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Coláiste na Tríonóide, Baile Átha Cliath

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**Investigation of Antibiotic Resistance and Biofilm
Formation in *Acinetobacter baumannii***

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University of Dublin

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DOCTOR OF PHILOSOPHY

by

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Declaration

I declare that this thesis has not been submitted as an exercise for a degree at this or any other university and it is entirely my own work. I confirm that the work has been completed in full compliance with relevant university policies, including the Academic Integrity policy, the Trinity Policy on Good Research Practice, and the guidance on AI and GenAI in Teaching, Learning, Assessment and Research.

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Summary

Acinetobacter baumannii is a multi-drug resistant Gram-negative bacterium of global concern. It commonly causes nosocomial infections such as ventilator-assisted pneumonia, bacteraemia, urinary tract infections, etc. (1). The genome of AB5075 consists of three plasmids (83 kbp, 8.7 kbp and 2 kbp) and a ~4 Mbp chromosome (2). It was recognized as the number one priority pathogen by the World Health Organization (WHO) in 2017 due to its multi-drug resistant status (3). *A. baumannii* is naturally resistant to chloramphenicol through a variety of different mechanisms such as regulation of membrane permeability, O-acetyltransferases and efflux pumps. Efflux pumps play an important role in antibiotic resistance and can convey drug resistance to multiple antibiotics or selective resistance to a single antibiotic (1). Two efflux pump genes *craA* and *cxpE* were investigated in *A. baumannii* and were shown to play a significant role in chloramphenicol resistance (4–7). However, the function, importance and regulation of these efflux pumps are poorly understood and there is conflicting evidence on which genes provide the largest contribution to chloramphenicol resistance in *A. baumannii* (4–7). In this study, we have determined that *craA* plays a role in the rapid adaptation to chloramphenicol exposure and that *cxpE* is required for the maintenance of growth in stationary phase in the presence of chloramphenicol. Transient chloramphenicol resistance was first identified in strain ATCC17978 (8). In this study, the transient resistance phenotype was shown to be conserved in strain AB5075 with *craA* playing a key role in this transient resistance phenomenon. CraA was proven to be present in the membrane throughout growth in minimal media, suggesting that CraA may lack the energy to rapidly and efficiently pump chloramphenicol out of the cell rendering a portion of the population sensitive to sub-inhibitory levels of chloramphenicol. The *cxpE* gene also appears to be involved in motility suggesting that *cxpE* has a broader role for *A. baumannii* physiology than just drug efflux. This study provides further insight into which genes are involved in chloramphenicol resistance in *A. baumannii* as well as a potential role for *cxpE* in the regulation of motility in *A. baumannii*.

The largest of the three plasmids “p1AB5075” harbors several antibiotic resistance genes (ARGs) *e.g.*, *aadB* and *strA* and numerous unidentified genes (9). Unfortunately, this plasmid has only been studied in terms of antimicrobial resistance (AR) specifically, investigating resistance island 2 (RI-2) to date (6, 10, 11). In this research we have examined 8 p1AB5075 individually; *aph(3')-VI*, *aaC(6')-Ib3*, *aadB*, *aadA2*, *strA*, *strB*, and *bla_{GES-11}* for their contribution to overall *A. baumannii* AB5075 resistance. Also, we demonstrate that p1AB5075 contributes to overall virulence by significantly influencing biofilm formation, adhesion and motility. Upon the loss of p1AB5075 there is a reduction of motility, adhesion capability to polystyrene plastic and an increase in biofilm formation. We hypothesized that the second copy of H-NS located on p1AB5075 is responsible for the observed change in biofilm formation. Upon reintroduction of *hns* into the Δp1AB5075 background, biofilm formation levels are restored to wildtype levels. The addition of *hns* to Δp1AB5075 and wildtype strains reveals a significant growth defect in L-broth and minimal media. RNA-seq also revealed evidence of severe dysregulation of cellular processes that may explain this reduction in bacterial fitness. Overall, the p1AB5075-borne copy of H-NS influences biofilm production in *A. baumannii*. This is important as dissemination of this plasmid into the environment may not alter just the AR profile but also, virulence factors already present in the recipient strain due to the presence of the global transcriptional regulator H-NS.

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I honestly don't know where to begin. This PhD has been the most challenging thing I have ever done but looking back it has also been the most rewarding journey of my life. I have made life long friends, got a chance to travel to new places, developed new hobbies and if I'm being honest, I might have gone a little insane.

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Publications

- **Plunkett, O.**, Ershova, A. S., Schauer, K., and Kröger, C. (2026). Contributions of plasmid p1AB5075-encoded antibiotic resistance genes to multidrug resistance of *Acinetobacter baumannii* AB5075. Doi: <https://doi.org/10.64898/2026.03.29.715119> preprint, BioRxiv.

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Chapter 1 - Introduction

1.1 *Acinetobacter baumannii* is a global health concern

Acinetobacter baumannii is a Gram-negative opportunistic nosocomial pathogen belonging to the class of Gammaproteobacteria. *A. baumannii* is a member of the ESKAPE pathogens. This group of bacterial pathogens is composed of *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *A. baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter sp.* ESKAPE pathogens are notorious for evading conventional therapies and their multidrug resistant status (12). *A. baumannii* has a high degree of genomic plasticity which allows the bacterium to develop resistance to a wide range of antibiotics at a rapid rate (13). Due to its global dissemination and multi-drug resistant (MDR) status in 2017, the World Health Organization (WHO) determined it to be the top-priority pathogen for the development of new antibiotics (14). The genome of the MDR strain *A. baumannii* AB5075 consists of three plasmids (~83kb, ~8.7kb and ~2kb) and a ~4Mbp chromosome. The largest of the three plasmids “p1AB5075” harbours “resistance island-2” including antibiotic resistance genes (ARGs) such as *dfrA7* and *bla_{GES-11}* (2). *A. baumannii* is a ubiquitous organism and can be found in environmental reservoirs *i.e.*, soil and water and human/animal reservoirs (15, 16). The ability of *A. baumannii* to form biofilms on biotic and abiotic surfaces allows for the persistence and transfer of the bacterium in the environment (17). For example, *A. baumannii* can colonise several different abiotic surfaces in hospitals such as glass and hydrophobic plastics commonly used in medical equipment (18). This allows for the rapid transfer of *A. baumannii* infection and multidrug resistance in a nosocomial setting (19). *A. baumannii* can cause a variety of diseases such as meningitis, bacteraemia, urinary tract infections and ventilator associated pneumonia (8). Most cases are as a result of hospital acquired infections (HAIs). However, community-acquired infections of *A. baumannii* have been occasionally reported (20). The average mortality rate for *A. baumannii* may be up to ~60% in vulnerable patients (21). Additional factors such as diabetes, smoking and alcoholism can impact the predisposition of *A. baumannii* infections (15, 22).

1.2 Pathogenesis of *Acinetobacter baumannii* development of disease

Many infections begin with the initial adhesion of *A. baumannii* to host cells. The main factors that influence bacterial attachment are pili, adhesins, the twin arginine (tat) system and outer membrane proteins (OMPs) (13, 23, 24). Pili are cell surface appendages found on many bacterial cells which aid in motility, adhesion and biofilm formation (16). Two key pili in *A. baumannii* strains are the Csu pili and the type IV pili. These pili provide the initial attachment of the bacterial cell to the host (13, 16, 18, 23, 25). Adhesins can also aid in the initial attachment of the cell through recognising different host cell structures. OmpA is an outer membrane protein that has been comprehensively studied in *A. baumannii* (26–28). OmpA binds to host surface factors such as fibronectin and integrins to aid in attachment and uptake of *A. baumannii* during infection (13). Another outer membrane protein CarO also aids in the adhesion and colonisation of *A. baumannii* in host infections (23). Bacterial adhesion is a multi-factorial system that relies on several adhesion associated proteins for the successful colonisation of the host (23).

A. baumannii invasion is not fully characterised to date. However, some studies have proposed that *A. baumannii* is internalised via receptor mediated entry (active invasion) into the host cell (13, 23). Phosphorylcholine (ChoP) residues are present on *A. baumannii* porins which interact with platelet-activating factor receptor (PAFR) located on human epithelial cells, this increases adhesion stability and activates signalling cascades in the host cell to activate bacterial endocytosis (23). Capsule presence and characteristics can influence the rate of phagocytosis e.g., capsule thickness (13). The survival time of *A. baumannii* localised within membrane bound host cell vacuoles is variable based on strain type (23). *A. baumannii* ATCC19606 has a short intracellular lifespan and is promptly degraded by the host immune system (29). Whereas, the AB5075-UW strain can have increased survival inside host cells due to being internalised inside host cell vacuoles before cell death via vacuole acidification (13).

Interestingly, studies have investigated an *A. baumannii* strain UPAB1 that is capable of replicating intracellularly in macrophages (30). This was the first case of an intracellular pathogenic *A. baumannii* isolate.

The UPAB1 strain requires type 1 secretion system (T1SS) for intracellular survival however, the exact mechanism behind this still need to be elucidated (30). Recently another *A. baumannii* isolate capable of replicating intracellularly was identified ABC141, which shows prolonged survival and replication inside of host epithelial cells (23, 29). ABC141 utilised both T1SS and type 2 secretion systems (T2SS) for bacterial multiplication and cell invasion respectively (23). This was the first time a T2SS was associated with internal colonisation of *A. baumannii* within host cells (31). This discovery of intracellularly replicating *A. baumannii* strains may have serve clinical consequences as it can increase the risk of reoccurring infections and antibiotic resistance (13).

1.3 Treatment of *Acinetobacter baumannii* infections; past, present and future options

Traditionally, *A. baumannii* infections were treated with penicillin until high levels of resistance were noted in isolates (15, 32). Currently, aminoglycosides, carbapenems, fluroquinolones, β -lactamase antibiotic combinations and cephalosporins are used for treatment of *A. baumannii* infections based on the isolate's resistance profile.

However, increased resistance is also noted for these antibiotics posing a challenge to the treatment of *A. baumannii* infections (15, 32). In extreme cases of multi-drug-resistant isolates, colistin has been approved for use as a drug of last resort. However, due to the adverse effects and toxicity its use has been limited (15, 21, 32). Another challenge for the treatment of *A. baumannii* infections is antibiotic heteroresistance. Antibiotic heteroresistance is a phenomenon where a small portion of a bacterial population display decreased susceptibility to a given antibiotic (11, 33–35). It causes challenges in selecting the correct antibiotic for treatment as the resistance profile of the isolates cannot be properly identified (33).

This can lead to an antibiotic being utilised that does not adequately kill off the bacterial population and the resistant cells cause treatment failure and can spread AMR genes (11, 35).

To combat the rise of pan-drug resistant *A. baumannii*, combination therapies have been implemented to limit the increase of antimicrobial resistance and provide effective treatment e.g., colistin/meropenem and colistin/sulbactam (32).

Additionally, research into bacteriophages and artificially engineered endolysins “artilysins” for alternative therapies are being investigated (32, 36, 37).

1.4 Molecular mechanisms of antimicrobial resistance

The remarkable ability of *Acinetobacter baumannii* to rapidly adapt to hostile environments has driven the emergence of strains that are extensively drug resistance (XDR) and pan drug resistance (PDR) has been recorded (38). Antibiotic resistance in *A. baumannii* is primarily mediated through four major mechanisms, the expression of efflux pumps, a reduction in membrane permeability, the modification of target sites and the use of drug modifying enzymes (39).

1.4.1 Efflux pumps

Efflux pumps are transport proteins that export substrates across the bacterial membrane to maintain the internal environment of the cell (39). They are involved in many cellular processes such as metabolism, antimicrobial resistance, pathogenicity and stress responses (40). During exposure to antibiotics, efflux pumps utilise an energy dependant concentration gradient to export the antibiotics out of the cell. This negatively impacts the antibiotics activity providing resistance to the cell (39).

Classification

There are six classes of efflux pumps all of which are found in *A. baumannii* (Figure 1.1). The major classes are Proteobacterial Antimicrobial Compound Efflux (PACE), ATP-Binding Cassette (ABC), Small Multidrug Resistance (SMR), Multidrug and Toxic Compound Extrusion (MATE), Resistance Nodulation Division (RND) and the Major Facilitator Superfamily (MFS) family (20).

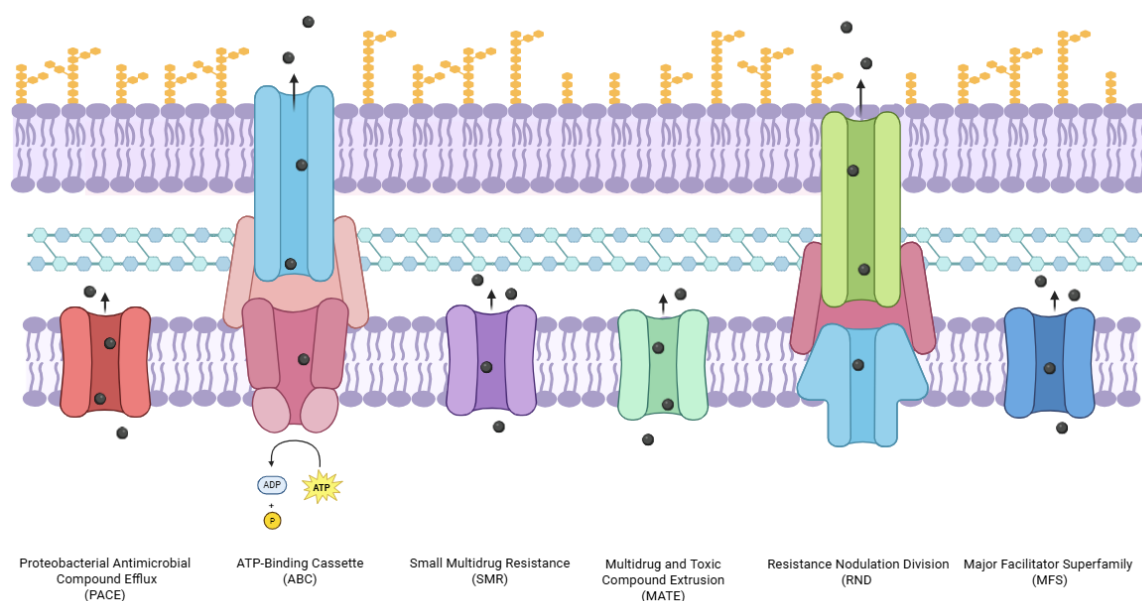


Figure 1.1 Efflux pump families in *A. baumannii* with examples. Efflux pump families in *A. baumannii* with examples. Abbreviations: PACE - Proteobacterial Antimicrobial Compound Efflux family, ABC - ATP-Binding Cassette, SMR - Small Multidrug Resistance, MATE - Multidrug and Toxic Compound Extrusion family, RND - Resistance Nodulation Division and MFS - Major Facilitator Superfamily.

Classification of efflux pumps into families is based on protein sequence similarity (21). Other traits for efflux characterization are; number of transmembrane domains, energy input and number of components e.g., RND pumps form tripartite system compared to SMR pumps which are single components (41). The most recently discovered class of efflux pumps are the PACE family. The mechanism of action and structural data is still unknown. PACE efflux pumps require a proton motive force for transport (42). The protein pumps are predicted to consist of four transmembrane domains, and they are often seen in biocide efflux e.g., Acel. Acel is a novel *Acinetobacter* sp. pump capable of conveying resistance to the disinfectant chlorhexidine (42, 43).

The ATP-binding cassette (ABC) family is the only class of efflux pumps to utilize free energy from ATP hydrolysis to transport substance across the cell membrane(s). This family characteristically contains proteins with membrane spanning domains and ATP hydrolysing domains. ABC efflux pumps can play a role in both importing and exporting substances across the bacterial cell membrane (44).

ABC pumps are involved in antimicrobial resistance and have also been shown to play a part in nutrient uptake and genetic mechanisms e.g., DNA repair. ABC pumps can appear as a singular component i.e., spanning the inner membrane or can appear as a tripartite system i.e., spanning two membranes. An example of an ABC efflux pump in *A. baumannii* is MacAB-TolC. This is a tripartite pump that utilizes the outer membrane protein TolC to span across the two membranes. MacAB-TolC conveys macrolide resistance (43).

Small multidrug resistance (SMR) efflux pumps are comprised of four transmembrane α -helical domains. SMR pumps require a proton motive force to operate (21). SMR protein also play a role in antibiotic resistance (AR) as seen with quaternary ammonium compounds (QAC) e.g., *qacE*. In addition, deletion of some SMR pumps e.g., A1S_0710 shows reduced motility and virulence. Therefore, SMR pumps play a significant role in cell physiology in addition to conveying antibiotic resistance. AbeS is a well-known SMR pump in *A. baumannii* which conveys resistance. AbeS has been shown to reduce susceptibility to detergents, chloramphenicol, erythromycin, novobiocin and fluroquinolones (43).

MATE efflux pumps are ubiquitous in all domains of life. These protein pumps consist of 12 transmembrane helical domains. These efflux pumps are associated with cationic drugs and work via a proton motive force (44). There is a lack of information on this family of efflux pumps in *A. baumannii*. To date only 3 MATE pumps are described in *A. baumannii* with AbeM being the pump most characterized. AbeM conveys resistance to chloramphenicol, trimethoprim as well as various fluroquinolones and aminoglycosides (21, 43).

In Gram-negative bacteria the most clinically significant family of efflux pumps is the Resistance Nodulation Division (RND) family. This is attributed to their broad substrate specificity and their capacity to transport substrates across both the inner and outer membranes. RND pumps are consistently organized as tripartite complexes, comprising of an inner membrane protein, a periplasmic adaptor protein and an outer membrane channel (21).

Interestingly, research has shown that mutations in RND efflux pump regulators that result in pump overexpression have been associated with increased antibiotic resistance in clinical isolates (45, 46). One example is mutations in *adeL* a LysR-type regulator of the RND efflux pump AdeFGH. AdeFGH is a well-known RND pump in *A. baumannii*. It conveys resistance to chloramphenicol, clindamycin, trimethoprim and fluoroquinolones (43).

The largest and most diverse class is the Major Facilitator Superfamily. This class utilizes the proton motive force and can be symporters, uniporters, or antiporters. In most cases these MFS pumps contain 12-14 transmembrane (TM) helical domains. MFS pumps can be a single component or tripartite efflux pump (43, 44). An example of an MFS efflux pump in *A. baumannii* is AmvA. AmvA prominently increases resistance to ciprofloxacin, novobiocin, norfloxacin, erythromycin, disinfectants, and dyes. AmvR regulates AmvA and it belongs to the TetR-type class (43).

Efflux pump inhibitors

Efflux pump inhibitors (EPIs) are molecules that disrupt substrate transport through two methods: inhibition of substrate binding or energy source dissipation. These are used in conjunction with antibiotics to increase the susceptibility of bacterial strains and improve treatment efficiency.

As efflux is an energy dependant process, some EPIs target the proton gradient used to power efflux pumps by decoupling oxidative phosphorylation e.g., carbonyl cyanide m-chlorophenylhydrazone (CCCP) (39). Most efflux pumps utilise a proton gradient as an energy source thus, CCCP can act on multiple different families of efflux pumps. However, CCCP has not been approved for clinical use due to its high level of toxicity (40).

Verapamil is an EPI that works by preventing the substrate from binding to the efflux pump for transport. Verapamil is a calcium channel blocker and has shown to increase tigecycline resistance in *A. baumannii* (40). Unfortunately, verapamil is not suitable for clinical application as it increases the Q-T interval of patients which puts the individual at significant risk of hypotension and shock (40).

Additionally, when used in conjunction with clarithromycin it can accumulate in the human body at toxic levels due to both compounds having the same cytochrome responsible for drug metabolism (40).

1.4.2 Reduced permeability

Porins are membrane proteins that function as transport channels for small molecules, including antibiotics (32). OmpA is a well-known porin in *A. baumannii* that plays a role in many cellular processes such as adhesion and antibiotic resistance (13, 28). Research has shown that loss of OmpA can increase sensitivity of *A. baumannii* strains to aztreonam, nalidixic acid and chloramphenicol. It is hypothesised that OmpA may enhance the activity of efflux pumps by exporting antibiotics from the periplasmic space across the outer membrane for efflux pump systems lacking a tripartite architecture, although the underlying mechanism remains unclear (28).

1.4.3 Modification of target sites

Antibiotics function by binding to a specific target protein inhibiting their activity. Cellular targets are usually proteins involved in essential cell processes such as protein synthesis, cell wall formation or nucleic acid synthesis. However, if the target site is altered, the antibiotic cannot bind efficiently leading to a reduction or a complete loss of antibiotic function (47). Modification through target site mutations can render the target protein functional but prevent antibiotic binding. This can be seen with fluoroquinolone resistance in *A. baumannii* where *gyrA* is modified through amino acid substitutions (48). Antimicrobial resistance can also arise through post-transcriptional modification of the target site.

Aminoglycoside resistance is mediated in *A. baumannii* through ArmA 16S rRNA methyltransferase modifying the 30S ribosome to prevent the antibiotic from binding and inhibiting protein synthesis (49). Thus, target site modification through structural or chemical changes to the antibiotic target site are a mechanism of antimicrobial resistance.

1.4.4 Drug modifying enzymes

Drug modifying enzymes represent another mechanism of antibiotic resistance, they function by degrading or inactivating the antibiotic so it can no longer affect the target protein (47). An example of degradation of antibiotics through drug modifying enzymes in *A. baumannii* is beta-lactamases. Beta-lactamases confer resistance to beta-lactam antibiotics e.g., carbapenems, by hydrolysing the beta-lactam ring, a structural component critical for their antibacterial activity (1).

Inactivation of antibiotics is achieved through chemical modification of the antibiotic structure by adding a chemical group to prevent binding of the antibiotic. Aminoglycoside modifying enzymes (AME) are a well-known resistance mechanisms in *A. baumannii* with several AMEs being found detected on both the chromosome and plasmids (11, 50, 51). AMEs are classified into three main groups based on the chemical group they add to the antibiotic for inactivation; phosphotransferases, nucleotidyltransferases and acetyltransferases (22).

1.4.5 Biofilm formation

Biofilms are an important physiological mechanism underlying the success of *A. baumannii* as a nosocomial pathogen. Biofilms aid in host cell attachment and provide protection from antibiotics, desiccation and the immune system which allows *A. baumannii* to persist in harsh environments and enhances its ability to cause infection (22). Sessile cells are more resistant to antibiotics than planktonic cells due to several lifestyle factors; a protective extracellular polysaccharide matrix, substantial gene expression heterogeneity and increased rates of genetic material exchange e.g., AMR genes (52). Biofilm formation has four stages of development: attachment, micro-colony formation, maturation and biofilm dispersion (Figure 1.2).

The first stage of biofilm development begins with adhesion of bacterial cells to a surface. In *A. baumannii* adhesion to abiotic surfaces is facilitated by the Csu pili . The Csu pilus is encoded by the *csu* operon (*csuA/B*, *csuA*, *csuB*, *csuC*, *csuD* and *csuE*) and is constructed through the chaperon-usher pathway (CUP) to produce an archaic-type pilus structure (53). Once the bacterial cells are adhered to the surface the cells begin to produce extracellular polymeric substances (EPS) and form a micro-colony. EPS aids in protection and exchange of genetic material and nutrients of the microbial community (54). Next the biofilm matures forming complex structures this is primarily mediated by biofilm-associated protein (bap) in *A. baumannii*. Bap plays a role in bacterial adhesion to host cells, controlling cell hydrophobicity and intracellular adhesion to strengthen the biofilm (19). The final stage of biofilm formation is dissemination/dispersal of sessile cells. This allows for further colonisation of hosts/surfaces and the acquisition of nutrients in a new location (54).

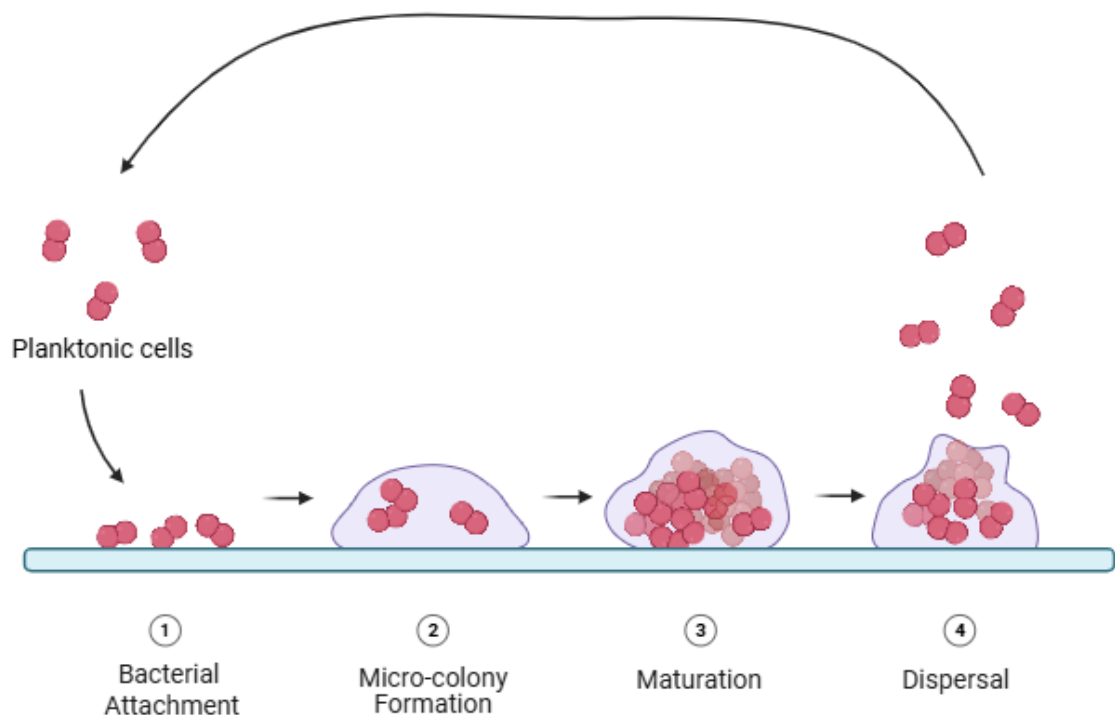


Figure 1.2. Biofilm life cycle. 1 – Bacterial attachment to surface, 2 – proliferation of cells forming a micro-colony, 3 - maturation of biofilm and 4 – dispersion of bacterial cells. Pink – bacterial cells and purple – extracellular matrix.

Biofilm formation can raise the antibiotic resistance profile of the bacteria by providing a protective physical barrier that restricts antibiotic penetration as well as the facilitating the exchange of AMR genes within the biofilm community (52). Additionally, the regulation of important biofilm associated genes can play a role in antibiotic resistance. For example, BfmRS, a two-component system, regulates the *csu* operon which plays a direct role in biofilm formation (19). BfmR is also known to affect meropenem resistance. Upon the loss of BfmR there is a decrease in meropenem resistance however, the exact mechanism/gene that is regulated by BfmRS that results in this sensitivity is not fully understood (55). Therefore, biofilm formation can influence the antibiotic resistance profile of a bacterial strain, either enhancing or reducing its susceptibility depending on the regulatory context (19). This highlights the importance of understanding the interconnected regulatory mechanisms involved in antimicrobial resistance and biofilm formation.

1.4.6 Capsule production

Antimicrobial resistance is also facilitated by capsule production in *A. baumannii*. Repeating interlinked sugar molecules form a protective layer around the bacterial cell which can increase the antimicrobial resistance and virulence of the cell (22). Interestingly in *A. baumannii* an increase in capsule production can be seen upon exposure to sub-MIC concentrations of chloramphenicol and erythromycin. This hyper mucoid state has been experimentally verified to be non-mutational and is driven by regulatory mechanisms (56). Hence, it is important to understand and consider *A. baumannii* cellular functions and how different antibiotic treatments may affect the virulence and antibiotic resistance profile of strains. Capsule regulation affecting resistance has also been seen in the absence of antibiotics causing “phase variation” within a population. This results in the production of opaque or translucent colonies with different antibiotic resistance profiles (57). Phase variation in *A. baumannii* strains is dependent on several regulatory mechanisms and is reversible allowing the bacterium to adapt to changing environments. Opaque colonies exhibit increased antibiotic resistance and motility but demonstrate impaired biofilm formation.

Additionally opaque cells are responsible for virulence in *Galleria mellonella* and mouse infections (10, 58). Conversely translucent colonies demonstrate a reduction in antibiotic resistance, virulence and motility. However, translucent colonies display greater biofilm forming capacity and are more suited to environmental persistence and colonisation beyond the host (57).

1.4.7 Regulation of antimicrobial resistance in *A. baumannii*

Local transcriptional regulators

The ability to rapidly react to bacterial stressors is a major contributor to *A. baumannii* capability to persist and resist. One mechanism of antimicrobial resistance is efflux pumps and their regulation is a tightly controlled complex system. Local transcriptional regulators control the expression of a single gene or operon. For example, AceI gene regulation is controlled by a chlorohexidine responsive negative feedback loop with the repressor AceR. AceR is a LysR-type. AceR binds to the AceI promoter region preventing transcription. However, when chlorohexidine is present in the cell it binds to AceR. This inhibits AceR from preventing transcription and the genes for the efflux pump are transcribed (42, 43, 59). Alterations in the regulation of these mechanisms can be highly advantageous to both antibiotic resistance and bacterial fitness in hostile environments. The regulation system controlling these transporters can be interconnected leading to a knock-on effect from targeting one regulator protein e.g., deletion of *acrB* causes AcrD and AcrF to be upregulated to compensate for the loss of AcrB (44).

Two component systems

Not all regulation mechanisms are fixed to controlling one efflux pump and may affect two or more pumps. Two component systems (TCS) are one example of a single regulatory system capable of influencing multiple efflux pumps expression for example, AdeRS regulates AdeABC and AdeIJK efflux pumps (16, 44). This system involves a sensor kinase and a regulator protein to switch on and off efflux pump genes. The sensor kinase recognizes environmental stimuli and phosphorylates a regulator protein to form a homodimer which can act as a transcriptional activator (16, 44).

However, the TCS BfmRS has been shown to alter antimicrobial resistance in *A. baumannii* through several other mechanisms such as; induction of β -lactamases, increasing expression of biofilm formation and capsule production associated genes (19). Similarly, GacSA does not alter the expression of efflux pumps and provides resistance through the regulation of porins e.g., *ompA* which limits the entry of the antibiotic into the bacterial cell (16).

Global transcriptional regulators

Another global transcriptional regulatory system are nucleoid-associated proteins. One of the most extensively studied of these is H-NS. H-NS functions as a global transcriptional repressor that inhibits gene expression by bending, stiffening or bridging DNA (Figure 1.3), therefore restricting RNA polymerase access to the target gene (60). H-NS binds to intrinsically curved AT-rich DNA regions, which are often located near gene promoters or within horizontally acquired genes (61, 62). H-NS has been shown to affect several cellular functions such as; metabolism, motility, type VI secretion system, extracellular DNA uptake, acquisition of transposable DNA and antimicrobial resistance (62–65). *A. baumannii* AB5075 carries two copies of H-NS in its genome; one on the chromosome and one on p1AB5075 plasmid (66). As previously stated the function of H-NS is known however, the copy residing on the p1AB5075 plasmid has not been studied to date exclusively in *A. baumannii* AB5075 (63, 65, 67).

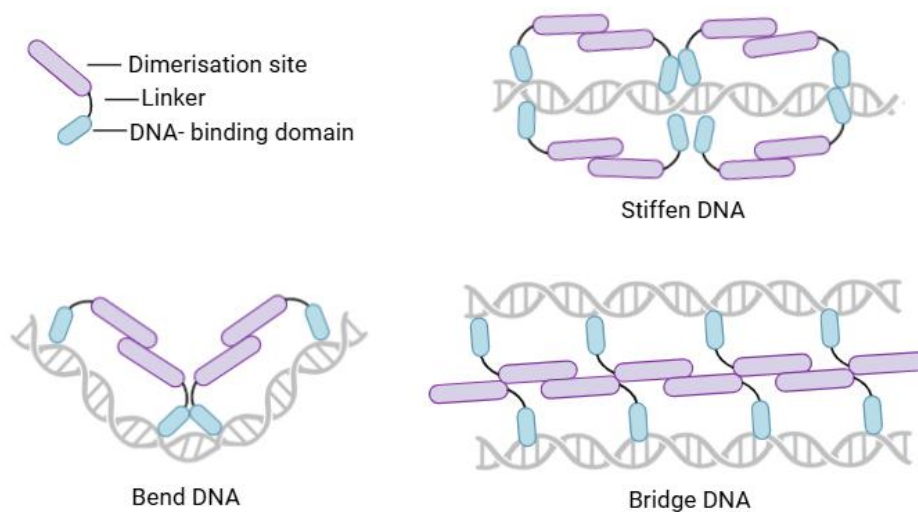


Figure 1.3 H-NS mediated silencing of AT-rich DNA. Purple – Dimerization site, Black – Flexible linker and Blue – DNA-binding domain.

Intrinsic chloramphenicol resistance

Chloramphenicol (CHL) is a broad-spectrum bacteriostatic antibiotic. CHL was first isolated in 1948 from *Streptomyces venezuelae*. It functions by binding to the 50S ribosomal subunit to inhibit protein synthesis (Figure 1.4). Upon binding to the ribosome CHL prevents the tRNA containing an amino acid from entering the A site. This blocks incoming amino acid residues from being added to an existing chain of amino acids and no new proteins can be made (68). Chloramphenicol was widely used due to its advantageous properties such as superb tissue penetration and capacity for oral administration. However, its widespread use in developed countries was halted due to adverse side effects (69).

Side effects can include severe haematological side effects, grey baby syndrome, ototoxicity, and neurotoxicity. These side effects can occur through systemic or topical administration of chloramphenicol (68). Regardless of these adverse side effects, CHL is still heavily utilized in developing countries. This is due to its low manufacturing cost, ease of availability and capacity to treat diseases such as; meningitis, typhoid fever and rickettsial infections (69).

A. baumannii is naturally resistant to chloramphenicol through several different resistance mechanisms such as; regulation of membrane permeability, O-acetyltransferases and efflux pumps (1). Major facilitator efflux pumps *craA* and *cmlA* are well-known chloramphenicol resistance genes in *A. baumannii* (1). CraA shares a 61% amino acid sequence similarity to the *Escherichia coli* MfdA efflux pump (48–50). MfdA exhibits resistance to a variety of antibiotics such as tetracycline, chloramphenicol, erythromycin, neomycin and kanamycin (71, 72). However, CraA appears to be specific for amphenicol, chlorhexidine and benzalkonium efflux (4, 5).

Cbl a LysR transcriptional regulator involved in sulphur acquisition and cysteine biosynthesis has been identified as a potential regulator of *craA*. Upon deletion of *cbl* a significant log₂-fold increase of 2.75 in *craA* expression was recorded (73). This is an indication that Cbl might also be involved in the direct regulation of the CraA efflux pump. However, to date the exact regulatory mechanisms and environmental conditions that influence *craA* expression are not fully understood. In 2018 an inner membrane permease ABUW_0982 *cxpE* was proposed to be a novel efflux pump that was the most significant contributor to chloramphenicol resistance in *A. baumannii* (7). This efflux protein shares low sequence homology with proteins that are members of the autoinducer-2 family and an *E. coli* permease TqsA (100% sequence identity observed across 23% of the protein sequence). It is predicted that the structure of *cxpE* is similar to TqsA with 8 transmembrane domains that reside in the inner membrane and span into the periplasm and cytoplasm (7, 74). It is currently unknown how *cxpE* is regulated and the mechanism in which it functions. It is hypothesized that tripartite efflux pumps work in tandem with *cxpE* for CHL efflux (7). The main mechanism of chloramphenicol resistance in *A. baumannii* remains unclear (4, 5, 7).

While *A. baumannii* is naturally resistant to this antibiotic CHL is still an important medicine used worldwide. It is currently on the WHO's list of essential medicines (75). Furthermore recent studies have shown that restoration of chloramphenicol sensitivity in *A. baumannii* ATCC17978 is possible in certain environmental conditions (8). Therefore, it is critical to have a comprehensive understanding of the mechanisms underlying antibiotic resistance and their regulatory pathways for developing strategies to restore the efficacy of existing antibiotics against resistant strains. This can result in repurposing currently available antibiotics reducing the urgent need for the development of novel antibiotics.

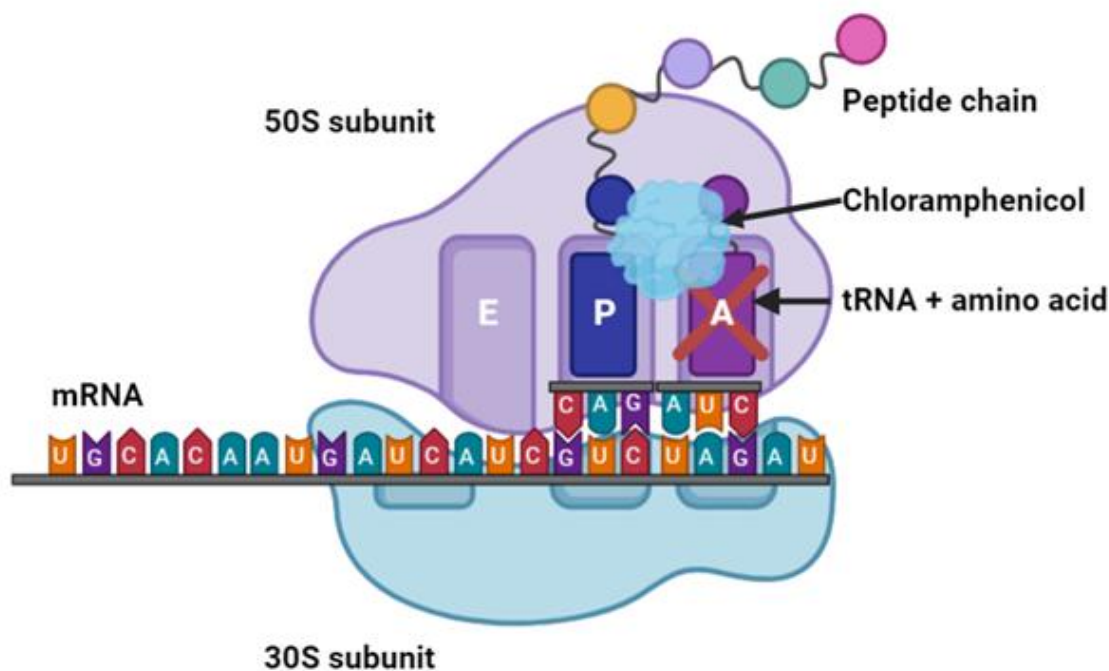


Figure 1.4. Chloramphenicol Mechanisms of action. A - aminoacyl site where the tRNA enters, P – peptidyl site where the peptide bond forms between the amino acid on the tRNA and the peptide chain, E – exit site where the empty tRNA leaves the ribosome.

1.5 Genetic architecture of p1AB5075 in *A. baumannii* AB5075

1.5.1 Structure and genetic overview of p1BA5075

Plasmid dissemination poses a significant challenge to combatting the spread of AMR due to efficient inter- and intra-species transfer accelerating the emergence and persistence of multi-drug-resistant strains (76). The largest plasmid “p1AB5075” in *A. baumannii* AB5075 is of concern as it carries resistance to several antibiotics including aminoglycosides and β -lactams. Plasmid p1AB5075 belongs to the F-type T4SS-encoding plasmid family which is transferred through conjugation (77).

Evidence of transfer between *A. baumannii* strains has been observed with either complete or partial transfer of the plasmid encoded genes. Plasmids pAB9098 and pK50a share 99% and 76% sequence identity with p1AB5075 respectively (50, 51).

Interestingly, p1AB5075 has also been shown to transferable to non *baumannii* strains providing increased antibiotic resistance profiles to *A. seifertii*, *A. baylyi*, *A. noscomialis* and *A. haemolyticus*. This is important as it shows the potential dissemination of resistance genes among species that are either emerging human pathogens or originate from environmental sources (77). Therefore, it is important to elucidate the role of individual plasmid encoded resistance genes in determining the overall antibiotic resistance of a strain. To date this has not been performed on p1AB5075 resistance genes except in cases where large deletions were analysed such as the removal of resistance island 2 (70). Plasmid dissemination is not only a concern for the transfer of antimicrobial resistance genes but also, for the potential impact on virulence (78, 79). The urinary isolate *A. baumannii* UPAB1 pAB5 plasmid has been shown to regulate chromosomal-encoded type Vi secretion system (T6SS) and biofilm associated genes (78, 79). It is critical to understand the function of plasmid-encoded genes and their impact through cross-talk regulation with the chromosome, to understand the severity of plasmid dissemination in *A. baumannii*.

1.5.2 Resistance mechanisms linked to p1AB5075

Plasmid p1AB5075 provides antimicrobial resistance to aminoglycosides, chloramphenicol, trimethoprim, disinfectants and cephalosporins through resistance island 2 (RI2). RI2 is located on the p1AB5075 plasmid and is made up of *aadB*, *cmlA5*, *aadA2*, *strA*, *strB*, *bla_{GES-11}*, *aacC4*, *qacΔE1* and *sul1* enclosed by class 1 integrons. Due to the presence of the integrons RI2 is able to undergo amplification resulting in increased antimicrobial resistance of the strain (11). This phenomenon complicates the treatment of *A. baumannii* as heterogeneity of antibiotic resistance can lead to treatment failure and persistence of *A. baumannii* infections. Phase variation regulation has also been linked to RI2 where a novel sRNA located on the 5' end of *aadB* is responsible for switching from opaque to translucent colony phenotypes (10). It is evident that p1AB5075 carries a variety of key regulatory mechanisms and antimicrobial resistance genes, highlighting the need for further study.

1.6 Aims of this study

Previously, a significant amount of research was performed using lab strains such as ATCC19606 and ATCC17978. However, these strains are no longer representative of the current state of *A. baumannii* infections due to the strains not having significant antimicrobial resistance. AB5075 is a more appropriate strain for current research as it is MDR and highly virulent (80). The primary objectives of this thesis were to investigate *craA* and *cxpE* as major contributors to chloramphenicol resistance and whether restoration of chloramphenicol sensitivity in *A. baumannii* AB5075 was possible as previously seen in *A. baumannii* ATCC17978. Additionally, this study investigated p1AB5075 to explore the contribution of individual antibiotic resistance genes and potential virulence regulatory mechanisms present on the plasmid. To accomplish this the following specific goals were investigated;

- To analyse the consequences of *craA* and *cxpE* deletions on antibiotic resistance through disk diffusion, minimum inhibitory concentration assays and growth experiments.
- To evaluate the impact of *craA* and *cxpE* on *A. baumannii* on motility and biofilm formation.
- To investigate whether transient chloramphenicol resistance is present in *A. baumannii* AB5075 and identify potential contributing genes.
- To explore the contribution of individual p1AB5075 plasmid encoded genes that influence the overall antibiotic resistance profile therefore providing a clearer understanding of the consequences of plasmid dissemination.
- To examine the implications of the loss of p1AB5075 on virulence in *A. baumannii* AB5075 to enhance the knowledge of plasmid mediated pathogenicity.
- To discover putative biofilm associated regulatory genes on the p1AB5075 plasmid through RNA-seq analysis of p1AB5075 deletion strains during biofilm formation.

Chapter 2 - Materials and Methods

2.1 Microbial culturing

2.1.1 Media

Media used in this study are listed in **Table 2.1**. Liquid media was stored at room temperature and agar plates were kept at 4°C for long term storage. Media was prepared using deionised water and was sterilised prior to use by autoclaving.

2.1.2 Bacterial strains

Bacterial strains used in this study are recorded in **Table 2.2**. Long term storage of strains was diluted in a ratio of 2:1 with 80% glycerol and kept at -80°C. For cultivation of strains cryo-stocks were streaked for isolation on L-agar plates supplemented with antibiotics if required and left at 37°C for 16 hours. Plates were kept for a maximum of one week. The primary strain *A. baumannii* AB5075 was isolated from a tibia osteomyelitis infection in the United States of America in 2008 (80).

2.1.3 Plasmids

All plasmids used in this study are detailed in **Table 2.3**. Plasmids were stored in *Escherichia coli* TOP10 and stored at -80°C. The streaking of plasmid strains was routinely performed with L-agar containing the appropriate selective antibiotic. Plates were discarded after one week. Isolated plasmids were kept at -20°C for long term storage.

Table 2.1 Media used in this study.

Media	Component	Concentration
<i>Lysogeny broth</i> (Lennox, L-broth)	Tryptone	10 g/L
	NaCl	5 g/L
	Yeast extract	5 g/L
<i>Lysogeny agar</i> (Lennox, L-agar) <i>Transformation media</i>	L-broth	
	Agar	1.5% (w/v) agar
	D3 Agarose	20 g/L
<i>Cation adjusted Mueller Hinton broth</i> (MH2)	Tryptone	2.5 g/L
	NaCl	2.5 g/L
	Beef extract	2 g/L
	Acid hydrolysate of casein	17.5 g/L
	Starch	1.5 g/L
	Agar	17 g/L
	Calcium Ca ²⁺	20 mg/L
<i>Mueller Hinton agar</i> (MH agar)	Magnesium Mg ²⁺	10 mg/L
	Beef extract	2 g/L
	Acid hydrolysate of casein	17.5 g/L
	Starch	1.5 g/L
	Agar	17 g/L
<i>M9 pyruvate</i>	M9	1X
	Magnesium sulfate (MgSO ₄)	1mM
	Calcium chloride (CaCl ₂)	0.2mM
	Pyruvate	0.02M
<i>M9 glucose</i>	M9	1X
	Magnesium sulfate (MgSO ₄)	1mM
	Calcium chloride (CaCl ₂)	0.2mM
	Glucose	2% (w/v)
<i>Congo Red agar</i>	Casamino acids	10 g/L
	Yeast extract	1.5 g/L
	Agar	5 g/L
	Congo red	80 µg/L
	Coomassie blue	20 µg/L
	Magnesium sulfate (MgSO ₄)	400 µM
<i>Coomassie blue agar 1</i>	Tryptone	10 g/L
	Yeast extract	5 g/L
	NaCl	5 g/L
	Glucose	10 g/L
	Agar	15 g/L
	Coomassie blue	200 mg/L
<i>Coomassie blue agar 2</i>	Tryptone	10 g/L
	Yeast extract	5 g/L
	NaCl	5 g/L
	Glucose	10 g/L
	Agar	15 g/L
	Congo red	400 mg/L
	Coomassie blue	200 mg/L
BM2 media	Phosphate buffer	31 mM
	Magnesium sulfate (MgSO ₄)	0.5 mM
	Ferrous sulfate (FeSO ₄)	10 µM
	Ammonium sulfate ((NH ₄) ₂ SO ₄)	70 mM
	Potassium glutamate	15 mM

Table 2.2. Bacterial strains used in this study.

Species	Strain	Genotype	Resistance	Source
<i>E. coli</i>	TOP10	F– <i>mcrA</i> $\Delta(mrrhsdRMSmcrBC)$ $\phi 80lacZ\Delta M15\Delta lacX74$ <i>nupG recA1 araD139</i> $\Delta(ara-leu)7697 galE15$ <i>galK16 rpsL (StrR)</i> <i>endA1</i> λ	-	Invitrogen
<i>A. baumannii</i>	AB5075	Wildtype	-	Salcedo Lab (80)
<i>A. baumannii</i>	AB5075	$\Delta craA$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta cxpE$	-	This study
<i>A. baumannii</i>	AB5075	$\Delta craA-\Delta cxpE$	-	This study
<i>A. baumannii</i>	AB5075	<i>craA::3XFLAG-aacC4</i>	Apra ^R	This study
<i>A. baumannii</i>	AB5075	<i>cxpE::3XFLAG-aacC4</i>	Apra ^R	This study
<i>A. baumannii</i>	AB5075	$\Delta cbl::sacB-aacC4$	Apra ^R	This study
<i>A. baumannii</i>	AB5075	$\Delta craA-\Delta cbl::sacB-$ <i>aacC4</i>	Apra ^R	This study
<i>A. baumannii</i>	AB5075	$\Delta cxpE-\Delta cbl::sacB-$ <i>aacC4</i>	Apra ^R	This study
<i>A. baumannii</i>	AB5075	$\Delta p1AB5075$	-	This study

Table 2.3 Plasmids used in this study.

Plasmid name	Description	Resistance	Reference
pMHL2	Contains a <i>sacB</i> - <i>aacC4</i> cassette used for generating deletion mutants	Apra ^R	(81)
pMHL2-3XFLAG	Contains 3XFLAG- <i>aaCC4</i> cassette utilized in generating FLAG tagged mutants for western blotting	Apra ^R	Kröger Lab
pWH1266	<i>E. coli</i> - <i>A. baumannii</i> shuttle vector	Tet ^R , Amp ^R	(82)
pWH1266- <i>craA</i>	CraA overexpression vector	Tet ^R	This study
pWH1266- <i>cxpE</i>	CxpE overexpression vector	Tet ^R	This study
pWH1266- <i>aadB</i>	AadB overexpression vector	Tet ^R	This study
pWH1266- <i>aph</i>	Aph(3')-VI overexpression vector	Tet ^R	This study
pWH1266- <i>aacA4</i>	AacA4 overexpression vector	Tet ^R	This study
pWH1266- <i>aadA2</i>	AadA2 overexpression vector	Tet ^R	This study
pWH1266- <i>strA</i>	StrA overexpression vector	Tet ^R	This study
pWH1266- <i>strB</i>	StrB overexpression vector	Tet ^R	This study
pWH1266- <i>bla</i> _{GES-11}	Bl _{GES-11} overexpression vector	Tet ^R	This study
pWH1266- <i>dfrA7</i>	DfrA7 overexpression vector	Tet ^R	This study
pWH1266- <i>hns</i>	H-NS (p1AB5075 copy) expression vector under control of its native promoter	Tet ^R	This study

2.2 Molecular techniques

2.2.1 Genomic DNA extraction

Chloroform extractions were performed on *A. baumannii* AB5075 overnight cultures to isolate genomic DNA for PCR reactions. For whole genomic sequencing DNA was extracted from overnight cultures using the Wizard® Genomic DNA Purification kit (Promega) as per the manufacturer's instructions. DNA concentrations were quantified using a NanoDrop™ 2000, adjusted to a working stock of 100 ng/μL. DNA was stored at -20°C for chloroform extracts and at 4°C for DNA extracted utilizing the Wizard® Genomic DNA Purification kit (Promega).

2.2.2 Plasmid isolation

Plasmids were isolated using the E.Z.N.A.® plasmid isolation kit (Omega Bio-Tek) and stored at -20°C. Plasmid concentrations were analysed using the NanoDrop™ 2000 (Thermo Scientific™) and adjusted to a working concentration of 10 ng/μL.

2.2.3 Polymerase Chain Reactions (PCR)

PCR fragments over 1 kb in length were performed using PCRBIO VeriFI™ Mix (PCR Biosystems) and PCRs under 1.5 kb were performed using Taq polymerase (Kröger Lab). PCR reactions were set up as per **Table 2.4** and the cycling conditions used in **Table 2.5**. All PCR products were analysed on 1% agarose gels to confirm the PCR fragment length and quality. Primers used in this study can be found in **Appendix I**.

Table 2.4. PCR reaction components

Component	Volume (μL)
<i>Polymerase mix</i>	25
<i>Template DNA (100 ng/μL)</i>	1
<i>Forward primer (10 μM)</i>	1
<i>Reverse primer (10 μM)</i>	1
<i>Water</i>	22
<i>Total</i>	50

Table 2.5. PCR cycling conditions

Stage	Temperature (°C)	Time	Cycles
<i>Denaturation</i>	95	2 min	1
<i>Denaturation</i>	95	30 s	35
<i>Annealing</i>	Variable	30 s	
<i>Extension</i>	72	2 min	
<i>Elongation</i>	72	5 min	1

2.2.4 Agarose gel electrophoresis

PCR products were analysed by agarose gel electrophoresis to confirm the predicted amplified fragment sizes. 2 μ L of PCR amplified DNA was mixed with 2 μ L of 2 $\times$ loading dye (40 % (v/v) Glycerol, 10 mM Tris-HCl (pH 7.6), 1 μ L, 60 mM EDTA, 0.25 % Xylene Cyanol FF, 0.25 % (w/v) Bromophenol blue (pH 8.0) and 0.25 % Orange G) and loaded into the agarose gel wells. A 1% (w/v) agarose gel was used for analysis of all PCR products and ran in 1 $\times$ TAE buffer (40 mM Tris-acetate, 1 mM EDTA) at 100 V for 25 min. The DNA ladder Generuler™ 1kb DNA ladder (Thermo Scientific™) was ran alongside the PCR products to compare fragment sizes. DNA bands were visualized by staining with SYBR™ Safe DNA gel stain (Thermo Scientific™) and viewed under a safeVIEW-MINI2 Blue Light Transilluminator (Cleaver Scientific).

2.2.5 PCR purification

PCR products were isolated using the E.Z.N.A.® cycle pure kit (Omega Bio-Tek) and stored at -20°C. DNA concentrations were analysed using the NanoDrop™ 2000 (Thermo Scientific™) and adjusted to a working concentration of 100 ng/ μ L.

2.2.6 *DpnI* digestion

Plasmids were linearized using Anza™ 10 *DpnI* restriction enzyme (Thermo Scientific™) as per the manufacturer's instructions. *DpnI* digested plasmids were stored at -20°C for long term storage.

2.2.7 Plasmid constructions

Plasmids were constructed using the SLiCE method as previously described (83). This method uses homologous recombination of the vector and insert fragment through complementary overhangs. The insert amplification primers were designed with ~20bp that overlap with the vector backbone. The SLiCE reaction was incubated at 37°C for one hour and stored at -20°C. *E. coli* TOP10 cells were transformed with the SLiCE product. The plasmids were then isolated, confirmed via Sanger sequencing before natural transformation into *A. baumannii* strains.

Table 2.6. SLiCE reaction components

Component	Quantity
<i>T4 DNA Ligase buffer (10X)</i>	1 µL
<i>SLiC Extract</i>	1 µL
<i>PCR purified linearised plasmid</i>	100 ng
<i>PCR purified DNA insert</i>	100 ng
<i>Water</i>	To 10 µL
<i>Total volume</i>	10 µL

2.3 Genetic manipulation of bacterial strains

2.3.1 Bacterial transformations

To prepare calcium-competent *E. coli* cells, an overnight culture inoculated with a single colony and 5 mL of L-broth was prepared. 50 μ L of the overnight culture was used to inoculate 50 mL of L-broth. The 50 mL flask was incubated at 37°C until the culture reached an OD₆₀₀ of 0.4 determined by GENESYS 10 UV-VIS spectrophotometer (Thermo Scientific™). The culture was then centrifuged at 4°C and 3220 $\times$ g for 8 min. The supernatant was removed, and the pellet was resuspended in 40 mL of ice-cold 0.1M CaCl₂. The resuspended cells were incubated on ice for 20 min and then centrifuged at 4°C and 3220 $\times$ g for 8 min. The supernatant was discarded, and the cells were resuspended in ice-cold 0.1M CaCl₂ and 1.15 mL 87% glycerol. The resuspended cells were aliquoted into 300 μ L volumes and stored at -80 °C for long term storage.

Calcium-competent *E. coli* was routinely transformed using a heat shock method at 42°C. This involves incubating the competent *E. coli* cells and DNA for 20 min on ice, then incubation at 42°C for 90 s. The cells were incubated on ice for 2 min before adding 800 μ L of L-broth and allowed to recover for 90 min at 37°C followed by plating on selective media. For *A. baumannii* transformations, natural transformation was used. *A. baumannii* cultures were grown in 2 mL L-broth to an OD₆₀₀ of 1. The culture was diluted with PBS to achieve an OD₆₀₀ of 0.1. Next, 5 μ L of the cells were mixed with 5 μ L of DNA (100-300 ng/ μ L) and spotted onto 1 mL of transformation media in 2 mL tubes. The transformation media tubes were incubated at 37°C (static) overnight. The next day, the bacteria were resuspended in 100 μ L of PBS and plated on selective L-agar plates (81).

2.3.2 Gene deletion using a linear DNA fragment

The Godeaux *et al.* (2020) scarless deletion protocol that utilises homologous recombination was implemented to generate deletion mutants (81). Up- and downstream regions of the selected genes were amplified by PCR from genomic DNA isolated from *A. baumannii* AB5075 using DNA oligonucleotides P1, P2, P3 and P4 (Figure 2.1).

In parallel, a resistance cassette containing two genes *sacB* and *aacC4* was amplified using DNA oligonucleotides P5 and P6 (Figure 2.1). The primers used for up- and downstream amplification *i.e.*, P2 and P3, were designed with an overhang. This overhang (green on P2 and red on P3) complements the *sacB-aacC4* resistance cassette (Figure 2.1). This allowed for an overlap extension PCR to be performed to generate an 8 kb-sized fragment “extension cassette”. This extension cassette was purified and then inserted through natural transformation into *A. baumannii* AB5075. Transformants were selected for on L-agar containing 60 µg/mL of apramycin. Insertion of the extension cassette was confirmed via colony PCR. The mutant strain carrying the insertion is referred to as the “knockout strain” as the gene of interest has been knocked out. A clean deletion mutant involves an additional transformation with a “clean deletion cassette.” This clean deletion cassette consisted of a 2 kb upstream and 2 kb downstream fragment that has undergone overlap extension PCR to generate a 4 kb fragment. The knockout strain is transformed with the clean deletion cassette and selected for on 20% sucrose. Colonies were re-streaked on apramycin and sucrose plates to confirm the loss of apramycin. Colony PCR was used to confirm gene deletion.

2.3.3 Curing of the p1AB5075 plasmid

In an attempt to accelerate the process of gene deletion mutant generation, a second approach employing the pALF12 suicide plasmid, as previously described (84), was implemented in *A. baumannii* AB5075. Although this method did not yield the intended deletion mutant strains, it resulted in the serendipitous acquisition of the Δ p1AB5075 strain. The use of a suicide vector system for gene deletion resulting in the expulsion of the p1AB5075 plasmid has been reported previously in *A. baumannii* AB5075 (70). Consequently, this suicide vector method was not used for the generation of any further deletion mutants. With the exception of the Δ p1AB5075 strain all other deletion mutants in *A. baumannii* were generated using the scarless deletion protocol outlined in section 2.3.2.

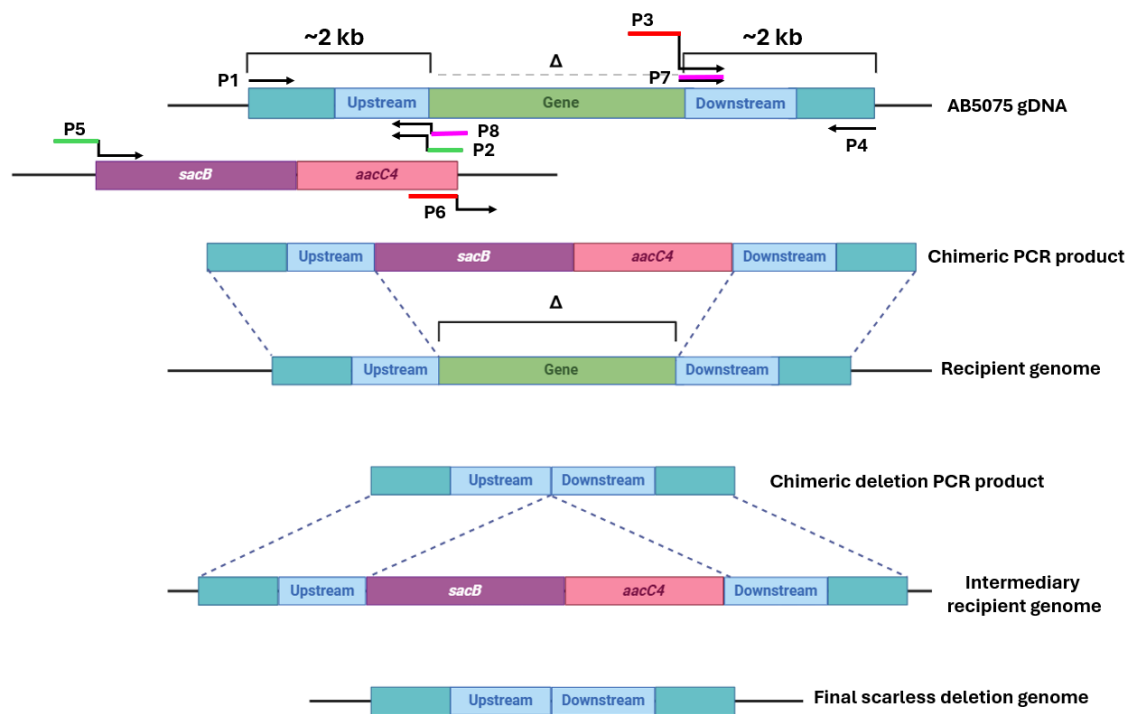


Figure 2.2. Designing a deletion cassette for a scarless gene deletion. A) amplification of the up and down stream fragments P1+P2 and P3+P4, respectively. P5 and P6 amplify a resistance cassette containing *sacB* and *aacC4*. P2+P5 and P3+P6 primers have complementary overhangs for extension PCR. B) A chimeric PCR product containing the up, down and resistance cassette was created using extension PCR and inserted into the recipient genome. Mutants are selected for using apramycin plates due to the *aacC4* gene conveying apramycin resistance. C) A second PCR product is generated containing the up and down stream fragments. This is inserted into the genome of the extension cassette mutant for a “clean deletion.” D) The clean deletion mutants are selected for using sucrose. The mutants containing the *sacB* gene will not grow as it renders the cells sucrose sensitive. Only clean deletion mutants will be recovered (81).

2.4 Analysis of antimicrobial susceptibility and virulence in *A. baumannii*

2.4.1 Antimicrobial susceptibility assays

Kirby-Bauer and minimum inhibitory (MIC) assays were performed as per the Clinical & Laboratory Standards Institute (CLSI) guidelines for *Acinetobacter sp* (85). Culture stocks are made from overnight cultures of each strain grown in cation adjusted Mueller-Hinton (MH2) which has been set to 0.5 McFarland standard. Kirby-Bauer assays were performed by spreading culture stocks over Mueller-Hinton (MH) plates to form a lawn of bacteria.

The plates were allowed to fully dry before addition of antibiotic disks (OXOID) to the MH plates. Kirby-Bauer plates were incubated upright for 22 h at 37°C before the zone of inhibition was measured. MIC assays were performed in 96 well plates using MH2 broth. Antibiotic concentrations were diluted 2-fold across the plate. A negative well was utilised as a blank. A positive well was used to serve as a growth reference (no antibiotic). 10 µL of culture stock (0.5 McFarland) was added to each well with the exception of the negative control. Plates were incubated at 37°C statically for 22 h before the plates were analysed by visual and OD₆₀₀ comparison.

2.4.2 Transient resistance growth analysis

Strains were grown overnight in 5 mL of L-broth supplemented with 25 µg/mL chloramphenicol. The next day, 1 mL samples were taken from each overnight and transferred into an Eppendorf tube. Samples were centrifuged at 13,000 × g for 1 minute, the supernatant was discarded, and the pellet was washed in 1 mL of PBS. This process was repeated 3 times. The OD₆₀₀ of each sample was determined by using a GENESYS 10 UV-VIS spectrophotometer (Thermo Scientific™). An aliquot of each sample was transferred to a flask containing 25 mL of M9 pyruvate media to obtain a final OD₆₀₀ of 0.025. Cultures were incubated at 37°C with 200 rpm for 5 days.

200 µL samples were taken at 0, 4, 24, 48, 72 and 96 h. 100 µL was used to determine the OD of the culture at the given time. The additional 100 µL were used for serial dilution for plating up to 10⁻⁸. CFU/mL was quantified using a “drip method”. The drip method entails spotting 10 µL of each serial dilution in triplicate on a square plate containing 0 µg/mL and 30 µg/mL chloramphenicol. The plate was then placed on its edge standing upright to allow the spots to flow down the surface of the plate. Colonies were counted in each lane to determine total CFU/mL (0 µg/mL) and resistant CFU/mL (30 µg/mL).

2.4.3 Permeability analysis of *A. baumannii* strains

Membrane permeability was assessed through an ethidium bromide cartwheel method as previously described (86). This method utilises the uptake of ethidium bromide into bacterial cells to assess the efflux capacity of different *A. baumannii* strains. Cultures were grown at 37°C, 220 rpm for 16 h. Next, the cultures were diluted to 0.5 McFarland standard for testing. The standardised cultures were swabbed onto L-agar containing ethidium bromide concentrations ranging from 0 to 2.5 µg/mL. Plates were incubated at 37°C for 16 h before visualization via ImageQuant™ LAS 4000 Luminescent Image Analyzer (GE Healthcare Life Sciences).

2.4.4 Analysis of bacterial biofilms in liquid media

Bacterial strains were incubated overnight in L-broth at 37°C and 220 rpm. OD₆₀₀ readings were taken, and the cultures were set to an OD₆₀₀ of 1 in PBS. Both nutrient rich media *i.e.*, L-broth and nutrient deficient media *i.e.*, M9 glucose media were used for biofilm analyses.

For analysis in 96 well plates (Fischer scientific Ltd), 10 µL of diluted culture was added to 90 µL of media and the plates were left at 30°C and 37°C statically for 24 h. The liquid culture was removed using a multi-channel micropipette and washed three times with 100 µL of PBS. Plates were put in a 60°C incubator for 10 min to fix the biofilm to the plate. 100 µL of 1:2 crystal violet solution (crystal violet : dH₂O) was added to each well and left for 15 min. The crystal violet solution was removed via a multi-channel micropipette and washed four times with PBS. The plates were dried for 10 min at 60°C. 100 µL of 95% EtOH was added, plates were agitated for 30 s and the OD was read at 575 nm in a Synergy™ HTX Multi-Mode microplate reader (BioTek). Crystal violet OD₅₇₅ readings were normalised to corresponding strain OD₆₀₀ readings to account for differences if any in bacterial growth and cell density.

For visual analysis and quantification, 2mL round bottom tubes composed of polypropylene (Falcon®) and polystyrene (Sarstedt) were utilised. Cultures were grown and diluted as previously prepared for 96 well plate analysis 400 µL of diluted culture was added to 2 mL of media and left to grow statically for 48 hours at 30°C and 37°C. The bacterial cultures were removed from the tubes using a 10 mL pipette and washed three times with 2 mL of PBS. The tubes were left at 60°C for 10 min before the addition of 2 mL 1:2 crystal violet solution. After 15 min, the crystal violet solution was removed, and the tubes were washed four times using 2 mL of PBS. The tubes were dried at 60°C for 10 min before being photographed. One mL of 95% EtOH was then added to each tube and agitated. 100 µL of this solution was then added into a 96 well plate and the OD was read at 575 nm in a Synergy™ HTX Multi-Mode microplate reader (BioTek). Crystal violet OD₅₇₅ readings were normalised to corresponding strain OD₆₀₀ readings to account for differences if any in bacterial growth and cell density.

2.4.5 Visualisation of biofilms through confocal microscopy

Confocal microscopy was performed for 3D visualisation of biofilms by the student in the Salcedo Lab (previously located in Lyon, France). Cells were grown overnight in L-broth at 37°C at 220 rpm. Cell cultures were adjusted to OD 0.01 with BM2 media. 500 µL of 0.01 OD₆₀₀ culture was transferred into two black 24 well plates and incubated statically at 37°C. Media was removed after 2 h and 3 d and the cells were fixed with 95% EtOH for 15 min. 95% EtOH was removed and the cells were washed three times with PBS. 500µL of DAPI (1:1000, Sigma) was added and left to stain for 30 min. Plates were examined using confocal microscope (Leica LP5).

2.4.6 Analysis of bacterial biofilms on solid media

For visualisation of biofilm formation on solid media, Congo red agar, Coomassie blue agars 1 and 2 were utilised. Agar was supplemented with appropriate antibiotics when necessary. *A. baumannii* single colonies were inoculated into 5 mL of L-broth and incubated at 37°C at 220 rpm for 16 h. The OD of overnight cultures were measured at 600 nm, diluted to an OD of 1. Three µL of diluted culture was spotted onto the different agar plates in duplicate and left to dry for 5 min.

Inoculated plates were sealed in a plastic bag to prevent drying out and incubated statically at 30°C and 37°C for 18 h. Plates were photographed at day 1, 5 and 7 for visual comparison.

2.4.7 Motility assay

Bacterial colonies were used to inoculate motility media plates (5 g/L tryptone, 0.5% (w/v) agarose). All plates were sealed in plastic bags to prevent drying out of the agarose. The plates were incubated upright statically for 5 d at 37°C. Next, all plates were left at 4°C for one hour to increase the visibility of motility interface. The motility interface was photographed alongside a ruler. All images were analysed using ImageJ for motility area calculation (87).

2.5 Analysis of proteins

2.5.1 Generation of FLAG-tagged *A. baumannii* strains

FLAG-tagged strains were constructed using a modification of the Godeaux deletion method (81). Instead of a “clean deletion cassette” being made a “FLAG cassette” containing ~1kb upstream of the gene, the gene of interest without its native stop codon and a 3×FLAG-*sacB-aacC4* fragment from pMHL2-3×FLAG plasmid was constructed. *A. baumannii* was then transformed with the FLAG cassette by natural transformation. The strains were validated by PCR, whole genome sequencing, and western blotting.

2.5.2 Protein sample preparation

For confirmation of the FLAG-tagged strain, cells were grown to an OD₆₀₀ of 0.3 before being diluted to an OD₆₀₀ of 0.1 for processing. Analysis of proteins throughout the growth phases were taken at specified timepoints alongside CFU/mL and OD₆₀₀ measurements. Samples were centrifuged at 4°C for 1 min at max speed and washed in PBS. Centrifugation was performed again at 4°C for 1 min at max speed. The pellets were washed twice in 200 µL PBS and retrieved via centrifugation at max speed and 4°C.

The washed pellets were resuspended in 25 μ L of 1 $\times$ Laemmli buffer (4% (w/v) SDS, 0.12M Tris-HCL (pH8.8), Bromophenol Blue 0.02% (w/v), glycerol 22% (v/v), DTT 0.2M) and 25 μ L of PBS before being boiled for 5 min. All samples were stored at -20°C.

2.5.3 Western blotting

Protein detection by Western blotting was performed using methods described previously (88). The SDS page gel was composed of a stacking layer *i.e.*, 5% polyacrylamide (acrylamide:bisacrylamide 6.6%, Tris-HCL (pH 6.8) 0.06M, SDS 0.15%, TEMED 0.06%, APS 0.1%) and a separating layer 15% polyacrylamide (acrylamide:bisacrylamide 12.5%, Tris-HCL (pH 6.8) 0.375M, SDS 0.1%, glycerol 7.6%, TEMED 0.067%, APS 0.1%). 10 μ L of each protein sample was loaded into the gel wells alongside the EZ-Run™ Pre-stained Rec Protein Ladder (Thermo Scientific™). The SDS gel was run for 2.5 hours at 100 V in 1 $\times$ running buffer (25 mM Tris, 192 mM Glycine, 0.1% SDS). The gel was then transferred to a nitrocellulose membrane using a Mini Trans-Blot® Cell (Bio-Rad) as per the manufacturers' instructions for 60 min at 150 V in 1 $\times$ transfer buffer (25 mM Tris, 0.19 M glycine). The membranes were blocked for 4 h at room temperature with blocking buffer (5% (w/v) skimmed milk powder, 0.9% (w/v) NaCl, 0.1% (v/v) Tween-20 and 10 mM Tris/HCL pH 7.5). The membrane was probed with the primary antibodies (anti-FLAG M2 mouse monoclonal antibody, cat no. F3165 1:10,000 dilution, Sigma) and anti-DnaK (mAb 8E2/2, *E.coli*, cat no. ADI-SPA-880-F, 1:5,000, Enzo) overnight at 4°C. The membrane was washed three times for 10 min each with PBST (PBS and 0.05% (v/v) Tween-20). Before the addition of the secondary antibody (rabbit anti-Mouse IgG horseradish-peroxidase, cat no. AP160P, 1:10,000 dilution, Thermo Scientific™) for 90 min. The membrane was washed again three times with PBST for 10 min each. Next 200 μ L of Pierce™ ECL Western Blotting Substrate (Thermo Scientific™) was added and the blot was visualised using an ImageQuant LAS400 instrument (GE Healthcare).

2.6 Analysis of RNA

2.6.1 Isolation of RNA from bacterial biofilms

A. baumannii strains were grown in 5 mL of L-broth at 37 °C and 220 rpm for 16 h. The OD600 of each overnight culture was determined and the strains were set to a final OD of 1 in PBS. 2 µL of diluted culture was added to 10 mL of M9 glucose media and incubated statically at 30°C for 2 d. The entire culture was centrifuged at 4°C and 3220 × g for 20 min. The pellet was resuspended in 4 mL of ice-cold 5% (w/v) phenol pH 4.3 and 95% (v/v) ethanol and incubated on ice for 30 min. The cultures were centrifuged at 4°C and 3220 × g for 20 min. The supernatant was discarded, and the pellet was resuspended in the residual liquid before transfer to a 1.5 mL Eppendorf tube. The cells were centrifuged at max speed for 1 min at 4°C. The supernatant was discarded, and the pellet was resuspended on ice in 1 mL of TRIzol™ Reagent (Thermo Scientific™). The cell mixture was transferred to phase-lock tubes (VWR) containing CHCl₃ and immediately shaken for 10 s. The tubes were spun at max speed for 30 min at room temperature. The aqueous phase was transferred to a 1.5 mL Eppendorf tube containing 450 µL of isopropanol and agitated for 10 s. The tubes were left for 30 min at room temperature before centrifugation at max speed for 30 min. The supernatant was discarded, and the pellet was washed with 350 µL of 75% EtOH. This was centrifuged at max speed for 10 min. The supernatant was discarded, and the RNA pellet was dried for 10 min. 20µL of RNase free water was added to the tubes before heating at 65°C and 900 rpm for 5 minutes to resuspend the pellet. RNA quantification was determined using the Qubit™ RNA Broad Range kit (Thermo Scientific™). RNA quality was analysed via agarose gel electrophoresis and stored at -80°C.

2.6.2 DNase treatment of RNA

DNase treatment was performed on RNA samples before RNA sequencing. Isolated RNA was diluted to a final concentration of 40 µg in 79 µL of RNase free water before heating at 65°C for 5 minutes. The samples were cooled on ice for 5 minutes before the addition of 10 µL 10× DNase I buffer (Fermentas), 1 µL Superase-In RNAase inhibitor (20 u/µL, Ambion) and 10 µL DNase I (1 u/µL, Fermentas).

This mixture was incubated at 37°C for 30 min before transfer to a phase-lock tube (VWR) containing 100 µL of ROTI®-Aqua-P/C/I (Sigma) and mixed vigorously for 15 s. The samples were centrifuged at 13,000 rpm for 12 min. The aqueous phase was transferred to a 1.5mL Eppendorf tube containing 300 µL of EtOH: 3 M Na-acetate mixture (30:1, pH 6.5) and stored overnight at -20°C. The samples were then centrifuged at 4°C and 13,000 rpm for 10 min. The supernatant was discarded, and the pellet was washed, resuspended in RNase free water, and quantified as previously described.

2.6.3 RNA sequencing analysis

RNA samples were sent to Azenta for RNA sequencing analysis. Library preparation, quality control and read analysis were examined with the help of Dr Karsten Hokamp (Smurfit Institute of Genetics, Trinity College Dublin) and Dr Anna Ershova (Moyne Institute of Preventive Medicine, Trinity College Dublin). Quality control was carried out through FastQC version 0.11.9 applied to the raw data files. The bowtie2 mapper version 2.4.2 was used with the 'very-sensitive-local' preset to align the short reads against the *A. baumannii* reference genome without plasmid p1. Only reads with the highest mapping quality (MAPQ $\geq$ 44) were kept. These were aggregated through featureCounts version 2.0.3. Parameters were set to work strand-specifically and to include reads that overlap more than one feature with fractional counts assigned. The resulting gene count matrix was analysed with DESeq2 version 1.48.1 from the Bioconductor package to detect differentially expressed genes. Strand-specific BigWig tracks scaled to the size of the smallest library were generated with bamCoverage version 3.5.5 from the deepTools package. BigWig files were utilised in Integrated Genome Browser (IGB) for visualisation of the RNA sequencing reads. Transcriptomic analysis consisted of volcano plots and GO analysis performed in R studio.

Chapter 3 – General Characterization of *craA* and *cxpE* in *A. baumannii* AB5075

3.1 Introduction

The substrates of *Acinetobacter baumannii* chromosomally-encoded efflux pumps *craA* and *cxpE* are well characterised (4, 5, 7, 70). However, significant gaps remain in our understanding of the regulatory mechanisms and environmental factors that influence their expression, this study aims to address these critical gaps in knowledge.

Prior work on *cxpE* states that it is the most significant contributor to chloramphenicol resistance in *A. baumannii* AB5075. Although besides substrate specificity and MIC analysis no other information is available on *cxpE* (7). In contrast, several studies have investigated the impact of *craA* and *cmlA* on a variety of *A. baumannii* strains and have concluded that *craA* plays a major role in maintaining intrinsic CHL resistance (4, 5, 70). Additionally, *craA* may export other substrates beyond amphenicols such as; benzalkonium and chlorhexidine (5). It is unclear whether *craA* is constitutively expressed in *A. baumannii* but, it is speculated that NaCl concentrations can upregulate the expression of *craA* (89, 90). In *A. baumannii* ATCC17978, it was identified by the Kröger group that chloramphenicol resistance is transient, likely involving CraA, suggesting that chloramphenicol resistance is regulated (8). Once ATCC17978 reaches the late stationary phase in minimal media it appears that a percentage of the population exhibits sensitivity to chloramphenicol. It is shown that depending on whether the growth environment is nutrient rich or nutrient deprived chloramphenicol resistance is conditional. Nutrient rich media allows for a highly resistant phenotype. However, when the bacteria are grown in minimal media a sensitive phenotype prevails as time progresses, there is a loss in resistance potential exhibited as a decrease of ~50% after 24 h. Thus, transient chloramphenicol resistance is present in *A. baumannii* ATCC17978.

Gene expression analysis suggested that down-regulation of efflux pump CraA may be responsible for this phenomenon (8). However, the regulatory factors influencing *craA* expression are unknown. A cysteine biosynthesis gene *cbl* has been proposed as a potential repressor for *craA* expression as upon the loss of the *cbl* gene *craA* is upregulated in *A. baumannii* (73).

Previously, a significant amount of research was performed using lab strains such as ATCC19606 and ATCC17978. However, these strains are no longer representative of the current state of *A. baumannii* infections due to the strains not having significant antimicrobial resistance. AB5075 is a more appropriate strain for current research as it is MDR and highly virulent. This project aims to re-evaluate the information on chloramphenicol resistance in the MDR strain AB5075 as well as tackling the gaps in knowledge in the genetic regulation of chloramphenicol resistance at a transcriptional level in *A. baumannii* AB5075.

3.2 Investigation into the biological role of *craA* and *cxpE* in *A. baumannii*

3.2.1 Construction of *craA* and *cxpE* complementation strains

To accurately assess the biological mechanisms that *craA* and *cxpE* influence, a scarless removal gene modification method was implemented (81), to generate gene deletion mutants that were used for analysis where possible. This refers to only the gene of interest being removed and no other significant genomic alteration being detected through whole genome sequencing. This allows for stability and reproducibility of results in this study. These deletion strains were generated using oligonucleotides to form a deletion fragment (Appendix I) and the natural homologous recombination method for transformation (81). All mutant strains generated underwent whole genome sequencing to ensure correct genotypes (Table 2.2).

To confirm that the loss of *craA* and *cxpE* was responsible for any research findings the gene of interest was reintroduced into the respective deletion mutant backgrounds to restore a wildtype phenotype. Complementation ensures that any observed phenotypic changes were specifically a result of losing either *craA* or *cxpE*. Gene complementation plasmids were constructed using the SLiCE method as previously described (83).

The gene of interest was inserted into the pWH1266 plasmid which contains a tetracycline resistance gene to enable selection of plasmid transformed mutants (Figure 3.1). The target gene is placed under control of the *bla* promoter present on the pWH1266 plasmid for constitutive expression (82). This system generates an overexpression of *craA/cxpE* as multiple copies of the plasmid may be present in the *A. baumannii* mutant strains and the wildtype strain only carries a single copy of *craA/cxpE* on the chromosome.

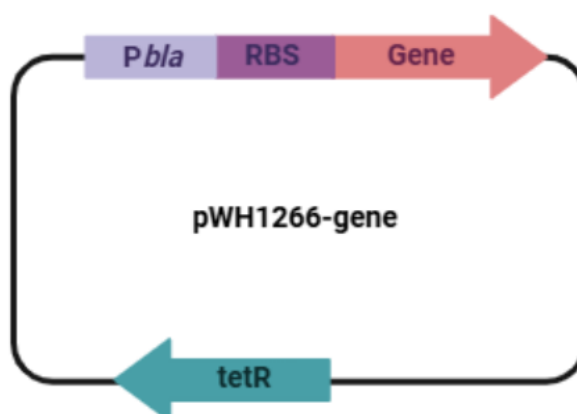


Figure 3.1 Construction of plasmids for mutant complementation utilising pWH1266. P-*bla* – beta-lactamase promoter, RBS – artificial ribosomal binding site “AGGAGG”, *tetR* – tetracycline resistance gene.

3.2.2 Phenotypic characterization of Δ *craA* and Δ *cxpE* mutants in *A. baumannii*

During preparation of this thesis, a large-scale RNA-seq analysis in *A. baumannii* AB5075 was carried out in the host lab by A. Bakheet, which included exposure of *A. baumannii* to a brief (15 min) exposure to a sub-inhibitory concentration of chloramphenicol and other stressors (91). The RNA-seq analysis of *A. baumannii* AB5075 revealed that the expression of *craA* in *A. baumannii* AB5075 is induced by exposure to 32 μ g/mL of chloramphenicol and 12 μ g/mL tetracycline.

Additionally, *cxpE*/ABUW_0982 is expressed highly in late exponential phase, early stationary phase, growth in 22°C and when exposed to a temperature shift from 22°C to 37°C in *A. baumannii* AB5075 (Figure 3.2).

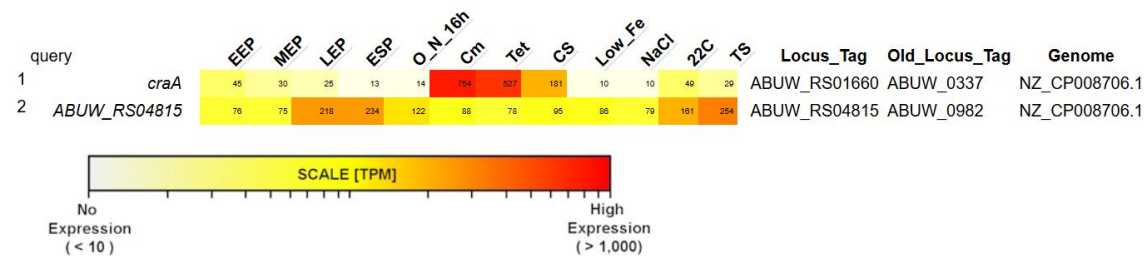


Figure 3.2. RNA-seq analysis of *cxpE* (ABUW_RS04815) and *craA* (ABUW_RS01660) under different environmental conditions. EEP – exponential phase, MEP – middle exponential phase, LEP – late exponential phase, ESP – early stationary phase, O_N_16 – overnight 16 hours, MEP – mid exponential phase, NaCl – salt shock, LowFe – iron limiting conditions, CS – cold shock, Tet – tetracycline, CM – chloramphenicol, 22C – 22°C, TS – temperature shift. Figure was derived from data analysis by Bakheet, Ali A. (2024) (91).

To assess the consequences of gene deletion of *craA* and *cxpE* on bacterial fitness, growth experiments were performed for both the wild-type strain and mutant strains Δ *craA*, Δ *cxpE* and the double deletion Δ *craA*- Δ *cxpE* (Figure 3.3).

The strains were analysed for growth defects in the absence (Figure 3.3.A) or presence of sub-inhibitory levels of chloramphenicol (Figure 3.3.B), a known substrate of both genes (4, 5, 7). Under optimal growth conditions, all strains exhibited comparable growth profiles, with no significant growth defects observed (Figure 3.3.A). This indicated that neither *craA* nor *cxpE* is essential for bacterial growth. Whole genome sequencing confirmed that the generation of mutant strains did not result in any unintended genomic alterations. In the presence of sub-inhibitory concentrations of chloramphenicol (25 µg/mL), Δ *craA* and Δ *cxpE* showed negatively impacted growth profiles compared to the wild-type strain (Figure 3.3.B). The strain Δ *craA* displayed an extended lag phase although, ultimately reached the same final optical density as the wildtype strain once the cells reached exponential phase. It is known that *craA* plays a role in chloramphenicol resistance (4, 5), and its expression is induced upon exposure to chloramphenicol (Figure 3.2).

This suggests that *craA* is required for the initial rapid adaptation to chloramphenicol exposure. However, the presence of other resistance mechanisms, likely the expression of *cxpE* and/or *cmlA* allows for growth after an extended period of time.

In contrast, Δ *cxpE* exhibited a similar growth profile to the wildtype strain until mid-exponential phase (approx. 11 hours) in the presence of sub-inhibitory concentrations of CHL (Figure 3.3.B). The Δ *cxpE* mutant strain prematurely entered stationary phase and achieved a lower final optical density in comparison to the wildtype strain. Interestingly, these are the growth phases *i.e.*, late exponential (LEP) and early stationary phase (ESP), where *cxpE* is highly expressed in *A. baumannii* AB5075 growth (Figure 3.2). This suggests that CpxE could be responsible for a sustained high-level of resistance once cells reach stationary phase.

Surprisingly, the double mutant Δ *craA*- Δ *cxpE* did not display a growth profile similar to either individual mutant strains as growth was comparable to the wildtype strain (Figure 3.3.B). This indicates that other CHL resistance mechanisms may be able to compensate upon the loss of *craA* and *cxpE* in *A. baumannii* AB5075. The mechanisms underlying this adaptation and survival are unclear and further investigation is required.

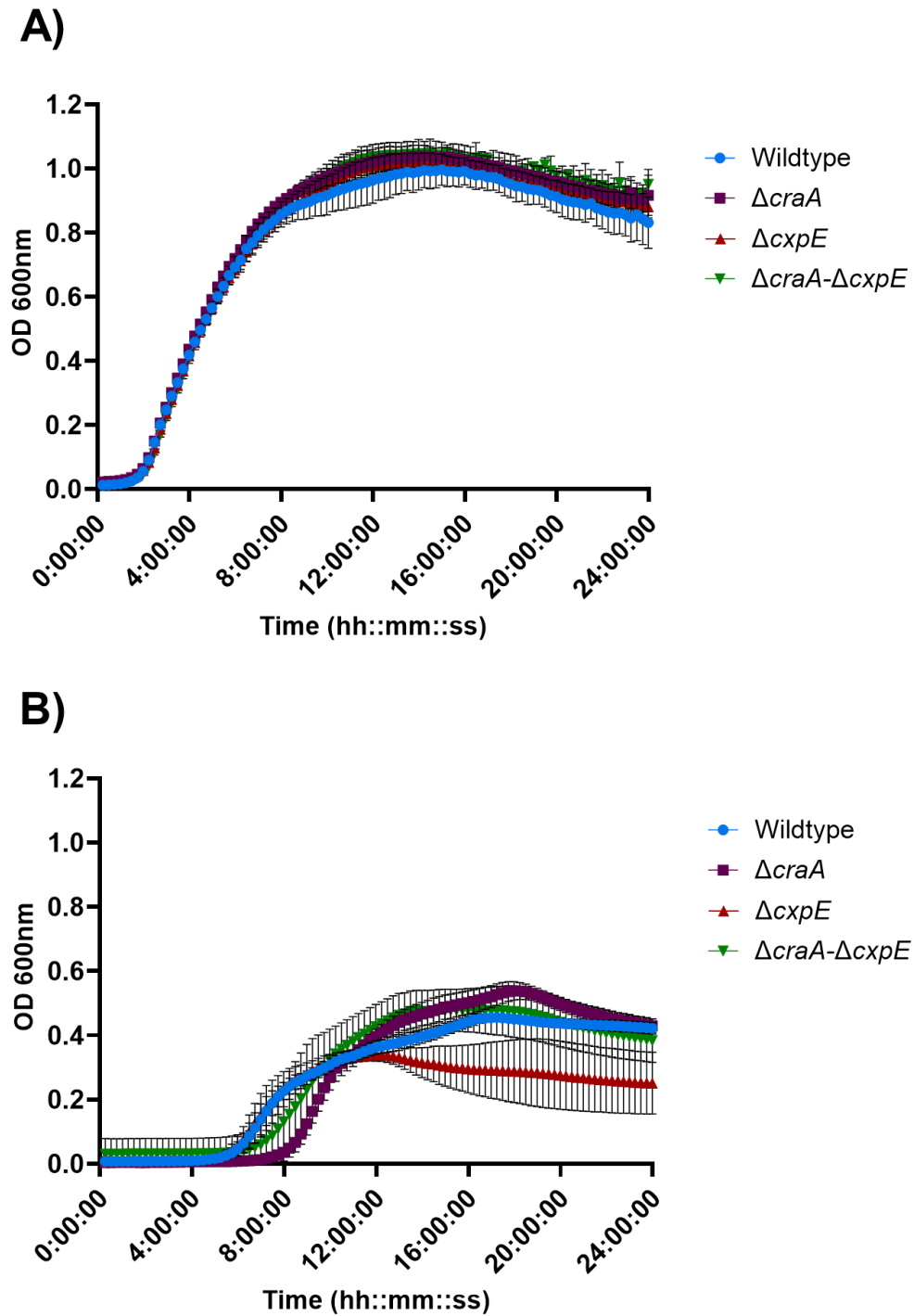


Figure 3.3. Growth experiment of wild-type AB5075, $\Delta craA$, $\Delta cxpE$ and $\Delta craA-\Delta cxpE$ in LB media. Overnight cultures of *A. baumannii* strains were diluted in PBS, standardised to an OD600 of 0.01 and incubated at 37°C with orbital shaking in A) LB 0 $\mu\text{g/mL}$ chloramphenicol and B) LB supplemented with 25 $\mu\text{g/mL}$ chloramphenicol. OD600 readings were taken at 15-minute intervals to evaluate bacterial growth over a 24-hour period (n=4).

3.2.3 Antimicrobial resistance of $\Delta craA$ and $\Delta cxpE$ mutants in *A. baumannii*

To investigate how *craA* and *cxpE* contribute to chloramphenicol resistance and to test other potential antibiotic substrates of the efflux pumps, the Kirby-Bauer disk diffusion method was performed (Table 3.1). This is a qualitative measurement used to analyse the resistance profile of a bacterial strain. It operates based on a zone of inhibition that indicated sensitivity of a bacterial strain to the corresponding antibiotic disk. All zones of inhibition were measured as per the CLSI guidelines and were compared to the publicly available *Acinetobacter sp.* data from the CLSI depository.

All strains showed resistance to the β -lactam antibiotics tested with the exception of cefoxitin (Table 3.1). However, for this class of antibiotics no difference in susceptibility levels was seen between the wildtype and mutant strains. This consistent resistance profile extended to carbapenems, aminoglycosides, quinolones, nitrofurantoin antibacterials, tetracyclines, folate pathway antagonists, polymyxins, cephamycin and cephalosporins, indicating that gene deletion did not alter antimicrobial susceptibility across the antibiotic classes evaluated. This was as expected as *craA* and *cxpE* have not been found to be involved in conferring resistance to any other antibiotic class besides aminoglycosides (4, 5, 7, 70). Despite the proven activity of *craA* and *cxpE* on chloramphenicol, no difference in chloramphenicol sensitivity was observed between the deletion strains and the wildtype when analysed for susceptibility through Kirby-Bauer assays.

Table 3.1. Kirby Bauer analysis of wildtype AB5075, Δ craA, Δ cxpE and Δ craA-cxpE. All results were colour coded based on CLSI resistance profile grading available in the CLSI M100 for *Acinetobacter* sp data (85). Red – resistant, Yellow -Intermediate, Green -sensitive and no colour indicates no comparative data available (n=3) .

Classes	Antibiotic (μ g)	Wildtype AB5075 Zone of inhibition (mm)	Δ craA Zone of inhibition (mm)	Δ cxpE Zone of inhibition (mm)
β-lactams	Aztreonam 30	0	0	0
	Cefoxitin 30	18	17	17
	Penicillin 2	0	0	0
	Ticarcillin 75	0	0	0
	Oxacillin 1	0	0	0
	Piperacillin/Tazobactam 110	0	0	0
Amphenicol	Chloramphenicol 30	8	9	9
Carbapenems	Imipenem 10	15	16	16
	Meropenem 10	13	12	13
	Doripenem 10	12	14	14
Aminoglycosides	Kanamycin 30	0	0	0
	Tobramycin 10	10	11	10
Quinolones	Ciprofloxacin 5	0	0	0
Nitrofurantoin antibacterials	Nitrofurantoin 100	0	0	0
Tetracyclines	Tigecycline 15	21	20	21
Folate pathway antagonists	Trimethoprim/ Sulfamethoxazole 25	0	0	0
Polymyxins	Colistin 50	19	18	18
Cephems	Cefepime 30	0	0	0
	Ceftazidime 30	0	0	0
Cephalosporins	Cefoperazone 30	0	0	0

Next, the chloramphenicol MICs were determined for wildtype and mutant strains (Table 3.2). The wildtype demonstrated chloramphenicol resistance with an MIC of 128 µg/mL (Table 3.2). For both $\Delta craA$, $\Delta cxpE$ and the double deletion mutant $\Delta craA\text{-}\Delta cxpE$ a 2-fold reduction in chloramphenicol MIC was observed *i.e.*, 64 µg/mL. This indicated that *craA* and *cxpE* are both important for maintaining a high level of chloramphenicol resistance in *A. baumannii* AB5075. However, when $\Delta craA$ and $\Delta cxpE$ mutant strains contained the pWH1266 plasmid required for accurate comparison to their respective complementation strains this reduction in MIC was undetectable from the wildtype. One hypothesis is that the addition of 12 µg/mL of tetracycline needed for plasmid retention, alongside chloramphenicol exposure induced other resistance mechanisms in the cell *e.g.*, alteration of membrane permeability, enabling the strain to persist under antibiotic stress.

Chlorhexidine MICs were also determined as in previous work in ATCC19606 $\Delta craA$ mutants showed a reduction in chlorhexidine resistance (5). The MIC for chlorhexidine in *A. baumannii* AB5075 wildtype pWH1266 was 8 µg/mL (Table 3.2). No difference in MIC was detected among the mutant strains with the exception of $\Delta craA$ pWH1266-*craA* which exhibited an increased MIC of 16 µg/mL. The increase in resistance to chlorhexidine in this complementation strain may be due to the overexpression of *craA*. As AB5075 wildtype only has one copy of *craA* on the chromosome and the exact pWH1266 plasmid copy number is unknown in *A. baumannii* AB5075, the increase in resistance can be attributed to an increased level of expression from having multiple plasmids carrying *craA*.

Table 3.2. Minimum Inhibitory concentration (MIC) assays of *craA* and *cxpE* mutants. MIC analysis was performed as per CLSI guidelines on *Acinetobacter* sp (85). NA – data not available (n=3).

Strain	Chlorhexidine (µg/mL)	Chloramphenicol (µg/mL)
AB5075 pWH1266	8	128
Δ <i>craA</i> pWH1266	8	128
Δ <i>craA</i> pWH1266- <i>craA</i>	16	128
Δ <i>cxpE</i> pWH1266	8	128
Δ <i>cxpE</i> pWH1266- <i>cxpE</i>	8	128
AB5075	NA	128
Δ <i>craA</i>	NA	64
Δ <i>cxpE</i>	NA	64
Δ <i>craA</i> - Δ <i>cxpE</i>	NA	64

To confirm if the growth defect of chloramphenicol on *A. baumannii* mutant strains was retained in mutant strains now carrying the pWH1266 plasmid, the growth experiment previously performed (Figure 3.2) was repeated. The same conditions were implemented with the addition of 12µg/mL of tetracycline for plasmid retention (Figure 3.4).

Under optimal growth conditions, growth defects were noticed in the Δ *craA* pWH1266-*craA* and Δ *cxpE* pWH1266 mutants compared to the wildtype pWH1266 strain (Figure 3.4.A). At first, the Δ *craA* pWH1266-*craA* had a growth pattern similar to the wildtype however, the complementation strain shows a decrease in optical density approximately after 15 hours resulting in a lower final OD, correlating to a lower bacterial density. Prolonged exposure to tetracycline in this experiment may cause *craA* to be expressed consistently which may result in a fitness cost through excess energy consumption needed to express CraA. This may explain the lower final optical density attributed to the Δ *craA* pWH1266-*craA* strain.

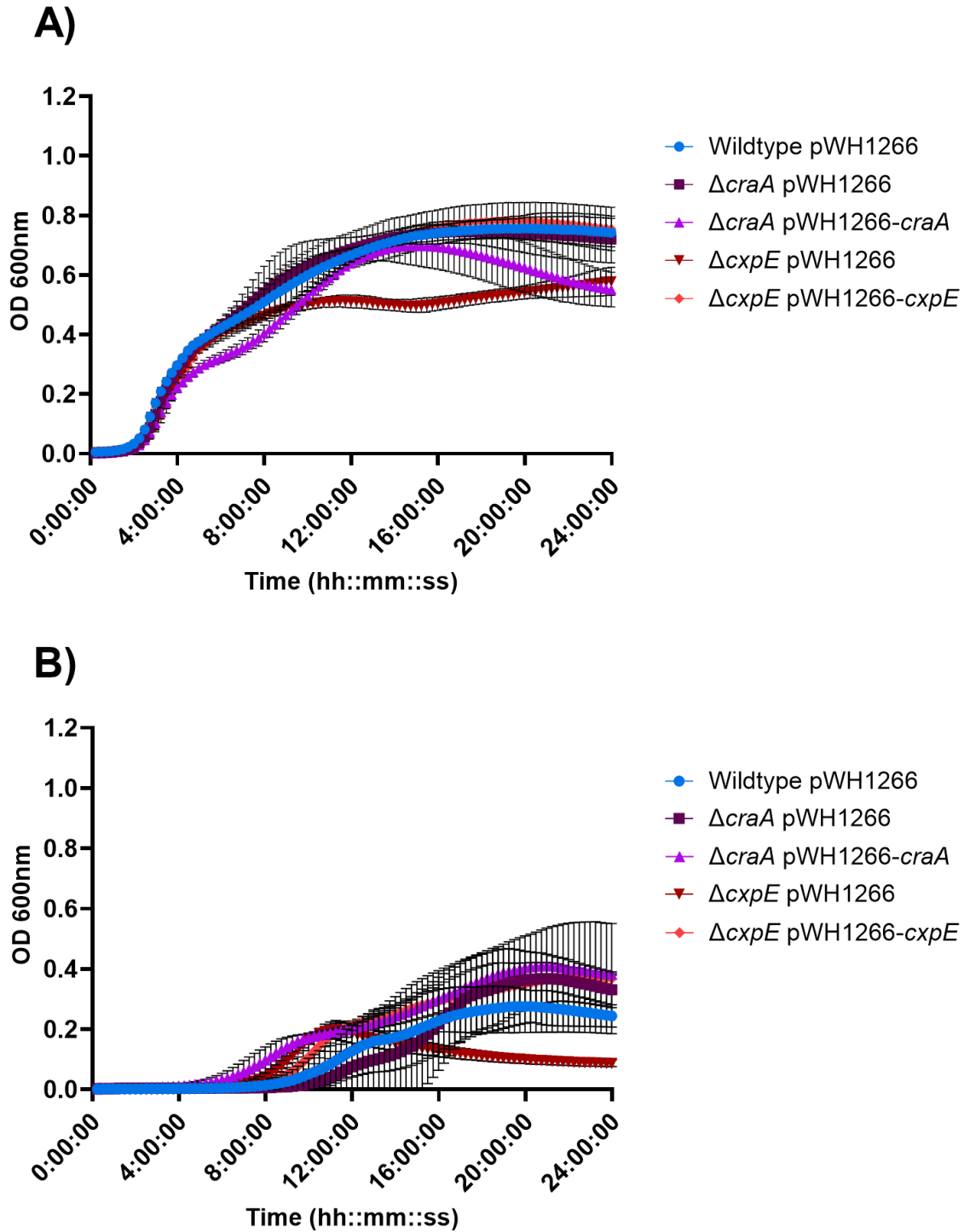


Figure 3.4. Growth experiment of *A. baumannii* AB5075 pWH1266 strains in LB media. Overnight cultures were grown in LB supplemented with 12 μ g/mL of tetracycline then, diluted and standardised to an OD600 of 0.01 in PBS and incubated at 37°C with orbital shaking in A) LB 0 μ g/mL chloramphenicol and 12 μ g/mL of tetracycline. B) LB supplemented with 25 μ g/mL chloramphenicol and 12 μ g/mL of tetracycline. OD600 readings were taken at 15-minute intervals to evaluate bacterial growth over a 24-hour period (n=4).

The $\Delta cpxE$ pWH1266 growth defect (Figure 3.4.A), resembles the previous $\Delta cpxE$ growth profile when exposed to sub-inhibitory levels of chloramphenicol *i.e.*, prematurely enters the stationary phase (Figure 3.3.B). The common experimental factor that results in this same growth profile is the exposure to a sub-inhibitory concentration of antibiotics (chloramphenicol, tetracycline) that target protein synthesis. The reoccurrence of this growth defect suggests that *cpxE* can efflux tetracycline as a substrate. Although *tetA*, a tetracycline efflux pump, is introduced into the cell through the pWH12066 plasmid comparable growth is not seen to the wildtype pWH1266 strain (Figure 3.4.A). While *cpxE* may efflux tetracycline directly it may also aid other efflux pumps in the enhancement efflux of antibiotics. This may explain the reduction in growth even though sufficient resistance genes are present for growth. The $\Delta cpxE$ pWH1266-*cpxE* shows no alteration in growth compared to the wildtype strain (Figure 3.4.A). Upon the reintroduction of *cpxE* the growth defect is eliminated. This reinforces the theory that *cpxE* is capable of direct or assistance of tetracycline efflux in *A. baumannii* AB5075.

Upon the addition of sub-inhibitory levels of chloramphenicol, the $\Delta craA$ pWH1266 shows a slight increase in lag phase compared to the wildtype (Figure 3.4.B). However, this is less pronounced than the increase in lag phase noted before in $\Delta craA$ (Figure 3.3.B). One reason for this improvement in rapid adaptation to CHL may be due to the presence of tetracycline in the media. Antibiotic resistance is often multifactorial and several AR genes may be altered in the presence of tetracycline which can consequently protect the cell from other antibiotic stressors like CHL for example, porin expression reduced upon exposure to tetracycline hence, limiting the uptake of chloramphenicol simultaneously. The reintroduction of the *craA* gene into the respective deletion background shows an increase in growth compared to the wildtype strain (Figure 3.4.B). As *craA* is overexpressed the mutant complementation strain outperforms the wildtype strain and enters into a extended exponential phase sooner and obtains a higher final bacterial concentration. This confirms that *craA* is important for the rapid adaptation of *A. baumannii* to chloramphenicol.

The growth defect seen in the presence of sub-inhibitory concentrations of chloramphenicol (Figure 3.3.B) and tetracycline (Figure 3.4.A) is more pronounced upon the exposure to both antibiotics simultaneously in $\Delta cxpE$ (Figure 3.4.B). The growth potential is significantly impaired in the $\Delta cxpE$ strain as the bacterial cells cannot combat the effects of the two antibiotics in tandem. This is a direct result of the loss of *cxpE* as the complementation strain vastly outperforms the wildtype strain in growth rate and final optical density reading (Figure 3.4.B). As the growth defect phenotype can be directly reversed upon the reintroduction of *cxpE* into *A. baumannii*, we can conclude that *cxpE* is important for maintaining chloramphenicol resistance in later stages of growth in *A. baumannii* AB5075.

3.2.4 The effect of *craA* and *cxpE* on membrane permeability in *A. baumannii*

To evaluate the effects of the loss of *craA* and *cxpE* on the overall efflux capacity of *A. baumannii* mutant strains, an ethidium bromide (EtBr) agar cartwheel analysis was performed (Figure 3.5). This EtBr agar cartwheel method is based on the uptake and active efflux of ethidium bromide by bacterial cells (92). EtBr is incorporated into the nutrient agar and is taken up through porins by the cells during bacterial growth in gram-negative bacteria. Plates are examined under a UV transilluminator for visual assessment. Bacterial strains with a high efflux capacity and low membrane permeability are seen as darker in appearance, as EtBr is effectively removed from the cell. Low efflux capacity and high membrane permeability bacterial strains can be seen as bright fluorescent streaks as the EtBr is retained intracellularly. Therefore, the visible fluorescence noted by the bacterial streaks serve as an indicator of efflux pump activity (92). *A. baumannii* AB5075 mutant strains $\Delta p1AB5075$ and $\Delta p1AB5075$ pWH1266-*hns* were included in this analysis as potential negative controls. Both strains were hypothesised to be sufficient negative controls due to the down regulation of numerous efflux pumps noted in the RNA sequencing analysis of these mutants (Appendix II). Across all tested EtBr concentrations, none of the *A. baumannii* mutant strains tested exhibited a significant change in fluorescence (Figure 3.5).

Unfortunately, $\Delta p1AB5075$ and $\Delta p1AB5075$ pWH1266-*hns* are inadequate negative controls as the wildtype showed no change in fluorescence from these strains. No other known negative controls were accessible for EtBr agar cartwheel analysis. However, no change was exhibited by any strain in comparison to the wildtype. Hence, we can speculate that the loss of *craA* and/or *cxpE* had no detrimental effect to the overall efflux capacity of *A. baumannii* AB5075.

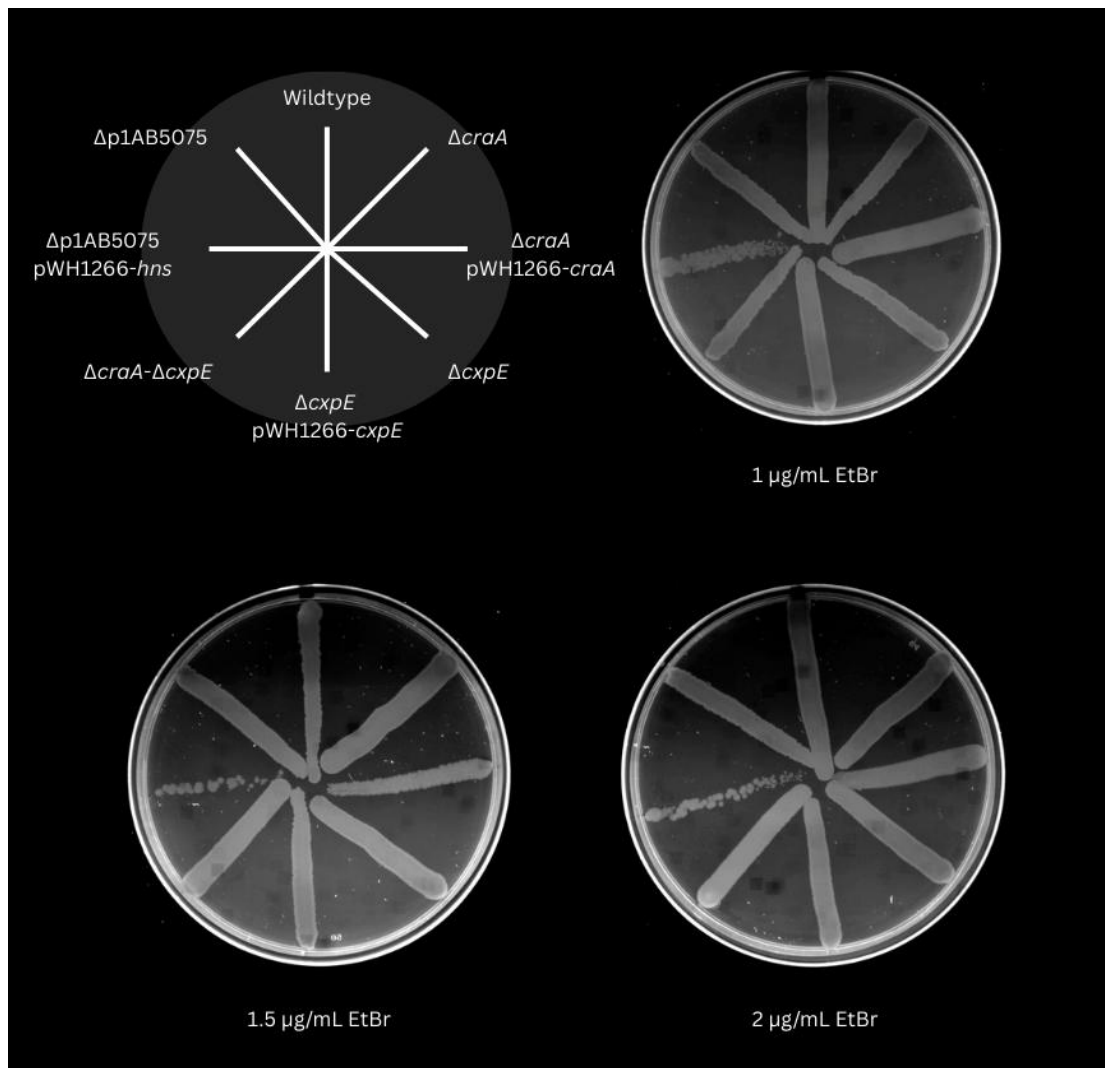


Figure 3.5. Ethidium bromide (EtBr) agar cartwheel analysis of *A. baumannii* AB5075 strains. Overnight cultures were diluted in PBS to a final OD of 0.5 McFarland, streaked onto agar plates containing 1-2 $\mu\text{g/mL}$ of EtBr and incubated overnight at 37°C. Plates were viewed using a UV transilluminator. This is a representative picture of each ethidium bromide concentration tested (n=3).

3.2.5 Analysis of *craA* and *cxpE* on motility and biofilm formation in *A. baumannii*

Bioinformatic analysis revealed that CxpE is a part of the AI-2 exporter superfamily (93). The AI-2 exporter superfamily has shown to be involved in a number of bacterial pathways e.g., quorum sensing, biofilm and motility (74). Thus, the role that *craA* and *cxpE* efflux pumps have on motility was assessed (Figure 3.6).

The Δ *craA* strain showed no significant decrease in motility compared to the wildtype strain. This result was not unexpected as previous studies on *craA* have not correlated the gene with a role in motility of *A. baumannii* strains (4, 5, 70). This result confirms that *craA* does not play a role in motility. Intriguingly, both mutant strains lacking the *cxpE* gene displayed a significant reduction in motility (Figure 3.6). This was not unexpected as AI-2 exporters are often involved in cellular signalling which can regulate motility (74, 94).

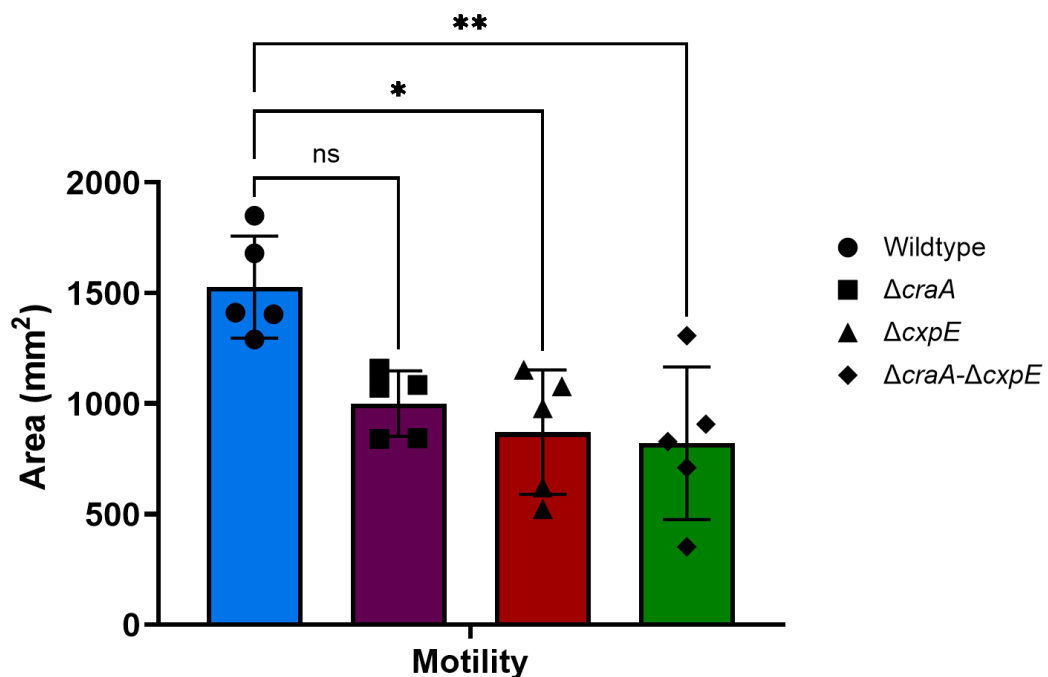


Figure 3.6. Impact of *craA* and *cxpE* on twitching interface motility. Single colonies were used to inoculate plates containing motility agar and incubated at 37°C for 5 days. The area of motility was analysed by measuring the zone of motility on each plate using ImageJ software (n=5). Statistical significance was determined by a nonparametric Kruskal-Wallis test where * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$.

To determine if *cxpE* is involved in other cellular functions besides motility, biofilm formation was assessed (Figure 3.7). Nutrient rich (L-broth) and nutrient limited (M9-glucose) media was used for biofilm analysis at 37°C and 30°C (Figure 3.7.A and Figure 3.7.B). In all conditions tested, the loss of *craA* had no significant effect on biofilm formation. A minor increase in biofilm production for the Δ *cxpE* strain was noted in minimal media at 30°C however, this result was not statistically significant (Figure 3.7.B). Similarly, Δ *cpxE* had no significant impact on biofilm in nutrient rich or nutrient limited media (Figure 3.7). While a slight increase in biofilm formation in low nutrient media incubated at 30°C was recorded (Figure 3.7.B), this result was not statistically significant. Thus, we can conclude that *cxpE* does not impact biofilm formation in *A. baumannii* AB5075.

The double deletion of *craA* and *cxpE* exhibited a decrease in biofilm formation upon comparison to the wildtype strain (Figure 3.7). Both nutrient rich and nutrient limiting conditions revealed a substantial reduction in Δ *craA*- Δ *cxpE* biofilm formation when incubated at 37°C (Figure 3.7.A). This statistically significant decrease in biofilm production was lost upon incubation at 30°C (Figure 3.7.B). This result was unexpected as both individual deletion strains did not exhibit a decrease in biofilm in any condition tested. Conversely, a slight increase in biofilm production was noted for both single mutant strains in minimal media grown at 30°C (Figure 3.7.B).

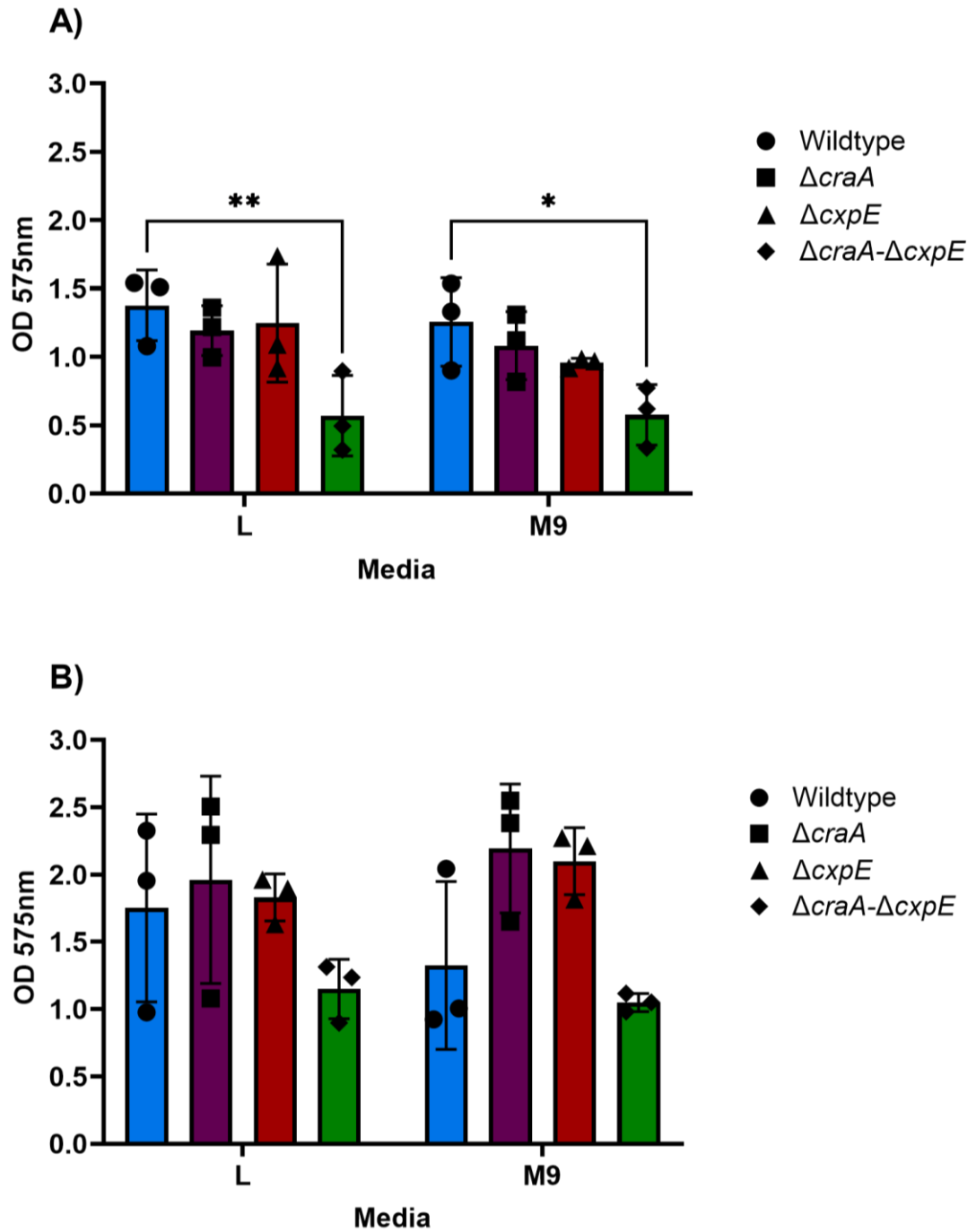


Figure 3.7. Biofilm formation of *A. baumannii* strains in nutrient rich (L-broth) and nutrient deprived (M9-glucose) conditions. A) Biofilm formation after 2 days in 37°C, B) Biofilm formation after 2 days in 30°C (n=3). Statistical significance was determined using a two-way ANOVA where * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$.

3.3 The impact of *craA* and *cxpE* on intrinsic chloramphenicol resistance in *A. baumannii* AB5075

3.3.1 The role of *craA* and *cxpE* on transient chloramphenicol resistance

To investigate if the transient chloramphenicol resistance phenotype was conserved in *A. baumannii* AB5075 the chloramphenicol sensitivity assay was repeated as previously described (Figure 3.8), with one exception of plating on 30 µg/mL of chloramphenicol instead of 10 µg/mL (8). This chloramphenicol concentration for selection was optimised for *A. baumannii* AB5075 as chloramphenicol resistance differs between *A. baumannii* strains (70, 95).

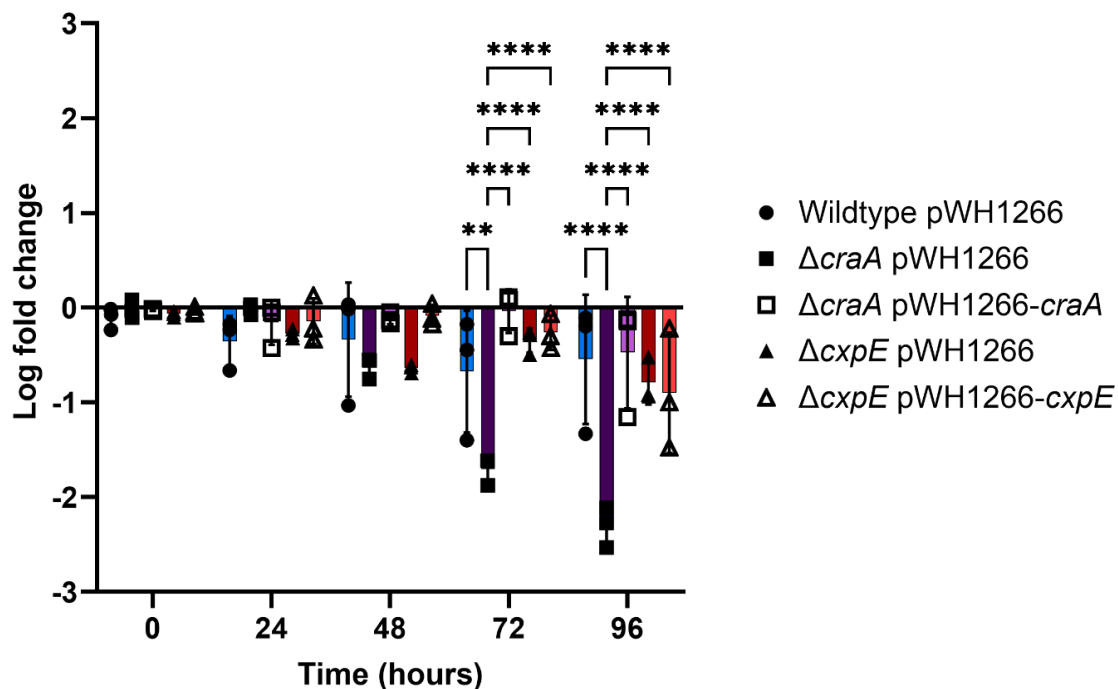


Figure 3.8. Investigation of transient resistant chloramphenicol resistance in *A. baumannii* mutant strains. Log fold change of the proportion of resistant cells to total cells across time points, illustrating changes in resistance prevalence. Strains were grown overnight in L-broth supplemented with 30 µg/mL chloramphenicol and 12 µg/mL of tetracycline. Overnight cultures were washed in PBS three times and used to set a 25 mL flask containing M9 supplemented with pyruvate to an OD of 0.025. The flasks were incubated at 37°C at 200 rpm for a total of 5 days. At time points 0, 4, 24, 48, 72, 96 h samples were taken, serially diluted and then plated on L-agar with 12 µg/mL of tetracycline in the presence and absence 30 µg/mL of chloramphenicol to compare total CFU/mL versus chloramphenicol resistant CFU/mL (n=3). Statistical significance was determined using a two-way ANOVA where where * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$.

At timepoint 0 there is no significant change in the amount of resistant cells compared to the total amount of cells in all strains tested (Figure 3.8). This indicates that at the beginning of the experiment all strains behave similarly and approximately 100% of the population is resistant to the sub-inhibitory levels of chloramphenicol. This is expected as 30 µg/mL of chloramphenicol is lower than the MIC values of all strains utilised (Table 3.2).

After 24 hours a slight reduction in fold change is seen for the wildtype pWH1266, $\Delta cxpE$ pWH1266 and $\Delta cxpE$ pWH1266-*cxpE* strains. The reduction in fold change is not statistically significant and correlates to previous work performed in ATCC 17978 where a slight decrease in the resistance population for the wildtype is seen after 24 hours (8).

After 48 hours the $\Delta craA$ pWH1266 and $\Delta cxpE$ pWH1266 both show a decreased fold change compared to the wildtype pWH1266 strain (Figure 3.8). A decrease in fold change directly correlates to a portion of the population that has become sensitive to the sub-inhibitory levels of chloramphenicol. While this result is not statistically significant at this timepoint, this indicates that *craA* or *cxpE* in the *A. baumannii* AB5075 strain may be required for the rapid adaptation to chloramphenicol exposure even at sub-inhibitory concentrations. The complementation strains of both *craA* and *perM* have a reduced fold change compared to the wildtype strain (Figure 3.8).

At 72 hours the $\Delta craA$ pWH1266 shows a significant decrease in fold change compared to the wildtype (Figure 3.8). A decrease in fold change of ~ 1.8 is noted for the $\Delta craA$ pWH1266 strain. Upon reintroduction of *craA* into the $\Delta craA$ background this significant decrease in fold change is lost (Figure 3.8). This reinforces that *craA* is needed for rapid adaptation to chloramphenicol exposure to maintain full resistance levels across the population. The $\Delta cxpE$ pWH1266 and $\Delta cxpE$ pWH1266-*cxpE* show no significant reduction in fold change compared to the wildtype. The *cxpE* gene may not be crucial for rapid response to chloramphenicol shock in *A. baumannii* AB5075. After 72 hours, the wildtype pWH1266 strain shows a slight reduction in the proportion of resistant cells to total cells in the population (Figure 3.8).

This result is comparable with previous studies showing that a portion of the *A. baumannii* ATCC17978 population becomes sensitive to sub-inhibitory concentrations of chloramphenicol when cultured in nutrient limiting media over time (8).

After growth for 96 hours in minimal media and exposure to sub-inhibitory levels of chloramphenicol, the Δ *craA* pWH1266 is the only strain that shows a significant decrease in log fold change compared to the wildtype pWH1266 strain (Figure 3.8). The Δ *craA* pWH1266 shows a significant decrease in the amount of resistant cells in the population. The Δ *craA* pWH1266-*craA* complementation strain lacks this reduction and behaves like the wildtype strain (Figure 3.8). Once again, we can conclude that *craA* is required to maintain full resistance levels of the population upon chloramphenicol shock. The wildtype pWH1266 and Δ *craA* pWH1266-*craA* display a decrease in log fold change of ~0.5 indicating that a small loss in the resistance population in this strain is present (Figure 3.8). The *cxpE* mutant strains both display and decreased fold change compared to the wildtype pWH1266 strain (Figure 3.8). However, as this reduction in fold change is not significant it appears that *cxpE* does not play a key role in this transient resistant phenotype. The results for the wildtype pWH1266, Δ *cxpE* pWH1266 and Δ *cxpE* pWH1266-*cxpE* strain correlates to work previously done in *A. baumannii* ATCC17978, this indicates that this transient resistance phenomenon is conserved in *A. baumannii* AB5075 and may be present in additional *A. baumannii* strains (8).

As the overnight cultures were grown in the presence of 30 μ g/mL of chloramphenicol before transfer to grow in minimal media, any genes involved in CHL resistance should be upregulated and functioning to compensate for the loss of *craA* e.g., *clmA5*. Although, we suspect that when the cells are grown in nutrient deprived media with no CHL present over time these genes are no longer upregulated as there is no physiological need and to conserve energy. The role *craA* plays on transient chloramphenicol resistance is confirmed as reintroduction of *craA* into the deletion background, which allows the mutant strain to behave like the wildtype strain (Figure 3.8).

Interestingly, upon visual inspection of the agar plates supplemented with a sub-inhibitory concentration of chloramphenicol, the $\Delta cxpE$ strain appears to be more mucoid than the wildtype and $\Delta craA$ strains (Figure 3.9). To determine resistant CFU/mL L-agar plates containing 30 $\mu\text{g/mL}$ of chloramphenicol were utilised. The wildtype and $\Delta craA$ strains displayed a low level of capsule production which is not unusual for *A. baumannii* strains exposed to sub-inhibitory concentrations of chloramphenicol (56).

However, $\Delta cxpE$ strain had altered colony morphology, characterized by increased translucency and enhanced mucoid production. It is unclear what is the cause of increased mucoid production is, it may be as a result of capsule production, but further analysis is required. This phenotype has not been associated with *cxpE* until this study. After 48 hours of growth in minimal media this phenotype is enhanced in $\Delta cxpE$ and is exacerbated by incubation at 4°C (Figure 3.9). The mechanisms behind this remarkable phenotype remain unclear and warrant further investigation into the interlinking mechanisms between *cxpE* and the antibiotic modulation of mucoid production in *A. baumannii*.

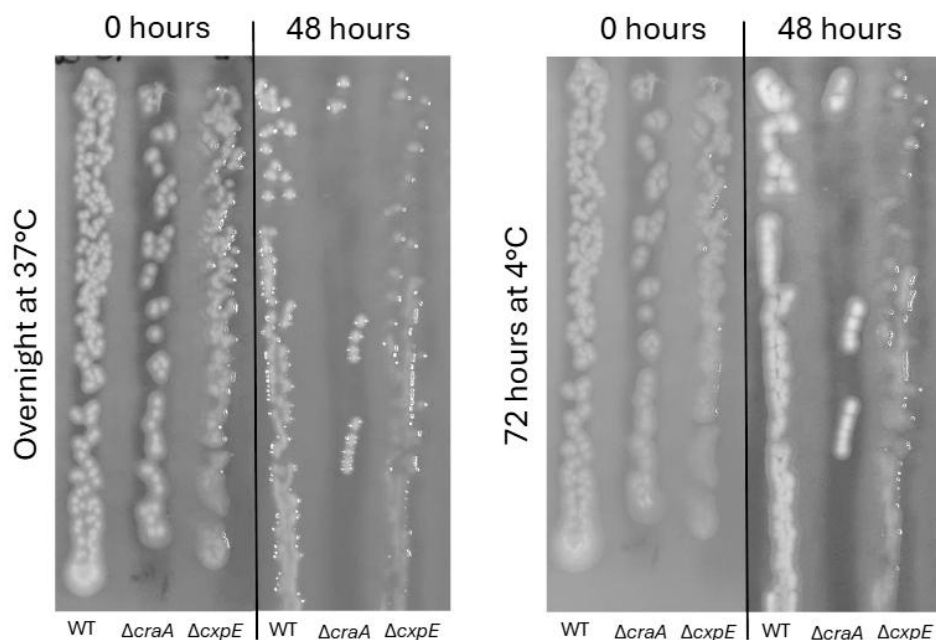


Figure 3.9. Phenotypic analysis of *A. baumannii* strains after 0 and 48 hours of growth in M9 minimal media and plated on L-agar supplemented with 30 $\mu\text{g/mL}$ chloramphenicol. Plates were incubated overnight at 37°C and kept at 4°C for 3 days. This is a representative picture of *A. baumannii* strains (n=3).

3.3.2 Expression of *craA* and *cxpE* during growth in minimal media

The level of expression of *craA* is reduced in stationary phase cultures (8). However, we do not know whether CraA or CxpE abundance changes over the course of the transient resistance growth experiment. The loss of resistance in stationary phase could be either due to the lack of CraA or if the efflux pump cannot be powered in the nutrient deprived environment.

To investigate this hypothesis, FLAG-tagged strains of the CraA and CxpE proteins were constructed to determine protein abundance at different time point during growth in minimal media (Table 2.2). C-terminal 3XFLAG-tagged strains were made by the Godeaux method utilising homologous recombination (81). The cassette used for FLAG-tagging is similar to the extension cassette with the exception that now the stop codon is deleted and replaced with the sequence encoding for the FLAG tag and two new stop codons.

To determine if the FLAG tag interfered with the function of CraA and CxpE a growth experiment in the presence and absence of chloramphenicol was performed (Figure 3.10). This experiment could identify any growth defect in the FLAG-tagged strains as seen with the sub-inhibitory growth curve in the deletion mutants (Figure 3.3).

Under optimal growth conditions, no change in growth profile was observed for FLAG-tagged *craA* or *cxpE* compared to the wildtype strain (Figure 3.10.A). This means that the generation of FLAG-tagged strains did not cause detrimental genomic changes to the *A. baumannii* strains. To examine whether the FLAG-tag impacted the function of *craA* or *cxpE* the strains were analysed for growth defects in chloramphenicol supplemented media (Figure 3.10.B). No significant growth defects were recorded in either CraA or CxpE FLAG-tagged strains upon exposure to chloramphenicol. If the FLAG-tag had impaired the CHL genes function a growth profile similar to that of the deletion mutants would be observed (Figure 3.3.B).

To examine whether the proteins were successfully tagged, a Western blot was performed (Figure 3.11.A). DnaK was used as a loading control to ensure the Western blot was performed successfully. The CraA and CxpE FLAG-tagged proteins are ~45kDa and 44kDa in size respectively.

These predicted protein sizes correlate with the bands present in the western blot indicating successful FLAG-tagging of *A. baumannii* strains (Figure 3.11.A). There appears to be an intermediate band in the CxpE-FLAG tag sample which may be a result of degradation or a possible precursor protein form of CxpE.

To assess whether CraA and CxpE were present in the cell during the growth experiment in M9 minimal media a Western blot analysis was performed (Figure 3.11.B and Figure 3.11.C). As shown previously, *craA* transcription gradually decreased throughout the M9 growth curve and is undetectable after ~48 hours (8), but the level of CraA protein was unclear. The Western blot analysis revealed that *craA* is still detectable in the membrane throughout the entire M9 experiment, however, at 96 hours at a much lower extent (Figure 3.11.B). Unfortunately, the DnaK loading control protein was not visible on the blot in samples taken from minimal media. The expression of DnaK in minimal media is unknown. Therefore, the absence of DnaK on the western blot may be a result of no DnaK being produced and not a failure of the DnaK antibody. Also, CxpE seems to be stable in the membrane throughout the M9 experiment (Figure 3.11). Further experimentation is needed to determine if CxpE plays a role in transient chloramphenicol resistance.

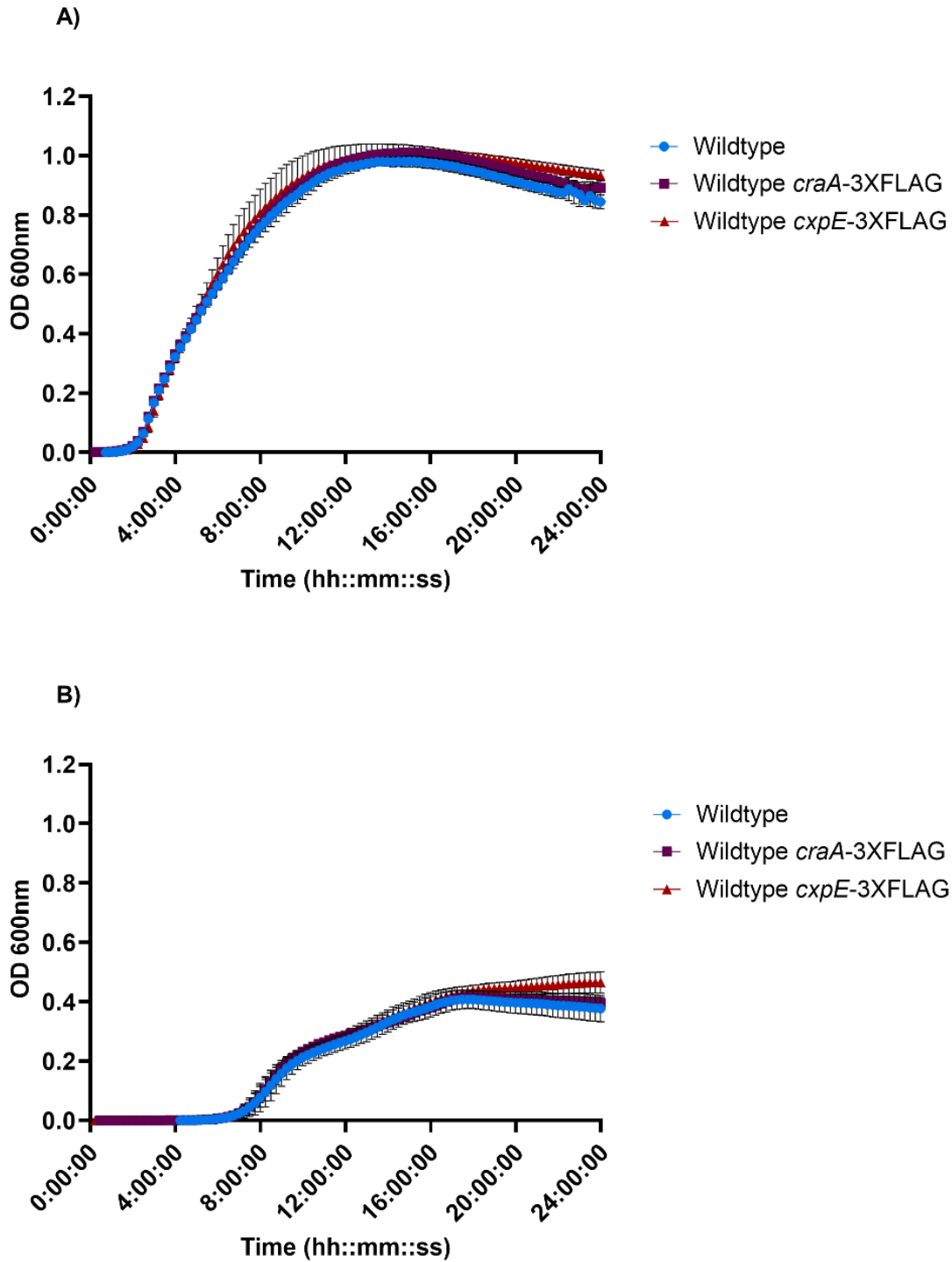


Figure 3.10. Growth experiment of wildtype AB5075 FLAG-tagged strains in LB media. Overnight cultures of *A. baumannii* strains were diluted in PBS, standardised to an OD600 of 0.01 and incubated at 37°C with orbital shaking in A) LB 0 µg/mL chloramphenicol and B) LB supplemented with 25 µg/mL chloramphenicol. OD600 readings were taken at 15-minute intervals to evaluate bacterial growth over a 24-hour period (n=3).

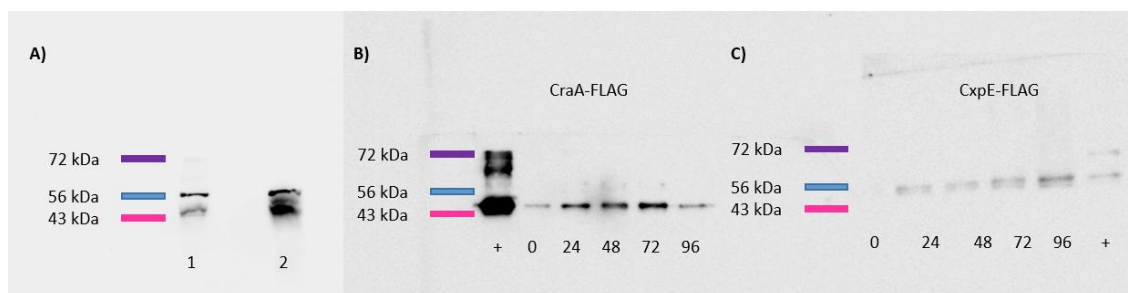


Figure 3.11. Western blot of flag-tagged strains. DnaK predicted size ~70kDa, CraA predicted size ~45kDa and CxpE predicted size ~44kDa. A) Confirmation of functional FLAG-tags. CraA-FLAG and CxpE-FLAG. All strains were grown to an OD of 0.3 in L-broth for analysis B) Western blot of CraA-FLAG during growth in minimal media timepoints ranging from 0-96 hours. C) Western blot of CxpE-FLAG during growth in minimal media timepoints ranging from 0-96 hours.

3.4 Identification of transcriptional regulators of *craA* and *cxpE* in *A. baumannii*

The regulators of *craA* and *cxpE* are currently unknown. However, a recent study proposed that *cbl*, a LysR type transcriptional regulator may be a regulator of *craA*. *Cbl* is involved in cysteine biosynthesis and sulphur metabolism. Upon its deletion the expression of *craA* displays an increased log₂-fold change of 2.75 (73). This suggests that *cbl* may play a role as a repressor of *craA* in *A. baumannii*.

To investigate if *cbl* was a potential regulator for *craA*, a deletion mutant of *cbl* was constructed and tested for antimicrobial susceptibility (Table 3.3). Removal of *sacB* and *aacC4* genes was unsuccessful, therefore this strain still possesses the selection and counter-selection genes. Minimum inhibitory concentration assays revealed no difference between *cbl* mutant strains and the wildtype strain, all strains had a chloramphenicol MIC of 128 µg/mL.

If the presence of *cbl* acted as a repressor of *cbl* as speculated (73), the loss of *cbl* could have increased the MIC as *craA* would be overexpressed and provide additional resistance to *A. baumannii* AB5075. As no alteration in chloramphenicol resistance was observed, it is unlikely that *cbl* directly regulates *craA* and potentially other regulatory mechanisms are present for *craA*.

Interestingly, the double deletion mutant of *cbl* and *craA* showed no reduction in chloramphenicol MIC compared to the wildtype (Table 3.3). Previously, the individual loss of *craA* resulted in a 2-fold reduction in the chloramphenicol MIC (Table 3.2). This was unexpected as the loss of chloramphenicol resistance linked to Δ *craA* was expected to be consistent across to the double deletion strain (Δ *cbl*::*sacB-aacC4*- Δ *craA*) carrying this mutation. If *cbl* does repress *craA* as seen in a previous RNA-seq analysis (73), *cbl* could potentially repress other CHL associated genes. Therefore, the loss of *cbl* would significantly enhance the expression of these genes when *craA* is absent from the genome. Similarly, for the Δ *cbl*::*sacB-aacC4*- Δ *cxpE* mutant, no difference in MIC is observed compared to the wildtype (Table 3.3). Were the previous hypothesis true that *cbl* regulates *craA* and potentially other CHL resistance genes the lack of reduction in chloramphenicol MIC for this strain would further support this theory. Likewise, as for the Δ *craA* mutant strain, the Δ *cxpE* mutant strain showed a reduction in MIC from 128 μ g/mL to 64 μ g/mL. The double deletion of *cbl* and *cxpE* did not show this resistance profile like Δ *cbl*::*sacB-aacC4*- Δ *craA*. Thus, further investigation is needed to assess the role of *cbl* in regulating *craA* and potentially other CHL resistance genes.

Table 3.3. Minimum inhibitory concentration (MIC) assays of *cbl* deletion mutants. MIC analysis was performed as per CLSI guidelines on *Acinetobacter* sp (n=3) (85).

Strain	Chloramphenicol (μ g/mL)
Wildtype AB5075	128
Δ <i>cbl</i> :: <i>sacB-aacC4</i>	128
Δ <i>cbl</i> :: <i>sacB-aacC4</i> - Δ <i>craA</i>	128
Δ <i>cbl</i> :: <i>sacB-aacC4</i> - Δ <i>cxpE</i>	128

To further investigate this hypothesis that *cbl* regulates *craA* subsequent testing was performed (Figure 3.12), using growth experiments in the presence and absence of CHL as previously described (Figure 3.2).

Under optimal growing conditions with no antibiotic present, Δ *cbl*::*sacB-aacC4* shows an increase in growth performance compared to the wildtype with a higher final OD (Figure 3.12.A).

The loss of *cbl* appears to be beneficial to *A. baumannii* AB5075 under ideal growth parameters. This has not been described in prior studies (73). Both $\Delta cbl::sacB-aacC4-\Delta craA$ and $\Delta cbl::sacB-aacC4-\Delta cxpE$ strains had growth patterns comparable to the wildtype strain (Figure 3.12.A). This was as expected as the individual mutants of all genes present displayed no growth defects prior in a stress-free environmental condition.

Growth in the presence of sub-inhibitory concentrations of chloramphenicol was performed to see if the *cbl* mutants carrying $\Delta craA$ or $\Delta cxpE$ exhibited altered growth profiles comparable to the individual $\Delta craA$ and $\Delta cxpE$ strains (Figure 3.12.B). There is a slight growth improvement of the $\Delta cbl::sacB-aacC4$ strain compared to wildtype. However, this improvement in growth through the potential upregulation of *craA* caused by the loss of *cbl* is limited (Figure 3.12.B), compared to the growth profile of the *craA* overexpression strain through plasmid complementation (Figure 3.3.B). The $\Delta cbl::sacB-aacC4-\Delta craA$ and $\Delta cbl::sacB-aacC4-\Delta cxpE$ strains displayed the same growth defects to the wildtype strain (Figure 3.12.B), as the $\Delta craA$ and $\Delta cxpE$ mutants (Figure 3.3.B). This refutes our earlier hypothesis that *cbl* regulates *craA* and other CHL resistance genes as no improvement in growth was noted for both strains. If our hypothesis was true, the growth defects noted would be reduced or the strains would grow similar to the wildtype. For example, the $\Delta cbl::sacB-aacC4-\Delta cxpE$ strain would not prematurely enter stationary phase as the upregulation of *craA* should compensate for the loss of *cxpE*. There is not enough evidence provided by these results to confirm that *cbl* regulates *craA* as previously suggested (73).

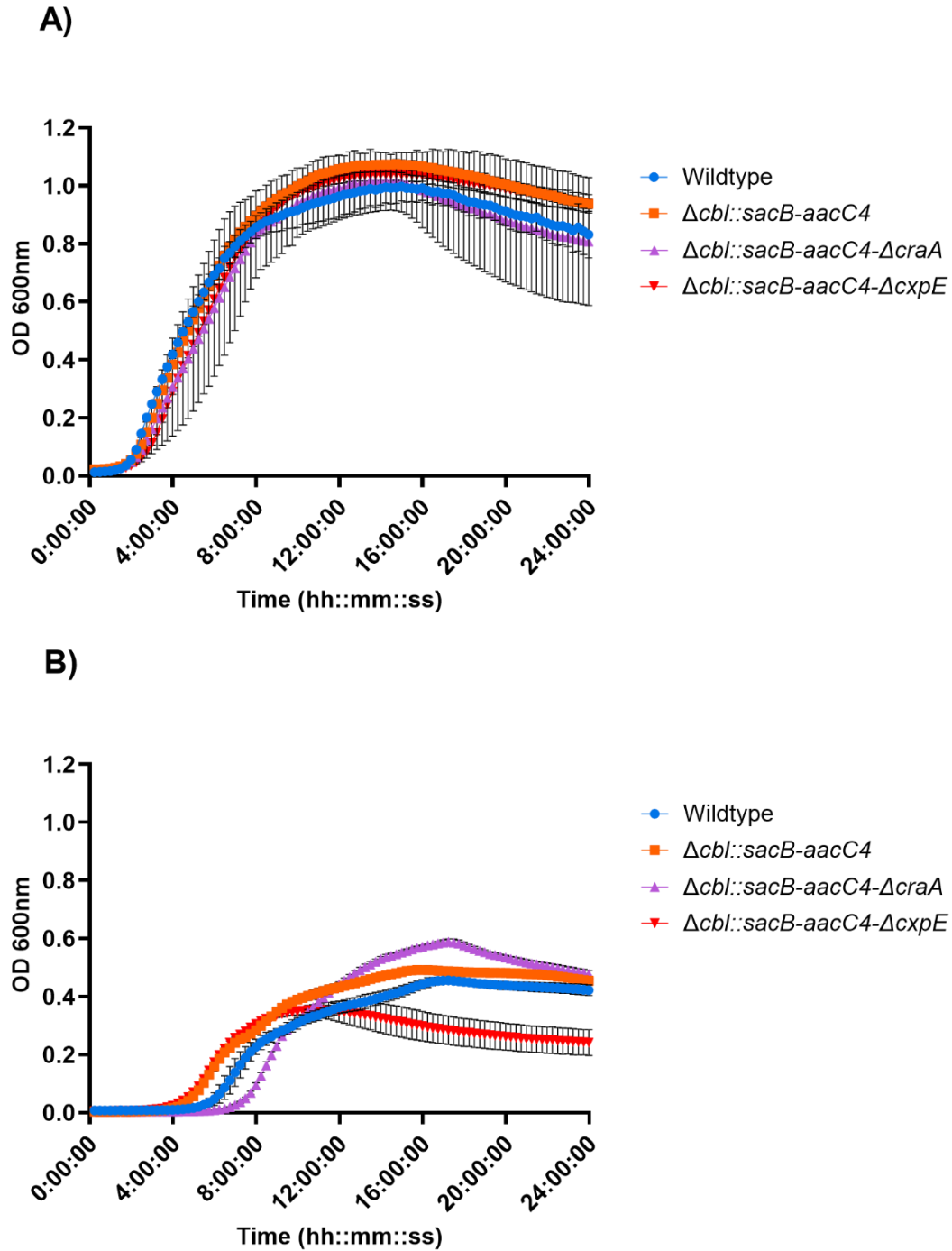


Figure 3.12. Growth experiment of *cbl* mutants in LB media. Overnight cultures of *A. baumannii* strains were diluted in PBS, standardised to an OD₆₀₀ of 0.01 and incubated at 37°C with orbital shaking in A) LB 0 µg/mL chloramphenicol and B) LB supplemented with 25 µg/mL chloramphenicol. OD₆₀₀ readings were taken at 15-minute intervals to evaluate bacterial growth over a 24-hour period (n=4).

Chapter 4 – Effects of Δ p1AB5075 on antimicrobial resistance in

A. baumannii AB5075

4.1 Introduction

A. baumannii is multi-drug-resistant strain that exhibits a high degree of genomic plasticity enhancing its ability to persist and resist in unfavourable environments. One method for the acquisition and spread of antimicrobial resistance in *A. baumannii* is horizontal gene transfer (52). The 83kb plasmid “p1AB5075” in *A. baumannii* AB5075 harbours several AR genes and is highly transmissible between *Acinetobacter* sp. This is of major concern as the AR genes on this plasmid provide resistance to clinically important antibiotic classes e.g., aminoglycosides and β -lactams (77). Resistance island 2 (RI2) is a region on the p1AB5075 plasmid containing several resistance genes and which has been shown in several studies to have a significant impact on the antibiotic resistance profile of the host strain (9, 11, 50, 70, 77). In previous literature, the focus has been on investigating the effects of RI2 as a whole on antibiotic resistance development in *A. baumannii*; this chapter aims to characterise the individual resistance genes located in RI2 and their respective contributions, if any, to the antibiotic resistance phenotype of *A. baumannii* AB5075.

4.2 Identification of antimicrobial resistance genes on p1AB5075

The genes *aaC(6')-Ib3*, *aadB*, *aadA2*, *strA*, *strB*, *cmlA5*, *blaGES-11* and *dfrA7* are located on the resistance island 2 and the *aph(3')-VI* is located on a different region of the plasmid outside the RI2 on the p1AB5075 plasmid (Figure 4.1). However, due to the nature of the majority of p1AB5075 AR genes being localized on RI2, the loss of these genes are investigated as a whole and have not been assessed for their individual contribution to *A. baumannii* AB5075 antibiotic resistance (11, 70, 77). This study aims to address this gap in the literature and the potential consequences that dissemination/presence of these genes may have on overall antibiotic resistance in *A. baumannii*.

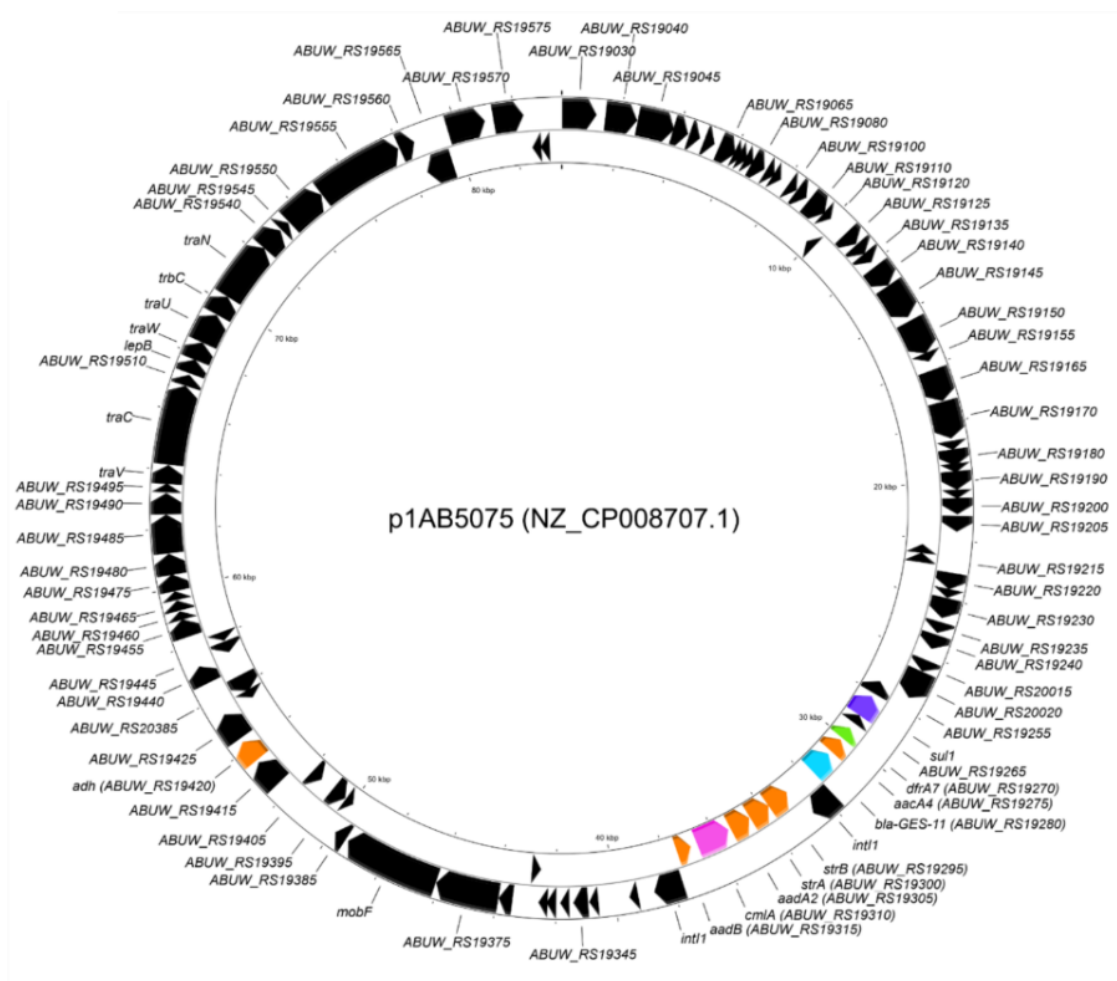


Figure 4.1. Map of *A. baumannii* AB5075 p1AB5075. Aminoglycoside genes are highlighted in orange, chloramphenicol resistance gene *cmIA5* in pink, sulphonamide resistance gene *sul1* in light green, beta-lactamase-encoding *bla_{GES-11}* in light blue and trimethoprim resistance gene *dfrA7* in purple. The map was created with Proksee.

4.2.1 Constructing an antimicrobial resistance gene overexpression in Δ p1AB5075

To analyse the contribution of AR genes identified on the plasmid p1AB5075, complementation plasmids were constructed (Figure 4.2). Eight antibiotic resistance genes were identified on the p1AB5075 plasmid: *dfrA7*, *bla_{GES-11}*, *aph(3')-VI*, *aadA2*, *aadB*, *aaC(6')-Ib3*, *strA* and *strB*. All genes were inserted into the pWH1266 backbone via SLiCE (83). The *bla* gene on the pWH1266 plasmid was replaced by the desired gene to ensure consistent expression from the *bla* promoter.

An artificial ribosomal binding site (RBS) “AGGAGG” was included for all complementation genes to ensure consistent translation. Additionally, 100 bp downstream of the coding sequence were included in the cloned fragments, which should ensure transcriptional termination.

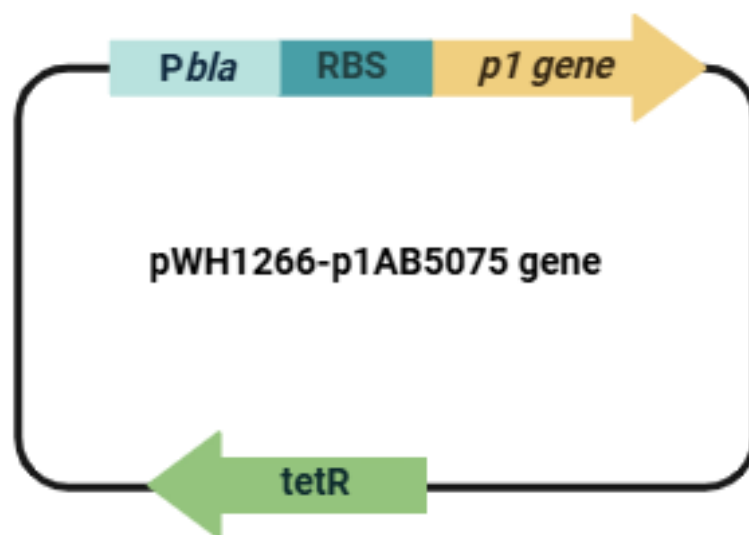


Figure 4.2. Construction of p1AB5075 antibiotic resistance gene overexpression vectors using pWH1266. *P-bla* – beta-lactamase promoter, RBS – artificial ribosomal binding site “AGGAGG”, *tetR* – tetracycline resistance gene.

4.2.2 Analysis of antimicrobial resistance in Δ p1AB5075

A literature review was performed to identify the potential substrates of the p1AB5075 antimicrobial resistance genes (Table 4.1). To verify the substrates of identified antibiotic genes; *dfrA7*, *bla_{GES-11}*, *aadB*, *aph(3')-VI*, *aadA2*, *aaC(6')-Ib3*, *strA* and *strB* complementation plasmids were constructed in the Δ p1AB5075 mutant strain and analysed for antibiotic sensitivity. To rapidly assess a wide range of antibiotic classes Kirby-Bauer disk diffusion analysis was carried out before validation using broth microdilution assays to determine the minimal inhibitory concentrations (Table 4.2, Figure 4.3).

No significant change in resistance between the Δ p1AB5075 *A. baumannii* mutants and the wildtype was seen for the following antibiotic families tested; β -lactams, glycopeptides, macrolides, nitrofurantoin antibacterials and tetracyclines.

These results correlate with the literature of known antibiotic resistance genes on the p1AB5075 plasmid (9). Interestingly, significant resistance profile changes were seen for all aminoglycosides tested, cefepime, ceftazidime, trimethoprim/sulfamethoxazole and a slight increase in sensitivity to chloramphenicol (Table 4.2).

Upon the loss of p1AB5075, *A. baumannii* AB5075 changed from resistant to sensitive to gentamicin, amikacin, tobramycin, kanamycin and streptomycin compared to the wildtype strain (Table 4.2). Full restoration of gentamicin resistance was mediated by the sole complementation of *aadB*. This agreed with the literature and *aadB* is a key contributor to gentamicin resistance in *A. baumannii* AB5075 (Table 4.1)(11). For amikacin resistance the overexpression of *aph(3')-VI* in the Δ p1AB5075 background produced an increased resistance phenotype surpassing the wildtype strain (Table 4.2). This result was as expected due to amikacin being associated with the *aph(3')-VI* gene in *A. baumannii* (96). Interestingly, only the *aph(3')-VI* strain altered the resistance profile for amikacin and the *aaC(6')-Ib3* complementation strain did not (Table 4.2). This was a surprising observation as previously *aaC(6')-Ib3* has been associated with amikacin resistance in *A. baumannii* (97).

Resistance to tobramycin was primarily mediated by *aadB* which fully restored resistance although, *aaC(6')-Ib3* restored an intermediate resistance profile to the Δ p1AB5075 strain (Table 4.2). Both *aadB* and *aaC(6')-Ib3* have been described to convey tobramycin resistance (Table 4.1) (97, 98). However, their contribution to *A. baumannii* AB5075 overall tobramycin resistance varies. Similarly, *aadB* plays a key role in providing kanamycin resistance to *A. baumannii* AB5075 and provides a resistance phenotype comparable to the wildtype (Table 4.2). Overexpression of *aph(3')-VI* can also restore the sensitive Δ p1AB5075 strain back to a fully kanamycin resistant profile (Table 4.2), as determined by the CLSI guidelines (85). These two genes have been shown to play a role in kanamycin resistance (96, 98).

The complementation strains containing *aadA2* and *strA* allowed for the reestablishment of streptomycin resistance comparable to the wildtype (Table 4.2). This agrees with the predicted substrates of these two genes (Table 4.1) (99, 100).

However, the overexpression of *strB* showed no decrease in the zone of inhibition to streptomycin. This was unusual as streptomycin resistance has been associated with this gene (100, 101).

This may be due to a non-functioning complementation plasmid or that in most cases *strA* and *strB* are often found encoded in tandem and investigated together (9, 101, 102). The reason that *strA* and *strB* are often studied in tandem is that they are usually encoded on the same operon (9, 102). Additionally, while *strA* and *strB* can provide resistance to streptomycin when expressed individually, this resistance increase is usually lower than when the two genes are expressed in tandem (101). Thus, while both genes can function independently, due to the high occurrence of co-expression these genes are usually investigated collectively.

Table 4.1. Antibiotic resistance genes on *A. baumannii* p1AB5075 (1, 9, 97–100, 103–105).

Gene	Locus ID	Annotation	Resistance prediction
<i>aph(3')-VI</i>	<i>ABUW_RS19420</i>	APH(3')-VI family aminoglycoside O-phosphotransferase	KAN, AMI
<i>aaC(6')-Ib3</i>	<i>ABUW_RS19275</i>	aminoglycoside N-acetyltransferase AAC(6')-Ib3	AMI, KAN, TOB
<i>aadB</i>	<i>ABUW_RS19315</i>	aminoglycoside nucleotidyltransferase ANT(2'')-Ia	DIB, GEN, KAN, SIS, TOB
<i>aadA2</i>	<i>ABUW_RS19305</i>	ANT(3'')-Ia family aminoglycoside nucleotidyltransferase	STR, SPE
<i>strA</i>	<i>ABUW_RS19300</i>	aminoglycoside O-phosphotransferase APH(3'')-Ib	STR
<i>strB</i>	<i>ABUW_RS19295</i>	APH(6)-I family aminoglycoside O-phosphotransferase	STR
<i>cmlA5</i>	<i>ABUW_RS19310</i>	CmlA family chloramphenicol efflux MFS transporter	CHL
<i>bla_{GES-11}</i>	<i>ABUW_RS19280</i>	Extended-spectrum class A beta-lactamase GES-11	FOX, CAZ, CEF, CTX, ATM, IMP, MER
<i>dfrA7</i>	<i>ABUW_RS19270</i>	Trimethoprim-resistant dihydrofolate reductase DfrA7	TMP

A significant zone of inhibition to trimethoprim/sulfamethoxazole was observed for Δ p1AB5075 compared to wildtype AB5075 (Table 4.2). The loss of *dfrA7* gene located on the p1AB5075 plasmid is most likely the cause of this increase in susceptibility (9, 104, 105). However, while construction of a complementation plasmid was successful in the Δ p1AB5075 background it does not restore trimethoprim/sulfamethoxazole resistance. This was not unexpected as trimethoprim/sulfamethoxazole is a combination treatment. The gene *dfrA7* can only provide resistance against trimethoprim, where as the *sul1* gene located on the p1AB5075 plasmid provides resistance against sulfamethoxazole. To fully restore resistance to this combination treatment both genes would have to be introduced into the Δ p1AB5075 strain.

In the absence of p1A5075, significant cefepime and ceftazidime susceptibility was recorded (Table 4.2). Upon re-introduction of the *bla_{GES-11}* gene full resistance to both cephalosporin antibiotics was achieved. This gene is a known facilitator of cefepime and ceftazidime resistance in *A. baumannii* and these results reflect its substrate specificity (Table 4.1) (103). It is important to note that the complementation strains *aadB*, *aph(3')-VI*, *aadA2* and *strA* all had an intermediate resistance profile as designated by the CLSI guidelines, which differed from the susceptible profile designated to Δ p1AB5075 (Table 4.2) (85). Although, these strains all had values closely corresponding to the resistance profile determining values set by the CLSI (85). Further investigation is needed to confirm whether these genes provide partial resistance to cefepime and ceftazidime in *A. baumannii* AB5075.

Lastly, a slight reduction in the zone of inhibition to chloramphenicol was noted for all Δ p1AB5075 strains (Table 4.2). This decrease is most likely associated to the *cmIA5* gene located on the p1AB5075 plasmid (9, 70). However, as outlines earlier in chapter 3 of this thesis chloramphenicol resistance in *A. baumannii* AB5075 is mediated by several AR genes both located on the chromosome and the plasmid. Thus, further investigation of the contribution of p1AB5075 plasmid to overall antibiotic resistance in *A. baumannii* AB5075 was performed with a focus on aminoglycosides and cephalosporins.

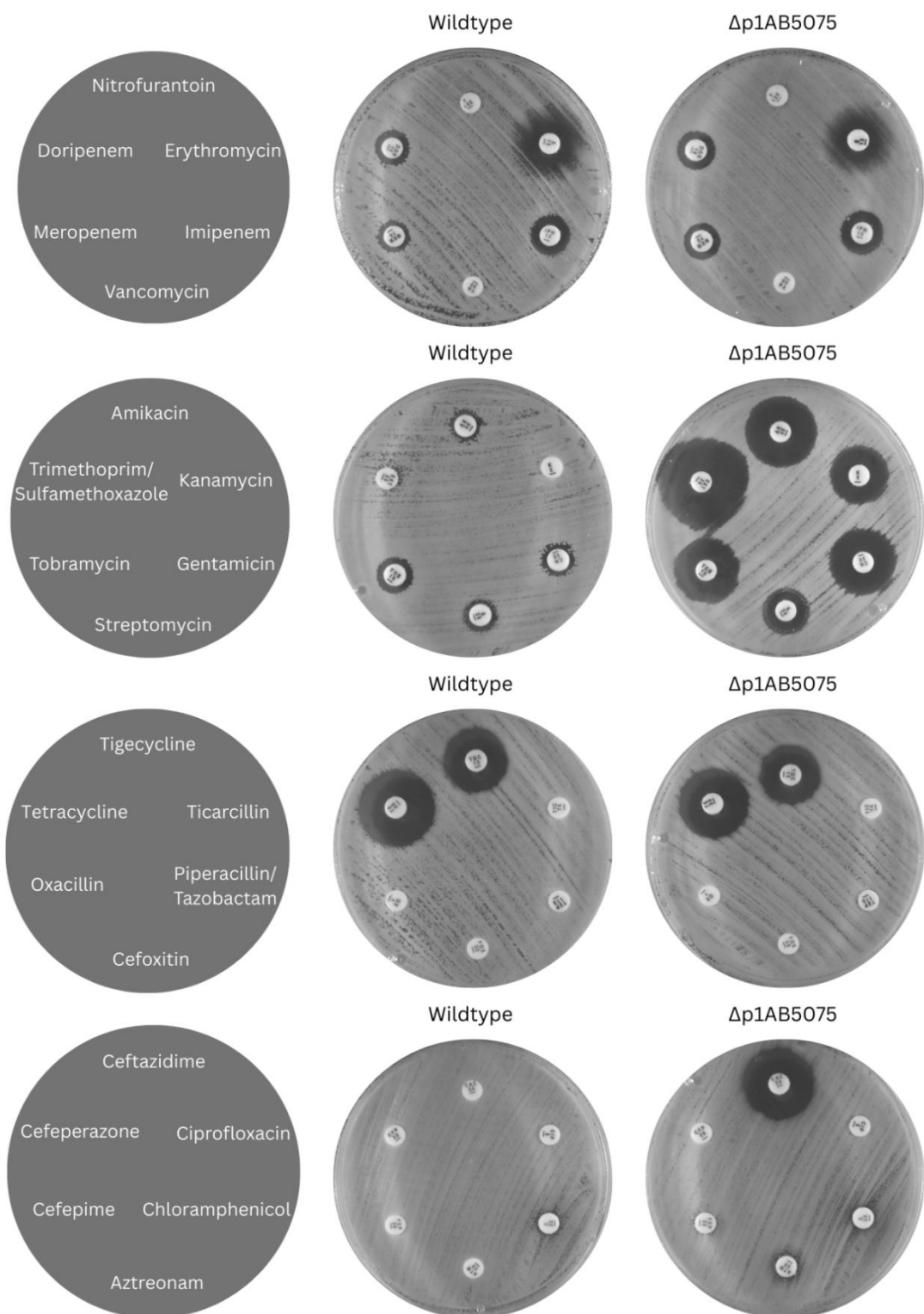


Figure 4.3. A Kirby-Bauer analysis of wildtype and $\Delta p1AB5075$ strains. Antibiotic families tested were β -lactams, amphenicols, aminoglycosides, glycopeptides, macrolides, quinolones, nitrofurantoin antibacterials, tetracyclines and folate pathway antagonists. This is a representative image of three biological replicates.

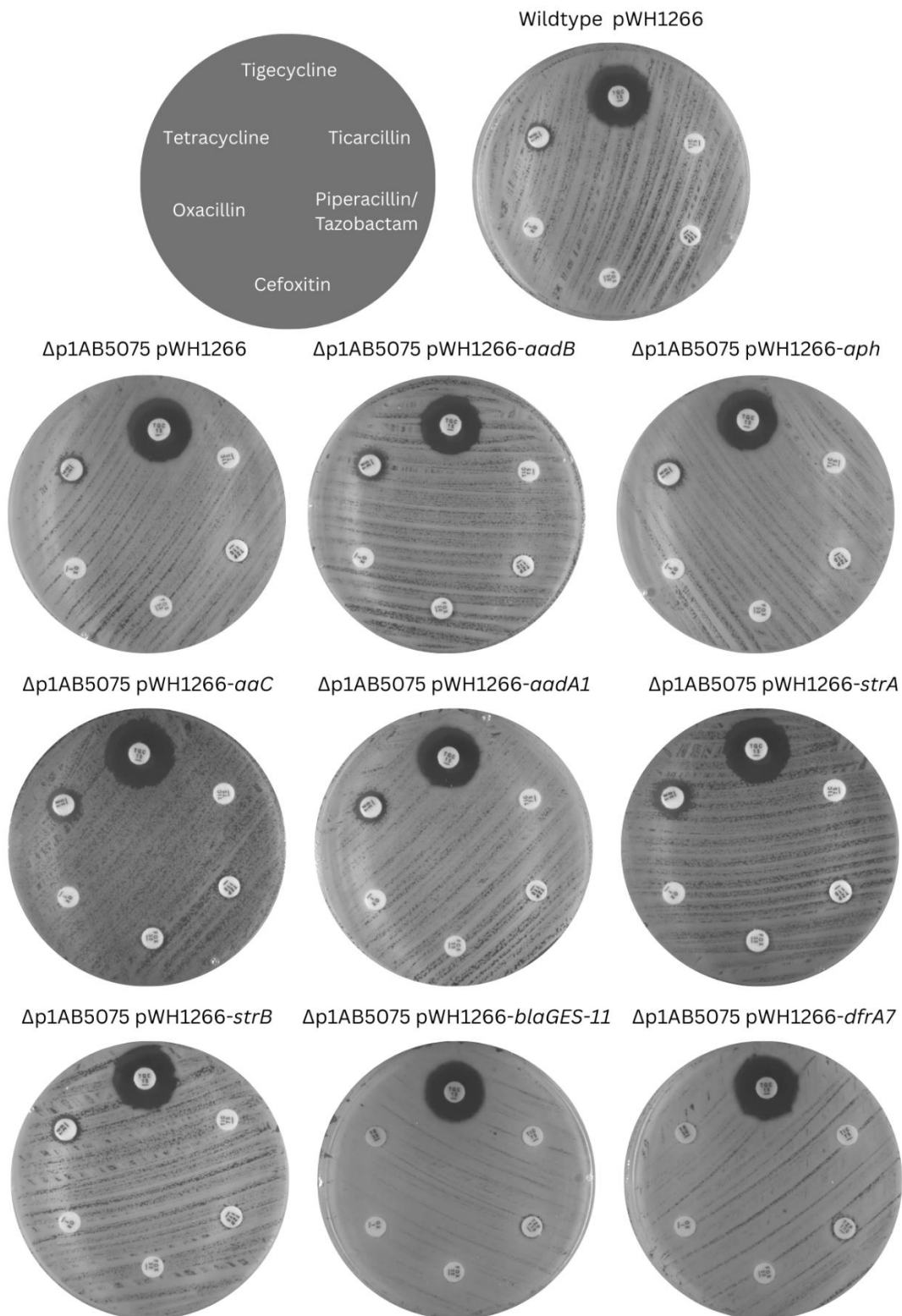


Figure 4.3.B Kirby-Bauer analysis wildtype and $\Delta p1AB5075$ mutant strains. Antibiotic families tested were β -lactams and tetracyclines. This is a representative image of three biological replicates.

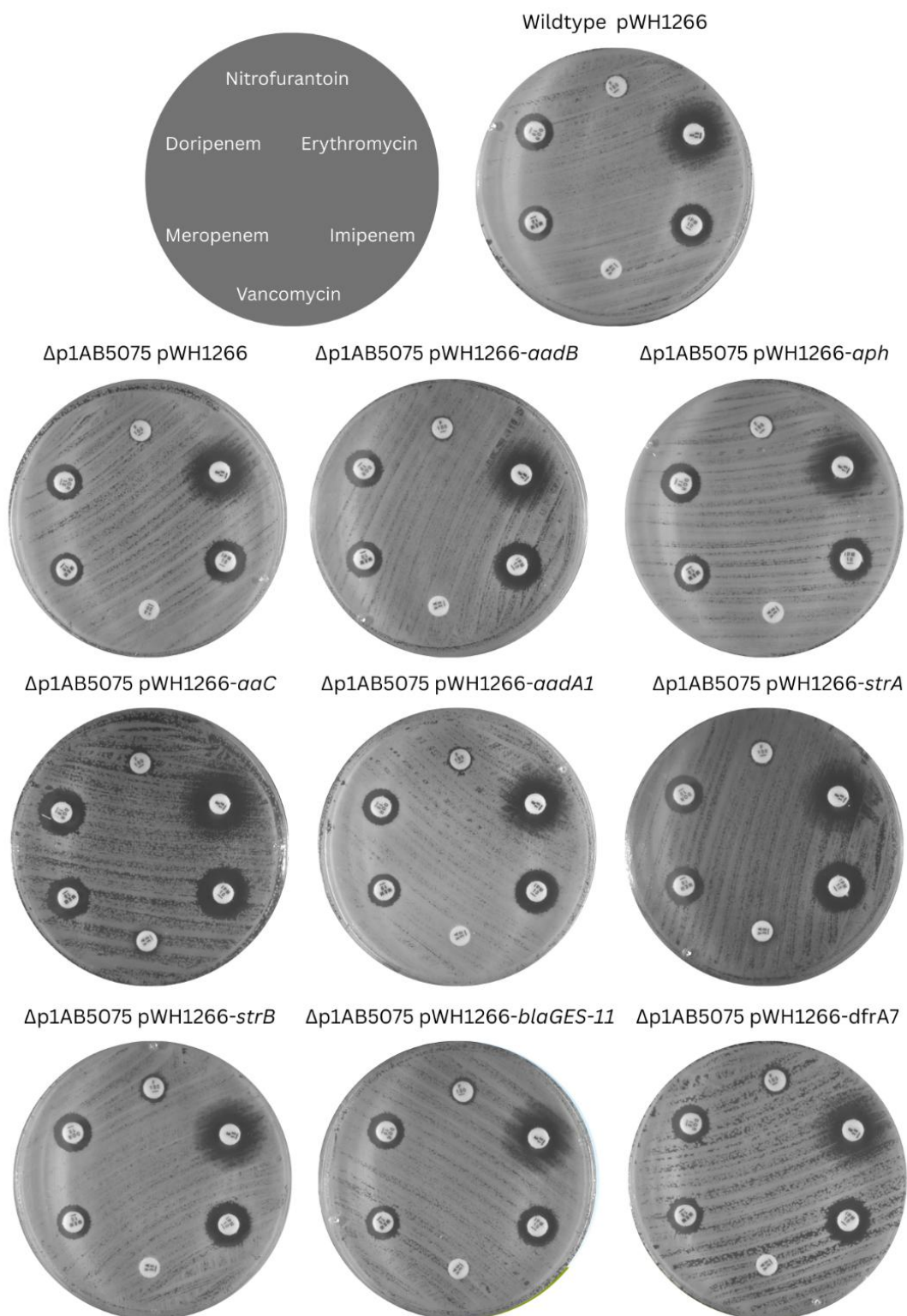


Figure 4.3.C Kirby-Bauer analysis of wildtype and $\Delta p1AB5075$ mutant strains. Antibiotic families tested were β -lactams, glycopeptides, macrolides and nitrofurantoin antibacterials. This is a representative image of three biological replicates.

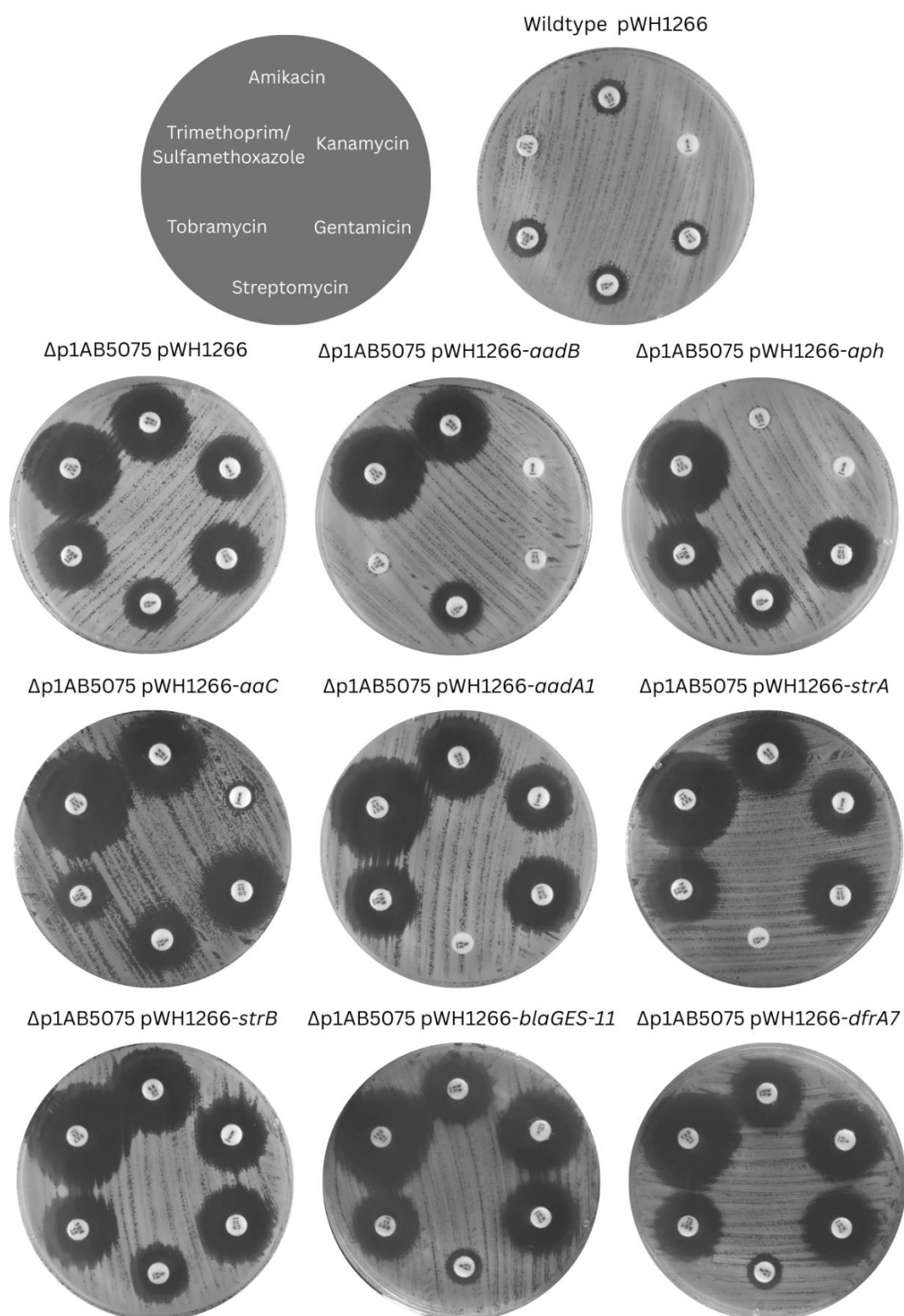


Figure 4.3.D Kirby-Bauer analysis of wildtype and Δ p1AB5075 mutant strains. Antibiotic families tested were aminoglycosides and folate pathway antagonists. This is a representative image of three biological replicates.

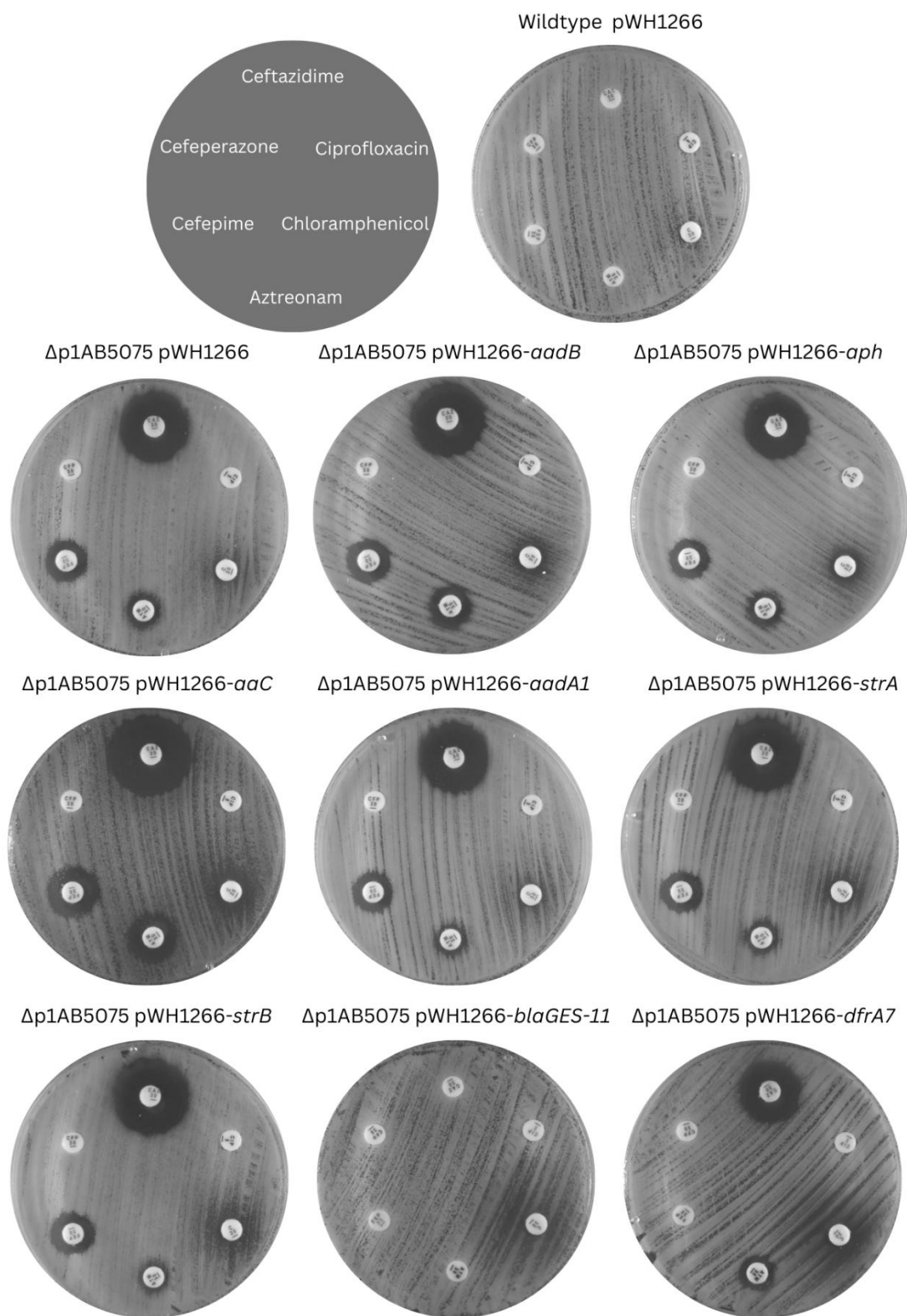


Figure 4.3.E Kirby-Bauer analysis of wildtype and $\Delta p1AB5075$ mutant strains. Antibiotic families tested were β -lactams, amphenicols and quinolones. This is a representative image of three biological replicate.

Table 4.2. Kirby-Bauer analysis of wildtype *A. baumannii* AB5075 mutants. All results were colour coded based on CLSI resistance profile grading available in the CLSI M100 for *Acinetobacter* sp. data (11). Red – resistant, Yellow -Intermediate, Green -sensitive and no colour indicates no comparative data available (n=3) .

Classes	Antibiotic (µg)	Wildtype pWH1266	Δp1AB5075 pWH1266	Δp1AB5075 aadB	Δp1AB5075 pWH1266- aph(3')-VI	Δp1AB5075 pWH1266 -aac(6')-Ib3	Δp1AB5075 pWH1266 -aadA2	Δp1AB5075 pWH1266 -strA	Δp1AB5075 pWH1266 -strB	Δp1AB507 5 pWH1266 -blacES-11	Δp1AB5075 pWH1266 -dfrA7
β-lactams	Aztreonam 30	0	8	10	9	11	10	10	12	0	11
	Cefoxitin 30	0	0	0	0	0	0	0	0	0	0
	Ticarcillin 75	0	0	0	0	0	0	0	0	0	0
	Oxacillin 1	0	0	0	0	0	0	0	0	0	0
Amphenicol	Piperacillin/ Tazobactam 110	0	0	0	0	0	0	0	0	0	0
	Chloramphenicol 30	0	7	10	9	12	8	10	11	8	9
Carbapenems	Imipenem 10	12	12	14	12	14	12	14	12	13	13
	Meropenem 10	10	9	10	10	14	10	10	10	10	11
	Doripenem10	12	12	13	12	14	11	12	11	12	12
	Gentamicin 30	10	21	0	23	20	22	25	23	23	21
Aminoglycosides	Amikacin 30	9.5	24	21	0	21	27	27	24	23	22
	Tobramycin 10	11	18	0	19	14	18	17	18	21	19
	Kanamycin 30	0	19	0	0	8	19	18	17	26	25
	Streptomycin 25	12	15	15	16	16	0	0	17	12	11
Glycopeptide	Vancomycin 30	0	0	0	0	6	0	0	0	0	0
Macrolide	Erythromycin 15	21	19	20	20	21	19	20	20	21	19
Quinolones	Ciprofloxacin 5	0	0	0	0	0	0	0	0	0	0
Nitrofurantoin	Nitrofurantoin 100	0	0	0	8	7	7	8	8	8	8
Tetracyclines	Tetracycline 30	10	10	10	10	9	9	11	10	0	0
	Tigecycline 15	18	19	15	16	18	15	18	15	17	19
Folate pathway antagonists	Trimethoprim/ Sulfamethoxazole	0	26	27	28	25	29	30	28	30	27
Cephalosporins	Ceftazidime 30	0	17	19	20	22	18	18	20	0	19
	Cefepime 30	0	18	15	17	19	17	15	19	0	18
	Cefoperazone80	0	0	0	0	0	0	0	0	0	0

To further analyse the contribution of the AR genes on the p1AB5075 plasmid to the overall antibiotic resistance profile in *A. baumannii* and to test whether resistance was returned to wild-type levels when expressing the AR genes from plasmids, broth microdilution assays were performed to determine minimum inhibitory concentrations (MICs) (Table 4.3). Amikacin, kanamycin, gentamicin, tobramycin, streptomycin and cefepime were used to analyse the contributions of the plasmid-encoded genes for cephalosporin and aminoglycoside resistance in *A. baumannii*. The carbapenems meropenem and imipenem were tested as Kirby-Bauer results showed subtle variations between mutant strains (Table 4.2).

The broth microdilution assays showed that amikacin resistance is mediated through *aph(3')-VI* and *aaC(6')-Ib3* increasing the MICs from 8 µg/mL to 2048 µg/mL (*aph(3')-VI*) and 32 µg/mL (*aaC(6')-Ib3*) respectively (Table 4.3). The likely overexpression of *aph(3')-VI* from pWH1266 resulted in an MIC surpassing the wildtype strain four-fold (512 µg/mL). Resistance to kanamycin in *A. baumannii* is primarily conveyed by *aph(3')-VI* which increases the MIC from 8 µg/mL to >4096 µg/mL, which is similar to the wild-type strain. However, the highest concentration measured was 4096 µg/mL, therefore it cannot be concluded from this data whether overexpression of *aph(3')-VI* also elevates the degree of resistance as observed for *aph(3')-VI* for amikacin resistance.

The genes *aadB* (2048 µg/mL) and *aaC(6')-Ib3* (512 µg/mL) also significantly mediate high-level kanamycin resistance (Table 4.3). Ectopic expression of *aadB* caused a high degree of gentamicin resistance increasing the MIC from 8 µg/mL to > 4096 µg/mL, which is far higher compared to the wild-type strain (256 µg/mL, Table 4.3). Surprisingly, *aaC(6')-Ib3* increased the MIC 4-fold from 8 to 32 µg/mL when overexpressed. This has not been shown before in *A. baumannii*, and this gene was not associated with gentamicin resistance (Table 4.1).

Upon loss of the p1AB5075 plasmid tobramycin resistance is decreased from 32 µg/mL to 0.5 µg/mL (Table 4.3). Upon complementation with *aadB* and *aaC(6')-Ib3* tobramycin resistance increased to 128 µg/mL and 32 µg/mL respectively. Overexpression of *aadB* leads to a 4-fold higher MIC than seen in the wildtype strain.

The MIC for streptomycin is 1024 µg/mL for the wildtype strain and upon loss of the p1AB5075 plasmid it is reduced to 256 µg/mL (Table 4.3). Upon overexpression of *aadA2* and *strA* the MIC is raised to >2048 µg/mL in each strain tested. Interestingly, no increase is observed in the *strB* complementation strain, which does not agree with the literature (101). Previously, *strB* expressed individually has been shown to convey low levels of streptomycin resistance to gram negative bacteria (101).

Cefepime resistance is significantly reduced from 512 µg/mL to 32 µg/mL upon the loss of the p1AB5075 plasmid (Table 4.3). The only gene tested that restored cefepime resistance was *bla_{GES-11}*. This gene is known to play a role in cephalosporin resistance (103). Also, this increase in resistance is also seen in the disk diffusion analysis (Table 4.2). The overexpression of *bla_{GES-11}* allows for resistance levels that exceed the wildtype strain two-fold.

No change in imipenem resistance was noted for any mutant strain tested compared to the wildtype strain (Table 4.3). This was not surprising as no known imipenem resistance gene is located on the p1AB5075 plasmid (9). However, a 2-fold reduction in meropenem MIC was seen in the Δp1AB5075 compared to the wildtype (Table 4.3). This result was consistent with all Δp1AB5075 based mutants and none of the complemented genes restored wildtype resistance levels. Therefore, other genes may be present on the p1AB5075 plasmid that contribute to meropenem resistance in *A. baumannii* AB5075.

Table 4.3. Minimum Inhibitory concentrations (MIC) of Δ p1AB5075 mutants. MIC analysis was performed as per CLSI guidelines on *Acinetobacter* sp (85). ND – not determined (n=3).

Strain	GEN	KAN	AMI	STR	TOB	FEP	IMP	MER
WT AB5075 pWH1266	256	> 4096	512	1024	32	512	64	16
Δp1AB5075 pWH1266	8	8	8	256	0.5	32	64	8
Δp1AB5075 pWH1266-<i>aadB</i>	> 4096	2048	8	256	128	32	64	8
Δp1AB5075 pWH1266-<i>aph(3')</i>-VI	8	>4096	2048	256	0.5	32	64	8
Δp1AB5075 pWH1266-<i>aadA1</i>	8	16	8	>2048	0.5	32	64	8
Δp1AB5075 pWH1266-<i>aaC(6')</i>-Ib3	32	512	32	256	32	32	64	8
Δp1AB5075 pWH1266-<i>strA</i>	8	16	8	>2048	0.5	32	64	8
Δp1AB5075 pWH1266-<i>strB</i>	8	16	8	256	0.5	32	64	8
Δp1AB5075 pWH1266-<i>bla</i>_{GES-11}	ND	ND	ND	ND	ND	1024	64	8

Chapter 5 – Impact of p1AB5075 on biofilm formation in *A. baumannii* AB5075

5.1 Introduction

Antimicrobial resistance is a multi-factorial phenomenon. While the presence of resistance genes largely determines the resistance profile of a bacterium, biofilms are another mechanism that plays a crucial role in allowing the bacteria to survive treatment and gradually develop increased resistance over time (19). Key biofilm formation genes such as *pgaABCD*, *csu* operon and *bap* are tightly regulated by the regulatory systems *bfmRS*, *gascSA*, *adeRS* and *abal-abaR* quorum sensing in *A. baumannii* (19, 106). However, these regulatory systems also regulate numerous antibiotic resistance efflux pumps and virulence genes, such as T6SS which enables the bacteria to endure host defence systems, survive antibiotic treatment and interbacterial competition during infection (52, 53, 106). Thus, the virulence and antimicrobial resistance status of bacteria are intertwined leading to increased complexity in treatment.

Crosstalk between plasmid-encoded regulatory genes and chromosomal genes has been seen before altering the resistance and virulence potential of *A. baumannii* strains (78, 79). Plasmid mediated biofilm regulation has been described before in the urinary isolate UPAB1 by a plasmid-encoded H-NS-encoding gene. Loss of H-NS revealed a significant increase in biofilm formation (79). Therefore, the contribution of the accessory genome to overall strain antimicrobial resistance and biofilm formation is crucial to understand. This regulatory crosstalk has not been investigated to date for p1AB5075 in the MDR strain *A. baumannii* AB5075. This study aims to address this gap in the literature and identify the potential contribution of p1AB5075 to overall physiology in *A. baumannii* AB5075.

5.2 Analysis of p1AB5075 on virulence in *A. baumannii* AB5075

To investigate the potential role of p1AB5075, different phenotypes were tested. Type IV pili in *A. baumannii* have been shown to affect motility, DNA uptake and adherence (107, 108).

A. baumannii acquires exogenous DNA during twitching motility by using the same extension and retraction dynamics that drive surface movement of the bacteria (108). A significant decrease in twitching motility was observed upon the loss of the p1AB5075 plasmid (Figure 5.1).

A. baumannii motility is facilitated by type IV pili and chromosomal known regulators of motility are the *BfmRS* two-component system and *AbaI-AbaR* (52). Therefore, on the p1AB5075 plasmid an unknown regulatory mechanism of motility may be present or a regulatory system that might interact with *BfmRS* or *AbaI-AbaR* regulatory systems, due to the reduction in motility observed, or motility could be affected through a new mechanism (Figure 5.1).

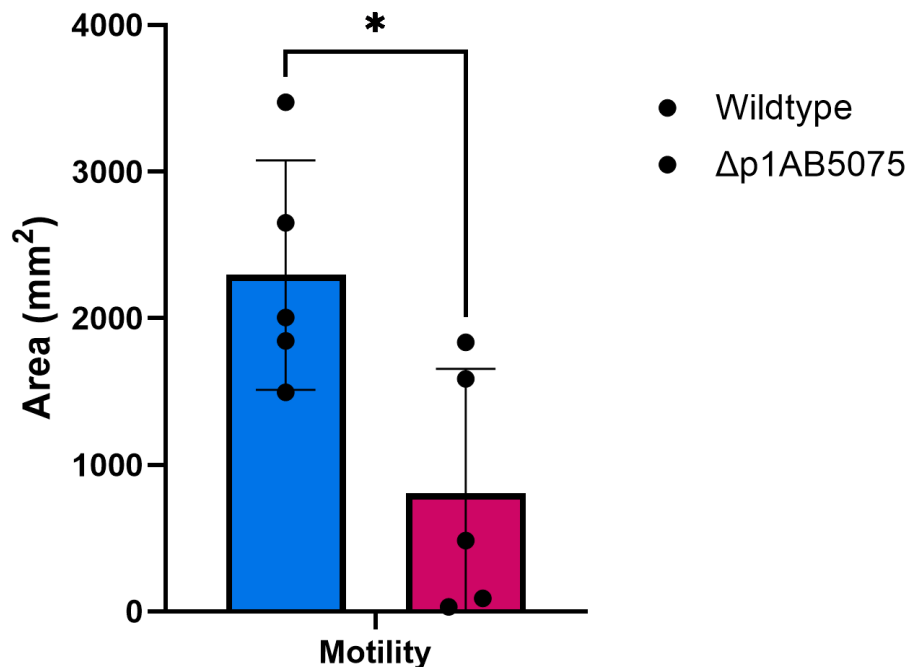


Figure 5.1. Impact of the loss of p1AB5075 on twitching interface motility. Single colonies were used to inoculate plates containing motility agar and incubated at 37°C for 5 days. Plates were analysed using ImageJ software (n=5). Statistical significance was determined by a nonparametric Mann-Whitney test where * = $P \leq 0.05$.

As type IV pili are involved in initial biofilm attachment and its regulators *BfmRS* and *AbaI-AbaR* are also involved in biofilm formation (52), the effect of $\Delta p1AB5075$ on biofilm formation was analysed (Figure 5.2). Growth in a nutrient rich environment *i.e.*, L-broth revealed that the loss of p1AB5075 significantly increased the biofilm formation in *A. baumannii* AB5075 (Figure 5.2). This result was surprising as no known biofilm associated genes have been identified on this plasmid to date.

Additionally, the reduction in motility associated with the $\Delta p1AB5075$ strain (Figure 5.1), would suggest that biofilm formation would also be impaired due to poor initial attachment to abiotic surfaces. In nutrient deprived conditions *i.e.*, M9-glucose media this increase in biofilm formation was seen in both strains compared to growth in L-broth *i.e.*, nutrient rich environment (Figure 5.2).

A significant increase in biofilm formation facilitated by the loss of p1AB5075 was exacerbated under nutrient deprived conditions compared to the wildtype strain (Figure 5.2). It is clear that p1AB5075 influences biofilm formation, due to the significant increase in biofilm mass detected upon loss of the plasmid *A. baumannii* AB5075.

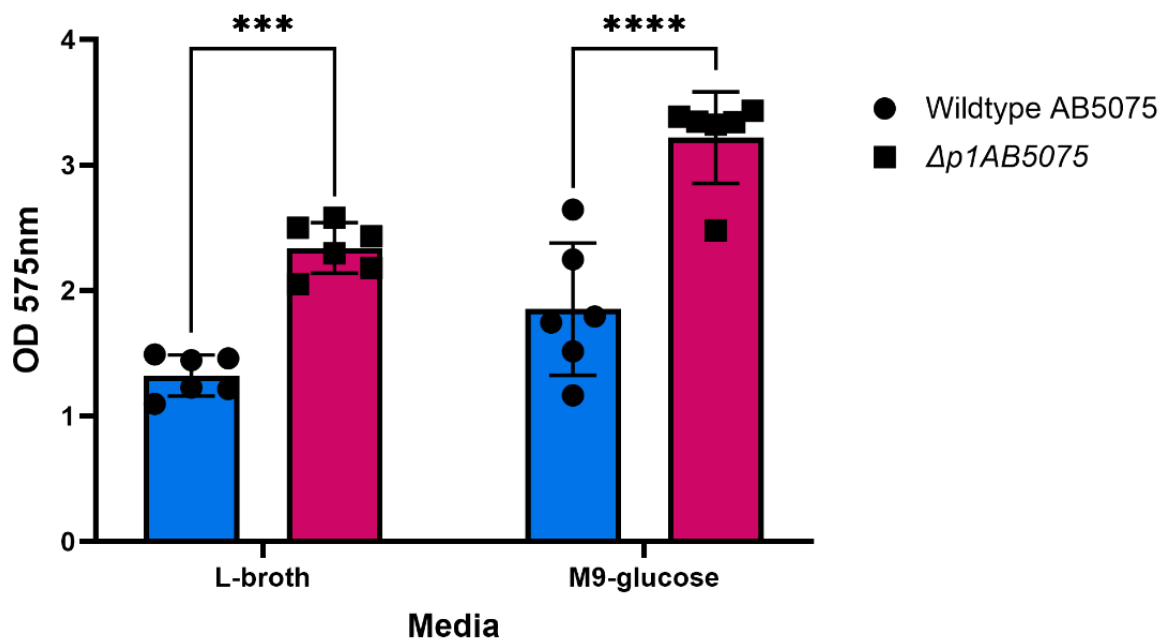


Figure 5.2. Consequences of the loss of p1AB5075 on *A. baumannii* AB5075 on biofilm formation in nutrient rich (L-broth) and nutrient deprived (M9-glucose) conditions at 37°C. Polystyrene based 96 well plates were utilised (n=6). Statistical significance was determined using a two-way ANOVA where * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$.

Biofilm formation was further analysed for the $\Delta p1AB5075$ strain through confocal microscopy (Figure 5.3). The wildtype and $\Delta p1AB5075$ strain underwent microscopy after 2 hours of growth to assess their adhesion capacity (Figure 5.3.A, Figure 5.3.B). It appears that the $\Delta p1AB5075$ is less adhesive to polystyrene plastic after 2 hours than the wildtype.

Interestingly, after 4 days there is a greater amount of biofilm biomass in the $\Delta p1AB5075$ than the wildtype (Figure 5.3.C, Figure 5.3.D). However, the biofilm architecture seems to be compromised. The wildtype biofilm is very dense, whereas the $\Delta p1AB5075$ biofilm while larger in size has a less dense or “fluffy” appearance. The increase in biofilm formation for $\Delta p1AB5075$ is consistent with previous findings in biofilm quantification (Figure 5.2). The reason for this change in phenotype is unclear and further analysis is needed.

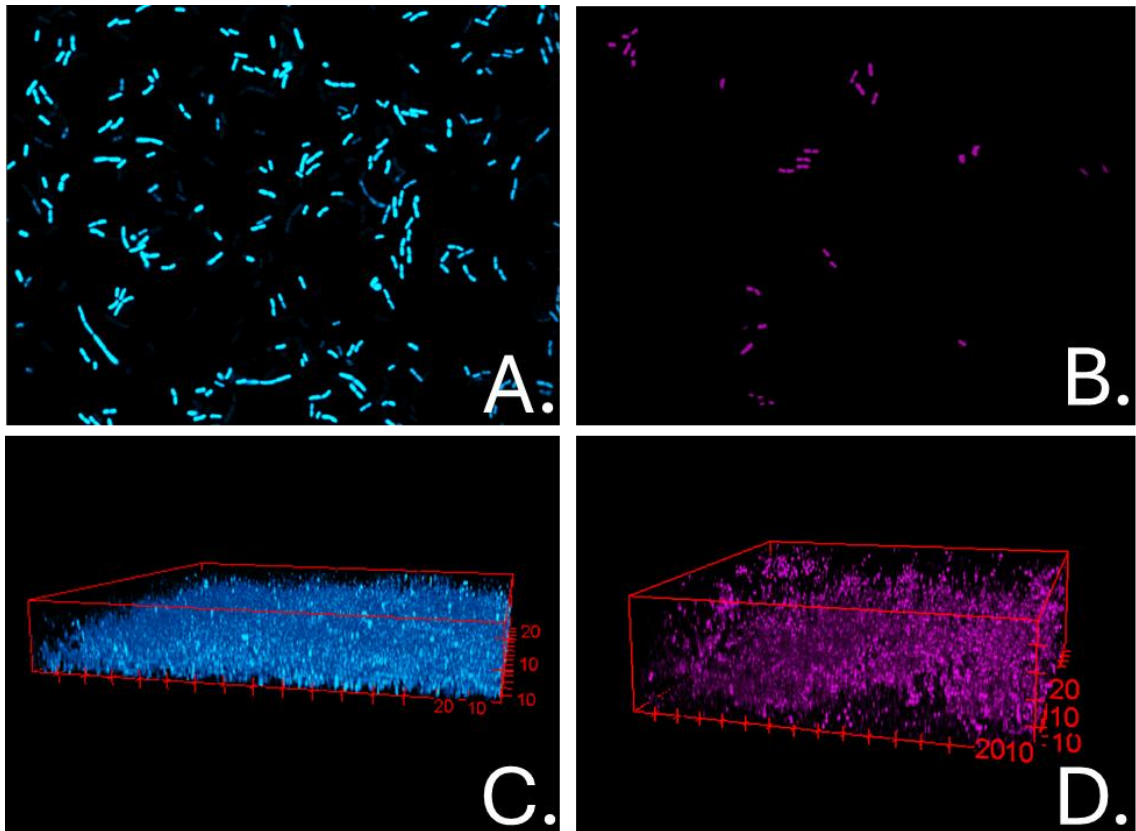


Figure 5.3. Adhesion to polystyrene plastic and biofilm formation of WT and $\Delta p1AB5075$. Confocal microscope 3D biofilm reconstruction of AB5075 strains stained with DAPI. WT (A) and $\Delta p1AB5075$ (B) adherence to a plastic surface after 2 hours. Biofilm formation of WT (C) and $\Delta p1AB5075$ (D) after 4 days. The $\Delta p1AB5075$ strain has less adhesion than the WT (A and B). Although fewer cells had adhered after 2 hrs, the $\Delta p1AB5075$ strain produces more biofilm with more loose architecture after 4 days (C and D).

5.3 Plasmid-encoded H-NS and biofilm formation in *A. baumannii* AB5075

5.3.1 Constructing H-NS complementation vectors in *A. baumannii*

To investigate what genes play a role in biofilm production on p1AB5075 the plasmid contents were analysed for any annotated genes of interest that are predicted regulators of gene expression. Only one gene was identified to encode a potential regulatory protein influencing biofilm formation, which is a H-NS-family protein (63, 65, 67, 79). In *A. baumannii* AB5075, two copies of *hns* are present, one is integrated into the chromosome and the other is located on the p1AB5075 plasmid (9, 80). Previous studies focus only on the *hns* copy on the chromosome whereas, this research is looking at the *hns* located on the p1AB5075 plasmid (63, 67).

Similar, to the previous complementation strains the Δ p1AB5075 background pWH1266 was utilised (Figure 5.4). However, the cloned gene was put under control of its native promoter and not the *bla* promoter on the pWH1266 plasmid. This was to ensure expression levels and regulation comparable to that of the wildtype strain, although due to copy number of the plasmid it would most likely be somewhat overexpressed.

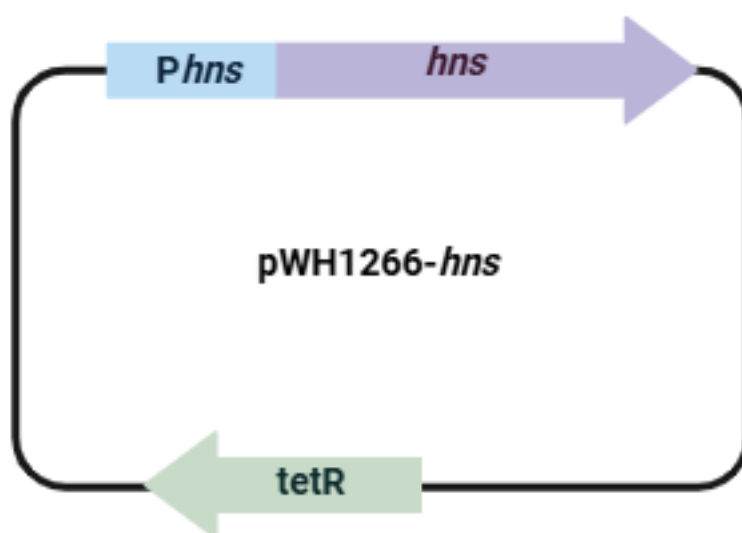


Figure 5.4. Construction of a *hns* overexpression model in *A. baumannii* AB5075. P-*hns*– native *hns* promoter, tetR – tetracycline resistance gene.

5.3.2 Comparison of H-NS proteins in *A. baumannii* AB5075

H-NS proteins are encoded on both the chromosome and p1AB5075 plasmid in *A. baumannii* AB5075 although their structural similarities are unknown (9). To analyse the structural differences between the two copies of H-NS a multiple sequence alignment (MSA) was performed including the H-NS protein from the pAB5 plasmid in the UPAB1 clinical isolate (Figure 5.5).

The UPAB1 H-NS protein is known to repress biofilm formation in *A. baumannii*, and, upon the loss of the pAB5 plasmid-encoded H-NS, a significant increase in biofilm formation is observed (79). This increase in biofilm formation is similar to that displayed by the loss of p1AB5075 H-NS in *A. baumannii* AB5075 and thus, was included for analysis (Figure 5.1). The MSA alignment revealed that all H-NS proteins investigated shared a low protein sequence similarity (Figure 5.5). This may indicate that each H-NS protein is capable of regulating different genes in the genome due to different structural binding sites.



Figure 5.5. Multiple sequence alignment of H-NS proteins in *A. baumannii*. UPAB1 – H-NS located on the pAB5 plasmid in UPAB1, Plasmid – H-NS located on the p1AB5075 plasmid in AB5075 and Chromosome – H-NS located on the AB5075 chromosome. Image was generated using ClustalW.

Table 5.1. Percentage identity of amino acid similarities between *A. baumannii* H-NS proteins. Values generated from ClustalW W.

Origin of <i>hns</i>	% identity to UPAB1 pAB5 <i>hns</i>	% identity to AB5075 chromosomal <i>hns</i>	% identity to AB5075 p1AB5075 <i>hns</i>
UPAB1 pAB5 <i>hns</i>	100	38.89	42.59
AB5075 chromosomal <i>hns</i>	38.89	100	59.16
AB5075 p1AB5075 <i>hns</i>	42.59	69.16	100

The H-NS molecule has an N-terminal used for oligomerization to other H-NS or regulatory proteins for stabilisation of the H-NS protein to accomplish gene silencing (61). Typically residues 1-46 are highly conserved in this area to provide stable protein-protein interactions (109). The N-terminal is followed by a linker region to the C terminal which is used for binding directly to DNA (61). The H-NS protein functions by binding to a region of AT rich DNA through the C terminal. Next, the N-terminal undergoes dimerization with other H-NS or H-NS like proteins to form filaments, which anchor the H-NS protein in place for effective gene silencing (109). Amino acid substitutions in the dimerization site have previously been linked to impaired gene regulation through the absence of H-NS protein stability (61).

To examine if the protein sequences generated similar protein structures, a 3-D rendering of the three H-NS proteins were created and aligned (Figure 5.6). Atoms that alter between the structures are displayed in red. It is clear that all H-NS proteins share a similar core structure however, they do not clearly align and several atoms are misaligned indicating differences in degrees of flexibility between the 3 proteins. Altered degrees of flexibility may coincide with varied substrate specificity.

To determine if the protein-protein interaction site of the three H-NS proteins were affected by the differences in protein flexibility, the protein binding site was identified and characterised (Figure 5.7). The protein binding site was located at residue 45 by the software PyMol (from metadata pdb files), for all H-NS proteins and the amino acid was identified (Table 5.2). The presence of valine in the protein binding site of the p1AB5075 H-NS protein indicates strong hydrophobicity for the stabilisation of protein-protein interactions through hydrophobic interactions (109–111). Due to asparagine being the main residue in the protein binding pocket for the AB5075 chromosome encoded H-NS protein, this indicates that protein interactions may be facilitated through hydrogen bonding with the amide group present (110).

Alanine in the UPAB1 H-NS protein is a non polar residue with low hydrophobicity and similar to p1AB5075 H-NS and relies on hydrophobic contacts for protein stability (109–111). These differences in binding properties influenced by the amino acid substitutions may indicate a difference in regulatory protein interactions.

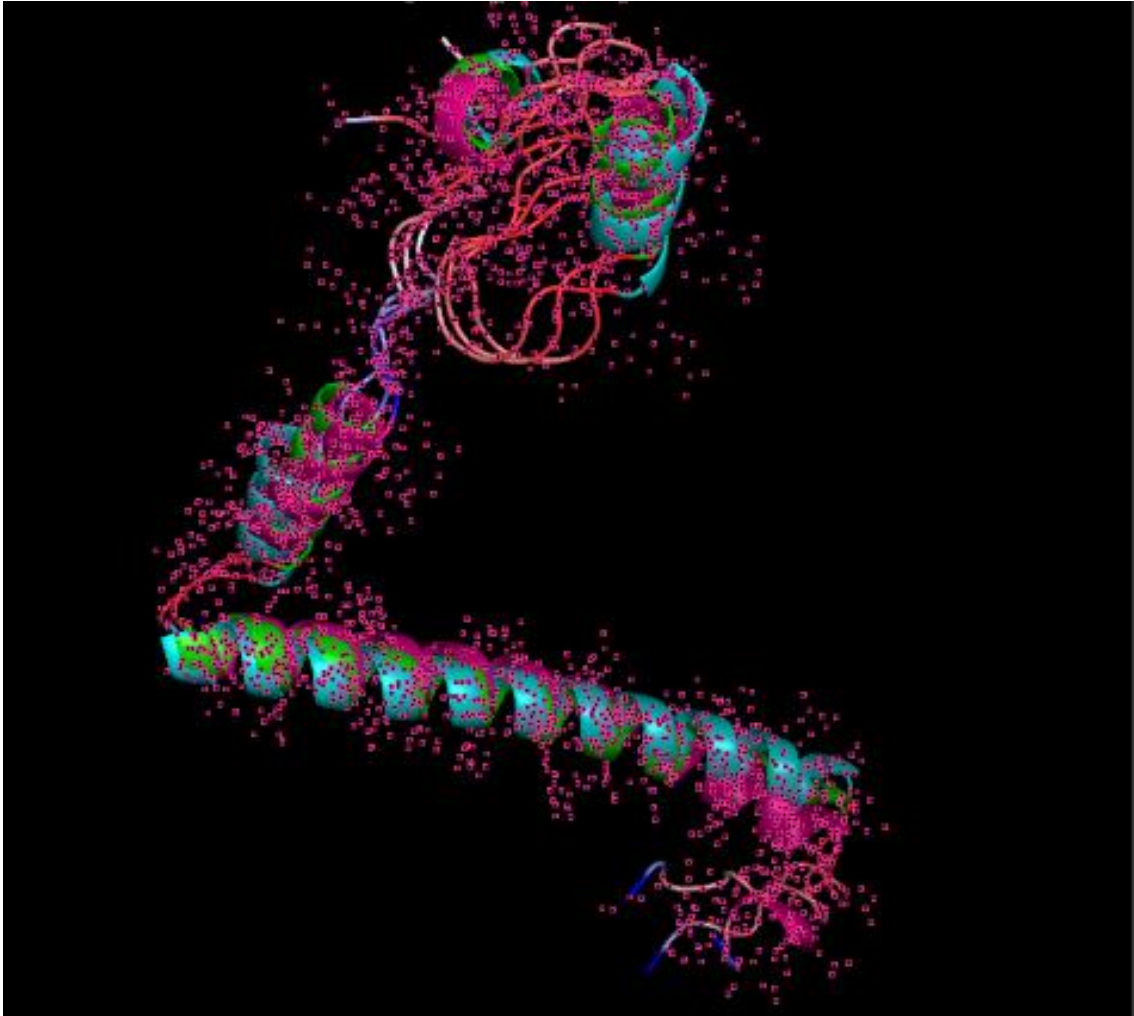


Figure 5.6. A 3-D model of H-NS proteins present in *A. baumannii*. H-NS proteins were aligned based on protein sequence and mismatched atoms are highlighted in red. Green - H-NS located on the pAB5 plasmid in UPAB1, Pink – H-NS located on the p1AB5075 plasmid in AB5075 and Blue – H-NS located on the AB5075 chromosome. Image was generated using PyMol.

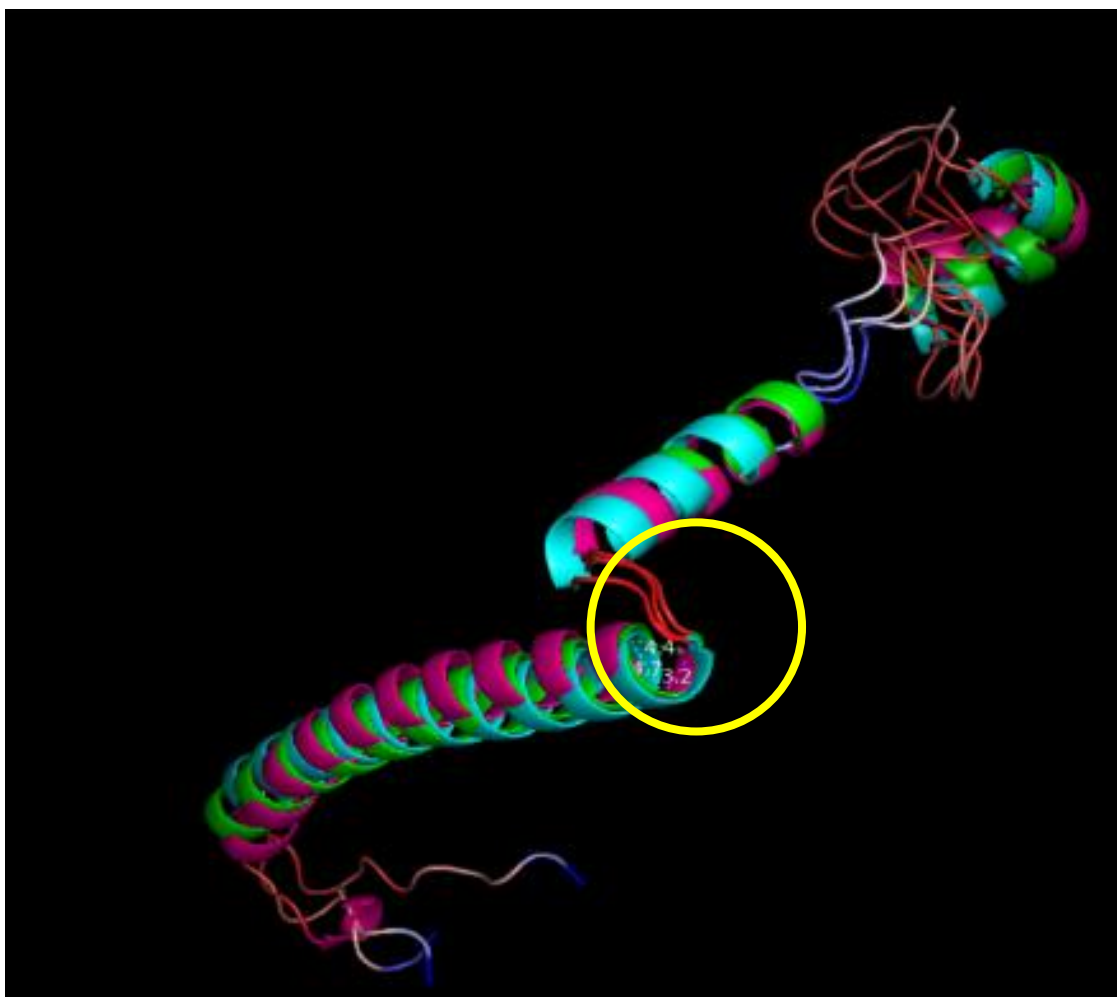


Figure 5.7. Structural comparison of three H-NS protein binding sites in *A. baumannii* strains.

Table 5.2. Properties of amino acids located in the protein binding site of *A. baumannii* H-NS proteins.

Property	H-NS p1AB5075	H-NS Chromosome	H-NS UPAB1
Amino Acid	Valine	Asparagine	Alanine
Side Chain	Branched (-CH(CH ₃) ₂)	Amide group (-CONH ₂)	Methyl group (-CH ₃)
Polarity	Nonpolar	Polar	Nonpolar
Charge at pH7	Neutral	Neutral	Neutral
Hydrophobicity	High	Low	Low

5.3.2 The role of H-NS on growth in *A. baumannii* AB5075

To examine the effects of overexpression of plasmid-encoded *hns* on *A. baumannii* AB5075 growth experiments were performed in nutrient rich and nutrient limited media (Figure 5.8). Under optimal growth conditions the $\Delta p1AB5075$ strain displays a slightly enhanced growth profile compared to the wildtype. The $\Delta p1AB5075$ strain has an extended log phase and has an increased final optical density (Figure 5.8.A). In contrast, both the *hns* complementation strains show negatively impacted growth compared to their respective strains (Figure 5.8.A). An increased lag phase and overall decreased final optical density is observed in both complementation strains. H-NS is a global transcriptional regulator which can impact several genes both on the chromosome and the accessory genome. Thus, having additional copies of *hns* may cause dysregulation of important cellular processes by the strains during growth (Figure 5.8.A). This demonstrates that the addition of multiple copies of *hns* can have a negative impact on *A. baumannii* growth.

In nutrient limited conditions, the $\Delta p1AB5075$ strain grows comparably to the wildtype strain (Figure 5.8.B). Similarly to growth under optimal conditions, the *hns* complementation strains show a negatively impacted growth profile (Figure 5.8.B). An increased lag phase and overall lower final bacterial density is exhibited by both strains potentially due to the same hypothesis stated previously. The reduction of bacterial growth in both media is also important to take into account for any future experiments, that the complementation strains have a reduced growth capacity. Therefore, normalisation of experiments based on growth is crucial to accurately attribute any changes in cellular processes to regulation by *hns* and not as a result of a lower bacterial concentration.

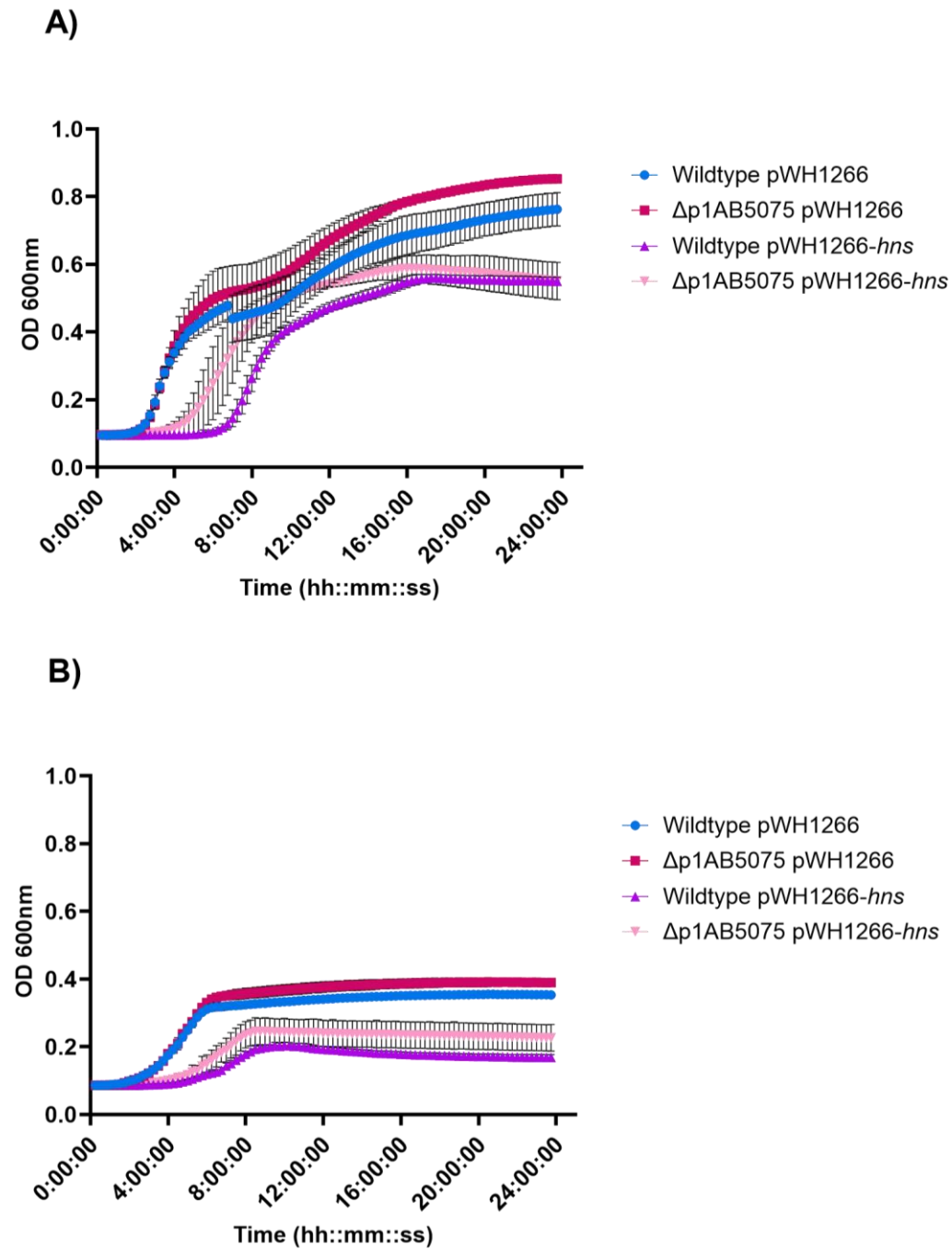


Figure 5.8. Growth experiment of *hns* mutants in *A. baumannii* AB5075. Overnight cultures of *A. baumannii* strains were diluted in PBS, standardised to an OD₆₀₀ of 0.01 and incubated at 37°C with orbital shaking in A) L-broth and B) M9 supplemented with 2% glucose. OD₆₀₀ readings were taken at 15-minute intervals to evaluate bacterial growth over a 24-hour period (n=3).

5.3.3 The impact of p1AB5075-encoded *hns* on biofilm formation in *A. baumannii*

To investigate if the plasmid-encoded *hns* plays a role in biofilm formation in *A. baumannii* AB5075, biofilm formation in minimal media was analysed (Figure 5.9). As biofilm formation was predominately different between Δ p1AB5075 and the wildtype in minimal media supplemented with glucose the same growth conditions were implemented for this investigation (Figure 5.2). The Δ p1AB5075 pWH1266 strain showed significantly increased biofilm formation compared to the wildtype pWH1266 strain in nutrient limited conditions at both 30°C and 37°C (Figure 5.9). This increase in biofilm production is not altered by the presence of the pWH1266 needed for accurate comparison to the complementation plasmids and reflects the results seen in previously in this study (Figure 5.2). Upon overexpression of p1AB5075 encoded *hns* in the wildtype strain, a significant increase in biofilm formation is only observed at 30°C, this increase in biofilm formation is absent in growth under optimal temperature conditions (Figure 5.9). The expression of *hns* in the Δ p1AB5075 background restores biofilm formation levels comparable to those displayed by the wildtype strain at 30°C and 37°C (Figure 5.9). This suggests that the levels of *hns* in the Δ p1AB5075 pWH1266-*hns* strain should be comparable to the levels of *hns* in the wildtype pWH1266 strain restoring the biofilm phenotype seen in the wildtype strain. Thus, we can suggest that the p1AB5075-encoded *hns* regulates biofilm associated genes present on the chromosome as seen previously in other *A. baumannii* strains (79).

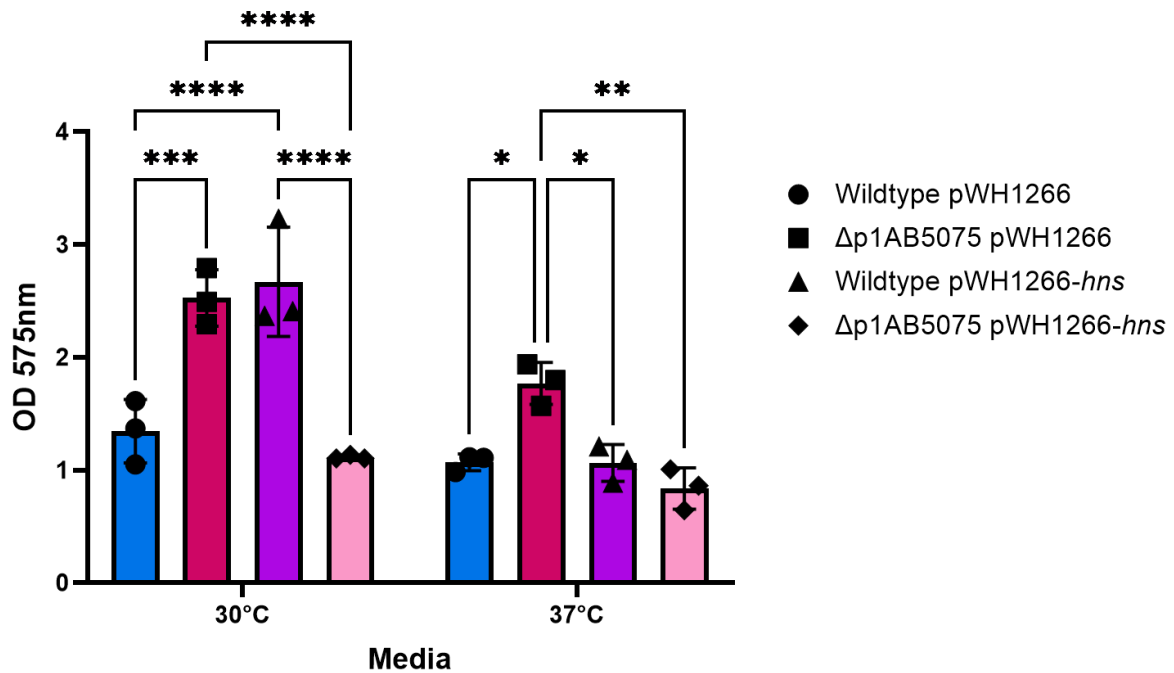


Figure 5.9. Biofilm analysis of wildtype AB5075 and Δp1AB5075 under nutrient limiting conditions in 96 well plates. Biofilm formation after 2 days in 30°C and 37°C in M9 supplemented with 2% glucose (n=3). Statistical significance was determined using a two-way ANOVA where * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$.

Biofilm formation analysis was repeated in a larger volume for better visualisation of the impact of Δp1AB5075 and the expression of plasmid-encoded *hns* on *A. baumannii* AB5075 (Figure 5.10). Upon visual analysis of biofilm formation in polypropylene tubes Δp1AB5075 has increased levels of biofilm compared to the wildtype (Figure 5.10.A). Subsequent analysis in polystyrene tubes also revealed a consistent increase in biofilm formation for Δp1AB5075 (Figure 5.9.B). Both *hns* complementation strains are comparable to the wildtype strain in both plastics analysed (Figure 5.10.A, Figure 5.10.B). The increase in biofilm for overexpression of *hns* in the wildtype background was lost when analysed at higher volumes than seen in the 96 well plate analysis (Figure 5.9). The reason for this is unknown however, we speculate that the as H-NS regulates may cellular factors including adherence, if adherence factors are upregulated in a small volume biofilm formation may appear inflated due to increased biofilm stability. This effect may have been normalised by the reduced surface area of the narrow plastic tubes used for analysis, along with the increased culture volume.

Quantitative analysis revealed that only $\Delta p1AB5075$ exhibited a significant increase in biofilm formation compared to the wildtype strain (Figure 5.10.C). As the re-introduction of *hns* into the $\Delta p1AB5075$ background restored biofilm formation to wildtype levels, it can be concluded that the plasmid-encoded *hns* regulates biofilm formation and stability in *A. baumannii* AB5075.

To further visualise differences between biofilm structural components in *A. baumannii* mutant strains, different agar media were utilised for visual analysis of colony phenotypes (Figure 5.11). Congo red was implemented for the detection of amyloid structures. At 37°C, *hns* complementation strains are comparable to the wildtype strain at day 1 (Figure 5.11.A). All strains display a dark red colony morphology which indicates a low degree of biofilm. The darker red pigment shows that Congo red is being bound to the cells efficiently. In contrast the $\Delta p1AB5075$ under the same conditions is paler in colour indicating that increased biofilm formation is masking the red colouration of cells at this timepoint (Figure 5.11.A). This suggests that *hns* may play a role in the regulation of biofilm formation in *A. baumannii*, upon the loss of the plasmid-encoded *hns* the red pigmentation is noticeably weaker correlating to increased biofilm production. By day 5 and 7 all strains have noticeably produced an extracellular matrix (Figure 5.11.A). The $\Delta p1AB5075$ strain shows a slight increase in biofilm production compared to the wildtype by day 5, consistent with the increase in biofilm formation noted in the crystal violet-based assays (Figure 5.9, Figure 5.10). Conversely, the *hns* complementation strains display a rough dry colony morphology compared to the wildtype strain at later timepoints at 37°C (Figure 5.11.A). Less biofilm is produced leading to the texturization of the *hns* strains. This may be as a result of dysregulation of biofilm genes and the growth defect leading to reduced biofilm production.

At 30°C a similar trend is seen across the *A. baumannii* strains (Figure 5.10.A). The $\Delta p1AB5075$ strain is noticeably paler than the wildtype strain but ultimately produces more biofilm and the *hns* strains have significantly altered colony morphology.

However, at 30°C the *hns* overexpression strains produce more biofilm compared to growth at 37°C. While the colony morphology has a rough appearance, the dryness of the colony surface is less pronounced at later timepoints.

At 30°C, the slowed growth may allow the cells to have more time to adapt and regulate the biofilm associated genes at an enhanced level compared to their higher growth rate in 37°C.

For the detection of protein abundance, Coomassie blue was used for protein visualisation. Similarly, throughout the course of the experiment Δ p1AB5075 displays a smooth, highly mucoid phenotype compared to the wildtype strain (Figure 5.11.B). At days 5 and 7, the biofilm obscures the Coomassie blue dye bound to proteins. This phenotype is enhanced at 30°C. Bacterial cells may have enhanced adaptation through slower growth. This phenomenon is comparable to the difference between the wildtype colonies at 37°C and 30°C (Figure 5.11.B). Biofilm is visible by day 5 and 7 at 37°C however, significantly more biofilm is noted in the same wildtype strain when grown at 30°C. Therefore, the lower temperature positively influences the production of biofilm formation. Both *hns*-expressing strains at days 1 and 5 have a stronger blue colour compared to the wildtype at 37°C and 30°C (Figure 5.11.B). This indicates that the higher degree of biofilm production in wildtype and the Δ p1AB5075 strain masks the blue colony colour, highlighting again that overexpression of *hns* represses biofilm production. At day 7 in 37°C the *hns* complementation strain in the Δ p1AB5075 background shows limited change to day 5 colony morphology at 37°C (Figure 5.11.B). In contrast, at day 7, when grown at 30°C, small pockets of biofilm production are visible on the edges of the Δ p1AB5075 pWH1266-*hns* colony. This phenotype might indicate that the plasmid is lost over time in some cells or that *hns* could have acquired inactivating mutations relieving repression of biofilm formation. Perhaps for the same reasons, the wildtype pWH1266-*hns* strain also exhibits a partial change in colony morphology at day 7 in both 37°C and 30°C (Figure 5.11.B). An increase in biofilm matrix is seen for this strain after prolonged incubation on the Coomassie blue agar.

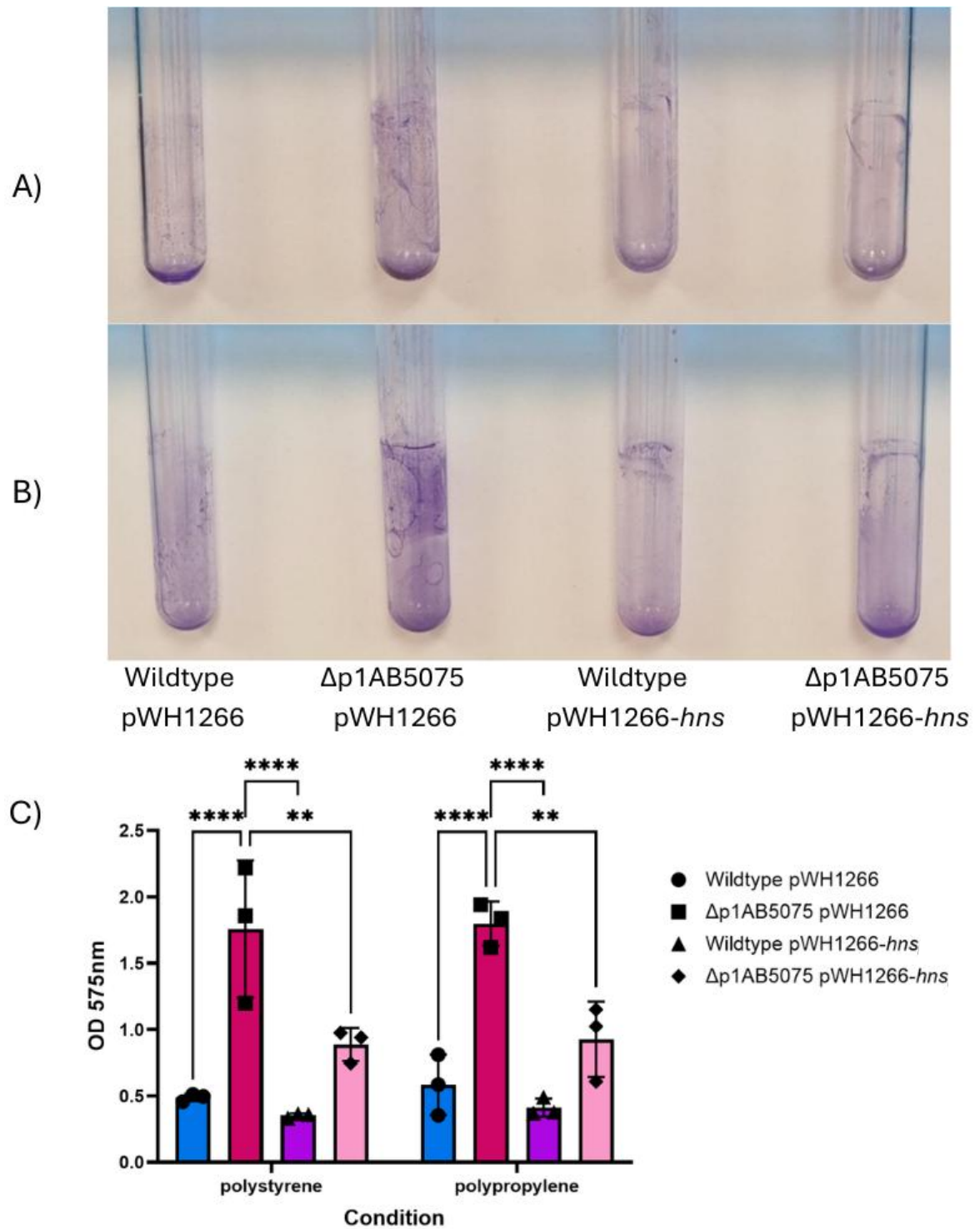


Figure 5.10. Biofilm analysis of wildtype AB5075 and Δ p1AB5075 mutants. A) in polypropylene and B) polystyrene after 2 days in 30°C in M9 supplemented with 2% glucose. C) OD575 nm readings of bacterial biofilms in A) polypropylene and B) polystyrene tubes (n=3). Statistical significance was determined using a two-way ANOVA where * = $P \leq 0.05$, ** = $P \leq 0.01$, *** = $P \leq 0.001$, **** = $P \leq 0.0001$.

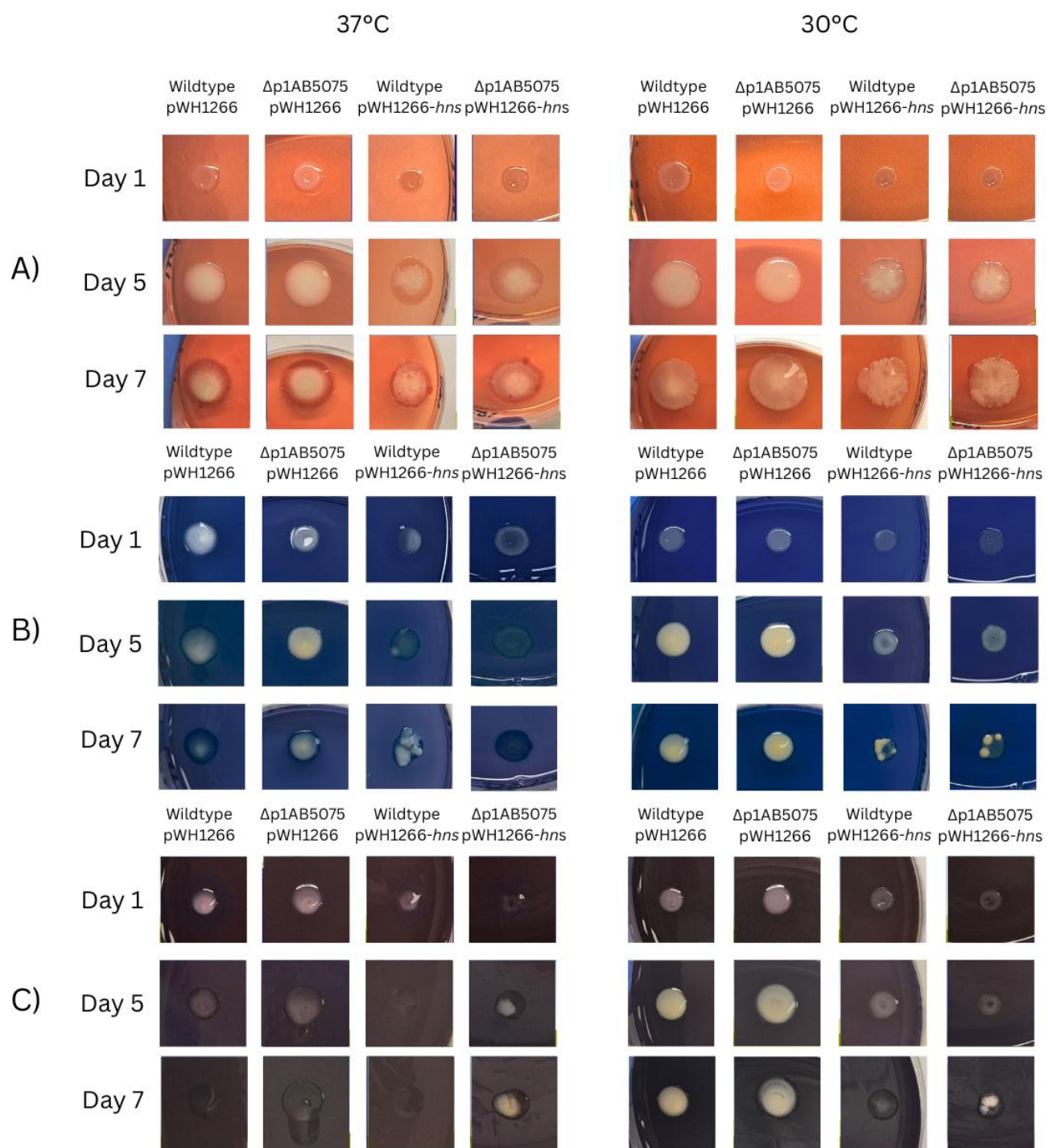


Figure 5.11. Biofilm analysis of *A. baumannii* plasmid encoded-hns mutants on solid media. A) Congo red agar B) Coomassie blue agar C) Congo red and Coomassie blue agar. Overnight *A. baumannii* cultures were diluted in PBS, standardised to OD an of 1 and spotted onto agar plates. Pictures were taken on days 1, 5 and 7 for visual analysis. This is a representative picture of each biofilm agar media analysed (n=3).

Agar plates containing both Congo red and Coomassie blue were utilised for the assessment of biofilm matrix abundance (Figure 5.11.C). At 37°C, $\Delta p1AB5075$ is comparable to the wildtype strain at day 1. Both strains display a light purple colour indicative of protein and low Congo red binding. At the later timepoints day 5 and 7, the increased biofilm formation again masks binding of Congo red and Coomassie blue in the $\Delta p1AB5075$ mutant compared to the wildtype (Figure 5.11.C). The wildtype pWH1266-*hns* strain has much less biofilm production from day 1 compared to the wildtype strain and the $\Delta p1AB5075$ mutant resulting in darker colony phenotypes. This phenotype is consistent throughout the timeline of the experiment (Figure 5.11.C). The stability and copy number of the pWH1266 complementation plasmid is unknown. The $\Delta p1AB5075$ pWH1266-*hns* plasmid strain could have a lower expression of *hnsP* due to plasmid loss or reduced copy number of *hnsP* producing this phenotype leading to sometimes mixed phenotypes at days 5 and 7.

At 30°C a similar colony morphology is seen for day 1, the wildtype and $\Delta p1AB5075$ strains produce more biofilm leading to a light purple colour (Figure 5.11.C). At days 5 and 7 a further increase in biofilm production is observed for both strains. This is shown through a pale white colony appearance meaning that pigment binding is significantly masked by the presence of increased biofilm. Similar to the 37°C phenotype trend, the wildtype pWH1266-*hnsP* strain is darker than the wildtype at all timepoints analysed at 30°C indicating that biofilm production is dramatically reduced (Figure 5.11.C). However, the colony is not as dark in pigment as it was at 37°C. A reduction in colour intensity signifies less visible pigment binding potentially due to an increase in biofilm formation.

This was also seen in the Coomassie blue plates, the wildtype pWH1266-*hnsP* strain shows a decrease in biofilm production when grown in lower temperatures (Figure 5.11.B). Again, the $\Delta p1AB5075$ pWH1266-*hnsP* colony is significantly darker than the other mutants tested at all timepoints at 30°C (Figure 5.11.C). At day 7, the colony is starting to produce patches of biofilm similar to the biofilm production of the $\Delta p1AB5075$ and wildtype strain. This is comparable to the increase in biofilm over time in the $\Delta p1AB5075$ pWH1266-*hnsP* strain at 37°C.

5.3.4 RNA-seq analysis of *A. baumannii* AB5075 biofilms

To investigate the effect of $\Delta p1AB5075$ and the role of plasmid-encoded H-NS on biofilm formation RNA-sequencing was performed (Appendix II). RNA samples were prepared from *A. baumannii* strains grown statically at 30°C in M9-glucose for 2 days. Principle component analysis (PCA) was used to visualise the transcriptional variation between strains (Figure 5.12). The PCA plot reveals a clustering of wildtype and $\Delta p1AB5075$ samples indicating that they share similar gene expression profiles. However, the H-NS complementation strains are located elsewhere showing a significant shift in gene expression profile. The wildtype pWH1266-*hns**p* is the only strain displaying a high degree of variation between biological replicates. This may be due to different plasmid copy numbers or a high degree of genetic heterogeneity.

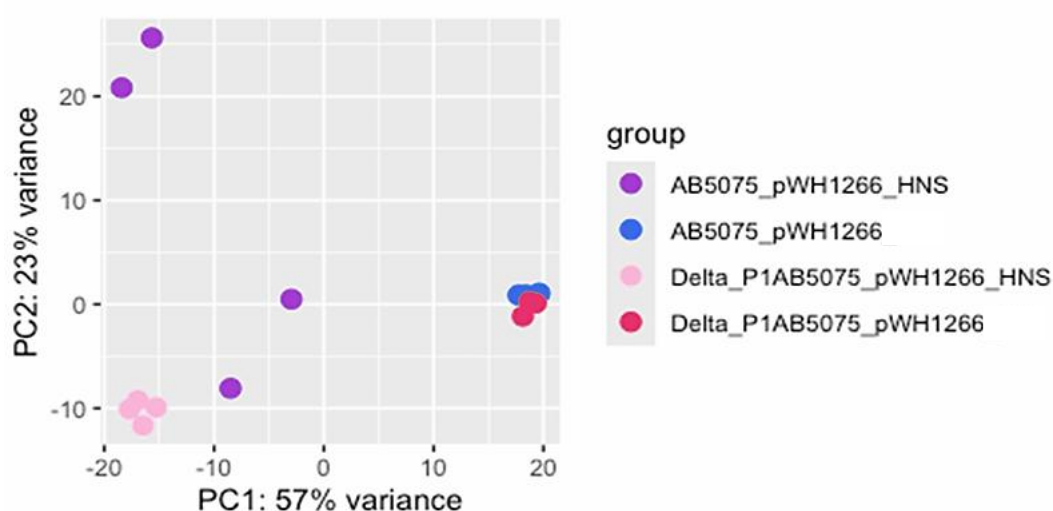


Figure 5.12. Principle component analysis (PCA) plot of transcriptomic profile for *A. baumannii* AB5075 strains under biofilm conditions. Overnight cultures were standardised to an OD of 1 and inoculated into 10mL of M9-glucose. Samples were grown for 2 days at 30°C before collection via centrifugation and prepped for RNA sequencing. Each symbol on the plot correlates to a biological replicate ($n = 3$ wildtype pWH1266 and $\Delta p1AB5075$ pWH1266, $n = 4$ wildtype pWH1266-*hns**p* and $\Delta p1AB5075$ pWH1266-*hns**p*).

The wildtype strain exhibited a gene expression profile similar to the $\Delta p1AB5075$ strain (Figure 5.13). Under ideal biofilm growth conditions, the wildtype had a total of three genes significantly upregulated and only one gene downregulated compared to the $\Delta p1AB5075$ strain (Table 5.3).

This result was surprising as significant phenotypic changes in biofilm production were previously seen (Figures 5.2, 5.3, 5.9-11) and the lack of differentially expressed genes was unexpected. The only gene significantly downregulated in the wildtype strain compared to the $\Delta p1AB5075$ strain was *otsB* (Table 5.4). This gene is a part of the *otsAB* regulatory pathway and has been known to play a role in stress response, capsule production and virulence in *A. baumannii* (112). Upregulated genes in the wildtype compared to $\Delta p1AB5075$ were *fimA*, molecular chaperone and a matrixin metalloprotease (Table 5.4). The type 1 pilin *fimA* is involved in host cell adherence and pellicle formation in other *A. baumannii* strains (113). This may explain the reduction in adherence in the $\Delta p1AB5075$ strain (Figure 5.3B). Metalloproteases are utilised by bacteria as a host defence mechanism (114), thus the consequence of the loss of *p1AB5075* may reduce virulence in *A. baumannii* AB5075, further investigation is required.

Table 5.3. Number of genes significantly upregulated and downregulated in *A. baumannii* mutant strains $\geq \pm 2$ -fold change.

Comparison	Upregulated	Downregulated
Wildtype pWH1266 vs. $\Delta p1AB5075$ pWH1266	3	1
$\Delta p1AB5075$ pWH1266- <i>hns</i> vs. $\Delta p1AB5075$ pWH1266	595	652
Wildtype pWH1266- <i>hns</i> vs. Wildtype pWH1266	607	457
Wildtype pWH1266- <i>hns</i> vs. $\Delta p1AB5075$ pWH1266- <i>hns</i>	583	310

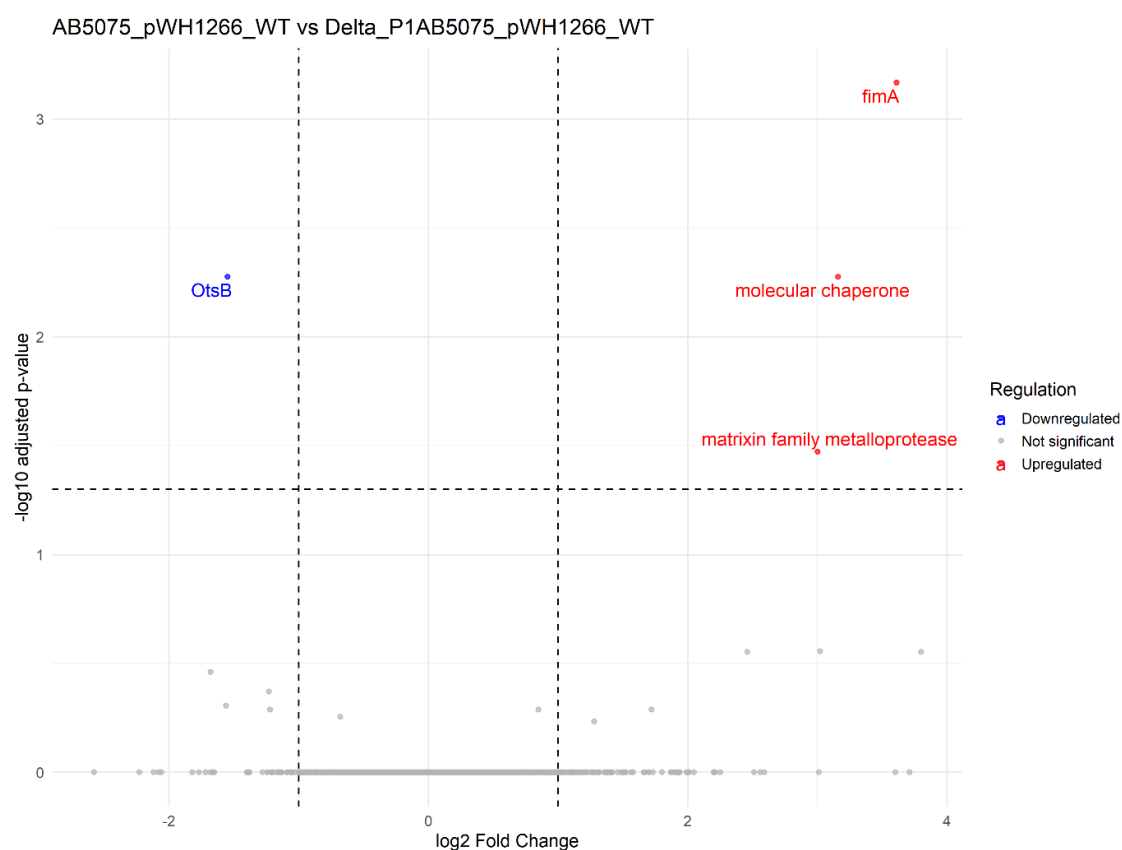


Figure 5.13. Transcriptomic analysis of wildtype pWH1266 in comparison to Δ p1AB5075 pWH1266 *A. baumannii* strain. Volcano plot visualises log₂-fold change on the x-axis and -log₁₀ adjusted p-value on the y-axis. Significantly differentially expressed genes displayed a minimum of a log₂-fold change of 1 and an adjusted p-value of <0.05. Upregulated genes are represented in red, non-significantly expressed genes in grey and downregulated genes are in blue.

Table 5.4. Differentially expressed genes between the wildtype pWH1266 in comparison to Δ P1AB5075 pWH1266 strain in biofilm conditions according to RNA sequencing.

Gene	product	Log 2-fold change	p-value adjusted	Regulation
ABUW_RS09965	FimA	3.61	2E-08	Upregulated
ABUW_RS09970	molecular chaperone	3.16	2E-14	Upregulated
ABUW_RS18900	matrixin family metalloprotease	3	8E-04	Upregulated
ABUW_RS15160	OtsB	-1.55	2E-05	Downregulated

Upon re-introduction of the plasmid-encoded *hns* into the $\Delta p1AB5075$ background increased diversity between the two strains is observed, with 595 genes upregulated and 652 genes downregulated with a minimum of a +/- 2-fold change (Table 5.3).

This change in genetic profiles during biofilm formation is visualised through transcriptomic analysis using volcano plots (Figure 5.14). There is an increase in the number of genes differentially expressed by +/- 2-fold when *hns* is present in the genome, compared to the analysis on wildtype pWH1266 vs. $\Delta p1AB5075$ pWH1266 (Figure 5.13 and 5.14). Thus, we can conclude that the plasmid-encoded *hns* regulates genes on the genome of *A. baumannii* AB5075.

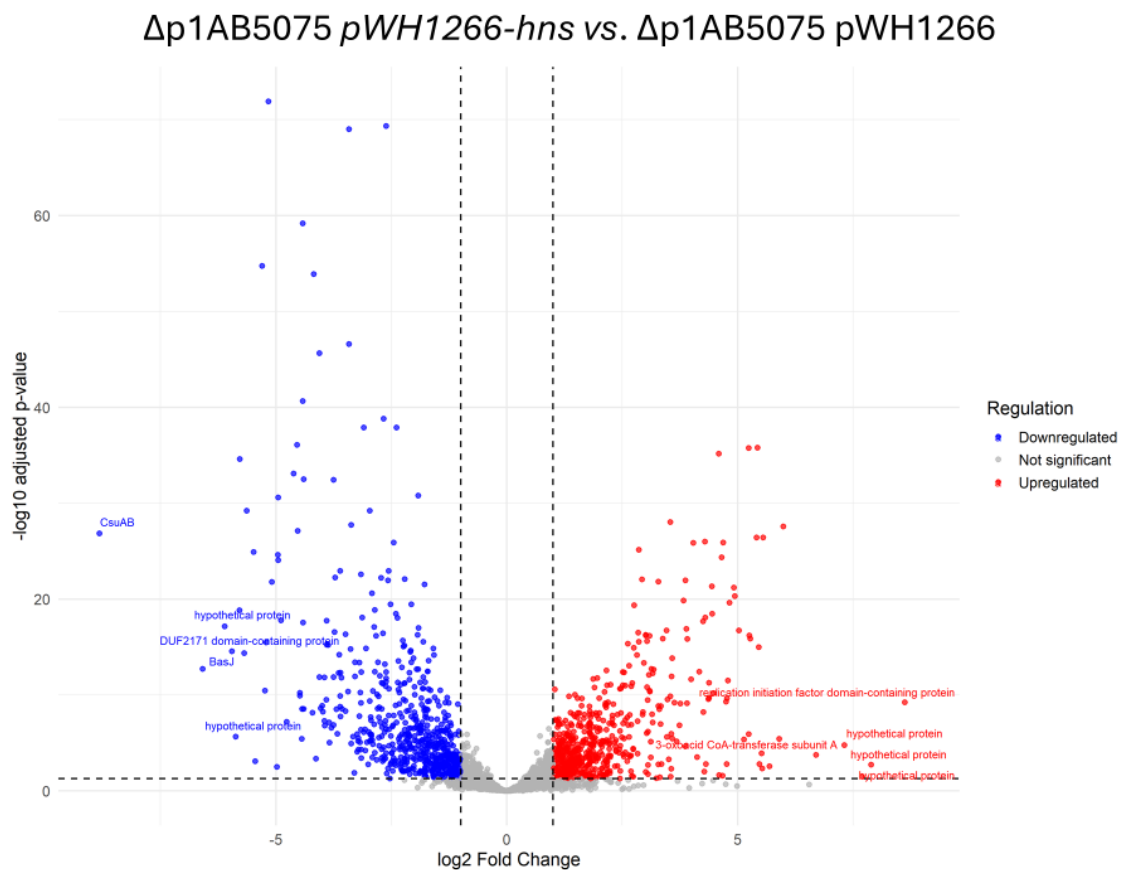


Figure 5.14. Transcriptomic analysis of $\Delta p1AB5075$ pWH1266-*hns* in comparison to $\Delta p1AB5075$ pWH1266 *A. baumannii* strain. Volcano plot visualises log2-fold change on the x-axis and -log10 adjusted p-value on the y-axis. Significantly differentially expressed genes displayed a minimum +/- 2-fold change and an adjusted p-value of <0.05. Upregulated genes are represented in red, non-significantly expressed genes in grey and downregulated genes are in blue.

The top five differentially expressed genes that were up and down regulated were summarised for analysis (Table 5.5). Unfortunately, 6 out of the 10 genes that were differentially expressed were hypothetical proteins with unknown functions. Therefore, their role in biofilm formation could not be deciphered and more characterisation of these genes is required for further analysis.

The two identified genes that were upregulated in the $\Delta p1AB5075$ pWH1266-*hns* background compared to the $\Delta p1AB5075$ pWH1266 were a replication initiation factor domain-containing protein and 3-oxoacid CoA-transferase subunit A (Table 5.5). These genes correspond to DNA replication and cell metabolism respectively indicating the negative consequences of overexpressing *hns* in *A. baumannii* AB5075 (115).

Table 5.5. Top 5 differentially expressed genes upregulated and downregulated between the $\Delta p1AB5075$ pWH1266-*hns* compared to $\Delta p1AB5075$ pWH1266 strain in biofilm conditions according to RNA sequencing.

Gene	product	Log 2-fold change	p-value adjusted	Regulation
ABUW_RS09760	replication initiation factor domain-containing protein	8.62	6E-10	Upregulated
ABUW_RS09705	hypothetical protein	7.89	2E-03	Upregulated
ABUW_RS09875	hypothetical protein	7.7	3E-02	Upregulated
ABUW_RS20455	hypothetical protein	7.31	2E-05	Upregulated
ABUW_RS09125	3-oxoacid CoA-transferase subunit A	6.7	2E-04	Upregulated
ABUW_RS07250	Csu fimbrial major subunit CsuAB	-8.82	1E-27	Downregulated
ABUW_RS05800	acinetobactin biosynthesis BasJ	-6.59	2E-13	Downregulated
ABUW_RS11870	hypothetical protein	-6.11	7E-18	Downregulated
ABUW_RS07145	DUF2171 domain-containing protein	-5.95	3E-15	Downregulated
ABUW_RS12415	hypothetical protein	-5.87	2E-06	Downregulated

Two identified genes *csuAB* and *basJ* were significantly downregulated in the Δ p1AB5075 pWH1266-*hns* mutant compared to the Δ p1AB5075 pWH1266 background (Table 5.5). The *csuAB* gene is involved in *csu* pili assembly and the *basJ* is a part of acinetobactin operon which encodes an iron acquisition siderophore (52). These results are in agreement with the biofilm formation experiments as Δ p1AB5075 pWH1266-*hns* produced less biofilm than the Δ p1AB5075 pWH1266 strain (Figure 5.9 and Figure 5.10). The *csu* pili are heavily involved in biofilm formation and the reduction in its expression correlates to the reduction in biofilm mass. The *basJ* gene encodes for part of the acinetobactin siderophore (*basA-J*).

To evaluate the global impact of plasmid-encoded *hns*, a GO analysis was performed to understand the cellular processes in the Δ p1AB5075 background (Figure 5.15). Several different metabolic processes were up and down regulated upon the re-introduction of *hns* into the Δ p1AB5075 background such as citric acid cycle and iron acquisition systems respectively (Figure 5.15). This indicates that cross-talk regulation by the plasmid-encoded *hns* gene and chromosomal metabolic genes is present. Interestingly, when plasmid-encoded *hns* is present some of the outer membrane proteins are downregulated (Figure 5.15). Previous work has seen that outer membrane proteins can affect biofilm formation in *A. baumannii* (17). This may explain the reduction of biofilm mass between the Δ p1AB5075 pWH1266-*hns* and Δ p1AB5075 pWH1266 strains (Figure 5.9 and Figure 5.10).

Δ p1AB5075 *pWH1266-hns* vs. Δ p1AB5075 *pWH1266*

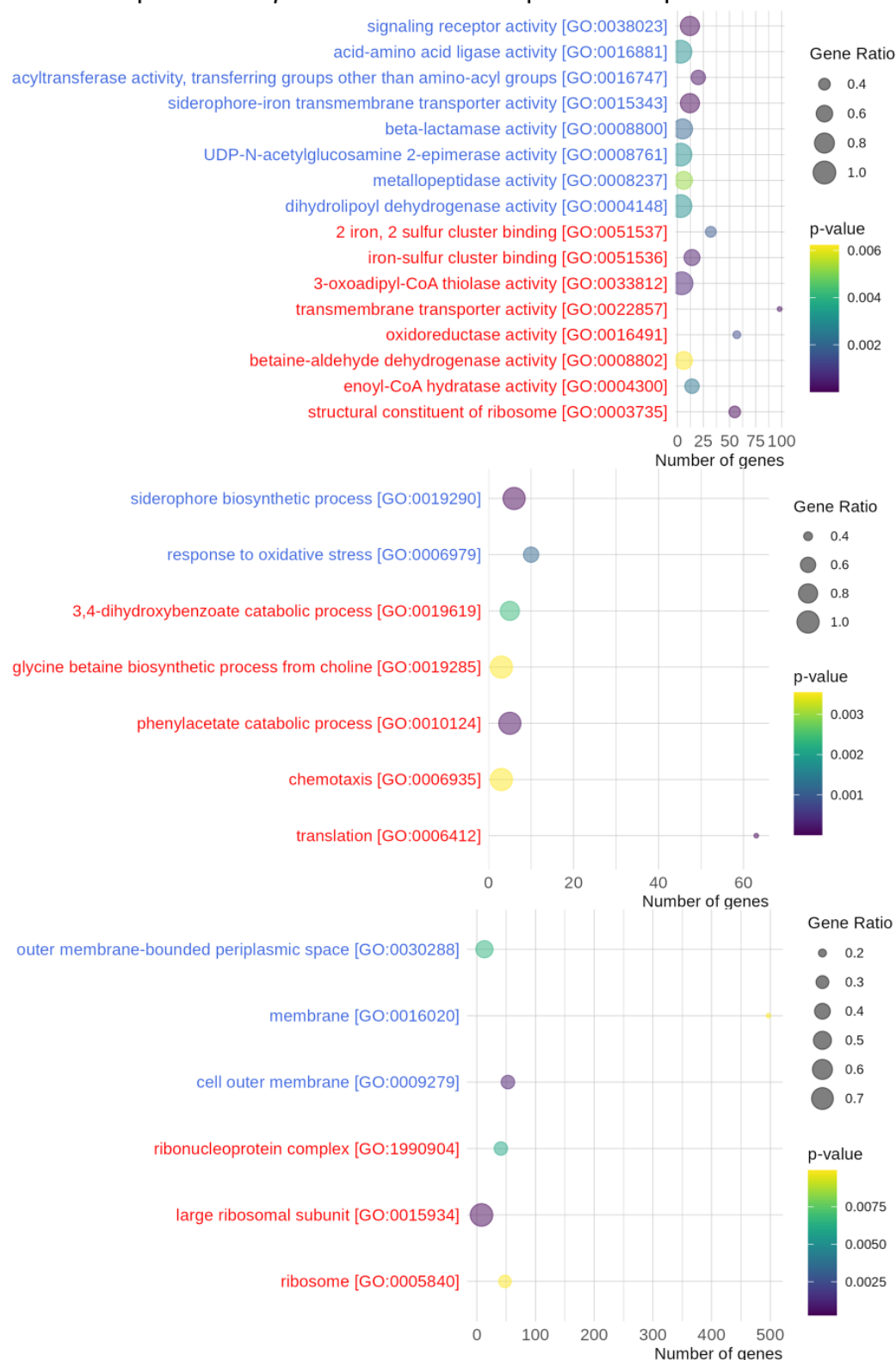


Figure 5.15. GO analysis of pathways upregulated and downregulated in the Δ p1AB5075 *pWH1266-hns* compared to Δ p1AB5075 *pWH1266*. Downregulated pathways are displayed in blue and upregulated pathways in red. The number of genes in the pathway are listed on the x-axis, where the symbol is located is the total number of genes in the indicated pathway. The size of the symbol correlates to the ratio of genes in that pathway that are affected and the colour denotes the p-value.

Similarly the introduction of plasmid-encoded *hns* significantly altered the differentially expressed genes in the wildtype background (Table 5.3). A total of 607 genes were upregulated and 457 genes were downregulated with a minimum of +/- 2-fold change in AB5075 pWH1266-*hns* compared to AB5075 pWH1266. This diversity in differentially expressed genes is clearly visualised through transcriptomic analysis (Figure 5.16). The top five differentially expressed genes that were upregulated and downregulated from this analysis were selected for and summarised for analysis (Table 5.6). Genes that were significantly upregulated in the wildtype AB5075 pWH1266-*hns* strain compared to the wildtype pWH1266 were a ChbG/HpnK family deacetylase, a TetR/AcrR family transcriptional regulator, an EamA family transporter, a hypothetical protein and glycosyltransferase family 2 protein (Table 5.5). ChbG/HpnK family deacetylases have been shown to be involved in the removal of an acetyl group from a polysaccharide, to form oligosaccharides that can be utilised by the bacteria for metabolism and depending on the polysaccharide cell wall synthesis in *E. coli* (116). Additionally, the glycosyltransferase family 2 proteins alter carbohydrate structures for cell metabolism, storage and cell wall synthesis (117). The upregulation of these two carbohydrate modifying enzymes indicate that the wildtype AB5075 pWH1266-*hns* metabolism pathways are dysregulated in this strain. This may provide an explanation for the growth defect of the wildtype AB5075 pWH1266-*hns* strain (Figure 5.8). Similarly the EamA family proteins are responsible for metabolite transport within the cell and reinforce the hypothesis that the wildtype AB5075 pWH1266-*hns* strain displays dysregulation of metabolism pathways crucial for growth compared to the wildtype pWH1266 strain. H-NS is a global transcriptional regulator and may regulate other regulatory mechanisms in *A. baumannii* (63). Thus an increase in other transcriptional regulators *i.e.*, TetR/AcrR family transcriptional regulator was not unexpected (Table 5.6). The most downregulated genes in the wildtype AB5075 pWH1266-*hns* strain compared to the wildtype pWH1266 strain all belong to the *csu* operon (Table 5.6). Similarly to the previous results on the overexpression of *hns* in the $\Delta p1AB5075$ background (Table 5.6), the plasmid-encoded *hns* appears to regulate the chromosomal encoded *csu* operon in *A. baumannii* AB5075.

The *csu* operon is important for biofilm formation and adherence in *A. baumannii* this might explain the reduction in biofilm formation seen by this strain on solid media (Figure 5.11).

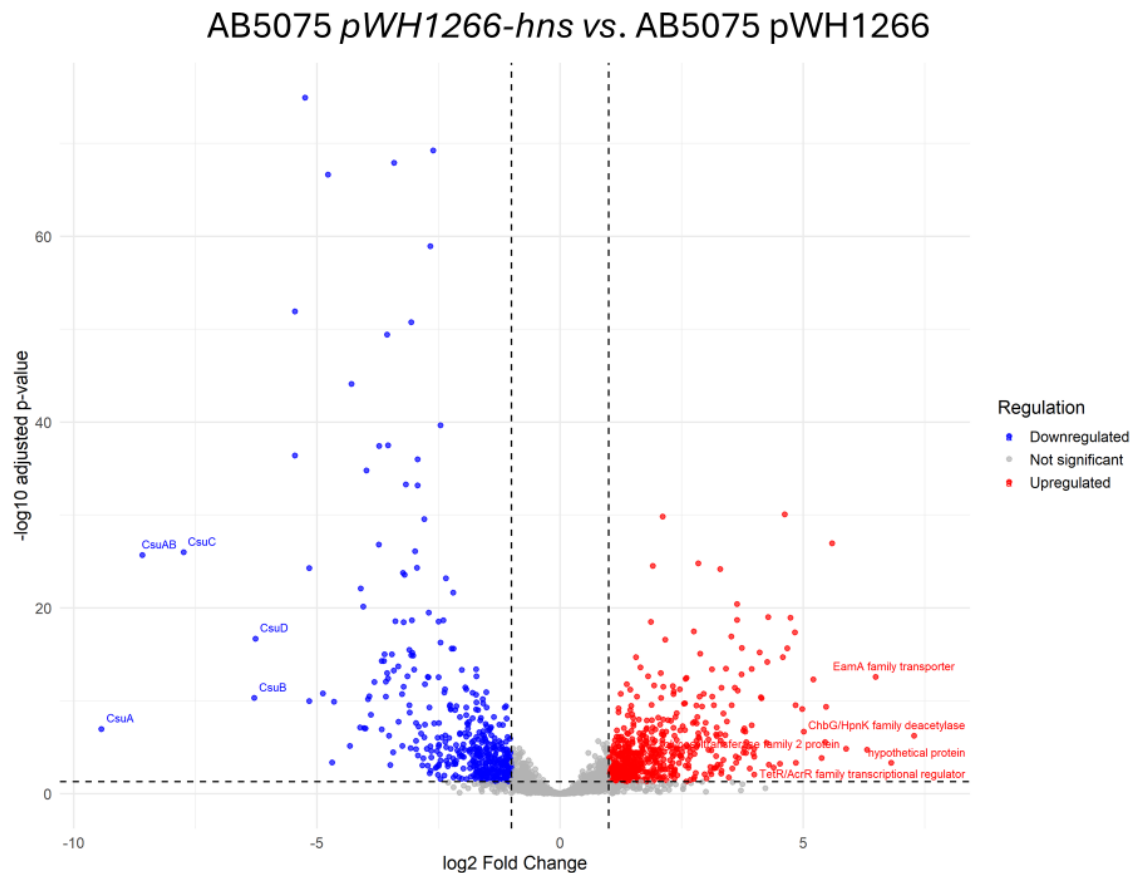


Figure 5.16. Transcriptomic analysis of AB5075 pWH1266-*hns* in comparison to AB5075 pWH1266 *A. baumannii* strain. Volcano plot visualises log₂-fold change on the x-axis and -log₁₀ adjusted p-value on the y-axis. Significantly differentially expressed genes displayed a minimum of a +/- 2-fold change of and an adjusted p-value of <0.05. Upregulated genes are represented in red, non-significantly expressed genes in grey and downregulated genes are in blue.

GO analysis was performed on the wildtype AB5075 pWH1266-*hns* strain in comparison to the wildtype pWH1266 strain to determine the cellular pathways that are significantly differentially expressed upon the over expression of *hns* (Figure 5.16). Similar to the Δ p1AB5075 pWH1266-*hns* overexpression strain, several metabolic pathways were differentially expressed (Figure 5.15 and 5.17). As both *hns* complementation strains displayed a negatively impacted growth profile (Figure 5.8), it is possible that the plasmid copy of *hns* dysregulates metabolism genes on the chromosome and that may result in the reduction of growth in *A. baumannii* AB5075.

Table 5.6. Top 5 differentially expressed genes upregulated and downregulated between the AB5075 pWH1266-hns in comparison to AB5075 pWH1266 strain in biofilm conditions according to RNA sequencing.

Gene	product	Log 2-fold change	p-value adjusted	Regulation
ABUW_RS04730	ChbG/HpnK family deacetylase	7.28	5.9E-07	Upregulated
ABUW_RS12615	TetR/AcrR family transcriptional regulator	6.81	4.6E-04	Upregulated
ABUW_RS01775	EamA family transporter	6.49	2.6E-13	Upregulated
ABUW_RS03650	hypothetical protein	6.31	1.8E-05	Upregulated
ABUW_RS04725	glycosyltransferase family 2 protein	5.88	1.4E-05	Upregulated
ABUW_RS07255	Csu fimbrial biogenesis protein CsuA	-9.43	1.1E-07	Downregulated
ABUW_RS07250	Csu fimbrial major subunit CsuAB	-8.59	2.0E-26	Downregulated
ABUW_RS07265	Csu fimbrial biogenesis chaperone CsuC	-7.74	9.5E-27	Downregulated
ABUW_RS07260	Csu fimbrial biogenesis protein CsuB	-6.29	5.0E-11	Downregulated
ABUW_RS07270	Csu fimbrial usher CsuD	-6.26	2.0E-17	Downregulated

Downregulation of the pilus assembly pathway in wildtype AB5075 pWH1266-*hns* compared to the wildtype pWH1266 strain is also recorded (Figure 5.17). This is most likely due to the downregulation of the *csu* operon as previously deciphered from transcriptomic analysis (Figure 5.16). Overall, plasmid-encoded *hns* from the p1AB5075 plasmid appears to regulate cell metabolism, outer membrane structure and pili assembly in *A. baumannii* AB5075.



Figure 5.17. GO analysis of pathways upregulated and downregulated in the AB5075 *pWH1266-hns* compared to AB5075 *pWH1266*. Downregulated pathways are displayed in blue and upregulated pathways in red. The number of genes in the pathway are listed on the x-axis, where the symbol is located is the total number of genes in the indicated pathway. The size of the symbol correlates to the ratio of genes in that pathway that are affected and the colour denotes the p-value.

The complementation of plasmid-encoded *hns* was performed in both the wildtype and the $\Delta p1AB5075$ background. However, the wildtype strain still harbours the p1AB5075 plasmid and thus, retains additional copies of the global transcriptional regulator *hns*. To investigate the differences in plasmid-encoded *hns* copy number on gene expression transcriptomic analysis was performed on wildtype pWH1266-*hns* compared to $\Delta p1AB5075$ pWH1266-*hns* (Figure 5.18). It is clear that the two strains have distinct gene expression profiles highlighted by the vast changes in differentially expressed genes. In the absence of the *hns* complementation this gene expression diversity is lost (Figure 5.13). A total of 583 genes were significantly upregulated and 310 genes were downregulated in the AB5075 pWH1266-*hns* strain in comparison to $\Delta p1AB5075$ pWH1266-*hns* strain (Table 5.3).

The top five upregulated genes in this comparison were three hypothetical proteins, *basJ* and ChbG/HpnK family deacetylase (Table 5.7). The three hypothetical proteins represent novel genes that were not previously identified in other strain comparisons however, their function is still unclear. The *basJ* gene encoding a siderophore in *A. baumannii* AB5075 was previously seen to be downregulated in the $\Delta p1AB5075$ pWH1266-*hns* strain when compared to the $\Delta p1AB5075$ pWH1266 strain (Table 5.5). The ChbG/HpnK family deacetylase is still significantly upregulated in the wildtype pWH1266-*hns* strain in this comparison (Table 5.7), as previously seen before (Table 5.6).

The downregulated genes in the wildtype pWH1266-*hns* compared to the $\Delta p1AB5075$ pWH1266-*hns* strain were a DNA replication protein, sRNA2 and three hypothetical proteins. This DNA replication protein is downregulated in the wildtype pWH1266-*hns* strain compared to $\Delta p1AB5075$ pWH1266-*hns* and this correlates with the wildtype pWH1266-*hns* strain entering stationary phase prior to the $\Delta p1AB5075$ pWH1266-*hns* strain. During stationary phase the cells cease to grow and thus, DNA replication is decreased due to a reduction in cellular division.

Further investigation is needed as the $\Delta p1AB5075$ pWH1266-*hns* strain only showed a slight improvement in growth compared to the wildtype pWH1266-*hns* strain in nutrient limiting conditions (Figure 5.8). Also, sRNA2 was downregulated in the wildtype pWH1266-*hns* strain however, no functional characteristics have been associated with this sRNA to date (Table 5.7).

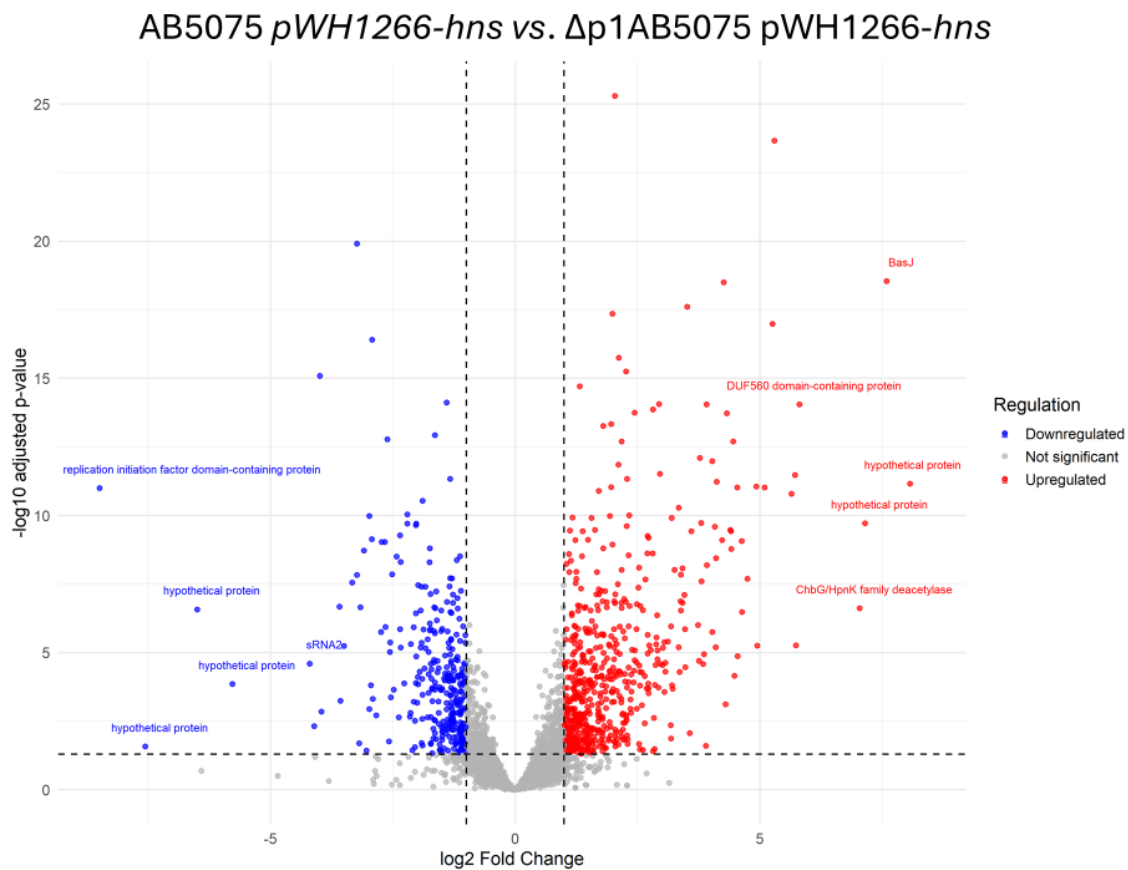


Figure 5.18 Transcriptomic analysis of AB5075 pWH1266-*hns* in comparison to $\Delta p1AB5075$ pWH1266-*hns* *A. baumannii* strain. Volcano plot visualises log2-fold change on the x-axis and -log10 adjusted p-value on the y-axis. Significantly differentially expressed genes displayed a minimum of a +/- 2-fold change of and an adjusted p-value of <0.05. Upregulated genes are represented in red, non-significantly expressed genes in grey and downregulated genes are in blue.

Table 5.7. Top 5 differentially expressed genes upregulated and downregulated between the AB5075 pWH1266-*hns* in comparison to Δ p1AB5075 pWH1266-*hns* strain in biofilm conditions according to RNA sequencing.

Gene	product	Log 2-fold change	p-value adjusted	Regulation
ABUW_RS11405	hypothetical protein	8.07	6.9E-12	Upregulated
ABUW_RS05800	acinetobactin biosynthesis BasJ	7.59	2.9E-19	Upregulated
ABUW_RS11230	hypothetical protein	7.15	1.9E-10	Upregulated
ABUW_RS04730	ChbG/HpnK family deacetylase	7.04	2.4E-07	Upregulated
ABUW_RS14485	DUF560 domain-containing protein	5.81	8.9E-15	Upregulated
ABUW_RS09760	replication initiation factor domain-containing protein	-8.49	1.0E-11	Downregulated
ABUW_RS09875	hypothetical protein	-7.56	2.7E-02	Downregulated
ABUW_RS09755	hypothetical protein	-6.5	2.7E-07	Downregulated
ABUW_RS20455	hypothetical protein	-5.78	1.4E-04	Downregulated
sRNA2	sRNA2	-4.2	2.5E-05	Downregulated

To investigate if any cellular processes were significantly affected by copy number of p1AB5075-encoded *hns* a GO analysis was performed (Figure 5.19). The increased number of p1AB5075-encoded *hns* in the wildtype pWH1266-*hns* strain revealed an upregulation in metabolism pathways. This was previously seen in the *hns* complementation strains in comparison to their respective background strains (Figure 5.15 and Figure 5.17). Interestingly, the type IV pilus assembly pathway is significantly downregulated upon the overexpression of *hns* (Figure 5.19). This may indicate that the p1AB5075-encoded *hns* directly regulates the type VI pili operon on the chromosome in *A. baumannii* AB5075. This highlights the importance of understanding the cross-talk interactions between the plasmid and the chromosome.

AB5075 *pWH1266-hns* vs. Δ p1AB5075 *pWH1266-hns*

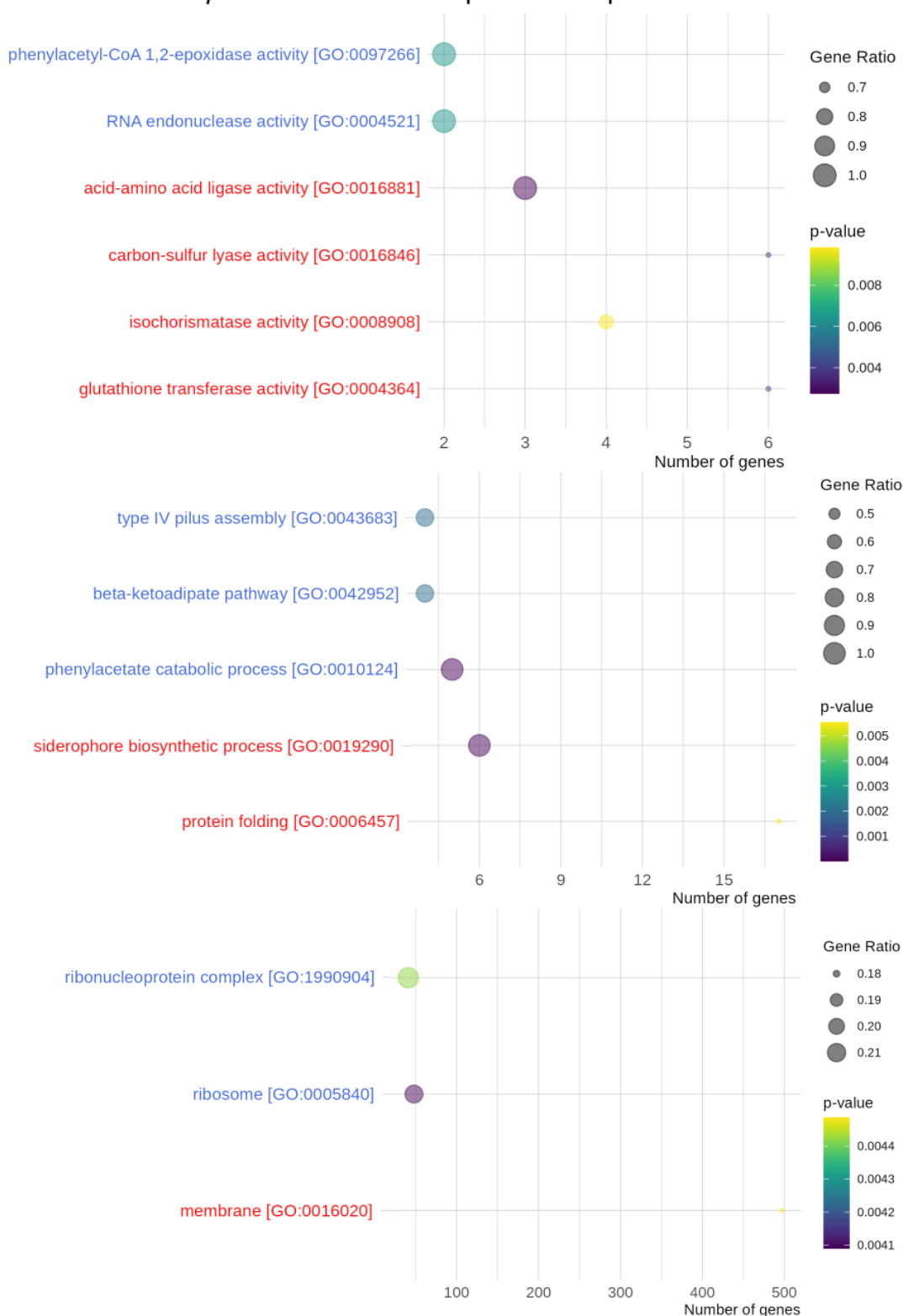


Figure 5.19. GO analysis of pathways upregulated and downregulated in the AB5075 *pWH1266-hns* compared to Δ p1AB5075 *pWH1266-hns*. Downregulated pathways are displayed in blue and upregulated pathways in red. The number of genes in the pathway are listed on the x-axis, where the symbol is located is the total number of genes in the indicated pathway. The size of the symbol correlates to the ratio of genes in that pathway that are affected and the colour denotes the p-value.

It is clear that plasmid-encoded *hns* regulates several genes on the chromosome, to further analyse this data RNA transcripts were examined for several biofilm associated genes such as *csu*, *pga*, type 1 fimbrial pili and type VI secretion system *hcp* showed alteration upon introduction of the *hns* gene (Appendix II). Firstly, RNA transcripts for the entire p1AB5075 plasmid were examined to ensure the deletion of p1AB5075 in the Δ p1AB5075 pWH1266 and Δ p1AB5075 pWH1266-*hns* strains (Figure 5.20). It is clear that both of the strains lacking the p1AB5075 plasmid show limited RNA transcripts mapping to the p1AB5075 plasmid as expected. Thereby, confirming the lack of the plasmid in the Δ p1AB5075 mutant strains. There were a small number of transcripts mapping to the p1AB5075 background in the Δ p1AB5075 pWH1266-*hns* strain (Figure 5.20). These mapped reads may be a result of reads misalignment or that this small section of the plasmid is also present elsewhere in the *A. baumannii* AB5075 genome.

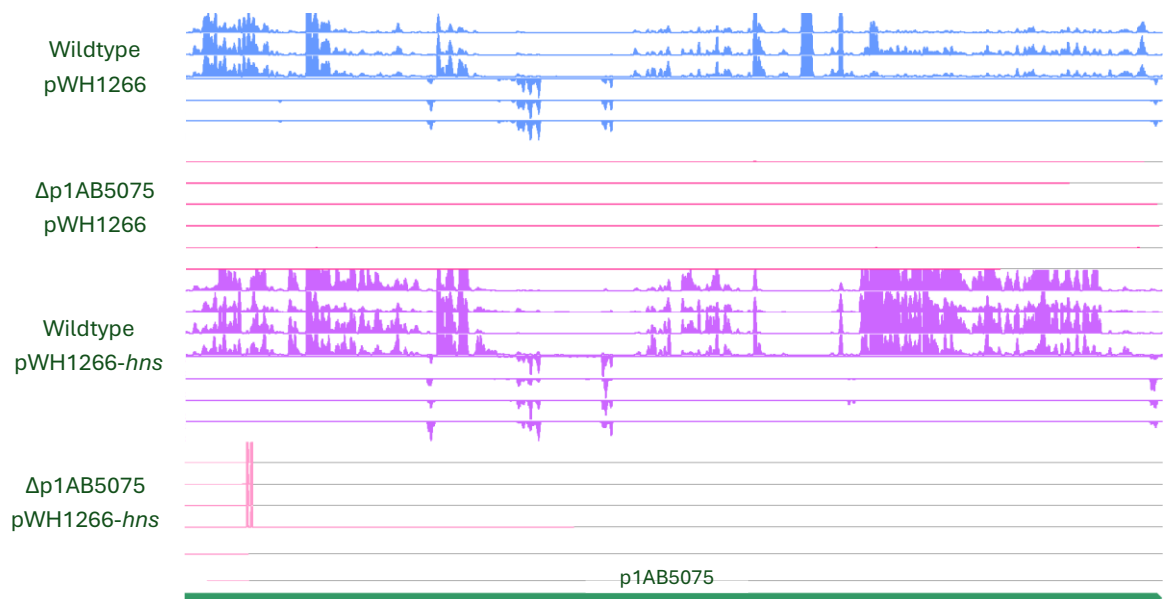


Figure 5.20. Transcripts per million (TPM) of the p1AB5075 plasmid in *A. baumannii* AB5075 strains. Blue – wildtype pWH1266, Dark pink - Δ p1AB5075 pWH1266, Purple – wildtype pWH1266-*hns*, Light pink - Δ p1AB5075 pWH1266-*hns*.

Next, to ensure the RNA quality of the biofilm samples, the expression of housekeeping genes *rpoB* and *rpoC* were analysed (Figure 5.21). No difference in RNA transcript abundance was recorded between the wildtype pWH1266 and Δ p1AB5075 pWH1266 strains. This was expected as housekeeping genes should have stable expression. This consistent expression of *rpoB/C* indicates that the RNA samples were of comparable quality and could be used for further analysis. In contrast, the transcript abundance of *rpoB/C* genes were altered upon the introduction of plasmid-encoded H-NS (Figure 5.21). This was not unexpected as the presence of multiple copies of H-NS may influence the expression of these housekeeping genes, due to its role as a global transcriptional regulator (62).

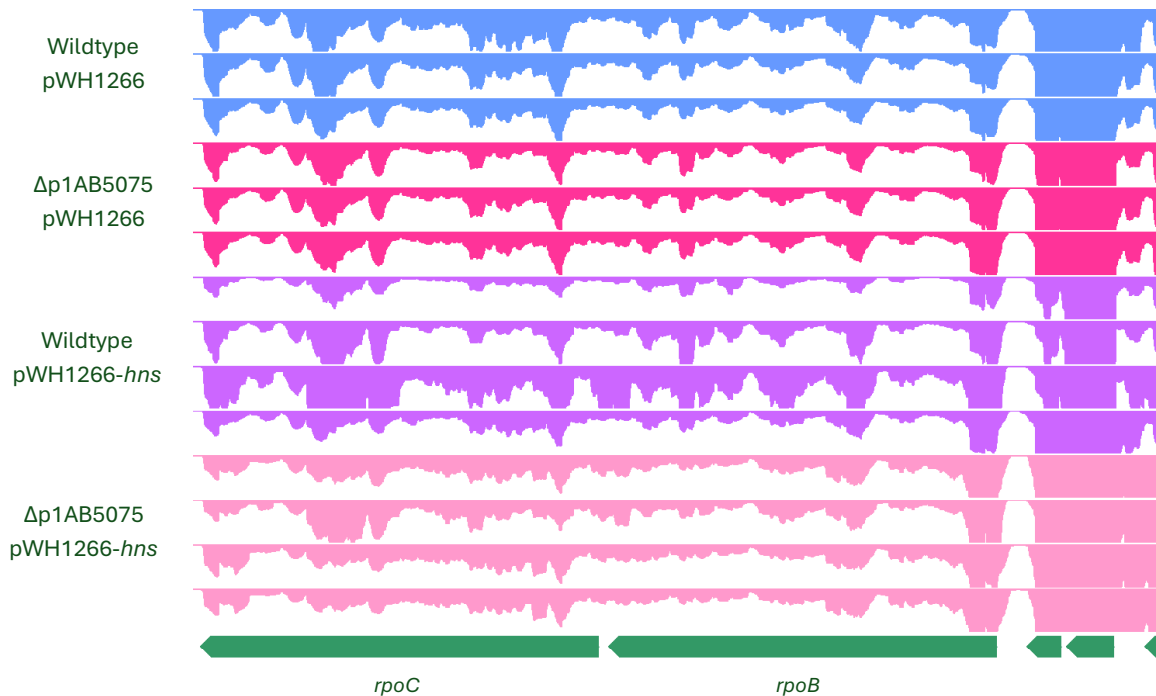


Figure 5.21. Transcripts per million (TPM) of the *rpoB* and *rpoC* genes in *A. baumannii* AB5075 strains. Blue – wildtype pWH1266, Dark pink - Δ p1AB5075 pWH1266, Purple – wildtype pWH1266-hns, Light pink - Δ p1AB5075 pWH1266-hns.

The *csu* operon was chosen for analysis as it is a key gene for optimal biofilm formation (Figure 5.22). Interestingly, a high degree of heterogeneity in gene expression for the *csu* operon was noted in the wildtype pWH1266 strain. This was unexpected as all RNA samples were isolated from the same condition thus, TPM values were expected to be consistent across sampling. However, this heterogeneity is not seen in the Δ p1AB5075 pWH1266 strain.

This may explain the patches of biofilm matrix on the Congo red and Coomassie blue plates (Figure 5.11). Upon the loss of the p1AB5075 plasmid *csu* gene expression appears to be stable (Figure 5.22). On average the *csu* operon has a lower level of expression in the Δ p1AB5075 pWH1266 strain compared to the wildtype. This may account for the reduction in adherence previously seen in this strain (Figure 5.3). For both strains overexpressing *hns*, the *csu* operon is significantly repressed (Figure 5.20). This was in agreement with previous biofilm formation experiments that showed that both strains produce much less biofilm (Figure 5.9-5.11).

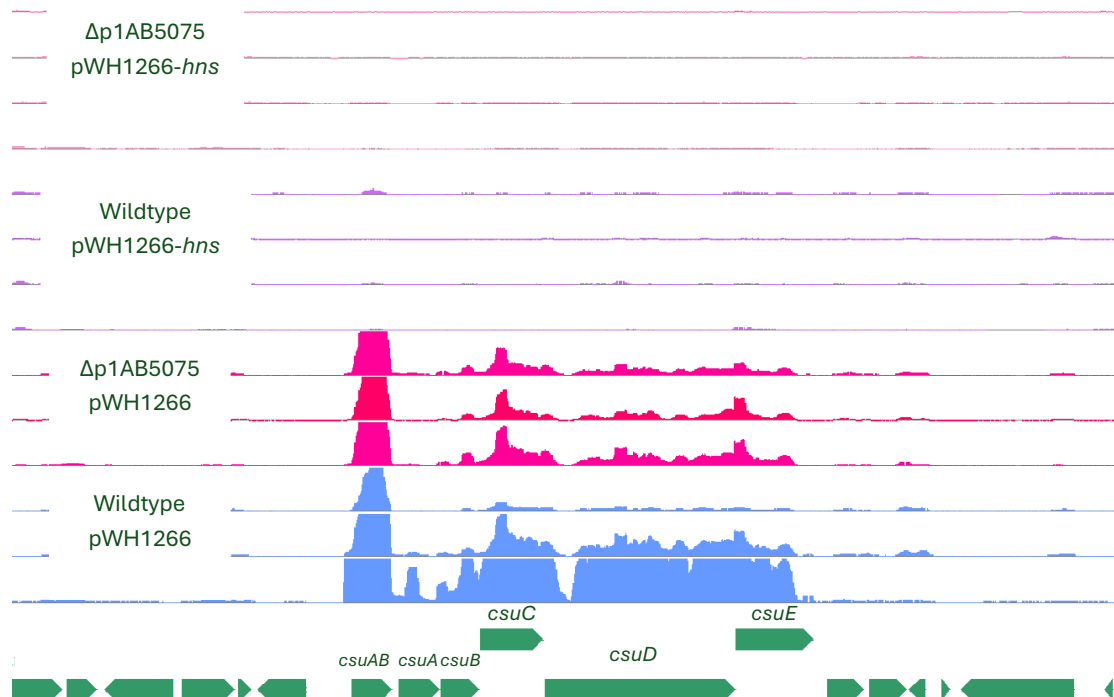


Figure 5.22. Transcripts per million (TPM) of the *csu* operon in *A. baumannii* AB5075 strains. Blue – wildtype pWH1266, Dark pink - Δ p1AB5075 pWH1266, Purple – wildtype pWH1266-*hns*, Light pink - Δ p1AB5075 pWH1266-*hns*.

The type 1 fimbrial pilus is also involved in *A. baumannii* adherence and hence, its expression was examined under biofilm expression (Figure 5.23). Similarly, the average TPM of wildtype pWH1266 revealed increased expression of the gene compared to Δ p1AB5075 pWH1266. However, the high degree of heterogeneity was also noted in the gene expression for wildtype pWH1266, this was not seen for Δ p1AB5075 (Figure 5.23). The reintroduction of *hns* into the Δ p1AB5075 background revealed increased expression of the type 1 fimbrial protein indicating a higher capacity for adherence. The same observation can be seen for *hns* in the wildtype background (Figure 5.23). While expression of this gene is increased the heterogeneity between wildtype pWH1266-*hns* samples is also seen similar to the wildtype pWH1266 strain. This indicates that upon loss of the p1AB5075 plasmid, heterogeneity of biofilm associated genes is limited.

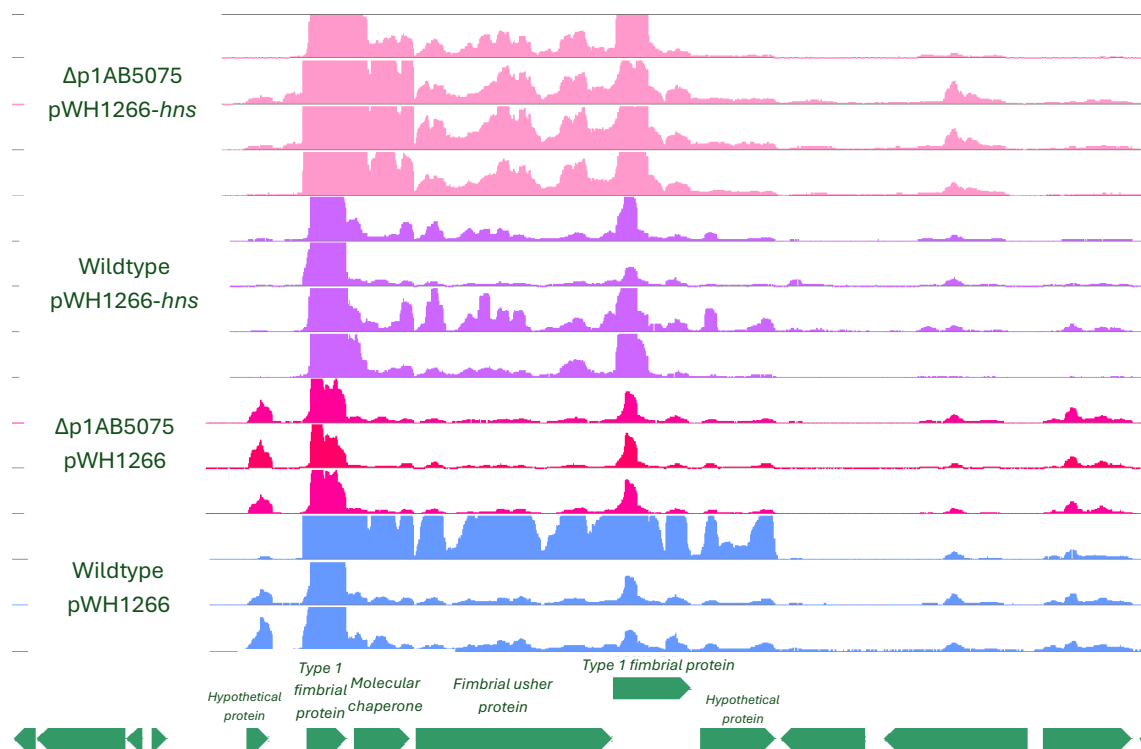


Figure 5.23 Transcripts per million (TPM) of type 1 fimbrial pilus operon encoding genes in *A. baumannii* AB5075 strains. Blue – wildtype pWH1266, Dark pink - Δ p1AB5075 pWH1266, Purple – wildtype pWH1266-*hns*, Light pink - Δ p1AB5075 pWH1266-*hns*.

The *pga* operon encoding PNAG an important factor of biofilm formation was examined (Figure 5.24). Overall, the *pga* operon were upregulated in the wildtype pWH1266 strain compared to Δ p1AB5075 pWH1266. However, a high degree of heterogeneity between samples is noted for the wildtype pWH1266 and the wildtype pWH1266-*hns* strains potentially skewing the data. This reinforces the hypothesis that the loss of p1AB5075 plasmid is linked to stable gene expression for biofilm associated genes. The Δ p1AB5075 pWH1266-*hns* strain exhibits a gene expression profile similar to the wildtype pWH1266 strain, with the exception of one wildtype pWH1266 sample (Figure 5.24).

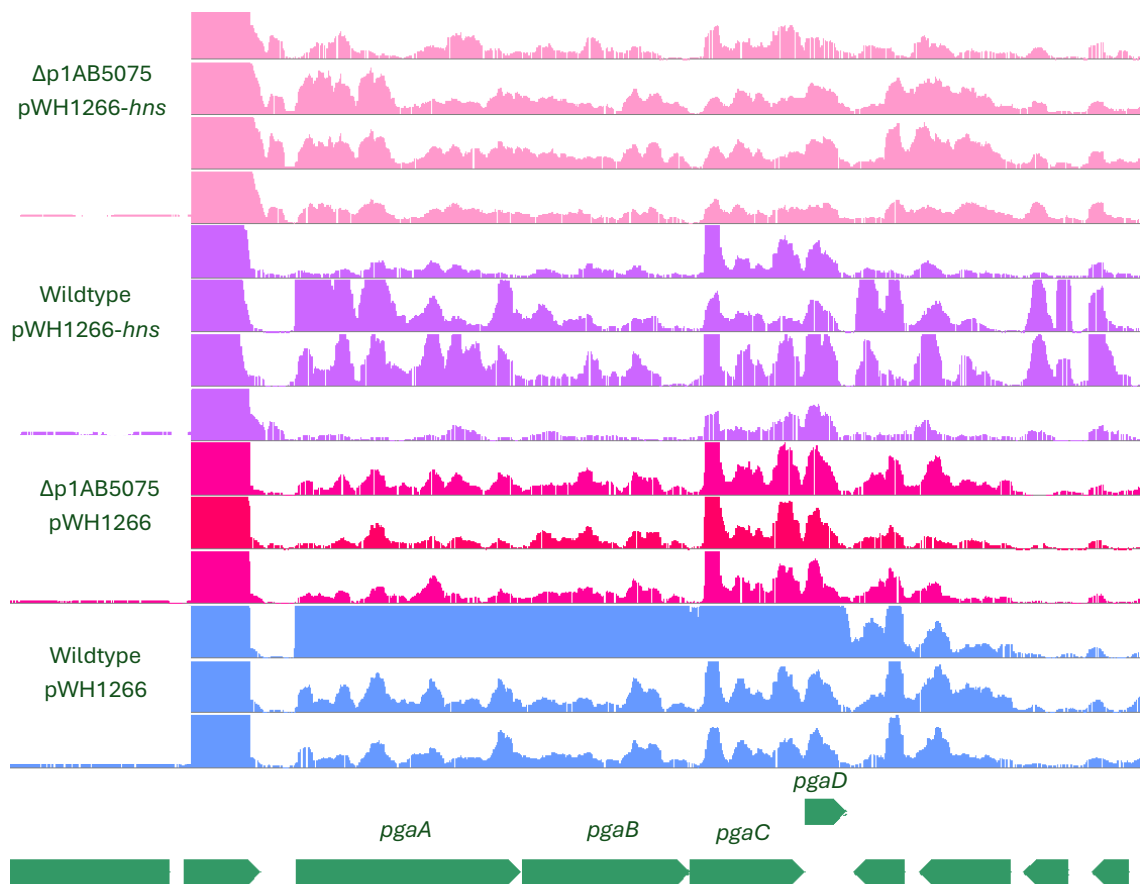


Figure 5.24 Transcripts per million (TPM) of *pga* operon in *A. baumannii* AB5075 strains. Blue – wildtype pWH1266, Dark pink - Δ p1AB5075 pWH1266, Purple – wildtype pWH1266-*hns*, Light pink - Δ p1AB5075 pWH1266-*hns*.

Due to the type VI secretion system showing differential expression between the *A. baumannii* strains (Appendix II), this gene was also examined as an important virulence factor in *A. baumannii* (Figure 5.25). Interestingly, the high degree of heterogeneity in gene expression was not seen in the wildtype pWH1266 strain as previously seen for other differentially expressed genes (Figure 5.22-5.24). Both the wildtype pWH1266 and Δ p1AB5075 pWH1266 expression levels are similar in comparison. Heterogeneity appears to be apparent in a select number of genes when the p1AB5075 plasmid is present. Both the *hns* overexpression strains show significant repression of the T6SS (Figure 5.25). This is important as genes on the accessory genome may directly influence major virulence factors located on the genome.

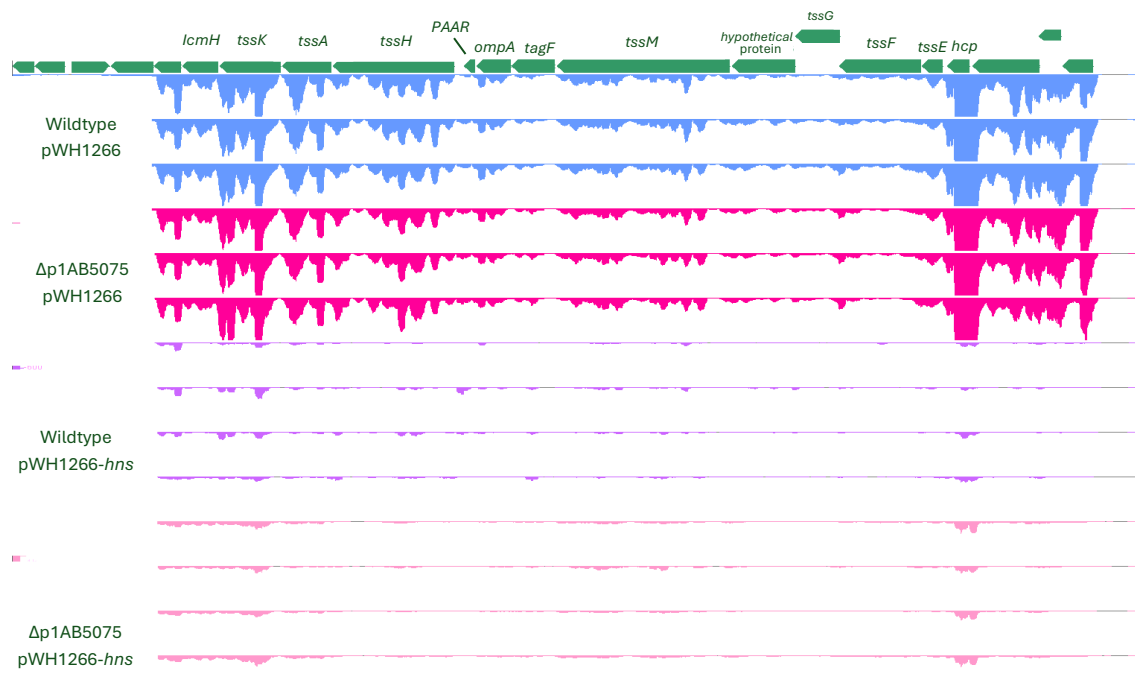


Figure 5.25 Transcripts per million (TPM) of type VI secretion system in *A. baumannii* AB5075 strains. Blue – wildtype pWH1266, Dark pink - Δ p1AB5075 pWH1266, Purple – wildtype pWH1266-*hns*, Light pink - Δ p1AB5075 pWH1266-*hns*.

Additionally, the expression of antimicrobial resistance genes present on the AB5075 chromosome are altered in the presence of plasmid-encoded H-NS and p1AB5075 (Appendix II). As *A. baumannii* AB5075 is notorious for its carbapenem resistance, the carbapenemase genes OXA-23 and OXA-51/69 and their associated insertion elements with potential promoter activity were examined further (Table 5.8). It appears that expression of these OXA genes are influenced by the overexpression of H-NS and whether p1AB5075 is present. In the Δ p1AB5075 background, H-NS overexpression resulted in a downregulation of both OXA-23 and OXA-51/69 (Table 5.8). This suggests that plasmid-encoded H-NS may act either directly or indirectly as a repressor for carbapenemase expression in the absence of p1AB5075. However, this repression was not observed when p1AB5075 was present (Table 5.8). These findings suggest that the p1AB5075 plasmid may encode a carbapenemase regulatory factor or that the presence of plasmid mitigates H-NS repression through competitive binding.

Several insertion elements also displayed altered expression in these strains such as ISAb1, ISAb26 and ISAb13 (Table 5.8). Insertion elements are known to carry promoters for carbapenemase resistance genes in *A. baumannii* (118). Upon the loss of p1AB5075 and the overexpression of p1AB5075-encoded H-NS, insertion elements ISAb1, ISAb26 and ISAb13 were upregulated compared to the Δ p1AB5075 background (Table 5.8). A similar effect was seen for ISAb1 in the wildtype background upon H-NS overexpression (Table 5.8). This is consistent with previous studies showing that H-NS regulates the transcription of horizontally acquired DNA and mobile genetic elements (62), suggesting that p1AB5075-encoded H-NS regulates IS element expression in *A. baumannii* AB5075. However, the ISAb23 and ISAb13 elements were downregulated in the wildtype pWH1266-*hns* strain compared to the wildtype pWH1266 (Table 5.8). It appears that the presence of p1AB5075 alongside the level of H-NS expression maintains the levels of insertion element expression.

Overall, these changes in insertion elements did not correlate with OXA expression suggesting that regulation is not solely attributed to IS elements. Instead the expression of H-NS and the presence of p1AB5075 plasmid play a role in regulating OXA carbapenemase genes in *A. baumannii* AB5075.

Table 5.8. Differentially expressed carbapenemase genes and ISA insertion elements in response to plasmid-encoded H-NS overexpression and p1AB5075 deletion under biofilm conditions.

product	Wildtype pWH1266-hns vs wildtype pWH1266 log2- fold change	Wildtype pWH1266-hns vs Δ p1AB5075 pWH1266-hns log2-fold change	Wildtype pWH1266 vs Δ p1AB5075 pWH1266 log2- fold change	Δ p1AB5075 pWH1266-hns vs Δ p1AB5075 pWH1266 log2- fold change
OXA-23	0.30	2.07	-0.21	-1.98
OXA-51/ OXA-69	-0.70	1.33	0.25	-1.79
ISAbal	2.33	0.44	-0.06	1.82
ISAbal26	-1.89	-3.04	0.28	1.43
ISAbal13	-1.76	-2.84	0.52	1.60

Chapter 6 – Discussion

6.1 Chloramphenicol resistance in *A. baumannii* AB5075

One of the reasons that chloramphenicol was chosen for antibiotic resistance analysis in *A. baumannii* was the presence of transient chloramphenicol resistance (8). While *A. baumannii* is genetically resistance to chloramphenicol, through nutrient deprivation a portion of the *A. baumannii* ATCC17978 population became sensitive to chloramphenicol (8). The functions of *craA* and *cxpE* have been determined to be chloramphenicol resistance efflux pumps (4, 5, 7, 70). However, there have been discrepancies on which gene is the major contributor of chloramphenicol resistance in different *A. baumannii* strains (7). Additionally, *cxpE* is predicted to be a member of the AI-2 exporter superfamily which has been shown to play a role in biofilm formation and motility (74, 93, 94). In this study, we aimed to clarify whether it is *craA* or *cxpE* that plays a key role in maintaining chloramphenicol resistance in *A. baumannii* AB5075 and if *cxpE* plays a role in any other cellular processes.

6.1.1 Investigation of *craA* and *cxpE* efflux pumps on antibiotic resistance in *A. baumannii* AB5075

Kirby-Bauer analysis was performed to test whether *craA* or *cxpE* that is a major contributor to intrinsic chloramphenicol resistance in *A. baumannii* (Table 3.1). Interestingly, both individual Δ *craA* and Δ *cxpE* mutant strains showed no difference to the wildtype strain. In a previous study a *cxpE* transposon mutant in *A. baumannii* AB5075 caused a difference in chloramphenicol resistance recorded through Kirby-Bauer analysis (7). As prior work was done in a transposon generated mutant and not a clean deletion mutant like in this study, it may account for the discrepancy of the result found in this study. This is due to the nature of transposon mutagenesis; additional unintended genomic alterations may arise from mutant construction that are undetected by sequencing the transposon insertion site alone. Additionally, *A. baumannii* strain ATCC19606 was primarily used in determining the substrate specificity of *craA*, while the *cxpE* work was carried out in AB5075 (4, 5). As AB5075 is used in this work, this may account for the phenotypic differences to chloramphenicol resistance as mechanisms can differ between the two strains.

For example, an additional chloramphenicol resistance gene *cmIA5*, which was described during the preparation of this work, is found on the p1AB5075 plasmid in AB5075 but is not present in the ATCC19606 or ATCC17978 strains which may compensate when *craA* is deleted (9). However, in the case of research performed by de Dios *et al.* (2022), *A. baumannii* AB5075 was utilised and a difference in chloramphenicol resistance was noted upon the deletion of *craA* (70). Although chloramphenicol susceptibility was determined by MIC assays which is performed in liquid media rather than Kirby-Bauer assays which utilize solid media.

This may cause the variability in chloramphenicol sensitivity results in *A. baumannii* AB5075, as bacterial cells grow and express genes differently when grown in liquid vs solid media and might compensate for each other to different degrees. Therefore, antimicrobial susceptibility testing of chloramphenicol resistance was repeated in liquid media using MIC assays (Table 3.2). Both the Δ *craA* and Δ *cxpE* strain showed a two-fold reduction in MIC compared to the wildtype *i.e.*, 64µg/mL compared to 128 µg/mL. A two-fold reduction in MIC is insufficient to classify *craA* and *cxpE* as major determinants of chloramphenicol resistance. As antibiotic resistance is often multi-factorial, further investigation involving the deletion of all known CHL resistance genes in this strain, is required before *craA* and *cxpE* can be determined as the primary contributors to CHL resistance. Overall, our results indicate that both *craA* and *cxpE* contribute to chloramphenicol resistance in *A. baumannii* AB5075. However, further in-depth analysis are required to establish the extent of their contribution and whether *craA* and *cxpE* can be classed as potential major chloramphenicol resistance determinants in *A. baumannii*.

Upon investigation into bacterial fitness the loss of *craA* and *cxpE* showed no significant alteration to the growth capacity of *A. baumannii* AB5075 under optimal growth conditions (Figure 3.3.A). However, when sub-inhibitory levels of chloramphenicol were added to the growth medium growth defects were prevalent once *craA* was absent from the cell. In the Δ *craA* strain an extended lag phase was recorded compared to the wildtype before a normal growth pattern resumed (Figure 3.3.B). This growth defect was absent in the Δ *craA* pWH1266-*craA* strain proving that this extended lag phase was a result of the loss of *craA* (Figure 3.4.B).

Ultimately, the $\Delta craA$ strain grows and has a final optical density value similar to the wildtype strain most likely due to the presence of other chloramphenicol resistance genes that needed additional time to be expressed and functioning in the cell. One hypothesis for this prolonged lag phase is that *craA* aids in the rapid adaptation to chloramphenicol exposure. Growth defects were noted in the $\Delta craA$ pWH1266-*craA* strain when grown in L-broth supplemented with 12 $\mu\text{g/mL}$ of tetracycline (Figure 3.4.A).

This was unusual as the $\Delta craA$ pWH1266 strains growth was comparable to wildtype pWH1266 (Figure 3.4.A). Tetracycline is required in the media for plasmid retention. The plasmid copy number of pWH1266 is unknown in *A. baumannii* therefore, multiple copies of the *craA* gene is present in the genome compared to the single copy of *craA* on the chromosome. One reason for this negative impact on growth is that *craA* is highly expressed upon exposure to chloramphenicol and tetracycline thus, extended exposure to tetracycline present in the media triggers the *craA* gene to be constitutively expressed which may impact bacterial fitness through excessive membrane protein production.

Similarly, the $\Delta cxpE$ strain only had a growth defect when sub-inhibitory concentrations of chloramphenicol were present in the media (Figure 3.3.B). Interestingly the $\Delta cxpE$ strain prematurely entered stationary phase compared to the wildtype strain and this is the growth phase that *cxpE* is most highly expressed in *A. baumannii* AB5075. Exponential phase is where the bacterial cells are most metabolically and proliferatively active, thus where the effects of the translational inhibition antibiotic chloramphenicol will be felt most in the bacterial cells. Other chloramphenicol resistance mechanisms can combat the effects of chloramphenicol in the early stages of growth e.g., *craA* (4, 5, 70). However, *cxpE* appears to play a significant role in the efflux of chloramphenicol in stationary phase, with the loss of *cxpE* the bacterial cell cannot combat the chloramphenicol stress and exits the exponential phase early. Normally a lack of nutrients would trigger the cells to enter stationary phase, this is not the case as the wildtype continues to grow. This indicates that this premature enter into stationary phase is based on the efficiency of chloramphenicol inhibiting protein synthesis.

These results suggest that upon exposure to chloramphenicol *cxpE* may play a role in maintaining sustained optimal growth of *A. baumannii* in antibiotic stress conditions through efflux, given the fitness cost exhibited by *A. baumannii* in this gene's absence.

The Δ *cxpE* pWH1266 also displayed a growth defect in sub-inhibitory levels of tetracycline (Figure 3.4.A), similar to the growth of Δ *cxpE* pWH1266 in sub-inhibitory concentrations of chloramphenicol (Figure 3.3.B).

The growth defect for the Δ *cxpE* pWH1266-*cxpE* strain was unexpected as *cxpE* expression is not altered in the presence of tetracycline and no data has indicated that tetracycline is exported by this protein (Figure 3.2)(7). Both conditions where the loss of *cxpE* results in a growth defect has an antibiotic that inhibits translation in the media. Previously, *cxpE* has been speculated to aid in the enhancement of other efflux pumps in *A. baumannii* (7). This data may reinforce this hypothesis as although the cells have been equipped with a tetracycline resistance gene on the plasmid *i.e.*, *tetA*, they still show a reduced growth capacity. This may be due to the lack of *cxpE* to help export the antibiotic across the inner membrane and aid other efflux pumps in their activity. Again, this growth defect arises once the cells reach late exponential phase and enter stationary phase prematurely where *cxpE* is expressed highly in *A. baumannii* (Figure 3.2).

This reinforces the hypothesis that *cxpE* aids in the long term adaptation to antibiotic stress in *A. baumannii*. Upon complementation of *cxpE* in the Δ *cxpE* background this growth defect is lost (Figure 3.4.A). In the presence of chloramphenicol, the Δ *cxpE* pWH1266 strain still retains the growth effect previously (Figure 3.3.B). However, upon complementation with *cxpE* this growth defect is eradicated (Figure 3.4.B). This indicates that *cxpE* is involved in maintaining chloramphenicol resistance in stationary phase in *A. baumannii* AB5075. Also, that *cxpE* may be advantageous in maintaining high levels of antibiotic resistance by aiding other efflux pumps in their activity as seen upon exposure to tetracycline.

In contrast, the $\Delta craA\text{-}\Delta cpxE$ strain displayed compared growth to the wildtype strain in the presence of sub-inhibitory levels of chloramphenicol. This suggests that when *craA* and *cpxE* are both absent from the cell, rapid adaptation and maintenance of chloramphenicol resistance is achieved by *A. baumannii* through alternative chloramphenicol resistance mechanisms, possibly by the p1AB5075-encoded *cmlA5* (9). The fact that the double deletion performed better than the individual mutants hints towards a complex regulatory network of multiple, interconnected and redundant chloramphenicol resistance mechanisms.

For example, amplification of a region between two intergrases on p1AB5075 containing *cmlA5* has been shown to undergo amplification causing aminoglycoside heteroresistance due to *aadB* (11). Thus, amplification of this region *i.e.*, *cmlA5* may compensate for the lack of *craA* and *cpxE*. Only a triple mutant of *craA*, *cpxE* and *cmlA5* can confirm this hypothesis. Both *craA* and *cpxE* are efflux pumps, although the loss of these genes showed no impact on membrane permeability in *A. baumannii* AB5075 (Figure 3.5). This result was not unexpected as many efflux pumps are encoded in the *A. baumannii* genome which may account for the lack of *craA* and *cpxE* efflux (21).

Overall, both *craA* and *cpxE* are contributors to chloramphenicol resistance in *A. baumannii*. The *craA* gene aids in rapid adaptation to chloramphenicol exposure. While the *cpxE* gene is beneficial for the maintenance of chloramphenicol resistance in late stages of growth in *A. baumannii* AB5075.

6.1.2 The effect of *craA* and *cpxE* on motility and biofilm formation in *A. baumannii*

Several cellular processes such as motility and biofilm formation are influenced by members of the AI-2 exporter superfamily (74, 94). It is important to note that motility and biofilm formation are complex mechanisms and are regulated on multiple levels in *A. baumannii*. The quorum sensing system *abaI-abaR* and two component system *bfmRS* has also been shown to play a role in regulation of biofilm and motility in *A. baumannii*. Motility was analysed to see if the loss of AI-2 exporter homolog *cpxE* had an impact in *A. baumannii*.

DNA uptake needed for horizontal gene transfer is dependant on twitching motility in *A. baumannii* (107, 108). Accordingly, alterations in motility may influence the future development of antimicrobial resistance potential of *A. baumannii*. The Δ *craA* strain showed no significant change in motility when compared to the wildtype (Figure 3.6). This was in line with previous work that showed that this efflux pump has no effect on motility (4, 5, 70). In contrast, both the Δ *cxpE* and Δ *craA*- Δ *cxpE* strains showed a significant reduction in motility (Figure 3.6). As AI-2 exporters are frequently involved in the regulation of motility this result was not suprising (74).

For example, TqsA which CxpE shows protein sequence similarity to acts as a repressor of motility and biofilm in *Escherchia coli* (94). *E. coli* utilises flagella for motility and can move in a series of runs and tumbles (119). In contrast, *A. baumannii* lacks flagella and instead relies on type IV pili for twitching motility. In this case *cxpE* may enhance bacterial movement, as the loss of *cxpE* demonstrates a reduction in motility (Figure 3.6). This suggests that *cxpE* contributes to the regulation of motility in *A. baumannii* AB5075. Interestingly, although TqsA and CxpE are related proteins and appear to influence motility, they are associated with distinct motility mechanisms in different bacterial species. Consequently, *cxpE* may also impact the ability to uptake exogenous DNA from the enviroment, influencing the antimicrobial resistance development *A. baumannii* AB5075 through horizontal gene transfer. Future analysis on the DNA uptake ability of Δ *cxpE* would be valuable to explore further.

As *cxpE* was shown to play a role in motility its ability to regulate biofilms was also assessed (Figure 3.7). No significant change in biofilm formation was noted for either Δ *craA* or Δ *cxpE* in both nutrient rich and nutrient deprived media. These results are in agreement with the literature for *craA* which does not play a role in other cellular processes beside antimicrobial efflux (4, 5, 70). In the case of Δ *cxpE*, this result was unexpected as it is a homolog of the AI-2 exporter TqsA (7). TqsA has been shown to influence biofilm formation in *E. coli* and *Klebsiella pneumoniae* through the regulation of polysaccharide synthesis and biofilm associated genes (74, 94, 120, 121).

However, our results indicate that CxpE does not play a major role in biofilm formation in *A. baumannii* AB5075. These findings suggest that although CxpE shares a domain with TqsA, its function is distinct in *A. baumannii* AB5075, contributing to motility but not biofilm formation.

Despite the individual mutants showing no effect on biofilm formation, the Δ *craA*- Δ *cxpE* double mutant strain showed a significant reduction in biofilm formation in nutrient rich and deprived media at 37°C (Figure 3.7). The combined interruption of membrane transport alteration and AI-2 signalling appears to amplify the biofilm defect. The mechanism behind this Δ *craA*- Δ *cxpE* biofilm phenotype is not understood and further investigation is needed to test whether there is a connection between *craA*-related efflux and quorum sensing.

6.1.3 Transient chloramphenicol resistance in *A. baumannii* AB5075

Transient chloramphenicol resistance is a phenomenon that has been identified in *A. baumannii* ATCC17978 (8). This phenomenon is where upon culturing of *A. baumannii* in minimal media a portion of the population becomes sensitive to sub-inhibitory levels of chloramphenicol over an extended period of time, this process is reversible and not due to gene mutation. One gene candidate speculated to be involved in this process was identified to be *craA* through qPCR analysis (8).

This transient resistance experiment was optimised in this study for analysis of *A. baumannii* AB5075 strains. No significant reduction in the resistance population for the *A. baumannii* mutant strains compared to the wildtype was detected for the first 48 hours of the experiment (Figure 3.8). However, after 72 and 96 hours a significant decrease in fold change of ~1.8 and ~2.5 correlating to the resistant population was seen for the Δ *craA* strain. The decrease in fold change correlates to a reduction in the proportion of resistant cells in the population. Upon reintroduction of *craA* into the Δ *craA* background, this phenotype is lost, and the strain behaves like the wildtype. This indicates that *craA* is required for the rapid adaptation to chloramphenicol exposure and may be responsible for the transient chloramphenicol resistance phenomenon. The wildtype also shows a decrease of ~0.5-fold change indicating that over time the proportion of the resistant population is declining in the wildtype *A. baumannii* AB5075 strain (Figure 3.8).

This was in agreement with published data as this decrease in the resistance population was also recorded for the *A. baumannii* ATCC17978 strain indicating that this transient resistance phenotype may be present in additional *A. baumannii* strains (8). One hypothesis for the reduction in fold change in the resistant population seen for the wildtype and complementation mutant strains, is lack of energy required to power chloramphenicol efflux pumps as many efflux pumps including *craA* rely on a proton motive force to provide chloramphenicol efflux. In *A. baumannii* grown in nutrient limited environments, chloramphenicol efflux proteins may be present in the cell, but may not be rapidly powered on upon exposure to chloramphenicol. It is also not known what the abundance and turnover rate for CraA and CxpE proteins in the membrane are when not exposed to chloramphenicol. While the absence of *cxpE* had no effect on the maintenance of the resistant population, the colony morphology of the Δ *cxpE* strain was altered compared to the wildtype (Figure 3.9). The Δ *cxpE* strain showed a mucoid colony phenotype although the mechanisms behind this still need to be elucidated.

CraA and CxpE proteins were visualised via western blot at each time point in the transient resistant growth experiment to see if they were present during growth in minimal media (Figure 3.11). Western blot analysis revealed that both CraA and CxpE were present during growth in minimal media over 96 hours. This concludes that CraA is present in the bacterial cells maybe be non-functional. This reinforces the hypothesis that CraA is present but cannot be powered likely due to a lack of energy required to power the proton motive force for the efflux of chloramphenicol, leading to the transient resistance phenomenon in *A. baumannii* AB5075. Future experiments could assess the differences in proton gradients across the membrane.

6.1.4 Investigation of *cbl* as a potential regulator for *craA* in *A. baumannii* AB5075

Currently, the regulation of both *craA* and *cxpE* are unknown in *A. baumannii* (4, 5, 7, 70), except for the cysteine biosynthesis gene *cbl*, which was identified as a potential regulator in *A. baumannii* (73). Previous work has recorded a 6.7-fold increase in expression of *craA* was recorded upon deletion of *cbl* in *A. baumannii* (73).

In this study, mutants of $\Delta cbl::sacB-aacC4$, $\Delta cbl::sacB-aacC4-\Delta craA$ and $\Delta cbl::sacB-aacC4-\Delta xcpE$ were constructed to investigate if *cbl* regulated either *craA* or *xcpE*. No significant change in chloramphenicol resistance was noted in the $\Delta cbl::sacB-aacC4$ deletion strain compared to the wildtype (Table 3.3). This was surprising as if *cbl* is absent from the cell, it is expected that *craA* should be upregulated and potentially increase the MIC of the strain based on previous findings (73). This indicates that *cbl* may still regulate *craA* however, other regulatory mechanisms may also regulate *craA* and act on the gene when *cbl* is not present. Surprisingly, the double deletion of $\Delta cbl::sacB-aacC4-\Delta craA$ also showed no change in MIC in comparison to the wildtype (Table 3.3). It was expected to see a reduction in MIC similar to the individual mutant of $\Delta craA$ (Table 3.2). One reason may be that if *cbl* regulates *craA* it may also regulate other chloramphenicol resistance genes which can compensate for the lack of *craA*.

Similarly, $\Delta cbl::sacB-aacC4-\Delta xcpE$ exhibited no reduction in MIC (Table 3.3). This would indicate that the hypothesis that *cbl* is a regulator of *craA* based on previous findings is true. If the deletion of *cbl* upregulates *craA* in $\Delta cbl::sacB-aacC4-\Delta xcpE$ mutant, it may compensate for the lack of *xcpE* and that is why a 2-fold reduction is not observed as previously seen for the $\Delta xcpE$ strain (Table 3.2).

To confirm if *cbl* regulates *craA* expression, growth in sub-inhibitory concentrations of chloramphenicol was analysed for growth defects (Figure 3.12.B). The $\Delta cbl::sacB-aacC4$ strain had a similar growth profile to the wildtype as expected. However, both the $\Delta cbl::sacB-aacC4-\Delta craA$ and $\Delta cbl::sacB-aacC4-\Delta xcpE$ showed the same growth defects as previously seen in the individual mutants $\Delta craA$ and $\Delta xcpE$ (Figure 3.3.B). If *cbl* did regulate *craA* the growth defect seen in $\Delta cbl::sacB-aacC4-\Delta xcpE$ should be reduced or eradicated as *craA* compensates for the lack of *xcpE*. This indicates that *cbl* is not a regulator of the chloramphenicol efflux pump *craA*.

6.2 Antimicrobial resistance genes on the p1AB5075 plasmid

On the p1AB5075 plasmid in *A. baumannii* AB5075 there are several antibiotic resistance genes (9). This study has chosen to focus on eight of p1AB5075 plasmid genes; *aph(3')-VI*, *aac(6')-Ib3*, *aadB*, *aadA2*, *strA*, *strB*, and *bla_{GES-11}* for their individual contribution to the MDR profile of *A. baumannii* AB5075. Rarely, these genes are assessed for their individual antimicrobial resistance potential and are often examined by complete deletion of resistance island 2 or as an operon (11, 70, 77, 102). Antimicrobial susceptibility testing was performed for each individual gene complemented into the Δ p1AB5075 background (Table 4.2-4.3). Upon loss of the p1AB5075 plasmid complete sensitivity to gentamicin, amikacin, tobramycin, kanamycin, streptomycin, trimethoprim-sulfamethoxazole, ceftazidime and cefepime was recorded compared to the wildtype strain. The gene *aadB* plays a role in kanamycin, gentamicin and tobramycin resistance. Amikacin and kanamycin resistance is primarily associated with *aph(3')-VI*. The role of *aacA4/aac(6')-Ib3* has been validated for amikacin, kanamycin and tobramycin. Additionally, an increase in gentamicin resistance was observed in overexpression of *aacA4/aac(6')-Ib3*. This has not been noted before in *A. baumannii*. The *aac(6')-Ib* family acetyltransferases are typically associated with resistance to amikacin but not gentamicin (122). However, *aac(6')-Ib* acetyltransferases isolated from *Pseudomonas aeruginosa* have been shown to have a high affinity for amikacin and only a weak affinity for gentamicin (122). Additionally, *aacA4/aac(6')-Ib3* was first reported as a plasmid-encoded acetyltransferase in *P. aeruginosa* (122).

It can be hypothesised that the copy of *A. baumannii* AB5075 *aac(6')-Ib3* may share the same substrate binding affinities. Therefore, the *aacA4/aac(6')-Ib3* may have a low affinity for gentamicin but the overexpression of this gene can compensate for the reduced affinity and provide low levels of gentamicin resistance in *A. baumannii*. Further investigation is required to determine the binding affinity of plasmid-encoded *aacA4* gene from *A. baumannii* AB5075 for gentamicin.

Both *aadA2* and *strA* play a crucial part in maintaining streptomycin resistance. No phenotype was associated with complementation of *strB* in the p1AB5075 deletion mutant.

This was unexpected as *strB* had been shown to convey low levels of streptomycin resistance when expressed as an individual gene in the gram-negative bacterium *Erwinia amylovora* (101). However, *E. amylovora* and *A. baumannii* are distinct bacterial species belonging to different genera and the regulation of resistance mechanisms can differ.

Finally, *bla_{GES-11}* is critical for cefepime resistance in *A. baumannii* AB5075. Overall, each of the genes investigated play crucial roles in maintaining antibiotic resistance in *A. baumannii* AB5075.

6.3 Plasmid-mediated biofilm formation in *A. baumannii* AB5075

6.3.1 The effect of Δ p1AB5075 on virulence in *A. baumannii*

Pili are filamentous structures located on the outside of bacterial cells that aid in motility, initial biofilm attachment and are essential for the uptake of DNA for horizontal gene transfer (18, 53, 107, 108). Upon deletion of the p1AB5075 plasmid a significant decrease in motility was observed (Figure 5.1). This indicates that pili genes are downregulated in the Δ p1AB5075 strain which may also affected biofilm formation. A similar response has been reported in *Vibrio parahaemolyticus*, where the absence of H-NS resulted in a reduced swimming motility due to insufficient activation of motility associated genes (124). One hypothesis is that a regulatory factor may be present on the p1AB5075 plasmid that directly controls pili expression or can interact with known motility regulatory systems such as *BfmRS* or *AbaI-AbaR* (52). Alternatively, the p1AB5075-encoded H-NS can directly influence the expression of motility genes in *A. baumannii* as previously observed in *V. parahaemolyticus* (124). Further investigation into the role of plasmid-encoded H-NS and motility in *A. baumannii* is required.

Previous work indicated that plasmid genes can interact with the chromosome and regulate cellular processes such as biofilm formation in *A. baumannii* (78). A significant increase in biofilm formation was noted in the Δ p1AB5075 strain compared to the wildtype on 96 well polystyrene plates (Figure 5.2).

This result was unexpected as no biofilm associated genes has been identified on the p1AB5075 plasmid to date. Also, the decrease in Δ p1AB5075 motility would indicate that biofilm formation may also be negatively affected due to poor initial attachment to surfaces.

Biofilm formation was increased for Δ p1AB5075 when grown in minimal media compared to L-broth as expected due to additional stress from a nutrient deprived environment on the cells (Figure 5.2). Confocal microscopy of biofilms revealed that adherence to polystyrene was reduced in the Δ p1AB5075 strain compared to the wildtype (Figure 5.3.A-B). Although after 2 days of growth on polystyrene plastic the Δ p1AB5075 strain ultimately produced more biofilm mass than the wildtype strain (Figure 5.3.B-C). However, the architecture of the biofilm was impaired and lacked the density of the wildtype biofilm.

6.3.2 H-NS encoded on the p1AB5075 plasmid engages in regulatory cross-talk with the chromosome to control biofilm formation in *A. baumannii* AB5075

In the urinary isolate *A. baumannii* UPAB, one copy of an H-NS-like gene is encoded on the pAB5 plasmid and has been shown to impact biofilm formation (79). Hence, the p1AB5075-encoded H-NS was chosen for analysis as a potential biofilm regulatory mechanism in *A. baumannii* AB5075. There are two copies of H-NS in the *A. baumannii* AB5075 genome (9, 80). Bioinformatic analysis revealed that the p1AB5075 H-NS shows low amino acid similarity with the AB5075 chromosomal H-NS and the pAB5 H-NS proteins (Figure 5.5-5.7). However, they do share a similar core structure with key amino acid substitutions which may affect the protein-protein interactions and stability that can alter the efficiency in gene silencing (109–111). Amino acid substitutions has been shown to affect biofilm formation in *E. coli*, highlighting the importance of the structure of H-NS and its role in the regulation of biofilm associated genes (125). Therefore, while plasmid-encoded H-NS represses biofilm formation through down regulation of PNAG production in *A. baumannii* UPAB1 (79), its regulatory effects in *A. baumannii* AB5075 may differ due to variations in H-NS structure.

Growth defects are apparent upon the expression of p1AB5075-encoded *hns* in the wildtype and Δ p1AB5075 backgrounds in optimal growth conditions (Figure 5.8.B). Both *hns* strains show an increase in the lag phase, a decrease in the length of the log phase and a lower final bacterial load compared to their respective background strains (Figure 5.8.A). This negatively impacted growth profile is exacerbated when grown in nutrient limiting conditions (Figure 5.8.B).

One hypothesis for this negatively impacted growth profile displayed by the *hns* complementation strains is due to large scale gene dysregulation interrupting normal cellular processes. As H-NS is a global transcriptional regulator and can influence a broad range of genes and thus cellular processes (63), the increased copy number of H-NS is detrimental to the cell.

As biofilm formation has been shown to be affected by H-NS proteins located on plasmids in *A. baumannii* biofilm analysis was performed in minimal media to see if this effect was conserved in *A. baumannii* AB5075 (Figure 5.9-5.11) (79).

The Δ p1AB5075 strain showed a significant increase in biofilm formation at 37°C and this effect was exacerbated when assessed at 30°C (Figure 5.9). Upon reintroduction of the *hns* gene into the Δ p1AB5075 background biofilm formation levels are restored to that of the wildtype strain (Figure 5.9). This indicates that p1AB5075-encoded *hns* is capable of regulating biofilm associated genes and is consistent with the literature which saw UPAB1 pAB5-encoded H-NS regulates biofilm formation (79). Although the UPAB1 pAB5-encoded H-NS and AB5075 p1AB5075-encoded H-NS share low sequence similarity, both regulatory proteins influence the expression of chromosomally-encoded biofilm genes (Table 5.1). This is intriguing as while both H-NS and plasmid content differs between the two strains, H-NS regulating biofilm formation is conserved between the *A. baumannii* strains. The wildtype pWH1266-*hns* strain only showed a significant increase in biofilm formation compared to the wildtype at 30°C (Figure 5.9). Biofilm formation is often induced to protect the bacteria from environmental stress.

We can suggest that from the increased biofilm seen in sub-optimal conditions (Figure 5.9) and the stress that the overexpression *hns* has on wildtype growth in minimal media (Figure 5.8), one hypothesis for this increase in biofilm formation could be due to increased expression of stress response genes, as this increase is only seen when media and temperature conditions are unfavourable to *A. baumannii*.

Biofilm formation was reassessed at a larger volume for visual and quantitative analysis (Figure 5.10). Once a larger volume was used for biofilm analysis the wildtype pWH1266-*hns* strain was comparable to the wildtype in minimal media. The exact mechanism behind this still needs to be elucidated. One reason for this may be the downregulation of adherence factors by H-NS. Biofilm formation may appear inflated due to increased biofilm stability in smaller volumes. Upon increasing to a larger volume with a reduced surface area the adherence of the biofilm is not strong enough to anchor the biomass to the abiotic surface. The Δ p1AB5075 showed increased biofilm formation on both polystyrene and polypropylene surfaces compared to the wildtype, so the effect was not specific to a certain type of plastic surface (Figure 5.10).

This increase in biofilm formation is eradicated with the complementation of *hns* which restores biofilm to wildtype levels (Figure 5.10). Visual analysis of biofilm formation was continued on Congo red and Coomassie blue agar plates (Figure 5.11). Overall the Δ p1AB5075 strain showed increased production of biofilm on the solid agar compared to the wildtype throughout the experiment. A similar colony in *V. parahaemolyticus* morphology was observed, where the loss of H-NS resulted in smooth colonies through alterations in *ci-di-GMP* signalling leading to an increase in EPS production (124, 126).

Both *hns* complementation strains showed a decrease in biofilm production displayed by a rougher and drier colony morphology compared to the wildtype and Δ p1AB5075 mutant (Figure 5.11). However, at 30°C small patches of biofilm was seen for both strains by day 7. This suggests the loss of the pWH1266 plasmid or mutation of the *hns* gene after a prolonged period of time.

Further investigation is required to determine the exact mechanism behind these patches of increased biofilm production.

In conclusion, the loss of p1AB5075 results in a significant increase in biofilm production in *A. baumannii* AB5075. The p1AB5075-encoded H-NS has been identified to be involved in regulatory cross-talk with the chromosome to regulate biofilm formation in *A. baumannii* AB5075.

6.3.3 RNA-sequencing analysis of *A. baumannii* mutants grown in biofilms

Transcriptomic analysis was implemented to better understand the impact of p1AB5075 and the p1AB5075-*hns* on the regulation of biofilm formation in *A. baumannii* AB5075 (Figure 5.13-19). Only three genes were significantly upregulated and one gene significantly downregulated in the wildtype strain compared to the Δ p1AB5075 in the conditions tested (Figure 5.13).

This result was unexpected as a larger change in differentially expressed genes was anticipated due to the significant difference in biofilm phenotypes previously seen (Figure 5.2-5.3, 5.9-5.11). One reason for the lack of diversity in gene expression may be due to the timepoint of sampling for RNA-seq. RNA samples were taken after 2 days of growth in minimal media. This is an extended period of time where the cells have been grown in nutrient limiting conditions and thus, the cells are not metabolically active *i.e.*, transcribing genes and this may reflect the lack of differential gene expression.

The three upregulated genes in the wildtype strain compared to the Δ p1AB5075 were *fimA*, a molecular chaperon and a matrixin family metalloprotease. As the type 1 pilus *fimA* is upregulated in the wildtype a lower rate of adherence is expected for the Δ p1AB5075 strain. Previously, a lack of adherence has been noted in the Δ p1AB5075 strain (Figure 5.3). Thus, we can speculate that reduced expression of the type 1 pilus *fimA* is the cause of the reduced adherence in the Δ p1AB5075 strain. Interestingly, a metalloprotease is downregulated in the Δ p1AB5075 strain. Metalloproteases are a key virulence factor and are utilised by the cell to evade host defence systems (114). This indicates that the virulence potential of Δ p1AB5075 may be impaired, however further testing is required.

The *otsA-otsB* pathway is used for stress response in bacteria (112), OtsB is downregulated in the wildtype strain which may indicate that the strain is operating efficiently and is capable of persisting in the nutrient deprived environment.

Upon the introduction of *hns* into the Δ p1AB5075 background, a total of 595 genes are upregulated and 652 genes are downregulated compared to the Δ p1AB5075 strain (Table 5.2). This shows that H-NS can influence numerous genes on the *A. baumannii* AB5075 chromosome. Out of the top 5 differentially expressed genes up and downregulated, 6 of these genes were hypothetical genes and could not be analysed further (Table 5.3). Upregulated genes that were affected were the replication initiation factor protein and 3-oxoacid coA transferase. These genes are involved in DNA replication and cell metabolism respectively. Downregulated genes were *basJ* and *csuAB*.

The gene *basJ* is a part of the acinetobactin siderophore operon used for iron scavenging in *A. baumannii* (52). This gene may be downregulated in the Δ p1AB5075 pWH1266-*hns* mutant due to low metabolism rates by the cells in late stationary phase. It has been shown that the Δ p1AB5075 pWH1266-*hns* strain has a lower bacterial fitness than the Δ p1AB5075 strain (Figure 5.8). The gene *csuAB* was significantly downregulated in the Δ p1AB5075 pWH1266-*hns* strain. This gene is a part of the *csu* operon which has been shown to directly influence biofilm formation in *A. baumannii* (53).

This reduction in *csu* expression correlates to the reduction in biofilm seen by the Δ p1AB5075 pWH1266-*hns* strain compared to the Δ p1AB5075 strain. GO pathway analysis revealed that several cellular processes such as; metabolism, siderophore biosynthesis, chemotaxis, translation and response to oxidative stress were affected in the Δ p1AB5075 pWH1266-*hns* strain. Due to a significant amount of cellular pathways and apparent growth defects in the Δ p1AB5075 pWH1266-*hns* we can conclude that the overexpression of *hns* in the *A. baumannii* strain causes dysregulation of critical genes in the cell.

A similar effect is seen when comparing wildtype pWH1266-*hns* to the wildtype strain (Figure 5.16). A total of 607 and 457 genes were up and down regulated respectively in the wildtype pWH1266-*hns* strain compared to the wildtype pWH1266 (Table 5.2). These include but are not limited to the upregulation of a ChbG/HpnK family deacetylase, EamA family transporter and a glycotransferase family 2 protein (Table 5.5). These genes are all involved in cellular metabolism and transport (116, 117) indicating the dysregulation of metabolism similar to the Δ p1AB5075 pWH1266-*hns* strain. The *csuA-D* genes were significantly downregulated in the wildtype pWH1266-*hns* strain compared to the wildtype (Table 5.5). This again signifies that the adherence and biofilm capability of the *hns* complementation strain may be impaired. This was only seen for wildtype pWH1266-*hns* biofilm formation on solid media (Figure 5.11).

A total of 583 genes were significantly upregulated, and 310 genes were significantly downregulated in the wildtype pWH1266-*hns* compared to the Δ p1AB5075 pWH1266-*hns* strain (Table 5.2). Several cellular pathways are also differentially expressed between the two *hns* complementation strains. Overall, reinforcing the fact that *hns* causes dysregulation of important cellular processes in the cell which may explain the reduction in growth capacity of these strains (Figure 5.8).

The TPM of the *csu* operon, type 1 fimbrial pilus, *pga* operon and T6SS were chosen for further analysis as important biofilm and virulence factors in *A. baumannii* (18, 53, 64). The *csu* operon was shown to be repressed by the p1AB5075-encoded *hns* (Figure 5.22). Interestingly, the wildtype strain showed heterogeneity in its expression of the *csu* operon. However, this heterogeneity was not seen in the Δ p1AB5075 strain. This may indicate that upon loss of the p1AB5075 plasmid, heterogeneity of biofilm associated genes is limited. This phenomenon was also seen for the wildtype and wildtype pWH1266-*hns* in the type 1 fimbrial operon (Figure 5.23). This heterogeneity was only seen in strains where p1AB5075 was absent. Overall, the expression of type 1 fimbrial protein was reduced in the Δ p1AB5075 strain compared to the wildtype and reintroduction of the *hns* gene into the Δ p1AB5075 background increase expression levels comparable to the wildtype.

As both the *csu* pili and the type 1 fimbrial pili are involved in adherence in *A. baumannii*, the down regulation of these operons in the Δ p1AB5075 strain may explain the reduction in adherence recorded to abiotic surfaces (Figure 5.3.A-B).

For the *pga* operon the Δ p1AB5075 appeared to be downregulated compared to the wildtype strain (Figure 5.24). However, a high degree of heterogeneity is observed for the wildtype pWH1266 and the wildtype pWH1266-*hns* strains. This reinforces the hypothesis that the loss of p1AB5075 plasmid is linked to stable gene expression for biofilm associated genes.

The T6SS is an important virulence factor in *A. baumannii* and previous data has seen that the chromosomal copy of ATCC 19606 H-NS represses the T6SS (64). Additionally H-NS has been shown to directly repress T6SS in *V. parahaemolyticus* (124). Both *hns* complementation strains display significant repression of the T6SS (Figure 5.25). These findings demonstrate the role of H-NS repressing T6SS is also seen in the *A. baumannii* AB5075 strain. Interestingly, the expression of the T6SS did not show a high degree of heterogeneity for strains that contained the p1AB5075 plasmid suggesting that the observed heterogeneous gene expression above is indicating true biological heterogeneity in gene expression and not differences in RNA isolation or the quality of RNA-sequencing. This indicates that this heterogeneity is only present for a select few genes in the *A. baumannii* AB5075 genome under these conditions. This is confirmed through analysis of RNA transcript abundance for housekeeping genes *rpoB/C* (Figure 5.21). No significant difference in expression is noted for *rpoB/C* in the Δ p1AB5075 compared to the wildtype. This is expected as housekeeping genes are constitutively expressed.

Overall, the loss of the p1AB5075 plasmid constitutes to high levels of biofilm formation compared to the wildtype. This phenotype can be rescued by the addition of p1AB5075-encoded H-NS protein. The H-NS protein can regulate a multitude of genes involved in crucial cellular processes and overexpression of H-NS can lead to gene dysregulation that is detrimental to the cell. The H-NS has been shown to regulate many important biofilm genes such as the *csu* operon, type 1 fimbrial protein, *pga* operon and the T6SS involved in *A. baumannii* virulence.

6.4 Conclusion

This research has expanded our understanding of chromosomal-encoded resistance mechanisms and plasmid-mediated regulatory cross-talk of biofilm formation in *A. baumannii* AB5075. This work has demonstrated that chloramphenicol resistance in *A. baumannii* is a multi-factorial process utilising distinct mechanisms that aid in bacterial survival at different stages of growth. Specifically, *craA* aids in the rapid adaptation to chloramphenicol exposure and is a key determinant in the transient resistance phenotype in *A. baumannii*. While *xcpE* appears to contribute to growth maintenance in the presence of antibiotics and may also influence motility. These findings provide a more comprehensive understanding of the role of these efflux pumps and help clarify their contribution to chloramphenicol in *A. baumannii*.

The role of p1AB5075 in conveying high levels of antimicrobial resistance was investigated and confirmed in *A. baumannii* AB5075. Interestingly, this research provided novel insights into the consequences of *aaCA4* overexpression, resulting in an expanded substrate profile and highlighting the potential consequences of the resistance island amplification events that can occur on p1AB5075.

In addition, this study revealed a previously unrecognised role for the p1AB5075 plasmid in the regulation of biofilm formation in *A. baumannii* AB5075. Loss of the p1AB5075 plasmid resulted in altered adhesion and biofilm formation demonstrating that the accessory genome can contribute to virulence associated phenotypes. Furthermore, plasmid-encoded H-NS was shown to engage in regulatory cross-talk with the AB5075 chromosome to regulate biofilm associated genes and the type VI secretion system. These findings suggest that the dissemination of the p1AB5075 plasmid can have consequences beyond the spread of antibiotic resistance genes.

Chapter 7 – References

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Chapter 8 – Appendices

Appendix I - Oligonucleotides in this study

Name	Sequences (5' – 3')	Purpose
sacB-aacC4 F	cgactcactatagggcgaattgggcc gctttccagtcgggaaacctg	P5 amplification of sacB-aacC4 selection cassette
sacB-aacC4 R	catatgccaccgacccgagcaaacc cgccagggtttcccagtcacgac	P6 amplification of sacB-aacC4 selection cassette
craA_UP_F	tgtctcagcaattcggac	P1 Deletion of craA in <i>A. baumannii</i>
craA_UP_R	ggcccaattcgccctatagtgcg aatagcggccactatgtc	P2 Deletion of craA in <i>A. baumannii</i>
craA_DOWN_F	gggtttgctcgggtcgggtggcatatg gaaagagttgcacaagacttac	P3 Deletion of craA in <i>A. baumannii</i>
craA_DOWN_R	attgctgctgcacttactg	P4 Deletion of craA in <i>A. baumannii</i>
craA_UP_R Clean deletion	aatagcggccactatgtc	P7 Deletion of craA in <i>A. baumannii</i>
craA_DOWN_F Clean deletion	gacatagtgccgctattgaaagagttgcacaagacttac	P8 Deletion of craA in <i>A. baumannii</i>
CraA F deletion check	tttgtgggctcagaaacc	Sanger sequencing check of craA fragment size
CraA R deletion check	ccctctcatttagaaaaagccg	Sanger sequencing check of craA fragment size
perM_UP_F	ttgaaggaggcagatgttccc	P1 Deletion of perM in <i>A. baumannii</i>
perM_UP_R	ggcccaattcgccctatagtgcg acggcgagctatagcatcttcg	P2 Deletion of perM in <i>A. baumannii</i>
perM_DOWN_F	gggtttgctcgggtcgggtggcatatg ccccgaatcttcagatcag	P3 Deletion of perM in <i>A. baumannii</i>
perM_DOWN_R	gaagcattgcctgtggagc	P4 Deletion of perM in <i>A. baumannii</i>
perM_UP_R Clean deletion	ggcgagctatagcatcttcg	P7 Deletion of perM in <i>A. baumannii</i>
perM_DOWN_F Clean deletion	aagatcgctatctgcgcgtccccgaatcttcagat	P8 Deletion of perM in <i>A. baumannii</i>
PerM F deletion check	ccgtgaagatgaagttgcg	Sanger sequencing check of perM fragment size
PerM R deletion check	caaactccctcatctgtactacc	Sanger sequencing check of perM fragment size
cbl_UP_F	ggaagccattctagaaatacca	P1 Deletion of cbl in <i>A.</i> <i>baumannii</i>
cbl_UP_R	ggcccaattcgccctatagtgcg gctacgt	P2 Deletion of cbl in <i>A.</i> <i>baumannii</i>
cbl_DOWN_F	gggtttgctcgggtcgggtggcatatgcacttttctcaaaaga ggtg	P3 Deletion of cbl in <i>A.</i> <i>baumannii</i>
cbl_DOWN_R	tacagggagaaatgtcacatg	P4 Deletion of cbl in <i>A.</i> <i>baumannii</i>

cbl F deletion check	cttcaaaagaataggtggtgtc	P7 Deletion of cbl in A. baumannii
cbl R deletion check	attgcaggtaccagcc	P8 Deletion of cbl in A. baumannii
pWH1266_SLiCE_F	tattgaagcatttatcaggg	Amplification of the pWH1266 backbone for complementation
pWH1266_SLiCE_R	cctcactgattaagcattgg	Amplification of the pWH1266 backbone for complementation
craA comp bla F	ccaatgcttaatcagtgagg aacaaatgagttattattag	Construction of craA complementation plasmid
craA comp bla R	ccctgataaatgcttcaata aggaggcacaactcatgaaaaatattc	Construction of craA complementation plasmid
perM comp bla F	ccaatgcttaatcagtgagg gcactgcatccactac	Construction of perM complementation plasmid
perM comp bla R	ccctgataaatgcttcaata aggagggtatttatgcaagatcgtatac	Construction of perM complementation plasmid
FLAG_apra_sacB_F	gactacaaagaccatgacgg	Amplification of FLAG-tag
pMHL2_FLAG_R	gttcccgactggaaagcacttogaagcagctccagc	Amplification of FLAG-tag
craA_up_FLAG_F	caaatactttacaaagtgaacg	Construction of craA-FLAG
craA_up_FLAG_R	ccgtcatggtctttgtagtc taagtcttgcaactctttc	Construction of craA-FLAG
craA_down_F	gggtttgctcgggtcggtggcatatg aaaataccggaatttatattccg	Construction of craA-FLAG
craA_down_R	gattgctgctgcacttac	Construction of craA-FLAG
perM_up_FLAG_F	aaagctctagaactggttttac	Construction of perM-FLAG
perM_up_FLAG_R	ccgtcatggtctttgtagtc tttctgatctgaaagattcgg	Construction of perM-FLAG
perM_down_F	gggtttgctcgggtcggtggcatatg ccaattcattatatgcgtcaac	Construction of perM-FLAG
perM_down_R	ctttatcagttgaattagcctg	Construction of perM-FLAG
AAC(6')-Ib3 F bla-pWH1266	ccaatgcttaatcagtgagg cagggccattaccgattacgcc	Construction of AAC(6')-Ib3 complementation plasmid
AAC(6')-Ib3 R bla-pWH1266	ccctgataaatgcttcaata aggagggcacgtgaccaacagcaacg	Construction of AAC(6')-Ib3 complementation plasmid
APH(3'')-Ib (StrA) F bla-pWH1266	ccaatgcttaatcagtgagg gtcttctatagtttcaatccc	Construction of strA complementation plasmid
APH(3'')-Ib (StrA) R bla-pWH1266	ccctgataaatgcttcaata aggaggctccattgaatcggacttat	Construction of strA complementation plasmid

APH(6)-I (StrB) F bla-pWH1266	ccaatgcttaatcagtgagg ccgctgctataggggtc	Construction of strB complementation plasmid
APH(6)-I (StrB) R bla-pWH1266	ccctgataaatgcttcaata aggaggggttgatgttcatgccgc	Construction of strB complementation plasmid
aadA2 F bla-pWH1266	ccaatgcttaatcagtgagg ccacgtcgaaaaacaaaatcac	Construction of aadA2 complementation plasmid
aadA2 R bla-pWH1266	ccctgataaatgcttcaata aggaggacatcatgagggtagcgg	Construction of aadA2 complementation plasmid
aadB F bla-pWH1266	ccaatgcttaatcagtgagg ctgctggctatctcatgattg	Construction of aadB complementation plasmid
aadB R bla-pWH1266	ccctgataaatgcttcaata aggagggccgcatggacacaac	Construction of aadB complementation plasmid
APH(3')-VI F bla-pWH1266	ccaatgcttaatcagtgagg ctcaagcattaatgcagtacgatc	Construction of APH(3')-VI complementation plasmid
APH(3')-VI R bla-pWH1266	ccctgataaatgcttcaata aggaggacttgatggaattgccaatatta	Construction of APH(3')-VI complementation plasmid
Blages 11 F bla-pWH1266	ccaatgcttaatcagtgagg gcctgagttaagccgcggtgc	Construction of BlaGES-11 complementation plasmid
Blages 11 R bla-pWH1266	ccctgataaatgcttcaata aggaggtcaccatgcgcttcattcacgcac	Construction of BlaGES-11 complementation plasmid
DfrA7 F bla-pWH1266	ccaatgcttaatcagtgagg ccgagttcagcggcagttttaag	Construction of DfrA7 complementation plasmid
DfrA7 R bla-pWH1266	ccctgataaatgcttcaata aggagg gttgaattgaaaatttcattgattctg	Construction of DfrA7 complementation plasmid
HNS (p1AB5075) F native-pWH1266	ccaatgcttaatcagtgagg ctggtaaaaccacaaaacc	Construction of hnsP complementation plasmid
HNS (P1AB5075) R native-pWH1266	ccctgataaatgcttcaata gccagccatttgagcaaagg	Construction of hnsP complementation plasmid

Appendix II – Differentially expressed genes in biofilm formation

Gene	product	Wildtype pWH1266- hns vs wildtype pWH1266 log2-fold change	Wildtype pWH1266- hns vs Δp1AB5075 pWH1266- hns log2- fold change	Wildtype pWH1266 vs Δp1AB5075 pWH1266 log2-fold change	Δp1AB5075 pWH1266- hns vs Δp1AB5075 pWH1266 log2-fold change
ABUW_RS00005	chromosomal replication initiator protein DnaA	-0.18	-0.40	-0.14	0.08
ABUW_RS00010	DNA polymerase III subunit beta	-0.02	-0.35	-0.22	0.11
ABUW_RS00015	DNA replication/repair protein RecF	-1.18	-0.85	0.37	0.04
ABUW_RS00020	DNA topoisomerase (ATP-hydrolyzing) subunit B	0.07	-0.15	-0.03	0.19
ABUW_RS00025	cytochrome b562	0.77	0.06	-0.44	0.28
ABUW_RS00030	VTT domain-containing protein	-1.14	-0.82	0.28	-0.04
ABUW_RS00035	ATP-binding cassette domain-containing protein	-0.08	-0.42	0.02	0.36
ABUW_RS00040	RND transporter	1.29	0.84	0.02	0.46
ABUW_RS00045	hypothetical protein	0.57	0.31	-0.05	0.22
ABUW_RS00050	hypothetical protein	0.25	0.66	0.57	0.17
ABUW_RS00055	iron-sulfur cluster insertion protein ErpA	1.38	1.20	-0.22	-0.03
ABUW_RS00060	alpha/beta fold hydrolase	0.96	-0.44	-0.08	1.32
ABUW_RS00065	anhydro-N-acetylmuramic acid kinase	0.97	0.61	-0.40	-0.04
ABUW_RS00070	tyrosine--tRNA ligase	-0.22	-0.21	-0.23	-0.24
ABUW_RS00100	glutathione S-transferase family protein TIGR04219 family outer membrane beta-barrel protein	-0.02	-0.02	-0.34	-0.34
ABUW_RS00105		-0.91	0.81	-0.47	-2.20
ABUW_RS00110	sodium-dependent transporter	-0.70	0.30	-0.08	-1.07
ABUW_RS00115	methionine/alanine import family NSS transporter small subunit	0.42	1.98	-0.95	-2.51
ABUW_RS00120	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	-0.70	-0.56	-0.01	-0.14
ABUW_RS00125	methionyl-tRNA formyltransferase	-0.35	-0.47	0.15	0.28
ABUW_RS00130	dihydroxy-acid dehydratase	0.16	-0.24	-0.07	0.32
ABUW_RS00135	hypothetical protein	-0.56	0.02	-0.03	-0.62
ABUW_RS00140	sulfite exporter TauE/SafE family protein	0.36	-0.10	-0.09	0.37
ABUW_RS00145	LysR family transcriptional regulator	-1.52	-0.47	0.42	-0.64
ABUW_RS00150	pyrimidine permease	-0.15	-0.06	-0.33	-0.42
ABUW_RS00155	phosphoenolpyruvate carboxylase	-1.03	-0.23	0.11	-0.69
ABUW_RS00160	TetR/AcrR family transcriptional regulator	-0.70	-0.74	0.17	0.21
ABUW_RS00165	efflux RND transporter periplasmic adaptor subunit	0.72	1.01	-0.26	-0.55
ABUW_RS00170	efflux RND transporter permease subunit	-0.26	0.61	0.03	-0.84
ABUW_RS00175	hypothetical protein	0.72	1.27	-0.28	-0.83
ABUW_RS00180	molecular chaperone DnaJ	0.14	0.99	-0.43	-1.27
ABUW_RS00185	hypothetical protein	1.69	2.69	0.52	-0.48
ABUW_RS00190	4-hydroxy-tetrahydrodipicolinate reductase	0.90	1.00	-0.55	-0.65
ABUW_RS00195	START domain-containing protein	0.53	1.43	-0.20	-1.10
ABUW_RS00200	MFS transporter	0.03	-1.75	0.02	1.80
ABUW_RS00205	2,5-didehydrogluconate reductase DkgB	-0.37	-1.54	0.29	1.46

ABUW_RS00210	LysR family transcriptional regulator	-0.57	-0.37	0.07	-0.13
ABUW_RS00215	hypothetical protein	-3.92	-2.00	0.43	-1.49
ABUW_RS00220	PLP-dependent aminotransferase family protein	0.52	-0.16	0.13	0.81
ABUW_RS00225	NAD(P)-dependent alcohol dehydrogenase	0.41	-0.42	-0.39	0.44
ABUW_RS00230	DNA-3-methyladenine glycosylase I	-0.19	-1.27	0.30	1.38
ABUW_RS00235	hypothetical protein	-0.47	-0.39	-0.27	-0.35
ABUW_RS00240	M23 family metalloproteinase	0.34	-0.43	-0.40	0.36
ABUW_RS00245	A/G-specific adenine glycosylase	0.30	-0.42	-0.05	0.67
ABUW_RS00250	HIT family protein	-1.13	-0.39	0.13	-0.61
ABUW_RS00255	dienelactone hydrolase family protein	-0.50	0.46	-0.09	-1.06
ABUW_RS00260	DUF1328 domain-containing protein	-1.57	3.01	0.18	-4.40
ABUW_RS00265	YcgN family cysteine cluster protein	0.92	1.69	0.04	-0.73
ABUW_RS00270	PQQ-dependent sugar dehydrogenase	0.31	0.33	-0.37	-0.39
ABUW_RS00275	replication-associated recombination protein A	0.54	0.12	-0.36	0.05
ABUW_RS00280	formate/nitrite transporter family protein	1.13	0.22	0.16	1.08
ABUW_RS00285	hypothetical protein	-0.15	1.04	0.93	-0.25
ABUW_RS00290	phosphoribosylaminoimidazolesuccinocarboxamide synthase	-1.07	-1.04	0.21	0.19
ABUW_RS00295	hypothetical protein	0.10	-1.08	-0.07	1.11
ABUW_RS00300	4-hydroxy-tetrahydrodipicolinate synthase	-0.12	-0.57	0.14	0.59
ABUW_RS00305	bifunctional nicotinamidase/pyrazinamidase	-0.07	-0.63	0.04	0.61
ABUW_RS00310	bile acid:sodium symporter family protein	0.58	-0.54	-0.37	0.75
ABUW_RS00315	MATE family efflux transporter	0.94	0.36	-0.17	0.40
ABUW_RS00320	DUF523 domain-containing protein	1.42	-0.15	-0.77	0.80
ABUW_RS00325	4-hydroxyphenylpyruvate dioxygenase	-0.12	-0.32	0.25	0.45
ABUW_RS00330	IcIR family transcriptional regulator	-0.52	-0.34	0.00	-0.18
ABUW_RS00335	VOC family protein	-1.60	-0.99	0.22	-0.39
ABUW_RS00340	maleylacetoacetate isomerase	-1.14	-1.09	0.57	0.52
ABUW_RS00345	fumarylacetoacetase	-0.30	-0.23	0.31	0.23
ABUW_RS00350	amino acid permease	-0.02	-0.90	-0.11	0.77
ABUW_RS00355	hypothetical protein	0.62	0.30	0.29	0.61
ABUW_RS00360	zinc metallochaperone GTPase ZlgA	1.38	0.01	0.37	1.75
ABUW_RS00365	acyltransferase	-2.25	0.25	-0.10	-2.61
ABUW_RS00370	histidine utilization repressor	-0.57	0.01	0.37	-0.21
ABUW_RS00375	HutD family protein	-0.84	-0.16	0.43	-0.25
ABUW_RS00380	urocanate hydratase	2.06	0.17	0.93	2.82
ABUW_RS00385	histidine ammonia-lyase	1.49	0.12	0.25	1.63
ABUW_RS00390	amino acid permease	1.77	0.55	-0.39	0.83
ABUW_RS00395	imidazolonepropionase	1.17	0.41	-0.03	0.73
ABUW_RS00400	formimidoylglutamase	0.25	-0.27	-0.01	0.51
ABUW_RS00405	DUF885 domain-containing protein	-0.09	0.69	0.10	-0.68
ABUW_RS00410	HAD family hydrolase	0.87	1.41	0.31	-0.23
ABUW_RS00415	glutamate racemase	-0.11	1.46	0.18	-1.39
ABUW_RS00420	hypothetical protein	2.36	1.73	0.53	1.17
ABUW_RS00425	DNA cytosine methyltransferase	-0.85	0.69	-0.03	-1.58

ABUW_RS00430	ATP-binding protein	-1.04	1.11	-0.03	-2.17
ABUW_RS00435	hypothetical protein	-1.59	0.66	0.04	-2.21
ABUW_RS00440	glutamine--fructose-6-phosphate transaminase (isomerizing)	0.11	0.89	-0.13	-0.91
ABUW_RS00445	bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlnU	-0.15	0.33	0.35	-0.12
ABUW_RS00450	phosphatidylglycerophosphatase A	1.38	0.57	-0.28	0.52
ABUW_RS00455	thiamine-phosphate kinase	-0.12	-0.55	0.11	0.55
ABUW_RS00460	transcription antitermination factor NusB	-1.27	-1.30	0.42	0.44
ABUW_RS00465	6,7-dimethyl-8-ribityllumazine synthase	-0.25	-0.09	-0.06	-0.22
ABUW_RS00470	bifunctional 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	0.26	-0.28	-0.10	0.44
ABUW_RS00475	hypothetical protein	-0.70	-0.42	0.09	-0.18
ABUW_RS00480	phosphoserine phosphatase SerB	0.74	0.00	-0.06	0.68
ABUW_RS00485	hypothetical protein	0.73	0.13	-0.57	0.03
ABUW_RS00490	hypothetical protein	0.59	0.37	-0.11	0.11
ABUW_RS00495	D-tyrosyl-tRNA(Tyr) deacylase	-0.45	-0.60	-0.07	0.08
ABUW_RS00500	nicotinate phosphoribosyltransferase	-0.37	0.05	0.17	-0.25
ABUW_RS00505	sulfurtransferase	-0.02	-0.83	0.06	0.87
ABUW_RS00510	phosphatidylserine decarboxylase	1.02	0.66	-0.94	-0.58
ABUW_RS00515	alpha/beta fold hydrolase	-0.52	-0.14	-0.11	-0.48
ABUW_RS00520	phosphate regulon sensor histidine kinase PhoR	-0.04	0.27	0.01	-0.30
ABUW_RS00525	phosphate regulon transcriptional regulator PhoB	1.12	0.71	0.32	0.73
ABUW_RS00530	TetR/AcrR family transcriptional regulator	-0.57	-0.93	0.31	0.67
ABUW_RS00535	SDR family NAD(P)-dependent oxidoreductase	0.83	0.64	-0.25	-0.05
ABUW_RS00540	MATE family efflux transporter	-0.33	-0.41	-0.02	0.06
ABUW_RS00545	pyridoxal phosphate-dependent aminotransferase	-0.01	0.22	-0.04	-0.28
ABUW_RS00550	DUF445 domain-containing protein	0.36	-0.16	-0.06	0.46
ABUW_RS00555	hypothetical protein	0.03	-0.23	0.02	0.28
ABUW_RS00560	DUF924 domain-containing protein	0.15	0.67	0.48	-0.04
ABUW_RS00565	glutamate--cysteine ligase	-0.05	0.00	-0.09	-0.13
ABUW_RS00570	disulfide bond formation protein B	1.17	1.42	-0.75	-0.99
ABUW_RS00575	type VI secretion system tip protein VgrG	-0.85	0.68	-0.37	-1.91
ABUW_RS00585	hypothetical protein	0.08	0.93	-0.92	-1.77
ABUW_RS00590	hypothetical protein	-0.75	1.35	-0.07	-2.17
ABUW_RS00595	DUF1311 domain-containing protein	0.81	0.07	-0.47	0.27
ABUW_RS00600	SH3 domain-containing protein	-0.38	0.36	-0.28	-1.03
ABUW_RS00605	hypothetical protein	0.43	-0.80	0.31	1.53
ABUW_RS00610	esterase	0.16	-0.63	0.11	0.90
ABUW_RS00615	DNA topoisomerase IV subunit B	0.22	-0.66	0.13	1.00
ABUW_RS00620	ureidoglycolate lyase	0.93	0.33	-0.38	0.22
ABUW_RS00625	allantoicase	0.63	0.14	0.16	0.65
ABUW_RS00630	FAD-dependent urate hydroxylase HpxO	1.17	1.19	0.25	0.23
ABUW_RS00635	ion channel protein Tsx	-0.17	0.33	-0.46	-0.96
ABUW_RS00640	purine permease	0.58	-0.43	-0.11	0.90
ABUW_RS00645	hydroxyisourate hydrolase	1.39	0.84	0.07	0.62

ABUW_RS00650	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	1.10	0.26	0.59	1.43
ABUW_RS00655	allantoinase PuuE	0.29	-0.12	0.02	0.43
ABUW_RS00660	HPF/RaiA family ribosome-associated protein	-0.38	0.57	0.24	-0.71
ABUW_RS00665	ankyrin repeat domain-containing protein	-0.03	1.04	0.40	-0.67
ABUW_RS00670	transporter	0.80	0.17	-0.31	0.32
ABUW_RS00675	protein-disulfide reductase DsbD	-0.50	-0.47	0.10	0.07
ABUW_RS00680	GGDEF domain-containing protein	-1.11	-0.01	0.23	-0.88
ABUW_RS00685	alpha/beta hydrolase	-0.94	-0.20	0.48	-0.26
ABUW_RS00690	DUF2147 domain-containing protein	-1.14	1.30	0.27	-2.17
ABUW_RS00695	arsenate reductase	-1.20	0.41	-0.01	-1.62
ABUW_RS00700	exodeoxyribonuclease III	0.06	-0.09	-0.02	0.14
ABUW_RS00705	orotate phosphoribosyltransferase	0.04	0.28	-0.37	-0.62
ABUW_RS00710	TonB-dependent siderophore receptor	-1.78	1.14	0.38	-2.55
ABUW_RS00715	DUF1737 domain-containing protein	-0.46	-0.26	0.46	0.26
ABUW_RS00720	glutathione synthase	0.18	0.72	-0.03	-0.56
ABUW_RS00725	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	0.98	0.93	-0.33	-0.27
ABUW_RS00730	UDP-N-acetylmuramate--L-alanine ligase	0.87	0.56	-0.21	0.09
ABUW_RS00735	D-alanine--D-alanine ligase	0.64	0.02	-0.12	0.49
ABUW_RS00740	cell division protein FtsQ/DivIB	0.05	-0.17	-0.02	0.20
ABUW_RS00745	cell division protein FtsA	0.59	0.39	-0.14	0.06
ABUW_RS00750	cell division protein FtsZ	0.09	-0.06	-0.07	0.07
ABUW_RS00755	UDP-3-O-acyl-N-acetylglucosamine deacetylase	0.70	0.15	-0.50	0.05
ABUW_RS00760	DUF721 domain-containing protein	0.00	-0.14	0.43	0.57
ABUW_RS00765	M23 family metalloproteinase	0.14	-0.59	-0.32	0.41
ABUW_RS00770	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	-0.78	0.47	0.41	-0.85
ABUW_RS00775	2-oxo acid dehydrogenase subunit E2	0.13	0.02	0.11	0.22
ABUW_RS00780	hypothetical protein	0.86	0.92	-0.68	-0.74
ABUW_RS00785	TMEM165/GDT1 family protein	0.18	-0.76	0.40	1.34
ABUW_RS00790	TonB-dependent siderophore receptor	-1.39	1.44	0.21	-2.62
ABUW_RS00795	MBL fold metallo-hydrolase	1.09	-0.59	-0.27	1.42
ABUW_RS00800	YkgJ family cysteine cluster protein	1.28	-0.43	0.09	1.80
ABUW_RS00805	IMP dehydrogenase	0.06	0.26	-0.29	-0.49
ABUW_RS00810	phosphoglucosamine mutase	0.37	1.04	-0.26	-0.93
ABUW_RS00815	pyridoxamine 5'-phosphate oxidase	0.28	0.57	0.19	-0.10
ABUW_RS00820	single-stranded-DNA-specific exonuclease RecJ	0.18	0.07	-0.14	-0.04
ABUW_RS00825	putative porin	-1.01	-1.39	0.29	0.67
ABUW_RS00830	peptide chain release factor 2	0.89	0.10	-0.32	0.47
ABUW_RS00835	helix-turn-helix transcriptional regulator	1.18	0.17	-0.23	0.78
ABUW_RS00840	alkene reductase	0.51	-0.05	0.13	0.70
ABUW_RS00845	3-deoxy-D-manno-octulosonic acid transferase	-0.42	-0.26	0.02	-0.14
ABUW_RS00850	16S rRNA (uracil(1498)-N(3))-methyltransferase	-0.51	-0.66	0.33	0.49
ABUW_RS00855	mechanosensitive ion channel family protein	-0.51	0.47	-0.26	-1.24
ABUW_RS00860	DUF805 domain-containing protein	-0.50	0.93	-0.02	-1.44

ABUW_RS00865	acetate--CoA ligase	-0.62	-0.46	-0.18	-0.34
ABUW_RS00870	cysteine hydrolase	-1.26	0.44	0.54	-1.16
ABUW_RS00875	winged helix-turn-helix transcriptional regulator	-1.43	-0.52	0.19	-0.72
ABUW_RS00880	dimethyl sulfone monooxygenase SfnG	0.62	0.19	-0.19	0.24
ABUW_RS00885	FMN reductase	-0.65	-0.69	0.04	0.08
ABUW_RS00890	response regulator transcription factor	-0.78	0.40	-0.15	-1.33
ABUW_RS00895	hypothetical protein	-1.13	0.54	0.34	-1.32
ABUW_RS00900	hybrid sensor histidine kinase/response regulator	-0.27	-0.75	-0.18	0.30
ABUW_RS00905	DUF485 domain-containing protein	-1.62	-0.51	0.17	-0.93
ABUW_RS00910	cation acetate symporter	-0.57	-0.54	-0.21	-0.24
ABUW_RS00915	hypothetical protein	0.14	1.02	0.02	-0.85
ABUW_RS00920	choline BCCT transporter BetT	-0.68	1.02	-0.28	-1.97
ABUW_RS00925	porin Omp33-36	-1.21	-1.09	-0.01	-0.13
ABUW_RS00930	GGDEF domain-containing protein	0.53	0.09	0.21	0.65
ABUW_RS00935	excinuclease ABC subunit UvrA	0.04	-0.31	0.12	0.47
ABUW_RS00940	TetR/AcrR family transcriptional regulator	3.09	2.11	0.26	1.24
ABUW_RS00945	zinc-binding dehydrogenase	1.25	0.54	-0.32	0.38
ABUW_RS00950	DUF1304 domain-containing protein	-0.26	0.19	-0.31	-0.76
ABUW_RS00955	GlpM family protein	0.11	0.31	-0.19	-0.39
ABUW_RS00960	thiaminase II	-1.51	0.09	0.10	-1.50
ABUW_RS00965	DUF475 domain-containing protein	0.69	0.94	-0.70	-0.96
ABUW_RS00970	MFS transporter	2.07	1.25	-0.27	0.54
ABUW_RS00975	single-stranded DNA-binding protein	1.02	-0.06	-0.17	0.91
ABUW_RS00980	AzID domain-containing protein	-0.59	-0.86	-0.07	0.20
ABUW_RS00985	AzIC family ABC transporter permease	0.84	-0.41	-0.49	0.75
ABUW_RS00990	helix-turn-helix transcriptional regulator	0.65	0.31	-0.35	-0.01
ABUW_RS00995	amino acid permease	0.89	-0.19	-0.15	0.93
ABUW_RS01000	PLP-dependent aminotransferase family protein	0.60	-0.35	-0.30	0.66
ABUW_RS01005	4-aminobutyrate--2-oxoglutarate transaminase	0.83	-0.41	0.44	1.68
ABUW_RS01010	NAD-dependent succinate-semialdehyde dehydrogenase	0.40	0.19	0.11	0.32
ABUW_RS01015	LysR family transcriptional regulator	-0.55	-0.20	0.13	-0.22
ABUW_RS01020	hydrolase	-1.00	1.07	0.19	-1.87
ABUW_RS01025	pirin family protein	2.57	0.93	-0.69	0.95
ABUW_RS01030	FAD-dependent oxidoreductase	-0.18	0.16	-0.25	-0.58
ABUW_RS01035	class I SAM-dependent methyltransferase	-0.36	-0.61	0.29	0.54
ABUW_RS01040	GFA family protein	0.32	0.64	-0.05	-0.36
ABUW_RS01050	MFS transporter	5.45	4.95	0.15	0.65
ABUW_RS01055	LysR family transcriptional regulator	-0.02	-0.26	0.09	0.33
ABUW_RS01060	DMT family transporter	-0.71	-0.38	-0.33	-0.66
ABUW_RS01065	hypothetical protein	-1.59	0.21	0.16	-1.65
ABUW_RS01070	hypothetical protein	-0.69	0.58	-0.24	-1.51
ABUW_RS01075	aldo/keto reductase	0.13	-0.44	0.11	0.68
ABUW_RS01080	AraC family transcriptional regulator	0.30	-0.43	0.34	1.07
ABUW_RS01085	TetR/AcrR family transcriptional regulator	1.78	2.15	-0.05	-0.42

ABUW_RS01090	carboxymuconolactone decarboxylase family protein	-0.61	0.25	0.22	-0.64
ABUW_RS01095	helix-turn-helix transcriptional regulator	-2.15	0.85	0.83	-2.16
ABUW_RS01100	hypothetical protein	-0.04	0.98	0.82	-0.20
ABUW_RS01105	hypothetical protein	-0.97	1.25	1.92	-0.30
ABUW_RS01110	helix-turn-helix transcriptional regulator	-0.32	0.42	0.65	-0.09
ABUW_RS01115	NAD(P)H-dependent oxidoreductase	-0.66	0.17	0.95	0.12
ABUW_RS01120	AraC family transcriptional regulator	-1.39	-1.09	0.74	0.45
ABUW_RS01125	GNAT family N-acetyltransferase	-0.12	2.54	0.16	-2.49
ABUW_RS01135	potassium transporter Kup	0.10	0.03	-0.41	-0.34
ABUW_RS01140	hypothetical protein	1.21	0.85	0.23	0.59
ABUW_RS01145	DNA/RNA non-specific endonuclease	0.60	0.12	0.08	0.56
ABUW_RS01150	LysE family translocator	-1.72	-0.40	0.28	-1.04
ABUW_RS01155	hypothetical protein	0.32	1.01	-0.25	-0.94
ABUW_RS01160	aquaporin Z	0.99	1.00	-0.20	-0.21
ABUW_RS01165	AraC family transcriptional regulator	-0.42	-0.26	0.40	0.24
ABUW_RS01170	hypothetical protein	-0.45	-1.95	0.72	2.23
ABUW_RS01175	imidazole glycerol phosphate synthase subunit HisF	1.00	0.49	-0.39	0.11
ABUW_RS01180	homoserine kinase	0.46	0.09	-0.30	0.07
ABUW_RS01185	DUF1294 domain-containing protein	0.33	-0.41	-0.05	0.69
ABUW_RS01190	membrane protein	0.82	1.59	0.14	-0.64
ABUW_RS01195	DMT family transporter	1.19	-0.37	-0.12	1.45
ABUW_RS01200	helix-turn-helix transcriptional regulator	0.93	-0.06	-0.18	0.81
ABUW_RS01205	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	-0.27	-0.23	-0.12	-0.16
ABUW_RS01210	3'-5' exonuclease domain-containing protein 2	-1.63	-0.81	0.26	-0.56
ABUW_RS01215	DUF805 domain-containing protein	-1.62	-0.04	0.29	-1.29
ABUW_RS01220	imidazole glycerol phosphate synthase subunit HisH	1.88	0.47	-0.58	0.83
ABUW_RS01225	imidazoleglycerol-phosphate dehydratase HisB	0.67	-0.06	-0.19	0.54
ABUW_RS01230	acetyl-CoA sensor PanZ family protein	0.93	0.21	-0.32	0.41
ABUW_RS01245	GNAT family acetyltransferase	0.44	0.92	-0.05	-0.52
ABUW_RS01250	acetyl-CoA hydrolase/transferase family protein	-0.92	-0.51	0.04	-0.37
ABUW_RS01255	HAMP domain-containing protein	-0.45	-0.87	0.05	0.48
ABUW_RS01260	two-component system response regulator OmpR	-0.32	-0.37	0.19	0.24
ABUW_RS01265	RNA-binding transcriptional accessory protein	0.31	0.55	-0.25	-0.50
ABUW_RS01270	bifunctional SulP family inorganic anion transporter/carbonic anhydrase	-0.92	0.18	0.81	-0.29
ABUW_RS01275	SDR family NAD(P)-dependent oxidoreductase	-1.05	-0.04	-0.09	-1.10
ABUW_RS01280	aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	-1.18	-0.27	0.21	-0.70
ABUW_RS01285	energy-dependent translational throttle protein EttA	0.57	0.34	-0.24	-0.01
ABUW_RS01290	hypothetical protein	-1.51	1.41	-0.13	-3.05
ABUW_RS01295	hypothetical protein	0.00	0.80	0.28	-0.51
ABUW_RS01300	hypothetical protein	-1.98	-1.37	0.32	-0.29
ABUW_RS01305	TolC family protein	-0.37	-0.48	-0.19	-0.08
ABUW_RS01310	efflux RND transporter periplasmic adaptor subunit	-0.71	0.27	-0.09	-1.07

ABUW_RS01315	CusA/CzcA family heavy metal efflux RND transporter	0.50	-0.21	-0.52	0.19
ABUW_RS01320	cation transporter	0.64	-0.14	-0.28	0.50
ABUW_RS01325	hypothetical protein	-0.48	1.17	-0.19	-1.84
ABUW_RS01330	hypothetical protein	-0.21	0.08	0.33	0.04
ABUW_RS01345	hypothetical protein	-0.16	-0.01	0.22	0.07
ABUW_RS01350	amino acid permease	-0.20	-1.04	-0.12	0.72
ABUW_RS01365	glutamate--tRNA ligase	-0.47	-0.36	0.31	0.20
ABUW_RS01370	hypothetical protein	-0.11	0.14	0.52	0.26
ABUW_RS01375	sulfate ABC transporter substrate-binding protein	0.39	-0.96	-0.04	1.31
ABUW_RS01380	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	1.39	0.65	-0.20	0.55
ABUW_RS01385	cell division protein FtsL	0.77	1.38	-0.52	-1.13
ABUW_RS01390	penicillin-binding protein PBP3	0.60	0.34	-0.30	-0.04
ABUW_RS01395	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	-0.10	0.21	0.08	-0.24
ABUW_RS01400	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	-0.06	0.05	-0.01	-0.12
ABUW_RS01405	phospho-N-acetylmuramoyl-pentapeptide-transferase	0.03	-0.05	-0.25	-0.18
ABUW_RS01410	hypothetical protein	1.52	1.82	0.04	-0.25
ABUW_RS01415	methyltransferase domain-containing protein	0.43	0.38	-0.28	-0.22
ABUW_RS01420	penicillin-binding protein PBP1a	0.09	0.43	-0.08	-0.42
ABUW_RS01425	pilus assembly protein PilM	0.41	-1.43	-0.06	1.78
ABUW_RS01430	PilN domain-containing protein	0.89	-1.38	-0.24	2.03
ABUW_RS01435	type 4a pilus biogenesis protein PilO	0.00	-1.73	0.20	1.94
ABUW_RS01440	pilus assembly protein PilP	0.67	-0.95	-0.21	1.41
ABUW_RS01445	type IV pilus secretin PilQ family protein	0.84	-1.10	0.02	1.96
ABUW_RS01450	shikimate kinase AroK	-0.02	0.16	-0.08	-0.26
ABUW_RS01455	3-dehydroquinate synthase	0.32	-0.02	-0.07	0.27
ABUW_RS01460	hypothetical protein	-0.03	0.50	-0.20	-0.74
ABUW_RS01465	glutamate synthase large subunit	1.44	0.30	-0.49	0.65
ABUW_RS01470	FAD-dependent oxidoreductase	1.36	0.10	-0.73	0.53
ABUW_RS01475	metal-dependent hydrolase	1.93	2.48	-0.05	-0.60
ABUW_RS01480	LemA family protein	-0.54	1.19	0.18	-1.55
ABUW_RS01485	TPM domain-containing protein	-0.43	0.31	0.28	-0.46
ABUW_RS01490	TPM domain-containing protein	-1.04	0.52	0.18	-1.37
ABUW_RS01495	pilin	2.74	-0.87	0.15	3.76
ABUW_RS01500	O-antigen ligase family protein	0.32	0.92	-0.51	-1.11
ABUW_RS01505	bacterioferritin	1.11	-0.19	0.23	1.54
ABUW_RS01510	bacterioferritin-associated ferredoxin	0.91	4.03	-0.50	-3.61
ABUW_RS01515	RidA family protein	-0.30	-1.49	0.24	1.43
ABUW_RS01520	bifunctional (p)ppGpp synthetase/guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	-1.04	-1.17	0.05	0.18
ABUW_RS01525	DNA-directed RNA polymerase subunit omega	-0.98	0.06	0.49	-0.55
ABUW_RS01530	guanylate kinase	-0.39	-0.55	0.21	0.37
ABUW_RS01535	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	0.83	0.62	-0.19	0.03
ABUW_RS01540	GspH/FimT family pseudopilin	1.45	0.02	0.35	1.78

ABUW_RS01545	type IV pilus modification protein PilV	2.09	-0.11	-0.29	1.91
ABUW_RS01550	PilW family protein	1.18	-1.22	-0.23	2.16
ABUW_RS01555	hypothetical protein	1.41	-0.52	-0.39	1.54
ABUW_RS01560	VWA domain-containing protein	0.32	-0.42	0.12	0.86
ABUW_RS01565	prepilin-type N-terminal cleavage/methylation domain-containing protein	0.07	-1.10	0.13	1.31
ABUW_RS01570	prepilin-type N-terminal cleavage/methylation domain-containing protein	0.36	-0.61	-0.14	0.83
ABUW_RS01575	30S ribosomal protein S16	0.06	-0.83	-0.31	0.58
ABUW_RS01580	ribosome maturation factor RimM	0.68	-0.85	-0.02	1.52
ABUW_RS01585	tRNA (guanosine(37)-N1)-methyltransferase TrmD	1.37	-0.65	-0.25	1.77
ABUW_RS01590	50S ribosomal protein L19	-0.48	-0.36	0.15	0.03
ABUW_RS01595	triacylglycerol lipase	0.53	0.44	0.30	0.39
ABUW_RS01600	lipase secretion chaperone	-0.95	0.52	0.78	-0.69
ABUW_RS01605	tRNA pseudouridine(55) synthase TruB	0.06	0.35	-0.14	-0.42
ABUW_RS01610	TSUP family transporter	0.19	0.18	-0.32	-0.31
ABUW_RS01615	hemerythrin domain-containing protein	-1.70	1.37	0.42	-2.65
ABUW_RS01620	EamA family transporter	-0.05	-0.20	-0.11	0.04
ABUW_RS01625	EamA family transporter	-0.22	-0.66	0.22	0.66
ABUW_RS01630	phosphoglycerate dehydrogenase	0.52	0.31	-0.34	-0.14
ABUW_RS01635	FAD-binding oxidoreductase	-0.03	-0.15	-0.05	0.07
ABUW_RS01640	hypothetical protein	-0.28	1.48	-0.09	-1.85
ABUW_RS01645	antibiotic biosynthesis monooxygenase	0.61	0.37	-0.50	-0.26
ABUW_RS01650	NAD(P)H-dependent oxidoreductase	1.21	0.20	-0.21	0.81
ABUW_RS01655	hypothetical protein	0.59	0.96	-0.51	-0.87
ABUW_RS01660	MFS transporter	-0.84	-0.92	0.57	0.66
ABUW_RS01665	TIGR01666 family membrane protein	-1.88	-0.19	0.23	-1.46
ABUW_RS01670	superoxide dismutase family protein	0.05	0.09	-0.21	-0.25
ABUW_RS01675	Al-2E family transporter	-0.24	-0.04	-0.26	-0.47
ABUW_RS01680	ParA family protein	-0.15	-0.07	0.03	-0.05
ABUW_RS01685	endonuclease	0.13	-0.03	-0.15	0.01
ABUW_RS01690	hypothetical protein	3.05	1.02	0.04	2.06
ABUW_RS01695	hypothetical protein	-0.76	0.62	0.17	-1.20
ABUW_RS01700	class I SAM-dependent methyltransferase	-0.27	0.75	0.28	-0.74
ABUW_RS01705	hypothetical protein	-0.80	-0.22	-0.35	-0.92
ABUW_RS01710	amino acid permease	-1.51	-0.58	-0.01	-0.94
ABUW_RS01715	Glu/Leu/Phe/Val dehydrogenase	-0.93	1.49	0.22	-2.20
ABUW_RS01720	aspartate aminotransferase family protein	-1.07	-0.23	0.09	-0.76
ABUW_RS01725	arginine N-succinyltransferase	-0.83	0.23	0.15	-0.91
ABUW_RS01730	succinylglutamate-semialdehyde dehydrogenase	-1.07	0.31	0.32	-1.06
ABUW_RS01735	N-succinylarginine dihydrolase	-1.03	0.12	0.11	-1.04
ABUW_RS01740	succinylglutamate desuccinylase	-0.28	-0.10	-0.14	-0.32
ABUW_RS01745	hypothetical protein	0.73	0.28	0.76	1.21
ABUW_RS01750	hypothetical protein	-0.03	0.41	0.85	0.41
ABUW_RS01755	S8 family serine peptidase	1.39	1.87	-0.07	-0.55
ABUW_RS01760	hypothetical protein	-0.07	1.70	-0.11	-1.87

ABUW_RS01765	hypothetical protein	0.93	2.32	-0.09	-1.48
ABUW_RS01770	LysR family transcriptional regulator	0.64	0.55	0.17	0.26
ABUW_RS01775	EamA family transporter	6.49	5.65	0.31	1.15
ABUW_RS01780	hypothetical protein	1.51	4.40	0.24	-2.66
ABUW_RS01785	DUF262 domain-containing protein	-0.70	0.43	-0.11	-1.23
ABUW_RS01790	hypothetical protein	-0.12	-0.26	-0.16	-0.02
ABUW_RS01795	glycine--tRNA ligase subunit beta	-0.42	-0.52	-0.01	0.10
ABUW_RS01800	glycine--tRNA ligase subunit alpha	-0.32	-0.75	0.00	0.44
ABUW_RS01805	tetracycline resistance MFS efflux pump	-0.39	-0.53	0.42	0.56
ABUW_RS01810	putative DNA modification/repair radical SAM protein	0.94	-0.42	-0.40	0.96
ABUW_RS01815	TIGR03915 family putative DNA repair protein	-0.35	-0.59	-0.03	0.21
ABUW_RS01820	HPP family protein	0.74	1.39	-0.41	-1.06
ABUW_RS01825	PspC domain-containing protein	1.00	4.42	0.20	-3.21
ABUW_RS01830	hypothetical protein	0.46	1.23	-0.23	-1.00
ABUW_RS01835	acyl-CoA dehydrogenase C-terminal domain-containing protein	-1.15	-0.15	0.49	-0.51
ABUW_RS01840	hypothetical protein	-1.66	0.29	-0.13	-2.07
ABUW_RS01845	shikimate dehydrogenase	-0.03	-0.99	0.29	1.24
ABUW_RS01850	oxygen-dependent coproporphyrinogen oxidase	0.20	-0.84	0.20	1.23
ABUW_RS01855	GTP cyclohydrolase II	0.67	0.42	-0.34	-0.09
ABUW_RS01860	1-deoxy-D-xylulose-5-phosphate synthase	0.98	-0.23	-0.24	0.97
ABUW_RS01865	inositol monophosphatase	0.92	-0.05	-0.66	0.31
ABUW_RS01870	DEAD/DEAH box helicase	-0.18	-0.97	0.25	1.04
ABUW_RS01880	ABC transporter ATP-binding protein	0.36	-0.11	0.15	0.62
ABUW_RS01885	lipid asymmetry maintenance ABC transporter permease subunit MlaE	1.00	-0.03	-0.29	0.73
ABUW_RS01890	outer membrane lipid asymmetry maintenance protein MlaD	1.55	0.41	-0.21	0.92
ABUW_RS01895	ABC transporter substrate-binding protein	1.59	0.66	0.47	1.41
ABUW_RS01900	STAS domain-containing protein	0.66	0.11	1.14	1.70
ABUW_RS01905	magnesium transporter	-0.10	0.21	-0.04	-0.36
ABUW_RS01910	TIGR00730 family Rossmann fold protein	0.83	0.30	-0.51	0.01
ABUW_RS01915	NUDIX domain-containing protein	-0.65	-0.21	0.07	-0.37
ABUW_RS01920	ComF family protein	-0.57	-0.46	0.02	-0.09
ABUW_RS01925	ATP-dependent DNA helicase RecG	-0.30	-0.04	0.14	-0.12
ABUW_RS01930	NAD(P)H-binding protein	0.52	0.72	-0.16	-0.36
ABUW_RS01935	putative multidrug efflux protein AdeT2	-0.36	-0.03	0.23	-0.09
ABUW_RS01940	glycerol-3-phosphate 1-O-acyltransferase PlsB	-0.08	0.36	-0.04	-0.48
ABUW_RS01945	acyl-CoA thioesterase II	0.02	-0.66	-0.07	0.61
ABUW_RS01950	dicarboxylate/amino acid:cation symporter	0.52	0.27	-0.25	-0.01
ABUW_RS01955	metal-dependent hydrolase	-0.25	-0.62	0.06	0.43
ABUW_RS01960	YihA family ribosome biogenesis GTP-binding protein	-0.59	-0.71	-0.02	0.10
ABUW_RS01965	Rrf2 family transcriptional regulator	0.75	0.03	-0.07	0.66
ABUW_RS01970	flavo-hemoprotein	-0.37	0.27	0.29	-0.35
ABUW_RS01975	DUF853 domain-containing protein	0.89	1.87	-0.04	-1.02
ABUW_RS01980	PLP-dependent transferase	-0.64	-0.50	0.26	0.12

ABUW_RS01985	type 1 glutamine amidotransferase	-0.10	-0.01	0.25	0.16
ABUW_RS01990	30S ribosomal protein S10	0.13	-0.28	0.06	0.47
ABUW_RS01995	50S ribosomal protein L3	0.95	-0.61	-0.05	1.51
ABUW_RS02000	50S ribosomal protein L4	0.74	-0.33	-0.15	0.92
ABUW_RS02005	50S ribosomal protein L23	0.95	0.01	-0.05	0.89
ABUW_RS02010	50S ribosomal protein L2	0.49	-0.54	0.01	1.04
ABUW_RS02015	30S ribosomal protein S19	0.24	-0.42	0.09	0.75
ABUW_RS02020	50S ribosomal protein L22	0.45	-0.40	0.16	1.01
ABUW_RS02025	30S ribosomal protein S3	0.21	-0.48	0.02	0.71
ABUW_RS02030	50S ribosomal protein L16	0.89	-0.01	-0.11	0.79
ABUW_RS02035	50S ribosomal protein L29	0.46	-0.23	0.03	0.71
ABUW_RS02040	30S ribosomal protein S17	-0.36	-0.21	0.30	0.14
ABUW_RS02045	50S ribosomal protein L14	-0.18	-0.63	0.18	0.63
ABUW_RS02050	50S ribosomal protein L24	-0.39	-0.31	0.23	0.15
ABUW_RS02055	50S ribosomal protein L5	0.07	-0.71	0.15	0.93
ABUW_RS02060	30S ribosomal protein S14	0.64	-0.44	-0.24	0.84
ABUW_RS02065	30S ribosomal protein S8	0.23	-0.25	-0.03	0.46
ABUW_RS02070	50S ribosomal protein L6	0.30	-0.21	0.04	0.54
ABUW_RS02075	50S ribosomal protein L18	-0.36	-1.07	0.33	1.04
ABUW_RS02080	30S ribosomal protein S5	0.61	-0.34	-0.05	0.90
ABUW_RS02085	50S ribosomal protein L30	0.64	-0.87	0.24	1.75
ABUW_RS02090	50S ribosomal protein L15	0.49	-0.54	0.14	1.18
ABUW_RS02095	preprotein translocase subunit SecY	0.94	-0.33	-0.23	1.04
ABUW_RS02100	50S ribosomal protein L36	-0.04	-0.02	-0.15	-0.18
ABUW_RS02105	30S ribosomal protein S13	0.55	-0.81	0.06	1.42
ABUW_RS02110	30S ribosomal protein S11	0.42	-0.82	-0.06	1.18
ABUW_RS02115	30S ribosomal protein S4	0.50	-0.79	-0.13	1.17
ABUW_RS02120	DNA-directed RNA polymerase subunit alpha	0.30	-1.14	0.11	1.55
ABUW_RS02125	50S ribosomal protein L17	-0.02	-0.62	0.14	0.74
ABUW_RS02130	NAD(P)/FAD-dependent oxidoreductase	0.24	-0.12	0.18	0.54
ABUW_RS02135	acyl-CoA dehydrogenase family protein	0.22	-0.09	0.13	0.43
ABUW_RS02140	succinate dehydrogenase assembly factor 2	-0.36	0.20	-0.07	-0.63
ABUW_RS02145	membrane protein	1.07	-0.38	-0.36	1.09
ABUW_RS02150	hypothetical protein	1.21	-0.31	-0.28	1.25
ABUW_RS02155	rhombosortase	0.78	-0.39	-0.19	0.99
ABUW_RS02160	TRAP transporter large permease subunit	0.32	-0.06	-0.21	0.17
ABUW_RS02165	hypothetical protein	-0.04	-0.94	0.24	1.14
ABUW_RS02170	YheV family putative metal-binding protein	1.83	1.81	-0.67	-0.65
ABUW_RS02175	M3 family metalloproteinase	-1.11	0.71	0.43	-1.39
ABUW_RS02180	ribonuclease R	-0.50	0.07	0.11	-0.46
ABUW_RS02200	HAD-IB family hydrolase	0.70	-0.12	0.10	0.91
ABUW_RS02205	hypothetical protein	-3.72	0.90	-0.54	-5.16
ABUW_RS02215	nitroreductase family protein	-0.73	0.32	0.51	-0.55
ABUW_RS02220	YcxB family protein	-0.82	0.58	-0.04	-1.45

ABUW_RS02225	fumarylacetoacetate hydrolase family protein	0.15	1.52	-0.71	-2.08
ABUW_RS02230	helix-turn-helix transcriptional regulator	-0.84	-0.03	0.53	-0.27
ABUW_RS02235	DMT family transporter	0.56	1.06	0.06	-0.44
ABUW_RS02240	YihY family inner membrane protein	-0.32	0.62	-0.26	-1.20
ABUW_RS02245	NAD(P)H:quinone oxidoreductase	0.09	0.04	-0.23	-0.18
ABUW_RS02250	xanthine phosphoribosyltransferase	0.32	-0.32	-0.07	0.56
ABUW_RS02255	DUF3108 domain-containing protein	1.08	0.59	0.36	0.85
ABUW_RS02260	hypothetical protein	-0.60	0.00	0.21	-0.39
ABUW_RS02265	energy transducer TonB	0.34	-0.59	-0.06	0.87
ABUW_RS02270	rRNA maturation RNase YbeY	-0.78	-1.02	0.32	0.56
ABUW_RS02275	PhoH family protein	-0.38	-0.58	0.22	0.42
ABUW_RS02280	tRNA (N6-isopentenyl adenosine(37)-C2)-methyltransferase MiaB	0.20	-0.46	-0.11	0.56
ABUW_RS02285	lytic transglycosylase domain-containing protein	0.26	0.60	0.01	-0.34
ABUW_RS02290	hypothetical protein	-0.27	-0.23	0.12	0.07
ABUW_RS02295	malate dehydrogenase	0.14	-0.14	0.00	0.27
ABUW_RS02300	DUF2789 domain-containing protein	1.04	3.81	-0.09	-2.86
ABUW_RS02305	hypothetical protein	-0.12	1.17	0.28	-1.01
ABUW_RS02310	2OG-Fe(II) oxygenase	0.12	0.17	-0.08	-0.13
ABUW_RS02315	23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ	0.13	-0.57	0.28	0.97
ABUW_RS02320	CDP-diacylglycerol--serine O-phosphatidyltransferase	0.82	-0.15	-0.44	0.53
ABUW_RS02325	hypothetical protein	-0.28	0.79	0.32	-0.75
ABUW_RS02355	GFA family protein	1.33	2.08	0.24	-0.51
ABUW_RS02360	DUF4256 domain-containing protein	1.11	1.48	0.56	0.19
ABUW_RS02365	acyl-CoA dehydrogenase family protein	2.05	2.13	0.52	0.44
ABUW_RS02370	TetR family transcriptional regulator	-0.38	-0.42	0.33	0.37
ABUW_RS02375	DUF1446 domain-containing protein	1.73	1.64	0.17	0.26
ABUW_RS02380	SDR family oxidoreductase	2.39	2.12	0.00	0.28
ABUW_RS02385	acetyl-CoA carboxylase carboxyltransferase subunit	1.49	1.54	0.40	0.35
ABUW_RS02390	acyl-CoA dehydrogenase family protein	0.97	2.10	0.34	-0.79
ABUW_RS02395	enoyl-CoA hydratase/isomerase family protein	1.86	0.66	-0.07	1.13
ABUW_RS02400	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	0.95	0.76	0.01	0.21
ABUW_RS02405	hypothetical protein	-0.76	0.30	0.04	-1.02
ABUW_RS02410	ClpXP protease specificity-enhancing factor	-1.10	-0.35	0.70	-0.05
ABUW_RS02415	glutathione S-transferase N-terminal domain-containing protein	-0.43	-0.48	0.34	0.38
ABUW_RS02420	30S ribosomal protein S9	-0.46	-1.66	0.20	1.41
ABUW_RS02425	50S ribosomal protein L13	-0.17	-1.07	0.53	1.43
ABUW_RS02430	4-hydroxythreonine-4-phosphate dehydrogenase PdxA	0.94	0.45	-0.26	0.22
ABUW_RS02435	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA	0.26	-0.37	-0.03	0.59
ABUW_RS02440	symmetrical bis(5'-nucleosyl)-tetrakisphosphate	0.47	0.42	-0.23	-0.18
ABUW_RS02445	DUF2147 domain-containing protein	0.54	0.82	-0.17	-0.45
ABUW_RS02450	LrgB family protein	-1.25	-0.84	0.26	-0.15
ABUW_RS02455	hypothetical protein	-1.14	-0.46	0.09	-0.60

ABUW_RS02460	GTPase HflX	-0.13	0.00	0.22	0.09
ABUW_RS02465	1-acyl-sn-glycerol-3-phosphate acyltransferase	-0.55	-0.11	-0.01	-0.44
ABUW_RS02470	phospholipase D family protein	-0.71	0.10	0.15	-0.66
ABUW_RS02475	metallophosphoesterase	-0.57	-0.18	0.20	-0.19
ABUW_RS02480	OmpA family protein	-0.05	0.29	-0.50	-0.85
ABUW_RS02485	diguanylate cyclase	-0.23	-0.02	-0.01	-0.23
ABUW_RS02490	YfiR family protein	0.15	0.84	-0.15	-0.84
ABUW_RS02520	dihydrolipoyl dehydrogenase	-1.72	0.30	-0.06	-2.08
ABUW_RS02525	hypothetical protein	-1.71	0.03	0.01	-1.74
ABUW_RS02530	TIGR01244 family phosphatase	-0.38	1.20	-0.14	-1.73
ABUW_RS02535	alpha/beta hydrolase	-0.22	0.48	0.31	-0.39
ABUW_RS02540	thioredoxin TrxC	0.00	0.44	0.07	-0.37
ABUW_RS02545	acyl-CoA thioesterase	0.95	0.47	-0.24	0.24
ABUW_RS02550	DUF4442 domain-containing protein	-0.86	0.02	0.52	-0.36
ABUW_RS02555	YajQ family cyclic di-GMP-binding protein	-0.16	1.17	0.28	-1.05
ABUW_RS02560	sulfurtransferase	-0.33	1.93	0.39	-1.87
ABUW_RS02565	bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC	-0.65	-0.56	0.22	0.13
ABUW_RS02570	hypothetical protein	0.10	-0.06	0.24	0.40
ABUW_RS02575	hypothetical protein	0.54	0.65	-0.17	-0.28
ABUW_RS02580	septation protein IspZ	0.27	-0.19	-0.06	0.40
ABUW_RS02585	PHP domain-containing protein	-0.11	0.28	0.38	-0.01
ABUW_RS02590	bestrophin	0.45	0.74	0.05	-0.25
ABUW_RS02595	DNA repair protein RadC	0.19	-1.13	0.23	1.55
ABUW_RS02600	bifunctional phosphopantothenoylecysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	0.46	0.00	-0.56	-0.10
ABUW_RS02605	protein translocase subunit SecF	-0.25	0.05	-0.11	-0.41
ABUW_RS02610	protein translocase subunit SecD	-0.43	-0.32	-0.12	-0.23
ABUW_RS02615	preprotein translocase subunit YajC	0.02	0.17	-0.49	-0.64
ABUW_RS02620	tRNA guanosine(34) transglycosylase Tgt	0.75	-0.35	-0.38	0.72
ABUW_RS02625	LemA family protein	-0.44	-0.53	-0.09	-0.01
ABUW_RS02630	hypothetical protein	-1.10	0.30	0.32	-1.07
ABUW_RS02635	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	0.32	0.36	-0.37	-0.42
ABUW_RS02645	site-specific integrase	-0.05	0.76	0.62	-0.19
ABUW_RS02650	hypothetical protein	-0.14	-0.91	-0.15	0.62
ABUW_RS02655	hypothetical protein	0.01	-1.34	-0.32	1.03
ABUW_RS02660	3'-5' exonuclease	-0.50	-0.61	0.29	0.40
ABUW_RS02665	single-stranded DNA-binding protein	0.41	-0.13	0.15	0.69
ABUW_RS02670	hypothetical protein	0.78	-0.13	-0.06	0.84
ABUW_RS02675	hypothetical protein	-0.50	-0.39	0.80	0.69
ABUW_RS02680	hypothetical protein	-1.06	0.69	0.64	-1.10
ABUW_RS02685	toprim domain-containing protein	0.66	-0.59	0.60	1.84
ABUW_RS02690	hypothetical protein	0.22	-1.21	1.72	3.15
ABUW_RS02695	helix-turn-helix transcriptional regulator	0.22	0.24	-0.34	-0.35

ABUW_RS02700	hypothetical protein	1.12	3.07	-0.58	-2.52
ABUW_RS02705	Rha family transcriptional regulator	-0.91	-1.39	0.29	0.77
ABUW_RS02710	hypothetical protein	-0.47	0.31	0.42	-0.36
ABUW_RS02715	BRCT domain-containing protein	-0.52	0.30	0.03	-0.79
ABUW_RS02720	hypothetical protein	0.25	0.52	-0.26	-0.54
ABUW_RS02730	TraR/DksA C4-type zinc finger protein	0.48	-0.21	0.46	1.15
ABUW_RS02735	ogr/Delta-like zinc finger family protein	1.26	2.28	0.32	-0.70
ABUW_RS02740	primase	-0.18	0.43	-0.17	-0.77
ABUW_RS02745	phage tail protein	-0.31	-0.53	0.03	0.25
ABUW_RS02750	phage tail tape measure protein	-0.09	0.06	0.16	0.01
ABUW_RS02765	carbapenem-hydrolyzing class D beta-lactamase OXA-23	0.30	2.07	-0.21	-1.98
ABUW_RS02770	ATP-binding protein	-0.07	-1.14	0.11	1.18
ABUW_RS02775	phage tail assembly protein	-0.14	0.99	0.88	-0.25
ABUW_RS02780	phage major tail tube protein	0.71	1.58	-0.01	-0.88
ABUW_RS02785	phage tail sheath protein	2.03	2.23	0.51	0.31
ABUW_RS02790	phage tail protein	-0.90	0.40	0.37	-0.93
ABUW_RS02795	phage tail protein I	-0.62	-0.50	0.62	0.50
ABUW_RS02800	baseplate J/gp47 family protein	-0.24	-0.52	0.97	1.26
ABUW_RS02805	GPW/gp25 family protein	0.32	0.09	3.01	3.24
ABUW_RS02810	phage baseplate assembly protein V	2.11	0.88	0.71	1.93
ABUW_RS02815	phage virion morphogenesis protein	-0.44	0.00	0.08	-0.36
ABUW_RS02820	phage tail protein	-0.05	0.49	-0.30	-0.84
ABUW_RS02825	DUF3380 domain-containing protein	0.16	0.69	-0.07	-0.60
ABUW_RS02830	phage holin family protein	-0.76	0.31	0.09	-0.97
ABUW_RS02835	membrane protein	-0.34	0.55	0.01	-0.89
ABUW_RS02840	tail protein X	0.97	0.91	0.66	0.72
ABUW_RS02845	head completion/stabilization protein	1.25	-0.45	-0.03	1.67
ABUW_RS02850	terminase	0.61	0.48	0.63	0.75
ABUW_RS02855	phage major capsid protein, P2 family	0.70	-0.24	0.36	1.29
ABUW_RS02860	GPO family capsid scaffolding protein	0.53	-0.18	0.60	1.30
ABUW_RS02865	terminase family protein	-0.02	-0.24	0.30	0.53
ABUW_RS02870	phage portal protein	0.38	0.16	-0.21	0.02
ABUW_RS02875	HAMP domain-containing histidine kinase bifunctional [glutamate--ammonia ligase]-adenylyl-L-tyrosine phosphorylase/[glutamate--ammonia-ligase] adenylyltransferase	-1.06	0.00	-0.06	-1.11
ABUW_RS02880		-0.39	-0.34	0.14	0.09
ABUW_RS02885	branched-chain amino acid transaminase	-0.86	-0.79	0.12	0.05
ABUW_RS02890	mitochondrial fission ELM1 family protein	0.28	0.32	-0.17	-0.21
ABUW_RS02895	glycosyltransferase family 1 protein	-0.02	0.05	-0.03	-0.10
ABUW_RS02900	polysaccharide deacetylase family protein	0.09	-0.04	-0.13	0.01
ABUW_RS02905	glycosyltransferase family 2 protein	-0.22	0.13	-0.17	-0.52
ABUW_RS02910	glycosyltransferase	0.17	0.43	-0.14	-0.41
ABUW_RS02915	hypothetical protein	-2.78	-0.75	0.34	-1.68
ABUW_RS02920	glycosyltransferase family 25 protein	-2.36	1.06	-0.45	-3.87
ABUW_RS02925	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-2.59	-0.35	0.10	-2.14

ABUW_RS02930	hypothetical protein	-1.14	-0.95	0.23	0.04
ABUW_RS02935	hypothetical protein	-0.78	0.50	-0.07	-1.35
ABUW_RS02940	aspartate--tRNA ligase	-1.00	-1.12	0.10	0.22
ABUW_RS02945	DUF4184 family protein	0.09	-0.02	-0.37	-0.26
ABUW_RS02950	zinc piracy TonB-dependent receptor ZnuD	0.25	0.99	-0.17	-0.91
ABUW_RS02955	phospholipase D family protein	-0.46	-0.77	0.21	0.52
ABUW_RS02960	hypothetical protein	-0.48	-0.86	0.20	0.58
ABUW_RS02965	RcnB family protein	3.54	2.53	0.92	1.93
ABUW_RS02970	phosphate-starvation-inducible PsiE family protein	-1.47	-0.41	0.26	-0.80
ABUW_RS02975	acyl-CoA dehydrogenase C-terminal domain-containing protein	-0.52	-0.26	0.24	-0.01
ABUW_RS02980	acyl-CoA dehydrogenase C-terminal domain-containing protein	-0.76	-0.94	0.40	0.59
ABUW_RS02985	hypothetical protein	2.09	1.13	1.22	2.18
ABUW_RS02990	sensor histidine kinase efflux regulator BaeS	0.12	0.22	0.19	0.09
ABUW_RS02995	response regulator	0.04	0.79	-0.09	-0.84
ABUW_RS03000	YdiU family protein	-0.35	-0.69	0.06	0.40
ABUW_RS03005	acyl-CoA desaturase	0.07	-0.29	-0.36	0.00
ABUW_RS03010	META domain-containing protein	0.46	0.39	-0.20	-0.14
ABUW_RS03015	glycerophosphodiester phosphodiesterase	-0.79	-0.49	0.09	-0.22
ABUW_RS03020	cob(I)yrinic acid a,c-diamide adenosyltransferase	1.59	0.77	-0.89	-0.08
ABUW_RS03025	TonB-dependent receptor	-0.50	0.28	0.07	-0.71
ABUW_RS03030	phosphoribosylanthranilate isomerase	0.46	-0.45	-0.20	0.72
ABUW_RS03035	tryptophan synthase subunit beta	0.18	-0.67	-0.11	0.74
ABUW_RS03040	DUF1543 domain-containing protein	0.94	0.11	-0.24	0.59
ABUW_RS03045	DUF2804 domain-containing protein	0.00	0.06	0.36	0.30
ABUW_RS03050	metal-dependent hydrolase	-2.28	-1.64	0.80	0.16
ABUW_RS03055	AraC family transcriptional regulator	0.34	-0.15	0.14	0.64
ABUW_RS03060	tryptophan synthase subunit alpha	0.53	-0.56	-0.12	0.96
ABUW_RS03065	acetyl-CoA carboxylase carboxyltransferase subunit beta	0.37	-0.25	-0.24	0.38
ABUW_RS03070	bifunctional tetrahydrofolate synthase/dihydrofolate synthase	0.37	-0.37	-0.03	0.71
ABUW_RS03075	SPOR domain-containing protein	0.05	1.25	-0.15	-1.36
ABUW_RS03080	dual specificity protein phosphatase family protein	-0.76	-0.02	0.24	-0.51
ABUW_RS03085	MBL fold metallo-hydrolase	0.42	0.55	-0.09	-0.22
ABUW_RS03090	peroxiredoxin	0.20	1.44	-0.26	-1.50
ABUW_RS03095	preprotein translocase subunit SecA	-0.09	1.11	-0.09	-1.29
ABUW_RS03100	hypothetical protein	1.06	0.96	-0.18	-0.08
ABUW_RS03105	MHS family MFS transporter	-0.52	-0.12	-0.06	-0.46
ABUW_RS03110	hemolysin III family protein	-0.42	0.22	-0.28	-0.91
ABUW_RS03115	SAM-dependent methyltransferase	-0.38	0.65	-0.01	-1.04
ABUW_RS03120	GNAT family N-acetyltransferase	-0.26	1.27	0.19	-1.35
ABUW_RS03125	patatin family protein	0.96	-0.11	-0.21	0.86
ABUW_RS03130	hypothetical protein	0.89	0.72	-0.55	-0.39
ABUW_RS03135	enoyl-CoA hydratase/isomerase family protein	0.02	-0.51	0.28	0.81
ABUW_RS03140	acetyl-CoA C-acetyltransferase	-0.04	-0.24	-0.01	0.19

ABUW_RS03145	AraC family transcriptional regulator	0.32	-1.10	0.25	1.67
ABUW_RS03150	CoA transferase	1.14	1.14	0.15	0.14
ABUW_RS03155	carbohydrate porin	-0.98	0.05	0.08	-0.95
ABUW_RS03160	glucose/quininate/shikimate family membrane-bound PQQ-dependent dehydrogenase	-0.26	0.77	-0.12	-1.15
ABUW_RS03165	nitrite/sulfite reductase	1.10	0.98	-0.25	-0.13
ABUW_RS03170	DUF934 domain-containing protein	0.54	0.06	-0.48	0.00
ABUW_RS03175	quaternary ammonium transporter	1.47	1.93	-0.69	-1.15
ABUW_RS03180	VOC family protein	1.54	2.89	-0.02	-1.37
ABUW_RS03185	thiolase family protein	0.07	0.34	0.16	-0.11
ABUW_RS03190	GspH/FimT family pseudopilin	-0.82	-0.63	0.56	0.37
ABUW_RS03195	OmpA family protein	-0.22	0.11	-0.01	-0.34
ABUW_RS03205	RtcB family protein	1.66	-0.03	-0.66	1.04
ABUW_RS03210	amino acid permease	0.25	-0.42	-0.33	0.35
ABUW_RS03215	methyltransferase	0.03	-0.78	-0.07	0.74
ABUW_RS03220	uracil-xanthine permease	0.00	-0.85	-0.45	0.40
ABUW_RS03225	translational GTPase TypA	0.47	-0.74	-0.26	0.95
ABUW_RS03230	large conductance mechanosensitive channel protein MscL	1.09	1.21	-0.10	-0.21
ABUW_RS03235	gamma-glutamylcyclotransferase	0.64	-0.16	-0.32	0.48
ABUW_RS03240	peptidylprolyl isomerase	0.06	-0.25	-0.22	0.09
ABUW_RS03245	bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase	0.48	0.25	-0.10	0.13
ABUW_RS03250	DNA-3-methyladenine glycosylase	-0.26	0.36	-0.09	-0.71
ABUW_RS03255	TonB-dependent receptor	0.22	0.31	-0.22	-0.31
ABUW_RS03260	NADH:flavin oxidoreductase/NADH oxidase	0.53	0.66	-0.25	-0.39
ABUW_RS03265	AEC family transporter	0.45	0.42	-0.12	-0.09
ABUW_RS03270	sel1 repeat family protein	0.26	0.95	0.60	-0.09
ABUW_RS03275	DsbC family protein	0.18	1.96	-0.28	-2.07
ABUW_RS03280	folate-binding protein YgfZ	-0.11	1.03	0.15	-0.99
ABUW_RS03285	SRPBCC family protein	0.93	1.54	0.02	-0.59
ABUW_RS03290	DUF488 domain-containing protein	0.08	0.78	0.01	-0.69
ABUW_RS03295	alkylphosphonate utilization protein	-0.20	0.12	0.27	-0.05
ABUW_RS03310	YegP family protein	0.28	0.86	-0.17	-0.75
ABUW_RS03315	proline--tRNA ligase	0.05	-0.21	0.16	0.42
ABUW_RS03320	efflux RND transporter permease subunit	-1.19	-0.01	0.15	-1.03
ABUW_RS03325	efflux RND transporter periplasmic adaptor subunit	-0.81	0.10	-0.06	-0.96
ABUW_RS03330	hypothetical protein	-0.62	0.29	0.68	-0.23
ABUW_RS03335	twitching motility response regulator PilG	-0.17	-1.03	-0.38	0.48
ABUW_RS03340	response regulator	0.29	-0.30	-0.39	0.21
ABUW_RS03345	purine-binding chemotaxis protein CheW	0.88	-0.90	-0.48	1.30
ABUW_RS03350	methyl-accepting chemotaxis protein	0.30	-1.51	-0.28	1.52
ABUW_RS03355	Hpt domain-containing protein	0.33	-1.17	-0.05	1.45
ABUW_RS03360	hypothetical protein	0.70	0.04	-0.72	-0.07
ABUW_RS03365	radical SAM protein	-4.05	-0.72	0.18	-3.15
ABUW_RS03370	alpha/beta fold hydrolase	-3.05	-1.00	-0.02	-2.07

ABUW_RS03375	succinyl-diaminopimelate desuccinylase	-0.58	-0.55	-0.07	-0.10
ABUW_RS03380	entericidin A/B family lipoprotein	0.34	2.43	0.79	-1.31
ABUW_RS03385	DUF1853 family protein	-0.70	-0.69	0.33	0.31
ABUW_RS03390	YbaN family protein	-0.09	-0.20	0.54	0.66
ABUW_RS03395	L,D-transpeptidase	0.40	0.51	-0.24	-0.35
ABUW_RS03430	YdcF family protein	0.24	0.46	-0.71	-0.93
ABUW_RS03435	PepSY domain-containing protein	-1.60	0.23	0.10	-1.73
ABUW_RS03440	Sdpl family protein	0.00	-0.43	-0.23	0.20
ABUW_RS03445	TIGR01666 family membrane protein	-0.20	-0.24	0.01	0.05
ABUW_RS03450	multidrug efflux MFS transporter	0.28	0.19	-0.13	-0.04
ABUW_RS03455	nitroreductase	-1.10	-0.56	0.03	-0.51
ABUW_RS03460	hypothetical protein	-0.60	-0.34	0.20	-0.06
ABUW_RS03465	alanine:cation symporter family protein	0.30	0.79	-0.62	-1.12
ABUW_RS03470	patatin-like phospholipase family protein	1.67	1.76	-0.52	-0.60
ABUW_RS03475	threonine ammonia-lyase	0.52	0.70	-0.07	-0.24
ABUW_RS03480	peptide antibiotic transporter SbmA	1.95	1.86	-0.54	-0.44
ABUW_RS03485	DUF4850 domain-containing protein	-1.84	-0.70	0.47	-0.67
ABUW_RS03490	DUF1176 domain-containing protein	-0.40	1.33	-0.06	-1.79
ABUW_RS03495	hypothetical protein	-0.08	0.54	0.18	-0.43
ABUW_RS03500	DJ-1/Pfpl family protein	-0.03	-0.06	-0.12	-0.09
ABUW_RS03505	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	0.27	0.11	-0.20	-0.04
ABUW_RS03510	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	0.04	-0.40	-0.20	0.25
ABUW_RS03515	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatC	-0.16	0.11	0.05	-0.22
ABUW_RS03520	rod shape-determining protein	0.54	0.01	-0.15	0.38
ABUW_RS03525	rod shape-determining protein MreC	0.25	-0.06	-0.13	0.18
ABUW_RS03530	rod shape-determining protein MreD	0.61	0.35	-0.25	0.01
ABUW_RS03535	Maf-like protein	-0.46	0.10	0.05	-0.50
ABUW_RS03540	ribonuclease G	-0.15	-0.07	-0.02	-0.10
ABUW_RS03550	wax ester/triacylglycerol synthase family O-acyltransferase	-0.25	-0.10	0.52	0.37
ABUW_RS03555	phosphoadenylyl-sulfate reductase bifunctional phosphoserine	0.81	-0.33	-0.25	0.89
ABUW_RS03560	phosphatase/homoserine phosphotransferase ThrH	-0.33	-0.23	-0.16	-0.26
ABUW_RS03565	outer membrane protein transport protein	-1.25	-0.90	0.13	-0.22
ABUW_RS03570	NAD(P)H-dependent oxidoreductase	-0.12	0.55	0.03	-0.64
ABUW_RS03575	AraC family transcriptional regulator	0.54	0.05	-0.16	0.32
ABUW_RS03580	fatty acid desaturase family protein	-0.06	1.30	0.57	-0.79
ABUW_RS03585	PaaX family transcriptional regulator	-1.03	0.43	0.42	-1.04
ABUW_RS03590	undecaprenyl-diphosphate phosphatase	1.06	2.18	-0.72	-1.84
ABUW_RS03595	AraC family transcriptional regulator	-0.01	0.51	0.31	-0.21
ABUW_RS03600	zinc-binding dehydrogenase	-0.04	0.84	-0.32	-1.20
ABUW_RS03605	protein deglycase HchA	-0.43	1.09	0.05	-1.48
ABUW_RS03610	AlpA family phage regulatory protein	1.60	1.56	0.88	0.92
ABUW_RS03615	hypothetical protein	2.32	2.45	-1.05	-1.18
ABUW_RS03620	hypothetical protein	1.34	1.98	0.26	-0.38

ABUW_RS03625	hypothetical protein	2.15	-0.61	-1.13	1.63
ABUW_RS03630	hypothetical protein	1.27	-0.58	0.22	2.07
ABUW_RS03635	hypothetical protein	2.34	-0.69	0.25	3.28
ABUW_RS03640	hypothetical protein	3.12	-0.17	0.18	3.46
ABUW_RS03650	hypothetical protein	6.31	-1.67	-2.08	5.90
ABUW_RS03655	hypothetical protein	4.14	0.57	0.34	3.90
ABUW_RS03660	hypothetical protein	4.83	1.26	0.41	3.99
ABUW_RS03665	hypothetical protein	3.30	0.16	1.25	4.38
ABUW_RS03670	N-6 DNA methylase	-1.73	0.52	0.00	-2.25
ABUW_RS03675	hypothetical protein	1.12	-0.18	-0.52	0.77
ABUW_RS03680	helix-turn-helix domain-containing protein	0.48	0.63	-0.33	-0.49
ABUW_RS03685	hypothetical protein	4.28	0.73	0.75	4.30
ABUW_RS03690	GntR family transcriptional regulator	4.74	0.31	0.40	4.82
ABUW_RS03695	AAA family ATPase	3.32	-0.49	0.10	3.91
ABUW_RS03705	hypothetical protein	2.10	0.31	0.28	2.07
ABUW_RS03710	hypothetical protein	1.18	-3.19	1.10	5.47
ABUW_RS03715	hypothetical protein	NA	NA	NA	NA
ABUW_RS03720	hypothetical protein	3.75	-1.14	-0.22	4.67
ABUW_RS03725	hypothetical protein	2.43	0.40	0.41	2.44
ABUW_RS03730	hypothetical protein	2.86	0.42	-0.09	2.36
ABUW_RS03735	VRR-NUC domain-containing protein	1.41	1.10	-0.37	-0.06
ABUW_RS03740	metallophosphoesterase	1.29	0.46	-0.13	0.70
ABUW_RS03745	hypothetical protein	0.76	3.07	0.01	-2.30
ABUW_RS03750	hypothetical protein	0.12	1.34	0.16	-1.06
ABUW_RS03760	DUF968 domain-containing protein	-0.01	0.28	1.07	0.79
ABUW_RS03765	hypothetical protein	0.39	0.51	0.42	0.30
ABUW_RS03770	RelA/SpoT domain-containing protein	0.66	0.21	-0.39	0.07
ABUW_RS03775	hypothetical protein	1.48	0.02	0.39	1.85
ABUW_RS03785	hypothetical protein	2.32	1.59	0.02	0.75
ABUW_RS03790	hypothetical protein	2.58	0.59	0.42	2.40
ABUW_RS03795	DUF2280 domain-containing protein	4.85	3.19	1.66	3.32
ABUW_RS03800	terminase family protein	3.22	0.96	-0.01	2.25
ABUW_RS03805	DUF4055 domain-containing protein	2.99	0.75	-0.27	1.97
ABUW_RS03810	minor capsid protein	2.13	0.32	-0.06	1.75
ABUW_RS03815	hypothetical protein	5.01	3.76	-1.68	-0.43
ABUW_RS03820	hypothetical protein	3.81	0.82	-0.16	2.83
ABUW_RS03825	hypothetical protein	2.80	0.65	0.06	2.21
ABUW_RS03830	hypothetical protein	2.92	0.24	-0.02	2.66
ABUW_RS03835	hypothetical protein	1.33	1.43	1.18	1.07
ABUW_RS03840	hypothetical protein	2.31	0.28	-0.35	1.68
ABUW_RS03845	hypothetical protein	3.62	-0.73	-1.24	3.12
ABUW_RS03850	hypothetical protein	-1.66	0.51	-0.14	-2.31
ABUW_RS03855	hypothetical protein	0.29	1.23	0.17	-0.77
ABUW_RS03860	hypothetical protein	-0.71	-0.53	0.62	0.44

ABUW_RS03865	hypothetical protein	NA	NA	NA	NA
ABUW_RS03870	hypothetical protein	NA	NA	NA	NA
ABUW_RS03875	hypothetical protein	-0.33	2.29	2.25	0.00
ABUW_RS03880	hypothetical protein	1.08	1.23	0.00	0.00
ABUW_RS03885	hypothetical protein	1.76	-0.05	-0.05	1.76
ABUW_RS03890	DUF4258 domain-containing protein	1.97	2.42	-0.03	-0.48
ABUW_RS03895	helix-turn-helix domain-containing protein	1.51	0.83	-0.13	0.56
ABUW_RS03900	DUF4236 domain-containing protein	0.69	1.20	-0.20	-0.71
ABUW_RS03905	hypothetical protein	-0.49	0.91	0.40	-1.01
ABUW_RS03910	hypothetical protein	-0.71	0.02	0.52	-0.21
ABUW_RS03915	Arc family DNA-binding protein	0.26	1.67	-0.12	-1.53
ABUW_RS03920	Arc family DNA-binding protein	0.68	0.39	-0.57	-0.27
ABUW_RS03925	KilA-N domain-containing protein	0.18	0.38	0.14	-0.06
ABUW_RS03930	hypothetical protein	3.82	0.17	1.49	5.14
ABUW_RS03935	tape measure protein	0.84	0.04	0.09	0.88
ABUW_RS03940	hypothetical protein	3.00	3.15	0.00	0.00
ABUW_RS03945	DUF1833 family protein	0.00	-2.36	0.00	2.50
ABUW_RS03950	hypothetical protein	3.32	1.52	0.46	2.26
ABUW_RS03955	hypothetical protein	3.30	2.24	0.50	1.55
ABUW_RS03960	hypothetical protein	2.67	0.51	-0.56	1.61
ABUW_RS03965	hypothetical protein	1.76	-0.97	-0.72	2.01
ABUW_RS03970	hypothetical protein	0.14	-0.35	0.27	0.76
ABUW_RS03975	hypothetical protein	0.14	-0.46	0.19	0.79
ABUW_RS03980	hypothetical protein	0.12	-0.43	0.11	0.67
ABUW_RS03990	integrase arm-type DNA-binding domain-containing protein	-0.23	0.46	-0.19	-0.87
ABUW_RS04000	amino acid permease	-0.20	-0.71	-0.31	0.21
ABUW_RS04005	2-methylnaconitate cis-trans isomerase PrpF	0.08	0.02	0.07	0.13
ABUW_RS04010	polyprenyl synthetase family protein	-0.32	0.20	0.22	-0.30
ABUW_RS04015	MmcQ/YjbR family DNA-binding protein	0.03	-0.07	0.12	0.22
ABUW_RS04020	SPFH/Band 7/PHB domain protein	-0.07	-0.29	-0.15	0.08
ABUW_RS04025	NfeD family protein	-0.16	-0.41	-0.14	0.11
ABUW_RS04030	patatin-like phospholipase family protein	0.36	0.09	-0.31	-0.04
ABUW_RS04035	1-acyl-sn-glycerol-3-phosphate acyltransferase	0.60	0.13	0.20	0.67
ABUW_RS04040	MFS transporter	-0.27	0.33	0.10	-0.51
ABUW_RS04045	porin	-1.33	0.26	-0.04	-1.63
ABUW_RS04050	phosphoethanolamine--lipid A transferase	3.11	4.55	0.19	-1.25
ABUW_RS04055	DNA-binding response regulator PmrA	2.40	2.61	-0.40	-0.61
ABUW_RS04060	two-component system sensor histidine kinase PmrB	1.34	1.54	-0.04	-0.24
ABUW_RS04065	phosphatase PAP2 family protein	3.97	4.10	0.28	0.15
ABUW_RS04070	ammonium transporter	3.40	1.93	-0.14	1.33
ABUW_RS04075	LysR family transcriptional regulator	0.49	-0.05	0.35	0.89
ABUW_RS04080	AEC family transporter	0.66	-0.61	0.12	1.38
ABUW_RS04085	molecular chaperone DnaJ	0.16	0.50	-0.28	-0.62
ABUW_RS04090	hypothetical protein	-0.75	1.45	-0.36	-2.55

ABUW_RS04095	valine--tRNA ligase	-0.28	-0.41	0.17	0.30
ABUW_RS04100	hypothetical protein	1.34	0.81	-0.28	0.26
ABUW_RS04105	SDR family NAD(P)-dependent oxidoreductase	0.62	0.35	-0.21	0.05
ABUW_RS04110	nuclear transport factor 2 family protein	1.25	0.83	0.00	0.42
ABUW_RS04115	YbjQ family protein	-0.64	-1.33	0.22	0.91
ABUW_RS04120	YbjQ family protein	0.16	-0.25	-0.18	0.23
ABUW_RS04125	multidrug efflux RND transporter outer membrane channel subunit AdeK	0.56	0.60	0.35	0.31
ABUW_RS04130	multidrug efflux RND transporter permease subunit AdeJ	1.01	1.37	0.12	-0.25
ABUW_RS04135	multidrug efflux RND transporter periplasmic adaptor subunit AdeI	1.62	1.22	-0.11	0.30
ABUW_RS04140	phosphatase PAP2 family protein	2.11	1.05	-0.02	1.05
ABUW_RS04145	site-specific recombinase	-0.69	-0.85	-0.04	0.13
ABUW_RS04150	polyprenyl synthetase family protein	0.09	-0.44	-0.03	0.49
ABUW_RS04155	hypothetical protein	-0.87	-1.02	1.99	2.14
ABUW_RS04160	50S ribosomal protein L21	0.72	-0.17	0.05	0.94
ABUW_RS04165	50S ribosomal protein L27	0.80	-0.24	-0.04	1.00
ABUW_RS04170	outer membrane lipoprotein chaperone LolA	1.26	0.09	0.41	1.57
ABUW_RS04175	DUF3298 domain-containing protein	0.50	1.17	-0.53	-1.20
ABUW_RS04180	serine--tRNA ligase	0.63	0.21	-0.21	0.20
ABUW_RS04185	uroporphyrinogen-III C-methyltransferase	0.59	0.59	-0.09	-0.08
ABUW_RS04190	tRNA (cytidine(34)-2'-O)-methyltransferase	-0.16	0.28	-0.10	-0.53
ABUW_RS04195	helix-turn-helix transcriptional regulator	-0.01	-0.51	0.66	1.16
ABUW_RS04200	flavodoxin family protein	0.04	1.32	-0.19	-1.48
ABUW_RS04205	APC family permease	-0.60	-0.54	0.10	0.03
ABUW_RS04210	iron-containing alcohol dehydrogenase	-1.03	-0.66	0.16	-0.21
ABUW_RS04215	hypothetical protein	0.05	-0.42	-0.29	0.18
ABUW_RS04220	lipoyl(octanoyl) transferase LipB	-1.13	-0.75	0.21	-0.17
ABUW_RS04225	DUF493 domain-containing protein	0.55	1.82	0.15	-1.12
ABUW_RS04230	RNA polymerase sigma factor RpoD	-0.38	-0.32	0.12	0.06
ABUW_RS04235	hypothetical protein	0.54	0.37	-0.10	0.08
ABUW_RS04240	YecA family protein	0.97	0.64	-0.49	-0.16
ABUW_RS04245	rhodanese-related sulfurtransferase	-0.01	0.22	0.18	-0.05
ABUW_RS04250	DUF1289 domain-containing protein	0.10	0.83	-0.09	-0.82
ABUW_RS04255	citrate (Si)-synthase	-1.00	-0.74	0.21	-0.05
ABUW_RS04260	succinate dehydrogenase, cytochrome b556 subunit	0.62	-0.18	-0.68	0.13
ABUW_RS04265	succinate dehydrogenase, hydrophobic membrane anchor protein	1.21	0.07	-0.94	0.19
ABUW_RS04270	succinate dehydrogenase flavoprotein subunit	0.20	-0.73	-0.16	0.77
ABUW_RS04275	succinate dehydrogenase iron-sulfur subunit	0.71	-0.96	-0.23	1.44
ABUW_RS04280	2-oxoglutarate dehydrogenase E1 component	0.04	0.35	0.32	0.02
ABUW_RS04285	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase	0.04	0.26	0.33	0.11
ABUW_RS04290	dihydrolipoyl dehydrogenase	0.38	1.19	-0.28	-1.09
ABUW_RS04295	ADP-forming succinate--CoA ligase subunit beta	0.33	1.41	-0.08	-1.17
ABUW_RS04300	succinate--CoA ligase subunit alpha	-0.74	0.38	0.38	-0.73
ABUW_RS04310	hypothetical protein	-0.93	0.10	0.00	-1.02

ABUW_RS04315	tryptophan--tRNA ligase	-0.77	0.31	-0.01	-1.09
ABUW_RS04320	DUF808 domain-containing protein	0.25	1.63	-0.44	-1.82
ABUW_RS04325	neutral zinc metallopeptidase	0.31	2.53	-0.54	-2.76
ABUW_RS04330	cation:proton antiporter	-0.80	0.73	-0.32	-1.84
ABUW_RS04345	hypothetical protein	-0.80	0.21	0.11	-0.90
ABUW_RS04350	CapA family protein	-1.07	-0.25	-0.01	-0.83
ABUW_RS04355	metalloprotease	-0.54	0.74	0.15	-1.12
ABUW_RS04360	MGMT family protein	-0.35	-0.01	0.24	-0.11
ABUW_RS04365	universal stress protein	0.09	0.74	0.19	-0.46
ABUW_RS04370	CatB-related O-acetyltransferase	0.34	0.37	0.01	-0.01
ABUW_RS04375	transcription elongation factor GreA	0.11	-0.79	0.03	0.93
ABUW_RS04380	carbamoyl-phosphate synthase large subunit	-0.88	-0.62	0.17	-0.09
ABUW_RS04385	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	0.18	-0.56	-0.19	0.55
ABUW_RS04390	hypothetical protein	-0.15	-1.22	-0.26	0.81
ABUW_RS04395	DOMON-like domain-containing protein	0.54	-1.01	0.45	1.99
ABUW_RS04400	ribosome assembly RNA-binding protein YhbY	0.63	0.05	0.09	0.67
ABUW_RS04405	23S rRNA (uridine(2552)-2'-O)-methyltransferase RlmE	0.77	0.91	0.10	-0.04
ABUW_RS04410	ATP-dependent zinc metalloprotease FtsH	1.06	0.36	-0.22	0.48
ABUW_RS04415	dihydropteroate synthase	0.79	1.04	-0.21	-0.45
ABUW_RS04420	hypothetical protein	1.43	-0.01	-0.06	1.38
ABUW_RS04425	hypothetical protein	-0.48	0.31	0.86	0.07
ABUW_RS04435	alkaline phosphatase D family protein	0.46	0.84	0.30	-0.08
ABUW_RS04450	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase Fld	0.24	-0.49	0.01	0.74
ABUW_RS04455	methyltransferase	0.16	-0.45	-0.03	0.59
ABUW_RS04460	hypothetical protein	-0.53	-0.64	0.01	0.11
ABUW_RS04465	MFS transporter	-0.88	0.61	-0.13	-1.62
ABUW_RS04470	glycerol kinase GlpK	0.50	0.78	-0.24	-0.51
ABUW_RS04475	glycerol-3-phosphate dehydrogenase	1.07	0.80	-0.11	0.16
ABUW_RS04480	phosphoenolpyruvate carboxykinase (GTP)	0.16	0.01	-0.01	0.14
ABUW_RS04485	NAD(+)/NADH kinase	-0.19	0.44	-0.07	-0.70
ABUW_RS04490	metallophosphoesterase	0.16	0.08	0.00	0.08
ABUW_RS04495	Ig-like domain repeat protein	-1.50	1.05	-0.25	-2.80
ABUW_RS04500	co-chaperone GroES	0.12	2.27	0.15	-2.00
ABUW_RS04505	chaperonin GroEL	0.12	1.53	-0.02	-1.43
ABUW_RS04510	diacylglycerol kinase	4.25	4.75	-0.01	-0.52
ABUW_RS04515	MBL fold metallo-hydrolase	-0.45	0.99	-0.27	-1.71
ABUW_RS04520	glycerophosphodiester phosphodiesterase	0.11	0.23	0.05	-0.07
ABUW_RS04525	multidrug efflux RND transporter permease subunit	0.38	0.25	-0.15	-0.03
ABUW_RS04530	DUF4112 domain-containing protein	-0.07	-0.39	-0.04	0.29
ABUW_RS04535	protease HtpX	-0.19	-0.47	0.14	0.42
ABUW_RS04540	lytic transglycosylase domain-containing protein	0.11	-1.02	0.13	1.26
ABUW_RS04545	tRNA 2-thiocytidine(32) synthetase TtcA	0.26	-0.28	-0.25	0.29
ABUW_RS04550	SCP2 sterol-binding domain-containing protein	1.05	0.62	-0.58	-0.15

ABUW_RS04555	transglycosylase SLT domain-containing protein	-1.56	-2.55	0.40	1.38
ABUW_RS04560	transcription elongation factor GreB	-0.21	0.10	0.38	0.08
ABUW_RS04570	SgcJ/EcaC family oxidoreductase	-0.95	-0.23	0.42	-0.29
ABUW_RS04575	non-ribosomal peptide synthetase	3.36	3.21	0.05	0.20
ABUW_RS04580	hypothetical protein	-0.62	1.63	-0.37	-2.63
ABUW_RS04590	hypothetical protein	-0.95	-1.45	-0.33	0.16
ABUW_RS04595	hypothetical protein	0.62	-0.79	-1.13	0.29
ABUW_RS04600	hypothetical protein	-1.66	-0.27	0.10	-1.30
ABUW_RS04605	helix-turn-helix transcriptional regulator	4.17	2.64	0.22	1.75
ABUW_RS04610	nitroreductase family protein	0.07	-1.31	0.11	1.48
ABUW_RS04615	SDR family oxidoreductase	0.33	-2.61	0.10	3.04
ABUW_RS04620	TetR/AcrR family transcriptional regulator	1.60	0.72	0.19	1.07
ABUW_RS04625	glycerate kinase	0.54	0.27	-0.04	0.23
ABUW_RS04630	FdhF/YdeP family oxidoreductase	1.11	0.59	0.17	0.68
ABUW_RS04635	formate dehydrogenase accessory sulfurtransferase FdhD	1.59	0.75	-0.06	0.78
ABUW_RS04640	DUF1232 domain-containing protein	1.21	1.46	0.17	-0.08
ABUW_RS04645	4-phosphoerythronate dehydrogenase	1.08	0.68	-0.02	0.37
ABUW_RS04650	EF-P lysine aminoacylase GenX	0.41	0.03	-0.27	0.11
ABUW_RS04655	Tim44 domain-containing protein	-0.12	-0.28	-0.03	0.13
ABUW_RS04660	DNA repair protein RadA	0.80	-0.05	-0.05	0.80
ABUW_RS04665	amino acid permease	-0.18	0.10	-0.32	-0.60
ABUW_RS04670	hypothetical protein	0.58	0.84	-0.09	-0.35
ABUW_RS04675	diaminopimelate decarboxylase	0.17	0.14	-0.14	-0.11
ABUW_RS04680	diaminopimelate epimerase	0.38	-0.23	-0.22	0.39
ABUW_RS04685	alpha/beta fold hydrolase	-0.09	-0.24	-0.01	0.15
ABUW_RS04690	LysE family translocator	-0.05	0.67	0.26	-0.46
ABUW_RS04695	tyrosine recombinase	-0.32	-0.17	0.03	-0.12
ABUW_RS04700	electron transfer flavoprotein subunit beta/FixA family protein	0.41	0.21	-0.02	0.18
ABUW_RS04705	FAD-binding protein	0.35	-0.17	-0.01	0.51
ABUW_RS04710	DNA gyrase subunit A	0.01	-0.11	0.08	0.20
ABUW_RS04715	glycosyltransferase family 39 protein	3.24	3.86	0.11	-0.52
ABUW_RS04720	GtrA family protein	4.39	4.30	0.96	1.05
ABUW_RS04725	glycosyltransferase family 2 protein	5.88	5.74	0.15	0.29
ABUW_RS04730	ChbG/HpnK family deacetylase	7.28	7.04	0.87	1.11
ABUW_RS04735	ABC transporter permease	-1.73	-0.34	0.51	-0.88
ABUW_RS04740	ABC transporter permease	-0.66	0.74	-0.02	-1.43
ABUW_RS04745	HlyD family secretion protein	-1.22	0.16	-0.12	-1.51
ABUW_RS04750	TolC family protein	-0.89	0.37	0.38	-0.87
ABUW_RS04755	3-phosphoserine/phosphohydroxythreonine transaminase	0.21	0.40	-0.34	-0.52
ABUW_RS04760	hypothetical protein	-1.84	1.06	0.62	-2.29
ABUW_RS04765	Yail/YqxJ family protein	-1.06	0.69	0.14	-1.61
ABUW_RS04770	EamA family transporter	-0.71	-0.04	-0.30	-0.97
ABUW_RS04775	lipoprotein-releasing ABC transporter permease subunit	0.57	0.53	-0.43	-0.39

ABUW_RS04780	lipoprotein-releasing ABC transporter ATP-binding protein LolD	-0.21	0.34	-0.27	-0.82
ABUW_RS04785	DNA internalization-related competence protein ComEC/Rec2	-0.94	-0.28	0.07	-0.60
ABUW_RS04790	lysophospholipid acyltransferase family protein	-1.18	-0.20	0.19	-0.80
ABUW_RS04795	signal peptide peptidase SppA	-0.21	0.68	-0.23	-1.12
ABUW_RS04800	alpha/beta hydrolase	-0.10	0.39	-0.54	-1.02
ABUW_RS04805	phosphoribosylglycinamide formyltransferase	0.12	-0.01	-0.01	0.12
ABUW_RS04810	phosphoribosylformylglycinamide cyclo-ligase	0.74	0.30	-0.28	0.16
ABUW_RS04815	AI-2E family transporter	0.27	0.57	-0.42	-0.73
ABUW_RS04820	DnaA regulatory inactivator Hda	-0.05	-0.23	-0.10	0.08
ABUW_RS04825	rhombotarget A	0.10	0.94	0.04	-0.80
ABUW_RS04830	CSLREA domain-containing protein	-0.79	0.20	0.31	-0.67
ABUW_RS04835	DUF3106 domain-containing protein	0.28	0.19	0.12	0.21
ABUW_RS04840	hypothetical protein	0.93	-0.27	-0.29	0.92
ABUW_RS04845	RNA polymerase sigma factor	0.99	0.28	-0.04	0.68
ABUW_RS04850	RNA methyltransferase	-0.85	-0.63	0.35	0.12
ABUW_RS04855	class 1 fructose-bisphosphatase	0.19	0.39	-0.25	-0.46
ABUW_RS04860	NF038105 family protein	1.32	3.34	-0.13	-2.16
ABUW_RS04865	peptidoglycan-associated lipoprotein Pal	0.68	0.31	-0.12	0.25
ABUW_RS04870	Tol-Pal system beta propeller repeat protein TolB	0.24	0.60	-0.09	-0.45
ABUW_RS04875	cell envelope integrity protein TolA	0.74	0.39	-0.51	-0.16
ABUW_RS04880	protein TolR	0.29	0.24	-0.36	-0.31
ABUW_RS04885	protein TolQ	0.83	0.81	-0.40	-0.38
ABUW_RS04890	tol-pal system-associated acyl-CoA thioesterase	0.46	0.12	0.06	0.40
ABUW_RS04895	amidohydrolase	-0.35	-0.63	0.00	0.29
ABUW_RS04900	Holliday junction branch migration DNA helicase RuvB	-0.18	-1.17	0.06	1.04
ABUW_RS04905	Holliday junction branch migration protein RuvA	-0.13	-0.93	0.18	0.99
ABUW_RS04910	deoxyguanosinetriphosphate triphosphohydrolase	-1.13	-0.98	0.44	0.28
ABUW_RS04915	phosphoribosylformylglycinamide synthase	0.54	0.00	-0.34	0.19
ABUW_RS04920	multidrug efflux MFS transporter	0.71	0.22	-0.13	0.36
ABUW_RS04930	NIF3 1	-0.14	-0.10	0.15	0.12
ABUW_RS04935	enoyl-CoA hydratase/isomerase family protein	-1.53	-0.25	0.51	-0.77
ABUW_RS04940	nicotinate-nicotinamide nucleotide adenyltransferase	0.61	0.31	-0.30	0.00
ABUW_RS04945	CAP domain-containing protein	-0.57	1.24	0.67	-1.13
ABUW_RS04950	peroxiredoxin	0.07	1.09	-0.01	-1.03
ABUW_RS04955	diphthine--ammonia ligase	0.27	-0.10	0.31	0.67
ABUW_RS04960	hypothetical protein	0.12	0.68	-0.15	-0.71
ABUW_RS04965	7-cyano-7-deazaguanine synthase QueC	-0.17	-0.28	0.01	0.11
ABUW_RS04970	7-carboxy-7-deazaguanine synthase QueE	0.25	-0.92	0.13	1.30
ABUW_RS04975	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	-0.11	0.16	-0.30	-0.57
ABUW_RS04980	ornithine uptake porin CarO type 3	0.63	-0.06	0.07	0.76
ABUW_RS04985	CysB family HTH-type transcriptional regulator	-0.54	-0.55	0.17	0.18
ABUW_RS04990	sulfate ABC transporter ATP-binding protein	0.05	0.01	-0.26	-0.22
ABUW_RS04995	sulfate ABC transporter permease subunit CysW	0.63	0.12	0.07	0.58

ABUW_RS05000	sulfate ABC transporter permease subunit CysT	0.60	-0.98	-0.03	1.55
ABUW_RS05005	alpha/beta hydrolase	0.32	-1.10	0.01	1.43
ABUW_RS05010	sulfate ABC transporter substrate-binding protein	1.90	-0.64	-0.37	2.17
ABUW_RS05015	aminodeoxychorismate lyase	0.72	1.41	-0.57	-1.26
ABUW_RS05020	endolytic transglycosylase MltG	0.21	0.69	-0.21	-0.69
ABUW_RS05025	dTMP kinase	0.43	0.56	-0.30	-0.44
ABUW_RS05030	Paal family thioesterase	-0.27	-0.12	0.23	0.08
ABUW_RS05035	L-aspartate oxidase	-0.87	-0.79	0.06	-0.03
ABUW_RS05040	Do family serine endopeptidase	1.32	1.43	-0.08	-0.19
ABUW_RS05045	acyl-CoA thioesterase	-0.12	0.00	-0.22	-0.33
ABUW_RS05050	elongation factor 4	0.38	0.23	-0.20	-0.05
ABUW_RS05055	signal peptidase I	0.56	0.61	-0.24	-0.30
ABUW_RS05060	DUF4845 domain-containing protein	0.10	-0.33	-0.15	0.28
ABUW_RS05065	ribonuclease III	-0.28	-0.43	-0.14	0.00
ABUW_RS05070	GTPase Era	0.49	0.31	-0.43	-0.25
ABUW_RS05075	NF038104 family lipoprotein	1.27	-0.03	-0.18	1.12
ABUW_RS05080	DNA repair protein RecO	0.29	-0.66	0.16	1.12
ABUW_RS05085	pyridoxine 5'-phosphate synthase	0.77	0.49	-0.57	-0.29
ABUW_RS05090	tRNA-(ms[2]io[6]A)-hydroxylase	0.22	0.07	-0.42	-0.27
ABUW_RS05095	SDR family oxidoreductase	-2.26	0.57	0.19	-2.64
ABUW_RS05105	hypothetical protein	-2.43	-2.13	0.94	0.64
ABUW_RS05110	Paal family thioesterase	-0.34	-0.69	0.37	0.72
ABUW_RS05115	GFA family protein	0.18	1.86	-0.48	-2.16
ABUW_RS05120	pyridoxal phosphate-dependent aminotransferase	0.32	0.46	-0.08	-0.22
ABUW_RS05125	hypothetical protein	0.41	2.36	0.09	-1.86
ABUW_RS05130	diguanylate cyclase	-1.02	0.29	0.30	-1.01
ABUW_RS05135	hypothetical protein	0.90	0.22	-0.26	0.42
ABUW_RS05140	excinuclease ABC subunit UvrB	0.81	1.59	0.05	-0.73
ABUW_RS05145	lipocalin family protein	-0.03	0.85	-0.15	-1.03
ABUW_RS05150	EamA family transporter RarD	0.46	1.01	-0.69	-1.24
ABUW_RS05155	glyceraldehyde-3-phosphate dehydrogenase	-0.61	-0.38	-0.21	-0.44
ABUW_RS05160	hypothetical protein	-0.08	0.95	-0.40	-1.44
ABUW_RS05165	hypothetical protein	-1.08	0.11	-0.01	-1.21
ABUW_RS05170	Obg family GTPase CgtA	0.80	0.47	-0.33	-0.01
ABUW_RS05175	glutamate 5-kinase	0.95	-0.01	-0.17	0.80
ABUW_RS05180	HAD-IB family hydrolase	-0.85	0.28	0.43	-0.70
ABUW_RS05185	DUF1615 domain-containing protein	0.26	-0.29	-0.08	0.46
ABUW_RS05190	tRNA dihydrouridine synthase DusB	0.44	-0.10	-0.15	0.39
ABUW_RS05195	nitronate monooxygenase	-1.24	-1.31	0.22	0.29
ABUW_RS05200	VIT family protein	-0.35	0.53	0.10	-0.79
ABUW_RS05205	hypothetical protein	0.27	1.94	0.15	-1.52
ABUW_RS05210	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-0.33	1.21	0.29	-1.25
ABUW_RS05215	hypothetical protein	-0.60	0.63	-0.13	-1.36
ABUW_RS05220	hypothetical protein	-1.35	0.59	0.24	-1.71

ABUW_RS05225	glycosyltransferase family 2 protein	-0.44	0.17	-0.14	-0.75
ABUW_RS05230	hypothetical protein	-0.98	-0.73	0.34	0.09
ABUW_RS05235	hypothetical protein	0.37	0.99	0.10	-0.52
ABUW_RS05240	deoxyribodipyrimidine photo-lyase	-1.47	-0.49	0.59	-0.39
ABUW_RS05245	peptidylprolyl isomerase	-0.47	-0.03	0.48	0.04
ABUW_RS05250	NAD(P)/FAD-dependent oxidoreductase	0.94	1.24	0.14	-0.16
ABUW_RS05255	D-alanyl-D-alanine carboxypeptidase PBP6B	0.30	0.45	-0.22	-0.37
ABUW_RS05260	M61 family metalloproteinase	-0.22	0.46	-0.19	-0.87
ABUW_RS05265	NADP-dependent isocitrate dehydrogenase	-0.51	0.40	0.16	-0.76
ABUW_RS05270	rRNA large subunit pseudouridine synthase E	0.17	0.39	-0.19	-0.40
ABUW_RS05275	NADP-dependent isocitrate dehydrogenase	0.72	1.32	-0.11	-0.71
ABUW_RS05285	hypothetical protein	-1.35	0.42	-0.09	-1.85
ABUW_RS05290	YbfB/YjiJ family MFS transporter	1.62	0.67	-0.24	0.71
ABUW_RS05295	LysR family transcriptional regulator	2.64	2.37	-0.02	0.26
ABUW_RS05300	L-cystine transporter	0.71	0.07	-0.30	0.34
ABUW_RS05305	PhzF family phenazine biosynthesis protein	-0.59	0.09	-0.47	-1.15
ABUW_RS05310	insulinase family protein	-0.83	0.55	-0.09	-1.47
ABUW_RS05315	DUF3144 domain-containing protein	1.96	1.24	-0.54	0.18
ABUW_RS05320	hypothetical protein	-1.11	0.07	0.32	-0.86
ABUW_RS05325	CYTH and CHAD domain-containing protein	-0.15	0.86	0.08	-0.93
ABUW_RS05330	DUF962 domain-containing protein	0.89	1.21	0.07	-0.24
ABUW_RS05335	type I-F CRISPR-associated endonuclease Cas1	0.47	0.05	0.10	0.52
ABUW_RS05340	type I-F CRISPR-associated helicase Cas3	-0.16	-0.19	0.14	0.17
ABUW_RS05345	type I-F CRISPR-associated protein Csy1	-0.41	0.05	-0.33	-0.80
ABUW_RS05350	type I-F CRISPR-associated protein Csy2	-1.43	0.04	0.17	-1.30
ABUW_RS05355	type I-F CRISPR-associated protein Csy3	-1.80	0.08	0.12	-1.76
ABUW_RS05360	type I-F CRISPR-associated endonuclease Cas6/Csy4	-0.62	0.45	-0.29	-1.36
ABUW_RS05365	thiamine phosphate synthase	0.06	-0.39	-0.03	0.43
ABUW_RS05370	glutamate-1-semialdehyde 2,1-aminomutase	-0.03	0.11	-0.19	-0.33
ABUW_RS05375	isochorismatase	0.25	1.55	0.12	-1.18
ABUW_RS05380	RluA family pseudouridine synthase	0.33	0.34	0.02	0.01
ABUW_RS05385	RNA polymerase-associated protein RapA	-0.33	-0.33	0.08	0.08
ABUW_RS05390	AI-2E family transporter	-0.89	-0.08	-0.02	-0.82
ABUW_RS05395	HTH-type transcriptional repressor FabR	-0.47	0.03	0.01	-0.48
ABUW_RS05400	ferredoxin reductase	-0.96	-0.91	-0.20	-0.26
ABUW_RS05405	acyl-CoA desaturase	-1.02	-1.27	-0.02	0.24
ABUW_RS05410	DUF4442 domain-containing protein	0.19	0.66	0.02	-0.46
ABUW_RS05415	TetR/AcrR family transcriptional regulator	0.78	1.68	-0.54	-1.44
ABUW_RS05420	SIMPL domain-containing protein	0.87	1.02	0.56	0.41
ABUW_RS05425	diaminobutyrate--2-oxoglutarate transaminase	0.01	-0.56	0.18	0.76
ABUW_RS05430	aspartate aminotransferase family protein	0.18	-0.07	0.02	0.27
ABUW_RS05435	aldehyde dehydrogenase family protein	1.22	-0.95	0.93	3.10
ABUW_RS05440	Lrp/AsnC family transcriptional regulator	-0.77	0.81	0.01	-1.58
ABUW_RS05445	alpha-keto acid decarboxylase family protein	0.65	-1.79	1.20	3.63

ABUW_RS05450	amino acid permease	1.23	-0.97	0.23	2.43
ABUW_RS05455	substrate-binding domain-containing protein	-0.51	1.01	0.30	-1.22
ABUW_RS05460	phosphate ABC transporter permease subunit PstC	-0.28	0.44	-0.30	-1.02
ABUW_RS05465	phosphate ABC transporter permease PstA	-0.49	0.16	-0.05	-0.70
ABUW_RS05470	phosphate ABC transporter ATP-binding protein	-0.03	-0.10	-0.06	0.02
ABUW_RS05475	protease SohB	-0.57	0.83	0.08	-1.32
ABUW_RS05480	BapA prefix-like domain-containing protein	-0.33	1.35	-0.09	-1.77
ABUW_RS05485	DUF2238 domain-containing protein	-0.10	1.23	0.29	-1.03
ABUW_RS05490	adenylosuccinate lyase	-0.43	-0.10	-0.06	-0.40
ABUW_RS05495	high frequency lysogenization protein HflD	-0.37	-0.49	-0.17	-0.04
ABUW_RS05500	tRNA 2-thiouridine(34) synthase MnmA	0.71	-0.18	-0.26	0.63
ABUW_RS05505	NUDIX hydrolase	1.44	-0.46	-0.10	1.81
ABUW_RS05510	gamma carbonic anhydrase family protein	0.19	-0.33	0.04	0.56
ABUW_RS05515	D-alanyl-D-alanine carboxypeptidase PBP5/6	-0.30	-0.48	0.17	0.35
ABUW_RS05520	hypothetical protein	0.31	0.47	0.17	0.01
ABUW_RS05525	hypothetical protein	-0.24	-1.35	0.00	1.11
ABUW_RS05530	5'/3'-nucleotidase SurE	-0.11	0.30	0.25	-0.16
ABUW_RS05535	peptidoglycan DD-metalloendopeptidase family protein	0.71	0.33	-0.42	-0.03
ABUW_RS05540	LysR family transcriptional regulator	0.59	0.24	-0.20	0.15
ABUW_RS05545	ATP-binding protein	-1.35	-0.08	0.37	-0.90
ABUW_RS05550	MFS transporter	-0.20	0.73	-0.22	-1.14
ABUW_RS05555	lactoylglutathione lyase	0.90	1.32	-0.96	-1.38
ABUW_RS05560	bile acid:sodium symporter	0.50	-0.07	-0.85	-0.28
ABUW_RS05565	50S ribosomal protein L31	1.92	2.32	-1.21	-1.61
ABUW_RS05570	EAL domain-containing protein	-0.51	-1.15	0.17	0.81
ABUW_RS05575	hypothetical protein	-0.70	-0.44	0.49	0.23
ABUW_RS05580	EF-P beta-lysylation protein EpmB	-0.30	0.23	0.20	-0.32
ABUW_RS05585	elongation factor P	-0.42	0.13	0.10	-0.45
ABUW_RS05590	carbon starvation protein A	0.71	0.12	-0.33	0.25
ABUW_RS05595	YbdD/YjiX family protein	1.05	-0.15	-0.53	0.67
ABUW_RS05605	LysR family transcriptional regulator	-0.85	0.31	0.22	-0.94
ABUW_RS05610	aminopeptidase P family protein	1.03	0.66	-0.26	0.12
ABUW_RS05615	BCCT family transporter	-0.87	-0.38	0.18	-0.30
ABUW_RS05620	BCCT family transporter	-0.45	-0.15	-0.04	-0.34
ABUW_RS05625	aromatic ring-hydroxylating dioxygenase subunit alpha	-0.58	-0.88	0.26	0.56
ABUW_RS05630	aldehyde dehydrogenase family protein	0.37	-0.55	0.15	1.08
ABUW_RS05635	FAD-dependent oxidoreductase	0.05	-0.67	0.22	0.94
ABUW_RS05640	FAD-binding oxidoreductase	-0.43	-0.62	0.03	0.22
ABUW_RS05645	ethanolamine utilization protein EutQ	0.03	2.21	-0.97	-3.15
ABUW_RS05650	hypothetical protein	0.14	0.85	0.33	-0.38
ABUW_RS05655	MarC family protein	0.32	-0.13	-0.37	0.08
ABUW_RS05660	aromatic amino acid DMT transporter YddG	-2.56	-0.54	0.82	-1.19
ABUW_RS05665	DMT family transporter	-1.44	-0.48	0.37	-0.59

ABUW_RS05670	type II toxin-antitoxin system Phd/YefM family antitoxin	-2.03	-0.21	-0.29	-2.11
ABUW_RS05675	TetR/AcrR family transcriptional regulator	-1.96	0.00	0.11	-1.85
ABUW_RS05680	hypothetical protein	-3.46	-0.05	-0.08	-3.49
ABUW_RS05685	hypothetical protein	-3.25	-0.37	0.68	-2.20
ABUW_RS05690	TetR/AcrR family transcriptional regulator	2.69	0.60	-0.82	1.27
ABUW_RS05695	pirin family protein	3.21	1.70	-0.55	0.97
ABUW_RS05700	threo-3-hydroxy-L-aspartate ammonia-lyase	-1.10	-0.04	0.32	-0.75
ABUW_RS05705	PAS domain-containing protein	0.07	0.63	0.41	-0.15
ABUW_RS05710	acinetobactin utilization protein BauF	-4.10	0.99	0.56	-4.53
ABUW_RS05715	acinetobactin non-ribosomal peptide synthetase subunit BasA	-3.58	2.14	0.23	-5.48
ABUW_RS05720	acinetobactin non-ribosomal peptide synthetase subunit BasB	-1.54	2.56	0.94	-3.16
ABUW_RS05725	ferric acinetobactin ABC transporter permease subunit BauD	-0.14	1.91	0.08	-1.97
ABUW_RS05730	ferric acinetobactin ABC transporter permease subunit BauC	-0.11	2.29	-0.07	-2.47
ABUW_RS05735	ferric acinetobactin ABC transporter ATP-binding protein BauE	-0.48	2.05	0.24	-2.28
ABUW_RS05740	siderophore-binding periplasmic lipoprotein BauB	0.15	3.05	-0.25	-3.15
ABUW_RS05745	TonB-dependent ferric acinetobactin receptor BauA	-1.51	2.91	0.39	-4.03
ABUW_RS05750	putative histamine N-monooxygenase	-0.52	2.90	0.49	-2.93
ABUW_RS05755	acinetobactin non-ribosomal peptide synthetase subunit BasD	-0.70	3.20	0.46	-3.44
ABUW_RS05760	(2,3-dihydroxybenzoyl)adenylate synthase BasE	0.19	3.42	0.01	-3.21
ABUW_RS05765	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-0.17	4.08	0.28	-3.98
ABUW_RS05770	acinetobactin biosynthesis histidine decarboxylase BasG	-0.05	3.92	0.13	-3.85
ABUW_RS05780	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-1.37	2.71	0.48	-3.60
ABUW_RS05785	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-1.31	2.71	0.53	-3.49
ABUW_RS05790	acinetobactin biosynthesis thioesterase Bash	-0.66	3.02	0.36	-3.33
ABUW_RS05795	acinetobactin biosynthesis phosphopantetheinyl transferase BasI	-0.90	2.19	0.43	-2.66
ABUW_RS05800	acinetobactin biosynthesis isochorismate synthase BasJ	0.83	7.59	0.17	-6.59
ABUW_RS05805	murein L,D-transpeptidase	-0.76	-0.19	0.06	-0.51
ABUW_RS05810	uroporphyrinogen decarboxylase	-0.68	-0.18	0.02	-0.48
ABUW_RS05815	DUF817 family protein	0.16	-0.60	-0.08	0.68
ABUW_RS05820	DUF3015 family protein	-2.01	2.81	-0.13	-4.95
ABUW_RS05825	DUF4105 domain-containing protein	-2.35	-0.39	0.25	-1.71
ABUW_RS05830	class C extended-spectrum beta-lactamase ADC-11	-1.36	0.84	-0.02	-2.21
ABUW_RS05835	GTP cyclohydrolase I FofE	0.40	-0.78	-0.10	1.08
ABUW_RS05840	xanthine dehydrogenase small subunit	0.45	0.41	-0.02	0.02
ABUW_RS05845	xanthine dehydrogenase molybdopterin binding subunit	0.86	0.27	-0.15	0.43
ABUW_RS05850	xanthine dehydrogenase accessory protein XdhC	0.71	-0.30	-0.22	0.79
ABUW_RS05855	Smr/MutS family protein	-0.41	-0.30	0.02	-0.10
ABUW_RS05860	indole-3-glycerol phosphate synthase TrpC	0.13	-0.04	0.11	0.28
ABUW_RS05865	anthranilate phosphoribosyltransferase	0.41	-0.28	-0.04	0.65
ABUW_RS05870	TonB-dependent receptor	-0.23	0.09	0.31	-0.01
ABUW_RS05875	M1 family metallopeptidase	-0.74	0.47	0.11	-1.09

ABUW_RS05880	aminodeoxychorismate/anthranilate synthase component II	0.04	-0.18	-0.15	0.08
ABUW_RS05885	aminopeptidase P family protein	-1.08	-1.19	0.23	0.34
ABUW_RS05890	peptide MFS transporter	-1.07	-0.67	-0.07	-0.46
ABUW_RS05895	type I glutamate--ammonia ligase	0.30	0.29	0.25	0.26
ABUW_RS05900	chorismate lyase	-0.63	-0.07	0.15	-0.41
ABUW_RS05905	4-hydroxybenzoate octaprenyltransferase	0.33	0.32	-0.49	-0.48
ABUW_RS05910	hypothetical protein	-0.66	0.65	-0.14	-1.45
ABUW_RS05915	hypothetical protein	1.11	1.32	-0.85	-1.05
ABUW_RS05920	DUF2726 domain-containing protein	0.32	-0.67	0.53	1.52
ABUW_RS05940	superoxide dismutase	-0.45	-0.68	0.06	0.30
ABUW_RS05945	Nif3-like dinuclear metal center hexameric protein	-0.94	0.05	-0.08	-1.06
ABUW_RS05950	trypsin-like peptidase domain-containing protein	0.44	0.92	-0.43	-0.91
ABUW_RS05955	multifunctional CCA addition/repair protein	0.93	-0.38	-0.33	0.98
ABUW_RS05960	NADP-dependent malic enzyme	-0.86	-0.02	0.22	-0.62
ABUW_RS05965	EAL domain-containing protein	-2.40	-0.31	0.40	-1.68
ABUW_RS05970	16S rRNA (uracil(1498)-N(3))-methyltransferase	-0.49	-0.42	0.03	-0.04
ABUW_RS05975	methylenetetrahydrofolate reductase [NAD(P)H]	-0.84	-0.59	0.31	0.06
ABUW_RS05980	adenosylhomocysteinase	-0.89	-0.60	0.25	-0.04
ABUW_RS05985	peptidase C39 carboxymuconolactone decarboxylase family protein	0.70	0.35	-0.60	-0.25
ABUW_RS05990		-1.27	-0.87	0.00	-0.40
ABUW_RS05995	acyl-CoA dehydrogenase	-0.16	1.23	-0.02	-1.42
ABUW_RS06000	lipoyl synthase	0.57	0.78	-0.04	-0.25
ABUW_RS06005	Si-specific NAD(P)(+) transhydrogenase	-0.28	0.39	-0.06	-0.73
ABUW_RS06015	MFS transporter	0.14	0.19	-0.14	-0.19
ABUW_RS06020	MFS transporter	1.33	-0.34	0.49	2.16
ABUW_RS06025	OmpW family protein	1.42	-0.17	0.21	1.79
ABUW_RS06030	type I methionyl aminopeptidase	0.46	0.41	-0.25	-0.20
ABUW_RS06035	30S ribosomal protein S2	-0.35	-1.64	0.33	1.62
ABUW_RS06040	elongation factor Ts	-0.17	-0.99	-0.01	0.81
ABUW_RS06045	DUF3465 domain-containing protein	0.85	0.38	-0.18	0.28
ABUW_RS06050	AraC family transcriptional regulator	-0.18	-0.35	0.21	0.39
ABUW_RS06055	AzIC family ABC transporter permease	-0.95	-0.67	0.38	0.11
ABUW_RS06060	AzID domain-containing protein	0.28	-0.73	-0.61	0.40
ABUW_RS06065	DUF962 domain-containing protein	0.53	0.91	0.24	-0.14
ABUW_RS06070	septal ring lytic transglycosylase RlpA family protein	-0.25	-1.21	-0.35	0.61
ABUW_RS06075	lytic murein transglycosylase B	-1.11	-0.42	0.00	-0.69
ABUW_RS06080	rod shape-determining protein RodA	0.81	0.51	-0.45	-0.15
ABUW_RS06085	hypothetical protein	-0.33	-0.75	0.18	0.60
ABUW_RS06090	NADPH-dependent 7-cyano-7-deazaguanine reductase QueF	-0.81	-0.45	0.06	-0.29
ABUW_RS06095	ABC transporter permease	-0.56	0.03	-0.16	-0.75
ABUW_RS06100	ABC transporter ATP-binding protein	-0.31	-0.07	0.06	-0.18
ABUW_RS06105	site-specific integrase	0.18	-0.16	-0.20	0.14
ABUW_RS06110	hypothetical protein	2.21	0.04	0.95	3.12

ABUW_RS06115	hypothetical protein	2.35	2.84	1.05	0.57
ABUW_RS06120	hypothetical protein	3.18	-0.35	-0.02	3.51
ABUW_RS06125	hypothetical protein	3.52	-0.23	-0.36	3.38
ABUW_RS06130	hypothetical protein	3.13	-0.44	0.02	3.58
ABUW_RS06135	hypothetical protein	3.01	-0.60	0.56	4.17
ABUW_RS06140	hypothetical protein	3.41	-0.88	0.41	4.69
ABUW_RS06145	PD-(D/E)XK nuclease-like domain-containing protein	3.53	-1.65	0.80	5.99
ABUW_RS06150	hypothetical protein	3.43	-0.61	1.00	5.03
ABUW_RS06155	hypothetical protein	4.10	-0.69	0.62	5.41
ABUW_RS06160	hypothetical protein	3.73	-0.46	0.26	4.45
ABUW_RS06165	hypothetical protein	2.46	-0.74	-0.34	2.86
ABUW_RS06180	hypothetical protein	0.85	-0.55	0.09	1.49
ABUW_RS06185	helix-turn-helix domain-containing protein	0.82	0.45	-0.03	0.34
ABUW_RS06190	hypothetical protein	4.26	0.85	0.12	3.54
ABUW_RS06195	hypothetical protein	3.64	-0.47	0.17	4.29
ABUW_RS06200	replication protein	3.65	-0.77	0.52	4.94
ABUW_RS06205	AAA family ATPase	2.95	-1.71	0.77	5.43
ABUW_RS06215	hypothetical protein	3.36	-1.03	0.38	4.77
ABUW_RS06220	hypothetical protein	0.00	-0.82	0.00	0.96
ABUW_RS06225	hypothetical protein	1.08	1.23	0.00	0.00
ABUW_RS06230	hypothetical protein	NA	NA	NA	NA
ABUW_RS06235	hypothetical protein	3.99	0.64	-0.72	2.63
ABUW_RS06240	hypothetical protein	2.30	-0.12	-0.06	2.36
ABUW_RS06245	DUF559 domain-containing protein	2.04	0.50	-0.24	1.31
ABUW_RS06250	hypothetical protein	0.56	0.71	0.04	-0.11
ABUW_RS06255	hypothetical protein	-2.11	-0.87	0.52	-0.72
ABUW_RS06260	hypothetical protein	-2.13	-0.36	0.25	-1.52
ABUW_RS06265	hypothetical protein	0.43	-0.30	0.47	1.20
ABUW_RS06270	hypothetical protein	-1.10	-0.26	0.01	-0.84
ABUW_RS06275	hypothetical protein	-2.92	-1.50	0.71	-0.71
ABUW_RS06280	hypothetical protein	-1.39	0.83	-0.22	-2.45
ABUW_RS06285	hypothetical protein	0.79	0.29	0.13	0.64
ABUW_RS06290	hypothetical protein	0.80	-0.15	0.38	1.34
ABUW_RS06295	DUF2280 domain-containing protein	2.84	0.59	0.11	2.35
ABUW_RS06300	phage terminase large subunit	2.55	0.18	0.34	2.70
ABUW_RS06305	DUF4055 domain-containing protein	2.88	0.14	0.27	3.01
ABUW_RS06310	minor capsid protein	2.58	-0.02	0.05	2.65
ABUW_RS06315	hypothetical protein	-0.99	-0.01	0.80	-0.18
ABUW_RS06320	hypothetical protein	-0.29	-0.76	0.15	0.62
ABUW_RS06325	hypothetical protein	3.05	-1.25	1.16	5.46
ABUW_RS06330	hypothetical protein	4.62	0.09	0.71	5.24
ABUW_RS06335	hypothetical protein	2.84	-0.01	0.00	2.86
ABUW_RS06340	stress-responsive nuclear envelope protein	3.64	0.18	0.41	3.87
ABUW_RS06345	hypothetical protein	2.76	0.92	-0.03	1.80

ABUW_RS06350	hypothetical protein	2.27	-1.02	1.46	4.75
ABUW_RS06355	hypothetical protein	2.07	0.41	0.25	1.90
ABUW_RS06360	hypothetical protein	2.02	1.28	-0.39	0.35
ABUW_RS06365	hypothetical protein	1.28	-0.28	-0.08	1.48
ABUW_RS06370	hypothetical protein	0.00	-0.21	0.00	0.35
ABUW_RS06375	hypothetical protein	NA	NA	NA	NA
ABUW_RS06380	hypothetical protein	NA	NA	NA	NA
ABUW_RS06385	hypothetical protein	1.08	1.23	0.00	0.00
ABUW_RS06390	hypothetical protein	NA	NA	NA	NA
ABUW_RS06395	DUF3800 domain-containing protein	1.26	1.27	-0.03	-0.05
ABUW_RS06400	ORF6N domain-containing protein	-0.88	-1.61	0.47	1.20
ABUW_RS06405	hypothetical protein	0.36	0.04	0.22	0.53
ABUW_RS06410	DUF4468 domain-containing protein	0.18	0.61	-0.48	-0.91
ABUW_RS06415	hypothetical protein	0.54	1.76	-0.58	-1.80
ABUW_RS06420	tape measure protein	0.53	0.50	0.05	0.08
ABUW_RS06425	hypothetical protein	0.21	0.33	-0.25	-0.38
ABUW_RS06430	hypothetical protein	0.05	0.55	-0.54	-1.04
ABUW_RS06435	hypothetical protein	-0.43	1.43	-0.43	-2.28
ABUW_RS06440	hypothetical protein	3.72	2.08	0.00	1.42
ABUW_RS06445	DUF1833 family protein	-0.67	2.29	2.59	0.00
ABUW_RS06450	hypothetical protein	1.64	-0.10	0.06	1.80
ABUW_RS06455	hypothetical protein	2.63	1.69	0.68	1.62
ABUW_RS06460	hypothetical protein	3.21	0.96	-0.38	1.88
ABUW_RS06465	hypothetical protein	2.68	1.25	0.25	1.68
ABUW_RS06470	lysozyme	0.90	0.33	0.04	0.61
ABUW_RS06475	DUF4760 domain-containing protein	-0.27	0.96	-0.06	-1.29
ABUW_RS06480	hypothetical protein	0.38	-2.15	1.05	3.58
ABUW_RS06490	hypothetical protein	-0.08	-0.27	0.64	0.83
ABUW_RS06495	DUF3820 family protein	-0.13	-0.03	0.00	-0.10
ABUW_RS06500	alpha/beta fold hydrolase	0.22	0.57	0.25	-0.09
ABUW_RS06505	serine hydroxymethyltransferase	-0.53	-0.44	-0.18	-0.26
ABUW_RS06510	multidrug efflux RND transporter outer membrane subunit AdeH	0.26	-0.66	-0.37	0.54
ABUW_RS06515	multidrug efflux RND transporter permease subunit AdeG	0.47	-0.98	-0.24	1.22
ABUW_RS06520	multidrug efflux RND transporter periplasmic adaptor subunit AdeF	1.11	-0.80	-0.35	1.56
ABUW_RS06525	multidrug efflux transcriptional repressor AdeL	1.27	-0.13	-0.48	0.92
ABUW_RS06530	ABC transporter substrate-binding protein	1.94	-0.06	0.21	2.22
ABUW_RS06535	histidine ABC transporter permease HisQ	1.84	-0.47	0.75	3.06
ABUW_RS06540	ABC transporter permease	1.18	-0.23	0.00	1.41
ABUW_RS06545	ATP-binding cassette domain-containing protein	0.97	0.91	-0.02	0.04
ABUW_RS06550	multidrug efflux SMR transporter AbeS	-2.34	-1.64	0.46	-0.24
ABUW_RS06555	YfhL family 4Fe-4S dicluster ferredoxin	-1.03	-2.51	0.10	1.58
ABUW_RS06560	tRNA 5-hydroxyuridine modification protein YegQ	-0.38	-1.20	0.39	1.21
ABUW_RS06565	PLP-dependent aminotransferase family protein	-0.25	-1.06	0.04	0.85

ABUW_RS06570	PhzF family phenazine biosynthesis protein	-0.13	-1.28	-0.42	0.73
ABUW_RS06575	ferredoxin--NADP reductase	1.03	0.75	0.07	0.35
ABUW_RS06580	tRNA (N6-threonylcarbamoyladenosine(37)-N6)-methyltransferase TrmO	0.00	-0.22	0.21	0.43
ABUW_RS06585	MgtC/SapB family protein	-0.22	0.08	0.45	0.15
ABUW_RS06590	Flp pilus assembly complex ATPase component TadA	0.44	-1.28	0.06	1.78
ABUW_RS06595	NirD/YgiW/YdeI family stress tolerance protein	-0.28	-1.59	0.18	1.49
ABUW_RS06600	response regulator transcription factor	-0.69	-1.32	0.43	1.06
ABUW_RS06605	GHKL domain-containing protein	0.09	-0.20	-0.13	0.16
ABUW_RS06610	hemin uptake protein HemP	-1.49	4.63	0.87	-5.24
ABUW_RS06615	thiamine phosphate synthase	0.58	0.19	-0.20	0.19
ABUW_RS06620	tetratricopeptide repeat protein	0.17	0.59	0.06	-0.36
ABUW_RS06625	penicillin-binding protein 1B	0.06	0.28	-0.08	-0.31
ABUW_RS06630	NAD(+) kinase	0.17	-0.40	-0.08	0.49
ABUW_RS06635	YeaC family protein	-0.27	-0.74	0.25	0.71
ABUW_RS06640	glycosyl transferase family protein	-0.05	0.61	-0.05	-0.71
ABUW_RS06645	dicarboxylate/amino acid:cation symporter	0.52	0.45	-0.42	-0.35
ABUW_RS06650	acyl-CoA dehydrogenase family protein	-0.53	0.50	0.03	-1.00
ABUW_RS06655	alpha/beta hydrolase	-2.79	-0.72	0.42	-1.65
ABUW_RS06660	prephenate dehydratase	-0.21	-0.32	-0.07	0.03
ABUW_RS06665	bifunctional prephenate dehydrogenase/3-phosphoshikimate 1-carboxyvinyltransferase	-0.84	-0.57	0.00	-0.27
ABUW_RS06670	hypothetical protein	-0.09	0.79	0.12	-0.76
ABUW_RS06675	aminoacyl-histidine dipeptidase	0.15	0.75	-0.06	-0.67
ABUW_RS06680	MBL fold metallo-hydrolase	0.02	0.52	0.16	-0.34
ABUW_RS06685	hydrolase	0.75	0.66	-0.18	-0.10
ABUW_RS06690	peroxide stress protein YaaA	-0.75	0.17	-0.51	-1.43
ABUW_RS06695	thiazole synthase	0.73	-0.29	-0.43	0.59
ABUW_RS06700	sulfur carrier protein ThiS	-0.07	-0.74	0.14	0.81
ABUW_RS06705	DUF423 domain-containing protein	0.29	-1.51	-0.19	1.61
ABUW_RS06710	RNA polymerase sigma factor RpoH	0.82	0.07	0.04	0.78
ABUW_RS06715	sulfurtransferase TusA family protein	-0.41	0.08	0.40	-0.08
ABUW_RS06720	cold-shock protein	-0.17	1.13	0.29	-1.01
ABUW_RS06725	ATP-dependent RNA helicase RhlB	0.45	-0.24	0.17	0.86
ABUW_RS06730	hypothetical protein	1.91	1.07	0.44	1.28
ABUW_RS06735	nitroreductase	-0.76	0.25	-0.05	-1.06
ABUW_RS06740	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	-0.80	0.02	0.01	-0.81
ABUW_RS06745	histidine phosphatase family protein	-0.32	0.35	-0.25	-0.91
ABUW_RS06750	site-specific integrase	0.00	0.82	0.13	-0.69
ABUW_RS06755	IS256-like element ISAbA26 family transposase	-1.89	-3.04	0.28	1.43
ABUW_RS06760	hypothetical protein	1.24	0.78	-0.64	-0.19
ABUW_RS06765	hypothetical protein	2.40	0.91	-1.13	0.36
ABUW_RS06770	hypothetical protein	1.40	-0.17	-0.58	0.99
ABUW_RS06775	hypothetical protein	1.46	-0.20	-0.75	0.91
ABUW_RS06780	hypothetical protein	0.57	-0.46	1.09	2.11

ABUW_RS06785	YqaJ viral recombinase family protein	1.54	-0.73	0.34	2.61
ABUW_RS06790	phage recombination protein Bet	1.88	-0.79	-0.13	2.54
ABUW_RS06795	hypothetical protein	0.28	-3.96	0.07	4.31
ABUW_RS06800	hypothetical protein	3.01	-1.76	0.74	5.52
ABUW_RS06805	hypothetical protein	4.67	0.22	-0.96	3.48
ABUW_RS06810	hypothetical protein	3.74	-0.56	0.14	4.44
ABUW_RS06815	hypothetical protein	2.25	-1.93	-0.29	3.89
ABUW_RS06820	hypothetical protein	2.61	-0.26	1.52	4.38
ABUW_RS06825	hypothetical protein	-0.73	-0.79	0.19	0.24
ABUW_RS06830	helix-turn-helix domain-containing protein	-1.06	0.07	0.25	-0.88
ABUW_RS06835	hypothetical protein	2.06	-0.51	0.46	3.03
ABUW_RS06840	ribbon-helix-helix protein, CopG family	2.51	0.01	-0.13	2.37
ABUW_RS06845	hypothetical protein	1.29	-1.21	0.44	2.93
ABUW_RS06850	hypothetical protein	1.88	-1.10	0.06	3.04
ABUW_RS06855	hypothetical protein	0.71	0.84	0.45	0.32
ABUW_RS06860	hypothetical protein	0.55	-0.94	0.33	1.82
ABUW_RS06865	hypothetical protein	1.94	-0.56	-0.19	2.32
ABUW_RS06870	hypothetical protein	0.60	-0.04	-0.11	0.53
ABUW_RS06875	hypothetical protein	0.85	1.89	0.46	-0.58
ABUW_RS06880	hypothetical protein	NA	NA	NA	NA
ABUW_RS06885	hypothetical protein	NA	NA	NA	NA
ABUW_RS06890	hypothetical protein	NA	NA	NA	NA
ABUW_RS06895	hypothetical protein	2.53	2.69	-1.77	-1.93
ABUW_RS06900	hypothetical protein	1.35	1.78	-0.53	-0.97
ABUW_RS06905	hypothetical protein	1.39	1.76	-0.81	-1.17
ABUW_RS06910	hypothetical protein	4.22	1.46	0.00	2.53
ABUW_RS06915	hypothetical protein	-1.35	-0.59	3.60	2.85
ABUW_RS06920	head-tail connector protein	0.46	-1.43	-0.12	1.78
ABUW_RS06925	hypothetical protein	0.57	-0.74	0.10	1.40
ABUW_RS06930	hypothetical protein	-0.12	0.21	0.32	-0.02
ABUW_RS06935	hypothetical protein	0.54	-0.62	-0.03	1.14
ABUW_RS06940	hypothetical protein	1.57	0.21	0.20	1.56
ABUW_RS06945	carbohydrate-binding protein	0.69	-0.46	0.09	1.24
ABUW_RS06950	GNAT family N-acetyltransferase	-0.64	-0.49	0.57	0.41
ABUW_RS06955	hypothetical protein	-0.10	-0.19	0.92	1.02
ABUW_RS06960	hypothetical protein	0.48	-0.04	-0.07	0.45
ABUW_RS06965	lytic transglycosylase domain-containing protein	0.13	-0.93	0.26	1.32
ABUW_RS06970	hypothetical protein	0.87	0.45	-0.14	0.29
ABUW_RS06975	hypothetical protein	1.48	2.00	-0.40	-0.92
ABUW_RS06980	hypothetical protein	0.59	-0.11	-0.04	0.66
ABUW_RS06990	hypothetical protein	0.73	1.75	0.18	-0.85
ABUW_RS06995	phage terminase large subunit	-0.01	-0.27	0.32	0.57
ABUW_RS07000	hypothetical protein	-0.68	0.40	0.21	-0.87
ABUW_RS07005	acyltransferase	-2.69	-1.32	-0.20	-1.57

ABUW_RS07010	hypothetical protein	-0.73	3.90	-0.36	-4.98
ABUW_RS07015	hypothetical protein	-1.61	-2.86	0.02	1.27
ABUW_RS07020	hypothetical protein	-0.51	-2.07	0.09	1.65
ABUW_RS07025	general secretion pathway protein GspL	0.35	-0.04	-0.16	0.23
ABUW_RS07030	type II secretion system protein M	-0.46	0.05	0.03	-0.48
ABUW_RS07035	quinone-dependent dihydroorotate dehydrogenase	1.15	0.62	-0.26	0.27
ABUW_RS07040	CvpA family protein	0.80	1.29	0.01	-0.48
ABUW_RS07045	amidophosphoribosyltransferase	0.54	0.85	-0.45	-0.76
ABUW_RS07050	M48 family metalloprotease	-0.70	0.26	0.10	-0.86
ABUW_RS07055	hypothetical protein	-0.56	0.49	0.26	-0.79
ABUW_RS07060	D-glycerate dehydrogenase	0.69	0.24	-0.37	0.08
ABUW_RS07065	M48 family metalloprotease	-0.14	0.19	0.17	-0.16
ABUW_RS07070	GatB/YqeY domain-containing protein	0.19	-1.12	-0.05	1.26
ABUW_RS07075	30S ribosomal protein S21 tRNA (adenosine(37)-N6)- threonylcarbamoyltransferase complex transferase subunit TsaD	-0.49	-1.29	0.11	0.91
ABUW_RS07080	hypothetical protein	1.04	0.29	-0.57	0.18
ABUW_RS07085	hypothetical protein	-1.61	-1.73	0.62	0.74
ABUW_RS07090	ATP-binding protein	-0.22	0.08	-0.08	-0.39
ABUW_RS07095	DUF3336 domain-containing protein	0.22	0.31	0.08	-0.01
ABUW_RS07100	protein kinase	0.17	-0.39	0.19	0.75
ABUW_RS07125	LysR family transcriptional regulator	-1.45	-1.03	0.61	0.20
ABUW_RS07130	aspartate aminotransferase family protein CoA-acylating methylmalonate-semialdehyde dehydrogenase	0.73	-1.19	0.09	2.01
ABUW_RS07135	amino acid permease	0.45	-0.47	-0.14	0.78
ABUW_RS07140	amino acid permease	-0.07	-1.05	0.09	1.07
ABUW_RS07145	DUF2171 domain-containing protein	0.64	4.93	-1.65	-5.95
ABUW_RS07150	hypothetical protein	-1.66	-0.20	-0.42	-1.88
ABUW_RS07155	PIG-L family deacetylase	-0.99	0.74	-0.75	-2.48
ABUW_RS07160	class I SAM-dependent methyltransferase	-0.80	0.80	-0.79	-2.39
ABUW_RS07165	glycosyltransferase	-0.50	0.45	-0.75	-1.70
ABUW_RS07170	NirD/YgiW/Ydel family stress tolerance protein	2.41	3.48	0.50	-0.58
ABUW_RS07175	BLUF domain-containing protein	-1.36	0.27	-0.17	-1.81
ABUW_RS07180	hypothetical protein	-4.03	-0.54	-0.73	-4.21
ABUW_RS07185	LysE family translocator	0.19	1.81	0.46	-1.16
ABUW_RS07190	AraC family transcriptional regulator	0.35	0.35	0.14	0.14
ABUW_RS07195	alpha/beta fold hydrolase	-0.14	-0.04	0.09	-0.01
ABUW_RS07200	sodium/glutamate symporter	-1.26	-0.43	-0.44	-1.27
ABUW_RS07205	cyclase family protein	0.55	-0.18	-0.53	0.21
ABUW_RS07210	LysR family transcriptional regulator	0.89	0.49	-0.07	0.33
ABUW_RS07215	aldo/keto reductase	1.70	0.21	-0.11	1.39
ABUW_RS07220	SDR family oxidoreductase	0.39	-0.11	0.02	0.52
ABUW_RS07225	SRPBCC family protein	-0.32	0.01	0.21	-0.12
ABUW_RS07230	ATP-binding protein	0.72	0.98	-0.06	-0.32
ABUW_RS07235	FadR family transcriptional regulator	-0.05	-0.30	0.50	0.75
ABUW_RS07240	hypothetical protein	-0.31	-0.33	0.43	0.46

ABUW_RS07245	TetR/AcrR family transcriptional regulator	-4.32	-2.10	1.02	-1.20
ABUW_RS07250	Csu fimbrial major subunit CsuAB	-8.59	1.79	1.56	-8.82
ABUW_RS07255	Csu fimbrial biogenesis protein CsuA	-9.43	-1.41	2.56	-5.45
ABUW_RS07260	Csu fimbrial biogenesis protein CsuB	-6.29	-0.27	1.58	-4.44
ABUW_RS07265	Csu fimbrial biogenesis chaperone CsuC	-7.74	-0.37	1.67	-5.69
ABUW_RS07270	Csu fimbrial usher CsuD	-6.26	-0.31	2.01	-3.94
ABUW_RS07275	Csu fimbrial tip adhesin CsuE	-4.65	0.68	1.38	-3.95
ABUW_RS07280	hypothetical protein	-2.20	3.19	0.18	-5.21
ABUW_RS07285	hypothetical protein	-1.86	0.49	0.21	-2.14
ABUW_RS07295	glycine betaine/L-proline transporter ProP	-1.00	-1.35	-0.45	-0.10
ABUW_RS07300	ADP-ribose pyrophosphatase	1.13	0.36	-0.04	0.73
ABUW_RS07305	TetR/AcrR family transcriptional regulator	2.97	1.64	0.52	1.85
ABUW_RS07310	DMT family transporter	-0.95	2.05	-0.68	-3.67
ABUW_RS07315	paraquat-inducible protein A	-1.03	0.49	-0.29	-1.81
ABUW_RS07320	paraquat-inducible protein A	-0.58	0.31	-0.43	-1.33
ABUW_RS07325	MCE family protein	-1.05	0.03	-0.22	-1.30
ABUW_RS07330	membrane integrity-associated transporter subunit PqiC	-1.90	-0.43	0.10	-1.36
ABUW_RS07335	hydroxyisourate hydrolase	-0.75	0.50	0.58	-0.67
ABUW_RS07340	heme-binding protein	0.46	0.77	1.01	0.69
ABUW_RS07345	heavy metal response regulator transcription factor	0.61	-0.18	0.05	0.84
ABUW_RS07350	heavy metal sensor histidine kinase	-0.77	-0.44	0.21	-0.12
ABUW_RS07355	lipocalin family protein	-1.03	0.08	-0.12	-1.23
ABUW_RS07360	acyl-CoA desaturase	0.60	0.64	0.51	0.47
ABUW_RS07365	FAD-dependent oxidoreductase	0.08	-0.60	0.27	0.95
ABUW_RS07370	DUF1365 domain-containing protein	0.11	-0.74	0.02	0.87
ABUW_RS07375	class I SAM-dependent methyltransferase	0.11	0.41	0.11	-0.19
ABUW_RS07380	DUF1295 domain-containing protein	0.88	0.61	-0.15	0.12
ABUW_RS07385	class I SAM-dependent methyltransferase	-0.33	1.14	-0.12	-1.59
ABUW_RS07390	HAMP domain-containing histidine kinase	0.05	0.20	-0.08	-0.24
ABUW_RS07395	response regulator transcription factor	-1.78	0.30	0.72	-1.37
ABUW_RS07400	chalcone isomerase family protein	-0.42	0.16	-0.40	-0.98
ABUW_RS07405	nuclear transport factor 2 family protein	-1.16	-0.35	0.32	-0.50
ABUW_RS07410	GNAT family N-acetyltransferase	-0.96	-0.18	0.00	-0.78
ABUW_RS07415	aspartate/glutamate racemase family protein	-0.37	1.08	0.09	-1.37
ABUW_RS07420	aromatic amino acid DMT transporter YddG	-2.93	-0.63	-0.15	-2.45
ABUW_RS07425	sorbose dehydrogenase family protein	-1.80	0.05	-0.16	-2.02
ABUW_RS07430	GNAT family N-acetyltransferase	-1.54	-0.69	-0.19	-1.04
ABUW_RS07435	MFS transporter	0.04	-0.28	0.17	0.49
ABUW_RS07440	TetR/AcrR family transcriptional regulator	-0.16	0.33	0.50	0.00
ABUW_RS07445	dicarboxylate/amino acid:cation symporter	-1.49	0.98	0.46	-2.01
ABUW_RS07450	hypothetical protein	0.38	3.39	0.10	-2.91
ABUW_RS07455	hydroxyacylglutathione hydrolase	-0.29	-0.13	0.00	-0.15
ABUW_RS07460	ABC transporter permease	0.85	-0.05	-0.43	0.47
ABUW_RS07465	methionine ABC transporter ATP-binding protein	0.05	-0.59	0.00	0.64

ABUW_RS07470	hypothetical protein	-0.11	-1.18	-0.23	0.84
ABUW_RS07475	phosphoribosylamine--glycine ligase bifunctional	0.04	0.12	-0.25	-0.33
ABUW_RS07480	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.33	0.26	-0.29	-0.22
ABUW_RS07485	DNA-binding transcriptional regulator Fis	0.17	-0.33	0.32	0.81
ABUW_RS07490	zinc-ribbon and DUF3426 domain-containing protein	-0.44	-0.67	0.46	0.69
ABUW_RS07495	50S ribosomal protein L11 methyltransferase	-0.04	-0.23	-0.01	0.18
ABUW_RS07500	hypothetical protein	1.10	2.65	1.02	-0.54
ABUW_RS07505	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	0.82	-0.17	-0.09	0.90
ABUW_RS07515	circularly permuted type 2 ATP-grasp protein	0.20	0.87	0.22	-0.45
ABUW_RS07520	alpha-E domain-containing protein	0.97	1.01	0.04	-0.01
ABUW_RS07525	transglutaminase family protein	0.75	2.03	-0.20	-1.47
ABUW_RS07530	proteasome-type protease	1.02	-0.01	-0.31	0.71
ABUW_RS07535	alanine racemase	-0.75	-0.66	0.04	-0.05
ABUW_RS07540	replicative DNA helicase	-0.53	-0.65	0.21	0.32
ABUW_RS07545	50S ribosomal protein L9	-0.39	-1.47	0.12	1.21
ABUW_RS07550	30S ribosomal protein S18	0.09	-0.67	-0.16	0.60
ABUW_RS07555	30S ribosomal protein S6	0.74	0.41	-0.55	-0.22
ABUW_RS07560	protoheme IX farnesyltransferase	0.07	-0.71	-0.13	0.65
ABUW_RS07565	cytochrome o ubiquinol oxidase subunit IV	1.24	-0.33	-0.29	1.28
ABUW_RS07570	cytochrome o ubiquinol oxidase subunit III	-0.83	-1.67	0.49	1.33
ABUW_RS07575	cytochrome o ubiquinol oxidase subunit I	0.39	-0.37	-0.13	0.63
ABUW_RS07580	ubiquinol oxidase subunit II	-0.06	-0.16	-0.40	-0.30
ABUW_RS07585	RDD family protein	-1.43	-1.07	0.10	-0.27
ABUW_RS07590	phosphoenolpyruvate synthase	-0.43	-0.12	0.06	-0.25
ABUW_RS07595	kinase/pyrophosphorylase	0.11	-0.46	-0.25	0.32
ABUW_RS07600	poly-beta-1,6 N-acetyl-D-glucosamine exporter porin PgaA	-2.30	0.67	3.80	0.83
ABUW_RS07605	poly-beta-1,6-N-acetyl-D-glucosamine N- deacetylase PgaB	-3.47	-0.29	3.23	0.05
ABUW_RS07610	poly-beta-1,6 N-acetyl-D-glucosamine synthase	-2.48	0.86	2.38	-0.97
ABUW_RS07615	poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD	-1.64	0.55	1.92	-0.27
ABUW_RS07620	hypothetical protein	0.56	-0.09	0.20	0.85
ABUW_RS07625	LLM class flavin-dependent oxidoreductase	2.76	0.19	0.17	2.74
ABUW_RS07630	hypothetical protein	3.88	2.18	0.30	2.01
ABUW_RS07640	hypothetical protein	3.22	1.73	-0.65	0.84
ABUW_RS07645	LysR family transcriptional regulator type 1 glutamine amidotransferase domain- containing protein	-0.43	0.02	0.42	-0.03
ABUW_RS07650		2.07	2.77	-0.18	-0.88
ABUW_RS07655	peptide chain release factor 1	0.46	0.23	-0.38	-0.15
ABUW_RS07660	peptide chain release factor N(5)-glutamine methyltransferase	-0.06	-0.06	-0.15	-0.15
ABUW_RS07665	ABC transporter permease	0.78	-0.19	0.28	1.25
ABUW_RS07670	aliphatic sulfonate ABC transporter substrate- binding protein	0.30	-0.50	0.28	1.07
ABUW_RS07675	AraC family transcriptional regulator	0.44	0.08	-0.16	0.20
ABUW_RS07680	3-hydroxyacyl-CoA dehydrogenase	1.76	0.95	0.06	0.86
ABUW_RS07685	acyl-CoA dehydrogenase family protein	2.09	0.02	-0.16	1.91

ABUW_RS07690	AMP-binding protein	1.35	0.13	-0.11	1.10
ABUW_RS07695	flavin reductase family protein	0.11	0.69	-0.18	-0.76
ABUW_RS07700	HesA/MoeB/ThiF family protein	1.58	1.16	-0.57	-0.14
ABUW_RS07705	AarF/ABC1/UbiB kinase family protein	0.70	0.10	-0.22	0.38
ABUW_RS07710	dihydroneopterin aldolase	-0.15	0.25	0.38	-0.02
ABUW_RS07715	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	0.32	-1.09	-0.01	1.40
ABUW_RS07720	potassium-transporting ATPase subunit KdpA	2.64	2.59	-0.34	-0.29
ABUW_RS07725	potassium-transporting ATPase subunit KdpB	0.86	0.40	0.11	0.57
ABUW_RS07730	potassium-transporting ATPase subunit KdpC	1.00	0.90	-0.18	-0.07
ABUW_RS07735	sensor histidine kinase KdpD	-0.07	0.12	-0.01	-0.20
ABUW_RS07740	response regulator transcription factor	-0.27	-0.29	0.10	0.11
ABUW_RS07745	glutamine synthetase	-0.79	0.22	0.18	-0.82
ABUW_RS07750	DUF2799 domain-containing protein	-1.85	2.02	-0.54	-4.41
ABUW_RS07755	2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinone monooxygenase	0.90	0.62	-0.40	-0.11
ABUW_RS07760	MFS transporter	-0.11	-0.29	0.01	0.19
ABUW_RS07765	outer membrane protein assembly factor	0.20	0.47	-0.14	-0.41
ABUW_RS07770	translocation/assembly module TamB domain-containing protein	-0.29	0.53	-0.07	-0.89
ABUW_RS07775	hypothetical protein	0.44	0.45	-0.48	-0.49
ABUW_RS07780	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	-0.36	-0.46	0.13	0.23
ABUW_RS07785	hypothetical protein	-2.49	0.71	-0.09	-3.29
ABUW_RS07790	ion transporter	-1.31	-0.17	0.07	-1.08
ABUW_RS07795	MFS transporter	-0.27	0.37	-0.06	-0.71
ABUW_RS07800	membrane protein	-0.45	1.45	0.01	-1.89
ABUW_RS07805	DUF4198 domain-containing protein	-1.21	3.39	0.12	-4.48
ABUW_RS07810	LysR family transcriptional regulator	-0.42	0.49	0.32	-0.59
ABUW_RS07815	DUF441 domain-containing protein	0.35	1.00	-0.03	-0.67
ABUW_RS07820	hypothetical protein	-0.24	0.87	0.21	-0.89
ABUW_RS07825	rRNA pseudouridine synthase	-0.35	0.41	0.18	-0.58
ABUW_RS07830	GNAT family N-acetyltransferase	0.00	0.43	0.30	-0.13
ABUW_RS07835	type II toxin-antitoxin system RelB/DinJ family antitoxin	-0.72	-0.75	0.40	0.43
ABUW_RS07840	pseudouridylate synthase	-0.80	-0.67	0.29	0.16
ABUW_RS07845	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	0.44	0.42	-0.25	-0.23
ABUW_RS07850	DNA mismatch repair endonuclease MutL	-0.08	0.05	0.17	0.04
ABUW_RS07855	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	1.31	0.73	-0.36	0.22
ABUW_RS07860	RNA chaperone Hfq	0.73	-0.36	1.00	2.10
ABUW_RS07865	DMT family transporter	0.07	0.01	-0.31	-0.25
ABUW_RS07870	oxygen-insensitive NAD(P)H nitroreductase	-0.38	0.57	0.08	-0.87
ABUW_RS07875	UDP-2,3-diacylglycerol glucosamine diphosphatase	0.58	-0.28	0.26	1.12
ABUW_RS07880	peptidyl-prolyl cis-trans isomerase	-0.32	-0.63	0.10	0.41
ABUW_RS07885	glutamine--tRNA ligase/YqeY domain fusion protein	0.59	-0.29	-0.04	0.85
ABUW_RS07890	glutamine amidotransferase	-1.03	-0.02	0.05	-0.96
ABUW_RS07895	ethanolamine ammonia-lyase subunit EutC	-0.50	-0.73	-0.08	0.14

ABUW_RS07900	ethanolamine ammonia-lyase subunit EutB	0.58	-1.03	0.25	1.86
ABUW_RS07905	ethanolamine permease	0.06	-2.02	-0.14	1.93
ABUW_RS07910	aldehyde dehydrogenase family protein	-0.27	-0.89	-0.22	0.39
ABUW_RS07915	transcriptional regulator	-0.06	-0.96	0.23	1.14
ABUW_RS07920	alpha/beta hydrolase	-0.74	-1.89	0.20	1.35
ABUW_RS07925	iron-containing alcohol dehydrogenase	0.50	-1.13	-0.31	1.31
ABUW_RS07930	AAA family ATPase	-0.83	-0.58	0.12	-0.13
ABUW_RS07935	5-carboxymethyl-2-hydroxymuconate Delta-isomerase	-0.33	0.16	-0.09	-0.59
ABUW_RS07940	hydroxyethylthiazole kinase	-0.63	-0.47	0.03	-0.13
ABUW_RS07945	hypothetical protein	-0.30	-0.05	0.43	0.19
ABUW_RS07950	hypothetical protein	0.95	1.43	0.56	0.08
ABUW_RS07955	aminopeptidase N	-1.10	0.99	0.31	-1.78
ABUW_RS07960	spore coat protein U domain-containing protein	-3.04	0.13	-1.23	-4.40
ABUW_RS07965	molecular chaperone	-2.71	0.06	-0.85	-3.61
ABUW_RS07970	fimbrial biogenesis outer membrane usher protein	-1.41	0.08	-0.87	-2.35
ABUW_RS07975	spore coat protein U domain-containing protein	-0.77	-0.05	-0.66	-1.38
ABUW_RS07980	glutathione S-transferase family protein	0.30	1.06	-0.10	-0.85
ABUW_RS07985	SDR family NAD(P)-dependent oxidoreductase	-0.39	-0.27	-0.10	-0.22
ABUW_RS07990	SDR family NAD(P)-dependent oxidoreductase	0.04	0.35	-0.39	-0.70
ABUW_RS07995	chorismate mutase	-0.17	-0.32	0.00	0.15
ABUW_RS08000	Lrp/AsnC family transcriptional regulator	-1.13	0.37	0.33	-1.16
ABUW_RS08010	hypothetical protein	-1.30	1.26	-0.33	-2.90
ABUW_RS08015	hypothetical protein	-4.69	-1.25	1.22	-2.22
ABUW_RS08020	hypothetical protein	-1.15	-0.34	-0.29	-1.10
ABUW_RS08025	hypothetical protein	-1.79	0.18	0.22	-1.75
ABUW_RS08030	TetR/AcrR family transcriptional regulator	3.55	-0.81	-2.12	2.24
ABUW_RS08035	TonB-dependent receptor	-2.46	-0.18	-0.11	-2.39
ABUW_RS08040	mechanosensitive ion channel	-1.55	0.59	0.15	-1.99
ABUW_RS08045	hypothetical protein	1.29	3.05	0.23	-1.52
ABUW_RS08050	hypothetical protein	0.58	1.00	-1.68	-2.09
ABUW_RS08055	hypothetical protein	-2.06	0.23	-0.07	-2.36
ABUW_RS08060	hypothetical protein	-2.16	-0.05	-0.72	-2.83
ABUW_RS08065	N-acetyltransferase	-0.38	-0.17	0.15	-0.06
ABUW_RS08070	TonB-dependent siderophore receptor	-1.37	2.14	-0.08	-3.60
ABUW_RS08075	OmpW family protein	2.81	2.37	-0.59	-0.16
ABUW_RS08085	hypothetical protein	-1.37	0.86	-0.93	-3.16
ABUW_RS08090	ABC-F family ATP-binding cassette domain-containing protein	0.37	-0.90	-0.13	1.14
ABUW_RS08095	universal stress protein	-0.10	0.05	0.07	-0.08
ABUW_RS08100	hypothetical protein	-0.28	-0.58	0.38	0.69
ABUW_RS08110	RDD family protein	-2.23	-0.17	-0.34	-2.40
ABUW_RS08115	magnesium-translocating P-type ATPase	0.05	0.21	-0.48	-0.64
ABUW_RS08120	MgtC/SapB family protein	0.06	0.28	-0.08	-0.31
ABUW_RS08125	benzoate/H(+) symporter BenE family transporter	-0.06	-0.31	-0.16	0.09
ABUW_RS08130	Lrp/AsnC family transcriptional regulator	1.40	-0.31	-0.09	1.62

ABUW_RS08135	leucine efflux protein LeuE	0.19	0.46	-0.23	-0.50
ABUW_RS08140	transaldolase	-0.54	0.14	0.06	-0.62
ABUW_RS08145	LysR family transcriptional regulator	-0.33	-0.37	0.29	0.33
ABUW_RS08150	chlorhexidine efflux PACE transporter Acel	0.42	0.16	-0.30	-0.04
ABUW_RS08155	acetyl-CoA C-acetyltransferase	-0.61	-0.75	0.50	0.64
ABUW_RS08160	3-oxoacyl-ACP reductase	0.07	-0.30	0.36	0.73
ABUW_RS08165	hypothetical protein	0.03	-0.09	0.10	0.21
ABUW_RS08170	serine hydrolase	0.10	0.35	0.08	-0.17
ABUW_RS08175	TetR family transcriptional regulator	1.24	0.22	-0.01	1.01
ABUW_RS08180	multidrug efflux MFS transporter AmvA	0.50	-0.63	-0.14	0.98
ABUW_RS08185	DNA polymerase III subunit gamma/tau	-0.77	-0.45	0.07	-0.25
ABUW_RS08190	phospholipase C, phosphocholine-specific	1.28	0.13	0.14	1.29
ABUW_RS08195	acyl-CoA thioesterase	-1.09	-0.37	0.08	-0.64
ABUW_RS08200	iron-containing alcohol dehydrogenase	-1.18	0.45	0.25	-1.38
ABUW_RS08205	lactonase family protein	-1.41	1.00	0.04	-2.37
ABUW_RS08210	low molecular weight phosphotyrosine protein phosphatase	0.33	0.65	0.10	-0.22
ABUW_RS08215	UDP-N-acetylmuramate dehydrogenase	0.23	0.17	-0.03	0.03
ABUW_RS08220	YdcF family protein	-0.18	0.26	0.07	-0.38
ABUW_RS08225	alpha/beta hydrolase	-0.55	0.17	0.12	-0.60
ABUW_RS08230	FMN-binding glutamate synthase family protein	-1.20	-0.21	-0.03	-1.02
ABUW_RS08235	PepSY domain-containing protein	-0.69	0.34	-0.23	-1.26
ABUW_RS08240	TetR/AcrR family transcriptional regulator	-3.82	-0.72	0.16	-2.94
ABUW_RS08245	iron-containing redox enzyme family protein	-1.53	2.88	-1.38	-5.79
ABUW_RS08250	MFS transporter	0.17	0.34	-0.13	-0.30
ABUW_RS08255	hypothetical protein	-1.52	1.45	0.23	-2.74
ABUW_RS08260	acetyl-CoA carboxylase biotin carboxylase subunit	-0.31	-0.74	0.04	0.47
ABUW_RS08265	acetyl-CoA carboxylase biotin carboxyl carrier protein	-0.11	-1.10	-0.08	0.91
ABUW_RS08270	type II 3-dehydroquinase dehydratase	0.95	0.28	-0.15	0.52
ABUW_RS08275	Y-family DNA polymerase	0.62	-1.18	0.40	2.19
ABUW_RS08280	ABC transporter substrate-binding protein	1.91	0.40	0.19	1.70
ABUW_RS08285	ANTAR domain-containing protein	3.09	1.00	0.05	2.14
ABUW_RS08290	hypothetical protein	5.38	2.55	-1.39	1.44
ABUW_RS08295	nitrite reductase large subunit	2.42	1.06	0.21	1.57
ABUW_RS08300	nitrite reductase small subunit NirD	2.18	0.39	-0.37	1.43
ABUW_RS08305	nitrate reductase	0.64	-0.22	-0.09	0.77
ABUW_RS08310	NTP transferase domain-containing protein	0.05	-0.63	-0.34	0.34
ABUW_RS08315	molybdopterin-dependent oxidoreductase	0.08	0.16	-0.11	-0.18
ABUW_RS08320	GTP 3',8-cyclase MoaA	0.58	0.16	0.26	0.69
ABUW_RS08325	MoaD/ThiS family protein	-0.14	0.18	0.18	-0.15
ABUW_RS08330	molybdenum cofactor biosynthesis protein MoaE	0.99	1.72	-0.54	-1.27
ABUW_RS08335	bifunctional molybdenum cofactor biosynthesis protein MoaC/MoaB	0.39	0.24	-0.03	0.12
ABUW_RS08340	molybdopterin molybdotransferase MoeA	0.32	0.34	-0.30	-0.32
ABUW_RS08345	helix-turn-helix transcriptional regulator	0.10	1.96	-0.34	-2.21

ABUW_RS08350	PLP-dependent aminotransferase family protein	0.51	-0.59	0.65	1.75
ABUW_RS08355	DMT family transporter	0.81	-0.06	0.04	0.91
ABUW_RS08360	TusE/DsrC/DsvC family sulfur relay protein	0.16	0.13	-0.18	-0.15
ABUW_RS08365	hypothetical protein	0.31	-1.31	-0.03	1.58
ABUW_RS08370	hypothetical protein	0.08	-0.80	-0.25	0.63
ABUW_RS08375	sulfurtransferase complex subunit TusD	0.44	-0.52	-0.01	0.94
ABUW_RS08380	SDR family NAD(P)-dependent oxidoreductase	0.76	0.21	0.37	0.92
ABUW_RS08385	class II fumarate hydratase	0.21	2.06	0.09	-1.76
ABUW_RS08390	hypothetical protein	0.06	1.88	0.42	-1.40
ABUW_RS08395	hypothetical protein	-1.44	-0.11	0.73	-0.60
ABUW_RS08400	hypothetical protein	-0.37	0.71	-0.15	-1.23
ABUW_RS08405	D-amino acid dehydrogenase	1.05	1.14	-0.23	-0.32
ABUW_RS08410	hypothetical protein	0.01	-0.08	0.38	0.48
ABUW_RS08415	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	-0.48	0.25	-0.13	-0.87
ABUW_RS08420	protein tyrosine phosphatase family protein	-1.73	-1.19	0.55	0.01
ABUW_RS08425	ornithine carbamoyltransferase	-0.29	-0.88	-0.30	0.29
ABUW_RS08430	multidrug efflux transcriptional repressor AdeN	0.60	-0.29	0.02	0.91
ABUW_RS08435	nitrogen regulation protein NR(I)	0.68	0.49	0.20	0.39
ABUW_RS08440	PAS domain-containing protein	0.53	0.11	0.43	0.85
ABUW_RS08445	30S ribosomal protein S12 methylthiotransferase RimO	1.21	0.21	-0.47	0.53
ABUW_RS08450	UMP kinase	0.81	1.28	-0.54	-1.01
ABUW_RS08455	ribosome recycling factor	0.75	0.45	-0.40	-0.11
ABUW_RS08460	di-trans,poly-cis-decaprenylcistransferase	0.75	0.31	-0.36	0.08
ABUW_RS08465	phosphatidate cytidyltransferase	0.86	-0.06	-0.30	0.62
ABUW_RS08470	1-deoxy-D-xylulose-5-phosphate reductoisomerase	-0.14	-0.63	0.19	0.68
ABUW_RS08475	RIP metalloprotease RseP	0.73	0.35	-0.22	0.15
ABUW_RS08480	outer membrane protein assembly factor BamA	0.27	0.89	-0.20	-0.82
ABUW_RS08485	OmpH family outer membrane protein	0.26	1.04	-0.23	-1.00
ABUW_RS08490	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	-0.41	0.50	0.07	-0.84
ABUW_RS08495	3-hydroxyacyl-ACP dehydratase FabZ	-0.25	-0.95	0.12	0.82
ABUW_RS08500	acyl-ACP--UDP-N-acetylglucosamine O-acyltransferase	0.61	-0.26	-0.46	0.41
ABUW_RS08505	tetratricopeptide repeat protein	-0.67	-0.05	-0.08	-0.70
ABUW_RS08510	regulatory protein RecX	0.30	0.30	-0.16	-0.16
ABUW_RS08515	recombinase RecA	0.39	-1.08	0.33	1.80
ABUW_RS08520	RNA-binding protein	0.79	2.02	0.29	-0.94
ABUW_RS08525	HAD-IA family hydrolase	-1.45	0.35	0.33	-1.46
ABUW_RS08530	hypothetical protein	-1.29	-0.26	0.23	-0.80
ABUW_RS08535	hypothetical protein	0.25	1.22	-0.78	-1.75
ABUW_RS08540	hypothetical protein	-2.49	-0.34	0.67	-1.48
ABUW_RS08545	GNAT family N-acetyltransferase	-0.59	0.58	-0.05	-1.22
ABUW_RS08550	Lrp/AsnC family transcriptional regulator	-0.04	1.49	0.91	-0.62
ABUW_RS08555	kynureninase	-0.17	-0.27	0.14	0.24
ABUW_RS08560	amino acid permease	-0.08	-0.24	0.11	0.27

ABUW_RS08565	alpha/beta hydrolase	-0.21	-0.20	-0.10	-0.11
ABUW_RS08570	S8 family peptidase	-0.25	0.77	-0.31	-1.34
ABUW_RS08575	SulP family inorganic anion transporter	-0.01	-0.48	-0.20	0.27
ABUW_RS08580	SOS response-associated peptidase family protein	0.11	1.50	0.84	-0.55
ABUW_RS08585	PQQ-dependent sugar dehydrogenase	-1.00	1.92	0.14	-2.78
ABUW_RS08590	universal stress protein	0.64	-1.20	0.09	1.93
ABUW_RS08595	GGDEF domain-containing protein	-1.25	0.89	0.27	-1.87
ABUW_RS08600	IS5-like element ISAb13 family transposase	-1.76	-2.84	0.52	1.60
ABUW_RS08605	hypothetical protein	-0.93	1.78	-0.05	-2.77
ABUW_RS08610	MarR family transcriptional regulator	-1.63	-0.95	0.27	-0.41
ABUW_RS08615	PEGA domain-containing protein	-0.40	0.88	0.02	-1.26
ABUW_RS08620	PTS transporter subunit EIIC	-1.29	0.08	-0.04	-1.41
ABUW_RS08625	1-phosphofructokinase	-1.58	-0.25	0.16	-1.16
ABUW_RS08630	phosphoenolpyruvate--protein phosphotransferase	-1.59	-0.04	0.08	-1.47
ABUW_RS08635	alpha/beta fold hydrolase	-1.29	-0.98	0.43	0.11
ABUW_RS08640	hypothetical protein	-0.67	0.61	-0.48	-1.76
ABUW_RS08645	hypothetical protein	-0.70	1.02	0.00	-1.72
ABUW_RS08650	heme-binding protein	-1.20	0.38	0.38	-1.20
ABUW_RS08655	branched-chain amino acid transport system II carrier protein	-1.38	-0.40	0.37	-0.61
ABUW_RS08660	type I methionyl aminopeptidase	-0.50	0.80	0.02	-1.29
ABUW_RS08665	LysR family transcriptional regulator	-0.51	0.14	-0.01	-0.66
ABUW_RS08670	hypothetical protein	-0.31	1.30	0.36	-1.26
ABUW_RS08675	Grx4 family monothiol glutaredoxin	-0.71	1.94	-0.11	-2.77
ABUW_RS08680	aspartate aminotransferase family protein	0.23	-0.38	-0.35	0.26
ABUW_RS08685	CBS domain-containing protein	-0.35	0.80	0.20	-0.95
ABUW_RS08690	DUF2750 domain-containing protein	1.39	2.29	-0.96	-1.86
ABUW_RS08695	hypothetical protein	0.01	0.80	1.22	0.44
ABUW_RS08700	hypothetical protein	0.66	1.49	0.52	-0.31
ABUW_RS08705	hypothetical protein	-0.07	-0.98	0.47	1.38
ABUW_RS08710	signal recognition particle-docking protein FtsY	0.57	-0.10	-0.28	0.39
ABUW_RS08715	nitroreductase family protein	1.14	1.09	0.07	0.12
ABUW_RS08720	DUF2057 domain-containing protein	0.16	1.53	0.29	-1.09
ABUW_RS08725	cyd operon YbgE family protein	-0.87	-1.49	-0.27	0.35
ABUW_RS08730	cytochrome bd-I oxidase subunit CydX	-0.87	-1.18	-0.35	-0.05
ABUW_RS08735	cytochrome d ubiquinol oxidase subunit II	-1.48	-1.27	-0.30	-0.52
ABUW_RS08740	cytochrome ubiquinol oxidase subunit I	-2.01	-2.07	-0.08	-0.02
ABUW_RS08745	hypothetical protein	-2.83	-1.91	1.41	0.50
ABUW_RS08750	DUF1449 family protein	0.18	-0.31	0.19	0.68
ABUW_RS08755	Rieske (2Fe-2S) protein	-0.18	-0.55	0.19	0.56
ABUW_RS08760	adenosine kinase	0.50	-0.03	-0.26	0.26
ABUW_RS08765	TonB-dependent siderophore receptor	-0.97	0.79	-0.16	-1.92
ABUW_RS08770	insulinase family protein	-0.64	-0.09	0.17	-0.38
ABUW_RS08775	phospholipase A	-0.54	0.32	0.05	-0.81
ABUW_RS08780	potassium uptake protein (TrkH)	-0.84	0.02	0.27	-0.60

ABUW_RS08785	TrkA family potassium uptake protein	0.09	0.83	-0.39	-1.13
ABUW_RS08790	threonine ammonia-lyase, biosynthetic	0.57	0.04	-0.33	0.21
ABUW_RS08795	ribose-5-phosphate isomerase RpiA	0.74	2.23	0.25	-1.24
ABUW_RS08800	M48 family metallopeptidase	0.03	-0.22	0.36	0.60
ABUW_RS08805	hypothetical protein	-0.32	0.44	0.34	-0.41
ABUW_RS08810	N-acetyl-gamma-glutamyl-phosphate reductase	0.81	0.56	-0.57	-0.33
ABUW_RS08815	hypothetical protein	0.58	0.35	-0.21	0.03
ABUW_RS08820	ATP-dependent Clp protease adapter ClpS	-0.02	-0.47	0.17	0.62
ABUW_RS08825	ATP-dependent Clp protease ATP-binding subunit ClpA	0.65	-0.03	-0.01	0.67
ABUW_RS08830	YnfA family protein	1.16	0.31	-0.31	0.53
ABUW_RS08835	3-deoxy-7-phosphoheptulonate synthase	-2.52	-0.47	-0.30	-2.34
ABUW_RS08840	alpha/beta hydrolase	-0.26	-0.10	0.33	0.16
ABUW_RS08845	PadR family transcriptional regulator	-0.68	-0.29	0.31	-0.08
ABUW_RS08850	NADPH-dependent 2,4-dienoyl-CoA reductase	0.88	0.91	-0.02	-0.06
ABUW_RS08855	nuclear transport factor 2 family protein	1.04	1.44	-0.30	-0.70
ABUW_RS08860	SGNH/GDSL hydrolase family protein	1.23	0.72	-0.36	0.15
ABUW_RS08865	alpha/beta hydrolase	-0.03	0.37	-0.24	-0.64
ABUW_RS08870	metal-dependent hydrolase	-0.41	-0.89	0.61	1.10
ABUW_RS08875	hypothetical protein	-1.61	1.40	0.30	-2.71
ABUW_RS08880	CTP synthase	0.68	0.01	-0.35	0.33
ABUW_RS08885	3-deoxy-8-phosphooctulonate synthase	-0.03	-0.20	-0.19	-0.02
ABUW_RS08890	phosphopyruvate hydratase	-0.51	-0.27	-0.05	-0.30
ABUW_RS08895	DUF421 domain-containing protein	-1.24	0.57	-0.02	-1.83
ABUW_RS08900	cell division protein FtsB	0.42	1.32	0.00	-0.89
ABUW_RS08905	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	0.27	0.09	-0.33	-0.15
ABUW_RS08910	3-oxoacid CoA-transferase subunit A	2.25	-1.13	1.37	4.76
ABUW_RS08915	CoA transferase subunit B	2.24	1.01	1.73	2.96
ABUW_RS08920	3-oxoadipyl-CoA thiolase	1.49	-0.59	0.38	2.46
ABUW_RS08925	3-carboxy-cis,cis-muconate cycloisomerase	0.96	-0.22	0.17	1.35
ABUW_RS08930	3-oxoadipate enol-lactonase	-0.64	-0.33	0.34	0.02
ABUW_RS08935	MFS transporter	0.81	-0.23	-0.21	0.83
ABUW_RS08940	4-carboxymuconolactone decarboxylase	0.76	-0.19	0.07	1.02
ABUW_RS08945	protocatechuate 3,4-dioxygenase subunit beta	0.67	-0.27	-0.24	0.69
ABUW_RS08950	protocatechuate 3,4-dioxygenase subunit alpha	0.87	-0.34	-0.27	0.94
ABUW_RS08955	type I 3-dehydroquinate dehydratase	0.37	-0.35	0.22	0.95
ABUW_RS08960	right-handed parallel beta-helix repeat-containing protein	0.75	0.07	-0.26	0.41
ABUW_RS08965	carbohydrate porin	1.34	0.40	-0.07	0.86
ABUW_RS08970	glucose/quininate/shikimate family membrane-bound PQQ-dependent dehydrogenase	0.99	0.23	-0.06	0.69
ABUW_RS08975	hypothetical protein	-1.69	-0.41	0.11	-1.17
ABUW_RS08980	YeeE/YedE family protein	1.85	1.23	-0.34	0.28
ABUW_RS08985	YeeE/YedE family protein	1.55	0.65	-0.62	0.27
ABUW_RS08990	MBL fold metallo-hydrolase	0.13	0.33	-0.34	-0.53
ABUW_RS08995	IcIR family transcriptional regulator PcaU	-0.31	0.04	0.06	-0.29

ABUW_RS09000	LysR family transcriptional regulator	-0.63	0.15	0.36	-0.42
ABUW_RS09005	acyl-CoA dehydrogenase family protein	0.22	-0.08	0.25	0.55
ABUW_RS09010	phosphotransferase family protein	0.59	0.01	0.03	0.61
ABUW_RS09015	histidine phosphatase family protein	0.06	-0.24	0.13	0.43
ABUW_RS09020	SDR family oxidoreductase	0.27	0.16	-0.36	-0.24
ABUW_RS09025	OprD family outer membrane porin	0.62	0.45	0.30	0.46
ABUW_RS09030	MFS transporter	2.81	0.74	0.15	2.22
ABUW_RS09035	winged helix-turn-helix transcriptional regulator	0.06	-0.34	0.17	0.57
ABUW_RS09040	amidase	4.98	0.98	-0.33	3.68
ABUW_RS09045	acyl-CoA dehydrogenase family protein	5.21	0.50	-1.15	3.56
ABUW_RS09050	hypothetical protein	4.84	1.02	-1.21	2.61
ABUW_RS09055	nuclear transport factor 2 family protein	3.79	-0.98	-0.41	4.37
ABUW_RS09060	aromatic ring-hydroxylating dioxygenase subunit alpha	4.13	-0.29	-1.09	3.33
ABUW_RS09065	aromatic-ring-hydroxylating dioxygenase subunit beta	3.94	-0.13	-1.40	2.67
ABUW_RS09070	SDR family oxidoreductase	3.36	-0.50	-0.56	3.30
ABUW_RS09075	oxidoreductase	3.16	-0.46	-0.99	2.63
ABUW_RS09080	flavin reductase family protein	1.90	-0.33	-0.51	1.72
ABUW_RS09085	transcriptional regulator FeaR	-0.90	-0.48	0.82	0.40
ABUW_RS09090	primary-amine oxidase	0.59	-0.29	-0.14	0.74
ABUW_RS09095	hypothetical protein	0.09	-0.84	0.42	1.35
ABUW_RS09100	NAD-dependent phenylacetaldehyde dehydrogenase	0.41	-0.33	-0.13	0.61
ABUW_RS09105	penicillin acylase family protein	0.68	-0.84	-0.33	1.20
ABUW_RS09110	3-oxoadipate enol-lactonase	-0.13	-1.24	-0.13	0.98
ABUW_RS09115	3-oxoadipyl-CoA thiolase	1.16	-1.21	0.20	2.57
ABUW_RS09120	CoA transferase subunit B	1.61	-2.05	-0.98	2.69
ABUW_RS09125	3-oxoacid CoA-transferase subunit A	-1.12	-4.11	3.71	6.70
ABUW_RS09130	catechol 1,2-dioxygenase	0.41	-1.35	0.37	2.13
ABUW_RS09135	muconolactone Delta-isomerase	0.64	-1.90	0.40	2.94
ABUW_RS09140	muconate cycloisomerase	0.86	-0.59	0.07	1.53
ABUW_RS09145	LysR family transcriptional regulator	0.06	-0.19	-0.05	0.19
ABUW_RS09150	hypothetical protein	-0.01	-0.12	0.06	0.17
ABUW_RS09155	FadR family transcriptional regulator	-0.61	-0.84	0.46	0.69
ABUW_RS09160	dihydroxy-acid dehydratase	1.09	-0.66	0.45	2.21
ABUW_RS09165	multidrug efflux MFS transporter AbaQ	1.02	-1.56	0.37	2.95
ABUW_RS09170	GguC protein	0.49	-1.99	0.01	2.49
ABUW_RS09175	aldehyde dehydrogenase (NADP(+))	0.29	-1.87	-1.82	0.34
ABUW_RS09180	hypothetical protein	-0.08	-1.32	0.32	1.56
ABUW_RS09185	alpha/beta hydrolase	0.54	0.85	-0.18	-0.49
ABUW_RS09190	NADH:flavin oxidoreductase/NADH oxidase family protein	0.23	-1.32	0.27	1.82
ABUW_RS09195	saccharopine dehydrogenase NADP-binding domain-containing protein	1.48	-0.18	-0.24	1.42
ABUW_RS09200	type 1 glutamine amidotransferase domain-containing protein	0.15	-0.94	0.28	1.37
ABUW_RS09205	MerR family transcriptional regulator	-0.17	-0.59	0.61	1.04

ABUW_RS09210	type 1 glutamine amidotransferase domain-containing protein	0.04	-0.02	-0.09	-0.04
ABUW_RS09215	FAD-dependent oxidoreductase	0.84	-1.22	0.39	2.45
ABUW_RS09220	Rrf2 family transcriptional regulator	0.88	-1.98	0.23	3.09
ABUW_RS09225	MBL fold metallo-hydrolase	1.59	-0.68	-0.05	2.22
ABUW_RS09230	TetR/AcrR family transcriptional regulator	0.44	-0.91	0.35	1.71
ABUW_RS09235	AraC family transcriptional regulator	-0.96	-1.33	0.28	0.64
ABUW_RS09240	SDR family oxidoreductase	1.33	-1.10	0.26	2.70
ABUW_RS09245	acetoacetate decarboxylase family protein	0.60	-1.40	0.02	2.01
ABUW_RS09250	metal-dependent hydrolase	0.08	-1.70	0.37	2.15
ABUW_RS09255	NADH:flavin oxidoreductase/NADH oxidase family protein	0.76	-0.91	0.14	1.81
ABUW_RS09260	sorbose dehydrogenase family protein	-3.33	-1.31	-0.07	-2.10
ABUW_RS09265	hypothetical protein	-3.89	-1.54	-0.59	-2.95
ABUW_RS09270	antibiotic biosynthesis monooxygenase	-0.50	-2.95	-0.22	2.23
ABUW_RS09275	hydrolase	-1.92	-2.38	0.29	0.76
ABUW_RS09280	LysR family transcriptional regulator	-0.35	-0.32	-0.22	-0.25
ABUW_RS09285	PQQ-dependent sugar dehydrogenase	-1.31	-1.14	-0.05	-0.22
ABUW_RS09290	cation:proton antiporter	-0.98	-0.89	0.00	-0.08
ABUW_RS09295	hypothetical protein	-1.78	-1.37	0.31	-0.09
ABUW_RS09300	amidohydrolase	0.62	-1.48	0.54	2.65
ABUW_RS09310	TetR/AcrR family transcriptional regulator	1.52	0.88	0.33	0.98
ABUW_RS09315	hypothetical protein	-0.06	-0.26	-0.30	-0.09
ABUW_RS09325	hypothetical protein	-1.62	-0.98	0.08	-0.56
ABUW_RS09330	DUF2247 family protein	-1.01	-0.74	-0.07	-0.34
ABUW_RS09335	SMI1/KNR4 family protein	-1.17	-1.12	-0.35	-0.41
ABUW_RS09345	hypothetical protein	-3.67	-2.14	0.55	-0.98
ABUW_RS09350	DUF2314 domain-containing protein	-2.53	-1.08	0.33	-1.12
ABUW_RS09355	MFS transporter	1.26	0.41	-0.16	0.69
ABUW_RS09360	amidohydrolase family protein	0.27	-0.80	0.79	1.86
ABUW_RS09365	SLC13 family permease	1.64	-0.35	0.06	2.04
ABUW_RS09370	GntR family transcriptional regulator	-0.58	-1.00	0.13	0.56
ABUW_RS09375	SMP-30/gluconolactonase/LRE family protein	0.54	-0.45	-0.19	0.79
ABUW_RS09380	MFS transporter	0.35	-0.37	-0.01	0.72
ABUW_RS09385	LysR family transcriptional regulator	-0.16	-1.12	0.41	1.36
ABUW_RS09390	DMT family transporter	2.28	-0.57	-0.39	2.45
ABUW_RS09395	DMT family transporter	1.66	-1.27	-0.65	2.28
ABUW_RS09400	HlyD family secretion protein	-0.58	-1.11	-0.16	0.37
ABUW_RS09405	MFS transporter	0.53	-0.54	-0.31	0.75
ABUW_RS09410	TetR/AcrR family transcriptional regulator	-0.66	-1.56	0.00	0.90
ABUW_RS09415	aldehyde dehydrogenase (NADP(+))	-0.63	-2.85	2.05	4.28
ABUW_RS09420	dihydroxy-acid dehydratase family protein	1.47	-0.88	-0.05	2.29
ABUW_RS09425	fumarylacetoacetate hydrolase family protein	0.04	-1.57	-0.04	1.57
ABUW_RS09430	LysR family transcriptional regulator	1.20	-0.85	-0.22	1.83
ABUW_RS09435	SDR family oxidoreductase	1.18	-1.38	-0.04	2.52
ABUW_RS09440	MFS transporter	0.06	-1.74	-0.13	1.67

ABUW_RS09445	NAD(P)-dependent oxidoreductase	0.53	-1.74	0.04	2.31
ABUW_RS09450	ribose-phosphate pyrophosphokinase	-1.36	-0.78	0.10	-0.48
ABUW_RS09455	nicotinate phosphoribosyltransferase	0.52	0.10	-0.19	0.23
ABUW_RS09460	NUDIX hydrolase	0.19	-0.70	0.21	1.10
ABUW_RS09465	methylenetetrahydrofolate reductase C-terminal domain-containing protein	0.74	-1.38	0.04	2.16
ABUW_RS09470	LuxR family transcriptional regulator	0.05	-0.41	-0.19	0.27
ABUW_RS09475	indoleacetamide hydrolase	0.56	-1.29	0.04	1.89
ABUW_RS09480	HlyD family secretion protein	-2.36	-1.26	-0.08	-1.18
ABUW_RS09485	DHA2 family efflux MFS transporter permease subunit	-1.87	-1.25	-0.27	-0.89
ABUW_RS09490	hypothetical protein	-1.73	-0.95	-0.05	-0.82
ABUW_RS09495	GH3 auxin-responsive promoter family protein	-1.59	-1.45	-0.10	-0.24
ABUW_RS09500	TolC family protein	-0.78	-1.49	0.03	0.73
ABUW_RS09505	hypothetical protein	-1.00	-1.77	0.46	1.23
ABUW_RS09510	acid phosphatase	0.22	-1.85	0.50	2.57
ABUW_RS09515	hypothetical protein	0.14	-2.03	0.23	2.40
ABUW_RS09520	HD domain-containing protein	-2.02	0.55	0.31	-2.26
ABUW_RS09525	DEAD/DEAH box helicase family protein	-3.22	-0.73	0.23	-2.27
ABUW_RS09530	TetR/AcrR family transcriptional regulator	1.20	0.65	0.48	1.02
ABUW_RS09535	hypothetical protein	-2.74	-2.27	-0.12	-0.59
ABUW_RS09540	endonuclease/exonuclease/phosphatase family protein	-4.00	-2.54	0.59	-0.86
ABUW_RS09545	hypothetical protein	-1.18	-0.08	0.03	-1.07
ABUW_RS09550	GNAT family N-acetyltransferase	-2.79	-1.17	0.25	-1.37
ABUW_RS09555	alpha/beta hydrolase	0.71	-2.03	0.10	2.85
ABUW_RS09560	LysR family transcriptional regulator	-0.70	-1.29	0.40	0.99
ABUW_RS09565	SDR family NAD(P)-dependent oxidoreductase	1.08	-1.14	0.06	2.28
ABUW_RS09570	SDR family NAD(P)-dependent oxidoreductase	2.14	-2.02	0.10	4.25
ABUW_RS09575	alpha/beta fold hydrolase	2.68	-2.74	-0.15	5.27
ABUW_RS09580	AraC family transcriptional regulator	1.01	-1.03	-0.04	2.00
ABUW_RS09585	hypothetical protein	0.68	0.13	-0.02	0.53
ABUW_RS09590	two-component sensor histidine kinase AdeS	0.25	-0.67	-0.20	0.72
ABUW_RS09595	efflux system response regulator transcription factor AdeR	-0.13	-0.02	0.06	-0.05
ABUW_RS09600	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	-0.59	-1.18	-0.51	0.08
ABUW_RS09605	multidrug efflux RND transporter permease subunit AdeB	-0.76	-0.95	-0.37	-0.18
ABUW_RS09610	multidrug efflux RND transporter outer membrane channel subunit AdeC	-0.84	-0.30	-0.31	-0.85
ABUW_RS09615	alpha/beta hydrolase	0.85	-1.40	0.51	2.75
ABUW_RS09620	NAD(P)/FAD-dependent oxidoreductase	1.12	-0.70	0.30	2.12
ABUW_RS09625	TetR/AcrR family transcriptional regulator	-0.19	0.33	-0.31	-0.83
ABUW_RS09630	FAD-binding oxidoreductase	3.29	0.21	0.46	3.54
ABUW_RS09635	hypothetical protein	2.28	-0.20	0.23	2.72
ABUW_RS09640	outer membrane protein transport protein	1.30	-1.28	0.60	3.18
ABUW_RS09645	hypothetical protein	-0.40	-1.07	0.96	1.63
ABUW_RS09650	helix-turn-helix transcriptional regulator	1.13	0.65	0.50	0.98

ABUW_RS09655	hypothetical protein	2.02	-1.29	0.95	4.26
ABUW_RS09660	replication initiation factor domain-containing protein	1.04	-1.70	0.35	3.09
ABUW_RS09665	hypothetical protein	0.82	-1.22	-0.71	1.34
ABUW_RS09670	hypothetical protein	1.97	-1.11	-0.25	2.83
ABUW_RS09675	hypothetical protein	0.55	-0.75	0.52	1.81
ABUW_RS09680	hypothetical protein	-1.62	-3.16	0.62	2.16
ABUW_RS09685	DUF2523 domain-containing protein	0.36	-2.34	-0.16	2.54
ABUW_RS09690	zonular occludens toxin	-1.24	-3.33	0.01	2.10
ABUW_RS09695	hypothetical protein	-1.31	-2.56	-0.05	1.20
ABUW_RS09700	hypothetical protein	-1.21	-3.23	0.21	2.24
ABUW_RS09705	hypothetical protein	2.00	-4.09	1.80	7.89
ABUW_RS09710	replication initiation factor domain-containing protein	NA	NA	NA	NA
ABUW_RS09715	hypothetical protein	NA	NA	NA	NA
ABUW_RS09720	hypothetical protein	NA	NA	NA	NA
ABUW_RS09725	hypothetical protein	NA	NA	NA	NA
ABUW_RS09730	hypothetical protein	NA	NA	NA	NA
ABUW_RS09735	DUF2523 domain-containing protein	NA	NA	NA	NA
ABUW_RS09740	hypothetical protein	NA	NA	NA	NA
ABUW_RS09745	phage coat protein	NA	NA	NA	NA
ABUW_RS09750	hypothetical protein	NA	NA	NA	NA
ABUW_RS09755	hypothetical protein	-1.62	-6.50	0.37	5.24
ABUW_RS09760	replication initiation factor domain-containing protein	0.00	-8.49	0.00	8.62
ABUW_RS09765	hypothetical protein	NA	NA	NA	NA
ABUW_RS09770	hypothetical protein	NA	NA	NA	NA
ABUW_RS09775	hypothetical protein	NA	NA	NA	NA
ABUW_RS09780	hypothetical protein	NA	NA	NA	NA
ABUW_RS09785	DUF2523 domain-containing protein	NA	NA	NA	NA
ABUW_RS09790	hypothetical protein	NA	NA	NA	NA
ABUW_RS09795	phage coat protein	NA	NA	NA	NA
ABUW_RS09800	hypothetical protein	NA	NA	NA	NA
ABUW_RS09805	hypothetical protein	NA	NA	NA	NA
ABUW_RS09810	replication initiation factor domain-containing protein	NA	NA	NA	NA
ABUW_RS09815	hypothetical protein	NA	NA	NA	NA
ABUW_RS09820	hypothetical protein	NA	NA	NA	NA
ABUW_RS09825	hypothetical protein	NA	NA	NA	NA
ABUW_RS09830	hypothetical protein	NA	NA	NA	NA
ABUW_RS09835	DUF2523 domain-containing protein	NA	NA	NA	NA
ABUW_RS09840	hypothetical protein	NA	NA	NA	NA
ABUW_RS09845	phage coat protein	NA	NA	NA	NA
ABUW_RS09850	hypothetical protein	NA	NA	NA	NA
ABUW_RS09855	hypothetical protein	NA	NA	NA	NA
ABUW_RS09860	replication initiation factor domain-containing protein	NA	NA	NA	NA
ABUW_RS09865	hypothetical protein	NA	NA	NA	NA

ABUW_RS09870	hypothetical protein	0.00	-6.41	0.00	6.55
ABUW_RS09875	hypothetical protein	0.00	-7.56	0.00	7.70
ABUW_RS09880	DNA replication protein	NA	NA	NA	NA
ABUW_RS09885	hypothetical protein	NA	NA	NA	NA
ABUW_RS09890	hypothetical protein	NA	NA	NA	NA
ABUW_RS09895	replication initiation factor domain-containing protein	NA	NA	NA	NA
ABUW_RS09900	hypothetical protein	NA	NA	NA	NA
ABUW_RS09905	hypothetical protein	NA	NA	NA	NA
ABUW_RS09910	hypothetical protein	2.06	-2.90	0.00	4.74
ABUW_RS09915	DNA replication protein	NA	NA	NA	NA
ABUW_RS09920	hypothetical protein	NA	NA	NA	NA
ABUW_RS09925	hypothetical protein	0.00	-4.85	0.00	4.99
ABUW_RS09930	DNA replication protein	0.00	-3.81	0.00	3.95
ABUW_RS09935	hypothetical protein	NA	NA	NA	NA
ABUW_RS09940	hypothetical protein	NA	NA	NA	NA
ABUW_RS09945	replication initiation factor domain-containing protein	NA	NA	NA	NA
ABUW_RS09950	hypothetical protein	NA	NA	NA	NA
ABUW_RS09955	hypothetical protein	1.03	-2.05	1.52	4.60
ABUW_RS09960	hypothetical protein	-3.43	-1.61	-0.44	-2.26
ABUW_RS09965	type 1 fimbrial protein	-0.87	-2.05	3.61	4.79
ABUW_RS09970	molecular chaperone	-1.17	-2.48	3.16	4.48
ABUW_RS09975	fimbrial biogenesis outer membrane usher protein	-1.32	-1.29	3.12	3.09
ABUW_RS09980	type 1 fimbrial protein	-0.59	-0.72	1.92	2.05
ABUW_RS09985	DUF4882 family protein	-1.74	-0.46	2.46	1.19
ABUW_RS09990	S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase	-0.60	-0.88	0.00	0.28
ABUW_RS09995	hypothetical protein	-2.19	0.12	-0.27	-2.57
ABUW_RS10000	catalase family protein	-1.43	-0.08	-0.13	-1.48
ABUW_RS10005	hypothetical protein	-4.11	-1.14	0.26	-2.71
ABUW_RS10010	hypothetical protein	1.07	1.63	-0.95	-1.50
ABUW_RS10015	phospholipase D family protein	-1.51	-0.37	0.30	-0.84
ABUW_RS10020	uracil-DNA glycosylase family protein	-2.50	-1.32	0.05	-1.13
ABUW_RS10025	hypothetical protein	-0.09	-0.53	-0.66	-0.22
ABUW_RS10035	dipeptidase	-1.07	-0.47	0.52	-0.08
ABUW_RS10040	pyrroloquinoline quinone biosynthesis protein PqqE	0.17	-0.07	0.16	0.40
ABUW_RS10045	pyrroloquinoline quinone biosynthesis peptide chaperone PqqD	0.86	0.41	0.17	0.62
ABUW_RS10050	pyrroloquinoline-quinone synthase PqqC	0.04	0.27	-0.02	-0.25
ABUW_RS10055	pyrroloquinoline quinone biosynthesis protein PqqB	0.46	0.19	0.07	0.34
ABUW_RS10060	polyphosphate kinase 1	-0.89	-0.39	0.17	-0.33
ABUW_RS10065	bifunctional metallophosphatase/5'-nucleotidase	0.44	-0.09	-0.10	0.43
ABUW_RS10070	transcriptional repressor	-0.10	3.47	-0.86	-4.43
ABUW_RS10075	isochorismatase family protein	-0.87	3.42	0.37	-3.91
ABUW_RS10080	SDR family oxidoreductase	-0.01	3.34	0.48	-2.87
ABUW_RS10085	ATP-binding cassette domain-containing protein	0.03	0.38	-0.02	-0.37

ABUW_RS10090	molybdate ABC transporter permease subunit	1.06	0.29	0.33	1.10
ABUW_RS10095	molybdate ABC transporter substrate-binding protein	0.57	0.54	0.15	0.18
ABUW_RS10100	LysR family transcriptional regulator	0.87	0.96	0.06	-0.04
ABUW_RS10105	anthranilate 1,2-dioxygenase large subunit	1.05	0.58	0.44	0.90
ABUW_RS10110	anthranilate 1,2-dioxygenase small subunit	0.02	-0.87	-0.22	0.67
ABUW_RS10115	anthranilate 1,2-dioxygenase electron transfer component AntC	0.63	-0.63	0.08	1.34
ABUW_RS10120	AraC family transcriptional regulator	0.84	-0.18	0.85	1.87
ABUW_RS10125	transporter	-0.62	-1.69	-0.32	0.76
ABUW_RS10130	flavin reductase family protein	0.13	-1.09	0.11	1.33
ABUW_RS10135	hypothetical protein	0.34	-1.08	0.36	1.79
ABUW_RS10140	SDR family oxidoreductase	0.85	-1.60	0.06	2.51
ABUW_RS10145	dienelactone hydrolase family protein	0.16	-1.52	0.19	1.87
ABUW_RS10150	MFS transporter	0.04	-1.02	0.25	1.30
ABUW_RS10155	AraC family transcriptional regulator	-0.79	-0.60	0.44	0.25
ABUW_RS10160	3-hydroxybutyrate dehydrogenase	0.00	0.01	-0.43	-0.44
ABUW_RS10165	GntP family permease	-0.16	-1.03	-0.50	0.37
ABUW_RS10170	hypothetical protein	0.78	0.19	-0.54	0.05
ABUW_RS10175	LysR family transcriptional regulator	-1.06	-0.50	0.17	-0.39
ABUW_RS10180	CoA transferase subunit A	2.06	0.96	-0.24	0.86
ABUW_RS10185	CoA transferase subunit B	1.26	-0.35	-0.22	1.39
ABUW_RS10190	short-chain fatty acid transporter	0.80	-0.03	0.46	1.29
ABUW_RS10195	thiolase family protein	0.62	0.02	0.14	0.73
ABUW_RS10200	LysR family transcriptional regulator	-2.46	-0.81	0.01	-1.64
ABUW_RS10205	LysR family transcriptional regulator	-1.33	0.17	-0.28	-1.77
ABUW_RS10210	hypothetical protein	-1.69	-0.49	3.02	1.82
ABUW_RS10215	hypothetical protein	-0.86	1.11	2.51	0.54
ABUW_RS10220	aspartate ammonia-lyase	-1.53	-1.83	1.28	1.57
ABUW_RS10225	TonB-dependent siderophore receptor	-0.81	-0.23	0.00	-0.57
ABUW_RS10230	MFS transporter	1.08	0.40	-0.33	0.35
ABUW_RS10235	DUF971 domain-containing protein	-0.54	-2.03	-0.58	0.91
ABUW_RS10240	HEAT repeat domain-containing protein	-0.32	-1.33	0.10	1.10
ABUW_RS10245	ABC transporter ATP-binding protein	0.51	-0.53	-0.25	0.79
ABUW_RS10250	ABC transporter permease	0.79	-0.19	-0.29	0.68
ABUW_RS10255	ABC transporter substrate-binding protein	0.35	0.20	0.01	0.15
ABUW_RS10260	ferredoxin family protein	-0.06	-0.51	-0.13	0.32
ABUW_RS10265	fumarate reductase/succinate dehydrogenase flavoprotein subunit	1.64	-0.12	-0.03	1.74
ABUW_RS10270	GntR family transcriptional regulator	0.40	-1.00	0.31	1.72
ABUW_RS10275	chromate efflux transporter	1.06	0.42	0.14	0.78
ABUW_RS10280	NAD(P)H-dependent oxidoreductase	-0.40	-1.13	0.33	1.06
ABUW_RS10290	AraC family transcriptional regulator	-0.21	-1.07	0.18	1.05
ABUW_RS10295	EamA family transporter	1.52	-0.88	-0.42	1.97
ABUW_RS10300	hypothetical protein	0.18	0.75	-0.01	-0.58
ABUW_RS10305	sulfite exporter TauE/SafE family protein	1.05	1.37	-0.52	-0.83

ABUW_RS10310	TIGR01244 family phosphatase	0.01	0.74	0.59	-0.14
ABUW_RS10315	MBL fold metallo-hydrolase	-0.69	0.89	0.72	-0.86
ABUW_RS10320	sigma-54-dependent Fis family transcriptional regulator	-0.21	-0.08	-0.05	-0.18
ABUW_RS10325	bestrophin	0.42	0.16	-0.15	0.11
ABUW_RS10330	2,3-butanediol dehydrogenase	-2.06	0.43	-0.22	-2.71
ABUW_RS10335	acetoin reductase	-1.60	0.27	-0.04	-1.91
ABUW_RS10340	dihydrolipoyl dehydrogenase	-3.32	-1.49	0.06	-1.77
ABUW_RS10345	2-oxo acid dehydrogenase subunit E2	-3.52	-1.33	0.14	-2.05
ABUW_RS10350	alpha-ketoacid dehydrogenase subunit beta	-2.54	-0.41	-0.38	-2.51
ABUW_RS10355	thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha	-2.81	-1.54	-0.01	-1.28
ABUW_RS10360	lipoyl synthase	-3.58	-2.93	-0.23	-0.87
ABUW_RS10365	transcriptional regulator	-0.40	-0.62	0.18	0.40
ABUW_RS10370	iron-containing redox enzyme family protein	1.17	0.33	-0.62	0.21
ABUW_RS10375	GGDEF domain-containing protein	-0.34	-0.05	-0.39	-0.68
ABUW_RS10380	chorismate synthase	0.24	-0.45	-0.40	0.29
ABUW_RS10385	50S ribosomal protein L3 N(5)-glutamine methyltransferase	-0.61	-1.27	0.06	0.72
ABUW_RS10390	tryptophan synthase subunit beta	-0.19	0.51	-0.21	-0.91
ABUW_RS10395	VWA domain-containing protein	-0.04	-0.09	0.09	0.14
ABUW_RS10400	MoxR family ATPase	-0.28	-0.59	0.34	0.64
ABUW_RS10405	hypothetical protein	-1.11	-0.78	0.26	-0.08
ABUW_RS10410	YcgL domain-containing protein	-1.47	-1.41	0.63	0.58
ABUW_RS10420	hypothetical protein	-0.76	-2.20	0.71	2.15
ABUW_RS10425	hypothetical protein	-2.51	-0.78	0.69	-1.04
ABUW_RS10430	HRDC domain-containing protein	-1.16	-0.35	0.07	-0.75
ABUW_RS10435	recombination protein RecR	-0.04	-0.43	0.01	0.40
ABUW_RS10440	YbaB/EbFC family nucleoid-associated protein	0.15	0.60	-0.03	-0.49
ABUW_RS10445	hypothetical protein	0.18	1.70	0.56	-0.96
ABUW_RS10450	O-succinylhomoserine sulfhydrylase	-0.45	0.12	-0.27	-0.84
ABUW_RS10455	alpha/beta fold hydrolase	-1.37	-1.16	0.58	0.38
ABUW_RS10460	methyltransferase domain-containing protein	-2.67	1.75	0.37	-4.06
ABUW_RS10465	cell envelope integrity protein TolA	-0.50	-1.77	-0.36	0.91
ABUW_RS10470	hypothetical protein	-0.76	-0.44	-0.49	-0.81
ABUW_RS10475	hypothetical protein	0.05	2.96	-0.82	-3.73
ABUW_RS10480	GFA family protein	-0.04	1.62	-0.56	-2.21
ABUW_RS10485	YARHG domain-containing protein	-0.65	1.59	-0.11	-2.35
ABUW_RS10490	HIT family protein	-1.16	1.17	0.03	-2.29
ABUW_RS10495	porin	-0.23	-0.93	0.40	1.09
ABUW_RS10500	DUF937 domain-containing protein	0.49	1.77	-0.48	-1.76
ABUW_RS10505	hypothetical protein	0.18	-0.76	0.31	1.25
ABUW_RS10510	DUF2797 domain-containing protein	0.68	-0.19	-0.09	0.78
ABUW_RS10515	lipid-A-disaccharide synthase	-0.16	-0.41	-0.30	-0.05
ABUW_RS10520	TonB-dependent siderophore receptor	-0.47	1.50	0.41	-1.55
ABUW_RS10525	hypothetical protein	2.05	2.20	-0.08	-0.22

ABUW_RS10530	PepSY domain-containing protein	0.25	1.61	0.48	-0.87
ABUW_RS10535	hypothetical protein	0.03	1.27	0.14	-1.10
ABUW_RS10540	sulfite exporter TauE/SafE family protein	0.73	0.67	-0.86	-0.80
ABUW_RS10545	3-deoxy-7-phosphoheptulonate synthase	-0.92	-0.50	0.05	-0.37
ABUW_RS10550	adenosylcobinamide-GDP ribazoletransferase	0.21	-0.25	-0.02	0.43
ABUW_RS10555	histidine-type phosphatase	-0.60	-0.40	0.49	0.29
ABUW_RS10560	histidine phosphatase family protein	-0.81	-1.00	0.18	0.37
ABUW_RS10565	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	0.37	-0.05	-0.18	0.25
ABUW_RS10570	bifunctional adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase	0.05	-1.25	0.03	1.32
ABUW_RS10575	2'-5' RNA ligase family protein	-0.78	-1.31	0.17	0.70
ABUW_RS10580	HAD family hydrolase	-1.18	-0.41	-0.04	-0.82
ABUW_RS10585	acetyltransferase	0.07	4.11	0.25	-3.80
ABUW_RS10590	hypothetical protein	-0.08	0.68	0.56	-0.21
ABUW_RS10595	PepSY domain-containing protein	0.26	1.79	0.33	-1.20
ABUW_RS10600	hypothetical protein	0.81	0.77	0.45	0.49
ABUW_RS10605	TonB-dependent receptor	0.20	1.56	0.43	-0.92
ABUW_RS10610	RraA family protein	0.70	3.46	0.56	-2.20
ABUW_RS10615	(2Fe-2S)-binding protein	0.74	2.27	0.74	-0.79
ABUW_RS10620	lucA/lucC family siderophore biosynthesis protein	1.13	4.41	0.22	-3.06
ABUW_RS10625	siderophore achromobactin biosynthesis protein AcsC	0.24	3.60	1.16	-2.21
ABUW_RS10630	DHA2 family efflux MFS transporter permease subunit	1.77	4.23	0.34	-2.12
ABUW_RS10635	SidA/lucD/PvdA family monooxygenase	0.76	4.33	0.61	-2.96
ABUW_RS10640	siderophore biosynthesis protein	0.64	3.80	0.67	-2.49
ABUW_RS10645	Cys-tRNA(Pro) deacylase	-0.88	3.91	-0.29	-5.09
ABUW_RS10650	hypothetical protein	-0.35	0.43	0.19	-0.60
ABUW_RS10655	AarF/ABC1/UbiB kinase family protein	-0.28	-0.11	0.00	-0.16
ABUW_RS10660	acyl-CoA dehydrogenase family protein	-1.34	-1.00	0.86	0.52
ABUW_RS10665	acyl-CoA dehydrogenase family protein	1.43	-0.05	-0.11	1.38
ABUW_RS10670	alkane 1-monooxygenase	-1.79	-0.43	0.19	-1.17
ABUW_RS10675	AraC family transcriptional regulator	-2.49	-0.21	0.69	-1.59
ABUW_RS10680	SurA N-terminal domain-containing protein	-0.27	0.08	-0.44	-0.79
ABUW_RS10685	HU family DNA-binding protein	-0.53	0.80	0.04	-1.29
ABUW_RS10690	phasin family protein	0.21	0.05	-0.06	0.10
ABUW_RS10695	hypothetical protein	-0.90	-0.10	0.39	-0.42
ABUW_RS10700	Rrf2 family transcriptional regulator	1.35	0.82	0.03	0.56
ABUW_RS10705	IscS subfamily cysteine desulfurase	0.49	0.21	-0.02	0.25
ABUW_RS10710	Fe-S cluster assembly scaffold IscU	0.97	-0.18	-0.12	1.03
ABUW_RS10715	iron-sulfur cluster assembly protein IscA	1.26	0.08	-0.27	0.92
ABUW_RS10720	Fe-S protein assembly co-chaperone HscB	0.62	-0.07	0.26	0.95
ABUW_RS10725	Fe-S protein assembly chaperone HscA	-0.11	-0.54	0.06	0.50
ABUW_RS10730	ISC system 2Fe-2S type ferredoxin	0.15	0.53	-0.61	-0.99
ABUW_RS10735	guanylate cyclase	-1.06	-0.44	0.15	-0.47
ABUW_RS10740	HIT domain-containing protein	-0.48	0.07	0.14	-0.42

ABUW_RS10745	transcription-repair coupling factor	-0.72	-0.18	0.10	-0.43
ABUW_RS10750	hypothetical protein	-1.68	-0.29	0.50	-0.89
ABUW_RS10755	Dyp-type peroxidase glutathione S-transferase N-terminal domain- containing protein	-0.29	1.11	-0.65	-2.05
ABUW_RS10760		0.33	0.42	-0.06	-0.15
ABUW_RS10765	ribonuclease E activity regulator RraA	0.48	1.95	-0.94	-2.41
ABUW_RS10770	nucleoside-diphosphate sugar epimerase	-0.53	0.16	0.35	-0.35
ABUW_RS10775	30S ribosomal protein S20	-1.34	0.50	0.05	-1.78
ABUW_RS10780	phosphoglycerate mutase family protein	0.44	-0.14	-0.19	0.40
ABUW_RS10785	3'(2'),5'-bisphosphate nucleotidase CysQ	0.12	-0.10	-0.34	-0.13
ABUW_RS10790	hypothetical protein	-0.26	0.44	0.09	-0.61
ABUW_RS10795	SOS response-associated peptidase family protein	1.02	-0.62	0.04	1.68
ABUW_RS10800	ABC transporter ATP-binding protein	-1.33	0.10	0.28	-1.16
ABUW_RS10805	ABC transporter permease	-0.68	0.84	-0.14	-1.66
ABUW_RS10810	ABC transporter permease	-1.47	0.64	0.02	-2.08
ABUW_RS10815	Zn-dependent oligopeptidase	-1.69	1.22	0.04	-2.87
ABUW_RS10820	ABC transporter substrate-binding protein	-1.95	0.45	0.17	-2.22
ABUW_RS10825	ABC transporter substrate-binding protein	-1.72	0.22	0.01	-1.93
ABUW_RS10830	TonB-dependent receptor	-0.56	0.02	0.09	-0.48
ABUW_RS10835	energy transducer TonB	-0.46	-1.71	0.33	1.57
ABUW_RS10840	MotA/TolQ/ExbB proton channel family protein	-0.99	-0.14	0.30	-0.55
ABUW_RS10845	biopolymer transporter ExbD	0.80	-0.55	-0.26	1.09
ABUW_RS10850	biopolymer transporter ExbD	-0.75	-0.74	0.13	0.12
ABUW_RS10855	hypothetical protein	-1.02	-0.98	0.17	0.14
ABUW_RS10860	malate synthase G	-0.45	0.75	0.04	-1.16
ABUW_RS10865	cell division protein ZapE	-0.43	-0.26	-0.28	-0.44
ABUW_RS10870	AraC family transcriptional regulator	-0.29	-0.21	0.04	-0.04
ABUW_RS10875	NAD(P)/FAD-dependent oxidoreductase	0.35	-0.36	0.01	0.73
ABUW_RS10880	lysine exporter LysO family protein	-1.62	0.01	-0.16	-1.78
ABUW_RS10885	orotidine-5'-phosphate decarboxylase	0.00	-0.47	-0.10	0.38
ABUW_RS10890	DUF1049 domain-containing protein	-0.32	-0.61	-0.01	0.28
ABUW_RS10895	integration host factor subunit beta	-0.53	0.43	0.10	-0.86
ABUW_RS10900	30S ribosomal protein S1	0.28	-0.68	0.06	1.02
ABUW_RS10905	(d)CMP kinase	0.53	0.82	0.09	-0.20
ABUW_RS10910	SRPBCC family protein	0.44	0.24	0.21	0.41
ABUW_RS10915	tRNA adenosine(34) deaminase TadA	-0.38	-0.66	-0.02	0.26
ABUW_RS10920	enoyl-CoA hydratase/isomerase family protein	-0.05	0.00	-0.17	-0.23
ABUW_RS10925	uracil-DNA glycosylase	-0.06	0.80	0.18	-0.69
ABUW_RS10930	6-carboxytetrahydropterin synthase	1.08	0.74	0.30	0.64
ABUW_RS10935	type II secretion system minor pseudopilin GspK	0.68	1.18	-0.60	-1.10
ABUW_RS10940	type II secretion system minor pseudopilin GspJ	-0.53	0.10	0.43	-0.21
ABUW_RS10945	type II secretion system minor pseudopilin GspI	-0.78	-0.38	0.18	-0.22
ABUW_RS10950	type II secretion system protein	-0.16	-1.09	0.09	1.01
ABUW_RS10955	TetR/AcrR family transcriptional regulator	0.45	0.27	-0.34	-0.16
ABUW_RS10960	TatD family hydrolase	-0.08	-0.58	0.02	0.52

ABUW_RS10965	PilZ domain-containing protein	-0.63	-0.22	0.30	-0.10
ABUW_RS10970	DNA polymerase III subunit delta'	0.31	0.54	0.07	-0.16
ABUW_RS10975	3-deoxy-manno-octulosonate cytidyltransferase	-0.31	0.03	-0.06	-0.39
ABUW_RS10980	tetraacyldisaccharide 4'-kinase	-0.03	0.04	0.02	-0.05
ABUW_RS10985	lipid A export permease/ATP-binding protein MsbA	0.81	0.44	-0.48	-0.12
ABUW_RS10990	biopolymer transporter ExbD	0.04	-0.73	-0.09	0.68
ABUW_RS10995	MotA/TolQ/ExbB proton channel family protein	0.61	-0.36	-0.44	0.53
ABUW_RS11000	ParB/RepB/Spo0J family partition protein	0.27	-0.37	-0.06	0.59
ABUW_RS11005	ParA family protein	0.46	0.20	-0.33	-0.07
ABUW_RS11010	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	0.60	0.20	-0.08	0.32
ABUW_RS11015	nucleotidyltransferase family protein	1.14	0.55	-0.62	-0.03
ABUW_RS11020	phosphotransferase	0.40	-0.18	-0.17	0.41
ABUW_RS11025	LPS-assembly protein LptD	-0.10	-0.40	0.01	0.31
ABUW_RS11030	peptidylprolyl isomerase	-0.16	0.33	-0.11	-0.60
ABUW_RS11035	fructose-bisphosphate aldolase class II	-0.46	-0.56	0.10	0.20
ABUW_RS11040	hypothetical protein	0.12	2.59	0.88	-1.59
ABUW_RS11045	phosphoglycerate kinase	-0.54	-0.10	0.03	-0.41
ABUW_RS11050	DUF2237 domain-containing protein	-0.42	-0.48	0.25	0.31
ABUW_RS11055	septum formation protein Maf	-0.53	-1.13	0.40	1.00
ABUW_RS11060	cupin domain-containing protein	-0.88	-0.95	0.20	0.26
ABUW_RS11065	TetR/AcrR family transcriptional regulator	-1.15	-0.23	0.15	-0.77
ABUW_RS11070	helix-turn-helix transcriptional regulator	0.03	1.79	0.49	-1.27
ABUW_RS11075	serine/threonine transporter SstT	-1.52	-0.29	-0.04	-1.27
ABUW_RS11080	DUF1275 domain-containing protein	-0.97	-1.11	0.09	0.24
ABUW_RS11085	DUF2058 domain-containing protein	-1.13	-0.46	0.01	-0.66
ABUW_RS11090	ABC transporter ATP-binding protein	-1.42	-0.28	0.02	-1.12
ABUW_RS11095	MaoC family dehydratase	-0.79	-0.31	0.22	-0.25
ABUW_RS11100	AraC family transcriptional regulator	-0.19	-0.44	0.26	0.51
ABUW_RS11105	glycine cleavage system protein GcvH	-0.82	1.25	-0.25	-2.31
ABUW_RS11110	NAD-dependent deacylase	-0.35	0.03	0.05	-0.34
ABUW_RS11115	sodium/proline symporter PutP	0.42	-0.35	-0.29	0.48
ABUW_RS11120	Lrp/AsnC ligand binding domain-containing protein trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	-0.47	-0.82	0.22	0.58
ABUW_RS11125		1.22	-0.72	0.34	2.28
ABUW_RS11130	GrpB family protein	-2.06	-0.85	0.51	-0.70
ABUW_RS11135	tRNA (uridine(54)-C5)-methyltransferase TrmA	-0.19	-0.35	-0.02	0.14
ABUW_RS11140	hypothetical protein	-0.08	2.55	-0.07	-2.71
ABUW_RS11145	phosphodiester glycosidase family protein	-0.27	0.83	-0.31	-1.41
ABUW_RS11150	lecithin retinol acyltransferase family protein	-0.41	0.11	0.18	-0.34
ABUW_RS11155	polyisoprenoid-binding protein	-1.07	0.47	0.23	-1.32
ABUW_RS11160	OsmC family protein	-0.76	0.23	0.07	-0.93
ABUW_RS11165	transketolase	0.02	0.17	-0.19	-0.34
ABUW_RS11170	methionine adenosyltransferase	0.04	-0.43	-0.32	0.15
ABUW_RS11180	hypothetical protein	-0.42	2.05	0.68	-1.78

ABUW_RS11185	FxsA family protein	-0.36	1.63	-0.13	-2.11
ABUW_RS11190	OXA-51 family carbapenem-hydrolyzing class D beta-lactamase OXA-69	-0.70	1.33	0.25	-1.79
ABUW_RS11195	N-acetyltransferase	0.82	0.09	-0.33	0.39
ABUW_RS11200	helix-turn-helix transcriptional regulator	1.41	0.37	-0.13	0.91
ABUW_RS11205	crossover junction endodeoxyribonuclease RuvC	0.82	0.36	-0.32	0.15
ABUW_RS11210	bifunctional ADP-dependent NAD(P)H-hydrate dehydratase/NAD(P)H-hydrate epimerase	0.18	-0.11	-0.07	0.21
ABUW_RS11215	tRNA epoxyqueuosine(34) reductase QueG	0.23	-0.66	0.18	1.06
ABUW_RS11220	biotin synthase BioB	-0.51	-1.07	-0.28	0.28
ABUW_RS11225	hypothetical protein	2.79	3.84	0.23	-0.82
ABUW_RS11230	hypothetical protein	3.90	7.15	0.72	-2.53
ABUW_RS11235	type 1 fimbrial protein	-1.73	1.49	-0.38	-3.61
ABUW_RS11240	fimbria/pilus periplasmic chaperone	-1.67	0.35	-0.10	-2.12
ABUW_RS11245	fimbrial biogenesis outer membrane usher protein	-1.93	-0.90	0.16	-0.87
ABUW_RS11250	fimbrial protein	-2.37	-0.57	0.19	-1.61
ABUW_RS11255	hypothetical protein	1.28	0.60	-0.96	-0.28
ABUW_RS11260	LysR family transcriptional regulator	0.08	-0.04	-0.22	-0.10
ABUW_RS11265	DMT family transporter	-0.32	-1.15	-0.11	0.73
ABUW_RS11270	hypothetical protein	0.44	1.13	0.01	-0.69
ABUW_RS11275	cytosine permease	0.05	-0.74	0.52	1.30
ABUW_RS11280	PACE efflux transporter	-2.06	-0.94	0.10	-1.02
ABUW_RS11285	LysR family transcriptional regulator	-1.09	-0.31	-0.02	-0.80
ABUW_RS11290	integrase family protein	-1.03	0.04	-0.17	-1.25
ABUW_RS11300	hypothetical protein	-3.00	0.05	0.19	-2.86
ABUW_RS11305	TetR/AcrR family transcriptional regulator	-2.91	-1.41	0.31	-1.19
ABUW_RS11310	1-acyl-sn-glycerol-3-phosphate acyltransferase YebC/PmpR family DNA-binding transcriptional regulator	-1.64	-0.85	-0.18	-0.97
ABUW_RS11315	regulator	-0.06	0.02	-0.05	-0.13
ABUW_RS11320	Lrp/AsnC family transcriptional regulator	0.56	1.34	-0.91	-1.69
ABUW_RS11325	hypothetical protein	0.19	-0.51	0.80	1.50
ABUW_RS11330	amino acid ABC transporter ATP-binding protein	-1.69	-0.12	-0.31	-1.88
ABUW_RS11335	amino acid ABC transporter permease	-1.32	-0.11	-0.54	-1.75
ABUW_RS11340	amino acid ABC transporter permease	-1.72	-0.33	-0.36	-1.75
ABUW_RS11345	amino acid ABC transporter substrate-binding protein	-1.93	0.36	0.03	-2.27
ABUW_RS11350	glutathione S-transferase	-0.53	1.38	0.19	-1.72
ABUW_RS11355	SfnB family sulfur acquisition oxidoreductase	0.25	-0.28	0.07	0.60
ABUW_RS11360	SfnB family sulfur acquisition oxidoreductase	-0.50	-0.93	0.16	0.59
ABUW_RS11365	LLM class flavin-dependent oxidoreductase	0.36	-0.05	-0.11	0.30
ABUW_RS11370	methionine transporter	-0.26	-0.34	-0.05	0.03
ABUW_RS11375	MetQ/NlpA family ABC transporter substrate-binding protein	0.29	-0.78	-0.21	0.86
ABUW_RS11380	ATP-binding cassette domain-containing protein	-0.52	-1.36	0.17	1.00
ABUW_RS11385	ABC transporter permease	-0.36	-0.87	-0.03	0.48
ABUW_RS11390	redox-regulated ATPase YchF	-0.01	-0.15	-0.30	-0.17
ABUW_RS11395	DUF962 domain-containing protein	0.21	-0.21	0.07	0.48
ABUW_RS11400	Crp/Fnr family transcriptional regulator	-0.37	0.01	-0.11	-0.49

ABUW_RS11405	hypothetical protein	4.52	8.07	0.25	-3.30
ABUW_RS11410	hypothetical protein	-0.37	0.71	-0.25	-1.34
ABUW_RS11415	AzIC family ABC transporter permease	-0.15	-0.24	0.21	0.30
ABUW_RS11420	L-valine transporter subunit YgaH	0.11	-0.07	-0.16	0.02
ABUW_RS11425	tautomerase family protein	-3.09	0.13	0.61	-2.61
ABUW_RS11430	formate-dependent phosphoribosylglycinamide formyltransferase	-0.76	-0.40	0.12	-0.24
ABUW_RS11435	[protein-Pil] uridylyltransferase	-0.66	-0.35	0.17	-0.14
ABUW_RS11440	succinyldiaminopimelate transaminase	-0.91	-0.28	-0.06	-0.68
ABUW_RS11445	LysE family translocator	0.08	-0.66	0.23	0.97
ABUW_RS11450	AraC family transcriptional regulator	0.62	-0.44	-0.10	0.96
ABUW_RS11455	glutathione peroxidase	0.93	0.96	-0.18	-0.21
ABUW_RS11460	peptide-methionine (R)-S-oxide reductase MsrB	0.91	0.82	-0.11	-0.02
ABUW_RS11465	pyridoxal phosphate-dependent aminotransferase	-0.34	-0.48	0.17	0.31
ABUW_RS11470	dicarboxylate/amino acid:cation symporter	-1.75	-1.36	0.70	0.31
ABUW_RS11475	type II asparaginase	-3.39	-1.59	0.09	-1.70
ABUW_RS11480	DNA polymerase III subunit alpha	-0.04	-0.40	0.02	0.37
ABUW_RS11485	RNA methyltransferase	0.39	-0.93	0.02	1.35
ABUW_RS11490	serine O-acetyltransferase	0.04	-0.93	-0.08	0.89
ABUW_RS11495	hypothetical protein	-0.93	-0.31	0.30	-0.32
ABUW_RS11500	alpha/beta fold hydrolase	-0.18	0.31	0.16	-0.33
ABUW_RS11505	alkyl hydroperoxide reductase subunit F	-0.82	-1.06	0.86	1.10
ABUW_RS11510	chromate transporter	2.60	1.33	0.37	1.64
ABUW_RS11515	chromate transporter	2.13	1.79	0.74	1.08
ABUW_RS11520	LysR family transcriptional regulator	0.90	-0.10	-0.17	0.83
ABUW_RS11525	ACR3 family arsenite efflux transporter	0.04	-0.65	-0.13	0.56
ABUW_RS11530	metalloregulator ArsR/SmtB family transcription factor	0.72	0.54	-0.16	0.03
ABUW_RS11535	arsenate reductase (glutaredoxin)	-0.29	-0.67	0.64	1.02
ABUW_RS11540	DUF1427 family protein	0.53	-0.95	-0.13	1.35
ABUW_RS11545	amidohydrolase	0.80	0.55	0.17	0.41
ABUW_RS11550	hydrolase	-0.89	0.08	0.50	-0.47
ABUW_RS11555	LysR family transcriptional regulator	-1.51	-0.21	0.12	-1.18
ABUW_RS11560	GntR family transcriptional regulator	-0.27	0.46	0.15	-0.58
ABUW_RS11565	NCS1 family nucleobase:cation symporter-1	0.59	-0.37	0.09	1.05
ABUW_RS11570	aspartate/glutamate racemase family protein	0.75	-0.47	-0.16	1.05
ABUW_RS11575	taurine dioxygenase	-0.04	-1.26	0.10	1.32
ABUW_RS11580	taurine ABC transporter permease TauC	1.03	-1.06	-0.23	1.86
ABUW_RS11585	ATP-binding cassette domain-containing protein	1.45	-1.06	-0.35	2.16
ABUW_RS11590	taurine ABC transporter substrate-binding protein	0.19	-1.66	-0.05	1.80
ABUW_RS11595	hypothetical protein	-1.02	-1.14	0.36	0.49
ABUW_RS11600	MFS transporter	0.28	-0.16	-0.32	0.12
ABUW_RS11605	LLM class flavin-dependent oxidoreductase	-0.01	-0.18	-0.40	-0.22
ABUW_RS11610	monooxygenase	-0.52	0.33	-0.09	-0.94
ABUW_RS11615	hypothetical protein	-0.03	0.82	0.00	-0.85
ABUW_RS11620	cytochrome ubiquinol oxidase subunit I	0.73	0.46	-0.07	0.20

ABUW_RS11625	cytochrome d ubiquinol oxidase subunit II	1.24	0.92	-0.67	-0.36
ABUW_RS11635	PLP-dependent aminotransferase family protein	-0.45	0.06	0.14	-0.37
ABUW_RS11640	LysR family transcriptional regulator	-0.54	-0.53	-0.41	-0.42
ABUW_RS11645	malonate transporter subunit MadM	0.75	-1.06	-0.31	1.50
ABUW_RS11650	malonate transporter subunit MadL	0.73	-0.94	-0.51	1.16
ABUW_RS11655	malonate decarboxylase subunit epsilon	0.65	-1.72	-0.53	1.84
ABUW_RS11660	malonate decarboxylase holo-ACP synthase	1.47	-1.45	-0.18	2.74
ABUW_RS11665	biotin-independent malonate decarboxylase subunit gamma	1.55	-2.35	-0.33	3.57
ABUW_RS11670	biotin-independent malonate decarboxylase subunit beta	1.14	-2.92	-0.02	4.04
ABUW_RS11675	malonate decarboxylase subunit delta	1.65	-3.99	-0.38	5.25
ABUW_RS11680	triphosphoribosyl-dephospho-CoA synthase	1.61	-3.23	-0.25	4.59
ABUW_RS11685	malonate decarboxylase subunit alpha	1.97	-2.66	0.01	4.65
ABUW_RS11690	MFS transporter	0.03	-0.46	0.08	0.57
ABUW_RS11695	GNAT family N-acetyltransferase	0.54	0.89	-0.01	-0.36
ABUW_RS11700	FMN-binding negative transcriptional regulator	-0.06	0.87	0.25	-0.69
ABUW_RS11705	PLP-dependent aminotransferase family protein	0.05	-1.26	0.18	1.49
ABUW_RS11710	LrgB family protein	1.19	-0.59	-0.19	1.59
ABUW_RS11715	CidA/LrgA family protein	1.36	-0.04	0.15	1.55
ABUW_RS11720	LysR family transcriptional regulator	-0.06	0.14	0.11	-0.09
ABUW_RS11725	glutathione transferase	0.55	1.20	0.36	-0.30
ABUW_RS11730	glutathione-dependent disulfide-bond oxidoreductase	0.74	0.92	0.02	-0.16
ABUW_RS11735	LysR family transcriptional regulator	0.28	-0.41	0.48	1.17
ABUW_RS11740	SDR family oxidoreductase	1.44	0.33	-0.09	1.03
ABUW_RS11745	rhodanese-like domain-containing protein	-1.99	-1.00	0.15	-0.84
ABUW_RS11750	serine acetyltransferase	0.91	-0.06	-0.78	0.20
ABUW_RS11755	hypothetical protein	-0.12	-0.30	0.52	0.70
ABUW_RS11760	cysteine desulfurase	-0.59	-0.77	0.27	0.45
ABUW_RS11765	LysE family translocator	2.02	1.41	0.03	0.64
ABUW_RS11770	LysR family transcriptional regulator	0.82	0.15	-0.05	0.61
ABUW_RS11775	cysteine ABC transporter substrate-binding protein	0.32	0.16	-0.15	0.01
ABUW_RS11780	transporter substrate-binding domain-containing protein	0.85	0.58	-0.57	-0.30
ABUW_RS11785	amino acid ABC transporter ATP-binding protein	0.37	-0.58	-0.10	0.85
ABUW_RS11790	amino acid ABC transporter permease	0.00	0.18	0.08	-0.09
ABUW_RS11795	amino acid ABC transporter permease	0.03	-0.38	0.05	0.46
ABUW_RS11800	N-acetyltransferase	0.85	2.82	-0.79	-2.75
ABUW_RS11805	response regulator transcription factor	0.62	0.18	0.00	0.44
ABUW_RS11810	response regulator	1.19	0.08	0.29	1.40
ABUW_RS11815	hypothetical protein	0.93	-0.41	-0.23	1.10
ABUW_RS11820	Lrp/AsnC family transcriptional regulator	0.44	-0.20	-0.30	0.33
ABUW_RS11825	LysE family translocator	-0.91	-2.65	-0.05	1.69
ABUW_RS11830	translesion error-prone DNA polymerase V autoproteolytic subunit	0.97	-0.99	-0.01	1.95
ABUW_RS11835	hypothetical protein	1.87	0.58	-0.02	1.27
ABUW_RS11840	stress-induced protein	0.14	-0.46	-1.72	-1.12

ABUW_RS11845	hypothetical protein	0.15	0.10	0.01	0.05
ABUW_RS11850	glucose 1-dehydrogenase	-2.15	-0.07	-0.98	-3.07
ABUW_RS11855	catalase HP11	-3.54	0.39	-0.50	-4.42
ABUW_RS11860	iron-containing redox enzyme family protein	-2.14	-0.23	-0.79	-2.71
ABUW_RS11865	CinA family protein	-1.44	1.16	-0.59	-3.18
ABUW_RS11870	hypothetical protein	-2.50	2.96	-0.65	-6.11
ABUW_RS11875	hypothetical protein	-1.66	1.74	-1.56	-4.96
ABUW_RS11880	hypothetical protein	-1.05	0.90	-0.28	-2.24
ABUW_RS11885	hypothetical protein	0.18	2.39	0.14	-2.06
ABUW_RS11895	hypothetical protein	-2.93	0.01	-0.47	-3.42
ABUW_RS11900	LysR family transcriptional regulator	1.00	0.23	-0.08	0.69
ABUW_RS11905	SGNH/GDSL hydrolase family protein	-0.66	-0.60	0.53	0.47
ABUW_RS11910	hypothetical protein	1.28	1.03	-0.19	0.07
ABUW_RS11915	class I SAM-dependent methyltransferase	1.88	0.51	-0.23	1.14
ABUW_RS11920	AMP-binding protein	1.96	0.64	0.18	1.50
ABUW_RS11925	TetR/AcrR family transcriptional regulator	1.91	1.19	-0.18	0.54
ABUW_RS11930	isovaleryl-CoA dehydrogenase	2.47	0.24	-0.13	2.10
ABUW_RS11935	methylcrotonoyl-CoA carboxylase	2.35	0.24	-0.07	2.03
ABUW_RS11940	enoyl-CoA hydratase/isomerase family protein	2.95	0.66	-0.50	1.79
ABUW_RS11945	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	1.83	0.50	0.02	1.36
ABUW_RS11950	hydroxymethylglutaryl-CoA lyase	1.06	-0.05	0.16	1.27
ABUW_RS11955	LysR family transcriptional regulator	-0.61	-0.44	0.14	-0.02
ABUW_RS11960	indolepyruvate ferredoxin oxidoreductase family protein	3.59	1.12	-0.13	2.34
ABUW_RS11965	thioesterase family protein	0.46	-0.34	-0.08	0.72
ABUW_RS11970	acyl-CoA dehydrogenase C-terminal domain-containing protein	0.86	0.16	0.48	1.18
ABUW_RS11975	Paal family thioesterase	0.95	0.50	0.50	0.95
ABUW_RS11980	MFS transporter	0.39	-0.79	0.09	1.27
ABUW_RS11985	hypothetical protein	-0.59	-0.35	0.40	0.17
ABUW_RS11990	3-oxoacid CoA-transferase subunit B	0.18	0.08	0.06	0.16
ABUW_RS11995	3-oxoacid CoA-transferase subunit A	0.76	-0.06	-0.03	0.80
ABUW_RS12000	MFS transporter	1.37	0.53	0.44	1.28
ABUW_RS12005	acyl-CoA dehydrogenase family protein	2.10	0.69	0.47	1.88
ABUW_RS12010	enoyl-CoA hydratase	3.21	1.92	0.90	2.20
ABUW_RS12015	SDR family oxidoreductase	1.37	0.60	-0.16	0.61
ABUW_RS12020	3-hydroxyacyl-CoA dehydrogenase	0.43	-0.53	0.12	1.08
ABUW_RS12025	3-oxoadipyl-CoA thiolase	0.56	-0.53	0.05	1.14
ABUW_RS12030	IclR family transcriptional regulator	0.36	-0.47	-0.01	0.82
ABUW_RS12035	MFS transporter	0.33	-0.68	0.03	1.04
ABUW_RS12040	nitronate monooxygenase	2.32	1.39	-0.05	0.88
ABUW_RS12045	enoyl-CoA hydratase	-0.24	-0.68	0.62	1.06
ABUW_RS12050	IclR family transcriptional regulator	0.89	0.11	-0.07	0.72
ABUW_RS12055	CoA transferase	2.10	0.10	-0.14	1.86
ABUW_RS12060	acyl-CoA dehydrogenase family protein	1.29	-0.81	0.10	2.19

ABUW_RS12065	MFS transporter	0.15	-1.18	-0.12	1.21
ABUW_RS12070	phosphonoacetaldehyde hydrolase	0.80	0.43	-0.27	0.10
ABUW_RS12075	2-aminoethylphosphonate--pyruvate transaminase	0.05	-0.24	0.21	0.49
ABUW_RS12080	TIGR03364 family FAD-dependent oxidoreductase	0.56	-0.11	0.55	1.22
ABUW_RS12085	putative 2-aminoethylphosphonate ABC transporter permease subunit	0.29	-0.45	-0.01	0.72
ABUW_RS12090	ATP-binding cassette domain-containing protein	-0.29	-0.81	0.71	1.24
ABUW_RS12095	putative 2-aminoethylphosphonate ABC transporter substrate-binding protein	-0.11	-0.06	0.44	0.39
ABUW_RS12100	UTRA domain-containing protein	-0.68	0.05	-0.35	-1.07
ABUW_RS12105	4-hydroxybenzoate 3-monooxygenase	2.28	1.00	-0.55	0.73
ABUW_RS12110	IcIR family transcriptional regulator PobR	0.81	0.03	0.28	1.06
ABUW_RS12115	NAD(P)H-dependent oxidoreductase	2.28	1.85	-0.15	0.28
ABUW_RS12120	LysR family transcriptional regulator	0.23	-0.71	0.16	1.11
ABUW_RS12125	carboxymuconolactone decarboxylase family protein	0.97	0.58	-0.45	-0.06
ABUW_RS12130	NAD-dependent succinate-semialdehyde dehydrogenase	1.33	1.01	-0.02	0.29
ABUW_RS12135	hypothetical protein	0.72	-0.04	0.06	0.83
ABUW_RS12140	cytosine permease	1.09	-0.04	0.06	1.19
ABUW_RS12145	aldehyde dehydrogenase	0.78	-0.60	-0.34	1.04
ABUW_RS12150	LLM class flavin-dependent oxidoreductase	0.79	-0.56	0.13	1.48
ABUW_RS12165	amino acid synthesis family protein	2.50	1.37	0.79	1.92
ABUW_RS12170	GntR family transcriptional regulator	-1.10	-1.13	0.36	0.39
ABUW_RS12175	DUF1330 domain-containing protein	-0.19	-1.26	-0.03	1.04
ABUW_RS12180	cytochrome b	-1.06	0.24	-0.35	-1.65
ABUW_RS12185	catalase family peroxidase	-0.93	1.23	-0.40	-2.56
ABUW_RS12190	MFS transporter	0.49	0.78	-0.93	-1.22
ABUW_RS12195	hydroxymethylglutaryl-CoA lyase	0.14	0.38	-0.35	-0.59
ABUW_RS12200	CoA transferase	-1.06	0.04	0.01	-1.09
ABUW_RS12205	LysR family transcriptional regulator	-1.87	0.11	0.03	-1.96
ABUW_RS12210	TetR/AcrR family transcriptional regulator	-1.61	-0.64	0.72	-0.26
ABUW_RS12215	hypothetical protein	-1.73	0.01	0.63	-1.10
ABUW_RS12220	hypothetical protein	0.57	0.62	-1.15	-1.20
ABUW_RS12225	cold-shock protein	-3.49	0.98	1.87	-2.60
ABUW_RS12230	hypothetical protein	0.09	0.59	-1.05	-1.55
ABUW_RS12245	hypothetical protein	-0.95	1.26	0.20	-2.00
ABUW_RS12250	TetR/AcrR family transcriptional regulator	2.75	1.92	1.42	2.26
ABUW_RS12255	ATP-dependent helicase	-1.67	0.24	0.34	-1.57
ABUW_RS12260	AAA family ATPase	-1.81	0.76	-0.22	-2.79
ABUW_RS12265	Paal family thioesterase	0.21	-0.56	0.63	1.40
ABUW_RS12270	carbonic anhydrase	0.36	-0.69	0.10	1.16
ABUW_RS12275	phenylacetic acid degradation operon negative regulatory protein PaaX	0.10	-0.97	0.07	1.14
ABUW_RS12280	phenylacetate--CoA ligase	0.60	-1.01	0.26	1.87
ABUW_RS12285	3-oxoadipyl-CoA thiolase	0.65	-1.51	0.46	2.62
ABUW_RS12290	3-hydroxyacyl-CoA dehydrogenase	0.68	-1.44	0.45	2.57
ABUW_RS12295	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	0.74	-1.11	0.63	2.47

ABUW_RS12300	enoyl-CoA hydratase/isomerase family protein	0.69	-2.34	0.80	3.83
ABUW_RS12305	phenylacetate-CoA oxygenase/reductase subunit PaaK	-0.19	-2.42	0.90	3.13
ABUW_RS12310	phenylacetate-CoA oxygenase subunit PaaJ	1.42	-1.49	0.43	3.34
ABUW_RS12315	phenylacetate-CoA oxygenase subunit PaaC	0.22	-1.93	1.02	3.16
ABUW_RS12320	1,2-phenylacetyl-CoA epoxidase subunit B	0.32	-1.79	0.86	2.97
ABUW_RS12325	1,2-phenylacetyl-CoA epoxidase subunit A	0.33	-1.31	0.52	2.17
ABUW_RS12330	phenylacetic acid degradation bifunctional protein PaaZ	-0.30	-1.65	0.90	2.25
ABUW_RS12335	L-serine ammonia-lyase	1.30	0.89	-0.05	0.36
ABUW_RS12350	APC family permease	4.58	1.41	0.00	3.16
ABUW_RS12355	aldehyde dehydrogenase (NADP(+))	2.12	-0.22	0.42	2.76
ABUW_RS12360	fosfomycin efflux MFS transporter AbaF	2.26	1.34	0.15	1.08
ABUW_RS12365	AraC family transcriptional regulator	0.17	-0.40	-0.09	0.48
ABUW_RS12370	NAD(P)/FAD-dependent oxidoreductase	1.15	-0.40	0.26	1.81
ABUW_RS12375	(2Fe-2S)-binding protein	2.34	-0.14	-0.13	2.34
ABUW_RS12380	FAD-binding oxidoreductase	1.15	-0.12	0.66	1.92
ABUW_RS12385	4-hydroxyproline epimerase	1.28	0.01	0.65	1.93
ABUW_RS12390	GntR family transcriptional regulator	0.17	0.65	0.26	-0.22
ABUW_RS12395	EamA family transporter	0.68	1.00	-0.38	-0.70
ABUW_RS12400	dihydrodipicolinate synthase family protein	2.82	1.43	-0.26	1.13
ABUW_RS12405	DUF333 domain-containing protein	-1.65	0.47	0.21	-1.92
ABUW_RS12410	redox-sensitive transcriptional activator SoxR	-1.57	0.67	-0.07	-2.31
ABUW_RS12415	hypothetical protein	-2.46	2.82	-0.60	-5.87
ABUW_RS12420	epoxyqueuosine reductase QueH	-3.61	0.07	-0.22	-3.90
ABUW_RS12425	GNAT family N-acetyltransferase	-2.65	-0.11	0.33	-2.21
ABUW_RS12430	winged helix-turn-helix domain-containing protein	0.39	0.91	-0.16	-0.68
ABUW_RS12435	cyanate transporter	0.48	0.02	0.05	0.51
ABUW_RS12440	nucleoside deaminase	-0.19	-0.29	0.03	0.13
ABUW_RS12445	ankyrin repeat domain-containing protein	1.13	1.07	-0.29	-0.24
ABUW_RS12450	LysR family transcriptional regulator	0.93	-0.63	-0.17	1.38
ABUW_RS12455	M15 family metalloproteinase	-0.57	-0.14	-0.41	-0.85
ABUW_RS12460	hypothetical protein	-2.20	-0.01	0.12	-2.07
ABUW_RS12465	type IVB secretion system protein IcmH/DotU	-3.02	-1.12	0.12	-1.77
ABUW_RS12470	type VI secretion system baseplate subunit TssK	-3.06	-0.34	0.04	-2.67
ABUW_RS12475	type VI secretion system protein TssA	-3.56	-0.32	0.14	-3.10
ABUW_RS12480	type VI secretion system ATPase TssH	-3.20	0.62	0.08	-3.75
ABUW_RS12485	PAAR domain-containing protein	-1.61	1.27	-0.31	-3.19
ABUW_RS12490	OmpA family protein	-2.98	-0.04	0.22	-2.72
ABUW_RS12495	type VI secretion system-associated protein TagF	-1.29	0.18	-0.16	-1.62
ABUW_RS12500	type VI secretion system membrane subunit TssM	-2.67	-0.62	0.12	-1.92
ABUW_RS12505	hypothetical protein	-2.70	-0.34	0.25	-2.11
ABUW_RS12510	type VI secretion system baseplate subunit TssG	-3.22	-0.70	0.19	-2.33
ABUW_RS12515	type VI secretion system baseplate subunit TssF	-2.94	-0.79	0.45	-1.71
ABUW_RS12520	type VI secretion system baseplate subunit TssE	-3.10	-0.42	0.07	-2.61
ABUW_RS12525	type VI secretion system tube protein Hcp	-5.45	-0.71	0.20	-4.54

ABUW_RS12530	type VI secretion system contractile sheath large subunit	-5.24	-0.97	0.21	-4.06
ABUW_RS12535	type VI secretion system contractile sheath small subunit	-4.77	-0.59	0.00	-4.18
ABUW_RS12540	hypothetical protein	-5.45	-0.32	0.18	-4.95
ABUW_RS12545	hypothetical protein	-2.24	0.08	0.19	-2.12
ABUW_RS12550	ABC transporter permease	-0.29	-0.50	0.20	0.41
ABUW_RS12555	ABC transporter ATP-binding protein	-0.30	-0.73	0.45	0.88
ABUW_RS12560	ABC transporter substrate-binding protein	0.64	0.18	-0.32	0.13
ABUW_RS12565	allophanate hydrolase	1.28	0.16	-0.11	1.01
ABUW_RS12570	transcriptional regulator	2.92	2.23	0.65	1.33
ABUW_RS12580	helix-turn-helix transcriptional regulator	2.19	4.64	0.63	-1.82
ABUW_RS12585	NAD(P)H-dependent oxidoreductase	-0.38	1.06	0.16	-1.28
ABUW_RS12590	urea carboxylase	1.56	-0.57	0.02	2.16
ABUW_RS12595	DUF1989 domain-containing protein	2.38	0.32	-0.54	1.51
ABUW_RS12600	DUF1989 domain-containing protein	1.57	0.35	-0.09	1.13
ABUW_RS12605	glutathione-dependent formaldehyde dehydrogenase	1.15	0.19	-0.77	0.19
ABUW_RS12610	SRPBCC family protein	-0.26	-1.03	0.50	1.27
ABUW_RS12615	TetR/AcrR family transcriptional regulator	6.81	1.06	0.00	5.53
ABUW_RS12620	hypothetical protein	-3.95	-0.04	0.35	-3.57
ABUW_RS12625	hypothetical protein	-3.54	0.45	0.10	-3.90
ABUW_RS12630	hypothetical protein	-0.37	-0.39	-0.02	0.00
ABUW_RS12635	sel1 repeat family protein	-1.21	0.55	0.75	-1.01
ABUW_RS12640	chloride channel protein	0.49	-0.27	0.67	1.43
ABUW_RS12645	ATP-grasp domain-containing protein	0.58	-0.16	-0.02	0.72
ABUW_RS12650	5-oxoprolinase/urea amidolyase family protein	1.54	0.48	0.02	1.07
ABUW_RS12655	putative hydro-lyase	0.98	0.20	0.42	1.19
ABUW_RS12660	LamB/YcsF family protein	1.63	0.11	-0.08	1.45
ABUW_RS12665	divalent metal cation transporter	1.76	1.23	-0.28	0.25
ABUW_RS12670	LysR family transcriptional regulator MumR	-0.82	-0.34	0.20	-0.27
ABUW_RS12675	hypothetical protein	-1.18	0.46	-0.19	-1.83
ABUW_RS12680	hypothetical protein	-2.96	-0.33	0.87	-1.76
ABUW_RS12685	hypothetical protein	-1.03	0.79	-0.30	-2.11
ABUW_RS12690	RHS domain-containing protein	-1.72	-0.05	0.17	-1.49
ABUW_RS12700	hypothetical protein	-1.63	-0.38	-0.34	-1.59
ABUW_RS12705	RHS domain-containing protein	-2.61	0.01	0.01	-2.61
ABUW_RS12710	type VI secretion system tip protein VgrG	-3.41	-0.11	-0.13	-3.42
ABUW_RS12715	serine hydrolase	-3.98	-0.55	0.27	-3.16
ABUW_RS12720	GNAT family N-acetyltransferase	-1.35	0.40	-0.56	-2.30
ABUW_RS12725	hypothetical protein	-1.85	-1.16	-0.32	-1.01
ABUW_RS12730	3-hydroxyacyl-CoA dehydrogenase	-1.22	1.04	-0.05	-2.31
ABUW_RS12735	DUF1826 domain-containing protein	-0.53	0.17	0.07	-0.64
ABUW_RS12740	exo-alpha-sialidase	-3.14	-0.07	-0.12	-3.19
ABUW_RS12745	DUF2147 domain-containing protein	-3.10	-0.19	0.29	-2.63
ABUW_RS12750	MFS transporter	-0.52	-0.02	0.28	-0.23

ABUW_RS12755	TetR/AcrR family transcriptional regulator	0.40	0.82	-0.48	-0.90
ABUW_RS12760	lauroyl acyltransferase	0.70	0.63	-0.18	-0.12
ABUW_RS12765	EAL domain-containing protein	-1.27	-0.67	0.28	-0.32
ABUW_RS12770	EamA family transporter	-0.28	-0.12	0.09	-0.07
ABUW_RS12775	Lrp/AsnC family transcriptional regulator	-0.96	-1.12	0.47	0.64
ABUW_RS12780	DNA mismatch repair protein MutS	-0.44	-0.53	0.07	0.16
ABUW_RS12785	GNAT family N-acetyltransferase	-1.99	-0.85	0.34	-0.80
ABUW_RS12790	ferredoxin family protein	1.27	1.95	0.17	-0.51
ABUW_RS12795	hypothetical protein	0.68	-0.26	-0.25	0.69
ABUW_RS12800	O-methyltransferase	-0.61	-0.73	0.00	0.12
ABUW_RS12805	universal stress protein	-0.49	0.20	0.06	-0.63
ABUW_RS12810	chloramphenicol acetyltransferase CAT	-0.15	0.75	-0.13	-1.03
ABUW_RS12815	YigZ family protein	-0.51	0.17	0.20	-0.48
ABUW_RS12820	HlyD family type I secretion periplasmic adaptor subunit	-0.74	0.20	-0.09	-1.03
ABUW_RS12825	type I secretion system permease/ATPase	-0.04	0.48	-0.21	-0.73
ABUW_RS12830	ToIC family protein	0.34	0.23	-0.23	-0.13
ABUW_RS12835	LPS export ABC transporter ATP-binding protein	0.38	0.09	-0.26	0.02
ABUW_RS12840	lipopolysaccharide transport periplasmic protein LptA	-0.04	0.20	0.33	0.08
ABUW_RS12845	LPS export ABC transporter periplasmic protein LptC	0.84	0.41	-0.42	0.02
ABUW_RS12850	HAD-IIIa family hydrolase	1.44	0.91	-0.58	-0.04
ABUW_RS12855	KpsF/GutQ family sugar-phosphate isomerase	0.02	0.04	0.31	0.30
ABUW_RS12860	cysteine--tRNA ligase	-0.44	-1.18	-0.04	0.70
ABUW_RS12875	site-specific integrase	0.01	-0.81	0.46	1.28
ABUW_RS12880	hypothetical protein	-0.41	0.65	-0.27	-1.34
ABUW_RS12885	hypothetical protein	-3.56	2.02	-0.20	-5.78
ABUW_RS12890	hypothetical protein	-4.29	-0.48	0.44	-3.37
ABUW_RS12895	hypothetical protein	-0.94	-0.81	0.49	0.37
ABUW_RS12900	DUF4882 family protein	-1.31	0.42	0.14	-1.58
ABUW_RS12905	hypothetical protein	0.55	0.76	-0.37	-0.58
ABUW_RS12910	right-handed parallel beta-helix repeat-containing protein	0.62	2.86	0.68	-1.55
ABUW_RS12915	fibronectin type III domain-containing protein	1.42	-0.45	-0.07	1.80
ABUW_RS12925	hypothetical protein	1.13	0.15	-0.78	0.20
ABUW_RS12930	DUF2213 domain-containing protein	0.96	1.02	0.05	-0.01
ABUW_RS12935	hypothetical protein	0.42	1.04	-0.38	-1.00
ABUW_RS12940	DUF2158 domain-containing protein	1.33	3.74	-0.41	-2.82
ABUW_RS12945	minor capsid protein	-0.31	-1.53	0.94	2.16
ABUW_RS12950	DUF1073 domain-containing protein	0.61	-0.19	0.16	0.96
ABUW_RS12955	phage terminase large subunit	0.71	-0.59	0.49	1.79
ABUW_RS12960	DUF2280 domain-containing protein	0.41	1.25	0.72	-0.12
ABUW_RS12965	transposase	0.67	0.46	0.24	0.46
ABUW_RS12970	hypothetical protein	0.49	0.13	-0.17	0.19
ABUW_RS12975	hypothetical protein	-0.51	1.19	-0.52	-2.22
ABUW_RS12980	hypothetical protein	-1.10	-1.12	-0.43	-0.41

ABUW_RS12990	hypothetical protein	-1.28	0.42	0.18	-1.51
ABUW_RS12995	hypothetical protein	-1.57	-0.71	-0.02	-0.87
ABUW_RS13000	hypothetical protein	-1.72	0.06	-0.08	-1.86
ABUW_RS13005	hypothetical protein	-1.50	1.70	0.25	-2.95
ABUW_RS13010	DUF4142 domain-containing protein	-0.07	1.39	-1.22	-2.68
ABUW_RS13015	hypothetical protein	-0.50	-0.65	0.23	0.37
ABUW_RS13020	helix-turn-helix transcriptional regulator	0.65	0.37	-0.16	0.12
ABUW_RS13025	MFS transporter	0.53	-1.30	-0.05	1.79
ABUW_RS13030	minor capsid protein	-1.76	-0.28	-0.53	-2.01
ABUW_RS13035	hypothetical protein	-1.11	-0.10	-0.97	-1.99
ABUW_RS13040	hypothetical protein	-0.02	1.35	-1.24	-2.61
ABUW_RS13045	NAD(P)-binding domain-containing protein	-3.06	0.29	-0.37	-3.72
ABUW_RS13050	hypothetical protein	-1.51	0.41	-0.30	-2.22
ABUW_RS13055	cold-shock protein	-2.65	0.83	-0.52	-4.00
ABUW_RS13060	LysE family translocator	-3.24	0.50	-0.74	-4.48
ABUW_RS13065	N-acetylmuramidase	1.52	2.36	0.45	-0.39
ABUW_RS13070	hypothetical protein	2.30	0.94	0.07	1.43
ABUW_RS13080	LexA family transcriptional regulator	0.74	0.04	0.09	0.80
ABUW_RS13085	transposase	-0.83	-1.66	0.97	1.80
ABUW_RS13095	exodeoxyribonuclease VII large subunit	-0.70	-0.02	0.32	-0.37
ABUW_RS13100	exodeoxyribonuclease VII small subunit	-1.11	-0.06	0.36	-0.70
ABUW_RS13105	hypothetical protein	-0.03	0.70	-0.33	-1.07
ABUW_RS13110	LysE family transporter	0.18	0.23	-0.53	-0.58
ABUW_RS13115	hypothetical protein	2.07	3.36	0.13	-1.16
ABUW_RS13120	four-helix bundle copper-binding protein	-0.93	-0.57	0.37	0.01
ABUW_RS13125	GFA family protein	0.08	-0.15	0.10	0.34
ABUW_RS13130	Cu(I)-responsive transcriptional regulator	0.29	-0.57	-0.42	0.44
ABUW_RS13135	copper-translocating P-type ATPase	0.17	-0.68	-0.18	0.68
ABUW_RS13140	heavy-metal-associated domain-containing protein	-0.49	-0.31	0.50	0.31
ABUW_RS13145	LysR family transcriptional regulator	0.91	0.17	-0.07	0.67
ABUW_RS13150	benzoate 1,2-dioxygenase large subunit	0.17	-0.74	0.51	1.43
ABUW_RS13155	benzoate 1,2-dioxygenase small subunit	0.20	-0.17	0.07	0.44
ABUW_RS13160	ring-hydroxylating dioxygenase ferredoxin reductase family protein	-0.18	-0.87	0.36	1.05
ABUW_RS13165	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	0.85	-0.98	0.01	1.83
ABUW_RS13170	benzoate/H(+) symporter BenE	0.03	-1.28	0.07	1.39
ABUW_RS13175	aromatic acid/H+ symport family MFS transporter	-0.88	-1.00	0.10	0.22
ABUW_RS13180	OprD family outer membrane porin	-1.06	-1.09	0.16	0.18
ABUW_RS13185	beta-ketoacyl-ACP synthase III	0.40	-0.38	-0.12	0.66
ABUW_RS13190	ATP-dependent RNA helicase HrpA	0.13	0.19	-0.02	-0.08
ABUW_RS13195	peroxiredoxin	-1.44	0.01	0.59	-0.87
ABUW_RS13200	KTSC domain-containing protein	-0.27	1.09	0.43	-0.93
ABUW_RS13205	O-methyltransferase	0.13	0.86	-0.08	-0.82
ABUW_RS13210	DUF1653 domain-containing protein	0.44	0.56	-0.15	-0.27
ABUW_RS13215	alkyl hydroperoxide reductase subunit F	-0.93	0.21	-0.08	-1.21

ABUW_RS13220	hypothetical protein	0.55	0.66	-0.14	-0.25
ABUW_RS13225	glutathione S-transferase N-terminal domain-containing protein	-1.47	2.06	-0.21	-3.75
ABUW_RS13230	ExeM/NucH family extracellular endonuclease	0.07	-0.36	-0.05	0.38
ABUW_RS13235	tRNA (guanosine(46)-N7)-methyltransferase TrmB	0.45	-0.25	-0.58	0.12
ABUW_RS13240	glutathione S-transferase	-1.19	-0.19	0.11	-0.90
ABUW_RS13245	DUF2520 domain-containing protein	-0.40	-0.10	0.01	-0.30
ABUW_RS13250	OmpA family protein	0.62	2.34	0.28	-1.43
ABUW_RS13255	aspartate carbamoyltransferase	0.45	0.30	-0.43	-0.28
ABUW_RS13260	aspartate carbamoyltransferase catalytic subunit	-0.01	0.29	-0.28	-0.58
ABUW_RS13265	hypothetical protein	-0.59	-0.33	1.27	1.01
ABUW_RS13270	bifunctional 23S rRNA (guanine(2069)-N(7))-methyltransferase RlmK/23S rRNA (guanine(2445)-N(2))-methyltransferase RlmL	-0.76	-0.25	0.04	-0.48
ABUW_RS13275	hypothetical protein	-0.07	1.54	-0.13	-1.75
ABUW_RS13280	CinA family protein	-1.43	0.35	-0.12	-1.90
ABUW_RS13285	ATP-dependent chaperone ClpB	0.60	2.07	0.23	-1.24
ABUW_RS13290	peptidoglycan DD-metalloendopeptidase family protein	0.26	1.16	-0.17	-1.08
ABUW_RS13295	GNAT family N-acetyltransferase	-0.16	0.27	0.53	0.10
ABUW_RS13300	OsmC family protein	-0.18	0.47	-0.35	-1.00
ABUW_RS13305	cAMP-activated global transcriptional regulator CRP	1.10	-0.13	-0.26	0.98
ABUW_RS13310	NADP(H)-dependent aldo-keto reductase	-1.48	-0.67	0.43	-0.39
ABUW_RS13315	M48 family metalloproteinase	0.78	0.35	-0.05	0.38
ABUW_RS13320	hypothetical protein	-0.09	-1.38	0.20	1.49
ABUW_RS13325	adenylosuccinate synthase	0.86	0.19	-0.61	0.06
ABUW_RS13330	ATP phosphoribosyltransferase regulatory subunit	0.67	-0.09	-0.33	0.44
ABUW_RS13335	type I glyceraldehyde-3-phosphate dehydrogenase	0.52	-0.31	-0.26	0.57
ABUW_RS13340	alanine--tRNA ligase	0.12	-0.62	0.04	0.78
ABUW_RS13345	aspartate kinase	-0.24	-0.81	-0.11	0.45
ABUW_RS13350	carbon storage regulator CsrA	0.06	0.22	0.03	-0.13
ABUW_RS13355	ribonuclease HII	-0.30	1.02	-0.26	-1.57
ABUW_RS13360	hypothetical protein	0.55	0.33	-0.12	0.10
ABUW_RS13365	cytochrome b	0.39	0.75	-0.30	-0.66
ABUW_RS13370	adenosine deaminase	-0.38	-0.65	0.03	0.30
ABUW_RS13375	NCS2 family permease	1.06	0.49	-0.49	0.07
ABUW_RS13380	hypothetical protein	-2.08	1.14	0.04	-3.17
ABUW_RS13385	NAD(P)/FAD-dependent oxidoreductase	0.34	0.01	-0.06	0.27
ABUW_RS13390	SDR family NAD(P)-dependent oxidoreductase	0.83	-0.40	-0.43	0.80
ABUW_RS13395	metal-dependent hydrolase	0.25	-0.19	0.83	1.27
ABUW_RS13400	pirin family protein	1.95	-0.04	0.53	2.52
ABUW_RS13405	TetR/AcrR family transcriptional regulator	0.31	0.18	0.09	0.22
ABUW_RS13410	metal-dependent hydrolase	0.18	-0.52	0.42	1.12
ABUW_RS13415	SDR family NAD(P)-dependent oxidoreductase	0.55	-0.59	-0.33	0.80
ABUW_RS13420	NAD(P)/FAD-dependent oxidoreductase	0.59	-0.26	0.08	0.93
ABUW_RS13425	class I SAM-dependent methyltransferase	-0.53	-0.34	0.43	0.24
ABUW_RS13430	AraC family transcriptional regulator	0.84	1.36	-0.04	-0.56

ABUW_RS13435	NAD(P)/FAD-dependent oxidoreductase	-0.88	-0.89	0.42	0.44
ABUW_RS13440	SDR family oxidoreductase	0.73	-0.44	-0.04	1.13
ABUW_RS13445	alpha/beta hydrolase	-1.55	-1.25	0.25	-0.05
ABUW_RS13450	GMC family oxidoreductase	-0.11	-0.81	0.12	0.82
ABUW_RS13455	OprD family outer membrane porin	1.24	0.72	0.33	0.85
ABUW_RS13460	MFS transporter	3.29	1.50	0.39	2.18
ABUW_RS13465	aromatic ring-hydroxylating dioxygenase subunit alpha	3.78	2.02	0.33	2.10
ABUW_RS13470	oxidoreductase	1.48	0.54	0.49	1.42
ABUW_RS13475	GntR family transcriptional regulator	0.05	-0.50	0.29	0.85
ABUW_RS13480	MarR family transcriptional regulator	-0.41	-0.31	0.55	0.45
ABUW_RS13485	3-(3-hydroxy-phenyl)propionate transporter MhpT	2.12	-0.10	-0.43	1.80
ABUW_RS13490	p-hydroxycinnamoyl CoA hydratase/lyase	2.57	0.78	-0.15	1.63
ABUW_RS13495	aldehyde dehydrogenase	1.10	-0.43	0.20	1.72
ABUW_RS13500	AMP-binding protein	0.59	-0.42	0.29	1.31
ABUW_RS13505	acyl-CoA dehydrogenase family protein	1.29	0.47	-0.09	0.74
ABUW_RS13510	OprD family porin	1.28	0.72	0.07	0.62
ABUW_RS13515	DUF3237 domain-containing protein	-0.38	-0.69	0.16	0.46
ABUW_RS13520	Paal family thioesterase	0.21	-0.46	0.24	0.91
ABUW_RS13525	tannase/feruloyl esterase family alpha/beta hydrolase	0.57	-0.21	0.11	0.90
ABUW_RS13530	FadR family transcriptional regulator	-0.28	-0.41	-0.05	0.08
ABUW_RS13535	aldehyde dehydrogenase (NADP(+))	1.25	0.29	-0.02	0.94
ABUW_RS13540	5-dehydro-4-deoxyglucarate dehydratase	1.80	1.43	0.06	0.43
ABUW_RS13545	glucarate dehydratase	0.98	0.58	0.17	0.56
ABUW_RS13550	MFS transporter	1.40	0.15	0.17	1.42
ABUW_RS13555	galactarate dehydratase	1.36	0.47	-0.26	0.63
ABUW_RS13560	DMT family transporter	-0.28	-0.20	0.07	-0.02
ABUW_RS13565	AraC family transcriptional regulator	0.43	0.10	0.22	0.55
ABUW_RS13570	coniferyl aldehyde dehydrogenase	-0.55	-0.28	0.33	0.05
ABUW_RS13575	hypothetical protein	-0.77	2.06	-0.54	-3.37
ABUW_RS13580	DUF4265 domain-containing protein	-2.38	0.29	0.10	-2.57
ABUW_RS13585	hypothetical protein	-2.86	1.51	-0.52	-4.89
ABUW_RS13590	amino acid permease	-0.77	-1.63	-0.81	0.06
ABUW_RS13595	arginine N-succinyltransferase	-0.55	-2.73	-1.09	1.09
ABUW_RS13600	aspartate aminotransferase family protein	1.39	-3.09	-1.20	3.28
ABUW_RS13605	Lrp/AsnC family transcriptional regulator	-0.24	0.07	0.03	-0.28
ABUW_RS13610	gamma-aminobutyraldehyde dehydrogenase	-0.19	-0.96	-0.05	0.73
ABUW_RS13615	nuclear transport factor 2 family protein	-0.43	0.06	0.20	-0.29
ABUW_RS13620	FadR family transcriptional regulator	0.27	-0.57	0.05	0.89
ABUW_RS13625	PDC sensor domain-containing protein	-0.02	1.55	0.05	-1.53
ABUW_RS13630	APC family permease	0.24	-0.49	0.25	0.98
ABUW_RS13635	FAD-binding oxidoreductase	0.11	-0.75	0.10	0.96
ABUW_RS13640	amino acid permease	0.71	-0.19	-0.51	0.39
ABUW_RS13645	hypothetical protein	1.06	1.00	0.08	0.14
ABUW_RS13650	ATP-binding protein	-2.50	-0.10	0.16	-2.24

ABUW_RS13655	hypothetical protein	-0.96	0.80	-0.34	-2.10
ABUW_RS13675	hypothetical protein	-0.15	1.03	-0.44	-1.61
ABUW_RS13680	RHS repeat protein	-3.23	0.10	0.65	-2.68
ABUW_RS13685	type VI secretion system tip protein VgrG	-2.02	0.26	0.19	-2.09
ABUW_RS13690	TetR/AcrR family transcriptional regulator	-0.26	1.89	1.11	-1.04
ABUW_RS13700	hypothetical protein	0.76	1.12	-0.41	-0.77
ABUW_RS13705	hypothetical protein	-1.52	-0.29	0.03	-1.19
ABUW_RS13715	NADPH-dependent 2,4-dienoyl-CoA reductase	0.54	0.39	0.19	0.34
ABUW_RS13720	argininosuccinate synthase	-0.47	-0.85	0.13	0.50
ABUW_RS13725	GGDEF domain-containing protein	-0.22	0.68	-0.19	-1.09
ABUW_RS13730	dihydroorotase	-1.01	-0.59	0.11	-0.30
ABUW_RS13735	ribonuclease T	-0.81	-1.40	-0.01	0.57
ABUW_RS13745	TonB-dependent receptor	-1.35	0.82	0.22	-1.95
ABUW_RS13750	hypothetical protein	0.14	2.44	-0.14	-2.44
ABUW_RS13755	RHS repeat-associated core domain-containing protein	-1.54	1.37	0.01	-2.90
ABUW_RS13760	RHS repeat protein	-3.17	-0.06	0.14	-2.97
ABUW_RS13765	hypothetical protein	-4.88	-1.72	0.67	-2.48
ABUW_RS13770	hypothetical protein	-2.96	-0.44	-0.18	-2.70
ABUW_RS13775	hypothetical protein	-5.16	-1.39	0.86	-2.91
ABUW_RS13780	NADH:flavin oxidoreductase/NADH oxidase family protein	-0.04	0.73	0.17	-0.60
ABUW_RS13785	ABC transporter ATP-binding protein	-0.28	-0.07	-0.10	-0.31
ABUW_RS13790	ABC transporter permease	0.76	0.43	-0.49	-0.16
ABUW_RS13795	microcin C ABC transporter permease YejB	0.33	-0.18	-0.22	0.30
ABUW_RS13800	ABC transporter substrate-binding protein	0.01	0.30	0.02	-0.27
ABUW_RS13805	LysM peptidoglycan-binding domain-containing protein	0.13	0.10	-0.12	-0.09
ABUW_RS13810	DNA polymerase III subunit epsilon	0.07	-0.10	0.04	0.22
ABUW_RS13815	hypothetical protein	-0.31	-1.24	-0.11	0.82
ABUW_RS13820	NAD(+) diphosphatase	-0.66	-0.03	0.33	-0.29
ABUW_RS13825	alpha/beta hydrolase	-0.07	-0.48	-0.19	0.22
ABUW_RS13830	BON domain-containing protein	0.43	0.64	-0.35	-0.56
ABUW_RS13835	YraN family protein	0.83	0.19	-0.24	0.40
ABUW_RS13840	16S rRNA (cytidine(1402)-2'-O)-methyltransferase	-0.56	-0.43	0.14	0.01
ABUW_RS13845	hypothetical protein	-0.40	-1.35	0.54	1.49
ABUW_RS13850	LysR family transcriptional regulator ArgP	0.38	1.03	-0.16	-0.81
ABUW_RS13855	amino acid transporter	1.17	-1.07	0.23	2.47
ABUW_RS13860	cation transporter	-0.87	0.75	-0.39	-2.01
ABUW_RS13865	MerR family transcriptional regulator	0.07	-0.12	-0.06	0.13
ABUW_RS13870	hypothetical protein	0.26	2.74	-0.19	-2.67
ABUW_RS13875	FAD-dependent monooxygenase	0.41	0.34	-0.20	-0.13
ABUW_RS13880	FAD-dependent monooxygenase	0.59	0.40	-0.34	-0.15
ABUW_RS13885	Xaa-Pro aminopeptidase	0.43	0.08	0.11	0.46
ABUW_RS13890	UPF0149 family protein	0.49	0.17	-0.25	0.08
ABUW_RS13895	hypothetical protein	-0.27	0.14	0.25	-0.17

ABUW_RS13900	cell division protein ZapA	0.31	-0.60	-0.04	0.87
ABUW_RS13905	hypothetical protein	0.08	1.76	1.30	-0.38
ABUW_RS13910	hypothetical protein	-1.30	0.88	0.40	-1.79
ABUW_RS13915	5-formyltetrahydrofolate cyclo-ligase	-0.91	-0.10	0.41	-0.40
ABUW_RS13920	endopeptidase La	-0.45	1.17	0.41	-1.21
ABUW_RS13925	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	0.22	0.73	0.49	-0.03
ABUW_RS13930	dioxygenase	0.88	-0.61	0.30	1.79
ABUW_RS13935	META and DUF4377 domain-containing protein	-2.50	-1.89	0.45	-0.16
ABUW_RS13940	NADP-specific glutamate dehydrogenase	-0.13	0.06	-0.47	-0.66
ABUW_RS13945	RnfABCDGE type electron transport complex subunit B	0.16	-1.13	-0.30	0.99
ABUW_RS13950	endonuclease III	-0.71	-0.76	-0.10	-0.05
ABUW_RS13955	adenylate kinase	0.42	-0.48	-0.32	0.59
ABUW_RS13960	membrane protein	0.18	0.30	-0.28	-0.40
ABUW_RS13965	hypothetical protein	-0.09	0.87	-0.11	-1.07
ABUW_RS13970	penicillin-binding protein 2	0.34	-0.38	-0.01	0.72
ABUW_RS13975	16S rRNA (guanine(966)-N(2))-methyltransferase RsmD	-0.44	-0.34	-0.02	-0.12
ABUW_RS13980	HupE/UreJ family protein	0.40	0.04	-0.33	0.03
ABUW_RS13985	urease accessory protein UreG	-0.33	1.01	0.18	-1.16
ABUW_RS13990	urease accessory protein	1.02	-0.08	-0.28	0.83
ABUW_RS13995	urease accessory protein UreE	0.60	0.41	-0.13	0.07
ABUW_RS14000	urease subunit alpha	1.40	1.57	-0.17	-0.34
ABUW_RS14010	urease subunit gamma	1.92	1.74	-0.58	-0.40
ABUW_RS14015	urease accessory protein UreD	1.68	1.86	-0.15	-0.34
ABUW_RS14020	hypothetical protein	0.21	0.17	0.39	0.43
ABUW_RS14025	copper resistance protein NlpE	-0.29	2.70	0.03	-2.97
ABUW_RS14030	isocitrate lyase	-0.23	-0.04	0.17	-0.02
ABUW_RS14035	LysR family transcriptional regulator	0.13	-0.32	0.10	0.55
ABUW_RS14040	HlyC/CorC family transporter	-0.38	0.16	-0.28	-0.82
ABUW_RS14045	CitMHS family transporter	-1.93	0.11	-0.48	-2.52
ABUW_RS14050	hypothetical protein	-0.62	0.74	0.20	-1.16
ABUW_RS14055	DUF2239 family protein	-0.61	-1.31	0.06	0.76
ABUW_RS14060	sulfate adenylyltransferase subunit CysN	-0.06	-0.29	0.01	0.24
ABUW_RS14065	sulfate adenylyltransferase subunit CysD	-0.33	-0.80	0.07	0.55
ABUW_RS14070	capsule assembly Wzi family protein	-1.96	0.55	-0.10	-2.61
ABUW_RS14075	lysine--tRNA ligase	-0.44	-0.43	-0.22	-0.24
ABUW_RS14080	esterase	-1.71	-1.64	0.19	0.13
ABUW_RS14085	SRPBCC domain-containing protein	-1.02	0.30	0.27	-1.05
ABUW_RS14090	rubredoxin	-1.23	0.77	0.15	-1.85
ABUW_RS14095	FAD-dependent oxidoreductase	-1.07	-0.04	0.02	-1.00
ABUW_RS14100	alpha/beta hydrolase	-0.68	-0.34	0.09	-0.25
ABUW_RS14105	hydrogen peroxide-inducible genes activator	-0.17	-1.07	-0.23	0.67
ABUW_RS14110	SPOR domain-containing protein	-0.32	1.19	0.20	-1.32
ABUW_RS14115	polyphosphate kinase 1	-0.03	0.40	-0.04	-0.47

ABUW_RS14120	monofunctional biosynthetic peptidoglycan transglycosylase	-0.31	0.39	0.13	-0.57
ABUW_RS14125	rhomboid family intramembrane serine protease	0.16	-0.57	-0.12	0.61
ABUW_RS14130	FtsX-like permease family protein	-0.04	-0.23	-0.12	0.07
ABUW_RS14135	ABC transporter ATP-binding protein	-0.05	-0.72	0.00	0.67
ABUW_RS14140	arylesterase	-0.20	-0.45	0.12	0.37
ABUW_RS14145	carbonic anhydrase	0.11	0.15	-0.41	-0.45
ABUW_RS14150	alpha/beta hydrolase	-0.24	0.11	0.25	-0.09
ABUW_RS14155	hypothetical protein	-1.07	-0.39	0.35	-0.33
ABUW_RS14160	TonB-dependent siderophore receptor	-2.31	-0.04	-0.19	-2.45
ABUW_RS14165	Fe-S biogenesis protein NfuA	0.20	1.39	-0.02	-1.21
ABUW_RS14170	rhomboid family intramembrane serine protease	-1.57	0.72	0.17	-2.11
ABUW_RS14175	arylsulfatase	-0.23	-0.53	0.67	0.97
ABUW_RS14180	formylglycine-generating enzyme family protein	1.07	0.49	-0.10	0.48
ABUW_RS14190	hypothetical protein	-0.27	-0.25	-0.64	-0.66
ABUW_RS14195	D-serine ammonia-lyase	-0.54	1.19	0.23	-1.50
ABUW_RS14200	inorganic phosphate transporter	0.16	0.49	-0.45	-0.78
ABUW_RS14205	methionine synthase	-0.20	-0.53	-0.13	0.20
ABUW_RS14210	transketolase	0.22	-0.24	-0.58	-0.12
ABUW_RS14215	transketolase	-0.37	-0.97	-0.11	0.48
ABUW_RS14220	MFS transporter	0.29	-1.21	-0.09	1.42
ABUW_RS14225	SDR family oxidoreductase	0.42	-0.59	-0.19	0.83
ABUW_RS14230	LysR family transcriptional regulator	-0.71	-1.83	0.42	1.53
ABUW_RS14235	hypothetical protein	-1.52	-0.54	0.29	-0.69
ABUW_RS14240	galactose mutarotase	-0.73	2.11	-0.08	-2.92
ABUW_RS14245	MFS transporter	0.57	0.94	-0.23	-0.60
ABUW_RS14250	helix-turn-helix transcriptional regulator	0.27	-0.08	0.16	0.51
ABUW_RS14255	glutaminase	1.19	1.02	-0.04	0.13
ABUW_RS14260	peptide deformylase	0.95	1.80	-0.44	-1.28
ABUW_RS14265	MFS transporter	0.92	0.62	-0.56	-0.26
ABUW_RS14270	hypothetical protein	-0.17	-0.26	0.31	0.41
ABUW_RS14275	thiamine pyrophosphate-binding protein	0.39	-0.36	0.19	0.94
ABUW_RS14280	aldehyde dehydrogenase	0.83	-0.37	-0.25	0.96
ABUW_RS14285	aspartate dehydrogenase	1.68	-0.39	-0.60	1.47
ABUW_RS14290	SDR family oxidoreductase	0.91	0.54	0.52	0.89
ABUW_RS14295	alpha/beta hydrolase	0.52	-0.36	0.70	1.57
ABUW_RS14300	cupin domain-containing protein	0.25	-0.54	0.07	0.85
ABUW_RS14305	MFS transporter	1.14	-0.43	-0.16	1.41
ABUW_RS14310	FAD-dependent oxidoreductase	1.93	0.46	0.01	1.48
ABUW_RS14315	VOC family protein	1.08	-0.21	0.35	1.64
ABUW_RS14320	SDR family oxidoreductase	3.11	0.22	-0.20	2.69
ABUW_RS14325	aromatic ring-hydroxylating dioxygenase subunit alpha	3.77	0.26	0.24	3.74
ABUW_RS14330	hypothetical protein	3.17	0.53	0.42	3.06
ABUW_RS14335	non-heme iron oxygenase ferredoxin subunit	3.99	1.31	0.68	3.35
ABUW_RS14340	lclR family transcriptional regulator	0.74	0.19	0.04	0.60

ABUW_RS14345	hypothetical protein	0.54	1.84	-1.03	-2.33
ABUW_RS14350	nicotinamide mononucleotide transporter	-0.62	-0.35	-0.35	-0.61
ABUW_RS14355	crotonase/enoyl-CoA hydratase family protein	-0.86	-0.27	0.13	-0.46
ABUW_RS14360	poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD	2.64	2.24	-0.35	0.05
ABUW_RS14365	poly-beta-1,6 N-acetyl-D-glucosamine synthase	2.02	0.98	-0.19	0.84
ABUW_RS14370	poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB	1.99	2.27	0.06	-0.23
ABUW_RS14375	FKBP-type peptidyl-prolyl cis-trans isomerase	0.39	1.25	-0.35	-1.21
ABUW_RS14380	YaeQ family protein	-0.90	1.48	0.65	-1.73
ABUW_RS14385	C4-dicarboxylate transporter DctA	-0.01	0.19	0.26	0.05
ABUW_RS14390	GTP-binding protein	0.42	0.25	0.42	0.59
ABUW_RS14395	hypothetical protein	-0.48	2.17	0.65	-2.01
ABUW_RS14400	acyl-CoA thioesterase	-0.42	0.06	0.04	-0.45
ABUW_RS14405	MarC family protein	-0.62	-0.04	-0.52	-1.10
ABUW_RS14410	choline transporter	-0.80	-0.34	-0.30	-0.76
ABUW_RS14415	BCCT family transporter	-0.38	-0.18	-0.21	-0.41
ABUW_RS14420	transcriptional regulator BetI	0.66	-0.51	-0.04	1.13
ABUW_RS14425	betaine-aldehyde dehydrogenase	0.08	-1.05	0.24	1.37
ABUW_RS14430	choline dehydrogenase	-0.11	-1.02	0.09	1.00
ABUW_RS14435	malate dehydrogenase (quinone)	-1.66	-0.47	0.21	-0.98
ABUW_RS14440	hypothetical protein	0.09	0.93	-0.22	-1.06
ABUW_RS14445	homocysteine S-methyltransferase family protein	-0.18	-0.78	0.15	0.75
ABUW_RS14450	amino acid permease	-0.15	-0.96	-0.05	0.76
ABUW_RS14455	alpha/beta fold hydrolase	0.19	-0.01	-0.08	0.12
ABUW_RS14460	DUF1275 domain-containing protein	0.71	2.05	0.10	-1.25
ABUW_RS14465	hypothetical protein	0.92	0.34	-0.07	0.51
ABUW_RS14470	YbaN family protein	0.65	3.78	0.64	-2.48
ABUW_RS14475	biliverdin-producing heme oxygenase	1.01	5.30	0.34	-3.95
ABUW_RS14480	energy transducer TonB	-0.11	4.26	0.73	-3.64
ABUW_RS14485	DUF560 domain-containing protein	2.14	5.81	0.43	-3.24
ABUW_RS14490	transferrin-binding protein-like solute binding protein	1.59	5.26	0.44	-3.24
ABUW_RS14495	TonB-dependent receptor	-0.37	3.52	0.50	-3.38
ABUW_RS14500	FecR domain-containing protein	-0.19	1.05	0.54	-0.69
ABUW_RS14505	sigma-70 family RNA polymerase sigma factor	-0.28	1.58	0.33	-1.54
ABUW_RS14510	LysR family transcriptional regulator	0.03	-0.19	0.34	0.56
ABUW_RS14515	dihydrodipicolinate synthase family protein	0.19	-0.54	-0.07	0.66
ABUW_RS14520	MFS transporter	0.45	-0.57	0.23	1.25
ABUW_RS14525	OprD family outer membrane porin	1.77	0.85	-0.17	0.75
ABUW_RS14530	hypothetical protein	2.54	0.74	0.61	2.41
ABUW_RS14535	hypothetical protein	0.36	-0.54	-0.50	0.40
ABUW_RS14540	DUF262 domain-containing protein	-1.01	-0.07	0.09	-0.85
ABUW_RS14545	hypothetical protein	-0.92	-0.15	0.16	-0.61
ABUW_RS14550	DEAD/DEAH box helicase family protein	-1.34	-0.03	0.10	-1.21
ABUW_RS14555	site-specific DNA-methyltransferase	-1.05	-0.12	0.27	-0.66

ABUW_RS14560	DUF4391 domain-containing protein	0.65	-0.96	-0.24	1.37
ABUW_RS14565	helicase	0.41	0.58	-0.31	-0.49
ABUW_RS14570	hypothetical protein	-3.42	-0.98	-0.13	-2.56
ABUW_RS14580	hypothetical protein	0.38	0.61	-0.55	-0.79
ABUW_RS14585	Fic family protein	-0.83	-0.37	0.17	-0.29
ABUW_RS14590	hypothetical protein	-0.55	0.77	0.05	-1.27
ABUW_RS14595	single-stranded DNA-binding protein	-0.55	-0.07	-0.25	-0.73
ABUW_RS14600	DUF927 domain-containing protein	0.17	-0.31	0.27	0.75
ABUW_RS14605	hypothetical protein	0.65	-0.14	0.27	1.06
ABUW_RS14610	hypothetical protein	0.45	0.02	0.30	0.73
ABUW_RS14615	hypothetical protein	0.11	-0.38	0.96	1.45
ABUW_RS14620	hypothetical protein	0.05	-0.59	0.41	1.05
ABUW_RS14625	DNA-binding protein	-0.97	-0.19	0.70	-0.08
ABUW_RS14630	hypothetical protein	-0.29	-0.52	1.00	1.23
ABUW_RS14635	hypothetical protein	-0.64	0.32	-0.10	-1.06
ABUW_RS14640	tyrosine-type recombinase/integrase	-0.38	0.53	0.65	-0.25
ABUW_RS14645	gamma-glutamyltransferase	-0.46	-0.20	-0.30	-0.56
ABUW_RS14650	DHA2 family efflux MFS transporter permease subunit	1.71	0.45	-0.45	0.81
ABUW_RS14655	EmrA/EmrK family multidrug efflux transporter periplasmic adaptor subunit	0.69	0.12	0.18	0.74
ABUW_RS14660	thioesterase family protein	1.37	-0.95	-0.32	2.00
ABUW_RS14665	prophobilinogen synthase	-0.38	-0.55	0.26	0.43
ABUW_RS14670	FAD-dependent oxidoreductase	0.08	-1.00	0.13	1.21
ABUW_RS14675	TIGR01777 family oxidoreductase	-0.52	-0.63	-0.07	0.05
ABUW_RS14680	ABZJ_00895 family protein	-0.07	0.58	-0.31	-0.95
ABUW_RS14685	VOC family protein	-0.17	-0.31	0.61	0.75
ABUW_RS14690	OsmC family protein	-1.21	0.27	0.26	-1.22
ABUW_RS14695	exonuclease SbcCD subunit D	-0.48	-0.37	0.46	0.35
ABUW_RS14700	AAA family ATPase	-0.34	0.31	0.16	-0.49
ABUW_RS14705	YggS family pyridoxal phosphate-dependent enzyme	0.35	-0.79	-0.10	1.04
ABUW_RS14710	type IV pilus twitching motility protein PilT	1.19	-1.91	-0.03	3.08
ABUW_RS14715	PilT/PilU family type 4a pilus ATPase	0.47	-1.13	-0.27	1.32
ABUW_RS14720	ferric iron uptake transcriptional regulator	0.16	-0.73	-0.35	0.54
ABUW_RS14725	outer membrane protein assembly factor BamE	1.35	0.93	0.15	0.56
ABUW_RS14730	RnfH family protein	-0.39	-0.84	0.04	0.49
ABUW_RS14735	hypothetical protein	-1.08	-0.69	-0.22	-0.61
ABUW_RS14740	bacteriohemerythrin	-2.19	2.05	0.40	-3.84
ABUW_RS14745	class II glutamine amidotransferase	-0.97	0.37	0.08	-1.26
ABUW_RS14750	GNAT family N-acetyltransferase	1.06	1.14	0.01	-0.07
ABUW_RS14755	acetylglutamate kinase	-0.17	1.21	0.03	-1.36
ABUW_RS14760	phosphomannomutase/phosphoglucomutase	-0.12	0.34	0.35	-0.11
ABUW_RS14765	dUTP diphosphatase	-0.23	-0.77	-0.37	0.18
ABUW_RS14770	DNA helicase Rep	-0.20	-0.31	0.03	0.14
ABUW_RS14775	OmpA family protein	1.03	1.04	-0.21	-0.22
ABUW_RS14780	acyltransferase	-0.90	0.14	0.07	-0.97

ABUW_RS14785	hypothetical protein	-0.66	-0.05	0.03	-0.58
ABUW_RS14790	septum site-determining protein MinC	-0.15	0.42	-0.11	-0.68
ABUW_RS14795	septum site-determining protein MinD	0.38	0.80	-0.19	-0.61
ABUW_RS14800	cell division topological specificity factor MinE	0.55	0.18	-0.19	0.18
ABUW_RS14805	PA4642 family protein	1.50	2.91	-0.15	-1.56
ABUW_RS14810	threonine export protein RhtC	-0.62	0.98	0.10	-1.49
ABUW_RS14815	DNA translocase FtsK	-0.22	0.23	0.14	-0.31
ABUW_RS14820	thioredoxin-disulfide reductase	0.32	0.06	0.16	0.42
ABUW_RS14825	leucyl/phenylalanyl-tRNA--protein transferase	-0.35	0.05	0.05	-0.36
ABUW_RS14830	arginyltransferase	-0.66	-1.12	0.35	0.81
ABUW_RS14835	ribosomal protein S18-alanine N-acetyltransferase	-0.10	0.59	0.14	-0.55
ABUW_RS14840	metal-dependent hydrolase	0.71	-1.72	0.03	2.46
ABUW_RS14845	metal-dependent hydrolase	0.29	-1.30	-0.04	1.54
ABUW_RS14850	elongation factor Tu	-0.53	-1.64	0.55	1.66
ABUW_RS14855	elongation factor G	0.30	-0.18	-0.05	0.43
ABUW_RS14860	30S ribosomal protein S7	0.84	-0.31	0.12	1.27
ABUW_RS14865	30S ribosomal protein S12	1.07	0.49	-0.15	0.43
ABUW_RS14870	EcsC family protein	-0.34	1.22	-0.15	-1.71
ABUW_RS14875	beta-ketoacyl-ACP synthase II	-1.91	-0.50	0.15	-1.25
ABUW_RS14880	protoporphyrinogen oxidase HemJ	-0.74	-0.71	-0.14	-0.18
ABUW_RS14885	pirin family protein	-0.67	0.06	0.61	-0.13
ABUW_RS14890	hypothetical protein	-0.93	0.28	0.11	-1.11
ABUW_RS14895	NAD+ synthase	-0.71	0.79	0.18	-1.32
ABUW_RS14900	hypothetical protein	-1.93	-0.31	0.43	-1.19
ABUW_RS14910	oxidoreductase	0.91	0.04	-0.30	0.57
ABUW_RS14915	NAD-dependent succinate-semialdehyde dehydrogenase	0.30	-0.71	-0.20	0.81
ABUW_RS14920	Rieske 2Fe-2S domain-containing protein	-0.07	-0.79	-0.12	0.60
ABUW_RS14925	alpha/beta hydrolase	0.86	-0.38	0.13	1.37
ABUW_RS14930	BCCT family carnitine transporter	0.85	-0.62	-0.21	1.26
ABUW_RS14935	tartrate dehydrogenase	0.31	-0.74	-0.18	0.87
ABUW_RS14940	LysR family transcriptional regulator	-0.91	-1.64	0.23	0.96
ABUW_RS14945	hypothetical protein	0.43	0.09	0.12	0.45
ABUW_RS14955	YfhL family 4Fe-4S dicluster ferredoxin	0.06	-0.50	0.46	1.02
ABUW_RS14960	pantetheine-phosphate adenylyltransferase	-0.17	-0.11	0.04	-0.02
ABUW_RS14965	SsrA-binding protein SmpB	-0.62	1.30	-0.03	-1.95
ABUW_RS14970	flavodoxin family protein	0.71	0.52	-0.01	0.18
ABUW_RS14975	peptidoglycan editing factor PgeF	-0.70	-0.76	0.29	0.35
ABUW_RS14980	23S rRNA pseudouridine(1911/1915/1917) synthase RluD	0.43	-0.04	0.01	0.48
ABUW_RS14985	outer membrane protein assembly factor BamD	-0.44	-0.02	0.03	-0.40
ABUW_RS14990	DNA primase	-0.35	0.06	0.06	-0.35
ABUW_RS14995	glutamyl-tRNA reductase	1.44	-0.07	0.09	1.59
ABUW_RS15000	tetratricopeptide repeat protein	-0.45	-0.27	0.26	0.08
ABUW_RS15005	outer membrane lipoprotein LolB	0.60	0.27	0.39	0.73

ABUW_RS15010	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	-0.49	-0.42	0.50	0.43
ABUW_RS15035	ribose-phosphate pyrophosphokinase	0.14	-1.43	-0.18	1.38
ABUW_RS15040	50S ribosomal protein L25	0.48	-0.40	-0.52	0.36
ABUW_RS15045	aminoacyl-tRNA hydrolase	0.73	-0.45	-0.11	1.07
ABUW_RS15050	aspartate 1-decarboxylase	0.95	0.72	-0.35	-0.11
ABUW_RS15055	GDYXXLY domain-containing protein	-0.44	0.67	-0.25	-1.36
ABUW_RS15060	DUF2157 domain-containing protein	-1.00	0.04	0.07	-0.96
ABUW_RS15065	3,4-dihydroxy-2-butanone-4-phosphate synthase	0.15	-0.09	-0.42	-0.18
ABUW_RS15070	HAD-IA family hydrolase	0.06	0.88	-0.32	-1.13
ABUW_RS15075	hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	-0.89	-0.06	-0.03	-0.85
ABUW_RS15080	peptidoglycan-binding protein LysM	1.23	3.38	-0.88	-3.03
ABUW_RS15085	acyl carrier protein	-0.03	-0.35	0.09	0.40
ABUW_RS15090	3-oxoacyl-ACP reductase FabG	-0.17	-1.07	-0.26	0.65
ABUW_RS15095	ACP S-malonyltransferase	0.62	-0.78	-0.22	1.17
ABUW_RS15100	50S ribosomal protein L32	0.73	-0.28	-0.01	1.00
ABUW_RS15105	DUF177 domain-containing protein	1.12	-0.91	0.06	2.09
ABUW_RS15110	elongation factor P hydroxylase	0.13	-0.08	-0.01	0.20
ABUW_RS15115	threonylcarbamoyl-AMP synthase	-0.19	-0.12	-0.14	-0.21
ABUW_RS15120	segregation/condensation protein A	0.04	-1.00	0.08	1.11
ABUW_RS15125	SMC-Scp complex subunit ScpB	-0.32	-1.09	0.09	0.86
ABUW_RS15130	23S rRNA pseudouridine(2605) synthase RluB	-0.34	-0.45	-0.13	-0.02
ABUW_RS15135	ATP-dependent dethiobiotin synthetase BioD	-0.01	0.38	-0.74	-1.14
ABUW_RS15140	malonyl-ACP O-methyltransferase BioC	-1.00	-1.03	-0.04	-0.01
ABUW_RS15145	8-amino-7-oxononanoate synthase	-0.31	-0.37	-0.22	-0.16
ABUW_RS15150	adenosylmethionine--8-amino-7-oxononanoate transaminase	-0.01	-0.25	0.06	0.30
ABUW_RS15155	alpha/beta fold hydrolase	-0.75	0.68	-0.43	-1.87
ABUW_RS15160	trehalose-phosphatase	-0.89	1.99	-1.55	-4.42
ABUW_RS15165	trehalose-6-phosphate synthase	-2.78	1.22	-0.62	-4.62
ABUW_RS15170	MFS transporter	2.22	1.32	-0.42	0.47
ABUW_RS15175	bacterioferritin	1.50	-0.11	-0.14	1.48
ABUW_RS15180	NAD-dependent DNA ligase LigA	0.58	0.59	-0.28	-0.29
ABUW_RS15185	cell division protein ZipA	0.99	0.73	-0.36	-0.09
ABUW_RS15190	chromosome segregation protein SMC	0.26	0.62	0.00	-0.35
ABUW_RS15195	GntR family transcriptional regulator	-0.50	0.38	0.38	-0.50
ABUW_RS15200	sulfite exporter TauE/SafE family protein	0.39	-1.31	-0.35	1.36
ABUW_RS15205	biotin--[acetyl-CoA-carboxylase] ligase	-1.10	-0.67	0.22	-0.21
ABUW_RS15210	pantothenate kinase	-0.74	-0.61	0.09	-0.04
ABUW_RS15215	signal recognition particle protein	0.22	0.04	-0.25	-0.06
ABUW_RS15220	cytochrome c biogenesis protein CcsA	-0.61	-1.26	0.40	1.04
ABUW_RS15225	tRNA-dihydrouridine synthase	-0.06	-1.29	-0.09	1.14
ABUW_RS15230	hypothetical protein	0.24	0.99	0.00	-0.74
ABUW_RS15235	hypothetical protein	-0.25	-0.46	0.08	0.29
ABUW_RS15240	hypothetical protein	0.33	-0.22	-0.15	0.40

ABUW_RS15245	hypothetical protein	-0.40	-0.22	0.39	0.21
ABUW_RS15250	hypothetical protein	0.17	0.85	0.13	-0.55
ABUW_RS15255	dCTP deaminase	-0.14	-0.09	-0.53	-0.58
ABUW_RS15260	LysE family transporter	-0.39	0.57	-0.43	-1.38
ABUW_RS15265	DUF2062 domain-containing protein	0.51	2.08	0.36	-1.21
ABUW_RS15270	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	-0.89	1.19	-0.26	-2.35
ABUW_RS15275	iron-sulfur cluster carrier protein ApbC	-0.18	0.09	0.28	0.01
ABUW_RS15280	hypothetical protein	0.26	2.73	0.00	-2.46
ABUW_RS15285	methionine--tRNA ligase	-0.58	-0.17	-0.13	-0.54
ABUW_RS15290	NF038215 family lipoprotein	1.08	2.73	0.50	-1.15
ABUW_RS15295	LysE family translocator	1.98	0.97	-1.17	-0.16
ABUW_RS15300	TetR/AcrR family transcriptional regulator	1.73	2.20	0.26	-0.21
ABUW_RS15305	MFS transporter	1.07	0.19	-0.05	0.83
ABUW_RS15310	HlyD family secretion protein	0.53	0.26	-0.34	-0.08
ABUW_RS15315	1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase	-0.42	-0.85	0.36	0.79
ABUW_RS15320	NAD(P)/FAD-dependent oxidoreductase	-0.15	-0.74	-0.09	0.51
ABUW_RS15330	mechanosensitive ion channel	0.30	1.47	-0.15	-1.32
ABUW_RS15335	hypothetical protein	1.15	2.55	0.11	-1.29
ABUW_RS15340	hypothetical protein	0.29	-0.87	0.71	1.87
ABUW_RS15345	ferredoxin--NADP reductase	0.23	-0.55	-0.35	0.43
ABUW_RS15350	LysR family transcriptional regulator GigC	0.32	-1.00	0.07	1.39
ABUW_RS15355	excalibur calcium-binding domain-containing protein	0.89	0.66	-0.17	0.06
ABUW_RS15360	cold shock domain-containing protein	0.37	1.52	-0.19	-1.34
ABUW_RS15365	uracil phosphoribosyltransferase	0.57	1.41	0.11	-0.73
ABUW_RS15370	NADH-quinone oxidoreductase subunit NuoN	0.03	-0.34	-0.44	-0.07
ABUW_RS15375	NADH-quinone oxidoreductase subunit M	-0.13	-0.12	-0.49	-0.51
ABUW_RS15380	NADH-quinone oxidoreductase subunit L	-0.39	0.09	-0.67	-1.14
ABUW_RS15385	NADH-quinone oxidoreductase subunit NuoK	-1.21	-0.52	-0.05	-0.73
ABUW_RS15390	NADH-quinone oxidoreductase subunit J	-0.64	-1.08	-0.33	0.11
ABUW_RS15395	NADH-quinone oxidoreductase subunit NuoI	-0.18	-0.24	-0.39	-0.34
ABUW_RS15400	NADH-quinone oxidoreductase subunit NuoH	0.11	-0.17	-0.43	-0.15
ABUW_RS15405	NADH-quinone oxidoreductase subunit NuoG	-0.59	-0.49	-0.09	-0.18
ABUW_RS15410	NADH-quinone oxidoreductase subunit NuoF	0.01	-0.63	-0.16	0.47
ABUW_RS15415	NADH-quinone oxidoreductase subunit NuoE	-0.55	-0.40	-0.24	-0.39
ABUW_RS15420	NADH-quinone oxidoreductase subunit C/D	-0.09	-0.51	-0.28	0.14
ABUW_RS15425	NADH-quinone oxidoreductase subunit B	0.63	-0.55	-0.65	0.54
ABUW_RS15430	NADH-quinone oxidoreductase subunit A	0.63	-0.39	-0.71	0.31
ABUW_RS15435	GGDEF domain-containing protein	-1.12	-0.40	0.30	-0.42
ABUW_RS15440	hypothetical protein	-1.14	0.64	0.86	-0.92
ABUW_RS15445	sensor histidine kinase BfmS	-0.25	-0.20	0.09	0.03
ABUW_RS15450	response regulator transcription factor BfmR	-0.57	0.67	0.43	-0.81
ABUW_RS15455	hypothetical protein	-0.12	1.54	1.50	-0.15
ABUW_RS15460	ribonucleoside-diphosphate reductase subunit alpha	-0.50	-0.29	0.37	0.16

ABUW_RS15465	hypothetical protein	0.70	-0.92	-0.28	1.35
ABUW_RS15470	ribonucleotide-diphosphate reductase subunit beta	-0.54	-0.30	0.29	0.04
ABUW_RS15475	hypothetical protein	-1.51	0.47	0.02	-1.96
ABUW_RS15480	PhzF family isomerase	-0.02	-0.18	-0.10	0.06
ABUW_RS15485	LysR family transcriptional regulator	0.43	0.87	-0.07	-0.52
ABUW_RS15490	hypothetical protein	-0.43	0.49	-0.77	-1.69
ABUW_RS15495	hypothetical protein	0.33	0.96	-1.15	-1.78
ABUW_RS15500	hypothetical protein	-2.31	0.08	0.23	-2.16
ABUW_RS15505	hypothetical protein	0.09	1.21	-0.64	-1.76
ABUW_RS15510	TetR/AcrR family transcriptional regulator	1.64	2.85	0.10	-1.11
ABUW_RS15515	flavin reductase	0.05	0.33	0.63	0.36
ABUW_RS15520	methionine synthase	-0.14	0.17	0.32	0.01
ABUW_RS15525	DUF1852 domain-containing protein	-0.13	0.66	0.36	-0.43
ABUW_RS15530	LysR family transcriptional regulator	-0.19	0.85	0.47	-0.56
ABUW_RS15535	LysE family translocator	0.12	-0.35	-1.00	-0.53
ABUW_RS15540	fatty acid desaturase	-0.32	-0.82	0.02	0.53
ABUW_RS15545	AraC family transcriptional regulator	-0.37	-0.19	0.40	0.21
ABUW_RS15550	amidohydrolase	-0.27	1.35	0.22	-1.39
ABUW_RS15555	hypothetical protein	-0.46	-0.45	0.32	0.31
ABUW_RS15560	LysR family transcriptional regulator	-0.31	-0.93	0.26	0.88
ABUW_RS15565	MFS transporter	2.83	0.37	-0.34	2.13
ABUW_RS15570	substrate-binding domain-containing protein	-0.65	-0.55	0.37	0.27
ABUW_RS15575	LysR family transcriptional regulator	1.35	0.81	-0.07	0.47
ABUW_RS15580	FAD-dependent tricarballoylate dehydrogenase TcuA	1.71	0.27	0.35	1.78
ABUW_RS15585	tricarballoylate utilization 4Fe-4S protein TcuB	-0.12	-1.32	0.02	1.22
ABUW_RS15590	CoA transferase	0.06	-0.49	0.17	0.72
ABUW_RS15595	MFS transporter	0.46	0.23	0.23	0.46
ABUW_RS15600	acyl-CoA dehydrogenase	1.83	1.26	-0.18	0.38
ABUW_RS15605	LysR family transcriptional regulator	-0.83	-0.78	0.19	0.14
ABUW_RS15610	zinc-binding dehydrogenase	0.26	-0.32	0.29	0.88
ABUW_RS15615	adenosine deaminase	-0.27	1.05	0.34	-0.99
ABUW_RS15640	quinolinate synthase NadA	1.27	0.19	-0.42	0.66
ABUW_RS15645	bifunctional glutamate N-acetyltransferase/ amino- acid acetyltransferase ArgJ	-0.08	-0.33	-0.07	0.19
ABUW_RS15650	methylated-DNA--[protein]-cysteine S- methyltransferase	0.52	-0.20	-0.31	0.42
ABUW_RS15655	multidrug efflux SMR transporter	1.30	-0.29	-0.54	1.04
ABUW_RS15660	cation transporter	1.67	1.40	-0.22	0.05
ABUW_RS15665	copper resistance protein B	0.32	-0.12	-0.37	0.08
ABUW_RS15670	copper resistance system multicopper oxidase	-0.18	-0.95	0.19	0.95
ABUW_RS15675	hypothetical protein	-0.68	-0.64	0.27	0.23
ABUW_RS15680	HAD family hydrolase	-0.17	0.35	0.05	-0.47
ABUW_RS15685	ribose-phosphate 3-epimerase	0.84	0.34	-0.52	-0.03
ABUW_RS15690	DUF2218 domain-containing protein	-0.31	0.46	0.12	-0.66
ABUW_RS15695	S-formylglutathione hydrolase	0.67	-0.12	-0.53	0.27
ABUW_RS15700	hypothetical protein	0.43	0.06	-0.39	-0.02

ABUW_RS15705	class I SAM-dependent methyltransferase tRNA (adenosine(37)-N6)- threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	0.18	-0.46	-0.10	0.54
ABUW_RS15710		-0.15	-0.42	-0.14	0.13
ABUW_RS15715	gamma carbonic anhydrase family protein	0.01	-0.30	-0.15	0.16
ABUW_RS15720	CoA pyrophosphatase	-0.26	-0.09	0.06	-0.10
ABUW_RS15725	NUDIX hydrolase	-0.28	0.47	0.22	-0.53
ABUW_RS15730	hypothetical protein	-0.81	0.61	0.02	-1.40
ABUW_RS15740	outer membrane protein transport protein	-0.65	-0.34	0.10	-0.21
ABUW_RS15745	hypothetical protein	-0.84	0.23	0.13	-0.94
ABUW_RS15750	C39 family peptidase	-1.89	-0.32	0.27	-1.30
ABUW_RS15755	hypothetical protein	2.16	1.78	-0.15	0.23
ABUW_RS15760	chorismate-binding protein	-0.96	0.01	-0.01	-0.98
ABUW_RS15765	histidinol-phosphate transaminase	0.50	0.43	-0.21	-0.14
ABUW_RS15770	histidinol dehydrogenase	0.50	0.20	-0.20	0.10
ABUW_RS15775	ATP phosphoribosyltransferase UDP-N-acetylglucosamine 1- carboxyvinyltransferase	0.59	0.44	-0.52	-0.36
ABUW_RS15780		0.53	0.33	-0.24	-0.04
ABUW_RS15785	BolA family iron metabolism protein IbaG	1.58	2.26	-0.64	-1.32
ABUW_RS15790	ribosome-associated translation inhibitor RaiA	1.04	1.99	0.24	-0.71
ABUW_RS15795	RNA polymerase factor sigma-54	-1.31	0.03	0.39	-0.94
ABUW_RS15825	VacJ family lipoprotein	0.54	0.19	0.06	0.40
ABUW_RS15830	RsbU family protein phosphatase GigA	-0.69	-0.36	0.41	0.07
ABUW_RS15835	anti-anti-sigma factor GigB	1.22	1.15	0.05	0.11
ABUW_RS15840	carbon-nitrogen hydrolase family protein	1.89	0.82	-0.11	0.96
ABUW_RS15845	DUF4951 domain-containing protein	1.65	0.90	0.27	1.02
ABUW_RS15850	MarR family transcriptional regulator	-0.09	0.69	0.57	-0.22
ABUW_RS15855	organic hydroperoxide resistance protein	0.76	4.12	0.60	-2.76
ABUW_RS15860	type II secretion system ATPase GspE	0.62	0.83	0.00	-0.21
ABUW_RS15865	hypothetical protein	0.71	2.16	0.13	-1.32
ABUW_RS15870	mechanosensitive ion channel family protein	-0.15	0.63	0.06	-0.73
ABUW_RS15875	DUF2339 domain-containing protein	0.78	1.57	-0.02	-0.81
ABUW_RS15880	DNA polymerase I	0.43	0.72	-0.01	-0.30
ABUW_RS15885	YggT family protein	0.64	0.10	-0.49	0.05
ABUW_RS15890	pyrroline-5-carboxylate reductase	0.68	0.33	-0.18	0.18
ABUW_RS15895	tRNA lysidine(34) synthetase TilS acetyl-CoA carboxylase carboxyltransferase subunit alpha	0.96	0.80	-0.25	-0.10
ABUW_RS15900		1.33	0.66	-0.53	0.13
ABUW_RS15905	exopolyphosphatase	0.64	0.71	-0.26	-0.33
ABUW_RS15910	thioredoxin	1.33	1.96	-0.09	-0.71
ABUW_RS15915	transcription termination factor Rho	0.17	-0.33	-0.16	0.34
ABUW_RS15920	hypothetical protein	0.43	1.20	0.45	-0.32
ABUW_RS15925	integration host factor subunit alpha	1.03	1.68	0.33	-0.32
ABUW_RS15930	phenylalanine--tRNA ligase subunit beta	1.07	0.89	0.05	0.23
ABUW_RS15935	phenylalanine--tRNA ligase subunit alpha	1.44	1.24	-0.27	-0.07
ABUW_RS15940	hypothetical protein	0.01	0.96	0.55	-0.40
ABUW_RS15945	hypothetical protein	0.90	0.85	-0.01	0.04

ABUW_RS15950	50S ribosomal protein L20	0.83	-1.40	-0.22	2.02
ABUW_RS15955	50S ribosomal protein L35	-0.32	-1.50	0.03	1.21
ABUW_RS15960	nickel resistance MFS transporter NreB	1.10	1.27	-0.40	-0.57
ABUW_RS15965	DedA family protein	1.44	1.28	-0.30	-0.14
ABUW_RS15970	glutathione S-transferase N-terminal domain-containing protein	0.65	1.79	-0.22	-1.36
ABUW_RS15975	translation initiation factor IF-3	0.48	-0.55	0.28	1.32
ABUW_RS15980	threonine--tRNA ligase	0.84	0.41	-0.03	0.40
ABUW_RS15985	acyl-CoA synthetase	-0.13	0.58	-0.04	-0.76
ABUW_RS15990	ribosome-associated protein	0.16	-0.05	0.29	0.50
ABUW_RS15995	HPr family phosphocarrier protein	0.28	1.15	0.30	-0.56
ABUW_RS16000	RNase adapter RapZ	0.89	0.17	0.27	0.99
ABUW_RS16005	pantoate--beta-alanine ligase	0.47	0.06	0.14	0.54
ABUW_RS16010	3-methyl-2-oxobutanoate hydroxymethyltransferase	0.91	0.53	-0.13	0.25
ABUW_RS16015	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	0.45	0.10	0.19	0.54
ABUW_RS16020	polynucleotide adenyltransferase PcnB	0.84	0.50	-0.09	0.25
ABUW_RS16025	ComEA family DNA-binding protein	1.01	0.89	0.00	0.11
ABUW_RS16030	nucleoside triphosphate pyrophosphohydrolase	1.03	1.32	0.43	0.14
ABUW_RS16035	SDR family oxidoreductase	1.54	1.27	-0.20	0.07
ABUW_RS16040	bifunctional (p)ppGpp synthetase/guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	0.86	1.06	-0.07	-0.27
ABUW_RS16045	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	1.20	0.96	-0.11	0.14
ABUW_RS16050	3'-5' exonuclease	1.78	0.83	-0.25	0.70
ABUW_RS16055	cysteine synthase CysM	2.33	1.23	-0.47	0.63
ABUW_RS16060	response regulator	-0.23	0.63	0.15	-0.70
ABUW_RS16065	crotonase/enoyl-CoA hydratase family protein	0.23	-0.03	0.29	0.54
ABUW_RS16070	NAD(P)-dependent oxidoreductase	0.35	-0.12	0.38	0.85
ABUW_RS16075	TIM barrel protein	0.72	1.09	0.06	-0.30
ABUW_RS16080	ribosome silencing factor	1.54	2.00	0.06	-0.40
ABUW_RS16085	SDR family NAD(P)-dependent oxidoreductase	0.46	0.21	0.58	0.84
ABUW_RS16090	NAD(P)(+) transhydrogenase (Re/Si-specific) subunit beta	0.58	0.65	-0.68	-0.75
ABUW_RS16095	NAD(P) transhydrogenase subunit alpha	0.86	0.32	-0.81	-0.27
ABUW_RS16100	Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha	0.79	0.40	-0.65	-0.26
ABUW_RS16105	DMT family transporter	0.88	0.57	0.04	0.35
ABUW_RS16110	RidA family protein	1.15	2.29	0.52	-0.62
ABUW_RS16115	MFS transporter	1.23	0.36	-0.29	0.59
ABUW_RS16120	hypothetical protein	0.03	0.01	0.15	0.17
ABUW_RS16125	ImmA/IrrE family metallo-endorpeptidase	-0.26	0.11	0.13	-0.24
ABUW_RS16130	copper resistance protein B	1.52	1.10	-0.47	-0.05
ABUW_RS16135	copper resistance system multicopper oxidase	0.88	1.18	-0.24	-0.54
ABUW_RS16140	hypothetical protein	1.01	2.32	-0.24	-1.56
ABUW_RS16145	heavy metal response regulator transcription factor	0.72	0.99	-0.13	-0.41
ABUW_RS16150	heavy metal sensor histidine kinase	0.12	1.12	-0.12	-1.12
ABUW_RS16155	heavy metal translocating P-type ATPase	0.78	1.19	-0.15	-0.56
ABUW_RS16160	copper resistance protein CopC	0.62	0.38	-0.10	0.13

ABUW_RS16165	CopD family protein	-0.06	0.28	0.04	-0.30
ABUW_RS16170	DUF932 domain-containing protein	1.15	0.61	0.22	0.76
ABUW_RS16175	hypothetical protein	1.35	1.24	-0.30	-0.20
ABUW_RS16180	hypothetical protein	2.14	2.21	-0.26	-0.33
ABUW_RS16185	hypothetical protein	1.60	1.82	0.16	-0.07
ABUW_RS16190	hypothetical protein	4.03	2.88	-0.61	0.54
ABUW_RS16195	hypothetical protein	3.55	3.06	-0.03	0.46
ABUW_RS16200	hypothetical protein	4.08	2.97	-0.06	1.05
ABUW_RS16205	hypothetical protein	-0.08	0.77	0.13	-0.73
ABUW_RS16210	hypothetical protein	-0.56	1.24	0.73	-1.07
ABUW_RS16215	inovirus-type Gp2 protein	0.49	0.23	0.17	0.43
ABUW_RS16220	hypothetical protein	0.44	0.05	0.21	0.59
ABUW_RS16225	pyocin activator PrtN family protein	1.20	0.56	-0.06	0.59
ABUW_RS16230	tyrosine-type recombinase/integrase	1.35	0.57	-0.41	0.37
ABUW_RS16235	tRNA dihydrouridine(20/20a) synthase DusA	1.69	0.38	-0.31	1.00
ABUW_RS16240	hypothetical protein	0.60	1.32	-0.08	-0.80
ABUW_RS16245	LysR family transcriptional regulator	0.44	0.47	0.13	0.10
ABUW_RS16250	tRNA threonylcarbamoyladenine dehydratase	2.37	1.62	-0.26	0.49
ABUW_RS16255	aconitate hydratase AcnA	1.20	0.89	0.13	0.43
ABUW_RS16260	TatD family hydrolase	0.77	0.06	0.19	0.90
ABUW_RS16265	DUF3298 domain-containing protein	0.94	1.37	-0.26	-0.70
ABUW_RS16270	hypothetical protein	0.79	0.83	-0.10	-0.14
ABUW_RS16275	peptide chain release factor 3	1.57	0.67	-0.43	0.47
ABUW_RS16280	hypothetical protein	-3.73	0.95	-0.63	-5.30
ABUW_RS16285	TetR/AcrR family transcriptional regulator	-3.67	-0.02	0.03	-3.63
ABUW_RS16290	TetR/AcrR family transcriptional regulator	1.19	0.98	0.04	0.26
ABUW_RS16295	EAL domain-containing protein	0.76	1.38	-0.03	-0.65
ABUW_RS16300	ketol-acid reductoisomerase	-1.35	0.75	0.37	-1.74
ABUW_RS16305	acetolactate synthase small subunit	-1.78	0.12	0.74	-1.17
ABUW_RS16310	acetolactate synthase 3 large subunit	-1.15	0.03	0.43	-0.75
ABUW_RS16315	DUF4124 domain-containing protein	0.71	0.87	0.68	0.52
ABUW_RS16320	leucine--tRNA ligase	-0.13	0.44	0.24	-0.32
ABUW_RS16325	hypothetical protein	0.78	0.96	-0.25	-0.43
ABUW_RS16330	DNA polymerase III subunit delta	-0.04	0.46	0.37	-0.14
ABUW_RS16335	MacA family efflux pump subunit	1.70	1.12	0.42	1.01
ABUW_RS16340	MacB family efflux pump subunit	0.72	0.05	0.17	0.84
ABUW_RS16345	AdeC/AdeK/OprM family multidrug efflux complex outer membrane factor	0.65	-0.07	0.11	0.83
ABUW_RS16350	enoyl-ACP reductase	0.38	0.78	-0.26	-0.66
ABUW_RS16355	Bax inhibitor-1/YccA family protein	1.14	1.04	-0.50	-0.40
ABUW_RS16360	oligoribonuclease	1.10	1.28	-0.13	-0.31
ABUW_RS16365	ribosome small subunit-dependent GTPase A	0.93	0.66	0.03	0.31
ABUW_RS16370	rhodanese-like domain-containing protein	1.42	2.04	0.01	-0.61
ABUW_RS16375	glutaredoxin 3	0.93	1.38	-0.17	-0.62
ABUW_RS16380	protein-export chaperone SecB	0.45	0.71	0.36	0.10

ABUW_RS16385	4'-phosphopantetheinyl transferase superfamily protein	1.17	0.99	0.02	0.20
ABUW_RS16390	ribosome biogenesis GTPase Der	1.16	0.50	-0.10	0.56
ABUW_RS16395	outer membrane protein assembly factor BamB	1.63	1.05	-0.43	0.15
ABUW_RS16400	tetratricopeptide repeat protein	1.09	1.47	-0.29	-0.67
ABUW_RS16405	histidine--tRNA ligase	1.59	1.88	-0.68	-0.97
ABUW_RS16410	flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	0.67	0.21	0.00	0.46
ABUW_RS16415	helix-turn-helix domain-containing protein	0.54	0.53	0.00	0.01
ABUW_RS16420	type IV pilus biogenesis/stability protein PilW	1.69	1.36	-0.47	-0.14
ABUW_RS16425	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN	1.27	0.78	0.06	0.55
ABUW_RS16430	nucleoside-diphosphate kinase	0.81	0.25	-0.09	0.47
ABUW_RS16435	Fe-S cluster assembly protein IscX	1.03	0.75	-0.60	-0.32
ABUW_RS16440	phosphatase PAP2 family protein	0.47	1.12	0.05	-0.60
ABUW_RS16445	glycosyltransferase family 1 protein	0.49	0.74	0.31	0.06
ABUW_RS16450	carboxy terminal-processing peptidase	0.92	0.92	-0.11	-0.10
ABUW_RS16455	beta-N-acetylhexosaminidase	0.92	1.14	-0.14	-0.37
ABUW_RS16460	class I SAM-dependent methyltransferase	0.23	-0.19	0.35	0.77
ABUW_RS16465	alpha/beta hydrolase	1.48	1.14	0.15	0.49
ABUW_RS16470	glutamate-5-semialdehyde dehydrogenase	1.16	0.29	-0.10	0.77
ABUW_RS16475	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-0.63	1.16	-0.33	-2.12
ABUW_RS16480	gluconokinase	-0.80	1.66	-0.39	-2.86
ABUW_RS16485	permease	-1.48	0.29	-0.17	-1.94
ABUW_RS16490	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase	-1.36	0.40	-0.40	-2.16
ABUW_RS16495	phosphogluconate dehydratase	-1.73	-0.07	-0.15	-1.81
ABUW_RS16500	acetate kinase	-1.58	-0.67	0.12	-0.79
ABUW_RS16505	phosphate acetyltransferase	-2.25	-1.47	0.23	-0.54
ABUW_RS16510	fumarate hydratase	1.11	-0.47	-0.35	1.22
ABUW_RS16515	DUF2059 domain-containing protein	0.39	0.74	0.06	-0.30
ABUW_RS16520	DUF2846 domain-containing protein	0.90	2.02	0.39	-0.72
ABUW_RS16525	ATP-dependent Clp protease ATP-binding subunit ClpX	0.18	0.90	0.17	-0.55
ABUW_RS16530	ATP-dependent Clp endopeptidase proteolytic subunit ClpP	0.76	0.97	-0.20	-0.41
ABUW_RS16535	trigger factor	0.27	0.03	0.11	0.35
ABUW_RS16540	TonB-dependent siderophore receptor	-0.73	0.19	0.20	-0.72
ABUW_RS16545	Fe2+-dependent dioxygenase	1.40	1.07	0.08	0.40
ABUW_RS16550	2-isopropylmalate synthase	-0.27	0.69	0.68	-0.28
ABUW_RS16555	homoserine O-acetyltransferase	0.23	-0.28	0.29	0.80
ABUW_RS16560	methionine biosynthesis protein MetW	1.14	-0.38	-0.09	1.44
ABUW_RS16565	sel1 repeat family protein	0.88	-0.15	-0.14	0.89
ABUW_RS16570	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	1.00	0.74	-0.42	-0.15
ABUW_RS16575	hypothetical protein	0.61	0.94	-0.47	-0.81
ABUW_RS16580	Sec-independent protein translocase subunit Tata	1.48	2.48	0.16	-0.83
ABUW_RS16585	twin-arginine translocase subunit TatB	1.05	0.89	0.24	0.40
ABUW_RS16590	twin-arginine translocase subunit TatC	0.44	0.48	0.45	0.41

ABUW_RS16595	DUF839 domain-containing protein	0.30	0.83	0.03	-0.50
ABUW_RS16600	PhoX family phosphatase	0.46	0.08	0.73	1.11
ABUW_RS16605	NRDE family protein	1.13	0.29	-0.19	0.65
ABUW_RS16610	prolipoprotein diacylglycerol transferase	1.29	0.66	-0.36	0.27
ABUW_RS16615	hypothetical protein	0.19	0.68	0.05	-0.44
ABUW_RS16620	hypothetical protein	1.14	0.35	0.69	1.47
ABUW_RS16625	thymidylate synthase	0.40	-0.03	0.00	0.43
ABUW_RS16630	dihydrofolate reductase	1.14	0.56	-0.23	0.34
ABUW_RS16635	DUF4105 domain-containing protein	-0.13	-0.11	0.32	0.31
ABUW_RS16640	peptide-methionine (S)-S-oxide reductase MsrA	1.04	1.38	-0.08	-0.42
ABUW_RS16645	biopolymer transporter ExbD	0.30	0.96	0.05	-0.61
ABUW_RS16650	MotA/TolQ/ExbB proton channel family protein	0.33	1.10	0.00	-0.78
ABUW_RS16655	energy transducer TonB	0.00	1.07	0.10	-0.97
ABUW_RS16660	formyltetrahydrofolate deformylase	0.85	-0.29	-0.01	1.13
ABUW_RS16665	TetR/AcrR family transcriptional regulator	1.25	0.40	-0.31	0.55
ABUW_RS16670	coniferyl aldehyde dehydrogenase	0.67	-1.31	0.15	2.14
ABUW_RS16675	50S ribosomal protein L28	-0.05	0.24	-0.04	-0.32
ABUW_RS16680	50S ribosomal protein L33	0.54	-1.56	-0.12	1.98
ABUW_RS16685	cation:proton antiporter	0.27	0.80	-0.33	-0.87
ABUW_RS16690	hypothetical protein	1.89	4.46	-0.40	-2.97
ABUW_RS16695	hypothetical protein	1.02	0.96	0.02	0.09
ABUW_RS16700	ASCH domain-containing protein	1.93	1.34	-0.54	0.06
ABUW_RS16705	RNA-binding protein	1.33	1.23	-0.36	-0.26
ABUW_RS16710	UvrD-helicase domain-containing protein	0.67	0.53	0.06	0.21
ABUW_RS16715	HdeD family acid-resistance protein	1.60	3.12	0.83	-0.69
ABUW_RS16720	hypothetical protein	1.33	0.99	-0.24	0.10
ABUW_RS16725	type I DNA topoisomerase	0.50	-0.30	0.01	0.81
ABUW_RS16730	hypothetical protein	0.77	0.18	-0.06	0.53
ABUW_RS16735	winged helix-turn-helix transcriptional regulator	1.00	-0.53	0.34	1.87
ABUW_RS16740	zinc-binding alcohol dehydrogenase family protein	0.51	0.22	0.22	0.51
ABUW_RS16745	SlyX family protein	0.27	-0.31	-0.16	0.42
ABUW_RS16750	ATP-binding cassette domain-containing protein	1.15	0.74	-0.19	0.23
ABUW_RS16755	LysE family translocator	0.70	0.89	0.29	0.10
ABUW_RS16760	LpxL/LpxP family Kdo(2)-lipid IV(A) lauroyl/palmitoleoyl acyltransferase	0.58	0.50	-0.06	0.02
ABUW_RS16765	glycosyltransferase family 4 protein	0.60	0.76	0.20	0.04
ABUW_RS16770	glutamate/aspartate:proton symporter GltP	0.54	0.61	-0.36	-0.43
ABUW_RS16775	endonuclease/exonuclease/phosphatase family protein	0.49	1.53	0.23	-0.81
ABUW_RS16780	aspartate-semialdehyde dehydrogenase	2.10	0.23	-0.47	1.39
ABUW_RS16785	hypothetical protein	0.30	-0.54	0.37	1.22
ABUW_RS16790	hypothetical protein	0.58	-0.58	-0.10	1.05
ABUW_RS16795	asparaginase	1.29	1.52	0.26	0.03
ABUW_RS16800	tRNA pseudouridine(38-40) synthase TruA	1.42	0.45	-0.16	0.81
ABUW_RS16805	AraC family transcriptional regulator	0.67	0.44	-0.22	0.01
ABUW_RS16810	translation initiation factor IF-1	0.05	1.22	0.00	-1.17

ABUW_RS16815	DUF1311 domain-containing protein	2.08	2.18	-0.58	-0.67
ABUW_RS16820	hypothetical protein	-0.43	0.77	0.58	-0.62
ABUW_RS16825	3-isopropylmalate dehydrogenase	-0.25	0.49	0.15	-0.59
ABUW_RS16830	hypothetical protein	0.57	0.80	-0.24	-0.47
ABUW_RS16835	3-isopropylmalate dehydratase small subunit	-1.52	1.04	0.31	-2.26
ABUW_RS16840	3-isopropylmalate dehydratase large subunit	0.36	2.21	0.29	-1.56
ABUW_RS16845	DUF2061 domain-containing protein	0.09	3.26	0.18	-2.99
ABUW_RS16850	LysR family transcriptional regulator	-0.47	0.38	0.40	-0.45
ABUW_RS16855	HAD-IB family hydrolase	1.62	0.98	-0.10	0.53
ABUW_RS16860	RNA pyrophosphohydrolase	0.89	0.25	0.21	0.85
ABUW_RS16865	phosphoenolpyruvate--protein phosphotransferase	0.45	0.65	0.02	-0.17
ABUW_RS16870	catalase/peroxidase HPI	-0.13	0.45	0.25	-0.34
ABUW_RS16875	MBL fold metallo-hydrolase	-0.84	0.41	-0.08	-1.33
ABUW_RS16880	DNA-binding transcriptional regulator HcaR	-3.62	0.37	0.71	-3.29
ABUW_RS16885	DUF1345 domain-containing protein	-2.27	0.81	-0.05	-3.13
ABUW_RS16890	glutathione S-transferase family protein	2.34	1.56	-0.16	0.62
ABUW_RS16895	YafY family transcriptional regulator	1.87	1.23	-0.35	0.29
ABUW_RS16900	HAD-IA family hydrolase	1.67	0.66	-0.38	0.63
ABUW_RS16905	RluA family pseudouridine synthase	1.05	1.18	-0.12	-0.25
ABUW_RS16910	hypothetical protein	0.50	0.95	0.01	-0.44
ABUW_RS16915	Rne/Rng family ribonuclease	-1.06	-1.18	0.53	0.65
ABUW_RS16920	long-chain-acyl-CoA synthetase	-0.37	0.43	0.38	-0.42
ABUW_RS16935	LysR family transcriptional regulator	0.40	-0.21	0.43	1.05
ABUW_RS16940	SDR family oxidoreductase	0.29	0.04	0.17	0.42
ABUW_RS16945	radical SAM family heme chaperone HemW	0.48	0.52	-0.02	-0.06
ABUW_RS16950	DMT family transporter	0.55	0.35	-0.04	0.16
ABUW_RS16955	multidrug efflux MATE transporter AbeM	0.83	0.14	-0.30	0.39
ABUW_RS16960	acyl-CoA dehydrogenase family protein	0.99	0.69	-0.13	0.17
ABUW_RS16965	SfnB family sulfur acquisition oxidoreductase	0.98	0.20	-0.16	0.62
ABUW_RS16970	ABC transporter	1.93	2.12	0.06	-0.13
ABUW_RS16975	type B 50S ribosomal protein L31	1.80	2.49	1.88	1.19
ABUW_RS16980	HopJ type III effector protein	-0.35	-0.02	0.38	0.04
ABUW_RS16985	fluoride efflux transporter CrcB	0.56	0.68	0.36	0.24
ABUW_RS16990	GFA family protein	1.66	1.80	-0.61	-0.75
ABUW_RS16995	TIGR03862 family flavoprotein	1.26	0.80	-0.32	0.13
ABUW_RS17000	SAM-dependent methyltransferase	0.17	-0.19	0.11	0.47
ABUW_RS17005	DNA gyrase inhibitor YacG	0.69	0.17	-0.30	0.22
ABUW_RS17010	MBL fold metallo-hydrolase	1.04	-0.73	-0.22	1.54
ABUW_RS17015	ferrochelatase	-0.12	-0.27	-0.03	0.12
ABUW_RS17020	DUF4062 domain-containing protein	1.49	0.42	0.24	1.31
ABUW_RS17025	glutamate racemase	1.52	0.65	0.14	1.00
ABUW_RS17030	DUF1285 domain-containing protein	-0.10	0.38	0.07	-0.41
ABUW_RS17035	electron transfer flavoprotein-ubiquinone oxidoreductase	0.71	0.45	-0.06	0.21
ABUW_RS17045	sulfurtransferase TusA	1.41	2.15	0.20	-0.54

ABUW_RS17050	CBS domain-containing protein	1.52	1.12	-0.44	-0.05
ABUW_RS17055	apolipoprotein N-acyltransferase	1.34	0.74	-0.17	0.43
ABUW_RS17060	tRNA-binding protein	0.41	0.73	-0.03	-0.35
ABUW_RS17065	hypothetical protein	0.76	0.89	-0.47	-0.61
ABUW_RS17070	type II secretion system major pseudopilin GspG	0.13	0.82	0.20	-0.50
ABUW_RS17075	type II secretion system inner membrane protein GspF	0.85	0.41	-0.12	0.32
ABUW_RS17080	primosomal protein N'	-0.26	-0.74	0.26	0.74
ABUW_RS17085	cation:proton antiporter	0.49	0.05	-0.14	0.30
ABUW_RS17090	Hsp33 family molecular chaperone HslO	0.63	1.06	0.06	-0.36
ABUW_RS17095	LysE family translocator	-0.64	1.05	0.01	-1.69
ABUW_RS17100	DnaJ domain-containing protein	0.87	2.73	0.55	-1.30
ABUW_RS17105	MerR family transcriptional regulator	0.62	-0.40	0.13	1.15
ABUW_RS17110	magnesium transporter CorA family protein	1.12	1.14	-0.27	-0.30
ABUW_RS17115	polyribonucleotide nucleotidyltransferase	-0.50	0.24	0.44	-0.30
ABUW_RS17120	30S ribosomal protein S15	-0.05	0.74	0.07	-0.72
ABUW_RS17125	EstA family serine hydrolase	0.02	0.12	0.46	0.36
ABUW_RS17130	exodeoxyribonuclease V subunit alpha	0.74	0.63	0.00	0.10
ABUW_RS17135	UvrD-helicase domain-containing protein	0.92	0.52	0.12	0.52
ABUW_RS17140	exodeoxyribonuclease V subunit gamma	0.71	0.31	-0.07	0.34
ABUW_RS17145	hypothetical protein	0.08	0.99	0.24	-0.67
ABUW_RS17150	polyphosphate--AMP phosphotransferase	1.02	1.84	0.08	-0.75
ABUW_RS17155	hypothetical protein	0.37	0.53	0.24	0.08
ABUW_RS17160	bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1,4-benzoquinol methylase UbiE	0.46	-0.43	0.13	1.02
ABUW_RS17165	hypothetical protein	0.27	-0.16	0.19	0.62
ABUW_RS17170	2-octaprenylphenol hydroxylase	0.12	0.07	0.10	0.15
ABUW_RS17175	FAD-dependent monooxygenase	0.33	0.85	0.35	-0.17
ABUW_RS17180	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase HisIE	0.58	0.62	0.31	0.27
ABUW_RS17185	AAA family ATPase	0.56	0.20	0.03	0.40
ABUW_RS17190	AAA family ATPase	0.88	0.82	-0.07	-0.01
ABUW_RS17195	monovalent cation/H+ antiporter subunit A	-1.72	-0.28	-0.11	-1.55
ABUW_RS17200	Na+/H+ antiporter subunit C	-1.46	-0.07	-0.29	-1.68
ABUW_RS17205	monovalent cation/H+ antiporter subunit D	-1.64	-0.33	0.04	-1.27
ABUW_RS17210	Na+/H+ antiporter subunit E	-2.72	-0.64	0.40	-1.68
ABUW_RS17215	monovalent cation/H+ antiporter subunit F	-1.21	-0.97	0.04	-0.19
ABUW_RS17220	Na+/H+ antiporter subunit G	0.63	0.29	-0.53	-0.19
ABUW_RS17225	ribosome-binding factor A	0.09	-0.21	-0.21	0.09
ABUW_RS17230	translation initiation factor IF-2	0.35	-0.15	0.09	0.60
ABUW_RS17235	transcription termination/antitermination protein NusA	0.23	0.12	0.06	0.17
ABUW_RS17240	ribosome maturation factor RimP	0.52	-0.44	-0.08	0.88
ABUW_RS17260	preprotein translocase subunit SecG	0.93	0.52	-0.16	0.25
ABUW_RS17265	triose-phosphate isomerase	1.20	0.87	-0.32	0.01
ABUW_RS17270	type IV-A pilus assembly ATPase PilB	1.29	-0.96	-0.19	2.06

ABUW_RS17275	type II secretion system F family protein	1.78	-0.40	-0.48	1.71
ABUW_RS17280	prepilin peptidase	1.02	0.00	-0.25	0.77
ABUW_RS17285	dephospho-CoA kinase	1.11	0.95	-0.22	-0.05
ABUW_RS17290	DMT family transporter	1.91	1.12	-0.21	0.58
ABUW_RS17295	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	1.56	0.68	-0.27	0.61
ABUW_RS17300	pyrimidine/purine nucleoside phosphorylase	1.38	1.70	-0.35	-0.67
ABUW_RS17305	hypothetical protein	1.20	2.33	-0.34	-1.48
ABUW_RS17310	DNA repair protein RecN	0.60	0.47	0.02	0.15
ABUW_RS17315	YqgE/AlgH family protein	0.30	-0.30	0.27	0.86
ABUW_RS17320	Holliday junction resolvase RuvX	0.04	-0.41	0.25	0.70
ABUW_RS17325	HlyD family secretion protein	1.36	1.29	-0.26	-0.19
ABUW_RS17330	DUF1656 domain-containing protein	1.77	1.71	-0.90	-0.84
ABUW_RS17335	FUSC family protein	2.40	1.50	-0.31	0.60
ABUW_RS17340	transcriptional regulator	1.31	1.29	0.20	0.22
ABUW_RS17345	alpha-ketoglutarate-dependent dioxygenase AlkB	0.26	0.00	0.14	0.40
ABUW_RS17350	methylated-DNA--[protein]-cysteine S-methyltransferase	1.48	0.49	-0.05	0.93
ABUW_RS17355	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	1.19	0.54	-0.30	0.35
ABUW_RS17360	thioesterase family protein	0.52	0.23	0.25	0.54
ABUW_RS17365	excinuclease ABC subunit UvrC	0.76	1.22	0.06	-0.40
ABUW_RS17370	peptidoglycan hydrolase	1.77	1.50	-0.69	-0.42
ABUW_RS17375	lipid A hydroxylase LpxO	0.92	0.97	-0.51	-0.56
ABUW_RS17380	hypothetical protein	-0.62	2.32	-0.16	-3.10
ABUW_RS17385	fatty acid oxidation complex subunit alpha FadB	0.73	0.32	0.17	0.58
ABUW_RS17390	acetyl-CoA C-acyltransferase FadA	0.18	0.26	0.27	0.19
ABUW_RS17395	hypothetical protein	0.43	1.71	0.05	-1.23
ABUW_RS17400	serine hydrolase family protein	1.04	2.18	-0.78	-1.92
ABUW_RS17405	MerR family transcriptional regulator	0.17	0.33	0.40	0.24
ABUW_RS17410	hypothetical protein	1.35	2.49	-0.42	-1.55
ABUW_RS17415	DsbA family oxidoreductase	1.93	2.52	0.04	-0.55
ABUW_RS17420	hypothetical protein	0.22	1.19	0.28	-0.69
ABUW_RS17425	hypothetical protein	2.44	2.38	0.14	0.20
ABUW_RS17430	molecular chaperone HtpG	0.59	2.94	0.08	-2.27
ABUW_RS17435	DUF1311 domain-containing protein	-0.55	0.10	0.03	-0.62
ABUW_RS17440	outer membrane beta-barrel protein	-1.76	-0.04	-0.22	-1.94
ABUW_RS17445	TRAP transporter large permease subunit	1.32	0.57	-0.45	0.30
ABUW_RS17450	alpha/beta fold hydrolase	0.90	1.32	0.36	-0.06
ABUW_RS17455	DUF4442 domain-containing protein	-0.52	0.76	0.32	-0.97
ABUW_RS17460	hypothetical protein	5.47	5.72	0.47	0.21
ABUW_RS17465	hypothetical protein	3.83	5.10	-0.18	-1.45
ABUW_RS17470	DNA-directed RNA polymerase subunit beta'	0.38	0.41	0.34	0.31
ABUW_RS17475	DNA-directed RNA polymerase subunit beta	0.70	0.32	0.15	0.53
ABUW_RS17480	50S ribosomal protein L7/L12	-0.55	-1.09	0.23	0.77
ABUW_RS17485	50S ribosomal protein L10	0.75	-0.53	-0.01	1.27

ABUW_RS17490	50S ribosomal protein L1	0.77	-0.56	-0.01	1.32
ABUW_RS17495	50S ribosomal protein L11	-0.03	-0.94	0.40	1.31
ABUW_RS17500	transcription termination/antitermination protein NusG	1.78	0.18	-0.21	1.39
ABUW_RS17505	preprotein translocase subunit SecE	1.39	0.46	-0.26	0.68
ABUW_RS17515	elongation factor Tu	0.79	-1.91	0.31	3.01
ABUW_RS17540	anthranilate synthase component I	1.20	1.17	0.06	0.08
ABUW_RS17545	phosphoglycolate phosphatase	1.37	1.10	-0.11	0.16
ABUW_RS17550	FHA domain-containing protein	1.72	1.18	-0.24	0.29
ABUW_RS17555	type II secretion system secretin GspD	0.71	0.82	0.04	-0.07
ABUW_RS17560	general secretion pathway protein	0.75	0.30	-0.15	0.30
ABUW_RS17565	type II secretion system protein N	1.06	1.81	-0.11	-0.86
ABUW_RS17570	H-NS histone family protein	-1.53	4.03	0.79	-4.77
ABUW_RS17575	acyl-CoA thioesterase	1.30	2.65	-1.06	-2.42
ABUW_RS17580	hypothetical protein	0.71	0.76	-0.20	-0.24
ABUW_RS17585	hypothetical protein	0.26	0.92	-0.15	-0.81
ABUW_RS17590	uroporphyrinogen-III synthase	1.32	0.30	0.03	1.05
ABUW_RS17595	hydroxymethylbilane synthase	0.74	0.23	0.01	0.51
ABUW_RS17600	response regulator transcription factor	0.66	1.31	-0.18	-0.84
ABUW_RS17605	histidine kinase	0.01	0.65	0.49	-0.15
ABUW_RS17610	argininosuccinate lyase	-0.02	0.46	0.01	-0.47
ABUW_RS17615	oxidative damage protection protein	-0.38	1.13	-0.02	-1.52
ABUW_RS17620	phosphate signaling complex protein PhoU	1.27	0.95	-0.04	0.28
ABUW_RS17625	TolC family outer membrane protein	0.41	1.08	0.00	-0.67
ABUW_RS17630	EamA family transporter	0.96	1.02	-0.18	-0.24
ABUW_RS17635	TetR/AcrR family transcriptional regulator	1.21	-0.02	0.02	1.25
ABUW_RS17640	hypothetical protein	1.40	1.64	0.09	-0.15
ABUW_RS17645	phosphomethylpyrimidine synthase ThiC	-0.10	1.48	0.08	-1.50
ABUW_RS17650	NUDIX domain-containing protein	-0.51	-0.86	0.49	0.84
ABUW_RS17655	3',5'-cyclic-AMP phosphodiesterase	-0.28	-0.50	0.26	0.48
ABUW_RS17660	RNA polymerase-binding protein DksA	1.14	0.39	-0.17	0.58
ABUW_RS17665	tRNA glutamyl-Q(34) synthetase GluQRS	0.34	-0.51	0.42	1.27
ABUW_RS17670	putative lipid II flippase FtsW	2.28	1.45	-0.70	0.13
ABUW_RS17675	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	1.20	1.42	-0.14	-0.35
ABUW_RS17680	hypothetical protein	0.32	2.28	-0.36	-2.33
ABUW_RS17685	ferrous iron transporter B	0.49	1.06	-0.16	-0.73
ABUW_RS17690	ferrous iron transport protein A	0.69	0.97	-0.16	-0.44
ABUW_RS17695	site-specific tyrosine recombinase XerD	-1.13	0.02	0.17	-0.98
ABUW_RS17700	DsbC family protein	1.21	1.29	-0.20	-0.28
ABUW_RS17705	homoserine dehydrogenase	0.65	0.01	0.01	0.65
ABUW_RS17710	threonine synthase	0.91	0.25	-0.29	0.38
ABUW_RS17715	D-alanyl-D-alanine endopeptidase PBP7/8	1.35	0.00	-0.07	1.28
ABUW_RS17720	response regulator	-0.54	-0.86	0.55	0.88
ABUW_RS17725	PAS domain-containing sensor histidine kinase	-0.34	-1.36	0.59	1.61

ABUW_RS17730	sigma-54-dependent Fis family transcriptional regulator	0.17	-1.40	0.33	1.90
ABUW_RS17735	peptidase S41	0.53	0.15	0.15	0.53
ABUW_RS17740	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	0.66	0.94	-0.19	-0.47
ABUW_RS17745	LPS export ABC transporter permease LptG	1.09	0.45	-0.34	0.30
ABUW_RS17750	LPS export ABC transporter permease LptF	1.46	0.89	-0.27	0.30
ABUW_RS17755	leucyl aminopeptidase	0.33	0.57	0.26	0.02
ABUW_RS17760	DNA polymerase III subunit chi	0.48	0.48	0.17	0.18
ABUW_RS17765	hypothetical protein	0.67	1.17	-0.18	-0.68
ABUW_RS17770	hypothetical protein	0.06	2.17	0.52	-1.60
ABUW_RS17775	riboflavin synthase	0.66	1.68	-0.15	-1.17
ABUW_RS17780	DNA adenine methylase bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD	0.97	0.55	0.01	0.43
ABUW_RS17785	transcriptional repressor NrdR	1.22	0.21	-0.12	0.89
ABUW_RS17790	ammonium transporter	2.16	0.17	-0.36	1.63
ABUW_RS17795	P-II family nitrogen regulator	1.65	0.63	-0.38	0.64
ABUW_RS17800	accessory factor UbiK family protein	0.56	1.80	0.00	-1.23
ABUW_RS17805	ATP-binding protein	0.09	1.46	0.64	-0.73
ABUW_RS17810	hypothetical protein	1.26	1.68	-0.17	-0.58
ABUW_RS17815	SulP family inorganic anion transporter	-1.53	0.46	0.18	-1.81
ABUW_RS17820	universal stress protein	0.81	0.51	-0.03	0.27
ABUW_RS17825	ISL3-like element ISPPu12 family transposase	1.46	0.62	-0.47	0.36
ABUW_RS17830	signal peptidase II	1.58	-0.11	-0.49	1.19
ABUW_RS17835	cation transporter	1.95	0.54	-0.88	0.53
ABUW_RS17840	Cd(II)/Pb(II)-responsive transcriptional regulator	2.13	0.53	-0.69	0.91
ABUW_RS17845	universal stress protein	2.33	0.47	-0.05	1.81
ABUW_RS17850	arsenate reductase (glutaredoxin) metalloregulator ArsR/SmtB family transcription factor	1.37	0.14	0.20	1.43
ABUW_RS17855	arsenate reductase ArsC	1.56	1.58	0.20	0.19
ABUW_RS17860	ACR3 family arsenite efflux transporter	1.03	0.18	0.09	0.94
ABUW_RS17865	arsenical resistance protein ArsH	1.07	0.82	-0.10	0.14
ABUW_RS17870	thioredoxin-disulfide reductase	1.79	0.58	-0.06	1.15
ABUW_RS17875	NAD(P)/FAD-dependent oxidoreductase	1.01	0.83	-0.06	0.13
ABUW_RS17880	TniQ family protein	1.10	0.63	0.12	0.59
ABUW_RS17885	TniB family NTP-binding protein	1.51	1.71	-0.21	-0.40
ABUW_RS17895	DDE-type integrase/transposase/recombinase heteromeric transposase endonuclease subunit TnsA	2.52	2.14	-0.15	0.24
ABUW_RS17900	ATP-binding protein	1.44	2.04	0.03	-0.58
ABUW_RS17905	PLP-dependent aminotransferase family protein	1.48	1.99	0.10	-0.42
ABUW_RS17910	aldolase	1.07	1.52	0.40	-0.05
ABUW_RS17915	dihydrodipicolinate synthase family protein	1.44	1.03	0.65	1.06
ABUW_RS17920	hypothetical protein	0.88	0.25	0.07	0.71
ABUW_RS17925	OprD family outer membrane porin	0.44	1.24	0.26	-0.54
ABUW_RS17930	hypothetical protein	-0.01	0.33	0.80	0.46
ABUW_RS17935	hypothetical protein	1.67	2.24	0.24	-0.33
ABUW_RS17940	hypothetical protein	0.13	0.59	-0.06	-0.52

ABUW_RS17945	inorganic diphosphatase	0.39	1.67	0.07	-1.20
ABUW_RS17950	MAPEG family protein	0.82	0.35	-0.33	0.15
ABUW_RS17955	hypothetical protein	0.96	1.03	-0.16	-0.22
ABUW_RS17960	long-chain-fatty-acid--CoA ligase	0.23	0.69	-0.02	-0.48
ABUW_RS17965	DNA topoisomerase IV subunit A	0.80	0.56	-0.04	0.20
ABUW_RS17970	MFS transporter	1.63	1.16	-0.34	0.14
ABUW_RS17975	trimeric intracellular cation channel family protein	2.12	1.47	-0.83	-0.18
ABUW_RS17980	YchJ family protein	0.32	1.10	0.18	-0.60
ABUW_RS17985	TerC family protein	0.84	1.15	-0.23	-0.54
ABUW_RS17990	TIGR00730 family Rossmann fold protein	1.91	1.34	-0.12	0.45
ABUW_RS17995	multidrug transporter subunit MdtD	0.55	0.98	0.06	-0.37
ABUW_RS18000	glycoside hydrolase family 25 protein	-0.01	0.46	0.21	-0.25
ABUW_RS18005	DNA polymerase IV	1.00	1.02	0.14	0.12
ABUW_RS18010	RidA family protein	-0.01	1.21	0.66	-0.56
ABUW_RS18015	DUF2726 domain-containing protein	0.79	1.82	0.28	-0.75
ABUW_RS18020	YgiQ family radical SAM protein	1.16	0.08	-0.30	0.79
ABUW_RS18025	esterase-like activity of phytase family protein	1.26	0.91	0.59	0.94
ABUW_RS18030	helix-turn-helix domain-containing protein	0.77	0.44	0.22	0.55
ABUW_RS18035	DUF2938 domain-containing protein	0.99	0.08	0.01	0.93
ABUW_RS18040	flavodoxin family protein	-0.56	-0.13	0.75	0.32
ABUW_RS18045	transglycosylase SLT domain-containing protein	1.52	1.60	-0.18	-0.26
ABUW_RS18050	cysteine synthase A	0.92	2.44	-0.19	-1.71
ABUW_RS18055	GNAT family N-acetyltransferase	1.61	1.74	0.67	0.53
ABUW_RS18085	TetR family transcriptional regulator	-1.27	-0.53	0.49	-0.26
ABUW_RS18090	DUF2236 domain-containing protein	0.08	-1.98	-0.28	1.78
ABUW_RS18095	hypothetical protein	0.86	2.72	-0.57	-2.43
ABUW_RS18100	TonB-dependent copper receptor	0.18	1.53	-0.43	-1.77
ABUW_RS18105	DUF2946 family protein	0.27	0.54	-0.31	-0.58
ABUW_RS18110	peptide deformylase	0.09	-0.17	-0.09	0.18
ABUW_RS18115	LysM peptidoglycan-binding domain-containing protein	1.06	-0.23	-0.41	0.88
ABUW_RS18120	DNA-processing protein DprA	0.24	-1.06	0.27	1.57
ABUW_RS18125	threonylcarbamoyl-AMP synthase	-1.04	-0.61	0.50	0.07
ABUW_RS18130	DMT family transporter	0.49	0.02	0.05	0.53
ABUW_RS18135	TetR/AcrR family transcriptional regulator	-0.03	-0.06	0.18	0.21
ABUW_RS18140	MFS transporter	0.86	0.06	0.00	0.80
ABUW_RS18145	helix-turn-helix domain-containing protein	-0.92	-0.67	0.99	0.74
ABUW_RS18150	glutathione peroxidase	-0.71	1.55	0.37	-1.89
ABUW_RS18155	hypothetical protein	1.59	2.49	0.63	-0.27
ABUW_RS18160	F0F1 ATP synthase subunit epsilon	0.12	0.24	-0.09	-0.21
ABUW_RS18165	F0F1 ATP synthase subunit beta	-0.52	-0.64	0.12	0.24
ABUW_RS18170	F0F1 ATP synthase subunit gamma	-0.23	-0.38	-0.10	0.05
ABUW_RS18175	F0F1 ATP synthase subunit alpha	-0.45	-0.68	0.08	0.31
ABUW_RS18180	F0F1 ATP synthase subunit delta	0.07	-0.47	0.00	0.54
ABUW_RS18185	F0F1 ATP synthase subunit B	1.34	-0.21	-0.43	1.12

ABUW_RS18190	F0F1 ATP synthase subunit C	0.64	0.26	-0.51	-0.14
ABUW_RS18195	F0F1 ATP synthase subunit A	0.19	-0.36	-0.29	0.26
ABUW_RS18200	ATP synthase subunit I	0.83	-0.83	0.05	1.71
ABUW_RS18205	zinc ABC transporter substrate-binding protein	0.49	-0.22	0.06	0.77
ABUW_RS18210	transcriptional repressor	0.38	-0.17	0.30	0.84
ABUW_RS18215	zinc ABC transporter ATP-binding protein ZnuC	0.39	-0.85	-0.09	1.15
ABUW_RS18220	zinc ABC transporter permease subunit ZnuB	0.04	-0.66	-0.28	0.42
ABUW_RS18225	LysE family transporter	-0.13	0.71	-0.07	-0.91
ABUW_RS18230	Dyp-type peroxidase	-0.03	0.69	-0.13	-0.84
ABUW_RS18235	NAD-dependent malic enzyme	-0.45	0.54	0.24	-0.75
ABUW_RS18240	arginine--tRNA ligase	-0.21	-0.47	0.21	0.47
ABUW_RS18245	SPOR domain-containing protein	-0.06	-0.02	-0.05	-0.09
ABUW_RS18250	glutathione S-transferase	1.08	1.13	-0.21	-0.26
ABUW_RS18255	OsmC family protein	0.30	0.42	0.10	-0.02
ABUW_RS18260	pirin family protein	1.34	-0.16	0.05	1.55
ABUW_RS18265	DUF3861 domain-containing protein	2.73	1.06	-0.08	1.58
ABUW_RS18270	PadR family transcriptional regulator	2.85	1.71	0.03	1.17
ABUW_RS18275	aminoglycoside nucleotidyltransferase ANT(3'')-IIa	0.52	1.65	-0.51	-1.64
ABUW_RS18280	glutamine-hydrolyzing GMP synthase	1.14	-0.31	-0.19	1.26
ABUW_RS18285	DUF445 family protein	0.13	-0.55	0.17	0.85
ABUW_RS18290	DoxX family protein	1.81	1.02	0.07	0.87
ABUW_RS18295	DedA family protein	-0.45	0.57	0.06	-0.96
ABUW_RS18300	LysE family transporter	-0.64	-0.79	-0.02	0.13
ABUW_RS18305	hypothetical protein	1.03	0.65	-0.53	-0.15
ABUW_RS18310	ParA family protein	1.07	0.76	-0.56	-0.25
ABUW_RS18315	SirB2 family protein	0.29	-1.02	-0.10	1.21
ABUW_RS18320	BoIA family transcriptional regulator	0.56	0.32	-0.22	0.03
ABUW_RS18335	4'-phosphopantetheinyl transferase superfamily protein	-0.49	-0.19	0.30	-0.01
ABUW_RS18340	alpha/beta fold hydrolase	-0.12	-0.64	0.13	0.65
ABUW_RS18345	hypothetical protein	-0.30	-0.79	0.16	0.65
ABUW_RS18350	outer membrane lipoprotein-sorting protein	-0.36	-0.61	-0.01	0.23
ABUW_RS18355	non-ribosomal peptide synthetase	0.41	-0.70	0.10	1.20
ABUW_RS18360	acyl carrier protein	0.29	-0.23	0.68	1.20
ABUW_RS18365	acyl-CoA dehydrogenase	1.10	0.08	-0.44	0.59
ABUW_RS18370	fatty acyl-AMP ligase	1.04	-0.44	0.46	1.95
ABUW_RS18375	LuxR family transcriptional regulator AbaR	-0.77	1.28	-0.15	-2.20
ABUW_RS18380	DUF4902 domain-containing protein	-1.37	-0.10	0.02	-1.25
ABUW_RS18385	acyl-homoserine-lactone synthase Abal	0.81	0.14	-0.36	0.31
ABUW_RS18390	MHS family MFS transporter	1.97	0.93	-0.21	0.83
ABUW_RS18395	enoyl-CoA hydratase/isomerase family protein	0.65	1.08	-0.03	-0.47
ABUW_RS18400	enoyl-CoA hydratase	1.78	1.51	-0.10	0.17
ABUW_RS18405	acyl-CoA dehydrogenase family protein	1.51	1.23	-0.17	0.12
ABUW_RS18410	AMP-binding protein	2.75	1.46	-0.08	1.21
ABUW_RS18415	3-hydroxyisobutyrate dehydrogenase	2.80	1.93	-0.06	0.82

ABUW_RS18420	CoA-acylating methylmalonate-semialdehyde dehydrogenase	2.87	2.17	-0.15	0.55
ABUW_RS18425	LysR family transcriptional regulator	0.22	-0.41	0.16	0.79
ABUW_RS18430	amino acid permease	1.32	0.84	-0.65	-0.17
ABUW_RS18435	amino acid permease	0.28	-0.11	0.14	0.52
ABUW_RS18440	RidA family protein	-0.79	0.86	0.37	-1.27
ABUW_RS18445	alanine racemase	1.38	0.11	0.36	1.63
ABUW_RS18450	D-amino acid dehydrogenase	2.54	1.18	-0.26	1.10
ABUW_RS18455	Lrp/AsnC ligand binding domain-containing protein	1.73	-0.06	-0.16	1.63
ABUW_RS18460	DUF1624 domain-containing protein	0.54	0.50	0.13	0.17
ABUW_RS18465	TonB-dependent siderophore receptor	0.00	0.21	0.08	-0.13
ABUW_RS18470	nuclear transport factor 2 family protein	0.69	0.66	0.32	0.34
ABUW_RS18475	ribonuclease E inhibitor RraB	1.50	1.56	-0.24	-0.30
ABUW_RS18480	RluA family pseudouridine synthase	-0.23	-0.83	0.31	0.91
ABUW_RS18485	DUF1003 domain-containing protein	0.30	1.76	0.14	-1.32
ABUW_RS18490	SDR family NAD(P)-dependent oxidoreductase	-0.72	0.35	0.42	-0.65
ABUW_RS18495	IS256-like element ISAb26 family transposase	-1.39	-3.59	0.45	2.65
ABUW_RS18505	DUF4844 domain-containing protein	-0.50	-0.57	0.13	0.19
ABUW_RS18510	IS5-like element ISAb13 family transposase	-0.77	-3.57	1.32	4.12
ABUW_RS18515	hypothetical protein	-1.38	-0.19	-0.09	-1.28
ABUW_RS18520	hypothetical protein	-2.96	0.39	0.43	-2.93
ABUW_RS18525	Fe/S-dependent 2-methylisocitrate dehydratase AcnD	0.57	0.06	0.03	0.54
ABUW_RS18530	2-methylcitrate synthase	0.01	0.57	0.42	-0.14
ABUW_RS18535	methylisocitrate lyase	0.66	0.63	-0.24	-0.21
ABUW_RS18540	GntR family transcriptional regulator	1.52	1.09	-0.03	0.41
ABUW_RS18545	aspartate/tyrosine/aromatic aminotransferase	-1.02	-1.25	0.17	0.40
ABUW_RS18550	D-lactate dehydrogenase	0.35	0.12	-0.15	0.08
ABUW_RS18555	FMN-dependent L-lactate dehydrogenase LldD	1.33	-0.40	-0.46	1.27
ABUW_RS18560	transcriptional regulator LldR	1.49	0.54	-0.33	0.62
ABUW_RS18565	L-lactate permease	0.61	0.02	-0.05	0.53
ABUW_RS18570	phosphomannomutase/phosphoglucomutase	-0.32	0.98	-0.12	-1.42
ABUW_RS18575	UDP-glucose 4-epimerase GalE	-0.21	1.61	-0.16	-1.98
ABUW_RS18580	glucose-6-phosphate isomerase	-0.63	0.66	-0.24	-1.54
ABUW_RS18585	UDP-glucose/GDP-mannose dehydrogenase family protein	-0.55	0.55	-0.06	-1.16
ABUW_RS18590	UTP--glucose-1-phosphate uridylyltransferase GalU	-1.42	-0.39	0.13	-0.89
ABUW_RS18595	polysaccharide biosynthesis protein DegT/DnrJ/EryC1/StrS aminotransferase family protein	-1.08	0.08	0.03	-1.13
ABUW_RS18600	protein	-1.25	-0.15	0.27	-0.84
ABUW_RS18605	acetyltransferase	-1.05	0.27	-0.20	-1.52
ABUW_RS18610	sugar transferase	-1.58	0.20	0.21	-1.56
ABUW_RS18615	glycosyltransferase family 4 protein	-1.10	0.56	-0.21	-1.87
ABUW_RS18620	oligosaccharide repeat unit polymerase	0.69	1.32	-0.58	-1.21
ABUW_RS18625	hypothetical protein	-0.56	1.22	-0.19	-1.97
ABUW_RS18630	oligosaccharide flippase family protein	0.57	1.26	-0.37	-1.06
ABUW_RS18635	UDP-N-acetyl-D-mannosamine dehydrogenase	-1.01	0.81	0.06	-1.77

ABUW_RS18640	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-0.59	1.03	-0.08	-1.69
ABUW_RS18645	Vi polysaccharide biosynthesis UDP-N-acetylglucosamine C-6 dehydrogenase TviB	-0.44	0.61	0.11	-0.94
ABUW_RS18650	polysaccharide biosynthesis/export family protein	-0.20	1.16	-0.35	-1.71
ABUW_RS18655	low molecular weight phosphotyrosine protein phosphatase	0.18	0.90	-0.56	-1.28
ABUW_RS18660	polysaccharide biosynthesis tyrosine autokinase	-0.93	0.87	-0.01	-1.81
ABUW_RS18665	FKBP-type peptidyl-prolyl cis-trans isomerase	-0.46	0.41	0.02	-0.85
ABUW_RS18670	FKBP-type peptidyl-prolyl cis-trans isomerase	-0.44	1.35	-0.21	-2.00
ABUW_RS18675	murein biosynthesis integral membrane protein MurJ	1.40	0.29	-0.53	0.58
ABUW_RS18680	1,6-anhydro-N-acetylmuramyl-L-alanine amidase	-0.44	-0.19	0.38	0.13
ABUW_RS18685	AmpD carboxylating nicotinate-nucleotide diphosphorylase	0.28	-0.12	-0.12	0.28
ABUW_RS18695	phospholipase C, phosphocholine-specific	1.47	0.54	-0.11	0.82
ABUW_RS18700	ribonuclease PH	0.36	0.13	-0.49	-0.27
ABUW_RS18705	acyl-CoA desaturase	0.55	-1.87	-0.12	2.29
ABUW_RS18710	ferredoxin reductase	0.70	-1.77	-0.59	1.89
ABUW_RS18715	TetR family transcriptional regulator	-0.49	-0.28	-0.14	-0.35
ABUW_RS18720	TetR/AcrR family transcriptional regulator	-0.02	-0.18	-0.01	0.15
ABUW_RS18725	thiol:disulfide interchange protein DsbA/DsbL	1.33	1.65	-0.39	-0.71
ABUW_RS18730	bifunctional 3-demethylubiquinone 3-O-methyltransferase/2-octaprenyl-6-hydroxy phenol methylase	0.36	0.23	0.04	0.17
ABUW_RS18735	HAD-IA family hydrolase	0.02	-0.06	0.09	0.18
ABUW_RS18740	YciK family oxidoreductase	0.96	-0.35	-0.19	1.12
ABUW_RS18745	RcnB family protein	3.67	1.85	0.33	2.15
ABUW_RS18750	RcnB family protein	4.29	2.61	1.38	3.06
ABUW_RS18755	amino-acid N-acetyltransferase	-0.42	0.05	0.22	-0.25
ABUW_RS18760	sulfonate ABC transporter substrate-binding protein	0.27	-0.32	0.33	0.93
ABUW_RS18765	sulfonate ABC transporter substrate-binding protein	0.80	-0.56	-0.02	1.33
ABUW_RS18770	FMNH2-dependent alkanesulfonate monooxygenase	0.33	-0.49	-0.04	0.78
ABUW_RS18775	aliphatic sulfonate ABC transporter permease SsuC	-0.02	-0.34	0.27	0.59
ABUW_RS18780	ATP-binding cassette domain-containing protein	0.41	-0.14	0.10	0.65
ABUW_RS18785	TetR/AcrR family transcriptional regulator	-0.40	-0.10	0.17	-0.13
ABUW_RS18790	5'-nucleosidase	-0.12	0.81	0.24	-0.69
ABUW_RS18795	TDT family transporter	1.11	1.77	0.79	0.13
ABUW_RS18800	bifunctional riboflavin kinase/FAD synthetase	0.02	-0.99	0.19	1.20
ABUW_RS18805	isoleucine--tRNA ligase	-0.86	-0.65	0.17	-0.04
ABUW_RS18810	signal peptidase II	-0.24	-0.23	0.32	0.30
ABUW_RS18815	peptidylprolyl isomerase	-0.13	0.77	0.00	-0.89
ABUW_RS18820	NAD(P)H-dependent oxidoreductase	-1.80	1.07	0.06	-2.81
ABUW_RS18825	ankyrin repeat domain-containing protein	1.06	1.08	0.52	0.49
ABUW_RS18855	peptidyl-prolyl cis-trans isomerase	0.64	1.29	-0.33	-0.98
ABUW_RS18860	alpha/beta hydrolase	0.42	1.31	-0.09	-0.97
ABUW_RS18865	hypothetical protein	3.47	3.57	0.90	0.81
ABUW_RS18870	hypothetical protein	2.04	2.71	-0.78	-1.45
ABUW_RS18875	MBL fold metallo-hydrolase	0.42	0.16	-0.11	0.15

ABUW_RS18880	LysR family transcriptional regulator	0.18	0.23	0.30	0.25
ABUW_RS18885	nucleotide exchange factor GrpE	-0.23	1.33	0.07	-1.49
ABUW_RS18890	molecular chaperone DnaK	-0.90	1.04	0.57	-1.37
ABUW_RS18895	matrixin family metalloprotease	-0.04	0.38	0.34	-0.08
ABUW_RS18900	matrixin family metalloprotease	-1.24	-1.72	3.00	3.47
ABUW_RS18905	hypothetical protein	-2.46	-1.61	1.11	0.25
ABUW_RS18910	lytic murein transglycosylase	-0.10	0.61	-0.25	-0.96
ABUW_RS18915	5-(carboxyamino)imidazole ribonucleotide synthase	1.40	0.39	-0.28	0.73
ABUW_RS18920	5-(carboxyamino)imidazole ribonucleotide mutase	1.41	1.01	-0.15	0.26
ABUW_RS18925	DMT family protein	1.23	1.35	0.20	0.08
ABUW_RS18930	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	0.76	0.72	-0.32	-0.27
ABUW_RS18935	low temperature requirement protein A	0.10	0.41	-0.25	-0.56
ABUW_RS18940	undecaprenyl-diphosphatase	-0.77	-0.10	0.14	-0.53
ABUW_RS18945	TerC family protein	1.14	0.43	0.32	1.03
ABUW_RS18950	hypothetical protein	-0.68	-0.50	0.55	0.37
ABUW_RS18955	glutathionylspermidine synthase family protein	0.01	0.11	0.16	0.05
ABUW_RS18960	aromatic ring-hydroxylating dioxygenase subunit alpha	0.47	0.21	0.27	0.52
ABUW_RS18965	guanine deaminase	-0.05	0.49	-0.09	-0.63
ABUW_RS18975	hypoxanthine phosphoribosyltransferase	0.36	-0.51	-0.11	0.76
ABUW_RS18980	GlsB/YeaQ/YmgE family stress response membrane protein	0.07	2.66	-0.05	-2.64
ABUW_RS18985	DsbC family protein	-0.16	0.21	0.33	-0.04
ABUW_RS18990	CDF family Co(II)/Ni(II) efflux transporter DmeF	0.24	-0.05	-0.02	0.27
ABUW_RS18995	metal/formaldehyde-sensitive transcriptional repressor	-0.07	0.89	0.49	-0.47
ABUW_RS19000	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE	0.17	-0.30	0.03	0.50
ABUW_RS19005	membrane protein insertase YidC	-0.40	-0.87	0.00	0.46
ABUW_RS19010	membrane protein insertion efficiency factor YidD	-0.74	-1.74	0.21	1.21
ABUW_RS19015	ribonuclease P protein component	-0.59	-1.63	0.01	1.05
ABUW_RS19020	50S ribosomal protein L34	-1.32	-2.35	0.28	1.32
ABUW_RS19590	replication initiation protein RepM	0.58	-0.28	0.17	1.04
ABUW_RS19595	helix-turn-helix domain-containing protein	-0.21	-0.68	0.53	0.99
ABUW_RS19600	sel1 repeat family protein	-0.46	-0.87	0.18	0.59
ABUW_RS19605	BrnT family toxin	3.61	2.20	0.30	1.70
ABUW_RS19610	BrnA antitoxin family protein	3.99	3.22	0.01	0.78
ABUW_RS19615	TonB-dependent receptor ZnuD2	-0.57	-0.64	0.18	0.25
ABUW_RS19620	DIP1984 family protein	-2.38	-1.11	0.45	-0.82
ABUW_RS19625	hypothetical protein	0.42	-0.56	-0.09	0.89
ABUW_RS19635	protein rep	0.15	-0.93	0.40	1.48
ABUW_RS19645	hypothetical protein	-0.53	0.84	-0.03	-1.40
ABUW_RS19650	LysM peptidoglycan-binding domain-containing protein	-1.35	0.81	-0.26	-2.41
ABUW_RS19680	IS4 family transposase ISAbA1	1.25	1.06	0.11	0.30
ABUW_RS19685	IS4 family transposase ISAbA1	0.57	-0.64	-0.15	1.05
ABUW_RS19690	hypothetical protein	3.77	0.85	0.95	3.87
ABUW_RS19705	hypothetical protein	0.61	1.97	-0.65	-2.01

ABUW_RS19715	hypothetical protein	1.25	4.54	-0.46	-3.75
ABUW_RS19720	Ig-like domain-containing protein	-1.07	-0.17	-0.27	-1.18
ABUW_RS19765	hypothetical protein	1.89	0.98	0.47	1.38
ABUW_RS19790	helix-turn-helix transcriptional regulator	0.19	-0.52	-0.13	0.57
ABUW_RS19795	GNAT family N-acetyltransferase	-1.40	-2.18	1.94	2.71
ABUW_RS19800	pyrroloquinoline quinone precursor peptide PqqA	0.49	-0.52	0.83	1.84
ABUW_RS19805	helix-turn-helix transcriptional regulator	1.09	0.16	-0.60	0.32
ABUW_RS19835	IS4 family transposase ISAb1	2.33	0.44	-0.06	1.82
ABUW_RS19865	hypothetical protein	-0.93	1.05	0.49	-1.49
ABUW_RS19890	hypothetical protein	-0.89	0.20	-0.54	-1.64
ABUW_RS19900	glutathione S-transferase	-2.72	-1.42	0.98	-0.32
ABUW_RS19925	single-stranded DNA-binding protein	-0.72	-0.69	0.18	0.15
ABUW_RS19995	hypothetical protein	1.26	1.49	0.19	-0.03
ABUW_RS20070	hypothetical protein	0.01	-1.80	0.08	1.89
ABUW_RS20075	transposase domain-containing protein	-1.98	-1.20	1.13	0.35
ABUW_RS20090	hypothetical protein	-0.41	0.01	0.88	0.46
ABUW_RS20095	hypothetical protein	-0.38	-0.76	0.67	1.04
ABUW_RS20100	hypothetical protein	0.03	-2.98	0.04	3.05
ABUW_RS20105	hypothetical protein	1.66	2.25	1.32	0.74
ABUW_RS20110	hypothetical protein	-0.19	-0.25	-0.40	-0.33
ABUW_RS20115	hypothetical protein	0.54	1.84	0.18	-1.11
ABUW_RS20120	hypothetical protein	-0.28	-0.13	0.25	0.10
ABUW_RS20125	hypothetical protein	0.69	0.74	-0.08	-0.13
ABUW_RS20135	hypothetical protein	-0.20	-0.05	-0.25	-0.39
ABUW_RS20140	hypothetical protein	2.14	1.71	0.36	0.80
ABUW_RS20145	hypothetical protein	0.69	2.93	0.02	-2.22
ABUW_RS20150	hypothetical protein	0.92	1.22	0.81	0.52
ABUW_RS20155	hypothetical protein	-1.18	1.40	0.34	-2.23
ABUW_RS20160	hypothetical protein	-0.37	-0.60	0.30	0.54
ABUW_RS20165	hypothetical protein	0.44	0.19	-0.37	-0.12
ABUW_RS20180	hypothetical protein	-0.24	-1.89	0.24	1.89
ABUW_RS20185	sulfite exporter TauE/SafE family protein	-0.99	-1.23	0.92	1.16
ABUW_RS20200	hypothetical protein	0.45	-0.20	-0.01	0.65
ABUW_RS20205	hypothetical protein	0.57	1.14	-0.49	-1.06
ABUW_RS20210	hypothetical protein	-1.22	-2.58	2.20	3.56
ABUW_RS20215	hypothetical protein	1.63	-0.22	1.70	3.55
ABUW_RS20220	flavin reductase family protein	0.20	-0.73	0.08	1.00
ABUW_RS20225	alpha/beta hydrolase	0.97	-0.23	0.17	1.38
ABUW_RS20230	hypothetical protein	-0.11	0.73	-0.94	-1.78
ABUW_RS20235	hypothetical protein	-2.19	-0.01	0.55	-1.62
ABUW_RS20240	hypothetical protein	-0.60	-2.52	0.74	2.65
ABUW_RS20245	hypothetical protein	3.31	3.18	0.25	0.39
ABUW_RS20260	hypothetical protein	-0.98	-0.82	0.10	-0.06
ABUW_RS20265	hypothetical protein	NA	NA	NA	NA

ABUW_RS20270	hypothetical protein	0.64	1.50	-0.29	-1.15
ABUW_RS20275	outer membrane assembly protein BamE	1.12	-0.62	-0.80	0.94
ABUW_RS20280	hypothetical protein	-0.01	-2.20	0.32	2.51
ABUW_RS20285	hypothetical protein	1.20	2.04	-0.87	-1.71
ABUW_RS20290	hypothetical protein	-1.29	-0.80	0.83	0.34
ABUW_RS20295	hypothetical protein	1.33	0.95	0.18	0.56
ABUW_RS20305	hypothetical protein	0.04	0.09	-0.32	-0.37
ABUW_RS20310	putative pilus assembly protein FilE	-0.92	0.45	0.04	-1.33
ABUW_RS20315	hypothetical protein	-0.01	1.85	0.91	-0.95
ABUW_RS20320	hypothetical protein	0.77	0.00	1.40	2.17
ABUW_RS20330	hypothetical protein	1.10	-0.49	-0.27	1.32
ABUW_RS20335	hypothetical protein	1.94	1.26	0.92	1.59
ABUW_RS20380	hypothetical protein	0.39	0.13	-0.25	0.00
ABUW_RS20390	hypothetical protein	-1.30	0.09	0.23	-1.15
ABUW_RS20420	hypothetical protein	-0.22	-1.30	0.35	1.42
ABUW_RS20425	hypothetical protein	0.76	0.17	-0.62	-0.03
ABUW_RS20430	hypothetical protein	5.59	-0.07	-0.11	5.55
ABUW_RS20435	hypothetical protein	1.19	-2.80	1.70	5.69
ABUW_RS20440	hypothetical protein	2.02	-2.43	0.00	4.23
ABUW_RS20445	hypothetical protein	-1.59	0.51	1.02	-1.08
ABUW_RS20450	hypothetical protein	3.94	-0.83	0.16	4.92
ABUW_RS20455	hypothetical protein	1.75	-5.78	0.00	7.31
ABUW_RS20460	hypothetical protein	0.15	4.48	0.20	-4.13
ABUW_RS20465	hypothetical protein	-0.25	0.08	-1.15	-1.48
ABUW_RS20475	hypothetical protein	-0.79	0.62	-0.09	-1.50
ABUW_RS20490	hypothetical protein	0.32	-0.14	0.37	0.82
ABUW_RS20495	hypothetical protein	0.82	0.19	0.06	0.69
ABUW_RS20500	GpE family phage tail protein	1.31	0.51	1.12	1.92
ABUW_RS20505	hypothetical protein	-2.15	1.31	0.77	-2.69
ABUW_RS20510	hypothetical protein	0.60	1.90	-0.67	-1.98
ABUW_RS20515	hypothetical protein	-3.07	-0.04	0.75	-2.28
ABUW_RS20520	hypothetical protein	-1.24	-1.70	0.02	0.47
ABUW_RS20525	hypothetical protein	-0.28	0.11	0.58	0.18
ABUW_RS20530	hypothetical protein	-1.51	-0.36	0.48	-0.67
ABUW_RS20535	hypothetical protein	-1.34	0.57	0.20	-1.71
ABUW_RS20540	hypothetical protein	-0.39	1.07	-0.74	-2.20
ABUW_RS20545	zinc ribbon-containing protein	-2.66	-1.25	0.29	-1.12
ABUW_RS20550	hypothetical protein	-1.71	-0.57	0.61	-0.52
ABUW_RS20555	WYL domain-containing protein	-0.07	-0.26	0.05	0.24
newcandsRNA1	NZ_CP008706.1	0.68	1.37	0.13	-0.56
sRNA1	NZ_CP008706.1	1.90	1.51	-0.09	0.29
sRNA10	NZ_CP008706.1	1.71	1.04	0.47	1.14
sRNA100	NZ_CP008706.1	-0.13	-0.50	0.02	0.40
sRNA101	NZ_CP008706.1	2.36	1.80	0.54	1.11

sRNA102	NZ_CP008706.1	2.48	2.25	-0.11	0.11
sRNA103	NZ_CP008706.1	2.26	1.62	0.34	0.98
sRNA104	NZ_CP008706.1	2.76	0.55	-2.23	-0.02
sRNA105	NZ_CP008706.1	0.79	1.34	2.00	1.44
sRNA106	NZ_CP008706.1	-1.62	1.13	0.63	-2.11
sRNA109	NZ_CP008706.1	0.91	-0.45	-0.40	0.96
sRNA110	NZ_CP008706.1	0.91	-0.45	-0.40	0.96
sRNA13	NZ_CP008706.1	1.78	0.94	-0.95	-0.12
sRNA14	NZ_CP008706.1	-0.25	0.39	0.28	-0.37
sRNA15	NZ_CP008706.1	0.01	0.70	-0.10	-0.79
sRNA17	NZ_CP008706.1	0.32	1.03	-0.32	-1.03
sRNA18	NZ_CP008706.1	-0.19	-0.63	0.72	1.16
sRNA19	NZ_CP008706.1	0.05	-0.90	-0.01	0.94
sRNA2	NZ_CP008706.1	-0.34	-4.20	-0.58	3.28
sRNA20	NZ_CP008706.1	0.21	-1.64	-0.14	1.72
sRNA21	NZ_CP008706.1	1.19	1.34	0.42	0.26
sRNA22	NZ_CP008706.1	2.53	-0.70	0.47	3.70
sRNA24	NZ_CP008706.1	-0.80	2.30	0.09	-3.00
sRNA25	NZ_CP008706.1	-2.07	-1.67	2.21	1.81
sRNA26	NZ_CP008706.1	-1.00	-0.05	-0.02	-0.97
sRNA27	NZ_CP008706.1	-2.14	-0.96	0.42	-0.75
sRNA28	NZ_CP008706.1	-2.47	-0.09	1.03	-1.35
sRNA29	NZ_CP008706.1	-0.51	-1.26	-2.58	-1.84
sRNA3	NZ_CP008706.1	-0.82	0.51	0.45	-0.88
sRNA30	NZ_CP008706.1	-1.30	-2.83	1.22	2.75
sRNA31	NZ_CP008706.1	0.92	0.80	0.21	0.33
sRNA32	NZ_CP008706.1	1.91	-0.65	0.18	2.74
sRNA37	NZ_CP008706.1	-0.71	-0.95	0.04	0.27
sRNA38	NZ_CP008706.1	-2.34	0.68	-0.56	-3.58
sRNA39	NZ_CP008706.1	-2.20	0.96	-0.53	-3.69
sRNA4	NZ_CP008706.1	0.82	-0.27	1.36	2.45
sRNA40	NZ_CP008706.1	0.00	-2.89	-2.06	1.19
sRNA42	NZ_CP008706.1	0.93	2.87	-1.28	-3.22
sRNA43_truncated	NZ_CP008706.1	1.86	-0.13	-0.24	1.75
sRNA44	NZ_CP008706.1	0.10	0.74	0.04	-0.61
sRNA46	NZ_CP008706.1	0.90	1.61	-0.34	-1.04
sRNA48	NZ_CP008706.1	0.10	-1.44	-0.08	1.45
sRNA49	NZ_CP008706.1	-1.01	-1.26	1.19	1.44
sRNA5	NZ_CP008706.1	-0.61	-2.36	0.09	1.84
sRNA50	NZ_CP008706.1	-0.44	-1.50	0.64	1.70
sRNA53	NZ_CP008706.1	-1.00	-0.24	0.69	-0.08
sRNA54	NZ_CP008706.1	-2.28	0.39	1.28	-1.39
sRNA55	NZ_CP008706.1	0.02	-0.43	-0.61	-0.16
sRNA56	NZ_CP008706.1	0.46	0.08	1.01	1.39

sRNA57	NZ_CP008706.1	0.89	-0.57	-1.66	-0.20
sRNA58	NZ_CP008706.1	0.15	-0.54	0.24	0.93
sRNA59	NZ_CP008706.1	-0.68	1.44	2.21	0.09
sRNA6	NZ_CP008706.1	1.79	-0.71	-0.36	2.13
sRNA60	NZ_CP008706.1	-0.70	-1.70	0.27	1.27
sRNA61	NZ_CP008706.1	-5.16	0.13	-0.35	-5.63
sRNA62	NZ_CP008706.1	-0.75	-2.91	-0.10	2.05
sRNA63	NZ_CP008706.1	-0.48	-0.85	0.45	0.82
sRNA64	NZ_CP008706.1	-2.08	-3.50	0.37	1.78
sRNA65	NZ_CP008706.1	-1.40	-1.13	0.48	0.22
sRNA69	NZ_CP008706.1	-1.58	0.37	0.73	-1.22
sRNA7	NZ_CP008706.1	0.44	-2.13	1.90	4.47
sRNA70	NZ_CP008706.1	1.15	-1.30	0.07	2.53
sRNA71	NZ_CP008706.1	-0.09	-0.37	0.83	1.11
sRNA72	NZ_CP008706.1	-2.18	0.48	0.11	-2.55
sRNA73	NZ_CP008706.1	-2.68	-2.98	1.93	2.23
sRNA74	NZ_CP008706.1	0.07	0.08	0.51	0.50
sRNA75	NZ_CP008706.1	-1.47	-1.90	0.70	1.14
sRNA76	NZ_CP008706.1	-0.47	-0.44	0.78	0.75
sRNA77	NZ_CP008706.1	1.18	1.35	0.54	0.36
sRNA8	NZ_CP008706.1	1.85	1.74	-0.83	-0.72
sRNA81	NZ_CP008706.1	-0.77	0.13	0.13	-0.77
sRNA84	NZ_CP008706.1	0.36	2.02	0.13	-1.53
sRNA85	NZ_CP008706.1	0.41	1.74	0.29	-1.04
sRNA86	NZ_CP008706.1	-0.44	0.29	0.81	0.08
sRNA87	NZ_CP008706.1	-0.26	-1.23	0.01	0.98
sRNA88	NZ_CP008706.1	1.38	2.30	-0.64	-1.56
sRNA89	NZ_CP008706.1	1.41	0.47	-0.51	0.42
sRNA9	NZ_CP008706.1	2.59	1.64	0.17	1.11
sRNA90	NZ_CP008706.1	-0.41	1.26	0.62	-1.05
sRNA91	NZ_CP008706.1	0.69	-0.89	0.11	1.70
sRNA92	NZ_CP008706.1	1.50	-0.70	0.82	3.01
sRNA93	NZ_CP008706.1	-0.37	-0.90	0.33	0.87
sRNA94	NZ_CP008706.1	1.05	-1.20	-0.47	1.78
sRNA95	NZ_CP008706.1	2.46	0.92	-0.02	1.53
sRNA96	NZ_CP008706.1	0.47	0.60	-0.11	-0.24
sRNA97	NZ_CP008706.1	1.10	0.32	-0.32	0.46
sRNA98	NZ_CP008706.1	-0.49	-0.71	0.86	1.09
sRNA99	NZ_CP008706.1	1.99	0.88	0.71	1.82