf19.891	AMP deaminase (by homology)
CA5973	1.4	1.0	0.6	1.0	1.7	1.1	IPF931	orf19.7567	unknown function
CA2760	1.4	1.0	1.0	0.9	1.0	1.0			
CA2292	1.4	1.6	0.9	0.9	1.0	1.0	VAC8	orf19.745	required for vacuole inheritance and protein targeting from the cytoplasm to vacuole (by homology)
CA5025	1.4	0.8	1.1	0.7	1.0	1.0	AMI3	orf19.6979	protein required for normal mitochondrial structure (by homology)
CA6100	1.4	1.5	1.0	1.1	2.1	1.1	IPF66	orf19.5956	unknown function
CA3991	1.4	0.9	0.8	0.8	0.7	0.8	VAM6.5f	orf19.1567	Vacuolar carboxypeptidase Y, 5-prime end (by homology)
CA3563	1.4	2.5	2.1	1.2	6.2	5.3	IPF7819	orf19.3130	unknown function
CA2372	1.4	1.1	1.3	1.0	0.8	0.9	IPF10335	orf19.1834	unknown function
CA5821	1.4	0.9	0.9	0.9	0.8	0.8	PHO81	orf19.7475	Cyclin-dependent kinase inhibitor (by homology)
CA2674	1.4	1.0	1.3	0.9	0.3	0.7	IPF5846	orf19.5495	unknown function
CA2351	1.4	1.0	0.8	1.1	1.3	1.3	IPF19947	orf19.4420	unknown function
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 end (by homology)
CA2834	1.4	1.0	0.6	0.9	1.4	1.1	IPF12093	orf19.4786	unknown function
CA0563	1.4	0.9	1.3	0.9	0.4	0.6	MNN11	orf19.2927	Mannosyltransferase complex component (by homology)
CA0961	1.4	1.6	0.7	0.9	2.2	1.2	IPF18822	orf19.3720	unknown function
CA0985	1.4	1.1	1.2	1.1	1.0	1.0	IPF4815.3f	orf19.3351	unknown Function
CA2130	1.4	3.6	1.2	1.0	1.2	1.1	RPS27A	orf19.413.1	ribosomal protein S27.e (by homology)
CA4519	1.4	1.2	0.7	0.8	0.9	0.8	IPF7088	orf19.486	similar to Saccharomyces cerevisiae Nip100p myosin-like protein, putative component of the dynactin complex
CA5221	1.4	1.1	1.0	1.0	1.2	0.8			
CA0125	1.4	1.4	0.8	0.9	1.0	1.0	IPF4119	orf19.2030	unknown function
CA0756	1.4	1.0	0.9	1.1	2.3	1.1	IPF14859	orf19.3488	acyl-coenzyme-A dehydrogenase (by homology)
CA1374	1.4	1.7	1.1	0.8	0.7	0.6	MIP1	orf19.1195	Mitochondrial intermediate peptidase (by homology)
CA2661	1.4	1.2	0.8	0.6	0.9	0.9	AAT1	orf19.3554	aspartate aminotransferase (by homology)
CA5742	1.4	1.3	0.8	0.8	1.1	1.0	FUN31	orf19.7451	Serine/threonine kinase (by homology)
CA4991	1.4	1.4	0.8	0.9	2.2	1.5	LCB4	orf19.5257	Sphingolipid long chain base kinase (by homology)
CA6089	1.4	1.3	1.0	0.9	0.9	1.2	RDI1	orf19.5968	Rho GDP dissociation inhibitor (by homology)
CA0356	1.4	1.2	0.9	0.9	1.0	1.1	IPF2532	orf19.6630	unknown function
CA3473	1.4	1.1	0.9	0.9	0.8	0.9	IPF6305	orf19.1668	unknown function
CA4160	1.4	1.0	1.3	1.1	0.9	1.2	IPF9294	orf19.5808	unknown function
CA0745	1.4	1.1	1.3	0.9	1.0	1.0	MTF1	orf19.1528	RNA polymerase specific factor, mitochondrial (by homology)
CA4066	1.4	1.4	1.1	1.0	0.8	0.9	IPF5925	orf19.444	RNA-binding protein (by homology)
CA5868	1.4	1.2	0.8	1.2	2.7	2.9	IPF351	orf19.7531	unknown function
CA0658	1.4	1.0	1.2	0.8	0.5	0.7	IPF16505	orf19.5575	Unknown function
CA3266	1.4	1.2	1.3	1.0	1.0	1.0	IPF5045	orf19.2703	unknown function
CA1138	1.4	2.3	0.7	0.9	0.9	1.1	IFN3	orf19.1978	glycerophosphoinositol transporter (by homology)
CA3955	1.4	1.4	1.0	1.0	1.1	1.1	IPF6712.5f	orf19.1414	unknown function, 5-prime end

CA0787	1.4	1.3	1.1	1.0	1.1	1.0	IPF7472	orf19.2447	unknown function
CA1318	1.4	0.7	1.7	1.2	0.8	1.1	IPF3147	orf19.4219	Nuclear valosin-containing protein-like (by homology)
CA2089	1.4	1.0	1.1	1.0	0.9	0.7	GNA1	orf19.837	Acetyltransferase
CA1231	1.4	1.1	0.9	1.0	0.9	0.9	IPF11817	orf19.4981	unknown function
CA0470	1.4	1.0	1.2	1.1	1.1	1.0	YPT32	orf19.2622	small GTP-binding protein essential for Golgi function (by homology)
CA3578	1.4	1.3	1.0	1.0	29.5	10.7	IPF11105	orf19.2262	probable quinone oxidoreductase
CA3729	1.4	1.0	1.1	1.0	1.1	1.0	IPF11901	orf19.4179	unknown function
CA0317	1.4	1.3	0.6	0.9	0.8	0.8	SSD1	orf19.3959	Protein phosphatase (by homology)
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 ligase (by homology)
CA1011	1.4	1.2	1.2	1.2	1.0	0.9	SRP101	orf19.3952	signal recognition particle receptor, alpha chain (by homology)
CA5338	1.4	1.0	0.7	1.0	1.2	0.8	IPF889	orf19.7213	ATP-dependent RNA helicase (by homology)
CA1429	1.4	1.1	1.2	1.0	0.9	1.0	IPF15123	orf19.5748	unknown function
CA5618	1.4	2.2	1.0	1.0	1.0	1.1	LEU2	orf19.7080	isopropyl malate dehydrogenase
CA3274	1.4	0.9	0.9	1.0	1.1	0.9	IPF12227.3f	orf19.6308	unknown function, 3-prime end
CA6001	1.4	1.2	1.1	1.1	4.2	3.8	IPF662	orf19.7601	unknown function
CA2766	1.4	1.0	1.1	1.1	1.0	0.8	IPF18416.5	orf19.5631	unknown function
CA3250	1.4	1.0	0.7	1.0	1.1	1.0	IPF4716	orf19.3735	unknown Function
CA2457	1.4	0.8	1.2	1.0	1.0	1.4	MCR1	orf19.3507	NADH-cytochrome-b5 reductase (by homology)
CA1493	1.4	0.8	1.3	1.0	0.3	0.7	FTH2	orf19.3227	iron transporter (by homology)
CA1609	1.4	1.0	1.1	1.0	1.1	0.9	TES11	orf19.4121	Thiosterase (by homology)
CA1830	1.4	0.8	0.8	1.1	1.1	0.9	IPF17177.5f	orf19.5185	similar to Saccharomyces cerevisiae Srm1p regulator of chromosome condensation, 5-prime end
CA3397	1.4	1.0	1.6	1.1	0.4	0.6	IPF13618	orf19.3972	unknown function
CA2131	1.4	2.6	0.9	1.0	1.0	1.1	IDP1	orf19.5211	isocitrate dehydrogenase, cytosolic (by homology)
CA1221	1.4	1.0	1.2	1.1	1.2	1.0	IPF14872	orf19.4133	unknown function
CA4399	1.4	1.7	1.2	1.3	1.1	3.8	PRA1	orf19.3111	pH-regulated antigen
CA1810	1.4	1.7	1.0	1.0	14.0	17.2	FDH2	orf19.1117	Formate dehydrogenase (by homology)
CA1702	1.4	0.7	1.6	1.0	0.7	0.9	HEL1	orf19.702	DNA helicase I (by homology)
CA2845	1.4	1.3	0.8	1.1	1.4	1.1	IPF10782	orf19.5730	unknown function
CA5389	1.4	1.0	0.8	1.1	1.0	1.1	IFA13	orf19.931	unknown function
CA2151	1.4	1.2	0.8	0.7	1.1	1.0	ERC2	orf19.6023	ethionine resistance protein (by homology)
CA4352	1.4	1.1	1.1	1.0	1.3	1.0	IPF3642	orf19.6726	Unknown function
CA2052	1.4	1.1	1.0	1.1	1.4	1.0	IPF11027	orf19.5722	unknown function
CA2638	1.4	0.8	0.6	0.8	1.4	3.2	GAP3	orf19.4304	General amino acid permease (by homology)
CA2199	1.4	1.4	1.0	1.0	0.7	0.6	IPF8113	orf19.2938	unknown function
CA0089	1.4	0.8	1.4	0.9	0.4	0.8	MRPL3	orf19.5064	ribosomal protein of the large subunit, mitochondrial (by homology)
CA2345	1.4	1.5	0.9	0.8	1.0	1.0	HNT1	orf19.2341	similarity to protein kinase C inhibitor-I (by homology)
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)
CA0499	1.4	1.0	0.9	1.0	1.0	1.1	IFA9	orf19.2663	unknown function
CA1517	1.4	1.1	0.8	0.9	0.5	0.6	IPF11045	orf19.4798	unknown function
CA5729	1.4	1.2	1.0	0.9	1.0	1.0	UBA1	orf19.7438	Ubiquitin-activating enzyme (by homology)
CA3679	1.4	1.1	0.7	0.9	1.2	0.8	IPF20142	orf19.730	unknown function
CA0012	1.4	3.0	0.9	1.0	0.5	0.9	IPF19448.5f	orf19.6019	similar to Saccharomyces cerevisiae Lro1p lecithin cholesterol acyltransferase-like gene
CA1821	1.4	1.3	0.8	0.9	0.8	1.0	IPF9527	orf19.4269	unknown function
CA1596	1.4	1.0	1.5	1.0	1.0	1.0	FAA21	orf19.272	long-chain-fatty-acid-CoA ligase (by homology)
CA4484	1.4	1.1	0.6	1.1	1.1	1.3	HEM15	orf19.1880	ferrochelatase precursor (by homology)
CA0176	1.4	1.3	1.0	1.0	0.6	0.8	IPF11388	orf19.652	unknown function

CA0958	1.4	1.5	1.0	1.0	0.7	0.9	SEC24	orf19.4732	component of COPII coat of ER-Golgi vesicles(by homology)
CA0393	1.4	1.1	1.0	1.1	1.7	1.6	IPF12758.3f	orf19.333.2	unknown function, 3-prime end
CA2806	1.4	1.0	0.8	1.0	1.0	1.0	IPF11702	orf19.5780	unknown function
CA1744	1.4	1.2	1.0	1.1	0.9	1.0	IPF10889	orf19.5052	unknown function
CA4473	1.4	1.2	0.9	1.0	1.0	1.1	IPF6447	orf19.1897	unknown function
CA4914	1.4	0.8	1.7	1.2	0.9	2.3	IPF1428	orf19.6054	Similar to ubiquitination protein Bul1p (by homology)
CA2914	1.4	1.0	0.8	1.0	1.6	1.1	IFA17.5f	orf19.4512	unknown function, 5-prime end
CA2413	1.4	1.1	1.9	0.9	0.8	1.0	IPF13756.5f	orf19.4480	unknown function, 5-prime end
CA3334	1.4	2.5	1.3	1.1	4.1	4.0	ALP1	orf19.2337	amino-acid permease (by homology)
CA5040	1.4	2.5	0.8	0.8	0.9	0.9	BAT22	orf19.6994	branched chain amino acid aminotransferase (by homology)
CA4962	1.4	1.1	1.0	1.1	1.3	1.0	TRL1	orf19.6511	tRNA ligase
CA2141	1.4	1.3	1.0	0.7	0.7	0.8	IPF19664	orf19.2511	unknown function
CA3527	1.4	2.1	1.5	1.6	1.0	1.4	IPF9934	orf19.988	unknown function
CA3891	1.4	1.0	0.9	1.0	0.9	1.0	BUD6	orf19.5087	bud site selection protein (by homology)
CA3309	1.4	1.4	2.5	1.8	3.5	2.4	IPF8806	orf19.2308	6-phosphofructose-2-kinase (by homology)
CA1356	1.4	1.5	0.5	0.3	1.9	2.0	IPF10138	orf19.409	unknown function
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)
CA5458	1.4	1.1	1.1	1.0	0.7	1.1	IPF274	orf19.3266	unknown function
CA4539	1.4	1.0	1.3	1.0	0.9	0.9	IFQ4	orf19.1464	Unknown function
CA5339	1.4	1.0	0.9	0.9	0.7	0.7	IPF885	orf19.7214	glucan 1,3-beta-glucosidase (by homology)
CA3289	1.4	1.0	1.1	1.1	1.0	1.1	HPA3	orf19.6323	histone and other protein acetyltransferase(by homology)
CA4138	1.4	1.0	1.1	1.0	1.6	1.5	IPF11954	orf19.4234	unknown function
CA1917	1.4	1.1	1.1	0.7	0.9	0.8	IPF7479.3f	orf19.2440	unknown function, 3-prime end
CA1631	1.4	1.0	2.2	1.0	1.2	1.1	IPF19582	orf19.1028	unknown function
CA5167	1.4	1.1	1.0	1.1	0.9	1.0	ERG8	orf19.4606	Phosphomevalonate kinase (by homology)
CA4249	1.4	1.4	1.0	0.9	1.0	1.0	IPF4293	orf19.538	similar to Saccharomyces cerevisiae Gpi2p N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein
CA0851	1.4	0.9	0.9	1.1	0.7	1.0	IPF16670	orf19.1746	unknown function
CA5425	1.4	0.6	0.8	0.7	0.9	1.0	BDF1	orf19.978	sporulation protein (by homology)
CA1279	1.4	1.4	0.8	0.9	1.0	0.8	RSP5	orf19.3628	ubiquitin-protein ligase (by homology)
CA2053	1.4	1.2	0.7	1.2	3.1	4.2	IPF11029	orf19.5720	unknown function
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 polymerization (by homology)
CA5378	1.4	1.9	1.2	1.2	1.2	1.2	MPR1	orf19.7264	26S proteasome regulatory subunit by homology
CA5661	1.4	1.5	1.6	1.5	0.8	0.9	KRE6	orf19.7363	Glucan synthase subunit
CA5964	1.4	1.0	1.2	0.9	0.9	0.9	IPF963	orf19.7553	unknown function
CA2932	1.4	1.2	1.2	0.9	0.9	1.0	NHX1	orf19.4201	NA+-H+ antiporter
CA2245	1.4	1.0	1.2	1.0	1.0	1.0	IPF7409	orf19.4668	unknown function
CA0048	1.4	0.7	1.1	1.0	0.9	1.0	TIF4631	orf19.3599	mRNA cap-binding protein (by homology)
CA3551	1.4	1.0	1.4	1.1	0.7	1.1	IPF13229	orf19.3876	unknown function
CA2191	1.4	1.1	1.3	1.1	0.6	1.1	IPF9417	orf19.4775	similar to Saccharomyces cerevisiae Hsf1p heat shock transcription factor (by homology)
CA3960	1.4	1.1	0.9	0.9	0.8	0.8	IPF11236.5f	orf19.1419	similar to Saccharomyces cerevisiae Sec15p component of the exocyst complex, 5-prime end (by homology)
CA2583	1.4	1.0	0.6	1.0	3.4	1.4	IPF9445	orf19.4372	unknown function
CA5192	1.4	1.0	2.9	1.4	1.1	1.0	HOK	orf19.7004	unknown function
CA2538	1.4	1.2	1.4	0.9	0.8	1.0	NAT1	orf19.3185	Protein N-acetyltransferase subunit (by homology)
CA4192	1.4	1.2	0.9	1.0	1.3	1.1	IPF7533	orf19.4533	unknown function
CA1102	1.4	1.2	1.1	1.2	1.2	0.8	AKR1	orf19.4950	ankyrin repeat-containing protein by homology
CA0324	1.4	0.7	0.7	0.9	1.0	0.8	STT4	orf19.1814	Phosphatidylinositol-4-kinase (by homology)

CA2575	1.4	0.8	0.8	1.0	0.8	0.9	SEC31	orf19.6217	Component of the COPII coat of ER-golgi vesicles (by homology).
CA1747	1.4	1.0	1.2	1.2	1.2	1.2	IPF10884	orf19.5049	unknown function
CA4139	1.4	0.8	1.0	1.0	1.0	1.0	THR4	orf19.4233	threonine synthase (by homology)
CA5001	1.4	1.2	0.9	1.0	1.5	1.1	IPF2022	orf19.5246	unknown function
CA4528	1.4	1.3	0.9	0.9	0.4	0.7	STT3	orf19.1478	oligosaccharyl transferase (by homology)
CA3978	1.4	1.6	1.1	1.1	1.0	1.0	CPR3	orf19.1552	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homology)
CA0334	1.4	1.0	1.5	1.0	1.0	1.1	IPF19562	orf19.194	unknown function
CA1225	1.4	1.1	1.0	1.0	1.0	1.1	SPS20	orf19.4157	peroxisomal 2,4-dienoyl-CoA reductase (by homology)
CA1270	1.4	0.8	1.1	1.0	1.0	0.9	IPF13504	orf19.3156	unknown function
CA2533	1.4	1.4	0.7	1.1	1.2	1.1	IPF12790	orf19.3180	inositol polyphosphate 5-phosphatase (by homology)
CA5115	1.4	1.1	1.3	1.2	0.8	0.8	IPF1331	orf19.6416	unknown function
CA4906	1.4	1.2	1.0	1.3	0.7	0.6	MOB2	orf19.6044	Required for maintenance in ploidy
CA5763	1.4	0.9	0.8	1.1	0.9	0.8	IFF10.5f	orf19.5404	unknown function, 5-prime end
CA3260	1.4	3.1	0.7	1.2	10.8	4.4	IPF7968	orf19.2693	unknown function
CA0644	1.4	0.9	0.9	1.0	7.0	1.0	IPF17131	orf19.69	unknown function
CA4216	1.4	0.9	1.0	1.0	1.2	0.7	IPF5806	orf19.815	unknown function
CA4386	1.4	1.6	1.3	1.2	1.1	1.2	IPF12412	orf19.3125	unknown function
CA2684	1.4	1.1	1.4	1.2	0.8	1.1	IFU3	orf19.2575	Unknown function
CA4883	1.4	0.9	1.1	0.8	0.8	0.8	IPF1649	orf19.6573	similar to Saccharomyces cerevisiae Bem2p GTPase-activating protein (by homology)
CA5328	1.4	1.0	1.0	1.0	0.9	0.9	RER1	orf19.7202	Required for correct localization of Sec12p (by homology)
CA4120	1.4	4.8	1.0	1.1	1.2	1.5	SOD1	orf19.2770.1	Cu,Zn-superoxide dismutase
CA4443	1.4	0.9	1.6	1.0	1.0	1.0	IPF3535	orf19.6840	unknown function
CA3544	1.4	0.9	1.1	0.8	0.7	0.7	BPT1.3f	orf19.6382	membrane transporter of the ATP-binding cassette (ABC) superfamily, 3-prime end (by homology)
CA4311	1.4	0.9	1.1	1.0	0.9	1.0	FAA23	orf19.4114	Long-chain-fatty-acid--CoA ligase (by homology)
CA2557	1.4	0.7	0.9	1.2	0.9	1.0	PGA7	orf19.5635	mycelial surface antigen precursor (by homology to Candida gene CSA1)
CA5082	1.4	2.1	0.8	1.0	1.7	1.6	SUA70	orf19.3059	TFIIB subunit (transcription initiation factor E)(by homology)
CA5034	1.4	1.2	0.9	0.7	0.5	0.6	OST1	orf19.6988	oligosaccharyltransferase
CA1595	1.4	1.8	1.0	1.0	0.6	1.0	IPF9544	orf19.273	unknown function
CA0431	1.4	1.3	1.6	1.1	4.3	2.1	IPF7927	orf19.1340	putative aldose reductase (by homology)
CA5038	1.4	1.2	1.4	1.1	2.7	4.2	QDR2	orf19.6992	putative antibiotic resistance proteins (by homology)
CA4131	1.4	1.0	1.1	1.0	0.7	1.0	IPF6886.3f	orf19.4243	unknown function, 3-prime end
CA1874	1.4	1.6	0.5	1.1	1.2	0.9	TPK2	orf19.2277	cAMP-dependent protein kinase 2 (by homology)
CA5182	1.4	0.8	0.9	1.0	1.0	0.9	IPF11093	orf19.4621	weak similarity to pig tubulin-tyrosine ligase
CA1954	1.4	1.1	0.8	0.8	0.9	1.0	IPF3897.5f	orf19.764	unknown function, 5-prime end
CA1288	1.4	1.2	0.7	1.2	1.1	0.8	KSP1	orf19.4432	SERINE/THREONINE-PROTEIN KINASE by homology
CA0466	1.4	1.0	0.7	0.8	1.1	1.0	URA4	orf19.1977	dihydroorotase (by homology)
CA0426	1.4	0.8	1.1	0.9	0.7	0.8	CFT1	orf19.2760	pre-mRNA 3 -end processing factor CF II (by homology)
CA2170	1.4	1.0	0.9	0.8	0.8	0.8	IPF4563.53f	orf19.912	similar to saccharomyces cerevisiae Tom1p E3 ubiqitin ligase required for G2/M transition, internal fragment
CA4742	1.4	1.2	0.9	0.9	1.0	1.0	SHY1	orf19.4841	SURF homologue protein (by homology)
CA1243	1.4	1.0	0.9	1.0	0.7	1.0	IPF7922	orf19.1343	unknown function
CA0711	1.4	1.1	0.7	0.9	1.1	1.0	VMA5	orf19.2166	H+-ATPase V1 domain 42 KD subunit (by homology)
CA5248	1.4	1.0	1.1	1.3	0.9	1.0	IPF1828	orf19.5014	unknown function
CA2064	1.4	1.2	0.8	0.9	1.4	1.2	IPF13024	orf19.2646	unknown function
CA4617	1.4	1.3	0.6	1.0	1.6	1.0	STB5	orf19.3308	SIN3 binding protein (by homology)
CA4436	1.4	1.9	0.9	1.4	1.9	1.5	IPF13868	orf19.5159	unknown function
CA5480	1.4	1.0	1.1	0.9	1.1	1.1	IPF8210	orf19.5312	unknown function

CA2394	1.4	1.0	1.3	1.0	0.6	0.8	IPF6424	orf19.3535	unknown function
CA2940	1.4	1.1	0.9	1.0	0.9	1.0	IPF8318	orf19.3323	unknown function
CA1960	1.4	1.0	1.0	1.0	1.2	0.9	IPF15232	orf19.2400	unknown function
CA1532	1.4	1.5	1.3	0.9	0.7	1.0	IPF9507.3f	orf19.1217	unknown function
CA4626	1.4	1.1	1.1	0.8	1.0	0.9	MRS7	orf19.3321	suppressor splicing defects (by homology)
CA1812	1.4	0.9	5.5	1.3	0.9	1.0	IPF13879	orf19.1120	unknown function
CA1895	1.4	1.2	0.9	1.0	1.2	1.1	PRE7.3f	orf19.2755.1	subunit of 20S proteasome, exon 2 (by homology)
CA4259	1.4	0.9	1.0	1.1	0.9	1.0	CDC10	orf19.548	cell division control protein
CA3310	1.4	1.6	1.1	1.2	0.7	1.0	PFS2	orf19.2307	Polyadenylation Factor I subunit (by homology)
CA1638	1.4	1.2	1.1	1.1	1.0	0.8	GRR1	orf19.3944	Required for glucose repression and for glucose and cation transport (by homology)
CA0987	1.4	0.9	1.1	1.2	0.9	0.9	RPB140	orf19.3349	DNA-dependent RNA polymerase II RPB140
CA1367	1.4	0.9	1.1	0.8	1.1	0.8	IPF16755	orf19.4966	unknown function
CA3385	1.4	1.8	0.8	1.0	0.8	0.4	DRS23	orf19.323	Membrane-spanning Ca-ATPase (by homology)
CA4185	1.4	1.0	1.0	1.2	1.2	1.1	HNM4	orf19.2946	Choline permease-like (by homology)
CA4565	1.4	1.0	0.7	0.9	0.9	0.9	VPS35	orf19.6875	Protein-sorting protein, vacuolar (by homology)
CA0783	1.4	1.4	1.0	1.1	1.1	1.0	ACR1	orf19.3931	Succinate-fumarate transporter (by homology)
CA5837	1.4	1.1	0.8	1.0	0.9	0.9	IPF426	orf19.7491	unknown function
CA3100	1.4	1.0	1.1	0.9	2.1	1.1	IPF6594	orf19.3863	unknown function
CA5431	1.4	1.2	1.1	0.9	1.1	1.0	IPF195	orf19.3233	unknown function
CA2909	1.4	1.0	1.3	0.9	0.7	0.7	IPF11424	orf19.4518	unknown function
CA2267	1.4	1.1	0.9	0.8	0.4	0.7	IFU1.5f	orf19.2600	Unknown function, 5-prime end
CA0530	1.4	1.6	0.7	0.6	0.7	0.9			
CA3227	1.4	1.4	1.5	1.5	0.8	1.1	AAT21	orf19.6287	aspartate aminotransferase (by homology)
CA2140	1.4	1.1	1.0	0.8	0.8	0.8	IPF19665	orf19.2510	unknown function
CA1061	1.4	1.1	1.1	1.0	0.6	1.1	IPF19720	orf19.4643	unknown function
CA5684	1.4	0.8	0.8	0.8	0.7	1.0	IPF3331	orf19.7386	unknown function
CA0233	1.4	1.1	1.0	0.9	1.1	0.6	URE2	orf19.155	Nitrogen catabolite repression regulator (by homology)
CA5004	1.4	0.9	1.0	0.9	1.0	1.0	TRP3	orf19.5243	Anthranilate synthase / indole glycerol phosphate synthase (by homology)
CA1836	1.4	1.5	1.3	1.0	1.2	1.0	IPF5773	orf19.3965	unknown function
CA0096	1.4	0.9	1.0	0.9	1.3	1.1	IPF13409	orf19.751	unknown function
CA3362	1.4	1.2	0.8	0.8	0.6	0.8	IPF9789	orf19.1933	unknown function
CA5917	1.4	1.2	1.0	1.0	0.9	0.9	IPF8923	orf19.6788	unknown function
CA2755	1.4	1.0	0.7	1.0	1.7	1.1	IFA12	orf19.5619	unknown function
CA0195	1.4	1.1	1.1	1.1	1.2	1.2	IPF12688	orf19.3921	unknown function
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)
CA6110	1.4	1.0	1.1	1.2	0.9	0.9	IPF91	orf19.5943	unknown function
CA4833	1.4	1.0	0.7	1.0	2.2	1.1	IPF1216	orf19.2064	unknown function
CA3858	1.4	1.4	1.0	1.2	0.9	1.0	TRP1	orf19.6096	phosphoribosylanthranilate isomerase
CA2581	1.4	1.2	3.6	2.8	19.0	11.5	IPF9450	orf19.4370	unknown function
CA4304	1.4	1.0	0.7	0.9	3.4	1.1	IPF6649	orf19.6704	unknown function
CA3049	1.4	1.9	1.0	0.8	1.6	1.2	IPF14990	orf19.2411	unknown function
CA1705	1.3	1.3	1.2	1.1	1.4	1.1	GCN5	orf19.705	Histone acetyltransferase (by homology)
CA3845	1.3	1.0	1.0	1.0	0.9	1.1	IPF7944	orf19.6605	unknown function
CA4737	1.3	1.1	0.7	0.9	0.8	0.9	SKI3	orf19.4848	antiviral protein
CA1563	1.3	1.0	1.0	1.0	1.0	0.9	IPF13855.5	orf19.4713	unknown function
CA5544	1.3	1.1	1.0	1.2	1.0	1.1	IPF5987	orf19.7306	unknown function

CA4351	1.3	0.7	1.3	1.2	1.0	1.0	FUM12.3f	orf19.6725	Fumarate hydratase, 3-prime end (by homology)
CA3835	1.3	0.8	1.8	1.5	1.5	1.6	RTA4	orf19.6595	Protein involved in 7-aminocholesterol resistance (by homology)
CA0962	1.3	1.6	2.2	1.3	2.8	1.3	IPF9145	orf19.6245	unknown function
CA6118	1.3	1.2	0.9	0.9	0.7	0.8	IPF126	orf19.5932	unknown function
CA2030	1.3	0.8	2.9	1.1	1.4	1.6	IPF13116	orf19.3463	unknown function
CA3079	1.3	1.1	0.9	1.0	1.5	1.2	RAM2	orf19.4817	geranylgeranyltransferase type I alpha subunit
CA2362	1.3	1.0	1.1	1.1	0.6	0.7	IPF10595	orf19.1287	unknown function
CA3267	1.3	1.0	1.6	1.4	2.3	1.0	RPS620a	orf19.6300	unknown function
CA5485	1.3	1.0	0.7	0.9	0.8	0.8	RAD1.53f	orf19.5319	UV endonuclease, component of the nucleotide excision repairosome, internal fragment (by homology)
CA3172	1.3	1.2	1.1	1.0	0.9	1.0	IPF7676	orf19.1400	unknown function
CA2277	1.3	1.4	0.9	1.1	0.5	0.7	DRS21.5eo	orf19.783	Membrane-spanning Ca-ATPase (by homology)
CA4711	1.3	1.1	0.9	1.3	1.5	1.1	PHB1	orf19.6944	Prohibitin, antiproliferative protein (by homology)
CA5307	1.3	1.1	1.0	1.0	1.0	1.0	IPF2172	orf19.7177	similar to Saccharomyces cerevisiae Kap120 nuclear transport factor, member of the karyopherin family (by homology)
CA5730	1.3	1.0	1.1	1.1	1.0	1.0	HST6	orf19.7440	ATP binding cassette protein
CA1234	1.3	1.0	1.0	1.0	1.5	0.8	IPF18732	orf19.711	histidine-rich glycoprotein precursor (by homology)
CA3569	1.3	1.6	1.0	1.1	1.0	1.1	IPF3268	orf19.3136	unknown function
CA4603	1.3	1.5	1.1	1.4	0.5	0.7	IPF6230	orf19.3293	unknown function
CA4119	1.3	1.2	0.9	0.8	0.6	0.6	BEM3	orf19.2771	GTPase-activating protein for Cdc42p and Rho1p (by homology)
CA2695	1.3	0.9	1.7	1.0	0.8	1.2	SEN2	0.00	tRNA splicing endonuclease beta subunit(by homology)
CA5844	1.3	1.1	1.3	1.2	0.4	0.7	PXA1	orf19.7500	long chain fatty acid ABC transporter (by homology)
CA0086	1.3	2.8	0.5	0.8	1.4	1.1	IPF16598	orf19.137	unknown function
CA5438	1.3	1.3	0.8	0.9	0.8	0.9	IPF223	orf19.3241	unknown function
CA1236	1.3	0.8	1.1	1.0	0.9	0.9	YPT6	orf19.714	GTP-binding protein of the rab family (by homology)
CA5304	1.3	1.1	1.1	1.0	1.0	0.9	IPF2178	orf19.7173	unknown function
CA4395	1.3	1.1	0.9	1.0	1.3	1.0	EXM2	orf19.3116	EXit from Mitosis (by homology)
CA5958	1.3	1.1	1.0	1.0	1.3	0.9	PIB1	orf19.7547	phosphatidylinositol(3)-phosphate binding protein (by homology)
CA3888	1.3	1.0	0.9	1.0	0.7	1.0	IPF12967	orf19.5092	unknown function
CA4599	1.3	1.0	1.0	0.9	0.9	0.9	IPF2200	orf19.6918	Unknown function
CA4915	1.3	1.1	0.4	0.7	1.5	1.8	IPF1427	orf19.6055	Similar to ubiquitination protein Bul1p (by homology)
CA2776	1.3	0.9	1.0	0.9	1.2	1.0	IPF10124	orf19.276	Alcohol acetyltransferase (by homology)
CA0880	1.3	1.1	0.8	0.9	1.1	1.2	IPF19542.3f	orf19.372	unknown function, 3-prime end
CA4181	1.3	1.1	1.1	1.2	0.9	1.1	HOM6	orf19.2951	homoserine dehydrogenase (by homology)
CA1405	1.3	1.0	0.7	1.0	1.0	1.0	IPF19554.3f	orf19.3371	unknown function, 3-prime end
CA3812	1.3	1.0	0.9	1.0	1.0	1.1	GSL22	orf19.2495	1,3-beta-D-glucan synthase subunit
CA2966	1.3	1.0	1.3	1.0	1.1	1.2	RPC34	orf19.5608	DNA-directed RNA polymerase III (by homology)
CA2884	1.3	0.8	0.7	0.9	0.6	0.8	IPF7201	orf19.2476	similar to Saccharomyces cerevisiae Ecm5p involved in cell wall biogenesis and architecture
CA4238	1.3	1.4	0.8	0.8	0.7	0.7	PIM1	orf19.522	mitochondrial ATP-dependent protease (by homology)
CA0998	1.3	1.3	0.5	1.0	0.8	0.9	IPF12369	orf19.4368	Putative dipeptidase (by homology)
CA0641	1.3	1.3	1.0	0.7	1.2	1.0	IPF15977	orf19.4698	unknown function
CA2651	1.3	1.2	1.0	0.7	0.7	0.8	HRD3	orf19.1191	involved in HMG-CoA reductase degradation (by homology)
CA3215	1.3	0.9	1.0	0.9	0.9	0.8	HCS1	orf19.6199	putative DNA helicase A (by homology)
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 homology)
CA2782	1.3	2.0	0.8	1.2	1.9	1.5	IPF3806	orf19.285	unknown function
CA4727	1.3	1.0	1.0	1.0	1.2	0.9	IPF12253	orf19.4861	unknown function
CA3596	1.3	1.1	0.8	0.8	0.7	0.9	IPF6085	orf19.4924	unknown function
CA4377	1.3	1.0	0.9	1.0	0.8	0.9	IPF11301	orf19.5669	unknown function

CA5762	1.3	0.9	0.6	1.0	0.9	0.9	IFF10.3f	orf19.5401	unknown function, 3-prime end
CA3137	1.3	1.2	0.9	0.9	1.0	1.0	IPF8976	orf19.1369	unknown function
CA2835	1.3	1.0	0.8	0.7	0.6	1.0	IPF12091	orf19.4787	Unknown function
CA1510	1.3	1.2	0.7	1.0	1.0	1.0	IPF9973	orf19.4523	similar to Saccharomyces cerevisiae Fau1p 5,10-methenyltetrahydrofolate synthetase (by homology)
CA1564	1.3	2.1	0.9	1.0	1.5	0.9	GAD1	orf19.1153	Glutamate decarboxylase (by homology)
CA2492	1.3	2.2	1.3	1.3	1.1	1.1	IPF7224	orf19.4045	putative telomere elongation protein (by homology)
CA0933	1.3	1.1	0.8	1.0	5.3	3.2	ATM1	orf19.1077	ATP-binding cassette transporter (by homology)
CA2946	1.3	1.0	1.2	1.3	1.1	1.4	IPF6296	orf19.1966	putative methyltransferase (by homology)
CA5883	1.3	1.0	1.2	1.0	0.9	0.8	IPF2425	orf19.6827	unknown function
CA4207	1.3	1.3	1.0	1.0	1.0	0.9	YAT1	orf19.4551	carnitine acetyltransferase (by homology)
CA3786	1.3	1.3	1.1	1.0	1.4	1.2	UFD1	orf19.5833	Ubiquitin fusion degradation protein (by homology)
CA2330	1.3	1.0	1.0	1.3	0.7	0.7	RIM2	orf19.4499	mitochondrial carrier protein (by homology)
CA1071	1.3	0.9	1.0	1.0	0.8	0.9	IPF16624	orf19.2534	unknown function
CA2721	1.3	1.0	0.7	1.0	3.5	1.2	IPF4799	orf19.3342	unknown Function
CA3733	1.3	1.3	1.0	1.1	1.3	1.1	IPF11897	orf19.4183	unknown function
CA1164	1.3	1.1	0.8	0.9	1.3	0.9	ARP8	orf19.3359	actin-related protein (by homology)
CA2828	1.3	1.4	0.8	1.0	1.0	1.1	IPF17026	orf19.1325	unknown function
CA4459	1.3	0.9	1.1	0.9	0.8	0.9	NSP49.3f	orf19.6856	nucleoporin, 3-prime end (by homology)
CA0717	1.3	1.1	0.9	0.8	0.6	0.7	IPF9785	orf19.3453	unknown function
CA4482	1.3	1.2	0.8	1.1	0.7	0.9	IPF9154	orf19.1883	similar to Saccharomyces cerevisiae Ycs4p subunit of condensin protein complex (by homology)
CA5952	1.3	1.0	1.1	1.1	0.8	1.0	IPF3503	orf19.6742	similar to Saccharomyces cerevisiae Fcp1p TFIIF interacting component of CTD phosphatase (by homology)
CA4036	1.3	0.9	1.5	1.0	0.8	0.9	IPF12042	orf19.3666	unknown function
CA1794	1.3	1.2	1.5	1.1	0.9	1.1	IPF18608.3f	orf19.5208	unknown function, 3-prime end
CA5291	1.3	0.7	1.2	0.8	0.6	0.8	LOS1	orf19.7153	pre-tRNA splicing protein (by homology)
CA5164	1.3	1.1	0.9	1.1	1.2	1.0	MDH1	orf19.4602	Mitochondrial malate dehydrogenase precursor (by homology)
CA1229	1.3	1.2	1.0	0.9	0.7	0.9	MLH1	orf19.4162	DNA mismatch repair protein (by homology)
CA0991	1.3	1.0	1.0	1.1	1.1	0.7	IPF11065	orf19.1393	unknown function
CA1361	1.3	1.1	0.7	0.9	1.0	0.9	PEP5	orf19.4403	vacuolar biogenesis protein (by homology)
CA2664	1.3	0.9	1.1	1.0	0.9	0.8	IPF13370	orf19.3551	unknown function
CA3264	1.3	1.1	1.1	1.0	0.9	1.0	IPF5035	orf19.2698	unknown function
CA2491	1.3	1.3	1.0	1.0	1.0	1.0	IPF7221	orf19.4046	unknown function
CA4763	1.3	1.1	0.8	0.9	0.9	0.9	IPF9645	orf19.3995	similar to Saccharomyces cerevisiae Rim13p calpain-like cysteine protease (by homology)
CA3051	1.3	0.9	1.1	1.1	1.1	1.2	IPF13043	orf19.2408	unknown function
CA5573	1.3	1.0	0.8	0.9	0.7	0.8			
CA2453	1.3	1.0	1.3	0.9	0.6	0.7	IPF9950	orf19.3501	unknown function
CA1775	1.3	2.4	1.0	1.1	4.1	3.2	GDH2	orf19.2192	NAD-specific glutamate dehydrogenase (NAD) (by homology)
CA3832	1.3	1.1	1.0	1.0	1.3	1.0	IPF8193	orf19.6591	unknown function
CA2975	1.3	2.3	0.9	0.8	7.6	14.3	ARO9	orf19.1237	aromatic amino acid aminotransferase II(by homology)
CA5137	1.3	1.1	1.3	1.1	0.8	1.1	IPF1032	orf19.4574	similar to probable membrane protein [S. cerevisiae]
CA2350	1.3	0.9	0.8	0.9	1.0	0.6	CWH41.5eo	orf19.4421	ER glucosidase I, 5-prime end (by homology)
6672.20	1.3	1.0	1.1	0.9	0.7	0.9			
CA3057	1.3	1.5	1.0	1.2	1.5	1.2	IPF2954	orf19.4293	unknown function
CA1104	1.3	2.1	0.5	0.9	0.7	0.8	IPF18761	orf19.4947	unknown function
CA1866	1.3	1.0	1.2	1.0	1.4	0.8	IPF7647	orf19.860	unknown function
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) FALSORF=SMALLORF
CA5118	1.3	1.0	1.1	1.1	0.8	1.0	IPF1321	orf19.6413	unknown function

CA5226	1.3	1.1	0.9	0.9	0.8	0.9	RIM15	orf19.7044	Protein kinase involved in the RIM pathway (by homology)
CA1709	1.3	0.6	1.1	0.9	0.5	0.6	HOL2	orf19.4889	Multidrug-resistance protein subfamily 1 (by homology)
CA1124	1.3	1.0	1.4	1.0	1.0	1.0	UBP12	orf19.6260	ubiquitin C-terminal hydrolase (by homology)
CA0652	1.3	1.3	1.0	0.9	1.2	1.0	SHP1	orf19.2550	potential regulatory subunit for Glc7p (by homology)
CA1439	1.3	0.9	0.9	0.9	0.9	0.9	IPF19602	orf19.4488	similar to Saccharomyces cerevisiae Swi3p transcription regulatory protein (by homology)
CA0529	1.3	1.2	1.0	0.9	0.8	0.8	SMC2	orf19.3623	chromosome segregation protein (by homology)
CA2262	1.3	1.0	1.2	1.1	0.6	1.0	IPF6857	orf19.1757	putative transcriptional regulator (unknown function)
CA1380	1.3	1.0	0.8	0.8	0.7	0.8	BCS1	orf19.458	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases (by homology)
CA1639	1.3	0.7	1.9	0.9	0.8	0.7	IPF18641.5f	orf19.1733	unknown function, 5-prime end
CA5648	1.3	1.2	1.2	1.1	0.9	1.1	UBC6	orf19.7347	E2 ubiquitin-conjugating enzyme (by homology)
CA2977	1.3	0.9	0.4	0.5	1.4	0.8	HOM3	orf19.1235	Aspartokinase (by homology)
CA0593	1.3	1.6	1.0	0.8	1.2	1.2	ARP6	orf19.4904	actin-related protein (by homology)
CA1192	1.3	1.0	0.7	0.9	1.0	1.0			
CA3668	1.3	1.3	0.9	2.1	0.8	0.8	DPP3	orf19.6459	Diacylglycerol Pyrophosphate Phosphatase by homology
CA3131	1.3	0.9	2.2	1.1	1.3	1.4	IPF8910	orf19.1362	unknown function
CA4118	1.3	1.8	1.1	1.0	1.2	0.8	IPF11952	orf19.2772	similar to Saccharomyces cerevisiae Hos3p putative histone deacetylase (by homology)
CA2882	1.3	0.9	1.2	0.8	0.6	0.8	STE13	orf19.5851	type IV dipeptidyl aminopeptidase (by homology)
CA5077	1.3	1.3	1.0	1.2	1.0	1.2	YPT1	orf19.3052	GTP-binding protein of the rab family (by homology)
CA3394	1.3	1.2	0.9	1.0	0.9	0.9	IPF6747	orf19.314	similar to Saccharomyces cerevisiae Stb2p involved Sin3p binding (by homology)
CA3621	1.3	1.0	0.9	0.9	0.8	1.0	IPF8942	orf19.204	unknown function
CA6076	1.3	0.8	1.3	1.2	1.2	1.0	PAC10	orf19.5985	Non-native Actin Binding Complex Component (by homology)
CA3387	1.3	3.6	0.8	1.0	3.3	0.9	MUP3	orf19.321	Very low affinity methionine permease
CA2365	1.3	0.8	1.4	1.1	0.6	0.9	CKS1	orf19.1282	cyclin-dependent kinases regulatory subunit (by homology)
CA4289	1.3	0.7	2.5	1.3	0.8	1.0	IPF6665	orf19.6686	unknown function
CA5294	1.3	1.0	0.9	0.9	0.7	1.0	IPF1952	orf19.7157	unknown function
CA4007	1.3	1.5	1.1	1.1	0.9	1.1	LAP41	orf19.1628	aminopeptidase yscl precursor (by homology)
CA2094	1.3	1.1	0.7	0.8	1.5	1.4	IPF11493	orf19.2393	unknown function
CA5503	1.3	1.5	1.1	1.0	1.2	1.1	DSK2	orf19.5345	ubiquitin-like protein (by homology)
CA3947	1.3	1.1	0.9	1.1	0.9	0.9	IPF14768	orf19.1994	unknown function
CA0044	1.3	1.0	0.9	0.7	1.1	1.5	IPF17347	orf19.6492	unknown function
CA0954	1.3	1.1	0.9	1.0	0.8	0.7	IPF13162	orf19.1142	unknown function
CA5188	1.3	1.3	1.2	1.0	1.5	1.1	TAP42	orf19.4626	Component of the Tor signaling pathway (by homology)
CA2788	1.3	1.3	0.9	1.1	1.1	1.2	RAD26	orf19.607	DNA repair and recombination protein (by homology)
CA3732	1.3	0.9	0.8	1.0	1.1	0.9	IPF11898	orf19.4182	unknown function
CA2632	1.3	1.1	1.1	1.1	3.6	1.7	NAR1	orf19.4757	Yeast nuclear architecture related protein (by homology)
CA3890	1.3	1.0	0.9	1.0	1.0	0.8	TERT2	orf19.5089	telomerase reverse transcriptase 2
CA0245	1.3	1.0	1.4	0.9	0.7	0.8	POL5.5f	orf19.5597	DNA polymerase V, 5-prime end (by homology)
CA4463	1.3	1.1	1.0	1.0	0.6	0.8	PIS1	orf19.6860	CDP diacylglycerol--inositol 3-phosphatidyltransferase (by homology)
CA1611	1.3	1.0	0.7	1.0	0.8	1.0	SPO72	orf19.4119	required for sporulation (by homology)
CA5927	1.3	0.9	0.8	0.8	0.6	0.6	DRS22	orf19.6778	Membrane-spanning Ca-ATPase (by homology)
CA0030	1.3	1.1	1.0	0.9	1.2	0.8	IPF17790.5	orf19.48	unknown function, 5-prime end
CA5207	1.3	1.0	0.8	0.9	0.9	1.1	IPF2359	orf19.7022	unknown function
CA0249	1.3	1.1	0.9	1.1	0.8	0.9	IPF19617	orf19.1350	unknown function
CA3418	1.3	0.9	1.1	1.2	0.6	0.9	IPF12777	orf19.6137	unknown function
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 homology)
CA0438	1.3	1.1	0.9	1.0	1.3	0.9	STE4	orf19.799	GTP-binding protein beta subunit of the pheromone pathway, 5-prime end (by homology)

CA3992	1.3	0.8	0.8	0.8	0.7	0.8	VAM6.3f	orf19.1568	Vacuolar carboxypeptidase Y, 3-prime end (by homology)
CA4439	1.3	0.7	0.9	1.1	0.6	0.8	IPF13865	orf19.5156	unknown function
CA2863	1.3	1.6	1.0	1.0	1.3	1.1	IPF20117	orf19.1058	unknown function
CA3730	1.3	1.1	1.0	1.0	1.2	1.1	IPF11900	orf19.4180	unknown function
CA5027	1.3	1.0	1.1	0.9	0.9	0.8	IPF2999	orf19.6981	unknown function
CA1428	1.3	0.8	1.2	1.1	0.7	0.8	MRP4	orf19.5747	Ribosomal protein of the small subunit mitochondrial (by homology)
CA0531	1.3	1.0	0.9	1.0	0.9	0.7	UBC1	orf19.1085	ubiquitin-conjugating enzyme by homology
CA0106	1.3	1.1	1.0	0.9	1.2	0.9	IPF16308	orf19.3851	unknown function
CA2022	1.3	0.8	1.2	0.9	0.7	1.0	CBK1	orf19.4909	serine/threonine protein kinase (by homology)
CA2902	1.3	0.9	1.3	0.9	0.9	0.9	HRR25	orf19.3476	casein kinase I (by homology)
CA4349	1.3	0.7	1.4	1.0	1.1	1.0	FUM12.5f	orf19.6724	Fumarate hydratase, 5-prime end (by homology)
CA0140	1.3	1.1	0.7	0.8	1.0	0.9	MDM1.3	orf19.2565	intermediate filament protein, 3-prime end (by homology)
CA3838	1.3	1.3	0.9	1.0	1.1	1.1	LAS17	orf19.6598	actin assembly factor (by homology)
CA2747	1.3	1.0	1.1	1.0	3.4	1.1	IPF11467	orf19.2367	unknown function
CA4348	1.3	1.0	1.1	0.8	0.5	0.8	IPF3638	orf19.6723	unknown function
CA3868	1.3	1.9	1.1	1.1	0.8	1.0	CCT1	orf19.401	component of chaperonin-containing T-complex (by homology)
CA2563	1.3	1.0	1.0	1.1	1.0	0.6	ECM7	orf19.5643	cell wall biogenesis and architecture (by homology)
CA0364	1.3	1.3	1.4	1.4	0.9	0.9	IPF15983	orf19.1525	unknown function
CA4644	1.3	1.2	0.9	1.1	1.3	1.0	IPF1497	orf19.351	unknown function
CA0114	1.3	1.3	1.2	1.1	1.3	1.1	SSU72	orf19.2402	suppressor of cs mutant of sua7(by homology)
CA0678	1.3	1.2	0.8	1.5	0.9	1.0	IPF13094	orf19.1183	unknown function
CA2113	1.3	1.3	1.2	0.8	0.8	1.2	ATP12	orf19.3686	F1F0-ATPase complex assembly protein (by homology)
CA0746	1.3	1.0	1.1	0.9	1.1	1.0	IPF14921	orf19.1527	unknown function
CA4762	1.3	1.0	1.0	1.0	0.5	0.6	IPF9647	orf19.3994	similar to Saccharomyces cerevisiae Ost3p oligosaccharyltransferase gamma subunit (by homology)
CA3273	1.3	0.9	0.9	1.1	1.0	1.1	IPF12227.5f	orf19.6307	unknown function, 5-prime end
CA0619	1.3	0.9	0.8	0.9	0.6	0.9	IPF18924	orf19.3146	unknown function
CA5757	1.3	1.2	1.1	1.1	1.3	0.9	IPF1067	orf19.5393	Putative glutamate decarboxylase (by homology)
CA2119	1.3	0.6	2.0	0.9	0.7	0.9	MTR4	orf19.1335	RNA Helicase (by homology)
CA4972	1.3	1.2	1.5	1.0	1.2	0.9	MUP1	orf19.5280	High affinity methionine permease (by homology)
CA4096	1.3	1.0	1.6	1.0	1.1	1.3	KRR1	orf19.661	involved in cell division and spore germination
CA0874	1.3	0.4	1.5	1.3	0.8	0.8	CPA1	orf19.4630	Arginine-specific carbamoylphosphate synthase, small chain
CA4309	1.3	1.1	1.0	0.9	0.8	1.0	IPF2127.3	orf19.4117	unknown function, 3-prime end
CA5474	1.3	0.9	1.8	1.1	1.0	1.6	IPF16944.3	orf19.3287	unknown function, 3-prime end
CA1161	1.3	1.1	1.3	1.2	1.0	1.0	GRX3	orf19.2727	glutaredoxin-like protein
CA3050	1.3	1.2	1.1	1.2	0.9	1.1	IPF13042	orf19.2410	similar to Saccharomyces cerevisiaeImh1p involved in vesicular transport (by homology)
CA1331	1.3	1.5	0.8	1.2	1.0	1.0	IPF11714	orf19.1150.1	unknown function
CA1886	1.3	1.1	0.9	0.9	0.7	0.9	RHO2.3f	orf19.2204.2	GTP-binding protein of the RHO subfamily, 3-prime end
CA1790	1.3	1.0	0.8	0.9	1.4	0.9	IPF13971	orf19.5204	unknown function
CA2334	1.3	1.0	0.9	1.0	1.0	1.0	ADH3.3f	orf19.4505	probable alcohol dehydrogenase, 3-prime end (by homology)
CA3985	1.3	0.9	1.0	1.1	1.0	1.0	POB3	orf19.1560	Binds DNA polymerase delta (by homology)
CA3967	1.3	1.0	1.0	1.0	0.5	0.9	IPF9377	orf19.1428	unknown function
CA3361	1.3	1.2	0.8	1.1	1.1	0.9	SNF1	orf19.1936	serine/threonine protein kinase
CA4579	1.3	1.1	1.1	1.0	14.2	12.2	IPF2234	orf19.6898	unknown function
CA3815	1.3	1.0	0.9	1.0	1.6	1.4	CYP7	orf19.2499	peptidyl-prolyl cis-trans isomerase cyp7 (ppiase)
CA2484	1.3	1.0	0.9	0.8	0.7	0.6	IPF9846	orf19.3202	unknown function
CA5744	1.3	1.1	0.8	1.0	0.8	1.0	IPF2898	orf19.7453	unknown function

CA3161	1.3	1.2	0.7	1.1	1.6	0.8	IPF13121.3	orf19.1584	unknown function, 3-prime end
CA2560	1.3	1.1	0.8	1.2	1.7	1.2	PEX5	orf19.5640	peroxisomal targeting signal receptor
CA5614	1.3	1.0	1.1	1.0	0.8	0.7	IPF522	orf19.7084	unknown function
CA4955	1.3	1.0	1.1	0.8	1.0	1.2	IPF4580	orf19.6522	putative allantoate permease (by homology)
CA3324	1.3	1.2	1.0	0.9	0.9	1.0	IPF6893	orf19.2675	unknown function
CA4936	1.3	1.1	1.3	3.1	0.5	0.6	IPF8369	orf19.6077	unknown function
CA0437	1.3	1.1	0.9	0.9	1.2	0.7	DIT1	orf19.1741	Spore wall maturation protein (by homology)
CA4899	1.3	0.9	0.6	0.7	0.8	0.9	IPF1460	orf19.6036	unknown function
CA0623	1.3	1.0	0.8	0.8	1.5	0.7	MSS4.3f	orf19.3153	phosphatidylinositol-4-phosphate 5-kinase, 3-prime end (by homology)
CA4376	1.3	1.2	1.0	1.1	0.9	1.1	IPF11307	orf19.5667	unknown function
CA2928	1.3	1.0	1.0	1.0	1.1	1.2	SME1	orf19.4205.1	Nuclear ribonucleoprotein E
CA2685	1.3	1.0	0.8	1.0	0.9	1.0	MSH4	orf19.2579	DNA mismatch repair protein
CA0103	1.3	1.0	0.7	0.9	1.3	0.9	IPF17515	orf19.749	unknown function
CA3900	1.3	0.9	1.1	0.8	1.0	1.0	IPF10092	orf19.5071	unknown function
CA0390	1.3	1.2	1.0	1.0	1.0	1.0	DCG1	orf19.244	involved in nitrogen-catabolite metabolism (by homology)
CA0884	1.3	0.9	0.4	0.9	1.7	1.1	CAN5	orf19.3641	basic amino acid permease (by homology)
CA0224	1.3	0.8	1.0	1.0	1.2	1.0	PRP31	orf19.1296	pre-mRNA splicing protein (by homology)
CA2985	1.3	0.8	1.0	0.9	0.5	0.7	SET1	orf19.6009	Chromatin regulatory protein (by homology)
CA3722	1.3	1.2	0.9	1.0	1.5	1.5	PHO13	orf19.4172	4-nitrophenylphosphatase (by homology)
CA4912	1.3	0.9	1.9	1.1	0.8	1.2	CNS1	orf19.6052	Cyclophilin Seven Suppressor (by homology)
CA2520	1.3	1.6	5.1	5.7	2.3	4.5	IPF20104	orf19.5517	alcohol dehydrogenase (by homology)
CA2283	1.3	0.7	1.6	1.7	1.3	1.2	MRT4	orf19.5550	required for mRNA decay (by homology)
CA0572	1.3	0.9	0.8	1.0	0.8	0.8	IPF14864	orf19.1804	unknown function
CA3644	1.3	1.1	1.4	1.0	0.9	0.9	IPF4126	orf19.2035	unknown function
CA3300	1.3	0.9	1.3	1.0	0.9	0.9	RTG3	orf19.2315	Probable bHLH/zip transcription factor that regulates CIT2 gene expression (by homology)
CA3048	1.3	0.8	1.0	1.1	1.4	0.9	IPF14991	orf19.2412	unknown function Unknown function
CA0606	1.3	0.9	0.9	0.8	0.9	0.8	COP1	orf19.1672	coatomer complex alpha chain of secretory pathway vesicles (by homology)
CA1795	1.3	1.1	1.0	0.9	0.6	0.9	IPF11261	orf19.5209	unknown function
CA2240	1.3	0.9	3.3	1.2	0.7	0.9			
CA3731	1.3	1.1	0.9	1.1	0.7	0.8	SPC2	orf19.4181	signal peptidase 18 kDa subunit (by homology)
CA1741	1.3	1.0	0.9	0.9	0.9	0.8	IPF12213	orf19.5057	unknown function
CA0391	1.3	1.0	1.2	1.0	1.0	0.9	DDC1	orf19.245	DNA damage checkpoint protein, delays the cell cycle at the G1/S boundary in response to UV irradiation,
CA1581	1.3	0.8	0.8	1.1	1.1	0.7	CWH41.3eo	orf19.4719	ER glucosidase I, 3-prime end (by homology)
CA3966	1.3	1.0	0.8	1.0	0.5	0.9	IPF9376	orf19.1427	unknown function
CA1699	1.3	0.9	1.4	1.0	1.0	0.9			
CA2693	1.3	1.2	1.2	0.9	0.9	1.0	IPF9173.5f	orf19.2733	similar to Saccharomyces cerevisiae Vps30p involved in vacuolar protein sorting and autophagy, 5-prime end
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)
CA3055	1.3	1.3	0.9	0.8	1.0	0.9	HIR2	orf19.4295	Histone transcription regulator (by homology)
CA3368	1.3	0.8	1.3	1.1	0.9	1.1	IPF4671	orf19.1849	unknown Function
CA2366	1.3	1.0	1.4	1.1	1.2	1.3	IPF10373	orf19.1281	unknown function
CA5695	1.3	1.7	0.9	0.8	0.7	1.1	IPF3310	orf19.7397	unknown function
CA1924	1.3	1.0	1.0	1.1	0.8	0.9	IPF9126	orf19.5537	unknown function
CA4242	1.3	1.0	1.0	0.9	0.7	0.9	SEC26	orf19.528	beta chain of secretory vesicles coatomer complex (by homology)
CA0770	1.3	1.0	1.2	0.9	0.9	0.8	IPF10963	orf19.2827	unknown
CA0508	1.3	1.0	1.0	0.9	1.0	0.8	IPF11991	orf19.3624	similar to Saccharomyces cerevisiae Msu1p 3'-5' exonuclease for RNA 3' ss-tail, mitochondrial (by homology)
CA2915	1.3	1.0	0.8	1.0	1.8	1.0	IFA17.3f	orf19.4511	unknown function, 3-prime end

CA3638	1.3	0.9	0.9	1.0	1.8	1.6	IPF9252	orf19.5134	unknown function
CA2148	1.3	1.0	1.1	1.0	1.4	0.9	AUT1	orf19.6020	essential for autophagocytosis (by homology)
CA0049	1.3	1.4	1.2	1.0	0.4	0.8	IPF3908	orf19.757	unknown function
CA4150	1.3	2.1	1.0	1.1	1.1	1.0	RPT3	orf19.5793	26S proteasome regulatory subunit
CA0773	1.3	1.0	1.0	1.2	1.0	1.1	UGA11.5f	orf19.854	4-aminobutyrate aminotransferase, exon 1 (by homology)
CA4587	1.3	1.4	1.4	0.9	2.1	1.1	IPF2223	orf19.6905	unknown function
CA3355	1.3	0.9	1.0	1.0	1.2	1.0	IPF11277	orf19.1943	unknown function
CA5255	1.3	1.2	1.1	1.1	1.0	1.0	ACT1	orf19.5007	actin (by homology)
CA4293	1.3	1.0	0.7	1.0	9.1	1.0	IFA8	orf19.6690	Unknown function
CA4678	1.3	1.1	0.6	0.9	0.8	1.0	IPF3670	orf19.894	unknown function
CA4538	1.3	1.2	1.0	1.0	1.0	1.1	IPF20018	orf19.1465	unknown function
CA5651	1.3	1.0	1.2	0.9	0.7	0.9	KIP3	orf19.7353	Kinesin-related protein required for nuclear migration (by homology)
CA2296	1.3	2.5	0.8	1.0	1.1	1.0	SCL1	orf19.5378	Proteasome subunit YC7alpha (by homology)
CA0102	1.3	1.0	1.1	1.0	1.1	0.9	IPF16695.5	orf19.736	unknown function
CA1446	1.3	0.8	1.1	0.8	0.7	0.9	YAL011	orf19.190	mitochondrial transit peptide (by homology)
CA1060	1.3	0.9	0.9	0.9	0.5	0.8	IPF11460	orf19.267	unknown function
CA5057	1.3	1.1	1.2	0.9	0.9	1.0	IPF3695	orf19.3023	similar to Saccharomyces cerevisiae Ngg1p general transcriptional adaptor or co-activator (by homology)
CA2121	1.3	2.3	0.9	0.9	1.1	1.2	IPF7930	orf19.1338	unknown function
CA5697	1.3	1.0	0.8	1.1	3.8	3.0			
CA4649	1.3	1.0	0.7	1.0	1.1	1.2	GPX4	orf19.4436	glutathione peroxidase (by homology)
CA1940	1.3	1.0	1.0	0.9	0.9	1.1	IPF7999	orf19.4190	unknown function
CA4677	1.3	0.9	0.8	1.1	1.1	1.0	HOG1	orf19.895	Ser/thr protein kinase of MAPK family
CA3370	1.3	1.0	0.8	1.0	1.0	1.0	IPF4674	orf19.1852	unknown Function
CA1838	1.3	1.6	1.1	1.1	1.4	1.3	IPF5777	orf19.3963	unknown function
CA5993	1.3	0.8	1.4	1.0	0.9	1.0	ASP1	orf19.7593	L-asparaginase (by homology)
CA4420	1.3	1.5	1.2	0.9	0.8	0.5	SSM4	orf19.5175	involved in mRNA turnover by homology
CA3318	1.3	1.1	0.8	0.8	0.5	0.6	WBP1	orf19.2298	Oligosaccharyl transferase beta subunit (by homology)
CA1046	1.3	1.0	1.0	1.1	0.9	1.0	IPF11617	orf19.1647	unknown function
CA4043	1.3	0.9	1.8	2.0	0.7	1.0	IPF5291	orf19.3674	UDP-glucose 4-epimerase (by homology)
CA0513	1.3	1.0	0.9	1.1	1.2	1.1	IPF13972	orf19.4955	unknown function
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 homology)
CA1621	1.3	1.0	0.8	1.0	1.0	1.0	IFF6	orf19.4072	unknown function
CA1203	1.3	1.1	2.2	3.4	1.4	1.6	IPF3937	orf19.868	Unknown function
CA5552	1.3	1.3	0.8	1.3	1.2	1.0	IPF5971	orf19.7316	unknown function
CA0506	1.3	0.9	1.1	1.0	0.7	1.2	IPF11988.5f	orf19.3626	unknown function, 5-prime end
CA0259	1.3	1.1	1.3	1.0	0.9	0.7	SOL1	orf19.1355	multicopy suppressor of los1-1
CA0167	1.3	1.0	1.1	1.0	0.8	0.8	IPF19160	orf19.1075	unknown function
CA5205	1.3	1.2	0.9	0.9	1.4	0.6	KEX1	orf19.7020	Carboxypeptidase-alpha (by homology)
CA1900	1.3	1.2	0.9	1.0	0.8	0.9	ARK1	orf19.2605	actin regulating serine/threonine kinase (by homology)
CA5443	1.3	1.4	1.2	0.8	1.9	0.9	IPF18105.5f	orf19.3246	unknown function, 3-prime end
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 rRNA (by homology)
CA2098	1.3	0.8	0.8	1.0	0.7	0.9	IPF11487	orf19.2387	unknown function
CA1806	1.3	0.8	1.3	1.0	1.3	1.1	IPF6329	orf19.1113	unknown function
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 homology)
CA4832	1.3	1.5	0.8	1.1	1.0	1.2	DAL2	orf19.2065	Allantoinase
CA1858	1.3	1.0	1.1	0.9	1.0	0.9	IPF15344	orf19.1500	unknown function

CA0203	1.3	1.1	0.8	1.0	0.9	0.7	MID1	orf19.3212	involved in Ca2+ influx during mating (by homology)
CA2827	1.3	0.8	0.9	0.8	0.7	0.6	RAD2	orf19.1324	structure-specific nuclease of the nucleotide excision repairosome (by homology)
CA4759	1.3	1.0	0.9	1.0	5.4	1.0	IPF9655	orf19.3988	unknown function
CA0213	1.3	0.9	1.2	1.0	0.7	0.6	CDS1	orf19.1279	CDP-diacylglycerol synthase (by homology)
CA0800	1.3	1.0	0.9	0.9	0.8	1.1	IPF14064	orf19.3494	similar to Saccharomyces cerevisiae Mcm21p involved in minichromosome maintenance
CA2650	1.3	1.9	0.6	0.8	1.0	1.0	STV1	orf19.1190	H+-ATPase V0 domain (by homology)
CA1116	1.3	2.1	1.1	1.3	0.9	1.0	CCT5	orf19.2288	T-complex protein 1, epsilon subunit (by homology)
CA5310	1.3	1.0	0.9	1.0	1.3	0.9	IPF2167	orf19.7181	unknown function
CA4430	1.3	0.6	1.0	1.2	0.9	0.9	IPF5577	orf19.5165	unknown function
CA1277	1.3	1.0	1.4	1.0	1.2	1.8	IPF10837	orf19.3630	unknown function
CA2793	1.3	0.8	1.0	1.1	0.6	1.1	TRK1.5f	orf19.600	Potassium transporter, 5-prime end
CA3313	1.3	1.5	1.3	1.2	1.0	1.0	IPF8811	orf19.2304	unknown function
CA4639	1.3	1.3	0.7	1.0	0.7	0.9	IPF1509	orf19.346	putative alanine transaminase (by homology)
CA4624	1.3	1.9	0.8	0.9	0.6	1.2	IPF5747	orf19.3318	unknown function
CA1495	1.3	0.9	1.0	0.8	0.6	0.8	IPF9686	orf19.3647	similar to Saccharomyces cerevisiae Sec8p Golgi - plasma membrane protein transport protein (by homology)
CA2883	1.3	0.9	0.7	0.8	0.6	0.9	IPF3790	orf19.5852	unknown function
CA5922	1.3	0.8	1.0	0.8	0.8	0.5	MRS6	orf19.6783	geranylgeranyltransferase regulatory subunit
CA3316	1.3	1.1	1.0	1.0	1.6	1.4	IPF8817	orf19.2301	putative proteasome subunit (by homology)
CA1620	1.3	1.4	1.3	1.0	0.8	1.0	MET10	orf19.4076	Sulfite reductase flavin-binding subunit (by homology)
CA3988	1.3	2.5	1.0	1.5	0.5	0.8	IPF7145	orf19.1564	unknown function
CA2599	1.3	1.0	0.8	0.8	1.1	0.7	IPF11176	orf19.52	similar to Saccharomyces cerevisiae Mmt2p mitochondrial iron transporter (by homology)
CA3530	1.3	0.9	1.0	0.9	1.0	1.0	IPF9926	orf19.984	alkaline phosphatase (by homology)
CA3485	1.3	1.2	0.9	1.0	0.8	1.2	IPF3213	orf19.3573	similar to Saccharomyces cerevisiae Pex6p peroxisomal assembly protein (by homology)
CA1382	1.3	0.9	0.9	0.9	0.9	0.9	IPF8421	orf19.928	unknown function
CA2243	1.3	0.9	1.1	0.9	0.5	0.9	IPF7414	orf19.4670	putative transcription factor (by homology)
CA0996	1.3	1.2	0.6	0.8	3.0	3.2	IPF10071	orf19.2283	catabolic 3-dehydroquinase (by homology)
CA3714	1.3	0.9	0.9	0.9	0.6	0.7	IPF16223	orf19.4163	unknown function
CA0507	1.3	1.4	1.0	1.0	1.0	1.0	IPF11989	orf19.3625	unknown function
CA2642	1.3	1.0	1.1	1.0	1.2	1.0	FTI1	orf19.4307	Rad52 inhibitor (by homology)
CA1258	1.3	2.2	0.9	0.9	1.8	1.2	RPN8	orf19.3168	26S proteasome regulatory subunit (by homology)
CA3898	1.3	1.9	1.1	0.9	0.8	1.0	UBA2	orf19.5074	ubiquitin-activating -like enzyme by homology
CA2644	1.3	8.1	2.0	1.4	2.1	2.0	GRP2	orf19.4309	Reductase (by homology)
CA5527	1.3	1.0	0.8	1.0	1.2	1.1	IPF2856	orf19.7285	unknown function
CA2694	1.3	1.4	1.1	1.1	1.0	0.9	IPF9171	orf19.2734	unknown function
CA0520	1.3	1.0	1.1	1.0	0.9	0.9	IPF4466	orf19.3531	unknown function
CA4982	1.3	1.4	1.0	1.1	1.0	1.0	NUT2	orf19.5268	Negative transcription regulator from artifical reporters (by homology)
CA3120	1.3	0.8	1.0	1.1	1.4	1.1	IPF5358	orf19.3007	unknown function
CA0675	1.3	0.9	0.8	1.0	1.0	0.9	IPF13098	orf19.1180	unknown function
CA4453	1.3	1.0	1.2	0.9	1.0	1.0	CHL4	orf19.6851	chromosome segregation protein (by homology)
CA1534	1.3	0.7	1.1	1.0	1.3	1.0	MAP2	orf19.1214	methionine aminopeptidase (by homology)
CA0680	1.3	0.9	0.8	0.9	1.2	0.9	IPF14511.5f	orf19.4699	unknown function, 5-prime end
CA4321	1.3	1.0	1.2	1.1	0.7	0.8	KAR3.3	orf19.4100	Kinesin-related protein, 3-prime end
CA3940	1.3	1.1	1.3	0.9	0.8	0.8	NIC96	orf19.2002	nuclear pore protein (by homology)
CA1045	1.3	1.0	1.0	1.0	0.7	0.8	IPF11620	orf19.1648	similar to Saccharomyces cerevisiae Rad50p DNA repair protein (by homology)
CA1588	1.3	0.9	1.0	1.1	0.9	0.9	SPT8	orf19.4312	transcriptional adaptor or co-activator (by homology)
CA5740	1.3	1.1	0.9	0.8	2.1	1.7	IPF20030	orf19.7450	unknown function

CA6087	1.3	1.1	0.9	0.8	0.8	0.7	YHV1	orf19.5971	unknown function
CA4721	1.3	0.9	0.8	0.9	0.7	0.6	CPP1	orf19.4866	probable protein-tyrosine phosphatase
CA0464	1.3	1.0	0.5	0.7	3.7	1.7	IPF14116	orf19.164	unknown function
CA5218	1.3	0.9	1.1	0.9	1.1	0.9	WHI2	orf19.7036	Growth regulation factor (by homology)
CA2951	1.3	2.1	0.8	1.0	0.9	1.0	SBP1	orf19.5854	RNA binding protein-like (by homology)
CA3438	1.3	1.3	1.0	1.0	0.6	0.6	IPF11330	orf19.2987	unknown function
CA1649	1.2	1.0	1.4	1.0	0.8	1.2	LAB1	orf19.5566	Lipoate biosynthesis by homology
CA2837	1.2	1.1	1.0	1.0	1.5	0.9	IPF8340	orf19.4789	unknown function
CA4616	1.2	1.7	0.5	0.9	1.3	1.2	IPF5761	orf19.3307	flavin-containing monooxigenase (by homology)
3692.20	1.2	1.2	0.8	0.9	2.2	2.1			
CA2641	1.2	1.1	1.0	1.1	1.5	1.2	IPF2929	orf19.4306	unknown function
CA2173	1.2	1.2	1.3	0.8	0.7	0.9	IPF18527	orf19.3764	unknown function
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 chromatin
CA4135	1.2	1.0	0.9	0.9	1.4	1.0	IPF20163	orf19.4239	unknown function
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 homology)
CA3676	1.2	1.3	0.9	1.0	0.9	1.1	RBP1	orf19.6452	rapamycin-binding protein
CA4999	1.2	0.9	1.1	0.9	0.8	0.9	IPF2024	orf19.5248	unknown function
CA1614	1.2	1.3	0.9	1.1	0.2	0.4	IPF18645	orf19.3216	unknown function
CA3954	1.2	1.1	0.7	0.9	1.2	1.0	YFH1	orf19.1413	Regulates mitochondrial iron accumulation (by homology)
CA1141	1.2	0.9	1.1	1.0	1.1	0.7	IPF17322.5f	orf19.4069	unknown function, 5-prime end
CA1000	1.2	1.0	1.8	0.9	1.0	0.9	IPF6011	orf19.1486	unknown function
CA4690	1.2	1.0	0.9	1.1	1.1	1.2	IPF3959	orf19.875	unknown function
CA5903	1.2	1.0	1.2	1.1	0.7	0.4	IPF5942	orf19.6803	transmembrane sugar transporter (by homology)
CA2176	1.2	0.6	1.3	0.8	0.2	0.3	CDC54	orf19.3761	cell division control protein (by homology)
CA3522	1.2	1.0	0.8	1.0	1.1	1.1	IPF20134	orf19.994	unknown function
CA1965	1.2	1.2	1.0	1.0	2.8	1.2	IPF14035	orf19.2395	Similar to serine/threonine protein kinase (by homology)
CA1117	1.2	1.2	0.7	0.9	1.1	1.1	ARP3	orf19.2289	actin related protein (by homology)
CA4717	1.2	1.0	1.4	1.0	0.8	0.6	IPF8663	orf19.6953	Unknown function
CA1839	1.2	1.2	0.7	0.9	1.0	1.2	IPF4435	orf19.4711	unknown function
CA0969	1.2	0.6	1.4	0.8	0.3	0.4	IPF9132	orf19.5541	unknown function
CA4885	1.2	1.3	1.2	1.1	1.1	2.6	IPF1636	orf19.6577	similar to Saccharomyces cerevisiae Tpo1p multidrug resistance protein
CA0296	1.2	1.0	0.9	1.0	1.4	1.0	IFA11	orf19.1596	Unknown function
CA0425	1.2	1.2	0.9	1.2	0.6	0.5	PPH21	orf19.1683	protein ser/thr phosphatase PP2A-1 (by homology)
CA2269	1.2	1.2	1.2	1.3	0.6	0.7	YOR100	orf19.2599	Putative mitochondrial carrier protein
CA1776	1.2	1.0	0.7	0.8	0.3	0.8	IPF14704	orf19.1823	unknown function
CA5893	1.2	1.1	1.0	1.1	0.9	1.0	IPF2392	orf19.6813	unknown function
CA4245	1.2	0.7	1.1	1.3	0.7	0.6	PGA21	orf19.532	unknown function
CA2489	1.2	1.0	0.8	0.8	1.0	0.9	IPF7217	orf19.4043	unknown function
CA3490	1.2	1.0	1.2	1.0	1.0	1.1	IPF3192	orf19.3565	unknown function
CA5327	1.2	1.6	0.9	0.8	0.8	0.7	SLA2	orf19.7201	Cytoskeleton assembly control protein
CA3220	1.2	1.0	0.8	1.0	0.8	0.9	IPF10001	orf19.6194	unknown function
CA3270	1.2	1.0	0.8	1.0	1.2	0.8	LYS5	orf19.6304	L-aminoadipate-semialdehyde dehydrogenase (by homology)
CA0051	1.2	0.9	1.4	1.0	0.8	0.8	IPF4443	orf19.4706	unknown function
CA5432	1.2	1.2	1.0	1.0	4.5	5.1	EBP5	orf19.3234	NADPH dehydrogenase (by homology)
CA3634	1.2	1.0	1.0	1.0	1.0	1.0	IFA25	orf19.5140	unknown function
CA4525	1.2	2.5	1.0	1.1	1.1	1.2	SEC22	orf19.479.2	synaptobrevin-type protein transport protein (by homology)

CA2868	1.2	1.4	0.8	1.0	3.0	1.0	IPF20118	orf19.2846	unknown function
CA0820	1.2	1.0	1.1	1.0	1.2	1.1	IPF12138	orf19.1950	unknown function
CA2036	1.2	1.3	1.0	0.9	1.0	0.8	MSP1	orf19.4362	40 kDa putative membrane-spanning ATPase
CA1734	1.2	1.2	0.8	0.9	0.7	0.8	IPF4988	orf19.2529	unknown function
CA4024	1.2	1.0	1.0	1.0	0.8	1.0	IPF7182	orf19.3439	unknown function
CA4416	1.2	1.1	1.3	1.0	1.5	1.3	IPF11888	orf19.5180	unknown function
CA1822	1.2	0.6	2.2	1.3	0.8	0.9	IPF9525	orf19.4268	unknown function
CA2000	1.2	1.4	0.8	1.2	1.0	1.0	IPF11796	orf19.2791	unknown function
CA3214	1.2	1.1	0.9	0.9	0.7	0.9	PUT3	orf19.6203	putative positive activator of the proline utilisation pathway
CA1212	1.2	1.0	1.0	1.0	0.8	0.8	IPF7033	orf19.131	unknown function
CA5306	1.2	1.7	1.0	1.0	1.1	1.1	NPT1	orf19.7176	Nicotinate phosphoribosyltransferase (by homology)
CA2555	1.2	0.9	0.7	1.0	1.0	1.0	IPF12105	orf19.5633	unknown function
CA4761	1.2	1.2	1.5	1.2	0.8	0.7	IPF9650	orf19.3991	lipase family protein containing serine active site (by homology)
CA2405	1.2	1.1	0.9	0.9	0.3	0.7	PGA18	orf19.301	unknown function
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 35S primary transcript, 3-prime end (by homology)
CA5658	1.2	1.1	1.1	1.0	1.0	1.0	IPF1242	orf19.7360	unknown function
CA1632	1.2	0.8	1.0	0.8	0.6	0.8	IPF10181	orf19.3938	similar to Saccharomyces cerevisiae Rsm26p protein of the small subunit of the mitochondrial ribosome (by homology)
CA1413	1.2	1.0	1.2	0.9	1.0	0.9	MTR3	orf19.168	Involved in mRNA transport (by homology)
CA2260	1.2	0.9	1.1	1.2	1.0	0.7	OST2	orf19.1761	Oligosaccharyltransferase epsilon subunit
CA4353	1.2	0.9	1.1	1.0	1.2	1.1	IPF3645	orf19.6727	similar to Saccharomyces cerevisiae Rit1p initiator tRNA phosphoribosyl-transferase (by homology)
CA0719	1.2	1.0	0.8	0.9	0.9	1.0	IPF9779.5	orf19.3456	serine/threonine protein kinase, 5-prime end (by homology)
CA2462	1.2	1.1	1.0	1.0	1.1	1.0	CDC16	orf19.1792	subunit of anaphase-promoting complex (by homology)
CA0939	1.2	0.9	1.7	1.2	1.1	1.4	DBP6	orf19.3704	RNA helicase required for 60S ribosomal subunit assembly (by homology)
CA5543	1.2	1.4	0.7	1.0	1.3	1.2	IPF5988	orf19.7305	unknown function
CA4901	1.2	1.0	1.0	1.0	1.1	1.3	IPF1457	orf19.6038	putative transcription activator (by homology)
CA0467	1.2	1.1	1.0	1.0	1.2	1.0	TRX2	orf19.1976	thioredoxin (by homology)
CA2136	1.2	1.1	0.9	0.9	0.6	0.8	VPS33	orf19.5214	VACUOLAR PROTEIN SORTING (by homology)
CA0839	1.2	1.0	1.1	1.0	1.2	1.0	IPF12492	orf19.1681	unknown function
CA3147	1.2	1.2	1.3	1.2	0.8	0.7	IPF9803	orf19.6160	unknown function
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)
CA5998	1.2	1.0	2.5	1.0	2.1	1.1	IPF670	orf19.7598	unknown function
CA3156	1.2	1.1	1.3	1.1	1.1	1.1	IPF14455	orf19.1589	similar to Saccharomyces cerevisiae Rrn7p polymerase I specific transcription initiation factor (by homology)
CA2320	1.2	1.0	0.8	1.1	1.0	1.1	SER1	orf19.5484	phosphoserine transaminase (by homology)
CA0345	1.2	1.7	1.0	1.0	1.0	0.9	ACH1	orf19.3171	acetyl-coenzyme-A hydrolase (by homology)
CA2255	1.2	1.0	1.1	1.1	2.1	1.6	CYC3	orf19.1957	cytochrome C heme lyase
CA0740	1.2	2.8	1.0	1.0	1.3	1.5	UMP1	orf19.3140.1	proteasome maturtion factor (by homology)
CA2095	1.2	1.0	0.7	0.8	1.6	1.6	IPF11492	orf19.2392	unknown function
CA5000	1.2	1.0	0.9	0.9	1.0	1.0	IPF2023	orf19.5247	unknown function
CA0384	1.2	1.0	1.0	0.9	0.9	0.9	PCL1	orf19.2649	cyclin, G1/S-specific (by homology)
CA4986	1.2	1.1	1.0	0.9	1.1	1.1	SER33	orf19.5263	Phosphoglycerate dehydrogenase (by homology)
CA2309	1.2	1.1	0.8	1.0	0.9	0.9	IPF9875	orf19.1374	unknown function
CA4606	1.2	1.0	0.9	1.0	0.8	0.9	IPF6224	orf19.3296	unknown function
CA1409	1.2	0.8	1.2	1.0	0.6	0.6	SPT16	orf19.2884	general chromatin factor (by homology)
CA3816	1.2	0.9	1.1	1.0	0.9	1.0	IPF4017	orf19.2500	unknown function
CA0269	1.2	0.8	0.8	0.8	1.1	1.0	PUF2.5f	orf19.4263	RNA-binding protein 5 prime end (by homology)
CA3917	1.2	1.1	0.8	1.0	1.1	1.0	IPF3273	orf19.4382	similar to Saccharomyces cerevisiae Ret3p coatomer complex zeta chain (by homology)

CA2749	1.2	1.0	1.0	1.0	1.6	1.4	IPF11465	orf19.2369	unknown function
CA0662	1.2	1.0	0.8	1.0	0.5	0.7	SPC97	orf19.708	spindle pole body component (by homology)
CA1158	1.2	1.6	0.8	0.6	1.6	1.8	IPF13275	orf19.4127	unknown function
CA0841	1.2	1.1	1.1	0.9	1.0	1.0	IPF15638	orf19.1050	unknown function
CA0779	1.2	1.0	1.0	0.9	1.3	1.1	IPF20065	orf19.3491	similar to Saccharomyces cerevisiae Yku70p high-affinity DNA-binding protein (by homology)
CA5046	1.2	0.9	1.0	0.8	1.0	1.0	YCK2	orf19.7001	casein kinase I (by homology)
CA5442	1.2	1.3	0.9	0.7	2.3	1.1	IPF18105.3f	orf19.3245	unknown function, 3-prime end
CA0260	1.2	0.7	1.7	0.9	0.4	0.7	IPF13683	orf19.2547	unknown function
CA3419	1.2	0.8	1.0	0.7	0.9	0.8	IPF12778	orf19.6136	ribosomal protein, mitochondrial (by homology)
CA1654	1.2	1.3	1.3	0.9	1.5	1.2	IPF19660	orf19.5559	unknown function
CA3557	1.2	0.9	1.1	1.0	0.9	1.0	IPF7763	orf19.3886	unknown function
CA2446	1.2	1.0	0.9	1.1	1.3	1.0	IPF2582	orf19.5504	unknown function
CA4385	1.2	1.7	1.1	1.0	0.9	1.0	CCT6	orf19.3126	component of chaperonin-containing T-complex (zeta subunit)(by homology)
CA3408	1.2	1.4	0.9	1.1	1.1	1.0	IPF9407	orf19.6151	similar to Saccharomyces cerevisiae Arc15p subunit of the ARP2/3 complex (by homology)
CA5995	1.2	1.0	1.3	1.1	1.3	1.0	IPF676	orf19.7595	unknown function
CA4872	1.2	0.8	1.1	1.0	0.6	0.7	SEC231	orf19.6558	Component of COPII coat (by homology)
CA3999	1.2	1.0	1.2	1.1	0.9	1.1	IPF10447	orf19.1637	unknown function
CA5751	1.2	1.3	0.9	0.9	0.5	0.7	VPS8	orf19.5387	Vacuolar sorting protein (by homology)
CA5183	1.2	1.0	1.1	0.9	1.0	0.9	IPF11090.5f	orf19.4622	weak similarity to glutenin, 5 prime end
CA5904	1.2	1.0	0.9	0.8	0.8	0.8	IPF5944	orf19.6802	Unknown function
CA2179	1.2	1.4	0.7	0.9	0.6	0.9	FAB1	orf19.1513	phosphatidylinositol 3-phosphate 5-kinase (by homology)
CA1931	1.2	1.0	0.9	0.8	0.7	0.7	IPF3905	orf19.759	similar to Saccharomyces cerevisiae Sec21p coatomer complex gamma chain
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 mitochondria (by homology)
CA2096	1.2	1.0	0.9	1.0	1.6	1.1	IPF11491	orf19.2391	unknown function
CA4368	1.2	1.7	1.1	1.1	0.9	1.1	PEX10.3f	orf19.5660	peroxisomal assembly protein, 3-prime end (by homology)
CA1320	1.2	1.0	1.0	1.1	0.9	1.0	IPF3143	orf19.4221	similar to Saccharomyces cerevisiae Orc4p subunit of origin recognition complex (by homology)
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)
CA5380	1.2	0.9	0.9	1.0	1.3	1.0	IPF5224	orf19.7267	unknown function
CA4333	1.2	1.6	1.2	1.1	1.4	1.2	IPF2083	orf19.4086	unknown function
CA5819	1.2	1.0	0.7	1.0	1.1	1.0	IFF4	orf19.7472	Unknown function
CA0483	1.2	1.5	1.1	0.6	1.6	1.3	SEC9	orf19.117	transport protein (by homology)
CA1999	1.2	0.9	1.9	1.0	0.8	1.0	IPF19513	orf19.6476	unknown function
CA1483	1.2	1.0	0.8	1.1	1.0	1.0	YHC3	orf19.4059	involved in cellular pH homeostasis (by homology)
CA0560	1.2	1.0	0.9	1.0	1.2	2.1	GPX3	orf19.87	glutathione peroxidase (by homology)
CA1743	1.2	1.5	1.0	1.0	0.9	1.1	IPF12209	orf19.5053	similar to Saccharomyces cerevisiae Eco1p involved in sister chromatid cohesion during replication (by homology)
CA0420	1.2	1.0	1.1	0.9	1.0	1.0	IPF9048	orf19.2229	unknown function
CA5743	1.2	1.0	1.0	1.0	0.8	1.0	IPF2895	orf19.7452	unknown function
CA3675	1.2	1.0	1.0	0.9	0.6	0.9	IPF19529.3f	orf19.6453	unknown function, 3-prime end
CA5141	1.2	1.1	1.1	1.0	1.0	1.1	CYT2	orf19.4578	holocytochrome-c1 synthase (by homology)
CA4012	1.2	1.1	0.9	0.9	0.8	0.7	GPA2	orf19.1621	nucleotide-binding regulatory protein GPA2
CA4910	1.2	1.0	0.9	1.0	0.9	0.7	IPF1437	orf19.6048	unknown function
CA4503	1.2	1.1	1.1	1.1	1.0	0.8	SRV2	orf19.505	adenylate cyclase-associated protein homolog
CA5272	1.2	1.0	1.0	0.9	0.8	1.0	IPF1770	orf19.4988	unknown function
CA5813	1.2	0.9	1.0	1.0	1.1	1.1	IPF2522	orf19.7460	unknown function
CA4299	1.2	1.0	0.8	0.9	1.0	1.0	IPF2598	orf19.6698	unknown function
CA1268	1.2	0.8	1.6	1.0	0.6	0.6	IPF14693	orf19.3159	unknown function

CA0241	1.2	0.9	1.1	0.9	0.9	0.9	IPF15630	orf19.3470	unknown function
CA2754	1.2	1.1	0.8	0.9	1.1	0.9	VPS45	orf19.5618	vacuolar protein sorting-associated protein (by homology)
CA3047	1.2	1.1	0.8	0.8	0.6	0.8			
CA3512	1.2	0.9	1.0	1.0	1.3	1.1	IPF11247	orf19.6359	unknown function
CA1800	1.2	1.0	1.0	1.0	1.0	1.0	IPF11445	orf19.2921	similar to Saccharomyces cerevisiae Pac2p involved in the stabilization of microtubles (by homology)
CA2450	1.2	1.0	0.7	1.0	3.8	1.0	IPF2589	orf19.5508	unknown function
CA6014	1.2	1.0	1.5	1.1	0.6	1.1	TRS31	orf19.7615	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic (by homology)
CA5465	1.2	1.0	1.1	1.1	1.3	1.4	IPF285.3f	orf19.3274	unknown function, 3-prime end
CA5537	1.2	2.4	0.9	1.1	0.3	0.7	CHS2	orf19.7298	Chitin synthase
CA2044	1.2	0.7	1.9	1.1	0.9	0.9	IPF10668	orf19.2930	unknown function
CA1841	1.2	0.8	0.9	1.3	0.7	0.9	CCA1	orf19.4705	tRNA nucleotidyltransferase (by homology)
CA2261	1.2	0.8	0.9	0.9	1.1	0.6	RAS1	orf19.1760	GTP-binding protein (by homology)
CA2536	1.2	1.1	1.0	1.1	0.9	1.1	IPF20107	orf19.3183	unknown function
CA3651	1.2	0.9	1.0	1.1	1.0	1.0	MSS1	orf19.2042	Mitochondrial GTPase involved in expression of COX1 (by homology).
CA1792	1.2	1.3	1.2	1.2	1.1	1.2	IPF13966	orf19.5206	unknown function
CA4961	1.2	1.2	0.7	1.1	0.8	1.0	IPF3916	orf19.6512	similar to Saccharomyces cerevisiae Exo70p 70 kDa exocyst component protein (by homology)
CA3493	1.2	1.0	1.1	1.0	0.7	0.8	CDC7	orf19.3561	serine/threonine protein kinase (by homology)
CA5035	1.2	1.0	1.0	1.1	1.1	1.0	IPF4531	orf19.6989	unknown function
CA1197	1.2	1.0	0.6	0.9	3.6	1.1			
CA1157	1.2	1.0	1.4	1.1	0.8	2.8	PZF1	orf19.4125	TFIIIA (transcription initiation factor) (by homology)
CA1938	1.2	0.7	1.8	1.1	0.8	0.8	NMD5	orf19.4188	putative Nam7p/Upf1p-interacting protein (by homolgy)
CA3595	1.2	1.2	0.9	1.0	1.0	1.0	IPF6079	orf19.4923	putative permease (by homology)
CA1378	1.2	1.1	0.8	1.0	0.9	0.9	ERK2	orf19.460	mitogen-activated protein kinase (MAP kinase)
CA5222	1.2	0.8	1.3	0.8	0.7	0.7	IPF3079	orf19.7041	similar to Saccharomyces cerevisiae Pta1p pre-tRNA processing protein (by homology)
CA4298	1.2	1.2	1.0	0.9	0.9	1.0	TIM9	orf19.6696	Mitochondrial inner membrane translocase (by homology)
CA2431	1.2	1.1	1.0	1.0	1.5	1.2	IPF12951	orf19.3401	unknown function
CA5564	1.2	1.6	0.7	0.9	1.0	0.9	IPF1980	orf19.7328	unknown function
CA4530	1.2	1.0	1.0	0.9	1.0	1.0	IME4	orf19.1476	positive transcription factor for IME2 (by homology)
CA6125	1.2	0.9	1.0	1.0	1.4	1.0	IPF138	orf19.5925	unknown function
CA0440	1.2	1.2	0.7	0.7	0.9	0.9			
CA2516	1.2	1.1	1.3	1.0	1.0	1.1	IPF4301	orf19.5513	unknown function
CA4695	1.2	1.9	0.9	1.4	1.3	1.0	IPF4229	orf19.6923	unknown function
CA4911	1.2	1.0	1.3	1.0	0.7	0.9	IPF1435	orf19.6049	unknown function
CA5006	1.2	1.2	1.1	0.7	0.5	0.8	IPF12584	orf19.5241	unknown function
CA0133	1.2	1.1	1.1	1.0	0.8	1.0	IPF3746	orf19.1007	unknown function
CA5018	1.2	1.1	0.8	0.9	0.8	0.7	IPF7558	orf19.6971	unknown function
CA1397	1.2	0.6	1.0	0.9	0.9	0.8	TOM72	orf19.3700	mitochondrial import receptor (by homology)
CA5532	1.2	1.2	0.9	1.1	0.9	1.0	ARP2	orf19.7292	actin-like protein (by homology)
CA4931	1.2	1.0	1.1	1.0	0.8	0.9	IPF8378	orf19.6072	unknown function
CA3059	1.2	1.8	1.2	1.1	6.9	4.2	TRR1	orf19.4290	Thioredoxin reductase (by homology)
CA0735	1.2	1.6	0.8	1.9	1.1	1.1	IPF8995	orf19.4633	unknown function
CA1837	1.2	1.4	1.3	1.0	1.1	0.9	IPF5776	orf19.3964	ash2-trithorax family protein (by homology)
CA3908	1.2	1.0	1.0	1.0	1.1	1.0	IPF3301	orf19.4394	unknown function
CA3974	1.2	1.0	0.8	0.9	0.9	1.0	IPF6507	orf19.1546	unknown function
CA5913	1.2	1.0	1.2	0.9	1.0	1.0	RRD1	orf19.6792	Phosphotyrosyl phosphatase activator involved in cell cycle progression (by homology)
CA4029	1.2	1.0	1.0	1.0	1.1	1.1	IPF7171.5f	orf19.3434	unknown function, 5-prime end

CA0248	1.2	1.1	1.0	0.9	1.2	1.0	IPF7262	orf19.2789	unknown function
CA5797	1.2	0.9	8.7	8.2	0.7	1.0	IPF4182	orf19.5446	unknown function
CA5597	1.2	0.9	0.9	0.9	1.5	1.0	IPF563	orf19.7103	unknown function
CA0149	1.2	1.5	1.3	1.1	0.8	1.1	VPS34	orf19.6243	1-phosphatidylinositol 3-kinase
CA2172	1.2	0.7	0.7	1.1	0.3	0.5	IPF15377	orf19.3765	probable membrane protein involved in bipolar budding (by homology)
CA0363	1.2	1.0	1.2	1.0	1.0	1.0	SPR3	orf19.1524	sporulation-specific septin (by homology)
CA4194	1.2	1.0	1.0	1.0	0.4	0.7	PTR3	orf19.4535	transcriptional regulator (by homology)
CA3671	1.2	1.0	1.2	1.0	1.0	0.9	IPF13933	orf19.6457	unknown function
CA3948	1.2	1.3	1.0	0.9	1.2	1.2	RPN9	orf19.1993	26S proteasome regulatory particle (by homology)
CA5752	1.2	1.0	0.8	1.1	1.4	0.8	IPF1055	orf19.5388	unknown function
CA2891	1.2	1.8	1.2	2.4	18.5	1.9	IFS4	orf19.2467	Pirin protein (by homology)
CA2482	1.2	0.9	1.2	1.0	0.7	1.0	IPF9841	orf19.3204	unknown function
CA4398	1.2	0.9	1.0	1.0	1.1	1.4	ZRT1	orf19.3112	high-affinity zinc transport protein (by homology)
CA4522	1.2	1.9	1.0	0.9	1.1	1.0	RPT4	orf19.482	26S proteasome regulatory subunit (by homology)
CA2698	1.2	2.5	1.1	0.8	0.9	1.0	SUL1	orf19.2738	High-affinity sulfate transport protein (by homology)
CA1793	1.2	1.2	2.2	1.1	0.9	1.0	IPF18608.5f	orf19.5207	unknown function, 5-prime end
CA5330	1.2	1.0	1.0	1.0	2.1	1.1	IPF2130	orf19.7204	similar to 2-nitropropane dioxygenases
CA4217	1.2	1.5	0.6	0.8	1.1	4.4	IPF5809	orf19.816	unknown function
CA4442	1.2	1.1	1.4	1.2	1.1	1.1	IPF3537	orf19.6838	unknown function
CA5031	1.2	1.0	1.0	1.0	1.1	1.0	IPF20023	orf19.6985	similar to Saccharomyces cerevisiae Tea1p activator of Ty1 enhance(by homology)
CA4720	1.2	1.5	1.0	1.0	1.3	1.0	ECM18	orf19.6958	Involved in cell wall biogenesis and architecture (by homology)
CA0445	1.2	1.3	1.1	0.7	0.9	0.9	IPF17429.5f	orf19.74	similar to Saccharomyces cerevisiae Sec5p required for exocytosis, 5-prime end
CA5556	1.2	1.0	0.8	0.9	1.0	1.0	LIP7	orf19.7320	Secretory lipase
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)
CA0944	1.2	1.0	0.7	1.0	1.0	1.0	IPF10280	orf19.1266	unknown function
CA1651	1.2	1.3	0.9	1.0	1.1	1.1	RNH12	orf19.5564	Ribonuclease H (by homology)
CA5231	1.2	0.8	1.1	1.1	1.0	1.0	IPF10422	orf19.5033	Similar to APG12, component of the autophagic system
CA5220	1.2	1.1	1.0	0.9	1.0	0.9	MVP1	orf19.7038	Required for vacuolar protein sorting (by homology)
CA1549	1.2	0.8	0.9	0.9	0.8	0.9	IPF8744	orf19.4278	unknown function
CA4995	1.2	1.0	0.9	1.0	1.0	0.9	IPF2032	orf19.5253	Ser/thr protein kinase (by homology)
CA2315	1.2	0.7	1.0	1.1	0.9	0.9	YEA4	orf19.1382	Golgi uridine diphosphate-N-acetylglucosamine transporter (by homology)
CA1165	1.2	0.9	0.7	1.1	3.0	1.3	IPF19902	orf19.3360	unknown function
CA0113	1.2	1.1	0.9	1.0	0.9	1.0	AUT2	orf19.2401	anchor protein mediateing attachment of autophagosomes to microtubules (by homology)
CA4965	1.2	1.0	1.1	1.0	1.2	1.0	IPF3921	orf19.6508	unknown function
CA4514	1.2	0.9	1.2	0.8	0.4	0.8	IPF20016	orf19.491	similar to Saccharomyces cerevisiae Sec63p ER protein-translocation complex subunit (by homology)
CA3811	1.2	0.9	0.9	0.9	1.1	0.8	PET112	orf19.2494	glutamyl-tRNA (GLN) amidotransferase subunit B (by homology)
CA0221	1.2	1.2	1.5	1.2	1.6	1.3	PUS4	orf19.1954	pseudouridine synthase (by homology)
CA4491	1.2	1.0	0.8	0.8	1.0	1.0	SWR1	orf19.1871	putative DNA helicase (by homology)
CA0419	1.2	1.4	0.9	0.7	0.9	1.0	IPF19864	orf19.2228	unknown function
CA0692	1.2	2.0	0.7	0.6	1.0	0.9	PGM2	orf19.2841	Phosphoglucomutase (by homology)
CA2722	1.2	1.3	0.9	0.9	1.2	1.1	IPF4801	orf19.3344	similar to Saccharomyces cerevisiae Vps17p vacuolar sorting protein (by homology)
CA1767	1.2	0.9	0.9	0.9	1.0	0.7	SIT4	orf19.5200	Ser/thr protein phosphatase
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 Pho4p and involved in pheromone response pathway,
CA6155	1.2	0.4	1.4	1.6	0.8	0.8	IPF1846	orf19.5884	unknown function
CA2918	1.2	0.9	1.0	1.0	1.2	1.0	IFA18.53f	orf19.4508	unknown function, 5 3-prime end
CA3143	1.2	1.0	1.0	1.1	0.8	1.4	IPF8295	orf19.3714	unknown function

CA4976	1.2	1.0	1.1	0.9	1.1	1.0	IPF4708	orf19.5276	unknown Function
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 tropicalis
CA4434	1.2	0.7	0.9	0.8	0.7	0.8	MRPL49	orf19.5161	ribosomal protein mitochondrial
CA5271	1.2	1.1	1.0	0.9	0.7	0.7	IPF1777	orf19.4991	similar to Saccharomyces cerevisiae Mpt5p multicopy suppressor of Pop2 required for glucose derepression
CA1784	1.2	1.1	1.9	1.2	0.7	0.9	ARO7	orf19.1170	chorismate mutase (by homology)
CA3956	1.2	1.6	1.0	1.0	1.0	1.2	IPF6712.3f	orf19.1414.2	unknown function, 3-prime end | Unknown function
CA2686	1.2	1.0	0.9	1.0	1.0	1.3	HST2	orf19.2580	Transcription regulatory protein
CA1728	1.2	1.1	0.8	0.9	0.5	0.8	WHI3	orf19.6494	Putative RNA binding protein (by homology)
CA2617	1.2	1.0	0.9	1.0	1.2	1.2	IPF3539	orf19.2813	unknown function
CA5516	1.2	0.9	1.2	1.1	0.9	1.1	IPF726	orf19.5364	rna binding protein (by homology)
CA3669	1.2	1.0	1.1	1.0	1.1	0.9	IPF19997	orf19.6458.1	by homology to S. cerevisiae: U6 snRNA associated protein
CA2697	1.2	1.5	2.9	2.6	0.9	0.8	IPF9167	orf19.2737	unknown function
CA0225	1.2	1.4	1.5	0.8	0.7	0.9	NUP84	orf19.1298	nuclear pore protein (by homology)
CA2800	1.2	1.1	1.1	1.0	1.1	1.0	IPF11366	orf19.1717	unknown function
CA5011	1.2	1.3	1.0	1.1	1.7	2.2	IPF13944	orf19.5236	unknown function
CA4557	1.2	1.3	1.0	1.0	0.9	1.1	IPF8043	orf19.6867	unknown function
CA1959	1.2	1.0	1.0	1.0	1.4	1.1	IFD2	orf19.771	putative oxidoreductase (by homology)
CA1390	1.2	1.2	1.1	1.1	1.0	0.9	IPF17474.5f	orf19.1768	unknown function
CA5977	1.2	2.0	1.2	1.0	1.3	1.2	UBC4	orf19.7571	E2 ubiquitin-conjugating enzyme (by homology)
CA2547	1.2	1.0	0.7	0.7	0.9	0.6	IPF14911	orf19.2832	unknown function
CA3655	1.2	1.1	1.0	1.1	2.3	1.1	POT13	orf19.2046	Acetyl-CoA C-acyltransferase, peroxisomal (by homology)
CA0789	1.2	1.0	1.1	0.9	0.6	0.7	ESP1	orf19.3356	Required for sister chromatid separation (by homology)
CA3097	1.2	1.3	1.5	1.2	0.8	0.9	IPF6600	orf19.3859	unknown function
CA5453	1.2	1.2	0.8	0.9	0.9	1.1	IPF256	orf19.3260	control of gene expression (by homology)
CA4011	1.2	0.9	1.2	1.1	0.9	1.1	IPF4240	orf19.1622	similar to Saccharomyces cerevisiae Ycg1p condensin G (by homology)
CA2183	1.2	1.1	1.1	1.0	1.2	1.1	IPF6872	orf19.4252	serine/threonine protein kinase (by homology)
CA0561	1.2	1.1	1.0	1.0	0.9	0.8	CIN4	orf19.2925	GTP-binding protein
CA2458	1.2	1.4	1.8	1.2	1.8	2.2	IPF12233	orf19.3508	unknown function
CA4257	1.2	2.2	1.0	0.9	1.3	1.1	PRE6	orf19.544.1	20S proteasome subunit
CA1319	1.2	1.0	0.9	1.0	1.1	1.2	IPF3144	orf19.4220	unknown function
CA5002	1.2	1.1	0.9	1.0	2.4	1.2	IPF2021	orf19.5245	unknown function
CA3005	1.2	1.0	1.4	1.1	0.7	0.4	CC43	orf19.6237	Cell Division Control -like (by homology)
CA3667	1.2	1.6	1.2	1.5	0.6	0.9	IPF16323	orf19.6460	similar to Saccharomyces cerevisiae Pex1p peroxisomal assembly protein (by homology)
CA3119	1.2	1.5	2.4	1.8	0.6	1.0	IPF5360	orf19.3007.2	unknown function
CA1584	1.2	1.0	1.0	1.0	1.0	1.0	IPF15824	orf19.6030	unknown function
CA5424	1.2	0.7	1.4	1.0	0.7	0.7	IPF1598	orf19.976	unknown function
CA3554	1.2	1.3	0.8	1.1	1.2	1.0	IPF7770	orf19.3881	unknown function
CA1872	1.2	1.0	0.7	0.9	0.6	0.8	IPF6700	orf19.2459	unknown function
CA2145	1.2	1.1	1.2	1.1	1.1	1.1	IPF12800	orf19.2514	unknown function
CA5003	1.2	1.0	1.0	0.9	0.4	0.5	MCD4	orf19.5244	Sporulation protein (by homology)
CA4390	1.2	1.2	1.0	1.0	1.5	1.2	HOD1	orf19.3122.2	regulator of G2/M progression (by homology)
CA5155	1.2	1.0	1.0	1.0	0.8	0.9	IPF995	orf19.4593.1	unknown function
CA0191	1.2	1.3	1.0	1.0	1.1	1.2	PEX7	orf19.89	peroxisomal import protein (by homology)
CA2293	1.2	0.9	1.1	0.9	0.9	1.0	IPF9748	orf19.746	unknown function
CA0886	1.2	0.9	1.3	1.2	1.2	1.3	IPF12382	orf19.1388	unknown function
CA5165	1.2	0.9	1.0	1.0	1.2	0.8	ARL1	orf19.4603	GTP-binding protein of the ARF family (by homology)

CA0016	1.2	1.0	0.7	1.0	1.4	1.0			
CA1090	1.2	1.1	1.0	0.8	0.8	1.0	COX18	orf19.3946	protein required for activity of mitochondrial cytochrome oxidase (by homology)
CA5043	1.2	1.0	0.9	1.0	1.5	1.1	FRP4	orf19.6997	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway regulator Gpr1p
CA4996	1.2	1.1	1.0	1.0	1.5	1.0	IPF2029	orf19.5251	unknown function
CA0887	1.2	1.5	0.6	0.9	1.4	1.6	IPF12383	orf19.1387	unknown function
CA0612	1.2	1.0	1.1	0.8	1.0	1.0	IPF17545	orf19.5579	unknown function
CA4241	1.2	0.9	0.9	0.9	1.0	1.0	IPF8177	orf19.527	unknown function
CA6145	1.2	1.1	0.8	0.8	0.8	0.8	IPF1869	orf19.5897	unknown function
CA5026	1.2	1.0	1.1	0.8	0.8	0.6	IPF3001	orf19.6980	serine/threonine protein kinase (by homology)
CA3121	1.2	1.2	0.9	0.8	1.0	0.9	GGA1	orf19.3006	Arf-binding protein
CA1947	1.2	1.2	0.9	0.9	3.1	0.9	IPF10637	orf19.4742	starvation protein -like (by homology)
CA0989	1.2	1.0	0.9	0.9	0.8	0.8	IPF11069	orf19.1391	unknown function
CA4797	1.2	1.0	1.0	1.0	0.9	1.0	PRP22	orf19.4033	RNA-dependent ATPase (by homology)
CA5053	1.2	1.0	1.0	1.1	0.7	0.9	IPF3707	orf19.3018	unknown function
CA2826	1.2	0.9	0.9	0.9	0.8	0.8	APL6	orf19.1323	AP-3 complex subunit, beta3-adaptin (by homology)
CA4834	1.2	1.0	0.7	0.9	0.6	1.6	IPF1217	orf19.2063	unknown function
CA4604	1.2	2.1	1.3	1.3	1.2	0.9	MBF1	orf19.3294	Multiprotein bridging factor mediates GCN4-dependent transcriptional activation (by homology)
CA3462	1.2	1.1	1.0	0.8	0.4	0.8	IPF14959	orf19.1265	similar to Saccharomyces cerevisiae Trs130p TRAPP subunit of 130 kDa
CA2425	1.2	1.0	0.7	1.0	0.6	0.9	IPF9907	orf19.3409	similar to Saccharomyces cerevisiae Sed4 protein of the endoplamic reticulum (by homology)
CA3968	1.2	1.1	1.2	1.1	0.8	1.0	IPF9378	orf19.1429	similar to Saccharomyces cerevisiae Soh1p suppressor of Hpr1p (by homology)
CA6039	1.2	1.0	1.8	1.3	1.0	1.1	CKA1	orf19.7652	casein kinase II, catalytic alpha chain (by homology)
CA1005	1.2	1.0	1.4	1.2	3.5	3.4	LPG7	orf19.3759	probable membrane protein (by homology)
CA1177	1.2	1.2	0.8	1.2	0.8	1.0	VMA7	orf19.806	vacuolar ATPase (by homology)
CA2468	1.2	1.0	1.8	1.1	3.9	3.3	IPF8723	orf19.1797	unknown function
CA2200	1.2	1.1	1.3	1.0	0.9	0.9	IPF8114	orf19.2939	unknown function
CA0116	1.2	1.0	1.0	1.0	1.3	0.9	IPF17975	orf19.915	unknown function
CA2621	1.2	0.9	1.1	0.9	1.0	0.8	IPF9499	orf19.2808	probable transcription factor (by homology)
CA1120	1.2	1.0	0.7	0.9	4.6	1.6	IPF7666	orf19.4056	unknown function
CA0766	1.2	1.0	0.9	1.0	0.8	1.0	IPF15335	orf19.4970	unknown function
CA1394	1.2	1.0	1.0	0.9	1.1	1.0	IFO2	orf19.1765	unknown function
CA4338	1.2	1.1	1.1	1.0	0.9	0.9	IPF3616.3e	orf19.6709	Unknown function, 3 prime end
CA4052	1.2	1.0	1.3	1.2	0.5	1.1	IPF10231.3f	orf19.427	unkown function, 3-prime end
CA1681	1.2	1.0	1.0	1.0	1.0	1.2	IPF12676	orf19.4914	unknown function
CA2876	1.2	0.9	1.0	0.8	2.3	1.3	RNR2	orf19.5845	Ribonucleotide reductase (by homology)
CA5471	1.2	1.1	1.0	1.0	1.1	1.0	IPF302	orf19.3283	short chain dehydrogenase/reductase (by homology)
CA0025	1.2	1.1	1.1	0.9	1.1	1.1	IPF17945	orf19.178	unknown function
4511.10	1.2	1.4	1.0	0.9	1.0	1.0			
CA2358	1.2	1.1	1.1	1.0	1.1	1.3	IPF8953	orf19.4895	unknown function
CA5643	1.2	0.9	1.0	1.0	1.0	1.0	IPF448	orf19.7051	unknown function
CA5772	1.2	0.9	0.8	1.0	1.6	1.0	ESA1	orf19.5416	Histone acetyltransferase (by homology)
CA5106	1.2	1.4	1.0	1.1	0.8	1.0	AFG2	orf19.6432	Member of the Sec18p, Pas1p, Cdc48p, TBP-1 family of ATPases (by homology)
CA3641	1.2	1.0	1.0	1.0	1.5	1.2	IPF4122	orf19.2032	unknown function
CA1869	1.2	0.7	1.2	1.0	0.9	0.7	IPF15822	orf19.2457	unknown function
CA4739	1.2	1.1	0.7	1.1	0.8	0.6	IPF4498	orf19.4845	unknown function
CA0275	1.2	1.1	0.9	0.9	1.1	0.9	NTA1	orf19.850	Amino-terminal amidase (by homology)
CA4648	1.2	0.9	1.1	0.9	0.5	0.8	IPF9864	orf19.4435	similar to Saccharomyces cerevisiae Stu1p mitotic spindle protein (by homology)

CA0760	1.2	1.0	1.0	1.0	1.2	0.9	IPF11161.3	orf19.3201	unknown function
CA2711	1.2	1.0	1.2	1.0	3.5	2.2	TFB3	orf19.567	Transcription/repair factor (by homology)
CA0234	1.2	1.0	1.0	1.1	1.1	1.0	IFA3	orf19.154	unknown function
CA1550	1.2	1.0	1.0	1.0	0.9	0.9	IPF8741.5f	orf19.4276	unknown function, 5-prime end
CA5590	1.2	1.0	1.0	1.0	0.9	1.1	TAD1	orf19.7110	Double-stranded rna specific adenosine deaminase by homology
CA2592	1.2	0.9	1.4	1.1	1.6	1.5	IPF18447	orf19.59	putative zinc-finger protein (by homology)
CA0628	1.2	1.0	1.5	1.2	1.1	1.4	IPF3878	orf19.773	unknown function
CA4113	1.2	1.0	1.8	1.5	0.4	0.7	CHO1	orf19.677	Phosphatidylserine synthase
CA0980	1.2	1.0	1.1	1.0	0.9	1.0	IPF17655	orf19.3600	unknown function
CA3302	1.2	1.3	1.3	1.0	1.2	1.4	IPF13784	orf19.2313	unknown function
CA5840	1.2	1.0	1.3	1.9	1.0	1.2	EBP6	orf19.7495	NADPH dehydrogenase (by homology)
CA2049	1.2	1.1	1.0	0.8	1.0	0.9	IPF12982.5f	orf19.5725	unknown function, 5-prime end
CA0946	1.2	1.0	1.1	1.0	1.5	1.1	IPF10277	orf19.1267.1	unknown function
CA2144	1.2	1.1	1.1	1.0	0.5	0.8	IPF12802	orf19.2513	unknown function
CA0942	1.2	1.4	0.7	0.8	2.9	2.4	IPF8619	orf19.3706	unknown function
CA2905	1.2	1.3	1.1	0.9	0.9	0.8	IPF12049	orf19.3473	unknown function
CA3420	1.2	1.0	1.0	1.0	1.1	1.0	SMX4	orf19.6135.1	U6 snRNA-associated Sm-like protein (by homology)
CA1623	1.2	0.9	1.0	0.8	0.9	0.8	STE7	orf19.469	MAP Kinase Kinase
CA3726	1.2	0.7	1.1	1.1	1.0	0.9	IPF6175	orf19.4176	unknown function
CA0084	1.2	1.1	1.2	1.3	1.0	0.8	NAB3	orf19.5530	polyadenylated RNA-binding protein (by homology)
CA2852	1.2	1.0	0.6	1.0	1.1	1.2	ALS5	orf19.5736	agglutinin-like protein
CA4877	1.2	1.6	1.0	0.8	0.6	0.7	IPF1667	orf19.6563	unknown function
CA1264	1.2	0.8	0.9	0.8	0.7	0.9	STH1	orf19.239	helicase related protein by homology
CA5457	1.2	1.0	2.2	1.2	0.9	1.0	TRM1	orf19.3265	N2,N2-dimethylguanine tRNA methyltransferase (by homology)
CA4535	1.2	1.0	1.2	1.0	1.1	0.8	CDC55	orf19.1468	B subunit of protein phosphatase 2A (by homology)
CA3445	1.2	1.1	1.1	1.0	2.4	1.4	IPF7325	orf19.2978	unknown function
CA2867	1.2	1.5	0.9	0.8	0.8	0.8	IPF11688	orf19.2844	similar to Saccharomyces cerevisiae Apl4p AP-1 complex subunit, gamma-adaptin, 94 KD (by homology)
CA1195	1.2	1.1	1.1	1.1	1.2	1.0			
CA3941	1.2	1.0	1.0	1.0	1.0	1.1	IPF4754	orf19.2001	unknown Function
CA5774	1.2	1.0	0.9	1.0	0.5	0.7	IPF1113	orf19.5418	unknown function
CA1309	1.2	1.0	0.8	0.9	0.7	1.0	IPF8627	orf19.3969	unknown function
CA5108	1.2	1.5	0.8	1.0	0.8	0.9	SKI2	orf19.6425	Antiviral protein and putative helicase
CA0992	1.2	1.1	0.9	1.0	1.6	1.1	IPF11063	orf19.1394	unknown function
CA1692	1.2	1.1	1.0	0.8	0.8	1.0	IPF17055.3	orf19.5036	unknown function, 3-prime end
CA3253	1.2	1.0	5.5	5.0	1.1	0.8	PGA23	orf19.3740	unknown Function
CA1153	1.2	1.0	1.1	1.0	1.0	1.0	IPF10455	orf19.104	unknown function
CA4076	1.2	0.7	0.9	0.9	1.0	0.9	IPF2542	orf19.6629	putative neutral sphingomyelinase (by homology)
CA5479	1.2	1.0	0.9	0.9	0.9	1.0	IPF8205	orf19.5311	unknown function
9290.20	1.2	0.9	0.9	1.2	0.8	1.0			
CA5486	1.2	0.9	0.8	1.1	1.0	0.9	IPF813	orf19.5320	unknown function
CA2823	1.2	1.5	0.8	0.9	0.7	0.8	IPF14554	orf19.1317	similar to Saccharomyces cerevisiae Osh3p oxysterol-binding protein (by homology)
CA1491	1.2	0.9	0.7	0.7	0.5	0.5	IPF166	orf19.3225	unknown function
CA6124	1.2	1.0	1.0	1.1	0.8	0.9	ARG11	orf19.5926	mitochondrial amino acid transporter (by homology)
CA4878	1.2	0.8	0.8	0.8	0.5	0.8	OXA1	orf19.6565	Cytochrome oxidase biogenesis protein (by homology)
CA0533	1.2	1.1	1.2	1.0	1.1	1.3	IPF19872	orf19.5067	unknown function
CA3753	1.2	1.0	1.0	0.9	0.7	1.0	IPF14743	orf19.3425	unknown function

CA5299	1.2	1.2	0.9	1.0	1.2	1.0	IPF2190	orf19.7164	putative serine/threonine protein kinase (by homology)
CA4902	1.2	1.2	1.1	1.1	1.1	0.9	SED5	orf19.6039	Syntaxin (by homology)
CA6138	1.2	0.9	0.9	0.9	1.3	1.1	TEC1	orf19.5908	unknown function
CA1135	1.2	0.9	1.0	1.1	1.1	0.9	IMP2	orf19.1981	mitochondrial inner membrane protease subunit (by homology)
CA5580	1.2	1.4	0.9	1.0	1.3	1.6	RVS161	orf19.7124	cytoskeletal binding protein (by homology)
CA3640	1.2	1.3	1.1	1.1	1.4	1.2	VPS24	orf19.2031	endosomal Vps protein complex subunit
CA2308	1.2	1.1	0.8	0.9	0.7	0.6	IPF9874.3	orf19.1373	similar to Saccharomyces cerevisiae Inp51p phosphatidylinositol phosphate 5-phosphatase, 3-prime end
CA4197	1.2	1.0	1.1	1.0	1.0	1.1	IPF8057	orf19.4538	similar to Saccharomyces cerevisiae Rna15p component of pre-mRNA 3'-end processing factor CF I (by homology)
CA6151	1.2	1.0	0.6	1.0	1.3	1.0	IPF1853	orf19.5890	unknown function
CA4450	1.2	1.4	0.9	0.7	0.7	0.8	IPF3518	orf19.6848	similar to Saccharomyces cerevisiae Vps16p vacuolar sorting protein (by homology)
CA4171	1.2	1.0	0.9	1.0	0.9	0.9	IPF7785	orf19.2962	unknown function
CA6114	1.2	0.9	1.2	0.9	0.6	0.8	SEN1	orf19.5938	positive effector of tRNA-splicing endonuclease (by homology)
CA2215	1.2	1.3	0.6	0.8	1.2	0.9	PFK26	orf19.4753	6-phosphofructose-2-kinase (by homology)
CA4871	1.2	0.8	0.8	0.9	1.0	0.9	IPF1680	orf19.6557	probable amidase
CA5888	1.2	1.3	1.0	0.8	1.1	0.9	IPF2414	orf19.6820	unknown function
CA2687	1.2	1.1	1.0	1.0	1.0	1.1			
CA3236	1.2	0.8	1.7	1.3	0.7	0.9	DEG1	orf19.6297	pseudouridine synthase (by homology)
CA3859	1.2	1.0	0.9	1.0	0.9	0.8	IPF4632	orf19.6094	similar to Saccharomyces cerevisiae Vps53p subunit of VP52-54 complex,
CA1486	1.2	1.0	1.3	1.0	1.0	1.0	IPF10521	orf19.4062	unknown function
CA1130	1.2	1.2	1.0	1.0	1.4	1.2	NAG1	orf19.2156	Glucosamine-6-phosphate deaminase
CA1906	1.2	1.0	1.0	0.9	1.1	1.0	IPF7271	orf19.2784	unknown function
CA2133	1.2	1.5	1.0	1.0	1.0	0.8	IPF5866	orf19.5213	unknown function
CA0673	1.2	0.7	0.9	0.9	0.7	1.0	AMO2	orf19.3152	amine oxidase (by homology)
CA0008	1.2	1.0	1.0	1.1	1.0	1.1	IPF12110	orf19.376	1,4-butanediol diacrylate esterase (by homology)
CA3400	1.2	1.0	1.1	0.9	1.0	0.9	JNM1	orf19.3976	mitosis protein, involved in nuclear migration (by homology)
CA0709	1.2	1.0	0.8	1.0	0.9	1.0	Zorro2a.3f	orf19.3387	Reverse transcriptase, 3-prime end
CA3268	1.2	1.0	1.6	1.6	2.2	1.1	RPS620b	orf19.6301	unknown function
CA5725	1.2	1.2	1.0	0.6	1.0	0.3	GLG2	orf19.7434	Self-glucosylating initiator of glycogen synthesis (by homology)
CA1129	1.2	1.0	1.1	0.9	2.4	1.1	IPF5197	orf19.3610	unknown function
CA3460	1.2	0.9	0.8	1.0	0.9	0.8	CFL1	orf19.1263	ferric reductase
CA4174	1.2	3.6	1.3	1.6	1.6	1.8	IPF4430	orf19.2959.1	unknown function
CA2706	1.2	1.0	1.2	0.8	0.7	0.8	IPF11006	orf19.4658	unknown function
CA4086	1.2	1.3	0.9	1.1	0.6	0.8	IPF5014	orf19.6642	unknown function
CA1583	1.2	1.1	1.1	1.2	0.3	0.8	ROT1	orf19.6029	Suppressor of TOR2 mutations (by homology)
CA0945	1.2	1.6	0.8	1.0	1.3	1.0	IPF10278	orf19.1267	DNA-J - like protein (by homology)
CA1474	1.2	1.0	0.9	1.2	0.7	0.9	IPF10208	orf19.1096	chloride channel-like protein (by homology)
CA0321	1.2	1.0	1.1	1.1	0.7	0.8	APL2	orf19.231	AP-1 complex subunit, beta1-adaptin (by homology)
CA6019	1.2	1.0	1.1	1.0	0.8	0.9	IPF625	orf19.7621	unknown function
CA5663	1.2	1.3	1.1	0.8	1.2	1.3	IPF1251	orf19.7365	unknown function
CA1175	1.2	1.0	0.9	1.0	0.9	0.8	ARG81	orf19.4766	transcription factor possibly involved in arginine metabolism, 3-prime end (by homology)
CA0372	1.2	1.3	0.9	0.9	0.7	0.7	IPF10062	orf19.1086	unknown function
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 homology)
CA3235	1.2	1.1	1.0	0.9	0.9	1.0	SNF8	orf19.6296	involved in glucose derepression (by homology)
CA3489	1.2	1.0	1.0	1.0	1.1	0.8	IPF3195	orf19.3567	unknown function
CA1920	1.2	1.3	0.8	0.7	0.9	0.9	IPF7476	orf19.2443	similar to Saccharomyces cerevisiae Rgd1p putative GTPase activating protein (by homology)
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)

CA1159	1.2	0.9	1.2	0.9	1.0	0.9	IPF13423	orf19.4128	unknown function
CA4402	1.2	1.0	1.0	1.0	1.3	1.1	MGT1	orf19.3108	O6-methylguanine DNA repair methyltransferase (by homology)
CA6119	1.2	1.0	1.0	1.0	0.8	0.8	ARV1	orf19.5931	involved in sterol uptake and distribution into the plasma membrane
CA5662	1.2	1.1	1.0	1.2	1.0	1.0	IPF1250	orf19.7364	Flavin-containing monooxygenase(by homology)
CA3359	1.2	1.0	0.9	1.0	2.0	1.1	IPF9566	orf19.1939	unknown function
CA3392	1.2	1.3	0.7	1.1	1.0	0.9	SEC13	orf19.316	Protein transport protein
CA4591	1.2	1.0	0.9	1.0	1.4	1.0	IPF2216	orf19.6908	putative folylpolyglutamate synthetase (by homology)
CA0643	1.2	1.4	0.7	1.0	0.7	1.0	IDP2	orf19.3733	isocitrate dehydrogenase, cytosolic (by homology)
CA2257	1.2	0.9	1.1	1.0	1.5	1.2	SHR5	orf19.1955	RAS suppressor (by homology)
CA3683	1.2	1.5	1.1	1.0	1.1	1.2	PPZ1	orf19.726	ser/thr phosphatase required for normal osmoregulation (by homology)
CA1355	1.2	1.5	0.4	0.3	1.7	1.7	IPF10140	orf19.408	unknown function
CA1847	1.2	1.0	0.9	1.0	0.9	0.9	IPF11127	orf19.639	unknown function
CA1453	1.2	1.0	0.8	1.1	0.9	0.8	HOS1	orf19.4411	Putative histon deacetylase (by homology)
CA5213	1.2	1.1	0.9	1.1	0.8	0.8	SSR1	orf19.7030	Secretory Stress Response protein 1 (by homology)
CA1751	1.2	0.8	0.9	0.9	1.4	1.0	ARO3	orf19.1517	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (by homology)
CA2799	1.2	1.1	0.9	0.9	0.9	1.0	IPF19769	orf19.1718	unknown function
CA2510	1.2	1.0	0.8	0.9	0.6	0.8	IPF1472	orf19.305	unknown function
CA2331	1.2	1.2	0.9	0.8	0.9	0.8	MOT1	orf19.4502	transcriptional accessory protein
CA3070	1.2	1.1	0.9	1.0	1.4	1.1	PPA2	orf19.4807	Mitochondrial inorganic pyrophosphatase
CA1860	1.2	1.0	1.0	1.0	1.3	1.2	UTR4	orf19.1495	unknown function
CA3907	1.2	1.5	0.7	1.0	1.0	0.9	IPF3304	orf19.4395	similar to Saccharomyces cerevisiae Aip1p actin cytoskeleton component (by homology)
CA4823	1.2	1.3	0.5	0.9	6.0	4.7	ERC3	orf19.2073	ethionine resistance protein (by homology)
CA3746	1.2	1.6	1.6	1.0	0.8	1.1	ARA1	orf19.2172	D-arabinose dehydrogenase (by homology)
CA4183	1.2	0.8	0.6	1.0	1.0	1.1	SNO1	orf19.2948	hisH-like protein (by homology)
CA5496	1.2	0.9	0.9	1.0	1.3	1.0	IPF779	orf19.5337	E2 ubiquitin conjugating enzyme (by homology)
CA0925	1.2	1.4	1.2	0.9	1.0	1.2	IPF17050	orf19.1049	unknown function
CA2550	1.2	1.1	0.9	1.0	1.1	0.9	IPF9099	orf19.2835	similar to Saccharomyces cerevisiae Aos1p activating enzyme for Smt3 (by homology)
CA3942	1.2	1.1	1.2	1.0	0.9	1.4	CHL1	orf19.2000	protein of the DEAH box family (by homology)
CA3925	1.2	1.0	2.2	1.2	0.8	1.0	IPF13257	orf19.5110	unknown function
CA3390	1.2	1.1	0.9	1.0	1.7	1.1	CAF17	orf19.318	Component of CCR4 transcriptional complex
CA4849	1.2	1.1	1.0	1.0	1.1	1.2	IPF6954	orf19.3818	unknown function
CA3723	1.2	0.7	1.2	1.4	1.2	1.0	DPH2	orf19.4173	Diphtheria toxin resistance protein (by homology)
CA5481	1.2	1.6	0.9	0.8	4.1	4.4	IPF19810	orf19.5313	unknown function
CA1736	1.2	0.9	1.1	1.1	1.0	1.0	IPF4983	orf19.2527	unknown function
CA2688	1.2	1.1	1.0	0.9	1.1	1.1	IFU6.5f	orf19.2581	Putative ortholog of S. cerevisiae Gre2p, 5-prime end
CA1732	1.2	1.0	1.0	1.0	0.9	1.0	ECM42	orf19.6500	Acetylornithine acetyltransferase (by homology)
CA5251	1.2	0.9	1.6	1.3	0.7	0.8	IPF1824	orf19.5011	unknown function
CA4981	1.2	1.0	1.2	1.0	1.0	1.0	IPF2057	orf19.5269	unknown function
CA4429	1.2	1.0	1.2	1.2	0.6	0.9	DBF4	orf19.5166	regulatory subunit for Cdc7 by homology
CA1097	1.2	0.8	1.1	0.9	0.6	1.1	IPF7575	orf19.4365	putative endo-exonuclease (by homology)
CA5259	1.2	0.6	0.8	0.9	0.7	1.0	OSM2	orf19.5005	Osmotic growth protein (by homology)
CA5233	1.2	1.1	0.9	1.1	0.8	1.0	SSK1	orf19.5031	Putative reponse regulator two-component phosphorelay gene
CA3897	1.2	1.5	1.0	1.0	0.9	1.0	PFY1	orf19.5076	BINDS TO ACTIN PROFILIN
CA4958	1.2	1.3	1.3	1.2	1.2	1.0	RAD14	orf19.6517	nucleotide excision repair protein (by homology)
CA4151	1.2	1.0	1.0	1.0	1.2	0.9	SHE9	orf19.5796	causes lethality when overexpressed
CA3761	1.2	2.5	0.9	1.0	2.0	2.2	IFR3	orf19.2908	unknown function

CA1750	1.2	1.1	0.8	0.9	0.8	0.8	IPF8252	orf19.1519	unknown function
CA5311	1.2	0.9	1.0	1.1	1.2	1.2	IPF2166	orf19.7182	unknown function
CA4518	1.2	1.1	0.8	1.0	0.9	1.0	SPT14	orf19.487	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein (by homology)
CA1145	1.2	0.8	0.8	0.8	0.9	0.8	GCS1	orf19.3683	ADP-ribosylation factor GTPase-activating protein (ARF-GAP) (by homology)
CA1524	1.2	1.3	0.9	1.0	1.0	1.2	SUR1	orf19.3794	Suppressor of ROK1
CA5944	1.2	1.2	1.0	1.0	1.4	1.1	IPF3491	orf19.6753	unknown function
CA0734	1.2	0.9	1.5	1.5	0.8	1.0	IPF8996	orf19.4634	unknown function
CA3449	1.2	0.9	1.1	1.0	0.9	1.0	IPF7320	orf19.2973	unknown function
CA5249	1.2	1.3	1.0	1.0	0.8	0.9	PCM1	orf19.5013	phosphoacetylglucosamine mutase (by homology)
CA4020	1.2	1.0	0.9	1.0	1.6	1.1	IPF5324	orf19.3444	putative transporter (by homology)
CA2050	1.2	1.0	1.0	1.0	0.9	0.9			
CA1082	1.2	0.9	1.2	1.0	0.8	1.1	IPF14797.5f	orf19.4818	unknown function
CA3197	1.2	1.1	1.0	1.2	0.4	0.7	SEC61	orf19.6176	ER protein-translocation complex subunit
CA3213	1.2	1.0	1.0	0.9	1.0	0.9	IPF8160	orf19.6205	unknown function
CA6075	1.2	0.9	1.2	1.2	1.3	1.1	THI4	orf19.5986	Thiazole biosynthetic enzyme precursor (by homology)
CA0510	1.2	0.4	0.4	0.8	1.8	0.8	ETF1	orf19.3175	ETF-UBIQUINONE OXIDOREDUCTASE (by homology)
CA4027	1.2	1.0	0.8	0.9	0.8	1.0	IPF7174	orf19.3436	unknown function
CA3552	1.2	1.0	0.8	1.0	1.7	1.0	IPF13231	orf19.3877	unknown function
CA5901	1.2	0.9	1.5	1.0	0.5	0.4	IPF2374	orf19.6805	unknown function
CA5013	1.2	1.0	0.8	0.8	0.9	0.7	IPF13941	orf19.5234	Unknown function
CA5641	1.2	0.9	1.0	0.9	0.9	0.9	GAC1	orf19.7053	ser/thr phosphoprotein phosphatase 1, regulatory chain (by homology)
CA1213	1.2	1.1	0.9	0.9	0.9	0.9	VPS15.5f	orf19.130	serine/threonine protein kinase, 5-prime end (by homology)
CA0850	1.2	1.0	0.8	1.0	3.0	1.0	IPF16671	orf19.1745	unknown function
CA1100	1.2	0.8	1.9	1.3	1.3	0.9	IPF5681	orf19.4952	unknown function
CA1899	1.2	0.9	1.0	0.9	1.0	0.8	HDA1	orf19.2606	Histone deacetylase (by homology)
CA1996	1.2	1.1	1.0	1.0	1.7	0.9	SEC1	orf19.6479	transport protein
CA0924	1.2	1.3	1.6	1.0	1.2	1.0	IFD5	orf19.1048	Putative aryl-alcohol dehydrogenase (by homology)
CA4109	1.2	1.2	1.0	1.0	1.1	1.0	IPF3967	orf19.673	unknown function
CA2466	1.2	1.0	0.8	1.0	1.1	1.0	IPF8725	orf19.1795.1	unknown function
CA0085	1.2	0.8	1.0	1.0	1.1	0.9	IPF16201	orf19.693	unknown function
CA3360	1.2	1.0	1.2	1.0	1.0	1.0	IPF9568	orf19.1938	unknown function
CA0348	1.2	0.9	0.9	1.0	1.1	0.9	IFK1	orf19.1523	probable monoxygenase (by homology)
CA2509	1.2	0.9	1.5	1.4	0.4	0.7	IPF1471	orf19.304	aminotriazole resistance protein (by homology)
CA3614	1.2	1.1	0.8	1.0	1.7	1.1	IPF8878	orf19.31	unknown function
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)
CA4632	1.2	1.3	0.9	1.0	0.8	0.8	IPF1531	orf19.338	unknown function
CA5139	1.2	1.0	1.0	1.0	1.1	1.0	IPF1027	orf19.4577	unknown function
CA0869	1.2	1.0	1.0	1.0	5.7	1.2	IPF14772	orf19.3589	unknown function
CA4037	1.2	1.0	1.2	0.9	0.8	0.8	KIP31	orf19.3667	kinesin-related protein required for nuclear migration (by homology)
CA5404	1.2	2.6	1.8	1.0	1.2	1.7	MET14	orf19.946	Adenylylsulfate kinase (by homology)
CA5796	1.2	1.1	1.2	1.2	0.8	1.1	GLO3	orf19.5445	zinc finger protein
CA5484	1.2	1.1	0.6	0.8	0.8	0.8	RAD1.3f	orf19.5318	UV endonuclease, component of the nucleotide excision repairosome, 3-prime end (by homology)
CA2965	1.2	1.1	1.3	1.0	0.8	1.1	IPF13174	orf19.5609	unknown function
CA0077	1.2	0.9	1.3	1.0	0.6	0.8			
CA0683	1.2	1.0	1.4	1.0	0.7	0.9	IPF14519.5f	orf19.4702	unknown function, 5-prime end
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)

CA4653	1.2	0.9	0.9	0.8	0.9	1.0	IPF3102	orf19.4440	similar to Saccharomyces cerevisiae Sec34p required for vesicle tethering to the yeast Golgi apparatus (by homology)
CA4831	1.2	1.0	1.2	1.1	1.2	1.2	IPF1212	orf19.2066	unknown function
CA5863	1.2	0.9	1.1	1.0	0.7	1.0	IPF370	orf19.7521	unknown function
CA0141	1.2	1.0	0.9	1.4	1.2	1.0	IPF17520.53	orf19.1021	unknown function, internal fragment
CA4767	1.2	1.1	1.0	1.0	0.6	0.9	IPF13054	orf19.3999	unknown function
CA5400	1.2	0.9	1.2	1.0	1.1	0.9	KRE62.3f	orf19.942.1	Glucan synthase subunit, 3-prime end (by homology)
CA2349	1.2	1.0	0.4	0.7	1.1	2.6	IFC3	orf19.3749	Unknown function
CA4371	1.2	1.2	0.8	1.0	1.1	1.0	PEP7	orf19.5662	vacuolar segregation protein by homology
CA4944	1.2	1.0	0.8	1.0	0.9	0.9	MSK1	orf19.6533	lysyl-tRNA synthetase by homology
CA4866	1.2	1.1	1.2	1.2	1.0	1.0	IPF4083	orf19.3843	similar to Saccharomyces cerevisiae Sec66p ER protein-translocation complex subunit(by homology)
CA0509	1.2	1.1	0.7	0.6	0.5	0.6	CDC24	orf19.3174	GTP/GDP exchange factor for Cdc42p (by homology)
CA0381	1.2	1.1	1.0	1.1	7.8	6.7	IPF16047	orf19.2825	unknown function
CA1411	1.2	1.0	0.4	0.9	0.8	1.0	IPF11858	orf19.1277	unknown function
CA4460	1.2	0.9	1.1	0.9	0.9	0.9	NSP49.5f	orf19.6857	nuclear pore protein, 5-prime end (by homology)
CA2812	1.2	0.7	1.9	1.2	0.9	1.0	TEM1	orf19.3001	GTP-binding protein of the RAS superfamily
CA0700	1.2	1.2	1.0	1.4	0.7	0.8	SHR3	orf19.3366	endoplasmatic reticulum membrane protein (by homology)
CA5372	1.2	1.1	1.1	1.0	1.1	1.0	MLH3	orf19.7257	DNA mismatch repair by homology
CA3893	1.2	0.7	1.5	1.2	1.1	1.1	FUN11	orf19.5083	putative GTP-binding protein (by homology)
CA0088	1.2	0.8	0.9	1.1	1.0	0.9	IPF7349	orf19.579	similar to Saccharomyces cerevisiae Fol1p dihydroneopterin aldolase,
CA4428	1.2	0.9	1.1	0.9	0.5	0.6	IFM1	orf19.5167	translation initiation factor 2 by homology
CA3247	1.2	1.9	1.1	1.0	0.7	0.8	IPF15832	orf19.4676	unknown function
CA4208	1.2	1.0	0.9	0.9	0.9	1.0			
CA4576	1.2	1.1	0.8	1.0	2.0	1.5	IPF9425.3	orf19.6888	unknown function
CA4283	1.2	1.0	1.1	1.1	1.0	0.9	IFJ4	orf19.6681	Unknown function
CA2767	1.2	0.9	1.0	1.0	0.7	1.0	TOA1	orf19.2682	transcription initiation factor IIA (by homology)
CA4812	1.2	0.9	0.7	0.9	1.6	1.3	IPF1171.3f	orf19.2089	Putative synaptobrevin (by homology)
CA3636	1.2	1.1	1.1	1.0	0.8	1.0	IFA21	orf19.5138	unknown function
CA0289	1.2	1.0	1.0	1.0	1.0	0.9	IPF13333	orf19.1590	unknown function
CA1520	1.2	1.0	0.9	1.0	1.2	1.2	IPF11035	orf19.4801	similar to Saccharomyces cerevisiae Mod5p tRNA isopentenyltransferase (by homology)
CA1511	1.2	1.0	0.9	1.0	1.0	1.1	IPF9972.3e	orf19.4522	unknown function, 3-prime end
CA5875	1.2	1.1	0.9	1.0	0.8	1.6	IPF324.3f	orf19.7545	unknown function, , 3-prime end
CA0124	1.2	1.1	1.1	1.1	1.1	1.2	RFC5	orf19.2029	DNA replication factor C (by homology)
CA1868	1.2	1.0	0.8	0.9	1.0	0.9	IPF14501.3f	orf19.2456	putative G-protein, -transducin type, 3-prime end (by homology)
CA2912	1.2	1.1	0.9	0.9	1.6	0.9	IPF11206	orf19.4515	unknown function
CA5782	1.2	1.0	0.9	0.9	0.8	0.9	IPF1127	orf19.5429	unknown function
CA5146	1.2	1.7	0.9	1.0	1.0	1.0	YMC2	orf19.4583	Carnitine/acylcarnitine translocase (by homology)
CA1551	1.2	1.0	0.9	0.9	0.8	1.0	IPF8741.3f	orf19.4275	unknown function, 3-prime end
CA0036	1.2	0.7	0.9	0.9	1.0	1.0	IPF19377	orf19.3336	unknown function
CA2669	1.2	1.8	0.8	0.9	1.0	1.0			
CA5072	1.2	1.0	0.5	0.8	0.9	0.6	IPF3598	orf19.3047	similar to Saccharomyces cerevisiae Sip3p protein which interacts with Snf1p protein kinase (by homology)
CA3656	1.2	1.2	0.5	1.0	1.9	0.9	IPF7456	orf19.2047	unknown function
CA0427	1.2	1.2	0.9	1.0	0.8	1.4	IPF11995	orf19.2761	unknown function
CA4411	1.2	0.9	1.1	1.0	1.0	1.0	BRR2	orf19.3098	RNA helicase-related protein (by homology)
CA0633	1.2	1.0	1.1	1.0	0.8	1.1	IPF16269	orf19.1771	unknown function
CA3933	1.2	1.1	1.2	0.9	1.3	1.2	IPF18281	orf19.2009	similar to Saccharomyces cerevisiae Pex12p peroxisome assembly (by homology)
CA3177	1.2	1.1	1.0	1.3	1.6	1.4	IPF11589	orf19.1405	similar to Saccharomyces cerevisiae Pho13p 4-nitrophenylphosphatase

CA0410	1.2	1.1	0.9	1.0	1.9	1.2	IPF15065	orf19.5757	unknown function
CA0807	1.2	1.1	1.0	1.0	1.0	1.2	IPF12564	orf19.3518	ADP/ATP carrier proteins (by homology)
CA5303	1.2	2.2	1.1	1.2	1.5	0.8	IPF2180	orf19.7170	unknown function
CA0769	1.2	1.2	1.1	1.0	1.0	1.0	IPF10967	orf19.2826	unknown function
CA4144	1.2	1.4	0.9	1.0	1.1	1.0	IPF13340	orf19.4228	unknown function
CA1509	1.2	1.0	0.5	0.9	0.9	0.9	IPF19920	orf19.4524	unknown function
CA2440	1.2	1.0	1.1	1.2	1.8	1.0	IPF7513	orf19.2196	unknown function
CA1487	1.2	1.2	1.0	1.0	1.0	1.1	GPT1	orf19.4063	polyamine transporter; GABA transporter
CA2778	1.2	1.5	0.9	1.1	2.3	1.3	MTR	orf19.278	neutral amino acid permease-like by homology
CA1224	1.2	1.0	0.8	0.9	0.9	1.0	IPF15662.5	orf19.4156	unknown function
CA4410	1.2	0.7	0.6	1.1	1.5	1.1	TRP4	orf19.3099	Anthranilate phosphoribosyltransferase
CA1083	1.2	0.9	1.0	1.0	1.1	1.0	IPF1034	orf19.4573	Similarity to transcription factors
CA4461	1.2	1.2	1.5	1.0	0.5	1.0	IPF8470	orf19.6858	unknown function
CA2188	1.2	1.1	1.0	1.1	0.4	0.6	SSU81	orf19.4772	protein involved in the HOG1 high-osmolarity signal transduction pathway (by homology)
CA3501	1.2	0.8	1.1	0.8	1.0	1.3	CDC40	orf19.6347	cell division control protein (by homology)
CA1779	1.2	1.1	4.5	1.5	0.5	0.8	IPF14510	orf19.1826	unknown function
CA4202	1.2	0.9	0.8	1.0	1.3	1.1	IPF8047	orf19.4544	unknown function
CA3163	1.2	1.0	1.0	0.9	1.1	1.0	HOL5.5f	orf19.1582	member of major facilitator superfamily multidrug-resistance protein subfamily 1, 5-prime end (by homology)
CA4388	1.2	1.0	1.0	1.0	1.1	1.0	IPF12416.3f	orf19.3123.2	cytidine deaminase, 3-prime end (by homology)
CA2757	1.2	1.0	1.0	0.9	0.8	1.0	IPF19767	orf19.5621	unknown function
CA1461	1.2	0.8	1.0	1.1	0.8	0.7	IPF6338	orf19.1109	unknown function Unknown protein
CA2110	1.2	1.1	1.1	1.0	0.9	0.9	IPF13749.3f	orf19.3689	unknown function, 3-prime end
CA5012	1.2	1.0	1.0	0.8	0.7	1.0	IPF13943	orf19.5235	Unknown function
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 acceptor (by homology)
CA5718	1.2	1.0	1.9	1.4	1.1	1.5	LCP5	orf19.7422	Ngg1p interacting protein (by homology)
CA3505	1.2	1.0	1.1	1.0	1.1	1.0	IPF11372	orf19.6351	unknown function
CA0465	1.2	0.9	1.0	0.9	1.0	0.9	IPF14113.5f	orf19.166	unknown function, 5-prime end
CA0477	1.2	1.0	1.2	1.1	0.9	1.0	IPF13839	orf19.6017	unknown function
CA2290	1.2	1.2	0.9	0.9	1.0	0.9	IPF16300	orf19.742	putative aldehyde dehydrogenase (by homology)
CA1937	1.2	0.9	0.9	1.0	1.0	0.9	MMM1	orf19.4187	mitochondrial outer membrane protein (by homology)
CA5912	1.2	1.1	1.0	1.0	0.9	0.8	IPF5966	orf19.6793	unknown function
CA4306	1.2	1.5	0.6	0.8	2.4	1.6	GYP7	orf19.6706	GTPase activating protein (by homology)
CA2497	1.2	0.7	0.7	0.7	0.7	0.9	TEL1	orf19.5580	Putative phosphatidylinositol kinase involved in controlling telomere lenght, (by homology)
CA3625	1.2	1.3	0.6	0.8	0.5	0.6	CYR1.3f	orf19.5151	adenylate cyclase, 3-prime end
CA3440	1.2	1.0	1.1	1.0	1.3	1.0	IPF11328	orf19.2985	unknown function
CA3607	1.2	0.4	4.1	1.8	1.4	1.2	RTA2	orf19.24	Unknown function
CA2305	1.2	1.3	0.9	1.0	1.3	1.3	MPA43	orf19.1686	Unknown function
CA3582	1.2	1.0	1.1	0.9	1.0	0.9	IPF15466	orf19.2258	unknown function
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)
CA4694	1.2	1.0	1.1	1.0	2.7	1.5	IPF3950	orf19.871	unknown function
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)
CA6132	1.1	1.0	1.0	1.1	1.1	0.9	DUR35.5f	orf19.5916	Urea transport protein, 5-prime end (by homology)
CA0729	1.1	1.0	0.9	1.0	1.1	1.0	IPF7338	orf19.3726	unknown function
CA5195	1.1	1.1	1.0	1.1	1.1	1.0	GRP8	orf19.7009	Similarity to dihydroflavonol-4-reductases
CA4726	1.1	1.2	0.9	1.0	1.0	0.9			
CA5563	1.1	0.9	1.4	1.1	0.3	0.6	PHO88	orf19.7327	Involved in phosphate transport (by homology)

CA5928	1.1	1.0	1.0	1.1	1.0	1.0	IPF2815	orf19.6777	unknown function
CA4734	1.1	0.9	1.4	1.0	1.0	1.0	TFA1	orf19.4851	Large subunit of transcription factor tfIIE
CA5061	1.1	1.0	0.9	0.8	1.2	1.0	IPF8495	orf19.3030	unknown function
CA0493	1.1	1.0	1.0	1.0	0.8	1.0	PRP39.3f	orf19.1492	pre-mRNA splicing factor, 3-prime end (by homology)
CA2495	1.1	1.0	0.9	0.8	1.0	1.0	CTA24	orf19.4054	transcriptional regulation (by homology)
CA5577	1.1	1.0	0.9	1.0	1.2	0.9	IPF12537	orf19.7344	unknown function
CA3857	1.1	1.2	1.1	1.4	0.9	1.0	CCT8	orf19.6099	component of chaperonin-containing T-complex
CA5830	1.1	0.7	0.8	0.7	0.8	0.8	MRPL9	orf19.7485	Mitochondrial ribosomal protein of the large subunit (by homology)
CA5473	1.1	1.1	1.1	0.9	0.6	0.8	IPF16947	orf19.3286	unknown function
CA3538	1.1	0.9	1.0	1.0	0.8	0.8	ATP10	orf19.6374	F1F0 ATPase complex assembly protein (by homology)
CA5074	1.1	1.0	1.0	1.0	1.0	0.9	IPF3607	orf19.3049	putative serine/threonine protein kinase
CA5886	1.1	1.0	0.7	0.8	1.2	1.0	IPF2417	orf19.6822	unknown function
CA2388	1.1	0.7	1.3	1.1	0.7	0.9	MCM6	orf19.2611	component of MCM initiator complex involved in DNA replication (by homology)
CA4384	1.1	1.0	1.0	1.1	1.0	1.0	DUR34	orf19.5677	Urea transport protein (by homology)
CA4555	1.1	1.1	0.9	0.9	1.0	1.0	IPF17555.3	orf19.1444	unknown function, 3-prime end
CA0146	1.1	1.3	1.1	1.0	1.1	1.0	IPF9689	orf19.3648	unknown function
CA2435	1.1	1.7	1.2	1.1	17.7	13.6	IPF9483	orf19.3395	probable permease (by homology)
CA5733	1.1	1.1	0.9	0.9	0.9	1.3	IPF2873	orf19.7443	unknown function
CA4468	1.1	0.9	0.9	1.0	0.8	0.9	TOR2.53eo	orf19.1905	phosphatidylinositol 3-kinase, internal fragment (by homology)
CA2567	1.1	0.8	1.0	1.0	0.9	0.9			
CA3765	1.1	0.4	0.8	1.0	0.7	0.6	IPF18298.5f	orf19.2904	unknown function, 5-prime end
CA4172	1.1	0.9	0.9	1.0	0.9	0.9	IPF4432	orf19.2961	unknown function
CA1402	1.1	1.0	1.0	1.0	0.9	1.0	ECE1	orf19.3374	Cell Elongation Protein
CA5184	1.1	0.9	1.1	1.1	1.0	1.0	IPF11090.3f	orf19.4623.2	weak similarity to glutenin, prime end
CA1978	1.1	1.0	1.2	1.0	0.8	0.9	IPF9580	orf19.687	unknown function
CA0753	1.1	1.0	0.9	1.0	1.4	1.1	IPF10359	orf19.3806	unknown function
CA2715	1.1	1.0	1.0	1.0	0.9	1.0	CTF8	orf19.576	putative) kinetochore protein (by homology)
CA0840	1.1	1.7	1.4	1.0	1.3	1.0			
CA2681	1.1	0.9	1.0	1.0	1.0	1.0	SEC4	orf19.2571	GTP-binding protein
CA5130	1.1	1.1	1.1	1.1	1.1	1.0	IFH2	orf19.6398	Dioxygenase (by homology)
CA0252	1.1	1.3	0.7	1.1	0.9	1.0			
CA0139	1.1	1.1	1.3	1.0	0.9	0.9	RUD3.5f	orf19.6894	Suppressor of uso1-1 transport defect, 5-prime end (by homology)
CA2762	1.1	1.0	1.1	0.9	0.9	1.1	IPF15012	orf19.5627	pre mRNA splicing factor (by homology)
CA5934	1.1	0.7	1.3	1.1	1.7	2.1	IPF2802	orf19.6769	unknown function
CA0904	1.1	1.0	1.2	1.0	1.0	1.0	IPF4403	orf19.1481	unknown function
CA3103	1.1	1.0	0.9	1.0	3.6	1.0			
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
CA0774	1.1	1.0	1.1	1.0	1.1	1.0	IPF11974	orf19.855	unknown function
CA1014	1.1	0.7	1.0	1.2	0.9	1.1	MES1	orf19.3955	methionyl-tRNA synthetase (by homology)
CA2919	1.1	0.9	1.0	1.0	1.5	1.0	IFA18.3f	orf19.4507	unknown function
CA2775	1.1	1.0	1.1	1.0	1.8	1.2	POP5	orf19.275	subunit of RNase P- like by homology
CA3833	1.1	1.0	1.0	1.0	1.0	1.1	IPF8192	orf19.6592	unknown function
CA0579	1.1	0.9	0.9	0.9	0.7	0.9	IPF3184	orf19.3559	unknown function
CA0803	1.1	1.0	1.0	1.0	1.3	1.1	IFL4	orf19.3512	unknown function
1977.20	1.1	0.8	1.0	1.0	1.1	1.0			
CA3681	1.1	1.1	0.6	0.9	0.8	0.8	IPF19787	orf19.728	unknown function

CA0859	1.1	1.0	1.2	1.0	1.1	0.8	IPF14495	orf19.4466	similar to Saccharomyces cerevisiae Erf2p involved in palmitoylation and localization of Ras2p
CA2208	1.1	0.8	1.0	0.9	1.2	0.9	IPF17255	orf19.696	similar to Saccharomyces cerevisiae Ste2p pheromone alpha-factor receptor
CA3498	1.1	1.0	1.0	0.9	1.0	1.0	RBK1	orf19.6344	Ribokinase (by homology)
CA5817	1.1	1.0	1.6	1.0	0.6	0.9	IPF2511	orf19.7468	unknown function
CA3472	1.1	1.1	1.0	0.9	1.0	0.7	IPF6306	orf19.1667.1	unknown function
CA0074	1.1	1.1	1.2	0.9	1.1	0.9	IFD7	orf19.629	Putative aryl-alcohol dehydrogenase (by homology)
CA2187	1.1	1.0	1.1	1.0	1.0	1.3	IPF11667	orf19.4771	unknown function
CA1399	1.1	0.9	1.0	1.0	0.9	1.0	IPF8069	orf19.3698	unknown function
CA1360	1.1	1.0	0.9	1.0	1.3	1.0	PGA49	orf19.4404	unknown function
CA5799	1.1	1.0	1.1	1.0	0.9	1.0	IPF4176	orf19.5449	unknown function
CA1531	1.1	1.3	0.9	1.1	1.1	0.8	RVS167	orf19.1220	(putative) cytoskeletal protein (by homology)
CA2683	1.1	0.9	0.8	1.1	1.1	1.0	IFU4	orf19.2574	Unknown function
CA0043	1.1	0.9	0.9	0.9	1.0	1.0	HRD1	orf19.719	Involved in degradation of Hmg2p
CA1209	1.1	1.1	1.1	0.9	0.9	1.1	ARG8.3f	orf19.3771	acetylornithine aminotransferase (by homology)
CA0982	1.1	1.3	0.8	0.4	3.4	1.8	IPF7397	orf19.1800	unknown function
CA2996	1.1	0.9	0.7	0.8	0.5	0.6	IPF9108	orf19.6124	similar to Saccharomyces cerevisiae Ace2p transcription factor (by homology)
CA3609	1.1	1.1	1.1	0.9	1.2	0.9	IPF3856	orf19.26	similar to Saccharomyces cerevisiae Png1P peptide:N-glycanase (by homology)
CA4465	1.1	0.9	1.3	1.1	0.8	1.4	IPF9829	orf19.6862	unknown function
CA4314	1.1	1.1	0.7	0.9	0.5	0.5	PMT4	orf19.4109	Mannosyltransferase (by homology)
CA2433	1.1	1.0	1.1	1.0	1.2	1.0	IPF12959	orf19.3399	unknown function
CA3622	1.1	1.0	0.8	0.9	1.0	0.9	IPF12022	orf19.206	extracellular alpha-1,4-glucan glucosidase (by homology)
CA2886	1.1	0.9	0.9	1.0	0.9	1.0	IPF7207	orf19.2473	unknown function
CA3560	1.1	1.0	3.1	1.0	1.6	1.2	CZF1	orf19.3127	canal zinc finger protein
CA1063	1.1	1.1	1.2	0.9	1.0	1.2	NMT1	orf19.4641	N-myristoyltransferase
CA3751	1.1	0.9	1.1	0.9	0.9	1.1	IPF7378	orf19.3427	unknown function
CA5321	1.1	1.1	1.1	1.0	0.9	0.8	RAD6.3f	orf19.7195	Ubiquitin protein ligase, 3-prime end
CA3887	1.1	0.9	0.8	1.0	1.1	1.1	IPF12964	orf19.5093	similar to Saccharomyces cerevisiae Sfh1p subunit of the RSC chromatin remodeling complex (by homology)
CA1099	1.1	1.3	5.4	1.3	5.9	3.8	IPF12312	orf19.5070	unknown function
CA3263	1.1	1.1	1.3	0.9	0.6	0.7	UBR12	orf19.2697	ubiquitin-protein ligase by homology
CA1612	1.1	0.9	1.0	0.7	0.9	0.9	IFJ6	orf19.3214	unknown function
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)
CA2553	1.1	1.2	0.6	0.9	0.9	1.0	IPF9096	orf19.2838	probable mannosidase (by homology)
CA1073	1.1	1.0	1.1	0.8	0.5	0.7	PRORS.3f	orf19.2533	prolyl-tRNA synthetase, 3-prime end
CA2006	1.1	1.0	0.7	0.8	0.7	0.7	IPF11801	orf19.2798	unknown function
CA1798	1.1	1.1	0.6	0.9	0.4	0.6	IPF11448	orf19.2923	unknown function
CA0490	1.1	0.8	0.8	1.0	0.9	0.8	COS161	orf19.2637	involved in manganese homeostasis (by homology)
CA4913	1.1	1.0	1.3	1.0	1.2	6.8	CIS2	orf19.6053	Gamma-glutamyltransferase (by homology)
CA3937	1.1	1.2	1.3	0.9	1.1	1.1	IPF14686	orf19.2006	unknown function
CA2875	1.1	1.0	1.0	1.0	1.0	1.0	MEI5	orf19.5844	meiotic protein (by homology)
CA4403	1.1	1.0	1.1	1.2	1.1	1.0	IPF8777	orf19.3107	unknown function
CA3010	1.1	0.7	1.6	1.0	1.6	1.0	IPF14568	orf19.6230	unknown function
CA1400	1.1	1.0	1.0	1.1	0.9	0.8	IPF8067	orf19.3697	unknown function
CA2717	1.1	1.1	1.0	0.9	0.8	0.7	MSB3	orf19.578	GTPase-activating protein for Sec4p (by homology)
CA5748	1.1	1.0	1.0	1.0	1.0	1.1	IPF2905	orf19.7457	unknown function
CA4452	1.1	1.0	0.8	1.0	1.1	0.8	IPF3514	orf19.6850	unknown function
CA3662	1.1	0.9	1.1	1.1	2.6	0.8	IPF17021	orf19.6464	unknown function

CA5839	1.1	1.0	0.9	0.9	0.3	0.6	IPF423	orf19.7494	unknown function
CA2481	1.1	1.0	1.0	0.9	0.6	0.9	MRPL36	orf19.3205	ribosomal protein YmL36 precursor, mitochondrial (by homology)
CA3549	1.1	1.4	1.0	1.1	0.7	1.0	ARC40	orf19.3873	subunit of the Arp2/3 complex involved in the control of actin polymerization (by homology)
CA3091	1.1	1.0	1.1	0.9	1.0	1.0	IPF9821.5f	orf19.4142	unknown function, 5-prime end
CA4774	1.1	1.1	0.8	1.1	1.1	1.0	IPF3341	orf19.4006	Unknown function
CA2506	1.1	1.0	1.1	0.9	1.0	1.3	IPF6794	orf19.5596	unknown function
CA1881	1.1	1.1	1.5	1.3	0.8	1.0	RCK2	orf19.2268	Ca/calmodulin-dependent ser/thr protein kinase (by homology)
CA3384	1.1	0.6	0.9	0.8	0.7	0.7	IPF8362	orf19.325	similar to Saccharomyces cerevisiae Cft2p involved in cleavage and polyadenylation specificity factor, part of CF II
CA0232	1.1	1.0	0.9	1.0	1.3	1.0	IFA1	orf19.156	Unknown function
CA1840	1.1	1.1	0.8	0.9	1.4	1.0	IFP3	orf19.4707	Unknown Function
CA5010	1.1	1.1	1.0	1.1	1.8	1.9	IPF13945	orf19.5236.1	Unknown function
CA1059	1.1	1.1	0.8	1.0	1.1	1.1	TRP2	orf19.2546	anthranilate synthase component I (by homology)
CA1139	1.1	1.1	0.8	0.9	0.8	0.8	IPF9466	orf19.4066	unknown function
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
CA2317	1.1	1.0	1.1	1.0	1.0	1.0	IPF13586	orf19.5479	unknown function
CA2258	1.1	2.8	0.9	0.9	7.4	15.1	IFR1	orf19.1763	Unknown function
CA1714	1.1	1.0	1.7	1.2	1.1	0.9	NAB2	orf19.3333	Nuclear poly(A)-RNA-binding protein (by homology)
CA2393	1.1	0.8	0.8	1.0	0.6	0.8	RHO3	orf19.3534	GTP-binding protein of the rho family
CA1255	1.1	1.2	0.8	0.9	1.3	1.0	IPF9030	orf19.1776	unknown function
CA5887	1.1	1.1	0.8	0.8	1.3	1.1	IPF2415	orf19.6821	similar to Saccharomyces cerevisiae Apc2p component of the anaphase promoting complex (by homology)
CA2033	1.1	0.9	1.1	1.0	0.6	0.8	SEC27	orf19.3467	coatomer complex beta chain (beta -cop) of secretory pathway vesicles (by homology)
CA0171	1.1	1.0	0.9	1.3	0.9	0.9	PGA56	orf19.1105.2	unknown function unknown function
CA3185	1.1	1.0	0.8	1.3	1.5	1.3	IPF13637	orf19.2137	unknown function
CA2439	1.1	1.2	1.3	1.1	1.1	1.1	IPF7514	orf19.2197	unknown function
CA1843	1.1	1.0	1.0	0.9	0.9	1.1	IPF11364	orf19.635	unknown function
CA4532	1.1	0.7	1.0	1.0	1.3	1.4	IPF4386	orf19.1473	unknown function
CA5449	1.1	1.0	1.2	1.0	1.0	1.0	DAL81	orf19.3252	Transcriptional activator for allantoin and GABA catabolic genes (by homology)
CA4928	1.1	1.0	1.1	1.0	1.0	1.1	IPF1399	orf19.6068	unknown function
CA4886	1.1	0.7	1.5	1.0	2.0	1.4	IPF1634	orf19.6578	unknown function
CA5841	1.1	0.9	1.2	0.9	1.0	1.0	IPF420	orf19.7497	unknown function
CA1682	1.1	1.0	0.8	1.0	1.0	1.0	Cirt3	orf19.4918	Putative transposase (by homology)
CA1274	1.1	0.9	1.5	1.2	1.0	1.0	SAS10	orf19.2717	Involved in silencing (by homology)
CA1468	1.1	1.0	1.0	0.9	1.3	1.0	SRB10	orf19.794	cyclin-dependent kinase by homology
CA1250	1.1	0.6	0.8	1.1	0.7	0.9	IPF9626	orf19.4959	unknown function
CA2983	1.1	0.9	1.1	1.0	0.9	1.0			
CA3518	1.1	1.0	0.9	0.6	0.9	0.6	AMYG2.5f	orf19.999	glucoamylase, 5-prime end
CA1893	1.1	0.9	1.0	1.2	0.9	1.0	TIM13	orf19.2754	subunit of mitochondrial protein import machinery-like by homology
CA5789	1.1	1.0	1.7	1.3	2.6	2.0	IPF1143	orf19.5438	Probable zinc-finger protein Unknown function
CA2997	1.1	1.2	1.2	1.2	1.3	1.3	KGD2	orf19.6126	2-oxoglutarate dehydrogenase complex E2 component (by homology)
CA0143	1.1	1.0	0.9	0.8	0.8	0.9	IPF19195.5f	orf19.153	putative amino acid or GABA permease, 5-prime end (by homology)
CA1948	1.1	1.1	1.0	1.1	1.1	1.1	IPF14022	orf19.4743	ATPase family gene (by homology)
CA0744	1.1	0.9	1.1	0.8	0.8	0.9	IPF14919.3f	orf19.1529	unknown function
CA2486	1.1	1.0	0.9	1.0	1.1	0.9			
CA3949	1.1	0.9	1.1	1.1	0.8	1.0	SIR21	orf19.1992	regulatory protein (by homology)
CA3379	1.1	1.3	1.0	1.1	1.0	1.0	IPF8350	orf19.331	putative methyltransferase (by homology)
CA3795	1.1	1.0	1.1	1.0	0.9	1.2	IPF5699	orf19.5824	Abhydrolase by homology

CA3439	1.1	1.0	1.0	1.0	1.1	0.9	IPF11329	orf19.2986	unknown function
CA0151	1.1	1.0	0.9	1.0	0.6	1.0	IPF15923.5	orf19.177	unknown function, 5-prime end
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 utilisation pathway (by homology)
CA2429	1.1	1.1	1.0	1.0	1.0	1.0	IPF9890	orf19.3404	unknown function
CA1650	1.1	1.0	1.0	0.9	1.1	1.0	IPF5389	orf19.5565	3-hydroxyisobutyrate dehydrogenase by homology
CA2639	1.1	1.0	0.9	1.0	1.4	1.0	IPF2932	orf19.4305	unknown function
CA0714	1.1	1.0	0.9	1.4	1.7	4.6	IPF9480	orf19.3394	unknown function
CA1208	1.1	1.0	1.0	1.0	0.9	1.0	IPF17195.3f	orf19.3772	unknown function
CA0484	1.1	1.2	1.1	1.0	1.1	1.0	IPF19622.5f	orf19.115	unknown function, 5-prime end
CA4247	1.1	1.1	1.0	1.0	0.8	0.9	TAF90	orf19.536	Probable transcription-associated factor protein
CA4228	1.1	1.0	1.3	1.0	0.9	1.0	IPF16057	orf19.831	unknown function
CA0521	1.1	1.1	1.2	1.1	1.2	1.4	CKA2	orf19.3530	casein kinase II alpha chain (by homology)
CA4015	1.1	1.1	1.1	0.9	0.8	0.8	IPF12268	orf19.1618.2	unknown function
CA6093	1.1	1.2	1.0	1.0	1.0	0.9	ARF22	orf19.5964	GTP-binding protein of the ARF family (by homology)
CA1658	1.1	1.2	1.1	1.0	0.8	0.8	IPF19924	orf19.4324	unknown function
CA0646	1.1	1.3	0.8	1.0	1.0	1.2	IPF19702.5f	orf19.4330	uknown function, 5-prime end
CA6156	1.1	1.0	0.7	0.8	1.1	0.9	GEF1.3f	orf19.5881	Voltage-gated chloride channel protein, 3-prime end (by homology)
CA4400	1.1	1.2	4.0	1.0	0.7	1.6	IPF14362	orf19.3110	unknown function
CA5982	1.1	1.2	1.0	1.1	1.0	0.9	IPF915	orf19.7578	unknown function
CA4282	1.1	1.3	0.9	1.1	1.5	1.0	IPF2319	orf19.6680	unknown function
CA3183	1.1	0.8	0.9	1.0	0.7	1.0	TSM1.3f	orf19.2135	component of TFIID complex, 3-prime end (by homology)
CA1336	1.1	1.2	1.0	1.0	1.1	1.1			
CA1126	1.1	1.3	1.0	0.9	0.5	0.9	IPF5203	orf19.3607	unknown function
CA4435	1.1	0.6	1.3	0.9	0.7	0.7	IPF5567	orf19.5160	phosphatase associated protein by homology
CA3780	1.1	1.0	1.0	1.0	0.9	1.0	IPF11222	orf19.5840	unknown function
CA4121	1.1	1.0	1.0	1.1	1.2	1.1	IPF7081	orf19.2770	unknown function
CA0309	1.1	1.0	1.2	1.0	0.8	0.9	IPF16935	orf19.1091	unknown function
9601.20	1.1	1.0	0.8	1.0	0.5	1.1			
CA0501	1.1	1.4	1.1	1.2	0.8	1.0	IPF16501	orf19.4795	unknown function
CA3654	1.1	0.8	1.3	1.3	0.6	0.8	IPF7452	orf19.2045	unknown function
CA1908	1.1	1.0	0.9	0.8	0.9	0.7	APL3	orf19.2786	AP-2 complex subunit, alpha-adaptin (by homology)
CA1342	1.1	1.0	1.1	0.9	0.9	1.0	IPF11347	orf19.4340.1	unknown function
CA3237	1.1	0.9	1.3	1.1	1.0	1.1	SPB4	orf19.6298	ATP-dependent RNA helicase of DEAH box family (by homology)
CA1152	1.1	1.0	1.0	0.9	1.0	1.0	IPF10457	orf19.103	
CA4625	1.1	1.5	0.8	0.9	0.9	1.2	IPF5742	orf19.3319	thioredoxin-like protein (by homology)
CA0552	1.1	1.1	0.8	1.0	0.8	1.0	IPF4343	orf19.5533	similar to Saccharomyces cerevisiae Vps9pvacuolar sorting protein
CA1882	1.1	2.4	0.8	1.0	0.8	1.9	IPF19934	orf19.2210	unknown function
CA5274	1.1	1.0	0.9	0.9	0.5	0.7	IPF1764	orf19.4985	similar to Saccharomyces cerevisiae Gup1p glycerol transporter (by homology)
CA2395	1.1	1.1	1.1	1.0	1.0	1.6	IPF6425	orf19.3536	unknown function
CA2325	1.1	1.0	1.1	1.0	1.0	1.1	IPF10977	orf19.5488	unknown function
CA1464	1.1	1.3	0.8	0.9	1.1	1.0	PYC2.3f	orf19.789	Pyruvate carboxylase 2, 3 prime end (by homology)
CA4992	1.1	1.0	1.0	1.0	1.0	1.0	IPF2036	orf19.5256	unknown function
CA4296	1.1	0.9	1.2	0.9	0.6	0.8	IPF2605	orf19.6693	unknown function
CA1777	1.1	1.0	1.1	0.9	0.9	1.0	PGA50	orf19.1824	unknown function
CA3463	1.1	1.1	0.9	1.0	0.5	0.6	ALG8	orf19.1659	glucosyltransferase (by homology)
CA2343	1.1	1.0	1.0	1.0	0.9	1.0	IPF8671	orf19.2343	unknown function

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 homology)
CA5421	1.1	1.1	1.1	1.1	0.9	1.1	SKN7	orf19.971	Transcription factor (by homology)
CA5428	1.1	0.7	1.0	0.9	0.8	0.9	BOI2	orf19.3230	budding protein (by homology)
CA5713	1.1	1.0	0.6	1.0	1.0	1.3	ALS6	orf19.7414	agglutinin-like protein
CA1163	1.1	1.3	1.0	1.3	1.0	1.0	IPF15357	orf19.2730	unknown function
CA2792	1.1	1.0	0.9	1.0	0.6	1.2	TRK1.3f	orf19.602	Potassium transporter, 3-prime end
CA5670	1.1	1.1	1.6	1.0	0.5	1.1	IPF1266	orf19.7372	Probable transcription factor
CA4091	1.1	1.0	1.2	1.0	1.0	0.9	IPF5005	orf19.6650	unknown function
CA2877	1.1	1.0	0.8	1.0	2.0	1.3	TFB2	orf19.5846	Transcription/repair factor (by homology)
CA4974	1.1	1.2	1.1	1.0	1.0	1.1	IPF4704	orf19.5278	unknown Function
CA4667	1.1	0.7	0.9	1.4	0.6	0.3	GAP5	orf19.4456	General amino acid permease (by homology)
CA4893	1.1	1.0	1.3	1.1	1.3	1.4	IPF1621	orf19.6585	unknown function
CA4868	1.1	1.2	1.1	1.1	0.8	1.1	IPF4078	orf19.3845	Unknown Function
CA5487	1.1	0.7	0.9	1.1	1.0	1.0	MET12	orf19.5321	methylenetetrahydrofolate reductase (by homology)
CA2126	1.1	1.0	0.9	1.0	1.1	0.8	IPF4896	orf19.417	unknown function
CA1648	1.1	1.0	1.2	1.2	1.1	1.2	IPF16662	orf19.5567	unknown function
CA2400	1.1	0.8	1.1	1.0	0.7	1.0	SUP45	orf19.3541	Translational release factor (by homology)
CA1488	1.1	1.2	0.9	0.8	0.6	0.7	IPF17402.5	orf19.4064	unknown function
CA0312	1.1	1.0	0.9	1.0	1.2	1.0	IPF6396	orf19.580	unknown function
CA1459	1.1	1.1	1.2	0.9	1.6	1.4	IPF6340	orf19.1107	unknown function
CA6025	1.1	1.1	0.9	0.9	0.9	0.9	IPF614	orf19.7629	unknown function
CA5422	1.1	1.0	1.0	1.0	0.9	1.0	IPF1588	orf19.972	unknown function
CA1969	1.1	1.1	1.0	1.0	1.0	1.1	IPF18579.3f	orf19.5221	unknown function, 3-prime end
CA3106	1.1	0.9	0.9	1.0	0.9	0.9	IPF11821	orf19.6552	unknown function
CA1296	1.1	1.0	4.0	1.9	0.9	0.9			
CA0235	1.1	0.9	1.2	1.0	2.4	1.8	HIS3	orf19.183	imidazole glycerol phosphate dehydratase
CA5881	1.1	1.0	1.1	1.1	0.5	0.8	SSS1	orf19.6828.1	ER protein-translocase complex subunit (by homology)
CA5353	1.1	1.2	0.5	0.9	1.7	0.9	IML2	orf19.7229	unknown function
CA0790	1.1	1.0	1.2	0.9	0.9	0.9	IPF14193	orf19.3357	unknown function
CA1910	1.1	1.1	0.8	1.1	0.8	1.0	IPF7260	orf19.2790	unknown function
CA2231	1.1	1.0	1.0	1.0	1.0	1.0	IPF10934	orf19.3926	similar to Saccharomyces cerevisiae Rny1 ribonuclease from the T2 family of ribonucleases (by homology)
CA2456	1.1	1.0	1.0	1.1	1.2	1.3	DBR1	orf19.3506	lariat-debranching enzyme (by homology)
CA1393	1.1	1.0	1.2	1.0	0.9	1.1	IFO3	orf19.1766	Similar to Streptomyces coelicolor putative hydrolase
CA3407	1.1	1.1	1.1	1.2	1.1	1.2	IPF9406	orf19.6152	unknown function
CA1217	1.1	1.1	1.0	1.0	1.1	1.4	IPF13909	orf19.123	Unknown function
CA5814	1.1	1.0	1.0	1.1	0.9	1.0	IPF2521	orf19.7463	putative protease (by homology)
CA0676	1.1	1.1	1.1	1.0	0.9	0.9	IPF13097	orf19.1181	unknown function
CA4337	1.1	0.9	1.1	0.8	1.1	1.0	IPF2071	orf19.4079	unknown function
CA3759	1.1	0.9	1.0	1.0	1.2	1.0	PGA43	orf19.2910	unknown function
CA0562	1.1	1.0	1.2	1.0	0.8	1.0	PSO2	orf19.2926	Interstrand crosslink repair protein (by homology)
CA2125	1.1	1.1	0.7	0.8	0.8	0.9	IPF4893	orf19.418	unknown function
CA5575	1.1	1.0	1.3	0.9	1.2	1.0	IPF19813	orf19.7342	unknown function
CA5533	1.1	1.1	1.0	1.0	0.4	0.6	IPF2846	orf19.7293	similar to Saccharomyces cerevisiae Mps1p serine/threonine/tyrosine protein kinase (by homology)
CA2487	1.1	1.0	0.7	1.0	0.9	0.9			
CA0435	1.1	1.4	0.9	0.7	0.3	0.8	UGP1	orf19.1738	UTP--glucose-1-phosphate uridylyltransferase (by homology)
CA5652	1.1	0.9	2.6	0.8	0.5	0.6	IPF19815	orf19.7354	longevity-assurance protein (by homology)

CA5634	1.1	0.9	0.9	1.1	1.0	1.0	IPF477	orf19.7061	unknown function
CA0429	1.1	1.0	1.0	1.0	1.1	1.0	IPF14827	orf19.1611	unknown function
CA6017	1.1	1.1	1.2	1.3	1.4	1.3	IPF629	orf19.7619	unknown function
CA4347	1.1	1.1	1.1	1.0	0.9	1.2	IPF3636	orf19.6722	similar to Saccharomyces cerevisiae Rad4p excision repair protein (by homology)
CA5075	1.1	0.8	0.8	0.8	0.9	0.8	IPF3610	orf19.3050	unknown function
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 homology)
CA2500	1.1	1.0	0.8	0.9	0.6	1.0	FIG4	orf19.5586	suppressor of sac1 mutation (by homology)
CA0247	1.1	1.1	1.1	1.0	1.2	1.0	RIB21	orf19.2788	DRAP deaminase (by homology)
CA2005	1.1	1.0	0.9	1.0	1.0	1.0	IPF11802	orf19.2797	unknown function
CA3643	1.1	1.0	1.1	1.0	1.0	1.0	IPF4124	orf19.2034	unknown function
CA0078	1.1	1.1	1.1	1.0	1.1	1.0	CTA27.5eoc	orf19.381	unknow function,5 -prime end
CA4056	1.1	1.3	1.0	0.9	1.5	0.8	IPF7721	orf19.431	unknown function
CA3395	1.1	0.9	1.2	0.9	1.0	1.0	IPF13616	orf19.3970	unknown function
CA3521	1.1	1.0	0.9	1.0	1.0	1.0	IFA15	orf19.996	unknown function
CA0469	1.1	1.0	1.1	1.0	1.2	1.1	IPF18977	orf19.2621	similar to Saccharomyces cerevisiae Smb1p associated with U1 snRNP
CA4122	1.1	1.2	1.1	1.0	1.1	1.1	PBI2	orf19.2769	proteinase B inhibitor 2 (by homology)
CA1684	1.1	1.0	1.0	0.9	1.0	1.0	IPF6070	orf19.4921	unknown function
CA5420	1.1	1.0	1.1	1.1	1.2	1.1	IPF1583	orf19.970	unknown function
CA1084	1.1	1.0	1.0	1.0	1.0	1.0	IPF1036	orf19.4571	unknown function
CA2077	1.1	1.0	0.9	1.0	1.9	1.1	IPF13353	orf19.4872	unknown function
CA5019	1.1	0.9	1.3	0.9	0.6	0.7	IPF7557	orf19.6972	similar to Saccharomyces cerevisiae Smi1p involved in beta-1,3-glucan synthesis (by homology)
CA3031	1.1	0.9	1.0	1.0	0.8	0.9	IPF12324	orf19.217	unknown function
CA5703	1.1	0.9	0.9	1.0	0.7	0.5	IPF2463	orf19.7403	unknown function
CA0947	1.1	1.5	1.0	1.2	1.3	0.9	CFL3	orf19.1270	ferric reductase-like protein
CA0187	1.1	1.0	1.0	0.9	0.9	1.0			
CA1785	1.1	1.1	1.4	1.1	1.2	1.0	IPF7631	orf19.1169	unknown function
CA5741	1.1	1.0	1.0	1.0	1.1	1.0	IPF2891.3f	orf19.7450.1	unknown function
CA1525	1.1	0.6	0.9	1.0	1.4	0.8	AGP3	orf19.3795	amino acid-permease (by homology)
CA1450	1.1	1.0	0.9	1.0	1.4	1.0	IPF6474	orf19.4414	unknown function
CA1324	1.1	0.6	1.7	0.9	0.8	0.6	IPF6676	orf19.1308	polytopic membrane protein involved in drug transport (by homology)
CA1604	1.1	1.1	1.1	1.0	0.9	1.0	IPF13653	orf19.4724	unknown function
CA2062	1.1	0.9	1.1	1.0	0.8	1.0	IPF7858	orf19.2563	similar to Saccharomyces cerevisiae Prp24p U4/U6 splicing factor (by homology)
CA3470	1.1	1.0	0.9	0.9	0.5	0.6	IPF6310	orf19.1666	unknown function
CA1970	1.1	1.0	1.0	0.9	0.8	1.2	IPF18579.5f	orf19.5222	unknown function, 5-prime end
CA4275	1.1	1.0	1.0	1.0	1.2	1.0	MDJ1	orf19.6672	Heat shock protein - chaperone (by homology)
CA2786	1.1	0.9	0.8	0.9	0.6	0.7	KRE5	orf19.290	UDP-glucose:glycoprotein glucosyltransferase,(by homology)
CA2859	1.1	0.9	0.6	1.0	0.9	0.7	IPF7056	orf19.1063	unknown function
CA3350	1.1	1.0	1.0	1.0	1.0	1.0			
CA0852	1.1	0.9	0.8	0.9	0.4	0.8	KIP2	orf19.1747	Kinesin-related protein required for nuclear migration (by homology)
CA4645	1.1	1.1	1.0	1.0	1.0	1.0	IPF1496	orf19.352	unknown function
CA0422	1.1	0.9	1.1	0.9	1.1	1.0	IPF9046	orf19.2231	unknown function
CA4668	1.1	1.1	0.7	0.6	1.0	1.0	ROM2	orf19.906	GDP/GTP exchange factor for Rho1p (by homology)
CA4488	1.1	1.0	1.0	1.1	1.0	0.9	MEK1.3f	orf19.1875	serine/threonine protein kinase, 3-prime end
CA0972	1.1	1.6	1.1	1.2	1.0	1.0	CYP1	orf19.6472	cyclophilin (peptidylprolyl isomerase), mitochondrial (by homology)
CA5598	1.1	1.1	0.9	0.9	1.2	0.8	IPF562	orf19.7101	unknown function
CA5825	1.1	1.0	1.1	1.0	1.1	1.0	IPF2489	orf19.7480	unknown function

CA3962	1.1	1.0	1.0	0.9	1.1	0.9	IPF11234	orf19.1421	similar to saccharomyces cerevisiae Dal3p ureidoglycolate hydrolase (by homology)
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)
CA0308	1.1	1.0	0.8	0.8	0.5	0.6	RHK1	orf19.1092	Mannosyltransferase (by homology)
CA2247	1.1	1.0	1.0	1.0	0.8	1.0	IPF7404	orf19.4665	unknown function
CA2319	1.1	1.1	0.8	0.8	0.8	0.9	GUF1	orf19.5483	GTP-binding protein (by homology)
CA4365	1.1	0.9	1.1	1.2	1.0	1.1	IPF5268	orf19.5656	choline monooxygenase, (by homology)
CA0634	1.1	1.0	1.2	1.0	0.6	0.9	IPF16267	orf19.1772	unknown function
CA4636	1.1	1.0	0.9	1.1	0.9	1.0	IPF1520	orf19.342	unknown function
CA6020	1.1	1.0	1.0	1.0	1.1	1.2	SPT3	orf19.7622	transcription factor
CA6077	1.1	0.9	2.2	1.6	0.6	0.7	IPF16	orf19.5984	unknown function
CA1227	1.1	0.5	1.3	0.9	0.6	0.8	IPF16082	orf19.4160	unknown function
CA0917	1.1	1.2	0.8	1.3	1.9	1.1	RAD16	orf19.2969	nucleotide excision repair protein (by homology)
CA3321	1.1	1.2	0.7	0.7	0.6	0.7	IPF6896.5f	orf19.2677	unknown function, 5-prime end
CA1038	1.1	1.0	1.0	0.9	1.5	1.3	IPF6159	orf19.1035	unknown function
CA4897	1.1	1.0	1.0	1.1	0.5	0.7	TUB2	orf19.6034	Beta-tubulin
CA4038	1.1	0.9	2.7	1.2	1.4	0.9	HGT12	orf19.3668	hexose transporter
CA3585	1.1	1.0	1.0	1.0	1.0	1.0	IFT1	orf19.2253	unknown function
CA5415	1.1	1.0	1.0	0.9	0.6	0.8	SMC4	orf19.964	Stable Maintenance of Chromosomes (by homology)
CA4709	1.1	1.1	0.8	1.1	1.4	0.7	IPF5895	orf19.6941	unknown function
CA2441	1.1	0.9	1.1	1.0	1.1	0.8	APM4	orf19.2194	AP-2 complex subunit, mu2 subunit (by homology)
CA0094	1.1	1.0	1.1	1.1	0.9	1.0	IPF12819	orf19.3213	unknown function
CA2063	1.1	0.9	0.9	1.0	1.1	1.1	IPF7859	orf19.2564	unknown function
CA1696	1.1	0.8	1.2	0.9	0.9	1.0	ASM4	orf19.5040	similar to Saccharmoyces cerevisiae Asm4p suppressor of temperature-sensitive mutations in Pol3p (by homology)
CA0028	1.1	1.1	1.3	1.0	1.4	1.1	IPF15345	orf19.1502	peptidyl-tRNA-hydrolase (by homology)
CA1930	1.1	0.9	1.3	0.9	0.9	0.5	IPF3906.3f	orf19.758	unknown function, 3-prime end
CA6036	1.1	1.1	1.0	0.9	0.9	1.0	IPF585	orf19.7646	unknown function
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. cerevisiae)
CA4725	1.1	1.0	1.0	1.0	0.9	1.0	PET100	orf19.4862.2	cytochrome-c oxidase assembly protein (by homology)
CA5147	1.1	1.1	0.8	1.0	0.8	0.9	PHO12	orf19.4584	Acid phosphatase, secreted (by homology)
CA4177	1.1	0.9	0.9	1.0	1.0	1.1	MGM101	orf19.2956	mitochondrial genome maintenance protein (by homology)
CA2622	1.1	1.5	0.9	1.2	0.9	0.8	PER3.3f	orf19.2806	peroxisomal import protein, 3-prime end (by homology)
CA3105	1.1	1.1	0.8	1.0	0.8	0.8	IPF12083	orf19.6553	unknown function
CA3906	1.1	1.2	1.2	1.2	1.0	0.9	IPF20149	orf19.4396	unknown function
CA2911	1.1	1.0	1.1	0.9	1.0	1.1	MET7	orf19.4516	folylpolyglutamate synthetase [Candida albicans]
CA4631	1.1	1.2	0.8	1.0	1.3	0.9	VTI1	orf19.337	v-SNARE involved in Golgi retrograde traffic (by homology)
CA0180	1.1	1.0	1.0	1.0	0.8	0.9	SPT20	orf19.422	transcription factor, member of the histone acetyltransferase SAGA complex (by homology)
CA4593	1.1	1.0	1.1	1.0	1.0	1.1	IPF2214	orf19.6910	unknown function
CA3231	1.1	1.3	0.9	1.1	1.3	1.1	IPF14348.3f	orf19.6293.1	unknown function, 3-prime end
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 pheromone induction of karyogamy genes
CA0059	1.1	1.4	1.3	1.1	1.0	1.1	IPF17840	orf19.566	unknown function
CA3166	1.1	1.1	0.9	1.0	0.8	0.9	IPF9634	orf19.1577	probable GATA zinc finger transcription factor (by homology)
CA3016	1.1	0.7	1.0	0.8	0.7	0.7	IPF10027	orf19.3914	unknown function
CA2585	1.1	1.0	1.3	1.1	1.3	1.2	IPF9438	orf19.4374	similar to Saccharomyces cerevisiae Prp42p U1 snRNP associated protein, required for pre-mRNA splicing
CA3543	1.1	0.8	1.0	1.1	0.8	0.9	IPF5428	orf19.6379	unknown function
CA3201	1.1	1.0	0.8	0.9	1.1	0.9	IPF3444.3f	orf19.6182	unknown function, 3-prime end
CA5767	1.1	1.0	0.8	1.0	1.2	1.1	IPF1098	orf19.5409	unknown function

CA3414	1.1	0.8	1.2	1.1	0.6	1.0	IPF9240	orf19.6141	probable permease
CA1251	1.1	1.0	1.0	1.0	0.8	0.9	IPF9624.5f	orf19.4957.1	similar to Saccharomyces cerevisiae Ecm25p involved in cell wall biogenesis and architecture, 5-prime end
CA5828	1.1	0.9	1.0	0.8	0.9	0.9	CRM1	orf19.7483	Nuclear export factor
CA5798	1.1	1.0	7.3	6.1	0.8	0.9	IPF4181	orf19.5447	putative permease (by homology)
CA2544	1.1	1.3	1.1	1.0	0.9	0.9	IPF16924	orf19.2829	unknown function
CA1471	1.1	1.0	0.9	1.0	0.9	1.0	ALS2.53feo	orf19.1098	agglutinin-like protein, internal fragment
CA0534	1.1	1.0	1.4	0.9	1.1	1.0	IPF15607	orf19.5066	unknown function
CA0041	1.1	0.9	1.0	1.1	0.7	0.9	IPF10360	orf19.3804	unknown function
CA4855	1.1	1.0	1.2	1.3	2.0	0.7	IPF5830	orf19.3826	unknown function
CA0715	1.1	0.9	2.5	1.3	1.4	1.4	DBP9	orf19.3393	dead box helicase
CA3345	1.1	1.2	1.0	1.3	1.4	1.0	IPF13357	orf19.2325	unknown function
CA4573	1.1	0.7	0.8	1.0	0.6	0.6	IPF9431	orf19.6884	unknown function
CA0580	1.1	0.9	1.1	0.8	0.8	0.9			
CA2397	1.1	1.0	1.1	1.0	1.5	1.0	CFL12	orf19.3538	Strong similarity to ferric reductase Fre2p (by homology)
CA0129	1.1	0.9	1.0	1.0	1.2	2.2	IPF10495	orf19.246	unknown function
CA4652	1.1	1.0	1.0	1.0	0.9	1.0	IPF3105	orf19.4439	Unknown function
CA1148	1.1	0.9	0.5	1.1	1.5	0.9	CAN1	orf19.97	amino acid permease (by homology)
CA3959	1.1	1.0	0.9	1.0	0.7	0.9	IPF11236.3f	orf19.1418	similar to Saccharomyces cerevisiae Sec15p component of the exocyst complex, 3-prime end (by homology)
CA1587	1.1	0.7	0.9	0.9	0.9	0.9	CMP2	orf19.6033	Calcineurin B, catalytic subunit (by homology)
CA0178	1.1	0.9	1.0	1.0	0.6	0.8			
CA3773	1.1	0.9	1.1	0.9	0.8	0.8	IPF11153	orf19.2893	unknown function
CA0198	1.1	1.2	1.1	1.0	1.4	0.5	IPF19685	orf19.1658	unknown function
CA2212	1.1	0.9	1.2	1.0	1.0	0.9	IPF13919	orf19.4750	unknown function
CA3565	1.1	1.3	0.7	0.7	1.1	1.1	MSC2	orf19.3132	Probable membrane protein
CA2008	1.1	0.5	1.1	1.2	0.6	0.9			
CA3566	1.1	1.0	1.0	0.8	1.3	1.2	GUT2	orf19.3133	Glycerol-3-phosphate dehydrogenase, mitochondrial (by homology)
CA4679	1.1	1.0	1.0	1.0	1.1	1.0	PGA17	orf19.893	unknown function
CA3212	1.1	0.9	1.1	0.9	0.5	0.8	MEF2	orf19.6208	translation elongation factor (by homology)
CA2790	1.1	1.1	1.0	1.0	0.9	1.2	IPF3562	orf19.604	Unknown function
CA4715	1.1	0.8	0.7	0.8	1.1	0.8	DPL1	orf19.6951	dihydrosphingosine phosphate lyase (by homology)
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)
CA5366	1.1	0.8	1.0	1.1	1.2	1.3	IPF823	orf19.7245	tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase
CA0485	1.1	1.0	1.3	0.9	1.0	1.0	IPF17574	orf19.3555	Unknown function
CA4698	1.1	1.4	0.7	0.9	0.6	0.7	CDC25	orf19.6926	cell division cycle protein
CA4280	1.1	1.0	1.1	1.1	1.2	1.1	IFJ5	orf19.6678	Unknown function
CA5783	1.1	0.9	1.1	1.0	1.2	1.1	IPF1128	orf19.5430	unknown function
CA4128	1.1	1.0	1.0	1.1	1.1	1.0	IPF6876	orf19.4250	unknown function
CA0538	1.1	1.0	1.0	1.2	1.2	1.1	IPF10901	orf19.2819	unknown function
CA3879	1.1	0.7	0.9	1.0	0.6	0.5	CDC42	orf19.390	Cell Division Control
CA1017	1.1	1.1	1.1	0.9	0.8	1.1	IPF11144	orf19.474	unknown function
CA4614	1.1	1.3	1.4	0.8	1.0	1.7	IPF7952	orf19.3305	unknown function
CA3952	1.1	1.0	1.0	1.0	1.8	1.1	IPF6716	orf19.1411	Phenylacetate 2-hydroxylase (by homology)
CA1598	1.1	0.7	1.0	1.2	1.0	1.1	SES1	orf19.269	seryl-tRNA synthetase (by homology)
CA5771	1.1	0.9	0.8	1.0	1.2	1.0	IPF1104	orf19.5413	similar to Saccharomyces cerevisiae Prp28p pre-mRNA splicing factor (by homology)
CA0742	1.1	1.0	0.7	1.0	1.3	0.9	IPF3259	orf19.3142	unknown function
CA2586	1.1	0.9	1.2	1.1	0.9	1.1	IPF9435	orf19.4375	unknown function

CA0428	1.1	1.2	1.0	0.8	1.1	0.8	ILV2	orf19.1613	acetolactate synthase (by homology)
CA5866	1.1	1.1	1.0	1.0	1.3	0.9	IPF361	orf19.7527	unknown function
CA2297	1.1	0.9	1.0	0.9	0.6	0.8	ERG4	orf19.5379	sterol C-24 reductase (by homology)
CA1819	1.1	1.0	1.2	1.0	0.4	0.9	IPF16549	orf19.4273	Unknown function
CA0556	1.1	1.0	1.0	1.0	1.0	1.0	IPF15920	orf19.4972	zinc-finger containing protein (by homology)
CA1826	1.1	1.1	1.2	1.0	1.3	1.3	UAP1	orf19.4265	UDP-N-acetylglucosamine pyrophosphorylase
CA1292	1.1	1.0	1.0	1.0	1.0	1.5	SRB2.3f	orf19.2711.1	DNA-directed RNA polymerase II holoenzyme and Kornberg s mediator (SRB) subcomplex subunit, 3-prime end
CA1171	1.1	1.0	0.9	0.9	0.8	1.2	IPF13264	orf19.2748	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type (by homology)
CA4561	1.1	1.0	0.7	1.1	1.1	1.1	IPF8031	orf19.6872	unknown function
CA1421	1.1	0.7	1.2	0.8	0.6	0.6	MRPL11	orf19.3797	Mitochondrial ribosomal protein (by komology)
CA4028	1.1	1.0	1.0	0.9	0.8	0.9	IPF7171.3f	orf19.3435	unknown function, 3-prime end
CA2626	1.1	1.0	0.9	1.2	0.9	0.9	PAN2	orf19.4764	component of Pab1p-stimulated poly(A)(by homology)
CA0571	1.1	1.0	1.1	0.9	0.9	0.8	CDC43	orf19.1803	geranylgeranyltransferase I
CA5673	1.1	0.8	0.9	1.0	0.8	0.7	IPF1272	orf19.7376	unknown function
CA1338	1.1	1.1	1.0	0.8	1.0	0.9	IPF5333	orf19.3449	unknown function
CA5342	1.1	1.2	1.1	1.0	1.5	0.7	YPT521	orf19.7216	GTP-binding protein of the rab/ypt family (by homology)
CA0922	1.1	1.0	1.1	1.0	1.2	1.0	IPF12991	orf19.1045	unknown function
CA4176	1.1	1.0	0.9	0.9	1.0	0.9	IFX2	orf19.2957	unknown function
CA3032	1.1	1.0	1.0	1.0	1.3	1.0	IPF12319	orf19.216	unknown function
CA2058	1.1	1.0	1.1	1.0	1.0	1.0	IPF7848	orf19.2558	unknown function
CA4212	1.1	1.0	1.0	1.0	1.3	1.0	HFM1	orf19.810	DNA/RNA helicase by homology
CA4582	1.1	1.1	1.0	1.0	1.1	1.0	MDM12	orf19.6900	Involved in mitochondrial inheritance (by homology)
CA1725	1.1	1.0	1.1	1.0	1.0	0.8	IPF15985	orf19.2650	unknown function
CA0806	1.1	1.5	1.1	1.0	1.1	0.8	IPF12567	orf19.3517	unknown function
CA4956	1.1	1.0	1.0	1.0	1.0	1.1	IPF4583	orf19.6520	putative allantoate permease (by homology)
CA5572	1.1	1.0	1.0	1.0	0.8	0.9	BGL22	orf19.7339	endo-beta-1,3-glucanase (by homology)
CA3374	1.1	0.9	1.2	1.1	1.2	0.9	IPF4683	orf19.1856	unknown Function
CA2432	1.1	1.0	0.8	1.0	1.0	1.2	COQ3	orf19.3400	3,4-dihydroxy-5-hexaprenylbenzoatemethyltransferase
CA1953	1.1	1.1	0.9	1.0	1.1	1.1	IPF3899	orf19.763	similar to Saccharomyces cerevisiae Cbc2p small subunit of the nuclear cap-binding protein complex CBC
CA1456	1.1	1.0	0.9	1.0	0.9	0.7			
CA1983	1.1	1.8	1.1	1.0	0.5	0.9	ILV5	orf19.88	ketol-acid reducto-isomerase (by homology)
CA4896	1.1	1.0	1.0	1.0	1.0	1.0	IPF18160	orf19.6588	unknown function
CA3950	1.1	1.1	0.8	0.9	0.5	0.7	PTM1	orf19.1991	Possibly involved in the TCA cycle (by homology)
CA0549	1.1	1.0	0.8	1.0	1.3	1.0	IPF14031	orf19.852	putative secreted aspartic protease (by homology)
CA1610	1.1	1.0	1.2	1.0	1.1	1.0	LAS1	orf19.4120	cell morphogenesis, cytoskeletal regulation and bud formation (by homology)
CA0047	1.1	1.0	1.0	1.0	0.8	0.8	PTC2	orf19.2538	Protein phosphatase type 2C (by homology)
CA4776	1.1	1.3	0.8	1.0	1.0	1.0	CNB1	orf19.4009	Protein phosphatase, Calcineurin B (by homology)
CA0932	1.1	0.7	1.2	1.2	0.4	0.5	EPT1	orf19.3695	alcohol phosphatidyl transferase (by homology)
CA5625	1.1	0.9	1.1	1.3	0.9	1.0	PEL1	orf19.7072	CDP-diacylglycerol-serine-O-phosphatidyltransfer ase (by homology)
CA1827	1.1	1.0	1.1	1.1	1.5	1.2	IPF9520	orf19.4264	unknown function
CA3291	1.1	1.0	1.1	1.0	0.9	1.0	IPF5730	orf19.6325.1	unknown function
CA0325	1.1	1.0	0.9	0.9	1.0	0.9	IPF15222	orf19.3781	Unknown function
CA1366	1.1	1.0	1.0	1.1	0.8	0.9	IPF11847	orf19.4457	unknown function
CA3006	1.1	0.7	1.6	1.3	1.1	1.2	IPF12152	orf19.6236	unknown function
CA0101	1.1	1.0	1.1	0.9	1.0	1.0	IPF10105	orf19.232	RNA polymerase-like (by homology)
CA1489	1.1	0.7	1.1	1.1	1.0	1.0	ATP3.3f	orf19.3223	F1F0-ATPase complex, F1 gamma subunit, 3-prime end (by homology)

CA1646	1.1	1.3	0.6	0.8	0.9	1.0	IPF9336	orf19.1725	unknown function
CA4685	1.1	0.8	0.8	1.0	0.9	0.8	IPF9013	orf19.881	unknown function
CA1590	1.1	1.0	2.3	1.0	0.9	1.0	IPF14665	orf19.4315	unknown function
CA5123	1.1	1.1	1.1	1.0	1.0	0.9	IPF1306	orf19.6405	unknown function
CA5514	1.1	1.0	1.0	0.9	1.1	0.9	IPF730	orf19.5362	unknown function
CA5301	1.1	1.7	1.4	1.2	3.2	1.9	IPF2186	orf19.7166	unknown function
CA2197	1.1	1.1	1.1	0.9	1.0	0.8	IPF8110	orf19.2936	unknown function
CA1815	1.1	1.0	1.0	0.9	1.1	1.0	IPF18606	orf19.138	unknown function
CA4108	1.1	1.0	1.0	1.0	1.3	1.3	IPF3968	orf19.672	similar to Saccharomyces cerevisiae pre-mRNA splicing factor RNA helicase of DEAD box family Prp28p
CA1283	1.1	1.0	1.0	1.1	1.0	1.0			
CA2078	1.1	1.0	0.9	0.9	1.4	1.0	IPF13352	orf19.4873	unknown function
CA4971	1.1	1.1	0.8	0.9	0.6	0.9	IPF4697	orf19.5281	similar to Saccharomyces cerevisiae Scp160p required for maintenance of exact ploidy (by homology)
CA2640	1.1	1.1	1.0	1.1	1.5	1.2	IPF2930	orf19.4305.1	Suppressor of PAB1 (by homology)
CA0994	1.1	1.1	1.0	1.0	1.2	1.2	IPF10077	orf19.2281	3-oxoacid CoA-transferase (by homology)
CA4277	1.1	1.4	1.1	1.1	1.6	1.2	BTS1	orf19.6674	Geranylgeranyl diphosphate synthase (by homology)
CA3301	1.1	0.8	1.4	1.2	1.2	1.2	IPF13782	orf19.2314	unknown function
CA0626	1.1	0.9	1.3	1.1	1.4	1.7	IPF3161	orf19.3161	Unknown function
CA5617	1.1	1.0	1.2	1.4	1.4	1.2	SPL1	orf19.7081	tRNA splicing protein
CA0396	1.1	0.9	1.0	0.9	1.3	1.0	SNM1	orf19.1927	RNA binding protein of RNase MRP (by homology)
CA5706	1.1	1.2	1.0	1.1	0.7	1.0	IPF2649	orf19.7406	unknown function
CA4661	1.1	1.0	1.1	0.9	0.7	0.9	IPF6561	orf19.4448	unknown function
CA4867	1.1	1.1	1.0	1.0	1.2	1.1	IPF4080	orf19.3844	similar to Saccharomyces cerevisiae Mrp8p ribosomal protein, mitochondrial (by homology)
CA0423	1.1	1.0	1.0	0.9	1.0	1.0	IPF15273	orf19.1822	unknown function
CA2600	1.1	0.4	0.9	0.6	0.8	0.6	IPF11177	orf19.51	similar to Saccharomyces cerevisiae Clu1p translation initiation factor eIF3 (p135 subunit) (by homology)
CA1125	1.1	0.9	1.6	1.2	1.1	1.4	RRP43	orf19.6259	rRNA processing protein (by homology)
CA2841	1.1	1.0	0.9	1.0	1.1	1.0	IPF12981	orf19.5727	unknown function
CA5036	1.1	1.0	0.8	1.0	1.2	1.1	CYP52	orf19.6990	Peptidyl-prolyl cis-trans isomerase D (by homology)
CA5550	1.1	1.6	4.0	1.9	3.8	8.0	SSU1	orf19.7313	Sulfite sensitivity protein (by homology)
CA1055	1.1	1.1	1.3	0.8	1.0	1.0	IPF17504	orf19.2541	unknown function
CA3594	1.1	1.1	0.8	0.9	1.2	1.0	IPF6076	orf19.4922	unknown function
CA5253	1.1	0.8	1.3	1.0	0.9	0.9	KEL3	orf19.5009	Kelch-repeat protein
CA5217	1.1	1.0	1.0	1.1	0.7	1.1	RFC2	orf19.7035	Replication factor (by homology)
CA3011	1.1	1.7	1.2	2.1	3.7	6.0	CTA1	orf19.6229	catalase A, peroxisomal(by homology)
CA0836	1.1	0.9	1.0	0.8	1.0	1.0	IPF12495	orf19.1679	unknown function
CA1371	1.1	0.9	1.1	1.0	1.0	1.1	IPF19731	orf19.4962	unknown function
CA4807	1.1	0.9	0.8	1.0	1.2	0.9	PDR6	orf19.2094	Pleiotropic drug resistance regulatory protein (by homology)
CA2437	1.1	0.9	0.9	0.9	1.0	1.0	PHO86	orf19.2199	inorganic phospate transporter by homology
CA2623	1.1	1.2	0.9	1.0	0.7	0.9	PER3.5f	orf19.2805	peroxisomal import protein, 5-prime end (by homology)
CA1327	1.1	0.9	1.1	1.0	1.0	1.0	IPF6680	orf19.1305	unknown function
CA2149	1.1	1.0	1.0	1.0	1.0	1.0	IPF10761	orf19.6021	unknown function
CA2196	1.1	0.8	1.0	0.9	0.5	0.7			
CA0978	1.1	1.0	1.0	0.9	0.9	0.8	IPF16222	orf19.3603	unknown function
CA0007	1.1	0.9	1.0	0.9	1.4	1.1	IPF12061.5f	orf19.174	zinc-finger containing protein, 5-prime end (by homology)
CA3114	1.1	1.0	1.1	1.0	0.7	1.0			
CA1680	1.1	1.3	1.0	1.0	0.8	0.9	IPF15649	orf19.4913	unknown function
CA2595	1.1	1.0	0.5	0.9	1.9	1.0	ARG2	orf19.56	acetylglutamate synthase (by homology)

CA3629	1.1	1.5	1.0	1.0	1.3	1.0	IPF18316	orf19.5145	related to flavin-containing monooxygenase (by homology)
CA0866	1.1	1.0	1.0	1.0	1.2	1.3	IPF14775	orf19.3585	unknown function
CA2467	1.1	1.0	1.3	1.0	1.8	1.1	IPF8724	orf19.1796	unknown function
CA1247	1.1	1.0	1.1	1.0	0.8	0.8	IPF3870	orf19.20	similar to Saccharomyces cerevisiae Rts1p potential regulatory subunit of protein phosphatase 2A
CA1618	1.1	1.0	1.0	1.0	1.2	1.1	RRP45	orf19.4078	Protein component of the exosome 3 -5 exoribonuclease complex (by homology)
CA0130	1.1	1.0	0.9	1.1	1.1	1.1	IPF4470	orf19.3533	unknown function
CA4266	1.1	1.2	0.4	0.6	6.6	3.6	IPF2283	orf19.6660	unknown function
CA4335	1.1	1.1	0.9	0.9	1.2	1.2	GAL83	orf19.4084	Glucose repression protein (by homology)
CA1519	1.1	1.2	0.6	0.9	1.1	1.2	RIM20	orf19.4800	Rim101 activating protein
CA6162	1.1	1.0	1.0	1.0	0.9	1.0	IPF1833	orf19.5874	similar to opaque phase protein OP4 (by homology)
5124.10	1.1	1.2	0.5	1.0	1.0	0.6			
CA4237	1.1	1.0	1.0	0.9	0.9	1.0	IPF6375	orf19.520	unknown function
CA5780	1.1	1.0	0.9	1.0	0.8	0.8	IPF1123	orf19.5426	unknown function
CA4615	1.1	1.0	1.0	0.9	1.3	1.3	IPF7955	orf19.3306	DNA binding protein (by homology)
CA5750	1.1	1.5	0.7	1.4	0.5	0.7	CHS8	orf19.5384	Chitin synthase (by homology)
CA5519	1.1	0.9	0.9	0.9	0.8	1.0	RDH54	orf19.5367	helicase required for mitotic diploid-specific recombination and repair (by homology)
CA2101	1.1	1.0	1.3	1.4	0.8	1.1	IPF9364	orf19.2384	unknown function
CA1780	1.1	1.0	1.1	1.0	1.5	0.8	IPF14509	orf19.1827	unknown function
CA4424	1.1	1.1	0.8	0.9	0.5	0.9	PMT1	orf19.5171	mannosyltransferase
CA1176	1.1	1.0	0.9	1.0	1.1	1.0	CHS5	orf19.807	Chitin biosynthesis protein
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 (by homology)
CA1454	1.1	0.8	1.0	0.9	0.9	0.9	ALG1	orf19.4410	beta-1,4-mannosyltransferase (by homology)
CA3613	1.1	0.9	1.0	0.8	0.3	0.7	SPF1	orf19.30	P-type ATPase
CA5245	1.1	1.0	0.9	1.0	1.2	1.1	DUR32	orf19.5017	Urea transport protein (by homology)
CA0013	1.1	1.1	0.7	0.9	1.2	1.0	MAK32	orf19.4548	sugar kinase (by homology)
CA1034	1.1	1.0	1.1	0.9	1.1	0.9	BET4.3f	orf19.1039	alpha subunit of geranylgeranyl transferase type 2, 3 prime end
CA1955	1.1	1.1	0.8	0.8	1.0	0.8	IPF3897.3f	orf19.765	unknown function, 3-prime end
CA3822	1.1	1.2	1.0	1.1	1.2	1.2	CUS2	orf19.5767	cold sensitive U2 snRNA Suppressor(by homology)
CA5215	1.1	0.9	1.0	0.8	0.7	0.6	PPS1	orf19.7033	protein tyrosine phosphatase (by homology)
CA6030	1.1	1.2	0.7	1.0	1.9	1.8	YHB2	orf19.7637	flavohemoprotein (by homology)
CA4318	1.1	1.1	1.1	0.9	1.1	1.0	IPF2106	orf19.4104	unknown function
CA3769	1.1	1.0	1.6	1.1	0.8	1.0	IPF13465	orf19.2898	Putative anion transport protein (by homology)
CA3162	1.1	1.1	0.9	0.9	1.2	0.9	HOL5.3f	orf19.1583	member of major facilitator superfamily multidrug-resistance protein subfamily 1, 3-prime end (by homology)
CA2174	1.1	1.0	0.9	1.1	0.9	0.9	IPF20096	orf19.3763	unknown function
CA5468	1.1	1.1	0.4	0.8	1.0	0.9	IFF7	orf19.3279	unknown function
CA3107	1.1	1.0	1.2	1.2	1.1	1.0	GOS1	orf19.6551	SNARE protein of Golgi compartment (by homology)
CA1118	1.1	0.8	0.9	1.0	0.8	1.0	IPF9987	orf19.2290	similar to phosphatidylinositol kinase (by homology)
CA0120	1.1	1.2	0.8	1.0	0.8	0.9	IPF19592	orf19.4353	similar to Saccharomyces cerevisiae Ulp1p Smt3-processing enzyme (by homology)
CA4145	1.1	0.9	0.8	1.0	1.1	1.0	IPF3130	orf19.4227	unknown function
CA0162	1.1	1.0	1.0	0.9	1.2	1.0	IPF19168	orf19.5616	unknown function
CA5768	1.1	1.0	0.9	1.0	0.9	0.9	PAC1	orf19.5410	Similarity to human LIS-1 protein (by homomology)
CA3599	1.1	0.6	0.7	0.6	0.4	0.4	IPF19785	orf19.4929	unknown function
CA2710	1.1	1.0	1.2	1.0	0.7	1.0	IPF7403	orf19.4664	unknown function
CA1742	1.1	1.4	0.7	1.0	1.0	1.0	IPF12210	orf19.5054	quinolinate phosphoribosyltransferase (by homology)
CA5873	1.1	1.0	1.0	1.0	0.9	0.6	PGA25	orf19.7542	GPI-anchored cell surface protein (by homology)
CA5574	1.1	1.0	1.0	1.0	0.8	0.9	IPF2007	orf19.7341	unknown function

CA5219	1.1	1.0	1.1	0.9	0.9	0.9	YAE1	orf19.7037	Essential protein
CA5235	1.1	1.1	0.8	0.9	1.2	1.1	IPF3015	orf19.5029	Similar to E.coli modF and photorepair protein phrA
CA5581	1.1	1.3	1.2	1.1	0.8	1.1	RAD3	orf19.7119	DNA helicase/ATPase by homology
CA4320	1.1	1.6	1.2	1.1	0.8	1.1	ECM17	orf19.4099	Putative sulfite reductase (by homology)
CA5212	1.1	1.0	1.1	1.1	1.2	1.0	IPF3050	orf19.7029	unknown function
CA1321	1.1	1.1	1.0	1.1	1.1	1.1	IPF3141	orf19.4222	similar to Saccharomyces cerevisiae Sst2p involved in desensitization to alpha-factor pheromone (by homology)
CA5162	1.1	1.0	1.0	0.9	0.6	0.9	IPF982	orf19.4600.1	Weakly similar to human dolichol-phosphate-mannose synthase
CA5690	1.1	0.9	0.8	0.9	0.6	0.4	OCH1	orf19.7391	Alpha-1,6-mannosyltransferase (by homology)
CA0713	1.1	1.0	1.2	1.0	1.2	1.2	IFJ2	orf19.2168	Unknown function
CA3135	1.1	1.0	0.9	0.9	0.9	1.0	IPF8990	orf19.1366	unknown function
CA3025	1.1	1.0	0.8	1.1	3.0	1.0	IPF11503	orf19.3902	unknown function
CA4346	1.1	3.4	0.7	0.6	1.6	1.3	IPF3634	orf19.6720	unknown function
CA2797	1.1	1.0	1.2	0.9	0.6	0.8	IPF8404	orf19.1720	putative helicase (by homology)
CA2067	1.1	1.0	1.0	1.1	1.0	1.1	IPF6976	orf19.2642	unknown function
CA1058	1.1	0.9	1.0	1.1	1.0	0.9	DOT6	orf19.2545	involved in derepression of telomeric silencing (by homology)
CA5166	1.1	1.0	1.1	1.0	1.2	1.1	TYR1	orf19.4605	Prephenate dehydrogenase (NADP+) (by homology)
CA4073	1.1	1.0	0.9	1.1	1.1	0.9	IPF2559.3	orf19.6626	unknown function, 3-prime end
CA2744	1.1	0.9	0.7	1.0	0.9	0.8	IPF10626	orf19.2101	unknown function
CA3094	1.1	1.1	1.1	0.7	1.3	2.1	IPF11548	orf19.3854	serine/threonine protein kinase (by homology)
CA3687	1.1	1.1	1.2	1.0	0.6	0.9	IPF4889	orf19.6264	unknown function
CA1719	1.1	1.3	1.0	0.9	0.9	0.9	ILV6	orf19.4650	acetolactate synthase, regulatory subunit (by homology)
CA0799	1.1	1.0	1.0	1.0	1.1	1.0	IPF14825	orf19.1610	unknown function
CA1026	1.1	1.1	0.9	1.0	1.9	1.2	TIP41.5f	orf19.3937	unknown function, 5-prime end
CA1052	1.1	0.9	1.0	1.0	0.9	0.9	IPF15861	orf19.3894	unknown function
CA5367	1.1	1.1	2.2	1.2	1.0	1.0	RIM101	orf19.7247	Zn finger transcription factor homolog; regulator of pH response
CA4824	1.1	1.0	0.9	1.0	1.0	1.0	HNM2	orf19.2072	Choline permease (by homology)
CA2963	1.1	1.1	1.0	1.0	2.2	1.0	GRP3	orf19.5611	dihydroflavonol-4-reductases (by homology)
CA0339	1.1	1.0	1.0	1.1	1.0	1.0	IPF13247	orf19.3376	unknown function
CA0196	1.1	1.0	0.9	0.8	1.3	1.2	IPF15799	orf19.1651	unknown function
CA5872	1.1	1.0	1.5	1.1	0.8	1.0	IPF333	orf19.7539	unknown function
CA5267	1.1	1.2	0.9	1.1	1.3	1.0	IPF1787.5f	orf19.4995	unknown function, 5-prime end
CA3373	1.1	1.0	1.1	1.0	1.2	0.8	SEO1	orf19.1855	suppressor of sulfoxyde ethionine resistance (by homology)
CA1712	1.1	0.6	1.0	1.2	0.9	1.0	ABC1	orf19.3331	ubiquinol--cytochrome-c reductase(by homology)
CA1174	1.1	1.1	1.4	1.0	0.8	1.0	IPF14255	orf19.4767	unknown function
CA5247	1.1	0.8	1.0	1.1	0.9	1.0	MYO2	orf19.5015	Myosin heavy chain (by homology)
CA1395	1.1	1.9	1.0	0.9	11.5	11.7			
CA2825	1.1	1.0	0.9	1.0	1.1	1.0	HWP1	orf19.1321	Hyphal wall protein
CA5189	1.1	0.7	0.9	0.8	0.8	0.8	IPF10158	orf19.4627	unknown function
CA5535	1.1	1.1	20.4	1.4	6.5	1.0	IPF2839	orf19.7296	unknown function
CA4417	1.1	1.0	1.0	1.0	1.2	0.9	LIP5	orf19.5179	Secretory lipase
CA3767	1.1	0.9	1.2	0.9	1.0	1.0	NUP60	orf19.2901	Putative nuclear pore protein (by homology)
CA2209	1.1	0.9	1.1	1.0	1.0	0.9	IPF18512	orf19.695	unknown function
CA2213	1.1	0.8	1.0	0.7	0.8	0.9	IPF16405	orf19.4751	similar to saccharomyces cerevisiae Rsm25p protein of the small subunit of the mitochondrial ribosome (by homology)
CA4401	1.1	1.0	1.1	1.2	1.0	1.1	IPF8780	orf19.3109	unknown function
CA0762	1.1	0.9	0.9	1.2	1.0	1.0	TAF67	orf19.1574	TFIID subunit (by homology)
CA3221	1.1	1.0	0.9	0.9	0.5	0.9	IPF10000.5	orf19.6193	unknown function, 5-prime end

CA4130	1.1	0.9	1.3	0.7	1.1	1.1	IPF20009	orf19.4245	Unknown function
CA1485	1.1	0.8	1.1	1.1	1.1	1.2	IPF20082	orf19.4061	unknown function
CA3175	1.1	0.7	1.8	1.3	1.1	0.8	IPF11587	orf19.1403	unknown function
CA3457	1.1	0.9	1.1	1.0	1.0	1.0	IPF8521	orf19.1260	unknown function
CA1512	1.1	1.0	1.0	1.0	0.9	1.0	IPF15255	orf19.4884	unknown function
CA1329	1.1	1.3	1.2	0.9	1.1	0.8	MRF2	orf19.1303	peptide chain release factor, mitochondrial (by homology)
CA1567	1.1	1.1	1.1	1.0	1.0	0.8	IPF7613	orf19.1156	unknown function
CA2169	1.1	0.9	1.0	1.0	0.9	0.9	IPF4563.5f	orf19.911	similar to saccharomyces cerevisiae Tom1p E3 ubiqitin ligase required for G2/M transition, 5-prime end (by homology)
CA4769	1.1	1.1	1.1	0.9	0.8	0.8	IPF9384	orf19.4001	similar to Saccharomyces cerevisiae Mss2p serine/threonine protein kinase (by homology)
CA3228	1.1	1.0	1.2	1.0	1.0	1.0	IPF9325	orf19.6288	unknown function
CA0145	1.1	1.1	1.1	0.8	1.0	1.0			
CA4628	1.1	1.1	1.2	1.0	1.2	0.8			
CA2894	1.1	1.1	1.3	1.0	26.6	2.5	IFS2	orf19.2462	Unknown function
CA1198	1.1	0.9	1.0	0.8	0.7	0.8	IPF10399	orf19.3367	unknown function
CA2112	1.1	1.1	1.1	0.9	1.1	1.0	PFD1	orf19.3687	Prefoldin subunit 1 (by homology)
CA6120	1.1	1.0	1.0	1.1	0.8	0.9	IPF132	orf19.5930	unknown function
CA3777	1.1	1.0	1.0	0.9	1.0	1.1	IPF10432	orf19.2889	unknown function
CA4031	1.1	1.0	0.9	1.1	1.2	0.9	IPF11077	orf19.3432	membrane transporter (by homology)
CA2980	1.1	0.8	1.1	1.0	0.4	0.6	GOG5	orf19.1232	GDP-mannose transporter (by homology)
CA4975	1.1	1.0	1.3	1.0	1.1	1.0	IPF4706	orf19.5277	unknown Function
CA5746	1.1	1.0	1.0	0.9	1.0	1.3	IPF2902	orf19.7455	unknown function
CA4938	1.1	1.1	1.1	0.9	0.9	1.0	IPF5166	orf19.6537	unknown function
CA0788	1.1	1.0	1.0	1.0	1.1	1.0	IPF14107	orf19.2449	unknown function
CA1796	1.1	0.9	1.1	1.0	0.8	1.2	IPF11259	orf19.5210	unknown function
CA2517	1.1	0.9	1.3	1.0	1.0	1.0	IPF4311	orf19.5514	unknown function
CA5961	1.1	1.0	0.9	1.0	8.1	1.0	IFA14	orf19.7550	unknown function
CA1601	1.1	1.0	0.9	1.0	1.1	1.1	IPF15728	orf19.4721	unknown function
CA4006	1.1	0.8	0.8	1.0	0.9	0.9	IPF4253	orf19.1630	unknown function
CA3806	1.1	0.9	0.9	0.9	0.7	0.9	IPF9224	orf19.2485	similar to Saccharomyces cerevisiae Nup170p nuclear pore protein (by homology)
CA2998	1.1	0.7	0.9	1.1	1.2	1.2	LPD1	orf19.6127	dihydrolipoamide dehydrogenase (by homology)
CA1108	1.1	1.1	1.0	1.0	1.0	2.3	IPF11273	orf19.5231	unknown function
CA5700	1.1	0.9	1.0	0.9	0.6	1.1	IPF2630	orf19.7399.3	unknown function
CA4291	1.1	1.0	0.9	1.1	1.0	1.1	IPF2615	orf19.6688	unknown function
CA2387	1.1	1.1	1.2	1.0	1.1	1.0	IPF8504	orf19.2612	unknown function
CA0543	1.1	1.4	1.1	1.0	1.2	1.1	IPF3255	orf19.2867	similar to Saccharomyces cerevisiae Vps5p involved in Golgi retention and vacuolar sorting (by homology)
CA1907	1.1	0.8	1.4	1.1	1.3	1.1	ATP7	orf19.2785	F1F0-ATPase complex, FO D subunit (by homology)
CA1498	1.1	1.0	1.0	1.0	1.5	1.0	IPF12371	orf19.3643	extracellular alpha-1,4-glucan glucosidase (by homology)
CA1334	1.1	1.0	0.9	0.9	1.1	0.9	IPF19912	orf19.1148	unknown function
CA4953	1.1	1.0	1.0	1.0	0.9	0.8	IPF4567.3f	orf19.6525	unknown function, 3-prime end
CA2824	1.1	1.1	1.0	0.9	0.7	0.9	IPF17888	orf19.1318	unknown function
CA2846	1.1	1.0	1.0	1.1	1.1	1.0	PAD1	orf19.5731	phenylacrylic acid decarboxylase (by homology)
CA3142	1.1	1.0	0.6	0.9	0.9	0.7	IPF9211.5f	orf19.3713	unknown function, 3-prime end
CA2927	1.1	1.1	0.9	1.1	1.5	1.0	RAD52	orf19.4208	Nuclear ribonucleoprotein E
CA3133	1.1	1.0	0.9	1.0	0.8	1.1	IPF16939	orf19.1364	unknown function
CA1154	1.1	1.1	0.9	1.0	1.3	1.2	MET221	orf19.105	protein ser/thr phosphatase (by homology)
CA2408	1.1	1.0	0.9	1.1	0.9	0.9	IPF3833	orf19.296	unknown function

CA3831	1.1	1.0	0.9	0.9	1.0	1.0	VMA22	orf19.6590	vacuolar ATPase assembly protein (by homology)
CA5254	1.1	0.9	1.0	1.1	1.0	1.0	IPF1820	orf19.5008.1	unknown function
CA4687	1.1	1.1	1.0	1.0	0.8	0.9	IPF9017	orf19.879	similar to Saccharomyces cerevisiae She4p required for mother cell-specific gene expression (by homology)
CA1412	1.1	1.0	0.9	0.9	1.1	1.0	IPF11854	orf19.1278	
CA1359	1.1	1.0	0.6	0.9	1.1	0.9	IPF11842	orf19.4405	unknown function
CA5448	1.1	1.6	0.9	0.8	1.1	1.0	ARC19.3f	orf19.3251	subunit of the Arp2/3 complex involved in the control of actin polymerization, exon 2 (by homology)
CA3674	1.1	1.0	1.0	1.0	0.8	0.9	IPF19529.5f	orf19.6454	unknown function, 5-prime end
CA4703	1.1	1.0	1.1	1.2	1.0	1.0	CLP1	orf19.6931	probable cleaveage/polyadenylation factor
CA3791	1.1	1.0	0.9	1.1	0.9	0.7	IPF11212	orf19.5827	similar to Saccharomyces cerevisiae Bub2 cell cycle arrest protein (by homology)
CA2604	1.1	1.0	1.0	0.9	0.9	0.9	IPF5469	orf19.5681	unknown function
CA3073	1.1	1.0	0.9	1.0	0.9	1.1	IPF6108	orf19.4811	putative tricarboxylate carrier (by homology)
CA4149	1.1	0.7	1.0	1.0	0.6	0.8	SMP3	orf19.5792	Protein kinase C pathway protein
CA4904	1.1	0.4	2.0	0.8	0.5	0.7	RPO41	orf19.6041	Mitochondrial DNA-directed RNA polymerase (by homology)
CA3695	1.1	1.0	1.0	0.9	0.9	0.9	IPF4872.5f	orf19.6270	unknown function, 5-prime end
CA5764	1.1	0.8	0.8	0.9	0.7	0.7	IPF20031	orf19.5406	similar to Saccharomyces cerevisiae Psr2p plasma membrane phosphatase required for sodium stress response
CA4146	1.1	0.7	0.8	0.8	1.0	0.9	LEU3	orf19.4225	Binds to UASs in promoters of LEU1, LEU2, LEU4, ILV2, ILV5, and GDH1 (by homology)
CA1506	1.1	1.0	3.2	1.1	1.4	1.0	HGT11	orf19.4527	hexose transporter
CA0131	1.1	1.0	1.3	1.0	0.8	0.7	IPF13402	orf19.36	unknown function
CA5911	1.1	0.8	1.2	0.9	0.9	0.9	IPF5965	orf19.6794	NADH-ubiquinone oxidoreductase (by homology)
CA0871	1.1	0.9	0.9	0.7	0.9	0.8	APE3	orf19.3591	aminopeptidase (by homology)
CA4724	1.1	1.0	1.0	0.8	0.9	0.8	PDC2	orf19.4863	pyruvate decarboxylase regulator
CA0707	1.1	1.1	1.2	0.9	1.4	0.9	IPF7711	orf19.681	related to Neurospora crassa AP-1-like transcription factor (by homology)
CA0523	1.1	0.9	1.1	1.0	1.1	1.1	IPF4459	orf19.3528	unknown function
CA5880	1.1	1.0	1.6	1.2	0.8	0.9	IPF12074	orf19.6829	unknown function
CA3829	1.1	1.0	1.1	1.0	1.1	1.2	PPQ1	orf19.5758	phosphoprotein phosphatase (by homology)
CA3537	1.1	0.9	1.2	0.8	0.9	0.8	PSU1	orf19.6373	suppressor of petit mutations by homology
CA1478	1.1	1.0	1.2	1.0	0.7	0.8	IPF16426	orf19.1251	similar to human BRRN1 (by homology)
CA1281	1.1	1.0	0.9	1.0	1.0	1.1	IPF10171	orf19.644	unknown function
CA2228	1.1	1.3	0.8	0.8	0.6	0.9	SCT12	orf19.5815	Suppresses a choline-transport mutant
CA0591	1.1	1.0	0.9	1.0	1.0	1.1	ALS3.5eoc	orf19.1816	agglutinin-like protein, 5-prime end
CA5769	1.1	1.0	0.9	1.0	1.2	1.2	UBC12	orf19.5411	E2 ubiquitin-conjugating enzyme (by homology)
CA3577	1.1	1.1	1.0	1.0	1.7	1.5	IPF11106	orf19.2263	unknown function
CA3404	1.1	0.9	1.1	1.0	0.9	1.0	MAL31	orf19.3981	maltose permease (by homology)
CA4140	1.1	1.0	1.3	1.0	0.9	1.0	IPF11959	orf19.4232	unknown function
CA2002	1.1	0.7	0.9	0.8	0.8	0.9	IPF16470	orf19.2794	unknown function
CA2783	1.1	1.2	1.0	1.0	1.0	1.0	IPF3808	orf19.286	unknown function
CA4568	1.1	0.9	0.8	1.0	0.8	0.7	IPF9554	orf19.6880	unknown function
CA4620	1.1	1.0	0.9	1.0	1.1	0.9	IFD3	orf19.3311	OXIDOREDUCTASE (by homology)
CA0110	1.1	0.6	0.8	0.6	0.4	0.6	IPF17190	orf19.3869	unknown function
CA3495	1.1	0.9	1.1	1.1	1.0	1.0	RIB7	orf19.6341	HTP reductase (By homology)
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)
CA4193	1.1	2.3	0.8	1.0	1.4	1.0	IPF7535	orf19.4534	unknown function
CA4598	1.1	1.0	1.2	1.0	0.8	1.2	IPF20019	orf19.6917	unknown function
CA3932	1.1	1.0	1.1	1.0	1.0	1.0	IPF20150	orf19.2010	unknown function
CA3258	1.1	1.0	0.5	0.9	1.1	2.7			
CA2254	1.1	1.0	1.1	1.0	1.0	1.0	IPF15487	orf19.1958	unknown function

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 oligosaccharides in the endoplasmic reticulum (by homology)
CA1855	1.1	1.0	1.1	1.1	0.9	1.0	GLN1	orf19.646	glutamate-ammonia ligase (by homology)
CA1804	1.1	0.9	1.0	1.0	1.0	1.0	TAF17	orf19.1111	TFIID and SAGA subunit (by homology)
CA2590	1.1	1.2	0.9	1.0	0.8	0.7	PPH32.3f	orf19.4378	protein serine/threonine phosphatase, 3-prime end (by homology)
CA1033	1.1	1.0	1.0	0.9	0.8	1.0	MAD2	orf19.1040	spindle checkpoint complex subunit (by homology)
CA5595	1.1	1.6	0.9	1.0	0.9	1.4	IPF568	orf19.7105	similar to Saccharomyces cerevisiae Far1p cyclin-dependent kinase inhibitor (CKI) (by homology)
CA2463	1.1	1.1	0.8	0.9	0.9	1.1	IPF8730	orf19.1793	unknown function
CA3684	1.1	1.0	0.9	1.0	1.1	1.0	IPF13613	orf19.725	unknown function
CA4766	1.1	1.0	0.9	0.9	1.1	1.0	IPF13056	orf19.3998	unknown function
CA2161	1.1	1.1	1.1	1.5	1.0	1.1	IPF11876	orf19.5295	unknown function
CA3468	1.1	1.0	0.6	1.0	1.3	0.9	IPF6318	orf19.1664	beta-glucosidase (by homology)
CA4994	1.1	1.0	0.9	1.0	1.1	1.0	IPF2033	orf19.5254	unknown function
CA0194	1.1	1.3	0.8	1.0	2.0	1.1	IPF16228	orf19.3922	unknown function
CA1406	1.1	0.9	1.5	1.1	0.5	0.6	DOT4	orf19.3370	derepression of telomeric silencing (by homology)
CA4681	1.1	0.9	0.6	1.0	1.1	0.9	IPF3679	orf19.889	similar to Saccharomyces cerevisiae Thi20p hydroxymethylpyrimidine phosphate (HMP-P) kinase (by homology)
CA0902	1.1	1.0	0.9	1.0	1.2	1.1	IPF12034	orf19.3413	unknown function
CA5675	1.1	1.0	0.8	0.9	0.9	0.7	SIS2	orf19.7378	Involved in cell cycle-specific gene expression (by homology)
CA0295	1.1	1.1	1.1	0.9	0.8	1.0	IPF15033.5	orf19.1595	unknown function, 5-prime end
CA4499	1.1	1.1	1.0	1.0	0.7	1.0	IPF11316	orf19.511	unknown function
CA3164	1.1	1.0	1.2	1.1	0.9	1.0	IPF13187	orf19.1580	unknown function
CA4612	1.1	0.9	1.4	1.0	1.5	1.7	PPM2	orf19.3303	carboxy methyl transferase; homolog of PPM1 (by homology)
CA4405	1.1	1.0	1.1	1.0	1.5	1.0	IPF8773	orf19.3105	putative cytochrome P450 (by homology)
CA0629	1.1	1.3	0.7	0.8	1.0	1.7	IPF3876	orf19.775	unknown function
CA4047	1.1	0.8	0.9	0.9	1.0	0.7	IPF9206	orf19.3678	unknown function
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 homology)
CA1449	1.1	1.0	1.0	0.9	1.1	1.2	IPF14730	orf19.193	unknown function
CA1533	1.1	1.1	1.2	0.9	0.6	1.0	IPF9510	orf19.1215	unknown function
CA5836	1.1	1.8	0.8	1.1	1.2	0.7	IPF428	orf19.7490	transport protein (by homology)
CA5777	1.1	1.1	1.0	1.2	1.3	1.1	IPF1118	orf19.5422	unknown function
CA0474	1.1	1.0	0.9	1.1	0.5	0.7	IPF12887	orf19.4780	Putative multidrug protein (by homology)
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 homology)
CA2029	1.1	1.0	0.8	0.9	0.7	1.1	SAR1.3f	orf19.3462	GTP-binding protein of the ARF family, 3-prime end (by homology)
CA2655	1.1	0.6	1.2	0.9	1.0	0.8	IPF8477	orf19.5704	unknown function
CA2972	1.1	1.1	0.8	1.0	0.7	0.9	MDL2.3f	orf19.5599	ATP-binding transporter, 3-prime end (by homology)
CA2357	1.1	1.2	1.0	0.9	1.0	1.0	IPF8957	orf19.4894	unknown function
CA1820	1.1	1.0	0.9	1.0	1.0	1.0	IPF9529	orf19.4270	probable mannosyltransferase (by homology)
CA1299	1.1	1.0	1.4	1.1	1.3	1.1	PTK2	orf19.3415	serine /threonine protein kinase involved in polyamine uptake (by homology)
CA5370	1.1	1.0	1.2	0.9	1.4	1.4	IPF5248	orf19.7254	unknown function
CA0479	1.1	1.0	1.2	1.0	0.9	0.9	IPF16191	orf19.2630	similar to Saccharomyces cerevisiae Rad59p recombination and DNA repair protein
CA4438	1.1	1.1	0.8	1.0	1.1	1.1	IPF13866	orf19.5157	unknown function
CA4634	1.1	1.3	0.9	0.9	1.3	1.1	IPF1526	orf19.340	unknown function
CA0888	1.1	1.2	0.9	1.2	1.0	1.3	BET1	orf19.1386	involved in ER-Golgi transport (by homology)
CA2259	1.1	1.1	1.2	0.9	1.1	1.3	IPF6845	orf19.1762	unknown function
CA0553	1.1	1.1	1.1	1.5	0.7	0.6	IPF16653	orf19.5534	unknown function
CA0728	1.1	1.0	0.7	1.0	0.7	0.9	IPF7345	orf19.3728	unknown function
CA0193	1.1	1.0	1.0	0.9	1.0	0.8	IPF6493	orf19.1541	unknown function

CA5792	1.1	1.0	1.3	1.0	0.7	0.9	IPF4195	orf19.5441	similar to Saccharomyces cerevisiae Ulp2p involved in ubiquitin-mediated protein degradation (by homology)
CA0604	1.1	1.0	1.0	1.0	1.0	1.0	VID21	orf19.3077	unknown function
CA0478	1.1	2.1	0.6	0.8	1.1	1.0	YAE8	orf19.6016	GTP-binding protein (by homology)
CA1079	1.1	1.0	1.0	0.9	1.2	1.1	LIP1	orf19.4821	Secretory lipase
CA1191	1.1	0.9	0.6	1.0	1.1	0.8	CAN2	orf19.111	amino acid permease (by homology)
CA3919	1.1	1.0	0.8	0.8	1.0	2.5	IFC5	orf19.5121	unknown function
CA3909	1.1	0.9	1.5	1.1	1.1	1.1	CIT1	orf19.4393	Citrate synthase
CA1788	1.1	1.5	1.0	1.3	0.8	1.0	EDE1	orf19.1166	Cytoskeletal-related transport protein, Ca++ binding (by homology)
CA0999	1.1	1.2	0.9	1.0	0.7	1.0	IPF12368	orf19.4369	unknown function
CA5884	1.1	1.0	1.2	1.0	1.0	0.8	SLF1	orf19.6826	Copper homeostasis protein (by homology)
CA3653	1.1	1.0	1.1	1.3	1.0	1.1	PGA27	orf19.2044	unknown function
CA0937	1.1	1.0	1.0	1.0	1.0	1.0	IPF19892	orf19.1082	unknown function
CA5720	1.1	1.1	1.0	0.9	0.7	1.0	UNG1	orf19.7425	Uracil-DNA glycosylase (by homology)
CA0379	1.1	0.9	0.9	1.0	1.0	1.0	SSP120	orf19.3173	secretory protein (by homology)
CA3562	1.1	1.1	1.1	0.9	1.4	1.3	IPF7823	orf19.3129	similar to Saccharomyces cerevisiae Rvb1p RuvB-like protein (by homology)
CA3170	1.1	1.0	0.9	1.0	0.8	0.9	IPF7685	orf19.1396	putative GTPase activating protein (by homology)
CA3670	1.1	1.0	1.1	1.0	1.0	1.0	IPF13934	orf19.6458	unknown function
CA1848	1.1	1.0	1.0	0.9	1.0	0.9	IPF11128	orf19.639.1	unknown function
CA1877	1.1	1.0	1.0	1.0	1.0	1.1	IPF10300	orf19.2274	unknown function
CA5227	1.1	1.8	1.2	1.3	1.6	1.6	IPF3087	orf19.7046	unknown function
CA3506	1.1	1.0	0.9	1.0	1.5	1.0	IFA5	orf19.6353	unknown function
CA1278	1.1	1.0	1.3	0.8	0.7	1.0	IPF10835	orf19.3629	unknown function
CA0072	1.1	1.0	0.9	1.0	1.0	1.1	IPF19284	orf19.625	unknown function
CA5548	1.1	1.0	0.9	1.1	1.1	1.0	IPF5978	orf19.7311	unknown function
CA0694	1.1	1.0	1.3	1.0	0.9	1.2	IPF12603	orf19.3289	unknown function
CA2668	1.1	0.9	1.2	1.2	1.0	1.0	IPF17553	orf19.3546	similar to Saccharomyces cerevisiae Pex2p peroxisomal protein (by homology)
CA1155	1.1	0.8	2.1	1.2	0.7	0.8	JA2	orf19.107	ATP-dependent RNA helicases-like (by homology)
CA0882	1.1	0.9	0.8	1.0	0.5	0.9	PHR3	orf19.377	surface glycoprotein (by homology)
CA0039	1.1	1.0	1.2	1.0	0.9	1.1			
CA5855	1.1	1.0	1.3	1.0	1.1	1.0	ALK3	orf19.7512	n-alkane inducible cytochrome P-450 (by homology)
CA3279	1.1	1.0	1.0	1.0	0.8	0.9	IPF6268	orf19.6313	unknown function
CA1144	1.1	0.7	1.1	0.9	0.9	1.0	SPS19.5f	orf19.3684	peroxisomal 2,4-dienoyl-CoA reductase (by homology)
CA2673	1.1	0.8	0.9	0.7	0.9	0.7	IPF5849	orf19.5496	unknown function
CA3663	1.1	1.8	1.9	1.6	2.9	2.4	IPF11432	orf19.6463	unknown function
CA3580	1.1	1.0	1.1	1.0	0.9	1.1	IPF16141	orf19.2260	unknown function
CA5994	1.1	1.1	1.2	1.0	1.0	1.0	IPF677	orf19.7594	unknown function
CA1223	1.1	1.2	0.9	0.8	0.4	0.7	IPF14870	orf19.4131	unknown function
CA1911	1.1	2.0	1.1	0.9	1.0	1.0	SSE1	orf19.2435	heat shock protein of HSP70 family (by homology)
CA2186	1.1	2.1	1.1	3.7	1.0	1.2	IPF6881	orf19.4246	putative phosphatidyl synthase
CA4313	1.1	0.9	1.0	0.8	1.0	0.9	IPF2121	orf19.4110	unknown function
CA0525	1.1	0.9	0.8	0.9	0.5	1.0	MSB1.5eoc	orf19.1133	Morphogenesis-related protein (by homology)
CA2285	1.1	1.4	0.6	0.9	1.0	0.7	IPF12629	orf19.5552	unknown function
CA2222	1.1	1.0	0.7	0.9	0.8	0.8	CCR4	orf19.5101	glucose-repressible alcohol dehydrogenase transcriptional effector
CA0080	1.1	1.0	0.9	1.0	1.0	0.8	IPF11378	orf19.632	unknown function
CA1297	1.1	1.2	1.1	1.2	0.8	0.8	ENG2	orf19.3417	endo-1,3-beta-glucanase
CA5181	1.1	1.0	0.9	0.9	1.2	1.1	TIM12	orf19.4620	subunit of the TIM22-complex (by homology) Mitochondrial transport

CA5902	1.1	0.8	1.7	0.8	0.9	0.9	SRP68	orf19.6804	SIGNAL RECOGNITION PARTICLE 68 (by homology)
CA3788	1.1	1.0	1.0	1.0	1.3	1.3	IPF16445	orf19.5831	unknown function
CA2704	1.1	1.1	1.0	1.0	0.9	1.0	IPF12195	orf19.4656	unknown function
CA3357	1.1	1.0	1.1	1.0	0.9	0.9	IPF9562	orf19.1941	similar to Saccharomyces cerevisiae Nuf2pspindle pole body protein
CA1294	1.1	1.0	1.1	1.1	1.0	1.1			
CA2380	1.1	1.0	0.9	1.0	1.0	1.0	IPF4072	orf19.2217	unknown function
CA5629	1.1	0.6	1.0	0.8	0.8	0.7	CTR9	orf19.7067	required for G1 cyclin expression (by homology)
CA4173	1.1	0.7	0.9	1.0	1.0	1.0	FRS2	orf19.2960	phenylalanine--tRNA ligase beta chain, cytosolic (by homology)
CA3775	1.1	0.7	1.1	0.9	0.7	0.9	AFG1	orf19.2891	ATPase family gene (by homology)
CA4035	1.1	1.0	1.4	0.8	0.8	0.9	IPF12040	orf19.3665	unknown function
CA0418	1.1	0.9	0.9	0.9	0.6	0.8	IPF9051.5e	orf19.2227	unknown function, 5-prime end
CA5214	1.1	1.0	1.2	1.1	0.9	1.0	IPF19807	orf19.7032	unknown function
CA0163	1.1	1.8	0.5	0.9	1.7	1.3	AYR2	orf19.5615	1-acyl dihydroxyacetone phosphate reductase (by homology)
CA2838	1.1	0.9	0.8	0.9	1.0	1.0	IPF8339	orf19.4791	unknown function
CA4887	1.1	1.0	1.2	1.3	0.4	0.7	IPF1632	orf19.6579	unknown function
CA4342	1.1	0.8	1.1	0.9	1.0	1.3	IPF3629	orf19.6716	RNA (guanine-N7-) methyltransferase
CA5793	1.1	1.4	1.5	1.2	1.1	1.4	IPF4192	orf19.5442	unknown function
CA2917	1.1	0.9	1.0	1.0	1.2	0.9	IFA18.5f	orf19.4509	Unknown function, 5-prime end
CA1007	1.1	0.9	1.1	1.0	1.0	1.0	DLH1.3f	orf19.3760	meiotic recombination protein, 3-prime end
CA1016	1.1	1.3	1.1	1.6	4.2	3.0	IPF11142	orf19.473	unknown function
CA1445	1.1	0.9	1.1	0.9	0.8	0.9	MRP51	orf19.185	Mitochondrial ribosomal protein of the small subunit (by homology)
CA3319	1.1	0.7	0.5	0.8	0.6	0.5	DRS25	orf19.2680	Probable ATPase, Potential phospholipid-transporting ATPase 5(by homology)
CA3856	1.1	1.7	1.0	1.2	0.8	0.8	IPF4641	orf19.6100	similar to Saccharomyces cerevisiae Crd1p cardiolipin synthase (by homology)
CA0304	1.1	1.0	1.4	1.1	0.6	1.2	IPF12829	orf19.721	unknown function
CA3762	1.1	1.0	1.0	1.0	1.1	1.0	PGA42	orf19.2907	unknown function
CA4688	1.1	1.1	0.9	1.0	1.0	1.0	NBN1	orf19.878	involved in chromatin remodeling and possibly transcription regulation (by homology)
CA1242	1.1	1.0	1.2	1.0	0.9	1.2	IPF19908	orf19.1344	unknown function
CA2452	1.1	1.2	1.7	1.0	1.1	1.1	IPF9955	orf19.3499	unknown function
CA1369	1.1	1.0	1.1	1.0	1.0	1.0	IPF15968	orf19.4964	unknown function
CA1086	1.1	1.0	1.0	1.2	1.0	1.1	IPF1039	orf19.4569	unknown function
CA0879	1.1	1.0	0.9	1.0	1.3	1.1	IPF19542.5f	orf19.371	unknown function, 5-prime end
CA3961	1.1	1.0	1.0	1.0	1.1	1.0	IPF11235	orf19.1420	unknown function
CA2220	1.1	1.0	1.0	1.0	1.1	1.0	NTG1	orf19.5098	endonuclease III-like glycosylase (by homology)
CA5630	1.1	0.9	1.1	0.9	0.8	1.0	IPF486	orf19.7065	unknown function
CA5524	1.1	1.0	1.2	1.1	1.1	1.0	IPF2861	orf19.7281	putative pyruvate dehydrogenase kinase
CA0266	1.1	0.9	1.0	0.9	1.0	0.9	IPF17773.5f	0.00	probable pseudogene, 5-prime end
CA1482	1.1	1.0	0.9	1.0	1.2	1.1	IPF15575	orf19.1247	unknown function
CA5216	1.1	1.0	1.0	0.8	0.9	0.9	IPF3069	orf19.7034	unknown function
CA2518	1.1	1.0	0.9	1.0	0.9	0.7	CBP3	orf19.5515	involved in cytochrome-c reductase assembly (by homology)
CA3774	1.1	1.0	0.8	1.0	0.5	0.7	IPF10437	orf19.2892	budding protein-like (by homology)
CA0330	1.1	1.3	0.7	0.9	1.3	1.1	BAT21	orf19.797	branched-chain amino acid transaminase (by homology)
CA4310	1.1	1.0	0.8	1.0	1.3	1.0	IPF2125	orf19.4116	unknown function
CA5778	1.1	1.0	0.9	1.1	1.4	1.0	IPF1119	orf19.5423	unknown function
CA5835	1.1	1.1	1.0	0.9	0.9	1.0	IPF429	orf19.7489.3	unknown function
CA1029	1.1	0.9	1.1	0.8	1.0	1.0	TLG2	orf19.1538	Syntaxin family of t-SNAREs (by homology)
CA2612	1.1	0.8	0.9	1.1	0.7	0.7	GAA1	orf19.5693	required for attachment of GPI anchor onto proteins by homology

CA5779	1.1	0.8	1.0	1.1	0.9	0.8	IPF1121	orf19.5425	unknown function
CA5206	1.1	1.1	0.7	0.6	0.7	1.0	GPH1	orf19.7021	Glycogen phosphorylase (by homology)
CA3230	1.1	1.0	0.9	1.2	0.7	0.9	EMP24	orf19.6293	component of the COPII-coated vesicles (by homology)
CA0319	1.1	1.1	1.3	1.0	0.6	0.8			
CA0546	1.1	1.0	1.0	1.1	1.4	1.1	IPF3250	orf19.2870	unknown function
CA5151	1.1	0.9	0.8	0.8	0.7	0.8	IPF1009	orf19.4590	Weak similarity to S. cerevisiae RFX1
CA3700	1.1	1.0	1.1	0.9	0.9	0.9	IPF4859	orf19.6276	unknown function
CA2702	1.1	1.1	1.0	1.0	0.8	0.9	EMP70	orf19.2746	Endosomal protein (by homology)
CA6113	1.1	1.1	0.8	1.0	1.0	0.7	IPF100.3f	orf19.5940	zinc finger protein, 3-prime end (by homology)
CA2829	1.1	1.0	1.0	1.0	1.2	1.0	IFA7	orf19.1326	unknown function
CA3696	1.1	1.0	1.0	1.0	0.9	0.9	IPF4868	orf19.6271	unknown function
CA2635	1.1	1.3	1.0	0.9	1.2	1.2	CKB22	orf19.4297	Casein kinase II, beta subunit (by homology)
CA2182	1.1	1.2	1.0	0.9	1.1	1.1	IPF6871	orf19.4253	unknown function
CA2398	1.1	1.0	1.0	1.0	1.1	1.5	IPF6431	orf19.3539	unknown function
CA1325	1.1	1.0	0.9	1.0	0.9	1.1	IPF6678	orf19.1307	unknown function
CA4013	1.1	1.0	1.0	0.9	1.0	1.0	IPF4234	orf19.1620	unknown function
CA0346	1.1	1.0	1.0	1.1	0.9	1.0	RFG1.3f	orf19.2824	regulator of filamentous growth and virulence, 3 prime end
CA5699	1.1	1.0	0.6	1.0	1.3	1.0	ALS7	orf19.7400	agglutinin-like protein
CA1340	1.1	1.1	1.0	1.1	1.2	1.4	VPS4	orf19.4339	vacuolar sorting protein by homology to S. cerevisiae
CA5462	1.1	1.0	0.8	1.1	0.7	0.9	GSL23.3f	orf19.3270	1,3-beta-D-glucan synthase subunit, 3-prime end
CA4200	1.1	1.0	0.9	1.0	1.1	1.2	CCL1	orf19.4542	cyclin (by homology)
CA1726	1.1	1.0	1.0	0.9	0.9	1.0	IPF13021	orf19.2647	unknown function
CA2396	1.1	1.0	1.0	1.1	19.9	12.7	IPF6428	orf19.3537	unknown function Unknown function
CA3647	1.1	1.0	1.0	1.2	1.2	1.2	IPF4129	orf19.2038	unknown function
CA1077	1.1	0.8	0.9	0.8	0.3	0.5	IPF13694	orf19.2238	unknown function
CA3672	1.1	1.0	1.1	1.0	0.8	1.0	IPF13669	orf19.6456	unknown function
CA0350	1.1	1.0	1.0	1.0	0.9	1.0	SNU114	orf19.144	snRNP-specific protein (by homology)
CA4048	1.1	1.0	0.8	0.8	0.9	0.7	IPF9207	orf19.3679	unknown function
CA1701	1.1	1.0	1.0	1.0	0.9	1.0	CFL11	orf19.701	Ferric reductase (by homology)
CA2102	1.1	1.1	0.8	0.9	1.0	1.0	IPF9363	orf19.2383	similar to Saccharomyces cerevisiae Yku80p component of DNA end-joining repair pathway (by homology)
CA2514	1.1	1.0	1.4	1.0	0.9	0.9	FUR4	orf19.313	Probable uracile or allantoin permease (by homology)
CA1040	1.1	0.9	1.1	1.0	1.0	0.9	IPF4010	orf19.2503	unknown function
CA0630	1.1	1.0	1.1	0.9	1.0	1.0	IPF3875	orf19.776	unknown function
CA3063	1.1	1.0	1.2	1.1	1.1	0.9	IPF2971	orf19.4284	unknown function
CA1918	1.1	1.1	1.2	0.9	0.8	0.8	IPF7479.5f	orf19.2441	unknown function, 5-prime end
CA4998	1.1	1.0	1.0	1.0	0.9	1.0	IPF2026	orf19.5249	unknown function
CA2074	1.1	1.1	1.0	1.0	1.0	1.0	IPF3733	orf19.5287	unknown function
CA2423	1.1	1.0	0.9	1.0	0.8	0.9	SDH41	orf19.4468	succinate dehydrogenase membrane anchor subunit for sdh2p (by homology)
CA1280	1.1	1.0	1.0	1.0	1.0	1.0	IPF10828	orf19.3627	unknown function
CA2970	1.1	1.1	1.0	0.9	1.1	1.0	IPF14448	orf19.5601	unknown function
CA1204	1.1	0.8	1.0	1.0	1.0	0.7	IPF14524	orf19.867	unknown function
CA0017	1.1	1.1	1.1	0.9	1.0	0.9	IPF17811	orf19.4169.1	
CA2742	1.1	1.1	1.1	1.3	1.7	1.2	JAC1	orf19.2104	molecular chaperone (by homology)
CA0409	1.1	0.9	1.2	1.0	1.1	1.0	PHO80	orf19.5755	Cyclin (by homology)
CA4078	1.1	1.0	1.0	1.0	1.0	1.0	VMA2	orf19.6634	H+-transporting ATPase (by homology)
CA5387	1.1	1.0	1.1	1.0	1.2	1.0	CTA213.3	orf19.7276.1	transcriptional activator, 3-prime end

CA1774	1.1	1.0	1.0	0.9	1.2	1.0	IPF7498	orf19.2191	unknown function
CA4496	1.1	0.9	1.0	1.0	1.1	0.7	IPF4062	orf19.1864	unknown function
CA0220	1.1	0.9	0.9	0.9	0.9	0.7	ABZ1	orf19.1291	para-aminobenzoate synthase (by homology)
CA3969	1.1	1.0	1.0	1.0	1.1	1.0	IPF9379.5e	orf19.1430	unknown function
CA4392	1.1	1.0	1.0	1.0	23.7	3.0	IPF12303	orf19.3121	glutathione-S-transferase (by homology)
CA3515	1.1	0.8	0.9	0.8	0.8	0.8	MRPL15	orf19.6363	mitochondrial ribosomal protein of the large subunit (by homology)
CA2971	1.1	0.8	0.9	1.2	0.8	0.9	MDL2.5f	orf19.5600	ATP-binding transporter, 5-prime end (by homology)
CA1056	1.1	1.0	1.1	1.1	1.1	1.1	IPF17503	orf19.2542	protein folding and stabilization (by homology)
CA4957	1.1	1.0	1.2	1.2	1.0	0.9	IPF4588	orf19.6518	putative aldehyde dehydrogenase (by homology)
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 homology)
CA0780	1.1	1.0	1.0	1.0	0.8	1.0	Cirt1a	orf19.3492	transposase (by homology)
CA2957	1.1	1.0	1.0	1.0	1.9	1.0	DAL53	orf19.5859	allantoate permease (by homology)
CA2230	1.1	1.0	1.1	1.0	0.7	0.8	IPF10936	orf19.3928	unknown function
CA0488	1.1	1.1	0.8	0.8	0.6	0.6	SEC59	orf19.261	Dolichol kinase (by homology)
CA6083	1.1	1.0	1.0	1.1	1.1	1.1	IPF26	orf19.5976	unknown function
CA2958	1.1	1.1	1.2	1.4	0.7	0.7	KRE9	orf19.5861	cell wall synthesis protein
CA2201	1.1	1.0	1.0	1.0	1.0	0.9	BOS1	orf19.2940	ER-to-Golgi v-SNARE (by homology)
CA1991	1.1	1.0	4.2	3.2	1.2	1.7			
CA2843	1.1	1.0	0.9	1.0	1.0	1.0	ALK5.5f	orf19.5728	n-alkane-inducible cytochrome P-450, 5-prime end
CA2185	1.1	1.1	0.7	1.1	0.9	0.9	IPF6880	orf19.4247	unknown function
CA1981	1.1	0.9	1.0	1.0	1.1	1.0	IPF9470	orf19.684	similar to Saccharomyces cerevisiae Pcf11p component of pre-mRNA 3'-end processing factor CF I (by homology)
CA3718	1.1	1.0	1.0	1.0	0.9	1.1	POP7	orf19.4168	Nuclear RNase P subunit (by homology)
CA0416	1.1	1.0	1.3	1.0	1.1	1.0	IPF17492	orf19.1225	unknown function
CA3241	1.1	0.9	1.0	1.0	0.9	0.9	IPF7493	orf19.4682	putative permease (by homology)
CA0598	1.1	1.0	1.0	0.9	1.2	1.0	IPF9703.5f	orf19.4880	unknown function, 5-prime end
CA4682	1.1	0.9	0.8	1.0	1.0	0.7	IPF3687	orf19.886	similar to Saccharomyces cerevisiae Pan1p actin-cytoskeleton assembly protein (by homology)
CA3536	1.1	1.0	1.1	1.0	0.7	1.0	IPF5414	orf19.6371	unknown function
CA5394	1.1	1.0	1.0	1.0	1.0	1.0	IPF9400	orf19.937	unknown function
CA3630	1.1	1.0	0.9	0.9	0.9	1.0	PGA28	orf19.5144	unknown function
CA3528	1.1	0.9	0.3	0.5	1.1	2.4	GLY1	orf19.986	L-threonine aldolase
CA0979	1.1	1.1	1.1	0.9	1.0	0.9	IPF19713	orf19.3601	unknown function
CA0848	1.1	0.7	0.9	0.9	0.7	0.7	ACS1	orf19.1743	acetyl-coenzyme-A synthetase (by homology)
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)
CA0021	1.1	1.0	1.0	1.0	1.0	1.0	IPF19425	orf19.161	unknown function
CA4464	1.1	1.0	0.9	0.9	0.7	0.8	IPF9828	orf19.6861	similar to Saccharomyces cerevisiae Apc5p component of the anaphase-promoting complex (by homology)
CA5352	1.1	1.4	0.7	1.2	1.7	0.8	IPF856	orf19.7228	unknown function
CA4646	1.1	1.0	0.9	1.0	1.1	0.9	IPF1495	orf19.353	unknown function
CA0906	1.1	0.9	1.0	0.9	0.8	1.0	IPF4406	orf19.1483	unknown function
CA6095	1.1	1.0	1.6	0.7	0.4	0.5	SNF3	orf19.5962	High affinity glucose transport protein (by homology)
CA3698	1.1	0.9	1.1	1.0	1.1	1.0	IPF4861	orf19.6274	unknown function
CA3904	1.1	0.8	1.5	1.3	1.2	1.4	IPF14888	orf19.4399	unknown function
CA5456	1.1	1.0	1.0	1.0	1.0	1.0	IPF267	orf19.3264	unknown function
CA2329	1.1	1.0	1.1	1.0	0.9	0.9	IPF4784	orf19.4498	unknown Function
CA0907	1.1	1.0	1.0	1.0	0.8	1.0	IPF19889	orf19.1484	Unknown Function
CA2925	1.1	1.0	1.1	1.1	0.9	1.0	IPF7827	orf19.4210	unknown function
CA4969	1.1	1.0	1.0	1.0	1.0	1.0	IPF3930	orf19.6502	unknown function

CA0279	1.1	0.9	1.1	1.0	1.1	1.1	IPF10568	orf19.1440	unknown function
CA1850	1.1	0.9	1.0	1.1	0.7	0.7	IPF14630	orf19.641	unknown function
CA5439	1.1	1.1	0.9	1.0	1.1	1.1	TAF25	orf19.3242	transcription initiation factor TFIID subunit (by homology)
CA1669	1.1	0.6	1.0	0.9	1.1	0.7	IPF11393	orf19.2852	unknown function
CA1433	1.1	1.1	0.9	1.0	0.7	0.9	IPF12464	orf19.1203.1	unknown function
CA3140	1.1	1.0	0.9	0.8	1.1	0.9	IPF9214	orf19.3711	unknown function
CA3982	1.1	1.0	0.9	0.9	0.8	0.9	SAC3.5f	orf19.1556	Leucine permease transcriptional regulator (by homology)
CA5529	1.1	1.1	2.3	1.1	1.0	0.9	IPF2852	orf19.7288	putative acetyl-coenzyme-A dehydrogenase
CA1442	1.1	0.7	0.9	0.8	1.0	1.0	ERG20	orf19.4491	farnesyl-pyrophosphate synthetase
CA0402	1.1	1.1	1.0	1.0	1.0	0.9	IPF15225	orf19.1990	Sorting nexin-like protein (by homology)
CA0108	1.1	0.8	1.2	1.1	0.7	0.8	HIK1	orf19.5181	histidine kinase
CA1098	1.1	1.1	4.7	1.2	12.9	3.5	IPF12316	orf19.5069	unknown function
CA4440	1.1	0.8	0.7	0.8	0.6	0.7	IPF13864	orf19.5155	similar to Saccharomyces cerevisiae Chs6p chitin biosynthesis protein (by homology)
CA1391	1.1	1.0	1.0	1.0	1.0	0.9	IPF17474.3f	orf19.1767.1	unknown function
CA4458	1.1	1.0	1.7	1.1	0.7	0.8	IPF8464	orf19.6855	unknown function
CA3082	1.1	1.0	1.0	1.0	0.9	1.0			
CA5237	1.1	1.6	1.8	1.5	1.4	2.9	ZMS1	orf19.5026	Zinc Finger Protein C2H2 (by homology)
CA1047	1.1	0.9	1.7	1.2	0.9	1.1	IPF11615	orf19.1646	RNA-binding proteins (by homology)
CA0217	1.1	1.1	0.9	1.0	0.9	1.0	MNN41	orf19.849	regulates the mannosylphosphorylation (by homology)
CA5810	1.1	1.0	1.2	1.1	1.0	1.1	IPF4137.3f	orf19.5468.1	unknown function, 3-prime end
CA6053	1.1	0.9	1.0	1.0	0.6	0.5	IPF4949	orf19.7670	unknown function
CA2701	1.1	1.0	1.0	1.1	0.8	1.0			
CA1922	1.1	1.0	1.0	1.0	1.1	1.0	DIP52	orf19.2445	Dicarboxylic amino acid permease (by homology)
CA3840	1.1	1.0	0.8	0.9	1.3	1.3	IPF12745	orf19.6600	unknown function
CA3889	1.1	1.0	1.0	1.0	0.8	0.9	TAD3	orf19.5090	tRNA-specific adenosine-34 deaminase subunit (by homology)
CA5337	1.1	1.1	0.5	0.9	1.4	0.9	APL1	orf19.7212	AP-2 complex subunit, beta2-adaptin (by homology)
CA2139	1.1	1.0	1.0	0.9	1.0	1.0	IPF15654	orf19.2509	unknown function,
CA6045	1.1	1.0	0.8	1.0	1.1	1.0	IPF4929	orf19.7661	similar to Saccharomyces cerevisiae Hmi1p mitochondrial DNA helicase (by homology)
CA3441	1.1	1.0	0.8	0.9	0.9	0.7	MST1	orf19.2984	mitochondrial threonyl tRNA synthetase [Candida albicans]
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)
CA1316	1.1	1.0	0.9	0.9	1.2	1.1			
CA0165	1.1	1.0	1.0	1.0	1.0	1.0			
CA4426	1.1	1.0	1.1	1.1	0.7	1.0	AMD21	orf19.5169	amidase (by homology)
CA0577	1.1	1.0	0.9	1.0	0.9	1.0	IPF16051	orf19.3068	unknown function
CA3508	1.1	0.7	1.4	1.1	1.2	1.2	RSA2	orf19.6355	Involved in ribosome biogenesis (by homology)
CA1244	1.1	0.9	1.0	0.8	1.1	0.7	IPF12767	orf19.2624	unknown function
CA0916	1.1	1.1	1.0	1.0	1.0	1.5	LYS2	orf19.2970	L-aminoadipate-semialdehyde dehydrogenase, large subunit
CA4784	1.1	1.0	1.0	1.2	1.0	1.1	IPF3359	orf19.4017	Unknown function
CA0257	1.1	1.0	0.9	1.1	0.9	1.0	IPF10079	orf19.2280	unknown function
CA5753	1.1	0.9	0.6	0.9	1.2	0.8	FKH2	orf19.5390	Fork head protein type transcription factor
CA6088	1.1	1.1	0.9	1.0	0.6	0.8	HPR5	orf19.5970	ATP-dependent DNA Helicase (by homology)
CA5444	1.1	1.6	0.7	0.8	0.8	0.8	IPF230	orf19.3247	unknown function
CA3033	1.1	1.2	1.0	0.9	0.9	1.1	IPF13202	orf19.215	unknown function
CA3391	1.1	1.2	0.8	1.0	1.5	1.2	PNP1	orf19.317	Purine Nucleoside Phosphorylase (by homology)
CA1928	1.1	1.0	1.2	1.0	0.7	0.9	MRPL37	orf19.755	Mitochondrial ribosomal protein YmL37 (by homology)
CA6085	1.1	1.1	0.9	0.9	0.9	0.8	IPF32	orf19.5974	similar to Saccharomyces cerevisiae Apg9p integral membrane protein required for Cvt and autophagy transport

CA3311	1.1	1.4	1.4	1.4	1.2	0.9	IPF8809	orf19.2306	unknown function
CA5383	1.1	1.0	0.8	1.0	1.0	1.0	Zorro1b.3f	orf19.7273	reverse transcriptase, 3-prime end (by homology)
CA0977	1.1	0.8	0.9	1.0	1.0	1.1	IPF18810	orf19.3604	unknown function
CA3184	1.1	1.0	1.0	1.0	0.7	0.8	TSM1.5f	orf19.2136	component of TFIID complex, 5-prime end (by homology)
CA3465	1.1	0.8	1.1	0.9	0.9	0.8	MRP1.3f	orf19.1661.1	Mitochondrial ribosomal protein of the small subunit, 3-prime end (by homology)
CA2872	1.1	1.0	0.6	1.0	0.8	0.9	APG13	orf19.2848	probable component of the autophagic system (by homology)
CA4017	1.1	1.0	1.0	1.0	1.3	1.1	PBN1	orf19.3447	protease by homology
CA3745	1.1	1.0	0.9	1.0	1.4	1.1	MAF1	orf19.2173	nuclear protein by homology
CA0768	1.1	1.4	0.9	0.8	0.9	0.9	COX19	orf19.4967	Protein required for cytochrome c oxidase activity (by homology)
CA2926	1.1	1.6	0.8	1.1	1.3	1.3	UBA3	orf19.4209	Ubiquitin-like protein activating enzyme
CA3182	1.1	1.0	0.9	1.0	1.8	1.0	LIP4	orf19.2133	secretory lipase
CA0920	1.1	0.9	1.1	1.1	1.3	1.1	IPF18833.3f	orf19.1042.1	unknown function
CA4230	1.1	1.0	1.1	0.9	1.0	1.1	IPF12481	orf19.513	unknown function
CA1313	1.1	1.1	1.0	1.1	1.0	1.1	PGA46	orf19.3638	unknown function
CA3513	1.1	1.0	1.0	1.0	1.0	1.1	IPF11246	orf19.6360	unknown function
CA4820	1.1	1.0	1.0	1.0	0.9	0.7	IPF1196	orf19.2077	unknown function Hypothetical Zn(2)-Cys(6) zinc-finger protein (by homology)
CA5656	1.1	1.0	1.3	0.9	0.7	0.8	IPF14683	orf19.7358	unknown function
CA4132	1.1	1.0	0.9	1.0	0.6	0.6	STE20	orf19.4242	serine/threonine-specific protein kinase
CA2232	1.1	1.0	1.0	1.0	1.0	1.0	IPF10929	orf19.3925	unknown function
CA1271	1.1	1.0	0.9	0.8	1.1	0.8	HIT1	orf19.2723	required for growth at high temperature (by homology)
CA3597	1.1	1.1	0.8	0.9	0.7	0.7	BNI1	orf19.4927	regulator of budding (by homology)
CA2376	1.1	1.0	1.0	1.0	0.7	0.9	IPF15506	orf19.2213	unknown function
CA1685	1.1	1.0	1.3	1.0	0.9	0.9	IPF12270.3	orf19.3660	unknown function
CA3632	1.1	0.9	0.9	1.0	1.0	1.0	DFR1	orf19.5142	dihydrofolate reductase
CA1364	1.1	1.4	0.6	0.9	0.9	0.7	IPF5561	orf19.4423	unknown function
CA1762	1.1	1.2	0.9	1.0	1.6	1.1	IPF20014	orf19.5194.1	oxidoreductase by homology
CA3478	1.1	1.0	0.9	0.9	0.7	1.0	IPF3227	orf19.3581	similar to Saccharomyces cerevisiae chromatin assembly complex, subunit p50 (by homology)
CA5722	1.1	1.5	1.4	1.0	0.4	1.0	IPF2446	orf19.7427	unknown function
CA1109	1.1	0.9	0.9	0.9	1.0	0.8	MRPS9	orf19.5230	ribosomal protein S9 small subunit precursor
CA5599	1.1	1.0	1.0	0.9	1.4	0.9	IPF560	orf19.7102	unknown function
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 homology)
CA0565	1.1	0.9	1.1	1.2	0.9	0.9	IPF13526	orf19.6250	unknown function
CA1092	1.1	1.1	1.0	0.9	1.0	1.0	YTA7	orf19.3949	26S proteasome subunit (by homology)
CA1259	1.1	1.0	1.0	1.0	0.8	0.5	IPF3174	orf19.3167	Farnesyl transferase (by homology)
CA0784	1.1	1.3	0.8	1.1	1.2	1.1	YUH1	orf19.3930	Putative ubiquitin carboxyl-terminal hydrolase-like protein (by homology)
CA5770	1.1	1.0	1.0	1.0	1.2	1.0	IPF1103	orf19.5412	unknown function
CA0159	1.1	1.0	0.9	1.0	0.8	1.0	TUB4	orf19.1238	gamma-tubulin
CA3132	1.1	1.1	1.7	1.2	3.0	1.9	IPF8904	orf19.1363	unknown function
CA4116	1.1	0.6	1.3	1.0	0.6	0.9	IDI1	orf19.2775	isopentenyl-diphosphate delta-isomerase (by homology) Lipid and fatty acid metabolism
CA1668	1.1	1.0	0.9	1.0	1.1	1.4	IPF11396	orf19.2853	unknown function
CA4232	1.0	0.9	1.1	1.0	1.2	1.1	IPF12484	orf19.515	unknown function
CA0229	1.0	1.0	1.1	0.9	0.9	0.9	IPF8147	orf19.6200	unknown function
CA4815	1.0	1.0	0.8	1.1	0.6	0.7	CDH1	orf19.2084	Substrate-specific activator of APC-dependent proteolysis (by homology)
CA5150	1.0	0.8	0.7	1.0	1.7	1.1	FMS1	orf19.4589	Similar to corticosteroid-binding protein CBP1 (by homology)
CA3990	1.0	0.4	3.9	1.5	0.6	0.9	IPF14782	orf19.1566	beta-transducin (by homology)
CA3496	1.0	1.0	1.2	1.1	1.0	1.0	IPF17064	orf19.6342	unknown function

CA2337	1.0	1.0	0.9	1.0	0.8	1.1	IPF13379	orf19.2352	unknown function
CA2178	1.0	0.9	1.0	0.9	1.0	0.8	IPF9282	orf19.1510	unknown function
CA5266	1.0	1.1	0.9	1.1	1.1	1.0	IPF1787.3f	orf19.4996	unknown function, 3-prime end
CA1076	1.0	0.9	0.7	0.8	0.4	0.7	IPF19721	orf19.2239	similar to Saccharomyces cerevisiae Lte1p GDP/GTP exchange factor
CA1266	1.0	1.0	0.9	1.0	1.1	1.0	SAP8	orf19.242	aspartic protease
CA3430	1.0	1.2	1.0	0.9	0.9	1.0	IPF6382	orf19.587	unknown function
CA2765	1.0	1.0	0.8	0.8	1.1	1.0	APA2	orf19.5630	ATP adenylyltransferase II (by homology)
CA3071	1.0	1.0	1.0	1.1	0.7	0.8	NUP188	orf19.4808	Nucleoporin
CA4467	1.0	1.0	2.6	1.1	0.9	0.9	IPF9833	orf19.6864	unknown function
CA4744	1.0	1.0	1.0	1.0	1.1	1.3	IPF4489	orf19.4837	unknown function
CA5054	1.0	0.9	1.3	1.0	0.8	1.0	IPF3704	orf19.3019	unknown function
CA4071	1.0	1.0	1.1	1.0	0.9	0.9	IPF2561	orf19.6624	unknown function
CA4040	1.0	0.9	1.6	1.5	1.2	1.0	GAL1	orf19.3670	galactokinase
CA3975	1.0	1.0	1.0	1.0	1.0	1.1	IPF20152	orf19.1547	unknown function
CA2420	1.0	1.1	1.1	1.0	1.9	0.8	SPC19	orf19.4473	spindle pole body protein (by homology)
CA0656	1.0	1.0	0.8	0.9	1.9	1.3	IPF12470	orf19.5573	unknown function
CA3517	1.0	1.0	0.6	1.0	0.9	1.0	IFA22	orf19.1002	Unknown function
CA0452	1.0	1.3	1.0	1.0	0.8	1.0	IPF13554	orf19.1301	Hypothetical acidic protein
CA4133	1.0	1.0	0.9	1.0	0.7	1.0	IPF7010	orf19.4241	unknown function
CA1093	1.0	1.0	1.0	1.0	0.8	0.9	MSM1	orf19.3950	mitochondrial methionyl-tRNA synthetase
CA1462	1.0	0.9	1.1	0.9	1.1	0.8	THI80	orf19.1110	Thiamin pyrophosphokinase (by homology)
CA1228	1.0	1.0	1.1	0.9	0.5	0.8	IPF16081	orf19.4161	unknown function
CA2527	1.0	1.0	0.7	1.0	1.4	1.0	IPF4331	orf19.5527	unknown function
CA3768	1.0	1.0	1.1	1.1	1.1	1.0	IPF13467	orf19.2899	Putative peroxisomal 2,4-dienoyl-CoA reductase (by homology)
CA0589	1.0	1.0	0.9	1.0	4.9	5.3	IPF13080	orf19.1162.1	unknown function
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 homology)
CA0650	1.0	1.0	0.9	0.9	1.0	0.8	IPF11566	orf19.11	unknown function
CA1667	1.0	1.4	1.1	1.2	0.9	0.8	SSL2	orf19.2857	by homology to S. cerevisiae: DNA helicase
CA3398	1.0	1.0	0.9	1.0	1.0	1.0	IPF13621	orf19.3973	unknown function
CA0995	1.0	1.0	0.9	0.9	3.8	1.9			
CA3738	1.0	0.9	1.2	1.1	0.7	0.8	IPF5526	orf19.2180	unknown function
CA3612	1.0	0.9	1.1	0.9	1.3	0.8	IPF3852	orf19.29	unknown function
CA5737	1.0	1.1	1.1	1.0	1.0	1.0	JEN1	orf19.7447	Carboxylic acid transporter protein (by homology)
CA5865	1.0	1.1	1.2	1.0	0.9	1.0	MKC1	orf19.7523	ser/thr protein kinase of MAP kinase family
CA5451	1.0	0.9	1.0	0.9	1.0	0.8	SLN1	orf19.3256	Two-component signal transducer histidine kinase component
CA3934	1.0	1.1	0.9	0.8	1.1	1.2	IPF17119	orf19.2008	unknown function
CA4383	1.0	1.3	0.6	1.1	1.1	1.1	IPF8573	orf19.5676	unknown function
CA4891	1.0	1.0	0.9	0.9	0.7	0.9	IPF1627	orf19.6583	unknown function
CA3998	1.0	1.0	1.0	1.0	0.9	0.9	IPF10443	orf19.1641	formamidase-like protein (by homology)
CA0517	1.0	1.0	1.0	1.1	1.0	1.0	HEM13	orf19.2803	by homology S. cerev.: coproporphyrinogen III oxidase
CA0227	1.0	0.9	1.0	0.9	0.8	1.0	PHO23	orf19.1759	Involved in transcriptional regulation of PHO5 (by homology)
CA3128	1.0	1.0	1.1	0.9	1.0	1.0	IPF8914	orf19.1360	unknown function
CA1602	1.0	1.1	1.0	1.1	1.5	1.0	RTG1	orf19.4722	basic helix-loop-helix transcription factor that regulates CIT2 gene expression (by homology)
CA0688	1.0	0.8	0.8	0.7	0.9	0.5			
CA5585	1.0	0.9	0.7	1.1	1.3	1.0	CSA1	orf19.7114	mycelial surface antigen by homology
CA2562	1.0	1.5	0.8	1.3	0.7	0.8	IPF19953	orf19.5642	unknown function

CA5571	1.0	1.0	0.9	0.9	0.6	1.1	IPF2001	orf19.7337	unknown function
CA0682	1.0	1.0	1.2	1.2	1.2	1.5	IPF14514	orf19.4701	unknown function
CA2485	1.0	1.0	1.0	1.0	1.2	1.2			
CA2761	1.0	0.8	0.8	0.7	1.0	0.9	IPF15013	orf19.5626	pyruvate decarboxylase regulatory protein (by homology)
CA2265	1.0	1.2	1.0	1.1	1.3	1.0	CMK2	orf19.1754	Ca2+/calmodulin-dependent ser/thr protein kinase, type II (by homology)
CA4422	1.0	1.0	1.0	0.9	1.1	0.9	LIP9.3f	orf19.5173	secretory lipase 9, 3-prime end
CA2147	1.0	0.9	1.1	0.9	1.0	0.8	IPF18533.5	orf19.2516	unknown function
CA1887	1.0	1.9	0.7	1.0	1.5	1.0	IPF5496	orf19.2204	unknown function
CA0258	1.0	1.0	1.3	0.9	1.2	0.9	IPF17112	orf19.1356	thiosulfate sulfurtransferase (by homology)
CA2472	1.0	0.9	1.5	1.0	0.8	0.9	IPF3239	orf19.2875	unknown function
CA5319	1.0	1.0	1.3	0.9	0.6	0.8	IPF2150	orf19.7193	similar to protein involved in ER function
CA3876	1.0	1.1	0.7	0.9	1.3	0.9	APS3	orf19.393	AP-3 complex subunit, sigma3 subunit (by homology)
CA3369	1.0	0.9	0.9	1.1	0.7	0.7	IPF4672	orf19.1850	unknown Function
CA3533	1.0	0.9	1.1	1.0	1.2	1.0	IPF13450	orf19.6366	unknown function
CA3779	1.0	1.0	1.1	1.0	0.6	0.8	IPF11221	orf19.5841	unknown function
CA4295	1.0	1.0	0.9	1.0	0.4	0.8	MNN7	orf19.6692	putative Golgi alpha-1,2-mannosyltransferase (by homology)
CA5395	1.0	1.0	0.9	1.0	1.0	0.9	IPF9401	orf19.938	unknown function
CA2127	1.0	1.0	1.0	1.0	1.1	1.0	IPF4897	orf19.416	unknown function
CA2504	1.0	1.0	1.0	1.0	1.0	1.0	IPF6803.3f	orf19.5593	unknown function, 3-prime end
CA5512	1.0	1.0	1.1	1.0	0.9	0.9	ORC2	orf19.5358	origin recognition complex subunit 2 (by homology)
CA5642	1.0	1.1	0.9	1.0	0.7	0.7	INP52	orf19.7052	phosphatidylinositol phosphate phosphatase (by homology)
CA4253	1.0	0.9	0.9	0.9	1.0	1.0	IPF4288.3f	orf19.541.1	unknown function
CA3451	1.0	1.1	1.0	1.0	1.0	1.1	IPF7316	orf19.2971	unknown function
CA2498	1.0	1.2	0.9	0.8	0.9	1.0	VPS181	orf19.5584	vacuolar membrane protein
CA6018	1.0	1.1	1.1	1.0	1.1	1.0	IPF627	orf19.7620	unknown function
CA2363	1.0	1.0	0.7	0.9	1.2	0.8	IPF10590	orf19.1285	unknown function
CA0487	1.0	1.0	0.9	1.0	1.1	1.0	IPF13724	orf19.259	unknown function
CA0900	1.0	1.1	0.9	1.1	1.1	1.0	IPF12031	orf19.3411	unknown function
CA1941	1.0	0.9	1.1	1.1	1.1	1.2	IPF7998	orf19.4191	Ribosomal protein L24 (by homology)
CA5601	1.0	1.0	0.9	1.0	0.9	1.2	IPF556	orf19.7098	transcriptional regulator (by homology)
CA5302	1.0	0.9	1.0	1.0	1.0	0.9	IPF20175	orf19.7167	unknown function
CA5093	1.0	1.0	1.2	1.0	1.2	1.0	IPF1390	orf19.6449	unknown function
CA1185	1.0	1.0	0.9	1.0	1.4	0.9	IPF19903.5f	orf19.3784	unknown function
CA4979	1.0	1.0	1.0	1.0	0.9	1.3	IPF2062	orf19.5271	unknown function
CA5241	1.0	1.0	0.7	1.0	0.4	0.3	SMF3	orf19.5022	Probable manganese transporter (by homology)
CA1147	1.0	1.0	1.2	0.9	0.5	0.8	KAP95	orf19.3681	karyopherin-beta protein (by homology)
CA5820	1.0	0.8	1.0	1.0	0.9	0.7	IPF2500	orf19.7473	unknown function
CA1878	1.0	0.7	1.0	0.9	0.8	0.6	IPF10298	orf19.2272	unknown function
CA2582	1.0	1.1	1.1	1.0	1.1	1.1	TAL1	orf19.4371	transaldolase (by homology)
CA4251	1.0	1.2	0.8	0.9	1.3	1.0	IPF4291	orf19.540	unknown function
CA3062	1.0	1.0	0.9	1.1	1.9	1.2	IPF2968	orf19.4286	unknown function
CA6102	1.0	1.0	1.0	0.9	1.0	1.0	SPO70.5f	orf19.5954	involved in meiosis and sporulation, 5-prime end
CA5554	1.0	1.9	0.7	1.0	0.9	1.0	IPF1960.5f	orf19.7318	putative transcriptional activator, 5-prime end
CA5559	1.0	1.7	1.2	1.1	0.8	1.1	CBP1	orf19.7323	Corticosteroid binding protein
CA0532	1.0	0.9	0.7	0.7	0.7	0.5	IRE1	orf19.5068	protein kinase (by homology)
CA2954	1.0	1.3	1.0	0.8	2.4	1.5	IPF10685	orf19.5856	unknown function

CA3742	1.0	1.0	0.8	1.0	1.9	1.0	IFM3	orf19.2176	2-hydroxyacid dehydrogenase by homology, Glycerate-formate-dehydrogenases-like
CA1659	1.0	1.0	1.1	1.0	0.9	1.0	IPF11054	orf19.4323	unknown function
CA3092	1.0	1.0	1.2	0.8	0.5	0.8	IPF9821.3f	orf19.4141	unknown function, 3-prime end
CA3807	1.0	1.0	1.1	1.0	0.8	1.1	IPF9225	orf19.2487	unknown function
CA2234	1.0	1.0	1.0	1.1	1.2	0.9	PGA37	orf19.3923	unknown function
CA2692	1.0	1.0	1.0	1.0	1.0	1.0	IPF9173.3f	orf19.2732	similar to Saccharomyces cerevisiae Vps30p involved in vacuolar protein sorting and autophagy, 3-prime end
CA4307	1.0	1.0	1.0	1.0	0.8	0.8	IPF20013	orf19.6707	Unknown function
CA2448	1.0	1.1	1.1	1.0	0.8	0.8	PLC1	orf19.5506	1-phosphatidylinositol-4,5-bisphosphatephosphodiesterase
CA5477	1.0	1.0	0.9	0.9	1.0	1.1	IPF18101	orf19.5306	unknown function
CA4345	1.0	0.9	0.8	0.9	0.9	0.8	IPF3633.3f	orf19.6719	similar to Saccharomyces cerevisiae Hir3p involved in cell cycle regulation of histone transcription, 3-prime end
CA5870	1.0	1.0	0.9	1.0	0.7	0.9	IPF345	orf19.7537	FH1/FH2 involved in cytokinesis and polarity (by homology)
CA0854	1.0	0.7	2.3	1.1	1.1	0.8	IPF8854	orf19.4900	similar to Saccharomyces cerevisiae Mnn1p alpha-1,3-mannosyltransferase (by homology)
CA4084	1.0	1.6	0.5	0.7	1.0	0.9	TPS1	orf19.6640	TREHALOSE-6-PHOSPHATE SYNTHASE
CA5478	1.0	1.0	1.0	1.0	1.1	1.1	JEN2	orf19.5307	carboxylic acid transporter protein (by homology)
CA5717	1.0	2.1	0.9	1.1	0.8	1.1	CYP51	orf19.7421	Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by homology)
CA0303	1.0	1.2	1.0	1.0	2.7	3.5	IPF17507	orf19.720	putative glutathione S-transferase (by homology)
CA2107	1.0	1.0	1.0	1.0	1.0	0.9	IPF10716	orf19.3691	unknown function
CA1854	1.0	0.9	0.8	0.9	0.8	0.6	IPF12611	orf19.649	unknown function
CA5434	1.0	1.4	0.8	0.7	1.1	1.1	IPF199	orf19.3235	F-actin capping protein alpha subunit (by homology)
CA2374	1.0	0.8	1.2	1.0	0.5	0.4	FCY23	orf19.1832	Putative purine-cytosine transport protein
CA4175	1.0	1.0	0.7	1.0	0.8	0.9	IFX1	orf19.2958	unknown function
CA0369	1.0	1.0	1.0	1.0	1.1	1.0	IPF13675	orf19.1656	unknown function
CA6074	1.0	0.7	1.8	1.3	1.1	1.0	IPF11	orf19.5987	unknown function
CA2490	1.0	1.4	0.4	0.8	1.5	0.9	MUM2	orf19.4044	ubiquitin C-terminal hydrolase (by homology)
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 (by homology)
CA2620	1.0	0.9	1.1	1.0	1.3	1.3	IPF9496	orf19.2809	carnitine O-acetyltransferase (by homology)
CA2137	1.0	0.9	0.8	0.8	0.6	0.9	ARP9	orf19.2507	actin-related protein (by homology)
CA2789	1.0	1.0	1.2	0.9	0.8	1.1	IPF3567	orf19.606	unknown function
CA5408	1.0	1.0	1.2	1.0	1.5	1.3	IPF1551	orf19.952	unknown function
CA0022	1.0	1.0	1.0	1.0	1.0	1.0	IPF19421.3	orf19.162	unknown function, 3-prime end
CA2378	1.0	0.9	1.3	1.1	1.0	1.0	GLE1	orf19.2215	RNA export mediator (by homology)
CA4531	1.0	1.0	0.7	0.9	0.8	0.9	SLA1	orf19.1474	cytoskeleton assembly control protein
CA2545	1.0	0.8	1.7	1.3	0.6	1.1	RRP9	orf19.2830	U3 small nucleolar ribonucleoprotein-associated protein involved in pre-ribosomal RNA processing (by homology)
CA2210	1.0	0.9	1.0	0.8	1.2	1.2	MSL1	orf19.4748	U2 snRNA-associated protein (by homology)
CA5210	1.0	1.0	0.8	1.0	0.9	0.9	IPF2373	orf19.7027	unknown function
CA0581	1.0	0.7	1.0	0.9	0.5	0.8	IPF3181	orf19.3558	similar to Saccharomyces cerevisiae Erp3p p24 protein involved in membrane trafficking (by homology)
CA0505	1.0	1.0	1.1	1.0	0.6	0.8	IPF11988.3f	orf19.3626.1	unknown function, 3-prime end
CA3894	1.0	0.9	1.0	1.2	0.8	1.0	YIF2	orf19.5081	general translation factor eIF2 homolog (by homology)
CA3293	1.0	1.1	1.0	1.2	0.8	1.0	IPF5726	orf19.6327	unknown function
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
CA2532	1.0	1.0	0.9	1.0	1.1	1.1	PRP9	orf19.3178	pre-mRNA splicing factor (snRNA-associated protein) (by homology)
CA0960	1.0	1.1	0.8	1.1	0.5	0.8	DPP1	orf19.656	Diacylglycerol Pyrophosphate Phosphatase by homology
CA4180	1.0	1.0	0.9	1.0	1.0	1.0	EXG2	orf19.2952	glucan 1,3-beta-glucosidase-like by homology
CA1572	1.0	0.9	1.0	1.0	0.7	0.4	POX4	orf19.1652	peroxisomal fatty acyl-CoA oxidase (by homology)
CA3701	1.0	1.1	1.0	1.1	0.9	1.0	IPF11936.3f	orf19.6277	unknown function, 3-prime end
CA5399	1.0	1.0	1.0	1.0	1.0	1.0	KRE62.5f	orf19.942	Glucan synthase subunit, 5-prime end (by homology)

CA3545	1.0	0.8	0.9	1.0	0.7	1.0	BPT1.5f	orf19.6383	membrane transporter of the ATP-binding cassette (ABC) superfamily, 5-prime end (by homology)
CA5895	1.0	1.0	0.9	1.0	3.3	1.4	ISA2	orf19.6811	Mitochondrial protein required for iron metabolism (by homology)
CA0436	1.0	1.1	0.9	0.9	0.8	1.0	RBL2	orf19.1738.1	Beta-tubulin binding protein (by homology)
CA0831	1.0	1.1	1.0	1.0	1.1	1.5	IPF10493	orf19.247	unknown function
CA4451	1.0	1.2	0.9	1.0	1.1	1.1	ELC1	orf19.6849	Transcription elongation factor (by homology)
CA2523	1.0	1.0	1.0	1.0	0.9	1.0	IPF4319	orf19.5520	unknown function
CA6000	1.0	1.7	0.9	0.8	2.3	2.0	FDH11	orf19.7600	glutathione-dependent formaldehyde dehydrogenase, (by homology)
CA0359	1.0	1.0	1.0	1.0	0.8	1.0	IPF17488.5	orf19.1820	unknown function, internal fragment
CA2512	1.0	1.0	0.9	1.1	1.0	1.1	HFI1	orf19.307	Putative transcriptional coactivator (by homology)
CA4543	1.0	1.0	1.0	1.0	1.0	0.9	PPE1	orf19.1459	Ribosomal protein of the small subunit, mitochondrial (by homology)
CA0582	1.0	0.9	1.1	1.0	0.9	1.0	IPF3180	orf19.3557	unknown function
CA2880	1.0	0.9	0.9	0.9	1.5	0.9	IPF3781	orf19.5849	unknown function
CA1523	1.0	0.8	1.0	1.0	0.8	1.0	PAT1	orf19.3792	Topoisomerase II-associated protein (by homology)
CA2976	1.0	1.0	0.7	1.1	1.2	0.9	IPF14676	orf19.1236	unknown function
CA1756	1.0	1.6	1.1	1.2	1.5	1.0	IPF14562	orf19.5129	unknown function
CA2856	1.0	1.1	1.5	1.4	1.4	1.2	IPF7062	orf19.1066	unknown function
CA5969	1.0	0.9	0.9	0.9	0.8	0.9	BET2	orf19.7563	beta subunit of geranylgeranyl transferase type2
CA2114	1.0	1.1	1.0	1.0	0.5	0.9	IPF13744	orf19.3685	protein involved in regulation of carbon metabolism (by homology)
CA6032	1.0	0.9	0.8	0.9	1.0	1.0	IPF596	orf19.7642	similar to Saccharomyces cerevisiae Vps3p vacuolar sorting protein
CA2241	1.0	1.0	0.9	1.0	1.4	0.9	IFQ1.3f	orf19.4674	Unknown function, 3-prime end
CA5653	1.0	1.1	1.2	1.0	1.0	1.0	SSN8	orf19.7355	C-type cyclin associated with the Ssn3p cyclin-dependent kinase (by homology)
CA5967	1.0	1.2	1.0	1.1	1.0	0.9	IPF955	orf19.7558	member of the AAA ATPase family of proteins (by homology)
CA5005	1.0	1.0	1.0	0.9	1.0	1.0	CDC62.5f	orf19.5242.1	Cell division control protein (by homology)
CA1257	1.0	1.1	0.9	1.0	2.0	1.2	IPF18725	orf19.3169	unknown function
CA1103	1.0	1.0	1.0	1.0	1.1	1.2	IPF5673	orf19.4948	imilar to Saccharomyces cerevisiae Rex3p RNA exonuclease (by homology)
CA0274	1.0	1.4	1.0	0.9	0.9	0.5	IPF15153	orf19.5867	unknown function
CA0052	1.0	1.1	1.4	1.0	1.3	1.8	IPF19567	orf19.475	Unknown function
CA0001	1.0	1.0	1.0	1.1	1.1	1.0			
CA3797	1.0	1.0	0.5	0.8	0.7	0.7	IPF5633	orf19.5821	unknown function
CA0797	1.0	1.0	1.0	1.2	0.9	1.0	IPF13564	orf19.1608	putative arylsulfatase (by homology)
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 homology)
CA1310	1.0	1.0	1.0	1.0	0.8	1.0	IPF14232	orf19.3631	unknown function
CA1408	1.0	1.0	1.0	0.8	1.4	1.1	IPF10513	orf19.2883	unknown function
CA5433	1.0	1.0	0.9	0.9	1.1	1.1	SFT1	orf19.3234.1	SNARE-like protein (by homology)
CA3784	1.0	0.9	1.2	1.1	1.1	1.0	IPF11229	orf19.5835	similar to Saccharomyces cerevisiae Rrp7p involved in pre-rRNA processing and ribosome assembly (by homology)
CA1220	1.0	1.0	1.0	1.0	0.6	1.0	IPF14985	orf19.4134	unknown function
CA3434	1.0	1.0	1.1	1.0	1.0	1.0	CCP2	orf19.584	Cytochrome-c peroxidase precursor (by homology)
CA4137	1.0	1.0	0.9	1.0	1.2	1.3	CNA1	orf19.4235	cyclic nucleotide phosphodiesterase
CA0757	1.0	0.7	0.6	0.8	2.2	2.0			
CA4701	1.0	1.0	0.8	0.9	1.2	1.4	IPF4214	orf19.6929	unknown function
CA2666	1.0	1.6	0.9	1.2	0.9	1.1	IPF16995	orf19.3548	unknown function
CA4556	1.0	0.9	0.9	0.8	0.9	0.9	IPF8044	orf19.6866	similar to Saccharomyces cerevisiae Snp1p U1 small nuclear ribonucleoprotein (by homology)
CA3381	1.0	0.9	1.2	1.0	0.8	1.0	NPR2	orf19.328	nitrogen permease regulator (by homology)
CA3126	1.0	1.2	1.0	0.9	1.2	1.2	GCN4	orf19.1358	transcriptional activator
CA5885	1.0	1.0	1.0	0.9	1.1	1.0	IPF2419	orf19.6824	unknown function
CA5916	1.0	0.8	1.0	0.9	0.7	0.7	IPF19818	orf19.6789	unknown function

CA0963	1.0	1.0	0.9	1.0	3.6	1.4	IPF9143	orf19.6246	similar to Saccharomyces cerevisiae Nat3p N-acetyltransferase (by homology)
CA0444	1.0	1.4	0.9	0.8	0.9	0.9	IPF17429.3f	orf19.75	similar to Saccharomyces cerevisiae Sec5p required for exocytosis, 3-prime end
CA2268	1.0	1.0	1.0	0.9	0.5	0.8	IFU1.3f	orf19.2599.3	Unknown function, 3-prime end
CA0336	1.0	1.1	0.8	0.9	0.8	0.9	IPF9869	orf19.1371	unknown function
CA6117	1.0	1.0	1.0	1.2	1.0	1.1	IPF122	orf19.5933	unknown function
CA2371	1.0	0.9	1.2	0.8	0.9	0.8	IPF10333	orf19.1835	unknown function
CA2606	1.0	1.1	0.8	1.0	1.3	1.1	IPF5466	orf19.5683	unknown function
CA2815	1.0	1.0	1.0	0.9	0.9	0.7	IPF5604	orf19.2996	unknown function
CA0264	1.0	1.0	1.0	1.0	1.0	1.1	IPF8434	orf19.1406.2	unknown function
CA0468	1.0	0.9	1.0	1.1	1.1	1.0	DIB1	orf19.1975	Component of the U4/U6.U5 snRNP (by homology)
CA5314	1.0	1.0	1.0	1.0	1.0	1.1	HAT2	orf19.7185	Subunit of the major yeast histone acetyltransferase (by homology)
CA3945	1.0	1.7	0.5	0.7	0.9	2.3	CHA12.3f	orf19.1996	L-serine/L-threonine deaminase (by homology)
CA2256	1.0	0.7	0.9	0.7	0.7	0.8	IPF14757	orf19.1956	unknown function
CA4816	1.0	1.0	1.0	1.0	1.0	1.0	IPF1183	orf19.2082	putative aspartyl protease (by homology)
CA4596	1.0	0.9	1.1	1.0	0.9	1.0	MRE11	orf19.6915	DNA repair and meiotic recombination protein (by homology)
CA0413	1.0	0.8	0.6	1.1	1.7	1.3	ALS12.3f	orf19.2122	agglutinin-like protein, 3-prime end
CA2444	1.0	1.1	1.2	0.9	1.0	1.0	IPF13883	orf19.5502	Unknown function
CA4507	1.0	1.1	1.1	1.3	1.0	1.5	IPF20015	orf19.499	unknown function
CA4156	1.0	1.0	1.2	1.0	0.9	1.0	IPF10990	orf19.5802	unknown function
CA2428	1.0	1.1	0.9	0.9	1.3	1.5	IPF9894	orf19.3405	possible zinc-finger protein
CA0905	1.0	1.0	0.9	0.9	0.8	0.9	IPF4405	orf19.1482	unknown function
CA3339	1.0	1.0	1.1	1.0	1.0	1.2	IPF20131	orf19.2332	unknown function
CA1530	1.0	0.9	1.0	1.0	0.6	0.6	ALG2.5	orf19.1221	mannosyltransferase, 5-prime end (by homology)
CA3023	1.0	1.0	1.0	1.1	1.0	0.7	IPF11508	orf19.3904	unknown function
CA0015	1.0	0.8	0.8	0.8	1.2	0.8			
CA5683	1.0	1.0	1.1	1.0	1.0	1.0	IPF3333	orf19.7385	unknown function
CA5734	1.0	1.1	1.0	0.9	2.2	1.0	IPF20029	orf19.7444	unknown function
CA5128	1.0	1.0	1.0	1.0	1.0	0.9	IPF5118	orf19.6400	unknown function
CA4267	1.0	1.0	1.0	0.9	1.3	1.0	IPF2286	orf19.6661	unknown function
CA1892	1.0	0.9	1.0	1.0	0.9	1.4	IPF10197	orf19.2753	Similarity to transcription factors
CA5377	1.0	0.7	1.1	1.2	1.0	1.2	IPF5234	orf19.7263	X-Pro dipeptidase (by homology)
CA3926	1.0	0.9	1.3	1.1	0.9	1.0	IPF16198	orf19.5107	possible regulatory protein
CA4638	1.0	1.1	0.9	0.9	1.2	1.1	UGA2	orf19.345	succinate-semialdehyde dehydrogenase (NAD(P)+) (by homology)
CA0855	1.0	1.0	0.6	0.8	0.9	0.4	AMYG1	orf19.4899	glucoamylase
CA3448	1.0	1.0	1.1	1.1	1.0	1.2	YKT6	orf19.2974	Endoplasmic Reticulum-Golgi transport (by homology)
CA3136	1.0	0.9	1.0	1.0	1.1	1.0	IPF8989	orf19.1367	unknown function
CA2777	1.0	0.8	1.0	0.9	1.6	0.9	THI6	orf19.277	thiamin-phosphate pyrophosphorylase and hydroxyethylthiazole kinase-like by homology
CA3312	1.0	1.2	1.2	1.1	0.9	1.1	IPF8810	orf19.2305	unknown function
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 glyoxylate pathway regulator Gpr1p
CA1358	1.0	0.9	0.9	1.0	1.2	1.1	NIF3	orf19.4406	Ngg1p-interacting factor 3 (by homology)
13882.10	1.0	1.0	1.1	1.0	0.9	0.9			
CA1889	1.0	1.1	1.0	0.8	0.9	0.9	CBP6	orf19.2201	apo-cytochrome B pre-mRNA processing protein (by homology)
CA5273	1.0	0.8	1.1	1.2	0.9	1.0	NUP49	orf19.4987	nuclear pore protein (by homology)
CA4234	1.0	1.0	0.9	1.0	1.0	1.1	HAP3	orf19.517	CCAAT-binding factor subunit (by homology)
CA2399	1.0	0.7	1.8	1.2	1.0	1.3	MAK5	orf19.3540	ATP-dependent RNA helicase (by homology)
CA5177	1.0	0.9	1.2	1.0	1.3	1.0	IPF11101	orf19.4615	Weak similarity to C. cerevisiae hypothetical protein (by homology)

CA2237	1.0	1.0	1.0	1.0	0.7	0.9	IPF10032.3f	orf19.3917	unknown function, 3-prime end
CA4107	1.0	1.1	1.3	0.9	0.6	0.8	IPF3970	orf19.671	unknown function
CA1065	1.0	1.0	1.0	1.0	0.9	1.0	IPF9002	orf19.4639	unknown function
CA2899	1.0	0.9	1.3	0.7	0.7	0.8	IPF17681	orf19.3480	similar to Saccharomyces cerevisiae Rsm23p involved in mitochondrial function (by homology)
CA5971	1.0	0.9	1.5	0.9	0.8	1.1	GNP2	orf19.7565	high affinity glutamine permease (by homology)
CA0463	1.0	1.0	1.1	0.9	0.8	0.9	IPF18979.5	orf19.163	unknown function
CA3871	1.0	0.9	1.0	0.9	0.8	0.8	IPF8828	orf19.398	unknown function
CA4630	1.0	1.1	0.9	0.9	2.4	2.1	IPF1537	orf19.336	putative adrenodoxin and ferrodoxin (by homolgy)
CA2718	1.0	0.9	1.0	1.1	1.6	1.3	IPF7374.3f	orf19.3338	unknown function
CA5851	1.0	1.3	0.8	1.4	0.8	0.8	KIN2	orf19.7510	ser/thr protein kinase (by homology)
CA2502	1.0	1.0	1.0	1.0	1.1	1.0	PGA60	orf19.5588	unknown function
CA5329	1.0	1.0	1.2	0.6	0.8	0.7	MRP7	orf19.7203	Mitochondrial ribosomal protein YmL2 precursor (by homology)
CA2690	1.0	1.0	0.9	1.0	1.0	1.0			
CA3764	1.0	1.0	0.9	1.1	1.0	1.0	IPF13072	orf19.2905	unknown function
CA4873	1.0	0.8	0.7	0.7	3.0	2.7			
CA1233	1.0	1.0	0.9	0.9	1.3	1.2	IPF11814	orf19.4983	unknown function
CA5450	1.0	1.1	1.6	1.0	0.8	0.9	IPF243	orf19.3254	unknown function
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-prime end (by homology)
CA4479	1.0	1.0	1.0	1.0	2.3	1.4	URH1	orf19.1888	Uridine ribohydrolase (by homology)
CA5174	1.0	0.9	1.0	1.2	1.3	1.3	PRS4	orf19.4611	Ribose-phosphate pyrophosphokinase 3 (by homology)
CA0891	1.0	1.2	0.9	1.0	0.9	1.0	IPF11764	orf19.4735	unknown function
CA0200	1.0	1.0	0.7	0.7	0.9	1.8	IPF15119	orf19.1534	unknown function
CA4822	1.0	1.6	0.8	1.2	0.8	0.8	DFG5	orf19.2075	Required for filamentous growth (by homology)
CA0292	1.0	1.0	1.1	1.1	0.9	1.0	IPF19855	orf19.6488	unknwon function
CA2605	1.0	0.7	0.9	1.2	0.9	0.9	SRP1	orf19.5682	alpha importin by homology
CA3712	1.0	1.0	1.1	1.0	1.0	1.0	IPF7891	orf19.4936	unknown function
CA0288	1.0	1.0	1.1	1.0	1.0	1.0	IPF14614	orf19.6080.1	unknown function
CA3056	1.0	0.9	1.1	0.9	0.7	0.8	IPF2953	orf19.4294	similar to Saccharomyces cerevisiae Cyc2p cytochrome-c mitochondrial import factor (by homology)
CA1031	1.0	1.1	0.9	0.9	0.8	0.9	IPF17469	orf19.3848	unknown function
CA1343	1.0	1.0	1.1	0.9	0.8	0.9	IPF14624	orf19.4341.2	unknown function unknown function | FALSORF=SMALLORF
CA3973	1.0	0.8	0.9	0.9	1.0	1.1	IPF6505	orf19.1545	unknown function
CA1423	1.0	1.2	1.0	0.9	0.6	0.8	IPF14247	orf19.3799	unknown function
CA1507	1.0	3.8	0.9	0.9	3.6	1.1	HSP30	orf19.4526	heat shock protein (by homology)
CA1926	1.0	1.1	0.8	0.9	1.0	0.5	IPF13407	orf19.753	Unknown function
CA0645	1.0	1.0	0.9	1.0	0.6	0.8			
CA3691	1.0	1.0	1.6	1.0	0.4	0.8	IPF4880	orf19.6266	unknown function
CA4134	1.0	0.9	0.9	0.9	0.4	0.6	COS162	orf19.4240	involved in manganese homeostasis (by homology)
CA3892	1.0	0.6	1.0	1.0	0.9	0.9	PSE1	orf19.5085	karyopherin-beta protein (by homology)
CA5719	1.0	1.0	1.5	1.2	1.2	1.4	IPF2441	orf19.7424	unknown function
CA3735	1.0	1.0	0.8	1.0	1.2	1.2	IPF5534	orf19.2184	5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxylase (by homology)
CA0672	1.0	1.5	1.6	1.4	1.2	1.0	GRP6	orf19.3151	Putative reductase (by homology)
CA0458	1.0	1.0	1.0	1.0	1.1	1.0	IPF15601	orf19.2433	unknown function
CA1607	1.0	1.0	1.1	1.0	1.4	1.1	IPF14916	orf19.4727	unknown function
CA1674	1.0	1.0	1.3	0.8	0.9	0.9	PAF1	orf19.3613	DNA-directed RNA polymerase II regulator by homology
CA5350	1.0	1.1	0.7	0.6	1.6	1.8	IPF859	orf19.7225	unknown function
CA3187	1.0	0.8	1.5	1.2	0.8	1.8	IPF17094	orf19.2143	unknown function

CA0973	1.0	1.5	2.1	1.6	1.3	1.3	IPF12662	orf19.6474	unknown function
CA4954	1.0	0.9	0.9	0.8	1.0	1.0	TOM40	orf19.6524	mitochondrial import receptor chain TOM40 (by homology)
CA0693	1.0	0.8	2.0	1.2	0.8	1.0	IPF12606.5	orf19.3288	unknown function, 5-prime end
CA3223	1.0	1.0	1.2	0.9	0.7	0.8	SRP102	orf19.6284	Signal recognition particle receptor (by homology)
CA5087	1.0	2.4	1.1	0.9	0.7	0.9	IPF20025	orf19.3062	unknown function
CA5800	1.0	1.1	0.9	1.1	0.8	1.1	IPF4175	orf19.5450	mitochondrial respiratory function (by homology)
CA3558	1.0	1.0	1.0	1.0	2.3	1.1	IPF7760	orf19.3887	unknown function
CA0705	1.0	1.0	1.0	1.0	0.9	1.0	IPF11804	orf19.2916	unknown function
CA4334	1.0	1.0	1.0	0.9	1.0	0.9	IPF2082	orf19.4085	unknown function
CA4143	1.0	1.2	0.9	1.1	1.0	1.1	DDP1	orf19.4229	diadenosine and diphosphoinositol polyphosphate phosphohydrolase (by homology)
CA0830	1.0	1.1	1.1	0.8	0.8	0.8	APL5	orf19.248	AP-3 complex subunit, gamma-adaptin (by homology)
CA1173	1.0	1.0	1.0	1.0	0.8	1.0	IPF14254	orf19.4768	unknown function
CA2679	1.0	1.0	1.0	1.0	1.7	1.2	IFU5	orf19.2568	Unknown function
CA3281	1.0	1.0	1.0	1.0	0.9	1.5	RPB8	orf19.6314	DNA-directed RNA polymerase I, II, III 16 KD subunit (by homology)
CA3692	1.0	1.0	1.1	1.0	0.9	1.0	IPF4876	orf19.6267	unknown function
CA5257	1.0	1.4	0.6	1.0	0.9	1.1			
CA6066	1.0	1.0	1.1	1.1	1.1	1.0	CDR1	orf19.6000	multidrug resistance protein (by homology)
CA4854	1.0	1.2	0.8	1.2	1.0	0.8	RCE1	orf19.3825	CAAX PRENYL PROTEASE 2 (by homology)
CA4859	1.0	0.8	1.0	1.0	0.6	0.8	IPF15927.5f	orf19.3833	similar to Saccharomyces cerevisiae Tfc3p transcription initiation factor TFIIIC, 5-prime end (by homology)
CA3393	1.0	1.2	1.0	1.0	0.9	0.9	IPF6748	orf19.315	unknown function
CA6137	1.0	1.0	1.4	0.9	0.5	0.8	IPF4356	orf19.5910	unknown function
CA2152	1.0	1.0	1.0	1.0	1.0	1.0	IPF7899	orf19.6024	unknown function
CA2807	1.0	1.2	0.6	0.8	1.2	1.1	IPF11965	orf19.5782	unknown function
CA3088	1.0	1.7	0.7	0.9	2.6	1.9	IPF9826	orf19.4145	unknown function
CA4061	1.0	1.0	1.1	0.7	1.1	0.8	IPF5935	orf19.438	Unknown function
CA3271	1.0	1.1	0.9	0.9	0.9	1.0	GLY2	orf19.6305	L-threonine aldolase, low-specific
CA5102	1.0	0.8	0.8	0.9	0.7	0.9	CDC23	orf19.6437	Subunit of anaphase-promoting complex (by homology)
CA0058	1.0	1.2	1.1	1.0	0.8	1.0			
CA4186	1.0	1.0	1.0	1.0	1.3	1.1	PUT4	orf19.2945	proline permease
CA0172	1.0	1.0	0.8	0.9	1.1	1.0	IPF19154	orf19.1126	unknown function
CA1687	1.0	0.9	0.5	0.8	0.7	0.7	IPF12275	orf19.3658	unknown function
CA2670	1.0	0.8	2.0	1.3	0.8	1.1	MAK16	orf19.5500	nuclear viral propagation protein (by homology)
CA2184	1.0	1.0	1.0	0.9	1.1	1.0	IPF6874.3f	orf19.4251	unknown function, 3-prime end
CA5381	1.0	0.9	1.2	1.1	1.0	1.0	IPF5222	orf19.7269	arylalkylamine n-acetyltransferase (by homology)
CA5009	1.0	1.4	0.9	1.0	1.9	2.1	VPH2	orf19.5237	H+-ATPase assembly protein (by homology)
CA0856	1.0	1.0	1.0	1.0	1.0	0.9	IFL1	orf19.4463	unknown function
CA2725	1.0	1.0	1.0	1.0	0.9	0.9	MRPL23A	orf19.3348	mitochondrial ribosomal protein L23 (by homology)
CA5199	1.0	0.9	0.9	1.0	1.0	1.0	IPF2334	orf19.7013	unknown function
CA4778	1.0	1.1	0.9	1.0	1.2	1.8	IFJ1	orf19.4011	Unknown function
CA2774	1.0	1.0	1.0	1.0	0.5	1.4	TFC4	orf19.274	transcription factor IIIC chain TFC4- like by homology
CA5396	1.0	0.6	1.1	0.8	0.7	0.8	NAM7	orf19.939	nonsense-mediated mRNA decay protein (by homology)
CA3801	1.0	1.0	1.0	1.0	0.9	1.0	UGA4	orf19.2479	GABA-specific transport protein
CA3633	1.0	1.0	0.9	0.9	1.1	1.2	IFA19	orf19.5141	unknown function
CA1799	1.0	1.0	1.0	1.0	1.0	1.1	IPF11446	orf19.2922	unknown function
CA6152	1.0	0.8	1.0	1.0	0.7	0.9	NUP85	orf19.5887	Nuclear pore protein (by homology)
CA2488	1.0	1.1	0.9	0.9	1.1	1.0			

CA1424	1.0	1.0	0.9	1.0	1.2	1.0	IPF9090	orf19.3801	unknown function
CA1311	1.0	1.1	1.0	0.9	1.0	1.1	IPF14233	orf19.3633	Putative transthyretin precursor (by homology)
CA2772	1.0	0.5	3.3	1.3	0.9	1.1	IPF20112	orf19.2688	unknown function
CA2353	1.0	0.9	0.9	0.9	0.8	0.8	VPS13	orf19.4416	involved in regulating membrane traffic (by homology)
CA3325	1.0	1.0	0.9	1.0	1.0	1.2	IPF6890	orf19.2674	unknown function
CA1929	1.0	1.0	1.9	1.6	0.9	0.7	SAP7	orf19.756	secreted aspartyl proteinase 7
CA0842	1.0	0.9	1.0	0.9	0.9	0.7	IPF15633	orf19.1053	similar to Saccharomyces cerevisiae Bst1p egative regulator of COPII vesicle formation
CA5048	1.0	1.0	1.1	1.0	0.6	1.1	IPF20024	orf19.3012	unknown function
CA5739	1.0	1.1	0.9	1.0	1.4	1.6	IPF2884	orf19.7449	unknown function
CA0222	1.0	1.0	1.0	1.0	1.3	1.2	IPF12141.3f	orf19.1952	unknown function
CA3652	1.0	1.0	1.0	0.9	1.0	1.4	NBP35	orf19.2043	Nucleotide-binding protein (by homology).
CA3727	1.0	1.0	0.7	1.1	1.4	1.1	HIS5.3f	orf19.4177	Histidinol-phosphate aminotransferase, 3-prime end (by homology)
CA4378	1.0	1.1	0.8	0.9	1.0	1.0	IPF11299	orf19.5671	unknown function
CA4673	1.0	1.0	0.7	1.0	1.4	1.3	IPF3661	orf19.899	unknown function
CA5745	1.0	0.9	1.1	1.0	0.8	1.1	TAF60	orf19.7454	TATA-binding protein-associated-factor (by homology)
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 glyoxylate pathway regulator Gpr1p
CA6026	1.0	1.1	1.0	0.9	0.8	1.0	IPF610	orf19.7631	unknown function
CA4470	1.0	0.8	2.1	1.5	1.1	1.1	IPF9717	orf19.1902	unknown function
CA3347	1.0	1.0	0.9	1.1	0.8	0.9	ERP5	orf19.2322.3	protein involved in membrane trafficking (by homology)
CA0062	1.0	1.0	1.0	1.0	1.0	1.0			
CA3276	1.0	1.0	0.9	1.0	0.8	1.0	IPF6263	orf19.6310	unknown function
CA1262	1.0	0.7	0.8	0.7	0.5	0.7	MDR1	orf19.1244	Mac1p interacting protein (by homology)
CA0679	1.0	1.0	1.1	1.0	1.3	1.2			
CA3944	1.0	1.1	0.7	0.9	1.1	1.1	IPF4750	orf19.1998	unknown Function
CA0337	1.0	1.0	1.0	0.9	0.9	1.0	IPF9867	orf19.1370	unknown function
CA0460	1.0	1.0	1.0	1.0	1.1	1.4	SEC17	orf19.2518	transport vesicle fusion protein (by homology)
CA0243	1.0	1.3	1.0	1.0	1.0	1.0	BSD2	orf19.5869	Metal homeostasis protein (by homology)
CA2705	1.0	1.0	1.0	1.0	0.9	1.1	NEM1	orf19.4657	required for nuclear morphology (by homology)
CA1420	1.0	0.8	0.7	1.1	1.2	1.0	RNT1	orf19.3796	Ribonuclease III (by homology)
CA3351	1.0	1.0	1.0	1.0	0.5	0.7			
CA2511	1.0	1.1	0.9	0.9	0.6	0.8	IPF1474	orf19.306	myosin-like protein
CA3096	1.0	1.0	1.0	1.0	1.0	1.0	IPF11551	orf19.3858	unknown function
CA6044	1.0	1.1	0.8	1.0	0.8	1.0	IPF4928	orf19.7660	similar to Saccharomyces cerevisiae Sac2p suppressor of actin mutation (by homology)
CA1671	1.0	1.0	0.7	0.9	0.7	0.9			
CA2878	1.0	0.7	1.1	1.1	1.1	0.9	RET1	orf19.5847	DNA-directed RNA polymerase III (by homology)
CA5655	1.0	1.2	1.0	1.0	0.7	0.8	IPF18080.3f	orf19.7357	unknown function
CA2995	1.0	1.0	0.6	0.7	1.0	0.9	IPF9113	orf19.6121	unknown function
CA1210	1.0	1.0	1.0	1.0	1.0	0.9	IPF7030	orf19.132	unknown function
CA4600	1.0	1.0	1.0	1.0	1.0	1.0	IPF2199	orf19.6919	unknown function
CA5047	1.0	1.0	1.0	0.9	1.0	1.1	IPF4504	orf19.7002	unknown function
CA1677	1.0	1.0	1.2	1.0	0.9	1.0	GTR1	orf19.3617	GTP-binding protein by homology
CA5628	1.0	1.0	1.0	1.0	1.5	0.9	MAC1	orf19.7068	putative metal-binding transcriptional regulator (by homology)
CA1537	1.0	1.0	0.9	1.0	1.6	1.0	IPF17483	orf19.450	unknown function
CA4731	1.0	1.0	1.0	1.0	1.0	1.0	LIP3	orf19.4856	Secretory lipase
CA1543	1.0	0.9	0.9	1.0	1.0	1.0	IPF1043	orf19.4567	Similar to hydroxyquinol 1,2-dioxygenase
CA0751	1.0	1.0	0.8	1.3	1.3	1.1	IPF6286	orf19.1971	unknown function

CA5723	1.0	1.0	1.0	1.1	1.1	0.8	APN1	orf19.7428	AP endonuclease, exonuclease III homologue (by homology)
CA0401	1.0	1.0	1.0	1.0	1.0	1.1	RTA1	orf19.6224	unknown function
CA3013	1.0	1.0	0.9	0.9	1.5	1.2	PET117	orf19.6225.1	cytochrome c oxidase assembly factor (by homology)
CA0594	1.0	1.0	1.0	0.9	1.1	0.7	IPF8860	orf19.4903	similar to Saccharomyces cerevisiae Gpi12p N-acetylglucosaminyl phosphatidylinositol deacetylase (by homology)
CA2549	1.0	1.1	1.0	0.9	1.3	0.8	RPD31	orf19.2834	histone deacetylase B (by homology)
CA0983	1.0	1.2	1.0	0.9	0.6	0.9	CBR1	orf19.1801	Cytochrome-b5 reductase (by homology)
CA2991	1.0	0.9	1.0	0.9	0.7	0.9	IPF5088	orf19.6013	unknown function
CA1852	1.0	1.0	1.0	1.0	0.9	1.0	IPF14628	orf19.642.1	unknown function
CA2122	1.0	1.0	1.0	1.0	0.7	0.9			
CA1001	1.0	1.0	1.0	1.0	1.0	0.9	IPF6006	orf19.1488	unknown function
CA3839	1.0	1.0	1.0	1.0	0.9	0.9	IPF12744	orf19.6599.1	unknown function
CA4487	1.0	1.1	1.1	1.1	1.2	1.0	IPF4039	orf19.1876	similar to Saccharomyces cerevisiae Nam8p recombination protein (by homology)
CA4605	1.0	1.0	1.0	1.3	0.6	0.7	IPF6226	orf19.3295	unknown function
CA1418	1.0	1.0	0.7	0.7	1.4	1.1	IPF12061.3f	orf19.173	zinc-finger containing protein, 3-prime end (by homology)
CA0073	1.0	1.0	1.0	1.0	1.0	1.0	IPF19283.5f	orf19.626.2	unknown function, 5-prime end
CA5129	1.0	1.1	1.1	1.0	1.1	1.1	ATS1	orf19.6399	alpha-tubulin suppressor (by homology)
CA4330	1.0	1.4	0.8	1.2	1.0	1.1	IPF2087	orf19.4090	unknown function
CA5491	1.0	1.0	0.9	1.0	0.9	1.0	IPF798	orf19.5326	transcriptional regulator (by homology)
CA1455	1.0	1.0	1.0	1.0	0.7	0.7	IPF15081	orf19.4409	phophodiesterase (by homology)
CA5472	1.0	1.0	1.0	1.0	0.9	1.0	IPF16948	orf19.3285	unknown function
CA5785	1.0	1.0	1.1	1.1	1.2	1.1	TPT1	orf19.5432	tRNA 2 -phosphotransferase (by homology)
CA1802	1.0	0.8	0.9	0.9	0.7	0.7	IPF11443	orf19.2919	unknown function
CA4407	1.0	0.9	0.9	1.1	1.0	1.0	RPO31	orf19.3103	DNA-directed RNA polymerase III (by homology)
CA0544	1.0	1.0	1.0	1.0	1.0	1.0	IPF3252	orf19.2868	unknown function
CA0453	1.0	1.2	1.3	0.8	0.6	0.7	IPF13552	orf19.1300	putative methyltransferase (by homology)
CA1754	1.0	1.3	0.7	0.7	1.3	1.1	IPF16320	orf19.5131	Unknown function
CA3792	1.0	1.0	1.1	1.0	1.0	1.0	UGA5	orf19.5826	GABA-SPECIFIC TRANSPORT PROTEIN by homology to S. cerevisiae
CA1966	1.0	1.1	1.0	1.0	1.0	1.0	IFR4	orf19.2394	unknown function
CA1853	1.0	1.3	0.9	1.1	1.3	0.9	LYP1	orf19.651	lysine-specific high-affinity permease (by homology)
CA0107	1.0	0.7	1.4	1.0	0.7	0.7	POL3	orf19.5183	DNA Polymerase III
CA5862	1.0	1.9	1.2	1.3	1.1	1.1	POT11	orf19.7520	peroxysomal 3-ketoacyl-CoA thiolase A (by homology)
CA4791	1.0	1.4	1.0	1.0	1.2	1.2	IPF3370	orf19.4025	similar to Saccharomyces cerevisiae Pre1p 20S proteasome subunit C11(beta4) (by homology)
CA4032	1.0	1.0	1.0	1.0	1.1	1.0	IPF11081.3f	orf19.3431.2	
CA2647	1.0	0.8	1.0	1.2	0.7	0.7	IPF13088	orf19.1186	unknown function
CA2442	1.0	0.7	1.7	1.3	1.2	1.5	PRS5	orf19.2193	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase)
CA5092	1.0	1.0	1.0	0.9	1.0	0.9	IPF1394	orf19.6450	unknown function
CA4287	1.0	1.1	1.0	1.0	1.1	1.2	IPF20011.3f	orf19.6684.1	similar to Saccharomyces cerevisiae Pnc1p pyrazinamidase and nicotinamidase, 3- prime end (by homology)
CA5145	1.0	1.0	0.8	1.0	1.4	1.4	SKI6	orf19.4582	3 ->5 exoribonuclease (by homology)
CA1263	1.0	1.0	1.0	1.1	0.8	0.9	IPF9880	orf19.1246	unknown function
CA4978	1.0	1.0	1.0	1.0	0.9	1.0	IPF2065	orf19.5274	unknown function
CA3591	1.0	1.0	1.0	1.0	0.9	0.8	IFT2	orf19.2247	unknown function
CA6033	1.0	0.9	0.7	1.1	1.0	0.8	COQ2	orf19.7643	para-hydroxybenzoate:polyprenyl transferase (by homology)
CA4396	1.0	1.0	0.7	1.0	2.1	1.1	IPF12294	orf19.3115	unknown function
CA4478	1.0	1.0	1.0	0.9	1.0	0.8	IPF6461	orf19.1889	unknown function
CA3939	1.0	0.9	3.2	1.1	0.4	0.8	HNM1	orf19.2003	Choline permease (by homology)
CA1829	1.0	0.9	0.8	1.1	1.2	1.0	IPF17177.3f	orf19.5184	similar to Saccharomyces cerevisiae Srm1p regulator of chromosome condensation, 3-prime end

CA4693	1.0	1.0	1.2	1.1	2.0	1.0	IPF3952	orf19.872	unknown function
CA3396	1.0	1.0	1.1	1.1	0.9	1.1	IPF13617	orf19.3971	unknown function
CA4647	1.0	0.9	0.6	1.1	0.7	0.7	IPF1493	orf19.354	X-Pro aminopeptidase II (by homology)
CA2409	1.0	0.9	1.1	1.3	1.0	1.1	IPF19948	orf19.291	unknown function
CA4448	1.0	0.9	0.8	1.1	1.1	1.1	PHO85	orf19.6846	Negative regulator of PHO system
CA4529	1.0	1.3	0.4	0.7	1.0	1.1	IPF4395	orf19.1477	unknown function
CA4760	1.0	1.0	1.1	0.9	0.9	1.1	IPF9652	orf19.3990	unknown function
CA0953	1.0	1.2	0.6	0.8	0.6	0.8	IPF13166	orf19.1144	unknown function
CA2242	1.0	1.0	0.9	1.0	1.0	0.9	IFQ1.5f	orf19.4673	Unknown function, 5-prime end
CA4239	1.0	1.0	0.8	1.1	2.0	1.3	IPF8174	orf19.524	unknown function
CA2609	1.0	1.2	0.9	1.0	0.9	0.9	IPF5457	orf19.5689	similar to Saccharomyces cerevisiae sec28p epsilon-COP coatomer subunit (by homology)
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)
CA3721	1.0	1.0	0.7	1.0	1.0	0.9	IPF6186	orf19.4171	unknown function
CA3586	1.0	1.0	1.0	1.0	0.9	1.0	IFT3	orf19.2252	Unknown function
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
CA4608	1.0	0.9	0.6	0.7	0.8	0.9	CCH1	orf19.3298	Calcium channel protein (by homology)
CA0635	1.0	0.9	1.1	0.9	0.9	0.9	IPF9036	orf19.1773	similar to Saccharomyces cerevisiae Rap1p DNA-binding protein with repressor and activator activity (by homology)
CA2836	1.0	0.9	1.3	1.1	0.7	0.8	ARG5,6	orf19.4788	acetylglutamate kinase and acetylglutamyl-phosphate reductase
CA1915	1.0	0.8	1.1	1.3	1.1	1.0	IPF16565	orf19.2439	unknown function
CA4060	1.0	0.9	1.0	0.9	1.0	1.0	GRS1	orf19.437	glycine-tRNA ligase (by homology)
CA1718	1.0	1.0	1.0	1.0	1.0	1.0	IPF9312	orf19.4649	unknown function
CA6142	1.0	0.8	0.9	0.9	0.5	0.4	IPF1879	orf19.5903	unknown function
CA1219	1.0	1.0	1.0	1.0	0.5	0.9	PRC2	orf19.4135	carboxypeptidase y precursor , serine-type protease (by homology)
CA2370	1.0	1.1	1.4	1.0	1.4	1.0	APN2	orf19.1836	AP endonuclease, exonuclease III homologue (by homology)
CA4446	1.0	0.9	2.6	1.2	35.2	2.7	ICL1	orf19.6844	Isocitrate lyase
CA3076	1.0	1.0	1.1	1.0	1.0	1.1	IPF6101	orf19.4814	unknown function,
CA0704	1.0	1.1	0.8	0.9	0.6	0.6	IPF11806	orf19.2915	similar to Saccharomyces cerevisiae Ynd1p nucleoside diphosphatase (by homology)
CA4559	1.0	7.2	0.9	1.6	1.0	1.6	IPF8041	orf19.6869	putative mitochondrial inner membrane protease (by homology)
CA3417	1.0	0.9	1.1	1.0	1.0	1.0	FRE41	orf19.6138	ferric reductase transmembrane component (by homology)
CA3847	1.0	0.8	1.2	1.0	1.5	1.1	IPF7942	orf19.6607	NADH-ubiquinone oxidoreductase
CA1151	1.0	1.0	0.9	1.0	1.0	1.1	IPF10459	orf19.102	unknown function
CA0424	1.0	1.0	1.1	0.8	2.2	1.0	IPF10795	orf19.2356	putative transcription factor (by homology)
CA1603	1.0	1.4	1.0	1.1	0.8	1.1	FAD1	orf19.4723	flavin adenine dinucleotide (FAD) synthetase (by homology)
CA2175	1.0	0.9	1.0	0.9	0.9	1.0	IPF8892	orf19.3762	unknown function
CA1112	1.0	1.0	1.0	1.0	1.0	1.0	IPF18758	orf19.2282	unknown function
CA5334	1.0	1.0	1.0	1.0	1.0	1.0	SMK1	orf19.7208	MAP kinase (by homology)
CA4758	1.0	1.0	1.2	1.0	1.0	1.0	PPR1	orf19.3986	transcription factor regulating pyrimidine pathway (by homology)
CA3928	1.0	0.9	0.8	1.0	0.7	0.9	GAL11	orf19.5105	DNA-directed RNA polymerase II holoenzyme and Kornberg s mediator (SRB) subcomplex subunit
CA2412	1.0	1.0	1.0	1.0	1.0	0.9	IPF13755	orf19.4481	unknown function
CA0741	1.0	0.7	0.8	0.7	0.7	0.8	IPF3261	orf19.3141	unknown function
CA5786	1.0	1.0	1.2	1.0	0.8	1.1	IPF1134	orf19.5433	unknown function Unknown function
CA0002	1.0	1.1	1.0	1.0	0.8	1.0	DOC1	orf19.5056	component of the anaphase promoting complex (by homology)
CA1809	1.0	1.0	0.9	1.0	0.7	1.1	IPF6325	orf19.1116	unknown function
CA5028	1.0	1.1	1.1	0.9	0.9	0.9	IPF2998	orf19.6982	unknown function
CA6042	1.0	1.0	1.1	1.0	1.0	1.0	IPF4924	orf19.7657	unknown function
CA0218	1.0	0.9	1.0	1.0	1.2	1.0	IPF15294	orf19.6238	unknown function

CA4112	1.0	0.7	1.1	1.1	0.5	0.6	BIM1	orf19.676	microtubule-binding protein (by homology)
CA5360	1.0	1.2	0.9	1.1	1.3	1.0	IPF839	orf19.7237	unknown function
CA5264	1.0	0.9	0.7	0.8	0.8	0.9	IPF1798	orf19.4998	unknown function
CA5615	1.0	1.0	1.0	1.0	1.0	1.1	IPF520	orf19.7083	unknown function
CA2907	1.0	1.2	0.9	1.1	1.1	0.8	IPF15525	orf19.4520	putative gluconokinase (by homology)
CA2952	1.0	1.0	1.0	0.9	1.1	1.0	IPF19671	orf19.5854.1	unknown function
CA3296	1.0	0.6	1.1	1.2	0.9	0.5			
CA2594	1.0	1.0	1.0	1.0	1.0	1.1	IPF12824	orf19.57	unknown function
CA2438	1.0	1.0	0.9	0.9	0.6	0.5	IPF5505	orf19.2198	unknown function
CA3902	1.0	1.0	1.3	1.1	1.2	1.3	YVH1	orf19.4401	protein tyrosine phosphatase (by homology)
CA5667	1.0	1.0	1.6	1.2	1.5	1.4	IPF1259	orf19.7369	Conserved hypothetical protein
CA1066	1.0	1.1	1.0	0.9	0.8	0.9	IPF9001	orf19.4638	
CA5088	1.0	1.0	1.1	1.0	0.9	1.0	IPF9758	orf19.3063	similar to Saccharomyces cerevisiae Dpb3p DNA-directed DNA polymerase epsilon, subunit C (by homology)
CA3666	1.0	1.0	1.0	1.0	1.0	0.8	IPF11435	orf19.6461	unknown function
CA5050	1.0	1.2	0.9	1.0	1.0	1.0	BMH2	orf19.3014	similar to Saccharomyces cerevisae Bmh2p suppressor of clathrin deficency (by homology)
CA1644	1.0	1.1	1.0	0.9	1.1	1.1	IPF9345	orf19.1728	unknown function
CA1553	1.0	1.0	1.0	1.0	1.5	1.0	PGA44	orf19.1714	unknown function
CA5845	1.0	1.1	1.0	1.0	1.2	1.0	NAP1	orf19.7501	nucleosome assembly protein (by homology)
CA3204	1.0	1.0	0.9	1.0	0.8	0.9	IPF3446	orf19.6186	Unknown function
CA5534	1.0	1.0	1.2	1.0	1.1	0.9	IPF2843	orf19.7295	unknown function
CA5871	1.0	0.9	0.8	1.1	0.9	1.0	PIF2	orf19.7538	DNA helicase (by homology)
CA3870	1.0	1.7	0.6	0.9	1.3	1.0	YPK1	orf19.399	ser/thr-specific protein kinase (by homology)
CA5152	1.0	0.9	0.9	0.8	0.2	0.3	CAT2	orf19.4591	carnitine O-acetyltransferase (by homology)
CA2787	1.0	0.8	0.8	0.6	0.5	0.7	EFG1	orf19.610	Enhanced filamentous growth factor
CA6065	1.0	1.0	1.1	1.1	1.0	1.0	SAP3	orf19.6001	secreted aspartyl proteinase
CA0034	1.0	1.1	1.1	1.0	0.9	1.0	IPF8016	orf19.1336.2	unknown function
CA2652	1.0	1.0	1.2	0.9	0.5	0.9	DNA2	orf19.1192	DNA helicase (by homology)
CA1335	1.0	0.7	0.9	0.9	0.8	0.7	TRA1.3eoc	orf19.3451	component of histone acetyltransferase, target for transcriptional activators, 3-prime end (by homology)
CA0190	1.0	0.9	1.1	0.8	1.3	0.8			
CA2627	1.0	1.0	0.9	0.8	0.9	1.2	IPF10916	orf19.4763	unknown function
CA1578	1.0	0.7	0.8	1.0	0.6	0.8	NUM11.5eo	orf19.4715	nuclear migration protein (by homology)
CA4836	1.0	0.9	1.0	0.9	2.7	2.0	PGA3	orf19.2060	Similar to superoxide dismutase (by homology)
CA3510	1.0	1.1	1.0	1.1	0.9	1.1	MAD1	orf19.6357	coiled-coil protein involved in the spindle-assembly checkpoint (by homology)
CA5437	1.0	1.2	0.8	1.0	0.6	1.1	ERG27	orf19.3240	3-keto sterol reductase (by homology)
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 processing
CA5320	1.0	1.0	1.0	1.0	0.9	0.9	IPF2147	orf19.7194	unknown function
CA0400	1.0	1.0	1.0	1.0	1.0	1.0	IPF7423.3f	orf19.6223	similar to Saccharomyces cerevisiae Spo22 involved in sporulation, 3-prime end
CA1214	1.0	1.0	1.0	0.8	0.9	0.8	VPS15.53f	orf19.129	serine/threonine protein kinase, internal fragment
CA1241	1.0	1.0	1.0	1.0	0.9	1.0	LIP8	orf19.1345	Secretory lipase
CA4552	1.0	1.0	0.9	1.0	0.5	0.9	IPF7869	orf19.1447	unknown function
CA3611	1.0	1.0	1.2	1.0	1.0	1.0	IPF3853	orf19.28	unknown function
CA4325	1.0	1.1	1.1	1.0	1.0	1.0	IPF2094	orf19.4094	unknown function
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
CA2118	1.0	1.0	0.7	0.9	0.5	0.7	IPF8024	orf19.1334	unknown function
CA4408	1.0	1.0	1.0	1.0	0.8	0.9	CTA6.3	orf19.3102	unknown function, 3-prime end
CA2276	1.0	1.1	0.8	1.0	1.5	1.1	HNM3	orf19.2587	Choline permease (by homology)

CA4288	1.0	1.1	1.1	1.1	1.2	1.3	IPF6662	orf19.6685	similar to Saccharomyces cerevisiae Isy1p pre-mRNA splicing factor (by homology)
CA4324	1.0	1.0	1.1	1.0	1.0	1.0	IPF2095	orf19.4095	unknown function
CA2610	1.0	1.2	1.0	1.1	0.9	1.0	CDC11	orf19.5691	septin by homology
CA0666	1.0	1.0	1.0	1.0	0.9	1.0	FIP1	orf19.4258	component of a pre-mRNA polyadenylation factor that interacts with poly(A) polymerase (by homology)
CA1862	1.0	1.0	1.0	1.1	1.1	1.0	NMD2	orf19.864	Nonsense-mediated mRNA decay protein 2 (by homology)
CA0360	1.0	1.0	1.0	1.0	1.0	1.4	IPF2328	orf19.1122	unknown function
CA3475	1.0	1.0	0.9	0.9	0.8	1.0	BRO1	orf19.1670	required for normal response to nutrient limitation (by homology)
CA1119	1.0	1.0	1.0	1.0	1.2	1.0	IPF7669.3f	orf19.4055.4	unknown function, 3-prime end
CA5935	1.0	0.7	1.2	1.1	0.9	1.2	IPF2798	orf19.6766	unknown function
CA0691	1.0	1.1	0.4	1.0	1.3	1.1			
CA1285	1.0	2.4	1.1	1.3	1.1	1.0	SKP1	orf19.4427	kinetochore protein complex CBF3 by homology
CA3429	1.0	1.1	1.0	1.0	0.9	1.1	IPF6380	orf19.588	unknown function
CA6144	1.0	0.8	0.8	1.2	0.8	0.7	PKC1	orf19.5901	Ser/thr protein kinase C
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
CA3148	1.0	1.0	1.0	0.9	1.1	1.0	IPF9808	orf19.6163	similar to Saccharomyces cerevisiae cse4p with strong similarity to histone H3 (by homology)
CA0921	1.0	1.0	0.6	0.9	1.0	1.0	IPF12992	orf19.1043	unknown function
CA4093	1.0	1.0	1.0	1.0	0.9	0.8	IPF5002	orf19.6653	GTP binding protein (by homology)
CA5999	1.0	1.1	1.7	1.2	1.1	1.1	IPF668	orf19.7599	unknown function
CA0657	1.0	0.8	1.0	1.0	1.4	1.4	IPF19877	orf19.5574	putative cysteine synthase (by homology)
CA1167	1.0	1.2	0.8	1.1	0.5	0.8	IPF16646	orf19.1782	unknown function
CA2427	1.0	1.3	0.7	0.6	0.8	2.2	IPF9898	orf19.3406	probable formate dehydrogenase (by homology)
CA0651	1.0	0.9	2.0	1.0	1.0	1.1	ALK8	orf19.10	n-alkane inducible cytochrome P-450 (by homology)
CA1330	1.0	3.4	1.0	1.6	1.0	1.0	IPF11713.3f	orf19.1151	unknown function, 3-prime end
CA0597	1.0	0.9	1.1	1.1	0.8	0.9	IPF9704	orf19.4882	similar to Saccharomyces cerevisiae Tfa2p TFIIE subunit (transcription initiation factor) (by homology)
CA2073	1.0	1.0	1.0	1.0	1.0	1.0	IPF6967	orf19.2638	unknown function
CA3803	1.0	1.0	1.0	1.0	1.0	1.0	IPF12407	orf19.2481	unknown function
CA1170	1.0	1.1	0.9	0.9	2.1	3.0	IPF13268	orf19.2749	unknown function
CA1844	1.0	0.9	1.0	1.0	1.1	0.9	IFL5.3	orf19.654	unknown function, 3-prime end
CA5578	1.0	1.0	1.0	1.1	0.9	1.0	IPF12536	orf19.7345	unknown function
CA3983	1.0	1.1	1.0	1.0	1.1	1.0	IPF7133	orf19.1557	unknown function
CA4610	1.0	2.0	2.6	1.5	2.5	1.7	IPF19802	orf19.3301	similar to Saccharomyces cerevisiae Met30p
CA3299	1.0	1.0	1.1	0.9	1.0	1.0	IPF13777	orf19.2317	unknown function
CA3435	1.0	1.8	0.9	1.4	1.3	1.2	IPF6391	orf19.583	indoleamine 2,3-dioxygenase (by homology)
CA2904	1.0	1.1	1.1	1.0	1.0	1.0	IPL1	orf19.3474	Ser/thr protein kinase (by homology)
CA1080	1.0	0.9	1.3	0.9	1.4	1.6	IPF14710	orf19.4820	unknown function
CA0018	1.0	1.0	1.0	1.1	1.1	1.0			
CA0056	1.0	1.1	1.0	1.0	0.3	0.7	IPF15839	orf19.556	unknown function
CA1998	1.0	1.0	1.2	1.1	1.4	0.9	IPF6605	orf19.6477	unknown function
CA5856	1.0	1.1	2.7	1.1	0.7	1.0	ALK2	orf19.7513	n-alkane inducible cytochrome P-450 (by homology)
CA2271	1.0	1.1	1.0	1.1	0.7	0.8	MRS2	orf19.2597	Mitochondrial RNA splicing protein (by homology)
CA1949	1.0	1.0	0.8	1.0	0.9	1.1	IPF14021	orf19.4744	dual specificity phosphatase (PTP/DSP) (by homology)
CA4925	1.0	1.2	0.8	1.0	1.1	1.0	IPF1408	orf19.6064	unknown function
CA0064	1.0	1.0	1.0	1.0	1.1	1.0	IPF19308.3f	orf19.618.1	unknown function
CA6041	1.0	1.0	1.0	1.0	1.0	0.8	RPO21	orf19.7655	DNA-directed RNA polymerase II, 215 KD subunit (by homology)
CA0718	1.0	1.0	0.9	0.9	0.8	0.9	IPF9782	orf19.3455	unknown function
CA0354	1.0	0.9	1.0	1.0	1.1	0.9	YAK1.5f	orf19.148	serine/threonine protein kinase, 5-prime end (by homology)

CA0853	1.0	1.0	1.3	1.0	0.9	1.0	IPF19640	orf19.1748	unknown function
CA1105	1.0	1.0	1.0	1.0	1.0	1.0	IPF18760.3	orf19.5232.1	unknown function, 3-prime end | FALSORF=falsorf
CA1695	1.0	0.9	1.6	1.1	1.0	1.4	RRP42	orf19.5039	rRNA processing protein (by homology)
CA0627	1.0	1.3	1.0	1.5	0.8	1.2	HSP12	orf19.3160	Heat shock protein (by homology)
CA0182	1.0	0.9	0.7	0.9	1.3	1.0	IFI1	orf19.1130	unknown function
CA1985	1.0	1.0	1.5	0.9	0.9	0.8	IPF9591	orf19.91	unknown function
CA5475	1.0	1.0	1.0	1.0	1.0	1.0	PGA30	orf19.5303	unknown function
CA1206	1.0	1.0	1.1	1.0	0.8	1.0	HUB1	orf19.3774.1	Unknown function
CA0545	1.0	1.1	1.0	1.0	0.9	1.0	IPF3251	orf19.2869	unknown function
CA3035	1.0	1.2	0.8	0.9	1.8	1.4	VPS28	orf19.212	involved in vacuolar traffic (by homology)
CA3482	1.0	0.8	0.7	0.8	1.0	0.9	COQ5	orf19.3577	C-methyltransferase (by homology)
CA3261	1.0	1.0	1.0	1.0	1.0	1.0	TYS1	orf19.2694	tyrosyl-tRNA synthetase by homology
CA0366	1.0	1.0	1.0	1.0	1.0	1.0	IPF19017	orf19.1351	unknown function
CA0293	1.0	1.0	1.0	0.9	1.1	0.9	IPF6624	orf19.6489	unknown function
CA2513	1.0	5.2	1.6	1.5	0.7	1.1	SNG1	orf19.308	Involved in nitroguanidine resistance (by homology)
CA1027	1.0	1.4	0.8	0.8	1.8	1.4	TIP41.3f	orf19.3937.2	unknown function, 3-prime end
CA5959	1.0	1.0	1.2	0.9	0.7	0.9	SRB7	orf19.7548	DNA-directed RNA polymerase II holoenzyme and kornberg s mediator (SRB) subcomplex subunit (by homology)
CA5727	1.0	1.0	0.9	1.0	1.1	1.1	ECM15	orf19.7436.1	Involved in cell wall biogenesis and architecture (by homology)
CA2662	1.0	0.9	1.1	1.1	1.0	1.0	IPF17139	orf19.3553	unknown function
CA0793	1.0	1.1	1.0	1.0	1.0	0.9	IPF16273	orf19.553	similar to Saccharomyces cerevisiae Dtr1p dityrosine transporter (by homology)
CA0447	1.0	1.1	1.0	1.0	1.0	0.9	IPF14275	orf19.2297	Probable ADP-ribosylation factors (by homology)
CA1992	1.0	1.0	1.0	1.0	1.0	1.0	IFW3	orf19.6484	unknown function, repeated protein
CA5024	1.0	1.2	0.5	0.8	0.5	0.6	IPF3009	orf19.6977	similar to Saccharomyces cerevisiae Gpi1p required for N-acetylglucosaminyl phosphatidylinositol synthesis
CA4427	1.0	1.0	1.0	1.1	1.0	1.0	IPF5584	orf19.5168	unknown function
CA2328	1.0	1.1	1.2	1.1	0.9	0.8	MED8	orf19.4497	transcriptional regulation mediator (by homology)
CA2528	1.0	1.0	1.0	1.0	1.1	1.0	MOB1	orf19.5528	required for completion of mitosis
CA1037	1.0	1.1	0.8	0.9	0.5	0.7	MNS1	orf19.1036	Alpha1,2-mannosidase (by homology)
CA4359	1.0	0.9	0.9	0.9	0.6	0.7	IPF6054	orf19.6736	unnown function
CA0976	1.0	1.0	0.9	1.0	1.5	1.1	PEX17	orf19.3605	Peroxisomal peripheral membrane protein (by homology)
CA5045	1.0	1.0	0.9	1.0	1.6	1.3	IPF4510	orf19.6999	unknown function
CA2279	1.0	1.0	0.9	1.0	0.8	1.0	DUR31	orf19.781	Urea transport protein (by homology)
CA0575	1.0	0.9	0.9	1.0	0.9	0.9	IPF15178.5	orf19.1808	Unknown function
CA6112	1.0	1.1	0.8	1.2	0.6	0.8	IPF97	orf19.5941	unknown function
CA4328	1.0	1.0	1.3	1.4	0.8	0.9	IPF2090	orf19.4091	similar to Saccharomyces cerevisiae Srb5p DNA-directed RNA polymerase II holoenzyme
CA1447	1.0	0.9	0.8	0.8	0.8	0.9	NRK1	orf19.191	Cdc31p-interacting ser/thr protein kinase (by homology)
CA1884	1.0	0.8	0.9	0.9	0.8	1.0	IPF5486	orf19.2208	unknown function
CA2601	1.0	0.9	1.2	0.7	1.2	0.8	IPF11181	orf19.50	unknown function
CA2959	1.0	1.1	1.0	1.2	1.0	1.1	IPF8591	orf19.5862	putative arginase family member (by homolgy)
CA3323	1.0	1.0	1.1	1.1	0.8	1.0	IKI1	orf19.2676	killer toxin insensitive protein
CA0433	1.0	0.8	1.1	1.4	0.9	1.0	SHM1	orf19.1342	Serine hydroxymethyltransferase precursor, mitochondrial (by homology)
CA3471	1.0	1.1	0.8	0.9	0.7	0.8	IPF6308	orf19.1667	unknown function
CA3020	1.0	1.0	1.1	1.1	1.0	0.9	IPF15492	orf19.3908	unknown function
CA5096	1.0	1.0	1.2	1.0	1.1	1.0	IPF1384	orf19.6445	similar to Saccharomyces cerevisiae Eci1p delta3-cis-delta2-trans-enoyl-CoA isomerase (by homology)
CA4672	1.0	1.7	0.9	1.0	0.9	0.9	IPF3659	orf19.900	similar to Saccharomyces cerevisiae Nsp1p nuclear pore protein (by homology)
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 homology)
CA2816	1.0	1.1	1.0	0.9	1.0	1.0	IPF5601	orf19.2995	unknown function

CA2426	1.0	0.9	0.8	0.8	1.1	1.1	IPF9901	orf19.3407	similar to Saccharomyces cerevisiae rad18p DNA repair protein (by homology)
CA1971	1.0	1.0	1.0	1.2	1.1	1.1	PKH2	orf19.5224	Ser/Thr protein kinase(by homology)
CA4841	1.0	0.6	1.2	1.1	0.7	0.9	IPF10355	orf19.3809	unknown function
CA4641	1.0	1.1	3.8	1.4	0.8	1.0	IPF1505	orf19.348	similar to saccharomyces cerevisiae Kre6p glucan synthase subunit (by homology)
CA1178	1.0	1.1	1.1	1.0	0.7	0.9	IPF5062	orf19.805	unknown function
CA1568	1.0	1.0	1.0	1.1	1.0	1.0	IPF7615	orf19.1158	unknown function
CA1961	1.0	0.7	1.2	1.0	0.8	1.2	IPF14284	orf19.2399	putative dnaJ-like protein (by homology)
CA2499	1.0	1.0	1.0	1.0	1.0	1.0	SAP5	orf19.5585	secreted aspartyl proteinase 5
CA5331	1.0	1.1	1.0	1.0	1.1	1.1	DUR33.5eo	orf19.7205	Urea transport protein (by homology)
CA3618	1.0	0.9	1.0	0.9	1.0	1.0	THO1	orf19.200	suppressor of the hpr1 ts phenotype (by homology)
CA3375	1.0	1.0	0.8	1.1	1.1	1.0	IPF4684	orf19.1857	unknown Function
CA0075	1.0	1.1	0.7	1.0	1.5	1.0			
CA2576	1.0	0.8	1.0	1.0	0.6	0.9	IPF7432	orf19.6219	unknown function
CA0157	1.0	1.0	1.0	1.0	1.0	1.0	IPF19178.3f	orf19.1072.4	unknown function, 3-prime end
CA2206	1.0	1.0	1.0	1.0	1.0	0.8	IPF12173	orf19.698	unknown function
CA4860	1.0	0.9	1.2	1.0	0.6	0.9	IPF19804	orf19.3835	unknown Function
CA2730	1.0	1.0	1.0	1.0	1.0	1.0	IPF10325	orf19.2115	molybdopterin-converting factor by homology
CA4548	1.0	0.9	0.9	1.0	1.0	1.0	IPF7862	orf19.1450	unknown function
CA1615	1.0	1.1	0.9	1.0	0.8	0.6	IPF14540	orf19.3218	putative multidrug protein (by homology)
CA5161	1.0	1.1	1.1	1.1	1.2	1.0	IPF983	orf19.4600	unknown function
14652.20	1.0	1.0	1.0	1.0	1.0	1.2			
CA1009	1.0	1.1	0.8	1.0	1.1	1.1	IPF14084	orf19.6255	unknown function
CA4968	1.0	0.9	0.9	0.9	0.9	0.8	IPF3928	orf19.6503	unknown function
CA1505	1.0	1.1	1.1	1.1	1.0	0.9			
CA3601	1.0	0.5	1.4	0.8	0.8	0.9	IPF15618	orf19.4931	cysteinyl-tRNA synthetase (by homology)
CA0231	1.0	1.0	1.1	1.1	1.0	1.0	RAD23	orf19.1494	nucleotide excision repair protein(ubiquitin-like protein) (by homology)
CA4773	1.0	1.0	0.9	1.0	1.1	1.0	IPF3340	orf19.4005	unknown function
CA4231	1.0	0.9	1.0	1.0	1.0	1.1	SNP3	orf19.514	snRNP-related protein (by homology)
CA2955	1.0	1.4	0.8	1.1	1.3	1.0	IPF15201	orf19.5857	Unknown function
CA3058	1.0	1.3	0.9	0.9	1.7	1.3	IPF2955	orf19.4292	unknown function
CA4327	1.0	1.0	1.2	1.1	1.0	1.2	IPF2091	orf19.4092	unknown function
CA1362	1.0	1.0	1.1	1.1	0.5	0.8	PEX3	orf19.4426	PEROXISOMAL MEMBRANE PROTEIN by homology
CA5853	1.0	1.0	1.1	0.9	1.1	1.1	LSM6	orf19.7509.2	U6 snRNA-associated Sm-like protein (by homology)
CA4937	1.0	1.0	1.1	1.2	0.7	0.7	TFP3	orf19.6538	H+-ATPase by homology
CA1901	1.0	0.8	1.2	1.3	1.0	1.2	IPF14135	orf19.2604	unknown function
CA2588	1.0	0.9	1.0	0.9	1.0	0.9	IPF15098	orf19.4376	Unknown function
CA6101	1.0	1.0	1.0	1.1	1.1	1.0	SPO70.3f	orf19.5955.1	involved in meiosis and sporulation, 3-prime end
CA4204	1.0	0.8	0.7	1.1	1.8	0.6	HOL4	orf19.4546	member of major facilitator superfamily multidrug-resistance protein subfamily 1 (by homology)
CA6013	1.0	1.0	1.3	1.0	1.2	0.9	IPF635	orf19.7614	unknown function
CA0786	1.0	1.1	1.0	0.9	1.5	1.0	IPF7473	orf19.2446	unknown function
CA5874	1.0	1.0	1.0	1.0	1.0	1.0	CTA23	orf19.7544	transcriptional activation
CA4252	1.0	0.9	0.8	1.0	2.2	1.3	IPF4290	orf19.541	unknown function
CA5246	1.0	0.8	0.9	1.0	0.8	1.0	IPF19808	orf19.5016	unknown function
CA2791	1.0	1.0	1.0	1.0	1.3	1.1	IMP4	orf19.603	Ribonucleoprotein (by homology)
CA5989	1.0	0.9	0.8	1.0	1.0	0.9	IPF692	orf19.7589	unknown function
CA3553	1.0	1.0	0.7	1.0	1.6	1.0	IFA27.5	orf19.3878	unknown function, 5-prime end

CA4892	1.0	0.7	1.4	0.9	0.9	0.9	PRT1	orf19.6584	Translation initiation factor eIF3 (by homology)
CA4045	1.0	0.8	1.4	1.1	1.1	1.2	ABP140	orf19.3676	putative methyltransferase (by homology)
CA0166	1.0	1.0	1.1	1.0	1.0	1.0			
CA3694	1.0	1.0	1.0	1.0	0.7	0.9	IPF4872.3f	orf19.6269	unknown function, 3-prime end
CA3386	1.0	0.9	1.1	1.0	1.2	0.8	IPF6758	orf19.322	unknown function
CA0449	1.0	1.0	1.0	1.0	0.9	1.0	MOT2.3f	orf19.2379	transcriptional repressor, 3-prime end (by homology)
CA1643	1.0	1.1	0.6	0.8	1.5	0.9	IPF9347	orf19.1729	unknown function
CA1816	1.0	1.0	0.8	1.0	1.5	1.1	IPF7020	orf19.136	unknown function
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 Pho4p and involved in pheromone response pathway,)
CA2525	1.0	1.0	1.1	1.1	0.9	1.0	IPF4324	orf19.5522	unknown function
CA2700	1.0	1.0	1.1	1.0	0.8	0.9	IPF1441	orf19.2740	unknown function
CA3004	1.0	1.1	0.8	1.0	1.2	1.1	KIN28	orf19.6239	cyclin-dependent ser/thr protein kinase (by homology)
CA4544	1.0	1.2	1.0	1.0	0.8	1.1	IPF6252	orf19.1458	similar to Saccharomyces cerevisiae Tad2p tRNA-specific adenosine deaminase 2 (by homology)
CA4564	1.0	0.9	0.5	0.5	0.6	0.8	IPF6572	orf19.6874	unknown function
CA3141	1.0	1.3	0.5	0.5	1.0	0.6	IPF9211.3f	orf19.3712	unknown function, 3-prime end
CA4751	1.0	0.8	0.5	0.9	1.3	0.9	IPF11473	orf19.4828	unknown function
CA0371	1.0	1.0	1.1	1.1	1.0	0.8	IPF19578	orf19.1087	unknown function
CA3783	1.0	0.8	1.0	1.0	1.3	1.2	IPF11226	orf19.5837	unknown function
CA1529	1.0	1.1	0.8	0.8	0.8	0.9	SPC105.5ec	orf19.4557	Spindle pole body protein (by homology)
CA3021	1.0	0.9	1.0	1.0	1.0	1.0	IPF17640	orf19.3906	unknown function
CA5117	1.0	1.0	1.1	0.9	0.7	0.8	IPF1323	orf19.6414	unknown function
CA5606	1.0	1.0	1.2	0.9	1.1	1.0	STL2	orf19.7093.2	sugar transporter (by homology)
CA0208	1.0	0.9	1.1	0.9	1.1	1.1	IPF19850	orf19.1227	unknown function
CA1363	1.0	1.0	1.1	1.0	1.1	1.1	IPF5556	orf19.4424	acid phosphatase (by homology)
CA1538	1.0	0.9	1.3	1.0	0.7	0.9			
CA4486	1.0	1.2	1.0	1.1	1.2	1.0	IPF9162	orf19.1877	unknown function
CA5482	1.0	0.8	0.8	0.9	0.3	0.5	IFV4.3f	orf19.5315	unknown function
CA5110	1.0	1.9	0.8	0.9	0.6	0.9	FBP26	orf19.6423	Fructose-2,6-bisphosphatase (by homology)
CA0727	1.0	1.1	1.1	1.0	0.7	1.0	IPF7347	orf19.3730	unknown function
CA5324	1.0	1.0	1.0	1.0	0.8	1.1	IPF2140	orf19.7198	unknown function
CA0164	1.0	1.8	1.0	1.0	0.9	1.0	IPF11694	orf19.4335	similar to Saccharomyces cerevisiae Tna1p high affinity nicotinic acid plasma membrane permease (by homology)
CA5761	1.0	1.0	0.7	1.0	0.8	0.9	IFF11	orf19.5399	unknown function
CA4718	1.0	0.7	2.5	1.4	1.2	1.0	IPF8661	orf19.6955	unknown function
CA0771	1.0	1.0	0.9	1.0	1.1	1.0	IPF11977	orf19.853	aspartic proteinase (by homology)
CA0093	1.0	1.0	1.1	0.9	1.7	1.1	IPF29954	orf19.100	putative lipase (by homology)
CA1993	1.0	1.0	1.0	1.1	1.0	1.1	IPF6614	orf19.6482	unknown function
CA1142	1.0	1.1	1.0	1.0	1.2	1.1	IPF9459	orf19.4070	unknown function
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)
CA0211	1.0	1.0	0.9	1.0	1.3	1.1	IPF4326	orf19.5524	unknown function
CA4840	1.0	1.0	2.1	1.1	0.6	1.0	IPF1235	orf19.2054	unknown function
CA2307	1.0	1.1	0.8	0.8	0.6	0.9	IPF18488	orf19.1684	unknown function
CA3561	1.0	1.0	0.8	1.1	1.3	0.9	SLY1	orf19.3128	hydrophilic suppressor of YPT1 and member of the Sec1p family (by homology)
CA2375	1.0	1.0	1.0	1.0	1.0	1.1	IPF15504	orf19.2211	unknown function
CA0158	1.0	1.0	1.0	1.0	1.0	1.0	IPF19178.53	orf19.1073	unknown function, internal fragment
CA1398	1.0	1.1	1.1	1.0	1.0	0.9	IPF19913	orf19.3699	unknown function
CA2653	1.0	1.0	1.0	1.0	0.8	0.6	IPF8472.3ec	orf19.5701	unknown function, 3-prime end

CA4019	1.0	1.3	0.9	0.9	0.8	0.8	HOC1	orf19.3445	GLYCOSYLTRANSFERASE by homology
CA2916	1.0	0.9	1.0	1.0	1.2	1.0	IFA4	orf19.4510	unknown function
CA3380	1.0	1.0	1.0	1.0	1.0	1.0	MSL5	orf19.329	branch point bridging protein (by homology)
CA1002	1.0	1.0	1.9	1.2	0.9	1.9	ROK1.3f	orf19.3756	RNA helicase, 3-prime end
CA0353	1.0	0.9	1.0	1.0	1.5	1.0	YAK1.3f	orf19.147	serine/threonine protein kinase, 3-prime end (by homology)
CA0251	1.0	1.0	2.5	1.0	2.1	1.0	IPF9146	orf19.6244	unknown function
CA3793	1.0	1.0	0.9	1.0	0.9	1.0	IPF5701	orf19.5825.1	unknown function
CA1166	1.0	1.0	1.0	1.0	1.0	1.0	IFO1	orf19.1780	Unknown function
CA4607	1.0	0.9	1.0	1.0	0.9	1.0	IPF6223	orf19.3297	unknown function Unknown function
CA0395	1.0	1.0	0.8	0.5	0.8	1.1	SEF11.5eoc	orf19.1926	Putative transcription factor, 5-prime end (by homology)
CA2364	1.0	1.1	0.6	0.7	0.5	0.7	MEC1	orf19.1283	cell cycle checkpoint protein (by homology)
CA2360	1.0	1.0	1.0	1.0	1.1	1.0	IPF8951	orf19.4897	unknown function
CA3130	1.0	0.9	1.5	1.0	0.7	0.8	TIM23	orf19.1361	mitochondrial inner membrane import translocase subunit (by homology)
CA5357	1.0	1.0	0.8	1.0	0.9	1.1	RSC8	orf19.7234	chromatin remodeling complex subunit (by homology)
CA6055	1.0	1.0	1.0	1.0	0.9	1.2	SMD1	orf19.7673	snRNA-associated protein (by homology)
CA6153	1.0	1.0	1.0	1.1	0.5	0.7	CUP5	orf19.5886	Vacuolar H+-ATPase (by homology)
CA1875	1.0	1.1	0.9	1.2	1.0	0.8	RPB9	orf19.2276	DNA-directed RNA polymerase II (by homology)
CA2689	1.0	1.1	1.0	0.9	0.6	1.0	IFU2	orf19.2582	Unknown function
CA1528	1.0	0.7	0.6	1.1	1.6	1.2	ALS4.3f	orf19.4556	agglutinin-like protein, 3-prime end
CA1571	1.0	1.0	0.8	0.9	0.9	0.8			
CA0811	1.0	1.0	1.0	1.0	1.0	1.0	IPF17625	orf19.1920	putative cell wall protein of the PIR family
CA3884	1.0	1.0	0.9	0.9	0.8	1.0	IPF6367	orf19.384	unknown function
CA0823	1.0	1.0	2.6	1.9	1.5	1.4	IPF11987.3e	orf19.692	unknown function, 3-prime end
CA1307	1.0	1.1	1.0	1.0	0.9	1.0	IPF13506.3e	orf19.4191.2	unknown function, 3-prime end
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 transduction pathway (by homology)
CA1458	1.0	1.0	1.0	1.0	0.9	0.9	IPF6342	orf19.1106	unknown function
CA2007	1.0	1.4	0.6	0.8	1.0	1.3	GPI8	orf19.2799	essential for GPI anchor attachment (by homology)
CA4951	1.0	1.8	1.7	3.7	5.4	2.0	IPF13607	orf19.6527	unknown function
CA5586	1.0	1.0	0.9	1.0	1.0	0.9	IPF5625	orf19.7112	unknown function
CA1535	1.0	0.9	1.1	1.0	0.9	0.8	IPF9515	orf19.1212	similar to Saccharomyces cerevisiae Scs2p required for inositol metabolism (by homology)
CA0653	1.0	1.1	1.0	1.1	1.0	1.0	MET6	orf19.2551	BY HOMOLOGY TO S.CEREV.: 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase
CA2566	1.0	1.1	1.0	1.1	0.9	0.9	IPF12122	orf19.5646	unknown function
CA4421	1.0	1.0	1.0	0.9	1.1	0.9	TAF19	orf19.5174	TBP-associated factor by homology
CA2561	1.0	1.6	1.2	1.5	0.8	0.9	CAR2	orf19.5641	ornithine aminotransferase (by homology)
CA1186	1.0	1.1	1.1	1.0	1.1	1.1	IPF6930	orf19.3785	unknown function
CA0148	1.0	1.0	1.2	1.1	0.9	1.1	POP1	orf19.2404	protein component of ribonuclease P and ribonuclease MRP (by homology)
CA5098	1.0	1.0	1.0	1.0	0.9	0.9	IPF1380	orf19.6443	delta3-cis-delta2-trans-enoyl-CoA isomerase (by homology)
CA2010	1.0	0.8	1.3	1.2	0.9	1.2	IPF1731	orf19.3088	unknown function
CA4640	1.0	1.0	1.0	1.0	1.0	1.0	IPF1506	orf19.347	unknown function
CA2352	1.0	1.0	1.0	1.0	1.1	1.1	FMT1	orf19.4418	Methionyl-tRNA Transformylase (by homology)
CA1282	1.0	1.0	1.0	1.1	1.0	1.0			
CA5619	1.0	1.0	1.0	1.0	0.8	1.0	IPF514	orf19.7079	similar to Saccharomyces cerevisiae Bud3p budding protein (by homology)
CA2660	1.0	0.9	1.0	1.0	1.0	1.0	SAP1	orf19.5714	secreted aspartyl proteinase
CA1050	1.0	0.9	1.0	1.0	1.0	1.0	IPF19897	orf19.3897	unknown function
CA6058	1.0	1.0	1.0	1.0	0.9	1.1	ATP16	orf19.7678	F1F0-ATPase complex, F1 delta subunit
CA2218	1.0	1.0	1.0	1.1	1.1	1.0	IPF18508	orf19.5375	unknown function

CA2021	1.0	1.1	0.6	0.5	1.2	2.1	IPF17283	orf19.4907	unknown function
CA4423	1.0	1.1	1.1	1.0	1.1	0.9	LIP9.5f	orf19.5172	secretory lipase 9, 5-prime end
CA5980	1.0	1.1	0.9	1.0	1.0	0.9	IPF918	orf19.7576	unknown function
CA5379	1.0	1.0	0.8	1.0	1.0	1.0	IPF5228.5	orf19.7265	similar to Saccharomyces cerevisiae Sad1p snRNP assembly factor required for pre-mRNA splicing, 5-prime end
CA3277	1.0	1.1	2.1	1.1	3.2	2.5	IPF6266	orf19.6311	unknown function
CA1088	1.0	1.0	1.0	1.1	0.8	0.9	IPF13319	orf19.740	unknown function
CA4803	1.0	1.0	1.7	1.0	1.4	1.0	PEX4	orf19.4041	E2 ubiquitin-conjugating enzyme -peroxin (by homology)
CA5252	1.0	0.8	1.7	1.4	0.9	1.2	DIM1	orf19.5010	rRNA (adenine-N6,N6-)-dimethyltransferase (by homology)
CA5677	1.0	1.0	1.0	1.0	0.8	0.9	IPF1286	orf19.7380	unknown function
CA4563	1.0	1.0	1.0	1.1	0.8	1.7	IPF6566	orf19.6873.1	unknown function
CA4864	1.0	0.8	0.9	0.8	1.0	1.0	IPF4087	orf19.3840	similar to Saccharomyces cerevisiae Pak1p protein kinase suppressing mutations in DNA polymerase alpha
CA3623	1.0	1.0	1.0	1.0	1.0	1.0			
CA3480	1.0	1.0	0.9	1.0	1.1	1.0	IPF3224	orf19.3578	unknown function
CA3118	1.0	1.2	0.8	0.9	0.9	1.0	COQ4	orf19.3008	ubiquinone biosynthesis
CA0253	1.0	0.8	1.1	1.0	0.9	1.1	FIL1	orf19.477	Putative mitochondrial ribosome recycling factor (by homology)
CA5290	1.0	1.0	1.2	1.1	1.3	1.2	IPF1943	orf19.7152	similar to Aspergillus (Emericella) nidulans cysteine synthase (by homology)
CA2879	1.0	1.1	0.8	0.9	1.0	1.0	IPF3779	orf19.5848	unknown function
CA4366	1.0	1.3	0.7	1.0	0.7	0.9	SWI1	orf19.5657	Transcription regulation by homology
CA0169	1.0	0.7	1.0	1.0	1.1	0.8	RBT7	orf19.2681	repressed by Tup1 protein 7, putative ribonuclease (by homology)
CA4332	1.0	1.2	1.5	1.4	1.5	1.2	GLO2	orf19.4088	Glyoxalase II (hydroxyacylglutathione hydrolase) (by homology)
CA4537	1.0	0.9	1.0	0.9	1.0	1.0	YNT2	orf19.1466	suppressor of rna12/yme2 (by homology)
CA4500	1.0	1.2	0.9	1.0	1.0	1.0	IPF11319	orf19.510	unknown function
CA3713	1.0	1.0	1.1	1.1	1.0	0.9	OPS4	orf19.4934	opaque - phase specific protein OP4, precursor (by homology)
CA4546	1.0	0.9	0.8	1.1	0.7	0.9	SPT5	orf19.1453	Transcription elongation protein
CA2294	1.0	2.5	1.1	1.1	7.7	9.1	IPF19946	orf19.747	similar to Saccharomyces cerevisiae Nbp35p nucleotide-binding protein
CA2709	1.0	1.0	1.1	1.0	1.0	1.0	IPF4828	orf19.4662	by homology to S. cerevisiae YEAST TRANSCRIPTION FACTOR RLM1
CA4619	1.0	1.0	1.0	1.0	1.1	0.8	IPF5756	orf19.3310	unknown function
CA1641	1.0	1.1	1.0	1.0	1.3	0.9	NHP10.3f	orf19.1731	unknown function, 3-prime end
CA0020	1.0	1.0	1.0	1.0	1.6	1.5	IPF7046	orf19.124	unknown function
CA5168	1.0	1.0	1.0	1.0	1.4	1.1	IPF6032	orf19.4607	unknown function
CA4092	1.0	1.0	1.0	1.0	1.0	1.3	DBP8	orf19.6652	DEAD box protein ATP-dependent RNA helicase (by homology)
CA4462	1.0	1.1	1.1	1.0	1.0	1.0	IPF17251	orf19.6859	unknown function
CA1939	1.0	1.0	1.0	1.1	1.1	1.1	IPF8000	orf19.4189	unknown function
CA1823	1.0	1.0	1.4	1.0	0.8	1.1	IPF9522.5f	orf19.4267	septin, 5-prime end (by homology)
CA0061	1.0	1.0	1.0	1.0	1.0	1.0			
CA5831	1.0	1.0	1.0	1.0	0.9	0.9	MRPL6	orf19.7486	ribosomal protein L6 precursor, mitochondrial (by homology)
CA1870	1.0	1.1	0.9	0.8	1.5	1.0			
CA5759	1.0	1.1	0.8	0.9	1.1	1.2	PET191	orf19.5394.1	Assembly of cytochrome oxidase (by homology) Respiration
CA4303	1.0	1.0	1.0	0.9	1.4	1.0	IFB1	orf19.6703	unknown function
CA0397	1.0	1.0	1.1	1.0	1.1	1.0	FRE31	orf19.1930	Ferric reductase (by homology)
CA2993	1.0	1.0	1.0	1.0	1.1	1.0	IPF9118	orf19.6118	unknown function
CA3673	1.0	1.0	1.1	0.9	1.4	0.8	IPF13667	orf19.6455	unknown function
CA2768	1.0	1.0	1.0	1.0	1.1	1.0	IPF17011	orf19.2684	similar to Saccharomyces cerevisiae Slk19p involved in control of spindle dynamics together with Kar3p (by homology)
CA1416	1.0	0.8	1.4	0.9	0.9	1.2			
CA1657	1.0	1.0	1.3	1.0	0.5	0.7	IPF16022	orf19.4325	unknown function
CA1817	1.0	1.3	0.9	0.8	1.2	0.9	IPF7021	orf19.135	similar to Saccharomyces cerevisiae Exo84p exocyst protein essential for secretion (by homology)

CA1049	1.0	1.0	1.0	0.9	0.9	0.9	TLG1	orf19.3898	tSNARE that affects a Late Golgi compartment (by homology)
CA2124	1.0	1.1	0.9	1.0	1.6	1.1	IPF10490	orf19.419	unknown function
CA2636	1.0	1.0	0.8	0.9	0.6	0.8	MSW1	orf19.4299	Mitochondrial tryptophanyl-tRNA synthetase (by homology)
CA2889	1.0	1.2	1.0	1.0	1.3	1.3	IPF13628	orf19.2469	putative DNA repair protein (by homology)
CA0370	1.0	1.1	0.9	1.2	1.3	1.0	IPF13678	orf19.1655.3	unknown function
CA5386	1.0	0.9	1.2	0.9	1.0	0.9	Zorro2b.5f	orf19.7277	Putative gag protein, 5-prime end
CA2224	1.0	1.0	1.0	1.1	1.0	1.1			
CA5531	1.0	0.9	1.2	1.2	1.3	1.1	GCD14	orf19.7291	Translational repressor of GCN4
CA2111	1.0	0.9	1.0	1.0	1.1	0.9	IPF13748	orf19.3688	Unknown function
CA2060	1.0	0.7	1.1	0.9	0.9	1.0	CDC61.3f	orf19.2560	Cytosolic leucyl-tRNA synthetase, 3-prime end
CA3365	1.0	0.9	0.6	0.7	0.5	0.5	ALG6	orf19.1843	glucosyltransferase (by homology)
CA3649	1.0	1.0	1.0	1.1	0.9	0.8	IPF4132	orf19.2040	unknown function
CA0838	1.0	1.1	1.0	1.1	0.5	0.8	TFP1.5f	orf19.1680	vacuolar ATPase subunit (by homology)
CA5232	1.0	1.0	1.0	1.1	0.4	1.0	SUN42	orf19.5032	Putative cell wall beta-glucosidase (by homology)
CA2322	1.0	0.8	1.0	1.0	1.1	0.8	YSH1	orf19.5486	component of pre-mRNA polyadenylation factor PF I (by homology)
CA3173	1.0	1.2	0.6	1.0	1.0	1.1	PGA47	orf19.1401	unknown function
CA0864	1.0	0.9	1.0	0.9	1.0	1.0	CYT1	orf19.3527	cytochrome-c1 (by homology)
CA1460	1.0	0.9	1.2	1.2	1.8	1.3	HAM1	orf19.1108	Controls 6-N-hydroxylaminopurine sensitivity and mutagenesis (by homology)
CA6098	1.0	0.7	1.9	1.4	0.8	0.9	IPF61	orf19.5959	unknown function
CA4055	1.0	0.8	1.1	1.0	1.2	0.9	YPT522	orf19.430	GTP-binding protein of the rab family(by homology)
CA6059	1.0	1.0	1.1	1.0	1.0	1.0	CTA26	orf19.7680	transcriptional activation
CA1673	1.0	3.1	1.2	1.0	1.6	3.0	PST21	orf19.3612	1,4-benzoquinone reductase by homology
CA3642	1.0	1.1	1.0	1.0	1.0	1.1	PGA19	orf19.2033	unknown function
CA3971	1.0	1.0	1.2	1.0	1.0	0.8	IPF6498	orf19.1543	unknown function
CA0202	1.0	0.8	0.5	0.9	0.9	1.0	IPF19126	orf19.1210	putative aminoacid transporter (by homology)
CA4329	1.0	1.0	1.0	1.0	1.0	1.0	VMA21	orf19.4090.1	Vacuolar H+-ATPase assembly (by homology)
CA5908	1.0	0.9	1.1	0.9	0.9	0.9	IPF5960	orf19.6797	unknown function
CA0126	1.0	0.9	0.9	0.9	1.3	1.1			
CA0144	1.0	1.0	1.0	1.0	0.9	1.0	IPF19195.3f	orf19.151	putative amino acid or GABA permease, 3-prime end (by homology)
CA4879	1.0	1.0	1.0	1.0	0.6	0.7	IPF1660	orf19.6566	unknown function
CA3456	1.0	0.8	0.9	0.7	0.7	0.8	IPF19986	orf19.1259	unknown function
CA0142	1.0	1.4	1.5	1.0	1.4	1.3	CSL4	orf19.1026	Involved in kinetochore-related function (by homology)
CA4789	1.0	0.9	1.0	1.0	0.9	1.0	IPF3366	orf19.4023	Mitochondrial ribosomal protein (by homology)
CA2850	1.0	1.0	0.9	1.2	0.7	0.7	CDC50	orf19.5735	cell division cycle mutant (by homology)
CA3935	1.0	1.0	0.8	0.9	0.9	0.8	IPF14688	orf19.2007	unknown function
CA0687	1.0	0.5	1.0	1.1	0.8	1.0	CPA2	orf19.3221	arginine-specific carbamoylphosphate (by homology)
CA5385	1.0	1.0	0.8	0.9	1.1	1.0	Zorro2b.3f	orf19.7275	reverse transcriptase, 3-prime end (by homology)
CA1023	1.0	1.3	1.5	1.4	1.1	1.2	IPF4817.3f	orf19.3351.1	unknown Function
CA4806	1.0	1.1	0.9	0.8	1.0	1.0	IPF1155	orf19.2095	Putative dipeptidase (by homology)
CA2318	1.0	0.7	0.6	1.1	1.1	1.0	ILV1	orf19.5480	Threonine dehydratase (by homology)
CA2848	1.0	0.5	2.5	1.4	1.2	1.1			
CA5607	1.0	1.0	1.1	1.0	1.0	1.0			
CA0338	1.0	1.0	0.9	1.0	1.1	1.2	IPF13252	orf19.3378	unknown function
CA4757	1.0	1.0	1.0	1.0	1.0	1.0	LIP10	orf19.4822	Secretory lipase
CA5429	1.0	1.4	0.7	0.7	0.7	1.0	CDC27	orf19.3231	subunit of anaphase-promoting complex (by homology)
CA2741	1.0	0.9	1.0	1.3	2.3	1.2	IPF10632	orf19.2105	unknown function

CA0250	1.0	1.0	1.0	1.0	1.0	1.0	IPF17661	orf19.1348	unknown function
CA3252	1.0	1.0	1.0	1.0	1.0	1.1	PGA22	orf19.3738	unknown Function
CA3790	1.0	1.0	0.9	1.1	0.8	0.9	IPF11215	orf19.5828	unknown function
CA4980	1.0	1.1	1.1	1.0	0.9	1.0	IPF2059	orf19.5270	unknown function
CA0877	1.0	1.0	1.0	1.1	0.5	0.7	CNH1	orf19.367	Na+/H+ antiporter
CA2032	1.0	0.7	1.7	0.8	0.5	0.6	IPF13112	orf19.3466	unknown function
CA2106	1.0	0.9	1.2	1.1	1.0	1.0	PGA5	orf19.3693	unknown function
CA2616	1.0	1.0	1.0	1.0	1.0	0.9	IPF3540	orf19.2814	unknown function
CA4095	1.0	1.0	1.2	1.0	0.5	0.8	IPF4002	orf19.660	unknown function
CA2275	1.0	1.0	0.9	0.9	1.1	1.0	BIO4	orf19.2590	dethiobiotin synthetase (by homology)
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 homology)
CA5918	1.0	0.7	1.3	1.3	0.3	0.6	ERV14	orf19.6787	membrane protein
CA1656	1.0	1.0	1.2	1.0	1.1	1.0	IPF16019	orf19.4326	unknown function
CA3196	1.0	1.0	1.6	1.4	1.1	1.2	IPF3428	orf19.6175	unknown function
CA1919	1.0	1.0	1.1	1.0	1.1	0.9	IPF7477	orf19.2442	unknown function
CA0294	1.0	0.9	1.2	0.8	0.8	1.0	IPF16061	orf19.1753	unknown function
CA4541	1.0	0.9	1.4	1.0	1.1	1.2	IPF6257	orf19.1461	unknown function
CA2944	1.0	1.0	1.0	1.0	1.0	1.0	IPF6294	orf19.1968	unknown function
CA2672	1.0	1.0	1.0	1.0	1.0	0.9	EFH1	orf19.5498	Transcription regulator
CA5520	1.0	1.0	1.0	0.9	1.0	1.0	IPF714	orf19.5368	unknown function
CA1573	1.0	1.0	1.0	1.0	1.0	1.0	IPF15087	orf19.1653	unknown function
CA5240	1.0	1.0	1.1	0.9	1.0	0.9	IPF3032	orf19.5023	allantoate permease (by homology)
CA0539	1.0	1.0	0.8	1.1	1.0	1.0	NUP57	orf19.2820	nuclear pore protein (by homology)
CA6007	1.0	1.1	1.0	1.0	1.2	0.9	IPF650	orf19.7608	unknown function
CA2987	1.0	1.0	1.1	1.0	0.9	0.9	RPB11.3f	orf19.6010.1	DNA-directed RNA polymerase II subunit, 3-prime end (by homology)
CA0019	1.0	0.9	1.7	0.8	0.9	1.7			
CA0873	1.0	0.9	1.1	0.8	0.9	0.9	BUL1	orf19.4629	Ubiquitin ligase binding protein
CA2116	1.0	0.7	0.6	1.0	0.6	0.7	SNG4	orf19.1332	Drug transporter (by homology)
CA0486	1.0	1.0	0.8	1.0	1.0	1.0	IPF15540	orf19.258	unknown function
CA2543	1.0	1.1	1.0	0.9	0.9	1.0	IPF16925	orf19.2828	unknown function
CA6008	1.0	1.0	0.9	1.0	1.5	1.0	PGA11	orf19.7609	unknown function
CA6108	1.0	1.1	0.8	0.9	0.7	0.8	SEC7	orf19.5947	Guanine nucleotide exchange protein for ADP-robosylation factor (by homology)
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)
CA2158	1.0	1.2	1.8	1.2	1.1	1.8	ECM1	orf19.5299	involved in cell wall biosynthesis (by homology)
CA0620	1.0	1.0	1.2	0.9	1.0	0.9	IPF17998	orf19.3147	unknown function
CA5986	1.0	0.9	0.6	1.0	0.6	0.7	INO1	orf19.7585	myo-inositol-1-phosphate synthase
CA3693	1.0	1.0	0.9	1.0	0.7	0.8	IPF4874	orf19.6268	unknown function
CA2132	1.0	1.0	1.0	1.0	1.0	1.0	IPF5865	orf19.5212	unknown function
CA2142	1.0	1.0	1.1	1.0	0.9	0.9	MRPL33	orf19.2511.1	ribosomal protein of the large subunit, mitochondrial (by homology)
CA0968	1.0	1.0	1.0	1.0	1.0	1.0	SAP6	orf19.5542	secreted aspartyl protease
CA3497	1.0	0.7	1.0	1.2	0.6	0.7	FEN11	orf19.6343	Fatty acid elongase required for sphingolipid formation (by homology)
CA2830	1.0	1.0	1.0	1.1	1.0	1.0	RBT1	orf19.1327	repressed by TUP1 protein 1
CA5260	1.0	1.1	0.8	0.9	0.8	0.8	RAD54	orf19.5004	DNA-dependent ATPase of the Snf2p family (by homology)
CA2274	1.0	1.0	0.9	1.0	1.0	0.9	BIO3	orf19.2591	DAPA aminotransferase (by homology)
CA2470	1.0	0.8	0.9	1.0	0.7	0.6	SDH12	orf19.2871	Succinate dehydrogenase (by homology)
CA3028	1.0	1.0	1.0	1.0	1.0	1.0			

CA0097	1.0	1.0	1.1	1.0	1.1	1.4	IPF13290	orf19.5314 unknown function
CA0897	1.0	1.0	1.0	1.0	0.7	1.1	IPF4902	orf19.413 unknown function
CA3037	1.0	1.0	0.8	1.1	1.3	0.7	IPF13442	orf19.210 unknown function
CA1182	1.0	0.9	1.1	1.0	0.6	1.0	IPF19724	orf19.801 similar to Saccharomyces cerevisiae Tbf1ptelomere repeat-binding factor 1
CA5281	1.0	0.9	1.2	1.0	1.1	1.0	SPT6	orf19.7136 Transcription elongation protein (by homology)
CA0503	1.0	0.9	0.8	1.3	0.5	0.6	PMT6	orf19.3802 protein mannosyltransferase
CA5490	1.0	1.0	0.9	1.1	0.8	1.0	KIN3	orf19.5325 G2-specific serine/threonine protein kinase (by homology)
CA4034	1.0	1.3	0.8	0.9	3.8	1.1	HSP31	orf19.3664 heat shock protein (by homology)
CA0496	1.0	1.1	1.0	0.9	1.3	1.0	IPF11644	orf19.2660 unknown function
CA0990	1.0	0.9	0.8	0.8	0.6	0.6	IPF11068	orf19.1392 unknown function
CA4719	1.0	1.0	0.8	1.0	1.7	1.0	DAL51	orf19.6956 allantoate permease (by homology)
CA2356	1.0	0.9	0.9	0.9	1.0	0.8	IPF12282	orf19.4893 unknown function
CA1344	1.0	1.0	0.5	1.0	0.8	1.0	IPF14623	orf19.4342 unknown function
CA3243	1.0	1.0	1.5	1.1	1.1	1.0	IPF7489	orf19.4680 unknown function
CA0071	1.0	0.9	1.0	1.0	1.0	1.0	IPF19290	orf19.621 unknown function,
CA2411	1.0	1.0	1.0	1.0	1.0	1.0	IFI3.3f	orf19.4483 Unknown function, 3-prime end
CA5850	1.0	0.8	0.9	1.3	0.9	0.7	IPF404.3f	orf19.7507 unknown function, 3-prime end
CA2809	1.0	1.0	0.9	1.2	0.8	1.1	AMO1	orf19.5784 amine oxidase (by homology)
CA0199	1.0	0.7	1.3	1.0	0.4	0.6	KAP104	orf19.3556 karyopherin-beta protein (by homology)
CA5846	1.0	1.0	1.0	1.0	0.8	1.2	IPF409	orf19.7502 unknown function
CA0754	1.0	0.9	1.2	1.2	1.1	0.9	IPF15880	orf19.3486 unknown function
CA0737	1.0	1.0	0.8	1.0	0.8	1.0		
CA4474	1.0	1.1	1.1	1.1	1.0	1.0	SSC1	orf19.1896 Mitochondrial heat shock protein 70-related protein (by homology)
CA4764	1.0	1.1	0.5	0.7	0.7	0.9	GPI10	orf19.3996 required for Glycosyl Phosphatdyl Inositol synthesis (by homology)
CA1160	1.0	1.4	1.5	1.0	2.3	1.6	IPF10262	orf19.2726 unknown function
CA2323	1.0	0.9	1.0	1.0	0.9	0.9	SMD2	orf19.5486.1 U1 snRNP protein of the Sm class protein (by homology)
CA1950	1.0	0.7	1.2	1.1	1.1	1.2	IPF14019	orf19.4746 unknown function
CA2960	1.0	1.0	1.0	1.3	1.1	1.2	IPF8590	orf19.5863 unknown function
CA1904	1.0	1.2	1.0	0.9	1.4	1.1	GRX5	orf19.2782 Glutaredoxin
CA0358	1.0	1.0	1.0	1.0	0.4	1.0	IPF17488.5f	orf19.1818 unknown function, 5-prime end
CA0050	1.0	1.0	1.1	1.0	1.0	1.0	CTA25	orf19.362 transcriptional activation
CA4195	1.0	1.1	1.0	1.0	1.0	1.1	CYS4	orf19.4536 cystathionine beta-synthase (by homology)
CA5996	1.0	1.0	1.0	1.0	1.1	1.0	IPF673	orf19.7596 unknown function
CA4110	1.0	1.0	1.3	1.1	2.1	1.4	IPF3965	orf19.674 unknown function
CA0865	1.0	1.0	0.8	1.0	1.3	1.0	IFM2	orf19.3584 Glycerate-formate-dehydrogenases (by homology)
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 homology)
CA5635	1.0	1.0	1.0	1.0	1.3	1.2	IPF474	orf19.7060 unknown Function
CA3356	1.0	1.0	1.1	1.3	1.1	0.9	IPF9560	orf19.1942 unknown function
CA0462	1.0	0.8	1.1	0.9	0.8	1.0	MRPS28	orf19.2520 ribosomal protein (by homology)
CA0849	1.0	0.9	0.7	0.9	1.4	1.2	HEM4	orf19.1744 uroporphyrinogen III synthase
CA1010	1.0	0.9	0.8	0.9	0.5	1.0	GLT1	orf19.6257 glutamate synthase (NAPDPH), (by homology)
CA2534	1.0	0.7	1.0	1.1	1.0	1.0	IPF12793	orf19.3182 similar to Saccharomyces cerevisiae Gis2p containing seven zinc finger motifs
CA3901	1.0	1.1	0.9	1.0	0.9	0.9	IPF3282.3e	orf19.4401.1
CA5136	1.0	1.0	1.0	1.0	1.0	1.1		
CA0936	1.0	0.9	1.0	1.0	1.1	1.0	IPF16291	orf19.1080 unknown function
CA1909	1.0	0.9	1.0	1.0	0.9	1.0	IPF20091	orf19.2787 unknown function

CA0326	1.0	1.0	1.0	1.0	0.8	1.0	IPF15220	orf19.3780	Unknown function
CA0814	1.0	1.0	0.9	1.0	1.1	1.1	IPF16233	orf19.1914	unknown function
CA4153	1.0	1.1	1.2	1.0	2.2	1.5	DNLI	orf19.5798	CANAL DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
CA3437	1.0	1.0	1.0	1.0	1.2	1.0	IPF15925	orf19.2988	unknown function
CA5647	1.0	0.9	1.5	0.8	0.7	0.9	RTF1.5f	orf19.7047.2	Nuclear protein regulating DNA binding properties of TATA Binding Protein, 5-prime end (by homology)
CA0918	1.0	1.0	1.0	1.1	1.0	1.0	IPF17881	orf19.1041	cyclin (by homology)
CA1683	1.0	1.0	1.1	0.9	1.3	1.0	Cirt5	orf19.4919	Probable transposase (by homology)
CA5140	1.0	1.0	0.9	0.9	0.9	1.2	TIM10	orf19.4577.3	Subunit of the Tim22-complex (by homology)
CA1015	1.0	1.0	0.6	0.9	1.3	1.2	IPF15547	orf19.3956	putative glutamyl-tRNA amidotransferase subunit A (by homology)
CA1757	1.0	0.6	1.7	0.8	0.8	0.7	IPF14559.5f	orf19.5128	unknown function, 5-prime end
CA5008	1.0	0.8	1.1	1.3	1.2	2.0	IPF12577	orf19.5238	unknown function
CA4637	1.0	1.0	1.2	1.0	2.8	1.5	IPF1514	orf19.344	unknown function
CA0026	1.0	1.1	0.8	0.9	2.7	1.5	IPF16843	orf19.2397.3	unknown function
CA2464	1.0	1.0	1.0	1.0	0.8	1.1	IPF8727	orf19.1794	unknown function
CA5827	1.0	1.1	1.0	1.0	0.9	0.9	IPF2485	orf19.7482	unknown function
CA4278	1.0	1.0	1.2	1.2	1.3	1.2	IPF2310	orf19.6675	unknown function
CA0926	1.0	1.6	0.7	1.1	1.5	1.0	IPF11335	orf19.3663	Member of the phosphate permease family (by homology)
CA6094	1.0	0.9	1.1	1.0	1.0	0.9	IPF53	orf19.5963	unknown function
CA3027	1.0	1.0	0.6	0.9	1.0	0.8	IPF20126	orf19.3900	putative chromosome segregation protein (by homology)
CA3436	1.0	0.8	1.0	0.9	1.1	0.9	NRD1	orf19.581	Involved in regulation of nuclear pre-mRNA abundance
CA2449	1.0	0.6	1.9	1.1	0.9	1.1	ENP1	orf19.5507	Essential nuclear protein (by homology)
CA3492	1.0	0.8	1.1	0.9	1.0	0.8	IPF3189	orf19.3563	unknown function
CA3529	1.0	0.9	1.0	0.8	0.6	0.8	IPF9929	orf19.985	unknown function
CA4542	1.0	1.1	1.0	0.7	1.1	1.0	IPF6255	orf19.1460	unknown function
CA1617	1.0	0.8	1.3	1.1	1.2	1.4	IPF14536	orf19.3220	unknown function
CA3295	1.0	0.9	1.0	1.1	0.8	0.9	IPF5723	orf19.6336	cell surface GPI-anchored protein, (by homology)
CA3110	1.0	1.0	1.1	1.2	2.4	1.3	LPI9	orf19.6544	Microtubule-associated protein (by homology)
CA4051	1.0	0.9	0.8	1.0	0.7	1.0	IPF10231.5f	orf19.426	unkown function, 5-prime end
CA1435	1.0	1.0	0.9	0.9	0.9	1.1	IPF7166	orf19.1202	unknown function
CA3567	1.0	1.0	1.0	1.0	1.0	1.0	IPF7804.5f	orf19.3134	unknown function, 5-prime end
CA2081	1.0	1.1	0.8	1.0	0.8	0.9	IPF9699	orf19.4878	unknown function
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 homology)
CA3927	1.0	0.7	3.4	1.3	0.7	0.8	DIP2	orf19.5106	beta transducin
CA0137	1.0	1.1	1.0	1.0	0.7	1.0	SEC232	orf19.1638	Component of COPII coat (by homology)
CA1032	1.0	1.0	0.9	0.8	1.2	1.0	IPF19896	orf19.3852	unknown function
CA0570	1.0	0.7	1.1	0.7	0.8	0.9	SVL3	orf19.1139	Involved in vacuole function (by homology)
CA2057	1.0	0.9	1.1	1.0	1.3	1.2	SEC65	orf19.2557	Recognition particle subunit (by homology)
CA1196	1.0	1.1	0.8	0.9	1.4	1.2	IPF10394	orf19.3364	unknown function
CA3509	1.0	1.2	1.0	1.0	0.7	1.1	PRP6	orf19.6356	snRNP(U4/U6)-associated splicing factor (by homology)
CA0993	1.0	1.0	0.6	0.9	2.2	2.4			
CA2974	1.0	1.1	1.0	1.0	1.0	1.0	IPF12540	orf19.1239	unknown function
CA2720	1.0	0.6	1.1	0.9	1.1	1.1	IPF7366	orf19.3341	Arginyl-tRNA synthetase
CA2165	1.0	1.0	1.0	1.0	0.7	0.8	IPF17024	orf19.5291	unknown function
CA1574	1.0	0.9	0.9	1.0	1.0	0.9	PXP2	orf19.1655	acyl-CoA oxidase peroxisomal (by homology)
CA4290	1.0	0.9	1.0	1.0	1.0	1.0	IPF2617	orf19.6687	unknown function
CA1381	1.0	1.0	1.0	1.0	1.0	1.0	IPF8420	orf19.929	unknown function

CA4379	1.0	1.1	0.9	1.0	1.0	1.0	MEP2	orf19.5672	high affinity low capacity ammonia (by homology)
CA4730	1.0	1.0	1.0	1.1	0.7	0.8	IPF7737	orf19.4857	unknown function
CA5854	1.0	0.9	1.0	1.1	0.7	0.9	IPF393	orf19.7511	similar to Saccharomyces cerevisiae Nup192p nucleoporin (by homology)
CA2903	1.0	0.5	0.9	0.8	0.8	0.9	IPF11725	orf19.3475	unknown function
CA3335	1.0	1.1	0.8	0.9	1.1	1.4	IPF8682	orf19.2336	unknown function
CA3336	1.0	1.5	0.8	0.8	1.1	1.3	IPF19983	orf19.2335	unknown function
CA3610	1.0	1.0	1.1	1.2	1.3	1.3	IPF3854	orf19.27	unknown function
CA5602	1.0	0.8	1.0	1.0	1.0	1.1	IPF554	orf19.7097	RNA binding protein (by homology)
CA5858	1.0	0.9	1.0	1.0	0.4	0.8	IPF380	orf19.7516	unknown function
CA1730	1.0	1.3	0.9	1.3	1.4	1.2	IPF8439	orf19.6498	unknown function
CA0876	1.0	0.9	0.9	1.0	1.0	1.1	VMA6	orf19.364	H+-ATPase V0 domain 36 KD subunit,vacuolar (by homology)
CA4714	1.0	0.9	1.0	1.0	0.8	0.9	IPF5912	orf19.6950	unknown function
CA5937	1.0	0.7	1.1	1.0	0.6	0.6	IPF2784	orf19.6760	unknown function
CA0957	1.0	0.9	0.8	0.9	1.5	1.0	IPF14322	orf19.4731	unknown function
CA4547	1.0	1.0	0.7	1.0	0.8	1.0	SRB9	orf19.1451	DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex subunit (by homology)
CA1368	1.0	0.9	1.0	1.0	1.0	1.0	IPF15969	orf19.4965	unknown function
CA0716	1.0	1.0	1.0	0.8	3.6	5.4	DOG2	orf19.3392	2-deoxyglucose-6-phosphate phosphatase (by homology)
CA2418	1.0	0.8	1.0	1.2	0.4	0.4	MNT4	orf19.4475	putative mannosyltransferase
CA3333	1.0	1.0	1.0	1.0	0.9	1.0	CDC48	orf19.2340	microsomal ATPase (by homology)
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)
CA5900	1.0	1.0	0.9	1.0	0.6	1.0	IPF2379	orf19.6806	unknown function
CA0209	1.0	1.0	1.1	0.9	1.0	1.0	HAP2	orf19.1228	CCAAT-binding factor subunit (by homology)
CA0554	1.0	0.5	1.3	1.1	1.3	1.2	HAS1	orf19.3962	ATP-DEPENDENT RNA HELICASE (by homology)
CA2942	1.0	0.9	0.9	0.9	0.7	0.8	IPF6291	orf19.1969	Secretory Stress Response protein (by homology)
CA3269	1.0	1.0	1.1	0.9	0.9	0.9	PGA39	orf19.6302	unknown function
CA2080	1.0	0.9	1.0	1.0	1.1	1.1	IPF9693	orf19.4875	unknown function
CA4355	1.0	0.9	1.1	1.1	1.3	1.4	IPF3649	orf19.6730	unknown function
CA6034	1.0	1.0	0.7	0.8	1.1	0.9	APC11	orf19.7644	subunit of the anaphase promoting complex (by homology)
CA1476	1.0	0.9	1.0	0.9	0.4	0.8	IPF10214	orf19.1093	unknown function
CA4316	1.0	1.0	0.9	1.1	1.3	0.9	IPF2111	orf19.4106	unknown function
CA3749	1.0	1.0	1.0	1.0	0.9	1.0	IPF7389	orf19.3429	unknown function
CA4710	1.0	0.9	1.1	1.0	0.7	0.8	ORC3	orf19.6942	Origin recognition complex (by homology)
CA4182	1.0	0.9	0.9	0.8	0.5	0.9	IPF19797	orf19.2949	unknown
CA4493	1.0	1.1	0.7	1.0	12.1	1.7	IPF4055	orf19.1867	unknown function
CA6071	1.0	0.8	1.0	0.9	1.0	1.0	IPF4835	orf19.5992	zinc finger protein (by homology)
CA2542	1.0	1.0	0.9	1.0	1.5	1.0	IPF16067	orf19.3190	unknown function
CA0755	1.0	1.2	1.0	0.9	1.2	1.0	IPF14861	orf19.3487	unknown function
CA3447	1.0	1.0	1.0	1.0	0.9	1.0	YPT70	orf19.2975	GTP-binding protein (by homology)
CA2769	1.0	0.8	0.9	0.8	0.4	0.5	PGA54	orf19.2685	unknown function
CA1518	1.0	1.0	1.0	1.0	1.3	1.3	IPF11040	orf19.4799	similar to Schizosaccharomyces pombe cdc5 myb-related protein required during G2/M transition (by homology)
CA4642	1.0	1.4	0.7	0.9	0.8	0.8	IPF1500	orf19.349	similar to Saccharomyces cerevisiae Nca2p regulating expression of mitochondrial ATP synthase (by homology)
CA1879	1.0	1.0	2.5	1.0	1.0	0.6	SMF12	orf19.2270	manganese transporter (by homology)
CA0383	1.0	1.0	0.5	0.8	1.1	0.9	IPF16028	orf19.1841	unknown function
CA4301	1.0	0.7	1.0	0.9	0.9	1.0	IPF2593	orf19.6701	amino acid-tRNA ligase homolog (by homology)
CA3486	1.0	1.1	1.4	1.0	0.9	0.9	IPF3206	orf19.3572	unknown function
CA4526	1.0	0.9	1.0	1.0	1.0	0.9	MON1.5f	orf19.479	unknown function, 5-prime end

CA2041	1.0	1.0	1.2	1.2	0.8	1.0	IPF12944	orf19.4355	unknown function
CA2999	1.0	1.1	0.9	0.9	0.8	0.8	MRPL8	orf19.6129	mitochondrial 60s ribosomal subunit (by homology)
CA4932	1.0	1.2	5.1	3.2	1.0	1.4	IPF8374	orf19.6073	unknown function
CA5413	1.0	0.9	0.9	1.0	0.9	1.0	IPF1567	orf19.961.2	mitochondrial ribosomal protein L34 (by homology)
CA1481	1.0	1.3	1.1	1.2	1.0	1.0	RPB3	orf19.1248	DNA-directed RNA-polymerase II (by homology)
CA2870	1.0	1.1	0.5	1.0	1.0	2.7	OPT2.53f	orf19.2847.1	Oligopeptide transporter, internal fragment (by homology)
CA1526	1.0	0.9	1.3	1.0	0.5	0.5	IPF13815	orf19.4553	unknown function
CA4923	1.0	0.9	1.2	1.2	1.1	1.1	IPF1413.3f	orf19.6062.3	unknown function, 3-prime end
CA4393	1.0	1.0	1.0	1.0	1.1	1.1	IPF12300	orf19.3120	unknown function
CA3865	1.0	1.0	1.2	1.2	0.9	1.0	IPF4608	orf19.6084	unknown Function
CA2298	1.0	1.2	0.8	1.0	0.8	1.0	IPF8224	orf19.5380	unknown function
CA2306	1.0	1.1	1.0	1.0	1.0	1.0	IPF6510	orf19.1685	unknown function
CA5030	1.0	0.9	0.8	0.8	1.0	1.0	IPF2988	orf19.6984	unknown function
CA5570	1.0	1.0	1.0	1.0	1.1	1.0	IPF1992	orf19.7336	putative MFS transporter
CA5925	1.0	1.1	1.0	0.9	1.0	1.0	MET8	orf19.6780	Siroheme synthase (by homology)
CA3830	1.0	0.9	1.4	1.1	1.3	1.2	SSF1.3eoc	orf19.6589	mating protein (by homology) 3 prime end
CA4909	1.0	0.8	0.7	0.9	0.9	1.0	TUF1	orf19.6047	Translation elongation factor TU (by homology)
CA2551	1.0	1.0	0.9	0.9	1.0	1.0	IPF9098	orf19.2836	unknown function
CA3224	1.0	0.9	0.9	0.9	0.9	0.8	GLC7	orf19.6285	Ser/thr phosphoprotein phosphatase 1 (by homology)
CA5436	1.0	1.0	1.0	0.9	0.6	0.8	CTF18	orf19.3239	chromosome transmission in mitosis and maintenance of telomere length (by homology)
CA5859	1.0	0.9	0.9	1.0	0.4	0.8	CHT1	orf19.7517	endochitinase 1 precursor
CA2780	1.0	1.1	0.8	1.2	1.1	1.1	IPF3831	orf19.281	unknown function
CA5867	1.0	1.0	1.0	1.0	1.0	0.8	EPL1	orf19.7529	DNA-binding protein (by homology)
CA1422	1.0	0.7	1.6	1.3	1.0	1.1	IPF14248	orf19.3798	putative methyltransferase (by homology)
CA1501	1.0	0.9	0.8	0.9	0.5	0.9	IPF13217	orf19.1698	unknown function
CA2238	1.0	1.1	1.0	1.0	0.7	0.9	IPF10032.5f	orf19.3916	unknown function, 5-prime end
CA2890	1.0	0.9	1.0	1.0	1.2	1.0	IPF13626	orf19.2468	Putative methyltransferase (by homology)
CA4966	1.0	1.0	1.0	1.0	1.1	1.1	IPF3923	orf19.6507	unknown function
CA3707	1.0	1.0	0.7	0.5	0.9	1.0	TYE7	orf19.4941	Basic helix-loop-helix transcription factor by homology
CA0100	1.0	1.0	0.9	1.2	0.5	0.7	IPF11569	orf19.9	unknown function
CA2908	1.0	0.8	1.1	0.8	0.9	0.8	SUV3	orf19.4519	ATP-dependent RNA helicase, mitochondrial (by homology)
CA1003	1.0	0.8	1.0	1.1	1.0	0.9	ATP20	orf19.3757	F1F0-ATPase complex, G subunit (by homology)
CA3426	1.0	1.1	0.8	1.1	1.2	1.0	IPF11869	orf19.592	unknown function
CA3911	1.0	1.0	1.2	1.0	1.0	1.0	IPF3292	orf19.4391	unknown function
CA1546	1.0	1.0	1.0	1.0	0.7	1.0	IPF6671	orf19.1311	unknown function
CA0975	1.0	1.0	1.1	1.1	1.0	0.9	IPF18811	orf19.3606	unknown function
CA5332	1.0	1.1	0.9	1.0	1.6	1.2	IPF900.3f	orf19.7206	unknown function, , 3-prime end
CA6097	1.0	1.0	1.1	1.1	1.0	1.0	NCE102	orf19.5960	secretion of proteins that lack classical secretory signal sequence (by homology)
CA4170	1.0	1.2	1.0	1.0	0.6	0.7	IPF7784	orf19.2963	unknown function
CA2831	1.0	1.3	1.1	1.0	8.0	23.6	IPF15706	orf19.4783	unknown function
CA0557	1.0	0.9	0.9	1.0	1.1	1.0			
CA5736	1.0	1.6	0.7	1.1	0.4	0.9	OPI3	orf19.7446	Methylene-fatty-acyl-phospholipid synthase (by homology)
CA1857	1.0	1.0	1.4	1.0	0.8	1.0	IPF15348	orf19.1504	unknown function
CA1426	1.0	1.1	0.4	1.0	2.2	1.1	ALS9.3f	orf19.5745	agglutinin-like protein, 3-prime end
CA4554	1.0	1.0	0.9	0.9	0.3	0.8	IPF7874	orf19.1445	similar to Saccharomyces cerevisiae Esc4p involved in chromatin silencing (by homology)
CA2530	1.0	1.1	0.9	1.0	0.8	0.6	IPF12782	orf19.3176	unknown function

CA2663	1.0	0.9	1.1	0.8	0.7	0.8	NUP133	orf19.3552	nuclear pore protein (by homology)
CA0473	1.0	1.0	1.0	1.0	1.3	1.5	GRP1	orf19.4781	dihydroflavonol-4-reductases (by homology)
CA3116	1.0	0.9	1.0	0.7	1.1	1.1	LAB2	orf19.3010	LIPOATE BIOSYNTHESIS PROTEIN by homology
CA5954	1.0	1.0	0.7	1.2	0.9	1.3	IPF3508	orf19.6740	unknown function
CA5402	1.0	1.1	0.9	1.2	0.9	0.9	IFG3.3	orf19.944	probable d-amino acid oxidase, 3-prime end (by homology)
CA5589	1.0	1.1	1.0	1.0	1.3	1.0	IPF5621	orf19.7111	unknown function
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 lipolytica glyoxylate pathway regulator Gpr1p
CA2556	1.0	1.0	0.7	1.0	0.8	0.9	FRE5	orf19.5634	ferric reductase transmembrane component (by homology)
CA1542	1.0	1.0	1.0	1.1	1.0	1.0	ROT11	orf19.4566	Putative membrane protein
CA0098	1.0	0.5	3.1	1.4	1.0	1.1	IPF16479	orf19.2319	unknown function
CA3255	1.0	1.1	1.1	1.3	1.0	0.9	IPF4729	orf19.3743	unknown Function
CA4875	1.0	0.7	1.1	0.9	1.1	1.1	LAT1	orf19.6561	Dihydrolipoamide S-acetyltransferase (by homology)
CA5133	1.0	0.7	1.2	1.4	0.8	1.0	IPF5129	orf19.6392	unknown function
CA4675	1.0	1.0	0.9	1.0	2.8	1.2	IPF3664	orf19.897	unknown function
CA1952	1.0	1.0	1.0	1.0	1.0	1.0	IFP1	orf19.762	Unknown function
CA3149	1.0	1.7	1.0	1.0	1.2	1.1	KGD1	orf19.6165	2-oxoglutarate dehydrogenase
CA4851	1.0	0.9	0.9	1.0	1.1	1.1	IPF5818	orf19.3821	unknown function
CA1676	1.0	0.6	0.5	0.8	1.0	1.0	ERG9	orf19.3616	farnesyl-diphosphate farnesyltransferase
CA5160	1.0	0.9	1.1	1.1	0.7	0.9	PHO89	orf19.4599	Na+-coupled phosphate transport (by homology)
CA5939	1.0	1.2	1.1	1.1	2.0	1.0	IPF3484	orf19.6758	aldo/keto reductase (by homology)
CA4363	1.0	0.8	0.8	1.0	0.5	0.8			
CA0014	1.0	1.0	0.9	1.0	1.0	1.0	IPF13368	orf19.3550	unknown function
CA3444	1.0	1.0	1.2	1.1	0.7	0.9	IPF11323	orf19.2980	unknown function
CA0298	1.0	1.0	1.0	1.0	0.7	0.8	PPT1	orf19.1673	Protein ser/thr phosphatase
CA4210	1.0	0.8	1.2	1.1	0.9	0.8			
CA4483	1.0	1.4	0.9	1.0	0.7	0.8	IPF9156	orf19.1881	unknown function
CA1496	1.0	0.5	0.8	0.9	3.9	2.5	CTR1	orf19.3646	copper transport protein
CA0329	1.0	0.8	0.9	1.0	0.6	0.8	IMG2	orf19.3777	Required for Integrity of Mitochondrial Genome (by homology)
CA0919	1.0	1.4	1.1	1.0	1.0	1.0	POR1	orf19.1042	mitochondrial outer membrane porin (by homology)
CA4540	1.0	1.1	0.9	1.0	0.9	0.8	SMP2	orf19.1462	Involved in plasmid maintenance, respiration and cell proliferation (by homology)
CA4098	1.0	0.9	1.1	1.0	0.9	0.9	IPF3988	orf19.664	unknown function
CA3036	1.0	1.0	0.9	1.1	1.8	0.8	IPF13443	orf19.211	unknown function
CA4308	1.0	1.1	0.9	1.0	1.1	1.2	IPF6660.5e	orf19.6708	unknown function
CA1035	1.0	1.0	0.8	1.0	1.3	1.0	IFI2.3f	orf19.1038	unknown function, 3-prime end
CA5410	1.0	1.1	0.9	1.1	0.8	0.9	IPF1557	orf19.954	similar to dnaJ proteins
CA1633	1.0	1.0	1.0	0.9	0.9	1.0	IPF10180	orf19.3940	unknown function
CA1932	1.0	1.0	1.0	0.9	0.8	0.9	IPF3903	orf19.760	unknown function
CA2961	1.0	1.0	1.1	1.1	1.4	1.2	URK1	orf19.5864	uridine kinase (by homology)
CA2624	1.0	1.0	1.0	1.0	1.0	1.0			
CA2703	1.0	1.0	1.0	1.0	0.8	1.0	IPF12193	orf19.4655	unknown function
CA1089	1.0	0.9	1.1	1.1	1.3	1.1	IPF13799	orf19.3945	unknown function
CA0986	1.0	1.1	1.0	1.0	0.8	0.7	IPF4814	orf19.3350	similar to Saccharomyces cerevisiae Mrp20p ribosomal protein of the large subunit, mitochondrial (by homology)
CA3015	1.0	1.4	1.1	1.0	0.9	1.1			
CA0291	1.0	1.1	0.9	0.9	0.9	1.0	IPF13328	orf19.1592	unknown function
CA0858	1.0	1.1	1.2	1.0	0.9	1.0	IPF14493	orf19.4465	unknown function
CA0883	1.0	0.6	1.0	1.2	0.3	0.6	SUN41	orf19.3642	Putative cell wall beta-glucosidase (by homology)

CA2104	1.0	0.9	0.9	1.1	0.9	0.9	IPF19939	orf19.2381	unknown function
CA1427	1.0	1.0	1.1	1.1	1.0	1.0	IPF9914	orf19.5746	alanyl-tRNA synthetase (by homology)
CA0516	1.0	1.0	1.0	1.0	1.1	1.0	IPF11526	orf19.2804	unknown function
CA1376	1.0	1.0	0.9	1.0	1.0	1.0	IPF7159	orf19.1198	unknown function
CA3648	1.0	0.9	0.7	0.8	0.7	0.9	MSF1	orf19.2039	phenylalanine--tRNA ligase
CA1773	1.0	1.2	0.9	1.1	0.8	1.2	VRP1	orf19.2190	verprolin (by homology)
CA1765	1.0	1.0	1.1	1.0	1.0	1.0	APE2	orf19.5197	aminopeptidase yscII
CA3608	1.0	0.9	1.8	1.3	1.5	1.4	IPF3857	orf19.25	unknown function
CA4444	1.0	1.1	0.8	1.0	3.1	1.1	IPF3533	orf19.6842	putative GDP/GTP exchange factor (by homology)
CA4001	1.0	1.2	1.0	1.0	0.9	1.1	RPL12	orf19.1635	ribosomal protein
CA1465	1.0	0.7	0.7	0.7	0.8	0.6	RIM11	orf19.791	Ser/thr protein kinase (by homology)
CA5992	1.0	0.5	1.2	0.8	1.0	1.0	FAA4	orf19.7592	long-chain fatty acid--CoA ligase and synthetase 4 (by homology)
CA0870	1.0	1.0	1.0	1.1	1.0	1.0	IPP1	orf19.3590	inorganic pyrophosphatase (by homology)
CA6121	1.0	1.0	1.0	1.0	1.1	0.9	IPF33	orf19.5929	unknown function
CA1149	1.0	1.1	0.8	1.1	1.5	1.1	MET223	orf19.99	protein ser/thr phosphatase (by homology)
CA2252	1.0	1.0	1.0	0.9	0.9	1.4	IPF12844	orf19.2362	unknown function
CA0267	1.0	1.0	0.6	1.0	1.0	1.0	PGA40	orf19.1616	extracellular alpha-1,4-glucan (by homology)
CA5113	1.0	0.8	1.9	1.4	1.0	1.0	IPF20026	orf19.6418	unknown function
CA2311	1.0	1.2	1.0	0.8	0.8	0.8	SSO2	orf19.1376	syntaxin (by homology)
CA3849	1.0	0.9	1.0	0.9	0.8	0.9	IPF7938	orf19.6610	similar to Saccharomyces cerevisiae Stu2p suppressor of cold-sensitive tubulin mutation (by homology)
CA4814	1.0	0.9	1.0	1.2	0.8	0.9	SAS2	orf19.2087	Zinc finger protein involved in silencing (by homology)
CA0625	1.0	0.9	1.0	0.9	1.0	1.0	IPF19637	orf19.3163	unknown function
CA4471	1.0	0.4	1.3	1.1	0.5	0.8	MCM3	orf19.1901	replication initiation protein (by homology)
CA1958	1.0	1.0	0.9	0.9	1.2	1.6	IFE1	orf19.769	Unknown function
CA2001	1.0	1.0	1.0	0.8	0.5	0.7	IPF17074	orf19.2792	unknown function
CA4601	1.0	0.9	1.0	1.1	1.5	1.0	IPF2195	orf19.6920	unknown function
CA5194	1.0	1.0	1.3	1.1	1.4	1.0	IPF11756	orf19.7006	unknown function
CA4659	1.0	0.8	1.0	1.2	0.8	0.7	IPF17754	orf19.4446	low affinity high capacity ammonium permease (by homology)
CA1008	1.0	1.0	1.1	1.0	1.1	1.0	IPF14083	orf19.6254	similarity to Saccharomyces cerevisiae carrier protein Flx1p (by homology)
CA3903	1.0	0.9	1.1	1.0	0.9	1.1	IPF14890	orf19.4400	unknown function
CA1012	1.0	1.0	0.8	0.9	1.4	1.0	PSD2	orf19.3954	phosphatidylserine decarboxylase 2, 5-prime end (by homology)
CA2065	1.0	0.9	1.1	0.9	1.0	1.1	QCR2	orf19.2644	Ubiquinol--cytochrome-c reductase 40KD chain II (by homology)
CA3823	1.0	0.9	1.1	1.1	0.9	0.9	IPF10651	orf19.5765	unknown function
CA0070	1.0	0.9	1.1	0.9	1.3	1.0	IPF19295.3f	orf19.6469	unknown function, 3-prime end
CA0038	1.0	1.3	1.0	1.1	1.0	1.1	CYC1	orf19.1770	cytochrome-c isoform 1 Respiration
CA3409	1.0	1.1	0.9	1.0	1.2	1.1	IPF9410	orf19.6148	similar to Saccharomyces cerevisiae Nuf1p spindle pole body component (by homology)
CA5198	1.0	1.0	1.3	1.0	0.7	0.7	LPA4	orf19.7012	Similar to ribosomal protein S16, mitochondrial (by homology)
CA4805	1.0	0.9	0.9	1.0	1.0	0.9	RAD5	orf19.2097	DNA helicase (by homology)
CA5250	1.0	1.1	1.5	1.0	0.8	1.0	IPF1826	orf19.5012	unknown function
CA1706	1.0	0.7	2.0	1.3	1.5	1.4	NMD3	orf19.706	RNA binding (by homology)
CA1128	1.0	1.0	1.7	1.1	1.1	1.6	IPF5198	orf19.3609	unknown function
CA0901	1.0	1.0	1.0	1.0	1.3	1.2	IPF12033	orf19.3412	unknown function
CA2524	1.0	1.5	4.6	2.3	6.8	3.8	IPF4322	orf19.5521	unknown function
CA3758	1.0	1.0	0.8	1.0	0.9	1.0	IPF8889	orf19.3418	putative arginase (by homology)
CA1048	1.0	1.0	0.9	0.9	0.9	1.0	IPF15394	orf19.3899	unknown function
CA5111	1.0	1.2	1.1	1.0	0.9	0.9	SSY5	orf19.6422	Involved in sulfonylurea herbicide sensitivity (by homology)

CA0352	1.0	1.1	1.1	0.8	0.9	1.2	RPB4.5f	orf19.146	DNA-directed RNA polymerase II, 32 kDa subunit, 5-prime end (by homology)
CA1689	1.0	1.0	0.9	1.1	1.1	1.5	IPF13030	orf19.3655	unknown function
CA6070	1.0	0.9	0.9	1.0	0.8	0.7	IPF4842	orf19.5994	similar to Saccharomyces cerevisiae Rsg1p ras-related GTP-binding protein (by homology)
CA4404	1.0	1.3	1.4	1.1	1.2	1.5	MET16	orf19.3106	3 -phosphoadenylylsulfate reductase (by homology)
CA2988	1.0	0.9	0.9	1.0	0.6	0.8	SIN3	orf19.6010.3	Histone deacetylase by homology
CA3819	1.0	1.1	1.0	1.1	1.1	1.0	IPF6993	orf19.5772	unknown function
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 (by homology)
CA5017	1.0	0.9	0.9	1.0	0.7	0.8	IPF7559	orf19.6970	unknown function
CA2658	1.0	2.0	0.8	0.7	0.7	0.7	IPF8105	orf19.5711	unknown function
CA4062	1.0	0.9	1.1	0.9	1.0	0.9	IPF5933	orf19.439	similar to Saccharomyces cerevisiae Mhr1p involved in mitochondrial homologous DNA recombination (by homology)
CA0170	1.0	0.8	1.1	0.9	0.9	0.8	IPF15959	orf19.1105	unknown function
CA4221	1.0	1.0	0.9	1.0	1.1	1.0	IPF8760	orf19.823	unknown function
CA3778	1.0	1.0	1.1	0.8	1.0	1.0	IPF10431	orf19.2888	unknown function
CA0622	1.0	1.1	1.0	1.2	1.1	1.0	IPF14171	orf19.3149	unknown function
CA2763	1.0	1.2	0.8	0.8	0.8	0.9			
CA0791	1.0	0.7	0.9	1.0	1.1	0.9	LSC1	orf19.3358	succinate-CoA ligase / synthetase (by homology)
CA1469	1.0	1.2	0.7	0.9	1.4	1.0	IPF5078	orf19.795	unknown function
CA4786	1.0	1.0	1.0	1.0	1.0	1.2	IPF3362	orf19.4019	Unknown function
CA4397	1.0	0.9	0.9	1.0	1.5	1.2	IPF14369	orf19.3114	unknown function
CA3363	1.0	1.0	1.1	0.9	1.0	0.9	FRE32	orf19.1932	ferric reductase (by homology)
CA3194	1.0	1.0	1.1	1.0	0.9	1.1	IPF3425	orf19.6171	unknown function
CA1594	1.0	1.0	1.0	1.0	1.1	1.1	IPF11051	orf19.4321	unknown function
CA1811	1.0	1.0	1.0	1.0	0.9	0.9	MTR10	orf19.1119	Involved in nuclear protein import
CA4666	1.0	0.7	1.1	1.1	0.8	0.8	IPF6542	orf19.4455	unknown function
CA1232	1.0	1.1	0.6	0.6	1.0	1.3	IPF11815	orf19.4982	similar to Saccharomyces cerevisiae Lys14 triacyglycerol lipase (by homology)
CA0287	1.0	1.0	1.2	1.2	0.9	0.8	IPF14615	orf19.6080	unknown function
CA1576	1.0	0.9	0.9	1.0	1.8	1.1	HYR1	orf19.4975	hyphally regulated protein
CA4126	1.0	1.0	0.9	0.8	0.5	0.7	IPF6631	orf19.2763	unknown function
CA1716	1.0	0.9	1.1	1.1	0.9	1.0	IPF17237	orf19.3335	unknown function
CA6148	1.0	1.0	1.0	1.0	1.0	1.0	IPF1862.3f	orf19.5894	unknown function, 3-prime end
CA2086	1.0	1.0	0.8	0.8	0.9	0.9	IPF3392	orf19.835	unknown function
CA5392	1.0	0.9	1.0	0.9	1.0	0.9	IPF10571	orf19.935	Unknown function
CA2535	1.0	1.2	1.0	0.9	1.0	1.1	NCE11	orf19.3181.1	involved in non-classical protein export pathway (by homology)
CA1873	1.0	0.7	1.0	1.1	0.9	0.9	IPF6696	orf19.2460	unknown function
CA3976	1.0	1.0	1.0	1.0	1.1	1.0	SNU23	orf19.1548	RNA binding zinc finger protein (by homology)
CA6082	1.0	1.2	1.3	1.1	0.9	0.9	CEM1	orf19.5977	3-oxoacyl-[acyl-carrier-protein]-synthase (by homology)
CA4843	1.0	1.2	0.7	0.9	0.7	0.6	GYP1	orf19.3811	GTPase activating protein (by homology)
CA5066	1.0	1.2	0.5	0.7	1.5	0.7	TPS2	orf19.3038	Threalose-6-phosphate phosphatase (by homology)
CA1863	1.0	0.8	1.0	0.7	0.7	1.0	MRPL35	orf19.863	Ribosomal protein of the large subunit, mitochondrial (by homology)
CA4165	1.0	1.7	1.0	1.1	1.0	1.0	IPF7774	orf19.2968	unknown function
CA3038	1.0	1.1	0.8	1.0	0.8	1.0	IPF13438	orf19.209	unknown function
CA3189	1.0	1.0	0.7	1.0	1.3	1.2	IPF11607	orf19.2149	unknown function
CA1345	1.0	1.4	0.8	1.1	0.6	0.8	IPF6003	orf19.1490	similar to Saccharomyces cerevisiae Msb2p multicopy suppressor of a CDC24 bud emergence defect (by homology)
CA2233	1.0	1.0	1.0	1.0	1.1	1.6	IFJ3	orf19.3924	unknown function
CA5636	1.0	1.0	1.0	1.0	1.0	1.2	IPF473	orf19.7059	unknown Function
CA3127	1.0	1.0	1.0	0.9	1.0	1.1	IPF8915	orf19.1359	unknown function

CA2962	1.0	1.0	0.9	1.1	1.0	1.0	PRP2	orf19.5865	RNA-dependent ATPase (by homology)
CA4100	1.0	1.0	1.2	1.0	0.8	0.9	IPF3985	orf19.666	unknown function
CA4223	0.9	0.8	1.1	0.8	0.8	0.9	IPF8757	orf19.826	unknown function
CA2316	0.9	1.0	0.9	0.9	0.7	1.0	IPF14542.3f	orf19.1384	unknown function, 3 prime end
CA4801	0.9	0.8	0.9	1.0	0.8	0.9	APM1	orf19.4036	AP-1 complex subunit, mu1 subunit (by homology)
CA3680	0.9	1.0	0.8	1.0	1.2	1.0	IPF8395	orf19.729	unknown function
CA4558	0.9	2.3	1.0	1.1	1.9	1.6	GRP5	orf19.6868	dihydroflavonol-4-reductases (by homology)
CA2346	0.9	1.0	0.9	0.9	0.9	0.9	SEF1	orf19.3753	Putative transcription factor1
CA2719	0.9	1.5	1.1	1.1	2.8	1.6	SOD2	orf19.3340	Manganese-superoxide dismutase
CA0092	0.9	1.0	1.0	1.1	0.9	1.1			
CA0504	0.9	1.0	1.6	1.0	0.9	0.9	IPF16466.5	orf19.2778	unknown function
CA0340	0.9	1.0	1.0	1.0	1.2	1.0	IPF19859	orf19.3375	unknown function
CA0282	0.9	1.1	1.1	1.0	1.2	1.0	IPF17417	orf19.4691	Unknown function
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-prime end (by homology)
CA4297	0.9	1.0	1.2	0.9	0.8	0.9	IPF2603	orf19.6694	unknown function
CA4825	0.9	1.0	0.9	0.9	1.0	1.0	IPF1205	orf19.2071	unknown function
CA3885	0.9	1.1	0.7	1.1	0.8	0.9	IPF19790	orf19.5095	oxysterol binding protein (by homology)
CA2676	0.9	1.0	1.1	1.0	1.0	1.1	YHC1	orf19.5492	SMALL NUCLEAR RIBONUCLEOPROTEIN C (by homology)
CA0361	0.9	1.1	1.1	1.0	1.0	1.0	IPF2326	orf19.1124	unknown function
CA3275	0.9	0.9	1.2	1.0	0.9	0.8	IPF17068	orf19.6309	unknown function
CA5525	0.9	0.7	1.2	1.0	0.7	0.8	PEX13	orf19.7282	Peroxisome import protein - peroxin (by homology)
CA0647	0.9	1.0	1.0	1.0	1.0	1.1	PGA58	orf19.4334	unknown function
CA3719	0.9	1.4	1.0	1.0	0.9	0.9			
CA1835	0.9	1.0	1.0	1.0	1.0	1.0	CRH12	orf19.3966	Cell wall protein (by homology)
CA1207	0.9	0.9	0.9	0.9	0.6	0.6	PPG1	orf19.3774	Phosphoprotein phosphatase PPG catalytic chain (by homology)
CA4813	0.9	1.0	1.1	1.1	0.9	1.0	DPB4	orf19.2088	DNA-directed DNA polymerase epsilon, subunit D (by homology)
CA2646	0.9	1.1	1.1	1.1	1.1	0.7	IPF13089	orf19.1185	unknown function
CA2808	0.9	0.8	1.0	1.2	1.1	1.2	IPF11966	orf19.5783	unknown function
CA6099	0.9	1.0	1.3	1.3	1.8	0.9	CDR2	orf19.5958	Candida albicans drug resistance protein 2
CA4922	0.9	1.0	0.9	0.9	0.9	1.0	IPF1415	orf19.6062	unknown function Unknown function
CA5860	0.9	1.2	0.8	1.0	0.9	0.9	IPF376	orf19.7518	transcriptional regulator (by homology)
CA1466	0.9	0.9	1.2	0.8	1.0	1.1	IPF13324	orf19.792	unknown function
CA5265	0.9	0.8	0.8	1.1	0.6	0.5	IPF1792	orf19.4997	unknown function
CA3190	0.9	1.1	1.0	0.9	0.8	1.0	IPF11603	orf19.2150	unknown function
CA5756	0.9	1.0	1.0	1.1	0.9	0.9	IPF1065	orf19.5392	unknown function
CA5518	0.9	0.9	1.1	1.1	0.8	0.8	IPF721.5f	orf19.5366	unknown function, 5-prime end
CA3007	0.9	0.8	1.8	1.4	1.1	1.4	IPF12148	orf19.6234	Unknown function
CA2072	0.9	0.9	1.0	1.1	0.8	1.0	IPF6970	orf19.2639	unknown function
CA3406	0.9	1.0	1.2	1.2	0.7	0.9	IPF9711	orf19.3983	unknown function
CA3763	0.9	1.0	0.9	0.9	1.1	1.0	PGA41	orf19.2906	unknown function
CA3259	0.9	1.0	1.2	1.5	1.8	1.5	IPF7970	orf19.2691	unknown function
CA5243	0.9	1.1	1.5	1.1	0.5	0.7	IPF3040	orf19.5020	unknown function
CA5405	0.9	0.8	1.2	1.0	0.9	0.9	MRP17	orf19.947	Mitochondrial ribosomal protein (by homology) Translation
CA0686	0.9	1.0	0.9	0.7	0.3	0.5	IPF162	orf19.3222	sulphate transporter (by homology)
CA5159	0.9	1.4	0.6	0.9	1.2	1.0	CAP2	orf19.4597	F-actin capping protein, beta subunit (by homology)
CA2226	0.9	1.3	0.9	0.9	1.1	1.5	BET3.3f	orf19.5817	targeting and fusion of ER to Golgi transport vesicles, (by homology)

CA2244	0.9	0.8	1.8	0.9	1.0	1.0	AAT22	orf19.4669	aspartate aminotransferase (by homology)
CA2570	0.9	1.0	1.4	1.4	1.0	1.1	PRO3	orf19.5650	delta 1-pyrroline-5-carboxylate reductase (by homology)
CA2389	0.9	1.0	1.1	1.0	1.7	1.0	IPF8500	orf19.2610	unknown function
CA3352	0.9	1.1	0.8	1.0	1.0	1.0	IPF16194	orf19.1946	unknown function
CA0442	0.9	1.2	0.5	0.8	1.1	2.6	IFC4	orf19.2292	unknown function
CA5632	0.9	0.9	1.4	1.1	0.9	1.2	IPF480	orf19.7063	unknown function
CA3754	0.9	0.7	1.0	0.9	0.8	1.0	TIF3	orf19.3423	translation initiation factor eIF4B (by homology)
CA0970	0.9	1.0	0.8	1.1	1.0	1.1	IPF10894	orf19.2822	unknown function
CA4141	0.9	1.0	1.0	1.0	1.0	1.0			
CA0201	0.9	1.1	1.3	0.7	0.6	1.8	IPF17419	orf19.1533	Unknown function
CA3216	0.9	1.1	0.9	1.0	0.8	0.8	IPF13038.3f	orf19.6198.1	unknown function
CA3113	0.9	1.0	0.9	0.9	1.2	1.4	IPF15737	orf19.6539	simailar to Saccharomyces cerevisiae Rvb2p RuvB-like protein (by homology)
CA2061	0.9	0.7	1.0	0.9	1.0	1.0	CDC61.5f	orf19.2562	Cytosolic leucyl-tRNA synthetase, 5-prime end
CA4127	0.9	1.6	0.7	0.9	0.9	0.9	IPF6629	orf19.2762	unknown function
CA2195	0.9	0.8	0.8	0.9	0.3	0.6	IPF18517	orf19.4349	unknown function
CA5312	0.9	1.1	0.9	1.0	1.2	1.1	IPF2165	orf19.7183	unknown function
CA0492	0.9	1.0	1.1	0.9	1.0	1.0	SNU71	orf19.1491	Associated with U1 snRNP (by homology)
CA1194	0.9	1.1	0.8	1.1	1.3	1.2			
CA4930	0.9	1.3	1.3	1.1	1.0	1.0	IPF8381	orf19.6071	similar to Saccharomyces cerevisiae Mdm20p
CA3382	0.9	0.9	1.0	1.2	1.0	0.8	HTA3	orf19.327	histone H2A F/Z variant (by homology)
CA4845	0.9	1.2	1.0	1.1	1.0	1.0	IPF6945.5f	orf19.3813	unknown function, 5-prime end
CA1783	0.9	0.9	0.9	0.9	0.9	1.0	IPF7635	orf19.1171	unknown function
CA3704	0.9	0.9	0.9	0.9	1.0	1.0	IPF5671	orf19.4946	unknown function
CA2759	0.9	1.2	1.0	0.8	0.8	0.8	ARP4.5f	orf19.5624	actin-related protein, 5-prime end (by homology)
CA1912	0.9	0.9	1.1	1.1	0.7	0.7	SKY1	orf19.2436	SRPK1 like protein kinase (by homology)
CA0242	0.9	1.0	1.0	1.1	1.0	1.0	IPF12047	orf19.3471	unknown function
CA3699	0.9	1.0	1.0	1.0	0.9	0.8	IPF4860	orf19.6275	similarity to ribosomal protein kinases (by homology)
CA4497	0.9	1.1	1.1	1.0	1.2	1.0	IPF4064.5f	orf19.1863	unknown function
CA5172	0.9	1.2	0.8	1.0	0.8	1.0	CPS2.5f	orf19.4610	Carboxypeptidase YSCS precursor, 5-prime end
CA4609	0.9	3.6	1.2	1.3	1.5	1.2	ZPR1	orf19.3300	Zinc finger protein (by homology)
CA2820	0.9	0.8	1.2	1.2	0.6	0.5	HOL1	orf19.2991	member of major facilitator superfamily multidrug-resistance protein subfamily 1 by homology
CA3964	0.9	1.2	1.0	1.0	0.8	0.9	IPF9370	orf19.1424	unknown function
CA5014	0.9	0.9	0.8	0.9	0.8	0.9	IPF11120	orf19.6966	similar to Saccharomyces cerevisiae Cki1p choline kinase (by homology)
CA4312	0.9	1.2	0.8	1.1	1.1	0.8	IPF2122	orf19.4112	similar to thiamin pyrophosphokinase
CA2740	0.9	1.1	1.0	1.2	1.9	1.2	IPF10633	orf19.2106	unknown function
CA0161	0.9	0.8	0.8	0.9	1.0	1.3	RMS1	orf19.2654	(putative) transcriptional regulator (by homology)
CA0315	0.9	1.0	1.0	1.0	1.0	1.0	ALS9.5f	orf19.5742	agglutinin-like protein, 5-prime end
CA0268	0.9	1.1	1.0	0.7	1.0	1.0	PUF2.3f	orf19.4262	RNA-binding protein, 3-prime end (by homology)
CA1480	0.9	1.0	1.0	1.0	1.1	0.9	HIS6	orf19.1249	5 Pro-FAR isomerase
CA2251	0.9	0.9	0.7	0.8	1.0	1.0	IPF12845	orf19.2363	unknown function
CA4218	0.9	1.1	0.9	1.0	1.1	1.0	ACP1	orf19.819	mitochondrial acyl carrier protein (by homology)
CA3581	0.9	0.9	1.0	0.9	0.8	0.9	IPF16143	orf19.2259	unknown function
CA0335	0.9	1.0	1.0	1.0	1.7	1.0	IFA2	orf19.195	unknown function
CA5153	0.9	1.0	1.0	1.1	0.4	0.5	IPF1003	orf19.4592	unknown function
CA5409	0.9	1.0	1.0	1.0	1.0	1.0	COF1.3f	orf19.953.1	cofilin (by homology) Budding, cell polarity and filament formation
CA3650	0.9	0.8	0.8	0.8	1.0	0.9	IPF4134	orf19.2041	unknown function

CA3503	0.9	1.0	0.7	1.0	1.0	1.0	IPF15890	orf19.6349	cytoskeletal binding protein (by homology)
CA0857	0.9	1.0	1.0	1.0	1.1	1.1	SEN15	orf19.4464	tRNA splicing endonuclease delta subunit(by homology)
CA3248	0.9	1.0	1.0	1.1	0.9	0.9	IPF15834	orf19.4675	unknown function
CA0825	0.9	0.9	1.1	1.1	1.1	0.9	PLB2	orf19.690	phospholipase B
CA6016	0.9	0.8	1.4	1.4	1.4	1.6	IPF630	orf19.7618	unknown function
CA5463	0.9	1.1	0.9	0.9	0.9	1.1	IPF284	orf19.3272	unknown function
CA2699	0.9	1.0	1.1	1.0	0.7	0.8	RLF2	orf19.2739	chromatin assembly complex, subunit p90 (by homology)
CA4702	0.9	1.2	1.2	1.3	0.7	0.6	IPF4213	orf19.6930	unknown function
CA4523	0.9	0.9	1.0	1.1	1.0	1.1	GCD1	orf19.481	translation initiation factor eIF2bgamma (by homology)
CA4705	0.9	1.1	0.8	1.0	0.8	1.2	IPF4206	orf19.6934	unknown function
CA0702	0.9	1.2	0.6	0.8	1.0	0.8	IPF11812.3f	orf19.2913	unknown function
CA4788	0.9	0.8	1.0	1.0	1.1	1.2	SDH42	orf19.4022	succinate dehydrogenase membrane anchor subunit for sdh2p (by homology)
CA3481	0.9	1.0	0.9	1.1	1.0	1.0	IPF3223	orf19.3577.1	unknown function
CA0278	0.9	1.1	1.0	1.0	1.0	1.1	IPF15772	orf19.4883.3	unknown function
CA1636	0.9	1.1	1.0	1.0	0.9	0.9	IPF20086	orf19.3942	unknown function
CA1586	0.9	1.0	1.3	1.0	1.0	1.0	ODC1	orf19.6032	Ornithine decarboxylase
CA5553	0.9	1.9	0.7	1.0	0.9	1.2	IPF1960.3f	orf19.7317	putative transcriptional activator, 3-prime end
CA3590	0.9	1.5	0.5	1.2	1.0	0.4	ARE2	orf19.2248	acyl-CoA sterol acyltransferase-like (by homology)
CA1024	0.9	2.6	2.3	1.3	1.6	1.8	CAR1	orf19.3934	arginase by homology
CA1727	0.9	0.9	1.0	1.0	0.9	0.8	IPF8448	orf19.6493	unknown function
CA1352	0.9	1.0	0.9	1.3	0.4	0.5	VCX1	orf19.405	Ca2+-transport by homology
CA1448	0.9	1.3	1.0	0.8	0.8	0.7	IPF14728	orf19.192	unknown function
CA0332	0.9	1.1	0.8	1.2	0.8	0.8	FEN2	orf19.5535	allantoate permease transporter (by homology)
CA0528	0.9	0.9	1.2	0.8	0.4	0.6	ANP1	orf19.3622	Golgi mannosyltransferase (by homology)
CA0344	0.9	1.0	1.1	1.0	1.1	1.0	IFF1.5eoc	orf19.1346	Unknown function, 5-prime end
CA5144	0.9	0.9	0.4	0.9	1.1	0.9	IPF1019	orf19.4581	unknown function
CA0837	0.9	1.0	1.0	0.9	1.0	1.0			
CA4350	0.9	0.9	1.3	1.0	1.3	1.1	FUM12.53f	orf19.6724.1	Fumarate hydratase, internal fragment (by homology)
CA0491	0.9	0.8	1.0	1.1	1.0	0.7			
CA3736	0.9	0.8	1.1	1.1	0.9	1.0	IPF5533	orf19.2183	ABC transporter (by homology)
CA1710	0.9	1.2	0.9	0.9	0.3	0.8	CLA4	orf19.4890	protein kinase homolog (by homology)
CA3317	0.9	1.1	1.1	1.0	1.0	1.0	URM1	orf19.2299	ubiquitin like protein (by homology)
CA0690	0.9	1.0	1.2	1.0	1.0	1.0			
CA2043	0.9	1.0	1.1	1.1	0.9	0.9	GSL21	orf19.2929	1,3-beta-D-glucan synthase subunit
CA5576	0.9	1.0	1.1	1.0	1.0	1.0	PRP4	orf19.7343	pre-mRNA-processing U4/U6 small nuclear ribonucleoprotein (by homology)
CA2286	0.9	1.8	0.8	1.1	1.4	1.4	IPF5369	orf19.5553	unknown function
CA3222	0.9	0.9	1.2	1.0	1.2	1.1	IPF15883	orf19.6283	unknown function
CA0053	0.9	1.1	1.1	1.0	1.1	0.9	IFA16	orf19.380	unknown function
CA2354	0.9	1.0	0.9	1.0	1.0	1.1	IPF18480	orf19.4415	unknown function
CA1686	0.9	1.2	0.7	0.8	2.1	1.5	IPF12272	orf19.3659	unknown function
CA0621	0.9	1.0	1.0	1.0	0.8	0.8	IPF17999	orf19.3148	unknown function
CA5388	0.9	1.0	1.0	1.1	1.0	1.0	PET9	orf19.930	ADP/ATP carrier protein (by homology)
CA3559	0.9	0.9	1.0	1.0	1.1	1.0	PGI1	orf19.3888	Glucose-6-phosphate isomerase
CA3200	0.9	1.1	0.7	1.2	0.8	0.9	IPF3439	orf19.6180	unknown function
CA1085	0.9	1.1	1.0	1.1	0.9	1.0	IPF1038	orf19.4570	unknown function
CA4592	0.9	0.9	1.0	1.1	1.2	1.0	IPF2215	orf19.6909	unknown function

CA6115	0.9	1.1	0.9	1.1	0.9	1.0	IPF112	orf19.5935	unknown function
CA0205	0.9	1.0	1.0	1.0	0.5	0.6	DBF2	orf19.1223	putative ser/thr protein kinase by homology
CA3423	0.9	1.2	0.9	1.5	1.3	1.0	IPF3549	orf19.597	unknown function
CA2474	0.9	1.0	1.1	1.1	1.0	1.0	PDC11	orf19.2877	Pyruvate decarboxylase (by homology)
CA4821	0.9	0.6	0.7	1.1	0.8	0.8	IPF1197	orf19.2076	unknown function
CA2552	0.9	0.9	1.2	0.9	0.6	0.4	ALG5	orf19.2837	dolichol-P-glucose synthetase (by homology)
CA3045	0.9	1.0	1.1	1.1	1.0	1.2	MLC1	orf19.2416.1	similar to Saccharomyces cerevisiae Mlc1p myosin ((Myo2p) light chain, (by homology)
CA3616	0.9	1.0	1.0	1.0	0.9	1.1	ASN1	0.00	asparagine synthetase (by homology)
CA4254	0.9	0.9	0.7	0.8	1.2	1.1	IPF18234.3f	orf19.542.2	Unknown Function, 3-prime end
CA5283	0.9	1.7	0.8	1.0	0.8	1.2	IPF1912	orf19.7140	putative catechol o-methyltransferase
CA3411	0.9	0.8	1.1	1.3	1.0	0.8	IPF9413	orf19.6146	unknown function
CA0602	0.9	1.0	1.1	1.0	1.0	1.0	CTA22	orf19.3074	Protein with putative transcription activation domain
CA1246	0.9	0.9	1.1	1.1	1.0	1.0	IMH3	orf19.19	IMP dehydrogenase
CA3115	0.9	1.0	1.1	1.1	1.0	1.0	ECM33.3f	orf19.3010.1	cell wall biogenesis, 3-prime end (by homology)
CA3483	0.9	1.0	1.1	1.1	1.0	1.0	CDC19	orf19.3575	pyruvate kinase (by homology)
CA5171	0.9	1.3	1.0	1.0	1.5	1.2	IPF6037	orf19.4609	Similar to Legionella pneumophila sbpA
CA1067	0.9	1.0	0.9	0.7	1.0	1.0	HXT62	orf19.2023	sugar transporter
CA1373	0.9	0.9	1.1	1.1	1.1	1.2	AGP1	orf19.1193	asparagine and glutamine permease (by homology)
CA0421	0.9	1.3	1.1	0.9	1.0	1.1	IPF9047	orf19.2230	unknown function
CA0214	0.9	0.9	0.5	0.7	0.7	0.7	SCT11	orf19.1289	Suppresses a choline-transport mutant
CA4431	0.9	1.1	0.8	0.9	0.5	0.6	ECM39	orf19.5164	cell wall biogenesis by homology
CA1322	0.9	0.9	1.2	0.9	1.2	1.1	GCD11	orf19.4223	Translation initiation factor eIF2 (by homology)
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 homology)
CA3809	0.9	0.8	1.1	1.1	1.0	1.0	KAP123	orf19.2489	karyopherin-beta protein (by homology)
CA0908	0.9	0.9	1.0	0.9	0.7	0.9	MRPL31	orf19.1485	Mitochondrial ribosomal protein
CA4743	0.9	1.0	1.1	1.1	0.5	0.8	IPF4491	orf19.4839	unknown function
CA3874	0.9	1.0	1.1	1.1	1.0	1.0	ENO1	orf19.395	Enolase I (2-phosphoglycerate dehydratase)
CA1556	0.9	1.0	0.7	0.7	1.2	0.9	END3	orf19.1711	required for endocytosis and cytoskeletal organization (by homology)
CA3024	0.9	0.9	1.0	1.0	1.1	1.1	IPF11506	orf19.3903	unknown function
CA4159	0.9	1.0	1.5	1.1	0.5	1.1	ALD5	orf19.5806	aldehyde dehydrogenase (NAD+) (by homology)
CA1300	0.9	1.0	2.1	1.4	3.9	1.2	SLY41	orf19.4199	vesicular transport (by homology)
CA2671	0.9	1.1	1.1	1.0	1.1	1.0	IPF5856	orf19.5499	4-hydroxyphenylpyruvate dioxygenase (by homology)
CA4835	0.9	0.9	1.0	1.0	1.0	1.5	PGA2	orf19.2062	Similar to superoxide dismutase (by homology)
CA4213	0.9	1.0	1.0	1.0	1.0	0.9	IPF5795	orf19.811	unknown function
CA0443	0.9	0.5	2.5	1.1	1.0	1.1	SPB1	orf19.76	Putative methyltransferase by homology
CA2737	0.9	1.0	0.9	1.1	1.1	0.9	PGA9	orf19.2108	putative superoxide dismutase (by homology)
CA5441	0.9	1.0	1.1	0.9	1.1	1.0	IPF227	orf19.3244	unknown function
CA1245	0.9	0.8	1.1	1.1	1.0	1.0			
CA0502	0.9	1.0	1.0	1.0	0.9	0.8	IPF16761	orf19.2664	unknown function
CA0455	0.9	1.1	0.9	1.0	1.3	1.0	Tca5a	orf19.2427	polyprotein of Tca5 retrotransposon
CA3186	0.9	0.9	1.1	1.0	1.0	1.0	ILS1	orf19.2138	isoleucyl-tRNA synthetase (by homology)
CA2300	0.9	1.0	1.1	1.1	1.0	1.0	PMA1	orf19.5383	plasma membrane H+-transporting ATPase 1
CA0362	0.9	1.0	1.1	1.1	1.0	1.0	TEF1	orf19.1435	translation elongation factor eEF1 alpha-A chain
CA5175	0.9	0.9	0.9	1.1	6.3	1.7	IPF6041	orf19.4612	Similar to Legionella pneumophila sbpA
CA5942	0.9	1.4	0.7	1.0	1.4	2.9	DLD2	orf19.6755	D-lactate ferrycytochrome C oxidoreductase (by homology)
CA4777	0.9	1.1	0.9	1.0	0.9	0.9	PAN3	orf19.4010	component of the Pab1p-dependent poly(A) ribonuclease (by homology)

CA0156	0.9	1.0	1.0	1.1	0.3	0.9	SCW1.3f	orf19.1779	glucanase (by homology)
CA4079	0.9	1.1	1.1	1.0	0.8	1.0	IPF2527	orf19.6635	unknown function
CA5749	0.9	0.7	0.4	0.4	0.8	1.0	IPF2908	orf19.7459	unknown function
CA5546	0.9	1.1	0.9	1.0	0.7	0.9	TUB1	orf19.7308	Alpha-1 tubulin
CA4472	0.9	1.0	1.0	1.0	1.0	1.0	IPF6444	orf19.1900	putative methyltransferase (by homology)
CA2012	0.9	1.0	1.0	1.0	0.8	0.9	SEC10	orf19.3086	Required for exocytosis (by homology)
CA0076	0.9	1.2	1.2	1.1	1.5	1.1	IPF8866	orf19.4906	unknown function
CA0781	0.9	1.6	1.8	1.2	1.6	1.9			
CA4900	0.9	1.1	0.6	0.9	1.4	0.9	IFP2	orf19.6037	unknown function
CA2451	0.9	1.0	1.0	1.0	1.1	0.9	IFB2	orf19.5509	unknown function
CA1437	0.9	0.9	0.8	1.0	1.2	1.0	IPF7163	orf19.1200	unknown function
CA0669	0.9	1.2	1.1	1.0	1.4	1.2	IPF5918	orf19.448	unknown function
CA3825	0.9	1.1	1.0	1.1	1.0	1.3	IPF10654	orf19.5763	D-arabinitol dehydrogenase-like (by homology)
CA6050	0.9	0.9	0.9	1.0	0.8	0.9	IPF4939	orf19.7666	similar to Saccharomyces cerevisiae Seo1p suppressor of sulfoxyde ethionine resistance (by homology)
CA4058	0.9	1.1	0.9	0.9	0.8	0.9	IPF7717	orf19.433	unknown function
CA1622	0.9	1.1	0.8	1.0	1.1	0.9	IPF10045	orf19.470	similar to Saccharomyces cerevisiae Taf61p TFIID and SAGA subunit (by homology)
CA0215	0.9	1.0	1.0	1.0	1.2	0.9	IPF15350	orf19.2745	putative zinc finger transcription factor (by homology)
CA3922	0.9	0.9	0.8	1.0	1.2	1.3	GRD19	orf19.5114	Probable golgi membrane protein-sorting protein (by homology)
CA4412	0.9	0.8	1.0	1.1	1.0	1.0	PDA1	orf19.3097	Pyruvate dehydrogenase alpha chain (by homology)
CA5665	0.9	0.7	1.4	0.9	0.6	0.8	UBP1	orf19.7367	Ubiquitin-specific protease (by homology)
CA0801	0.9	1.0	1.1	1.1	1.0	1.0	CHC1	orf19.3496	clathrin heavy chain (by homology)
CA3841	0.9	1.0	1.0	1.1	1.0	1.0	IPF16640	orf19.6601	unknown function
CA5089	0.9	0.9	0.9	0.8	0.8	1.0	MRPL27	orf19.3064	ribosomal protein (by homology)
CA2027	0.9	1.0	0.8	0.9	0.6	0.5	MCK1	orf19.3459	ser/thr/tyr protein kinase (by homology)
CA3678	0.9	0.9	0.9	1.1	0.6	0.7	IPF8392	orf19.731	unknown function
CA3979	0.9	1.0	0.9	0.9	0.8	0.8	ENT3.3f	orf19.1553	putative endocytosis and cytoskeleton protein, 3-prime end (by homology)
CA3546	0.9	0.9	1.1	1.1	1.0	1.0	ACO1	orf19.6385	aconitate hydratase (by homology)
CA2478	0.9	1.1	0.9	1.0	1.0	1.0	DAL52	orf19.3208	allantoate permease (by homology)
CA1432	0.9	0.9	0.8	1.0	0.9	0.9	APM3	orf19.1204	AP-3 complex subunit, mu3 subunit (by homology)
CA5295	0.9	1.0	0.9	1.0	1.3	1.1	IPF1954	orf19.7158	putative transporter (by homology)
CA1647	0.9	1.1	1.0	1.0	1.1	1.2	IPF16663	orf19.5568	unknown function
CA3810	0.9	1.0	1.0	0.9	1.2	0.8	IPF9230	orf19.2492	similar to Saccharomyces cerevisiae Ste3p pheromone a-factor receptor (by homology)
CA4317	0.9	0.9	1.1	1.0	1.1	1.0	IPF2109	orf19.4105	unknown function
CA3504	0.9	1.1	1.0	1.0	1.0	1.0	IPF11369	orf19.6350	unknown function
CA0404	0.9	1.2	1.1	1.2	1.0	1.1	LYS14	orf19.5548	transcription factor involved in lysine biosynthesis (by homology)
CA0772	0.9	1.1	1.0	1.0	0.9	1.0	UGA11.3f	orf19.853.3	4-aminobutyrate aminotransferase, exon 2 (by homology)
CA5323	0.9	0.7	2.5	1.2	0.7	1.1	IPF2142	orf19.7197	unknown function
CA0794	0.9	1.0	1.1	1.0	1.0	1.0	IPF15639	orf19.552	unknown function
CA4357	0.9	1.1	1.0	1.1	1.0	1.0	IPF19800	orf19.6732	unknown function
CA3053	0.9	1.0	0.8	1.0	1.2	1.3	GTR2	orf19.2406	GTP-binding protein (by homology)
CA1306	0.9	0.8	1.0	1.1	0.4	0.5	CDC14	orf19.4192	protein phosphatase
CA2273	0.9	1.1	1.0	1.0	1.0	0.9	BIO2	orf19.2593	biotin synthetase (by homology)
CA3146	0.9	0.9	1.0	0.9	0.9	0.9	IPF9797	orf19.6156	unknown function
CA2736	0.9	1.2	1.0	1.5	1.0	0.9	ATE1	orf19.2110	arginyl tRNA transferase (by homology)
CA1078	0.9	1.0	1.0	1.1	0.9	0.9	SPR1	orf19.2237	exo-1,3-beta-glucanase precursor (by homology)
CA5899	0.9	0.5	1.1	0.9	1.0	1.0	IPF2382	orf19.6807	unknown function

CA0160	0.9	0.8	0.6	0.8	2.2	2.1	GAP7	orf19.3195	general amino acid permease
CA2678	0.9	1.1	1.2	1.0	0.6	0.9	IPF5834	orf19.5491	unknown function
CA1832	0.9	1.0	0.8	1.0	0.6	1.1	IPF17727	orf19.5190	unknown function
CA0522	0.9	0.9	0.8	1.0	0.8	0.9	IPF4463	orf19.3529	unknown function
CA5686	0.9	0.7	1.2	1.1	0.6	0.8	IPF3329	orf19.7388	similar to Saccharomyces cerevisiae Pbs2p tyrosine protein kinase of the MAP kinase kinase family (by homology)
CA4039	0.9	1.1	0.4	0.3	1.0	1.0	SKS1	orf19.3669	serine/threonine kinase by homology
CA0761	0.9	1.0	1.1	0.9	1.0	0.8	IPF8267	orf19.1573	P-type ATPase
CA1284	0.9	1.1	1.0	1.0	0.6	1.0	IPF10168	orf19.643	unknown function
CA4520	0.9	0.9	0.9	0.9	1.1	0.7	CDC31	orf19.485	spindle pole body component, centrin (by homology)
CA5765	0.9	0.9	1.6	1.1	1.2	1.5	SOF1	orf19.5407	Involved in 18S pre-rRNA production (by homology)
CA1521	0.9	0.9	1.0	1.0	0.9	1.0	FTH1	orf19.4802	iron transporter
CA3144	0.9	1.0	1.0	1.0	0.9	1.0	ASF1	orf19.3715	anti-silencing protein (by homology)
CA3202	0.9	1.1	1.0	0.9	1.2	1.0	IPF3444.5f	orf19.6184	unknown function, 5-prime end
CA1377	0.9	0.9	0.5	0.8	1.0	1.0	IPF18690.5	orf19.461	unknown function
CA3068	0.9	0.9	1.0	1.0	1.0	1.0	LIP2	orf19.4804	Secretory lipase
CA5776	0.9	0.8	1.0	1.0	0.8	0.8	RML2	orf19.5420	Ribosomal L2 protein, mitochondrial (by homology)
CA4950	0.9	1.0	0.9	1.0	1.7	1.2	IPF5143	orf19.6528	Unknown function
CA4918	0.9	1.0	1.3	1.2	1.7	1.8	GLO1	orf19.6058	Glyoxalase I (by homology)
CA3946	0.9	1.0	1.0	1.1	1.0	1.0	MNN2	orf19.1995	Golgi alpha-1,2-mannosyltransferase (by homology)
CA1914	0.9	0.9	1.0	0.7	1.0	1.0	IPF16564	orf19.2438	putative mitochondrial ribosomal protein S12
CA0732	0.9	0.8	1.0	1.1	0.9	0.9	IPF9000	orf19.4636	unknown function
CA4948	0.9	1.0	1.0	1.0	1.2	1.0	IPF5149	orf19.6530	unknown function
CA4863	0.9	1.2	1.1	1.1	1.5	1.4	SAP10	orf19.3839	secretory aspartyl proteinase
CA0373	0.9	1.0	1.0	0.9	1.0	1.1			
CA4224	0.9	0.9	1.1	0.9	1.2	1.1	IPF8755	orf19.827	unknown function
CA2384	0.9	1.1	0.6	0.8	1.0	0.8	MDL1	orf19.2615	ATP-DEPENDENT PERMEASE
CA0749	0.9	0.9	1.1	0.9	0.8	0.9	HAP5	orf19.1973	CCAAT-binding factor subunit (by homology)
CA4466	0.9	0.8	0.9	1.1	0.8	0.7	VPH1	orf19.6863	H+-ATPase V0 domain subunit (by homology)
CA2055	0.9	1.0	1.0	1.0	1.0	1.0	SAP4	orf19.5716	secreted aspartyl proteinase
CA5624	0.9	1.1	0.9	1.0	0.9	1.0	IPF501	orf19.7073	unknown function
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 homology)
CA2753	0.9	0.9	1.1	1.1	1.4	1.2	IPF16806	orf19.5617	unknown function
CA4375	0.9	1.0	1.0	1.1	1.2	1.0	IPF11309	orf19.5666	unknown function
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
CA4080	0.9	1.0	0.8	1.0	1.0	1.1	IPF2524	orf19.6636	unknown function
CA2143	0.9	0.9	0.9	0.9	0.8	0.8	IPF12803	orf19.2512	unknown function
CA1540	0.9	0.9	1.2	1.5	0.9	1.6	IPF1047	orf19.4563	unknown function
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 homology)
CA2611	0.9	1.1	0.9	1.0	0.8	1.0	IPF5453	orf19.5692	unknown function
CA5963	0.9	0.9	1.3	0.9	1.1	1.0	IPF966	orf19.7552	unknown function
CA4651	0.9	1.7	0.6	0.7	1.9	2.0	IPF3121	orf19.4438	unknown function
CA1733	0.9	0.9	1.0	1.0	1.0	1.1	IPF3931	orf19.6501	Unknown function
CA5522	0.9	0.9	1.0	1.0	0.8	0.9	IPF708	orf19.5370	unknown function
CA2559	0.9	1.0	1.0	1.2	1.0	1.1	HIS4	orf19.5639	Histidine biosynthesis trifunctional protein
CA2531	0.9	0.9	1.0	1.0	0.8	0.8	RIB2	orf19.3177	DRAP deaminase (by homology)
CA2507	0.9	1.1	1.0	1.0	1.0	1.0			

CA5801	0.9	1.0	1.0	1.1	1.0	1.4	DAL1	orf19.5454	allantoinase
CA2248	0.9	0.9	1.0	0.9	0.9	0.9	IPF11469	orf19.2366	unknown function
CA2554	0.9	1.0	0.6	1.2	1.1	1.1	Cirt4	orf19.2839	probable transposase (by homology)
CA6128	0.9	1.0	1.9	0.8	0.3	0.5	IPF152	orf19.5919	unknown function
CA0223	0.9	0.4	1.1	1.0	1.0	1.0	VAS1	orf19.1295	valyl-tRNA synthetase (by homology)
CA1249	0.9	0.9	1.7	1.3	1.3	1.2	SPE4	orf19.4960	spermine synthase (by homology)
CA5393	0.9	1.0	1.0	1.0	0.9	1.0	IPF9398	orf19.936	unknown function
CA4049	0.9	1.9	0.9	1.2	1.1	1.0	IPF10482	orf19.424	unknown function
CA3306	0.9	0.9	1.1	1.0	1.0	0.9	IPF11738	orf19.2310	unknown function
CA5239	0.9	1.1	1.0	0.8	1.3	1.3	GND1	orf19.5024	6-phosphogluconate dehydrogenase
CA0459	0.9	1.0	1.0	1.0	1.0	1.2	HOL3	orf19.2517	member of major facilitator superfamily multidrug-resistance protein subfamily 1 (by homology)
CA5947	0.9	0.7	1.1	1.0	1.0	1.1	KRS1	orf19.6749	Lysyl-tRNA synthetase (by homology)
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)
CA0500	0.9	1.0	1.4	1.2	0.9	2.0	IPF20058	orf19.4793	unknown function
CA5715	0.9	1.1	0.9	1.1	1.4	1.3	HNT2	orf19.7419	Diadenosine polyphosphate hydrolase
CA5755	0.9	1.1	1.0	1.0	0.8	0.8	IPF1063	orf19.5391	Spliceosomal protein SAP 130 (by homology)
CA4300	0.9	1.2	0.8	0.9	1.0	1.0	HIS2	orf19.6699	Histidinol phosphatase (by homology)
CA1990	0.9	0.9	1.4	1.0	0.6	0.9	TOP1	orf19.96	CANAL DNA TOPOISOMERASE I
CA5126	0.9	1.0	1.0	1.0	0.8	1.0	SLS1	orf19.6403	Endoplasmic translocation machinery by homology
CA3688	0.9	0.9	1.7	1.2	0.4	0.7	YIP3	orf19.6264.3	protein of unknown function, (by homology)
CA0105	0.9	1.0	0.9	1.0	1.0	1.0	IPF17529.3	orf19.786	unknown function, 3-prime end
CA2046	0.9	0.9	1.1	0.9	0.8	0.9	IPF8108	orf19.2934	unknown function
CA5158	0.9	1.1	0.8	1.0	1.3	1.1	IPF992	orf19.4596	unknown function
CA5470	0.9	1.0	1.2	1.0	0.5	0.9	IPF300	orf19.3282	unknown function
CA0331	0.9	0.8	0.8	1.0	0.9	1.0	ANC1	orf19.798	TFIIF subunit, transcription initiation factor (by homology)
CA2943	0.9	1.0	1.0	0.9	0.7	0.7	MAK31	orf19.1968.1	Involved in stability of L-A dsRNA-containing particles (by homology)
CA5910	0.9	1.4	1.0	1.0	0.9	0.9	IPF5964	orf19.6795	unknown function
CA0461	0.9	1.0	1.0	1.0	0.9	1.1	IPF4972	orf19.2519	unknown function
CA5376	0.9	0.9	1.0	1.0	0.9	1.2	GDI1	orf19.7261	GDP dissociation inhibitor by homology
CA4790	0.9	1.3	1.1	1.1	0.8	1.0	IPF3367	orf19.4024	Riboflavin synthase (by homology)
CA0342	0.9	1.1	1.0	0.9	0.8	1.0	IPF10470	orf19.1789	unknown function
CA2198	0.9	1.5	0.9	0.9	0.6	0.7	PMM1	orf19.2937	phosphomannomutase
CA0306	0.9	0.8	1.1	1.0	1.6	0.9	HEM3	orf19.1742	porphobilinogen deaminase
CA1074	0.9	1.1	1.1	0.8	0.5	0.6	PRORS.5f	orf19.2532	prolyl-tRNA synthetase, 5-prime end
CA5403	0.9	1.4	1.0	1.1	1.1	1.1	IPF1542	orf19.945	unknown function
CA3938	0.9	1.0	1.0	0.9	0.9	1.0	IPF4764	orf19.2005	unknown Function
CA4775	0.9	1.1	1.0	1.1	1.1	1.0	IPF3342	orf19.4007	Unknown function
CA4939	0.9	0.6	0.5	0.8	0.4	0.7	IQG1	orf19.6536	RAS GTPase-activating-like protein by homology
CA3282	0.9	1.0	1.0	1.0	0.4	0.9	IPF6272	orf19.6315	unknown function
CA1430	0.9	1.2	0.9	1.0	0.9	1.0	PGA8	orf19.3380	Probable extracellular alpha-1,4-glucan glucosidase (by homology)
CA2476	0.9	1.0	1.0	1.0	0.9	1.0	IFF5	orf19.2879	unknown function
CA5891	0.9	1.8	0.6	0.2	1.8	1.2	IPF2400	orf19.6816	putative aldehyde reductase (by homology)
CA1122	0.9	0.9	1.2	0.9	0.9	0.8	PMS1.3eoc	orf19.1605	DNA mismatch repair protein, 3-prime end (by homology)
CA3461	0.9	0.5	1.2	1.1	1.4	0.9	CFL2	orf19.1264	ferric reductase (by homology)
CA0952	0.9	0.9	0.9	1.1	0.6	0.7			
CA0923	0.9	0.8	1.7	1.4	0.9	1.1	IPF12987	orf19.1047	unknown function

CA6024	0.9	1.1	0.9	0.9	1.0	1.0	IPF615	orf19.7627	unknown function
CA2168	0.9	1.0	1.2	0.9	1.1	1.5	IPF4558	orf19.910	similar to Saccharomyces cerevisiae Prp3p splicing factor (by homology)
CA4508	0.9	1.0	1.0	0.8	0.8	0.8	NAM9	orf19.498	mitochondrial ribosomal protein
CA3631	0.9	0.5	0.9	1.1	0.8	1.0	TIM54	orf19.5143	Translocase for the insertion of proteins into the mitochondrial inner membrane(by homology)
CA6116	0.9	0.9	1.0	1.0	0.7	0.9	TOP3	orf19.5934	DNA topoisomerase III (by homology)
CA6060	0.9	0.8	1.3	0.9	0.6	0.7	IPF8301	orf19.6008	unknown function
CA0305	0.9	1.0	0.8	0.7	1.3	1.0	INO80	orf19.1734	DNA helicase (by homology)
CA0810	0.9	0.9	1.5	1.0	0.8	1.2	RRN3	orf19.1923	RNA polymerase I specific transcription factor (by homology)
CA2281	0.9	1.0	2.0	1.5	1.0	1.1	HAT1	orf19.779	histone acetyltransferase (by homology)
CA5440	0.9	1.1	1.0	0.9	0.8	0.9	SRP54	orf19.3243	54 kD signal recognition particle subunit
CA3646	0.9	1.0	1.1	1.0	0.8	0.9	IPF4128	orf19.2037	unknown function
CA2860	0.9	1.0	1.1	1.0	1.0	1.0	IPF7054	orf19.1062	unknown function
CA3703	0.9	1.0	0.9	0.8	1.0	1.0	IPF11945	orf19.6281	unknown function
CA0940	0.9	1.0	1.0	1.0	0.8	0.9	IPF8616	orf19.3704.1	similar to Saccharomyces cerevisiae Rsm19p ribosomal protein (by homology)
CA2696	0.9	1.4	1.5	1.1	0.8	0.8	IPF9169	orf19.2736	similar to Saccharomyces cerevisiae Bur6p functional homolog of human NC2alpha (by homology)
CA2897	0.9	0.9	1.1	1.1	1.7	1.1	IPF14979	orf19.3482	similar to Saccharomyces cerevisiae Npy1p NADH pyrophosphatase (by homology)
CA4584	0.9	1.0	1.6	1.0	1.2	1.0	IPF2228	orf19.6902	similar to Saccharomyces cerevisiae Dbp7p RNA helicase required for 60S ribosomal subunit assembly (by homology)
CA4623	0.9	1.0	0.7	1.0	0.6	0.8	CTA9	orf19.3315	Putative transcriptional regulator
CA1979	0.9	1.3	1.3	1.1	0.9	1.0	IPF9577	orf19.686	unknown function
CA5229	0.9	1.0	1.0	1.1	0.8	1.0	IPF10425	orf19.5035	unknown function
CA1419	0.9	0.9	1.0	1.1	1.1	1.1	IPF17296	orf19.175	unknown function
CA3828	0.9	1.2	1.7	1.1	1.6	1.2	SNQ2	orf19.5759	multidrug resistance protein (by homology)
CA5262	0.9	1.0	1.1	0.8	1.0	0.9	IPF1804	orf19.5001	putative transcription factor (by homology)
CA4454	0.9	0.9	0.9	1.0	0.9	1.0	IPF15160	orf19.6852	unknown function
CA3117	0.9	1.1	1.0	1.0	0.7	1.0	IPF5363	orf19.3009	unknown function
CA4586	0.9	0.9	1.3	1.1	1.4	1.1	GCN3	orf19.6904	Translation initiation factor eIF2B alpha subunit (by homology)
CA3519	0.9	1.0	0.9	0.9	1.0	1.1	IPF6787	orf19.998	unknown function
CA4214	0.9	1.0	1.1	1.1	1.0	1.1	IPF5796	orf19.812	unknown function
CA5411	0.9	1.0	0.9	0.9	0.9	0.9	IPF1558	orf19.955	unknown function
CA5500	0.9	1.1	0.9	0.9	1.0	0.8	IPF768	orf19.5342	unknown function
CA4881	0.9	0.8	1.1	1.1	1.0	0.9	IPF1652	orf19.6569	putative purine nucleoside permease (by homology)
CA2475	0.9	1.0	1.0	1.0	1.7	1.0	PGA15	orf19.2878	unknown function
CA3089	0.9	1.1	0.7	1.0	1.4	0.9	IPF9825	orf19.4144	unknown function
CA3770	0.9	1.1	2.5	1.4	0.9	1.1	SOU2	orf19.2897	Sorbitol utilization protein Sou2p [Candida albicans]
CA4837	0.9	1.1	0.9	1.0	2.0	1.1	IPF1228	orf19.2059	unknown function
CA2155	0.9	1.0	1.0	0.9	1.0	0.9	IPF7903	orf19.6027	unknown function
CA3405	0.9	1.1	0.9	1.1	1.1	1.1	IPF8644	orf19.3982	maltase (by homology)
CA2037	0.9	1.0	0.6	1.0	0.9	0.8	IFF3	orf19.4361	unknown function
CA3388	0.9	1.1	1.0	1.0	1.4	1.0	IPF6755	orf19.320	unknown function
CA0765	0.9	0.8	0.8	0.9	0.6	0.9	IPF9040	orf19.2236	similar to Saccharomyces cerevisiae Fhl1p transcriptional activator of the forkhead/hnf3 family (by homology)
CA3366	0.9	0.9	0.8	1.0	1.0	0.9	FRE43.3f	orf19.1845	ferric reductase-like (by homology)
CA2205	0.9	0.9	1.0	1.0	1.1	0.8	SEO2	orf19.700	suppressor of sulfoxyde ethionine resistance
CA6084	0.9	1.0	1.1	1.0	0.9	1.0	IPF29	orf19.5975	zinc finger protein (by homology)
CA0067	0.9	0.8	0.9	1.0	0.9	1.0	IPF13904	orf19.120	farnesyl cysteine carboxyl-methyltransferase (by homology)
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 end (by homology)
CA2003	0.9	0.4	1.5	1.1	1.4	1.2	IPF16471	orf19.2795	putative RNA binding protein by homology

CA4341	0.9	1.0	0.6	0.9	1.0	0.8	IPF3624	orf19.6713	unknown function
CA1722	0.9	1.0	1.1	1.1	0.9	1.2	TEF41	orf19.2652	Probable translation elongation factor (by homology)
CA1665	0.9	1.1	0.6	0.9	3.6	5.4	RIB1	orf19.2862	GTP cyclohydrolase II by homology to S.cerevisiae
CA4811	0.9	0.6	2.0	1.2	1.0	1.0	ECM16	orf19.2090	RNA helicase (by homology)
CA1414	0.9	0.6	1.2	0.9	0.5	0.5	CHO2	orf19.169	phosphatidylethanolamine N-methyltransferase (by homology)
CA5335	0.9	1.1	0.9	1.0	1.1	0.9	IPF894	orf19.7209	unknown function
CA5707	0.9	1.0	0.9	1.1	0.7	0.9	ERV25	orf19.7409	Component of COPII-coated vesicles (by homology)
CA6047	0.9	1.0	0.9	1.2	1.1	1.0	IPF4933	orf19.7663	unknown function
CA0060	0.9	1.1	1.2	1.0	0.8	0.9	IPF13661	orf19.1699	unknown function
CA2034	0.9	1.1	1.7	1.1	0.8	1.0			
CA0237	0.9	1.0	1.0	1.0	0.6	1.0	IPF13416.5f	orf19.188	Unknown function, 5-prime end
CA1484	0.9	0.7	1.1	1.0	1.0	1.0	ARO4	orf19.4060	3-dehydro-deoxyphosphoheptonate aldolase, tyrosine-inhibited (by homology)
CA2935	0.9	0.8	1.7	1.0	0.5	0.5	IPF11521	orf19.3328	unknown function
CA5943	0.9	1.0	1.6	1.0	0.9	1.2	IPF3490	orf19.6754	unknown function
CA4382	0.9	0.9	0.6	0.9	0.9	0.5	IPF8576	orf19.5675	similar to Saccharomyces cerevisiae Ris1p DNA helicase (by homology)
CA1043	0.9	1.0	0.8	0.9	1.0	1.0	TOM6	orf19.1650	mitochondrial outer membrane import receptor subunit (by homology)
CA3169	0.9	1.3	0.4	0.8	1.9	3.9	IPF7686	orf19.1395	putative mitochondrial phosphate carrier protein (by homology)
CA1968	0.9	0.9	1.0	1.0	0.9	1.3	IPF10864	orf19.5220	similar to Saccharomyces cerevisiae Rex4p member of the 3-prime to 5-prime exonuclease family (by homology)
CA5555	0.9	1.7	1.0	1.0	1.3	1.1	SUC1	orf19.7319	Putative zinc finger protein Suc1
CA1407	0.9	0.9	2.1	1.4	0.9	0.7	UAPC	orf19.2882	purine permease (by homology)
CA3283	0.9	0.9	0.8	1.1	0.7	0.9	IPF6274	orf19.6316	unknown function
CA3852	0.9	1.1	1.0	1.3	0.8	1.0	TUP1	orf19.6109	general transcription repressor
CA6072	0.9	0.9	2.5	1.1	1.0	1.2	DBP10	orf19.5991	Putative ATP-dependent RNA helicase (by homology)
CA3195	0.9	1.1	1.2	1.1	0.7	0.8	IPF3426	orf19.6173	unknown function
CA3706	0.9	2.2	0.7	0.8	1.1	1.0	PSA2	orf19.4943	mannose-1-phosphate guanyltransferase by homology
CA0230	0.9	1.1	0.9	0.9	1.0	1.0	TOM37	orf19.1532	Mitochondrial outer membrane import receptor subunit (by homology)
CA4419	0.9	1.3	0.8	1.0	1.4	1.1	IFA6	orf19.5177	Unknown function
CA0281	0.9	1.0	1.1	1.0	1.1	1.1	IPF10565	orf19.1438	unknown function
CA1967	0.9	0.9	0.7	1.1	1.0	0.8	IPF10866	orf19.5219	GTPase-activator protein (by homology)
CA2071	0.9	1.0	1.1	1.0	1.0	1.0	IPF6971	orf19.2639.2	
CA3826	0.9	1.1	1.0	1.0	1.0	1.0	PGA61	orf19.5762	unknown function
CA5063	0.9	0.5	2.2	1.1	0.7	0.8	IPF8493	orf19.3034	putative member of nontransporter group of ATP-binding cassette (ABC) superfamily (by homology)
CA1769	0.9	1.0	0.9	1.1	1.1	1.0	IPF7581.5e	orf19.5203	unknown function
CA3997	0.9	1.0	1.3	1.0	1.0	1.2	LOC1	orf19.1642	putative double-stranded RNA-binding protein (by homology)
CA5965	0.9	1.1	0.9	0.9	7.6	6.7	IPF961	orf19.7554	drug resistance protein (by homology)
CA2117	0.9	0.4	0.7	1.2	0.9	0.5	SNG3	orf19.1333	Drug transporter (by homology)
CA6035	0.9	1.9	1.2	1.2	0.6	0.8	BPL1	orf19.7645	biotin holocarboxylase synthetase (by homology)
CA3080	0.9	1.1	1.0	0.8	1.0	1.6	IPF14634	orf19.4153	APP-binding protein 1 (by homology)
CA4947	0.9	1.0	1.0	1.1	0.9	0.9	NUC2	orf19.6531	NADH-UBIQUINONE OXIDOREDUCTASE (by homology)
CA1383	0.9	1.1	0.9	1.0	0.8	1.1	IPF8422	orf19.927	unknown function
CA3615	0.9	1.0	1.0	1.1	1.1	0.7	GIT1	orf19.34	glycerophosphoinositol transporter (by homology)
CA2618	0.9	1.1	1.0	1.0	1.2	1.0	SNG2	orf19.2812	drug transporter (by homology)
CA2526	0.9	1.0	0.7	1.0	1.2	1.0	SEC20	orf19.5526	secretory pathway protein
CA0057	0.9	0.8	1.6	1.3	1.4	1.6			
CA3970	0.9	1.0	1.0	1.0	1.2	1.0	IPF6497	orf19.1542	unknown function
CA4545	0.9	1.0	1.0	1.1	0.9	1.0	SSL1	orf19.1457	TFIIH subunit (transcription initiation factor), factor B

CA5455	0.9	0.9	1.2	1.0	0.9	1.2	IPF263.3	orf19.3263	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate pathway regulator Gpr1p
CA2040	0.9	1.3	2.7	1.5	0.9	0.6	IPF12946	orf19.4356	unknown function
CA2162	0.9	0.5	1.1	1.0	1.0	0.9	PDB1	orf19.5294	pyruvate dehydrogenase (by homology)
CA5897	0.9	0.6	0.6	0.5	1.5	0.9	IPF2384	orf19.6809	unknown function
CA5731	0.9	1.1	1.1	1.1	0.7	0.8	IPF2870	orf19.7441	unknown function
CA5105	0.9	0.7	1.3	1.2	1.1	1.0	PEX19	orf19.6434	Required for biogenesis of peroxisomes (by homology)
CA1711	0.9	1.1	1.1	1.0	1.0	1.0	POX18.5f	orf19.3330.4	Lipid-transfer protein, 5-prime end (by homology)
CA0764	0.9	1.0	1.0	1.0	1.0	1.0	PRE2	orf19.2233	20S proteasome subunit (beta5)
CA3507	0.9	0.9	1.3	0.9	1.0	0.9	IPF11375	orf19.6354	unknown function
CA1401	0.9	0.8	1.0	0.9	1.0	0.7	TOM22	orf19.3696	mitochondrial outer membrane import receptor complex subunit (by homology)
CA5909	0.9	1.5	0.9	1.0	1.0	1.4	YSA1	orf19.6796	sugar-nucleotide hydrolase (by homology)
CA1698	0.9	0.9	0.9	1.0	6.3	3.5	IPF15681	orf19.5045	unknown function
CA2087	0.9	1.2	0.9	1.0	1.0	1.2	IPF3393	orf19.836	unknown function
CA3343	0.9	0.8	1.1	1.0	0.7	1.0	IPF13360	orf19.2328	unknown function
CA3995	0.9	0.7	1.9	1.3	1.0	1.2			
CA5156	0.9	1.0	0.9	0.9	1.2	1.1	CLC1	orf19.4594	clathrin light chain (by homology)
CA0434	0.9	0.9	1.0	1.0	1.0	1.0	IPF13577	orf19.1735	unknown function
CA3592	0.9	0.9	1.1	1.1	1.0	1.1	IPF12900	orf19.2246	unknown function
CA1597	0.9	1.1	1.0	1.1	1.0	1.0	IPF9538	orf19.271	unknown function
CA1703	0.9	1.2	0.8	1.0	1.4	1.6	IPF7987	orf19.703	unknown function
CA5488	0.9	1.1	1.0	1.1	0.5	0.4	IPF810	orf19.5322	unknown function
CA2608	0.9	0.6	1.1	1.0	0.9	1.1	THS1	orf19.5685	threonyl tRNA synthetase by homology
CA2781	0.9	0.8	0.9	1.2	0.8	0.8	IPF3821	orf19.284	unknown function
CA4358	0.9	1.0	1.0	0.9	0.8	0.9	IPF6067	orf19.6734	putative transcription factor (by homology)
CA2723	0.9	1.0	0.7	1.0	0.6	0.9	IPF4805	orf19.3345	unknown Function
CA1354	0.9	0.8	0.9	1.0	0.9	0.9	GCD6	orf19.407	Guanine nucleotide exchange factor (by homolgy)
CA3781	0.9	0.9	1.4	1.2	1.0	1.2	IPF11224	orf19.5839	similar to Saccharomyces cerevisiae Pdr16p protein involved in lipid biosynthesis and multidrug resistance
CA2934	0.9	1.1	1.0	1.1	0.5	0.6	IPF11515	orf19.3329	similar to Saccharomyces cerevisiae Lcb3p sphingoid base-phosphate phosphatase (by homology)
CA1351	0.9	0.9	1.1	1.0	0.4	0.7	PCL2	orf19.403	G1/S specific cyclin
CA3280	0.9	1.0	1.0	1.0	1.0	1.0	IPF6269	orf19.6313.2	unknown function
CA3292	0.9	1.1	1.1	1.0	0.7	1.1	IPF5729	orf19.6326	unknown function
CA5611	0.9	0.6	1.4	1.1	0.9	1.3	SUA5	orf19.7088	translation initiation protein (by homology)
CA0365	0.9	1.0	0.9	1.0	1.0	1.0	IPF15177	orf19.750	Unknown function
CA1069	0.9	0.9	1.0	0.6	1.1	1.0	HXT5.3f	orf19.2021	sugar transporter, 3-prime end
CA0244	0.9	1.1	1.0	1.0	1.0	1.0			
CA4655	0.9	1.5	0.5	0.9	0.6	0.8	IPF3098	orf19.4442	Putative mannosyltransferase (by homology)
CA3824	0.9	1.2	0.8	1.1	1.2	1.2	SKI8	orf19.5764	antiviral protein-like (by homology)
CA0136	0.9	1.1	1.1	1.0	1.0	1.1	IFH1.5f	orf19.1639	Dioxygenase (by homology)
CA2728	0.9	1.2	1.3	1.4	0.7	0.9	IPF10322	orf19.2117	putative mitochondrial carrier protein (by homology)
CA5806	0.9	1.0	1.1	1.0	0.9	1.0	IPF4149	orf19.5465	unknown function
CA2422	0.9	1.0	1.0	1.0	0.9	1.0	IPF14997.5f	orf19.4470	unknown function, 5-prime end
CA0285	0.9	1.1	1.0	1.0	0.9	1.0	IPF14392	orf19.1535	unknown function
CA6067	0.9	0.9	0.8	1.0	0.7	0.9	DYN1	orf19.5999	dynein heavy chain, cytosolic (by homology)
CA3315	0.9	1.1	1.6	1.5	1.0	1.0	IPF8814	orf19.2302	unknown function
CA5515	0.9	1.0	0.9	1.1	1.2	1.0	SAT2	orf19.5363	putative glycosyl-transferase involved in osmotolerance (by homology)
CA2929	0.9	1.0	1.0	1.0	0.9	1.1	IPF7838	orf19.4206	similar to Saccharomyces cerevisiae Mus81p involved in DNA repair, interacts with Rad54p (by homology)

CA6031	0.9	0.9	0.6	1.1	1.4	1.0	PRO1	orf19.7638	glutamate 5-kinase (by homology)
CA2847	0.9	0.6	4.0	1.3	1.1	1.2	NOG2	orf19.5733	unknown function Nuclear/Nucleolar GTP-binding protein, by homology
CA4413	0.9	0.9	1.2	0.9	0.7	1.0	MSH2	orf19.3093	DNA mismatch repair protein (by homology)
CA1797	0.9	0.6	0.6	0.8	0.6	0.9	NUM12	orf19.2924	nuclear migration protein (by homology)
CA0216	0.9	0.5	1.1	1.1	1.0	1.0	IPF11681	orf19.1682	unknown function
CA3766	0.9	0.5	0.7	0.9	0.7	0.8	IPF18298.3f	orf19.2903	unknown function, 3-prime end
CA0931	0.9	1.1	1.0	1.1	1.0	1.1	IPF3748	orf19.562	unknown function
CA0439	0.9	1.1	0.7	0.9	0.8	0.9	SCRC1	orf19.5569	unknown function
CA4273	0.9	0.9	1.0	1.0	0.8	0.9	CAC2	orf19.6670	Chromatin assembly complex, subunit p60 (by homology)
CA3851	0.9	1.0	1.0	0.8	1.0	1.0	CTA21	orf19.6112	transcriptional activation
CA3052	0.9	0.7	1.0	1.1	1.0	1.3	DPS1	orf19.2407	aspartyl-tRNA synthetase (by homology)
CA4158	0.9	0.9	0.9	0.9	0.7	1.6	DLD3	orf19.5805	D-lactate ferrycytochrome C oxidoreductase (by homology)
CA1475	0.9	0.7	1.0	1.2	1.0	1.0	GLE2	orf19.1095	nuclear pore complex structure and function-like protein (by homology)
CA4753	0.9	0.7	1.1	1.2	1.3	1.2	IDH1	orf19.4826	isocitrate dehydrogenase (NAD+) subunit1, mitochondrial (by homology)
CA3484	0.9	1.0	0.9	0.9	1.2	0.9	IPF3214	orf19.3574	HSP-mitochondrial chaperone (by homology)
CA1415	0.9	0.7	1.5	1.1	1.1	0.8	DBP2	orf19.171	ATP-dependent RNA helicase of DEAD box family
CA0349	0.9	0.9	0.7	1.0	0.4	0.5	IPF19026	orf19.1813	unknown function
CA4246	0.9	1.0	1.6	1.6	1.3	1.1	PGA20	orf19.535	unknown function
CA5631	0.9	0.7	1.1	1.0	1.2	1.1	GLN4	orf19.7064	glutaminyl-tRNA synthetase (by homology)
CA0681	0.9	1.1	1.0	1.1	1.0	1.0			
CA0578	0.9	0.9	0.6	0.7	1.2	0.6	IPF9605	orf19.3071	similar to Saccharomyces cerevisiae Mih1p M-phase inducing protein tyrosine phosphatase
CA5284	0.9	0.9	1.0	1.1	1.3	1.0	UFE1	orf19.7141	Endoplasmic reticulum t-SNARE (by homology)
CA1745	0.9	1.0	0.9	1.0	0.3	0.6	IPF10888	orf19.5051	unknown function
CA4179	0.9	0.6	1.0	1.0	0.9	0.9	TOM20	orf19.2953	mitochondrial outer membrane import receptor subunit, 20 kD (by homology)
CA5148	0.9	1.0	0.8	1.0	1.0	1.0	TFG1	orf19.4585	RNA pol.II transcription initiation factor TFIIF (by homology)
CA1323	0.9	1.0	1.0	1.0	1.0	1.1	IPF6675	orf19.1309	unknown function Unknown fnction
CA1903	0.9	1.0	0.9	1.0	1.2	1.0	IPF2754	orf19.2601.1	unknown function
CA5716	0.9	1.1	0.9	1.1	1.1	1.5	MED6	orf19.7420	RNA polymerase II transcriptional regulation mediator (by homology)
CA0777	0.9	1.1	0.5	0.6	1.3	1.8	IPF11777	orf19.4778	unknown function
CA4104	0.9	0.9	1.0	1.0	1.1	1.0	IPF20157	orf19.669	unknown function
CA5384	0.9	1.0	0.8	1.0	1.1	1.1	Zorro1b.5f	orf19.7274	reverse transcriptase, 5-prime end (by homology)
CA2814	0.9	0.9	1.4	1.3	1.3	1.2	IPF5607	orf19.2998	unknown function
CA2770	0.9	1.1	0.7	1.2	0.6	0.8	CPS1	orf19.2686	Carboxypeptidase YSCS precursor, second fragment (by homology)
CA4018	0.9	1.0	1.1	0.9	1.2	1.1	MOG1	orf19.3446	Ran-Binding Protein by homology
CA0725	0.9	1.0	1.0	1.1	1.2	0.9	IPF20063	orf19.1749	unknown function
CA0514	0.9	1.0	0.9	1.0	1.0	1.1	BEM1	orf19.4645	bud emergence mediator (by homology)
CA1396	0.9	1.0	1.1	0.9	1.0	0.9	IPF8075	orf19.3701	unknown function
CA2103	0.9	0.8	0.6	0.7	0.6	0.6	ISM1	orf19.2382	isoleucyl-tRNA synthetase (by homology)
CA1386	0.9	0.8	0.5	1.0	1.0	1.1	THR1	orf19.923	homoserine kinase
CA2164	0.9	0.9	0.9	0.8	0.7	0.6	AXL2	orf19.5292	similar to saccharomyces cerevisiae Axl2p required for axial pattern of budding (by homology)
CA3153	0.9	0.8	1.4	1.0	1.1	1.0	FRP2	orf19.6169	member of the FRP family of proteins related to Yarrowia lipolytica glyoxylate
CA5847	0.9	1.1	1.0	1.0	1.1	1.0	CDA2	orf19.7503	chitin deacetylase (by homology)
CA1856	0.9	1.0	1.9	1.0	1.2	1.8	IPF13689	orf19.1505	unknown function
CA4712	0.9	1.1	1.0	1.1	4.0	1.1	GTT1	orf19.6947	glutathione S-transferase (by homology)
CA5869	0.9	1.0	1.0	1.0	1.1	1.0	MIS12	orf19.7534	mitochondrial C1-tetrahydrofolate synthase precursor (by homology)
6532.20	0.9	0.9	0.6	0.8	2.3	2.1			

CA5300	0.9	1.0	1.1	1.1	1.2	1.0	IPF2189	orf19.7165	unknown function
CA4336	0.9	1.1	1.8	1.5	0.6	0.9	DDR48	orf19.4082	stress protein (by homology)
CA3920	0.9	0.9	1.0	1.0	1.0	1.0	SDS24	orf19.5118	Similar to S. cerevisiae YBR214w which presents strong similarity to hypothetical protein YGL056c
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 homology)
CA3192	0.9	1.1	0.8	1.3	1.1	1.0	IPF11598	orf19.2154	by homology to S. cerv.:hexokinase I
CA1599	0.9	1.0	0.9	1.0	1.5	0.9	IPF11452	orf19.268	unknown function
CA5805	0.9	1.1	0.9	1.2	1.0	1.1	IPF4153	orf19.5463	similar to Saccharomyces cerevisiae Sec6p protein involved in Golgi to plasma membrane protein transport
CA0179	0.9	1.1	0.9	1.0	1.1	1.1	DCP1	orf19.423	mRNA decapping enzyme (by homology)
CA4085	0.9	1.1	0.6	0.9	1.3	1.0	IPF5015	orf19.6641	unknown function
CA3157	0.9	1.4	1.0	1.3	1.5	1.7	IPF14456	orf19.1588	unknown function Unknown function
CA5279	0.9	1.4	1.0	1.0	0.8	0.8	SYS1	orf19.7128	Similar to ypt6 suppressor in S. cerevisae (by homology)
CA2714	0.9	1.0	0.6	1.0	1.1	1.0	IFF2	orf19.575	unknown function
CA5639	0.9	0.8	0.8	1.0	0.9	0.9			
CA4880	0.9	1.0	1.2	0.9	0.3	0.6	RHC18	orf19.6568	Recombination repair protein (by homology)
CA5626	0.9	1.1	0.9	1.0	1.1	1.5	IPF498	orf19.7071	unknown function
CA1781	0.9	1.0	1.5	1.0	1.7	0.8	IPF14508	orf19.1828	unknown function
CA1514	0.9	1.0	0.8	1.1	1.1	1.0	IPF7539	orf19.4886	unknown function
CA5209	0.9	0.9	1.4	1.2	0.4	0.6	MCM1	orf19.7025	Transcription factor of the MADS box (by homology)
CA1645	0.9	0.8	1.0	0.9	0.6	0.6	PMC1	orf19.1727	Ca2+-transporting P-type ATPase (by homology)
CA5620	0.9	1.1	0.7	1.0	0.9	1.0	IPF511	orf19.7078	unknown function
CA5754	0.9	0.9	0.6	0.9	1.3	0.8			
CA3905	0.9	1.3	0.8	1.0	1.0	1.3	IPF19792.5f	orf19.4398	unknown function, 5-prime end
CA6046	0.9	1.0	1.1	1.0	1.1	1.1	IPF4931	orf19.7662	unknown function
CA3413	0.9	1.0	1.1	1.0	0.9	1.0	IPF9239	orf19.6142	unknown function
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 homology)
CA1559	0.9	0.9	1.1	1.0	0.9	1.2	IPF16533	orf19.1708	unknown function
CA2844	0.9	1.1	0.6	1.0	1.2	1.1	IPF13158	orf19.5729	unknown function
CA5726	0.9	0.9	1.0	1.0	2.0	1.1	AAF1	orf19.7436	Adhesion and aggregation mediating surface antigen
CA2355	0.9	1.2	0.9	0.8	2.2	1.4	TPK1	orf19.4892	cAMP-dependent protein kinase 2 (by homology)
CA5701	0.9	0.7	1.2	0.8	0.5	0.7	ISW2	orf19.7401	Chromatin remodeling complex (by homology)
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) by homology
CA1042	0.9	0.9	0.9	0.9	0.8	0.9	IPF18784	orf19.2506	unknown function
CA3717	0.9	0.9	0.8	0.9	0.8	0.9	IPF6192	orf19.4167	unknown function
CA1457	0.9	1.1	0.9	1.0	0.9	1.0	IPF8287	orf19.612	unknown function
CA5623	0.9	1.0	0.9	1.0	1.0	1.0	IPF502	orf19.7074	unknown function
CA2321	0.9	1.2	0.9	1.0	1.8	1.0	MEC3	orf19.5485	G2-specific checkpoint protein (by homology)
CA4124	0.9	0.9	1.2	1.1	1.0	1.0	PGA59	orf19.2767	unknown function
CA5163	0.9	1.0	1.0	1.0	1.0	1.0	TFC1	orf19.4601	Transcription initiation factor TFIIIC 95 kD subunit (by homology)
CA3532	0.9	1.1	1.0	1.0	1.1	1.1	IPF13448	orf19.6365	similar to Saccharomyces Ptp1p protein tyrosine phosphatase (by homology)
CA3603	0.9	0.5	0.9	0.6	0.5	0.7	MEF1	orf19.4932	mitochondrial translation elongation factor G (by homology)
CA1054	0.9	0.8	1.1	1.0	1.1	1.0	SAS3	orf19.2540	silencing protein (by homology)
CA6080	0.9	1.0	0.8	0.9	1.2	1.1	IPF21	orf19.5980	unknown function
CA4002	0.9	1.0	1.2	0.9	1.0	0.8	IPF4258	orf19.1634	unknown function
CA1286	0.9	0.9	1.2	1.0	0.9	0.9	IPF5546	orf19.4428	unknown function
CA0778	0.9	0.8	0.6	0.3	3.2	2.7	IPF12884	orf19.4779	unknown function
CA3524	0.9	1.3	0.9	0.9	1.1	0.9	LKH1.3f	orf19.992	PROBABLE LEUKOTRIENE A-4 HYDROLASE (LTA-4 HYDROLASE) (LEUKOTRIENE A(4) HYDROLASE),

CA0498	0.9	1.1	1.0	1.0	0.9	1.0	CTA211.3f	orf19.2661	transcriptional activator, 3-prime end (by homology)
CA3145	0.9	1.3	0.8	1.1	0.8	0.8	CDC9	orf19.6155	DNA ligase (by homology)
CA0648	0.9	1.0	1.0	1.1	1.0	1.0	IPF12399	orf19.3210	unknown function
CA3785	0.9	0.7	1.1	0.9	0.5	0.8	IPF19788	orf19.5834	similar to Saccharomyces cerevisiae Sxm1p putative beta-karyopherin (by homology)
CA4895	0.9	1.1	1.3	1.0	0.8	1.3	IPF18161	orf19.6587	unknown function
CA3029	0.9	1.0	0.6	0.9	1.7	1.1	IPF13825	orf19.223	serine/threonine protein kinases (by homology)
CA5119	0.9	1.0	0.8	1.0	0.8	0.6	IPF1320	orf19.6411	unknown function
CA5972	0.9	0.8	1.8	1.0	1.5	1.2	GNP1	orf19.7566	high affinity glutamine permease (by homology)
CA5452	0.9	1.2	0.7	1.0	0.8	0.8	SEC11	orf19.3259	signal peptidase subunit (by homology)
CA1934	0.9	0.9	0.9	1.0	1.0	0.8			
CA1240	0.9	1.0	1.2	1.0	0.8	1.0	IPF14026	orf19.718	similar to Saccharomyces cerevisiae Rrn11p involved in RNA polymerase I specific transcription (by homology)
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 homology)
CA4802	0.9	0.8	0.9	1.0	0.7	1.0	ILV3	orf19.4040	dihydroxyacid dehydratase (by homology)
CA5447	0.9	1.0	1.3	1.0	0.8	0.9	IPF234	orf19.3250	similar to Saccharomyces cerevisiae Prp40p splicing factor (by homology)
CA3548	0.9	1.0	1.0	1.1	0.4	0.8	IPF12179	orf19.3872	unknown function
CA5244	0.9	1.0	1.3	0.9	1.0	1.2	IPF3043	orf19.5019	unknown function
CA1291	0.9	0.7	1.6	1.2	0.9	1.1	IPF16752	orf19.2711	unknown function
CA1675	0.9	1.0	0.9	1.0	1.3	1.3	IPF5192	orf19.3615	unknown function
CA3661	0.9	1.0	1.0	1.0	1.1	1.0	IPF17991	orf19.6465	unknown function
CA5949	0.9	1.1	0.8	1.2	1.8	1.4	IPF3498	orf19.6747	unknown function
CA5833	0.9	0.9	1.2	1.1	1.2	1.5	IMP3	orf19.7488	U3 small nucleolar ribonucleoprotein (by homology)
CA2713	0.9	1.0	1.0	1.0	1.1	1.0	IFF8	orf19.570	unknown function
CA2593	0.9	0.8	2.1	1.1	1.1	1.1	RRP6	orf19.58	involved in 5.8S rRNA processing (by homology)
CA1720	0.9	1.0	0.9	1.1	0.9	1.0	PGA53	orf19.4651	unknown function unknown function
CA1028	0.9	1.0	1.0	1.0	0.9	0.9	IPF6488	orf19.1539	unknown function
CA3491	0.9	0.6	1.5	1.1	1.3	1.4	RPC40	orf19.3564	RNA polymerase (by homology)
CA0177	0.9	1.1	1.0	1.1	1.1	0.9	IFL2	orf19.555	unknown function
CA2017	0.9	0.9	0.5	0.7	0.7	0.6	IPF3414	orf19.846	putative serine/threonine protein kinase
CA5905	0.9	1.0	0.8	0.9	0.9	1.0	RPD32	orf19.6801	histone deacetylase B (by homology)
CA5070	0.9	1.2	1.0	1.1	0.9	1.2	IPF3594	orf19.3043	triglyceride lipase (by homology)
CA3179	0.9	0.7	0.9	1.1	0.9	0.9	YLF2	orf19.2128	GTP-binding protein
CA5988	0.9	0.8	0.9	1.0	1.1	0.8	IPF693	orf19.7588	unknown function
CA0055	0.9	1.3	1.2	1.0	0.7	0.9	IPF12442	orf19.3414	unknown function
CA5430	0.9	1.0	0.9	1.0	1.0	1.0	IPF191	orf19.3232	putative permease (by homology)
CA1172	0.9	1.1	1.2	0.9	1.0	1.0	RGT1	orf19.2747	Regulator of glucose-induced genes (by homology)
CA4511	0.9	0.9	1.3	1.0	0.8	1.0	IPF8966	orf19.494	unknown function
CA0867	0.9	0.9	1.1	1.0	1.1	0.9	IPF14773.3f	orf19.3586	unknown function, 3-prime end
CA0590	0.9	0.6	1.0	0.9	2.8	3.6	IPF13079	orf19.1163	unknown function
CA1582	0.9	0.8	1.1	0.8	0.8	0.9	CLN21	orf19.6028	G1 cyclin (by homology)
CA1933	0.9	1.0	1.0	0.9	1.0	1.0	IPF18586	orf19.761	Unknown function
CA4415	0.9	1.0	1.1	1.1	0.6	0.8			
CA4014	0.9	1.0	1.1	1.0	1.2	0.8	CTK1	orf19.1619	probable cell division protein kinase
CA2015	0.9	1.1	1.1	1.0	0.9	1.1	PGA16	orf19.848	Hypothetical protein unknown function
CA0730	0.9	0.7	1.2	1.1	1.6	1.5	IPF7334	orf19.3724	unknown function
CA0927	0.9	1.3	2.7	1.1	7.1	2.1	IPF11332	orf19.3661	unknown function
CA2153	0.9	1.0	1.0	1.0	0.8	1.0	IPF7900	orf19.6025	unknown function

CA6027	0.9	1.1	0.8	1.0	0.8	1.0	IPF609	orf19.7632	unknown function
CA1443	0.9	0.8	1.5	1.0	1.1	1.1	IPF4776	orf19.4492	unknown Function
CA1694	0.9	0.8	2.6	1.1	0.5	0.9	TRM3	orf19.5038	2 -O-ribose methyltransferase (by homology)
CA4046	0.9	1.1	0.8	1.0	1.1	1.0	IPF9205	orf19.3677	similar to Saccharomyces cerevisiae Apg5p involved in autophagy and nutrient starvation (by homology)
CA5955	0.9	1.1	0.6	0.8	0.8	0.8	IPF3510	orf19.6739	unknown function
CA1951	0.9	0.9	0.4	0.8	1.0	0.7	HEM14	orf19.4747	Mitochondrial protoporphyrinogen oxidase (by homology)
CA5039	0.9	1.0	1.4	1.5	1.0	1.2	GAP2	orf19.6993	general amino acid permease (by homology)
CA1570	0.9	0.9	0.7	1.1	0.7	0.6	IPF7617	orf19.1160	unknown function
CA4945	0.9	1.0	1.0	1.0	0.9	1.3	FLX1	orf19.6532	MITOCHONDRIAL FAD CARRIER by homology
CA5790	0.9	1.0	1.4	1.2	1.7	1.6	IPF1144	orf19.5439	unknown function
CA5261	0.9	0.9	1.3	0.8	1.0	1.2	IPF1805	orf19.5003	unknown function
CA1749	0.9	1.0	0.7	0.9	0.3	0.7	IPF8257.3f	orf19.1518.3	unknown function, 3-prime end
CA2282	0.9	1.0	1.0	0.9	1.0	1.0	IPF14438	orf19.5549	unknown function
CA5322	0.9	1.7	0.8	1.5	0.5	0.4	PRB1	orf19.7196	Protease B, vacuolar (by homology)
CA3067	0.9	1.0	0.8	1.0	0.8	1.1	IPF15811	orf19.4280	unknown function
CA3972	0.9	1.0	1.0	0.9	1.1	1.1	IPF6504	orf19.1544	unknown function
CA2430	0.9	1.3	1.1	1.0	1.5	1.0	IPF12950	orf19.3402	unknown function
CA3450	0.9	0.9	0.9	1.0	1.3	1.4	PDE2	orf19.2972	Nucleotide phosphodiesterase
CA3600	0.9	1.0	0.8	0.8	0.6	0.7	SPC3	orf19.4930	signal peptidase subunit (by homology)
CA4654	0.9	1.1	1.0	1.0	1.3	1.2	IPF3101	orf19.4441	unknown function
CA3046	0.9	0.9	1.2	0.8	0.4	0.6	IPF7295	orf19.2417	unknown function
CA1655	0.9	1.0	1.5	0.9	1.5	0.8	CCC2	orf19.4328	putative copper-transporting ATPase (by homology)
CA5892	0.9	1.0	1.1	1.1	1.0	1.0	GAP1	orf19.6814	Glyceraldehyde-3-phosphate dehydrogenase
CA5015	0.9	1.0	1.1	1.0	0.9	0.8	IPF11118	orf19.6967	unknown function
CA2503	0.9	1.1	0.9	1.0	1.0	1.1	IPF6803.5f	orf19.5592	unknown function, 5-prime end
CA3855	0.9	1.0	1.0	1.0	1.0	0.9	IPF4645	orf19.6103	unknown Function
CA5292	0.9	0.5	2.7	1.4	0.9	1.1	IPF1948	orf19.7154	unknown function
CA2801	0.9	0.6	1.0	0.9	0.9	0.9	URA3	orf19.1716	orotidine-5 -monophosphate decarboxylase [Candida albicans]
CA5099	0.9	1.1	0.9	1.0	0.8	1.0	PRP8	orf19.6442	U5 snRNP protein, pre-mRNA splicing factor (by homology)
CA4674	0.9	0.8	0.7	1.3	1.2	1.1	HEM2	orf19.898	Porphobilinogen synthase (by homology)
CA5672	0.9	1.0	1.0	1.0	1.2	1.5	IPF1271	orf19.7375	Small nuclear ribonucleoprotein (by homology)
CA3340	0.9	1.0	2.5	1.0	0.7	1.0	ADA2	orf19.2331	general transcriptional adaptor or co-activator (by homology)
CA4858	0.9	0.9	1.1	1.1	1.0	1.1	IPF15927.3f	orf19.3831	similar to Saccharomyces cerevisiae Tfc3p transcription initiation factor TFIIIC, 3-prime end (by homology)
CA4432	0.9	1.0	0.9	0.8	0.5	0.8	IPF5574	orf19.5163	unknown function
CA1760	0.9	0.9	0.9	1.0	1.0	1.0	IPF17914.3	orf19.5124	unknown function
CA3628	0.9	1.5	0.8	0.9	1.3	1.1			
CA0138	0.9	1.0	1.2	1.1	1.2	1.0			
CA3129	0.9	1.0	1.1	1.0	0.9	0.9	OST4	orf19.1360.1	oligosaccharyltransferase subunit
CA1417	0.9	0.6	1.9	1.2	1.2	1.4	IPF16126	orf19.172	similar to Saccharomyces cerevisiae Rpc19p DNA-directed RNA polymerase I,III 16 KD subunit (by homology)
CA0118	0.9	0.9	1.0	1.1	1.1	1.0	IPF16430	orf19.913.2	similar to Saccharomyces cerevisiae Qcr6p ubiquinol-cytochrome-c reductase 17K protein (by homology)
CA0152	0.9	0.8	0.9	1.0	1.4	1.1	IPF16368.3f	orf19.254	unknown function, 3-prime end
CA0063	0.9	1.0	1.0	1.0	1.0	1.0	IPF19310.3f	orf19.617.3	unknown function, 3-prime end
2566.20	0.9	1.0	0.4	0.9	1.1	1.1			
CA1916	0.9	1.0	1.0	1.0	1.2	1.0	IPF16566.3	orf19.2439.1	unknown function,
CA1053	0.9	0.7	0.8	0.7	0.3	0.5	SCW11.3eo	orf19.3893	glucanase gene family member, 3-prime end (by homology)
CA5685	0.9	0.5	1.8	1.0	0.9	0.9	HPA1	orf19.7387	RNA polymerase II-associated Histone acetyltransferase (by homology)

CA3328	0.9	0.9	0.9	1.1	1.0	1.0	IPF10564	orf19.2671	unknown function
CA5603	0.9	1.0	0.4	0.7	0.8	0.7	IPF553	orf19.7096	unknown function
CA0576	0.9	1.8	0.4	0.8	1.4	1.0	NPR1	orf19.6232	nitrogen permease reactivator protein (by homology)
CA1888	0.9	1.0	0.9	0.9	1.0	0.9	IPF18594	orf19.2202	unknown function
CA4935	0.9	1.1	0.9	1.1	0.9	1.0	VPS29	orf19.6076	vacuolar protein sorting protein (by homology)
CA5100	0.9	1.5	0.5	0.8	1.1	0.8	IPF1372	orf19.6440	unknown function
CA1729	0.9	0.9	0.9	1.1	1.4	1.1	IPF8440	orf19.6496	similar to Saccharomyces cerevisiae Trs33p TRAPP subunit of 33 kDa involved in targeting and fusion of ER
CA1057	0.9	0.8	1.2	1.1	0.9	1.1	IPF17031	orf19.2544	unknown function
CA5696	0.9	1.0	1.6	1.3	1.4	1.7	IPF3309.3e	orf19.7398	unknown function, 3-prime end
CA0941	0.9	1.0	0.8	1.0	1.3	1.6	IPF8617	orf19.3705	unknown function
CA3378	0.9	1.0	1.0	1.0	1.0	1.3	RUB1	orf19.330.1	ubiquitin-like protein (by homology)
CA6023	0.9	0.9	1.0	1.2	1.2	1.2	CDC33	orf19.7626	translation initiation factor eIF4E, cap binding protein
CA5280	0.9	0.9	1.0	1.0	1.0	1.1	IPF1899	orf19.7131	unknown function
CA5347	0.9	1.1	1.0	1.0	1.0	1.4	IPF864	orf19.7222	unknown function
CA4903	0.9	1.2	1.1	1.1	1.6	1.0	SNF7	orf19.6040	Class E Vps protein (by homology)
CA0649	0.9	0.9	0.9	1.2	0.9	1.0	RFC3	orf19.3211	DNA replication factor C, 40 kDa subunit (by homology)
CA0066	0.9	1.1	0.9	0.9	0.9	0.9	IPF15051	orf19.1258	unknown function
CA2327	0.9	1.0	1.0	1.0	0.7	0.7	IPF4782	orf19.4496	probable membrane protein (by homology)
CA4785	0.9	0.9	1.2	0.8	0.8	0.9	IPF3361	orf19.4018	putative mitochondrial ribosomal protein S7 (by homology)
CA5278	0.9	1.0	1.0	1.0	1.2	1.1	CTA29.3f	orf19.7127.1	Protein with putative transcription activation domain, 3-prime end
CA2501	0.9	1.1	0.9	1.0	1.3	1.0	IPF6812	orf19.5587	unknown function
CA1605	0.9	1.0	1.5	1.1	0.5	0.9	SWI6	orf19.4725	Transcription factor (by homology)
CA3083	0.9	1.2	1.2	1.1	0.7	1.0	IPF11262	orf19.4150	unknown function
CA3262	0.9	1.1	0.9	1.0	0.9	0.9	UBR11.3f	orf19.2695	ubiquitin-protein ligase, 3-prime end (by homology)
CA2373	0.9	0.5	1.0	1.0	1.1	1.1	CBF5	orf19.1833	centromere/ microtubule binding protein
CA0747	0.9	1.0	0.8	0.8	0.7	0.9	SNF2	orf19.1526	component of SWI/SNF global transcription activator complex (by homology)
CA2613	0.9	0.6	1.0	0.9	0.7	0.9	IPF5446	orf19.5698	putative ribosomal protein (by homology)
CA0206	0.9	1.0	1.7	1.1	1.0	1.0	IPF14089	orf19.2781	putative serine/threonine protein kinase
CA5297	0.9	0.9	1.3	1.2	1.5	1.2	YAR1	orf19.7160	Ankyrin repeat-containing protein (by homology)
CA4003	0.9	0.7	2.6	1.5	0.9	0.9	IPF4257	orf19.1633	unknown function
CA6081	0.9	1.1	1.0	1.0	1.2	1.0	IPF24	orf19.5978	reductase (by homology)
CA3568	0.9	1.0	1.3	0.9	1.2	0.8	IPF7804.3f	orf19.3135	unknown function, 3-prime end
CA5960	0.9	0.8	0.8	0.8	0.6	0.7	PMT5	orf19.7549	protein mannosyltransferase (by homology)
CA4480	0.9	1.7	0.7	1.1	1.5	1.4	IPF6464	orf19.1887	putative triacylglycerol lipase (by homology)
CA1624	0.9	0.9	1.0	0.9	0.9	0.8	IPF10055	orf19.467	unknown function
CA0568	0.9	1.1	0.8	1.0	1.3	1.0	APS2	orf19.1136	AP-2 complex subunit, sigma2 subunit, 17KD (by homology)
CA5584	0.9	1.1	1.6	1.0	0.7	0.8	SAC7	orf19.7115	GAP for RHO1 by homology
CA2324	0.9	0.9	1.3	0.9	0.5	0.4	CDC46	orf19.5487	cell division control protein (by homology)
CA2921	0.9	0.9	1.1	1.1	1.0	1.1	IPF17037	orf19.4214	unknown function
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)
CA3799	0.9	0.7	1.1	0.9	0.7	0.9	IPF7198	orf19.2478	unknown function
CA0087	0.9	1.2	1.9	0.9	1.0	0.6	SMF11	orf19.4690	manganese transporter (by homology)
CA1963	0.9	0.8	0.8	0.9	1.0	0.9	IPF14040	orf19.2397	probable transporter (by homology)
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)
CA2615	0.9	1.0	1.0	1.0	1.0	1.0	CTA241.5f	orf19.5700	transcriptional activator, 5-prime end
CA4706	0.9	1.1	1.0	1.0	0.8	0.8	RAD53	orf19.6936	protein kinase

CA4331	0.9	1.2	1.1	0.9	0.9	1.1	IPF2086	orf19.4089	unknown function
CA3188	0.9	1.0	1.1	1.0	0.6	0.7	IPF11610	orf19.2146	similar to Saccharomyces cerevisiae Hat2 subunit of the major yeast histone acetyltransferase (by homology)
CA1808	0.9	1.2	1.1	0.9	1.0	1.5	GUK1	orf19.1115	Guanylate kinase (by homology)
CA0664	0.9	0.6	1.1	1.2	1.0	1.0	LSC2.3eoc	orf19.710	succinate-CoA ligase beta subunit, 3-prime end (by homology)
CA2901	0.9	1.0	1.0	1.0	1.0	1.0	PUS1	orf19.3477	pseudouridine synthase 1 (by homology)
CA5978	0.9	0.9	0.8	1.0	0.8	1.0	SPT7	orf19.7572	transcription factor, member of the histone acetyltransferase SAGA complex (by homology)
CA2385	0.9	1.0	1.0	1.0	0.8	0.7	RSR1	orf19.2614	GTP-binding protein
CA1134	0.9	0.9	0.8	0.9	0.7	0.9	IPF2702	orf19.2163	unknown function
CA0631	0.9	2.0	1.1	0.8	4.2	4.5	IPF11698.5f	orf19.4338	similar to Saccharomyces cerevisiae Esbp6p probable monocarboxylate permease, 5-prime end (by homology
CA3924	0.9	0.8	1.1	1.3	1.1	1.1	TKL1	orf19.5112	transketolase 1
CA0624	0.9	1.0	1.2	0.9	1.3	0.8	IPF312	orf19.3154	unknown function
CA3677	0.9	1.2	1.0	1.1	1.3	1.5	SOU3	orf19.732	putative sorbitol utilization protein (by homology)
CA4700	0.9	1.0	1.0	1.0	2.3	1.6	SAP9	orf19.6928	aspartyl proteinase 9 (by homology)
CA2893	0.9	0.9	1.0	1.0	2.8	1.2	IFS3	orf19.2463	Unknown function
CA0519	0.9	0.9	0.8	0.9	0.7	0.9	MRPL10.3	orf19.3532	ribosomal protein, 3-prime end (by homology)
CA4781	0.9	1.1	0.7	0.8	0.7	0.6	IPF3355	orf19.4014	similar to Saccharomyces cerevisiae Cdc1 cell cycle protein involved in ion homeostasis (by homology)
CA1724	0.9	1.0	1.0	0.9	0.9	1.0	MRP10	orf19.2650.1	Mitochondrial ribosomal protein (by homology)
CA3421	0.9	1.0	0.9	1.0	1.2	1.0	IPF19782	orf19.6135	unknown function
CA0913	0.9	1.1	0.8	1.1	0.6	0.8	IPF14810	orf19.2016	unknown function
CA0299	0.9	1.0	0.9	1.0	1.1	1.0	IPF3765.3e	orf19.1597	unknown function
CA1552	0.9	1.1	0.9	1.0	0.7	1.0	PUT1	orf19.4274	proline oxidase (by homology)
CA4521	0.9	0.9	1.2	0.8	0.6	0.9	MRPL40	orf19.484	Putative mitochondrial ribosomal protein (by homology)
CA3744	0.9	1.0	0.9	1.0	0.9	1.0	RAD57	orf19.2174	DNA-repair like protein
CA2729	0.9	3.2	1.0	1.1	0.9	0.7	NAT2	orf19.2116	N-acetyltransferase for N-terminal methionine (by homology)
CA5492	0.9	0.6	1.0	1.1	0.9	1.0	GCN1.3f	orf19.5328	translational activator, 3-prime end (by homology)
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 export (by homology)
CA5097	0.9	0.8	1.7	1.1	0.9	1.1	IPF1382	orf19.6444	unknown function
CA0399	0.9	1.0	0.7	0.8	0.8	0.7	CDC45	orf19.1988	Chromosomal DNA replication initiation protein (by homology)
CA4846	0.9	1.3	1.1	1.1	1.1	1.2	IPF6945.3f	orf19.3814	unknown function, 3-prime end
CA5085	0.9	0.9	1.1	1.0	1.0	1.0			
CA5710	0.9	1.0	1.0	1.0	0.9	1.3	OAC1	orf19.7411	Mitochondrial oxaloacetate transport protein (by homology)
CA3715	0.9	0.9	1.0	0.9	1.2	1.2	IPF6205	orf19.4164	unknown function
CA0835	0.9	1.0	0.8	1.0	0.8	0.9	IPF12498.5	orf19.1677.1	unknown function, internal fragment
CA0111	0.9	1.0	1.0	1.0	1.1	1.1	IPF16830	orf19.4151	similar to Saccharomyces cerevisiae Spo1p transcriptional regulator involved in sporulation (by homology)
CA0316	0.9	1.0	1.2	0.9	14.1	2.0	ALS1	orf19.5741	agglutinin-like protein
CA2035	0.9	1.4	2.0	1.0	0.7	0.9	SGD1	orf19.4363	involved in the HOG pathway (by homology)
CA1226	0.9	1.1	1.1	0.9	0.4	0.7	IPF15660	orf19.4159	putative mitochondrial carrier (by homology)
CA1787	0.9	1.0	0.9	1.1	3.6	1.0	IFH3	orf19.1167	Dioxygenase (by homology)
CA1589	0.9	0.9	1.1	1.0	0.8	1.1			
CA0181	0.9	0.8	1.1	0.8	0.8	0.9	NOT3	orf19.2012	GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION, SUBUNIT 3 (by homology)
CA2229	0.9	1.1	0.9	1.0	0.8	0.9	IPF5682	orf19.5814	unknown function
CA5561	0.9	1.1	0.6	0.7	0.8	1.0	SCO1	orf19.7325	Inner mitochondrial membrane protein (by homology)
CA3720	0.9	0.9	0.8	1.0	0.9	1.0	IFL3	orf19.4170	unknown function
CA1201	0.9	1.0	0.9	1.1	0.9	1.0	IPF19906	orf19.4869	unknown function
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)
CA2401	0.9	1.1	0.9	1.2	0.8	0.8	LEM3	orf19.3542	cell division cycle mutant (by homology)

CA1818	0.9	1.0	1.3	0.9	0.5	1.0	IPF7023.3f	orf19.134	unknown function, 3-prime end
CA2028	0.9	0.9	1.0	0.8	0.9	0.9			
CA1984	0.9	1.3	2.5	1.1	0.8	0.7	IPF9592	orf19.90	unknown function
CA3389	0.9	0.9	1.0	1.0	1.3	1.0	IPF6754	orf19.319	unknown function
CA0703	0.9	1.0	0.7	0.9	1.0	1.2	IPF11807	orf19.2914	unknown function
CA4082	0.9	1.3	0.5	0.8	1.3	0.7	PTC4	orf19.6638	ser/thr protein phosphatase PP2C(by homology)
CA0040	0.9	0.8	0.9	0.9	0.8	0.9	IPF15632	orf19.3469	unknown function
CA2079	0.9	0.5	0.7	0.8	0.4	0.5	MNN3	orf19.4874	Golgi alpha-1,2-mannosyltransferase (by homology)
CA3205	0.9	1.1	0.7	1.0	0.9	0.9	IPF3448	orf19.6185	Unknown function
CA4916	0.9	0.9	0.8	1.0	1.4	1.3	IPF1425	orf19.6056	Hypothetical phosphoglycerate mutase (by homology)
CA2649	0.9	1.0	0.5	1.0	3.3	2.1	IPF9057	orf19.1189	unknown function
CA3348	0.9	0.9	2.4	1.2	0.7	1.2	RIO1	orf19.2320	unknown function
CA3138	0.9	1.1	1.0	1.0	1.0	1.0	SAP2	orf19.3708	aspartic protease
CA5059	0.9	0.9	0.8	1.0	1.2	1.2	IPF3691	orf19.3027	unknown function
CA4302	0.9	0.4	0.9	0.9	0.9	1.1	DED81	orf19.6702	Asparaginyl-tRNA synthetase (by homology)
CA2288	0.9	0.8	0.7	0.9	1.0	0.9	IPF5376	orf19.5557	unknown function
CA5275	0.9	1.0	0.8	0.9	0.9	1.0	IPF1760.3f	orf19.4984	unknown function
CA6056	0.9	1.0	1.0	1.0	1.3	0.9	IPF4955	orf19.7675	similar to Saccharomyces cerevisiae Mrpl25p ribosomal protein YmL25, mitochondrial (by homology)
CA5567	0.9	0.9	0.8	1.0	1.5	1.0	FCY24	orf19.7331	Putative purine-cytosine transport protein
CA3943	0.9	1.0	1.0	1.1	1.0	1.1	IPF4751	orf19.1999	unknown Function
CA5898	0.9	0.8	0.7	0.7	1.1	0.9	IPF2383	orf19.6808	unknown function
CA2445	0.9	0.9	1.1	1.1	1.1	0.9	IPF13885	orf19.5503	unknown function
CA1096	0.9	1.0	1.1	1.0	0.9	1.0	IPF7578	orf19.4366	unknown function
CA4740	0.9	0.9	1.2	1.1	1.1	1.1	IPF4497	orf19.4844	unknown function
CA5593	0.9	1.1	1.1	1.1	1.6	1.2	IPF5615	orf19.7107	unknown function
CA3314	0.9	1.0	1.2	1.1	0.8	0.9	IPF8812	orf19.2303	unknown function
CA3572	0.9	1.1	1.0	1.0	1.0	1.0			
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)
CA2312	0.9	0.9	0.9	0.9	1.0	1.0	IPF16498	orf19.1377	similar to Saccharomyces cerevisiae Arg82p arginine metabolism transcription factor
CA0949	0.9	1.1	0.9	1.0	0.9	1.1	IPF10269	orf19.1273	Gim complex component-like by homology
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)
CA5549	0.9	1.0	1.0	0.9	0.8	1.1	ERG13	orf19.7312	3-hydroxy-3-methylglutaryl coenzyme A synthase (by homology)
CA4243	0.9	1.1	0.6	0.9	0.8	0.9	IPF16491	orf19.529	unknown function
CA5712	0.9	1.1	0.9	1.1	1.0	1.2	IPF2657	orf19.7413	unknown function
CA1087	0.9	1.1	0.9	1.0	1.2	0.8	MYO5	orf19.738	Myosin I (by homology)
CA5416	0.9	0.9	1.0	1.3	1.2	1.2	IPF1576	orf19.966	unknown function
CA4699	0.9	1.2	0.8	1.1	1.4	1.3	IPF4220	orf19.6927	similar to Saccharomyces cerevisiae Pep8p involved in vacuolar protein sorting/targeting (by homology)
CA3994	0.9	0.7	1.1	1.4	0.7	0.9	ERG7	orf19.1570	lanosterol synthase
CA5423	0.9	1.0	0.7	1.0	0.4	0.5	ROT2	orf19.974	Glucosidase II, catalytic subunit (by homology)
CA5990	0.9	0.4	1.5	0.8	0.8	0.8	IPF690.5f	orf19.7590	NADH dehydrogenase (ubiquinone) 78K chain precursor, 5-prime end (by homology)
CA2082	0.9	1.1	0.9	1.1	1.0	1.0	NTF2	orf19.4879.2	nuclear transport factor (by homology)
CA4765	0.9		1.1	1.1	1.0	1.0	ADH1	orf19.3997	alcohol dehydrogenase (by homology)
CA5234	0.9	1.0	0.9	1.0	1.2	1.1	IPF3014	orf19.5030	weak similarity to S. cerevisiae DOS2 involved in genome stability
CA5469	0.9	1.1	0.6	0.9	1.1	1.0	IPF298	orf19.3281	unknown function
CA4792	0.9	0.9	1.0	1.1	1.1	1.3	HIS1	orf19.4026	ATP phosphoribosyltransferase
CA0956	0.9	1.1	1.1	1.2	0.8	0.9	IPF14914.5f	orf19.4728	putative ankyrin, 5-prime end (by homology)

CA2569	0.9	0.7	1.1	1.2	0.8	1.0	IPF12117	orf19.5648	unknown function
CA3575	0.9	0.9	0.9	1.0	0.9	1.0	IPF11108	orf19.2265	unknown function
CA2156	0.9	3.0	3.7	12.9	1.0	4.2	PGA31	orf19.5302	unknown function
CA4394	0.9	0.7	0.8	0.9	0.9	0.7	IPF12297	orf19.3117	mycelial surface antigen (by homology)
CA1091	0.9	1.0	1.0	0.9	1.1	0.9	SPT4	orf19.3947	transcription elongation protein (by homology)
CA2436	0.9	1.1	0.9	1.0	0.6	0.7	IPF5500	orf19.2200	unknown function
CA3555	0.9	1.0	1.0	1.1	1.1	1.1	IPF7766	orf19.3884	unknown function
CA3124	0.9	0.9	1.1	1.0	0.6	0.8	IPF5353	orf19.3003	unknown function,
CA0301	0.9	1.0	1.0	1.0	0.8	1.0	IPF19688	orf19.1606	unknown function
CA3041	0.9	0.9	1.1	0.9	0.9	0.8	IPF7303	orf19.2423	unknown function
CA5368	0.9	0.9	1.1	0.9	1.1	1.0	IPF5257	orf19.7250	unknown function
CA3065	0.9	0.7	1.1	0.9	0.6	0.8	IPF19775	orf19.4282	unknown function
CA0733	0.9	0.5	1.3	0.8	0.7	0.8	NIP1	orf19.4635	translation initiation factor subunit
CA4372	0.9	0.8	0.6	0.9	0.8	1.0	IPF5282	orf19.5663	unknown function
CA5071	0.9	1.0	0.8	1.0	0.9	1.1	IPF3597	orf19.3045	similar to Saccharomyces cerevisiae Ald4p mitochondrial aldehyde dehydrogenase (by homology)
CA3989	0.9	0.9	1.1	1.2	0.8	1.0	IPF7147	orf19.1565	unknown function
CA1864	0.9	1.1	1.1	1.0	0.8	0.9	IPF7644	orf19.862	unknown function
CA0238	0.9	0.8	1.1	1.0	1.1	1.0	PHA2.3	orf19.234	prephenate dehydratase, 3-prime end (by homology)
CA0965	0.9	0.9	1.0	0.9	2.9	1.0	IPF9139	orf19.6248	unknown function
CA1831	0.9	0.7	0.7	1.1	0.4	0.5	CHS1	orf19.5188	Chitin synthase (by homology)
CA3514	0.9	0.6	1.1	0.8	0.7	0.8	IPF11245	orf19.6362	similar to Saccharomyces cerevisiae Spa2p involved in cell polarity (by homology)
CA5608	0.9	1.1	0.9	0.9	1.5	1.2	IPF539	orf19.7092	unknown function
CA1634	0.9	1.0	1.0	0.9	1.4	1.1	IPF10179	orf19.3939	unknown function
CA3087	0.9	1.1	1.1	1.1	2.2	2.1	SMD3	orf19.4146	core snRNP protein (by homology)
CA5604	0.9	1.0	0.6	0.9	1.1	0.9	IPF549	orf19.7095	unknown function
CA0284	0.9	0.9	1.2	1.0	0.5	0.9	IPF14657	orf19.1441	unknown function
CA3951	0.9	1.1	1.2	1.1	0.6	0.9	VAC7.3	orf19.1409	Vacuolar protein, 3-prime end (by homology)
CA0318	0.9	0.9	0.9	0.9	1.1	1.3	FOL2	orf19.3957	GTP cyclohydrolase (by homology)
CA1499	0.9	0.9	0.9	0.8	0.4	0.7			
CA6133	0.9	1.0	1.1	1.0	1.0	1.1	DUR35.3f	orf19.5915	Urea transport protein, 3-prime end (by homology)
CA1436	0.9	0.9	0.5	1.0	1.2	1.0	IPF7165	orf19.1201	similar to Saccharomyces cerevisiae Dia4p seryl-tRNA synthetase (by homology)
CA4550	0.9	0.9	1.0	1.1	1.1	1.2	DYN2.3f	orf19.1448.2	Dynein light chain 1, cytosolic, 3-prime end
CA2945	0.9	0.8	1.0	0.6	0.7	0.9	IMG1	orf19.1967	Ribosomal protein, mitochondrial (by homology)
CA4101	0.9	1.0	1.2	1.0	0.8	0.9	IPF3984	orf19.667	unknown function
CA2459	0.9	0.9	2.2	1.3	1.2	1.1	IPF12234.5	orf19.3509	unknown function, 5- prime end
CA2496	0.9	0.9	0.8	1.0	0.9	1.1	IPF3468	orf19.4055	unknown function
CA2070	0.9	0.9	1.0	0.9	1.0	1.0			
CA0536	0.9	0.8	0.9	0.8	0.7	0.9	PAN6.3f	orf19.2815	pantothenate synthetase, 3-prime end (by homology)
CA4477	0.9	1.2	1.2	1.1	1.2	1.8	IPF6459	orf19.1890	unknown function
CA3108	0.9	0.8	0.9	0.9	1.3	1.2	IPF11826	orf19.6550	unknown function
CA1905	0.9	1.0	1.3	1.0	1.0	1.0	IPF7274	orf19.2783	unknown function
CA3660	0.9	1.2	1.2	1.0	1.1	1.0			
CA2159	0.9	1.1	1.0	0.8	0.9	0.9	IPF19753	orf19.5297	similar to Saccharomyces cerevisiae Tfb1p transcription initiation factor (by homology)
CA0767	0.9	0.9	0.9	0.9	0.8	0.8	KEM1.3	orf19.4969	multifunctional nuclease, 3-prime end (by homology)
CA4187	0.9	0.9	0.8	1.0	0.8	0.9	IPF7524	orf19.4528	unknown function
CA4633	0.9	0.8	0.7	0.8	1.5	1.2	NDH1	orf19.339	Mitochondrial NADH dehydrogenase

CA3748	0.8	0.9	0.8	1.0	1.0	1.0	IPF7385	orf19.3430	unknown function
CA0398	0.8	0.8	0.9	1.0	1.1	1.1	ARO2	orf19.1986	chorismate synthase (by homology)
CA4374	0.8	1.0	0.8	1.2	0.7	1.1	IPF5288	orf19.5665	Unknown function
CA3329	0.8	2.9	0.3	0.9	1.3	1.3	IPF12162	orf19.2670	Unknown function
CA1156	0.8	0.7	1.0	0.9	0.7	0.9	RLR1	orf19.4123	hypothetical regulatory protein (by homology)
CA4756	0.8	1.1	0.8	1.0	0.8	1.2	LIP6	orf19.4823	Secretory lipase
CA5285	0.8	0.7	1.1	1.1	1.0	1.1	HBS1	orf19.7144	Translation elongation factor eEF-1 alpha chain homolog, (by homology)
CA0588	0.8	1.0	0.9	0.9	9.5	8.2	IPF13081	orf19.1162	unknown function
CA5103	0.8	1.0	1.1	1.0	1.1	1.1	IPF1367	orf19.6436	unknown function
CA0173	0.8	1.0	1.0	0.9	0.7	0.6	IPF6913	orf19.3793	unknown function
CA2013	0.8	1.0	0.8	0.9	0.8	0.8	CDC1	orf19.3083	Cell division control protein (by homology)
CA0283	0.8	0.8	1.2	1.0	0.9	1.0	MDN1	orf19.4697	midasin (by homology)
CA2377	0.8	0.6	1.1	0.7	0.8	0.8	MRPL7	orf19.2214	Ribosomal protein of the large subunit, mitochondrial (by homology)
CA1106	0.8	0.7	1.7	1.3	1.2	1.5	IPF11270	orf19.5232	unknown function
CA5932	0.8	1.0	1.0	1.0	1.0	1.0	UBI4	orf19.6771	Polyubiquitin
CA2982	0.8	1.0	1.0	1.0	1.0	1.0	CSE1.53f	orf19.1230	Importin-beta-like protein, internal fragment (by homology)
CA5418	0.8	0.8	1.1	1.2	1.0	1.0	PGA14	orf19.968	unknown function
CA1539	0.8	0.6	0.9	0.8	0.8	0.9	BFR1	orf19.4560	Similar to Saccharomyces cerevisiae Bfr1p involved in the maintenance of normal ploidy (by homology)
CA4114	0.8	0.9	1.2	1.0	0.8	0.8	IPF7704	orf19.679	unknown function
CA3206	0.8	1.1	0.7	1.1	0.9	1.0	IPF3454	orf19.6187	unknown function
CA0712	0.8	0.7	1.7	1.2	1.2	1.2	IPF13717	orf19.2167	unknown function
CA2515	0.8	1.0	1.6	0.9	0.6	0.8	IPF19759	orf19.5510	Unknown Function
CA5566	0.8	1.1	0.8	1.0	0.9	1.1	PET18	orf19.7330	Putative transcriptional regulator (by homology)
CA5681	0.8	1.1	1.0	1.0	0.4	0.6	MNN9	orf19.7383	Required for complex N-glycosylation
CA4244	0.8	1.0	1.1	1.0	0.7	1.0	IPF4305	orf19.530	unknown function
CA2128	0.8	0.9	0.8	1.1	1.4	1.0	IPF4898	orf19.415	unknown function
CA6143	0.8	1.1	0.9	1.0	4.2	4.5	IPF1873	orf19.5902	putative GTP-binding protein (by homology)
CA1814	0.8	0.7	0.9	0.9	0.6	0.8	TRA1.5eoc	orf19.139	component of histone acetyltransferase, target for transcriptional activators, 5-prime end (by homology)
CA1897	0.8	0.9	0.7	0.9	1.4	1.0	IPF12002	orf19.2757	unknown function
CA3232	0.8	1.1	0.8	1.0	0.8	1.0			
CA0045	0.8	0.7	0.4	0.9	0.7	1.0	IPF8985	orf19.1368	unknown function
CA3760	0.8	1.0	0.7	1.0	1.0	1.0	ERG26	orf19.2909	C-3 sterol dehydrogenase (C-4 decarboxylase) (by homology)
CA2953	0.8	0.9	0.7	0.9	0.9	1.0	MBP1	orf19.5855	transcription factor (by homologgy)
CA1861	0.8	0.8	1.1	1.2	1.3	1.0	RAD32	orf19.866	DNA repair protein (by homology)
CA2657	0.8	1.1	0.9	1.0	0.9	0.9	IPF8486	orf19.5710	unknown function
CA4949	0.8	0.7	0.5	1.0	2.1	0.9	CDC34	orf19.6529	Ubiquitin-conjugating enzyme (by homology)
CA1179	0.8	0.9	1.0	1.0	0.8	0.9	IPF5064	orf19.804	ADP/ATP carrier protein (by homology)
CA0826	0.8	1.0	1.0	1.0	0.9	1.0	IPF19885.5f	0.00	unknown function, 5-prime end
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)
CA4908	0.8	1.2	0.8	0.9	0.7	0.8	IPF1445	orf19.6046	similar to Saccharomyces cerevisiae Apc1p subunit of anaphase-promoting complex
CA0587	0.8	0.9	0.8	0.9	0.9	0.6	PLD1	orf19.1161	phospholipase D
CA1845	0.8	0.8	1.1	1.1	1.3	0.9	IPF11123	orf19.637	similar to Saccharomyces cerevisiae Sdh2p succinate dehydrogenase iron-sulfur protein subunit (by homology)
CA5346	0.8	0.9	1.1	0.8	0.6	0.9	IPF867	orf19.7221	unknown function
CA0024	0.8	0.8	1.0	0.9	1.0	1.2			
CA3467	0.8	0.9	1.0	1.1	0.5	0.6	MNT2	orf19.1663	Alpha-1,2-mannosyltransferase (by homology)
CA2794	0.8	1.0	1.0	1.1	1.2	1.0	IPF8408	orf19.1724	unknown function

CA2289	0.8	0.7	1.1	1.0	0.8	0.7	RBF1.3	orf19.5558	RPG-BOX-BINDING FACTOR, 3-prime end
CA6038	0.8	1.2	1.8	1.2	1.1	1.6	LTV1	orf19.7650	low-temperature viability protein (by homology)
CA1328	0.8	1.0	1.2	1.0	1.1	1.3	RRP4	orf19.1304	3 ->5 exoribonuclease required for 3 end formation of 5.8S rRNA (by homology)
CA3002	0.8	0.9	1.1	0.9	0.6	0.7	PIF1	orf19.6133	mitochondrial DNA helicase (by homology)
CA4148	0.8	0.7	1.0	1.0	1.3	1.3	IDH2	orf19.5791	socitrate dehydrogenase (NAD+) subunit 2, mitochondrial (by homology)
CA4770	0.8	0.9	0.9	1.0	0.7	0.8	IPF9382.3	orf19.4002	similar to Saccharomyces cerevisiae Dun1p protein kinase (by homology)
CA2598	0.8	1.0	0.9	1.0	0.9	0.9	IPF13142	orf19.53	unknown function
CA4747	0.8	1.0	1.1	1.2	1.0	1.0	IPF4484	orf19.4834	unknown function
CA1772	0.8	1.0	0.8	0.9	0.4	0.5	ALG7	orf19.2187	UDP-N-acetylglucosamine-1-phosphate transferase (by homology)
CA5109	0.8	1.1	0.9	1.0	0.9	1.0	UBC9	orf19.6424	E2 ubiquitin-conjugating enzyme (by homology)
CA2066	0.8	1.3	1.2	1.4	1.2	1.2	RPO26	orf19.2643	DNA-directed RNA polymerase I, II, III 18 KD subunit (by homology)
CA2287	0.8	1.0	0.8	1.0	0.5	0.9	IPF5373	orf19.5555	unknown function
CA4848	0.8	1.0	1.0	1.0	1.1	1.5	RTS2	orf19.3817	Unknown function
CA3150	0.8	1.0	1.1	0.9	0.7	1.0	IPF4035	orf19.6166	unknown function
CA4686	0.8	0.8	0.8	0.9	0.8	0.8	IPF9015	orf19.880	unknown function
CA4067	0.8	0.8	1.3	0.9	0.6	0.5	IPF5924	orf19.445	unknown function
CA3257	0.8	1.1	0.3	0.7	1.0	2.4	IFC1	orf19.3746	Unknown Function
CA5621	0.8	0.4	1.2	0.9	6.1	6.9	FRE7	orf19.7077	Ferric reductase transmembrane component (by homology)
CA1107	0.8	0.8	1.1	1.0	1.0	1.0	IPF11271	orf19.5231.2	by homology to S. cerevisiae: ATP19 subunit K of the dimeric form of mitochondrial F1F0-ATP synthase
CA3576	0.8	0.9	1.0	0.9	0.9	0.9	IPF11107	orf19.2264	probably stearoyl-CoA desaturase by homology to S. cerevisiae
CA4198	0.8	0.9	0.7	1.0	0.9	1.0	IPF8055	orf19.4539	unknown function
CA3520	0.8	0.8	1.0	1.1	0.7	0.7	IPF6785	orf19.997	unknown function
CA4741	0.8	0.6	0.9	0.9	1.2	1.2	IPF4496	orf19.4843	unknown function
CA0738	0.8	0.8	0.7	0.9	1.1	1.1			
CA3320	0.8	0.8	0.7	0.8	0.4	0.7	IPF6898	orf19.2678	similar to Saccharomyces cerevisiae Bub1p serine/threonine kinase (by homology)
CA3069	0.8	0.7	1.9	2.1	0.6	0.7	IPF6117	orf19.4805	unknown function
CA2804	0.8	0.9	0.7	0.9	1.1	1.0	IPF19961	orf19.5777	unknown function
CA0184	0.8	0.5	1.0	0.7	1.0	0.8	IPF19142	orf19.3984	unknown function
CA4281	0.8	1.1	1.3	1.1	1.0	1.1	IPF2314	orf19.6679	unknown function
CA5721	0.8	1.0	1.1	1.1	0.5	0.8	IPF2443	orf19.7426	similar to Saccharomyces cerevisiae Ost6p N-oligosaccharyltransferase complex subunit (by homology)
CA3645	0.8	1.0	1.3	1.0	0.9	1.2	IPF4127	orf19.2036	putative dimeric dihydrodiol dehydrogenase (by homology)
CA5664	0.8	1.1	1.1	0.9	1.0	0.9	IPF1252	orf19.7366	Conserved hypothetical protein
CA4271	0.8	1.0	1.0	1.0	1.2	1.1	IPF2297	orf19.6667	Subunit of the histone deacetylase B complex (by homology)
CA1305	0.8	1.1	0.9	1.0	0.8	1.0	IPF13508.3f	orf19.4193	unknown function
CA0798	0.8	0.9	1.7	1.0	1.1	1.1	IPF13565	orf19.1609	unknown function
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
CA2099	0.8	0.8	1.8	1.1	1.1	1.1	IPF11484	orf19.2386	unknown function
CA0541	0.8	1.0	1.1	1.2	1.0	1.2	IPF14574	orf19.1083	unknown function
CA1640	0.8	0.7	2.2	0.9	0.7	0.9	IPF18641.3f	orf19.1732	unknown function, 3-prime end
CA4274	0.8	1.2	1.3	1.0	1.2	1.2	LAP42	orf19.6671	Aminopeptidase yscI precursor, vacuolar (by homology)
CA2266	0.8	0.6	0.4	0.6	1.4	1.0	HEM1	orf19.2601	5-aminolevulinic acid synthase
CA0611	0.8	1.0	0.6	1.0	1.1	1.0	IPF17542	orf19.5578	unknown function
CA5056	0.8	0.7	1.3	0.8	0.8	0.9	IPF3698	orf19.3022	similar to Saccharomyces cerevisiae Rsm24p mitochondrial ribosomal protein (S24) (by homology)
CA0750	0.8	0.7	1.4	1.1	1.0	1.1	IPF6284	orf19.1972	unknown function
CA2930	0.8	0.8	1.4	0.8	0.9	0.8	IPF7840	orf19.4204	similar to Saccharomyces cerevisiae Pet123p ribosomal protein, mitochondrial (by homology)
CA4549	0.8	0.9	1.0	1.0	1.1	1.0	IPF7863	orf19.1449	unknown function

CA2591	0.8	1.2	0.8	0.9	0.4	0.7	IPF18448.3	orf19.60	unknown function, 3-prime end
CA2047	0.8	0.7	1.0	1.1	1.3	1.3	RPL10	orf19.2935	Ribosomal protein L10 (by homology)
CA3377	0.8	1.0	0.9	1.2	0.9	0.8	CLF1	orf19.332	pre-mRNA splicing factor (by homology)
CA2691	0.8	1.1	0.9	1.0	0.8	1.0	PTR2	orf19.2582.1	Peptide transporter for di- and tripeptides
CA4656	0.8	1.1	1.5	1.1	2.5	1.5	IPF3095	orf19.4443	unknown function
CA2223	0.8	1.0	0.7	0.8	0.6	0.8	PLB5	orf19.5102	putative phospholipase B precursor
CA1946	0.8	1.0	0.8	1.0	1.2	1.1	IPF19937	orf19.4740	putative peptidyl-tRNA hydrolases (by homology)
CA1600	0.8	1.3	0.8	1.0	2.6	2.0	CTR2	orf19.4720	copper transport protein (by homology)
CA2336	0.8	1.0	1.1	1.1	0.5	0.7	IPF13383.5	orf19.2353	unknown function, 5 prime end
CA6161	0.8	1.0	0.9	1.0	1.1	1.1	IPF1834	orf19.5875	probable syntaxin (by homology)
CA2392	0.8	1.2	0.5	1.1	2.1	1.2	IPF15672	orf19.2607	unknown function
CA3285	0.8	1.2	0.8	1.0	0.9	0.8	IPF6280	orf19.6318	unknown function
CA3432	0.8	0.7	1.0	0.7	0.8	0.8	MRPL17	orf19.585	ribosomal protein of the large subunit (YmL30), mitochondrial (by homology)
CA2025	0.8	1.0	0.8	1.0	2.1	1.3	IPF9618	orf19.4911	unknown function
CA3176	0.8	0.7	1.5	1.2	1.4	1.2	IPF11588	orf19.1404	unknown function
CA5406	0.8	0.9	1.0	1.1	0.3	0.9	IPF1547	orf19.949	unknown function
CA1150	0.8	1.0	0.8	1.0	0.9	1.0	RIM9	orf19.101	regulator for sporulation and invasive growth
CA3658	0.8	1.1	0.6	1.1	1.5	1.0	TGL1	orf19.2050	Triacylglycerol lipase (by homology)
CA3090	0.8	1.0	1.1	1.0	1.2	1.5	IPF18385	orf19.4143	unknown function
CA5069	0.8	1.0	1.0	1.1	0.9	1.0	IPF3593	orf19.3042	unknown function
CA3593	0.8	1.0	1.0	1.0	1.2	1.1	YPT71	orf19.2245	GTP-binding protein of the RAB family (by homology)
CA5823	0.8	0.9	1.1	0.8	0.7	0.8	COQ1	orf19.7478	Hexaprenyl pyrophosphate synthetase (by homology)
CA3915	0.8	1.0	0.8	1.0	0.7	0.9			
CA3526	0.8	0.6	0.9	0.8	0.8	0.8	MRPS5.5f	orf19.989	Probable ribosomal protein S5, mitochondrial (by homology)
CA5180	0.8	0.9	1.1	1.1	1.0	1.0	FBA1	orf19.4618	fructose-bisphosphate aldolase (by homology)
CA3019	0.8	1.1	0.8	1.5	0.9	0.9	IPF15494	orf19.3910	putative ribonuclease (by homology)
CA5132	0.8	1.3	0.9	1.0	1.0	1.0	GTS1	orf19.6393	Transcription factor by homology
2262.10	0.8	1.0	1.7	1.7	1.9	1.2			
CA1851	0.8	1.0	0.9	1.0	0.7	0.9	IPF14629	orf19.642	Cell cycle protein, interacts with Sit4 (by homology)
CA1133	0.8	1.1	1.0	1.1	0.8	1.1	IFY1	orf19.2160	putative permease (by homology)
CA5288	0.8	0.7	1.0	0.7	1.0	0.9	IPF1928	orf19.7149	unknown function
CA2390	0.8	0.9	1.0	0.8	1.0	0.9	CET1	orf19.2609	mRNA 5 -triphosphatase (capping enzyme, beta subunit)
CA4585	0.8	0.9	1.6	1.2	1.2	1.3	IPF2227	orf19.6903	unknown function
CA2421	0.8	0.9	1.2	0.9	0.9	0.9	IPF14998	orf19.4471	unknown function
CA5325	0.8	1.2	1.0	0.9	0.8	1.0	IPF2138	orf19.7199	unknown function
CA6048	0.8	1.1	1.0	1.1	1.1	1.1	IPF4934	orf19.7664	unknown function
CA4861	0.8	1.0	1.1	1.1	1.1	1.2	IPF4094	orf19.3836	unknown function
CA4229	0.8	0.7	1.3	1.2	0.8	0.8			
CA0377	0.8	0.9	1.0	1.1	1.3	1.3	IPF14356	orf19.2708	unknown function
CA5526	0.8	1.2	4.8	1.9	1.1	1.0	IPF2857	orf19.7284	unknown function
CA3337	0.8	1.0	0.7	0.9	1.7	1.6	IPF13583	orf19.2334	unknown function
CA6147	0.8	1.0	0.9	1.0	1.0	1.0	IPF1862.5f	orf19.5895	unknown function, 5-prime end | Unknown function
CA3916	0.8	1.1	1.0	1.1	1.3	1.3	IPF3274	orf19.4383	Unknown function
CA1740	0.8	1.0	1.0	1.1	0.9	1.0	SMI1	orf19.5058	beta-1,3-glucan synthesis protein (by homology)
CA0006	0.8	1.0	1.0	0.9	1.0	1.0	IPF2072	orf19.4080	unknown function
CA4088	0.8	1.1	0.7	1.0	0.9	0.7	HMO1	orf19.6645	High-mobility protein 1 by homology

CA2068	0.8	1.0	0.9	1.1	0.9	1.0	ARP1	orf19.2641	centractin (by homology)
CA2339	0.8	0.8	0.7	1.6	2.3	1.4	IPF13377	orf19.2350	unknown function
CA4689	0.8	0.7	1.0	1.3	0.8	0.8	PGA33	orf19.876	unknown function
CA0758	0.8	1.3	1.0	1.1	0.8	0.9	PAP11	orf19.3197	poly(A) polymerase by homology to S. cerevisiae
CA4087	0.8	1.1	0.9	1.0	0.8	1.1	IPF5013	orf19.6643	similar to Saccharomyces cerevisiae Mct1p malonyl-CoA:ACP transferase (by homology)
CA5781	0.8	1.2	0.8	1.1	0.8	1.0	IPF1126	orf19.5428	unknown function
CA4083	0.8	0.8	0.8	0.7	0.9	0.8	IPF5018	orf19.6639	unknown function
CA3000	0.8	1.0	0.9	1.1	1.1	1.1	TSC1.5	orf19.6131	3-ketosphinganine reductase, 5-prime end (by homology)
CA1184	0.8	0.9	1.1	1.0	1.0	0.9	IPF14802	orf19.3782.2	unknown function
CA1500	0.8	0.8	2.3	1.0	1.0	1.1	IPF13221	orf19.1697	unknown function
CA1350	0.8	0.8	1.6	1.2	0.3	0.6	MCM2	orf19.4354	replication licensing factor (by homology)
CA1871	0.8	0.9	0.9	0.7	1.6	0.9	IPF16981	orf19.2458	unknown function
CA2381	0.8	0.9	0.9	0.9	0.8	0.7	YCK3.3f	orf19.2221	casein kinase I, 3-prime end (by homology)
CA2619	0.8	1.0	0.9	1.0	1.0	1.2	IPF9490	orf19.2810	amino acid permease (by homology)
CA1115	0.8	1.0	0.9	1.1	1.0	1.3	RPA12	orf19.2287	DNA-directed RNA polymerase I (by homology)
CA5906	0.8	0.8	0.7	0.8	0.8	0.7	IPF5949	orf19.6800	unknown function
CA1713	0.8	1.0	1.0	1.3	0.5	0.3	IPF19743	orf19.3332	unknown function
CA6073	0.8	0.7	1.1	1.0	1.2	1.0	HRP1	orf19.5989	Nuclear polyadenylated RNA-binding protein (by homology)
CA4839	0.8	0.9	1.2	1.0	0.9	1.1	NPL6	orf19.2055	Nuclear protein localization factor (by homology)
CA5609	0.8	1.1	0.8	1.0	1.0	1.1	IPF538	orf19.7091	unknown function
CA3344	0.8	0.9	1.1	1.1	0.9	0.9	IPF13359	orf19.2326	unknown function
CA5517	0.8	1.2	1.1	1.1	0.8	1.1	IPF721.3f	orf19.5365	unknown function, 3-prime end
CA4853	0.8	1.0	0.7	0.8	0.8	0.8	IPF5823	orf19.3823	similar to Saccharomyces cerevisiae Zds1p involved in negative regulation of cell polarity (by homology)
CA4075	0.8	0.9	1.1	0.9	0.9	1.0	IPF2555	orf19.6628	unknown function
CA1513	0.8	0.5	1.0	1.1	1.0	1.0	MIR1	orf19.4885	phosphate transport protein, mitochondrial (MCF) (by homology)
CA2735	0.8	0.8	1.4	1.0	1.2	0.9	TFG2	orf19.2111	transcription initiation factor TFIIF middle subunit (by homology)
CA5915	0.8	1.0	1.0	0.9	0.9	1.0	IPF10735	orf19.6790	negative growth regulatory RNA-binding protein (by homology)
CA4819	0.8	0.9	0.6	0.9	1.3	2.0	IPF1194	orf19.2078	Similar to clathrin coat proteins
CA2645	0.8	1.1	1.7	1.2	1.0	1.1	YNK1	orf19.4311	Nucleoside diphosphate kinase (by homology)
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)
CA3716	0.8	1.0	1.1	1.1	0.4	0.9	IPF6203	orf19.4166	unknown function
CA0910	0.8	1.0	0.8	0.7	0.8	0.9	MRPL16	orf19.2019	ribosomal protein
CA3410	0.8	0.9	1.1	1.0	1.0	0.9	IPF9411	orf19.6147	unknown function
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)
CA3664	0.8	1.1	1.1	1.1	0.8	0.9	IPF11434	orf19.6461.1	unknown function,
CA5678	0.8	1.0	1.0	0.8	0.9	2.0	IPF1292	orf19.7381	unknown function Hypothetical zinc-finger protein
CA2105	0.8	1.0	1.0	1.0	0.6	0.8	IPF10711	orf19.3694	unknown function
CA0955	0.8	0.9	0.9	0.9	1.0	1.1	IPF13160	orf19.1140	unknown function
CA5565	0.8	1.1	0.7	1.0	1.0	0.8	QRI8	orf19.7329	E2 ubiquitin-conjugation enzyme (by homology)
CA5208	0.8	1.0	1.0	1.0	1.7	1.0	IPF2361	orf19.7023	unknown function
CA5505	0.8	1.2	0.6	0.7	0.7	0.8	TPS3	orf19.5348	alpha,alpha-trehalose-phosphate synthase, regulatory subunit (by homology)
CA5414	0.8	0.8	1.4	1.1	1.3	1.2	IPF1568	orf19.962	unknown function
CA4884	0.8	1.1	0.7	1.0	0.9	1.0	ALK6	orf19.6574	n-alkane inducible cytochrome P-450 (by homology)
CA4572	0.8	0.7	0.9	0.9	0.9	1.1	KES1	orf19.6883	involved in ergosterol biosynthesis (by homology)
CA0495	0.8	1.0	0.2	0.5	1.1	1.0	IPF20056	orf19.2659	unknown function
CA4356	0.8	1.1	1.1	1.2	1.1	1.0	IPF3651	orf19.6731.1	unknown function

CA1444	0.8	0.8	1.4	1.1	0.6	0.7	KTR2	orf19.4494	mannosyltransferase (by homology)
CA4905	0.8	0.8	0.9	0.9	0.9	1.1	DLD1	orf19.6043	D-lactate ferricytochrome C oxidoreductase (by homology)
CA4279	0.8	0.7	1.0	1.4	1.2	1.0	DPH51	orf19.6676	Diphthamide methyltransferase (by homology)
CA4125	0.8	1.2	1.1	1.0	1.0	1.0	PGA62	orf19.2765	unknown function
CA5224	0.8	1.6	0.7	1.0	5.4	0.7	IPF3081	orf19.7043	unknown function
CA5498	0.8	0.9	1.1	1.2	1.2	0.9	IPF772	orf19.5340	unknown function
CA4129	0.8	1.2	0.8	1.1	1.0	1.2	IPF6878	orf19.4248	unknown function
CA2603	0.8	1.4	0.8	1.0	1.4	1.0	IPF5471	orf19.5680	unknown function
CA0351	0.8	1.0	1.1	0.9	0.9	1.3	RPB4.3f	orf19.145	DNA-directed RNA polymerase II, 32 kDa subunit, 3-prime end (by homology)
CA6057	0.8	2.0	0.5	0.9	1.3	1.2	IPF4959	orf19.7676	D-xylulose reductase (by homology)
CA1341	0.8	1.0	1.0	0.9	1.3	1.0	IPF11344	orf19.4340	unknown function
CA1666	0.8	0.6	2.6	1.7	1.0	1.0	SRP40	orf19.2859	RNA I and II supressor (by homology)
CA2864	0.8	1.2	0.9	1.0	1.3	1.0	IPF17234.3f	orf19.1057	unknown function, 3-prime end
CA3122	0.8	1.2	0.5	1.0	1.3	1.2	IPF5356	orf19.3004	unknown function
CA3209	0.8	0.9	1.1	1.0	1.3	1.0	CTA210.3f	orf19.6190.2	transcriptional activator, 3-prime end
CA0860	0.8	0.9	0.8	0.9	1.0	0.9	IPF17272.3f	orf19.3522	unknown function
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 homology)
CA3776	0.8	1.2	0.9	1.1	0.6	0.9	IPF10435	orf19.2890	unknown function
CA3843	0.8	1.0	0.6	0.8	0.9	1.0	IPF7947	orf19.6602	unknown function
CA1807	0.8	1.0	1.0	1.0	0.8	1.1	IPF6328	orf19.1114	unknown function
CA4364	0.8	0.8	1.0	1.0	0.9	1.0			
CA3873	0.8	0.9	0.8	0.8	0.9	1.1	IPF8825	orf19.396	unknown function
CA4575	0.8	0.8	2.0	1.2	0.9	1.4	IPF9428	orf19.6886	unknown function
CA3286	0.8	1.0	1.0	1.0	1.2	1.2	UBP3.3eoc	orf19.6319	Ubiquitin-specific proteinase, 3-prime end (by homology)
CA1522	0.8	0.9	1.1	1.2	1.0	1.1	IPF6916	orf19.3791	unknown function
CA1825	0.8	0.8	1.3	1.2	2.0	1.6	IPF9522.3f	orf19.4266.1	septin, 3-prime end (by homology)
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 homology)
CA2630	0.8	0.9	0.9	1.1	1.0	0.9	COX5A	orf19.4759	cytochrome-c oxidase chain V.A precursor (by homology)
CA5371	0.8	1.1	1.1	1.0	1.0	1.2	RPC10	orf19.7255	DNA-directed RNA polymerases small subunit by homology
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 homology)
CA5610	0.8	0.9	0.8	1.0	0.7	0.7	PMR1	orf19.7089	calcium/mangenease P-type ATPase
CA2019	0.8	1.0	1.0	1.0	0.6	0.6	IPF3409	orf19.843	unknown function
CA2614	0.8	1.1	1.0	1.0	1.1	1.0	CTA241.3f	orf19.5699.1	transcriptional activator, 3-prime end
CA5962	0.8	1.2	0.7	0.9	1.2	1.0	ALO1	orf19.7551	D-arabinono-1,4-lactone oxidase (by homology)
CA6006	0.8	1.3	1.0	1.2	1.1	1.2	IPF652	orf19.7606	unknown function
CA0290	0.8	0.8	1.1	0.9	0.9	1.0	POT14	orf19.1591	acetyl-CoA acetyltransferase (by homology)
CA2936	0.8	0.8	1.4	1.2	0.6	0.7	IPF8326	orf19.3327	similar to Saccharomyces cerevisiae Rnc1p endo-exonuclease (by homology)
CA5084	0.8	1.0	0.8	1.1	0.8	0.9	IMP1	orf19.3061	protease, mitochondrial (by homology)
CA6141	0.8	0.5	1.1	1.1	1.1	1.0	RPL19A	orf19.5904	Ribosomal protein L19.e (by homology)
CA6049	0.8	0.9	0.9	1.1	1.0	1.2	IPF4935	orf19.7665	unknown function
CA4339	0.8	0.7	1.9	1.3	1.1	0.9	IPF3618	orf19.6710	Unknown function
CA2519	0.8	0.8	1.3	0.9	1.0	0.9	SRP72	orf19.5516	signal recognition particle protein SRP72 (by homology)
CA3044	0.8	1.1	0.9	1.0	1.2	1.1	IPF7298	orf19.2418	unknown function
CA3225	0.8	1.0	1.5	0.9	1.2	1.0	IPF9329	orf19.6286	unknown function
CA3583	0.8	0.7	0.8	0.9	0.7	0.8	IPF20137	orf19.2257	unknown function
CA1132	0.8	1.0	1.0	1.3	0.9	0.9	IFY2.5f	orf19.2159	putative permease, 5-prime end (by homology)

CA4692	0.8	0.8	0.9	1.1	0.9	1.1	COX6	orf19.873.2	cytochrome-c oxidase subunit VI (by homology)
CA1020	0.8	1.1	0.7	1.1	1.8	1.0	IPF4824	orf19.3355	unknown function
CA4907	0.8	0.9	0.6	1.1	0.9	0.9	PSD1	orf19.6045	Phosphatidylserine decarboxylase 1 (by homology)
CA2217	0.8	1.0	1.0	1.0	1.0	1.1	POL0	orf19.5373	pol polyprotein, reverse transcripase
CA3383	0.8	1.1	0.9	0.9	1.1	0.9	IPF8359	orf19.326	unknown function
CA1697	0.8	1.0	1.1	1.0	1.0	1.0	IPF16758	orf19.5043	unknown function
CA3353	0.8	0.8	0.4	0.7	1.5	1.4	AUR1	orf19.1945	aureobasidin-resistance protein
CA1761	0.8	1.8	0.7	1.0	2.0	1.6	IPF7602	orf19.5193	oxidoreductase (by homology)
CA4211	0.8	0.9	1.6	1.3	1.2	1.5	IPF5052	orf19.809	RNA-binding protein (by homology)
CA4070	0.8	1.1	0.8	0.9	1.2	1.2	IPF2562	orf19.6623	unknown function
CA4485	0.8	0.9	0.8	1.0	1.1	1.0	IPF9160	orf19.1878	similar to Saccharomyces cerevisiae Med4ptranscription regulation mediator (by homology)
CA4755	0.8	1.0	0.8	1.2	0.8	0.7	IPF11480	orf19.4824	unknown function
CA6063	0.8	1.1	1.5	1.0	1.0	1.0	IPF8311	orf19.6003	unknown function
CA1312	0.8	1.1	0.8	0.7	0.5	0.7	IPF14241	orf19.3635	unknown function
CA0212	0.8	1.0	0.7	1.1	1.2	1.2	IPF4325	orf19.5523	unknown function
CA1470	0.8	0.9	0.6	0.8	1.2	1.0	IPF17942	orf19.796	unknown function
CA5190	0.8	0.6	1.0	0.9	1.2	1.1	IPF10155	orf19.4628	unknown function
CA1691	0.8	1.2	1.0	0.9	1.0	1.0	PGK1	orf19.3651	Phosphoglycerate kinase
CA5919	0.8	0.9	1.4	0.9	0.6	0.9	IPF8926.3	orf19.6786	unknown function, 3-prime end
CA4248	0.8	1.0	1.1	1.0	1.0	0.9	IPF4294	orf19.537	unknown function
CA4946	0.8	0.9	1.0	1.0	0.7	1.0	TOM71	orf19.6531.1	Translocase of the outer mitochondrial membrane (by homology)
CA4796	0.8	1.0	0.8	1.0	1.0	1.2	IPF3380	orf19.4031	unknown function
CA1516	0.8	0.9	0.9	1.0	1.0	0.9	IPF16764	orf19.4796	unknown function
CA3193	0.8	1.1	1.1	1.1	0.9	1.0	IPF3418.5e	orf19.6170	unknown function
CA1717	0.8	0.9	1.0	0.9	1.0	1.0	IPF9315	orf19.4647	putative CCAAT-binding factor subunit (by homology)
CA5483	0.8	0.9	0.5	0.9	0.5	0.7	IPF817	orf19.5316	unknown function
CA0912	0.8	0.8	1.2	1.2	1.2	1.1	RPA49	orf19.2017	DNA-directed RNA polymerase A (by homology)
CA1962	0.8	1.0	0.5	0.9	2.1	1.6	IPF14285	orf19.2398	unknown function
CA0555	0.8	0.8	1.2	1.0	0.7	1.0	HYS2	orf19.3960	DNA-directed DNA polymerase delta (by homology)
CA5122	0.8	0.9	1.2	0.9	0.8	0.9	IPF1308	orf19.6406	Similarity to ribosomal protein S13 (by homology) Translation
CA3589	0.8	1.5	0.8	1.2	1.4	1.1	IPF10113	orf19.2249	unknown function
CA1786	0.8	1.1	1.8	1.1	1.0	1.0	IPF7629	orf19.1168	unknown function
CA4940	0.8	1.0	1.0	1.0	0.9	1.0	CRN1.3f	orf19.6535	actin-binding protein, 3-prime end (by homology)
CA3488	0.8	1.1	0.9	1.0	0.7	0.7	IPF3198	orf19.3568	unknown function
CA5287	0.8	1.0	1.0	0.9	1.0	1.7	IPF1922	orf19.7148	similar to multidrug resistance proteins
CA1265	0.8	0.8	1.3	1.0	1.0	0.6	IPF10510	orf19.240	unknown function
CA4072	0.8	0.9	1.1	1.0	1.1	1.0	IPF2560	orf19.6625	unknown function
CA5445	0.8	1.0	1.0	1.0	1.2	1.2	IPF232	orf19.3248	unknown function
CA1642	0.8	1.0	1.0	0.9	1.1	0.9	NHP1.5f	orf19.1730	unknown function, 5-prime end
CA5803	0.8	1.0	1.5	1.0	0.8	1.3	IPF4163	orf19.5457	unknown function
CA4262	0.8	1.1	1.4	1.3	0.6	1.7	IPF2275.5e	orf19.6654	unknown function
CA3772	0.8	1.1	0.9	1.1	0.9	0.8	VMA8	orf19.2895	CANAL VACUOLAR ATP SYNTHASE SUBUNIT D
CA0405	0.8	1.1	1.0	1.0	1.2	1.2			
CA0451	0.8	1.1	1.0	1.1	0.9	0.9	IPF13556	orf19.1302	unknown function
CA3066	0.8	0.5	1.1	1.0	0.6	0.8	IPF15813	orf19.4281	unknown function
CA2333	0.8	1.0	0.7	0.9	1.0	1.0	ADH4	orf19.4504	probable alcohol dehydrogenase (by homology)

CA4941	0.8	0.8	0.8	1.0	0.9	0.9	CRN1.53f	orf19.6534.3	actin-binding protein, 5-prime end (by homology)
CA2849	0.8	1.0	0.9	1.0	1.2	1.2	POP2	orf19.5734	required for glucose derepression (by homology)
CA4817	0.8	0.8	0.9	0.8	0.5	0.6	POM152	orf19.2081	Nuclear pore membrane glycoprotein (by homology)
CA0079	0.8	1.0	1.1	1.0	1.2	1.1	IPF14323	orf19.4730	unknown function
CA4166	0.8	0.8	1.0	1.0	1.0	1.1	TIF34	orf19.2967	Translation initiation factor eIF3, p39 subunit
CA2745	0.8	0.9	0.6	1.2	0.8	0.7	HIR1.3f	orf19.2099	Histone transcription regulator (by homology)
CA4449	0.8	0.7	1.3	0.8	1.1	1.2	IPF3520	orf19.6847	unknown function
CA5523	0.8	1.0	1.2	1.1	0.9	1.0	NIT2	orf19.7279	Nitrilase (by homology)
CA2332	0.8	0.9	1.2	1.0	1.1	0.8	IPF4792	orf19.4503	unknown Function
CA3466	0.8	0.7	1.1	0.8	0.8	0.9	MRP1.5f	orf19.1662	mitochondrial ribosomal protein of the small subunit, 5-prime end (by homology)
CA1739	0.8	1.1	0.9	1.0	0.7	0.9	IPF4976	orf19.2522	unknown function
CA1127	0.8	0.9	1.2	0.8	0.5	1.1	MSH3	orf19.3608	DNA mismatch repair by homology
CA2088	0.8	0.9	1.0	1.0	0.9	0.9	IPF3394	orf19.836.1	probable small nuclear ribonucleoprotein G (SNRNP-G)
CA2160	0.8	1.0	0.9	0.8	0.7	0.9	IPF15664	orf19.5296	unknown function
CA3910	0.8	0.9	0.9	1.0	0.9	1.1	IPF3293	orf19.4392	unknown function
CA5822	0.8	0.8	1.2	0.9	1.2	1.0	YRB1	orf19.7477	GTPase-activating protein (by homology)
CA0535	0.8	0.9	1.4	1.0	0.6	0.6	IPF15606	orf19.5065	similar to Saccharomyces cerevisiae Erd1p required for retention of luminal ER proteins
CA4580	0.8	0.8	1.0	1.0	1.7	2.0	IPF2233	orf19.6898.1	unknown function
CA5398	0.8	0.7	1.1	0.9	1.0	1.0	SEC14	orf19.941	phosphatidylinositol(PI)/phosphatidylcholine(PC)transfer
CA4155	0.8	0.5	1.0	0.5	0.5	0.7	RNR21	orf19.5801	ribonucleoside-diphosphate reductase (by homology)
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 mutations (by homology)
CA1652	0.8	1.0	0.7	1.0	0.6	1.0	RNH11	orf19.5563	Ribonuclease H (by homology)
CA0376	0.8	0.9	0.9	0.9	0.9	1.1	QCR9	orf19.2707.1	ubiquinol--cytochrome-c reductase subunit 9(by homology)
CA2922	0.8	0.7	0.9	1.2	1.0	0.9	FET31	orf19.4213	cell surface ferroxidase (by homology)
CA5654	0.8	1.1	1.0	1.0	1.0	1.0	IPF15543	orf19.7356	unknown function
CA0862	0.8	0.9	1.0	0.8	0.5	0.6	CRK1.5f	orf19.3524	Protein kinase, 5-prime end
CA2406	0.8	1.0	0.9	0.9	1.0	1.0	AIP2	orf19.300	actin interacting protein 2 (by homology)
CA5375	0.8	1.1	0.9	1.0	1.1	1.1	IPF5239	orf19.7260	similarity to aldose reductase (by homology)
CA5277	0.8	1.0	1.0	1.0	1.0	1.0	CTA29.5f	orf19.7127	Protein with putative transcription activation domain, 5-prime end
CA2629	0.8	1.1	1.8	1.1	1.2	1.1	IPF10911	orf19.4760	unknown function
CA0885	0.8	1.0	1.1	1.0	0.9	0.9	IPF12381	orf19.1389	unknown function
CA3965	0.8	1.0	1.0	1.0	0.4	0.8	IPF9375	orf19.1426	unknown function
CA2677	0.8	0.9	1.1	1.1	1.2	1.1			
CA1883	0.8	1.5	0.9	1.0	0.7	0.7	IPF5479	orf19.2209	unknown function
CA5211	0.8	0.9	0.8	0.8	1.0	0.9	IPF18125	orf19.7028	similar to glutenin and glutamine-rich proteins
CA4506	0.8	0.6	1.4	1.4	1.2	1.0	GCD10	orf19.500	translation initiation factor eIF3 RNA-binding subunit (by homology)
CA1565	0.8	0.9	1.0	1.0	0.9	1.0	EGD1	orf19.1154	GAL4 DNA-binding enhancer protein (by homology)
CA5929	0.8	0.7	1.0	1.0	1.1	1.1	GCD2	orf19.6776	Translation initiation factor eIF2B, 71 kDa (delta) subunit (by homology)
CA2093	0.8	1.1	1.5	1.2	0.7	0.9	IPF3406	orf19.841	unknown function
CA4746	0.8	0.7	1.5	1.4	1.0	1.1	IPF4485	orf19.4835	unknown function
CA3808	0.8	1.1	1.5	1.2	1.1	1.6	FAL1	orf19.2488	ATP-dependent RNA helicase
CA1678	0.8	0.5	1.0	1.0	0.9	0.8	PGA24	orf19.3618	putative cell wall protein (by homology)
CA0095	0.8	1.0	1.5	0.7	0.2	0.6	ALG11	orf19.3468	required for asparagine-linked oligosaccharide assembly (by homology)
CA0981	0.8	0.7	0.6	1.0	1.9	1.3	GAP4	orf19.1799	general amino acid permease (by homology)
CA4233	0.8	0.9	1.0	1.1	0.4	0.7	RFT1	orf19.516	nuclear division protein (by homology)
CA0812	0.8	0.7	0.7	1.1	0.7	0.9	IPF3348	orf19.1917	unknown function

CA1626	0.8	1.3	1.6	1.4	1.3	1.1	STR2	orf19.1033	O-succinylhomoserine (thiol)-lyase (by homology)
CA0154	0.8	0.9	1.2	0.9	1.3	1.1	CPH1	orf19.4433	Transcription factor
CA1766	0.8	0.6	2.0	1.2	1.2	1.3	NOP4	orf19.5198	Nucleolar protein
CA0009	0.8	1.0	1.0	1.0	1.4	1.1	IPF11382	orf19.634	unknown function
CA1670	0.8	1.0	0.9	1.1	0.8	1.0	IPF11392	orf19.2851	unknown function
CA3012	0.8	0.9	1.3	1.1	0.7	0.8	IPF14013	orf19.6227	unknown function
CA3502	0.8	1.0	1.1	0.7	0.9	0.9	IPF14485	orf19.6348	unknown function
CA0878	0.8	0.7	1.1	1.0	0.5	0.7			
CA5412	0.8	1.3	0.7	0.9	0.5	0.8	IPF1566	orf19.956	unknown function
CA2771	0.8	0.8	0.8	1.1	0.9	1.0	RPB10	orf19.2687.1	DNA-directed RNA polymerase II (by homology)
CA2221	0.8	0.8	1.0	0.9	0.5	0.7	IPF9670	orf19.5100	membrane transporter of the ATP-binding cassette (ABC) superfamily involved in metal resistance (by homology)
CA6165	0.8	0.9	0.8	0.9	0.8	0.8	SNF5.3f	orf19.5871	Component of SWI/SNF transcription activator complex, 3-prime end (by homology)
CA0386	0.8	1.2	1.8	1.4	3.2	1.6	IPF4065	orf19.1862	unknown function
CA3454	0.8	1.0	0.9	1.0	0.9	1.0	IPF10533.5f	orf19.1255	unknown function, 5-prime end
CA6012	0.8	0.7	1.0	1.4	1.2	1.1	HCR1	orf19.7613	putative translation initiation factor 3 subunit (by homology)
CA1545	0.8	0.7	0.9	0.9	0.7	0.7	CDR3	orf19.1313	ABC transporter, multidrug resistance protein
CA5838	0.8	1.0	0.8	0.9	0.9	0.8	IPF424	orf19.7492	unknown function
CA5637	0.8	0.9	0.9	1.1	0.5	0.7	IPF472	orf19.7058	unknown Function
CA5568	0.8	0.4	2.0	1.0	1.2	1.0	ELF1	orf19.7332	Elongation-like factor
CA3072	0.8	1.2	0.9	1.0	0.4	0.8	ERG12	orf19.4809	Mevalonate kinase (by homology)
CA3881	0.8	1.0	0.8	0.9	0.8	0.7	GCR3	orf19.387	Large subunit of the nuclear cap-binding protein complex CBC (by homology).
CA5116	0.8	0.8	1.3	1.1	1.0	0.9	TPM2	orf19.6414.3	Tropomyosin
CA0174	0.8	0.7	1.2	0.8	1.2	0.8			
CA4090	0.8	1.0	1.1	1.2	1.3	1.2	BRF1	orf19.6649	TFIIIB subunit
CA5282	0.8	1.0	1.0	1.0	1.0	1.0	IPF1911	orf19.7139	unknown function
CA3342	0.8	0.7	1.7	1.4	0.7	1.1	IPF13361	orf19.2330	unknown function
CA3064	0.8	0.8	1.2	0.9	0.8	1.1	IPF2973	orf19.4283	unknown function
CA5849	0.8	1.1	1.1	1.4	0.9	0.7	IPF404.5f	orf19.7506	unknown function, 5-prime end
CA4227	0.8	1.0	2.1	1.1	0.8	1.2	SCH9	orf19.829	protein kinase (by homology)
CA0430	0.8	1.5	1.4	1.4	0.8	0.9	PRC1	orf19.1339	Carboxypeptidase Y precursor
CA3165	0.8	0.6	1.3	1.1	0.9	1.0	FMI1	orf19.1578	processing of pre-ribosomal RNA
CA6104	0.8	0.9	1.1	1.1	1.7	1.1	IPF65	orf19.5952	unknown function
CA2304	0.8	0.6	2.1	1.3	0.8	1.4	PRP43	orf19.1687	RNA-dependent ATPase (by homology)
CA1566	0.8	0.8	1.4	1.0	0.7	0.7	DPP2	orf19.1155	Diacylglycerol pyrophosphate phosphatase (by homology)
CA5530	0.8	0.8	1.4	1.0	1.1	1.1	SPB8	orf19.7290	Suppressor of PAB1 (by homology)
CA1935	0.8	1.2	0.6	1.0	1.0	1.0	IPF19936	orf19.4185	unknown function
CA5417	0.8	0.9	0.9	1.1	1.0	1.0	NUC1	orf19.967	Nuclease, mitochondrial
CA2163	0.8	1.2	0.8	1.0	1.0	0.6	IPF11879	orf19.5293	unknown function
CA1936	0.8	1.0	0.7	1.0	1.0	1.0	PCT1	orf19.4186	cholinephosphate cytidylyltransferase (by homology)
CA6051	0.8	1.0	0.8	1.1	0.7	0.9	IPF4940	orf19.7667	unknown function
CA2984	0.8	0.6	2.1	1.2	0.8	0.9	IPF12606.3	orf19.6008.1	
CA0614	0.8	0.8	0.8	0.9	0.5	0.7	IPF19700	orf19.1600	unknown function
CA1375	0.8	0.8	0.9	0.9	0.9	0.8	IPF7158	orf19.1196	putative serine/threonine kinase
CA2707	0.8	1.0	1.1	0.9	1.1	1.3	IPF11003	orf19.4659	by homology pre-mrna splicing factor
CA0411	0.8	1.0	1.4	1.0	0.4	0.8	IPF17676	orf19.1507	similar to Saccharomyces cerevisiae Cst13p involved in chromosome stability (by homology)
CA0228	0.8	1.0	1.6	1.1	0.5	0.7	IPT1.5f	orf19.4769	Mannosyl diphosphorylinositol ceramide, 5-prime end (by homology)

CA4033	0.8	1.0	1.0	1.0	0.7	1.0	IPF19795	orf19.3431	similar to Saccharomyces cerevisiae Mip1p DNA-directed DNA polymerase gamma catalytic subunit, mitochondrial)
CA5787	0.8	0.8	2.4	1.3	1.1	0.9	IPF1136	orf19.5436	unknown function
CA5760	0.8	1.1	0.8	0.9	0.8	1.0	IPF1072	orf19.5397	unknown function
CA2743	0.8	0.7	0.9	1.0	1.4	1.1	CKB21	orf19.2102	Casein kinase II, beta subunit (by homology)
CA3861	0.8	1.0	1.0	1.0	0.9	1.0	RIM8	orf19.6091	regulator of PH response
CA0959	0.8	0.7	1.1	1.1	1.0	1.1	SAM2	orf19.657	S-adenosylmethionine synthetase 2
CA5276	0.8	1.0	0.9	1.0	0.9	1.0			
CA4567	0.8	0.9	1.0	1.0	1.0	1.1	IPF9555	orf19.6879	unknown function
CA4583	0.8	1.1	1.1	1.0	1.0	1.1	IPF2229	orf19.6901	unknown function
CA0724	0.8	1.0	1.4	1.0	3.0	1.4	IPF13398	orf19.35	protein kinase (by homology)
CA5946	0.8	0.9	1.1	1.1	1.0	1.2	IPF3493	orf19.6751	unknown function
CA4387	0.8	0.7	1.8	1.0	1.4	1.2	MAP1	orf19.3124	methionine aminopeptidase, isoform 1 (by homology)
CA4196	0.8	1.1	1.1	1.0	1.1	1.2	DST1	orf19.4537	RNA polymerase II elongation factor (by homology)
CA5513	0.8	0.9	1.0	1.0	1.0	1.1	RPC11	orf19.5360	RNA polymerase III C11 subunit (by homology)
CA2596	0.8	1.1	0.7	0.9	0.8	0.9	IPF19546	orf19.55	unknown function
CA4373	0.8	0.6	0.7	1.0	0.3	0.5	IPF5287	orf19.5664	signal transduction protein (by homology)
CA2931	0.8	0.9	0.7	0.9	0.5	0.9	IPF7841	orf19.4203	similar to Saccharomyces cerevisiae Ndc1p nuclear envelope protein (by homology)
CA0573	0.8	1.3	1.2	1.0	0.9	0.9	PEX14	orf19.1805	peroxisomal protein (by homology)
CA6103	0.8	0.9	1.2	1.4	1.1	1.1	SFP1	orf19.5953	zinc finger protein (by homology)
CA4099	0.8	0.4	2.1	1.2	0.7	1.0	IPF3986	orf19.665	unknown function
CA4509	0.8	1.0	1.1	1.0	0.8	0.9	IPF8973	orf19.497	unknown function
CA0759	0.8	1.2	1.0	1.1	0.9	0.8	IPF11167	orf19.3198	unknown function
CA0616	0.8	1.0	0.3	0.9	2.5	1.0	PHO11	orf19.2619	Secreted acid phosphatase
CA1758	0.8	0.5	2.0	0.7	0.9	0.8	IPF14559.3f	orf19.5126	unknown function, 3-prime end
CA0569	0.8	1.0	1.0	0.9	1.2	1.1	CDC8	orf19.1137	dTMP kinase (by homology)
CA5263	0.8	1.2	0.5	1.0	1.0	0.9	CYB3	orf19.5000	Lactate dehydrogenase cytochrome b2 (by homology)
CA3326	0.8	1.0	1.5	1.1	0.7	1.0	IPF6889	orf19.2673	unknown function
CA4154	0.8	1.7	1.7	1.5	0.7	1.6	IPF20010	orf19.5799	unknown function
CA2803	0.8	1.2	0.6	0.9	0.9	1.0	IPF11711	orf19.5776	ubiquitin-protein ligase (by homology)
CA3755	0.8	1.1	0.6	0.7	1.0	1.0	IPF17743	orf19.3421.1	Unknown function
CA0027	0.8	0.6	2.3	1.5	1.1	1.2	RCL1	orf19.1886	RNA 3 -terminal phosphate cyclase (by homology)
CA2796	0.8	0.6	1.8	1.3	1.3	1.1	IPF8405	orf19.1721	similar to Saccharomyces cerevisiae Nce103p involved in non-classical protein export pathway (by homology)
CA1735	0.8	1.1	1.3	1.0	0.7	1.0	IPF4986	orf19.2528	similar to Saccharomyces cerevisiae Tfc5p TFIIIB subunit, 90 kD (by homology)
CA1660	0.8	0.8	2.2	1.2	0.8	0.5	DAP2	orf19.4322	dipeptidyl aminopeptidase B (by homology)
CA4256	0.8	0.8	0.9	1.1	1.0	1.0	IPF4282	orf19.544	unknown function
CA4209	0.8	0.9	1.3	1.2	0.8	0.8	DEP1	orf19.808	Regulator of phospholipid metabolism (by homology)
CA6009	0.8	1.0	1.3	1.0	1.2	1.7	IPF643	orf19.7610	similar to Saccharomyces cerevisiae Ptp3p protein tyrosine phosphatase (by homology)
CA5644	0.8	0.8	2.1	1.2	1.1	1.1	IPF447	orf19.7050	unknown function
CA3442	0.8	0.9	0.9	1.0	1.0	0.8	IPF11326	orf19.2983	similar to Saccharomyces cerevisiae (by homology)
CA2833	0.8	1.2	0.7	1.1	1.2	1.3	PTC1	orf19.4785	protein serine/threonine phosphatase 2c (by homology)
CA3061	0.8	1.7	0.5	0.9	1.7	0.8	IPF2965	orf19.4287	unknown function
CA5358	0.8	1.2	0.6	0.9	2.1	1.4	IPF846	orf19.7235	WD-repeat protein, beta-transducin (by homology)
CA4457	0.8	0.7	1.1	1.0	1.0	1.0			
CA5236	0.8	0.5	0.8	0.7	0.4	0.6	LCB2	orf19.5027	Palmitoyl transferase (by homology)
CA4089	0.8	0.6	1.5	1.2	0.9	0.8	IPF5009	orf19.6648	unknown function
CA3499	0.8	0.7	1.1	0.9	1.0	1.0	RPG1	orf19.6345	Translation initiation factor eIF3 (by homology)

CA6022	0.8	0.9	3.3	1.2	0.4	0.4	PGA1	orf19.7625	GPI-anchored cell surface protein (by homology)
CA2992	0.8	0.9	2.0	1.3	1.2	1.7	RRS1	orf19.6014	Regulator for ribosome synthesis (by homology)
CA5974	0.8	0.9	1.0	1.0	1.0	1.0	IPF930	orf19.7568	unknown function
CA5504	0.8	0.9	1.0	1.0	1.4	0.9	TAF65	orf19.5346	subunit of transcription factor TFIID (by homology)
CA1842	0.8	0.6	0.9	1.1	0.8	0.8	ARO1	orf19.4704	arom pentafunctional enzyme (by homology)
CA5815	0.8	0.9	1.0	1.0	1.0	1.0	IPF2517	orf19.7464	putative protease (by homology)
CA5591	0.8	1.3	0.9	1.0	1.1	1.1	IPF5618	orf19.7109	unknown function
CA1410	0.8	1.1	0.4	1.0	1.0	1.1	GAT1	orf19.1275	nitrogen regulation (by homology)
CA0389	0.8	1.0	1.0	1.1	0.9	1.0	IPF14465	orf19.1910	unknown function
CA4077	0.8	0.6	0.9	1.0	1.0	1.0	ACO2	orf19.6632	aconitate hydratase (by homology)
CA0489	0.8	1.3	1.5	1.5	0.7	1.8	IPF6960	orf19.2636	
CA4735	0.8	1.3	0.6	0.7	1.5	1.1	IPF7726	orf19.4850	unknown function
CA4635	0.8	3.1	2.1	1.6	1.9	0.5	IPF1524	orf19.341	putative multidrug resistance protein (by homology)
CA6015	0.8	0.9	1.2	1.2	1.1	1.1	ARD1	orf19.7617	protein N-acetyltransferase subunit (by homology)
CA0388	0.8	1.1	0.8	1.0	0.8	0.8	IPF14468	orf19.1907	unknown function
CA4574	0.8	0.9	1.2	0.9	0.5	0.4	IPF9430	orf19.6885	similar to Saccharomyces cerevisiae Spo7p meiotic protein (by homology)
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)
CA2340	0.8	0.7	0.7	1.1	0.6	0.6	MNN5	orf19.2347	Golgi alpha-1,2-mannosyltransferase (by homology)
CA1039	0.8	0.8	1.7	0.9	0.5	0.5	IPF4012	orf19.2501	Unknown Function
CA3272	0.8	1.1	2.0	1.0	0.7	1.1	ALD4	orf19.6306	aldehyde dehydrogenase, mitochondrial (by homology)
CA4973	0.8	0.9	1.2	0.9	0.8	0.9	IPF4703	orf19.5279	unknown Function
CA2732	0.8	0.7	0.9	0.8	0.5	0.6	IPF10327	orf19.2113	unknown function
CA2607	0.8	0.9	0.9	0.8	0.9	0.9	MRPL38	orf19.5684	ribosomal protein of the large subunit(L14), mitochondrial, by homology
CA0246	0.8	0.8	1.0	1.0	1.2	1.1			
CA6166	0.8	0.9	0.6	1.1	1.7	0.9	CTP1.3f	orf19.5870	Citrate transport protein (by homology)
CA4964	0.8	0.9	0.9	1.0	1.2	1.1	IPF3920	orf19.6509	unknown function
CA0950	0.8	1.0	1.0	1.0	0.9	1.0	IPF3737	orf19.1012	similar to Saccharomyces cerevisiae Aps1p AP-1 complex subunit, sigma1 subunit (by homology)
CA1591	0.8	0.9	1.3	1.1	0.9	1.0	IPF14663	orf19.4316	unknown function
CA5795	0.8	0.7	1.0	0.9	1.0	1.0	TIM44	orf19.5444	mitochondrial inner membrane import receptor
CA1202	0.8	0.7	1.4	1.0	1.1	1.3	DBP3	orf19.4870	ATP-dependent RNA helicase, helicase CA3 (by homology)
CA4869	0.8	1.0	0.7	1.0	1.0	1.0	LYS4	orf19.3846	homoaconitate hydratase
CA4527	0.8	1.1	0.6	1.0	0.7	0.9	IPF4398	orf19.1479	unknown function
CA2056	0.8	0.8	1.0	0.8	1.2	1.5	URA5	orf19.2555	Orotate phosphoribosyltransferase (by homology)
CA1095	0.8	0.5	1.3	0.9	0.4	0.7	SMC1	orf19.4367	Chromosomal ATPase family member (by homology)
CA6037	0.8	0.6	1.4	1.2	0.7	1.0	ERC4	orf19.7648	ethionine resistance protein (by homology)
CA1834	0.8	0.6	0.9	0.8	1.0	1.0	PFK1	orf19.3967	6-phosphofructokinase, alpha subunit
CA3598	0.8	1.0	0.6	0.9	0.9	1.1	SEC2	orf19.4928	GDP/GTP exchange factor (by homology)
CA1385	0.8	0.8	0.9	0.9	0.7	0.9	IPF8424	orf19.925	unknown function
CA5970	0.8	0.7	1.1	0.8	0.6	0.8	DPB2	orf19.7564	DNA-directed DNA polymerase epsilon, subunit B (by homology)
CA1801	0.8	1.3	0.9	1.2	1.1	1.3	IPF11444	orf19.2920	unknown function
CA4768	0.8	1.0	1.9	0.9	1.7	0.8	IPF9385	orf19.4000	similar to Saccharomyces cerevisiae Pho2p homeobox-domain containing transcription factor (by homology)
CA1778	0.8	1.0	1.7	1.0	0.3	1.0	IPF13810	orf19.1825	unknown function
CA0029	0.8	0.9	0.9	1.0	1.0	1.2	PET56	orf19.182	ribosomal RNA methylase (by homology)
CA1064	0.8	0.9	1.5	1.1	1.0	1.0	PWP1	orf19.4640	beta-transducin superfamily (by homology)
CA3085	0.8	0.8	1.6	1.9	1.0	1.2	IPF17086	orf19.4148	unknown function
CA4967	0.8	0.8	0.7	0.9	1.0	0.8	IPF3927	orf19.6506	unknown function

CA3820	0.8	0.8	1.1	0.9	1.3	1.0	PBP2	orf19.5771	PAB1 binding protein (by homology)
CA3074	0.8	0.6	1.0	1.1	0.9	1.1	IPF6106	orf19.4812	similar to Bacillus halodurans holo-(acyl carrier protein) synthase Unknown function
CA5373	0.8	1.1	0.9	1.0	1.0	1.0	IPF5243	orf19.7256	snRNP (by homology)
CA4115	0.8	0.6	1.0	0.7	0.9	0.9	IPF7706	orf19.680	putative plasma membrane phosphatase (by homology)
CA1218	0.8	0.7	0.7	0.7	0.3	0.4	CDC20	orf19.122	anaphase promoting complex subunit (by homology)
CA5157	0.8	1.0	0.4	1.0	1.4	1.0	IPF993	orf19.4595	unknown function
CA3930	0.8	0.9	0.9	0.9	1.1	1.0			
CA0574	0.8	0.9	1.1	1.1	0.9	1.0	IPF15183	orf19.1806	unknown function
CA3043	0.8	0.9	0.9	1.0	1.3	1.1	DOM34	orf19.2419	probable involvement in meiotic and mitotic divisions (by homology)
CA1715	0.8	0.6	1.1	1.1	1.1	1.1	RPS21	orf19.3334	ribosomal protein (by homology)
CA3500	0.8	0.9	1.4	1.1	1.0	1.2	IPF14487	orf19.6346	unknown function
CA5489	0.8	1.0	0.7	1.0	0.8	0.8	MDH12	orf19.5323	mitochondrial malate dehydrogenase (by homology)
CA1768	0.8	0.7	1.4	0.8	0.7	0.8	IPF7585	orf19.5201	unknown function
CA5907	0.8	0.6	1.1	1.2	0.8	0.9	SSN6	orf19.6798	transcriptional repressor (by homology)
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)
CA3542	0.8	1.1	1.1	1.1	1.0	1.2	IPF5426	orf19.6378	putative methyltransferase (by homology)
CA3913	0.8	1.0	0.9	1.0	1.0	0.9	IPF3283	orf19.4388	unknown function
CA1944	0.8	1.0	0.4	0.9	1.2	0.6	IPF10645	orf19.4738	unknown function
CA3476	0.8	1.2	1.0	1.0	1.2	1.1	YRB2.3eoc	orf19.3583	Ran-GTPase-binding protein involved in nuclear export, 3-prime end (by homology)
CA1022	0.8	0.9	1.7	1.9	0.8	0.6	IPF4820.5f	orf19.3353	putativecomplex I intermediate associated protein CIA30 (by homology)
CA3584	0.8	0.9	1.4	1.0	1.1	1.3	IPF15468	orf19.2256	unknown function
CA4920	0.8	0.6	1.0	1.0	0.9	0.9	GCN20	orf19.6060	Positive effector of Gcn2p (by homology)
CA1515	0.8	1.0	0.4	0.8	2.4	1.6			
CA1994	0.8	0.8	0.8	1.0	0.8	1.1	IPF6613	orf19.6481	unknown function
CA1479	0.8	0.8	1.4	1.2	1.1	1.2	IPF16428	orf19.1250	unknown function
CA1748	0.8	0.9	0.6	0.9	0.3	0.7	IPF8257.5f	orf19.1522	unknown function, 5-prime end
CA5364	0.8	0.9	0.9	1.1	1.0	1.1	DCD1	orf19.7243	deoxycytidylate deaminase (by homology)
CA2571	0.8	0.5	1.6	1.2	1.1	0.7	IPF13769	orf19.6209	unknown function
CA4240	0.8	0.9	1.0	1.2	1.4	1.3	NHP2	orf19.526	nucleolar rRNA processing protein (by homology)
CA4898	0.8	0.7	0.9	0.9	1.0	1.1	IPF1461	orf19.6035	putative NADH dehydrogenase (ubiquinone) (by homology)
CA4716	0.8	1.0	0.7	1.1	1.3	0.8	IPF8666	orf19.6952	unknown function
CA2407	0.8	0.8	0.8	1.2	0.7	0.7	ECM14	orf19.299	carboxypeptidase involved in cell wall biogenesis and architecture (by homology)
CA0188	0.8	1.0	1.0	1.1	0.7	0.9	PGA52	orf19.1911	unknown function
CA4921	0.8	1.1	1.1	1.1	1.2	0.6	IPF1416	orf19.6061	unknown function
CA5382	0.8	0.6	0.9	0.9	0.9	0.6	IPF5217	orf19.7270	unknown function
CA4510	0.8	1.2	0.9	0.9	0.5	0.6	IPF8970	orf19.496	similar to Saccharomyces cerevisiae Msh1p DNA mismatch repair protein, mitochondrial (by homology)
CA5984	0.8	1.0	0.8	1.1	1.1	1.0	CUS1	orf19.7581	spliceosome associated protein (by homology)
CA0951	0.8	1.1	1.0	1.0	0.6	0.6	MNN6	orf19.1011	putative golgi alpha-1,2-mannosyltransferase (by homology)
CA3860	0.7	1.0	1.1	1.0	0.8	1.1	KEL1	orf19.6092	involved in cell fusion and morphology (by homology)
CA2042	0.7	0.9	0.8	0.8	0.3	0.5			
CA1828	0.7	0.8	1.2	1.1	0.7	0.7			
CA1303	0.7	0.9	1.2	1.1	1.2	0.9	TFB4	orf19.4194	component of RNA polymerase transcription initiation TFIIH factor (by homology)
CA5029	0.7	1.0	1.0	0.9	0.4	0.6	IPF2997	orf19.6983	unknown function
CA6140	0.7	0.7	1.6	1.2	0.6	1.2	IPF1882	orf19.5905	unknown function Unknown function
CA0023	0.7	0.8	1.1	1.0	0.9	1.0	IPF6922	orf19.3788	unknown function
CA0081	0.7	1.9	0.6	0.8	2.5	0.9	IPF11379	orf19.633	unknown function

CA3846	0.7	0.7	0.9	1.0	0.8	0.9	IPF7943	orf19.6606	unknown function
CA2631	0.7	0.9	1.2	0.9	1.1	1.0	IPF14389	orf19.4758	ubiquinone oxidoreductase subunit NUIM (by homology)
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)
CA0341	0.7	1.8	0.3	1.3	1.1	1.7	XKS1	orf19.1788	xylulokinase (by homology)
CA6146	0.7	0.7	0.9	1.2	0.8	0.9	IPF1863	orf19.5896	unknown function
CA5953	0.7	0.6	1.0	0.4	0.4	0.3	IPF3506	orf19.6741	unknown function
CA3303	0.7	0.8	1.4	1.0	1.0	0.9	FRE42	orf19.2312	ferric reductase (by homology)
CA4494	0.7	1.2	1.1	0.9	1.2	1.2	VMA1	orf19.1866	vacuolar ATPase V1 domain subunit G
CA3872	0.7	0.8	0.9	0.8	0.9	0.9	MRPL28	orf19.397	mitochondrial ribosomal protein of the large subunit (by homology)
CA1558	0.7	1.1	3.2	2.1	0.8	1.0	IPF15679	orf19.1709	lipid transfer protein (by homology)
CA1974	0.7	0.8	0.7	1.0	2.1	1.6	IPF10410	orf19.5227	unknown function
CA5090	0.7	0.8	1.2	1.2	0.7	0.7	IFG4	orf19.3065	probable d-amino acid oxidase (by homology)
CA5861	0.7	1.1	0.9	1.0	1.5	1.1	IPF373	orf19.7519	unknown function
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)
CA4360	0.7	1.1	0.9	1.0	0.4	0.8	IPF6050	orf19.6737	unknown function
CA3278	0.7	0.7	1.0	1.1	1.0	1.0	RPS3E	orf19.6312	Ribosomal protein S3.e (by homology)
CA0795	0.7	0.9	1.2	1.3	1.0	1.2	IPF15641	orf19.551	unknown function
CA4738	0.7	0.9	1.0	1.0	0.7	0.8	IPF4500	orf19.4846	putative GTP-binding protein (by homology)
CA5991	0.7	0.5	1.4	1.1	1.0	1.0	IPF690.3f	orf19.7591	NADH dehydrogenase (ubiquinone) 78K chain precursor, 3-prime end (by homology)
CA0813	0.7	0.7	1.9	1.3	1.3	0.8	MPP10	orf19.1915	component of the U3 small nucleolar ribonucleoprotein (by homology)
CA3040	0.7	0.8	0.8	1.0	0.4	0.7	IPF7306	orf19.2425	putative permease (by homology)
CA4063	0.7	0.8	0.8	1.0	0.8	0.8	SDH11	orf19.440	Succinate dehydrogenase (by homology)
CA3556	0.7	0.8	1.0	1.0	1.0	1.0	IPF7764	orf19.3885	unknown function
CA4258	0.7	1.0	1.3	0.9	1.1	1.3	IPF4279	orf19.547	unknown function
CA4826	0.7	0.8	0.9	0.8	0.9	1.0	IPF1206	orf19.2070	unknown function
CA4009	0.7	0.8	1.1	1.1	1.2	1.0	IPF4247	orf19.1625	unknown function
CA5605	0.7	1.0	0.4	0.9	1.1	1.0	SNF31	orf19.7094	high-affinity glucose transporter (by homology)
CA3635	0.7	1.1	0.6	1.0	0.6	1.0	IFA20	orf19.5139	unknown function
CA5348	0.7	0.6	1.3	1.1	0.8	1.2	IPF863	orf19.7223	involved in inositol biosynthesis (by homology)
CA2746	0.7	1.0	0.9	1.0	1.2	1.0			
CA1200	0.7	0.9	0.7	0.8	0.6	0.8	IPF10223	orf19.4867	putative serine/threonine kinase
CA3794	0.7	0.9	0.9	1.0	1.2	1.2	NCB2	orf19.5825	Transcriptional repressor by homology
CA0031	0.7	1.1	0.9	0.9	1.0	1.1	COX7	orf19.227	Subunit VII of cytochrome c oxidase (by homology)
CA0480	0.7	0.8	1.3	0.9	1.1	0.7	IPF8610	orf19.2633	permease (by homology)
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, cell division, DNA synthesis
CA5318	0.7	0.7	1.4	0.9	0.8	1.1	OGG1	orf19.7190	8-oxoguanine DNA glycosylase (by homology)
CA1876	0.7	0.7	0.9	0.8	0.9	1.0	IPF10301	orf19.2275	putative 60S ribosomal protein L7/L12 homolog, mitochondrial precursor
CA5951	0.7	0.9	0.9	0.9	1.2	1.1	IPF3500	orf19.6744	unknown function
CA0450	0.7	0.9	0.8	1.1	0.6	0.9	IPF9353	orf19.2378	unknown function
CA2455	0.7	0.8	1.2	0.8	0.9	1.1	IPF12228	orf19.3505	unknown function
CA5016	0.7	1.2	1.3	0.9	0.5	0.6	IPF7561	orf19.6968	unknown function
CA0526	0.7	1.4	0.3	0.7	1.0	1.0	BUB3	orf19.2655	cell cycle arrest protein (by homology)
CA4754	0.7	1.0	1.0	1.0	1.2	1.5	IPF11479	orf19.4825	unknown function
CA3882	0.7	0.8	0.8	1.1	1.1	1.1	IPF7279	orf19.386	putative cobalamin-dependent homocysteine S-methyltransferase (by homology)
CA4808	0.7	1.1	1.1	1.3	0.9	1.2	RFA1	orf19.2093	DNA replication factor A, 69 KD subunit (by homology)
CA2994	0.7	0.9	0.6	0.9	0.6	0.5	IPF9116	orf19.6119	unknown function

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)
CA4059	0.7	0.9	0.7	0.6	0.8	1.2	PRD1	orf19.434	Proteinase (by homology)
CA3001	0.7	1.0	0.9	1.1	1.4	1.1	IPF8841	orf19.6132	unknown function
CA4560	0.7	0.8	1.2	0.8	0.5	0.9	IPF8038	orf19.6871	unknown function
CA5508	0.7	0.8	0.8	0.9	0.6	0.7	IPF745	orf19.5352	unknown function
CA2479	0.7	1.1	1.3	1.1	0.1	0.5	CCN1	orf19.3207	G1 cyclin
CA3850	0.7	1.1	0.9	0.6	0.9	1.0	IPF7932	orf19.6612	similar to Saccharomyces cerevisiae Etf-beta electron-transferring flavoprotein, beta chain (by homology)
CA1290	0.7	1.1	0.9	1.0	1.5	1.0	IPF16212	orf19.2710	unknown function
CA4733	0.7	0.9	1.0	0.9	0.6	0.6	IPF7732	orf19.4853	similar to Saccharomyces cerevisiae Hcm1p transcription factor with fork head domain (by homology)
CA2727	0.7	0.8	1.3	1.2	0.9	1.1	IPF10318	orf19.2119	similar to Saccharomyces cerevisiae Ndt80p meiosis-specific protein (by homology)
CA2821	0.7	0.4	0.7	0.9	0.4	0.5			
CA4004	0.7	0.7	3.4	1.5	1.1	0.7	IPF4256	orf19.1632	unknown function
CA6139	0.7	0.6	1.3	1.3	1.0	1.1	ADE2	orf19.5906	phosphoribosylaminoimidazole carboxylase
CA0512	0.7	0.8	1.5	1.5	1.0	1.0	VMA16	orf19.4954	H+-ATPase 23 KD subunit, vacuolar (by homology)
CA3540	0.7	0.9	1.2	1.1	1.2	0.7	PTC5	orf19.6376	Type 2C Protein Phosphatase by homology
CA0032	0.7	0.9	0.9	1.0	0.8	0.8	IPF15248	orf19.229	zinc finger protein (by homology)
CA3912	0.7	1.0	0.6	0.8	0.2	0.7	IPF3288	orf19.4390	unknown function
CA4010	0.7	0.9	1.2	0.7	0.8	0.7	MAK10.3f	orf19.1624	glucose-repressible protein, 3-prime end (by homology)
CA5101	0.7	0.5	0.9	1.0	0.7	0.7	LCB1	orf19.6438	Serine C-palmitoyltransferase subunit (by homology)
CA3349	0.7	0.8	1.0	1.3	0.5	0.8	IPF19588	orf19.2318.1	unknown function
CA0197	0.7	0.9	2.3	2.0	0.4	0.6	IPF9787	orf19.1934	similar to Saccharomyces cerevisiae Hst3p silencing protein (by homology)
CA0132	0.7	0.8	0.9	1.0	1.0	1.0	SPT10	orf19.2361	Transcription regulatory protein (by homology)
CA4984	0.7	0.9	0.9	1.1	0.7	1.1	IPF2052	orf19.5266	unknown function
CA4588	0.7	0.8	1.1	1.1	1.0	1.0	BEL1	orf19.6906.1	protein of the 40S ribosomal subunit (by homology)
CA5824	0.7	1.0	1.3	1.2	1.2	0.9	NTH1	orf19.7479	Neutral trehalase
CA3009	0.7	1.0	0.9	0.9	0.7	0.8	MRPL19	orf19.6231	Ribosomal protein (by homology)
CA4284	0.7	0.9	1.0	1.4	1.1	1.1	DPH52.3eo	orf19.6682	Diphthamide methyltransferase, 3-prime end (by homology)
CA0599	0.7	0.9	1.5	1.2	1.1	1.1	IPF12428	orf19.2667	unknown function
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)
CA5705	0.7	1.1	0.4	1.0	3.3	1.1	IPF2645	orf19.7405	unknown function
CA5121	0.7	0.8	1.6	1.2	1.0	0.9	IPF1310	orf19.6407	unknown function
CA4000	0.7	0.9	1.2	1.0	0.8	0.9	IPF4262	orf19.1636	similar to Saccharomyces cerevisiae Ste50p pheromone response pathway protein (by homology)
CA4178	0.7	0.6	1.0	1.1	1.0	1.0	IPF4421	orf19.2954	unknown function
CA5242	0.7	0.5	0.8	0.9	1.2	0.9	PDX1	orf19.5021	Pyruvate dehydrogenase complex protein X (by homology)
CA5095	0.7	1.1	1.1	1.2	0.9	1.0	ARF21	orf19.6447	GTP-binding protein of the ARF family (by homology)
CA5645	0.7	0.3	1.0	1.0	0.3	0.5	CYB5	orf19.7049	Cytochrome b5 (by homology)
CA4960	0.7	0.8	0.7	0.7	1.2	1.8	IPF3912	orf19.6514	unknown function
CA1030	0.7	0.9	1.1	0.9	0.8	0.6	ZRC1.3f	orf19.1537	Zinc and cadmium resistance protein (by homology)
CA1865	0.7	1.2	0.7	1.1	1.9	1.2	IPF7646	orf19.861	putative transcription factor (by homology)
CA0566	0.7	0.8	1.2	1.0	1.2	1.1	IPF13522	orf19.6252	unknown function
CA5080	0.7	1.0	0.9	0.9	0.9	1.1	SRB4	orf19.3055	probable DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit
CA3993	0.7	0.3	2.4	1.0	0.7	0.7	IPF8275	orf19.1569	unknown function
CA2069	0.7	0.7	0.8	1.2	1.0	1.1	FUR1	orf19.2640	Uracil phosphoribosyltransferase (by homology)
CA4344	0.7	0.8	0.8	0.9	1.1	1.2	IPF3631	orf19.6718	unknown function
CA2150	0.7	1.0	0.8	0.7	0.3	0.7	IPF19940	orf19.6022	unknown function
CA2313	0.7	0.6	1.0	1.0	1.0	1.0	ERF3	orf19.1378	translation release factor 3

CA2211	0.7	0.9	1.3	1.2	0.8	0.8	IPF13921	orf19.4749	Unknown function
CA5938	0.7	0.9	0.9	1.1	0.6	0.7	IPF3481	orf19.6759	unknown function
CA2637	0.7	0.8	1.1	1.0	0.4	0.9	IPF19954	orf19.4301	unknown function
CA1704	0.7	1.2	0.8	1.1	1.0	1.1	SOL3	orf19.704	weak multicopy suppressor of los1-1 (by homology)
CA2097	0.7	1.1	0.9	0.9	0.9	1.0	IPF11489	orf19.2389	unknown function
CA5521	0.7	0.6	0.9	0.8	0.8	1.0	HEM12	orf19.5369	uroporphyrinogen decarboxylase (by homology)
CA3787	0.7	0.9	1.3	1.2	1.4	1.2	HPT1	orf19.5832	hypoxanthine guanine phosphoribosy transferase(by homology)
CA5804	0.7	0.9	1.0	1.0	0.8	1.0	IPF4160	orf19.5459	unknown function
CA1606	0.7	1.1	1.0	1.0	1.3	1.0	NCS1	orf19.4726	Calcium binding protein (by homology)
CA0121	0.7	1.0	1.0	1.1	0.7	0.7	IPF17048	orf19.983	unknown function
CA3487	0.7	0.9	0.8	0.9	0.6	0.9	IPF3203	orf19.3569	unknown function
CA0475	0.7	0.8	0.9	0.9	0.8	0.9	IPF2580	orf19.454	unknown function
CA4660	0.7	0.9	1.0	1.5	0.7	1.4	YMC1	orf19.4447	mitochondrial carrier protein (MCF) (by homology)
CA4188	0.7	1.0	1.1	0.9	1.1	1.0	IPF7525	orf19.4529	unknown function
CA3455	0.7	0.9	1.0	1.0	0.9	1.0	IPF10533.3f	orf19.1256	unknown function, 3-prime end
CA5124	0.7	0.7	1.2	1.1	1.0	0.9	GSH2	orf19.6404	Glutathione synthetase (by homology)
CA3986	0.7	0.8	1.0	0.9	1.5	1.9	IPF7141	orf19.1562	unknown function
CA3931	0.7	0.9	0.5	1.0	1.1	1.1	IPF12719	orf19.5103	unknown function
CA5674	0.7	0.9	0.6	0.9	0.4	0.6	IPF1274	orf19.7377	similar to Saccharomyces cerevisiae Ase1p component of the anaphase spindle midzone (by homology)
CA5467	0.7	1.5	0.8	0.5	1.2	0.8	GSY1	orf19.3278	UDP glucose--starch glucosyltransferase, glycogen synthase (by homology)
CA2665	0.7	0.7	1.0	1.2	0.9	1.1	CDC21	orf19.3549	thymidylate synthase (by homology)
CA5114	0.7	0.7	3.1	1.5	0.7	1.0	IPF1334	orf19.6417	Conserved hypothetical protein
CA3477	0.7	1.0	1.3	1.0	1.3	1.1	IPF3229	orf19.3582	unknown function
CA3452	0.7	1.0	0.9	1.0	0.2	0.9	IPF10541	orf19.1253	unknown function
CA0834	0.7	1.2	0.9	0.9	0.8	1.1	IPF12498.3f	orf19.1677	unknown function, 3-prime end
CA1403	0.7	0.7	1.1	1.1	0.8	1.0	IPF14155	orf19.3373	similar to Saccharomyces cerevisiae Rim4p involved in sporulation (by homology)
CA4650	0.7	0.7	0.9	0.8	0.6	0.7	ISW1	orf19.4437	ATPase component of a four subunit chromatin remodeling complex, (by homology)
CA3953	0.7	1.0	1.0	1.0	0.9	1.1	IPF6714	orf19.1412	
CA2680	0.7	1.0	1.1	1.1	1.2	1.1	MCI4	orf19.2570	NADH dehydrogenase (ubiquinone)
CA5363	0.7	1.4	0.9	1.2	0.6	0.7	NCR1	orf19.7242	Polytopic membrane protein involved in sterol homeostasis and trafficking (by homology)
CA5258	0.7	1.0	0.8	1.0	1.0	1.1	GCV3	orf19.5006	Glycine decarboxylase, subunit H (by homology)
CA5340	0.7	0.4	1.2	1.5	0.8	0.9	IPF883	orf19.7215	unknown function
CA0731	0.7	0.8	1.0	1.0	1.1	1.0	IPF7333	orf19.3722	unknown function
CA4147	0.7	0.5	1.0	1.0	1.0	1.2	ADE8	orf19.5789	Phosphoribosylglycinamide formyltransferase (GART)
CA4362	0.7	1.0	1.3	1.2	1.0	1.1	ATP2	orf19.5653	F1F0-ATPase complex, F1 beta subunit (by homology)
CA2810	0.7	0.6	1.1	1.1	1.0	1.0			
CA0239	0.7	0.8	1.1	1.1	0.8	1.0	RPL9B	orf19.236	RPL9B ribosomal protein L9 by homology
CA1770	0.7	0.6	1.8	1.3	1.3	1.4	IPF12457	orf19.2185	unknown function
CA2270	0.7	0.9	1.0	1.2	0.9	1.0	VMA4	orf19.2598	H+-transporting ATPase E chain
CA4455	0.7	0.7	1.0	0.7	0.7	1.0	IPF8454	orf19.6853	unknown function
CA3425	0.7	1.3	0.8	0.9	0.9	0.9	IPF11873	orf19.593	similar to Saccharomyces cerevisiae Swa2p clathrin-binding protein required for normal clathrin function
CA0903	0.7	0.8	0.7	0.9	1.0	0.9	IPF4401	orf19.1480	putative succinate dehydrogenase (by homology)
CA3914	0.7	1.4	0.8	1.1	0.7	1.1	IPF3277	orf19.4386	hexose transporter (by homology)
CA5104	0.7	1.0	1.0	1.1	1.1	1.1	IPF1364	orf19.6435	unknown function Unknown function
CA1763	0.7	1.1	0.9	1.1	1.2	1.1	URA6	orf19.5195	Uridine-monophosphate kinase(by homology)
CA1187	0.7	0.9	1.2	1.5	1.1	1.0	QRI7	orf19.3787	putative glycoprotease (by homology)

CA2779	0.7	1.0	0.9	1.0	1.3	1.0	IPF3836	orf19.279	unknown function
CA0119	0.7	1.0	1.8	1.4	1.7	1.7	RMT2.5eoc	orf19.920	N-delta-arginine methyltransferase (by homology)
CA3619	0.7	0.6	1.1	0.9	0.4	0.6	CDC47	orf19.202	cell division control protein, ,(by homology)
CA5975	0.7	0.4	1.1	1.1	1.2	1.2	SIK1	orf19.7569	nucleolar protein involved in pre-rRNA processing (by homology)
CA2764	0.7	0.6	1.1	0.8	1.0	1.0	QCR7	orf19.5629	ubiquinol--cytochrome-c reductase subunit 7 (by homology)
CA5143	0.7	1.2	0.8	1.2	1.2	1.1	IPF1020	orf19.4580	Weak similarity to N. crassa hypothetical protein
CA3203	0.7	0.9	1.0	1.0	0.9	0.7	IPF3445	orf19.6183	Unknown function
CA2193	0.7	0.8	0.8	0.8	0.4	0.6	IPF14273	orf19.4347	Probable ser/thr protein kinase (by homology)
CA5890	0.7	0.9	0.4	0.7	1.5	1.9	FCR1	orf19.6817	Zinc cluster transcription factor
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 homology)
CA6090	0.7	0.9	0.9	1.1	0.7	0.8	IPF44	orf19.5967	unknown function
CA4787	0.7	0.7	1.3	1.2	1.3	1.1	IPF3364	orf19.4021	Unknown function
CA0827	0.7	0.8	0.7	1.0	1.7	1.3			
CA4272	0.7	1.2	0.9	1.0	0.8	0.9	CUE1	orf19.6668	Involved in ubiquitination and degradation at the ER surface (by homology)
CA2648	0.7	0.8	0.7	1.0	1.1	1.0	CPH2	orf19.1187	myc-type bHLH transcription factor CpH2
CA4780	0.7	0.9	0.4	0.9	0.8	0.9	IPF3352	orf19.4013	unknown function
CA4340	0.7	0.9	1.0	0.9	0.9	0.8	IPF3621	orf19.6712	unknown function
CA1041	0.7	0.6	2.4	1.1	0.9	1.2	BMS1	orf19.2504	probable membrane protein involved in bud site selection (by homology)
CA4074	0.7	1.3	0.9	1.1	0.9	0.9	IPF2557	orf19.6627	unknown function
CA1791	0.7	1.2	0.4	1.1	1.0	1.1	IPF13967	orf19.5205	unknown function
CA2910	0.7	0.8	1.2	0.8	0.9	1.1	IPF11421	orf19.4517	unknown function
CA5945	0.7	0.9	1.1	0.9	0.7	0.9	IPF3492	orf19.6752	unknown function
CA6043	0.7	0.9	1.1	1.0	1.0	1.1	RFC4	orf19.7658	DNA replication factor C (by homology)
CA1140	0.7	1.0	1.3	0.9	0.4	1.0	IPF17322.3f	orf19.4068	unknown function, 3-prime end
CA0385	0.7	1.5	0.7	1.1	3.6	3.0	IPF4071	orf19.1861	unknown function
CA5702	0.7	0.6	0.9	0.8	0.5	0.7	PCH1	orf19.7402	Putative ATPase (by homology)
CA4236	0.7	1.0	1.0	1.0	1.0	1.2	IPF8166	orf19.519	unknown function
CA5889	0.7	0.7	1.5	1.1	0.6	0.8	IPF2409	orf19.6818	RNA-dependent ATPase (by homology)
CA0441	0.7	1.7	0.3	0.9	0.5	1.0	IPF12472	orf19.5572	unknown function
CA0815	0.7	0.9	1.0	1.0	1.1	1.2	IPF16231	orf19.1913	unknown function
CA0685	0.7	0.7	0.7	1.0	0.9	0.8	ADO1	orf19.5591	adenosine kinase (by homology)
CA0263	0.7	3.0	0.5	0.5	0.9	0.4	GLK1	orf19.13	aldohexose specific glucokinase (by homology)
CA4566	0.7	1.8	0.6	0.7	1.0	0.9	IPF19801	orf19.6877	unknown function
CA5671	0.7	1.2	0.6	1.2	3.6	1.8	CTA4	orf19.7374	Probable transcription factor
CA5506	0.7	1.0	0.6	1.0	0.9	1.0	IPF748	orf19.5350	unknown function
CA2667	0.7	0.4	2.0	1.3	1.1	1.1	IPF16996	orf19.3547	unknown function
CA0069	0.7	1.0	1.4	1.0	1.6	1.0	IPF19295.5f	orf19.6468	unknown function, 5-prime end
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 end (by homology)
CA3294	0.7	0.9	1.0	1.0	0.8	1.0	IPF5725	orf19.6328	unknown function
CA0567	0.7	0.7	1.0	1.0	1.0	1.0	RPS23.5f	orf19.6253	Ribosomal protein S23, 5-prime end (by homology)
CA2235	0.7	0.9	1.0	1.0	0.8	0.9	MPD1	orf19.3920	disulfide isomerase related protein (by homology)
CA5187	0.7	0.8	0.9	1.0	1.4	1.0	TOA2	orf19.4625	TFIIA subunit 13.5 kD (by homology)
CA3977	0.7	0.6	1.2	1.0	1.2	1.2	IPF20153	orf19.1549	unknown function
CA2348	0.7	0.6	0.5	0.6	0.2	0.3	IPF12811	orf19.3751	putative serine/threonine kinase
CA3125	0.7	0.8	0.6	0.9	1.5	1.0	FCY21.5f	orf19.1357.1	Purine-cytosine permease (by homology) , 5-prime end
CA0829	0.7	0.5	0.8	0.6	0.7	0.7	SLC1	orf19.250	fatty acyltransferase (by homology)

CA4827	0.7	1.2	0.4	0.8	0.8	0.8	SMF2	orf19.2069	Manganese transporter (by homology)
CA2973	0.7	0.8	1.0	1.1	1.1	1.0	IPF14452	orf19.5598.2	F1-ATPase epsilon subunit (by homology) Respiration
CA4250	0.7	1.0	0.5	0.9	0.6	1.5	IPF4292	orf19.539	bleomycin Hydrolase
CA0832	0.7	0.8	1.3	1.4	0.5	0.4	IPF14225	orf19.1675	unknown function
CA5289	0.7	0.9	0.9	0.9	1.4	2.4	NRG1	orf19.7150	similar to transcriptional repressor Nrg1p/Nrg2p
CA5829	0.7	0.6	0.9	1.1	1.0	1.0	ADE1	orf19.7484	phosphoribosyl-amidoimidazole-succinocarboxamidesynthetase
CA4367	0.7	0.8	0.8	1.1	0.6	0.7	MNN10	orf19.5658	galactosyltransferase (by homology)
CA3003	0.7	0.4	0.6	0.9	0.5	0.5	IPF15741.5f	orf19.6242	similar to Saccharomyces cerevisiae Cyk3p possibly involved in cytokinesis, 5-prime end (by homology)
CA0548	0.7	0.9	0.6	0.7	1.2	0.4	PHO87	orf19.2454	Member of the phosphate permease family (by homology)
CA0300	0.7	0.7	0.9	1.0	0.4	0.6	ERG24	orf19.1598	C-14 sterol reductase (by homology)
CA4795	0.7	0.9	1.0	1.0	0.8	1.1	IPF3378	orf19.4030	similar to Saccharomyces cerevisiae Pri1p DNA-directed DNA polymerase alpha 48kDa subunit (DNA primase)
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 homology)
CA4748	0.7	1.3	2.1	2.3	4.1	4.5	MLS1	orf19.4833	malate synthase
CA3869	0.7	0.8	0.9	0.9	1.1	1.0	IPF8831	orf19.400	unknown function
CA5708	0.7	0.8	1.0	1.0	0.9	0.9	MRPL39	orf19.7409.1	Mitochondrial 60S ribosomal protein (by homology)
CA1357	0.7	0.9	0.6	0.8	1.5	1.0	ARH1	orf19.410	adrenodoxin reductase and ferredoxin-NADP+ reductase (by homology)
CA1301	0.7	1.1	1.3	1.2	1.0	1.0	YHM2	orf19.4197	mtDNA stabilizing protein (by homology)
CA2202	0.7	0.6	0.9	1.2	0.7	0.9	SCW4	orf19.2941	cell wall glucanase (by homology)
CA5094	0.7	0.9	1.0	0.8	1.0	1.0	IPF1387	orf19.6448	unknown function
CA4215	0.7	0.8	0.6	0.9	1.1	1.4	SSY1	orf19.814	Regulator of transporters (by homology)
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 end (by homology)
CA5579	0.7	1.0	0.8	1.0	0.8	0.7	IPF5661	orf19.7125	unknown function
CA1898	0.7	0.4	0.7	0.6	0.5	1.0	PGA38	orf19.2758	unknown function
CA5186	0.7	0.9	0.6	0.7	1.2	0.9	HRT2	orf19.4624	Similar to ScHRT2 (by homology)
CA0833	0.7	1.0	1.2	1.5	0.9	0.8	IPF12501	orf19.1676	unknown function
CA5933	0.7	1.0	0.3	0.7	1.5	2.9	IPF2804	orf19.6770	unknown function
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)
CA2731	0.7	1.0	2.0	1.3	1.0	1.0	URIC	orf19.2114	uricase (urate oxidase) (by homology)
CA3827	0.7	0.8	0.9	1.0	1.1	1.0	PGA36	orf19.5760	unknown function
CA0327	0.7	0.7	1.9	1.4	1.1	1.1	IPF15217.5f	orf19.3779	WD-repeat protein, 5-prime end (by homology)
CA0192	0.7	1.0	1.0	1.1	1.0	1.0	IPF15134	orf19.1177	Unknown function
CA5956	0.7	0.7	0.9	0.9	0.4	0.5	VAN1	orf19.6738	Vanadate resistance protein
CA0090	0.7	1.0	0.7	0.9	0.8	1.0	UBP13	orf19.2026	ubiquitin carboxyl-terminal hydrolase (by homology)
CA4888	0.7	1.0	1.4	1.1	1.1	1.2	IPF1631	orf19.6580	unknown function
CA0804	0.7	1.4	0.7	0.8	1.2	1.3	BNA1	orf19.3515	3-hydroxyanthranilic acid dioxygenase (by homology)
CA4818	0.7	0.9	0.8	0.7	1.2	1.5	IPF1193	orf19.2079	unknown function Unknown function
CA0153	0.7	1.1	1.0	1.1	1.5	1.0	IPF16368.5f	orf19.255	Unknown function, 5-prime end
CA5419	0.7	0.7	1.2	1.4	0.9	1.2	PRS1	orf19.969	Ribose-phosphate pyrophosphokinase
CA5202	0.7	1.0	1.2	0.9	0.5	0.8	YOX1	orf19.7017	Similar to homoeodomain protein (by homology)
CA4505	0.7	0.4	1.1	1.2	1.1	1.0	NOP2	orf19.501	nucleolar protein (by homology)
CA4117	0.7	0.7	0.7	1.0	1.0	1.1	LAB5	orf19.2774	lipoic acid synthase (by homology)
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 lipolytica glyoxylate pathway regulator Gpr1p
CA2675	0.7	1.1	1.0	1.2	0.8	1.0	GSP1	orf19.5493	GTP-binding protein (by homology)
CA3747	0.7	0.9	1.1	0.9	0.7	1.1	IPF10153	orf19.2170	membrane transporter by homology
CA1771	0.7	0.9	1.0	1.1	0.9	1.0	SEH1	orf19.2186	nuclear pore protein (by homology)
CA1688	0.7	0.6	0.3	0.6	0.8	0.5	COX15	orf19.3656	cytochrome oxidase assembly factor (by homology)

CA4752	0.7	0.6	0.8	1.0	0.8	1.0	ADE12	orf19.4827	adenylosuccinate synthetase (by homology)
CA4671	0.7	0.8	0.9	0.9	1.0	1.0	GPM1	orf19.903	phosphoglycerate mutase (by homology)
CA4268	0.7	0.8	1.0	1.0	1.0	1.0	IPF2287	orf19.6662	unknown function
CA4097	0.7	0.8	1.3	0.9	0.2	0.5	GIN4	orf19.663	ser/thr protein kinase (by homology)
CA5940	0.7	1.5	1.9	1.1	4.3	0.9	IPF3485	orf19.6757	aldo/keto reductase (by homology)
CA2216	0.7	0.9	1.0	1.0	0.7	1.3	IPF6235	orf19.5372	Candida albicans Tca2 retrotransposon
CA4222	0.7	0.8	1.4	1.0	1.0	1.2	GCD7	orf19.825	translation initiation factor eIF2b subunit (by homology)
CA0387	0.7	0.8	1.0	1.0	1.0	1.0	IPF14475.5	orf19.1904.2	
CA1982	0.7	0.6	1.0	0.8	0.9	1.1	ADK1	orf19.683	adenylate kinase, cytosolic (by homology)
CA0603	0.7	1.3	1.0	1.1	1.0	0.9	IPF1709	orf19.3076	unknown function
CA5359	0.7	0.5	1.2	1.1	1.1	1.0	TIF35	orf19.7236	translation initiation factor eIF3, p33 subunit (by homology)
CA5588	0.7	1.0	1.1	1.0	1.1	1.0			
CA5023	0.7	0.7	2.1	1.0	0.4	0.6	IPF7547	orf19.6976	unknown function
CA4370	0.7	0.8	0.9	1.1	1.0	0.8	IPF5279	orf19.5661	unknown function
CA3208	0.7	0.9	0.9	1.1	1.0	1.1	PSA1	orf19.6190	GDP-mannose pyrophosphorylase
CA4380	0.7	2.9	0.8	1.1	1.1	2.1	IPF12736	orf19.5673	unknown function
CA3123	0.7	0.6	1.1	1.1	1.1	1.0	RPL6	orf19.3003.1	ribosomal protein
CA2986	0.7	0.5	0.7	0.9	0.2	0.3	CDC5	orf19.6010	Cell-cycle protein kinase (by homology)
CA2784	0.7	0.8	1.0	1.1	1.0	1.0	IPF3810	orf19.287	unknown function
CA2752	0.7	1.0	1.0	0.9	1.0	1.0	IPF6238	orf19.2374	GAG protein of retrotransposon pCal
CA5923	0.7	0.4	1.1	0.7	0.7	0.3	IFQ2	orf19.6782	Unknown function
CA6028	0.7	0.9	1.0	0.8	0.3	0.8	IPF607	orf19.7634	unknown function
CA0861	0.7	0.9	0.9	1.0	0.6	0.8	CRK1.3f	orf19.3523	Protein kinase, 3-prime end
CA5068	0.7	1.0	0.6	1.1	0.9	1.5	IPF3592	orf19.3041	unknown function
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 primase) (by homology)
CA3240	0.7	0.6	1.4	1.1	0.6	0.8	IPF10559	orf19.4683	myosin-like protein (by homology)
CA3896	0.7	0.6	1.2	1.0	0.9	1.3	IPF10339	orf19.5077	unknown function
CA5112	0.7	3.0	1.2	1.3	0.7	1.3	PGA13	orf19.6420	Similarity to mucin proteins
CA0046	0.7	0.9	0.7	0.7	0.4	0.3	IPF14850	orf19.2452	Hypothetical protein
CA1326	0.7	0.9	0.8	1.1	0.9	1.3	IPF6679	orf19.1306	unknown function
CA3588	0.7	0.5	1.2	1.1	1.3	1.1	SPE3	orf19.2250	putrescine aminopropyltransferase by homology
CA3424	0.7	0.9	1.0	1.1	1.0	0.9	NOP10	orf19.596.1	Nucleolar rRNA processing protein (by homology)
CA3752	0.7	0.7	1.1	1.2	1.0	1.0	TIF51.3f	orf19.3426	translation initiation factor eIF-5A, 3-prime end
CA1619	0.7	0.6	1.6	1.5	0.6	0.6	IPF2067	orf19.4077	Required for mannosylation of sphingolipids (by homology)
CA2477	0.7	1.3	1.0	0.8	1.5	2.1	MNN4	orf19.2881	regulates the mannosylphosphorylation (by homology)
CA0684	0.7	1.0	0.3	0.9	1.1	1.1			
CA4708	0.7	1.0	1.8	1.1	1.2	1.1	MEU1	orf19.6938	regulator of ADH2 expression (by homology)
CA3866	0.7	0.7	0.7	1.3	0.9	0.8	IPF4606	orf19.6082	unknown Function
CA5766	0.7	0.7	0.4	0.7	1.5	1.0	IPF1097	orf19.5408	serine/threonine protein kinase (by homology)
CA0696	0.7	0.6	1.1	1.4	1.2	1.1	HMT1	orf19.3291	hnRNP methyltransferase (by homology)
CA3541	0.7	0.8	1.0	0.8	1.0	1.1	IPF5425	orf19.6377	similar to Saccharomyces cerevisiae Ppm1p carboxy methyltransferase (by homology)
CA0270	0.7	1.4	0.8	1.2	1.9	1.5	PRB2	orf19.2242	Protease B, vacuolar (by homology)
CA0667	0.7	1.0	1.1	0.8	0.8	1.1	TIF5	orf19.4261	Translation initiation factor eIF5 (by homology)
CA3957	0.7	0.9	1.0	0.9	0.9	0.9	RBT2	orf19.1415	Repressed by TUP1 protein 2; Rbt2p, Ferric reductase (by homology)
CA0189	0.7	0.4	0.5	0.6	1.2	0.9	IPF12201	orf19.4118	Na+-nucleoside cotransporter (by homology)
CA4578	0.7	0.7	0.9	0.8	0.8	0.8	RFC1	orf19.6891	DNA replication factor C (by homology)

CA2359	0.7	0.6	1.7	1.2	0.8	1.0	IPF8952	orf19.4896	similar to Saccharomyces cerevisiae Rpa34p nonessential component of RNA-polI (by homology)
CA0432	0.7	0.5	1.0	1.1	0.9	0.9	IPF7926	orf19.1341	putative protein kinase (by homology)
CA4105	0.6	1.0	0.7	1.0	1.1	1.2	SMT3	orf19.670	Ubiquitin-like protein (by homology)
CA2858	0.6	0.4	1.0	0.8	1.0	1.0	ACS2	orf19.1064	acetyl-coenzyme-A synthetase (by homology)
CA5446	0.6	0.6	1.5	0.9	0.5	0.7	LAG1	orf19.3249	longevity-assurance protein (by homology)
CA2004	0.6	0.7	1.0	0.7	0.6	0.8	POL12	orf19.2796	DNA-directed DNA polymerase alpha (by homology)
CA3307	0.6	0.7	1.1	1.1	1.1	1.0	RPL2	orf19.2309.2	ribosomal protein L8, 3-prime end (by homology)
CA3154	0.6	0.9	2.0	0.9	1.8	1.0	FUN34.5eoc	orf19.6169.2	unknown function, 5-prime end
CA5493	0.6	0.4	0.9	0.8	0.7	0.8	GCN1.5f	orf19.5333	translational activator, 5-prime end (by homology)
CA2795	0.6	1.1	0.6	0.9	0.9	1.1	IPF8407	orf19.1723	unknown function
CA2573	0.6	0.6	1.2	1.1	1.1	1.1	SUI2	orf19.6213	translation initiation factor eIF2, alpha chain (by homology)
CA3587	0.6	1.2	0.8	1.5	3.6	1.0	AAH1	orf19.2251	adenosine deaminase (by homology)
CA5948	0.6	0.8	1.1	0.9	1.0	1.0	IPF3496	orf19.6748	unknown function
CA5073	0.6	1.0	0.8	0.9	0.2	0.6	IPF3603	orf19.3048	unknown function
CA4830	0.6	0.8	1.1	1.0	1.4	1.0	ATP8	orf19.2066.1	F1F0-ATPase complex, Atp8 subunit (by homology) Respiration
CA3782	0.6	0.9	1.0	1.0	1.0	1.2	SER2	orf19.5838	phosphoserine phosphatase by homology to S. cerevisiae
CA0948	0.6	1.1	0.9	1.9	1.1	1.0	IPF10270	orf19.1272	unknown function
CA2941	0.6	0.9	1.3	1.1	0.7	0.6	CVB1	orf19.1970	vacuole biogenesis component
CA3198	0.6	1.0	1.0	1.2	1.4	0.9	IPF3432	orf19.6177	Unknown function
CA4569	0.6	1.6	0.5	0.9	3.3	2.3	IPF9552	orf19.6881	unknown function
CA3358	0.6	0.9	0.6	1.0	1.0	1.2	IPF19984	orf19.1940	similar to Saccharomyces cerevisiae Cat5p involved in coenzyme Q (ubiquinone) biosynthesis (by homology)
CA5582	0.6	0.9	1.1	1.1	1.1	0.9	ADK2	orf19.7118	adenylate kinase, mitochondrial (by homology)
CA5298	0.6	0.5	1.1	1.2	1.0	1.0	SUI3	orf19.7161	Translation initiation factor eIF2 beta subunit (by homology)
CA4495	0.6	1.1	0.9	0.8	0.7	0.7	IPF4059	orf19.1865	aldehyde dehydrogenase (by homology)
CA4235	0.6	0.4	1.1	1.0	1.0	1.1	NCL1	orf19.518	Probable proliferating-cell nucleolar antigen (by homology)
CA3606	0.6	1.0	4.6	1.9	1.4	2.0	RTA3	orf19.23	Unknown function
CA3095	0.6	1.4	1.0	1.0	0.8	1.1	CDC28	orf19.3856	CELL DIVISION CONTROL PROTEIN 28 -protein kinase
CA4536	0.6	0.6	1.1	1.1	1.0	1.0	COX13	orf19.1467	cytochrome-c oxidase chain VIa (by homology)
CA3805	0.6	1.1	0.8	1.1	0.8	1.0	IPF12403	orf19.2484	unknown function
CA0037	0.6	1.0	0.7	1.0	0.9	1.0	IPF17652.3	orf19.6078	reverse transcriptase, 3-prime end (by homology)
CA4732	0.6	0.8	1.1	1.1	0.9	0.9	IPF7733	orf19.4855	unknown function
CA2572	0.6	0.8	0.7	1.0	1.2	1.0	IPF13766	orf19.6211	unknown function
CA5362	0.6	0.8	1.3	1.0	0.9	0.6	IPF836.3	orf19.7239	regulation of G-protein function, (by homology)
CA0127	0.6	0.9	0.8	0.4	1.0	1.0	HXK2	orf19.542	hexokinase II (by homology)
CA2949	0.6	0.9	1.3	1.0	0.5	0.8	IPF14506	orf19.1961	unknown function
CA3229	0.6	0.9	1.8	1.1	0.5	0.9	FUN30	orf19.6291	helicases of the Snf2/Rad54 family(by homology)
CA4054	0.6	0.7	1.9	1.0	0.9	1.0	TRF4	orf19.429	Topoisomerase I-related protein
CA2522	0.6	0.7	1.0	1.1	0.9	1.1	GCV1	orf19.5519	glycine cleavage T protein (by homology)
CA2326	0.6	0.6	1.1	0.9	0.8	0.8	NUBM	orf19.4495	nucleotide-binding respiratory complex I subunit (by homology)
CA1490	0.6	0.7	1.1	1.0	1.1	1.0	IPF165	orf19.3224.1	unknown function
CA2090	0.6	0.7	1.0	1.1	1.0	1.0	IPF3398.3f	orf19.837.2	unknown function, 3-prime end
CA5802	0.6	0.9	1.0	1.4	0.5	0.9	IPF4164	orf19.5455	similar to Saccharomyces cerevisiae Vtc1p negative regulator of Cdc42p (by homology)
CA2682	0.6	0.6	0.9	0.9	0.9	1.1	FRS1	orf19.2573	Phenylalanyl-tRNA synthetase
CA1548	0.6	1.1	0.5	0.9	1.5	1.0	IPF8746	orf19.4279	putative alpha-1,3-mannosyltransferase (by homology)
CA0403	0.6	0.9	0.8	1.1	0.5	0.6	PGA51	orf19.1989	unknown function
CA0368	0.6	0.9	0.2	0.9	1.0	0.9	IPF11646	orf19.1353	unknown function

CA5201	0.6	0.9	1.1	0.9	0.2	0.6	IPF2349	orf19.7016	similar to human sphingomyelin
CA5081	0.6	0.8	0.8	1.1	0.8	0.9	COQ6	orf19.3058	monooxygenase (by homology)
CA2813	0.6	0.8	1.5	1.0	0.9	0.9	ORC1	orf19.3000	Origin recognition complex protein 1
CA4476	0.6	1.6	1.1	1.2	0.8	1.1	APR1	orf19.1891	aspartyl protease
CA1973	0.6	0.5	1.4	0.9	1.0	1.1	WRS1	orf19.5226	tryptophan--tRNA ligase
CA0895	0.6	1.3	1.0	1.0	0.9	1.0	SHM2	orf19.5750	Serine hydroxymethyltransferase precursor, mitochondrial (by homology)
CA4475	0.6	0.9	0.8	0.8	1.2	0.9	IPF6455	orf19.1893	unknown function
CA4963	0.6	0.8	1.0	1.0	1.2	1.1	IPF3919	orf19.6510	unknown function
CA3757	0.6	0.8	0.2	0.3	0.5	0.5	MAE1	orf19.3419	mitochondrial malic enzyme (by homology)
CA2628	0.6	1.1	1.1	1.2	0.9	1.1	SIR22	orf19.4761	canal regulatory protein (by homology)
CA4844	0.6	0.4	1.2	1.2	1.0	1.2	PDR13	orf19.3812	Drug resistance
CA4498	0.6	0.4	1.4	1.4	0.9	1.0	IPF11315	orf19.512	unknown function
CA1593	0.6	0.9	1.0	0.8	1.0	1.0	MIG1	orf19.4318	transcriptional regulator
CA6061	0.6	0.6	2.3	1.2	0.4	0.4	IPF8302	orf19.6007	unknown function
CA3573	0.6	0.8	1.1	1.0	1.1	1.2	RFA2	orf19.2267	DNA replication factor by homology to S. cerevisiae
CA5704	0.6	1.7	0.5	0.9	1.2	1.2	CHA11	orf19.7404	L-serine/L-threonine deaminase (by homology)
CA1114	0.6	0.6	0.9	1.2	1.1	1.2	IPF9995	orf19.2286	unknown function
CA2892	0.6	1.0	1.2	1.0	0.9	1.4	IPF6688	orf19.2465	unknown function
CA2802	0.6	1.0	0.8	0.8	0.9	0.8	IPF11363	orf19.1715	unknown function
CA4189	0.6	1.1	0.5	1.0	1.0	1.0	IPF7527	orf19.4530.1	unknown function
CA1211	0.6	1.1	0.7	0.8	0.6	0.5	IPF7031.3f	orf19.131.2	unknown function, 3-prime end
CA3469	0.6	0.7	0.8	1.0	0.5	0.9	MNT1	orf19.1665	Mannosyltransferase involved in n-linked and o-linked glycosylation
CA0585	0.6	0.7	1.0	1.1	1.0	1.0	ADE5,7.5f	orf19.5062	phosphoribosylamine-glycine ligase and phosphoribosylformylglycinamidine cyclo-ligase, 5-prime end (by homology)
CA4094	0.6	0.7	1.2	0.9	0.4	0.8	IPF4004	orf19.658	unknown function
CA2839	0.6	0.6	1.9	0.7	3.9	2.3	IPF8336	orf19.4792	unknown function
CA3433	0.6	1.0	0.9	1.0	0.8	1.1	IPF6387.3f	orf19.584.3	unknown function, 3-prime end
CA4943	0.6	1.0	0.8	1.0	0.8	1.2	IPF5158	orf19.6534	unknown function
CA2135	0.6	0.7	0.9	1.0	1.0	1.0	COX9	orf19.5213.2	CYTOCHROME C OXIDASE (by homology)
CA2785	0.6	1.7	0.6	0.9	0.9	1.0	MET13	orf19.288	Methylene tetrahydrofolate reductase (by homology)
CA3014	0.6	0.9	1.0	0.8	1.5	0.9	IPF11915	orf19.6225	similar to Saccharomyces cerevisiae Pcl7p cyclin like protein interacting with Pho85p (by homology)
ATP6	0.6	0.8	1.0	1.4	2.0	1.1			
CA3834	0.6	0.8	0.6	0.9	1.0	0.7	PLB3	orf19.6594	phospholipase B (by homology)
CA2471	0.6	0.9	1.2	1.1	0.7	0.9	TOP2	orf19.2873	Topoisomerase II
CA5021	0.6	0.4	1.1	1.0	1.0	1.0			
CA5693	0.6	1.0	1.3	1.0	0.4	0.8	GDA1	orf19.7394	Golgi guanosine diphosphatase (by homology)
CA1927	0.6	0.6	1.0	1.1	1.0	1.0	YBN5	orf19.754	Putative purine nucleotide-binding protein (by homology)
CA2881	0.6	0.5	1.7	1.1	1.1	1.1	RAD4	orf19.5850	Excision repair protein (by homology)
CA4515	0.6	0.7	0.9	0.9	1.0	0.8	IPF16652	orf19.490	unknown function
CA1925	0.6	1.0	0.7	0.8	1.3	1.0	IPF18587	orf19.752	putative methyltransferase (by homology)
CA4970	0.6	1.0	0.7	0.6	2.2	3.6	IPF4696	orf19.5282	unknown Function
CA4876	0.6	1.0	1.0	1.1	1.0	0.6	RNH35	orf19.6562	RNase H (by homology)
CA0695	0.6	0.7	1.1	1.0	1.4	1.1	IPF12601	orf19.3290	unknown function
CA2250	0.6	0.4	0.8	0.7	1.0	0.9	MIS11	orf19.2364	mitochondrial C1-tetrahydrofolate synthase precursor (by homology)
CA0286	0.6	1.0	0.8	1.1	0.9	1.1	IPF14618	orf19.6079	unknown function
CA2822	0.6	1.0	0.6	0.9	1.4	0.9	IPF14550	orf19.1314	unknown function
CA4276	0.6	1.1	0.9	1.1	1.1	1.2	HEX1	orf19.6673	_-N-acetylglucosaminidase

CA5627	0.6	0.8	1.1	1.1	0.9	1.2	IPF495	orf19.7069	unknown function
CA1976	0.6	0.5	1.0	0.9	0.8	0.8	IPF9582	orf19.688	similar to Saccharomyces cerevisiae Mrps18p ribosomal protein of the small subunit, mitochondrial (by homology)
CA4409	0.6	0.7	0.8	0.8	0.5	0.7	IPF13151	orf19.3100	unknown function
CA3399	0.6	3.7	1.1	1.5	0.6	1.0	PUT2	orf19.3974	1-pyrroline-5-carboxylate dehydrogenase (by homology)
CA1557	0.6	1.0	0.8	1.0	1.1	1.0	IPF15677	orf19.1710	probable NADH-ubiquinone oxidoreductase (by homology)
CA4315	0.6	0.8	0.7	1.1	1.3	0.9	PPX1	orf19.4107	Exopolyphosphatase (by homology)
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)
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)
CA1923	0.6	0.8	1.0	0.9	1.1	1.0	IPF9130	orf19.5539	unknown function
CA3102	0.6	0.7	2.3	1.2	1.4	1.6	RLP7	orf19.3867	ribosomal-like proteins
CA1672	0.6	0.9	1.1	1.0	1.4	1.0	IPF5196	orf19.3611	unknown function
CA5724	0.6	0.9	0.7	1.1	1.0	1.0	NUP116	orf19.7433	nuclear pore protein (by homology)
CA3877	0.6	0.9	0.6	0.7	0.9	0.8	CBP4	orf19.392	Ubiquinol--cytochrome-c reductase assembly factor (by homology)
CA4456	0.6	0.4	1.0	1.0	0.9	1.0	ATP1	orf19.6854	F1F0-ATPase complex, F1 alpha subunit
CA4167	0.6	2.1	0.8	1.0	0.9	1.1	IPF7778	orf19.2966	putative carboxymethylenebutenolidase (dienelactone hydrolase, DLH) (by homology)
CA5315	0.6	0.8	0.7	1.2	0.5	0.7	CYB2	orf19.7186	B-type cyclin
CA4481	0.6	1.1	1.1	1.2	1.1	1.2	IPF9150	orf19.1885	similar to Saccharomyces cerevisiae Mpt1p required for protein synthesis (by homology)
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)
CA1629	0.6	2.2	1.2	1.5	1.4	1.3	NPI46	orf19.1030	proline cis-trans isomerase (by homology)
CA4225	0.6	0.6	1.1	0.9	1.0	1.0	RPL39	orf19.827.1	ribosomal protein L39
CA1289	0.6	0.5	1.1	1.0	1.2	1.1	ZUO1	orf19.2709	Zuotin, a putative Z-DNA binding (by homology)
CA3535	0.6	0.5	1.5	1.2	0.9	0.9	IPF13458	orf19.6369	unknown function
CA0104	0.6	0.8	0.7	1.1	0.3	0.8	RBT4	orf19.6202	repressed by TUP1 protein
CA3570	0.6	0.6	1.1	1.2	0.9	0.9	NOP1	orf19.3138	Fibrillarin
CA5052	0.6	1.0	1.1	1.2	0.9	1.0	IPF3708	orf19.3016	unknown function
CA1438	0.6	0.4	1.4	1.2	1.2	1.1	NOP58	orf19.1199	nucleolar protein required for pre-18S rRNA processing
CA0109	0.6	0.8	0.3	0.6	1.0	1.0	IPF13723	orf19.260	unknown function
CA2347	0.6	0.9	0.9	1.1	1.2	1.2	RAD51	orf19.3752	DNA repair protein by homology
CA6131	0.6	0.9	0.5	0.8	0.7	0.9	IPF4369	orf19.5917	similar to Saccharomyces cerevisiae Stp2p involved in pre-tRNA splicing (by homology)
CA4255	0.6	0.6	1.0	1.0	1.0	0.9	FUM11	orf19.543	fumarate hydratase
CA5064	0.6	0.8	1.0	1.0	0.9	0.9	CHD1	orf19.3035	transcriptional regulator (by homology)
CA5775	0.6	0.7	1.1	1.2	0.9	0.9	ATP5	orf19.5419	F1F0-ATPase complex, OSCP subunit (by homology)
CA3804	0.6	1.1	0.8	1.0	1.1	1.1	RIM1	orf19.2483	telomere-binding protein (by homology)
CA5694	0.6	1.0	0.5	0.9	1.1	0.8	IPF3311	orf19.7396	unknown function
CA2602	0.6	0.7	1.0	1.1	1.0	0.8	IPF5473.5e	orf19.5679	unknown function
CA2383	0.6	1.3	0.6	1.0	0.7	1.2	IPF18474	orf19.2222.2	unknown function
CA2979	0.6	0.5	1.2	0.7	0.8	0.8	ADE4	orf19.1233	amidophosphoribosyltransferase (by homology)
CA4361	0.6	0.9	0.8	0.9	0.9	1.0	IPF16104	orf19.5651	unknown function
CA4926	0.6	1.1	0.6	0.9	0.8	1.0	IPF1404	orf19.6065	unknown function
CA0272	0.6	0.7	0.8	0.7	0.7	0.8	DPB11	orf19.1434	DNA polymerase II complex (by homology)
CA4369	0.6	0.9	1.1	1.1	1.0	0.9	TIM11	orf19.5660.1	subunit e of mitochondrial F1F0- ATPase by homology
CA4749	0.6	0.6	1.0	0.8	0.4	0.8	IPF4481	orf19.4831	unknown function
CA3771	0.6	2.2	4.7	2.6	0.9	1.0	SOU1	orf19.2896	Sorbitol utilization protein Sou1p [Candida albicans]
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 isomerase(by homology)
CA3743	0.6	1.0	0.6	1.1	1.5	1.5	IPF19998	orf19.2175	unknown function
CA0276	0.6	0.5	0.9	0.7	0.5	0.9	IPF15015	orf19.5612	unknown function

CA0670	0.6	1.6	0.5	0.7	6.4	5.3	IPF5915	orf19.449	phosphatidyl synthase (by homology)
CA5204	0.6	0.5	1.1	0.7	0.7	0.9	YML6	orf19.7019	Ribosomal protein, mitochondrial (by homology)
CA4828	0.6	1.4	0.7	0.9	0.9	1.0	IPF1209	orf19.2068	unknown function
CA2505	0.6	0.7	1.2	1.0	0.6	0.7	IPF6796	orf19.5595	unknown function
CA2214	0.6	0.8	0.3	0.6	1.2	0.8	IPF9939	orf19.4752	similar to Saccharomyces cerevisiae Msn4p transcriptional activator (by homology)
CA5460	0.6	0.7	0.9	1.1	0.8	0.8	IPF277	orf19.3268	human IgE-dependent histamine-releasing factor homolog (by homology)
CA4670	0.6	1.1	0.5	0.8	1.3	2.8	IPF4536	orf19.904	unknown function
CA3308	0.6	0.8	2.2	1.0	0.6	1.0	PET127.5f	orf19.2309	component of mitochondrial translation (by homology)
CA2253	0.6	0.9	1.6	1.2	0.9	0.8	IPF15485	orf19.1959	unknown function
CA4226	0.6	0.6	1.3	0.7	0.7	0.8	IPF8752	orf19.828	similar to Saccharomyces cerevisiae Mrpl24p ribosomal protein of the large subunit, mitochondrial (by homology)
CA5638	0.6	0.4	0.9	1.1	0.9	1.0	IPF470	orf19.7057	putative glutamine-tRNA ligase (by homology)
CA3534	0.6	0.2	1.0	0.9	1.0	1.0	SSB1	orf19.6367	heat shock protein 70
CA3042	0.6	0.6	1.0	1.1	1.1	1.2	ARC1	orf19.2422	G4 nucleic acid binding protein (by homology)
CA4810	0.6	0.5	1.1	0.9	1.1	1.1	IPF1164	orf19.2091	Subunit NUHM of NADH:Ubiquinone Oxidoreductase (by homology)
CA4206	0.6	0.8	0.4	0.8	1.2	0.6	IPF9079	orf19.4550	Membrane transporter (by homology)
CA3207	0.6	1.0	0.8	1.0	0.9	1.2	IPF3456	orf19.6189	unknown function
CA2989	0.6	1.0	0.7	0.9	0.6	1.0			
CA5852	0.6	0.8	1.0	1.0	1.2	1.2	ATP17	orf19.7509.1	F1F0-ATPase complex, F1 delta subunit f (by homology)
CA4952	0.6	0.9	1.8	1.6	0.6	0.7	IPF13609	orf19.6526	unknown function
CA0659	0.6	0.7	0.8	0.6	0.4	0.4	IPF16189.3f	orf19.5576	panthotenate kinase, 3-prime end (by homology)
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)
CA6134	0.6	0.6	1.3	1.1	0.8	0.8	MAK21	orf19.5912	Ribosome biogenesis protein (by homology)
CA5495	0.6	0.9	0.9	0.9	0.5	1.1	SGS1	orf19.5335	ATP-dependent DNA helicase (by homology)
CA2303	0.6	0.5	0.9	1.2	0.8	0.7	TOS1	orf19.1690	putative Anchor subunit of a-agglutinin (by homology)
CA2521	0.6	0.9	1.2	1.3	0.6	0.9	IPF4317	orf19.5518	unknown function
CA0540	0.6	0.7	1.1	1.1	1.4	1.1	IPF10896	orf19.2821	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor (by homology)
CA2733	0.6	0.7	1.2	1.1	0.9	0.8	PRP18	orf19.2112	U5 snRNA-associated protein (by homology)
CA4441	0.6	1.1	1.4	1.9	1.3	0.9	IPF2268.3f	orf19.6834.3	unknown function, 3-prime end
CA5914	0.6	1.0	0.9	0.9	0.7	1.0	HHT3	orf19.6791	histone H3
CA5369	0.6	1.0	1.2	1.1	0.9	0.8	WSC4	orf19.7251	Cell wall integrity by homology
CA3158	0.6	0.6	0.8	1.4	1.1	1.0	IPF13131.3	orf19.1587	unknown function, 3-prime end
CA5794	0.6	0.8	0.6	1.0	0.7	0.7	IPF4191	orf19.5443	unknown function
CA2134	0.6	0.8	0.9	1.1	1.0	1.0	COX8	orf19.5213.1	CYTOCHROME C OXIDASE (by homology)
CA0701	0.6	0.8	1.0	1.0	1.0	1.0	IPF10397	orf19.3366.1	unknown function
CA3112	0.6	0.4	0.8	0.6	1.1	1.0	PFK2	orf19.6540	6-phosphofructokinase, beta subunit
CA0524	0.6	0.7	1.0	1.0	0.9	1.0			
CA4627	0.6	0.6	1.0	1.0	0.5	1.1	DUT1	orf19.3322	dUTP pyrophosphatase
CA4874	0.6	0.6	0.6	0.5	1.8	1.4	IPF1674	orf19.6559	putative transcription initiation factor (by homology)
CA4081	0.6	1.1	0.4	0.9	0.9	1.0	IPF2523	orf19.6637	unknown function
CA0035	0.6	1.2	0.7	1.0	0.7	1.0	PRC3	orf19.2474	Carboxypeptidase Y precursor (by homology)
CA3923	0.6	1.2	0.7	0.8	0.8	1.0	ADH2	orf19.5113	alcohol dehydrogenase I (by homology)
CA4570	0.6	1.2	0.8	0.5	1.0	1.1	IPF9550	orf19.6882	similar to Saccharomyces cerevisiae Osm1p osmotic growth protein
CA1679	0.6	0.9	1.0	1.1	0.9	1.0			
CA0414	0.6	1.1	0.9	0.8	1.6	1.2	IPF4068	orf19.2164	reverse transcriptase
CA0367	0.6	0.9	0.4	1.0	1.4	0.9	TIM22	orf19.1352	Mitochondrial import inner membrane translocase subunit (by homology)
CA0660	0.6	0.8	0.7	0.6	0.5	0.4	IPF16189.5f	orf19.5577	panthotenate kinase, 5-prime end (by homology)

CA5078	0.6	1.1	0.8	0.8	1.5	1.3	IPF15297	orf19.3053	unknown function
CA5501	0.6	0.8	0.9	1.2	0.9	1.0	MTR2.3f	orf19.5342.1	mRNA transport protein, 3-prime end (by homology)
CA6029	0.6	0.5	1.7	1.3	1.1	1.5	DRS1	orf19.7635	ATP dependent RNA helicase (by homology)
CA2950	0.6	0.7	0.3	0.8	0.1	0.4	CLN2	orf19.1960	G1/S-SPECIFIC CYCLIN CLN2
CA1789	0.6	0.5	1.2	1.2	1.2	1.1	GAR1	orf19.1164	Nucleolar rRNA processing protein (by homology)
CA3346	0.6	1.4	0.6	1.1	1.8	1.2	IPF13356	orf19.2324	molybdopterin biosynthesis (by homology)
CA2368	0.6	0.6	1.2	1.2	0.9	1.0	RPA190	orf19.1839	DNA-directed RNA polymerase I (by homology)
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 homology)
11759.20	0.6	1.2	0.2	0.3	1.4	1.5			
CA3018	0.5	0.5	1.0	1.1	1.0	1.0	SAH1	orf19.3911	S-adenosyl-L-homocysteine hydrolase by homology
CA2708	0.5	0.3	1.2	1.0	1.1	1.0	RPS6A	orf19.4660	ribosomal protein S6 (by homology)
CA4005	0.5	0.6	1.1	1.1	0.2	0.5	ERG6	orf19.1631	sterol transmethylase
CA5179	0.5	0.7	0.5	0.6	2.5	1.6	MAK3	orf19.4617	N-acetyltransferase (by homology)
CA4590	0.5	0.5	1.1	1.0	0.9	0.9	IPF2218	orf19.6907	unknown function
CA0890	0.5	1.0	0.5	1.0	1.2	1.3	IPF11766	orf19.4734	unknown function
CA1803	0.5	0.6	1.8	1.2	1.1	1.2	IPF16748	orf19.2917	unknown function
CA4326	0.5	0.4	1.5	1.3	1.2	1.3	IPF2093	orf19.4093	nuclear protein of unknown function (by homology)
CA3604	0.5	0.6	2.1	1.8	0.3	0.4	IPF12942	orf19.4933	delta-12 fatty acid desaturase (by homology)
CA2832	0.5	3.3	0.4	0.8	1.3	2.1	CRD1	orf19.4784	Cu-transporting P1-type ATPase
CA3111	0.5	0.3	1.1	1.1	1.1	1.1	RPL5	orf19.6541	ribosomal protein (by homology)
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)
CA1121	0.5	1.1	0.7	0.8	1.4	1.0	IPF6730	orf19.1604	Unknown function
CA5666	0.5	0.6	0.8	1.0	0.5	0.6	PUB1	orf19.7368	Major polyadenylated RNA-binding protein (by homology)
CA5921	0.5	0.8	1.2	1.0	0.9	0.9	PGA32	orf19.6784	unknown function
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 homology)
1615.20	0.5	0.7	0.9	1.0	1.0	0.8			
CA5583	0.5	0.9	1.3	1.1	1.0	1.0	IPF5644	orf19.7116	unknown function
CA5600	0.5	0.7	0.6	1.0	0.4	0.5	IPF559	orf19.7100	unknown function
CA3081	0.5	0.5	1.1	1.1	1.1	1.0	EFT3	orf19.4152	translation elongation factor 3
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
CA4203	0.5	0.7	0.7	0.6	0.6	0.8	SWI4.3f	orf19.4545	transcription factor (by homology)
CA3376	0.5	0.5	1.0	1.3	1.0	0.9	LSC2.5eoc	orf19.1857.1	succinate-CoA ligase beta subunit, 5-prime end (by homology)
CA3987	0.5	0.9	0.6	1.0	0.4	0.7	ECM3	orf19.1563	Involved in cell wall biogenesis and architecture (by homology).
CA6154	0.5	0.3	1.6	1.4	1.0	1.0	IPF1848	orf19.5885	similar to Saccharomyces cerevisiae Snu13p U4/U6.U5 snRNP associated protein (by homology) | Unknown function
CA1541	0.5	1.1	0.9	1.1	0.9	1.0	BGL21	orf19.4565	endo-beta-1,3-glucanase (by homology)
CA3539	0.5	0.4	1.1	1.1	1.1	1.0	RPS20	orf19.6375	ribosomal protein (by homology)
CA0697	0.5	0.7	0.5	0.9	0.7	0.4	VTC4	orf19.3363	putative polyphosphate synthetase (by homology)
CA0586	0.5	0.7	1.2	1.3	1.2	1.0	IPF13493	orf19.5063	Unknown function
CA5843	0.5	0.9	0.7	0.7	0.8	1.0	IPF416	orf19.7499	unknown function
CA5067	0.5	0.9	1.9	1.6	1.5	1.2	IPF3589	orf19.3040	putative alcohol acyl transferase (by homology)
CA4270	0.5	0.3	1.0	0.9	0.6	0.7	NUP2	orf19.6665	Nuclear pore protein (by homology)
CA3867	0.5	0.8	0.9	1.5	0.9	0.7	PHR2	orf19.6081	pH-regulated protein 2
CA3181	0.5	1.0	0.7	1.0	1.5	1.3	IPF12241	orf19.2132	unknown function
CA6079	0.5	0.5	1.1	1.0	1.0	1.0	RPL18	orf19.5981.1	Ribosomal protein L18B (large subunit), (by homology)
CA4191	0.5	0.5	0.9	1.1	1.3	1.2	IPF7531	orf19.4532	unknown function
CA5596	0.5	0.9	1.1	1.0	1.0	1.1	IPF564	orf19.7104	unknown function

CA2898	0.5	0.6	2.0	0.9	0.6	0.8	IPF15646	orf19.3481	putative ATP-dependent RNA helicase (by homology)
CA4553	0.5	0.7	0.5	0.7	0.4	0.6	CYB1	orf19.1446	G2/Mitotic-specific cyclin
CA0674	0.5	0.9	0.8	1.0	1.0	1.1	IPF19608	orf19.1179	unknown function
CA1302	0.5	0.9	0.9	1.1	1.5	1.5	FCA1	orf19.4195.1	cytosine deaminase
CA5691	0.5	0.5	1.4	1.2	0.7	0.5	DED1	orf19.7392	RNA helicase (by homology)
CA2379	0.5	0.8	1.3	1.0	0.5	0.7	IPF4073	orf19.2216	similar to Saccharomyces cerevisiae CaPds5p regulation of dissociation of sister chromatids (by homology)
CA5682	0.5	0.5	1.9	0.9	1.0	1.0	NOG1	orf19.7384	Nucleolar G-protein (by homology)
CA3756	0.5	0.8	0.4	0.6	0.4	0.7	IPF8884	orf19.3422	unknown function
CA5170	0.5	1.0	0.5	0.9	0.6	0.9			
CA5051	0.5	0.3	2.5	1.4	1.2	1.2	IPF3709	orf19.3015	unknown function
CA3523	0.5	1.2	0.8	0.9	0.7	1.1	IPF20135	orf19.993	unknown function
CA4343	0.5	0.7	0.9	1.1	0.9	1.1	IPF3630	orf19.6717	unknown function
CA3579	0.5	1.0	0.5	1.0	1.0	1.5	HSH49	orf19.2261	spliceosome-associated essential protein [Candida albicans]
CA3168	0.5	0.5	1.3	1.4	1.3	1.3	PRS3	orf19.1575	ribose-phosphate pyrophosphokinase
CA2956	0.5	0.6	0.9	1.2	1.3	1.1	EGD2	orf19.5858	Nascent polypeptide associated complex protein alpha subunit (by homology)
CA4850	0.5	1.1	0.6	1.0	0.9	1.1	Cirt2	orf19.3820	Transposase
CA3479	0.5	0.8	1.1	1.2	1.0	1.0	ATP4	orf19.3579	F1F0-ATPase complex, F0 subunit B (by homology)
CA0824	0.5	0.9	1.9	7.6	2.9	1.8	GPD2	orf19.691	Glycerol 3-phosphate dehydrogenase (by homology)
CA0689	0.5	0.3	1.5	1.4	0.3	0.3	IPF14119	orf19.4688	unknown function
CA5507	0.5	0.5	1.1	1.0	1.0	0.9	TIF11	orf19.5351	translation initiation factor eIF1a (by homology)
CA4260	0.5	0.8	0.9	0.9	0.8	0.9	IPF4276	orf19.549	similar to Saccharomyces cerevisiae Mrpl32p putative mitochondrial ribosomal protein (by homology)
CA4696	0.5	0.4	0.9	0.7	0.6	0.8	HTA1	orf19.6924	Histone H2A (by homology)
CA3848	0.5	1.0	0.6	0.9	0.7	1.0	IPF7940	orf19.6608	unknown function
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) (by homology)
CA4381	0.5	0.8	0.5	0.7	0.8	0.6	PGA10	orf19.5674	unknown function
CA5351	0.5	0.6	0.7	0.8	2.3	2.1	IPF857	orf19.7227	unknown function
CA3854	0.5	0.6	0.8	1.0	0.9	1.2	IPF4649	orf19.6102	unknown Function
CA5494	0.5	0.7	0.5	0.6	0.9	0.9	IPF85	orf19.5334	similar to Saccharomyces cerevisiae Tis11p tRNA-specific adenosine deaminase 3 (by homology)
CA0938	0.5	0.6	1.0	1.0	1.1	1.1	COX12	orf19.1082.1	cytochrome-c oxidase, subunit VIB (by homology)
CA5497	0.5	0.4	1.2	0.7	1.9	1.0	IPF776	orf19.5338	transcriptional activator (by homology)
CA3705	0.5	0.9	1.1	1.0	0.3	0.7	MSH6	orf19.4945	DNA mismatch repair protein by homology
CA1388	0.5	1.0	0.7	0.8	1.2	0.9	IPF16514	orf19.921	unknown function
CA2091	0.5	0.6	1.0	1.0	0.8	0.9	IPF3401	orf19.839	unknown function
CA2939	0.5	0.4	1.0	1.0	1.0	1.0	TIF1	orf19.3324	translation initiation factor
CA0928	0.5	0.8	0.8	1.0	0.6	0.9	IPF19891	orf19.557	unknown function
CA4102	0.5	0.6	1.1	1.1	1.1	1.0	RPL37B	orf19.667.1	Ribosomal protein
CA3327	0.5	0.7	0.6	0.7	0.5	0.7	NCP1	orf19.2672	NADPH-cytochrome P450 reductase
CA1723	0.5	0.6	1.0	1.0	1.1	1.1	TEF4	orf19.2651	translation elongation factor eEF1 (by homology)
CA5680	0.5	0.4	1.0	0.9	1.0	1.0			
CA4745	0.5	0.6	0.6	1.0	0.8	0.6	URA1	orf19.4836	dihydroorotate dehydrogenase
CA0302	0.5	0.9	1.2	1.4	0.7	0.6	MEP3	orf19.1614	low affinity high capacity ammonium permease (by homology)
CA2885	0.5	0.6	0.9	0.9	0.3	0.8	PGA26	orf19.2475	unknown function
CA3895	0.5	1.0	0.3	0.4	1.1	2.7	CDR4	orf19.5079	Multidrug resistance protein
CA4445	0.5	0.9	1.1	1.1	1.5	1.2	IPF3530	orf19.6843	unknown function
CA2249	0.5	0.6	0.9	0.7	0.5	0.7	POL2	orf19.2365	DNA-directed DNA polymerase epsilon, catalytic subunit A (by homology)
CA3880	0.5	1.0	0.3	0.7	1.9	1.0	CAF16	orf19.388	ABC ATPase (by homology)

CA5197	0.5	0.4	1.3	1.2	1.0	0.8	IPF2342	orf19.7011	unknown function
CA3242	0.5	0.6	1.8	1.2	0.7	0.9	RAT1	orf19.4681	5 -3 Exoribonuclease (by homology)
CA2493	0.5	0.4	0.9	0.8	0.9	0.8	IPF7227	orf19.4048	putative fatty acid desaturase (by homology)
CA1737	0.5	0.8	0.6	1.1	1.0	0.9	LYS12	orf19.2525	homo-isocitrate dehydrogenase (by homology)
CA2280	0.5	1.0	0.3	1.0	0.7	0.9	DUR1,2	orf19.780	urea amidolyase (by homology)
CA1663	0.5	0.6	1.3	1.1	0.9	1.0	IPF7309	orf19.2864	unknown function
CA2558	0.5	0.5	0.6	0.8	0.8	0.7	RBT5	orf19.5636	repressed by TUP1 protein 5
CA5735	0.5	1.0	0.6	0.8	1.6	0.9	IPF2878	orf19.7445	unknown function
CA1384	0.5	0.8	0.9	1.0	0.6	0.8	IPF8423	orf19.926	similar to Saccharomyces cerevisiae Dhs1p exonuclease (by homology)
CA1956	0.5	0.6	0.9	0.8	0.4	0.5	ERG3	orf19.767	C5,6 desaturase
CA4501	0.5	1.3	0.1	0.1	0.6	0.9	QDR1	orf19.508	putative antibiotic resistance proteins (by homology)
CA4551	0.5	0.5	1.1	1.1	1.2	1.2	APT1	orf19.1448	adenine phosphoribosyltransferase
CA5594	0.5	1.3	0.8	1.1	0.6	1.1	IPF19814	orf19.7106	folate hydrolase (by homology)
CA3853	0.5	0.5	0.9	1.0	0.8	1.0	MVD1	orf19.6105	mevalonate pyrophosphate decarboxylase
CA1503	0.5	0.4	2.0	1.6	1.0	1.1	RKI1	orf19.1701	D-ribose-5-phosphate ketol-isomerase (by homology)
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 lipolytica glyoxylate pathway regulator Gpr1p
CA3918	0.5	0.5	0.6	1.1	0.5	0.7	VTC2	orf19.4381	putative polyphosphate synthetase (by homology)
CA2263	0.5	0.6	0.6	0.6	2.2	1.2	GPD1	orf19.1756	Glycerol-3-phosphate dehydrogenase (by homology)
CA3574	0.5	0.5	1.1	1.0	0.9	1.2	IPF19584	orf19.2266	unknown function
CA4783	0.5	0.5	1.0	1.0	1.0	1.0	IPF3358	orf19.4016	ubiquinol-cytochrome-c reductase (by homology)
CA4490	0.5	0.7	1.0	1.1	0.8	1.1	IPF4045	orf19.1872	unknown function
CA4418	0.5	0.6	0.8	1.0	0.7	0.8	ERG5	orf19.5178	C-22 sterol desaturase by homology
CA6109	0.5	0.5	1.1	1.1	1.0	1.0	IPF89.3f	orf19.5943.1	unknown function, 3-prime end
CA3883	0.5	0.2	1.0	1.3	0.2	0.4	GCV2	orf19.385	Glycine decarboxylase P subunit
CA2314	0.5	0.8	0.4	0.8	1.9	1.0	IPF14545	orf19.1381	unknown function
CA2024	0.5	0.5	0.9	1.0	0.7	0.3	PGA35	orf19.4910	unknown function
CA2181	0.5	0.6	0.6	0.9	0.5	0.9	ECM331	orf19.4255	Involved in cell wall biogenesis and architecture (by homology)
CA1989	0.4	0.8	0.9	0.8	0.8	0.9	IPF16596	orf19.95	unknown function
CA3287	0.4	0.9	0.9	1.0	1.0	1.1	PGA48	orf19.6321	putative Sed1p-like cell surface protein (by homology)
CA2923	0.4	0.3	1.0	1.4	1.0	0.8	FET32	orf19.4212	cell surface ferroxidase (by homology)
CA2948	0.4	0.9	1.6	0.9	0.5	0.8	GDS1	orf19.1963	nam9-1 suppressor (by homology)
CA0207	0.4	0.4	1.9	1.0	1.0	0.7	IPF18002	orf19.1226	Unknown function
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 homology)
CA3739	0.4	0.2	0.9	0.9	0.9	0.9	RPS10	orf19.2179.2	ribosomal protein
CA4513	0.4	0.3	1.0	1.1	1.0	1.0	ADE17	orf19.492	5-aminoimidazole-4-carboxamide ribotide transformylase (by homology to S. cerev.)
CA2924	0.4	0.5	1.0	1.3	1.2	0.8	FET33	orf19.4211	cell surface ferroxidase (by homology)
CA6149	0.4	0.6	1.1	0.9	1.1	1.0	RIP1	orf19.5893	Ubiquinol cytochrome-c reductase (by homology)
CA6129	0.4	0.6	0.9	1.1	1.0	0.8			
CA0642	0.4	0.3	1.3	1.4	0.4	0.4	ERG25	orf19.3732	C-4 sterol methyl oxidase
CA1494	0.4	0.8	0.6	0.8	0.9	0.7	IPF171	orf19.3228	unknown function
CA5622	0.4	0.8	0.8	0.9	1.1	1.1	GBP2.3f	orf19.7076	single-strand telomeric DNA-binding protein, 3-prime end (by homology)
CA2494	0.4	0.6	0.8	1.1	0.9	1.1	HTS1	orf19.4051	histidine tRNA synthetase (by homology)
CA6122	0.4	0.5	1.2	1.1	1.1	1.0	RPP2B	orf19.5928	acidic ribosomal protein (by homology)
CA5968	0.4	1.0	0.6	1.0	1.4	1.0	IPF946	orf19.7561	unknown function
CA1635	0.4	0.3	0.8	1.3	0.9	1.1	URA7	orf19.3941	CTP synthase 1 (by homology)
CA0964	0.4	0.6	0.8	0.9	0.4	0.6	IPF9141	orf19.6247	similar to Saccharomyces cerevisiae Ctf4p DNA-directed DNA polymerase alpha-binding protein (by homology)

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
CA5857	0.4	1.2	0.4	0.6	0.6	0.7	PCK1	orf19.7514	phosphoenolpyruvate carboxykinase
CA3075	0.4	0.3	1.0	1.3	1.0	1.0	IPF6105	orf19.4813	similar to Saccharomyces cerevisiae Gua1p GMP synthase (glutamine-hydrolyzing) (by homology)
CA2154	0.4	1.3	1.2	1.1	0.4	0.7	ERG2	orf19.6026	C-8 sterol isomerase
CA5091	0.4	0.4	0.5	0.7	0.2	0.6	ENG1	orf19.3066	endo-1,3-beta-glucanase
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 major facilitator superfamily (by homology
CA4589	0.4	0.5	1.1	1.0	1.0	1.0			
CA2969	0.4	0.2	0.4	0.6	0.6	0.5	IPF19772	orf19.5602	unknown function
CA2391	0.4	1.3	0.4	0.8	0.8	1.0	ADH5	orf19.2608	probable alcohol dehydrogenase (by homology)
CA0736	0.4	0.2	1.0	1.1	1.0	1.0	RPL20B	orf19.4632	ribosomal protein (by homology)
CA4263	0.4	0.2	1.1	0.9	0.5	0.4	IPF2277	orf19.6656	unknown function
CA0375	0.4	1.1	1.1	0.8	0.7	0.6	CRH11	orf19.2706	Probable membrane protein (by homology)
CA0984	0.4	0.5	0.5	0.7	0.8	0.8	IPF7400	orf19.1802	unknown function
CA1625	0.4	0.9	0.6	0.7	1.5	1.0	IPF6156	orf19.1034	similar to C.elegans LIM homeobox protein
CA5065	0.4	0.3	1.0	1.0	0.8	1.0	IPF3584	orf19.3037	similar to Saccharomyces cerevisiae Pab1p mRNA polyadenylate-binding protein (by homology)
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)
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 Phr3 (by homology)
CA0899	0.4	0.9	0.6	0.7	1.6	1.7	IPF4905	orf19.411	unknown function
CA3338	0.4	0.7	0.4	0.9	1.4	1.5	IPF13582	orf19.2333	unknown function
CA1298	0.4	0.3	1.0	1.1	0.9	1.0	RPL32	orf19.3415.1	ribosomal protein L32
CA5317	0.4	0.3	1.0	1.1	1.0	1.0	RPP1B	orf19.7188	Acidic ribosomal protein L44 (by homology)
CA2587	0.4	0.6	1.1	1.1	1.0	1.0	RPS30	orf19.4375.1	40S ribosomal protein S30(by homology)
CA2739	0.4	1.0	1.3	1.2	1.5	1.6	MUQ1	orf19.2107	choline phosphate cytidylyltransferase (by homology)
CA1502	0.4	0.4	1.1	1.1	1.0	1.0	RPS7A	orf19.1700	ribosomal protein (by homology)
CA4862	0.4	0.3	1.0	1.0	1.0	1.0	EFB1	orf19.3838	translation elongation factor eEF1beta
CA1070	0.4	0.6	0.7	0.4	1.0	0.9	HXT61	orf19.2020	sugar transporter
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 homology)
CA5612	0.4	1.3	0.7	0.8	0.8	0.7	KAP114	orf19.7086	putative RAN-binding protein/importin (by homology)
CA0357	0.4	0.6	0.5	0.9	0.8	0.4	FCY22	orf19.333	purine-cytosine permease (by homology)
CA1975	0.4	0.8	0.7	1.0	0.7	0.8	PLB1	orf19.689	phospholipase B
CA2578	0.4	0.5	1.1	0.9	0.6	0.9	MMD1	orf19.6220.3	Maintenance of mitochondrial DNA (by homology)
CA5476	0.4	4.2	0.7	0.8	2.7	1.8	PGA29	orf19.5305	unknown function
CA5950	0.4	0.6	0.8	0.7	1.0	1.0	TPI1	orf19.6745	Triose phosphate isomerase
CA5076	0.4	0.3	0.9	0.6	0.4	0.8	IPF15301	orf19.3051	unknown function
CA2473	0.4	0.8	0.6	0.8	0.4	0.4	CBF1	orf19.2876	putative centromere binding factor 1
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
CA5178	0.4	0.5	1.0	1.0	0.9	1.1	POL30	orf19.4616	Proliferating Cell Nuclear Antigen (by homology)
CA2597	0.4	0.3	0.8	0.7	1.0	0.5	IFQ3	orf19.54	unknown function
CA4163	0.4	1.0	0.9	0.8	1.1	0.8	IPF9301	orf19.5812	unknown function
CA4657	0.4	1.1	0.7	1.1	2.3	1.2	IPF3094	orf19.4444	4-nitrophenyl phosphatase (by homology)
CA3864	0.4	0.3	1.0	1.0	1.0	1.0	RPL16A	orf19.6085	ribosomal protein (by homology)
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 lipolytica glyoxylate pathway regulator Gpr1p
CA4611	0.4	1.1	0.2	0.7	1.8	1.7	IPF10727	orf19.3302	unknown function
CA3284	0.4	0.4	0.9	0.9	1.0	1.0	ADE6	orf19.6317	5 -phosphoribosylformyl glycinamidine synthetase (by homology)
CA5987	0.4	0.7	0.6	0.7	0.7	0.5	CHT3	orf19.7586	chitinase 3 precursor
CA2861	0.4	0.6	0.8	0.9	0.7	1.0	HHT21	orf19.1061	Histone H3

CA2574	0.4	1.5	0.4	1.1	0.8	1.2	ATH1	orf19.6214	acid trehalase, vacuolar
CA0665	0.4	0.3	0.6	0.7	0.6	0.8	INT1	orf19.4257	integrin-like protein alpha chain
CA2938	0.4	0.8	0.5	0.7	0.6	0.4	IPF8321	orf19.3325	similar to Saccharomyces cerevisiae Glg2p self-glucosylating initiator of glycogen synthesis (by homology)
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 homology)
CA4571	0.4	0.2	1.0	1.1	1.0	1.1	RPL33	orf19.6882.1	ribosomal protein L35a
CA4008	0.4	0.4	0.9	1.0	1.0	1.0	DYS1	orf19.1626	deoxyhypusine synthase
CA0254	0.4	0.4	0.9	1.1	2.3	0.9	IPF14968	orf19.3461	unknown function
CA4533	0.4	0.5	0.9	1.3	0.9	1.0	COX4	orf19.1471	cytochrome-c oxidase (by homology)
CA4852	0.4	0.5	0.6	0.7	0.9	0.8	SCS7	orf19.3822	Required for hydroxylation of ceramide (by homology)
CA0210	0.4	1.1	0.7	1.1	1.3	1.3	IPF4328	orf19.5525	unknown function
CA5042	0.4	0.6	0.5	0.9	2.0	5.6	IPF4514	orf19.6996	putative alpha-1,3-mannosyltransferase (by homology)
CA0322	0.4	0.3	1.0	1.0	1.0	1.0	RPS9B	orf19.838.1	Ribosomal protein
CA2454	0.3	0.3	1.1	1.0	1.1	1.0	RPL23B	orf19.3504	ribosomal protein L23.e (by homology)
CA3547	0.3	0.4	0.8	1.0	0.8	1.0	ADE13	orf19.3870	adenylosuccinate lyase (by homology)
CA3862	0.3	0.4	1.3	1.6	1.4	1.0	NSR1	orf19.6090	nuclear localization sequence binding protein (by homology)
CA2855	0.3	0.8	0.5	0.8	1.8	1.4	GPM2	orf19.1067	phosphoglycerate mutase (by homology)
CA3602	0.3	0.4	1.0	1.0	1.0	0.9	RPL14B	orf19.4931.1	ribosomal protein L14B (by homology)
CA3637	0.3	0.9	0.2	0.5	1.8	1.3	IPF9255	orf19.5136	unknown function
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 homology)
CA6135	0.3	0.7	0.4	0.8	1.0	0.6	CMK1	orf19.5911	Ca2+/calmodulin-dependent ser/thr protein kinase (by homology)
CA4512	0.3	0.3	1.0	0.9	1.1	1.1			
CA5407	0.3	1.1	0.3	0.5	0.9	0.8	IPF1548	orf19.951	unknown function
CA0752	0.3	1.4	0.6	0.5	0.6	1.3	MNN22	orf19.3803	Golgi alpha-1,2-mannosyltransferase (by homology)
CA3372	0.3	0.5	1.0	0.9	0.4	0.6	HHF22	orf19.1854	histone H4 (by homology)
CA0875	0.3	0.4	1.0	1.0	0.7	0.5	ERG251	orf19.4631	C-4 sterol methyl oxidase (by homology)
CA3226	0.3	0.3	1.2	1.1	1.0	1.0	RPS27	orf19.6286.2	ribosomal protein S27 (by homology)
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)
CA4261	0.3	1.1	0.5	0.8	1.0	0.8	PDX3	orf19.550	pyridoxamine-phosphate oxidase (by homology)
CA0472	0.3	0.3	14.5	5.6	1.8	1.5	STL1	orf19.5753	sugar transporter (by homology)
CA5816	0.3	0.3	1.0	0.8	1.0	1.1	ACC1	orf19.7466	acetyl-coenzyme-A carboxylase (by homology)
CA5354	0.3	0.4	1.0	1.2	0.6	0.7	FTR2	orf19.7231	high affinity iron permease
CA4707	0.3	0.7	0.9	0.9	1.1	1.1	PTR21	orf19.6937	peptide transporter
CA1315	0.3	0.3	0.8	0.9	1.0	0.9	URA2	orf19.2360	multifunctional pyrimidine biosynthesis protein, (by homology)
CA1062	0.3	0.2	0.6	0.4	1.0	1.2	IPF14165	orf19.4642	unknown function
CA3239	0.3	0.3	1.1	1.3	0.9	1.0	IPF10558	orf19.4684.2	unknown function
CA0763	0.3	0.2	1.1	1.1	0.9	0.9	RPL11	orf19.2232	60S ribosomal protein (by homology)
CA4882	0.3	0.3	0.7	0.9	0.5	0.8	IPF1651	orf19.6570	purine nucleoside permease (by homology)
CA2805	0.3	0.4	0.7	0.8	0.7	0.8	RNR1	orf19.5779	ribonucleoside-diphosphate reductase (by homology)
CA1387	0.3	0.4	0.7	0.7	0.8	0.9	ERG11	orf19.922	cytochrome P450 lanosterol 14a-demethylase
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 homology)
CA0380	0.3	0.3	0.8	1.1	0.6	0.5	PGA45	orf19.2451	unknown function
CA3921	0.3	0.2	1.0	1.1	1.0	1.0	OLE1	orf19.5117	Stearoyl-CoA desaturase (by homology)
CA2031	0.3	0.2	1.0	1.1	1.0	1.0	RPL10A	orf19.3465	L10A ribosomal protein
CA2937	0.3	0.3	1.2	1.1	1.1	1.0	RPS21B.3f	orf19.3325.3	ribosomal protein S21, 3- prime end
CA4697	0.3	0.4	0.8	0.8	0.6	0.8	HTB1	orf19.6925	Histone H2B (by homology)
CA1902	0.3	1.1	0.4	1.1	1.0	1.0	OPT1	orf19.2602	oligopeptide transporter

CA5200	0.3	0.3	1.1	1.1	1.0	1.0	RPL10E	orf19.7015	Ribosomal protein L10, cytosolic (by homology)
CA2819	0.3	0.4	1.1	1.1	1.0	1.0	RPA1	orf19.2992	60S ribosomal protein
CA5343	0.3	0.2	1.0	1.0	1.0	1.0	RPL4B	orf19.7217	Ribosomal protein L4B (by homology)
CA0311	0.3	0.9	0.4	1.5	0.9	1.1			
CA5344	0.3	0.4	0.6	2.3	0.3	0.5	PRY2	orf19.7218	putative pathogen related proteins (by homology)
CA1977	0.3	0.3	0.9	1.0	0.9	1.0	RPL25	orf19.687.1	ribosomal protein L23a (by homology)
CA6163	0.3	0.3	1.0	0.8	0.4	0.8	POL1	orf19.5873	DNA-directed DNA polymerase alpha (by homology)
CA4492	0.3	0.9	0.2	0.7	1.3	1.1	RNR22	orf19.1868	ribonucleoside-diphosphate reductase (by homology)
CA2734	0.3	0.5	1.2	1.1	1.0	0.9	RPL38	orf19.2111.2	ribosomal protein L38 (by homology)
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 homology
CA0273	0.3	0.9	0.3	0.5	1.0	0.6	IPF19066	orf19.1433	unknown function
CA4516	0.3	0.5	0.3	0.5	1.3	0.8	IPF18207	orf19.489	unknown function
CA0083	0.3	0.1	1.0	1.1	0.6	0.2	PHO84.5eo	orf19.655	high-affinity inorganic phosphate/H+ symporter by homology
CA2862	0.3	0.5	0.8	0.9	0.2	0.6	HHF21	orf19.1059	histone H4
CA1662	0.3	0.2	0.9	1.0	1.0	1.0			
CA5499	0.3	0.2	1.1	1.1	1.0	1.0	RPS4A	orf19.5341	ribosomal protein S4
CA3740	0.3	0.8	1.0	1.0	0.8	0.8	SIT1	orf19.2179	Ferrioxamine B permease by homology
CA1304	0.3	0.3	1.1	1.0	1.0	1.0	RPS13.3	orf19.4193.1	ribosomal protein (by homology)
CA3341	0.2	0.2	1.1	1.0	1.0	1.0	RPS17	orf19.2329.1	Ribosomal protein S17 (by homology)
CA2738	0.2	1.2	0.4	0.8	2.5	1.6	STF2	orf19.2107.1	ATP synthase regulatory factor (by homology)
CA6123	0.2	0.2	1.0	1.0	1.0	1.0	RPS15	orf19.5927	40S ribosomal protein S15, (by homology)
CA2011	0.2	0.4	1.3	1.4	1.1	1.1	RPS31	orf19.3087	Ubiquitin fusion protein
CA1188	0.2	0.2	1.2	1.0	1.0	1.0	RPL30.3f	orf19.3788.1	RNA binding (by homology)
CA0632	0.2	0.2	1.3	1.1	1.0	1.0	RPS5	orf19.4336	ribosomal protein S5.e (by homology)
CA5345	0.2	0.3	1.1	1.2	1.0	0.9	FTR1	orf19.7219	high affinity iron permease
CA5203	0.2	0.2	1.0	1.2	0.9	1.0	RPS18	orf19.7018	Ribosomal protein S18 (by homology)
CA2625	0.2	0.9	0.7	0.9	0.2	0.3	PGA6	orf19.4765	Putative glycosylphosphatidylinositol-modified protein
CA0186	0.2	0.7	0.7	0.7	0.6	0.7	PLB4.3f	orf19.1443	phospholipase, 3-prime end (by homology)
CA1189	0.2	0.2	1.0	1.0	1.0	1.0	RPL24A	orf19.3789	ribosomal protein L24 (by homology)
CA1440	0.2	0.5	1.2	0.9	1.0	1.1	RPL17B	orf19.4490	RPL17B ribosomal protein L17.e
CA4983	0.2	0.7	0.6	1.2	0.4	0.5	IPF2053	orf19.5267	unknown function
CA1972	0.2	0.3	1.3	1.1	0.9	1.0	RPL27A	orf19.5225.2	ribosomal protein L27
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
CA3689	0.2	0.2	1.1	1.1	0.9	1.0	RPS22A	orf19.6265	ribosomal protein S15a.e.c10 (by homology)
CA0185	0.2	0.7	0.7	0.6	0.5	0.8	PLB4.5f	orf19.1442	Phospholipase, 5-prime end (by homology)
CA0482	0.2	0.6	0.6	0.9	0.5	0.4	IPF14763	orf19.118	delta-12 fatty acid desaturase (by homology)
CA4269	0.2	0.2	0.9	1.1	0.9	1.0	RPS25B	orf19.6663	Cytosolic ribosomal protein (by homology)
CA2811	0.2	0.3	1.1	1.0	1.0	1.0	RPS3A	orf19.3002	Ribosomal protein 10
CA4842	0.2	0.5	0.7	1.2	0.9	0.8	MTD1	orf19.3810	methylenetetrahydrofolate dehydrogenase
CA6064	0.2	0.2	1.0	0.9	0.9	1.0	RPL81	orf19.6002	60S ribosomal protein L7a.e.B (by homology)
CA2092	0.2	0.2	1.0	1.0	0.9	1.0	RPL21A	orf19.840	Ribosomal protein (by homology)
CA2817	0.2	0.2	1.1	1.1	1.0	1.0	RPS16	orf19.2994.1	ribosomal protein
CA5807	0.2	0.2	1.1	1.0	0.9	1.0	RPS24	orf19.5466	ribosomal protein S24.e
CA5426	0.2	0.2	1.0	0.8	1.0	1.0	FAS1	orf19.979	Fatty-acyl-CoA synthase, beta chain.
CA1353	0.2	0.3	0.4	0.5	0.7	1.0	ERG1	orf19.406	squalene epoxidase
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)

CA2075	0.2	0.5	0.5	0.7	1.3	1.1	IFE2	orf19.5288	Unknown function
CA3304	0.2	0.2	1.0	0.9	0.9	1.0	RPL82	orf19.2311	60S ribosomal protein L7a.e.B (by homology)
CA3160	0.2	1.0	0.2	0.7	0.4	0.6	ZRT2	orf19.1585	zinc transport protein (by homology)
CA4562	0.2	0.3	0.9	1.1	1.0	1.0	RPS8A	orf19.6873	ribosomal protein (by homology)
CA5920	0.2	0.2	1.0	1.0	1.2	1.0	RPS12	orf19.6785	acidic ribosomal protein S12 (by homology)
CA6092	0.2	0.3	1.2	0.9	1.1	1.0	RPL35	orf19.5964.2	Ribosomal protein L35A, (by homology)
CA3030	0.2	0.6	1.2	0.9	0.9	1.3	IPF19968	orf19.220	putative cell wall protein of the PIR family
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 homology)
CA2818	0.2	0.2	1.1	1.1	1.1	1.0	RPL13	orf19.2994	Ribosomal protein
CA3690	0.2	0.2	1.0	1.0	1.0	0.9	RPS14B	orf19.6265.1	ribosomal protein (by homology)
CA6068	0.2	0.2	1.2	1.2	1.0	1.0	RPS19A	orf19.5996.1	ribosomal protein S19.e (by homology)
CA2108	0.2	0.2	0.9	0.9	1.0	1.0	RPL26A.3f	orf19.3690.2	ribosomal protein, 3-prime end (by homology)
CA5125	0.2	0.2	1.0	1.2	1.0	1.0	RPP2	orf19.6403.1	acidic ribosomal protein by homology
CA2947	0.2	0.3	0.7	0.5	0.5	0.7	IPF6298	orf19.1964	unknown function
CA4103	0.2	0.4	1.0	1.0	1.1	1.0	IPF3980	orf19.668	unknown function
CA1782	0.2	0.1	0.9	1.0	0.5	0.2	PHO84.3eo	orf19.1172	Inorganic phosphate transport protein, 3-prime end (by homology)
CA3878	0.2	0.3	0.5	0.6	0.5	0.5	IPF7289	orf19.391	similar to Saccharomyces cerevisiae Upc2p RNA polymerase II transcription factor
CA2579	0.2	0.2	1.3	1.0	1.1	1.0			
CA1637	0.2	0.2	1.0	1.1	1.0	1.0	RPL43A	orf19.3942.1	ribosomal protein (by homology)
CA3084	0.1	0.2	1.0	1.1	1.0	1.1	IPF11625	orf19.4149	unknown function
CA2920	0.1	0.2	1.0	1.1	0.9	0.7	FET5.5eoc	orf19.4215	multicopy oxidase (by homology)
CA4534	0.1	0.2	1.2	0.9	1.1	1.1	RPS26A	orf19.1470	ribosomal protein S26.e.A, cytosolic (by homology)
CA3305	0.1	0.2	1.2	1.0	1.1	0.9	RPL29	orf19.2310.1	ribosomal protein, cytosolic(by homology)
CA3244	0.1	0.2	1.9	1.6	3.3	1.0	AGP2	orf19.4679	amino-acid permease (by homology)
CA0943	0.1	0.5	0.4	0.4	0.9	1.1	YHB1	orf19.3707	flavohemoglobin (by homology)
CA5788	0.1	0.6	1.1	1.8	1.7	1.0	RHR2	orf19.5437	DL-glycerol phosphatase
CA1051	0.1	0.3	0.7	0.9	1.0	1.0	CHT2	orf19.3895	chitinase 2 precursor
CA1579	0.1	2.0	0.6	1.3	0.5	1.2	GDH3	orf19.4716	NADP-glutamate dehydrogenase (by homology)
CA2302	0.1	0.6	0.3	0.6	0.1	0.3	IPF6518	orf19.1691	unknown function