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**Transcriptomic and Functional Analysis of Two-
Component Systems AdeRS, BaeRS, GacAS in
Acinetobacter baumannii AB5075**

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

Maha Mohammed Sulimani

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The Moyne Institute of Preventive Medicine

Department of Microbiology

Trinity College

University of Dublin

Declaration

I hereby declare that this thesis is my own, independent work that has never before been submitted for credit toward a degree at this or any other university, with the exception of instances where it is properly recognized in the text. I acknowledge that Trinity College Dublin's librarian may choose to lend or copy this thesis.

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Summary

Antimicrobial resistance constitutes one of the most significant global health challenges of our era, with *Acinetobacter baumannii* becoming a key priority pathogen owing to its extraordinary capacity to withstand various classes of antibiotics. A primary factor contributing to this resilience is the function of regulatory proteins, especially Two-Component Systems (TCSs), which allow the bacterium to detect environmental cues and swiftly modify gene expression. Nevertheless, the overarching regulatory networks of these systems are still not well comprehended. The objective of this thesis was to examine the regulatory functions of specific two-component systems (TCSs) AdeRS, BaeRS, and GacSA in *A. baumannii* AB5075, as well as to investigate their roles in antimicrobial resistance and various adaptive phenotypes. Through transcriptomic analysis (RNA-seq), I detected genome wide expression alterations in mutant strains that lacked these regulators when compared to the wild-type during exponential and stationary growth phases. Phenotypic assays, which included minimum inhibitory concentration (MIC) determination, disk diffusion, phenotypic microarrays and growth assays, were conducted to establish a correlation between transcriptional changes and antibiotic susceptibility and metabolism. In order to delve deeper into gene regulation, transcriptional start sites (TSSs) were delineated through differential RNA-seq, which facilitated the identification of promoter motifs and offered insights into the structure of transcriptional regulation in *A. baumannii*. Moreover, chromatin immunoprecipitation coupled with sequencing (ChIP-seq) was utilized to comprehensively map the binding sites of essential transcription factors (AdeR, BaeR, and GacA), uncovering their direct regulons and preferences for DNA binding.

The results outlined in this thesis enhance our comprehension of TCS mediated regulation in *A. baumannii*. They reveal that AdeRS, BaeRS, and GacSA are responsible not only for the regulation of antibiotic resistance factors but also for affecting wider physiological mechanisms that aid in bacterial survival and adaptation. A comparative transcriptomic analysis of the *adeRS*, *baeRS*, and *gacSA* two-component systems has unveiled distinct regulatory effects on gene expression in *Acinetobacter baumannii* AB5075. Both *adeR* and *adeS* mutants exhibited numerous

transcriptional alterations, particularly a downregulation of the *adeABC* efflux pump genes, thereby confirming their involvement in the regulation of antibiotic resistance. In the *baeRS* system, *baeS* demonstrated a more extensive transcriptomic influence compared to *baeR*, especially under the Late Stationary Phase LSP condition, where *baeR* was found to regulate only two genes. The *gacA* and *gacS* mutants revealed the highest number of differentially expressed genes across all systems, with *gacA* notably regulating the small RNAs sRNA100 and sRNA99, as indicated by peaks observed in chip seq data. The phenotypic characterization conducted through Kirby–Bauer disk diffusion assays indicated that all *adeRS*, *baeRS*, and *gacSA* mutants displayed measurable inhibition zones against specific antibiotics, implying partial changes in their susceptibility profiles. Nevertheless, minimum inhibitory concentration (MIC) testing revealed that these mutants continued to exhibit resistance, suggesting that although the regulatory disruptions influenced gene expression, they were not adequate to completely undermine the antibiotic resistance phenotypes.

Differential RNA-seq analysis has revealed a total of 9,428 transcription start sites (TSSs) throughout the *A. baumannii* AB5075 genome, thereby creating a detailed map of promoter regions. This dataset serves as a crucial resource for comprehending transcriptional regulation and provides valuable insights into the potential role of two-component systems in modulating gene expression at the promoter level. To ascertain the genome-wide binding profiles of the response regulators AdeR, BaeR, and GacA, chromatin immunoprecipitation followed by sequencing (ChIP-seq) was employed. AdeR demonstrated a pronounced binding peak in the intergenic region situated between *adeR* and *adeA*, which aligns with its function in the regulation of the *adeABC* efflux operon. GacA displayed unique binding peaks linked to sRNA100, sRNA99, and sRNA91, reinforcing its role in post-transcriptional regulation via small RNAs. BaeR revealed a notable binding site located between *fabR* (*ABUW_RS05395*) and *ABUW_RS05400*, indicating a potential novel regulatory connection between fatty acid metabolism and stress response mechanisms.

Through the integration of transcriptomic, genetic, and phenotypic analyses, this research pinpoints potential regulatory targets that may guide the creation of innovative antimicrobial approaches to combat this challenging pathogen.

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Publications and Conferences

Publications:

- Shaban, L., Ershova, A.S., Hamrock, F.J., Shaibah, A., **Sulimani, M.M.**, Amin, M.R., et al. (2021) Draft Genome Sequence and Annotation of *Acinetobacter soli* AS15, Isolated from an Irish Hospital. *Microbiol Resour Announc* 10: e0061121.
- Hamrock, F. J., Ryan, D., Shaibah, A., Ershova, A. S., Mogre, A., **Sulimani, M.M.**, Ben Taarit, S., Hokamp, K., Westermann, A. J., & Kröger, C. (2024). Global analysis of the RNA–RNA interactome in *Acinetobacter baumannii* AB5075 uncovers a small regulatory RNA repressing the virulence-related outer membrane protein CarO. *Nucleic Acids Research*, 1–18.

Conferences:

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Table of Contents

Declaration.....	2
Summary.....	3
Acknowledgements.....	5
Publications and Conferences.....	7
Table of Contents.....	8
List of Figures.....	11
List of Tables.....	14
Chapter 1: General Introduction.....	17
1.1 <i>Acinetobacter baumannii</i> as a Global Threat.....	17
1. Taxonomic classification of <i>Acinetobacter</i> species.....	17
2. Mechanisms of Antibiotic Resistance in <i>Acinetobacter baumannii</i>	18
1.2 Virulence and Persistence Factors.....	20
1. Outer membrane proteins (OMPs).....	20
2. Biofilm formation.....	20
3. Efflux pumps.....	21
4. Lipopolysaccharides	21
5. Quorum sensing.....	22
6. Siderophore-mediated iron acquisition systems.....	22
7. Two-Component Systems in Bacteria.....	23
1.3 Existing Knowledge Deficiencies and Prospective Pathways.....	24
1. The number of TCSs across different bacteria.....	25
2. Transcriptional Regulation and Two-Component Systems in <i>A. baumannii</i>	26
3. The Abundance and Diversity of TCSs in <i>A. baumannii</i>	27
4. AdeRS Two-Component System.....	30
5. Types of Signals Detected by AdeRS.....	31
6. Possible Interaction between AdeRS and Other Two-Component Systems..	31
7. BaeSR Two-Component System.....	31
8. GacSA Two-Component System.....	32
1.4 Identifying Knowledge Gaps and Justifying Research.....	32

1.5 Aims and Objectives.....	34
Chapter 2: Material & Methods	35
2.1 Microbial culturing.....	35
1. Media.....	35
2. Bacterial strains.....	36
3. Plasmids.....	37
4. Bacterial Culture Conditions.....	37
5. Preparation of antibiotics.....	38
2.2 General molecular techniques.....	38
1. Isolation of genomic DNA from <i>Acinetobacter baumannii</i> AB5075.....	38
2. Plasmid preparations.....	39
3. Polymerase chain reaction (PCR).....	39
4. Agarose gel electrophoresis.....	43
5. Purification of PCR products.....	43
6. Natural transformation of <i>A. baumannii</i>	44
7. Creating deletion mutants in <i>A. baumannii</i> AB5075.....	44
8. Sanger sequencing.....	46
2.3 Phenotypic analyses.....	46
1. The Antibiotic Disk Diffusion (Kirby-Bauer).....	46
2. Broth microdilution assay (MIC determination).....	47
3. Colourimetric method for the determination of metabolisable sources of <i>A. baumannii</i>	47
2.4 Transcriptomic analysis.....	48
1. RNA Isolation.....	48
2. Bioinformatic analysis of RNA seq	49
3. Differential RNA Sequencing.....	49
4. RNA Treatments.....	49
5. Terminator Exonuclease (TEX) Library.....	50
6. Whole Transcriptome Library.....	50
7. cDNA Synthesis and Library Construction.....	51

8. Bioinformatic analysis of dRNA-seq data and determination of transcriptional start sites.....	51
9. Identification of –10 and –35 sigma factor motifs.....	51
2.5 Analysis of proteins.....	52
1. Preparation of whole cell lysates.....	52
2. Protein detection by Western blotting.....	52
3. Chromatin Immunoprecipitation for ChIP-seq.....	54
Chapter 3: Transcriptomic analysis of two component system mutants in <i>Acinetobacter baumannii</i> AB5075.....	57
3.1 Introduction.....	57
3.2 Selection of growth conditions.....	58
3.3 Quality control of RNA and RNA-seq.....	58
3.4 RNA-seq.....	59
3.5 Testing for Mutant Strains.....	59
3.6 Results.....	65
1. $\Delta adeR$ - $\Delta adeS$	65
2. RNA-seq Analysis of $\Delta adeR$ and $\Delta adeS$ Mutan.....	65
3. The overlap between $\Delta adeR$ and $\Delta adeS$	77
4. $\Delta baeR$ - $\Delta baeS$	81
5. RNA-seq Analysis of $\Delta baeR$ and $\Delta baeS$ Mutant.....	81
6. The overlap between $\Delta baeR$ and $\Delta baeS$	92
7. $\Delta gacA$ - $\Delta gacS$	94
8. RNA-seq Analysis of $\Delta gacA$ and $\Delta gacS$ Mutant.....	94
9. The overlap between $\Delta gacA$ and $\Delta gacS$	106
3.7 Regulation of small RNAs in TCS mutant strains.....	109
3.8 Pathway analyses using transcriptomic data of TCS mutants.....	111
Chapter 4: The dRNA-seq and ChIP-seq methodologies uncover the regulatory framework of <i>Acinetobacter baumannii</i> AB5075.....	120
4.1 Introduction.....	120
4.2 Differential RNA sequencing.....	121

4.3 Identification of –10 and –35 sigma factor motifs.....	124
4.4 Global location of AdeR, BaeR, and GacA in <i>Acinetobacter baumannii</i> using ChIP-seq.....	128
4.5 Verification of FLAG-tagged Response Regulators.....	129
4.6 Chip- seq data overview.....	131

Chapter 5: Phenotypic Characterization of Two-Component System Mutants in *Acinetobacter baumannii* 137

5.1 Introduction.....	137
5.2 Growth curve experiments comparing wild-type (WT) and mutant strains.....	137
5.3 Kirby-Bauer Disk Diffusion.....	139
5.4 Results.....	140
1. $\Delta adeR$ - $\Delta adeS$	140
2. $\Delta baeR$ - $\Delta baeS$	143
3. $\Delta gacA$ - $\Delta gacS$	145
5.5 Minimum inhibitory concentration (MIC) determination.....	147
5.6 Results.....	147
1. $\Delta adeR$ - $\Delta adeS$	147
2. $\Delta baeR$ - $\Delta baeS$	149
3. $\Delta gacA$ - $\Delta gacS$	149
5.7 Colorimetric method for the determination of metabolisable sources in AB5075.....	150

Chapter 6: Discussion.....168

List of Figures

Chapter 1

Figure 1.1. Mechanisms of antibiotic resistance in <i>Acinetobacter baumannii</i>	19
Figure 1.2. A summary of the identified two-component systems (TCSs) in <i>Acinetobacter baumannii</i>	26
Figure 1.3. Two-Component Regulatory Systems.....	28
Figure 1.4. TCSs are pathways for signal transduction.....	29

Chapter 2

Figure 2.1. PCR-based genome editing of transformable <i>A. baumannii</i> . Taken from (Godeux et al., 2020).....	45
Figure 2.2. Overview of Chromatin Immunoprecipitation (ChIP) Workflow for ChIP-seq in <i>A. baumannii</i>	56
Chapter 3	
Figure 3.1. Analysis of RNA integrity utilizing the Agilent Bioanalyzer.....	58
Figure 3.2. Visualization of RNA-seq read coverage for <i>adeR</i> and <i>adeS</i> in wild-type (WT) and deletion mutants as analyzed using JBrowse.....	60
Figure 3.3. Visualization of RNA-seq read coverage for <i>baeR</i> and <i>baeS</i> in wild-type (WT) and deletion mutants as analyzed using JBrowse.....	61
Figure 3.4. Visualization of RNA-seq read coverage for <i>gacA</i> in wild-type (WT) and deletion mutants as analyzed using JBrowse.....	62
Figure 3.5. Visualization of RNA-seq read coverage for <i>gacS</i> in wild-type (WT) and deletion mutants as analyzed using JBrowse.....	63
Figure 3.6. Principal Component Analysis (PCA) of transcriptomic profiles for <i>A. baumannii</i> AB5075 wild-type (WT) and TCS mutants under MEP and LSP conditions.....	64
Figure 3.7. Transcriptomic analysis was conducted on the $\Delta adeR$ and $\Delta adeS$ mutant in comparison to the wild-type <i>A. baumannii</i> AB5075 under two different growth conditions.....	66
Figure 3.8. Venn diagrams illustrating the comparison of $\Delta adeR$ and $\Delta adeS$ transcriptomes in MEP.....	79
Figure 3.9. Venn diagrams illustrating the comparison of $\Delta adeR$ and $\Delta adeS$ transcriptomes in LSP.....	80
Figure 3.10. A transcriptomic analysis was performed on the $\Delta baeR$ and $\Delta baeS$ mutants in comparison to the wild-type <i>A. baumannii</i> AB5075 under two distinct growth conditions.....	84
Figure 3.11. Venn diagram of upregulated genes in $\Delta baeR$ and $\Delta baeS$ during MEP.....	93

Figure 3.12. Transcriptomic analysis was conducted on the $\Delta gacA$ and $\Delta gacS$ mutant in comparison to the wild-type <i>A. baumannii</i> AB5075 under two different growth conditions.....	96
Figure 3.13. Venn diagrams illustrating the transcriptomes of $\Delta gacA$ and $\Delta gacS$ during the MEP.....	108
Figure 3.14. Venn diagrams illustrating the transcriptomes of $\Delta gacA$ and $\Delta gacS$ during LSP.....	109
Figure 3.15. A heat map illustrating the differentially expressed sRNA (DEGs) between the wild-type (WT) and mutant strains of <i>Acinetobacter baumannii</i>	115
Figure 3.16. Heat map showing overall sRNA expression profiles of <i>Acinetobacter baumannii</i> mutant strains based on TPM.....	117
Figure 3.17. GO analysis (BP) of WT versus $\Delta adeR$ (A & B) and $\Delta adeS$ (C & D) in MEP (A & C) and LSP (B & D).....	117
Figure 3.18. GO analysis (BP) of WT versus $\Delta baeR$ (A & B) and $\Delta baeS$ (C & D) in MEP (A & C) and LSP (B & D).....	118
Figure 3.19. GO analysis (BP) of WT versus $\Delta gacA$ (A & B) and $\Delta gacS$ (C & D) in MEP (A & C) and LSP (B & D).....	119
Chapter 4	
Figure 4.1. Categories of Transcriptional start sites (TSS) identified by dRNA-seq.....	123
Figure 4.2. Promoter motifs (–35 and –10) derived from upstream regions of transcriptional start sites (TSSs) mapped by dRNA-seq in <i>Acinetobacter baumannii</i> AB5075.....	125
Figure 4.3. Visualization of transcriptional start sites (TSS) using JBrowse for selected Two-Component System genes in <i>Acinetobacter baumannii</i> AB5075.....	127
Figure 4.4. The protein level of strains with inserted chromosomal (A) <i>adeR</i> ::FLAG, (B) <i>baeR</i> ::FLAG, and (C) <i>gacA</i> ::FLAG fusions in the wild-type (WT) strain were assessed through western blotting.....	130
Figure 4.5. A comprehensive view of ChIP-seq data aligned to the <i>Acinetobacter baumannii</i> AB5075 reference genome and plasmids via JBrowse.....	132

Figure 4.6. (A), a significant enrichment peak that is absent from the control samples is found in the AdeR immunoprecipitated (IP) sample.....	136

Chapter 5

Figure 5.1. Growth curves of <i>A. baumannii</i> AB5075 wild type and TCS mutants in LB and M9 media.....	138

Figure 5.2: An example 96-well plate displaying the colorimetric results of metabolic activity after incubation with various carbon sources.....	152

Figure 5.3: Analysis of phenotypic microarrays regarding amino acid utilization in <i>A. baumannii</i> wild-type and mutant strains at 24 hours and 48 hours.....	158

List of Tables

Chapter 1

Table 1.1. Taxonomic classification of <i>Acinetobacter</i> species.....	18

Table 1.2. List of common Two-Component Systems identified in <i>A.baumannii</i> AB5075.....	30

Chapter 2

Table 2.1 Media recipes.....	35

Table 2.2 Bacterial strains used in this study.....	36

Table 2.3 Plasmids used in this study.....	37

Table 2.4 Composition of a typical PCR reaction.....	39

Table 2.5 primers used in this study.....	39

Table 2.6 PCR cycling conditions.....	42

Table 2.7 Colony PCR cycling conditions.....	43

Table 2.8 Buffers and solutions for western blotting.....	53

Chapter 3

Table 3.1: List of genes significantly upregulated or downregulated in the $\Delta adeR$ and $\Delta adeS$ mutant compared to wild-type AB5075.....	68

Table 3.2: Top 20 upregulated and top 20 downregulated genes in the $\Delta adeR$ mutant compared to wild-type AB5075 under MEP conditions.....	69
Table 3.3: The 20 genes exhibiting the highest levels of upregulation and the 20 genes showing the most significant downregulation in the $\Delta adeR$ mutant relative to the wild-type AB5075 under LSP conditions.....	71
Table 3.4: Top 20 upregulated and downregulated genes in the $\Delta adeS$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under MEP conditions.....	73
Table 3.5: Top 20 upregulated and downregulated genes in the $\Delta adeS$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under LSP conditions.....	75
Table 3.6: List of genes significantly upregulated or downregulated in the $\Delta baeR$ and $\Delta baeS$ mutant compared to wild-type AB5075.....	84
Table 3.7: Top 20 upregulated and downregulated genes in the $\Delta baeR$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under MEP conditions.....	85
Table 3.8: Differentially expressed genes in the $\Delta baeR$ mutant under LSP condition.....	87
Table 3.9: Top 20 upregulated and downregulated genes in the $\Delta baeS$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under MEP conditions.....	88
Table 3.10: Top 20 upregulated and downregulated genes in the $\Delta baeS$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under LSP conditions.....	90
Table 3.11: List of genes significantly upregulated or downregulated in the $\Delta gacA$ and $\Delta gacS$ mutant compared to wild-type AB5075.....	97
Table 3.12: Top 20 upregulated and downregulated genes in the $\Delta gacA$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under MEP conditions.....	98
Table 3.13: Top 20 upregulated and downregulated genes in the $\Delta gacA$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under LSP conditions.....	100
Table 3.14: Top 20 upregulated and downregulated genes in the $\Delta gacS$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under MEP conditions.....	102

Table 3.15: Top 20 upregulated and downregulated genes in the $\Delta gacS$ mutant compared to wild-type <i>A. baumannii</i> AB5075 under LSP conditions.....	104

Chapter 4

Table 4.1. Different conditions the RNA was isolated from.....	123

Table 4.2. TSS prediction statistics: All Primary Secondary Internal Antisense Orphan in AB5075 strain.....	124

Table 4.3. Summary of the number of peaks identified for AdeR, BaeR, and GacA in <i>Acinetobacter baumannii</i> AB5075.....	131

Chapter 5

Table 5.1: Measurement of inhibition zones (cm) in Kirby-Bauer disk diffusion tests of <i>adeRS</i>	142

Table 5.2: Antibiotic susceptibility profiles determined by Kirby-Bauer disk diffusion assay of <i>baeRS</i>	144

Table 5.3. Kirby-Bauer disk diffusion results for multiple antibiotics tested against wild-type and mutant strains <i>gacAS</i>	146

Table 5.4: The Minimum Inhibitory Concentration (MIC) values for specific antibiotics against <i>Acinetobacter baumannii</i> wild-type (WT), $\Delta adeR$, and $\Delta adeS$ strains are presented.....	149

Table 5.5: The Minimum Inhibitory Concentration (MIC) values for specific antibiotics against <i>Acinetobacter baumannii</i> wild-type (WT), $\Delta gacS$ strains are presented....	150

Table 5.6: List of Amino Acids Tested as Sole Carbon Sources in the Colorimetric Metabolism Assay of <i>A. baumannii</i> AB5075.....	151

Table 5.7: Heatmap illustrating the metabolic activity of <i>A. baumannii</i> wild-type and TCS mutants over a specified duration.....	152

Chapter 1

General Introduction

1.1 *Acinetobacter baumannii* as a Global Threat

Acinetobacter baumannii is an opportunistic, Gram-negative, non-fermentative coccobacillus that has emerged as a significant contributor to healthcare-associated infections globally. Its capacity to endure on non-living surfaces, withstand drying, and persist in hospital settings has rendered it a challenging nosocomial pathogen. Frequently linked to ventilator-associated pneumonia, bloodstream infections, urinary tract infections, and wound infections, *A. baumannii* primarily impacts critically ill and immunocompromised individuals (Howard *et al.*, 2012; Kyriakidis *et al.*, 2021). *A. baumannii* is characterized by its extraordinary ability to develop resistance against various classes of antibiotics. The rise of multidrug-resistant extensively drug-resistant and even pan drug resistant strains has significantly restricted treatment alternatives creating substantial difficulties in clinical management. Given its clinical significance and resistance characteristics, the World Health Organization (WHO) has classified *A. baumannii* as a Priority #1 critical pathogen, highlighting the pressing necessity for innovative therapeutic approaches and a more profound comprehension of its resistance mechanisms (McConnell *et al.*, 2013; Abdi *et al.*, 2020; Kyriakidis *et al.*, 2021; Sati *et al.*, 2025).

1. Taxonomic classification of *Acinetobacter* species

Phylogenetic analysis is crucial for understanding the emergence of pathogenic species, as genera frequently encompass pathogens, commensals, and free living (environmental) bacteria. A pertinent example is the genus *Acinetobacter*, which comprises a diverse array of biochemically and physiologically adaptable bacteria that inhabit various natural ecosystems and are increasingly implicated in opportunistic human infections (Touchon *et al.*, 2014). Due to recent progress in our understanding of the composition of *Acinetobacter* spp. through next generation sequencing (NGS)

based genome sequencing, the nomenclature of *Acinetobacter* species has experienced considerable taxonomic changes over time (Diancourt *et al.*, 2010; Touchon *et al.*, 2014). The taxonomic classification of *A. baumannii*, the bacterium examined in this thesis, is illustrated in **Table 1.1**.

Table 1.1 Taxonomic classification of *Acinetobacter* species.

Domain	Bacteria
Phylum	Proteobacteria
Class	Gamma-proteobacteria
Order	Pseudomonadales
Family	Moraxellaceae
Genus	<i>Acinetobacter</i>
Species	<i>baumannii</i>

2. Mechanisms of Antibiotic Resistance in *Acinetobacter baumannii*

The antibiotic resistance seen in *A. baumannii* is a complex issue, stemming from both intrinsic and acquired factors. These factors encompass the production of β -lactamases (such as OXA-type carbapenemases), mutations at target sites, decreased membrane permeability due to the loss or alteration of porins, and the active expulsion of antibiotics through multidrug efflux pumps (Xu *et al.*, 2019; Abdi *et al.*, 2020) (**Figure 1.1**). Among these factors efflux pumps are pivotal in the development of multidrug resistance. Numerous efflux systems from the resistance-nodulation-division (RND) family have been identified in *A. baumannii* with the AdeABC, AdeFGH, and AdeIJK pumps being the most prominent. The AdeABC pump is particularly noteworthy because of its significant role in conferring resistance to aminoglycosides, fluoroquinolones, and tetracyclines. The overexpression of these pumps results in lower intracellular concentrations of antibiotics which in turn reduces the effectiveness of the drugs (Xu *et al.*, 2019; Abdi *et al.*, 2020; Kyriakidis *et al.*, 2021). The regulation of these pumps is managed by transcriptional regulators which are frequently part of Two-Component Systems (TCSs)(Kröger *et al.*, 2017). For instance,

the AdeRS TCS is responsible for regulating the expression of the AdeABC pump, while BaeSR and GacSA are involved in broader stress response mechanisms and the regulation of multidrug resistance. Gaining insight into how these regulatory systems influence efflux activity is crucial for developing effective strategies to address antibiotic resistance in *A. baumannii* (Xu *et al.*, 2019; Lee *et al.*, 2020; Abdi *et al.*, 2020).

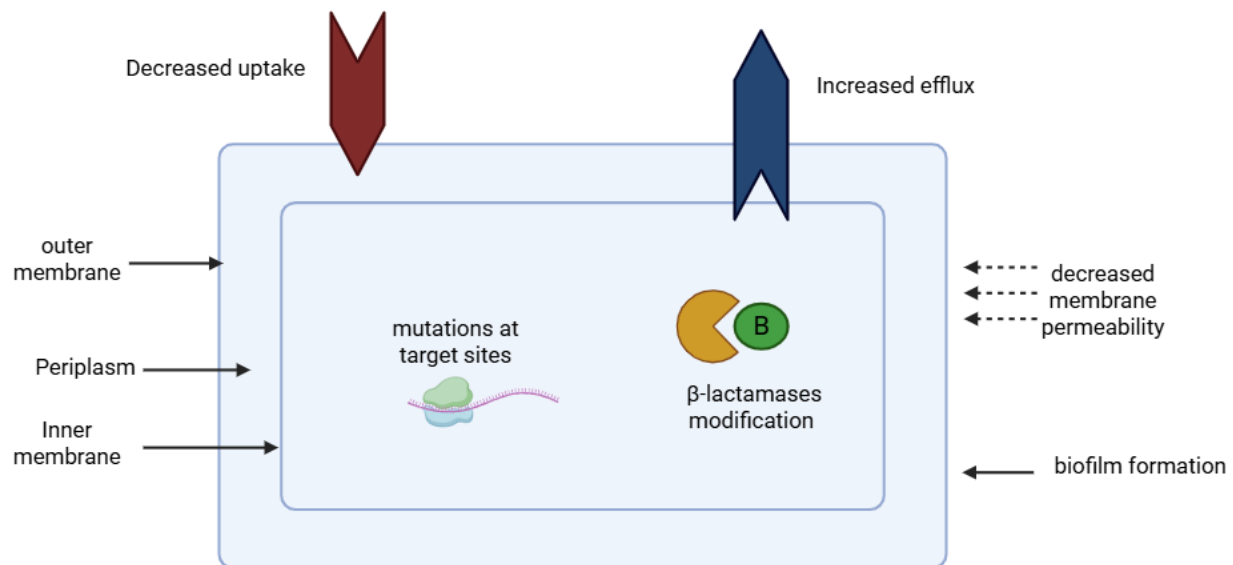


Figure 1.1 Mechanisms of antibiotic resistance in *Acinetobacter baumannii*. Efflux pumps, such as AdeABC, AdeIJK, and AdeFGH, function to actively transport antibiotics out of the cell, thereby decreasing the concentrations of drugs within the cell. The enzymatic inactivation of antibiotics occurs through β -lactamases, which encompass OXA-type carbapenemases and β -lactamases. The loss or alteration of porins leads to a reduction in membrane permeability, consequently restricting the entry of antibiotics, especially β -lactams. Modification of targets via point mutations (for instance, in *gyrAB* or *parCE*) that reduce the binding affinity of fluoroquinolones. The formation of biofilms, which establishes a protective environment that hinders antibiotic penetration and promotes persistence. Collectively, these mechanisms play a role in the multidrug-resistant (MDR) phenotype of *A. baumannii*, thereby complicating treatment in clinical environments.

1.2 Virulence and Persistence Factors

Multidrug-resistant microorganisms are expected to present the most considerable challenge to healthcare in the 21st century. In recent years, species belonging to the genus *Acinetobacter* have emerged as opportunistic bacterial pathogens, particularly recognized as significant nosocomial pathogens due to the rapid emergence of antimicrobial resistance. Although our current biological understanding of virulence mechanisms is limited, an increasing number of researchers are focused on identifying virulence factors and exploring antibiotic resistance (Kröger *et al.*, 2017; Monem *et al.*, 2020). In addition to its remarkable antimicrobial resistance, *A. baumannii* possesses a diverse range of virulence factors that bolster its survival, persistence, and pathogenicity, particularly within hospital settings. These virulence factors facilitate host colonization, enable evasion of the immune response, and cause damage to host tissues (Lee *et al.*, 2017).

1. Outer membrane proteins (OMPs)

Outer membrane protein A (OmpA), a principal element of outer membrane proteins (OMPs) in Gram-negative bacteria, serves as a crucial virulence factor that facilitates bacterial biofilm formation, infection of eukaryotic cells, antibiotic resistance, and immunomodulation (Choi *et al.*, 2008; Woo *et al.*, 2025). The functions of the OmpA protein in *A. baumannii* have begun to be elucidated by researchers in recent years. They have identified novel treatment strategies for treating *A. baumannii* infections, described the structure and activities of the *A. baumannii* OmpA protein (AbOmpA), and highlighted the possibility of using AbOmpA as a promising therapeutic target (Morris *et al.*, 2019; Nie *et al.*, 2020; Monem *et al.*, 2020).

2. Biofilm formation

The capacity to develop biofilms on non-living surfaces enables *A. baumannii* to withstand unfavourable conditions, including desiccation and exposure to detergents. Pili, which are protein filaments, are essential for adhering to surfaces, thereby facilitating prolonged survival on medical equipment and surfaces within healthcare settings (Eze *et al.*, 2018; Elkheloui *et al.*, 2020). The assembly of pili and the

synthesis of the Bap surface-adhesion protein are crucial for the initiation and maturation of biofilms following the initial attachment to non-biological surfaces (Elkheloui *et al.*, 2020; Pompilio *et al.*, 2021). The regulation governing the formation and progression of these biofilms is as varied as the surfaces on which this bacterium thrives, as well as the cellular components involved in this intricate multistep process (Gaddy and Actis, 2009). Certain extracellular signals may be detected by two-component regulatory systems, such as BfmRS (Geisinger and Isberg, 2015; Pompilio *et al.*, 2021). This transcriptional regulatory system triggers the expression of the usher-chaperone assembly system, which is essential for the production of pili necessary for cell attachment and biofilm development on polystyrene surfaces (Gaddy and Actis, 2009; Palethorpe *et al.*, 2022).

3. Efflux pumps

Antibiotic resistance is a significant issue not only attributed to *A. baumannii* but is also regarded as a primary challenge posed by numerous other pathogens. Various elements, including the efflux pump, are linked to antibiotic resistance, biofilm formation, and genetic mutations (Abdi *et al.*, 2020). Bacterial efflux systems are tripartite systems that span the membrane and demonstrate a wide range of substrate specificity, facilitating the expulsion of potentially harmful compounds from the periplasm to the external environment (Morris *et al.*, 2019). Each efflux pump is composed of three elements: the outer membrane channel, the periplasmic lipoprotein, and the inner membrane transporter. Four categories of efflux pumps, namely the major facilitator superfamily (MFS), the resistance-nodulation cell division (RND) family, the small multidrug resistance (SMR) family, and the multidrug and toxic compound extrusion (MATE) family, are linked to the antimicrobial resistance observed in *A. baumannii* (Sun *et al.*, 2014; Abdi *et al.*, 2020).

4. Lipooligosaccharides

Gram-negative bacteria exhibit resistance to antibiotics due to their outer membrane, which is strengthened by lipooligosaccharides (LOS). In the case of *Acinetobacter baumannii*, resistance to colistin may develop through the depletion of lipid LOS, underscoring their significance in survival and as prospective targets for antimicrobial

intervention (Boll *et al.*, 2016). Recent studies indicate that *Acinetobacter baumannii* is capable of surviving in the absence of lipid A biosynthesis and the outer membrane lipooligosaccharide (LOS), which marks a notable deviation from the behavior of most Gram-negative bacteria (Powers and Trent, 2018), because it is usually lethal to cells, but it confers resistance to the polymyxin colistin. This deficiency in LOS affects various aspects such as cell envelope integrity, bacterial physiology, antibiotic resistance, and virulence, with evidence suggesting that the elongasome pathway involved in peptidoglycan synthesis is essential for this survival strategy (Moffatt *et al.*, 2010; Powers and Trent, 2018; Yehya *et al.*, 2025).

5. Quorum sensing

Quorum sensing represents an advanced communication mechanism that allows bacteria to synchronize group behaviours essential for their survival and pathogenicity (Zhong and He, 2021). In *A. baumannii*, the quorum sensing system, primarily governed by Abal/AbaR, is instrumental in biofilm development, resistance to antibiotics, and virulence. Gaining insights into and addressing quorum sensing components paves the way for innovative strategies in anti-virulence therapy (Saipriya *et al.*, 2020; Zhao *et al.*, 2020). The manifestation of pathogenicity and virulence via the QS system generally encompasses the following stages: (I) the synthesis of QS signal molecules; (II) the release of these signal molecules into the environment; (III) the detection and binding of the signal molecules to membrane receptors at elevated cell densities; (IV) the internalization of the receptor-signal complex and its subsequent binding to the promoter region; and (V) the transcription of genes associated with pathogenicity (Zhong and He, 2021).

6. Siderophore-mediated iron acquisition systems

Iron is crucial for the survival and virulence of bacteria; however, it is tightly bound by host proteins within vertebrate tissues. To address this challenge, *A. baumannii* utilizes specialized systems for iron acquisition that are mediated by siderophores to extract iron from the host environment (Cook-Libin *et al.*, 2022). *A. baumannii* produces as many as ten unique siderophores, which are encoded by three separate loci: acinetobactin and pre-acinetobactin, baumannoferrins A and B, and fimsbactins

A-F (Sheldon and Skaar, 2020). The primary siderophore synthesized by *A. baumannii* is acinetobactin, which is a catechol-type siderophore produced and released in conditions where iron is scarce. Acinetobactin exhibits a strong affinity for ferric iron (Fe^{3+}) and facilitates its transport back into the bacterial cell through a specific receptor-mediated uptake mechanism (Dorsey *et al.*, 2004; Sheldon and Skaar, 2020). Moreover, aside from acinetobactin, certain strains of *A. baumannii* are capable of utilizing additional iron sources, such as heme and transferrin, via alternative receptors, implying the existence of redundant or complementary pathways for iron acquisition (Zhang *et al.*, 2025). Research indicates that the removal of acinetobactin biosynthetic genes results in a marked reduction of virulence in animal infection models, underscoring its critical role in pathogenesis (Sheldon and Skaar, 2020).

7. Two-Component Systems in Bacteria

Two-component systems represent cellular signalling networks that gained significant attention in the early 1980s, particularly following their identification in the model organism *Escherichia coli* (Nixon *et al.*, 1986; Paul Golby, 1999). These systems enable organisms to detect and convert a variety of input signals, facilitating adaptive responses to alterations in both extracellular and intracellular environments (Olivera *et al.*, 2010; Papon and Stock, 2019).

Two-component systems typically consist of a duo of proteins that are part of the histidine kinase and response regulator families, coordinating a singular phosphotransfer event. In standard systems, the histidine kinase, which is generally dimerized and frequently spans the membrane, functions as a sensor protein that detects the input signal and undergoes autophosphorylation on a conserved histidine residue. Subsequently, the phosphoryl group is transferred to a conserved aspartate residue of the corresponding response regulator, thereby activating it to initiate a response often involving the transcriptional regulation of specific genes (Mitrophanov and Groisman, 2008; Lin *et al.*, 2015; Francis *et al.*, 2017). Two-component systems (TCSs) are crucial in governing a variety of bacterial functions, including motility, virulence, nutrient uptake, responses to osmotic stress, antibiotic resistance, and

biofilm development, including in *A. baumannii*. These systems are often conserved across prokaryotic organisms and can be essential for survival in challenging or variable environments. Given their fundamental regulatory functions and their lack of presence in humans, TCSs are viewed as promising targets for the development of new antibacterial treatments (Olivera *et al.*, 2010; Sánchez de la Nieta *et al.*, 2022; Hu *et al.*, 2024).

1.3 Existing Knowledge Deficiencies and Prospective Pathways

TCSs are involved in the adaptive responses of bacteria, which can result in changes to their susceptibility to antibiotics and their virulence. Therefore, it is essential to investigate these systems to comprehend the mechanisms underlying antibiotic resistance and virulence in bacterial species (Kröger *et al.*, 2017; De Silva and Kumar, 2019). Despite comprehensive studies on two-component systems (TCSs), numerous critical elements are still inadequately understood, especially in clinically significant pathogens such as *Acinetobacter baumannii*. A significant deficiency exists in the functional characterization of many anticipated TCSs. Although genomic investigations have revealed a multitude of TCS-encoding genes, the precise signals they recognize and their downstream regulatory targets are unidentified in the majority of instances (Papon and Stock, 2019; Rajeev *et al.*, 2020).

Another domain that necessitates additional investigation is the degree of cross-talk and regulatory intricacy present within TCS networks. Although these networks have historically been perceived as one to one signalling pathways, it has become increasingly clear that sensor kinases can phosphorylate non-cognate response regulators, resulting in intricate and interrelated networks that remain inadequately charted (Agrawal *et al.*, 2016; Ali and Abdel Aziz, 2024).

Moreover, the molecular mechanisms underlying signal recognition by sensor histidine kinases remain largely unexplored across numerous systems. Determining the specific environmental signals that initiate TCS activation, such as those derived from hosts or related to stress, continues to pose a considerable challenge (Mascher *et al.*, 2006; Bleul *et al.*, 2021). Compounding the complexity, numerous bacteria possess non-canonical two-component systems (TCSs), including orphan response

regulators or kinases, hybrid kinases, and phosphatases that diverge from traditional models and may operate via alternative signalling pathways. These unusual systems remain inadequately studied in *A. baumannii* and other multidrug-resistant species (Laub *et al.*, 2007; Wuichet *et al.*, 2010; Zschiedrich *et al.*, 2016).

Although Two-Component Systems (TCSs) represent promising candidates for novel antimicrobial agents owing to their critical role in pathogens and their non-existence in humans, no drug targeting TCSs has been approved for clinical application to date. Additional research is required to create specific inhibitors and evaluate their efficacy and safety (Bem *et al.*, 2015; Murugaiyan *et al.*, 2022). Addressing these gaps collectively will be crucial for the complete utilization of TCSs as diagnostic markers and therapeutic targets, particularly regarding antimicrobial resistance in *A. baumannii*.

1. The number of TCSs across different bacteria

Two-component systems (TCSs) are widely found in bacteria, exhibiting considerable variation in their numbers across different species. For instance, certain bacteria such as *E. coli* contain approximately 29 TCS sets, whereas others, including *Pseudomonas aeruginosa*, have a notably higher count, featuring at least 64 response regulators and 63 histidine kinases (Sultan *et al.*, 2021). *Acinetobacter baumannii* harbours numerous two-component systems (TCSs) that regulate genes important for its survival and virulence. Although the precise count may differ slightly among strains and research, genomic studies generally reveal approximately 20 distinct genes or operons that encode TCSs in well-studied clinical isolates. These systems play a vital role in detecting and reacting to a range of environmental signals, influencing antibiotic resistance, biofilm development, and various other virulence determinants (**Figure 1.2**) (De Silva and Kumar, 2019).

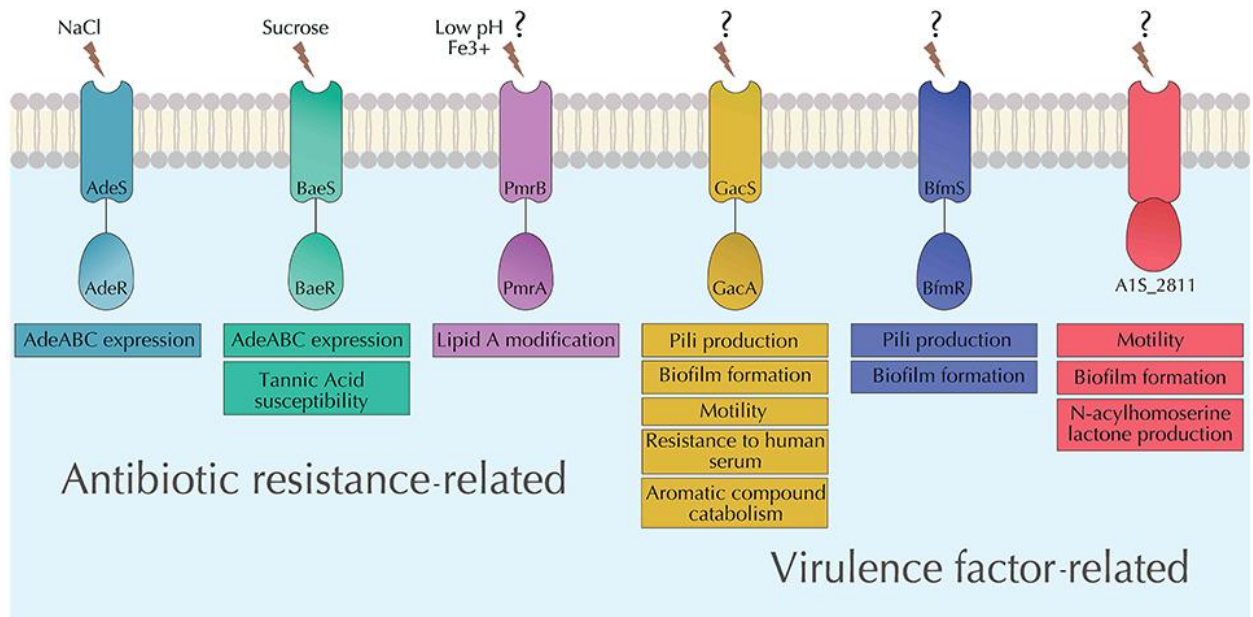


Figure 1.2 A summary of the identified two-component systems (TCSs) in *Acinetobacter baumannii*. The roles of each characterized TCS in *A. baumannii* (AdeRS, BaeSR, PmrAB, GacSA, BfmRS, and A1S_2811) along with their recognized stimuli are illustrated. Taken from (De Silva and Kumar, 2019).

2. Transcriptional Regulation and Two-Component Systems in *A. baumannii*

Bacterial adaptation to environmental stress is primarily facilitated by the precise and dynamic regulation of gene expression. Two-Component Systems (TCSs), which consist of a histidine kinase sensor and its corresponding response regulator, allow bacteria to detect and adjust to changes in their environment. (Bhagirath *et al.*, 2019; Song *et al.*, 2022). Upon activation by an environmental or physiological stimulus, the sensor kinase transmits this signal by phosphorylating a corresponding response regulator (**Figure 1.3**). This response regulator acts as a transcription factor, which experiences a conformational alteration upon phosphorylation, thereby enhancing its ability to bind to DNA (Bourret and Silversmith, 2010; Zschiedrich *et al.*, 2016b).

In *A. baumannii*, two-component systems (TCSs) are essential for the regulation of significant biological processes such as antibiotic resistance, biofilm formation, motility, and virulence (**Figure 1.4**). For instance: The AdeRS TCS represents the

most thoroughly characterized regulatory system in *A. baumannii*. AdeRS system regulates the AdeABC efflux pump and directly contributes to resistance against aminoglycosides and fluoroquinolones (Richmond *et al.*, 2016a; Kröger *et al.*, 2017).

The BaeSR TCS is involved in the envelope stress response and is linked to the regulation of various efflux systems (Lin *et al.*, 2015). GacSA is recognized for regulating genes associated with virulence and may influence resistance under specific stress conditions (Song *et al.*, 2022). Despite the established roles of these systems (**Table 1.2**), the comprehensive regulatory functions of TCSs, their target genes, and the mechanistic pathways they affect are not fully elucidated. A more thorough exploration of these TCSs is vital for uncovering new regulatory networks.

3. The Abundance and Diversity of TCSs in *A. baumannii*

The genomic examination of *A. baumannii* strains, such as ATCC 17978 and AB5075, indicates the presence of approximately 25-30 two-component systems (TCSs). These TCSs are located on both the chromosome and plasmids (**Figure 1.3**), and they are anticipated to regulate a variety of bacterial functions, including antibiotic resistance, membrane integrity, virulence, iron acquisition, and biofilm development. A significant number of these TCSs have yet to be characterized (Casella *et al.*, 2017; Zhu *et al.*, 2020; Nasser *et al.*, 2024).

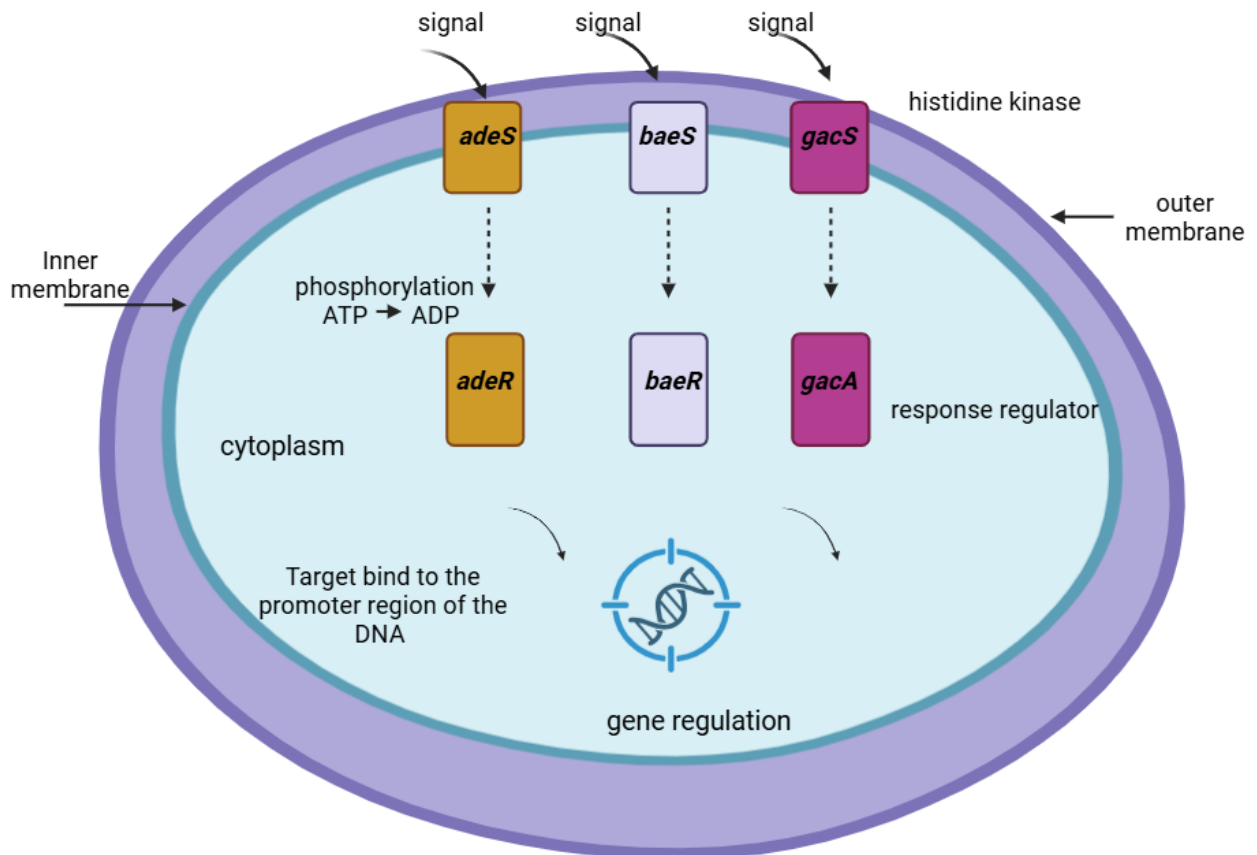


Figure 1.3 Two-Component Regulatory Systems. **Sensor Kinase:** Typically located in the bacterial inner cell membrane, it is composed of an extracytoplasmic sensing domain, a transmembrane region, and an intracellular kinase domain. **Response Regulator:** The response regulator usually consists of a receiver domain, which gets phosphorylated by the sensor kinase, and an output domain, which typically has DNA-binding activity. **Phosphotransferase:** The phosphate group from the phosphorylated histidine residue of the sensor kinase is transferred to an aspartate residue on the response regulator. **Regulation of Gene Expression:** The phosphorylated response regulator undergoes a conformational change that allows it to bind to specific DNA sequences, leading to the activation or repression of target genes.

Two component system (TCSs)

Genomic location:

- Chromosomal TCS
- Plasmid TCS

Functional roles of TCSs in *A. baumannii*:

- Antibiotic Resistance: regulate efflux pumps & resistant genes.
- Membrane Integrity: preserve envelope structure.
- Virulence: control expression of toxins, adhesins.
- Iron acquisition: regulate iron uptake genes.
- Biofilm formation: initiate and maintain biofilm state

Figure 1.4 TCSs are pathways for signal transduction. In *A. baumannii*, TCSs are found on either the bacterial chromosome or plasmids and are crucial for adapting to the environment. Their predicted functions involve regulating antibiotic resistance, maintaining membrane integrity, controlling virulence factors, acquiring iron, and forming biofilms. These systems are vital for the bacterium's survival in harsh conditions, such as during infections and antibiotic therapies.

Table 1.2 List of common Two-Component Systems (TCSs) identified in *A.baumannii* AB5075.

system	type	Function
<i>adeRS</i>	Two-component system	Controls the expression of the AdeABC drug efflux pump. Essential for biofilm development.
<i>baeRS</i>	Two-component system	The process of deletion leads to a diminished expression of the AdeABC, AdeIJK, and MacAB-TolC drug efflux pumps, thereby enhancing susceptibility to tannic acid.
<i>gacAS</i>	Two-component system	The GacS/GacA system regulates genes associated with virulence, such as those involved in biofilm formation, motility, and secretion systems.
<i>pmrAB</i>	Two-component system	Controlling resistance to the antibiotic colistin, along with other elements such as surface motility and biofilm development. Regulates lipid A modification genes.
<i>bfmRS</i>	Two-component system	controlling different cellular activities, such as biofilm development, motility, and reactions to stress

4. AdeRS Two-Component System

The AdeRS two-component system represents one of the most thoroughly investigated regulatory mechanisms in *A. baumannii*, particularly recognized for its direct regulation of the AdeABC efflux pump, which is essential in the context of multidrug resistance. This TCS is composed of: AdeS a membrane-associated sensor histidine kinase that identifies environmental cues (including antibiotic stress), and AdeR a cytoplasmic response regulator that influences gene expression following phosphorylation (Ruzin *et al.*, 2007; Sun *et al.*, 2012). The *adeRS* operon is situated next to the *adeABC* operon, indicating a close regulatory relationship. In response to antibiotic stress or other challenging conditions, AdeS experiences autophosphorylation and subsequently transfers the phosphate group to AdeR, which then interacts with the promoter region of *adeABC*, thereby initiating its transcription. The excessive production of the AdeABC efflux pump in *A. baumannii*, which effectively exports aminoglycosides, tetracyclines, fluoroquinolones, and tigecycline, is a recognized mechanism of resistance. This overexpression is often caused by mutations in the AdeRS two-component regulatory system. For example, point

mutations like Pro116Leu in AdeR or Gly103Asp in AdeS have been demonstrated to maintain elevated levels of pump expression (Marchand *et al.*, 2004; Sun *et al.*, 2012; Subhasree Roy, 2022). RNA-Seq analysis demonstrated that the absence of AdeRS or AdeB substantially modified the transcriptional profile, leading to altered expression levels of numerous genes, particularly those linked to antimicrobial resistance and virulence interactions (Richmond *et al.*, 2016).

5. Types of Signals Detected by AdeRS

Although the precise signals recognized by AdeS remain incompletely defined, numerous studies indicate that it predominantly reacts to membrane stress or the existence of specific antibiotics. Suggested stimuli encompass exposure to antibiotics, particularly Aminoglycosides, Fluoroquinolones, Tigecycline, Membrane-disrupting agents, including disinfectants or detergents also environmental stressors such as variations in pH, osmolarity and envelope integrity (De Gaetano *et al.*, 2023; Brand *et al.*, 2025).

6. Possible Interaction between AdeRS and Other Two-Component Systems

Although two-component systems (TCSs) are typically regarded as separate signal transduction pathways, there is evidence indicating that cross-talk and regulatory overlap take place particularly in intricate stress responses. In *A. baumannii*, the AdeRS and BaeSR systems, which both react to envelope stress and play a role in antibiotic resistance, exemplify the possible interactions between various TCSs (Lin *et al.*, 2014; Palethorpe *et al.*, 2022). Previous research has shown that BaeSR affects tigecycline susceptibility in *A. baumannii* by regulating the *adeAB* genes, which are typically thought to be controlled by AdeRS (Lin *et al.*, 2014). The shared regulons of AdeRS and BaeSR may suggest that BaeSR operates through interaction with AdeRS (Kröger *et al.*, 2017).

7. BaeSR Two-Component System

The BaeSR two-component system represents a conserved regulatory mechanism found in Gram-negative bacteria, which serves as a conserved mechanism for responding to stress in the cell envelope (Powers and Trent, 2018). In *A. baumannii*,

BaeSR is involved in the regulation of multidrug resistance, however, its regulatory framework is not as clearly defined as that of AdeRS (Lin *et al.*, 2015). This system consists of BaeS, a sensor histidine kinase associated with the membrane that likely identifies stress signals within the periplasm or membrane. And BaeR, a cytoplasmic response regulator that upon phosphorylation influences the transcription of genes related to stress (Liu *et al.*, 2023).

BaeS or BaeR additionally regulates the expression of *csu* and *paa* genes, thereby affecting biofilm development, surface motility, and virulence in *A. baumannii* (Liu *et al.*, 2023). BaeSR is an envelope system that reacts to stress induced by external stimuli, serving as a global regulator that affects the transcription of *adeAB* and, consequently, the susceptibility of *A. baumannii* to tigecycline.

8. GacSA Two-Component System

The GacSA is a global activator of antibiotic and carbon utilization, two-component system represents a highly conserved regulatory module found across numerous Gram-negative bacteria. In contrast to *adeRS* and *baeRS*, *gacSA* are not encoded in an operon, but in different locations on the genome, although they have been shown to work together (Cerqueira *et al.*, 2014). In *A. baumannii*, the GacS (sensor kinase) and GacA (response regulator) together constitute a global regulatory system that influences a wide array of physiological processes and those associated with virulence (Cerqueira *et al.*, 2014; Bhagirath *et al.*, 2019). In *A. baumannii*, GacS also influences the expression of CsrA-binding sRNAs CsrB (sRNA97), CsrC (sRNA104) and CsrD (sRNA109) and is therefore indirectly involved in post-transcriptional regulation (Singh *et al.*, 2025) and switching from virulent opaque (VIR-O) to avirulent translucent (AV-T) cell types. In other bacteria, such as *P. aeruginosa*, the phenotypes governed by the GacS/GacA system may be regulated not solely at the transcription initiation level by the response regulator, but also through the action of the small RNAs RsmY and RsmZ, which are regulators of the RNA-binding protein RsmA, which is a homologue of CsrA (Brencic *et al.*, 2009).

1.4 Identifying Knowledge Gaps and Justifying Research

Worldwide, there is a growing prevalence of bacteria that have developed resistance to antibiotic treatments, with numerous reports indicating the presence of multi-drug resistant (MDR) bacteria. AMR is typically depicted as a binary classification of antimicrobial sensitivity versus antimicrobial resistance, this oversimplification fails to capture the range of resistance phenotypes that emerge from the intricate and varied nature of resistance mechanisms. In other terms, the sensitivity or resistance of a bacterium may hinge on the manner in which environmental factors and their influence on transcriptional regulation of antimicrobial resistance genes (ARGs) and impact the complex interplay of inherent physiology and metabolic processes to either evade or eliminate antimicrobials. A potentially highly effective strategy for AMR involves analysing the conditions and mechanisms through which bacteria shift between sensitive and resistant phenotypes by modulating the expression of ARGs. The elements that influence ARG expression can serve as innovative targets for drug development (Salam *et al.*, 2023; Muteeb *et al.*, 2023).

In my research on AMR in *A. baumannii*, I will utilize the highly virulent MDR strain *A. baumannii* AB5075 as a model strain, which is not only clinically significant but also remains genetically accessible. It shows high-level resistance to several classes of antibiotics, particularly β -lactams (carbapenems), aminoglycosides, and fluoroquinolones (Jacobs *et al.*, 2014a; Godeux *et al.*, 2020a). Although specific elements of antibiotic resistance in *A. baumannii*, including the AdeABC efflux pump and its regulatory component AdeRS, have been documented, the comprehensive regulatory frameworks that encompass Two-Component Systems (TCSs) are still not well comprehended (Barrow and Kwon, 2009; Lin *et al.*, 2014). The majority of research has concentrated on individual genes or particular conditions, resulting in a deficiency in our knowledge regarding the global responses of these systems to environmental factors or antibiotic induced stress.

Moreover, there exists a scarcity of information regarding the specific regulatory targets of essential response regulators like AdeR, BaeR, and GacA, particularly at the genome-wide scale and in different environmental conditions and whether there

is cross-talk between different TCS. In addition, the transcriptional start sites and promoters of numerous genes linked to resistance and virulence have not been thoroughly delineated in *A. baumannii* AB5075. In light of the clinical urgency to address multidrug-resistant *A. baumannii*, it is imperative to elucidate the mechanistic foundations of TCS-mediated gene regulation, as this may uncover new targets for the development or intervention of antimicrobial strategies (Kröger *et al.*, 2018; Ibrahim *et al.*, 2021).

1.5 Aims and Objectives

The primary objective of this thesis is to explore the global regulatory functions of specific Two-Component Systems (TCSs) namely AdeRS, BaeSR, and GacSA in *Acinetobacter baumannii* AB5075, concentrating on their influence on gene expression, antibiotic resistance, and phenotypic characteristics. To accomplish this, the following specific goals were investigated:

- To conduct transcriptomic analysis (RNA-seq) of both wild-type and TCS mutant strains to pinpoint differentially expressed genes across various genetic backgrounds.
- To evaluate the phenotypic consequences of TCS deletion on antibiotic susceptibility, growth, and stress response through MIC assays, disk diffusion, and growth curves.
- To delineate transcriptional start sites and promoter regions in *A. baumannii* via differential RNA-seq to enhance the understanding of gene regulation.
- To identify the genome-wide DNA binding sites of AdeR, BaeR, and GacA through ChIP-seq to discover direct regulatory targets.

By employing this comprehensive approach, the research seeks to offer novel insights into the regulatory networks that govern antimicrobial resistance and stress adaptation in *A. baumannii*. Additionally, it aims to uncover and characterize regulatory factors associated with antibiotic resistance in *A. baumannii* that could serve as potential new targets for the development of antimicrobial drugs in the future.

Chapter 2

Material & Methods

2.1 Microbial culturing

1. Media

The recipes for media can be found in **Table 2.1**. All media were prepared using deionized water. Sterilization of media was achieved through autoclaving or filtration with 0.2 µm polyether sulfone (PES) membrane filters (Fisher Scientific). Agar plates were made by melting Lennox agar (LA, L-agar) by autoclaving, cooling it to 50°C, and then adding antibiotics (if needed) before pouring. Agar plates were stored at 4°C. Antibiotic-containing L-agar plates were prepared by mixing the necessary antibiotics with cooled molten L-agar and then pouring the mixture into petri dishes.

Table 2.1 Media recipes

Medium	Reagent	Concentration	Reference
Lysogeny broth (Lennox, L-)	Bacto-Tryptone	10 g/L	(Lennox, 1955)
	NaCl	5 g/L	
	Bacto-Yeast extract	5 g/L	
Lennox Agar	Lennox broth Bacto-Agar	L-broth+ 1.5% (w/v) agar	(Lennox, 1955)
Mueller Hinton Broth	Dehydrated infusion	300 g/L	
	Casein hydrolysate	17.5 g/L	
	Starch	1.5 g/L	
Mueller Hinton Agar	Dehydrated infusion	300 g/L	
	Casein hydrolysate	17.5 g/L	
	Starch	1.5 g/L	
	Agar	17 g/L	
Minimal Medium (M9)	Na ₂ HPO ₄ × 7H ₂ O	64 g/L	
	KH ₂ PO ₄	15 g/L	
	NaCl	2.5 g/L	
	NH ₄ Cl	5 g/L	
Motility Media	Agarose – D3	20 g/L	(Godeux <i>et al.</i> , 2018)
	Tryptone	5 g/L	
	Sodium chloride	2.5 g/L	

IF-MM	NaCl	4 g	
	Kolliphor	0.3 g	
	Phytigel Plant	0.2 g	
	Tetrazolium violet (Dye)	0.1 g	
	Autoclave for 15 min at 121°C, cool down to RT		
	M9 (10x)	100 mL	
	0,2 M MgSO ₄ (final concentration 2 mM)	10 mL	
	1 mM CaCl ₂ (final concentration 0.1 µM)	0.1 mL	

2. Bacterial strains

The bacterial strains used in this research are detailed in **Table 2.2**. To maintain bacterial stocks for an extended period, overnight cultures were mixed with 30% sterile glycerol in L-broth (**Table 2.1**) and stored at -80°C. Single colonies of the strains were streaked on LA plates with the suitable antibiotics and grown at either 30°C or 37°C as required. These plates were kept at 4°C for a maximum of one week.

Table 2.2 Bacterial strains used in this study.

Species	Strain	Genotype	Source/References
<i>A. baumannii</i>	AB5075	wildtype	S. Salcedo lab (Lyon) (Jacobs <i>et al.</i> , 2014b)
<i>E. coli</i>	TOP10	F– <i>mcrA</i> $\Delta(mrr-hsdRMS-mcrBC)$ $\phi 80lacZ\Delta M15$ $\Delta lacX74$ <i>nupG</i> <i>recA1</i> <i>araD139</i> $\Delta(ara-leu)7697$ <i>galE15</i> <i>galK16</i> <i>rpsL(Str^R) endA1</i> λ^-	Invitrogen
<i>A. baumannii</i>	AB5075	$\Delta adeR$	This study
<i>A. baumannii</i>	AB5075	$\Delta adeS$	This study

<i>A. baumannii</i>	AB5075	$\Delta baeR$	This study
<i>A. baumannii</i>	AB5075	$\Delta baeS$	This study
<i>A. baumannii</i>	AB5075	$\Delta gacS$	This study
<i>A. baumannii</i>	AB5075	$\Delta gacA$	This study

3. Plasmids

The strains of all plasmids utilized in this investigation can be found in **Table 2.3**.

Table 2.3 Plasmids used in this study.

Plasmid	Description	Resistance	Source/References
pMHL-2	Template for amplification of <i>aacC4</i> and <i>sacB</i> genes	Apramycin	X. Charpentier (Lyon) (Godeux <i>et al.</i> , 2020b)
pWH1266	<i>E. coli</i> - <i>A. baumannii</i> shuttle vector	Tetracycline, ampicillin	(Hunger <i>et al.</i> , 1990)

4. Bacterial Culture Conditions

Growth in Lennox Broth

The L-broth and L-agar plates were placed in an incubator set at a temperature of 37°C. To initiate the overnight cultures, 5 mL of L-broth was inoculated with a single colony and then cultivated in an environmental incubator shaker for a duration of 16-18 h (37°C and 220 rpm). In order to inoculate larger culture volumes in L-broth, bacterial cultures were sub-inoculated at a ratio of 1:1000 in 25 mL of L-broth within a 250 mL Erlenmeyer flask and the cultures were cultivated with agitation at a speed of 220 rpm. This process took place at a temperature of 37°C using an Innova 3100 water-bath shaker manufactured by New Brunswick Scientific. Additionally, agar plates were incubated at 37°C using a Memmert INB200 Incubator Oven.

Growth in Minimal Media

To achieve growth in minimal media, overnight cultures were cultivated with the following procedure. A volume of 1 mL of the overnight culture was collected through centrifugation at maximum speed in a microcentrifuge, then subjected to three washes

in minimal media. Subsequently, the culture was sub-inoculated at a ratio of 1:500 into 25 mL of minimal media within a 250 mL Erlenmeyer flask.

Monitoring Bacterial Growth

The optical density at a wavelength of 600 nm (OD₆₀₀) was assessed using a Biomate 3S spectrophotometer (Thermo Scientific) to monitor the growth of bacterial cultures. Prior to measurement, cultures exhibiting an OD₆₀₀ exceeding approximately 0.5 were diluted tenfold in the suitable medium.

5. Preparation of antibiotics

The antibiotics apramycin (60 µg/mL) and tetracycline (12 µg/mL) were added to growth media with indicated final concentrations. The antibiotics were dissolved in dH₂O (apramycin) or 70% ethanol (for tetracycline) to prepare antibiotic stock solutions, which were 1000× concentrated (i.e., apramycin (60 mg/mL), tetracycline (12 mg/mL). These solutions dissolved in dH₂O were then sterilized by filtration through a 0.22 µm filter pore. Antibiotic stocks were stored long-term at -20°C.

2.2 General molecular techniques

1. Isolation of genomic DNA from *Acinetobacter baumannii* AB5075

Overnight cultures were prepared as previously outlined. A volume of 400 µL of the culture was collected through centrifugation at 8,000 × g for 1 min at room temperature. The resulting cell pellet was resuspended in 200 µL of sterile dH₂O and subjected to boiling at 100°C for 5 min, followed by vortexing for 30 s to ensure thorough lysis. Cell debris was removed by centrifugation at 8,000 × g for 5 min, and the supernatants were combined with an equal volume of chloroform and vortexed for 30 s. The organic and aqueous phases of the mixture were separated by centrifugation at 8,000 × g for 10 min at 4°C. To eliminate chloroform contamination, 75% of the aqueous layer was transferred to a new 1.5 mL tube. The DNA present in the aqueous phase was quantified using the Nano Drop ND-1000 Spectrophotometer

(Thermo Scientific), and the concentration was adjusted to 100 ng/μL then stored at -20°C for use as a PCR template.

2. Plasmid preparations

All plasmids were obtained from *E. coli* utilizing the E.Z.N.A. Plasmid DNA Mini Kit from Omega Bio-Tek. The plasmids were extracted from overnight cultures grown in L-broth, with antibiotics added as necessary. Following this, the cultures were centrifuged at 13,000 × g to pellet the cells, and the plasmids were isolated and purified in accordance with the manufacturer's instructions provided by Omega Bio-Tek. The concentration and purity of the plasmids were measured using the NanoDrop ND-1000 Spectrophotometer (Thermo Scientific).

3. Polymerase chain reaction (PCR)

In this study, PCR was employed with the primers listed in **Table 2.5**. VeriFi™ polymerase (PCRBIO Systems) was used for amplifying products in accordance with the manufacturer's guidelines. For the PCR template, 100 ng of chromosomal DNA, 1-10 ng of plasmid DNA, or a single colony resuspended in 200 μL of sterile dH₂O was utilized. The components and conditions for these reactions are detailed in **Tables 2.4, 2.5, 2.6, and 2.7**.

Table 2.4 Composition of a typical PCR reaction.

Components	Standard PCR	Control
2x VeriFi mix	25 μL	25 μL
Forward primer (10 μM)	1 μL	1 μL
Reverse primer (10 μM)	1 μL	1 μL
Template DNA (100 ng/μL)	1 μL	-
dH ₂ O	22 μL	23 μL
Total volume	50 μL	50 μL

Table 2.5 primers used in this study.

Primer Name	Primer Sequence (5'→3')	Description
P1-adeR-up-R	ATGCCTTCCGGTAAATTTAGC	2kb up reverse for <i>adeR</i> deletion
P2-adeR-up-F	GGCCCAATTCGCCCTATAGTGAGTCGCATCATACGCTAAATTATCCG	2Kb up forward for <i>adeR</i> deletion
P3-adeR-down-R	GGGTTTGCTCGGGTCGGTGGCATATGCTAGCTGTAA AAGATGATGC	2Kb down reverse for <i>adeR</i> deletion
p4-adeR-down-F	TATACTGAATATGTAGAGCTTTC	2Kb down forward for <i>adeR</i> deletion
P5-aacC4-F	CCGAGATCCGTTGATCTTCC	For amplify the cassette
P6-sacB-R	CAAACGCTTGAGTTGCGCCTC	For amplify the cassette
p7-adeR	CTGTAAAAGATGATGC	For clean deletion
p8-adeR	GCATCATCTTTTACAGATACGCTAAATTATCCG	For clean deletion
P9-adeR-up-F	GCCACAATTGCTGGAATAAGC	~200bp to check the deletion
P10-adeR-down-R	GAACCGTGGCCTAAAGCAG	~200bp to check the deletion
adeR_flag_up_F	ATCTGTTGAATGGTTGCC	For Chip seq
adeR_flag_up_R	CCGTCATGGTCTTTGTAGTCGGCATCATCTTTTACAG C	For Chip seq
adeR_flag_down_F	GGGTTTGCTCGGGTCGGTGGCATATGATAATATTTAAA AAATAGCTAGGGAATATTTTATG	For Chip seq
adeR_flag_down_R	TCTACCTCTGAAGTAACAG	For Chip seq
P1-adeS-up-R	GAAGATCGCGATAACCCAAG	2Kb down forward for <i>adeS</i> deletion
P2-adeS-up-F	GGCCCAATTCGCCCTATAGTGAGTCGCTTTTCATAAA ATATTCCCTAGC	2Kb down forward for <i>adeS</i> deletion
P3-adeS-down-R	GGGTTTGCTCGGGTCGGTGGCATATGGAAGAGATGG GGTAATTCGC	2Kb down forward for <i>adeS</i> deletion
P4-adeS-down-F	GTTCAATTGCCATGCTAGATG	2Kb down forward for <i>adeS</i> deletion
p7-adeS	GAAGAGATGGGGTAATTCGC	For clean deletion
p8-adeS	GCGAATTACCCCATCTCTTCCTTTTCATAAAATATTCC CTAGC	For clean deletion
P9-adeS-up-F	GGCACAGATGTGGAAATGGC	~200bp to check the deletion

P10-adeS-down-R	GACATCATACGCTATTACCCGG	~200bp to check the deletion
P1-baeR-up-F	CATTGACTGGTGGTTGAGGAC	2Kb down forward for <i>baeR</i> deletion
P2-baeR-up-R	GGCCCAATTCGCCCTATAGTGAGTCGAACATAATATG TTTCATGGGCC	2Kb down forward for <i>baeR</i> deletion
P3-baeR-down-F	GGGTTTGCTCGGGTCGGTGGCATATGATAACCACAA TGTTATCCACAG	2Kb down forward for <i>baeR</i> deletion
P4-baeR-down-R	GAGGGTTACCACAACATATCACC	2Kb down forward for <i>baeR</i> deletion
p7-baeR	ATAACCACAATGTTATCCACAG	For clean deletion
p8-baeR	CTGTGGATAACATTGTGGTTATAACATAATATGTTTCA TGGGCC	For clean deletion
P9-baeR-up-F	GTATTGTGGCATATCGGGTTCC	~200bp to check the deletion
P10-baeR-down-R	CGATCATTCTCCATCTGAACCAG	~200bp to check the deletion
P1-baeR-Flag	GGTGAAAGATTCATATTCATAC	For Chip seq
P2-baeR-Flag	CCGTCATGGTCTTTGTAGTCTTCTTCTGGATATTCGAA GCG	For Chip seq
p1-baeS-up-F	TAAGGGCGCTTTGTATTGTG	2Kb down forward for <i>baeS</i> deletion
p2-baeS-up-R	GGCCCAATTCGCCCTATAGTGAGTCGGCACTCTCTCA TTTTTACTCTA	2Kb down forward for <i>baeS</i> deletion
p3-baeS-down-F	GGGTTTGCTCGGGTCGGTGGCATATGCTGACCTTTA AAAAGCAGAG	2Kb down forward for <i>baeS</i> deletion
p4-baeS-down-R	TATCTTACGTAACCATATGG	2Kb down forward for <i>baeS</i> deletion
p7_baeS	CTGACCTTTAAAAAGCAGAG	For clean deletion
p8_baeS	CTCTGCTTTTTAAAGGTCAGGCACTCTCTCATTTTTAC TCTA	For clean deletion
P1-gacS-up-F	GAGTGCCTGTTCAACATCTG	2Kb down forward for <i>gacS</i> deletion
P2-gacS-up-R	GGCCCAATTCGCCCTATAGTGAGTCGCTACATCAGAT TGATCTCTCTG	2Kb down forward for <i>gacS</i> deletion

P3-gacS-down-F	GGGTTTGCTCGGGTCGGTGGCATATGCATCAAATTTT AGTCATACCAG	2Kb down forward for <i>gacS</i> deletion
P4-gacS-down-R	GCAATAGGAGTATTACGATC	2Kb down forward for <i>gacS</i> deletion
p7_gacS	CATCAAATTTTAGTCATACCAG	For clean deletion
p8_gacS	CTGGTATGACTAAAATTTGATGCTACATCAGATTGATC TCTCTG	For clean deletion
P9-gacS-up-F	GCACACCTATTCGAGCACG	~200bp to check the deletion
p10-gacS-down-R	GCGAAATCGTGAGAATTAGACACG	~200bp to check the deletion
P1-gacA-up-F	CGCAAGCCATGATGTATGG	2Kb down forward for <i>gacA</i> deletion
P2-gacA-up-R	GGCCCAATTCGCCCTATAGTGAGTCGACTGTAATCAA GAAGACCTCCTTTC	2Kb down forward for <i>gacA</i> deletion
P3-gacA-down-F	GGGTTTGCTCGGGTCGGTGGCATATGCGTTTGATC AAGCCATAACC	2Kb down forward for <i>gacA</i> deletion
P4-gacA-down-R	GGTTACTCAGCCGATGAACC	2Kb down forward for <i>gacA</i> deletion
p7-gacA	CGGTTTGATCAAGCCATAACC	For clean deletion
p8-gacA	GGTTATGGCTTGATCAAACCGACTGTAATCAAGAAGA CCTCCTTTC	For clean deletion
p9-gacA-up-F	GAAGGCAACACCCCTCTC	~200bp to check the deletion
P10-gacA-down-R	GAGGTCCATAACGTGAATACGG	~200bp to check the deletion
P1-gacA-Flag-F	TGACTAGCATCCGCTGCAGACC	For Chip seq
P2-gacA-Flag-R	CCGTCATGGTCTTTGTAGTCTGGCTTGATCAAACCGT AACG	For Chip seq

All PCR reactions were conducted in 0.2 ml PCR tubes and subsequently positioned in the SimpliAmp™ Thermal Cycler, following the cycles detailed in **Table 2.6**. The annealing temperature and extension duration are subject to variation based on the primer sequences and the sizes of the amplicon fragments.

Table 2.6 PCR cycling conditions.

Step	Temperature	Time	Cycles
Denaturation	95°C	2 min	1
Denaturation	95°C	15 s	35
Annealing	Variable	30 s	
Extension	72°C	Variable	
Extension	72°C	2 min	1

For colony PCR, cells of a single colony were added to the reaction mix and the initial denaturation step was extended (**Table 2.7**). The cycling conditions and primers utilized for colony PCR are detailed in **Table 2.7**.

Table 2.7 Colony PCR cycling conditions.

Step	Temperature	Time	Cycles
Denaturation	95°C	10 min	1
Denaturation	95°C	15 s	35
Annealing	Variable	30 s	
Extension	72°C	Variable	
Extension	72°C	2 min	1

4. Agarose gel electrophoresis

Agarose gel electrophoresis was employed for the separation of DNA and RNA molecules based on size. DNA samples were combined with a DNA loading dye consisting of 40% (v/v) glycerol, 60 mM EDTA, 10 mM Tris-HCl (pH 7.6), 0.25% (w/v) bromophenol blue, 0.25% (w/v) xylene cyanol FF, and 0.25% (w/v) orange G. These samples were routinely subjected to electrophoresis in a 1-2.5% (w/v) agarose gel using 1× Tris Acetate Ethylenediaminetetraacetic acid (TAE) buffer at a voltage of 100 V. For RNA samples, an RNA loading dye was prepared, containing 0.025% (w/v) xylene cyanol FF, 0.025% (w/v) bromophenol blue, 18 mM EDTA (pH 8.0), 0.025% (w/v) SDS, and 95% (v/v) formamide. The RNA samples were heat denatured at 65°C for 5 min and subsequently separated by electrophoresis in a 2.5% (w/v) agarose gel in 1× Tris Borate EDTA (TBE) buffer

at 90 V. The gels were stained with SafeView Nucleic Acid Stain (NBS Biologicals) before visualization under ultraviolet light using the ImageQuant™ LAS 4000 (GE Healthcare Life Sciences) or blue light using the safeVIEW-MINI2 Blue Light Transilluminator (Cleaver Scientific). The molecular size of the DNA fragments that were electrophoresed was estimated by comparison with HyperLadder™ I (Bioline) or O'GeneRuler™ 1 kb DNA Ladder (Thermo Scientific).

5. Purification of PCR products

PCR products, which were confirmed through agarose gel electrophoresis, were purified with PCR purification kits to eliminate excess primers and other PCR reagents. This process utilized the E.Z.N.A.® Cycle Pure Kit (Omega Bio-Tek). The samples were handled according to the manufacturer's guidelines (Omega Bio-Tek). The concentration of the purified PCR products was assessed using the Nanodrop™ (Thermo Scientific). DNA was stored at -20°C.

6. Natural transformation of *A. baumannii*

A natural transformation protocol previously described by Godeux *et al.* was utilized to introduce plasmid DNA or chimeric PCR products to delete genes into *A. baumannii* AB5075 (Godeux *et al.*, 2020). Initially, a single colony of the *A. baumannii* AB5075 strain was used to inoculate 2 ml of L-broth in a test tube, which was then incubated at 37°C until it reached an OD600 of approximately 1.0. This culture was subsequently diluted to an OD600 of 0.01 in PBS. An aliquot of 5 µL from this dilution was combined with 5 µL of plasmid DNA (around 10 ng) or purified chimeric PCR products when creating a deletion mutant. A volume of 2.5 µL from this mixture was then used to inoculate 1 ml of *A. baumannii* transformation medium, composed of 2% Euromedex agarose D3, 5 g/L tryptone, and 2.5 g/L NaCl, and incubated overnight at 37°C. The next day, the *A. baumannii* cells were resuspended in 100 µL of PBS and plated on L-agar supplemented with the necessary antibiotic. For the generation of clean deletion mutants, the transformation medium was incubated at 37°C for 6 h prior

to resuspension and plating on L-agar plates containing 20% (w/v) sucrose, which were then incubated overnight at 30°C.

7. Creating deletion mutants in *A. baumannii* AB5075

Deletion mutants were created using the gene replacement method outlined by Godeux, a PCR-based genome editing approach suitable for naturally transformable *A. baumannii* AB5075 (Godeux *et al.*, 2020). This involved amplifying ~2000 bp regions both upstream and downstream of the gene targeted for deletion, followed by confirming the correct DNA size via agarose gel electrophoresis. After verifying the sizes of the DNA fragments, purification was carried out with a PCR clean-up kit to prepare for the overlap-extension PCR, which aimed to construct the complete deletion cassette (**Figure 2.1**). This overlap-extension PCR employed the plasmid pMHL-2, which contains a counter-selectable cassette with the *sacB* gene that induces sucrose sensitivity, along with the *aacC4* gene that provides resistance to apramycin. The resulting chimeric product features the *sacB_aacC4* gene cassette flanked by two ~2000 bp homologous regions that enable the recombination of the chimeric PCR product into the genome of the recipient cell. Insertion mutants were identified by their resistance to apramycin and sensitivity to sucrose. A precise deletion was accomplished through a two-step assembly PCR of products containing the homologous regions adjacent to the deleted gene, leading to cells that displayed resistance to sucrose and sensitivity to apramycin.

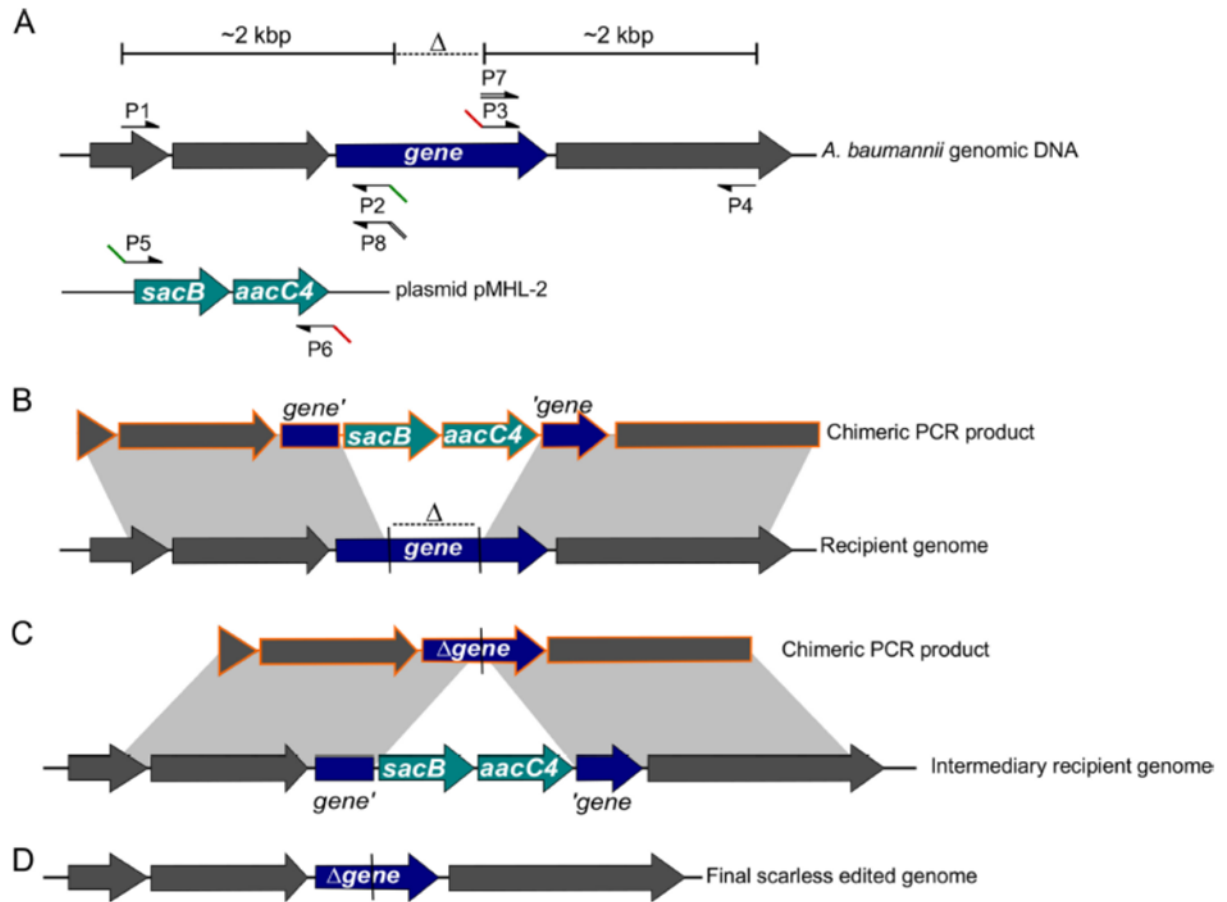


Figure 2.1 PCR-based genome editing of transformable *A. baumannii*. Taken from (Godeux *et al.*, 2020a). Schematic representations of steps for gene inactivation (dark blue gene) using natural transformation. (A) Annealing sites for primers of PCR assemblies on their respective templates: either *A. baumannii* genomic DNA for amplifications of ~2000 bp upstream and downstream of the deleted region (Δ) or the plasmid pMHL-2 that bears the counterselectable cassette (light blue) with a *sacB* gene conferring sucrose sensitivity and the *aacC4* gene encoding resistance to apramycin. Note that primers P2, P3, and P7 share annealing sequences with primers P5, P6, and P8, respectively. (B) Chimeric PCR product (orange) obtained after two-step PCR assembly of products P1 _ P2 with P5 _ P6 and P3 _ P4. This chimeric product bears the *sacB_aacC4* cassette flanked by two ~2000 bp-long regions of homology with the recipient cell's genome (grey areas). These homologous regions allow the recombination of the chimeric PCR product into the recipient cell's genome, resulting, upon apramycin selection of the transformants, in the intermediary genotype represented in panel C. (C) Chimeric PCR product obtained after two-step assembly PCR of products P1 _ P8 with P7 _ P4 bearing the deleted gene flanked by homologous regions (gray areas), allowing

recombination and replacement of the counter selectable cassette in the intermediary recipient genome. (D) The transformants are selected based on their sucrose resistance resulting in the final scarless edited genome.

8. Sanger sequencing

PCR amplicons spanning the deleted region of $\Delta adeR$, $\Delta adeS$, $\Delta baeR$, $\Delta baeS$, $\Delta gacA$, and $\Delta gacS$ mutants and the complementation of these mutants were sent as templates for Sanger sequencing with appropriate primers to Eurofins Genomics. The results were analysed using a local alignment program.

2.3 Phenotypic analyses

1. The Antibiotic Disk Diffusion (Kirby-Bauer)

The Kirby-Bauer Disk Diffusion Method was employed to assess antibacterial susceptibility using the agar disk diffusion technique. Overnight cultures of *A. baumannii* AB5075 WT and the mutants were prepared, ensuring the turbidity matched the 0.5 McFarland standard on Muller Hinton Medium (MHA). A sterile cotton swab was immersed in the adjusted bacterial suspension, and the swab was used to inoculate a Muller Hinton agar (MH) plate by streaking it across the entire surface. Antibiotic discs were placed evenly on the agar, ensuring adequate spacing between them. Simultaneously, tests for the unknown sensitivity organism mutants and the control organism of known sensitivity (WT) were conducted under identical conditions on the same plate. The plates were incubated at 37°C for 16-18 hours, after which the zones of inhibition were carefully measured in millimetres (mm) using a ruler.

2. Broth microdilution assay (MIC determination)

The minimum inhibitory concentration (MIC) of antibiotics was established using the broth microdilution technique. Initially, 100 μ L of Mueller-Hinton broth (MHB) was added to each well of a 96-well microplate leaving out column 12. Subsequently, 200 μ L of the antibiotic solution at its highest concentration was introduced into the wells of column 12. The contents of these wells were mixed thoroughly by pipetting up and

down five times with a multichannel pipette. Then, 100 μ L was transferred to the next wells in column 11, and the mixing process was repeated, continuing this dilution process sequentially until reaching column 3. The final 100 μ L from column 3 was discarded, ensuring that each well from columns 12 to 3 contained 100 μ L of the final volume. Following this, all wells from columns 12 to 2 were inoculated with 5 μ L of an overnight culture of *A. baumannii*, which had been adjusted to a McFarland standard of 0.5. This culture was prepared by taking 50 μ L of the overnight culture and diluting it in 4.95 mL of Phosphate Buffered Saline (PBS), followed by thorough vortexing. The diluted culture was then transferred to a reservoir, and using a multichannel pipette, 5 μ L was inoculated into each well of the microplate, excluding column 1, which served as a negative control. The microplate was incubated at 37°C for 18 hours, after which the results were recorded.

3. Colourimetric method for the determination of metabolisable sources of *A. baumannii*.

To identify the metabolisable substrates in *A. baumannii* AB5075 through a colorimetric approach (Kröger and Fuchs, 2009), overnight cultures of the test strains are established in 4–5 mL of L-broth and incubated at 37°C with shaking at 220 rpm for a duration of 16 to 17 h. Following this, the cultures are centrifuged in 2 mL tubes at $10,000 \times g$ for 2 min at room temperature, utilizing 1.6 mL aliquots, and the supernatant is discarded. This procedure is repeated with the remaining culture. The resultant pellet is washed twice by resuspending in 1 mL of PBS and subjected to another centrifugation at $10,000 \times g$ for 2 min at room temperature. The optical density at 600 nm (OD_{600}) is then measured, followed by an additional centrifugation step. The pellet is gently resuspended in 1 mL of IF-MM solution, taking care to avoid vortexing to prevent the formation of air bubbles. The bacterial suspension is diluted to $OD_{600} = 0.3$ and 0.2 in 4 mL of IF-MM, respectively. For the assay, 90 μ L of the bacterial suspension is added to each well of a microplate, followed by 10 μ L of the test substrate per well, ensuring that no bubbles are present. The initial OD_{600} ($t=0$) is recorded using a plate reader (Synergy HTX). The plates are then incubated at 37°C in a humid chamber (such as a box lined with a moist paper towel) for a period of 24

to 48 hours, after which the OD₆₀₀ is measured again at 24 hours (t=24h) and 48 hours (t=48h).

2.4 Transcriptomic analysis

1. RNA Isolation

Total RNA was extracted using TRIzol from cells cultured aerobically at specific growth stages, namely mid-exponential phase (MEP) with an OD₆₀₀ of 0.3 and late stationary phase (LSP) after 16 h of incubation in Lennox (L)-broth. Cells equivalent to 4 OD₆₀₀ per ml ($\sim 4 \times 10^9$ cells) of *ΔbaeR* cells were collected, combined with 2/5 volume of an ice-cold stop solution [19% ethanol, 1% acidic phenol (pH 4.3)], and kept on ice for 30 minutes to inhibit RNA degradation (Tedin and Bläsi, 1996). The cells were then centrifuged for 10 min at $3,220 \times g$ and 4°C. Most of the supernatant was removed, and the cell pellet was resuspended in the remaining liquid before being transferred to a 2 mL Eppendorf tube. The cell suspension underwent centrifugation for 1 min at $20,000 \times g$ and 4°C, after which the supernatant was discarded. The cell pellet was resuspended in 1 mL of TRIzol and placed in a 2 mL heavy phase-lock tube, followed by the addition of 400 μL chloroform, which was mixed immediately for 10 s. After a 2-min incubation at room temperature, the mixture was centrifuged for 15 min at $20,000 \times g$. The upper phase containing the RNA (approximately 500 μL) was transferred to a 1.5 mL Eppendorf tube, and 450 μL isopropanol was added. The mixture was inverted to mix and incubated at room temperature for 30 min. The RNA was pelleted by centrifugation for 30 min at $20,000 \times g$, and the supernatant was discarded. The pellet was washed with 350 μL of 70% ethanol and centrifuged again for 10 min at $20,000 \times g$. After discarding the supernatant, the pellet was air-dried and resuspended in RNase-free water by shaking at 900 rpm for 5 min in a heat block set to 65°C, then stored at -80°C until needed. RNA quality was assessed using an Agilent Bioanalyzer 2100 or agarose gel electrophoresis, and RNA concentration was determined using a NanoDrop™.

2. Bioinformatic analysis of RNA seq

Quality control was performed using FastQC version 0.11.9 on the raw data files. The bowtie2 mapper version 2.4.2 was employed with the 'very-sensitive-local' preset to align the short reads to the *A. baumannii* reference genome. Reads that had multiple hits were eliminated by discarding results that included the 'XS:i' tag (alignment score of the next-best hit). The remaining reads were compiled using featureCounts version 2.0.3. The parameters were configured to operate strand-specifically, exclude low-quality mappings, include reads that overlap with more than one feature, and assign fractional counting based on the largest overlap. The resulting gene count matrix was analyzed using DESeq2 version 1.48.1 from the Bioconductor package to identify differentially expressed genes. BigWig tracks were created with bamCoverage version 3.5.5 from the deepTools package. Library preparation and sequencing the obtained reads were analysed with the help of Dr. Karsten Hokamp (Smurfit Institute, Department of Genetics, TCD) and Dr. Anna Ershova (Moyne Institute of Preventive Medicine, Department of Microbiology, TCD).

3. Differential RNA Sequencing

Differential RNA Sequencing (dRNA-seq) was performed by Vertis Biotechnology AG located in Freising, Germany, which involved the preparation of RNA libraries and subsequent sequencing. This methodology facilitates the accurate identification of transcriptional start sites (TSS) by distinguishing between primary and processed transcripts, thus offering a more detailed understanding of the transcriptional landscape in *Acinetobacter baumannii* AB5075.

4. RNA Treatments

Initially, total RNA underwent treatment with Turbo DNase (Ambion) to eliminate any remaining DNA contamination. Subsequently, the RNA was fragmented through ultrasound sonication, applying four 30-second pulses at a temperature of 4°C, which resulted in smaller RNA fragments appropriate for

subsequent processing. The fragmented RNA was then divided into two portions to facilitate the development of two separate libraries: the Terminator Exonuclease (TEX) library and the whole transcriptome library. Each library employed distinct enzymatic treatments aimed at enriching primary transcripts and analyzing the complete RNA population, respectively.

5. Terminator Exonuclease (TEX) Library

In one portion of the RNA sample, fragments possessing 5' monophosphate ends underwent initial treatment with T4 Polynucleotide Kinase (New England Biolabs). This procedure was essential for preparing the RNA fragments for subsequent exonuclease digestion by ensuring that any unphosphorylated RNA ends were modified to the correct phosphorylation state. Following this, the fragments were exposed to degradation by Terminator Exonuclease (Epicentre), which specifically targets and degrades RNA fragments with 5' monophosphate ends. This process effectively enriches the sample for RNA molecules characterized by 5' triphosphate (5'PPP) ends, which are indicative of primary transcripts. In the final step, the 5'PPP ends were converted to 5' monophosphate through the action of RNA 5' Polyphosphatase (Epicentre), thereby preparing the RNA for subsequent adapter ligation and sequencing.

6. Whole Transcriptome Library

In the latter portion of the fragmented RNA processing, Antarctic Phosphatase (New England Biolabs) was employed to dephosphorylate the RNA, effectively eliminating any pre-existing 5' phosphate groups. This step was crucial in mitigating potential interference with subsequent enzymatic reactions. Following this, T4 Polynucleotide Kinase was utilized for re-phosphorylation, which facilitated the establishment of consistent 5' phosphate ends throughout the RNA sample. This comprehensive treatment enabled the sequencing of both primary and processed RNA fragments, thereby encompassing the entire transcriptome.

7. cDNA Synthesis and Library Construction

In the preparation of both libraries, oligonucleotide adapters were attached to the 5' and 3' termini of the RNA fragments. The synthesis of first-strand complementary DNA (cDNA) was conducted utilizing Moloney Murine Leukemia Virus (M-MLV) reverse transcriptase, with the 3' adapter functioning as the primer. The resultant cDNAs underwent amplification via polymerase chain reaction (PCR) employing a high-fidelity DNA polymerase to guarantee precise replication of the RNA sequences. Subsequent to amplification, the cDNA libraries were purified utilizing the Agencourt AMPure XP system (Beckman Coulter Genomics) to eliminate contaminants and fragments of inappropriate size. Ultimately, the quality and size distribution of the cDNA were evaluated through capillary electrophoresis.

8. Bioinformatic analysis of dRNA-seq data and determination of transcriptional start sites

The obtained sequence reads from the MEP and LSP conditions of dRNA-seq were analysed with READemption using default settings which includes generation of normalised coverage tracks for downstream identification of transcriptional start sites (Fo, 2014). The location and classification of transcriptional start sites was determined using TSSpredator with default settings (Dugar *et al.*, 2013). This analysis was carried out by Dr Carsten Kröger.

9. Identification of –10 and –35 sigma factor motifs

DNA sequences upstream of all transcription start sites were extracted in two blocks of nucleotides: between position –3 to –18 (–10 block) and between –16 to –50 (–35 block). Each block was searched with the unbiased motif finding program MEME 5.5.8 (Bailey *et al.*, 2015). Each sequence block was searched with the following settings: one occurrence per sequence with a width of 6–12

bp (–10 motif) or 4–10 bp (–35 motif). This analysis was carried out by Dr Carsten Kröger.

2.5 Analysis of proteins

1. Preparation of whole cell lysates

Whole cell lysates were prepared from *A. baumannii* AB5075 by cultivating 25 ml cultures at 37°C until the desired growth phase was reached. Typically, *A. baumannii* cells were grown to mid exponential phase (MEP, OD600 = 0.3) and late stationary phase (LSP, approximately 16 hours of growth) before lysate preparation. To obtain whole cell lysates, cells corresponding to an OD600 of 0.1 were harvested by centrifugation in 1.5 ml Eppendorf tubes at 2,500 x g for 5 min at 4°C. The resulting pellets were washed twice with PBS and centrifuged again under the same conditions. The pellets were then resuspended in 1× Laemmli buffer and heated at 95°C for 10 min. Following this, the tubes were centrifuged at maximum speed at 4°C for 1 min. The prepared whole cell lysates were either used immediately for western blotting or stored at -20°C for future applications.

2. Protein detection by Western blotting.

Western blotting involved the separation of whole lysates (0.03 OD600 units per lane) using a discontinuous SDS-polyacrylamide gel. This gel consisted of a stacking layer (5% polyacrylamide) and a separating layer (15% polyacrylamide). The whole cell lysates were electrophoresed alongside the EZ-Run™ Prestained Rec Protein Ladder (Fisher Scientific) for comparison purposes. The gels were initially run at 80 V until the dye front entered the separating layer, after which they were run at 120 V until the dye front reached the bottom of the separating layer. Subsequently, the gels were washed with deionised water and equilibrated in 1× transfer buffer (25 mM Tris, 0.19 M glycine) for 10 minutes, along with 0.45 µm Amersham™ Protran® nitrocellulose membranes (Merck) and 3 mm filter paper (Whatman). These components were assembled into 'sandwiches' within gel holder cassettes, and proteins were blotted (300 mA, 90 min)

onto the nitrocellulose membranes using a Mini Trans-Blot Electrophoretic Transfer Cell (Bio-Rad) with an ice pack. After blotting, the uniform transfer of proteins onto the membranes was routinely evaluated by staining the membranes with Ponceau S (Sigma) until the bands became visible.

Subsequently, the membranes were rinsed with deionised water to eliminate Ponceau S staining, followed by a two-hour blocking period in a blocking buffer composed of 5% (w/v) skimmed milk powder, 0.9% (w/v) NaCl, and 10 mM Tris/HCl at pH 7.5 to inhibit non-specific antibody binding. The membranes underwent two washes of ten minutes each in an antibody buffer containing 0.5% (w/v) skimmed milk powder, 0.9% (w/v) NaCl, 0.1% (v/v) Tween-20, and 10 mM Tris/HCl at pH 7.5. They were then incubated overnight at 4°C in antibody buffer with primary antibodies (anti-FLAG from Sigma, diluted 1:10,000; anti-DnaK from *E. coli*, Enzo, diluted 1:5,000). Following this, the membranes were washed four times for ten minutes each in PBST (PBS with 0.05% (v/v) Tween-20). Afterward, they were treated for 90 minutes with an antibody wash containing the secondary antibody (anti-Mouse IgG Fc, horseradish-peroxidase from Thermo Fisher Scientific, diluted 1:10,000). The membranes were then washed three times for ten minutes each in PBST and subsequently covered with ECL chemiluminescent HRP substrate from Pierce. Chemiluminescent imaging was conducted using an ImageQuant LAS4000 imager from GE Healthcare.

Table 2.8 Buffers and solutions for western blotting

Name	Reagent	Concentration
RNA loading dye	Xylene cyanol FF	0.025% (w/v)
	Bromophenol blue	0.025% (w/v)
	EDTA pH 8.0	18 mM
	SDS 0.025% (w/v)	0.025% (w/v)
	Formamide	95% (v/v)
20 SSC	NaCl	3 M
	Sodium Citrate	0.3 M
Stringency wash I	SSC	2x
	SDS	0.1% (w/v)
	H ₂ O	
Stringency wash II	SSC	0.5x

	SDS	0.1% (w/v)
	H ₂ O	
Maleic acid buffer pH 7.5	Maleic acid	0.1 M
	NaCl	0.15 M
Washing buffer	Maleic acid buffer	1x
	Tween-20	0.3% (v/v)
1 Blocking buffer	Casein Blocking Solution (Roche)	1x
	Maleic acid buffer	1x
Detection buffer pH 9.5	Tris-HCl	0.1 M
	NaCl	0.1 M

3. Chromatin Immunoprecipitation for ChIP-seq

On Day -1, 4 mL of overnight cultures of the selected strains were cultivated in LB medium at 37°C with shaking at 200 rpm. On Day 1, these cultures were diluted 1:1000 into 25 mL of fresh LB and allowed to grow until the desired optical density at 600 nm (OD₆₀₀) was reached. The cells were then harvested by centrifugation at 4,000 rpm for 10 minutes at room temperature (RT), resuspended in 50 mL of pre-warmed 1×PBS, and transferred to a 250 mL conical flask containing a sterile magnetic stirrer. Formaldehyde (1355 µL of 37%) was added dropwise while stirring to achieve a final concentration of 1% for crosslinking, which was allowed to proceed for 10 min. The crosslinking reaction was quenched by the addition of 3.425 mL of ice-cold 2 M glycine while stirring for an additional 5 min. The cells were collected again by centrifugation at 4,000 rpm for 10 min at 4°C, and the resulting pellet was resuspended in 600 µL of lysis buffer and incubated on ice for 10 min. Following this, 1.4 mL of IP dilution buffer was added, and the sample was transferred to a sonication tube. Sonication was conducted at a 10-micron amplitude in 30-second bursts (12 cycles), with 1-min ice incubation between each burst. The sonicated chromatin was then centrifuged at 13,000 rpm for 10 min at 4°C, and the supernatant was transferred to a 15 mL Falcon tube. A 5 µL aliquot was set aside for gel electrophoresis to verify successful chromatin shearing, which typically appears as a smear centered around 500 bp. To the remaining chromatin, 1 mL of IP dilution buffer was added, mixed gently, and stored at –80°C.

On the second day, the thawed chromatin underwent pre-clearing by the addition of 100 μ L of normal rabbit IgG, followed by incubation on a rotating wheel for one h at 4°C. Subsequently, 100 μ L of protein G agarose was incorporated and incubated for three h under identical conditions. After centrifugation at 4,000 rpm for two min at 4°C to pellet the beads, the supernatant was utilized to initiate the ChIP reactions. Three immunoprecipitations (IPs) were established in 2 mL tubes: 200 μ L of chromatin preserved as input (–20°C), 1350 μ L of chromatin combined with 10 μ L of normal mouse IgG as a mock IP, and 1350 μ L of chromatin with 5–10 μ g of the experimental antibody (for instance, 10 μ g of anti-c-Myc for Fis::8xMyc). The tubes were sealed with parafilm and incubated overnight at 4°C on a rotating wheel.

On the third day, immunoprecipitation samples were subjected to centrifugation at 13,000 rpm for a duration of 5 min at a temperature of 4°C, after which the supernatants were carefully transferred to new tubes. Each sample was treated with 100 μ L of protein G agarose and rotated for 3 hours at 4°C. Subsequently, the beads were pelleted at 7,500 rpm for 2 min at 4°C, briefly placed on ice, and washed four times with 750 μ L of CSH IP wash buffer, followed by two washes with TE buffer at pH 8.0. For the elution process, 225 μ L of elution buffer was added to each sample, which was then rotated for 1 min, centrifuged, and this step was repeated; the eluates were combined. Input samples were thawed and enhanced with 250 μ L of H₂O and NaCl to achieve a final concentration of 0.3 M. All samples were incubated at 65°C for 6 h, followed by treatment with 9 μ L of 10 mg/mL proteinase K and an overnight incubation at 45°C (**Figure 2.2**).

On the fourth day, PCR purify samples with Qiagen PCR purification kit, Elute in water.

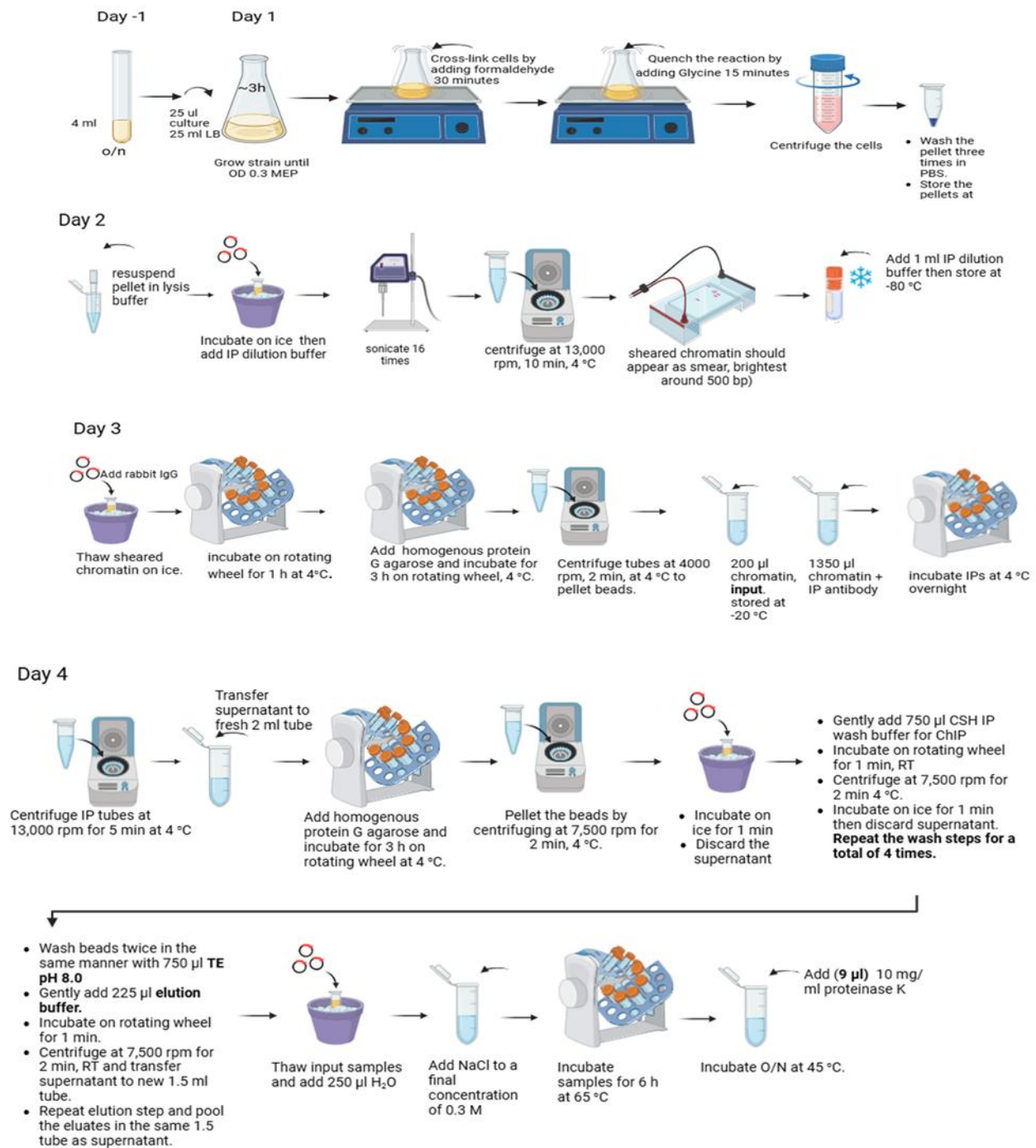


Figure 2.2 Overview of Chromatin Immunoprecipitation (ChIP) Workflow for ChIP-seq in *A. baumannii*. A step-by-step schematic representation of the ChIP-seq protocol used for identifying DNA-protein interactions in *A. baumannii*.

Chapter 3

Transcriptomic analysis of two component system mutants in *Acinetobacter baumannii* AB5075

3.1 Introduction

Acinetobacter baumannii is a hospital-acquired pathogen that is becoming increasingly concerning on a global scale due to its resistance to multiple drugs and its ability to endure in adverse environments (Howard *et al.*, 2012; Kyriakidis *et al.*, 2021). Among the various strategies this bacterium utilizes to adapt and survive, Two-Component Systems (TCSs) are essential for detecting changes in the environment and adjusting gene expression accordingly. These signal transduction systems generally comprise a sensor kinase located in the membrane and a cytoplasmic response regulator that, when activated, influence the transcription of target genes related to stress responses, antibiotic resistance, virulence, and metabolic adaptation (Bhagirath *et al.*, 2019; Song *et al.*, 2022). In the *A. baumannii* strain AB5075, multiple two-component systems (TCSs) have been identified as playing a role in the regulation of essential adaptive mechanisms. Specifically, the AdeRS, BaeSR, and GacSA systems are recognized or anticipated to participate in the modulation of efflux pump expression, responses to envelope stress, and overarching regulatory networks. Nevertheless, the comprehensive transcriptional effects of these TCSs are still not fully elucidated (Lin *et al.*, 2015; Richmond *et al.*, 2016b).

To explore the regulatory functions of these systems, we conducted RNA-sequencing (RNA-seq) analysis on single-deletion mutants of *adeR*, *adeS*, *baeR*, *baeS*, *gacS*, and *gacA*, comparing them with the wild-type AB5075 under specific *in vitro* conditions. This methodology facilitates a thorough evaluation of gene expression alterations that arise from the disruption of individual TCS response regulators.

The objective of this chapter is to:

1. Identify genes that are differentially expressed (DEGs) in the mutants compared to the wild-type strain during exponential growth and in stationary phase.

2. Infer possible regulatory pathways and target genes that are affected by each TCS.
3. Offer transcriptomic insights into the molecular mechanisms that support TCS-mediated regulation in *A. baumannii* and whether there is cross-talk between systems under investigation.

3.2 Selection of growth conditions

To determine the global gene expression patterns of *A. baumannii*, total RNA was extracted from two distinct environmental conditions (biological replicates n=3). The total RNA was obtained from varying optical densities in L-broth, encompassing growth stages from the mid exponential phase to the late stationary phase: OD600 0.3 (Mid Exponential Phase, MEP) and after 16 hours of growth (Late Stationary Phase, LSP).

3.3 Quality control of RNA and RNA-seq

To obtain high-quality RNA for RNA sequencing (RNA-seq), we assessed the integrity of the RNA using the Agilent Bioanalyzer. **(Figure 3.1)** illustrates examples of the $\Delta baeS$ mutant isolated from the MEP condition. The presence of sharp peaks at higher molecular weights corresponds to the 16S and 23S rRNA, while the absence of peaks at lower molecular weights indicates that the RNA is highly intact. RNA from three biological replicates, selected based on their quality, was subjected to RNA-seq across the two environmental conditions.

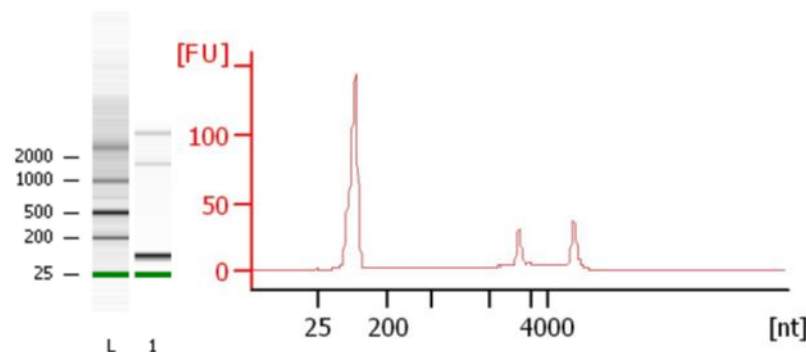


Figure 3.1 Analysis of RNA integrity utilizing the Agilent Bioanalyzer. Total RNA obtained from *Acinetobacter baumannii* AB5075 $\Delta baeS$ was evaluated with the Agilent 2100 Bioanalyzer. The electropherogram (on the right) and the associated gel-like image (on the left) reveal three prominent peaks that correspond to tRNA/small RNA, 16S rRNA, and 23S rRNA. The distinct peaks for 16S and 23S rRNA, along with minimal degradation of RNA, suggest that the RNA is of high quality and intact, making it suitable for subsequent RNA-seq analysis.

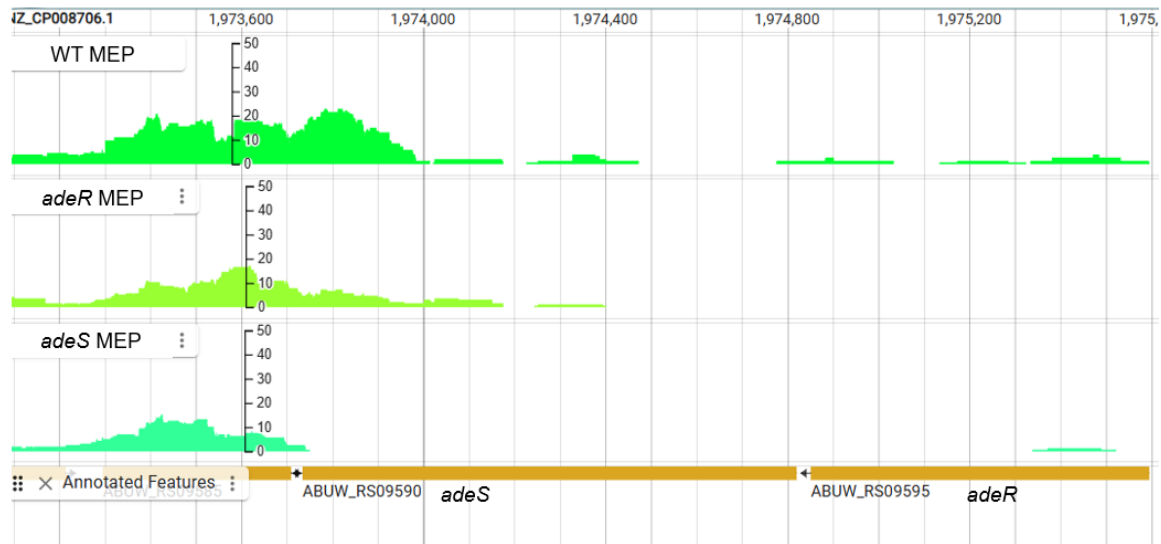
3.4 RNA-seq

RNA was extracted from samples and subsequently analyzed through RNA sequencing at Azenta Life Sciences. Following DNase treatment, ribosomal RNA was removed, and the processes of library preparation and sequencing were conducted at Azenta Life Sciences. The resulting reads were evaluated with the assistance of Dr. Karsten Hokamp from the Smurfit Institute, Department of Genetics at TCD, and Dr. Anna Ershova from the Moyne Institute of Preventive Medicine, Department of Microbiology at TCD. Each sample yielded between thirteen and twenty-four million reads, which is adequate for comprehensive coverage of the bacterial transcriptome.

3.5 Testing for Mutant Strains

All of the mutant strains used in this study were verified prior to RNA-seq in order to ensure the accuracy of the transcriptome analysis. PCR and whole genome sequencing were used to confirm that the target genes (*adeR*, *adeS*, *baeR*, *baeS*, *gacS*, and *gacA*) were successfully deleted. In each case, the wild-type strain showed the original gene, and the mutant showed the expected banding pattern. **Figures 3.2–3.5** show the exemplary verification results for each mutant from the subsequent RNA-seq data to assess whether deletions caused a polar effect on neighboring genes.

(A)



(B)

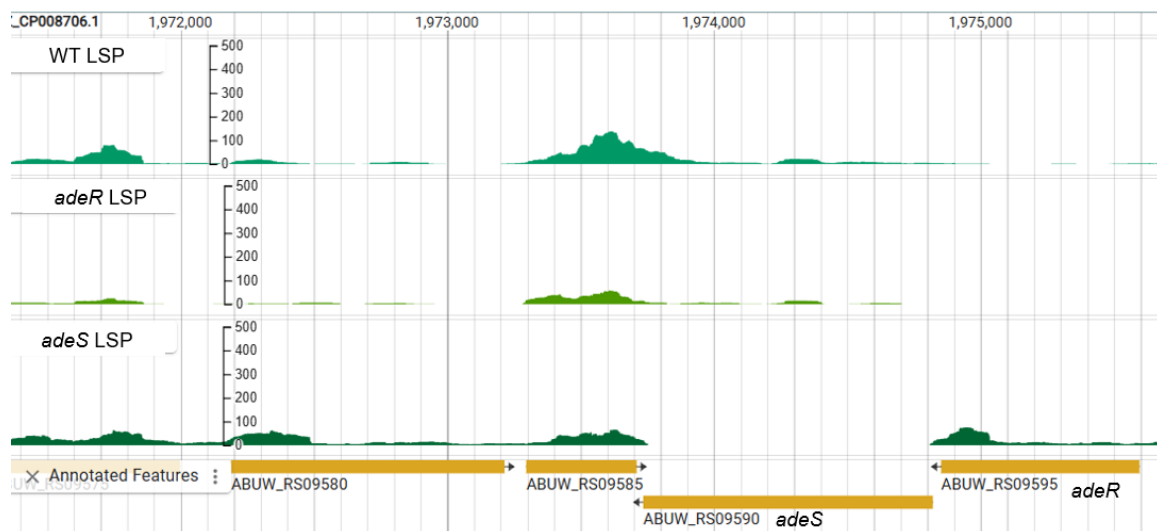
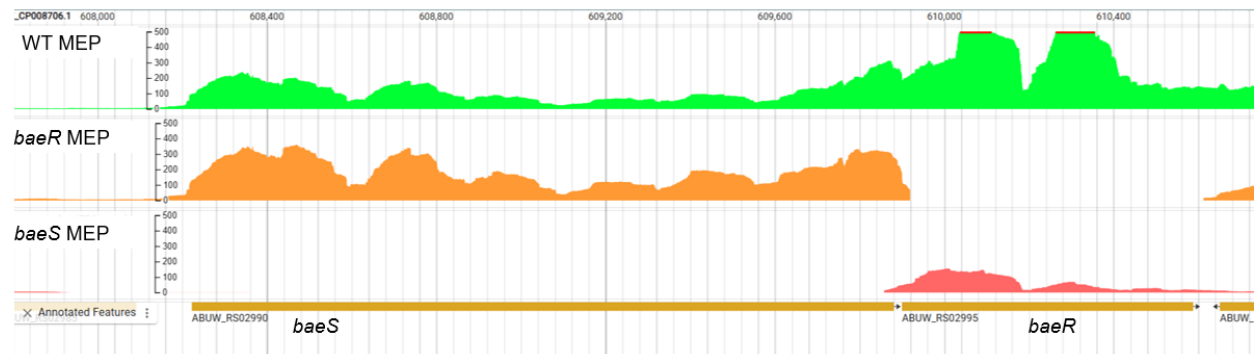


Figure 3.2 Visualization of RNA-seq read coverage for *adeR* and *adeS* in wild-type (WT) and deletion mutants as analyzed using JBrowse. RNA-seq reads were aligned to the reference genome of *A. baumannii* AB5075. The wild-type strain (WT) exhibits read coverage throughout the [*adeR* and *adeS*] locus in MEP (A) and LSP (B), which is indicative of intact transcription. Conversely, the corresponding deletion mutant's $\Delta adeR$ and $\Delta adeS$ demonstrate a complete absence of coverage at the target locus, thereby confirming the successful deletion of the gene. The neighboring genes maintain normal coverage, suggesting that the deletion was specific to the intended gene and did not impact adjacent regions.

(A)



(B)

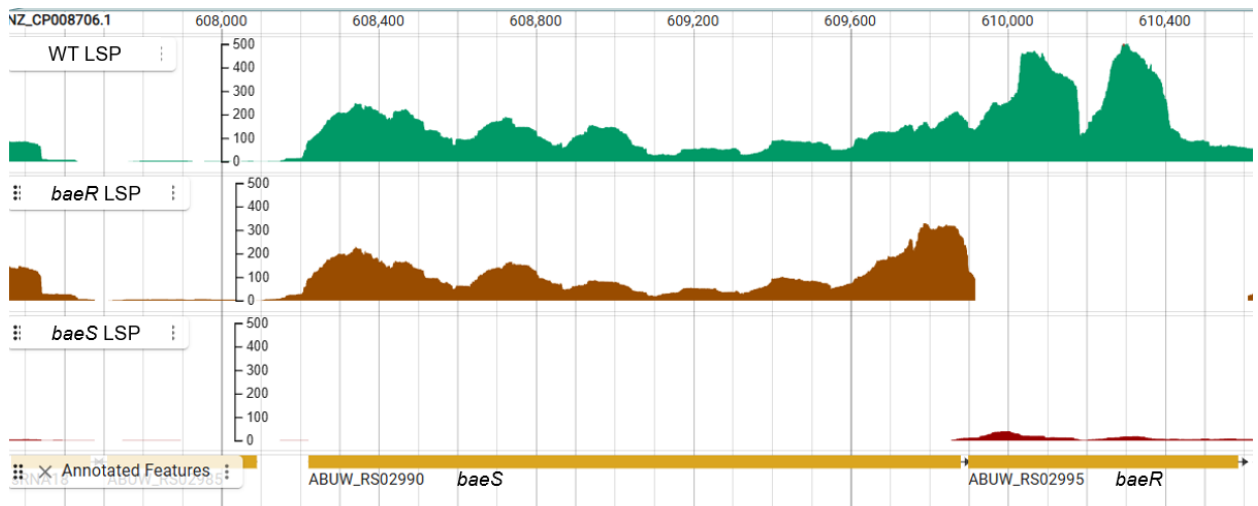
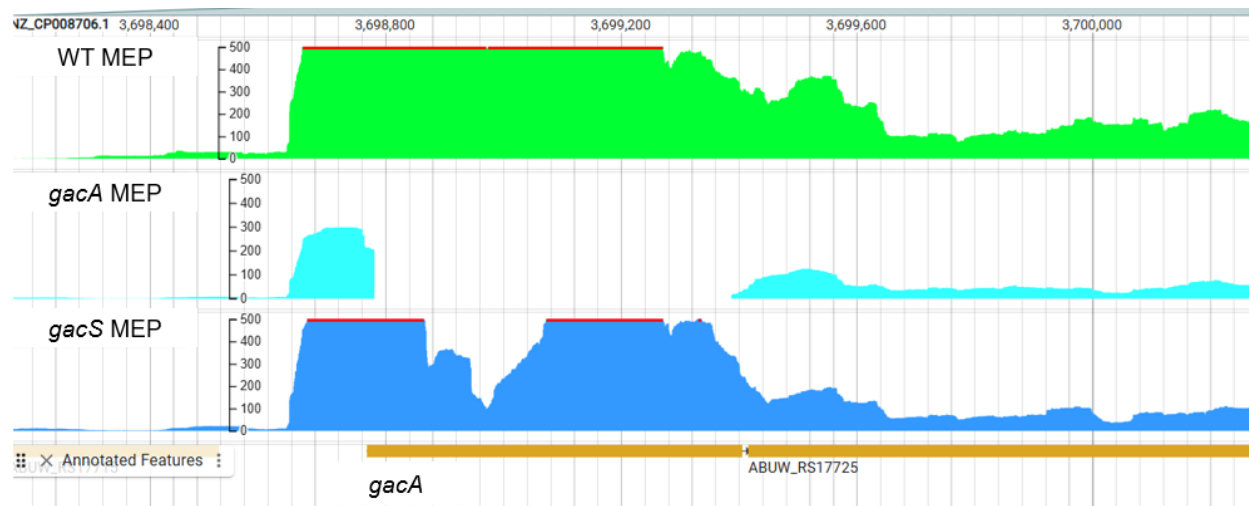


Figure 3.3 Visualization of RNA-seq read coverage for *baeR* and *baeS* in wild-type (WT) and deletion mutants as analyzed using JBrowse. RNA-seq reads were aligned to the reference genome of *A. baumannii* AB5075. The wild-type strain (WT) exhibits read coverage throughout the [*baeR* and *baeS*] locus in MEP **(A)** and LSP **(B)**, which is indicative of intact transcription. Conversely, the corresponding deletion mutant's Δ *baeR* and Δ *baeS* demonstrate a complete absence of coverage at the target locus, thereby confirming the successful deletion of the gene. The neighboring genes maintain normal coverage, except for expression of *baeR* in the Δ *baeS* strain, in which the expression is lower compared to WT.

(A)



(B)

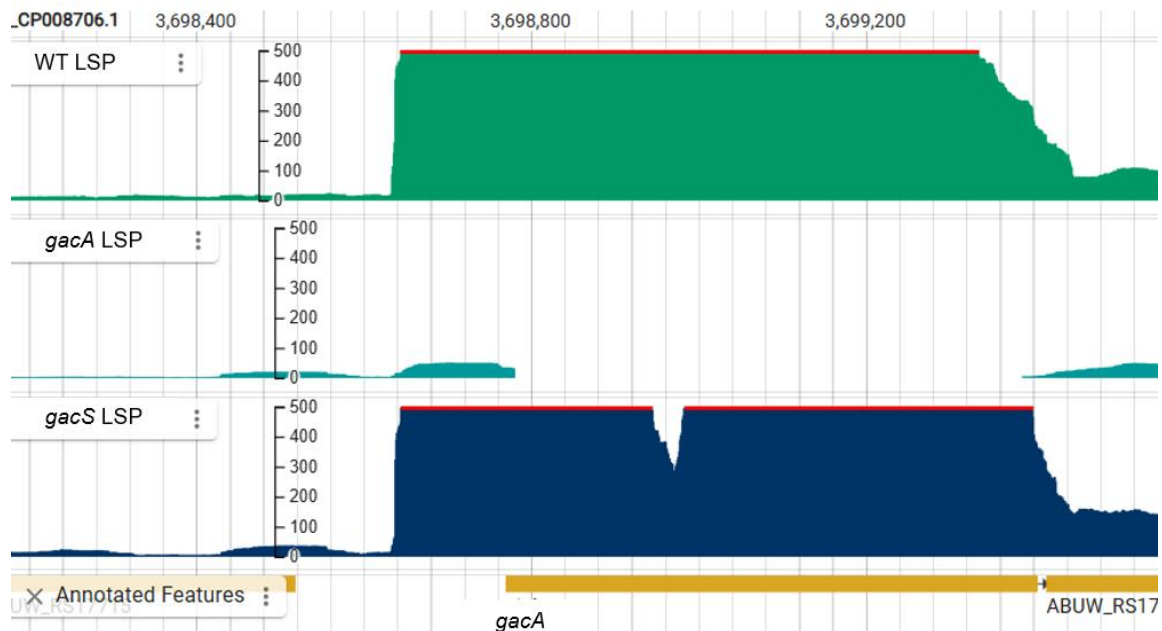
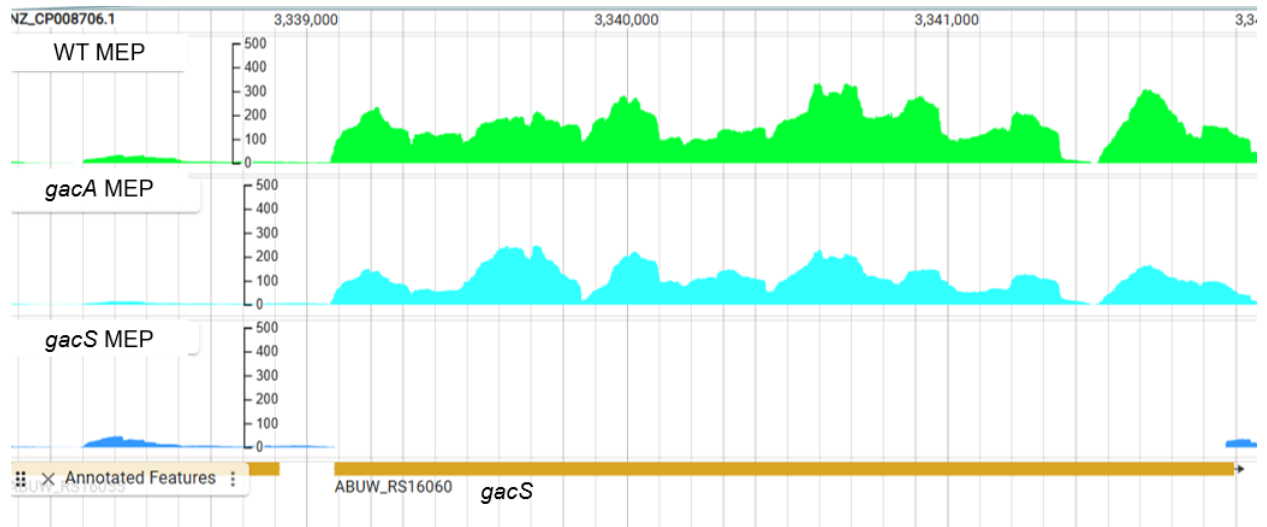


Figure 3.4 Visualization of RNA-seq read coverage for *gacA* in wild-type (WT) and deletion mutants as analyzed using JBrowse. RNA-seq reads were aligned to the reference genome of *A. baumannii* AB5075. The wild-type strain (WT) exhibits read coverage throughout the [*gacA*] locus in MEP (A) and LSP (B), which is indicative of intact transcription. Conversely, the corresponding deletion mutant's $\Delta gacA$ demonstrate a complete absence of coverage at the target locus, thereby confirming the successful deletion of the gene. The neighboring genes maintain normal coverage, suggesting that the deletion was specific to the intended gene and did not impact adjacent regions.

(A)



(B)

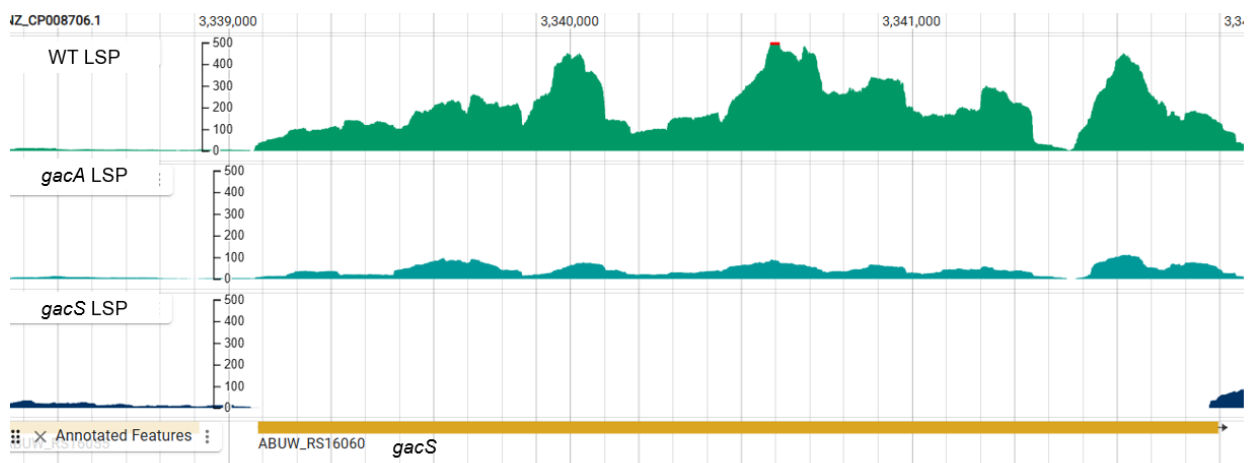


Figure 3.5 Visualization of RNA-seq read coverage for *gacS* in wild-type (WT) and deletion mutants as analyzed using JBrowse. RNA-seq reads were aligned to the reference genome of *A. baumannii* AB5075. The wild-type strain (WT) exhibits read coverage throughout the [*gacS*] locus in MEP (A) and LSP (B), which is indicative of intact transcription. Conversely, the corresponding deletion mutant's $\Delta gacS$ demonstrate a complete absence of coverage at the target locus, thereby confirming the successful deletion of the gene. Expression of *gacA* appears to be lower in the $\Delta gacS$ strain compared to WT, but not absent.

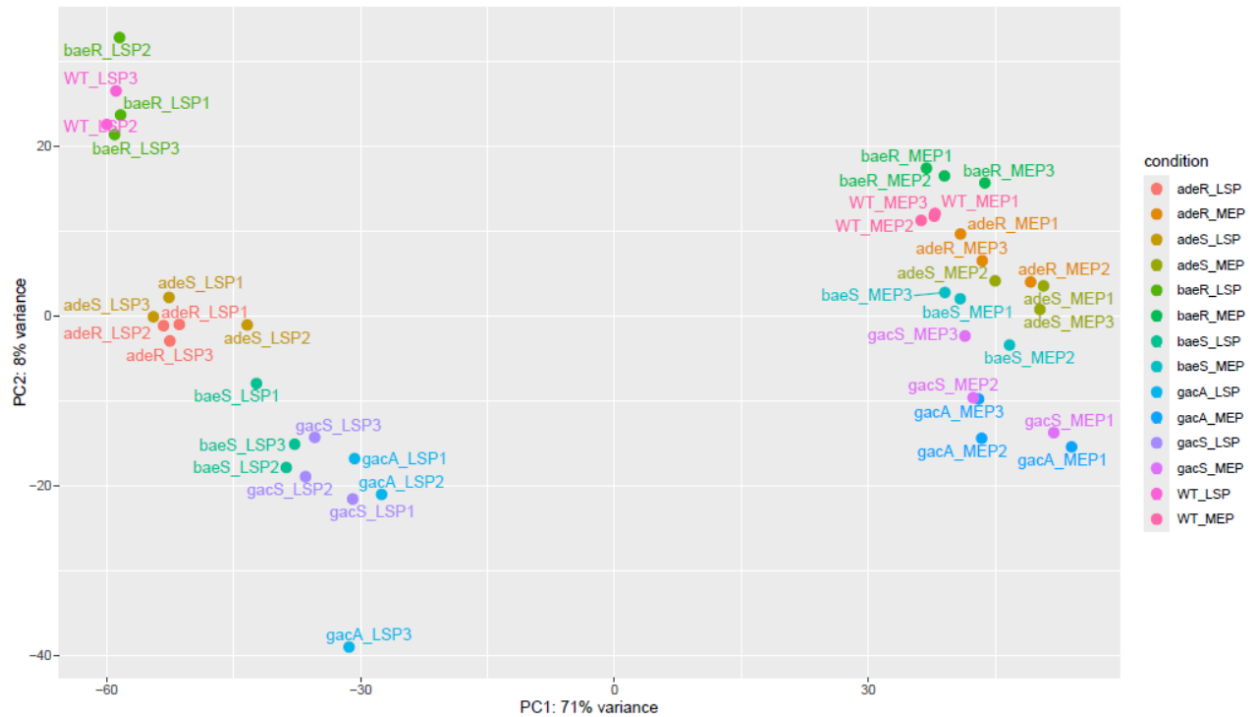


Figure 3.6 Principal Component Analysis (PCA) of transcriptomic profiles for *A. baumannii* AB5075 wild-type (WT) and TCS mutants under MEP and LSP conditions. Principal Component Analysis (PCA) was conducted on normalized RNA-Seq expression data to illustrate the global transcriptomic variation among wild-type (WT) and mutant strains ($\Delta adeR$, $\Delta adeS$, $\Delta baeR$, $\Delta baeS$, $\Delta gacA$, and $\Delta gacS$) of *Acinetobacter baumannii* AB5075. Each point on the plot represents an independent biological replicate, and the clustering indicates the overall similarity in gene expression profiles. The PCA plot reveals a clear separation between MEP (mid-exponential phase) and LSP (late stationary phase) samples along the first principal component (PC1), signifying significant transcriptional shifts between the growth phases. The separation along PC2 differentiates WT from the respective mutants, emphasizing strain-specific transcriptional variations.

3.6 Results:

1. $\Delta adeR$ - $\Delta adeS$

The AdeRS two-component system is recognized as one of the most thoroughly studied regulators of antibiotic resistance in *Acinetobacter baumannii*. It governs the expression of the AdeABC resistance-nodulation-division (RND) efflux pump, which provides resistance against a diverse array of antibiotics, such as aminoglycosides, tetracyclines, and tigecycline. AdeS functions as the sensor kinase, whereas AdeR serves as the response regulator that directly activates the *adeABC* operon in reaction to environmental signals. Despite comprehensive investigations into its role in efflux regulation, the wider transcriptomic consequences of AdeRS disruption remain inadequately examined (Lee *et al.*, 2020; Subhasree Roy, 2022).

2. RNA-seq Analysis of $\Delta adeR$ and $\Delta adeS$ Mutant

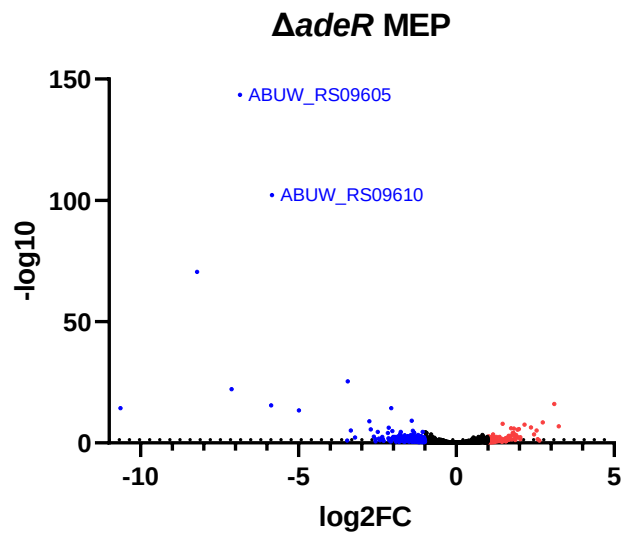
To investigate the global regulatory role of AdeRS, RNA-sequencing was performed on the $\Delta adeR$ and $\Delta adeS$ mutants compared to the wild-type AB5075. A total of **4033** were analyzed to identify the significantly differentially expressed genes (≥ 2 -fold) in MEP and LSP, including upregulated and downregulated genes (**Table 3.1**) ($\log_2FC \geq 1$ or ≤ -1 , adjusted p-value < 0.05). Interestingly, the RNA-seq analysis indicated that the *adeABC* operon was one of the most significantly downregulated loci in the $\Delta adeR$ and $\Delta adeS$ mutants in the MEP condition. In contrast, under LSP conditions, it was also downregulated, albeit to a lesser degree and not as severely affected as in MEP mainly because AdeABC are not as highly expressed in LSP. Both results confirm the established role of AdeRS as a positive regulator of the AdeABC efflux system.

In the MEP condition, a total of **219** genes exhibited differential expression the $\Delta adeR$ mutant compared to the wild-type strain comprising **71** genes that were upregulated and **148** genes that were downregulated (**Figure 3.7A**). Conversely, the effects of $\Delta adeR$ deletion on the transcriptome were significantly greater in the LSP condition, where **691** genes showed differential expression, including **323** that were upregulated and **368** that were downregulated (**Figure 3.7B**). This indicates that the regulatory function of AdeR is wide-ranging and broadens when cells are grown to LSP, which

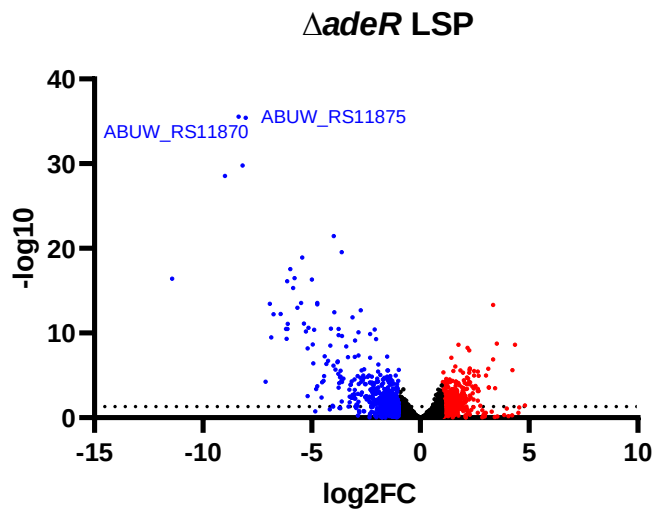
suggests that more indirect regulatory effects manifest when cells are grown for several hours longer into another growth phase.

In the absence of *adeS*, a total of **588** genes demonstrated differential expression in MEP condition, with **262** genes being upregulated and **326** genes downregulated (**Figure 3.7C**). Under LSP conditions, **533** genes exhibited differential expression, comprising **307** upregulated genes and **226** downregulated genes (**Figure 3.7D**).

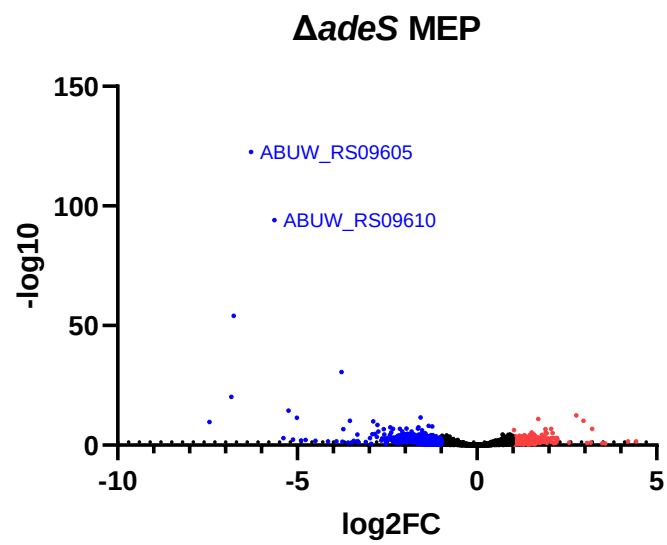
(A)



(B)



(C)



(D)

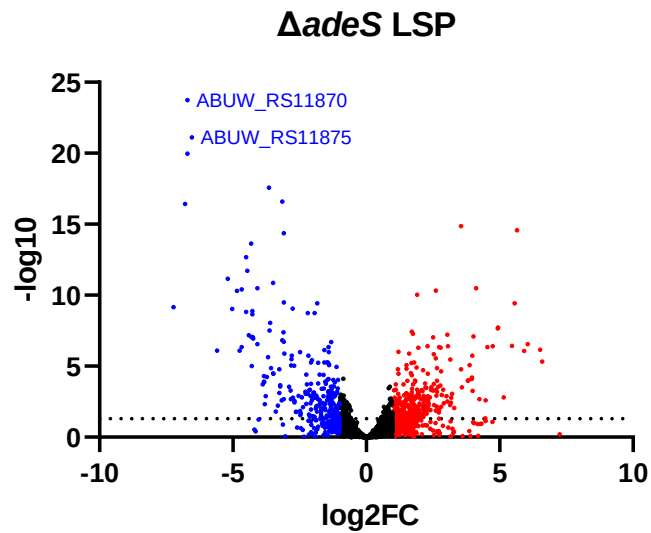


Figure 3.7 Transcriptomic analysis was conducted on the $\Delta adeR$ and $\Delta adeS$ mutant in comparison to the wild-type *A. baumannii* AB5075 under two different growth conditions: MEP (Panel **A&C**) and LSP (Panel **B&D**). Each volcano plot illustrates the log₂ fold change (x-axis) versus the $-\log_{10}$ adjusted p-value (y-axis) for all identified genes. Genes exhibiting $|\log_2 \text{fold change}| \geq 1$ and an adjusted p-value < 0.05 were deemed significantly differentially expressed. Upregulated genes are represented in red, downregulated genes in blue, and non-significant genes in black.

Table 3.1 List of genes significantly upregulated or downregulated in the $\Delta adeR$ and $\Delta adeS$ mutant compared to wild-type AB5075.

	$\Delta adeR$		$\Delta adeS$	
(up/down)	MEP	LSP	MEP	LSP
up	71	323	262	307
down	148	368	326	226

Table 3.2 Top 20 upregulated and top 20 downregulated genes in the ***ΔadeR*** mutant compared to wild-type AB5075 under **MEP** conditions. Differentially expressed genes were ranked based on absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The upregulated genes. **(B)** The downregulated genes.

(A)

Gene	Gene Name	Function	<i>adeR</i> MEP vs WT MEP log2FC
<i>ABUW_RS01510</i>		bacterioferritin-associated ferredoxin	3.24
<i>ABUW_RS16540</i>		TonB-dependent siderophore receptor	3.10
<i>ABUW_RS11440</i>	<i>dapC</i>	succinyldiaminopimelate transaminase	2.74
<i>ABUW_RS10220</i>		aspartate ammonia-lyase	2.58
<i>ABUW_RS10600</i>		hypothetical protein	2.54
<i>ABUW_RS11470</i>		dicarboxylate/amino acid:cation symporter	2.46
<i>ABUW_RS07720</i>	<i>kdpA</i>	potassium-transporting ATPase subunit KdpA	2.36
<i>ABUW_RS16655</i>		energy transducer TonB	2.16
<i>ABUW_RS10525</i>		hypothetical protein	2.03
<i>ABUW_RS17830</i>		ISL3-like element ISPpu12 family transposase	2.03
<i>ABUW_RS07725</i>	<i>kdpB</i>	potassium-transporting ATPase subunit KdpB	1.98
<i>ABUW_RS17840</i>		cation transporter	1.95
<i>ABUW_RS08035</i>		TonB-dependent receptor	1.94
<i>ABUW_RS00790</i>		TonB-dependent siderophore receptor	1.89
<i>ABUW_RS20540</i>		hypothetical protein	1.88
<i>ABUW_RS17835</i>		signal peptidase II	1.86
<i>ABUW_RS17685</i>		ferrous iron transporter B	1.83
<i>ABUW_RS07730</i>	<i>kdpC</i>	potassium-transporting ATPase subunit KdpC	1.82
<i>ABUW_RS18235</i>		NAD-dependent malic enzyme	1.81
<i>ABUW_RS11435</i>	<i>glnD</i>	[protein-Pil] uridylyltransferase	1.79

(B)

Gene	Gene Name	Function	adeR MEP vs WT MEP log2FC
ABUW_RS09595	<i>adeR</i>	efflux system response regulator transcription factor AdeR	-10.64
ABUW_RS09600	<i>adeA</i>	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	-8.21
ABUW_RS10105	<i>antA</i>	anthranilate 1,2-dioxygenase large subunit	-7.12
ABUW_RS09605	<i>adeB</i>	multidrug efflux RND transporter permease subunit AdeB	-6.85
ABUW_RS10110	<i>antB</i>	anthranilate 1,2-dioxygenase small subunit	-5.87
ABUW_RS09610	<i>adeC</i>	multidrug efflux RND transporter outer membrane channel subunit AdeC	-5.84
ABUW_RS10115	<i>antC</i>	anthranilate 1,2-dioxygenase electron transfer component AntC	-4.99
ABUW_RS05745	<i>bauA</i>	TonB-dependent ferric acinetobactin receptor BauA	-3.44
ABUW_RS05740	<i>bauB</i>	siderophore-binding periplasmic lipoprotein BauB	-3.34
ABUW_RS12215		hypothetical protein	-3.21
ABUW_RS15175	<i>bfr</i>	bacterioferritin	-2.76
ABUW_RS17065		hypothetical protein	-2.71
ABUW_RS00335		VOC family protein	-2.61
ABUW_RS15160	<i>otsB</i>	trehalose-phosphatase	-2.56
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-2.49
ABUW_RS13055		cold-shock protein	-2.45
ABUW_RS11275		cytosine permease	-2.36
ABUW_RS00340	<i>maiA</i>	maleylacetoacetate isomerase	-2.35
ABUW_RS05735	<i>bauE</i>	ferric acinetobactin ABC transporter ATP-binding protein BauE	-2.33
ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-2.17

Table 3.3 The 20 genes exhibiting the highest levels of upregulation and the 20 genes showing the most significant downregulation in the ***ΔadeR*** mutant relative to the wild-type AB5075 under **LSP** conditions. The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>adeR</i> LSP vs WT LSP log2FC
ABUW_RS03795		DUF2280 domain-containing protein	4.81
ABUW_RS19125		hypothetical protein	4.35
ABUW_RS19235		hypothetical protein	4.23
ABUW_RS15150	<i>bioA</i>	adenosylmethionine--8-amino-7-oxononanoate transaminase	3.52
ABUW_RS19355		hypothetical protein	3.43
ABUW_RS19220		hypothetical protein	3.34
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	3.34
ABUW_RS08395		hypothetical protein	3.15
ABUW_RS19350		hypothetical protein	3.15
ABUW_RS15145		8-amino-7-oxononanoate synthase	3.12
ABUW_RS20385		hypothetical protein	3.02
ABUW_RS09450		ribose-phosphate pyrophosphokinase	2.75
ABUW_RS05140	<i>uvrB</i>	excinuclease ABC subunit UvrB	2.68
ABUW_RS08495	<i>fabZ</i>	3-hydroxyacyl-ACP dehydratase FabZ	2.67
ABUW_RS19360		hypothetical protein	2.64
ABUW_RS19230		hypothetical protein	2.64
ABUW_RS14845		metal-dependent hydrolase	2.64
ABUW_RS19205		hypothetical protein	2.63
ABUW_RS19140		ParA family protein	2.54
ABUW_RS12620		hypothetical protein	2.47

(B)

Gene	Gene Name	Function	<i>adeR</i> LSP vs WT LSP log2FC
ABUW_RS09595	<i>adeR</i>	efflux system response regulator transcription factor AdeR	-11.42
ABUW_RS15580	<i>tcuA</i>	FAD-dependent tricarballoylate dehydrogenase TcuA	-8.99
ABUW_RS11875		hypothetical protein	-8.37
ABUW_RS15585	<i>tcuB</i>	tricarballoylate utilization 4Fe-4S protein TcuB	-8.18
ABUW_RS11870		hypothetical protein	-8.04
ABUW_RS20145		hypothetical protein	-7.13
ABUW_RS13010		DUF4142 domain-containing protein	-6.93
ABUW_RS08050		hypothetical protein	-6.86
ABUW_RS15565		MFS transporter	-6.76
ABUW_RS05765	<i>basF</i>	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-6.43
ABUW_RS12975		hypothetical protein	-6.18
ABUW_RS05730	<i>bauC</i>	ferric acinetobactin ABC transporter permease subunit BauC	-6.16
ABUW_RS10635		SidA/IucD/PvdA family monooxygenase	-6.13
ABUW_RS13040		hypothetical protein	-6.12
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-6.10
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-5.99
ABUW_RS05720	<i>basB</i>	acinetobactin non-ribosomal peptide synthetase subunit BasB	-5.85
ABUW_RS11855	<i>katE</i>	catalase HP11	-5.79
ABUW_RS05760	<i>basE</i>	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.67
ABUW_RS10640		siderophore biosynthesis protein	-5.50

Table 3.4 Top 20 upregulated and downregulated genes in the Δ *adeS* mutant compared to wild-type *A. baumannii* AB5075 under **MEP** conditions. The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>adeS</i> MEP vs WT MEP log2FC
sRNA92	sRNA92	sRNA92	4.43
sRNA48	sRNA48	sRNA48	4.20
ABUW_RS01510		bacterioferritin-associated ferredoxin	3.20
ABUW_RS11440	<i>dapC</i>	succinyldiaminopimelate transaminase	2.96
ABUW_RS16540		TonB-dependent siderophore receptor	2.76
ABUW_RS14395		hypothetical protein	2.24
ABUW_RS20110		hypothetical protein	2.22
ABUW_RS03460		hypothetical protein	2.20
ABUW_RS17830		ISL3-like element ISPpu12 family transposase	2.13
ABUW_RS07720	<i>kdpA</i>	potassium-transporting ATPase subunit KdpA	2.10
ABUW_RS01820		HPP family protein	2.07
ABUW_RS16655		energy transducer TonB	2.06
ABUW_RS17835		signal peptidase II	2.04
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	1.99
ABUW_RS17840		cation transporter	1.97
ABUW_RS20540		hypothetical protein	1.95
ABUW_RS18235		NAD-dependent malic enzyme	1.94
ABUW_RS17255		tRNA-Leu	1.93
ABUW_RS07725	<i>kdpB</i>	potassium-transporting ATPase subunit KdpB	1.91
ABUW_RS07730	<i>kdpC</i>	potassium-transporting ATPase subunit KdpC	1.90

(B)

Gene	Gene Name	Function	<i>adeS</i> MEP vs WT MEP log2FC
ABUW_RS09590	<i>adeS</i>	two-component sensor histidine kinase AdeS	-7.45
ABUW_RS10105	<i>antA</i>	anthranilate 1,2-dioxygenase large subunit	-6.84
ABUW_RS09600	<i>adeA</i>	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	-6.77
ABUW_RS09605	<i>adeB</i>	multidrug efflux RND transporter permease subunit AdeB	-6.29
ABUW_RS09610	<i>adeC</i>	multidrug efflux RND transporter outer membrane channel subunit AdeC	-5.64
ABUW_RS12215		hypothetical protein	-5.39
ABUW_RS10115	<i>antC</i>	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.25
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-5.12
ABUW_RS10110	<i>antB</i>	anthranilate 1,2-dioxygenase small subunit	-5.01
ABUW_RS20235		hypothetical protein	-4.90
ABUW_RS12220		hypothetical protein	-4.77
ABUW_RS12230		hypothetical protein	-4.50
ABUW_RS19790		helix-turn-helix transcriptional regulator	-4.15
ABUW_RS12225		cold-shock protein	-3.91
ABUW_RS05745	<i>bauA</i>	TonB-dependent ferric acinetobactin receptor BauA	-3.77
ABUW_RS11675		malonate decarboxylase subunit delta	-3.75
ABUW_RS05740	<i>bauB</i>	siderophore-binding periplasmic lipoprotein BauB	-3.72
ABUW_RS17065		hypothetical protein	-3.54
ABUW_RS04595		hypothetical protein	-3.43
ABUW_RS00380	<i>hutU</i>	urocanate hydratase	-3.33

Table 3.5 Top 20 upregulated and downregulated genes in the $\Delta adeS$ mutant compared to wild-type *A. baumannii* AB5075 under **LSP** conditions. The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>adeS</i> LSP vs WT LSP log2FC
ABUW_RS20020		TniB family NTP-binding protein	6.59
ABUW_RS19340		hypothetical protein	6.52
ABUW_RS19240		hypothetical protein	6.05
ABUW_RS20015		Mu transposase C-terminal domain-containing protein	5.92
ABUW_RS19125		hypothetical protein	5.65
ABUW_RS19355		hypothetical protein	5.56
ABUW_RS19130		SAM-dependent DNA methyltransferase	5.46
ABUW_RS10215		hypothetical protein	5.15
ABUW_RS19235		hypothetical protein	4.94
ABUW_RS19345		molecular chaperone DnaJ	4.93
ABUW_RS19360		hypothetical protein	4.74
ABUW_RS19135		hypothetical protein	4.54
ABUW_RS02145		membrane protein	4.47
ABUW_RS03860		hypothetical protein	4.46
ABUW_RS19175		hypothetical protein	4.24
ABUW_RS19220		hypothetical protein	4.12
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	4.02
ABUW_RS09970		molecular chaperone	3.98
ABUW_RS19350		hypothetical protein	3.97
ABUW_RS19030		replication initiation protein	3.96

(B)

Gene	Gene Name	Function	<i>adeS</i> LSP vs WT LSP log2FC
<i>ABUW_RS09590</i>	<i>adeS</i>	two-component sensor histidine kinase AdeS	-7.23
<i>ABUW_RS15580</i>	<i>tcuA</i>	FAD-dependent tricarballoylate dehydrogenase TcuA	-6.79
<i>ABUW_RS11870</i>		hypothetical protein	-6.71
<i>ABUW_RS15585</i>	<i>tcuB</i>	tricarballoylate utilization 4Fe-4S protein TcuB	-6.71
<i>ABUW_RS11875</i>		hypothetical protein	-6.54
<i>ABUW_RS08050</i>		hypothetical protein	-5.59
<i>ABUW_RS10635</i>		SidA/lucD/PvdA family monooxygenase	-5.19
<i>ABUW_RS10585</i>		acetyltransferase	-5.03
<i>ABUW_RS10640</i>		siderophore biosynthesis protein	-4.85
<i>ABUW_RS15565</i>		MFS transporter	-4.75
<i>ABUW_RS05765</i>	<i>basF</i>	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-4.67
<i>ABUW_RS10630</i>		DHA2 family efflux MFS transporter permease subunit	-4.67
<i>ABUW_RS10625</i>		siderophore achromobactin biosynthesis protein AcsC	-4.51
<i>ABUW_RS05720</i>	<i>basB</i>	acinetobactin non-ribosomal peptide synthetase subunit BasB	-4.51
<i>ABUW_RS05750</i>	<i>basC</i>	putative histamine N-monooxygenase	-4.46
<i>ABUW_RS05755</i>	<i>basD</i>	acinetobactin non-ribosomal peptide synthetase subunit BasD	-4.41
<i>ABUW_RS14490</i>		transferrin-binding protein-like solute binding protein	-4.32
<i>ABUW_RS05770</i>	<i>basG</i>	acinetobactin biosynthesis histidine decarboxylase BasG	-4.31
<i>ABUW_RS05735</i>	<i>bauE</i>	ferric acinetobactin ABC transporter ATP-binding protein BauE	-4.29
<i>ABUW_RS07500</i>		hypothetical protein	-4.27

3. The overlap between $\Delta adeR$ and $\Delta adeS$

Because the number of differentially expressed genes differed in the $\Delta adeR$ and $\Delta adeS$ mutants, this suggests that they either of the components might work with one or more other TCS. In order to analyze the transcriptional alterations resulting from the absence of the response regulator AdeR and the sensor kinase AdeS during mid-exponential growth (MEP) and late stationary phase (LSP), we created Venn diagrams clarify the overlap of up-regulated and down-regulated genes in each mutant to identify genes that are not be under the control by the one or other regulatory gene.

Upregulated genes in MEP: In the MEP condition, the removal of the sensor kinase AdeS led to a more extensive transcriptional activation compared to the deletion of the response regulator AdeR. The $\Delta adeS$ mutant exhibited **262** upregulated genes, while the $\Delta adeR$ mutant showed **71** upregulated genes. Among these, **60** genes were found to be commonly activated in both mutants, indicating a shared core of genes regulated by AdeRS. The remaining **202** genes uniquely upregulated in $\Delta adeS$ and **11** uniquely upregulated in $\Delta adeR$. The lack of AdeS disrupts additional regulatory pathways that extend beyond those directly governed by AdeR.

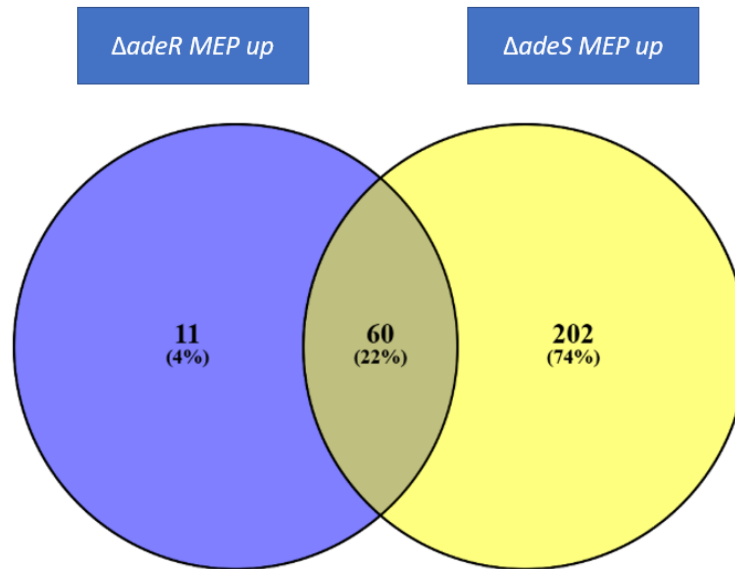
Downregulated genes in MEP: A comparable pattern was noted for downregulated genes. $\Delta adeS$ exhibited 326 downregulated genes in contrast to **148** in $\Delta adeR$, with **133** genes common to both. Consequently, **193** genes were specifically downregulated in $\Delta adeS$, while **15** genes were uniquely downregulated in $\Delta adeR$. This further demonstrates that the lack of AdeS exerts a more extensive influence on overall transcription compared to the simple absence of AdeR.

Upregulated genes in LSP: During the late stationary phase (LSP), both $\Delta adeS$ and $\Delta adeR$ mutants exhibited significant transcriptional activity. The $\Delta adeS$ mutant showed **307** genes that were upregulated, while the $\Delta adeR$ mutant had **323** upregulated genes. Among these, **133** genes were induced in both mutants, highlighting the common AdeRS dependent regulon. Nevertheless, $\Delta adeS$ uniquely upregulated **174** genes, in contrast to $\Delta adeR$, which uniquely upregulated **190** genes. This indicates that in the LSP, both mutants contribute to large but only partially overlapping regulons.

Downregulated genes in LSP: In the case of down-regulated transcripts, both $\Delta adeS$ and $\Delta adeR$ exhibited distinct yet overlapping expression profiles. Specifically, $\Delta adeS$ was associated with **226** downregulated genes, whereas $\Delta adeR$ had **368**, with **184** genes being common to both. Consequently, there were **42** genes that were uniquely downregulated in $\Delta adeS$ and **184** that were uniquely downregulated in $\Delta adeR$. This indicates that during LSP, the lack of AdeR has a more pronounced effect on gene repression compared to the lack of AdeS.

The low overlap of 25-42% of genes that are regulated by individual deletions of *adeR* and *adeS* was surprising. This suggests that both, AdeR and AdeS, might also be activated in the case of AdeR or activate in the case of AdeS by other TCS. However, the most strongly differentially expressed genes were regulated commonly, suggesting that for their regulation is the AdeRS system directly responsible. Among the commonly upregulated genes were the gene encoding for the bacterioferritin-associated ferredoxin and genes encoding for potassium-transporting ATPase subunits Kdp. The overlap also includes the downregulations of the AdeABC efflux pump, the genes *antA-C* involved in anthranilate metabolism, tricarballoylate metabolism genes and *bau* and *bas* genes, which are required to produce the *Acinetobacter*-specific siderophore Acinetobactin. Therefore, the AdeRS system controls multiple parts of the *A. baumannii* physiology, from metabolic pathways, transporters and virulence factors such as the production of the siderophore Acinetobactin.

(A)



(B)

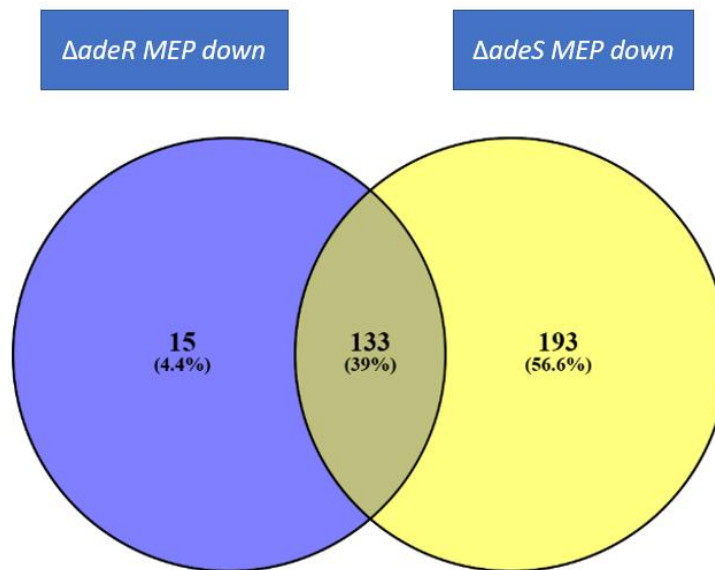
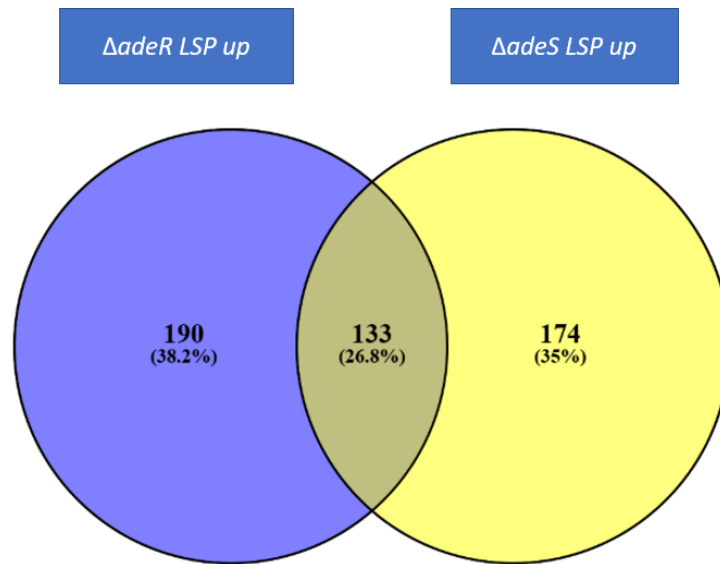


Figure 3.8 Venn diagrams illustrating the comparison of $\Delta adeR$ and $\Delta adeS$ transcriptomes in MEP. (A) The overlap of up-regulated genes in $\Delta adeS$ (262) and $\Delta adeR$ (71) reveals 60 shared genes. (B) The overlap of down-regulated genes in $\Delta adeS$ (326) and $\Delta adeR$ (148) indicates 133 shared genes. In both instances, $\Delta adeS$ demonstrates a greater number of unique differentially expressed genes, which aligns with a more extensive influence on transcription relative to $\Delta adeR$.

(A)



(B)

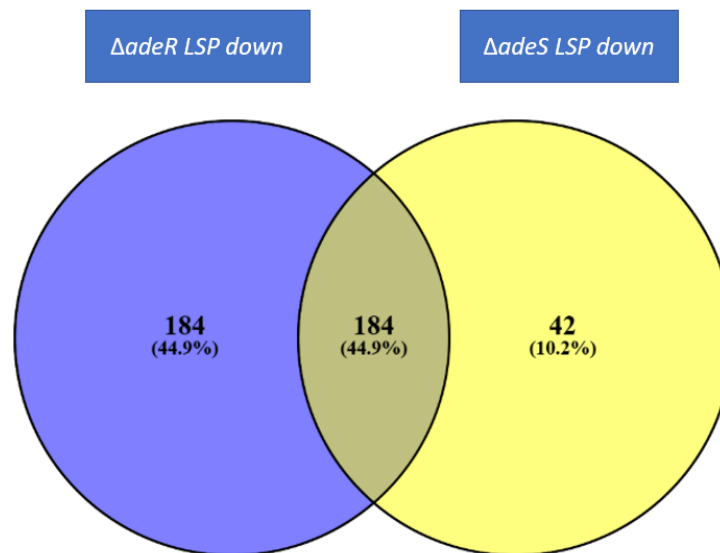


Figure 3.9 Venn diagrams illustrating the comparison of $\Delta adeR$ and $\Delta adeS$ transcriptomes in LSP. **(A)** The intersection of up-regulated genes in $\Delta adeS$ (307) and $\Delta adeR$ (323) reveals 133 shared genes. **(B)** The intersection of down-regulated genes in $\Delta adeS$ (226) and $\Delta adeR$ (368) indicates 184 shared genes. In contrast to MEP, where $\Delta adeS$ exhibited a more extensive influence, both mutants displayed significant yet distinct regulons in LSP, with $\Delta adeR$ exerting a more pronounced effect on repression.

4. $\Delta baeR$ - $\Delta baeS$

The BaeSR two-component system is recognized for its role in regulating the envelope stress response, efflux systems, and potentially conferring resistance to antimicrobial agents in Gram-negative bacteria (Lin *et al.*, 2015). The removal of *baeSR* in *A. baumannii* resulted in a marked decrease in the expression of key efflux pumps, including AdeABC, AdeIJK, and MacAB-TolC, which in turn led to heightened susceptibility to tigecycline. The regulons of AdeRS and BaeSR exhibit overlap. This suggests that BaeSR might operate through crosstalk with AdeRS (Kröger *et al.*, 2016; Bhagirath *et al.*, 2019).

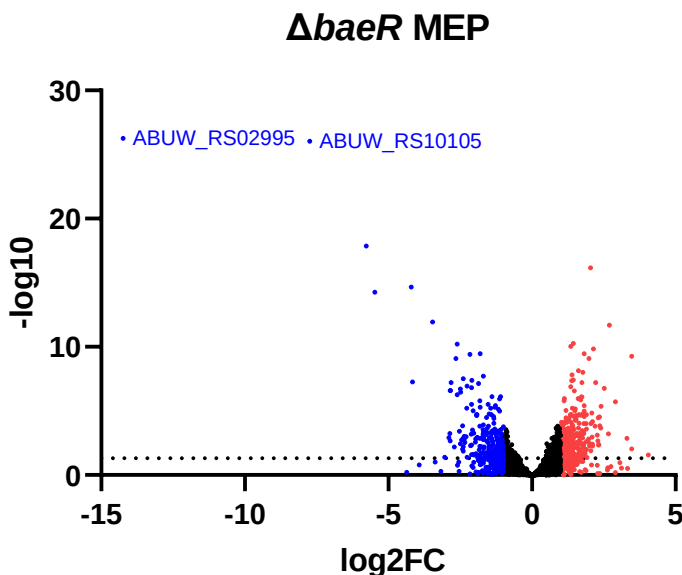
5. RNA-seq Analysis of $\Delta baeR$ and $\Delta baeS$ Mutant

To investigate the global regulatory effects of *baeR* and *baeS* in *Acinetobacter baumannii* AB5075, transcriptomic profiling was conducted utilizing RNA-seq on $\Delta baeR$ and $\Delta baeS$ mutants in comparison to the wild-type strain across the two growth conditions MEP and LSP. An analysis of differential gene expression was conducted to pinpoint genes that exhibit significant upregulation or downregulation in the absence of *baeR* or *baeS*. A total of **4033** were analyzed to identify the significantly differentially expressed genes in MEP and LSP, which encompasses both upregulated and downregulated genes (**Table 3.6**) ($\log_2FC \geq 1$ or ≤ -1 , with an adjusted p-value of less than 0.05). In the absence of *baeR* a total of **488** genes demonstrated differential expression in **MEP** conditions, with **284** genes being upregulated and **204** genes downregulated. Under **LSP** conditions, when the differential expression analysis was conducted for the $\Delta baeR$ mutant in LSP conditions, only two genes were found to be significantly downregulated (adjusted p < 0.05), one of which was *baeR* itself, confirming that the gene was successfully deleted. After testing the data, no other genes were significantly regulated. The principal component analysis (PCA) plot (**Figure 3.6**) revealed little separation between WT LSP and $\Delta baeR$ LSP samples, suggesting that the global transcriptional differences between these conditions were quite subtle. In contrast, a greater transcriptional variation was noted for the $\Delta baeS$ mutant under the same conditions. Because there were so few differentially expressed genes in the $\Delta baeR$ mutant, an overlap analysis between *baeR* and *baeS* under LSP conditions could not be conducted. These results imply that the regulatory effect of BaeR under LSP is minimal, or that any changes are too subtle to be

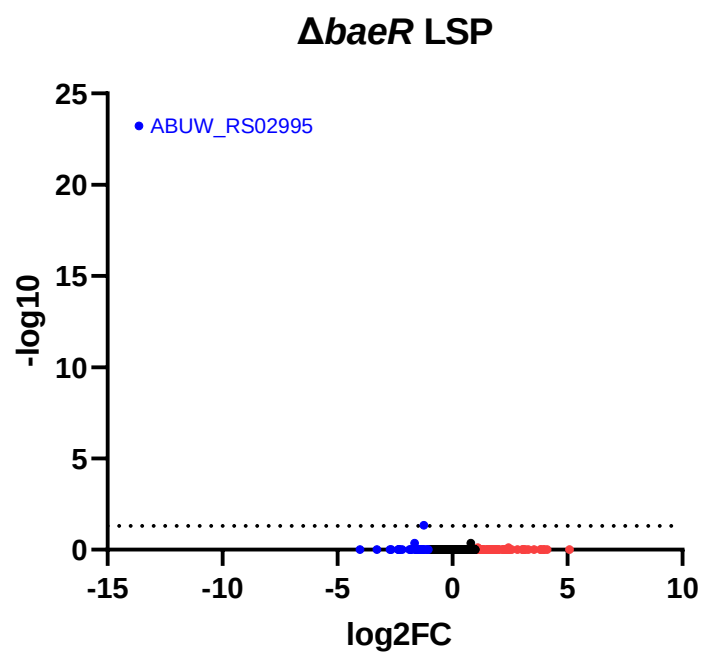
detected with the current sample set showing that the BaeR does not appear to have any significant role in LSP and that all transcriptomic changes seen in MEP are recovered.

In the absence of *baeS*, a total of **280** genes exhibited differential expression under MEP conditions, with **98** genes being upregulated and **182** genes being downregulated. Conversely, in the LSP conditions, a greater number of genes displayed differential expression, totaling **1179**. Among these, **714** genes were upregulated while **465** genes were downregulated (**Table 3.6**). In the $\Delta baeS$ mutant, the quantity of differentially expressed genes under MEP conditions was similar to that of the $\Delta baeR$ mutant, exhibiting a relatively even distribution between upregulated and downregulated genes. Notably, under LSP conditions, the overall number of differentially expressed genes in the $\Delta baeS$ mutant rose in comparison to MEP, indicating that BaeS assumes a more significant regulatory function during stress or stationary phase conditions. Furthermore, the quantity of differentially expressed genes was far greater in the $\Delta baeS$ mutant in comparison to the $\Delta baeR$ mutant LSP, while there was a greater effect in the $\Delta baeR$ in the MEP conditions. While the $\Delta baeR$ mutant exhibited only a restricted range of transcriptional alterations, the removal of the sensor kinase BaeS led to a more extensive transcriptomic response.

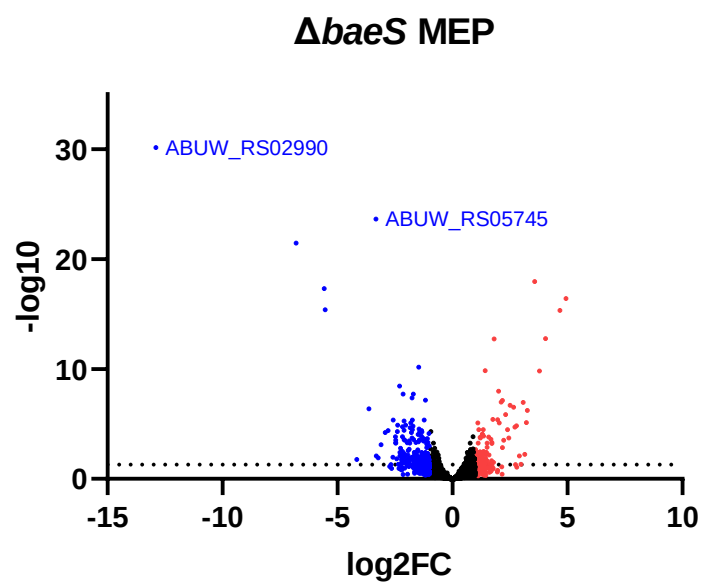
(A)



(B)



(C)



(D)

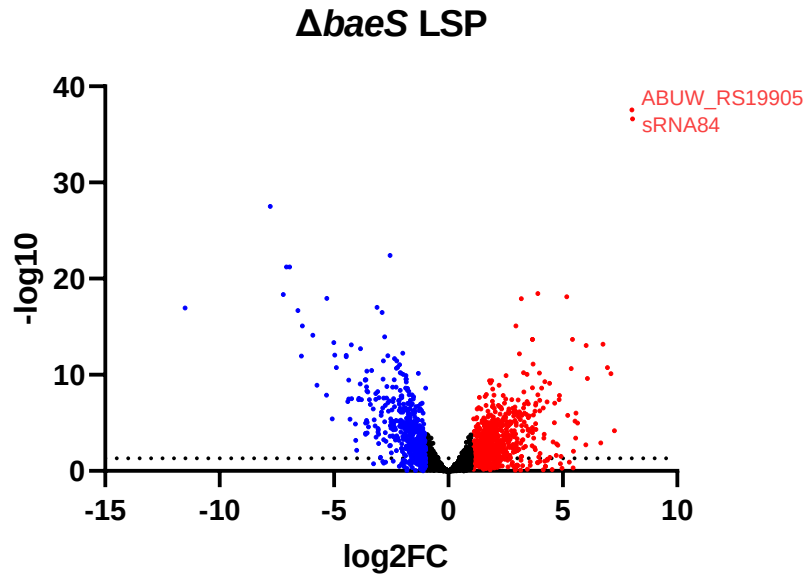


Figure 3.10 A transcriptomic analysis was performed on the $\Delta baeR$ and $\Delta baeS$ mutants in comparison to the wild-type *A. baumannii* AB5075 under two distinct growth conditions: MEP (Panel **A&C**) and LSP (Panel **B&D**). Each volcano plot displays the log2 fold change (x-axis) against the $-\log_{10}$ adjusted p-value (y-axis) for all identified genes. Genes with $|\log_2 \text{fold change}| \geq 1$ and an adjusted p-value < 0.05 were considered to be significantly differentially expressed. Upregulated genes are indicated in red, downregulated genes in blue, and non-significant genes in black.

Table 3.6 List of genes significantly upregulated or downregulated in the $\Delta baeR$ and $\Delta baeS$ mutant compared to wild-type AB5075.

	$\Delta baeR$		$\Delta baeS$	
(up/down)	MEP	LSP	MEP	LSP
up	284	0	98	714
down	204	2	182	465

Table 3.7 Top 20 upregulated and downregulated genes in the Δ *baeR* mutant compared to wild-type *A. baumannii* AB5075 under **MEP** conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>baeR</i> MEP vs WT MEP log2FC
newcandsRNA1	newcandsRNA1	newcandsRNA1	4.05
sRNA2	sRNA2	sRNA2	3.47
ABUW_RS11230		hypothetical protein	3.47
ABUW_RS10220		aspartate ammonia-lyase	3.30
ABUW_RS01510		bacterioferritin-associated ferredoxin	2.91
ABUW_RS16540		TonB-dependent siderophore receptor	2.69
ABUW_RS05285		hypothetical protein	2.66
ABUW_RS10595		PepSY domain-containing protein	2.52
ABUW_RS11620		cytochrome ubiquinol oxidase subunit I	2.41
ABUW_RS20540		hypothetical protein	2.40
ABUW_RS10590		hypothetical protein	2.36
ABUW_RS11625	<i>cydB</i>	cytochrome d ubiquinol oxidase subunit II	2.35
ABUW_RS10070		transcriptional repressor	2.33
ABUW_RS10170		hypothetical protein	2.32
ABUW_RS10600		hypothetical protein	2.31
ABUW_RS20550		hypothetical protein	2.29
ABUW_RS10530		PepSY domain-containing protein	2.27
ABUW_RS09650		helix-turn-helix transcriptional regulator	2.22
sRNA72	sRNA72	sRNA72	2.20
ABUW_RS06655		alpha/beta hydrolase	2.14

(B)

Gene	Common Gene Name	Function	<i>baeR</i> MEP vs WT MEP log2FC
ABUW_RS02995		response regulator	-14.24
ABUW_RS10105	<i>antA</i>	anthranilate 1,2-dioxygenase large subunit	-7.74
ABUW_RS10115	<i>antC</i>	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.77
ABUW_RS10110	<i>antB</i>	anthranilate 1,2-dioxygenase small subunit	-5.47
ABUW_RS01005	<i>gabT</i>	4-aminobutyrate--2-oxoglutarate transaminase	-4.21
ABUW_RS00380	<i>hutU</i>	urocanate hydratase	-4.16
ABUW_RS01010		NAD-dependent succinate-semialdehyde dehydrogenase	-3.46
ABUW_RS09115	<i>pcaF</i>	3-oxoadipyl-CoA thiolase	-3.04
ABUW_RS12300		enoyl-CoA hydratase/isomerase family protein	-2.89
ABUW_RS15525		DUF1852 domain-containing protein	-2.86
ABUW_RS17065		hypothetical protein	-2.85
ABUW_RS12295		2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	-2.85
ABUW_RS15515		flavin reductase	-2.84
ABUW_RS15520		methionine synthase	-2.82
ABUW_RS13600		aspartate aminotransferase family protein	-2.71
ABUW_RS00385	<i>hutH</i>	histidine ammonia-lyase	-2.65
<i>sRNA6</i>	<i>sRNA6</i>	<i>sRNA6</i>	-2.61
ABUW_RS18550	<i>dld</i>	D-lactate dehydrogenase	-2.61
ABUW_RS00340	<i>maiA</i>	maleylacetoacetate isomerase	-2.53
ABUW_RS01870		DEAD/DEAH box helicase	-2.50

Table 3.8 Differentially expressed genes in the $\Delta baeR$ mutant under LSP condition. Only two genes were identified as significantly downregulated (adjusted $p < 0.05$) compared to the WT LSP strain, including *baeR* itself. No upregulated genes were detected after correction. The results indicate minimal transcriptional changes between $\Delta baeR$ and WT under LSP conditions, consistent with the subtle differences observed in PCA analysis.

(A)

Gene	Gene Name	Function	baeR LSP vs WT LSP log2FC
<i>ABUW_RS02995</i>	<i>baeR</i>	response regulator	-13.63
<i>ABUW_RS07640</i>		hypothetical protein	-1.25

Table 3.9 Top 20 upregulated and downregulated genes in the Δ *baeS* mutant compared to wild-type *A. baumannii* AB5075 under **MEP** conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>baeS</i> MEP vs WT MEP log2FC
sRNA84	sRNA84	sRNA84	4.94
<i>ABUW_RS19905</i>	<i>ssrS</i>	6S RNA	4.68
<i>ABUW_RS17840</i>		cation transporter	4.05
<i>ABUW_RS17830</i>		ISL3-like element ISPpu12 family transposase	3.78
<i>ABUW_RS13860</i>		cation transporter	3.57
<i>ABUW_RS17835</i>		signal peptidase II	3.25
<i>ABUW_RS09655</i>		hypothetical protein	3.21
sRNA24	sRNA24	sRNA24	3.15
sRNA1	sRNA1	sRNA1	3.07
sRNA2	sRNA2	sRNA2	2.98
<i>ABUW_RS07110</i>		tRNA-Trp	2.91
<i>ABUW_RS11470</i>		dicarboxylate/amino acid:cation symporter	2.78
<i>ABUW_RS01510</i>		bacterioferritin-associated ferredoxin	2.71
sRNA42	sRNA42	sRNA42	2.66
sRNA96	sRNA96	sRNA96	2.51
<i>ABUW_RS09675</i>		hypothetical protein	2.45
<i>ABUW_RS07005</i>		acyltransferase	2.39
<i>ABUW_RS11440</i>	<i>dapC</i>	succinyldiaminopimelate transaminase	2.31
sRNA100	sRNA100	sRNA100	2.23
sRNA15	sRNA15	sRNA15	2.18

(B)

Gene	Gene Name	Function	<i>baeS</i> MEP vs WT MEP log2FC
ABUW_RS02990	<i>baeS</i>	sensor histidine kinase efflux regulator BaeS	-12.89
ABUW_RS10105	<i>antA</i>	anthranilate 1,2-dioxygenase large subunit	-6.80
ABUW_RS10115	<i>antC</i>	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.58
ABUW_RS10110	<i>antB</i>	anthranilate 1,2-dioxygenase small subunit	-5.54
ABUW_RS20235		hypothetical protein	-4.16
ABUW_RS05740	<i>bauB</i>	siderophore-binding periplasmic lipoprotein BauB	-3.63
ABUW_RS05745	<i>bauA</i>	TonB-dependent ferric acinetobactin receptor BauA	-3.33
ABUW_RS07260	<i>csuB</i>	Csu fimbrial biogenesis protein CsuB	-3.31
ABUW_RS07255	<i>csuA</i>	Csu fimbrial biogenesis protein CsuA	-3.23
ABUW_RS05735	<i>bauE</i>	ferric acinetobactin ABC transporter ATP-binding protein BauE	-3.10
ABUW_RS05720	<i>basB</i>	acinetobactin non-ribosomal peptide synthetase subunit BasB	-2.92
ABUW_RS08730	<i>cydX</i>	cytochrome bd-I oxidase subunit CydX	-2.80
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-2.67
ABUW_RS15565		MFS transporter	-2.59
ABUW_RS19040		zeta toxin family protein	-2.58
ABUW_RS20485		hypothetical protein	-2.48
ABUW_RS11870		hypothetical protein	-2.47
ABUW_RS08725		cyd operon YbgE family protein	-2.46
ABUW_RS02840		tail protein X	-2.46
ABUW_RS13055		cold-shock protein	-2.43

Table 3.10 Top 20 upregulated and downregulated genes in the Δ *baeS* mutant compared to wild-type *A. baumannii* AB5075 under **LSP** conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>baeS</i> LSP vs WT LSP log2FC
sRNA84	sRNA84	sRNA84	8.05
ABUW_RS19905	<i>ssrS</i>	6S RNA	8.02
ABUW_RS07105		tRNA-Leu	7.25
ABUW_RS07110		tRNA-Trp	7.10
ABUW_RS09970		molecular chaperone	6.95
sRNA77	sRNA77	sRNA77	6.76
ABUW_RS12755		TetR/AcrR family transcriptional regulator	6.66
ABUW_RS09965		type 1 fimbrial protein	6.08
ABUW_RS08150	<i>aceI</i>	chlorhexidine efflux PACE transporter AceI	6.02
ABUW_RS15030		tRNA-Gln	6.01
ABUW_RS19340		hypothetical protein	5.64
ABUW_RS19240		hypothetical protein	5.58
sRNA81	sRNA81	sRNA81	5.56
ABUW_RS15025		tRNA-Gln	5.54
ABUW_RS06940		hypothetical protein	5.47
ABUW_RS19125		hypothetical protein	5.42
ABUW_RS09655		hypothetical protein	5.37
ABUW_RS14535		hypothetical protein	5.21
sRNA100	sRNA100	sRNA100	5.18
sRNA62	sRNA62	sRNA62	4.92

(B)

Gene	Gene Name	Function	<i>baeS</i> LSP vs WT LSP log2FC
ABUW_RS02990	<i>baeS</i>	sensor histidine kinase efflux regulator BaeS	-11.51
ABUW_RS10640		siderophore biosynthesis protein	-7.78
ABUW_RS15580	<i>tcuA</i>	FAD-dependent tricarballylate dehydrogenase TcuA	-7.21
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-7.07
ABUW_RS15585	<i>tcuB</i>	tricarballylate utilization 4Fe-4S protein TcuB	-6.94
ABUW_RS05755	<i>basD</i>	acinetobactin non-ribosomal peptide synthetase subunit BasD	-6.58
ABUW_RS05765	<i>basF</i>	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-6.42
ABUW_RS10585		acetyltransferase	-6.38
ABUW_RS05760	<i>basE</i>	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.92
ABUW_RS15565		MFS transporter	-5.75
ABUW_RS10525		hypothetical protein	-5.32
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-5.31
ABUW_RS08050		hypothetical protein	-5.07
ABUW_RS11870		hypothetical protein	-5.01
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-4.97
ABUW_RS05720	<i>basB</i>	acinetobactin non-ribosomal peptide synthetase subunit BasB	-4.90
ABUW_RS05750	<i>basC</i>	putative histamine N-monooxygenase	-4.47
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-4.47
ABUW_RS06610		hemin uptake protein HemP	-4.39
ABUW_RS05770	<i>basG</i>	acinetobactin biosynthesis histidine decarboxylase BasG	-4.35

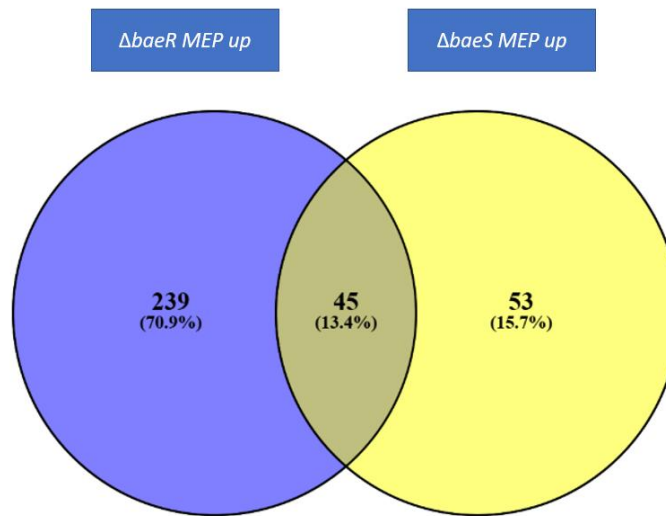
6. The overlap between $\Delta baeR$ and $\Delta baeS$

To explore the similarities and distinctions in transcriptional regulation between the response regulator BaeR and its corresponding sensor kinase BaeS during MEP and LSP, Venn diagrams were created to analyze the gene sets that were upregulated and downregulated in each mutant.

Upregulated genes in MEP: In the MEP condition, the removal of the response regulator $\Delta baeR$ led to a greater number of upregulated genes in comparison to the deletion of the sensor kinase $\Delta baeS$. Specifically, $\Delta baeR$ exhibited **284** upregulated genes, whereas $\Delta baeS$ displayed **98** upregulated genes, with **45** genes being common to both mutants. Consequently, **239** genes were uniquely upregulated in $\Delta baeR$, and **53** were uniquely upregulated in $\Delta baeS$. This suggests that although both mutants share a sizable subset of induced targets, BaeR plays a more extensive role in transcriptional activation during exponential growth.

Down-regulated genes in MEP: A comparable pattern was noted for downregulated transcripts. $\Delta baeR$ displayed **204** downregulated genes, whereas $\Delta baeS$ showed **184**, with **67** genes in common. This indicates that **137** genes were uniquely suppressed in $\Delta baeR$ and **115** uniquely suppressed in $\Delta baeS$. These findings suggest that while both mutants affect overlapping gene sets, the deletion of $\Delta baeR$ has a more pronounced impact on both activation and repression in MEP.

(A)



(B)

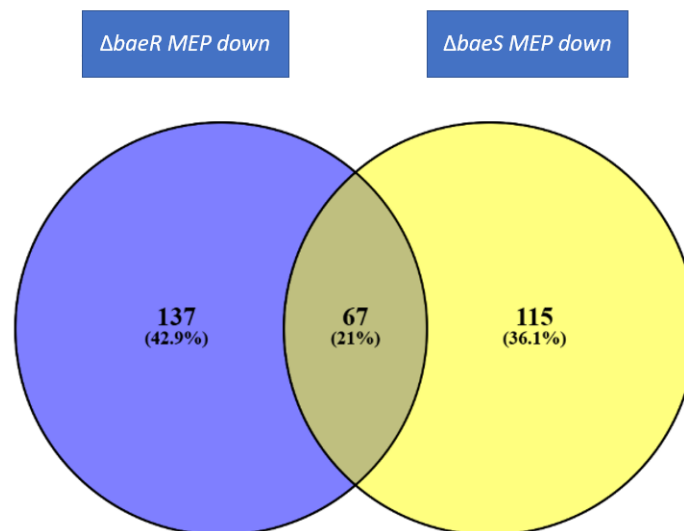


Figure 3.11 Venn diagram of upregulated genes in $\Delta baeR$ and $\Delta baeS$ during MEP. (A) $\Delta baeR$ exhibited 284 upregulated genes, $\Delta baeS$ exhibited 98, with 45 genes shared between the two mutants. The larger number of unique genes in $\Delta baeR$ indicates a broader role for BaeR in transcriptional activation compared to BaeS under exponential growth conditions. (B) In down regulate, $\Delta baeR$ exhibited 204 downregulated genes, $\Delta baeS$ exhibited 182, with 67 genes shared between the two mutants.

7. $\Delta gacA$ - $\Delta gacS$

The GacS/GacA two-component system is a thoroughly studied global regulatory mechanism found in numerous Gram-negative bacteria, where it is crucial for the regulation of secondary metabolism, motility, biofilm development, and adaptation to stress. In *Pseudomonas* sp., GacS (the sensor kinase) and GacA (the response regulator) constitute a pivotal element within intricate regulatory networks that govern the expression of small RNAs and various genes associated with virulence (Gotoh *et al.*, 2010; Bhagirath *et al.*, 2019; Song *et al.*, 2022).

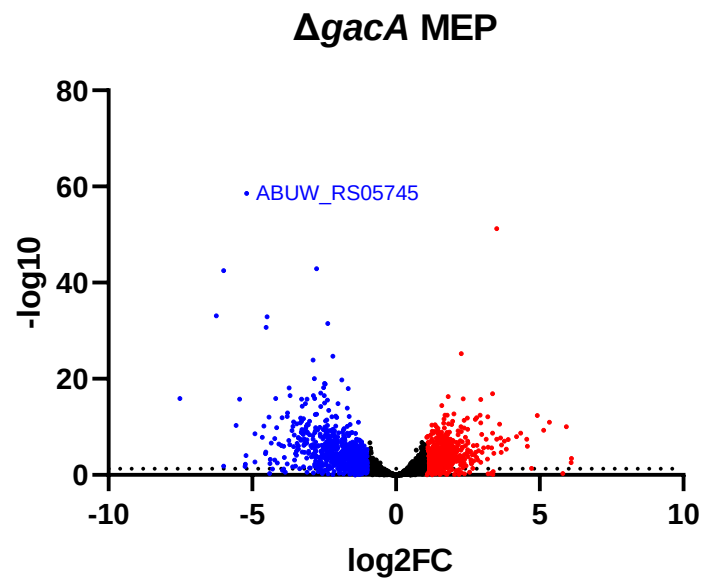
To explore its possible regulatory roles, we conducted RNA-seq analysis on the $\Delta gacA$ and $\Delta gacS$ mutants within the *A. baumannii* AB5075 background, under both (MEP) and (LSP) conditions. The objective of this analysis was to identify genes that are dependent on GacA/GacS and to ascertain how this system influences gene expression in reaction to varying environmental conditions.

8. RNA-seq Analysis of $\Delta gacA$ and $\Delta gacS$ Mutant

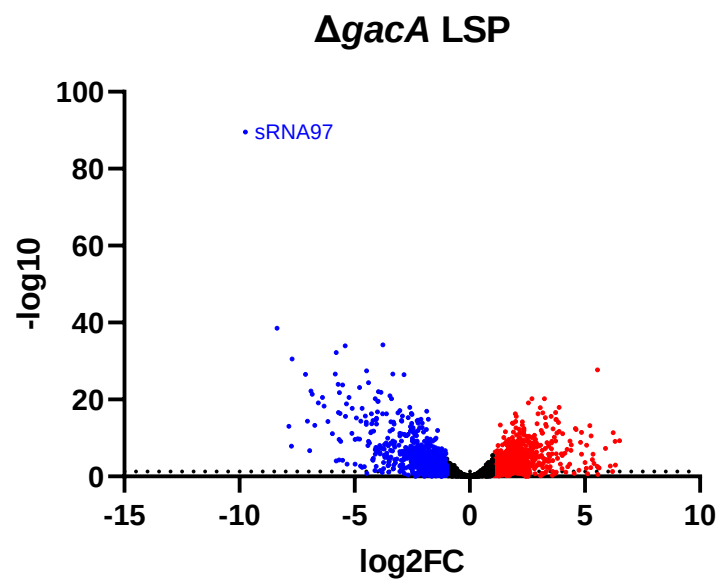
In the $\Delta gacA$ mutant, RNA-seq analysis conducted under MEP conditions identified a total of **1320** genes that were significantly differentially expressed when compared to the wild-type strain, comprising **670** genes that were upregulated and **650** genes that were downregulated. Under LSP conditions, the count of differentially expressed genes rose to **1524**, with **846** genes being upregulated and **678** genes downregulated, indicating that GacA has a more significant regulatory function during stationary-phase or stress conditions. In a similar manner, the $\Delta gacS$ mutant displayed **1038** differentially expressed genes in MEP, comprising **532** genes that were upregulated and **506** genes that were downregulated. Conversely, in LSP, there was a total of **1398** genes, with **807** being upregulated and **591** downregulated (**Table 3.11**).

The findings suggest that GacS and GacA work together to regulate gene expression in *A. baumannii*, with their regulatory influence being more significant during LSP. This may indicate that environmental signals trigger the activation of the GacS/GacA system during this phase.

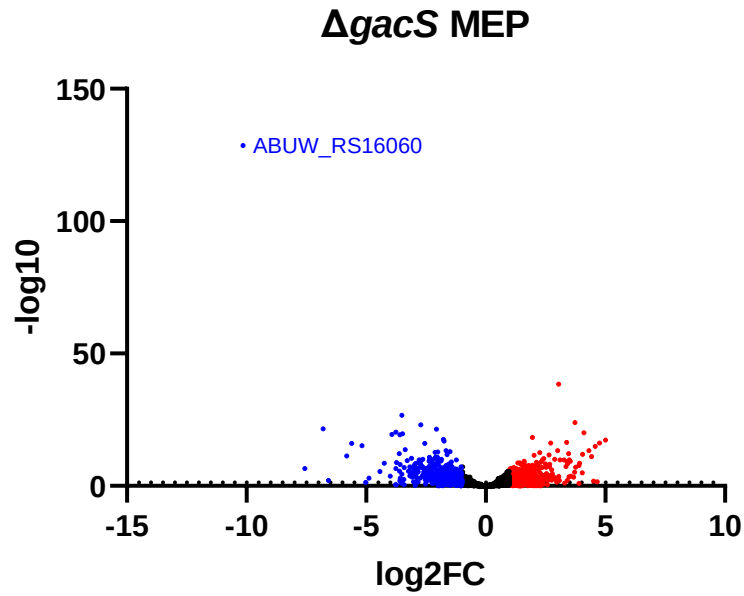
(A)



(B)



(C)



(D)

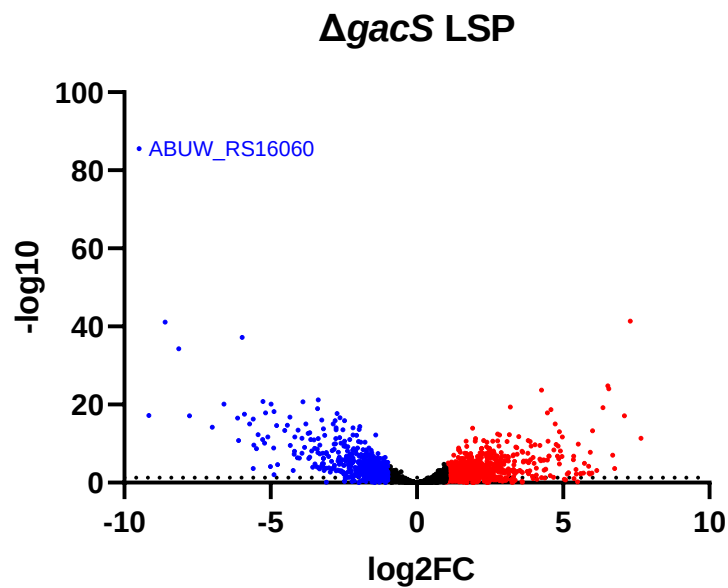


Figure 3.12 Transcriptomic analysis was conducted on the $\Delta gacA$ and $\Delta gacS$ mutant in comparison to the wild-type *A. baumannii* AB5075 under two different growth conditions: MEP (Panel **A&C**) and LSP (Panel **B&D**). Each volcano plot illustrates the log2 fold change (x-axis)

versus the $-\log_{10}$ adjusted p-value (y-axis) for all identified genes. Genes exhibiting $|\log_2 \text{ fold change}| \geq 1$ and an adjusted p-value < 0.05 were deemed significantly differentially expressed. Upregulated genes are represented in red, downregulated genes in blue, and non-significant genes in black.

Table 3.11 List of genes significantly upregulated or downregulated in the $\Delta gacA$ and $\Delta gacS$ mutant compared to wild-type AB5075.

	$\Delta gacA$		$\Delta gacS$	
(up/down)	MEP	LSP	MEP	LSP
up	670	846	532	807
down	650	678	506	591

Table 3.12 Top 20 upregulated and downregulated genes in the $\Delta gacA$ mutant compared to wild-type *A. baumannii* AB5075 under MEP conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). (A) The genes that are upregulated. (B) The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>gacA</i> MEP vs WT MEP log2FC
sRNA92	sRNA92	sRNA92	6.10
ABUW_RS09120		CoA transferase subunit B	6.09
ABUW_RS11825		LysE family translocator	5.93
ABUW_RS10185		CoA transferase subunit B	5.34
ABUW_RS10190		short-chain fatty acid transporter	5.14
ABUW_RS11715		CidA/LrgA family protein	4.92
sRNA94	sRNA94	sRNA94	4.72
ABUW_RS10180		CoA transferase subunit A	4.57
ABUW_RS13600		aspartate aminotransferase family protein	4.55
ABUW_RS09140		muconate cycloisomerase	4.34
ABUW_RS10195		thiolase family protein	4.19
ABUW_RS09130	<i>catA</i>	catechol 1,2-dioxygenase	3.91
ABUW_RS09135	<i>catC</i>	muconolactone Delta-isomerase	3.84
ABUW_RS10160		3-hydroxybutyrate dehydrogenase	3.77
ABUW_RS10165		GntP family permease	3.67
ABUW_RS18435		amino acid permease	3.66
ABUW_RS13855		amino acid transporter	3.64
ABUW_RS11710		LrgB family protein	3.61
ABUW_RS10150		MFS transporter	3.51
ABUW_RS03465		alanine:cation symporter family protein	3.50

(B)

Gene	Gene Name	Function	<i>gacA</i> MEP vs WT MEP log2FC
ABUW_RS01495	<i>pilA</i>	pilin	-7.52
ABUW_RS12745		DUF2147 domain-containing protein	-6.25
sRNA29	sRNA29	sRNA29	-6.00
sRNA97	sRNA97	sRNA97	-5.99
ABUW_RS07180		hypothetical protein	-5.56
ABUW_RS05740	<i>bauB</i>	siderophore-binding periplasmic lipoprotein BauB	-5.44
sRNA64	sRNA64	sRNA64	-5.25
ABUW_RS20520		hypothetical protein	-5.24
sRNA99	sRNA99	sRNA99	-5.22
ABUW_RS05745	<i>bauA</i>	TonB-dependent ferric acinetobactin receptor BauA	-5.19
ABUW_RS12225		cold-shock protein	-4.90
ABUW_RS13655		hypothetical protein	-4.90
ABUW_RS08535		hypothetical protein	-4.65
ABUW_RS00905		DUF485 domain-containing protein	-4.59
ABUW_RS07255	<i>csuA</i>	Csu fimbrial biogenesis protein CsuA	-4.54
ABUW_RS12215		hypothetical protein	-4.53
ABUW_RS11425		tautomerase family protein	-4.52
ABUW_RS01215		DUF805 domain-containing protein	-4.48
ABUW_RS14740		bacteriohemerythrin	-4.42
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-4.38

Table 3.13 Top 20 upregulated and downregulated genes in the $\Delta gacA$ mutant compared to wild-type *A. baumannii* AB5075 under **LSP** conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>gacA</i> LSP vs WT LSP log2FC
ABUW_RS19295		APH(6)-I family aminoglycoside O-phosphotransferase	6.51
ABUW_RS01355		tRNA-Glu	6.32
ABUW_RS19300	aph(3'')-Ib	aminoglycoside O-phosphotransferase APH(3'')-Ib	6.31
ABUW_RS19305		ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2	6.23
sRNA26	sRNA26	sRNA26	6.20
ABUW_RS06940		hypothetical protein	6.11
ABUW_RS07110		tRNA-Trp	5.89
ABUW_RS12755		TetR/AcrR family transcriptional regulator	5.62
ABUW_RS06215		hypothetical protein	5.59
ABUW_RS01305		TolC family protein	5.55
ABUW_RS07105		tRNA-Leu	5.53
sRNA81	sRNA81	sRNA81	5.39
ABUW_RS19240		hypothetical protein	5.36
ABUW_RS02145		membrane protein	5.33
ABUW_RS19310		CmlA family chloramphenicol efflux MFS transporter	5.27
ABUW_RS08015		hypothetical protein	5.25
ABUW_RS11765		LysE family translocator	5.21
ABUW_RS19255		GNAT family N-acetyltransferase	5.08
ABUW_RS03860		hypothetical protein	5.06
ABUW_RS20020		TniB family NTP-binding protein	5.01

(B)

Gene	Gene Name	Function	<i>gacA</i> LSP vs WT LSP log2FC
sRNA97	sRNA97	sRNA97	-9.75
ABUW_RS11870		hypothetical protein	-8.37
ABUW_RS08050		hypothetical protein	-7.85
sRNA106	sRNA106	sRNA106	-7.74
ABUW_RS11875		hypothetical protein	-7.71
ABUW_RS07500		hypothetical protein	-7.13
ABUW_RS12975		hypothetical protein	-7.05
ABUW_RS20235		hypothetical protein	-6.95
ABUW_RS10640		siderophore biosynthesis protein	-6.90
ABUW_RS15585	<i>tcuB</i>	tricarballylate utilization 4Fe-4S protein TcuB	-6.84
ABUW_RS13040		hypothetical protein	-6.73
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-6.58
ABUW_RS18865		hypothetical protein	-6.39
ABUW_RS05720	<i>basB</i>	acinetobactin non-ribosomal peptide synthetase subunit BasB	-6.32
ABUW_RS15580	<i>tcuA</i>	FAD-dependent tricarballylate dehydrogenase TcuA	-6.16
ABUW_RS05765	<i>basF</i>	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-5.97
ABUW_RS01615		hemerythrin domain-containing protein	-5.84
sRNA99	sRNA99	sRNA99	-5.80
ABUW_RS03310		YegP family protein	-5.80
ABUW_RS09210		type 1 glutamine amidotransferase domain-containing protein	-5.72

Table 3.14 Top 20 upregulated and downregulated genes in the $\Delta gacS$ mutant compared to wild-type *A. baumannii* AB5075 under **MEP** conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>gacS</i> MEP vs WT MEP log2FC
sRNA84	sRNA84	sRNA84	5.01
ABUW_RS19905	ssrS	6S RNA	4.75
ABUW_RS09120		CoA transferase subunit B	4.66
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	4.57
sRNA92	sRNA92	sRNA92	4.50
ABUW_RS09655		hypothetical protein	4.43
ABUW_RS09675		hypothetical protein	4.31
sRNA96	sRNA96	sRNA96	4.11
ABUW_RS01510		bacterioferritin-associated ferredoxin	4.05
ABUW_RS07110		tRNA-Trp	4.03
ABUW_RS18100		TonB-dependent copper receptor	3.92
ABUW_RS11715		CidA/LrgA family protein	3.90
ABUW_RS09670		hypothetical protein	3.75
ABUW_RS16540		TonB-dependent siderophore receptor	3.73
ABUW_RS16925		tRNA-Lys	3.71
ABUW_RS07105		tRNA-Leu	3.67
ABUW_RS11825		LysE family translocator	3.56
ABUW_RS11475		type II asparaginase	3.53
ABUW_RS17840		cation transporter	3.49
sRNA24	sRNA24	sRNA24	3.48

(B)

Gene	Gene Name	Function	<i>gacS</i> MEP vs WT MEP log2FC
<i>ABUW_RS16060</i>		response regulator	-10.15
sRNA99	sRNA99	sRNA99	-7.56
<i>ABUW_RS10105</i>	<i>antA</i>	anthranilate 1,2-dioxygenase large subunit	-6.80
sRNA29	sRNA29	sRNA29	-6.57
<i>ABUW_RS07180</i>		hypothetical protein	-5.81
<i>ABUW_RS10110</i>	<i>antB</i>	anthranilate 1,2-dioxygenase small subunit	-5.61
<i>ABUW_RS10115</i>	<i>antC</i>	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.17
<i>ABUW_RS12210</i>		TetR/AcrR family transcriptional regulator	-4.88
<i>ABUW_RS01495</i>	<i>pilA</i>	pilin	-4.42
<i>ABUW_RS00905</i>		DUF485 domain-containing protein	-4.25
<i>ABUW_RS07260</i>	<i>csuB</i>	Csu fimbrial biogenesis protein CsuB	-3.99
sRNA97	sRNA97	sRNA97	-3.93
<i>ABUW_RS13655</i>		hypothetical protein	-3.76
<i>ABUW_RS12745</i>		DUF2147 domain-containing protein	-3.76
<i>ABUW_RS00910</i>		cation acetate symporter	-3.73
<i>ABUW_RS14080</i>		esterase	-3.62
<i>ABUW_RS01250</i>		acetyl-CoA hydrolase/transferase family protein	-3.61
<i>ABUW_RS20235</i>		hypothetical protein	-3.59
<i>ABUW_RS11425</i>		tautomerase family protein	-3.59
<i>ABUW_RS08730</i>	<i>cydX</i>	cytochrome bd-I oxidase subunit CydX	-3.58

Table 3.15 Top 20 upregulated and downregulated genes in the Δ *gacS* mutant compared to wild-type *A. baumannii* AB5075 under **LSP** conditions. . The differentially expressed genes were organized according to their absolute log2 fold change and statistical significance (adjusted p-value < 0.05). **(A)** The genes that are upregulated. **(B)** The genes that are downregulated.

(A)

Gene	Gene Name	Function	<i>gacS</i> LSP vs WT LSP log2FC
<i>ABUW_RS19240</i>		hypothetical protein	7.66
<i>ABUW_RS11925</i>		TetR/AcrR family transcriptional regulator	7.29
<i>ABUW_RS19235</i>		hypothetical protein	7.09
<i>ABUW_RS15030</i>		tRNA-Gln	6.76
<i>ABUW_RS19340</i>		hypothetical protein	6.70
sRNA84	sRNA84	sRNA84	6.56
<i>ABUW_RS19905</i>	<i>ssrS</i>	6S RNA	6.53
<i>ABUW_RS19125</i>		hypothetical protein	6.36
<i>ABUW_RS07105</i>		tRNA-Leu	6.15
<i>ABUW_RS08150</i>	<i>acel</i>	chlorhexidine efflux PACE transporter Acel	6.00
<i>ABUW_RS12755</i>		TetR/AcrR family transcriptional regulator	5.98
<i>ABUW_RS14535</i>		hypothetical protein	5.93
<i>ABUW_RS03965</i>		hypothetical protein	5.92
<i>ABUW_RS19415</i>		IS30-like element ISAb125 family transposase	5.88
<i>ABUW_RS10215</i>		hypothetical protein	5.87
<i>ABUW_RS14335</i>		non-heme iron oxygenase ferredoxin subunit	5.73
<i>ABUW_RS03795</i>		DUF2280 domain-containing protein	5.70
<i>ABUW_RS06940</i>		hypothetical protein	5.61
<i>ABUW_RS01355</i>		tRNA-Glu	5.59
<i>ABUW_RS19355</i>		hypothetical protein	5.52

(B)

Gene	Gene Name	Function	<i>gacS</i> LSP vs WT LSP log2FC
<i>ABUW_RS16060</i>		response regulator	-9.50
<i>ABUW_RS08050</i>		hypothetical protein	-9.16
<i>ABUW_RS11870</i>		hypothetical protein	-8.61
<i>ABUW_RS11875</i>		hypothetical protein	-8.14
<i>ABUW_RS12975</i>		hypothetical protein	-7.77
<i>ABUW_RS13010</i>		DUF4142 domain-containing protein	-7.00
<i>ABUW_RS10640</i>		siderophore biosynthesis protein	-6.60
<i>ABUW_RS10635</i>		SidA/lucD/PvdA family monooxygenase	-6.13
<i>ABUW_RS13040</i>		hypothetical protein	-6.10
sRNA97	sRNA97	sRNA97	-5.97
<i>ABUW_RS11855</i>	<i>katE</i>	catalase HPII	-5.89
<i>ABUW_RS15585</i>	<i>tcuB</i>	tricarballoylate utilization 4Fe-4S protein TcuB	-5.72
<i>ABUW_RS07500</i>		hypothetical protein	-5.60
sRNA99	sRNA99	sRNA99	-5.59
<i>ABUW_RS05765</i>	<i>basF</i>	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-5.57
<i>ABUW_RS15565</i>		MFS transporter	-5.48
<i>ABUW_RS05760</i>	<i>basE</i>	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.43
<i>ABUW_RS05755</i>	<i>basD</i>	acinetobactin non-ribosomal peptide synthetase subunit BasD	-5.27
<i>ABUW_RS15330</i>		mechanosensitive ion channel	-5.26
<i>ABUW_RS15580</i>	<i>tcuA</i>	FAD-dependent tricarballoylate dehydrogenase TcuA	-5.21

9. The overlap between $\Delta gacA$ and $\Delta gacS$

To investigate the connection between the response regulator GacA and its corresponding sensor kinase GacS throughout MEP, Venn diagrams were created to analyze the groups of upregulated and downregulated genes in each mutant.

Upregulated genes in MEP: In the MEP condition, the deletion of the response regulator $\Delta gacA$ led to the upregulation of **670** genes, whereas the deletion of the sensor kinase $\Delta gacS$ resulted in **532** upregulated genes. Among these, **420** genes were common to both mutants, indicating a significant core set of genes that are similarly affected. Nevertheless, **250** genes were specifically upregulated in $\Delta gacA$, and **112** were uniquely upregulated in $\Delta gacS$, suggesting that while both mutants significantly impact overlapping targets, they also exhibit distinct transcriptional effects. These variations may illustrate the broader function of GacA as a transcriptional regulator, whereas the disruption of GacS might modify the signaling balance and initiate indirect regulatory alterations.

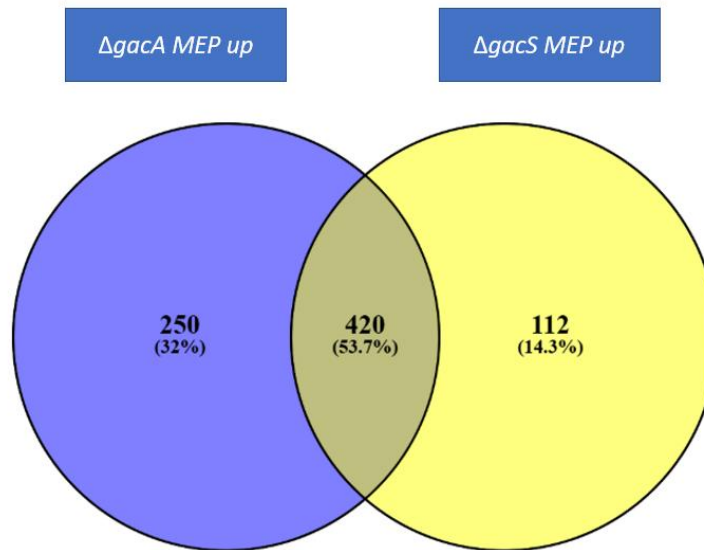
Downregulated genes in MEP: In the case of the downregulated genes, $\Delta gacA$ exhibited **650** instances, whereas $\Delta gacS$ displayed **506**, resulting in **445** genes being shared between the two. Notably, the majority of the differentially expressed genes were found to be common to both mutants; however, $\Delta gacA$ presented **205** unique downregulated genes in contrast to the **61** that were unique to $\Delta gacS$. Overall, these findings indicate that $\Delta gacA$ and $\Delta gacS$ possess a significant core group of regulated targets within the MEP pathway, aligning with their roles as a cognate pair. Nevertheless, the existence of unique gene sets in each mutant implies that the lack of the regulator compared to the sensor kinase results in different transcriptional effects, which may represent varying degrees of direct transcriptional regulation by GacA in contrast to the signaling disruptions resulting from the absence of GacS.

Upregulated genes in LSP: In the LSP condition, the upregulated genes for $\Delta gacA$ were **846**, whereas $\Delta gacS$ exhibited **807**, resulting in a significant overlap of **448** genes. Despite this shared regulon, there were **398** genes that were uniquely upregulated in $\Delta gacA$ and **360** that were uniquely upregulated in $\Delta gacS$, suggesting that both mutants elicited extensive yet partially distinct transcriptional responses.

Downregulated genes in LSP: In the case of the downregulated genes, *ΔgacA* exhibited a total of **678**, whereas *ΔgacS* presented **591**, with **403** genes being common to both. Consequently, there were **275** genes that were uniquely downregulated in *ΔgacA* and **188** that were uniquely down-regulated in *ΔgacS*.

Collectively, these findings indicate that in LSP, both *ΔgacA* and *ΔgacS* mutants influence a diverse range of transcripts, exhibiting a significant common core alongside extensive groups of unique genes. In contrast to MEP, the overlap between *ΔgacA* and *ΔgacS* is relatively diminished, implying that the consequences of impairing either element of the GacAS system become more distinct during the stationary phase, probably due to intricate signaling interactions and extensive physiological reorganization.

(A)



(B)

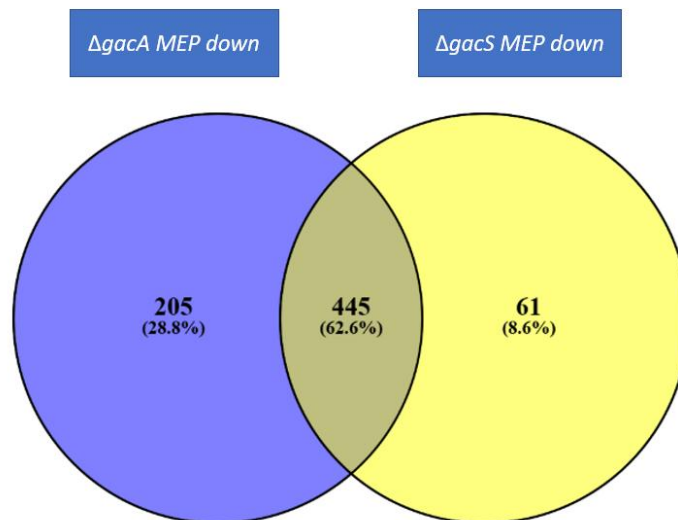
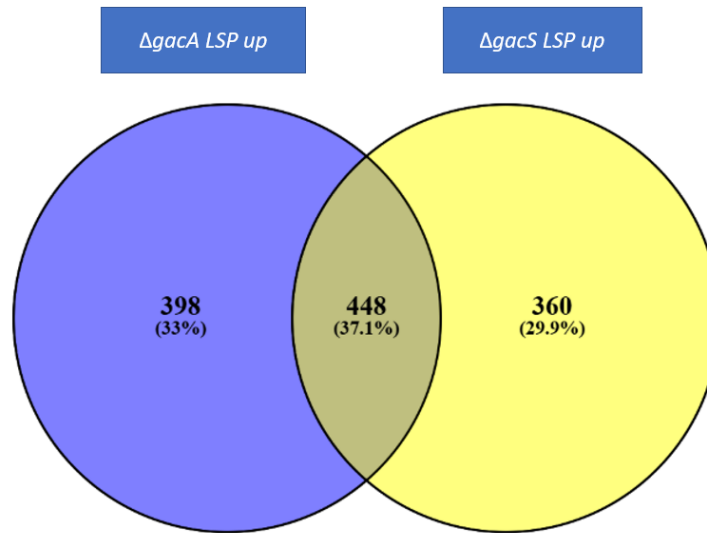


Figure 3.13 Venn diagrams illustrating the transcriptomes of $\Delta gacA$ and $\Delta gacS$ during the MEP process. (A) Genes that are up-regulated: $\Delta gacA$ (766), $\Delta gacS$ (628), with 489 genes being common to both. (B) Genes that are down-regulated: $\Delta gacA$ (758), $\Delta gacS$ (625), with 537 genes shared. The significant overlaps underscore the presence of a shared GacAS regulon, whereas the distinct sets suggest that the deletion of either the sensor or the regulator can lead to different transcriptional outcomes.

(A)



(B)

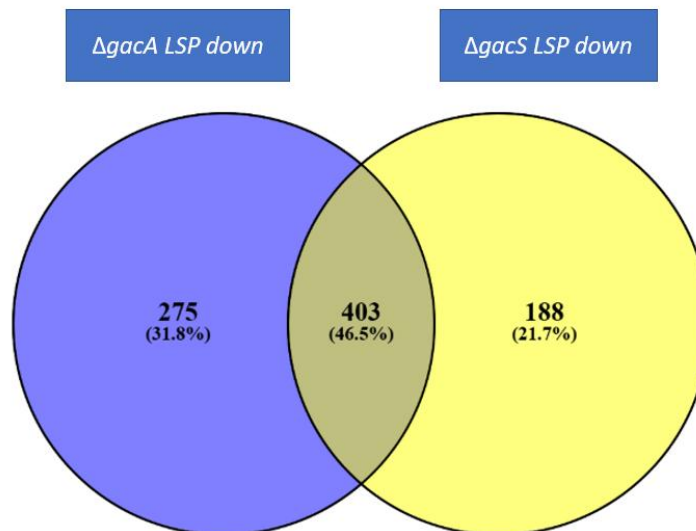


Figure 3.14 Venn diagrams illustrating the transcriptomes of $\Delta gacA$ and $\Delta gacS$ during LSP. **(A)** Genes that are upregulated: $\Delta gacA$ (846) and $\Delta gacS$ (807), with 448 genes in common. **(B)** Genes that are downregulated: $\Delta gacA$ (678) and $\Delta gacS$ (591), with 403 genes in common. Despite the mutants sharing a significant number of differentially expressed genes, each also exhibits considerable unique subsets, suggesting a greater divergence in transcriptional effects during LSP as opposed to MEP.

3.7 Regulation of small RNAs in TCS mutant strains.

Although transcriptomic data exists for the TCS mutants from previous work, none of them has focused on the expression of small RNAs, because they are not part of the standard NCBI annotation and but were annotated in a few publications from transcriptomic data (Weiss *et al.*, 2016; Kröger *et al.*, 2018). The data for this study was not specifically generated for the expression of sRNAs and they are often lost during standard RNA-seq library preparation. Therefore, the data have to be analyzed and interpreted with care. Confirmatory experiments of expression via northern blotting or qRT-PCR should be conducted. Nevertheless, the expression of sRNAs was part of the transcriptomic analyses and are shown in Figures 3.15 (differential gene expression; DESeq2 data) and 3.16 (TPM values).

A previous reported that the sRNA Aar (sRNA21), was mildly upregulated in the $\Delta adeR$ mutant and downregulated in the $\Delta gacS$ mutant (Fergal J. Hamrock *et al.*, 2024). The transcriptomic data agreed for the $\Delta gacS$ mutant (Fergal J. Hamrock *et al.*, 2024), which was 2.7-fold downregulated in LSP confirming that GacS appears to be an activator of Aar. The effect was even stronger in the $\Delta gacA$ mutant in LSP (18-fold downregulated). For the $\Delta adeR$ deletion strain, a downregulation was also observed which was opposite to the published data. Further experiments are required to clarify the regulation.

The CsrB (sRNA97), CsrC (104), CsrD (sRNA109) sRNAs were all reported to be downregulated in the $\Delta gacA$ mutant (Singh *et al.*, 2025). This was confirmed for CsrB and CsrC most prominently in LSP (861-fold and 11.7-fold downregulated), which CsrD showed a slight (2.3-fold) upregulation. The effect in the $\Delta gacS$ mutant was similar for CsrB and CsrC (63-fold and 5.6-fold downregulated) and no change for CsrD. Therefore, there was a good but not fully consistent overlap with published data.

In the $\Delta adeR$ mutant, the largest differences in gene expression of sRNAs was in the LSP condition (Figure 3.15). Two small RNAs (sRNA7 and sRNA44) were strongly upregulated (16.5-fold and 14.5-fold), where AdeR acts as a repressor. The sRNA7 is of unknown function and would require further investigation. For sRNA44, there is preliminary data that it might be a regulator of the biofilm-associated protein Bap

(Mogre et al., 2025). The Bap protein is not only involved in biofilm production but also in adhesion to surfaces, therefore AdeR might be indirectly involved in controlling biofilm production and adhesion via sRNA44 control of Bap. Highly downregulated sRNAs, where AdeR acts as an activator are sRNA65 (30-fold), sRNA74 (37-fold) and sRNA103 (29-fold). None of these have been investigated in detail, though. Curiously, all regulatory effects in the $\Delta adeR$ mutant were not observed in the $\Delta adeS$ mutant.

For the BaeRS TCS, as described earlier, larger effects on gene expression were observed in the $\Delta baeS$ mutant at LSP. Here, BaeS appears to mostly act as a repressor of sRNA expression. No small RNA was highly downregulated in the $\Delta baeS$ or $\Delta baeR$ mutants. However, a few sRNAs showed very strong upregulation upon deletion of *baeS* suggesting that BaeS represses their expression. Most strongly upregulated were sRNA26 (39-fold), sRNA77 (108-fold), sRNA81 (47-fold), 6S (sRNA84, 265-fold) and sRNA100 (56-fold). Again, none of the sRNAs have been described in detail, however, 6S RNA has been studied in many bacteria, most prominently in *E. coli* as an sRNA that binds to RNA polymerase in stationary phase to mimic promoter structures and sequester RNA polymerase (Wassarman, 2018).

The GacSA TCS had the most prominent effect on sRNA gene expression and in contrast to AdeRS and BaeRS, the effects of deleting *gacA* or *gacS* were largely similar (Figure 3.15). Apart from the mentioned effects above, sRNA97 (861-fold in $\Delta gacA$, 48-fold in $\Delta gacS$), sRNA99 (56-fold in $\Delta gacA$, 48-fold in $\Delta gacS$) and sRNA100 (13-fold in $\Delta gacA$, 4-fold in $\Delta gacS$) were among the most downregulated genes upon deletion of *gacA* or *gacS* indicating that they are activators of their expression. Multiple sRNAs were strongly upregulated (> 15-fold) in both mutants, including sRNA24, sRNA26, sRNA53, sRNA77, sRNA81, 6S (sRNA84), sRNA92 and sRNA94, suggesting that both proteins are repressors of transcription of a large number of sRNAs. None of the sRNAs mentioned above are described in any mechanistic detail. Of course, all the effects of differences in sRNA expression could be indirect responses to changes in cell physiology when TCSs are deleted. Whether any of the response regulators are directly regulating the expression of the sRNAs will be investigated in Chapter 4.

3.8 Pathway analyses using transcriptomic data of TCS mutants.

To contextualize the transcriptomic data and to acquire a better understanding of the global patterns in the data, a gene ontology (GO) analysis was carried out to assess whether differences in gene regulation could be functionally grouped. The GO analysis was provided by Dr. Anna Ershova (Department of Microbiology, TCD). The analysis was focused on the “Biological Processes (BP)” pathways and comparing wildtype and mutant strains in MEP and LSP.

Comparing biological processes between WT and $\Delta adeR$ and $\Delta adeS$ mutants, the number of processes changing in the $\Delta adeS$ mutant compared to WT is greater than for the $\Delta adeR$ mutant (**Figure 3.17**), which is reflected by the larger number of genes showing differential gene expression (**Table 3.1**).

Upregulated processes at MEP $\Delta adeR$ and $\Delta adeS$ mutants have in common are lysine biosynthetic process via diaminopimelate [GO:0009089] and ‘*de novo*’ IMP biosynthetic process [GO:0006189], while at LSP, it was biotin biosynthetic process [GO:0009102] and nucleobase-containing compound metabolic process [GO:0006139]. Downregulated processes at MEP that $\Delta adeR$ and $\Delta adeS$ mutants have in common are organonitrogen compound metabolic process [GO:1901564], histidine catabolic process to glutamate and formate [GO:0019557] and glutamate and formamide [GO:0019566], as well as iron ion transport [GO:0006826] and intracellular iron homeostasis [GO:0006879]. In LSP, siderophore biosynthetic process [GO:0019290], acetyl-CoA biosynthetic process [GO:0006085] and trehalose biosynthetic process [GO:0005992] were commonly down-regulated. Therefore, there is large overlap of biological processes that are commonly regulated by AdeRS. Several processes are related to central metabolism such as amino acid metabolism, synthesis of acetyl-CoA and iron homeostasis. Regulation of iron metabolism and siderophore biosynthesis are also like to affect virulence of *A. baumannii*.

Biological pathways differentially expression between WT and $\Delta baeR$ and $\Delta baeS$ mutants are shown in **Figure 3.18**. It is apparent that in the $\Delta baeR$ mutant pathways are only downregulated at MEP (**Figure 3.18A**), while, as seen before, there is hardly any change at LSP, where only *baeR* itself shows no gene expression which can be

seen as the phosphorelay signal transduction system [GO:0000160] process (**Figure 3.18B**). In common between $\Delta baeR$ and $\Delta baeS$ in MEP are only downregulated pathways at MEP: iron ion transport [GO:0006826], and histidine catabolic process to glutamate and formate [GO:0019557] and glutamate and formamide [GO:0019566]. Interestingly, several processes in the $\Delta baeS$ mutant in MEP and LSP were in relation to cell division and cell wall biosynthesis. At MEP the processes diaminopimelate biosynthetic process [GO:0019877] and lysine biosynthetic process via diaminopimelate [GO:0009089] were upregulated which could be involved in creating building blocks for peptidoglycan. At LSP, potentially the consequences can be seen as upregulated processes are cell wall organization [GO:0071555], cell division [GO:0051301], peptidoglycan biosynthetic process [GO:0009252], regulation of cell shape [GO:0008360] and cell cycle [GO:0007049] (**Figure 3.18C&D**). Of note is also that processes histidine catabolic process to glutamate and formate [GO:0019557] and glutamate and formamide [GO:0019566] are downregulated at MEP but then upregulated at LSP in the $\Delta baeS$ mutant suggesting a dysregulation of these pathways across both growth phases and a dual role (up- and downregulation) of BaeS for their regulation.

Comparison of differentially expressed biological processes between WT and $\Delta gacA$ and $\Delta gacS$ mutants revealed a large overlap (**Figure 3.19**). Multiple processes were upregulated in both mutants at MEP (**Figure 3.19A&C**): arginine catabolic process to succinate [GO:0019545] and glutamate [GO:0019544], arginine biosynthetic process [GO:0006526] 'de novo' UMP [GO:0044205] and IMP [GO:0006189] biosynthetic processes, iron-sulfur cluster assembly [GO:0016226], lysine biosynthetic process via diaminopimelate [GO:0009089] tricarboxylic acid cycle [GO:0006099] and translation [GO:0006412]; and downregulated at MEP: type IV pilus assembly [GO:0043683], pilus assembly [GO:0009297] and chemotaxis [GO:0006935]. There was much less overlap of biological processes at LSP (**Figure 3.19B&D**). Upregulated was the biological process one-carbon metabolic process [GO:0006730] and downregulated was the response to oxidative stress [GO:0006979]. Potentially, GacS and GacA work predominantly as a TCS in MEP, while at LSP more specific effects of the individual deletion are observed. At MEP, GacSA appears to control multiple biological

processes in relation to amino acid and nucleotide metabolism and the TCA cycle, suggesting that is a regulator of central metabolic flux.

	adeR		adeS		baeR		baeS		gacA		gacS	
	MEP	LSP	MEP	LSP	MEP	LSP	MEP	LSP	MEP	LSP	MEP	LSP
sRNA1			1.02				3.07	4.21	2.69	3.08	3.39	4.87
sRNA2			2.19	2.6	3.47		2.98	1.69	-1.62	-4.12		-4.88
sRNA3								1.12				2.14
sRNA4		1.27		1.7		1.25	-2.14	3.95	-3.91	-1.75		5.18
sRNA5			-1.35		-1.29				-1.18	-1.75		3.01
sRNA6		-2.26			-2.61		1.00	-1.92	2.15			
sRNA7		4.05		1.8	2.28			2.93				3.29
sRNA8			-1.05					1.02	-1.92		-1.11	
sRNA9			1.86		-1.07			2.74	1.47		1.29	2.03
sRNA10					1.27			-1.93	-2.40			1.42
sRNA13		-1.41						-2.31	1.32			-2.29
sRNA15	1.15		1.16				2.18	3.13	1.52	1.98	2.53	2.84
sRNA17								-1.10				
sRNA18								-1.35	-1.38	-1.28		
sRNA20		-1.14		1.6	3.12				1.74	1.73	2.07	3.22
sRNA21		-3.26			-1.25		-1.65	-1.66	-1.34	-4.20		-1.43
sRNA22									2.51		1.85	1.71
sRNA24			1.75		-1.79		3.15	4.17	2.95	3.94	3.48	4.87
sRNA25					-1.40			1.82			1.42	1.59
sRNA26								5.28	1.77	6.20	1.42	5.37
sRNA27	-1.20		-2.18						-2.83	-2.74	-1.54	
sRNA28									-1.68	-2.07		
sRNA29		-1.12			-1.34				-6.00		-6.57	-1.49
sRNA30		-2.35						-1.44		-1.97		-1.07
sRNA31		-1.77					-2.23	-1.87	-2.41	-1.60	-1.61	-1.25
sRNA32		-1.25			-1.49			-1.21	-2.71		-2.52	
sRNA37		-1.43						2.06	1.94	3.75	1.71	3.32
sRNA38		-1.94						1.58		1.67	1.48	2.13
sRNA39		-1.33			1.26			1.66		1.86		1.55
sRNA40		2.08										
sRNA42		-2.70			1.29		2.66		1.73		3.10	1.34
sRNA44		3.86		1.8					-2.56		-3.75	2.43
sRNA46					-1.40		1.58	4.31	1.05	1.68	1.81	3.64
sRNA48		2.93	4.20		2.75				2.18		3.30	
sRNA49	-1.12			1.8				2.36				2.88
sRNA50				1.6	-1.26			1.01	-1.56	-1.23		1.06
sRNA53				2.7				4.32		4.74		5.45
sRNA54		1.50		1.9				2.43		-1.49	1.49	2.23
sRNA55		-1.11	1.60		2.07		1.37		2.19	2.59	1.79	
sRNA56		-2.81							-2.48	-1.64	-2.25	
sRNA57			-2.54		1.85	1.22			-1.52			2.05
sRNA58				2.3				1.71	1.00	-1.07		1.44
sRNA59		-1.07									1.80	2.06
sRNA60					-1.01			2.71		1.28		3.77
sRNA61		-1.20		1.0				2.08	-3.21	2.47	-2.19	2.65
sRNA62		1.75				-2.34		4.92	2.56	3.13	2.28	4.26
sRNA63							1.28					1.59
sRNA64		-1.14				-2.33			-5.25	1.70	-3.53	1.68
sRNA65	-1.06	-4.80							-2.20	-3.23	-1.00	-1.60
sRNA69					1.26				-1.40	-1.06		
sRNA70					-1.40				3.31	3.09	1.13	2.46
sRNA71		-1.64										1.75
sRNA72					2.20				-1.14	-2.08		
sRNA73									-1.42			3.27
sRNA74		-5.19										
sRNA75			-1.78						-3.70		-2.63	1.41
sRNA76					-1.17		-1.78	1.47	-1.20		-1.26	1.36
sRNA77		1.77	-1.20	2.1				6.76		3.61	2.51	4.80
sRNA81	1.08	1.05	1.58				2.80	5.56	2.67	5.39	3.41	5.44
sRNA84							4.94	8.05	2.59	4.62	5.01	6.56
sRNA85		-1.16						2.13	-3.35		-1.76	-1.54
sRNA86					-1.18		-2.21			-1.25		1.07
sRNA87		1.39		1.1	-1.51				-3.16	-1.84		
sRNA88			1.59		-2.04		1.70	3.48		3.39	1.53	3.13
sRNA89		1.55			-1.07			3.67		3.74		1.89
sRNA90							1.60	1.35		-2.54	1.65	
sRNA91									1.06			
sRNA92		-1.75	4.43		2.64			2.80	6.10	3.33	4.50	4.08
sRNA93					-1.13			3.32				2.00
sRNA94		-1.13			-1.40			2.61	4.72	3.72	3.90	2.39
sRNA95		1.44		1.5				2.09		4.26		1.56
sRNA96	1.19	-2.05	1.36		1.33		2.51		3.19		4.11	
sRNA97								1.20	-5.99	-9.75	-3.93	-5.97
sRNA98								-1.21				
sRNA99		1.66	1.26		1.05				-5.22	-5.80	-7.56	-5.59
sRNA100		1.71		1.2			2.23	5.18	-1.58	-3.70		-2.00
sRNA101		-3.00						1.11	1.84		1.67	
sRNA102		-2.26					1.43		1.56	2.22	2.08	2.62
sRNA103		-4.84			-2.54				-1.83	-4.46		-1.28
sRNA104		-1.22	-1.22		1.26		1.04			-3.55		-2.49
sRNA105								1.67		-2.35		2.27
sRNA106		1.71		2.3	-1.26		1.95		1.24	-7.74	2.31	-5.01
sRNA109			-1.23							1.23		
sRNA110			-1.23							1.23		

Figure 3.15 A heat map illustrating the differentially expressed sRNA (DEGs) between the wild-type (WT) and mutant strains of *Acinetobacter baumannii*, as analyzed using DESeq2. The color gradient signifies normalized expression levels, with red denoting upregulation and blue signifying downregulation in comparison to the average expression across the samples.

	adeR MEP	adeR-LSP	adeS MEP	adeS LSP	baeR MEP	baeR LSP	baeS MEP	baeS LSP	gacA MEP	gacA LSP	gacS MEP	gacS LSP
sRNA1												
sRNA2												
sRNA3												
sRNA4												
sRNA5												
sRNA6												
sRNA7												
sRNA8												
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sRNA109												
sRNA110												
newcandsRNA1												

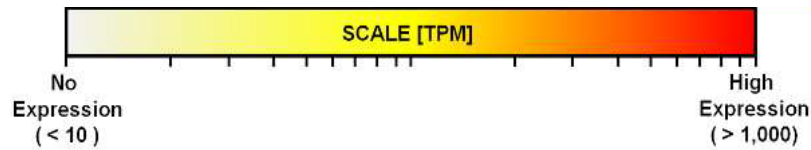
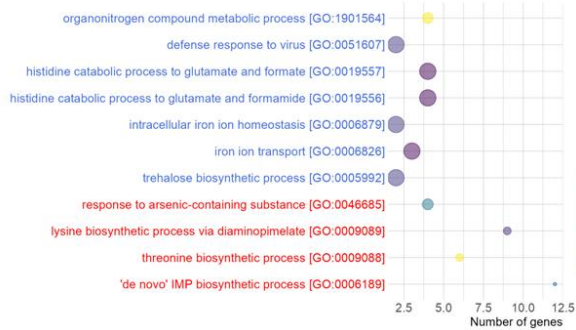
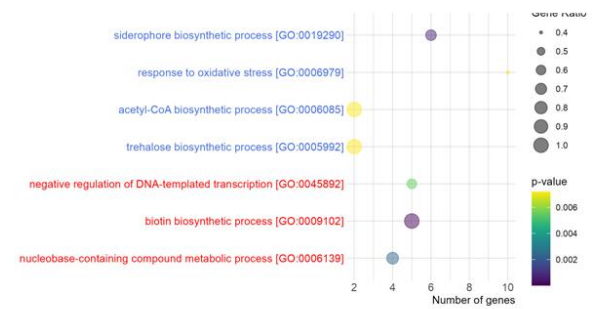


Figure 3.16 Heat map showing overall sRNA expression profiles of *Acinetobacter baumannii* mutant strains based on TPM (Transcripts Per Million) values. TPM normalization accounts for both gene length and sequencing depth, allowing visualization of absolute expression abundance for each sRNA across samples. The color scale represents where darker shades indicate higher transcript abundance. This heat map illustrates the general expression patterns of the analyzed genes but does not reflect statistical significance between conditions.

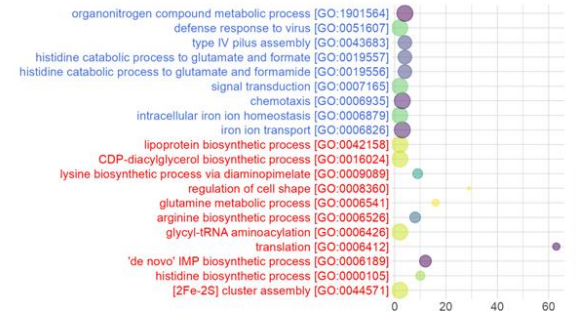
A - WT vs $\Delta adeR$ - MEP



B - WT vs $\Delta adeR$ - LSP



C - WT vs $\Delta adeS$ - MEP



D - WT vs $\Delta adeS$ - LSP

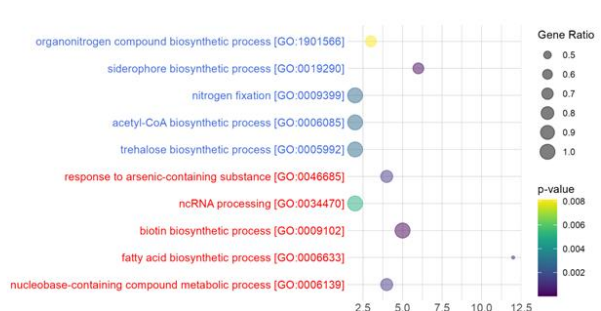


Figure 3.17 GO analysis (BP) of WT versus $\Delta adeR$ (A & B) and $\Delta adeS$ (C & D) in MEP (A & C) and LSP (B & D). Biological processes upregulated are highlighted in red and downregulated in blue. Gene ratio shows percentage of genes with differential gene expression for each pathway. Color of circles indicate p values.

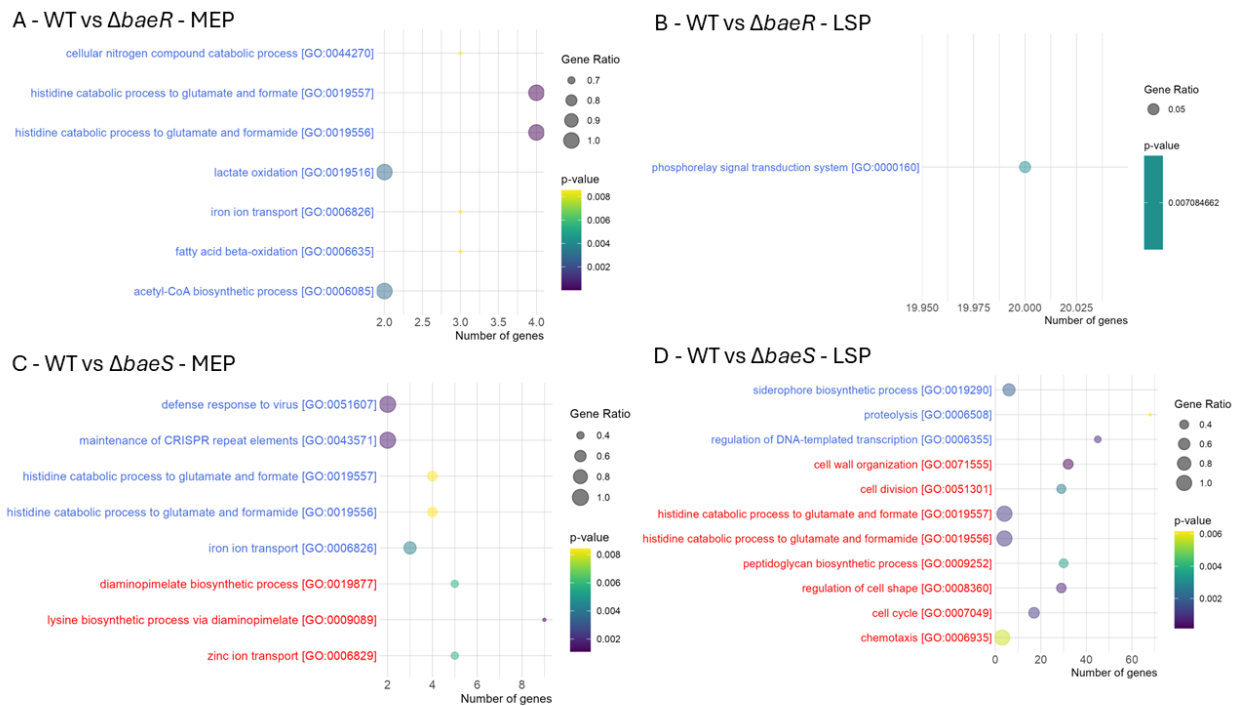
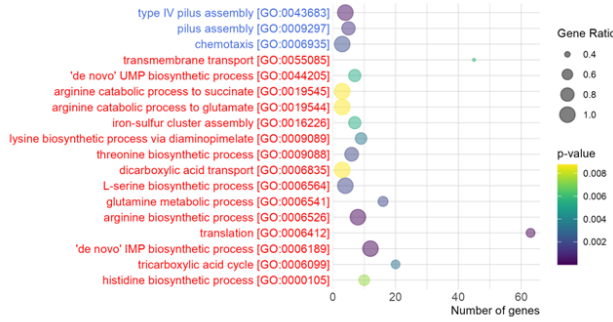
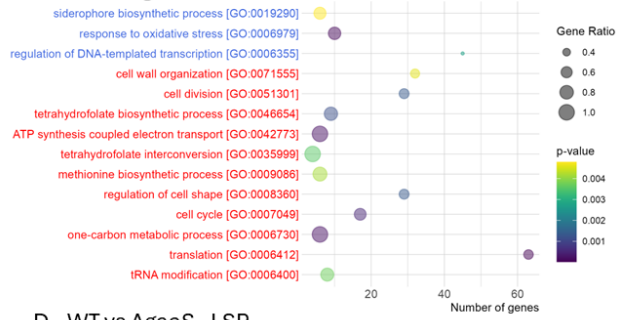


Figure 3.18 GO analysis (BP) of WT versus $\Delta baeR$ (A & B) and $\Delta baeS$ (C & D) in MEP (A & C) and LSP (B & D). Biological processes upregulated are highlighted in red and downregulated in blue. Gene ratio shows percentage of genes with differential gene expression for each pathway. Color of circles indicate p values.

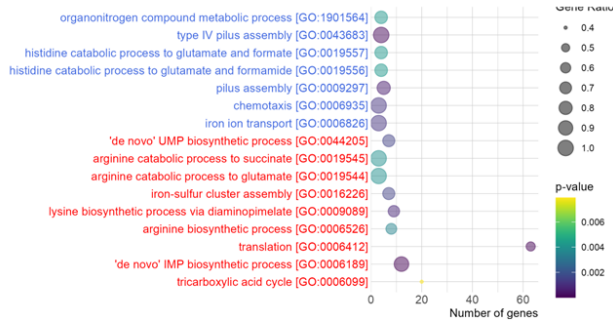
A - WT vs Δ gacA - MEP



B - WT vs Δ gacA - LSP



C - WT vs Δ gacS - MEP



D - WT vs Δ gacS - LSP

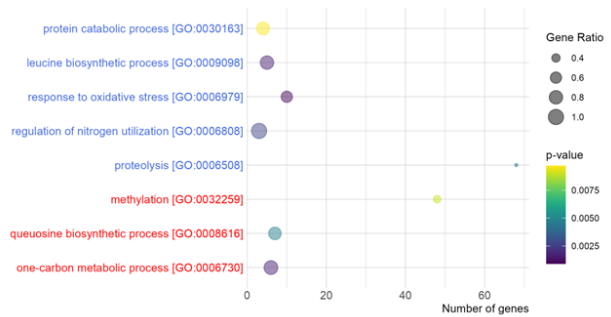


Figure 3.19 GO analysis (BP) of WT versus Δ gacA (A & B) and Δ gacS (C & D) in MEP (A & C) and LSP (B & D). Biological processes upregulated are highlighted in red and downregulated in blue. Gene ratio shows percentage of genes with differential gene expression for each pathway. Color of circles indicate p values.

Chapter 4

The dRNA-seq and ChIP-seq methodologies uncover the regulatory framework of *Acinetobacter baumannii* AB5075

4.1 Introduction

Acinetobacter baumannii is an opportunistic pathogen of high priority that flourishes in hospital settings and is well known for its ability to acquire, express, and manage various antibiotic resistance factors (Howard *et al.*, 2012). In addition to the existence of resistance genes, the timing and extent of their expression play a crucial role in determining phenotypes, including adaptive resistance, and persistence (Rokes *et al.*, 2025; Goncalves *et al.*, 2025). Therefore, it is vital to decode the transcriptional programs and the regulatory elements that connect them to comprehend how *A. baumannii* endures antibiotic exposure and to identify potential intervention points (Allen *et al.*, 2020). Bacterial transcription is regulated at two closely linked levels: (i) genomic characteristics that determine the initiation points of transcription (promoters and transcriptional start sites, TSS), and (ii) regulatory proteins that influence the timing and intensity with which these promoters activate in reaction to environmental signals (Bischler *et al.*, 2015; Wood *et al.*, 2018).

This chapter combines two complementary genomic methodologies to create a high-resolution map of transcription and its regulation in the multidrug resistant strain AB5075. Differential RNA sequencing (dRNA-seq) utilizes the enzymatic distinction between primary transcripts that possess 5'-triphosphate ends and processed RNAs that contain 5'-monophosphates (Sharma *et al.*, 2010; Bischler *et al.*, 2015). Through the comparison of libraries that have been treated with a 5'-monophosphate-dependent exonuclease (+TEX) and those that have not been treated (–TEX), dRNA-seq enhances the identification of primary start sites and facilitates accurate, single-nucleotide mapping of transcription start sites (TSSs). When integrated with motif analysis and metrics related to promoter architecture (such as –10/–35 elements and the distances between TSS and start codon), dRNA-seq produces a comprehensive genome-scale promoter atlas, thereby elucidating the structure and diversity of

transcription initiation in AB5075 (Kröger *et al.*, 2012; Dugar *et al.*, 2013; Kröger *et al.*, 2013; Wicke *et al.*, 2020).

Chromatin immunoprecipitation coupled with sequencing (ChIP-seq) enhances the transcript centric perspective by mapping the DNA occupancy of regulatory proteins throughout the genome. In this study, we examine the binding profiles of three response regulators, AdeR, BaeR, and GacA, which respond to different environmental conditions and manage stress adaptation in *A. baumannii*. Conducting ChIP-seq with DNA-binding transcription factors like response regulator strains allows the identification of the location of high-confidence binding peaks, the delineation of consensus motifs, and the correlation of binding events with the activity of adjacent promoters.

When examined independently, each dataset offers significant biological insight with dRNA-seq identifying transcription initiation sites, whereas ChIP-seq uncovers the locations where regulatory proteins bind to the genome. The integration of these elements can facilitate the identification of direct regulation of promoters that contain regulator binding sites and initiate transcription. In practical terms, this synthesis differentiates between direct and indirect effects identified in transcriptome studies, emphasizing candidate promoters regulated by response regulators under investigation.

4.2 Differential RNA sequencing

Identifying the location of bacterial promoters is crucial for understanding how genes are controlled. Differential RNA sequencing an effective method for locating each promoter in a bacterial genome (**Figure 4.1**). Knowledge of the location of transcriptional start sites (TSSs) identifies the promoters of genes, which specify where RNA polymerase begins transcription, and how genes are turned on/off, consequently influencing both the timing and magnitude of gene expression (Zhu *et al.*, 2024). Precise mapping of promoters offers essential understanding of bacterial regulatory networks, encompassing those that govern virulence and antimicrobial resistance (Kröger *et al.*, 2018). This methodology has been effectively utilized across various bacterial species, including *Escherichia coli*, *Salmonella enterica*, and

Helicobacter pylori among others where it has yielded detailed transcriptional maps and enhanced our comprehension of gene regulation (Sharma *et al.*, 2010; Kröger *et al.*, 2012; Thomason *et al.*, 2015).

Despite the increasing availability of genomic and transcriptomic data, our understanding of the transcriptional structure of *A. baumannii*, particularly regarding the positioning of promoters and regulatory elements, is still inadequate. This information is essential for analyzing the regulatory networks governed by transcription factors and two-component systems that play a role in its pathogenesis and multidrug resistance (Fiester and Actis, 2013). In this chapter, we first utilized dRNA-seq on the multidrug-resistant strain *A. baumannii* AB5075 to create a comprehensive genome-wide map of transcriptional start sites and promoters.

Differential RNA-seq has been conducted in *A. baumannii* ATCC17978 (Kröger *et al.*, 2018). In this study, I performed this analysis with the multidrug resistant *A. baumannii* AB5075 strain (Jacobs *et al.*, 2014a). RNA was isolated from cells grown in L-broth of the two environmental conditions MEP and LSP as shown in **(Table 4.1)**. The primary objective is to pinpoint the positions of promoters, as this may uncover the regions on the genome where different transcription factors may bind to promoters. The dRNA-seq technique differentiates between primary and processed 5' ends through the sequencing of distinct cDNA library pairs: one library is labeled (TEX-) and is derived from untreated total bacterial RNA, while the other library (TEX+) is enriched for primary transcripts following treatment with a terminator exonuclease, which degrades 5' monophosphate (5'P) RNA but leaves 5' triphosphate (5'PPP) RNA intact. The sequencing reads acquired through dRNA sequencing were aligned to the genome by Dr. Carsten Kröger (see Material and Methods). The location of the TSS were predicted with the TSS Predator software (Dugar *et al.*, 2013; Kröger *et al.*, 2018).

In total, we identified 9428 transcription start sites (TSS) using the TSS software with its default settings **(Table 4.2)**. Among these, 2273 are categorized as primary TSS, indicating their location upstream (within 400 base pairs) of a coding sequence. The counts of primary TSS are 1878 in (MEP) and 2137 in (LSP). However, we noted a number of antisense TSS, with 3952 in LSP compared to 3538 in MEP, as well as a

greater number of internal TSS in LSP (3380 in LSP versus 1853 in MEP). The reason for this increase remains unclear, nevertheless, a visual inspection of several of these transcription start sites (TSS) indicates that most are producing short, lowly expressed transcripts, which may be non-functional. A total of 443 TSS were identified exclusively in MEP and not in LSP, while 2482 were found solely in LSP and absent in MEP. Among these, 136 are classified as primary TSS in MEP, and 395 are primary TSS in LSP, suggesting that these represent specifically active promoters for each condition (**Table 4.2**). The genes regulated by these promoters may be considered condition-specific for MEP or LSP. Furthermore, we have identified several orphan TSS, totaling 164. A more thorough analysis is required to understand their functions. Some of these may produce novel non-coding RNAs, or it is possible that a gene was missed during the annotation process.

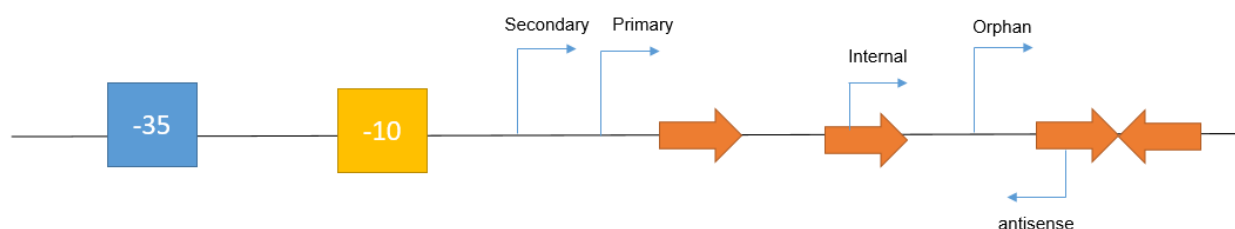


Figure 4.1 Categories of Transcriptional start sites (TSS) identified by dRNA-seq. TSS were divided into five groups according to their genomic position and expression pattern. Primary TSS: the most highly expressed TSS found ≤ 400 upstream of a coding region or noncoding RNA gene. Secondary TSS: extra upstream TSS for the same gene with lower expression levels. Internal TSS: TSS found within a coding region on the sense strand. Antisense TSS: TSS located within or opposite a coding region on the antisense strand. Orphan TSS: TSS that cannot be linked to any nearby annotated gene.

Table 4.1 Different conditions the RNA was isolated from.

Name	Growth Conditions
MEP (Mid Exponential Phase)	L-broth, OD = 0.3
LSP (Late Stationary Phase)	L-broth, 16h of growth (o/n)

Table 4.2 TSS prediction statistics: All Primary Secondary Internal Antisense Orphan in AB5075 strain.

TSS prediction statistics	All	Primary	Secondary	Internal	Antisense	Orphan
Complete number of detected TSS	9428	2273(24%)	1034(11%)	3567(38%)	4050(43%)	164(2%)
Number of TSS detected in all strains/conditions	6503	1742(27%)	594(9%)	1666(26%)	3440(53%)	112(2%)
Number of TSS detected in MEP	6946	1878(27%)	717(10%)	1853(27%)	3538(51%)	118(2%)
Number of TSS detected in LSP	8985	2137(24%)	911(10%)	3380(38%)	3952(44%)	158(2%)
Number of TSS only detected in MEP	443	136(31%)	123(28%)	187(42%)	98(22%)	6(1%)
Number of TSS only detected in LSP	2482	395(16%)	317(13%)	1714(69%)	512(21%)	46(2%)
Number of TSS only missing in MEP	2482	395(16%)	317(13%)	1714(69%)	512(21%)	46(2%)
Number of TSS only missing in LSP	443	136(31%)	123(28%)	187(42%)	98(22%)	6(1%)

4.3 Identification of –10 and –35 sigma factor motifs

Sigma factors are proteins found in bacteria that help RNA polymerase locate the right promoter by identifying the conserved –10 and –35 motifs, which ensures transcription starts accurately. DNA sequences located upstream of all transcription start sites were gathered in two segments of nucleotides: one from position (–10 block) and the other from (–35 block). Each segment was analyzed using the unbiased motif discovery tool MEME (**Figure 4.2**).

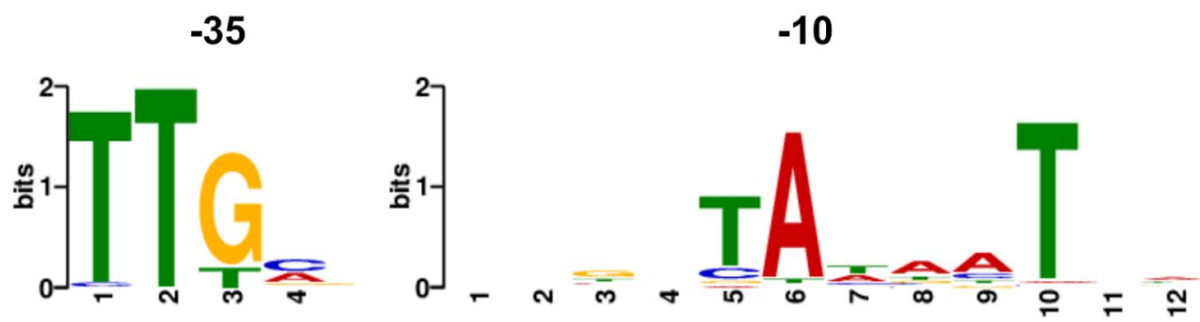
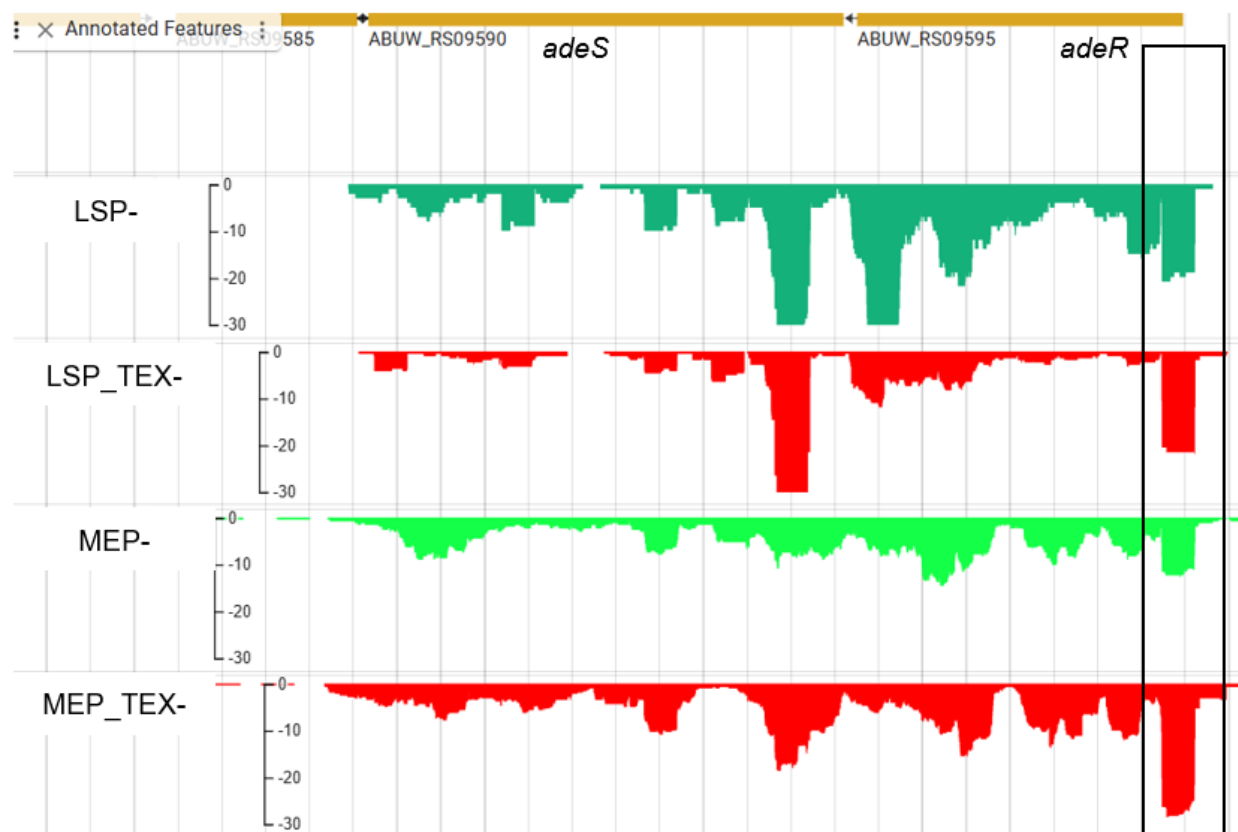
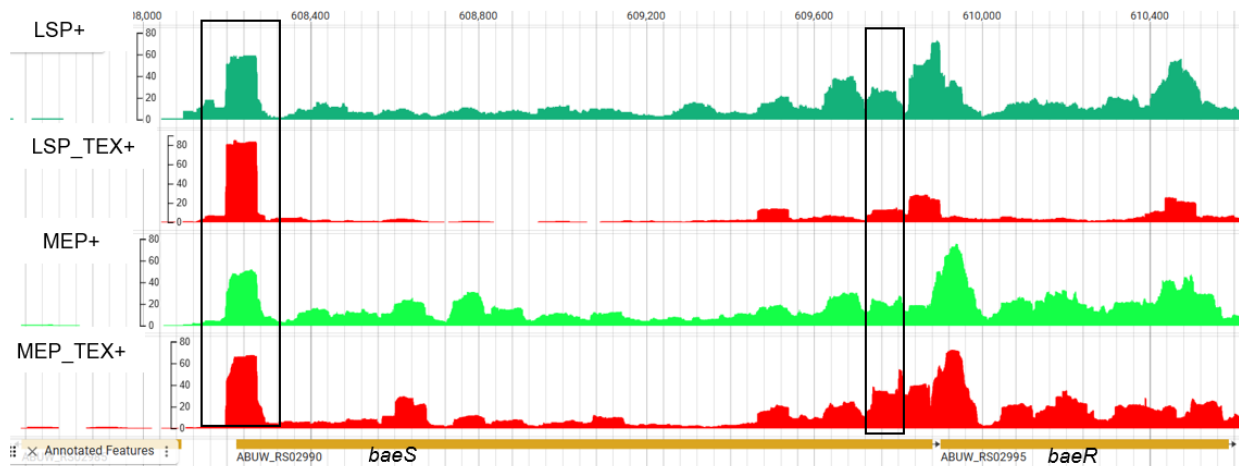


Figure 4.2 Promoter motifs (-35 and -10) derived from upstream regions of transcriptional start sites (TSSs) mapped by dRNA-seq in *Acinetobacter baumannii* AB5075.

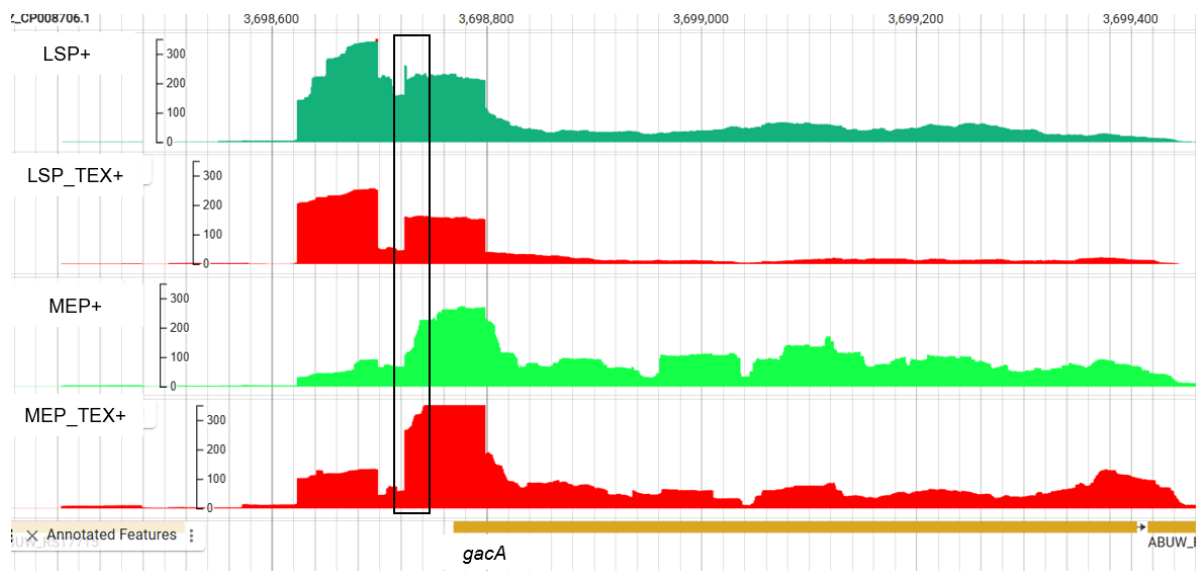
(A)



(B)



(C)



(D)

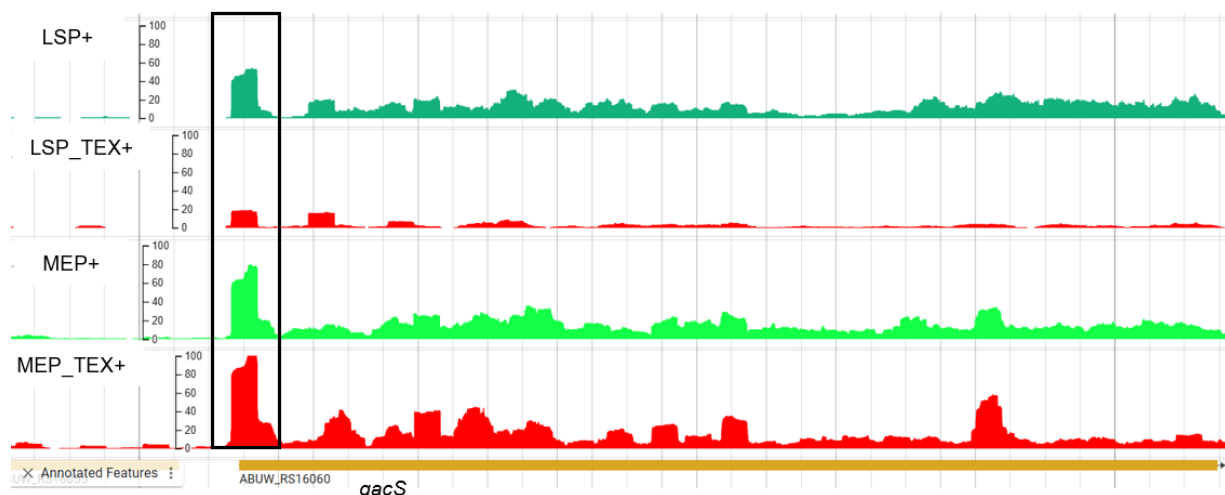


Figure 4.3 Visualization of transcriptional start sites (TSS) using JBrowse for selected Two-Component System (TCS) genes in *Acinetobacter baumannii* AB5075. Coverage plots from differential RNA-seq (dRNA-seq) are displayed for both (+TEX) and (–TEX) libraries, where TEX treatment enhances the detection of primary transcripts. The distinct peaks of enrichment in the +TEX libraries show the locations of transcriptional start sites before the *adeRS*, *gacSA*, and *baeRS* genes. These peaks verify the existence of active promoters that control each of these TCS regions. The highlight peaks show where the gene start sites are.

4.4 The binding sites of AdeR, BaeR, and GacA in *Acinetobacter baumannii* using ChIP-seq

Bacteria depend on transcriptional regulation to adapt rapidly changing environments, particularly under stress conditions faced during infections or antibiotic therapies. At the heart of this regulation are response regulators (RRs) associated with two-component systems (TCSs), which influence gene expression in reaction to environmental signals (Stock *et al.*, 2000; Tiwari *et al.*, 2017). RRs generally act as DNA-binding proteins that either activate or inhibit transcription following phosphorylation by their corresponding sensor kinases (Song *et al.*, 2022; Shaw *et al.*, 2022). Consequently, identifying the DNA-binding sites of response regulator is

crucial for comprehending the regulatory networks that control bacterial physiology and antibiotic resistance. Chromatin immunoprecipitation followed with sequencing (ChIP-seq) has emerged as a powerful technique for the global identification of proteins. This method is based on the *in vivo* crosslinking of proteins to DNA, followed by the immunoprecipitation of the target protein using a specific antibody, and the subsequent high-throughput sequencing of the associated DNA fragments (Johnson *et al.*, 2007; Park, 2009). In bacterial systems, ChIP-seq has been extensively utilized to delineate the binding sites of transcription factors and sigma factors, thus uncovering their regulons and direct target genes but only few studies exist that used ChIP-seq in *A. baumannii* (Raustad *et al.*, 2024). The examination of TCSs in *A. baumannii* holds significant relevance, as this opportunistic pathogen has become a primary contributor to multidrug resistant infections within hospital environments (Cerqueira *et al.*, 2014). Among the response regulators (RRs), AdeR regulates the *adeABC* efflux pump, a critical factor in multidrug resistance (Ruzin *et al.*, 2007; Lee *et al.*, 2020). BaeR is linked to resistance against envelope stress and plays a role in the regulation of efflux systems (Lin *et al.*, 2015). GacA is involved in the management of virulence and adaptation to environmental changes (Song *et al.*, 2022). In spite of their clinical significance, the genome wide DNA binding profiles of these (RRs) in *A. baumannii* are still largely uncharted in the strain AB5075.

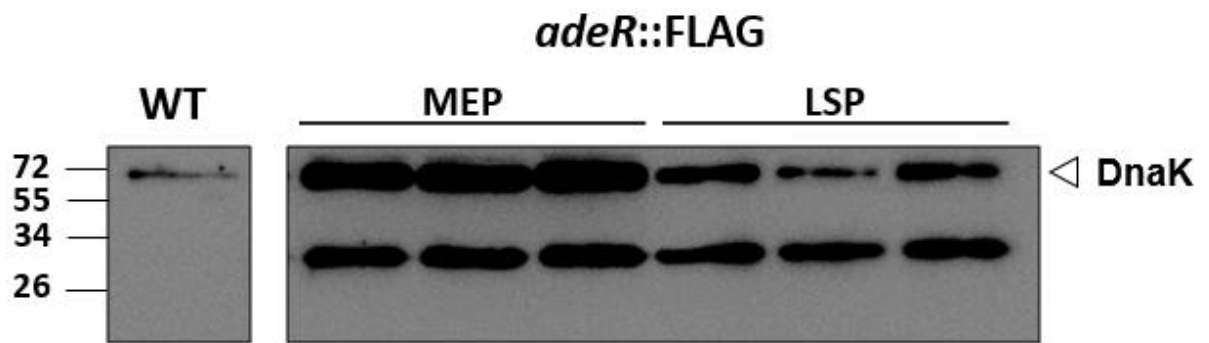
In this chapter, we developed FLAG tagged variants of AdeR, BaeR, and GacA in *A. baumannii* AB5075, confirmed their expression through Western blotting, and conducted ChIP-seq to delineate their genome wide binding profiles. This methodology offers the initial comprehensive perspective on the DNA-binding targets of these clinically significant response regulators (RRs), illuminating their regulatory functions in antibiotic resistance, stress response, and virulence.

4.5 Verification of FLAG-tagged Response Regulators

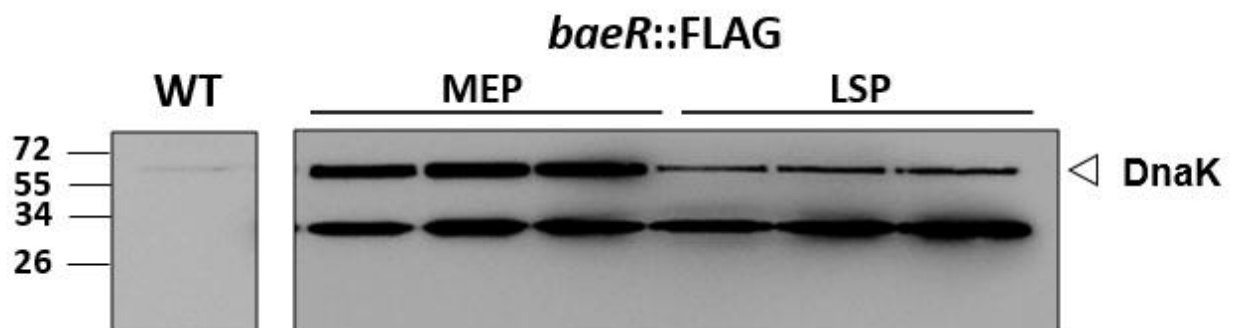
In order to enable the immunoprecipitation of the response regulators AdeR, BaeR, and GacA, we created FLAG tagged versions of each protein in *A. baumannii* AB5075. The functionality of these tagged proteins was initially verified by evaluating their expression levels through Western blotting. Whole cell lysates derived from FLAG

tagged strains, along with the untagged wild-type control, were analyzed using an anti-FLAG antibody. Distinct bands were observed at the anticipated molecular weights: ~27.2 kDa for AdeR-FLAG, ~26.7 kDa for BaeR-FLAG, and ~23.1 kDa for GacA-FLAG (**Figure 4.4**). The bands corresponded with the anticipated molecular weights of the native proteins plus the FLAG tag (2.73). The absence of a FLAG-reactive signal in the wild-type strain validated the specificity of the detection. Individual bands devoid of notable degradation products suggests that the FLAG-tagged proteins were expressed stably in *A. baumannii*. These findings confirm the successful implementation of FLAG-tagging and establish a foundation for the ChIP-seq experiments.

(A)



(B)



(C)

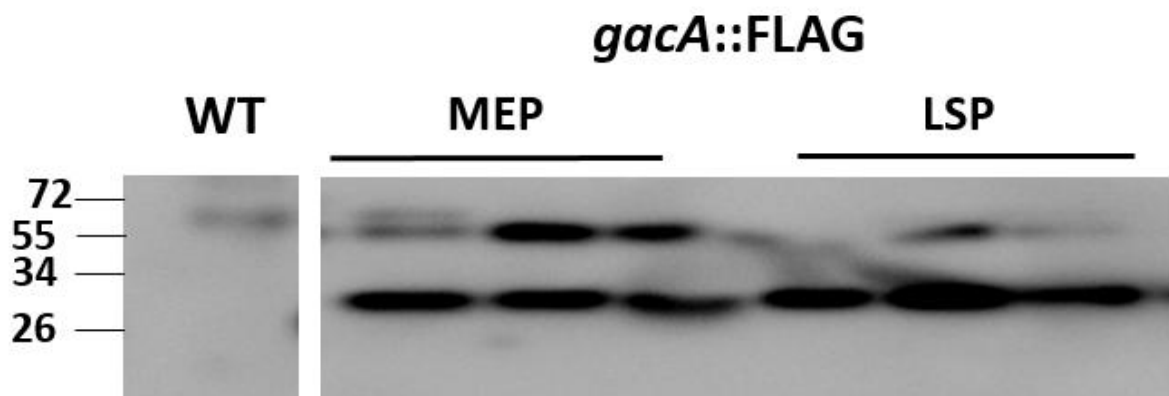


Figure 4.4 The protein level of strains with inserted chromosomal (A) *adeR*::FLAG, (B) *baeR*::FLAG, and (C) *gacA*::FLAG fusions in the wild-type (WT) strain were assessed through western blotting. Whole cell lysates were obtained from *A. baumannii* cultured to mid-exponential phase (MEP) and late stationary phase (LSP). Three independent biological replicates were loaded onto the gels. The numbers displayed in the western blotting results indicate the sizes of the protein ladder measured in kilodaltons (kDa). The protein abundance of AdeR-FLAG, BaeR-FLAG, and GacA-FLAG, along with the loading control DnaK, was detected using anti-FLAG and anti-DnaK antibodies, respectively.

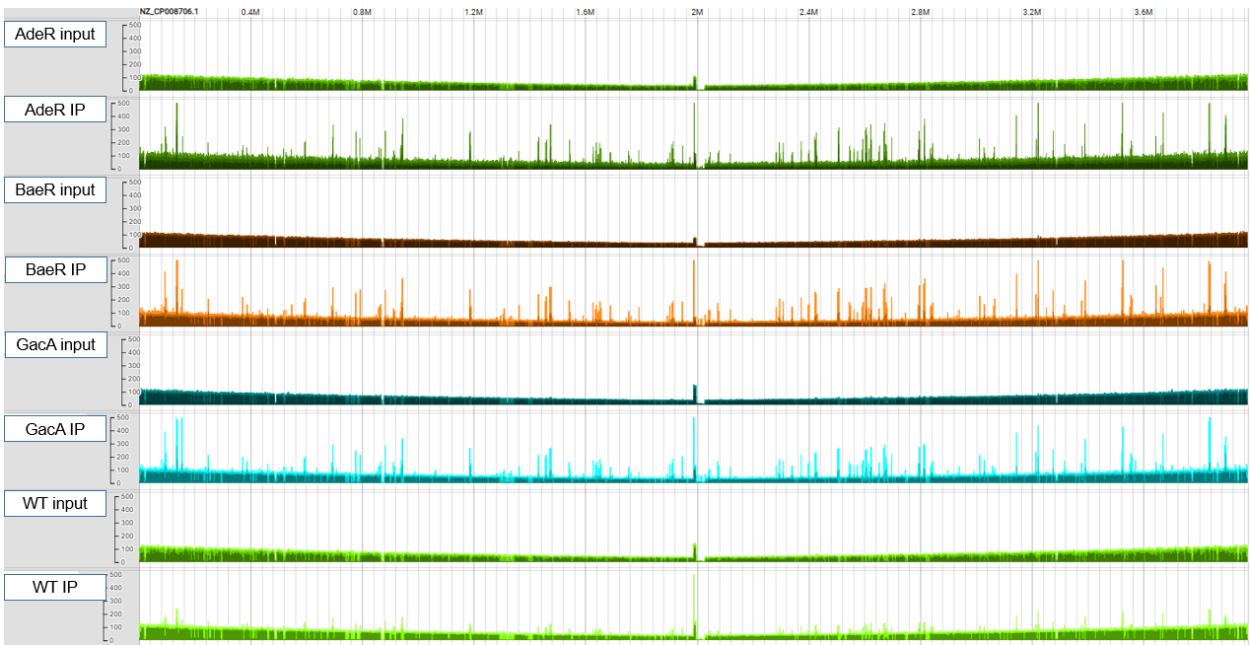
4.6 Chip- seq data overview

To explore the genome-wide DNA binding characteristics of the response regulators AdeR, BaeR, and GacA in *A. baumannii* AB5075, we conducted chromatin immunoprecipitation coupled with high-throughput sequencing (ChIP-seq) on FLAG-tagged strains in the MEP condition. The ChIP-seq data obtained from the FLAG-tagged AdeR and GacA strains demonstrated numerous enriched regions (peaks) throughout the *A. baumannii* genome **Table 4.3**. Given the extensive number of identified binding sites, only select examples that exhibit clear and distinct enrichment patterns are showcased here. Although biological duplicates were sent for sequencing, only one sample per strain gave high-quality results. However, this limits statistical analysis of the data. Because the ChIP-seq experiments were only carried out at the very end of the thesis, only a very preliminary analysis was carried out. To illustrate the distribution of ChIP-seq peaks throughout the complete *Acinetobacter baumannii* AB5075 genome and its plasmids, the aligned reads were mapped and presented using JBrowse (**Figure 4.5**).

Table 4.3 Summary of the number of peaks identified for AdeR, BaeR, and GacA in *Acinetobacter baumannii* AB5075. The table presents the total number of peaks detected for each response regulator (AdeR, BaeR, and GacA) based on ChIP-seq analysis. Peaks were identified using (MACS3 peak detection analysis). The results indicate the genome-wide binding sites of each transcription factor under the tested conditions.

Protein	peaks number
AdeR	115
BaeR	148
GacA	154

(A)



(B)

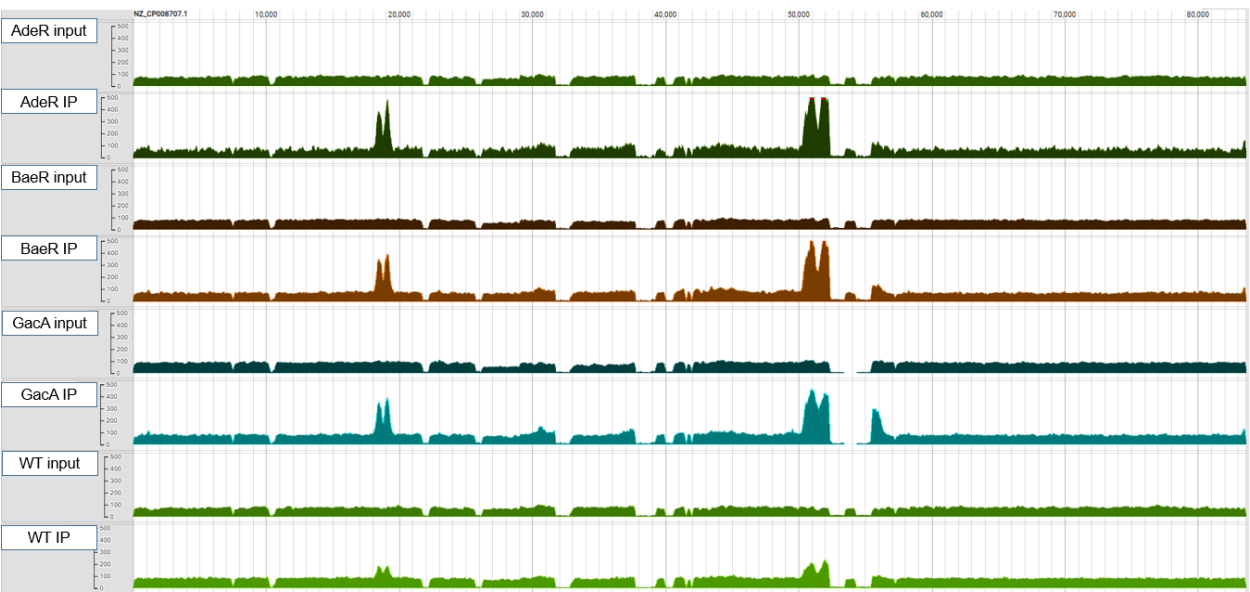


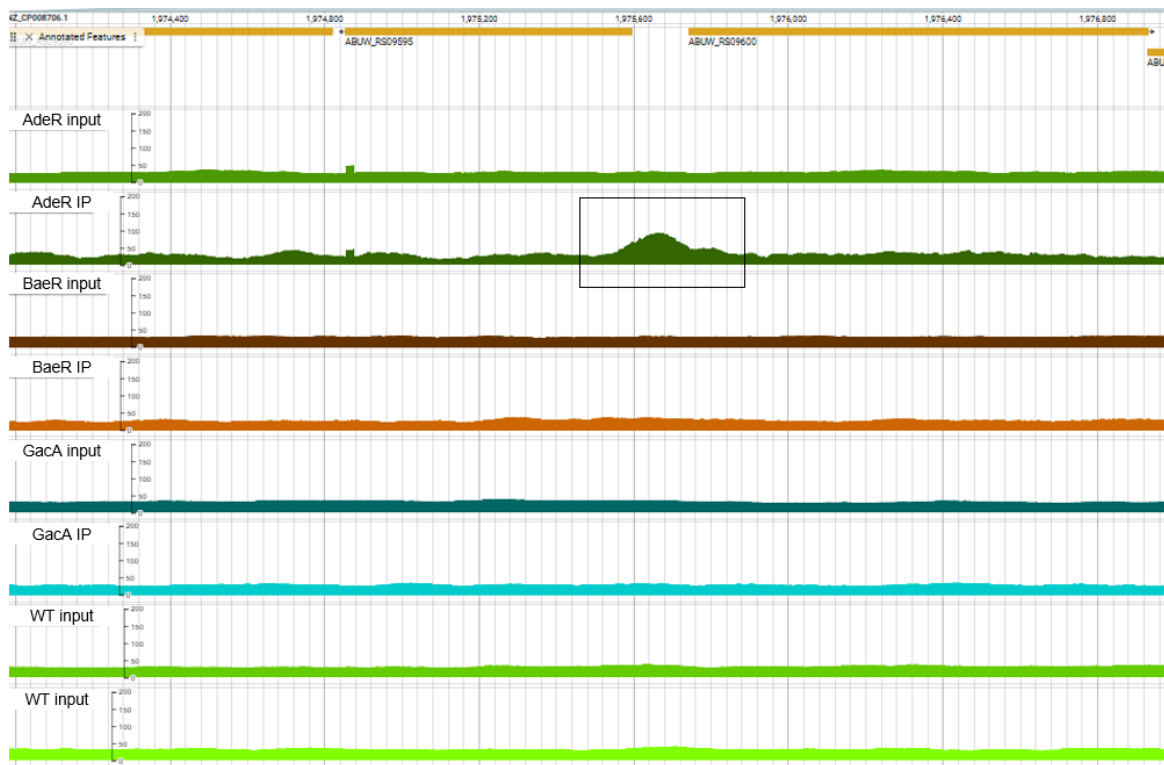
Figure 4.5 A comprehensive view of ChIP-seq data aligned to the *Acinetobacter baumannii* AB5075 reference genome and plasmids via JBrowse. The tracks display the aligned ChIP-seq reads for each sample, illustrating coverage throughout the chromosome and plasmids. Peaks suggest possible binding areas for the target response regulators. A genome-wide view of ChIP-seq data aligned to the *Acinetobacter baumannii* AB5075 reference sequence using JBrowse. **(A)** Coverage of ChIP-seq reads across the whole chromosomal genome. **(B)** Coverage of ChIP-seq reads across the plasmids.

As a positive control, we inspected regions where DNA binding events were expected. One such instance is that the AdeR RR should bind its own promoter and the promoter of AdeABC, which are in the same intergenic region. In **Figure 4.5 (A)**, a notable enrichment peak is identified in the **AdeR** immunoprecipitated (IP) sample, which is not present in the control samples. This peak is situated in the intergenic region that lies between *adeR* and *adeA*, centrally located between these two genes. Such positioning implies that AdeR could directly interact with the common promoter region that governs the *adeABC* efflux operon, thus modulating the transcription of *adeABC* and auto regulating the expression of *adeR* as well. This also confirmed the validity of the ChIP-seq data for AdeR. In **Figure (D)**, a notable peak was observed in the AdeR immunoprecipitated (IP) sample, which was not present in the control samples. This peak is situated in the intergenic region upstream of *ABUW_RS05385 (rapA)*, which encodes the RNA polymerase-associated protein RapA. This finding implies that AdeR could directly interact with the regulatory region of *rapA*, possibly affecting its transcriptional activity. The gene expression of these gene in the RNA seq data of $\Delta adeR$ was not change.

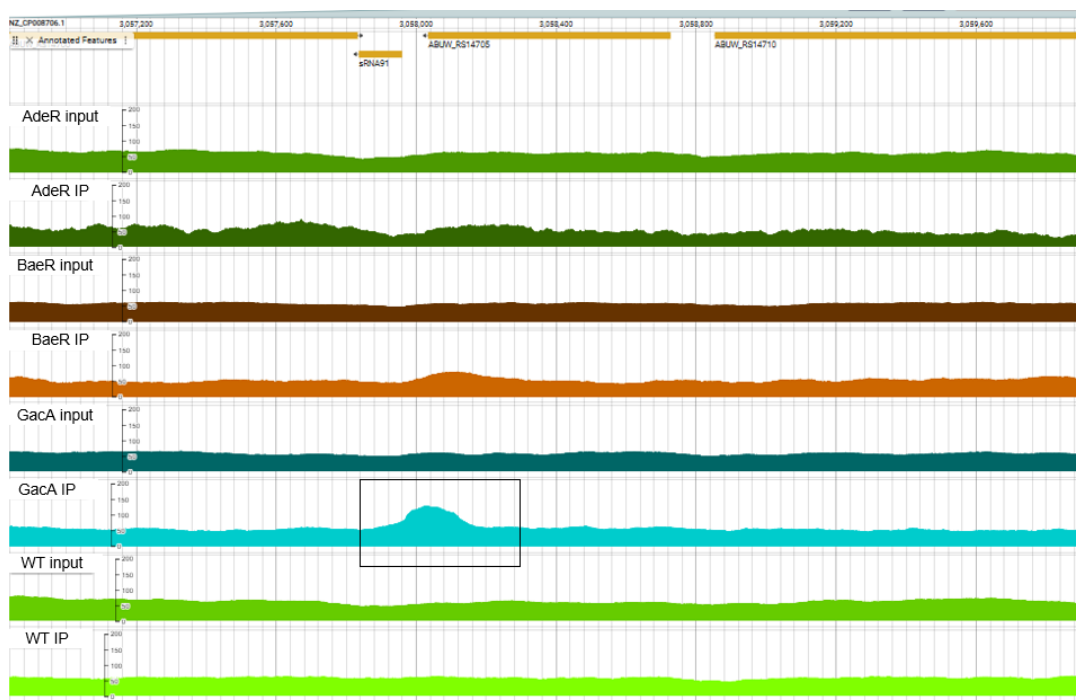
In Figures **(B, C)** distinct peaks are observed in the GacA IP strain corresponding to sRNAs 91, 99, and 100, indicating that GacA might directly associates with the promoter regions of these small RNAs. The gene expression of these genes in the RNA seq data of $\Delta gacA$ were downregulated. These examples represent that might GacA works as activator but need more replicates.

In **Figure (D)**, a notable peak was observed in the BaeR immunoprecipitated (IP) sample, which was not present in the control samples. This peak is situated within the intergenic region between *ABUW_RS05395* (*fabR*) and *ABUW_RS05400*, the latter of which encodes a ferredoxin reductase. The *fabR* gene encodes an HTH-type transcriptional repressor that plays a role in the regulation of unsaturated fatty acid biosynthesis. The detection of this peak indicates that BaeR may have a direct interaction with the promoter region that is common to these two genes, potentially affecting the expression of *fabR*, *ABUW_RS05400*, or both. The gene expression of these genes in the RNA seq data of $\Delta baeR$ were not change.

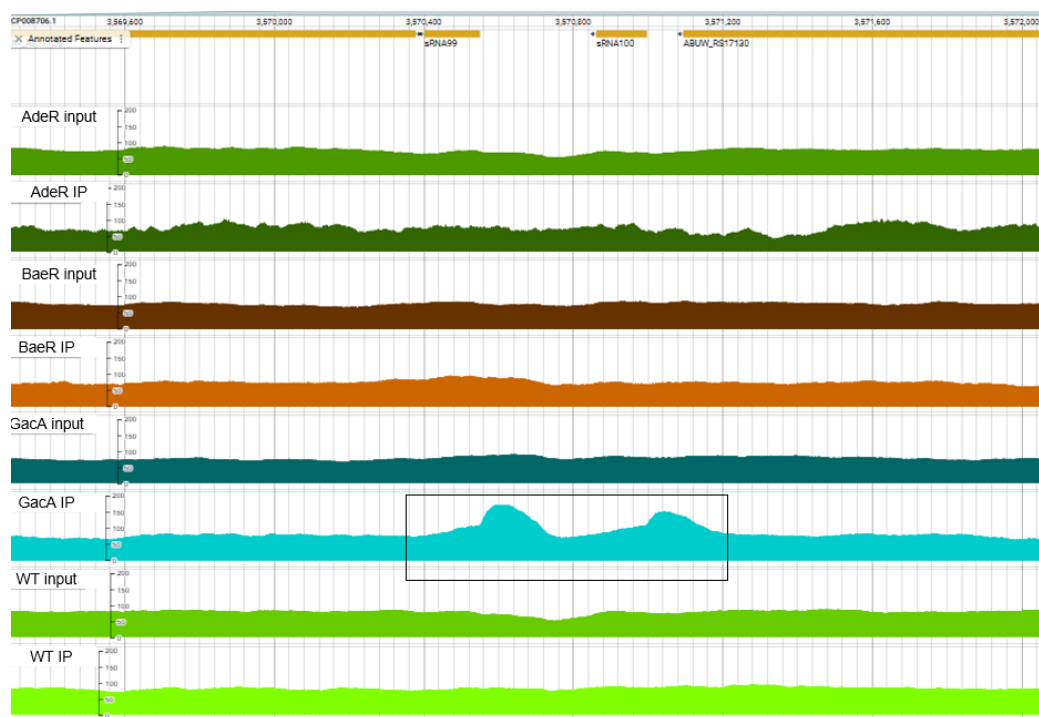
(A)



(B)



(C)



(D)

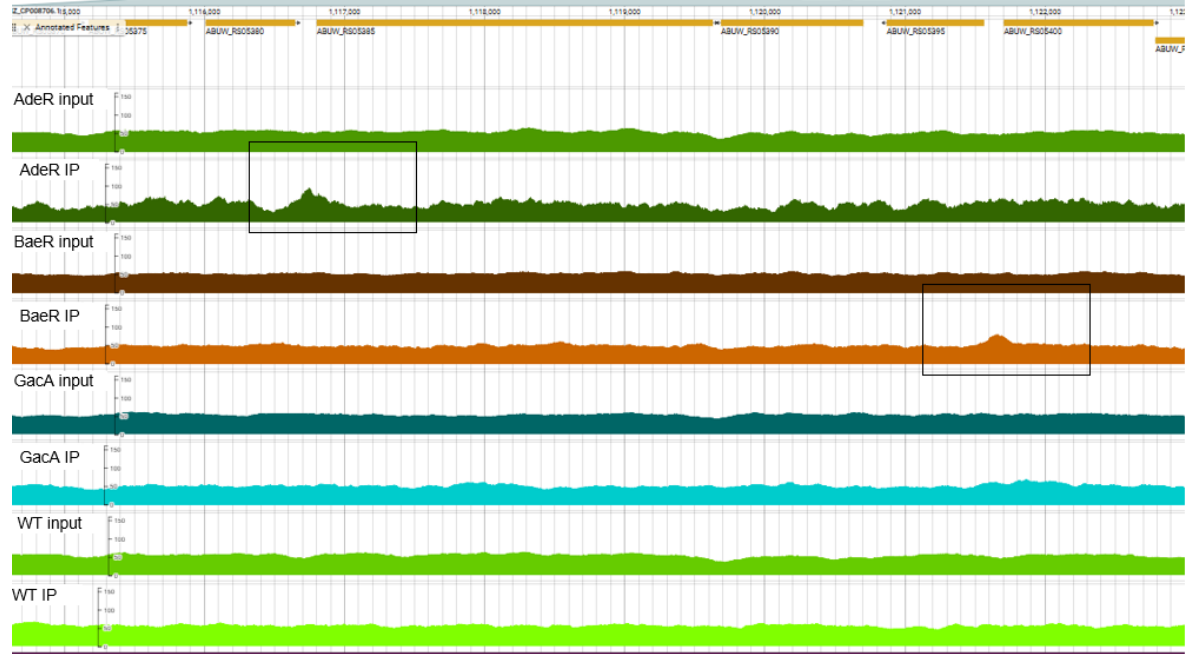


Figure 4.6 (A), a significant enrichment peak that is absent from the control samples is found in the AdeR immunoprecipitated (IP) sample. This peak is found in the area in the middle of the genes *adeR* and *adeA*. **(B, C)** The GacA IP strain exhibits discrete peaks that correlate to sRNAs 91, 99, and 100. **(D)**, The BaeR immunoprecipitated (IP) sample showed a significant peak that was absent from the control samples. The intergenic region between *ABUW_RS05395* (*fabR*) and *ABUW_RS05400* contains this peak. One prominent peak in the AdeR was found to be located in the intergenic region upstream of *ABUW_RS05385* (*rapA*), which codes for the RNA polymerase-associated protein RapA.

Chapter 5

Phenotypic Characterization of Two-Component System Mutants in *Acinetobacter baumannii*

5.1 Introduction

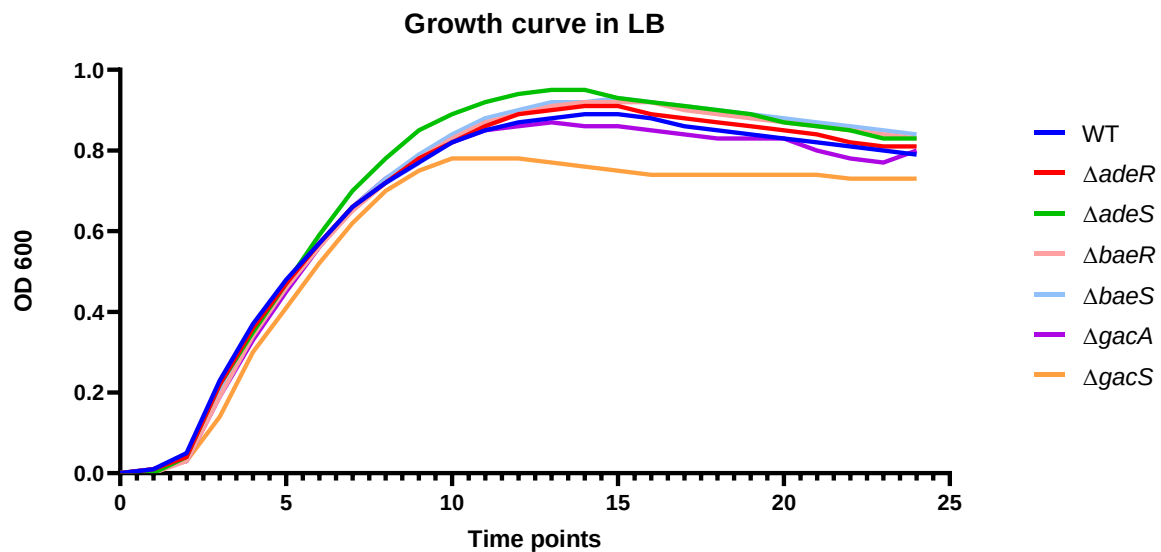
Two-component systems (TCSs) are frequently employed by pathogenic bacteria to detect environmental signals and play a role in disease progression (Gotoh *et al.*, 2010). Understanding the phenotypic effects of gene deletion or change is crucial to determining the functions of bacterial regulatory systems. The physiological effects of altering important response regulators from *Acinetobacter baumannii* AB5075 two-Component Systems (TCSs) were evaluated in this chapter. AdeRS, BaeSR, and GacSA are among the systems known to control cellular stress responses and antibiotic resistance. Based on the transcriptomic data, Kirby-Bauer disk diffusion assay and Minimum Inhibitory Concentration (MIC) were used to determine antibiotic susceptibility tests to assess the impact of TCS mutations on antibiotic resistance. Furthermore, the ability to use amino acids as carbon substrates during respiration was assessed.

5.2 Growth curve experiments comparing wild-type (WT) and mutant strains

To evaluate the effects of gene deletion on the fitness and nutrient utilization of bacteria, growth curves were performed for both the wild-type strain *A. baumannii* AB5075 and various mutant strains $\Delta adeR$, $\Delta adeS$, $\Delta baeR$, $\Delta baeS$, $\Delta gacA$ and $\Delta gacS$, in rich and minimal media. Lysogeny broth (Lennox, LB) served as the nutrient-rich medium, whereas M9 minimal medium added to it Sodium pyruvate was employed to assess growth in nutrient-limited environments. In LB, all strains demonstrated similar growth profiles indicating no major defects in nutrient-rich conditions except for the $\Delta gacS$ mutant, which exhibited slightly delayed in exponential phase and reached a lower final optical density (**Figure 5.1A**). In M9 minimal medium, the wild type (WT), as well as the mutants $\Delta adeR$, $\Delta adeS$, $\Delta baeR$, and $\Delta baeS$, exhibited comparable growth patterns (**Figure 5.1B**). In comparison to the wild type, the *gacS* mutant

demonstrated a reduced growth rate in M9 media. Despite the impaired growth characteristics of *gacS*, it outperformed the *gacA* mutant, which exhibited a more pronounced growth deficiency. Importantly, the *gacA* mutant did not perform a clear phase of exponential (log) growth, suggesting a considerable disruption in its capacity to adapt and multiply under the experimental conditions.

(A)



(B)

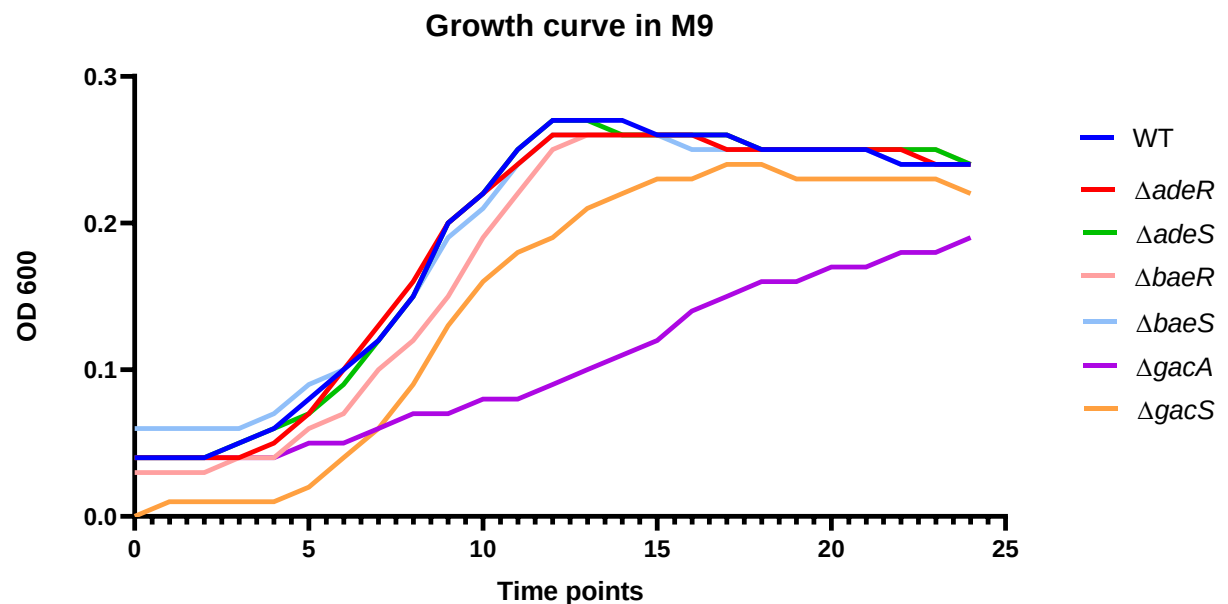


Figure 5.1 Growth curves of *A. baumannii* AB5075 wild type and TCS mutants in LB and M9 media. Overnight cultures of both the wild type (WT) and mutant strains $\Delta adeR$, $\Delta adeS$, $\Delta baeR$, $\Delta baeS$, $\Delta gacA$ and $\Delta gacS$ were diluted to a standardized initial OD₆₀₀ and incubated at 37°C with shaking in (A) LB and (B) M9 minimal medium. The optical density at 600 nm (OD₆₀₀) was measured at regular intervals to track bacterial growth over time.

5.3 Kirby-Bauer Disk Diffusion

To examine the phenotypic impacts of specific gene deletions on antibiotic resistance in *Acinetobacter baumannii* AB5075, the Kirby-Bauer Disk Diffusion method was utilized. This technique is commonly employed to assess bacterial sensitivity to antibiotics by evaluating the diameter of the inhibition zone surrounding antibiotic-impregnated paper disks placed on a Mueller Hinton agar plate that has been inoculated with a standardized bacterial suspension. It offers a comparative and qualitative evaluation of resistance or susceptibility.

This study utilized a range of antibiotic classes to evaluate the antimicrobial susceptibility profiles of both wild-type and mutant strains of *Acinetobacter baumannii*, emphasizing agents that are effective against Gram-negative bacteria. Among the bactericidal antibiotics, beta-lactams such as penicillins, cephalosporins, carbapenems, and monobactams function by inhibiting cell wall synthesis through their binding to penicillin-binding proteins (PBPs), which ultimately results in bacterial lysis and death (Kohanski *et al.*, 2010). Cephalosporins, especially those from the third and fourth generations, along with carbapenems like imipenem and meropenem, demonstrate significant efficacy against Gram-negative bacteria, including strains resistant to multiple drugs. Monobactams, such as aztreonam, are a specific class of beta-lactams that focus on Gram-negative bacteria and are frequently utilized in cases of beta-lactam allergies (Pfeifer *et al.*, 2010). Monobactams like aztreonam are specialized beta-lactams targeting Gram-negative species. Aminoglycosides, such as gentamicin and amikacin, exhibit bactericidal properties, they irreversibly attach to the 30S ribosomal subunit, thereby interfering with protein synthesis and leading to the misreading of mRNA. Fluoroquinolones, including ciprofloxacin and levofloxacin,

obstruct the enzymes responsible for bacterial DNA replication and are especially potent against Gram-negative bacteria (Kyriakidis *et al.*, 2021). Polymyxins, such as polymyxin B and colistin, serve as last-resort treatments that compromise the structural integrity of the outer membrane in Gram-negative bacteria, leading to swift cell death (Baran *et al.*, 2023). Furthermore, nitrofurans such as nitrofurantoin demonstrate bactericidal effects by causing harm to bacterial DNA, RNA, and proteins, especially in cases of urinary tract infections.

In contrast, bacteriostatic antibiotics prevent the growth and reproduction of bacteria without directly eliminating the cells, thereby enabling the host's immune system to eradicate the infection. Tetracyclines and glycylcyclines such as tigecycline function by attaching to the 30S ribosomal subunit and inhibiting aminoacyl-tRNA binding, which consequently interrupts protein synthesis. Although tetracyclines are generally bacteriostatic, glycylcyclines demonstrate improved efficacy against resistant Gram-negative strains. Sulfonamides, including sulfamethoxazole, and antifolates such as trimethoprim, impede consecutive stages in folate biosynthesis, which is crucial for nucleotide synthesis. When used individually, they exhibit bacteriostatic properties, however, when combined as trimethoprim-sulfamethoxazole, they can produce a synergistic bactericidal effect. These bacteriostatic agents offer significant alternatives for addressing Gram-negative pathogens, particularly when utilized in combination or as components of combination therapies (Kyriakidis *et al.*, 2021; Baran *et al.*, 2023).

5.4 Results:

1. $\Delta adeR$ - $\Delta adeS$

To evaluate the antibiotic susceptibility profiles of the mutants, disk diffusion assays were performed using a panel of many antibiotics with different mechanisms of action. The inhibition zone diameters were measured in centimeters (cm), and resistance was recorded as “R” (resistant) if there was no visible zone of inhibition.

The data presented in **Table 5.1** show the results from three biological replicates of each strain group. All strains were resistant to multiple antibiotics, including oxacillin, ticarcillin, sulphafurazole, trimethoprim/sulfamethoxazole, nalidixic acid, and trimethoprim, Ceftazidime, Cefepime, Cefoperazone and Aztreonam as indicated by

“R” in all replicates. The zones of inhibition for cefoxitin were uniform across all strains, measuring between 1.4 and 1.6 cm, which suggests a consistent level of intermediate susceptibility or resistance. Tetracycline demonstrated a moderate level of activity, exhibiting larger inhibition zones in the $\Delta adeS$ (3.2 cm), which may suggest heightened sensitivity in this mutant. Ciprofloxacin displayed slightly increased inhibition in the $\Delta adeS$ (1.6 cm in $\Delta adeS$ 1) compared to WT and $\Delta adeR$, suggesting altered susceptibility.

Significantly, WT exhibited complete resistance to all aminoglycosides evaluated (gentamicin, kanamycin, amikacin), whereas $\Delta adeR$ and $\Delta adeS$ demonstrated minor inhibition zones (1.0–2.2 cm), suggesting a partial recovery of sensitivity in these mutant strains. The reaction to amikacin was notably pronounced $\Delta adeR$ exhibited stable regions between 1.0 and 1.9 cm, while $\Delta adeS$ demonstrated reduced sensitivity (0.8 cm), indicating a possible regulatory function of the mutant gene in aminoglycoside resistance.

The inhibition zones for tobramycin were a small extent greater in the $\Delta adeR$ and $\Delta adeS$ mutants (1.2–1.5 cm) compared to the wild type (WT) (1.0–1.1 cm), indicating a tendency for heightened sensitivity in these mutants. The wild-type and $\Delta adeR$ strains demonstrated full resistance to nitrofurantoin. In contrast, the $\Delta adeS$ mutant showed a minor inhibition zone. This indicates that the deletion of *adeS* could potentially diminish resistance to nitrofurantoin. In the classes of carbapenem antibiotics (doripenem, imipenem), no differences were observed between the wild-type (WT) and the mutant strains, as all exhibited a minimal inhibition zone. Conversely, the wild-type strain demonstrated a distinct zone of inhibition when exposed to Meropenem, whereas the mutant strain displayed total resistance.

In the case of Tigecycline, colistin sulphate, piperacillin-tazobactam, and Chloramphenicol, both the wild-type strain and all examined mutant $\Delta adeR$, $\Delta adeS$ displayed comparable inhibition zones (around 1–1.7 cm). This observation indicates that the removal of these regulatory genes did not have a significant impact on susceptibility to the aforementioned antibiotics. Consequently, it implies that these

genes are not directly implicated in the modulation of resistance to these antibiotics in *A. baumannii* under standard conditions.

Table 5.1 Measurement of inhibition zones (cm) in Kirby-Bauer disk diffusion tests. The letter "R" denotes the absence of an inhibition zone (resistant phenotype). Each value corresponds to a separate biological replicate. The differences have been highlighted.

Antibiotic classes	Antibiotics	Concentration	WT1	WT2	WT3	$\Delta adeR$ 1	$\Delta adeR$ 2	$\Delta adeR$ 3	$\Delta adeS$ 1	$\Delta adeS$ 2	$\Delta adeS$ 3
Beta-lactam	Oxacillin	Ox1 (1 μ g)	R	R	R	R	R	R	R	R	R
	Cefoxitin	Fox30 (30 μ g)	1.5	1.5	1.6	1.5	1.5	1.5	1.4	1.6	1.6
Tetracycline	Ticarcillin	TIC (75 μ g)	R	R	R	R	R	R	R	R	R
	Tetracycline	TE 30 (30 μ g)	2.5	2.8	2.6	3	3	3	3	3.2	3.2
Sulfonamide	Sulphafurazole	SF300 (300 μ g)	R	R	R	R	R	R	R	R	R
	Trimethoprim/sulfamethoxazole	SXT (25 μ g)	R	R	R	R	R	R	R	R	R
Quinolone	Nalidixic acid	NA30 (30 μ g)	R	R	R	R	R	R	R	R	R
Fluoroquinolone	Ciprofloxacin	CIP (5 μ g)	1.1	1.5	1	1.4	1.3	1.4	1.6	1.5	1.5
Antifolate	Trimethoprim	W1.25 (1.25 μ g)	R	R	R	R	R	R	R	R	R
Aminoglycoside	Gentamicin	CN10 (10 μ g)	R	R	R	1.4	1.2	1.1	1	1.2	1
	Kanamycin	K (30 μ g)	R	R	R	1.5	1	2.2	R	R	R
	Amikacin	AK (30 μ g)	R	R	R	1.9	1	1.9	0.8	1.1	1
	Tobramycin	TOB (10 μ g)	1	1.1	1	1.5	1.2	1.3	1.2	1.2	1.4
Nitrofurantoin	Nitrofurantoin	F100 (100 μ g)	R	R	R	R	R	R	0.9	1	0.9
Cephalosporin	Ceftazidime	CAZ (30 μ g)	R	R	R	R	R	R	R	R	R
	Cefepime	FEP (30 μ g)	R	R	R	R	R	R	R	R	R
	Cefotaxime	CTX(30 μ g)	R	R	R	R	R	R	R	R	R
	Cefoperazone	CFP (30 μ g)	R	R	R	R	R	R	R	R	R
Carbapenem	doripenem	DOR (10 μ g)	1.5	1.5	1.3	1	0.8	0.9	1.1	1.1	0.8
	Meropenem	MEM (10 μ g)	1.3	1.3	1.2	R	R	R	R	R	R
	Imipenem	IPM (10 μ g)	1.4	1.5	1.4	1.5	1.4	1.6	1.7	1.8	1.6
Glycylcycline	Tigecycline	TGC (15 μ g)	3	2.7	2.8	2.8	3	3	3	3.1	3.1
Polymyxin	Colistin sulphate	CT (50 μ g)	2	1.7	2	1.9	1.7	1.8	2	2	1.8
Monobactam	Aztreonam	ATM (30 μ g)	R	R	R	R	R	R	R	R	R
Penicillins and beta-lactamase	Piperacillin-tazobactam	TZP (110 μ g)	1	1.2	1	1.2	1	1.2	0.9	1	1
Phenicol	Chloramphenicol	C (30 μ g)	1.7	1.5	1.7	1.3	0.9	1	1.1	1.2	1.2

2. $\Delta baeR$ - $\Delta baeS$

All strains were resistant to multiple antibiotics, including oxacillin, ticarcillin, nalidixic acid, trimethoprim, Gentamicin, Kanamycin, Ceftazidime, Cefepime, Cefotaxime and Aztreonam as indicated by (R) in all replicates.

Additionally, all strains exhibited an inhibin zone with no significant differences observed between the wild type (WT) and mutants in the presence of Tetracycline, Meropenem, Imipenem, colistin sulphate, and piperacillin-tazobactam.

In the case of Cefoxitin and Ciprofloxacin, the table 5.2 indicated that the wild type (WT) exhibited resistance to these antibiotics, whereas the mutants displayed an inhibition zone of 1 to 1.5 cm. This may suggest that the mutants have become more sensitive.

Tobramycin and doripenem, the $\Delta baeS$ strain, exhibited resistance to these antibiotics similarly to the wild type (WT). In contrast, the $\Delta baeR$ strain demonstrated a minor inhibition zone measuring between 1 and 1.8 cm.

In the case of Nitrofurantoin and Cefoperazone, both the WT and the $\Delta baeR$ strains exhibited complete resistance to these antibiotics, however, the $\Delta baeS$ strain displayed a minor inhibition zone ranging from 0.8 to 1 cm, which is also classified as resistant. All strains exhibited a distinct inhibition zone when treated with tigecycline, however, the diameter of this inhibition zone was greater in the mutants than in the wild type.

Table 5.2 Antibiotic susceptibility profiles determined by Kirby-Bauer disk diffusion assay. Inhibition zones are presented in centimeters. “R” indicates a resistant phenotype with no observable zone of inhibition. Each value corresponds to a separate biological replicate. The differences have been highlighted.

Antibiotic classes	Antibiotics	Concentration	WT1	WT2	WT3	$\Delta baeR1$	$\Delta baeR2$	$\Delta baeR3$	$\Delta baeS1$	$\Delta baeS2$	$\Delta baeS3$
beta-lactam	Oxacillin	Ox1 (1 µg)	R	R	R	R	R	R	R	R	R
	Cefoxitin	Fox30 (30 µg)	R	R	R	1.5	1.5	1.5	0.9	0.9	R
Tetracycline	Ticarcillin	TIC (75 µg)	R	R	R	R	R	R	0.6	0.5	0.5
	Tetracycline	TE 30 (30 µg)	2.5	2.5	2.5	2.5	2.8	2.8	2.5	2.5	2.5
Quinolone	Nalidixic acid	NA30 (30 µg)	R	R	R	R	R	R	R	R	R
fluoroquinolone	Ciprofloxacin	CIP (5 µg)	R	R	R	1.2	1.3	1.1	1	0.9	0.9
antifolate	Trimethoprim	W1.25 (1.25 µg)	R	R	R	R	R	R	R	R	R
aminoglycoside	Gentamicin	CN10 (10 µg)	R	R	R	R	R	R	R	R	R
	Kanamycin	K (30 µg)	R	R	R	R	R	R	R	R	R
	Tobramycin	TOB (10 µg)	R	R	R	1	1.1	1.1	R	R	R
nitrofurantoin	Nitrofurantoin	F100 (100 µg)	R	R	R	R	R	R	1	1	0.8
cephalosporin	Ceftazidime	CAZ (30 µg)	R	R	R	R	R	R	R	R	R
	Cefepime	FEP (30 µg)	R	R	R	R	R	R	R	R	R
	Cefotaxime	CTX (30 µg)	R	R	R	R	R	R	R	R	R
	Cefoperazone	CFP(30 µg)	R	R	R	R	R	R	1	0.9	0.9
carbapenem	doripenem	DOR (10 µg)	R	R	R	1.4	1.5	1.8	R	R	R
	Meropenem	MEM (10 µg)	1.4	1.3	1.4	1.3	1	1	1.8	1.7	1.6
	Imipenem	IPM (10 µg)	1.6	1.5	1.6	1.5	1.6	1.5	2	1.7	1.9
glycylcycline	tigecycline	TGC (15 µg)	2	2	2	3	3	2.8	2.8	3.2	3
polymyxin	colistin sulphate	CT (50 µg)	1.7	1.7	1.8	2	2.2	1.7	2.1	2.2	2
monobactam	Aztreonam	ATM (30 µg)	R	R	R	R	R	R	0.8	0.6	R
penicillins and beta-lactamase	piperacillin-tazobactam	TZP (110 µg)	1	1	1	1	1	1.1	1.3	1	0.9

3. $\Delta gacA$ - $\Delta gacS$

All strains demonstrated resistance to various antibiotics, such as Oxacillin, Ticarcillin, Kanamycin, Ceftazidime, Cefepime, and Aztreonam. All strains displayed an inhibition zone, with no significant differences noted between the wild type (WT) and mutants when exposed to Tetracycline, Colistin sulphate, Piperacillin-tazobactam, Chloramphenicol, and Imipenem. Both the wild-type AB5075 and the $\Delta gacS$ mutant strains consistently exhibited resistance to Tobramycin and Trimethoprim/sulfamethoxazole, however, the $\Delta gacA$ mutant presented a variable phenotype across replicates. Two biological replicates showed distinct inhibition zones indicating partial sensitivity, while one replicate remained resistant. Regarding Ciprofloxacin, Nitrofurantoin, and Cefoperazone, a minor inhibition zone was observed (0.5-1), which is inadequate to conclude that the $\Delta gacS$ has become sensitive to these antibiotics, while both the WT and the $\Delta gacA$ remained resistant. When evaluated for its response to Doripenem, the wild-type strain continued to exhibit resistance, as evidenced by the absence of a visible inhibition zone. The $\Delta gacS$ mutant demonstrated a minor enhancement in sensitivity, resulting in a small inhibition zone measuring between 0.7 and 0.8 cm. Conversely, the $\Delta gacA$ mutant revealed a considerably larger inhibition zone of approximately 1.5 cm, indicating a significantly elevated level of susceptibility. These results imply that GacA has a more critical role than GacS in influencing resistance to Doripenem. In the instance of Meropenem, both the wild type (WT) and the $\Delta gacA$ mutant exhibited similar inhibition zones ranging from 1 to 1.4, whereas the $\Delta gacS$ mutant demonstrated resistance across the three replicates.

Upon exposure to Tigecycline, all strains tested, including the wild-type AB5075, exhibited inhibition zones, which indicate a fundamental level of susceptibility. Nevertheless, both the $\Delta gacS$ and $\Delta gacA$ mutants showed significantly larger inhibition zones in comparison to the wild type, implying heightened sensitivity. These results suggest a role for the GacS/GacA two-component system in the development of Tigecycline resistance. The increased susceptibility observed in the mutants indicates that GacS/GacA may positively influence one or more mechanisms associated with intrinsic resistance such as the expression of efflux pumps or modifications to the cell envelope that diminish antibiotic effectiveness.

Table 5.3 Kirby-Bauer disk diffusion results for multiple antibiotics tested against wild-type and mutant strains. Values indicate the diameter of the inhibition zone in centimeters. "R" represents complete resistance, with no zone of inhibition detected. Each measurement was obtained from an independent biological replicate. The differences have been highlighted.

Antibiotic classes	Antibiotics	Concentration	WT1	WT2	WT3	$\Delta gacS1$	$\Delta gacS2$	$\Delta gacS3$	$\Delta gacA1$	$\Delta gacA2$	$\Delta gacA3$
Beta-lactam	Oxacillin	Ox (1 μ g)	R	R	R	R	R	R	R	R	R
Tetracycline	Ticarcillin	TIC (75 μ g)	R	R	R	R	R	R	R	R	R
	Tetracycline	TE (30 μ g)	2.5	2.5	2.5	2.8	3	2.7	2.6	2.5	2.2
Sulfonamide	Trimethoprim/sulfamethoxazole	SXT(25 μ g)	R	R	R	R	R	R	1.2	1	R
Fluoroquinolone	Ciprofloxacin	CIP (5 μ g)	R	R	R	0.5	0.7	0.8	R	R	R
aminoglycoside	Kanamycin	K (30 μ g)	R	R	R	R	R	R	R	R	R
	Tobramycin	TOB (10 μ g)	R	R	R	R	R	R	1	1	R
Nitrofurantoin	Nitrofurantoin	F(100 μ g)	R	R	R	1.1	1.2	1	R	R	R
Cephalosporin	Ceftazidime	CAZ (30 μ g)	R	R	R	R	R	R	R	R	R
	Cefepime	FEP (30 μ g)	R	R	R	R	R	R	R	R	R
	Cefoperazone	CFP(30 μ g)	R	R	R	1	0.7	0.5	R	R	R
Carbapenem	Doripenem	DOR (10 μ g)	R	R	R	0.8	0.7	0.8	1.5	1.5	1.3
	Meropenem	MEM (10 μ g)	1.4	1.3	1.4	R	R	R	1	1.2	1
	Imipenem	IPM (10 μ g)	1.6	1.5	1.6	2.2	2.1	2.3	1.7	1.7	1.3
Glycylcycline	Tigecycline	TGC (15 μ g)	2	2	2	3.5	3	2.5	2.5	3.2	2.7
Polymyxin	Colistin sulphate	CT (50 μ g)	1.7	1.7	1.8	2.3	2.3	2.4	1.9	2.2	2
Monobactam	Aztreonam	ATM (30 μ g)	R	R	R	R	R	R	R	R	R
Penicillins and beta-lactamase	Piperacillin-tazobactam	TZP (110 μ g)	1	1	1	1	1	1	1	1	1.1
Chloramphenicol	Chloramphenicol	C(30 μ g)	1.3	2	1	1.5	1.5	1.6	1	2	1.7

5.5 Minimum inhibitory concentration (MIC) determination

The Minimum Inhibitory Concentration (MIC) refers to the smallest concentration of an antimicrobial agent that prevents visible bacterial growth following a specified incubation period, usually lasting 16–20 hours. This quantitative measure is extensively utilized to evaluate the susceptibility of bacterial isolates to different antibiotics. MIC testing yields more accurate data compared to disk diffusion assays, especially when analyzing phenotypic variations between wild-type and mutant strains. In this research, MIC determination was employed to assess the effect of particular gene deletions on antibiotic susceptibility in *Acinetobacter baumannii* AB5075.

5.5 Results:

1. $\Delta adeR$ - $\Delta adeS$

In light of the noted discrepancies in antibiotic susceptibility between the wild-type strain and the mutants as observed in the Kirby-Bauer disk diffusion assay, we advanced to ascertain the Minimum Inhibitory Concentration (MIC) for the identical antibiotics. This methodology was designed to quantitatively evaluate the degree of bacterial growth inhibition at reduced antibiotic concentrations and to confirm the phenotypic differences noted in the disk diffusion outcomes.

As per the CLSI M100 (2023) guidelines, resistance to Meropenem in *Acinetobacter baumannii* is characterized by a minimum inhibitory concentration (MIC) of ≥ 8 $\mu\text{g/mL}$ and a disk diffusion zone diameter of ≤ 19 mm. In our investigation, all strains tested including the wild-type, $\Delta adeR$ mutant, and $\Delta adeS$ mutant demonstrated MIC values of 16 $\mu\text{g/mL}$, categorizing them as resistant. This finding was corroborated by the disk diffusion assay, where the wild-type displayed a minimal inhibition zone (~ 13 mm), while the mutants exhibited no measurable zone. The correlation between MIC and disk diffusion suggests that Meropenem resistance is evident in all strains, likely due to intrinsic or acquired mechanisms such as efflux pump activity or alterations in porins. The absence of *adeR* and *adeS*, which are regulators of the AdeABC efflux system, did not lead to enhanced susceptibility to Meropenem, indicating that these

genes may not significantly influence Meropenem resistance in this strain background or that compensatory mechanisms may be operational.

In addition to Meropenem, the susceptibility of *A. baumannii* strains to Doripenem and Imipenem was also evaluated. All strains tested, including the wild-type, $\Delta adeR$ and $\Delta adeS$ mutant, displayed increased MIC values of ≥ 32 $\mu\text{g/mL}$ for both Doripenem and Imipenem, which aligns with resistance as per CLSI M100 (2023) breakpoints of ≥ 8 $\mu\text{g/mL}$. These results indicate that the resistance to carbapenems in this strain background is not dependent on the *adeR* and *adeS* regulatory genes and likely involves other intrinsic or acquired mechanisms. The observation that the deletion of *adeR* or *adeS* did not change carbapenem susceptibility further reinforces the idea that the AdeABC efflux system may not be the main factor contributing to carbapenem resistance in this scenario.

In light of the varying sizes of inhibition zones noted in the Kirby-Bauer disk diffusion assay between the wild-type (WT) strain and the mutants when subjected to aminoglycoside antibiotics, minimum inhibitory concentration (MIC) assays were conducted to assess bacterial growth inhibition across a wider spectrum of concentrations. The WT strain demonstrated a high level of resistance to Gentamicin, Kanamycin, and Amikacin, with bacterial growth continuing even at concentrations reaching 1024 $\mu\text{g/mL}$, which indicates a strongly resistant phenotype. Notably, the $\Delta adeR$ and $\Delta adeS$ mutants displayed a partial enhancement in susceptibility (Table 5.4). For Kanamycin, the MIC remained comparably elevated across all strains, implying that the deletion of *adeR* and *adeS* did not significantly influence resistance to this antibiotic. Conversely, with Gentamicin, both mutants exhibited inhibition at 32 $\mu\text{g/mL}$, suggesting a certain level of increased susceptibility relative to the WT. Nevertheless, according to CLSI M100 (2023), *A. baumannii* is classified as resistant to Gentamicin at MICs of ≥ 16 $\mu\text{g/mL}$, thus the mutants still remain within the resistant category. Regarding Amikacin, the mutants showed inhibition at 128 $\mu\text{g/mL}$, whereas the WT strain remained uninhibited up to 1024 $\mu\text{g/mL}$. Following CLSI guidelines (resistance defined as ≥ 64 $\mu\text{g/mL}$), all strains continue to be categorized as resistant. However, the alteration in MIC for Gentamicin and Amikacin in the mutants indicates

that the deletion of *adeR* or *adeS* may partially compromise the functionality of the AdeABC efflux pump, which has been associated with aminoglycoside resistance.

Table 5.4 The Minimum Inhibitory Concentration (MIC) values for specific antibiotics against *Acinetobacter baumannii* wild-type (WT), $\Delta adeR$, and $\Delta adeS$ strains are presented. The MIC values are measured in $\mu\text{g/ml}$. Interpretations are derived from the CLSI M100 (2023) breakpoints for *Acinetobacter*. The MIC assays were conducted in triplicate, and the reported values reflect the mode of three independent experiments. The differences have been highlighted.

antibiotic	WT1	WT2	WT3	$\Delta adeR$ 1	$\Delta adeR$ 2	$\Delta adeR$ 3	$\Delta adeS$ 1	$\Delta adeS$ 2	$\Delta adeS$ 3
Meropenem	16 μg	16 μg	16 μg	16 μg	16 μg	16 μg	16 μg	16 μg	16 μg
Doripenem	64 μg	64 μg	32 μg	64 μg	64 μg	32 μg	64 μg	64 μg	32 μg
Imipenem	32 μg	32 μg	32 μg	32 μg	32 μg	32 μg	16 μg	32 μg	32 μg
Gentamicin	1024 μg	1024 μg	1024 μg	32 μg	32 μg	32 μg	32 μg	32 μg	32 μg
Kanamycin	1024 μg	1024 μg	1024 μg	1024 μg	1024 μg	1024 μg	1024 μg	1024 μg	1024 μg
Amikacin	1024 μg	1024 μg	1024 μg	128 μg	128 μg	128 μg	128 μg	128 μg	128 μg

2. $\Delta baeR$ - $\Delta baeS$

Given that the $\Delta baeR$ and $\Delta baeS$ mutants consistently exhibited minimum inhibitory concentrations (MICs) comparable to those of the wild type, especially for antibiotics that demonstrated only minor differences in the Kirby-Bauer disk diffusion assay, these MIC findings were considered non-informative and are consequently not included in this presentation.

3. $\Delta gacA$ - $\Delta gacS$

Since, given that the *gacA* mutant exhibited no discernible differences when compared to the wild type in the disk diffusion assay, MIC testing was deemed unnecessary for this strain. According to the CLSI M100 (2023) guidelines, *Acinetobacter baumannii* exhibits resistance to Meropenem and Doripenem when the minimum inhibitory concentration (MIC) is $\geq 8 \mu\text{g/ml}$. The wild-type *A. baumannii* remains resistant to Doripenem and Meropenem, as previously described. The $\Delta gacS$ mutant showed

elevated MIC values of ≥ 8 $\mu\text{g/mL}$ for both Doripenem and Meropenem (Table 5.5), which is consistent with the resistance criteria outlined in the CLSI M100 (2023) breakpoints of ≥ 8 $\mu\text{g/mL}$. This indicates that the removal of *gacS* does not result in heightened vulnerability to these carbapenems, suggesting that GacS may not significantly contribute to carbapenem resistance in this particular strain. The MIC analysis of Gentamicin against the $\Delta gacS$ mutant strain indicated a value of 512 $\mu\text{g/mL}$, which is considerably higher than the CLSI M100 (2023) resistance breakpoint of ≥ 16 $\mu\text{g/mL}$ for *Acinetobacter* spp. This finding suggests that the $\Delta gacS$ mutant demonstrates a high level of resistance to Gentamicin. Given that this level of resistance is similar to the wild-type strain, it implies that the deletion of *gacS* does not reduce resistance to Gentamicin. These findings suggest that the GacS sensor kinase does not function as a negative regulator of resistance under the conditions tested, and that other elements such as efflux systems or aminoglycoside-modifying enzymes could be significantly influencing Gentamicin resistance.

Table 5.5 The Minimum Inhibitory Concentration (MIC) values for specific antibiotics against *Acinetobacter baumannii* wild-type (WT), $\Delta gacS$ strains are presented.

antibiotic	WT1	WT2	WT3	$\Delta gacS$ 1	$\Delta gacS$ 2	$\Delta gacS$ 3
Doripenem	16 μg	16 μg	16 μg	8 μg	8 μg	8 μg
Meropenem	16 μg	16 μg	16 μg	8 μg	8 μg	8 μg
Gentamicin	1024 μg	1024 μg	1024 μg	512 μg	512 μg	512 μg

5.7 Colorimetric method for the determination of metabolisable sources in AB5075

In order to assess the carbon source utilization profile and examine the metabolic versatility of *A. baumannii* AB5075, a colorimetric assay utilizing tetrazolium violet dye reduction was implemented (**Figure 5.2**). This technique identifies metabolically active cells by means of the colorimetric reduction of tetrazolium dye into a purple formazan product, which can be seen from the plates.

The assay was conducted utilizing wild-type AB5075 along with the TCS mutant strains. Overnight cultures were cultivated in LB broth at a temperature of 37 °C with agitation, subsequently washed and adjusted to a suitable optical density prior to inoculation. A total of 20 amino acids were evaluated, each supplied as the exclusive carbon source in minimal medium augmented with tetrazolium violet dye. Each experimental condition was assessed in triplicate. The rise in absorbance was regarded as a sign of metabolic activity and the use of substrates. This assay enabled the comparative screening of substrate utilization patterns between wild-type and mutant strains of *A. baumannii*, providing insights into the metabolic impact of specific gene disruptions.

Table 5.6 List of Amino Acids Tested as Sole Carbon Sources in the Colorimetric Metabolism Assay of *A. baumannii* AB5075.

Abbreviation	Name	Abbreviation	Name
Ala	Alanine	Leu	Leucine
Arg	Arginine	Lys	Lysine
Asn	Asparagine	Met	Methionine
Asp	Aspartic acid	Phe	Phenylalanine
Cys	Cysteine	Pro	Proline
Glu	Glutamic acid	Ser	Serine
Gln	Glutamine	Thr	Threonine
Gly	Glycine	Trp	Tryptophan
His	Histidine	Tyr	Tyrosine
Ile	Isoleucine	Val	Valine

Phenotypic microarray analysis was conducted to evaluate the metabolic profiles of the wild-type *A. baumannii* AB5075 along with the $\Delta adeR$, $\Delta adeS$, $\Delta baeR$, $\Delta baeS$, $\Delta gacA$, and $\Delta gacS$ deletion mutants. The findings indicated no significant variations in the utilization of a several amino acids, specifically cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, threonine and valine. All strains exhibited similar color development in the respective wells, reflecting comparable levels of metabolic activity and suggesting that the AdeRS, GacAS and BaeRS two-component systems do not significantly influence the regulation of amino

acid metabolism under the conditions and at the times tested (**Figure 5.3**). However, notable differences were observed for the tested strains in the presence of alanine, arginine, asparagine, aspartic acid, phenylalanine, proline, serine, tryptophan and tyrosine (**Figure 5.3**).

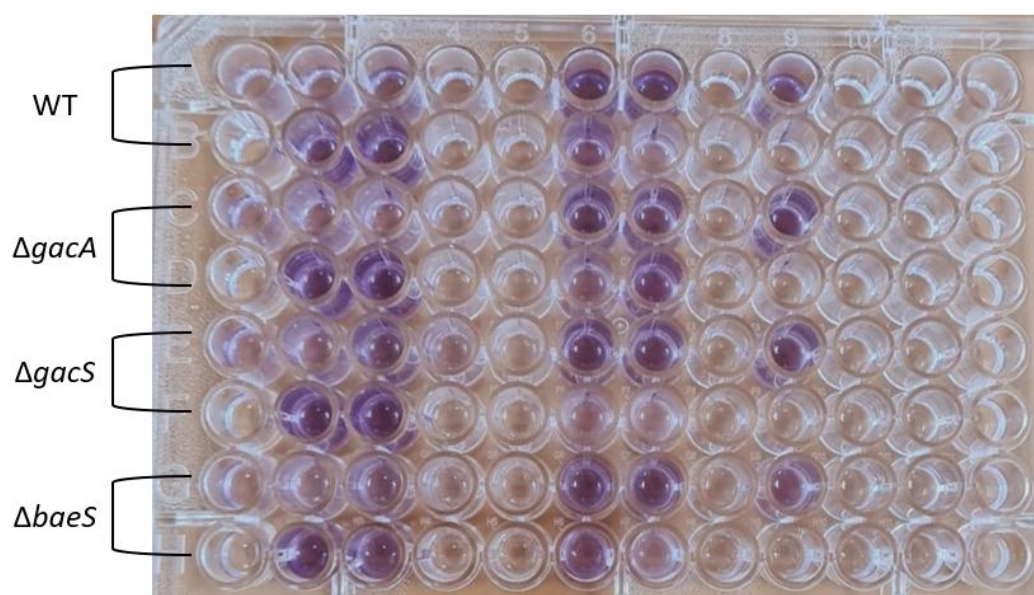


Figure 5.2 An example 96-well plate displaying the colorimetric results of metabolic activity after incubation with various carbon sources. Each well contains a redox-sensitive dye that changes to purple in reaction to bacterial respiration, signifying the use of the respective compound. A greater color intensity reflects increased metabolic activity. Rows A–H and columns 1–12 correspond to different substrates. Clear or faint wells suggest minimal or absent metabolic activity. A deep purple hue indicates significant utilization of the corresponding substrate. The experiment was incubated at 37 °C for 48 hours.

Table 5.7 Heatmap illustrating the metabolic activity of *A. baumannii* wild-type and TCS mutants over a specified duration. The heatmap depicts the colorimetric metabolic activity of *A. baumannii* AB5075 wild-type (WT) and various mutant strains ($\Delta gacA$, $\Delta gacS$, $\Delta baeR$, $\Delta baeS$, $\Delta adeR$, and $\Delta adeS$) at 24 h, and 48 h, as determined by optical density (OD) measurements from phenotypic microarray plates. Each cell within the heatmap corresponds to the metabolic activity recorded in a particular well, with color coding based on OD values:

green (<0.05) signifies no or minimal activity, yellow (0.05–0.2) denotes moderate activity, and red (>0.2) represents high metabolic activity.

Amino Acid	Time (h)	WT	$\Delta adeR$	$\Delta adeS$	$\Delta baeR$	$\Delta baeS$	$\Delta gacA$	$\Delta gacS$
Alanine	24	0.29	0.32	0.29	0.23	0.27	0.33	0.41
	48	0.23	0.32	0.28	0.19	0.31	0.48	0.53
Arginine	24	0.32	0.28	0.31	0.29	0.33	0.15	0.16
	48	0.30	0.35	0.34	0.41	0.35	0.45	0.45
Asparagine	24	0.44	0.56	0.52	0.38	0.45	0.50	0.67
	48	0.38	0.58	0.54	0.52	0.48	0.50	0.68
Aspartic acid	24	0.19	0.26	0.24	0.17	0.19	0.29	0.34
	48	0.17	0.25	0.25	0.16	0.22	0.28	0.36
Cysteine	24	0.11	0.12	0.10	0.10	0.11	0.15	0.14
	48	0.10	0.12	0.11	0.10	0.13	0.14	0.14
Glutamic acid	24	0.83	0.96	1.00	0.96	0.81	0.76	0.75
	48	1.13	1.02	0.96	1.22	0.74	0.77	0.84
Glutamine	24	0.66	0.74	0.79	0.62	0.67	0.60	0.70
	48	0.84	0.96	0.98	0.83	0.64	0.69	0.71
Glycine	24	0.12	0.11	0.10	0.10	0.14	0.15	0.14
	48	0.10	0.10	0.08	0.09	0.13	0.15	0.09
Histidine	24	0.52	0.43	0.47	0.42	0.52	0.27	0.52
	48	0.75	0.54	0.54	0.54	0.61	0.75	0.83
Isoleucine	24	0.13	0.11	0.11	0.10	0.14	0.14	0.16
	48	0.08	0.09	0.09	0.09	0.14	0.14	0.14
Leucine	24	0.14	0.12	0.11	0.10	0.13	0.15	0.15
	48	0.08	0.09	0.09	0.08	0.16	0.16	0.14
Lysine	24	0.15	0.14	0.14	0.10	0.14	0.15	0.14
	48	0.05	0.05	0.08	0.04	0.16	0.17	0.13
Methionine	24	0.13	0.12	0.11	0.10	0.12	0.14	0.11
	48	0.06	0.12	0.10	0.10	0.15	0.15	0.15
Phenylalanine	24	0.33	0.33	0.35	0.23	0.42	0.16	0.17
	48	0.59	0.79	0.69	0.77	1.25	0.87	0.74
Proline	24	0.81	0.73	0.73	0.83	0.75	0.41	0.71
	48	1.34	0.90	0.90	1.13	0.78	0.95	1.09
Serine	24	0.14	0.13	0.14	0.12	0.11	0.14	0.13
	48	0.22	0.23	0.29	0.21	0.16	0.16	0.14
Threonine	24	0.12	0.11	0.11	0.10	0.10	0.14	0.13
	48	0.07	0.07	0.11	0.09	0.15	0.16	0.13
Tryptophan	24	0.25	0.19	0.18	0.17	0.28	0.15	0.15
	48	0.37	0.31	0.27	0.27	0.61	0.37	0.35
Tyrosine	24	0.30	0.45	0.47	0.22	0.38	0.26	0.27
	48	0.46	0.71	1.21	0.45	0.47	0.49	0.39

Valine	24	0.13	0.10	0.11	0.10	0.13	0.14	0.15
	48	0.06	0.10	0.09	0.09	0.17	0.11	0.11

5.8 Variations in amino acid usage were observed between wild-type (WT) and mutant strains at both 24 hours and 48 hours

Alanine

A. baumannii appears to be able to use alanine as the single carbon source for respiration (**Table 5.7**). After 24 h, there was no difference between wild-type and mutants, however, after 48 h of incubation, the $\Delta gacA$ and $\Delta gacS$ mutant strains showed a statistically higher value compared to the wild-type (**Figure 5.3**). It is unclear from the transcriptomic data, how alanine catabolism is de-repressed in the $\Delta gacA$ and $\Delta gacS$ mutant strains, and there is little known about how alanine is catabolized in *A. baumannii*. For cell wall peptidoglycan biosynthesis, L-alanine has to be converted to D-alanine through alanine racemase, and potentially, the pool of L-alanine is depleted quicker in the $\Delta gacA$ and $\Delta gacS$ mutant strains compared to the WT or other mutants. This might contribute to the observed growth defects in the $\Delta gacA$ and $\Delta gacS$ mutant strains in minimal media, but increased L-alanine catabolism. In the transcriptomic data, where L-alanine should be available in L-broth, the $\Delta gacS$ mutant grows slightly worse and alanine racemase is 5.6-fold downregulated in LSP (but not in the $\Delta gacA$ mutant, which grows normally) suggesting that mismanagement of L-alanine-D-alanine pools could contribute to the observed growth defect in L-broth.

Arginine

Both the $\Delta gacA$ and $\Delta gacS$ mutants utilized less arginine at 24 hours, however both mutant strains caught up with the WT at 48 hours. This agrees with a recently published work that showed that the *A. baumannii* strain ATCC17978 $\Delta gacA$ was not able to grow in M9 medium with arginine as the carbon source and that the ability to utilize arginine is essential for *A. baumannii* survival in a mouse pneumonia model (Devnath *et al.*, 2025). Here, we add that this phenotype is conserved in *A. baumannii* AB5075 and extend it to the $\Delta gacS$ mutant. Interestingly, there was no difference after 48 h, suggesting that arginine utilization is not completely inhibited but impaired

(**Figure 5.3**). The transcriptomic data generated from L-broth listed arginine catabolic processes to succinate [GO:0019545] and glutamate [GO:019544] and arginine biosynthetic processes [GO:0006526] are significantly upregulated in MEP in the $\Delta gacA$ and $\Delta gacS$ mutants compared to WT (**Figure 3.19**). This could mean that GacA and GacS not only act as activators of arginine metabolism in minimal medium but also repressors in rich medium.

Asparagine

Asparagine is metabolized by all strains, however, after 24 h the $\Delta gacS$ mutant utilizes asparagine significantly quicker compared to the wild-type strain (**Figure 5.3**). This coincides with up-regulation (11.3-fold, $p_{adj} < 0.05$) of asparaginase (ABUW_RS11475) in the $\Delta gacS$ mutant strain at MEP which is required for conversion to aspartate (aspartic acid) and then further into the TCA cycle, however, again it must be noted that the growth media are different. However, the upregulation might indicate GacS represses asparagine catabolism.

Aspartic acid (aspartate)

In agreement with the better utilization of asparagine in the $\Delta gacS$ mutant strain, the use of aspartic acid is also increased in the $\Delta gacS$ mutant strain compared to the wild-type strain (**Figure 5.3**). There are five predicted aspartate aminotransferase family proteins in *A. baumannii* AB5075, and three out of five are upregulated in the $\Delta gacS$ mutant strain (ABUW_RS05430, 3.5-fold, ABUW_RS08680 3-fold, and ABUW_RS01720 2.9-fold, all $p_{adj} < 0.05$). As asparagine is converted to aspartic acid by asparaginase and further to oxaloacetate and glutamate by aspartate aminotransferase, the upregulation of all the above enzymes in the $\Delta gacS$ mutant strain at MEP could contribute to better asparagine and aspartic acid utilization. The expression pattern in the $\Delta gacA$ mutant strain is different, with the ABUW_RS13600 aspartate aminotransferase family protein as highest up-regulated enzyme of this family (23-fold, $p_{adj} < 0.05$), which does not change significantly in the $\Delta gacS$ mutant (1.8-fold, $p_{adj} = 0.37$). This highlights that the regulation of asparagine and aspartic acid metabolism is different in $\Delta gacS$ and $\Delta gacA$ mutant strains.

Phenylalanine

The catabolic pathway of phenylacetic acid which is derived from phenylalanine is an important virulence factor in *A. baumannii*. Phenylacetate acts as a chemoattractant for neutrophils (Bhuiyan *et al.*, 2016). Both the $\Delta gacA$ and $\Delta gacS$ mutants showed significant reduction of phenylalanine utilization at 24 hours suggesting that both are required for full phenylalanine utilization (**Figure 5.3**). Previously, and in line with the findings of this work, it was shown in *A. baumannii* ATCC17978 that the phenylacetic acid (*paa*) catabolic pathway was downregulated in the $\Delta gacS$ mutant (Cerqueira *et al.*, 2014). Here, show that the downregulation of *paa* genes observed in the $\Delta gacA$ mutant also leads to reduced phenylalanine utilization. At the 48 h timepoint, there was no difference between any of the mutants and the wildtype strain any more indicating that the utilization of phenylalanine is not completely abolished in the $\Delta gacA$ and $\Delta gacS$ mutants but delayed.

Proline

Together with glutamic acid, proline showed the best respiration rates in the phenotypic microarray leading to the highest OD₆₀₀ readings after 48 h (**Figure 5.3**). There were no statistically significant differences between the wildtype and all mutants except for the $\Delta gacA$ mutant which showed significantly reduced respiration. None of the genes or pathways annotated as part of the proline metabolism showed changes in gene expression in $\Delta gacA$ mutant, except for the sodium/proline symporter PutP (ABUW_RS11115) which is even 5-fold upregulated in the $\Delta gacA$ mutant. This might hint to increased uptake of proline in the $\Delta gacA$ mutant which is counter to the decreased proline utilization. Here again, this could be caused by the different growth media in the two experiments and would require further experimentation. It is notable though, that also for proline, there's a different response of deleting *gacA* or *gacS* indicating that they might not operate as a cognate two-component system in regulation of the metabolism of several amino acids.

Serine

Serine utilization was not different between wildtype and mutants at 24 h, however, a statistically higher value ($p < 0.05$) was measured for the $\Delta adeS$ mutant at 48 h

(**Figure 5.3**). A similar trend was observed for the $\Delta adeR$ mutant, however, the difference was not statistically significant ($p > 0.05$). The current data would therefore support that deletion of *adeS* de-represses serine utilization compared to the wildtype. None of the obvious enzymes for serine catabolism are upregulated in the transcriptomic data of the $\Delta adeS$ mutant.

Tryptophan

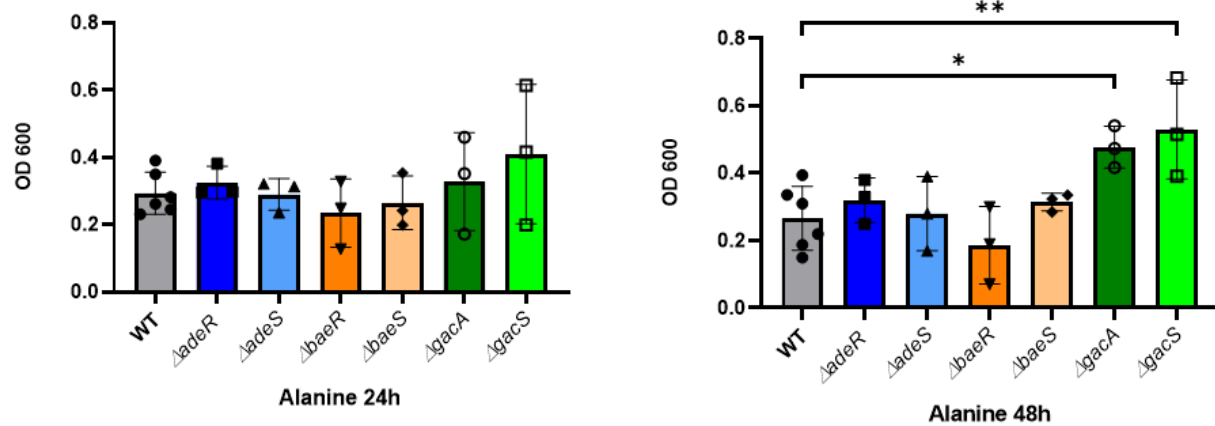
Tryptophan is utilized by *Acinetobacter calcoaceticus* by the beta-ketoadipate pathway, which could be conserved in *A. baumannii* (Wheelis, 1972). In a multi-enzymatic pathway with intermediates via kynurenine and later catechol, it can be converted to succinic acid and acetyl-CoA and from there funneled into the TCA cycle. Annotated in *A. baumannii* is kynureninase (KynU) which is essential and specific for kynurenine conversion to catechol (Wheelis, 1972). The $\Delta baeR$ and $\Delta adeS$ mutants showed significantly lower utilization of tryptophan at LSP (**Figure 5.3**). Gene expression at LSP showed 4.9-fold upregulation of *kynU* in the $\Delta adeS$ mutant and no change in the $\Delta baeR$ mutant, which do not explain the difference in tryptophan catabolism. Further experiments are required to investigate these phenotypes.

Tyrosine

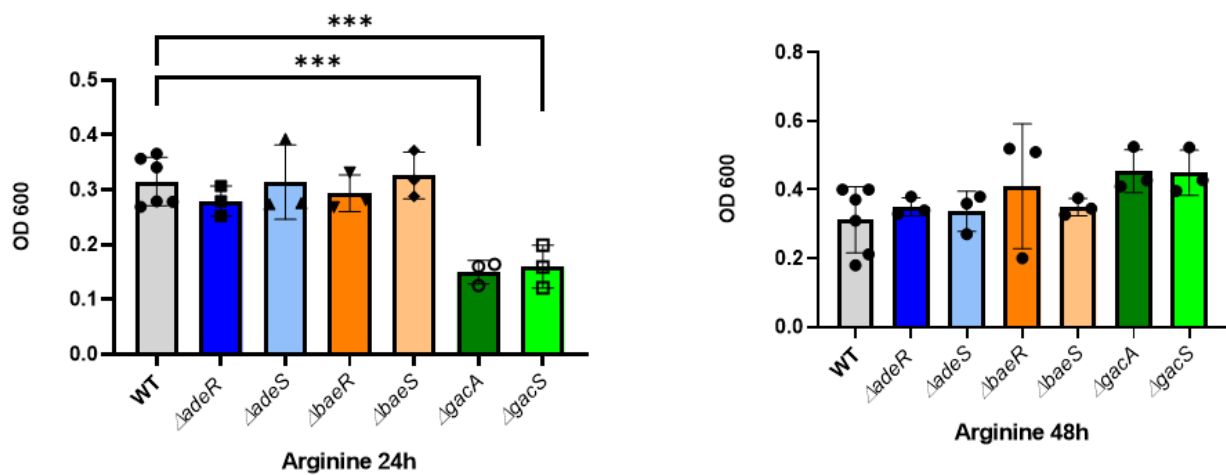
Tyrosine catabolism is significantly increased after 24 in both $\Delta adeR$ and $\Delta adeS$ mutants compared to the wildtype. This effect is sustained in the $\Delta adeS$ mutant at 48 h. None of the gene expression of pathway analysis easily explains this marked difference, therefore further experimentation is required here, too.

Figure 5.3 Analysis of phenotypic microarrays regarding amino acid utilization in *A. baumannii* wild-type and mutant strains at 24 hours and 48 hours. Growth and metabolic activity were evaluated with 20 amino acids serving as the exclusive carbon and nitrogen source. The data presented are mean values recorded at 24 hours and 48 hours. Graphs were created utilizing GraphPad Prism. Statistical comparisons between wild-type and mutant strains were conducted using one-way ANOVA ($p < 0.05$).

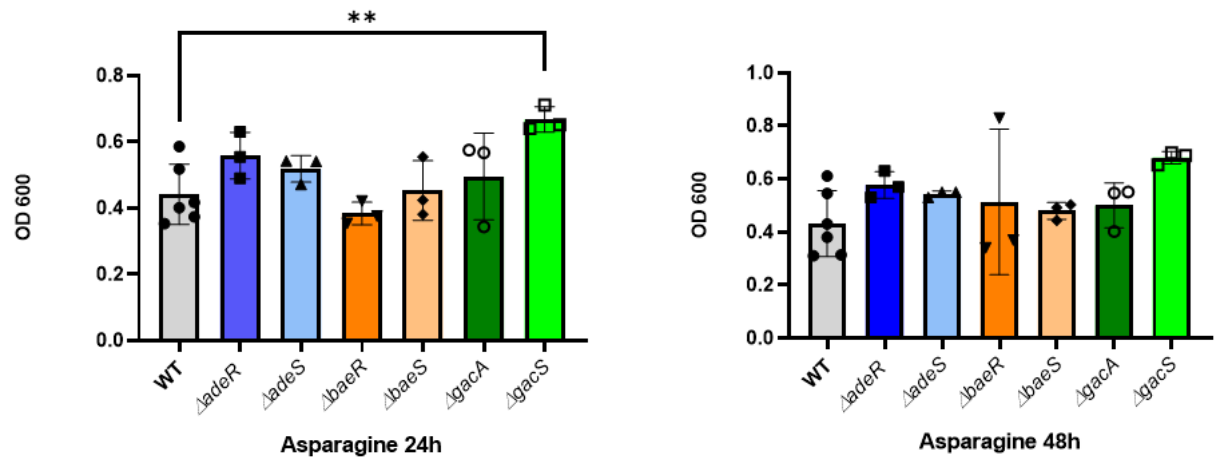
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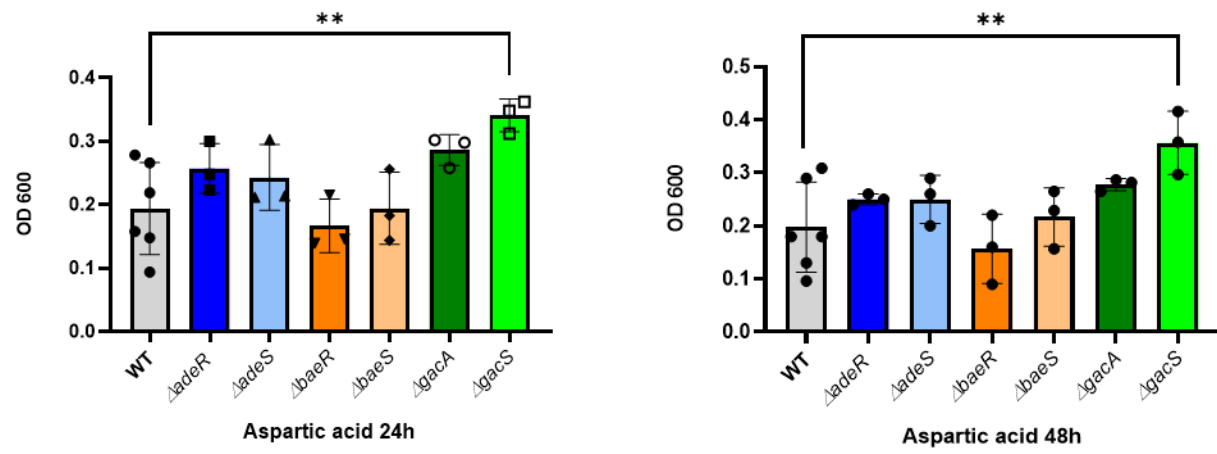
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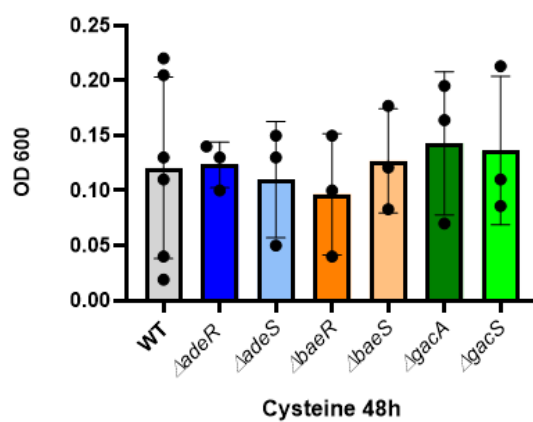
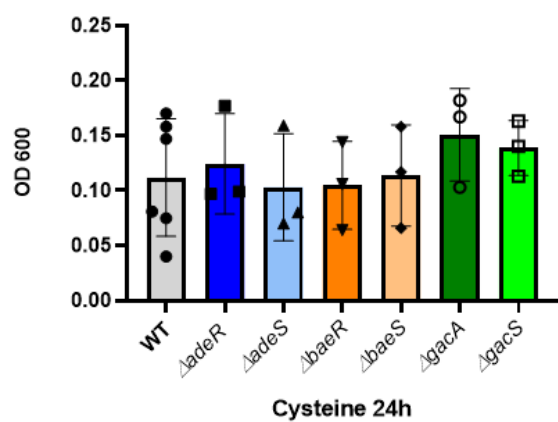
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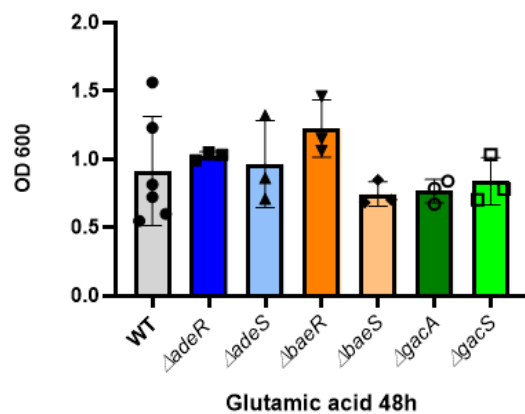
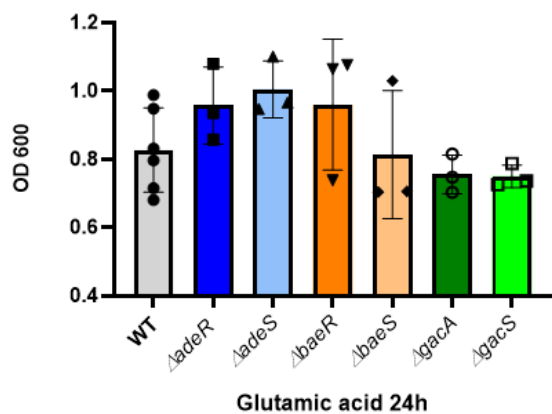
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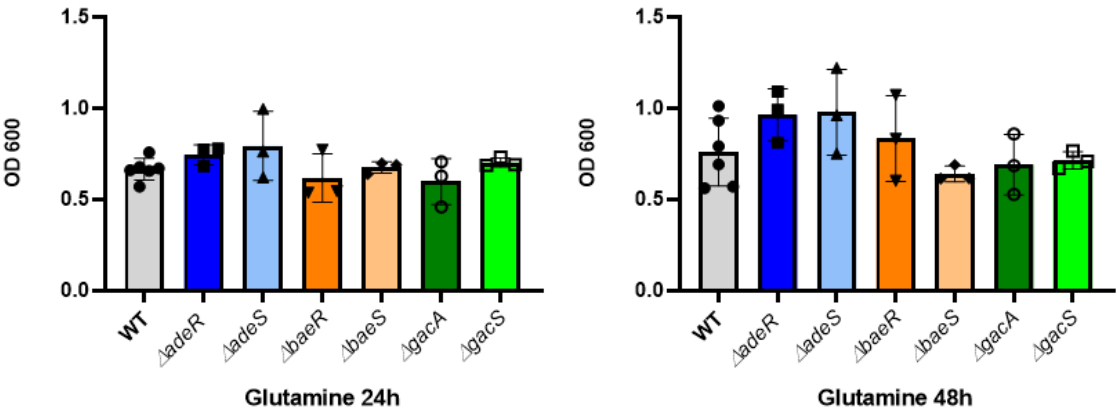
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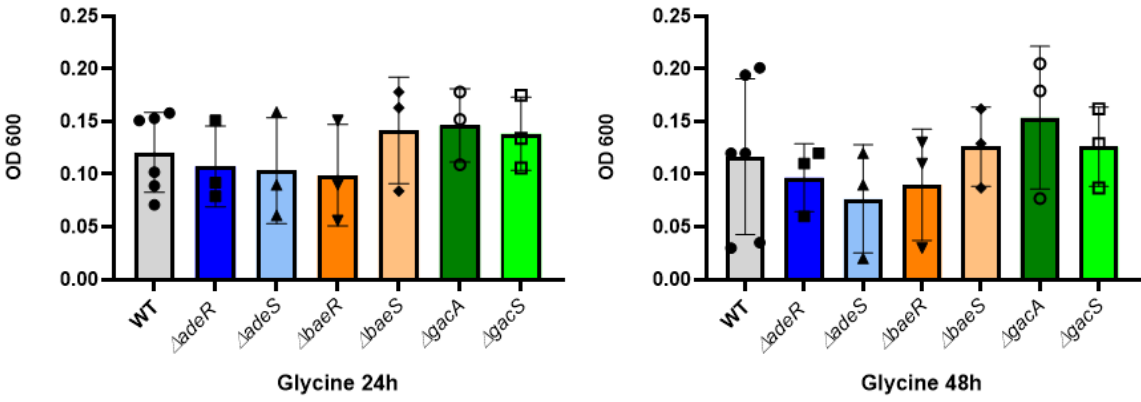
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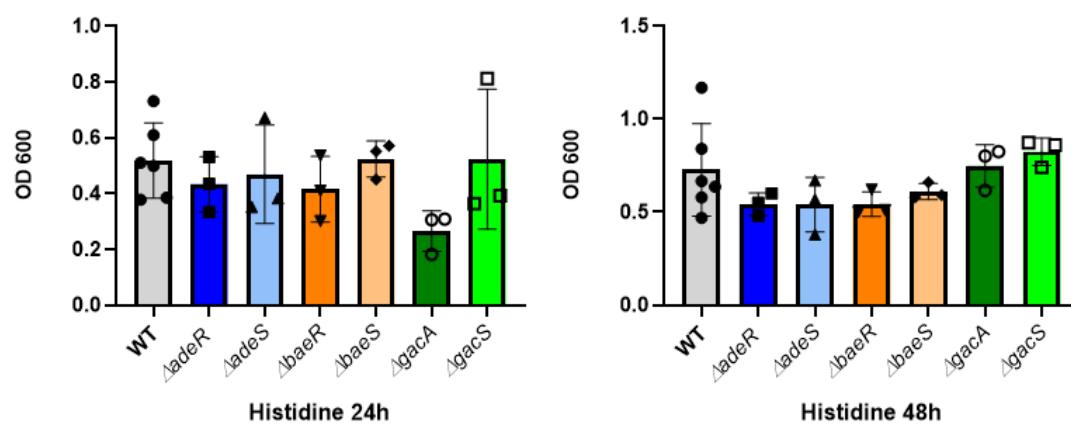
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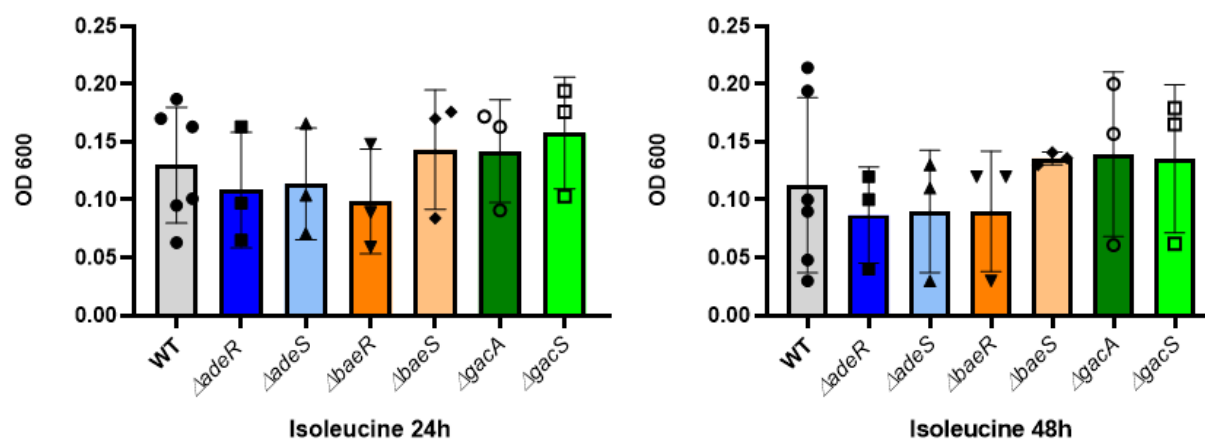
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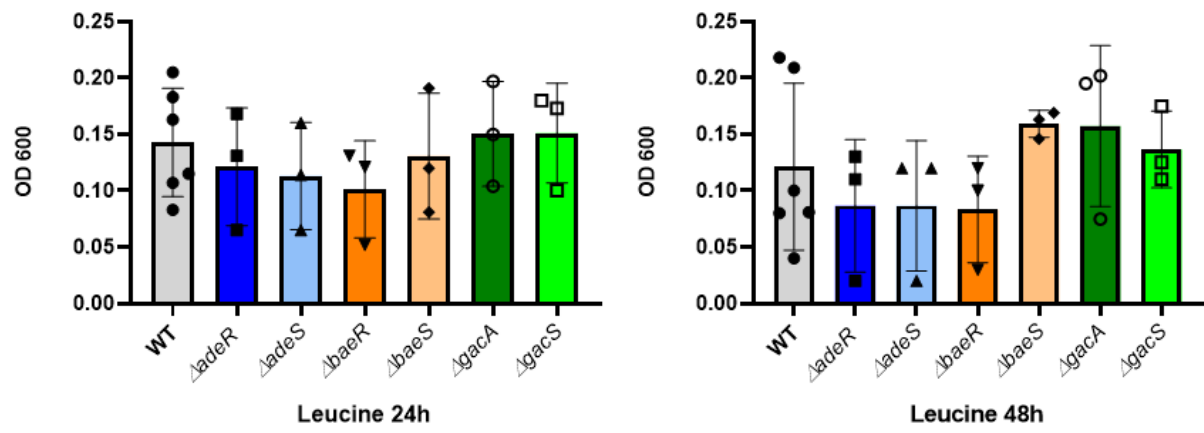
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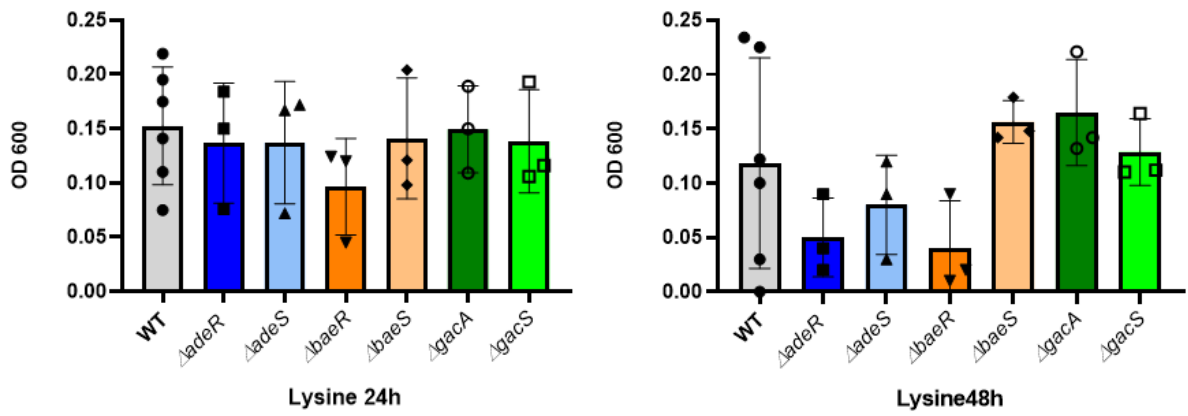
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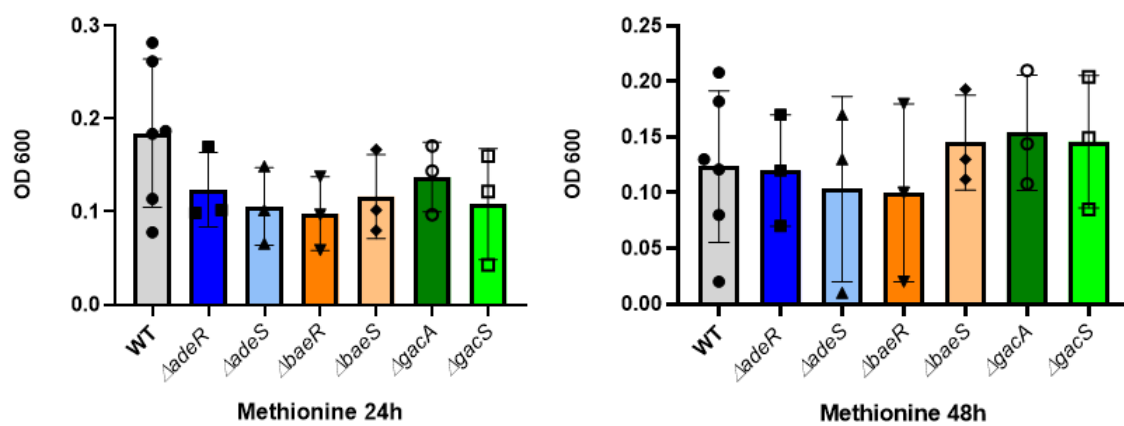
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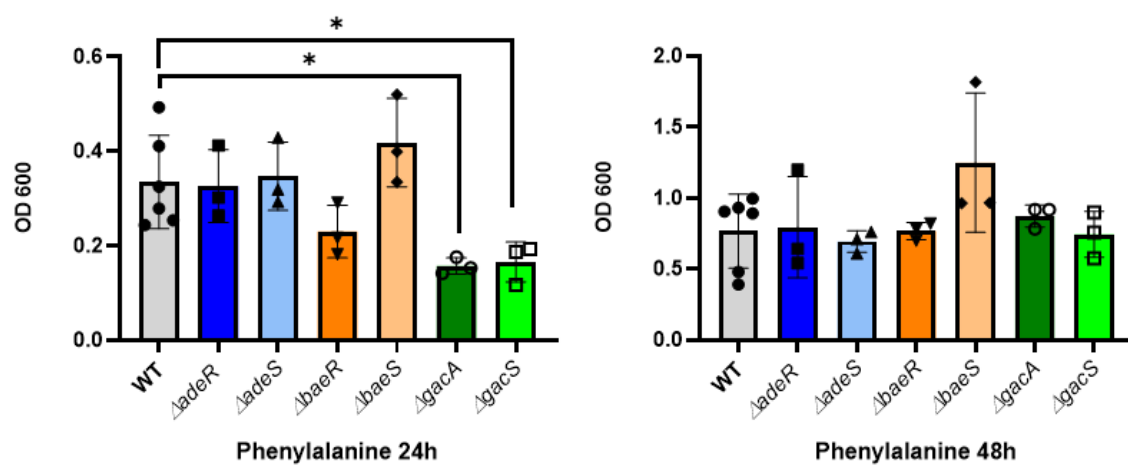
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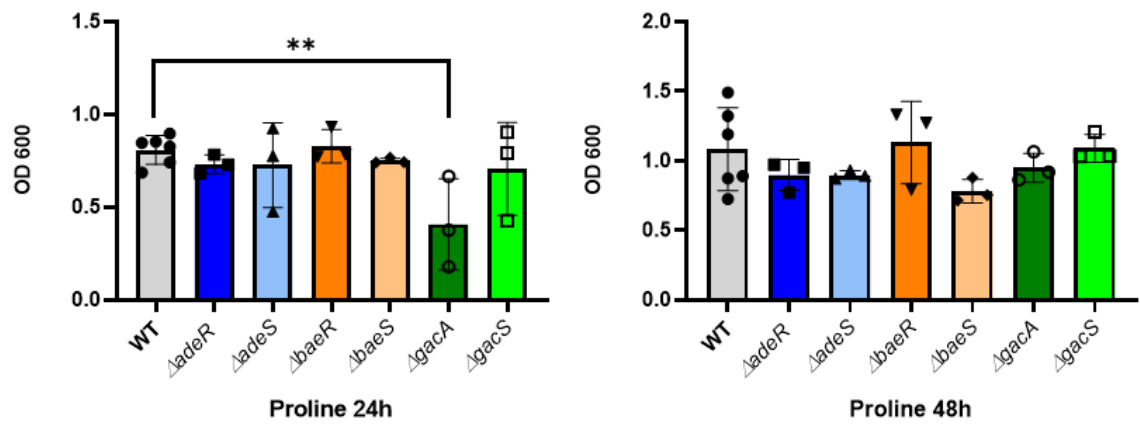
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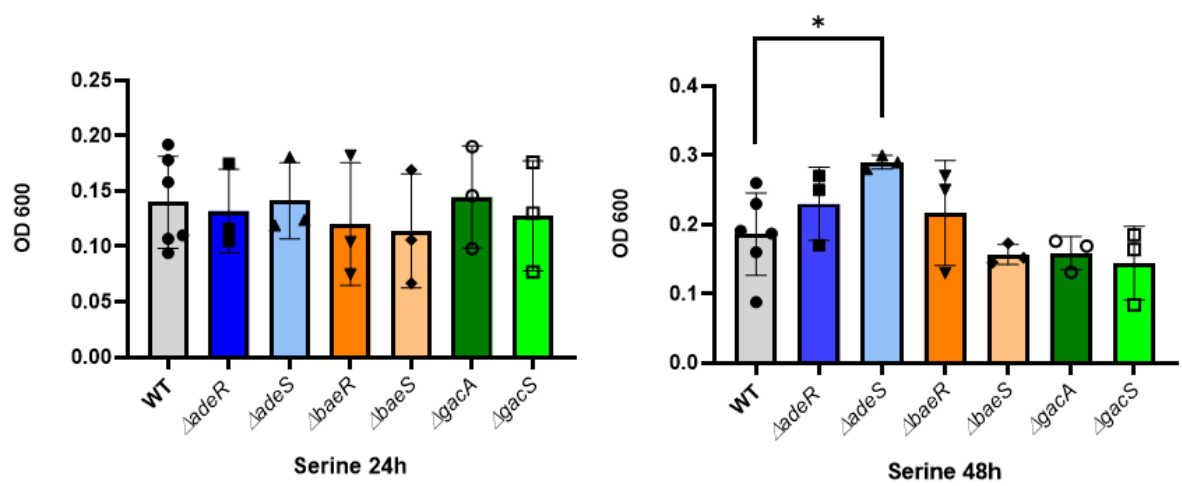
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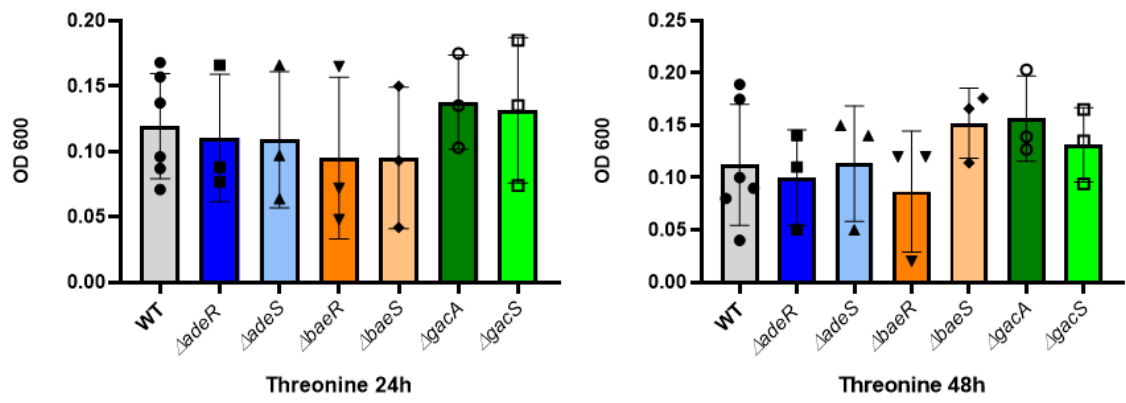
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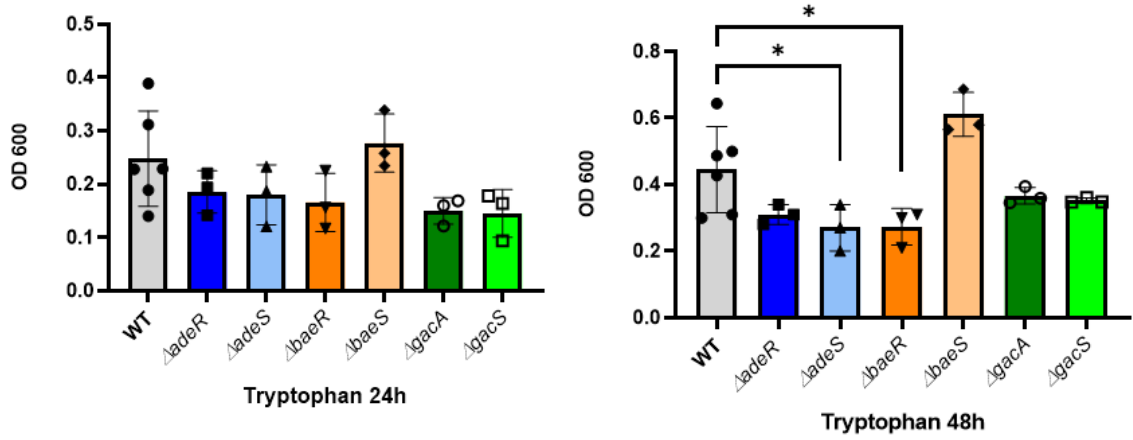
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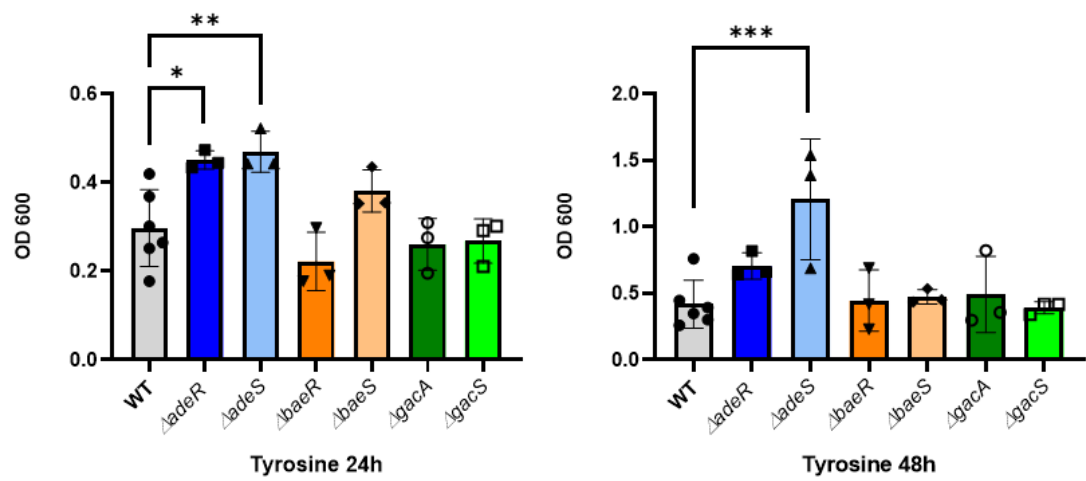
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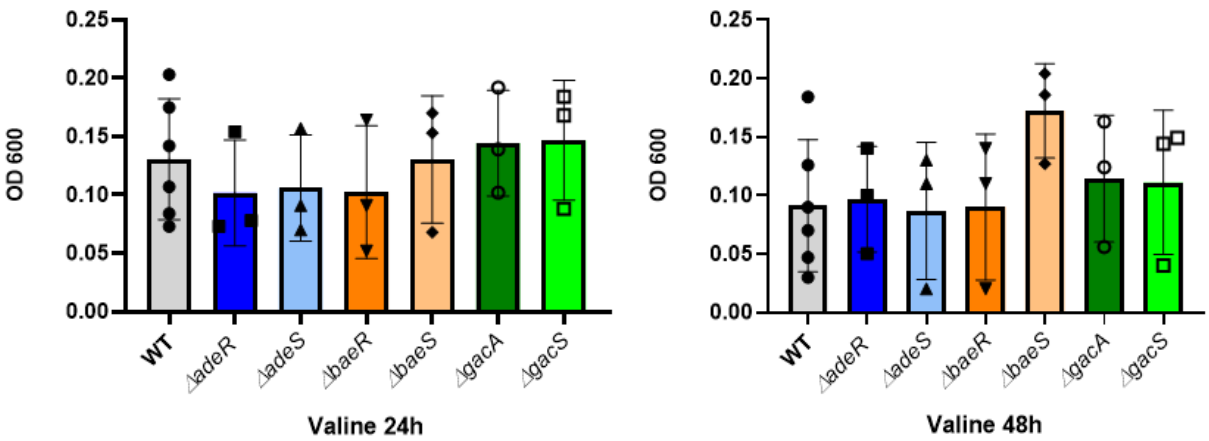
(18)



(19)



(20)



Chapter 6

Discussion

6.1. Overview of transcriptional changes under MEP and LSP conditions

Global transcriptomic analysis of the *A. baumannii* $\Delta adeR$, $\Delta adeS$, $\Delta baeR$, $\Delta baeS$, $\Delta gacS$, and $\Delta gacA$ mutants under MEP and LSP conditions demonstrated distinct gene regulation patterns in comparison to the wild type strain. In general, the quantity of differentially expressed genes (DEGs) fluctuated based on the specific two-component system and growth condition, underscoring the intricate and condition dependent characteristics of bacterial regulatory networks. Typically, a greater number of genes were differentially expressed under the LSP condition, suggesting that late stationary phase cells display more pronounced transcriptional responses to the absence of these regulators than mid-exponential phase cells. The genes impacted were mainly linked to stress response, efflux transporters, metabolism, and cell envelope processes, emphasizing the extensive regulatory impact of these systems.

6.2. Regulatory overlap and coordinated control by the AdeRS system

The AdeRS system exhibited strong and consistent transcriptional effects under both MEP and LSP conditions. In the MEP condition, a total of 71 genes were upregulated and 148 genes were downregulated in the $\Delta adeR$ mutant, while 262 upregulated and 326 downregulated genes were identified in the $\Delta adeS$ mutant. Comparative analysis revealed a substantial overlap between the two mutants, with 60 genes commonly upregulated and 133 genes commonly downregulated.

Under LSP conditions, a total of 323 genes were upregulated and 368 genes were downregulated in the $\Delta adeR$ mutant, while 307 upregulated and 226 downregulated genes were identified in the $\Delta adeS$ mutant. Comparative analysis revealed a substantial overlap between the two mutants, with 133 genes commonly upregulated and 184 genes commonly downregulated. This significant overlap suggests that AdeR and AdeS control a shared regulon, thus enhancing their collaborative role in the

regulation of gene expression in *A. baumannii*. The consistent regulatory pattern observed under both growth conditions implies that the AdeRS system manages a core set of genes vital for adaptive responses, encompassing those associated with stress tolerance, efflux pump regulation, and antimicrobial resistance. Collectively, these findings underscore the essential role of AdeRS in synchronizing transcriptional programs that support the persistence and multidrug-resistant traits of *A. baumannii* (Richmond *et al.*, 2016b; Lari *et al.*, 2018; Kyriakidis *et al.*, 2021).

6.3 Role of the AdeRS Two-Component System in regulating the *adeABC* Efflux operon under different growth conditions

The RNA-seq analysis indicated that the *adeABC* was one of the most significantly downregulated loci in both the $\Delta adeR$ and $\Delta adeS$ mutants in (MEP) conditions. This pronounced repression of *adeABC* expression reinforces the established function of the AdeRS two-component system as a positive regulator of the *adeABC* efflux operon (Marchand *et al.*, 2004; Yoon *et al.*, 2013). The AdeRS system detects environmental signals and initiates the transcription of *adeABC*, which encodes the RND-type efflux pump that confers resistance to various classes of antibiotics, such as aminoglycosides, β -lactams, and fluoroquinolones (Marchand *et al.*, 2004; Lee *et al.*, 2020).

Interestingly, under conditions of LSP, the *adeABC* operon was also found to be downregulated in the mutants, albeit to a lesser degree than in MEP. This reduced effect may be ascribed to the lower basal expression levels of *adeABC* in LSP, indicating that environmental factors play a significant role in influencing the transcriptional activity of the efflux operon. Prior research has demonstrated that the expression of *adeABC* is affected by environmental stresses, including osmolarity, pH, and exposure to antibiotics, which can modify AdeRS-mediated signal transduction (Marchand *et al.*, 2004; Peleg *et al.*, 2008; Coyne *et al.*, 2011). Overall, the persistent downregulation of *adeABC* in both $\Delta adeR$ and $\Delta adeS$ mutants emphasizes the significance of AdeRS as a regulatory mechanism governing multidrug resistance in *A. baumannii*. These results corroborate earlier studies indicating that the disruption

of the AdeRS TCS results in diminished expression of *adeABC* and heightened vulnerability to various antibiotics (Wen *et al.*, 2017; Xu *et al.*, 2019; De Gaetano *et al.*, 2023).

6.4. Regulatory overlap and coordinated control by the BaeRS system

The BaeRS system also influenced global gene expression. In the MEP condition, 284 genes were upregulated and 204 genes were downregulated in the $\Delta baeR$ mutant, while 98 upregulated and 182 downregulated genes were identified in the $\Delta baeS$ mutant. Comparative analysis revealed a substantial overlap between the two mutants, with 45 genes commonly upregulated and 67 genes commonly downregulated. Under LSP conditions, the $\Delta baeS$ mutant demonstrated a significantly wider transcriptional response, with 714 genes being upregulated and 465 genes downregulated. This indicates that BaeS has a more pronounced regulatory influence during stress or stationary-phase conditions. Conversely, the $\Delta baeR$ mutant under LSP conditions revealed only two genes that were significantly downregulated (including *baeR* itself) and did not show any upregulated genes after correction, suggesting a minimal change in transcriptional activity. Overall, these results imply that although BaeR and BaeS function as a two component system, BaeS seems to have a more prominent role in regulating gene expression, especially under LSP conditions.

6.5. Regulatory overlap and coordinated control by the GacAS system

The GacAS system displayed broad transcriptional effects under both MEP and LSP conditions, indicating its role as a global regulator in *A. baumannii*. In the MEP condition, a total of 670 genes were upregulated and 650 genes were downregulated in the $\Delta gacA$ mutant, while 532 upregulated and 506 downregulated genes were identified in the $\Delta gacS$ mutant. Comparative analysis revealed a substantial overlap between the two mutants, with 420 genes commonly upregulated and 445 genes commonly downregulated. Under LSP conditions, transcriptional changes remained extensive, with 846 genes upregulated and 678 genes downregulated in the $\Delta gacA$

mutant, and 807 upregulated and 591 downregulated genes in the $\Delta gacS$ mutant. The overlap analysis showed 448 genes commonly upregulated and 403 genes commonly downregulated in both mutants. The significant overlap observed under both growth conditions indicates that GacA and GacS work together to control a common set of genes, aligning with their functions as the response regulator and sensor kinase within the same two-component system. The GacAS regulon includes genes that play a role in metabolic adaptation, oxidative stress response, and cellular signaling, thereby reinforcing its role as a global regulator that harmonizes transcriptional programs vital for persistence and survival in varying environmental conditions (Wei *et al.*, 2013; Cheng *et al.*, 2016; Song *et al.*, 2022).

6. 6 Transcriptional Landscape of *Acinetobacter baumannii* AB5075 using dRNA-seq

Our dRNA-seq analysis of *Acinetobacter baumannii* AB5075 offers a significant opportunity to examine the transcriptional landscape of a contemporary multidrug resistant clinical isolate in comparison to the previously published primary transcriptome of the laboratory reference strain ATCC 17978 (Kröger *et al.*, 2018). Although both studies underscore the intricate nature of transcriptional organization in *A. baumannii*, various notable similarities and differences arise, yielding fresh insights into the strain specific regulation of virulence and antimicrobial resistance.

To start, regarding global transcriptional architecture, both AB5075 and ATCC 17978 show a wide range of transcriptional start sites (TSSs), which include primary, secondary, and antisense TSSs. However, there is a significant difference in the total number and distribution of TSSs between the two strains, with AB5075 (9428) having almost three times as many TSSs as ATCC 17978 (3731). This difference might be caused by increased spurious transcription in AB5075, as mostly an increased number of antisense start sites was detected. In *E. coli*, spurious transcription is suppressed by the H-NS protein (Singh *et al.*, 2014). In AB5075, there is an additional H-NS on plasmid p1AB5075 compared to ATCC17978, and perhaps this difference in H-NS protein content could be investigated whether it is the cause of the increased

spurious transcription. Even with these differences, the key -10 and -35 promoter motifs were preserved in both strains, indicating that the basic process of sigma factor driven transcription initiation is still common. Therefore, although the main promoter structure is consistent, the unique variations in TSS count, sRNA collections, and promoter application probably contribute to the greater pathogenic ability of AB5075 in comparison to the lab reference strain.

In bacteria, small RNAs (sRNAs) serve as important post transcriptional regulators that affect nearly all aspects of cell metabolism and are especially crucial for controlling virulence (Koo *et al.*, 2011; Gottesman and Storz, 2011). In ATCC17978, dRNA-seq found 110 sRNAs (Kröger *et al.*, 2018), many of which play a role in managing efflux pumps and stress responses. In comparison, our study of AB5075 revealed 88 sRNAs that are conserved with ATCC17978. In $\Delta baeS$, there was a significant change in the expression of various sRNAs, resulting in the top 20 upregulated sRNAs, including sRNA 84, 24, 1, 2, 42, 96, 100, and 15. In the cases of $\Delta gacA$ and $\Delta gacS$, numerous sRNAs exhibited changes in expression, either upregulated or downregulated. Notably, sRNA 99 was identified as the most downregulated gene in both instances, and we observed a peak in the ChIP-seq data for GacA at positions 99 and 100.

6.7 Chip seq analysis

The findings from ChIP-seq offered initial insights into the possible genomic targets of the response regulators AdeR, GacA, and BaeR in *A. baumannii*.

A specific AdeR binding peak was found in the intergenic area between *adeR* and *adeA*, indicating that AdeR interacts directly with the promoter that regulates the *adeABC* efflux operon. This finding aligns with earlier studies showing that the AdeRS two-component system controls the expression of the AdeABC multidrug efflux pump, which plays a significant role in antibiotic resistance in *A. baumannii* (Lari *et al.*, 2018; Xu *et al.*, 2019; Lee *et al.*, 2020). The peak's central location suggests that AdeR not only promotes *adeA* transcription but might also regulate its own expression to adjust efflux activity. This type of autoregulatory feedback is typical among response regulators, allowing for flexible control of gene expression in response to changing

environmental conditions. Additionally, another AdeR binding site was identified upstream of *rapA* (*ABUW_RS05385*), which codes for the RNA polymerase-associated protein RapA that is involved in transcription recycling and reinitiation. The existence of this peak indicates that AdeR could affect global transcriptional control, possibly connecting efflux regulation to wider stress response pathways. These results broaden the functional role of AdeR beyond just regulating antibiotic resistance.

For GacA, distinct peaks were found in or around small RNAs (sRNA99, sRNA91, and sRNA100), suggesting that GacA might directly engage with non-coding RNA data. This finding implies that GacA could play a role in adjusting post-transcriptional regulatory networks, alongside its established function in gene regulation. The detection of binding signals close to sRNAs points to a potential cross-regulatory mechanism by which GacA affects adaptive stress responses and the fine-tuning of gene expression.

The ChIP-seq analysis showed a specific BaeR binding site in the intergenic area between *fabR* (*ABUW_RS05395*) and *ABUW_RS05400*, which codes for a ferredoxin reductase. Given that FabR acts as a transcriptional repressor for genes related to fatty acid metabolism, BaeR binding in this area indicates a possible regulatory link between BaeR and lipid balance. This connection implies that BaeR could play an indirect role in altering membrane composition or adapting to stress.

In summary, these results offer important initial evidence of the direct regulatory roles played by AdeR, GacA, and BaeR in *A. baumannii*. However, more replicates need to be sure of these findings, as they are based on a small number of biological replicates. To verify the consistency of these peaks and to differentiate real binding events from background noise, more independent ChIP-seq experiments are necessary. Increasing the number of replicates would improve statistical reliability and clarify each regulator's binding specificity and consensus sequence. Future validation using qPCR, gene expression tests, and promoter-reporter studies will be vital to confirm these interactions and to better understand the wider regulatory systems governed by these two-component systems.

6.8 Kirby-Bauer disk diffusion assay and Minimum inhibitory concentration (MIC) determination highlights the role of regulatory systems in antibiotic susceptibility

$\Delta adeR$ - $\Delta adeS$

In our Kirby-Bauer disk diffusion assays, all strains (WT and $\Delta adeR$ - $\Delta adeS$) exhibited resistance to a range of β -lactams, including oxacillin, ticarcillin, ceftazidime, cefepime, cefoperazone, and aztreonam. This includes β -lactams such as Penicillins, Cephalosporins, and Monobactams. This extensive resistance phenotype signifies a broad multidrug resistance (MDR) profile, aligning with numerous previous studies. For example, clinical *A. baumannii* isolates in South Africa displayed resistance rates surpassing 60–70% for ceftazidime and cefepime (Lowings *et al.*, 2015). Likewise, isolates from Slovakia (2019–2022) exhibited markedly increased resistance rates to ceftazidime, cefepime, aztreonam, and co-trimoxazole (Lari *et al.*, 2018; Jalali *et al.*, 2023). In the United States, there is a growing report of resistance to cephalosporins and carbapenems in clinical strains of *A. baumannii* (Adams-Haduch *et al.*, 2011). These observations suggest that (i) the regulatory mutants do not possess any notable susceptibility advantage over WT and (ii) our laboratory WT strain is already significantly resistant.

Carbapenems: The influence of AdeRS disruption on carbapenem resistance was subsequently examined. Although deletions of *adeR* and *adeS* resulted in minor effects on aminoglycoside susceptibility, no significant differences were noted for imipenem and doripenem, all strains exhibited minimal inhibition zones and increased MICs. This emphasizes that carbapenem resistance in *A. baumannii* is predominantly driven by carbapenemases. Notably, meropenem displayed strain specific differences in the disk diffusion assay: the wild-type strain presented a partial inhibition zone, whereas the $\Delta adeR$ and $\Delta adeS$ mutants showed complete resistance. However, this trend was not replicated in MIC assays, where all strains continued to exhibit resistance. This discrepancy underscores the methodological sensitivity of disk diffusion in comparison to MIC testing. The absence of partial susceptibility in mutants indicates that AdeRS may have a subtle, indirect influence on meropenem

susceptibility, potentially through efflux or membrane associated factors. Previous research has similarly indicated that AdeRS regulated AdeABC efflux activity can influence carbapenem MICs, although carbapenemases primarily dictate resistance outcomes (Marchand *et al.*, 2004; Yoon *et al.*, 2013).

Aminoglycosides: Differences in susceptibility to aminoglycosides between wild-type (WT) and $\Delta adeR$ and $\Delta adeS$ mutants underscore the significant function of the AdeRS two-component system in modulating resistance to this antibiotic class. AdeRS is a thoroughly investigated regulator of the AdeABC efflux pump, which is crucial for aminoglycoside resistance. Our WT strain demonstrated exceptionally high resistance to gentamicin, kanamycin, and amikacin, showing no inhibition even at concentrations of 1024 $\mu\text{g/mL}$, aligning with previous findings regarding aminoglycoside resistant *A. baumannii* (Magnet *et al.*, 2001; Leus *et al.*, 2020; Lucaßen *et al.*, 2021). The deletion of either *adeR* or *adeS* resulted in a partial restoration of susceptibility, especially for gentamicin (32 $\mu\text{g/mL}$) and amikacin (128 $\mu\text{g/mL}$). Although these susceptibility values remain within the resistant category according to CLSI standards (M100, 2023), they indicate that the efflux regulated by *adeRS* significantly contributes to high-level resistance. Nevertheless, full susceptibility was not achieved, suggesting that additional mechanisms such as aminoglycoside modifying enzymes are also involved. Therefore, solely targeting AdeABC may not be adequate to reverse aminoglycoside resistance.

Other Agents (Tetracyclines, Polymyxins, Combination β -lactams, and Phenicol) the susceptibility profiles of tigecycline, colistin sulfate, piperacillin-tazobactam, and chloramphenicol revealed no significant differences between wild-type (WT) and $\Delta adeR$ and $\Delta adeS$ mutants, as all strains displayed comparable inhibition zones. Resistance to tigecycline is frequently associated with the overexpression of the AdeABC efflux pump, however, this generally necessitates gain of function mutations in *adeS* (Ruzin *et al.*, 2007). Given that our mutants were characterized by loss of function deletions, no enhancement in susceptibility was detected. Likewise, colistin resistance in *A. baumannii* is predominantly governed by lipid A modifications that are regulated by the PmrAB system (Adams *et al.*, 2009), which accounts for the absence

of AdeRS involvement. The susceptibility to piperacillin-tazobactam and chloramphenicol also remained stable, further underscoring that the AdeRS system primarily influences aminoglycosides and, to a lesser extent, meropenem.

$\Delta baeR$, $\Delta baeS$

β -lactams (including penicillins, cephalosporins, monobactams, and carbapenems) all strains (WT, $\Delta baeR$, $\Delta baeS$) demonstrated resistance to oxacillin, ticarcillin, ceftazidime, cefepime, cefotaxime, and aztreonam, which aligns with the prevalent multidrug resistance phenotype observed in *A. baumannii*. This indicates that BaeRS does not significantly influence the regulation of resistance to these β -lactams. Notably, cefoxitin and cefoperazone exhibited slight variations, while both WT and $\Delta baeR$ were completely resistant, $\Delta baeS$ presented a minor inhibition zone (0.8–1 cm), yet it remained classified as resistant. These subtle effects may indicate an indirect modulation of outer membrane permeability or stress-response pathways by BaeRS (Lin *et al.*, 2014). Within the carbapenem category, $\Delta baeS$ exhibited resistance similar to WT (resistant to imipenem, meropenem, and doripenem), whereas $\Delta baeR$ displayed partial susceptibility to doripenem (1–1.8 cm zone). Given that BaeRS has been associated with efflux regulation (Henry *et al.*, 2012; Lin *et al.*, 2014), the heightened susceptibility of $\Delta baeR$ may result from a compromised efflux capacity for doripenem, underscoring that the response regulator *baeR* has a more prominent role than *baeS* in mediating these phenotypes.

Aminoglycosides: WT and $\Delta baeS$ exhibited resistance to gentamicin, kanamycin, and tobramycin, while $\Delta baeR$ showed a minor inhibition zone against tobramycin (1–1.8 cm). Prior research has indicated that *baeRS* may modulate the AdeABC, AdeIJK, and MacAB-TolC efflux pumps (Henry *et al.*, 2012; Lin *et al.*, 2015), which are associated with aminoglycoside resistance. The phenotype noted in $\Delta baeR$ may thus indicate a reduction in efflux regulation. Given that $\Delta baeS$ did not demonstrate this effect, the findings support the notion that the response regulator *baeR* has a more direct role in the efflux-mediated resistance to aminoglycosides.

Fluoroquinolones: In the case of ciprofloxacin, the wild type (WT) exhibited resistance, whereas both mutants displayed minor inhibition zones (1–1.5 cm), indicating a slight

enhancement in sensitivity. This observation is consistent with the involvement of efflux pumps, specifically AdeIJK and MacAB-TolC, in the resistance to fluoroquinolones, which have been suggested to be regulated by BaeRS (Henry *et al.*, 2012; Lin *et al.*, 2015). Consequently, the deletion of either *baeR* or *baeS* may hinder the complete efflux capacity, thereby elucidating the minor shifts in susceptibility.

Other antibiotic classes: No notable differences were observed for tetracycline, colistin sulfate, piperacillin-tazobactam, chloramphenicol, and imipenem, suggesting that *baeRS* does not play a significant regulatory role for these antibiotics. Like resistance to colistin is generally controlled by the PmrAB system (Adams *et al.*, 2009), while tigecycline resistance is frequently associated with AdeRS-mediated efflux rather than BaeRS (Ruzin *et al.*, 2007).

Nitrofurantoin and Tigecycline, In the case of nitrofurantoin, the $\Delta baeS$ mutant exhibited a minor inhibition zone measuring between 0.8 and 1 cm, whereas both the wild type (WT) and $\Delta baeR$ mutants displayed resistance. This observation implies that the absence of *baeS* may activate compensatory stress responses. Conversely, Tigecycline demonstrated the most significant variations, with inhibition zones being more extensive in both mutant strains compared to the WT. Given that *baeRS* has been associated with the regulation of efflux pumps (Lin *et al.*, 2015), it is plausible that this phenotype arises from diminished efflux activity in the mutants. This finding aligns with previous studies indicating that BaeRS plays a role in stress tolerance and the survival of antibiotics (Chusri *et al.*, 2009; Lin *et al.*, 2015).

$\Delta gacA$, $\Delta gacS$

The antibiotic susceptibility assessment of the $\Delta gacA$ and $\Delta gacS$ mutants indicated that the GacAS system does not have a widespread function in resistance, however, it seems to selectively influence resistance to specific antibiotics.

β -lactams: Both mutants, along with the wild type (WT), exhibited resistance to oxacillin, ticarcillin, ceftazidime, cefepime, and aztreonam, which are recognized as ineffective against multidrug resistant *A. baumannii*. These findings imply that *gacAS* does not play a role in the regulation of resistance to these agents. In the case of

piperacillin-tazobactam, no notable differences were detected between the WT and the mutants. Among the carbapenems, distinct patterns were observed. For imipenem, no differences were noted among the strains. Conversely, doripenem and meropenem exhibited varying effects. The WT maintained full resistance to doripenem, whereas $\Delta gacS$ showed only a minor increase in sensitivity (0.7–0.8 cm inhibition zone) and $\Delta gacA$ exhibited a significantly larger inhibition zone (~1.5 cm), suggesting that *gacA* is more crucial in sustaining resistance to this compound. In contrast, for meropenem, both WT and $\Delta gacA$ demonstrated comparable inhibition zones (1–1.4 cm), while $\Delta gacS$ remained resistant. These results indicate that GacA, functioning as the response regulator, may modulate specific resistance determinants, and that the differences observed between doripenem and meropenem reflect drug-specific interactions with the GacAS regulatory system. Interestingly, our findings reveal that the $\Delta gacA$ mutant exhibited heightened susceptibility to doripenem. This increased sensitivity may stem not only from changes in efflux or membrane-associated genes but also from regulatory effects on motility. Previous studies have demonstrated that GacAS is involved in the regulation of bacterial motility, which has been linked to multidrug resistance traits in metabolically active swarming cells (Song *et al.*, 2022). Although there have been no direct studies confirming this relationship in *A. baumannii*, our results imply that the disruption of *gacA* could impair motility-related resistance mechanisms, thereby increasing sensitivity to carbapenems.

Aminoglycosides: In the case of kanamycin, all strains exhibited resistance, showing no observable impact from the deletion of *gacA* or *gacS*. The findings regarding tobramycin were more complex: both the wild type (WT) and the $\Delta gacS$ strains consistently displayed resistance, whereas the $\Delta gacA$ strain presented a variable phenotype across different replicates, two experiments indicated partial inhibition zones, while one remained resistant. This inconsistency suggests that *gacA* might indirectly influence susceptibility through stochastic effects on efflux regulation or membrane permeability.

Fluoroquinolones and others: The $\Delta gacS$ mutant exhibited minimal inhibition zones (0.5–1 cm) when tested with ciprofloxacin, nitrofurantoin, and cefoperazone, which is

inadequate to indicate significant sensitivity, whereas both WT and $\Delta gacA$ continued to show resistance. These slight variations may indicate minor regulatory influences of *gacS* on outer membrane activities, yet they are improbable to hold clinical relevance.

Tetracyclines: There was no significant difference in tetracycline susceptibility between wild-type (WT) strains and mutants. **Polymyxins:** The inhibition zones for colistin sulfate were comparable among all strains, aligning with previous findings that indicate colistin resistance in *A. baumannii* is predominantly governed by the PmrAB two-component system (Adams *et al.*, 2009). **Phenolics:** The susceptibility to chloramphenicol remained consistent between WT strains and mutants. Previous research has underscored the multifaceted roles of the *gacA* and *gacS* two-component system in *A. baumannii*. In addition to its initial identification in citrate metabolism (Dorsey *et al.*, 2002), GacSA has been associated with the regulation of virulence, which encompasses pili synthesis, motility, biofilm development, resistance to human serum, and the metabolism of aromatic compounds (Cerqueira *et al.*, 2014; Bhuiyan *et al.*, 2016). These characteristics are intricately linked to antibiotic resistance, as motility and biofilm behavior affect drug tolerance, while metabolic regulation can influence susceptibility. Our finding that the $\Delta gacA$ mutant showed heightened susceptibility to doripenem indicates that *gacA* may influence resistance indirectly by modulating pathways related to virulence or metabolic functions, rather than directly regulating resistance genes. In summary, these findings reinforce the notion of *gacSA* as a comprehensive regulator in *A. baumannii*, with significant implications for both virulence and antibiotic resistance.

6.9 Insights from Phenotypic Microarray on metabolic and stress adaptations of *Acinetobacter baumannii*

1. Amino Acid Utilization in the $\Delta gacA$ and $\Delta gacS$ Mutants

Phenotypic microarray analysis showed that mutations in the *gacA* and *gacS* genes led to different uses of several amino acids. This indicates that the GacS/GacA two component system (TCS) plays a role in regulating amino acid metabolism in *Acinetobacter baumannii*. While the GacS/GacA system is known as a major regulator

of virulence, secondary metabolism, and stress responses in Gram-negative bacteria (Heeb and Haas, 2001; Wei *et al.*, 2013; Song *et al.*, 2022), its specific role in amino acid utilization has not been reported before.

Both $\Delta gacA$ and $\Delta gacS$ mutants showed a much higher use of L-alanine than the wild-type strain, which suggests increased breakdown activity for this substrate. This could indicate a lack of proper control over alanine metabolism or a change in carbon-nitrogen flow without the GacS/GacA regulatory system. Interestingly, even with this higher alanine breakdown, both mutants had growth issues in minimal media, suggesting that the imbalance in alanine use might harm cellular metabolic balance. To our knowledge, no prior research has shown a direct regulatory link between GacS/GacA and alanine metabolism in *A. baumannii*, making this a potentially new discovery.

In contrast, the use of arginine was postponed in both $\Delta gacA$ and $\Delta gacS$ mutants, as they displayed lower activity at 24 hours but reached wild-type levels by 48 hours. This trend indicates that GacS/GacA affects the initial phases of arginine breakdown or absorption. These findings align with a recent study showing that the *A. baumannii* ATCC 17978 $\Delta gacA$ mutant could not grow in minimal medium when arginine was the only carbon source, and that arginine use is crucial for bacterial survival in a mouse pneumonia model (Devnath *et al.*, 2025). Overall, these results suggest that the GacS/GacA system is significant in regulating arginine metabolism, impacting both nutrient uptake and disease progression.

The absence of GacS also influenced the use of asparagine. While all strains could use asparagine, the $\Delta gacS$ mutant showed a significantly quicker utilization rate after 24 hours than the wild type. However, there have been no prior studies that have directly connected GacS/GacA to asparagine metabolism in *A. baumannii* AB5075. Thus, this finding might indicate a new metabolic phenotype related to GacS in regulating amino acid use, which requires more research.

Increased use of aspartic acid was also seen in the $\Delta gacS$ mutant. Transcriptomic data backed this observation, indicating that the aspartate aminotransferase family protein was significantly upregulated in the $\Delta gacA$ mutant, while it stayed the same in

the $\Delta gacS$ mutant. This difference implies that GacA and GacS might control different groups of genes in the same metabolic pathway, potentially through separate or compensatory regulatory methods.

For proline, most strains showed no significant differences, except for the $\Delta gacA$ mutant, which had a notable decrease in respiration. This suggests that GacA, instead of GacS, has a more direct influence on proline metabolism or energy production related to proline oxidation.

Overall, these findings show that the GacS/GacA TCS affects amino acid metabolism more than was previously understood. Although there are no direct regulatory connections identified between GacS/GacA and particular amino acid breakdown pathways in *A. baumannii* AB5075, the noticeable phenotypic variations in $\Delta gacA$ and $\Delta gacS$ mutants indicate that this system influences metabolic flexibility and may align nutrient use with environmental or stress signals. This regulatory adaptability might help the organism endure in nutrient scarce environments and during infections.

2. Amino Acid Utilization in the $\Delta adeS$, $\Delta adeR$ and $\Delta baeR$ Mutants

For serine, there was no difference in utilization between the wild type and mutants at 24 hours. However, at 48 hours, the $\Delta adeS$ mutant showed a significantly increased level of respiration ($p < 0.05$), while the $\Delta adeR$ mutant displayed a similar trend that was not statistically significant ($p > 0.05$). These findings indicate that the AdeRS system might have a secondary or time dependent role in controlling serine utilization, possibly by affecting membrane transporters or metabolic enzymes that are active during extended incubation.

Besides the amino acids mentioned earlier, there were also significant differences noted in how tryptophan is used. The $\Delta baeR$ and $\Delta adeS$ mutant strains showed much lower metabolic activity with tryptophan after 48 hours when compared to the wild-type strain. This decrease indicates that both BaeR and AdeS response regulators might play a role in managing tryptophan transport or breakdown. Since tryptophan metabolism is closely tied to redox balance and the production of secondary metabolites, the reduced utilization seen in these mutants could indicate a weakened

ability to sustain metabolic balance in nutrient-poor environments. The current results imply that these systems might also have wider impacts on cellular metabolism in *A. baumannii*.

The breakdown of tyrosine was significantly higher in both the $\Delta adeR$ and $\Delta adeS$ mutant strains compared to the wild type after 24 hours. This increase continued in the $\Delta adeS$ mutant at 48 hours. This greater utilization of tyrosine indicates that the AdeRS two-component system is involved in negatively regulating tyrosine catabolism or its related transport processes. The ongoing increase in the $\Delta adeS$ mutant suggests that AdeS, acting as the sensor kinase, may exert a stronger regulatory effect on tyrosine-related pathways than AdeR.

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Appendix

Table A1. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta adeR$ MEP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta adeR$ MEP vs WT MEP log2FC
ABUW_RS01510		bacterioferritin-associated ferredoxin	3.24
ABUW_RS16540		TonB-dependent siderophore receptor	3.10
ABUW_RS11440	dapC	succinyl-diaminopimelate transaminase	2.74
ABUW_RS10220		aspartate ammonia-lyase	2.58
ABUW_RS10600		hypothetical protein	2.54
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	2.46
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	2.36
ABUW_RS16655		energy transducer TonB	2.16
ABUW_RS10525		hypothetical protein	2.03
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	2.03
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.98
ABUW_RS17840		cation transporter	1.95
ABUW_RS08035		TonB-dependent receptor	1.94
ABUW_RS00790		TonB-dependent siderophore receptor	1.89
ABUW_RS20540		hypothetical protein	1.88
ABUW_RS17835		signal peptidase II	1.86
ABUW_RS17685		ferrous iron transporter B	1.83
ABUW_RS07730	kdpC	potassium-transporting ATPase subunit KdpC	1.82
ABUW_RS18235		NAD-dependent malic enzyme	1.81
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	1.79
ABUW_RS00710		TonB-dependent siderophore receptor	1.76
ABUW_RS06655		alpha/beta hydrolase	1.73
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	1.72
ABUW_RS20110		hypothetical protein	1.69
ABUW_RS13745		TonB-dependent receptor	1.67
ABUW_RS08720		DUF2057 domain-containing protein	1.67
ABUW_RS16645		biopolymer transporter ExbD	1.66
ABUW_RS10595		PepSY domain-containing protein	1.64
ABUW_RS07435		MFS transporter	1.63
ABUW_RS17680		hypothetical protein	1.60
ABUW_RS17690		ferrous iron transport protein A	1.57
ABUW_RS17430	htpG	molecular chaperone HtpG	1.56
ABUW_RS01820		HPP family protein	1.53
ABUW_RS03465		alanine:cation symporter family protein	1.47
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	1.45
ABUW_RS17870	arsB	ACR3 family arsenite efflux transporter	1.37
ABUW_RS11115	putP	sodium/proline symporter PutP	1.27
ABUW_RS09360		amidohydrolase family protein	1.27
ABUW_RS02370		TetR family transcriptional regulator	1.24
ABUW_RS01470		FAD-dependent oxidoreductase	1.22
ABUW_RS18915		5-(carboxyamino)imidazole ribonucleotide synthase	1.20
ABUW_RS05430		aspartate aminotransferase family protein	1.20
sRNA96	sRNA96	sRNA96	1.19
ABUW_RS16495		phosphogluconate dehydratase	1.19
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.19
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.18
ABUW_RS04205		APC family permease	1.17
ABUW_RS07475	purD	phosphoribosylamine-glycine ligase	1.16
ABUW_RS08680		aspartate aminotransferase family protein	1.16
ABUW_RS17865		arsenate reductase ArsC	1.16
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	1.15

ABUW_RS02590		bestrophin	1.14
ABUW_RS13345		aspartate kinase	1.13
ABUW_RS17905		DDE-type integrase/transposase/recombinase	1.13
ABUW_RS01350		amino acid permease	1.10
ABUW_RS14250		helix-turn-helix transcriptional regulator	1.10
ABUW_RS16800	truA	tRNA pseudouridine(38-40) synthase TruA	1.08
ABUW_RS17900		TniB family NTP-binding protein	1.08
ABUW_RS17215		monovalent cation/H+ antiporter subunit F	1.08
ABUW_RS08000		Lrp/AsnC family transcriptional regulator	1.07
ABUW_RS11080		DUF1275 domain-containing protein	1.07
ABUW_RS17630		EamA family transporter	1.06
ABUW_RS07480	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.04
ABUW_RS08765		TonB-dependent siderophore receptor	1.04
ABUW_RS13930		dioxygenase	1.04
ABUW_RS14375		FKBP-type peptidyl-prolyl cis-trans isomerase	1.03
ABUW_RS16620		hypothetical protein	1.02
ABUW_RS06685		hydrolase	1.02
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.02
ABUW_RS06105		site-specific integrase	1.00
ABUW_RS07870	nfsB	oxygen-insensitive NAD(P)H nitroreductase	1.00

Gene	Gene Name	Function	Δ adeR MEP vs WT MEP log2FC
ABUW_RS09595	adeR	efflux system response regulator transcription factor AdeR	-10.64
ABUW_RS09600	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	-8.21
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	-7.12
ABUW_RS09605	adeB	multidrug efflux RND transporter permease subunit AdeB	-6.85
ABUW_RS10110	antB	anthranilate 1,2-dioxygenase small subunit	-5.87
ABUW_RS09610	adeC	multidrug efflux RND transporter outer membrane channel subunit AdeC	-5.84
ABUW_RS10115	antC	anthranilate 1,2-dioxygenase electron transfer component AntC	-4.99
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-3.44
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-3.34
ABUW_RS12215		hypothetical protein	-3.21
ABUW_RS15175	bfr	bacterioferritin	-2.76
ABUW_RS17065		hypothetical protein	-2.71
ABUW_RS00335		VOC family protein	-2.61
ABUW_RS15160	otsB	trehalose-phosphatase	-2.56
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-2.49
ABUW_RS13055		cold-shock protein	-2.45
ABUW_RS11275		cytosine permease	-2.36
ABUW_RS00340	maiA	maleylacetoacetate isomerase	-2.35
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-2.33
ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-2.17
ABUW_RS02785		phage tail sheath protein	-2.15
ABUW_RS02860		GPO family capsid scaffolding protein	-2.14
ABUW_RS07265	csuC	Csu fimbrial biogenesis chaperone CsuC	-2.10
ABUW_RS00380	hutU	urocanate hydratase	-2.09
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	-2.06
ABUW_RS12320	paaB	1,2-phenylacetyl-CoA epoxidase subunit B	-2.04
ABUW_RS00385	hutH	histidine ammonia-lyase	-2.03
ABUW_RS00345	fahA	fumarylacetoacetase	-2.00
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-1.99
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	-1.95
ABUW_RS11780		transporter substrate-binding domain-containing protein	-1.95
ABUW_RS11355		SfnB family sulfur acquisition oxidoreductase	-1.94
ABUW_RS12325	paaA	1,2-phenylacetyl-CoA epoxidase subunit A	-1.92

ABUW_RS12315	paaC	phenylacetate-CoA oxygenase subunit PaaC	-1.90
ABUW_RS12330	paaZ	phenylacetic acid degradation bifunctional protein PaaZ	-1.88
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-1.87
ABUW_RS19040		zeta toxin family protein	-1.85
ABUW_RS11360		SfnB family sulfur acquisition oxidoreductase	-1.85
ABUW_RS11575	tauD	taurine dioxygenase	-1.81
ABUW_RS11750		serine acetyltransferase	-1.79
ABUW_RS11370		methionine transporter	-1.79
ABUW_RS07135		CoA-acylating methylmalonate-semialdehyde dehydrogenase	-1.78
ABUW_RS05750	basC	putative histamine N-monooxygenase	-1.77
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	-1.76
ABUW_RS00515		alpha/beta fold hydrolase	-1.75
ABUW_RS13445		alpha/beta hydrolase	-1.74
ABUW_RS03310		YegP family protein	-1.73
ABUW_RS13005		hypothetical protein	-1.72
ABUW_RS20105		hypothetical protein	-1.72
ABUW_RS08725		cyd operon YbgE family protein	-1.70
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-1.67
ABUW_RS07515		circularly permuted type 2 ATP-grasp protein	-1.67
ABUW_RS10615		(2Fe-2S)-binding protein	-1.66
ABUW_RS07270	csuD	Csu fimbrial usher CsuD	-1.65
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-1.64
ABUW_RS11425		tautomerase family protein	-1.64
ABUW_RS09295		hypothetical protein	-1.62
ABUW_RS11785		amino acid ABC transporter ATP-binding protein	-1.61
ABUW_RS19070		hypothetical protein	-1.59
ABUW_RS07130		aspartate aminotransferase family protein	-1.58
ABUW_RS09985		DUF4882 family protein	-1.58
ABUW_RS05230		hypothetical protein	-1.56
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-1.56
ABUW_RS12745		DUF2147 domain-containing protein	-1.54
ABUW_RS12725		hypothetical protein	-1.53
ABUW_RS00405		DUF885 domain-containing protein	-1.53
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-1.51
ABUW_RS02850		terminase	-1.49
ABUW_RS12760		lauroyl acyltransferase	-1.47
ABUW_RS13250		OmpA family protein	-1.47
ABUW_RS13045		NAD(P)-binding domain-containing protein	-1.45
ABUW_RS05685		hypothetical protein	-1.44
ABUW_RS03605	hchA	protein deglycase HchA	-1.44
ABUW_RS16440		phosphatase PAP2 family protein	-1.44
ABUW_RS07960		spore coat protein U domain-containing protein	-1.44
ABUW_RS01505	bfr	bacterioferritin	-1.41
ABUW_RS05540		LysR family transcriptional regulator	-1.41
ABUW_RS12900		DUF4882 family protein	-1.39
ABUW_RS12635		sel1 repeat family protein	-1.39
ABUW_RS03180		VOC family protein	-1.39
ABUW_RS00390		amino acid permease	-1.38
ABUW_RS14030		isocitrate lyase	-1.38
ABUW_RS07965		molecular chaperone	-1.37
ABUW_RS07520		alpha-E domain-containing protein	-1.37
ABUW_RS16890		glutathione S-transferase family protein	-1.37
ABUW_RS19065		hypothetical protein	-1.36
ABUW_RS09525		DEAD/DEAH box helicase family protein	-1.34
ABUW_RS12520	tssE	type VI secretion system baseplate subunit TssE	-1.34
ABUW_RS05225		glycosyltransferase family 2 protein	-1.34
ABUW_RS05340	cas3f	type I-F CRISPR-associated helicase Cas3	-1.33

ABUW_RS00395		imidazolonepropionase	-1.32
ABUW_RS16720		hypothetical protein	-1.32
ABUW_RS19080		thermonuclease family protein	-1.32
ABUW_RS15165		trehalose-6-phosphate synthase	-1.29
ABUW_RS04495		Ig-like domain repeat protein	-1.29
ABUW_RS11380		ATP-binding cassette domain-containing protein	-1.29
ABUW_RS00260		DUF1328 domain-containing protein	-1.28
ABUW_RS16715		HdeD family acid-resistance protein	-1.26
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	-1.26
ABUW_RS13685		type VI secretion system tip protein VgrG	-1.26
ABUW_RS11375		MetQ/NlpA family ABC transporter substrate-binding protein	-1.25
ABUW_RS13450		GMC family oxidoreductase	-1.25
ABUW_RS09290		cation:proton antiporter	-1.25
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.24
ABUW_RS07250	csuAB	Csu fimbrial major subunit CsuAB	-1.24
ABUW_RS10580		HAD family hydrolase	-1.23
ABUW_RS01615		hemerythrin domain-containing protein	-1.22
ABUW_RS08700		hypothetical protein	-1.21
ABUW_RS05910		hypothetical protein	-1.21
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	-1.21
ABUW_RS05480		BapA prefix-like domain-containing protein	-1.21
ABUW_RS07985		SDR family NAD(P)-dependent oxidoreductase	-1.20
sRNA27	sRNA27	sRNA27	-1.20
ABUW_RS02855		phage major capsid protein, P2 family	-1.19
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.19
ABUW_RS14645	ggt	gamma-glutamyltransferase	-1.19
ABUW_RS15615	add	adenosine deaminase	-1.18
ABUW_RS13760		RHS repeat protein	-1.18
ABUW_RS05825		DUF4105 domain-containing protein	-1.17
ABUW_RS16445		glycosyltransferase family 1 protein	-1.17
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	-1.15
ABUW_RS04990		sulfate ABC transporter ATP-binding protein	-1.15
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.14
ABUW_RS05220		hypothetical protein	-1.14
ABUW_RS01215		DUF805 domain-containing protein	-1.14
ABUW_RS10770		nucleoside-diphosphate sugar epimerase	-1.14
ABUW_RS04895		amidohydrolase	-1.13
ABUW_RS03630		hypothetical protein	-1.12
ABUW_RS00375		HutD family protein	-1.12
ABUW_RS05355	csy3	type I-F CRISPR-associated protein Csy3	-1.11
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.10
ABUW_RS14885		pirin family protein	-1.08
ABUW_RS05205		hypothetical protein	-1.08
ABUW_RS04355		metalloprotease	-1.08
ABUW_RS05345	csy1	type I-F CRISPR-associated protein Csy1	-1.07
ABUW_RS00400	hutG	formimidoylglutamase	-1.06
ABUW_RS09550		GNAT family N-acetyltransferase	-1.05
ABUW_RS15055		GDYXXLXY domain-containing protein	-1.05
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.05
ABUW_RS09260		sorbose dehydrogenase family protein	-1.05
ABUW_RS12430		winged helix-turn-helix domain-containing protein	-1.04
ABUW_RS12510	tssG	type VI secretion system baseplate subunit TssG	-1.03
ABUW_RS18770	ssuD	FMNH2-dependent alkanesulfonate monooxygenase	-1.02
ABUW_RS04910		deoxyguanosinetriphosphate triphosphohydrolase	-1.02
ABUW_RS04365		universal stress protein	-1.02
ABUW_RS12830		TolC family protein	-1.02
ABUW_RS17100		DnaJ domain-containing protein	-1.02

ABUW_RS19085		H-NS histone family protein	-1.01

Table A2. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta adeR$ LSP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta adeR$ LSP vs WT LSP log2FC
ABUW_RS03795		DUF2280 domain-containing protein	4.81
ABUW_RS19125		hypothetical protein	4.35
ABUW_RS19235		hypothetical protein	4.23
ABUW_RS15150	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	3.52
ABUW_RS19355		hypothetical protein	3.43
ABUW_RS19220		hypothetical protein	3.34
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	3.34
ABUW_RS08395		hypothetical protein	3.15
ABUW_RS19350		hypothetical protein	3.15
ABUW_RS15145		8-amino-7-oxononanoate synthase	3.12
ABUW_RS20385		hypothetical protein	3.02
ABUW_RS09450		ribose-phosphate pyrophosphokinase	2.75
ABUW_RS05140	uvrB	excinuclease ABC subunit UvrB	2.68
ABUW_RS08495	fabZ	3-hydroxyacyl-ACP dehydratase FabZ	2.67
ABUW_RS19360		hypothetical protein	2.64
ABUW_RS19230		hypothetical protein	2.64
ABUW_RS14845		metal-dependent hydrolase	2.64
ABUW_RS19205		hypothetical protein	2.63
ABUW_RS19140		ParA family protein	2.54
ABUW_RS12620		hypothetical protein	2.47
ABUW_RS11290		integrase family protein	2.47
ABUW_RS15140	bioC	malonyl-ACP O-methyltransferase BioC	2.45
ABUW_RS19120		hypothetical protein	2.43
ABUW_RS09295		hypothetical protein	2.40
ABUW_RS18720		TetR/AcrR family transcriptional regulator	2.39
ABUW_RS18515		hypothetical protein	2.31
ABUW_RS14875		beta-ketoacyl-ACP synthase II	2.29
ABUW_RS10410		YcgL domain-containing protein	2.27
ABUW_RS12010		enoyl-CoA hydratase	2.27
ABUW_RS00925	omp33-36	porin Omp33-36	2.25
ABUW_RS10200		LysR family transcriptional regulator	2.25
ABUW_RS06830		helix-turn-helix domain-containing protein	2.24
ABUW_RS18130		DMT family transporter	2.24
ABUW_RS11530		metalloregulator ArsR/SmtB family transcription factor	2.24
ABUW_RS08270	aroQ	type II 3-dehydroquinate dehydratase	2.24
ABUW_RS18680	ampD	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD	2.19
ABUW_RS17025	murI	glutamate racemase	2.17
ABUW_RS08500	lpxA	acyl-ACP--UDP-N-acetylglucosamine O-acyltransferase	2.14
ABUW_RS04620		TetR/AcrR family transcriptional regulator	2.13
ABUW_RS01505	bfr	bacterioferritin	2.13
ABUW_RS17440		outer membrane beta-barrel protein	2.11
ABUW_RS19510		hypothetical protein	2.10
ABUW_RS17835		signal peptidase II	2.09
ABUW_RS07085		hypothetical protein	2.07
ABUW_RS19490		DsbC family protein	2.06
ABUW_RS15980	thrS	threonine--tRNA ligase	2.06
ABUW_RS06110		hypothetical protein	2.05
ABUW_RS04945		CAP domain-containing protein	2.04
ABUW_RS11770		LysR family transcriptional regulator	2.04
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	2.03

ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	2.00
ABUW_RS08410		hypothetical protein	2.00
ABUW_RS04360		MGMT family protein	2.00
ABUW_RS17705		homoserine dehydrogenase	2.00
ABUW_RS16515		DUF2059 domain-containing protein	1.99
ABUW_RS03440		Sdpl family protein	1.99
ABUW_RS11465		pyridoxal phosphate-dependent aminotransferase	1.98
ABUW_RS10485		YARHG domain-containing protein	1.97
ABUW_RS14145		carbonic anhydrase	1.96
ABUW_RS16350		enoyl-ACP reductase	1.96
ABUW_RS07455	gloB	hydroxyacylglutathione hydrolase	1.95
ABUW_RS19705		hypothetical protein	1.95
ABUW_RS19520	traW	type-F conjugative transfer system protein TraW	1.94
ABUW_RS02790		phage tail protein	1.94
ABUW_RS04760		hypothetical protein	1.94
ABUW_RS19315	aadB	aminoglycoside nucleotidyltransferase ANT(2'')-Ia	1.94
ABUW_RS07035		quinone-dependent dihydroorotate dehydrogenase	1.92
ABUW_RS05240		deoxyribodipyrimidine photo-lyase	1.91
ABUW_RS15135	bioD	ATP-dependent dethiobiotin synthetase BioD	1.90
ABUW_RS12060		acyl-CoA dehydrogenase family protein	1.89
ABUW_RS15675		hypothetical protein	1.88
ABUW_RS13060		LysE family translocator	1.87
ABUW_RS04460		hypothetical protein	1.87
ABUW_RS18520		hypothetical protein	1.85
ABUW_RS19145		ParB/RepB/Spo0J family partition protein	1.85
ABUW_RS10490		HIT family protein	1.85
ABUW_RS11350		glutathione S-transferase	1.84
ABUW_RS11325		hypothetical protein	1.83
ABUW_RS16315		DUF4124 domain-containing protein	1.83
ABUW_RS03330		hypothetical protein	1.82
ABUW_RS08065		N-acetyltransferase	1.82
ABUW_RS13395		metal-dependent hydrolase	1.81
ABUW_RS12055		CoA transferase	1.80
ABUW_RS07910		aldehyde dehydrogenase family protein	1.80
ABUW_RS13080		LexA family transcriptional regulator	1.79
ABUW_RS08635		alpha/beta fold hydrolase	1.79
ABUW_RS13480		MarR family transcriptional regulator	1.77
ABUW_RS14635		hypothetical protein	1.76
ABUW_RS08265	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein	1.75
ABUW_RS10865		cell division protein ZapE	1.75
ABUW_RS17910		heteromeric transposase endonuclease subunit TnsA	1.75
ABUW_RS16775		endonuclease/exonuclease/phosphatase family protein	1.74
ABUW_RS04170	lolA	outer membrane lipoprotein chaperone LolA	1.74
ABUW_RS00500	pncB	nicotinate phosphoribosyltransferase	1.73
ABUW_RS15750		C39 family peptidase	1.72
sRNA100	sRNA100	sRNA100	1.71
ABUW_RS11925		TetR/AcrR family transcriptional regulator	1.70
ABUW_RS15515		flavin reductase	1.70
ABUW_RS17310	recN	DNA repair protein RecN	1.69
ABUW_RS08655	brnQ	branched-chain amino acid transport system II carrier protein	1.69
ABUW_RS02965		RcnB family protein	1.69
ABUW_RS18125		threonylcarbamoyl-AMP synthase	1.69
ABUW_RS01425		pilus assembly protein PilM	1.68
ABUW_RS02035	rpmC	50S ribosomal protein L29	1.68
ABUW_RS16470		glutamate-5-semialdehyde dehydrogenase	1.68
ABUW_RS01435		type 4a pilus biogenesis protein PilO	1.68
ABUW_RS14190		hypothetical protein	1.67

ABUW_RS07100		protein kinase	1.67
ABUW_RS03585		PaaX family transcriptional regulator	1.67
ABUW_RS07070		GatB/YqeY domain-containing protein	1.66
ABUW_RS18990	dmeF	CDF family Co(II)/Ni(II) efflux transporter DmeF	1.66
ABUW_RS02985		hypothetical protein	1.65
ABUW_RS00875		winged helix-turn-helix transcriptional regulator	1.65
ABUW_RS20425		hypothetical protein	1.65
ABUW_RS04195		helix-turn-helix transcriptional regulator	1.64
ABUW_RS03850		hypothetical protein	1.63
ABUW_RS11040		hypothetical protein	1.62
ABUW_RS12670	mumR	LysR family transcriptional regulator MumR	1.62
ABUW_RS17385	fadB	fatty acid oxidation complex subunit alpha FadB	1.62
ABUW_RS01920		ComF family protein	1.61
ABUW_RS03290		DUF488 domain-containing protein	1.60
ABUW_RS11220	bioB	biotin synthase BioB	1.60
ABUW_RS11705		PLP-dependent aminotransferase family protein	1.59
ABUW_RS19375		type IV secretion system DNA-binding domain-containing protein	1.59
ABUW_RS00100		glutathione S-transferase family protein	1.58
ABUW_RS14425	betB	betaine-aldehyde dehydrogenase	1.57
ABUW_RS18135		TetR/AcrR family transcriptional regulator	1.56
ABUW_RS19930	ssrA	transfer-messenger RNA	1.55
sRNA89	sRNA89	sRNA89	1.55
ABUW_RS17800	glnK	P-II family nitrogen regulator	1.55
ABUW_RS01210		3'-5' exonuclease domain-containing protein 2	1.55
ABUW_RS17315		YqgE/AlgH family protein	1.53
ABUW_RS01935	adeT2	putative multidrug efflux protein AdeT2	1.53
ABUW_RS16230		tyrosine-type recombinase/integrase	1.52
ABUW_RS10100		LysR family transcriptional regulator	1.51
ABUW_RS12590	uca	urea carboxylase	1.51
ABUW_RS16335		MacA family efflux pump subunit	1.51
ABUW_RS01955		metal-dependent hydrolase	1.51
ABUW_RS19600		sel1 repeat family protein	1.50
ABUW_RS16030	mazG	nucleoside triphosphate pyrophosphohydrolase	1.50
sRNA54	sRNA54	sRNA54	1.50
ABUW_RS15690		DUF2218 domain-containing protein	1.49
ABUW_RS15850		MarR family transcriptional regulator	1.49
ABUW_RS09145		LysR family transcriptional regulator	1.49
ABUW_RS02040	rpsQ	30S ribosomal protein S17	1.49
ABUW_RS08400		hypothetical protein	1.48
ABUW_RS05510		gamma carbonic anhydrase family protein	1.48
ABUW_RS17785	ribD	bifunctional diaminoxyhydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD	1.48
ABUW_RS09650		helix-turn-helix transcriptional regulator	1.47
ABUW_RS04695		tyrosine recombinase	1.47
ABUW_RS10405		hypothetical protein	1.47
ABUW_RS09035		winged helix-turn-helix transcriptional regulator	1.47
ABUW_RS02695		helix-turn-helix transcriptional regulator	1.46
ABUW_RS15115		threonylcarbamoyl-AMP synthase	1.46
ABUW_RS08175		TetR family transcriptional regulator	1.46
ABUW_RS19620		DIP1984 family protein	1.45
ABUW_RS09000		LysR family transcriptional regulator	1.44
ABUW_RS16735		winged helix-turn-helix transcriptional regulator	1.44
ABUW_RS06525	adeL	multidrug efflux transcriptional repressor AdeL	1.44
ABUW_RS07095		DUF3336 domain-containing protein	1.43
ABUW_RS00565		glutamate--cysteine ligase	1.42
ABUW_RS14880	hemJ	protoporphyrinogen oxidase HemJ	1.42
ABUW_RS15480		PhzF family isomerase	1.42

ABUW_RS16880	hcaR	DNA-binding transcriptional regulator HcaR	1.42
ABUW_RS05375		isochorismatase	1.42
ABUW_RS14010	ureA	urease subunit gamma	1.41
ABUW_RS14400		acyl-CoA thioesterase	1.40
ABUW_RS17380		hypothetical protein	1.40
ABUW_RS14420	betI	transcriptional regulator BetI	1.40
ABUW_RS00320		DUF523 domain-containing protein	1.40
ABUW_RS08835		3-deoxy-7-phosphoheptulonate synthase	1.40
sRNA87	sRNA87	sRNA87	1.39
ABUW_RS07630		hypothetical protein	1.39
ABUW_RS10555		histidine-type phosphatase	1.39
ABUW_RS16145		heavy metal response regulator transcription factor	1.38
ABUW_RS13530		FadR family transcriptional regulator	1.38
ABUW_RS12790		ferredoxin family protein	1.38
ABUW_RS08975		hypothetical protein	1.37
ABUW_RS15760		chorismate-binding protein	1.35
ABUW_RS01040		GFA family protein	1.35
ABUW_RS06570		PhzF family phenazine biosynthesis protein	1.35
ABUW_RS07645		LysR family transcriptional regulator	1.34
ABUW_RS17650		NUDIX domain-containing protein	1.34
ABUW_RS05900		chorismate lyase	1.34
ABUW_RS06360		hypothetical protein	1.34
ABUW_RS13095		exodeoxyribonuclease VII large subunit	1.34
ABUW_RS00465	ribE	6,7-dimethyl-8-ribityllumazine synthase	1.34
ABUW_RS17790	nrdR	transcriptional repressor NrdR	1.34
ABUW_RS12910		right-handed parallel beta-helix repeat-containing protein	1.33
ABUW_RS17110		magnesium transporter CorA family protein	1.33
ABUW_RS04125	adeK	multidrug efflux RND transporter outer membrane channel subunit AdeK	1.32
ABUW_RS18785		TetR/AcrR family transcriptional regulator	1.31
ABUW_RS06505		serine hydroxymethyltransferase	1.31
ABUW_RS07875		UDP-2,3-diacylglucosamine diphosphatase	1.31
ABUW_RS07050		M48 family metalloprotease	1.31
ABUW_RS00460	nusB	transcription antitermination factor NusB	1.31
ABUW_RS00790		TonB-dependent siderophore receptor	1.30
ABUW_RS12450		LysR family transcriptional regulator	1.30
ABUW_RS00275		replication-associated recombination protein A	1.30
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.30
ABUW_RS17320	ruvX	Holliday junction resolvase RuvX	1.30
ABUW_RS15740		outer membrane protein transport protein	1.29
ABUW_RS02165		hypothetical protein	1.28
ABUW_RS08135	leuE	leucine efflux protein LeuE	1.28
ABUW_RS07885		glutamine--tRNA ligase/YqeY domain fusion protein	1.28
ABUW_RS01520		bifunctional (p)ppGpp synthetase/guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	1.28
ABUW_RS08375	tusD	sulfurtransferase complex subunit TusD	1.28
ABUW_RS02005	rplW	50S ribosomal protein L23	1.28
ABUW_RS17780	aamA	DNA adenine methylase	1.28
ABUW_RS07055		hypothetical protein	1.28
ABUW_RS14660		thioesterase family protein	1.28
ABUW_RS09005		acyl-CoA dehydrogenase family protein	1.27
ABUW_RS07540	dnaB	replicative DNA helicase	1.26
ABUW_RS13650		ATP-binding protein	1.26
ABUW_RS17710		threonine synthase	1.26
ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	1.26
ABUW_RS10455		alpha/beta fold hydrolase	1.26
ABUW_RS00210		LysR family transcriptional regulator	1.25
ABUW_RS02070	rplF	50S ribosomal protein L6	1.25

ABUW_RS02990	baeS	sensor histidine kinase efflux regulator BaeS	1.25
ABUW_RS09160		dihydroxy-acid dehydratase	1.24
ABUW_RS05555	gloA	lactoylglutathione lyase	1.24
ABUW_RS04250		DUF1289 domain-containing protein	1.24
ABUW_RS07460		ABC transporter permease	1.24
ABUW_RS17360		thioesterase family protein	1.23
ABUW_RS10205		LysR family transcriptional regulator	1.23
ABUW_RS10735		guanylate cyclase	1.23
ABUW_RS09105		penicillin acylase family protein	1.23
ABUW_RS07045	purF	amidophosphoribosyltransferase	1.22
ABUW_RS17225		ribosome-binding factor A	1.22
ABUW_RS15635		tRNA-Pro	1.22
ABUW_RS03250		DNA-3-methyladenine glycosylase	1.20
ABUW_RS13970	mrda	penicillin-binding protein 2	1.20
ABUW_RS08490	lpxD	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	1.20
ABUW_RS16615		hypothetical protein	1.20
ABUW_RS13820	nudC	NAD(+) diphosphatase	1.19
ABUW_RS04820	hda	DnaA regulatory inactivator Hda	1.19
ABUW_RS17285		dephospho-CoA kinase	1.19
ABUW_RS15350	gigC	LysR family transcriptional regulator GigC	1.18
ABUW_RS00060		alpha/beta fold hydrolase	1.18
ABUW_RS00680		GGDEF domain-containing protein	1.18
ABUW_RS13810	dnaQ	DNA polymerase III subunit epsilon	1.18
ABUW_RS18230		Dyp-type peroxidase	1.17
ABUW_RS16520		DUF2846 domain-containing protein	1.16
ABUW_RS18800	ribF	bifunctional riboflavin kinase/FAD synthetase	1.16
ABUW_RS01205	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1.15
ABUW_RS15960	nreB	nickel resistance MFS transporter NreB	1.15
ABUW_RS12740		exo-alpha-sialidase	1.15
ABUW_RS10740		HIT domain-containing protein	1.14
ABUW_RS13560		DMT family transporter	1.14
ABUW_RS04920		multidrug efflux MFS transporter	1.14
ABUW_RS09155		FadR family transcriptional regulator	1.14
ABUW_RS05870		TonB-dependent receptor	1.14
ABUW_RS17085		cation:proton antiporter	1.13
ABUW_RS10545		3-deoxy-7-phosphoheptulonate synthase	1.12
ABUW_RS06000	lipA	lipoyl synthase	1.12
ABUW_RS06630		NAD(+) kinase	1.12
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	1.12
ABUW_RS18700	rph	ribonuclease PH	1.12
ABUW_RS18235		NAD-dependent malic enzyme	1.12
ABUW_RS16545		Fe2+-dependent dioxygenase	1.12
ABUW_RS19805		helix-turn-helix transcriptional regulator	1.12
ABUW_RS01635		FAD-binding oxidoreductase	1.11
ABUW_RS00470		bifunctional 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	1.11
ABUW_RS03245	mutM	bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase	1.11
ABUW_RS14990		DNA primase	1.11
ABUW_RS17365	uvrC	excinuclease ABC subunit UvrC	1.11
ABUW_RS11110		NAD-dependent deacylase	1.11
ABUW_RS08750		DUF1449 family protein	1.11
ABUW_RS07775		hypothetical protein	1.11
ABUW_RS00805	guaB	IMP dehydrogenase	1.11
ABUW_RS06035	rpsB	30S ribosomal protein S2	1.10
ABUW_RS02310		2OG-Fe(II) oxygenase	1.10
ABUW_RS08660	map	type I methionyl aminopeptidase	1.10

ABUW_RS10785		3'(2'),5'-bisphosphate nucleotidase CysQ	1.10
ABUW_RS18240		arginine--tRNA ligase	1.09
ABUW_RS11720		LysR family transcriptional regulator	1.09
ABUW_RS14665	hemB	prophobilinogen synthase	1.09
ABUW_RS17970		MFS transporter	1.09
ABUW_RS11430	purT	formate-dependent phosphoribosylglycinamide formyltransferase	1.09
ABUW_RS16620		hypothetical protein	1.08
ABUW_RS12715		serine hydrolase	1.08
ABUW_RS00930		GGDEF domain-containing protein	1.08
ABUW_RS04390		hypothetical protein	1.08
ABUW_RS06965		lytic transglycosylase domain-containing protein	1.08
ABUW_RS14670		FAD-dependent oxidoreductase	1.08
ABUW_RS18270		PadR family transcriptional regulator	1.08
ABUW_RS15645	argJ	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ	1.08
ABUW_RS07075	rpsU	30S ribosomal protein S21	1.08
ABUW_RS07810		LysR family transcriptional regulator	1.08
ABUW_RS10175		LysR family transcriptional regulator	1.07
ABUW_RS00455	thiL	thiamine-phosphate kinase	1.07
ABUW_RS00960	tenA	thiaminase II	1.07
ABUW_RS18210		transcriptional repressor	1.07
ABUW_RS17565	gspN	type II secretion system protein N	1.07
ABUW_RS05295		LysR family transcriptional regulator	1.07
ABUW_RS14585		Fic family protein	1.07
ABUW_RS08800		M48 family metalloproteinase	1.07
ABUW_RS07930		AAA family ATPase	1.06
ABUW_RS00970		MFS transporter	1.06
ABUW_RS14035		LysR family transcriptional regulator	1.06
ABUW_RS11050		DUF2237 domain-containing protein	1.06
ABUW_RS02315		23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ	1.05
ABUW_RS04010		polyprenyl synthetase family protein	1.05
ABUW_RS13160		ring-hydroxylating dioxygenase ferredoxin reductase family protein	1.05
ABUW_RS16020	pcnB	polynucleotide adenyltransferase PcnB	1.05
ABUW_RS00355		hypothetical protein	1.04
ABUW_RS16120		hypothetical protein	1.04
ABUW_RS18350		outer membrane lipoprotein-sorting protein	1.03
ABUW_RS07710	folB	dihydroneopterin aldolase	1.03
ABUW_RS06050		AraC family transcriptional regulator	1.03
ABUW_RS16055	cysM	cysteine synthase CysM	1.03
ABUW_RS00305	pncA	bifunctional nicotinamidase/pyrazinamidase	1.03
ABUW_RS15865		hypothetical protein	1.02
ABUW_RS14040		HlyC/CorC family transporter	1.02
ABUW_RS08525		HAD-IA family hydrolase	1.02
ABUW_RS15220	ccsA	cytochrome c biogenesis protein CcsA	1.01
ABUW_RS04560	greB	transcription elongation factor GreB	1.01
ABUW_RS03575		AraC family transcriptional regulator	1.01
ABUW_RS13930		dioxygenase	1.01
ABUW_RS01030		FAD-dependent oxidoreductase	1.00
ABUW_RS10430		HRDC domain-containing protein	1.00
ABUW_RS11205	ruvC	crossover junction endodeoxyribonuclease RuvC	1.00

Gene	Gene Name	Function	$\Delta adeR$ LSP vs WT LSP log2FC
ABUW_RS09595	adeR	efflux system response regulator transcription factor AdeR	-11.42
ABUW_RS15580	tcuA	FAD-dependent tricarballylate dehydrogenase TcuA	-8.99
ABUW_RS11875		hypothetical protein	-8.37

ABUW_RS15585	tcuB	tricarballylate utilization 4Fe-4S protein TcuB	-8.18
ABUW_RS11870		hypothetical protein	-8.04
ABUW_RS20145		hypothetical protein	-7.13
ABUW_RS13010		DUF4142 domain-containing protein	-6.93
ABUW_RS08050		hypothetical protein	-6.86
ABUW_RS15565		MFS transporter	-6.76
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-6.43
ABUW_RS12975		hypothetical protein	-6.18
ABUW_RS05730	bauC	ferric acinetobactin ABC transporter permease subunit BauC	-6.16
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-6.13
ABUW_RS13040		hypothetical protein	-6.12
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-6.10
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-5.99
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-5.85
ABUW_RS11855	katE	catalase HP11	-5.79
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.67
ABUW_RS10640		siderophore biosynthesis protein	-5.50
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-5.44
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-5.36
ABUW_RS10585		acetyltransferase	-5.28
ABUW_RS18445	alr	alanine racemase	-5.20
sRNA74	sRNA74	sRNA74	-5.19
ABUW_RS18440		RidA family protein	-5.15
ABUW_RS11860		iron-containing redox enzyme family protein	-5.00
ABUW_RS10010		hypothetical protein	-4.95
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-4.93
ABUW_RS07145		DUF2171 domain-containing protein	-4.89
sRNA65	sRNA65	sRNA65	-4.80
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-4.75
ABUW_RS05750	basC	putative histamine N-monooxygenase	-4.75
newcandsRNA1	newcandsRNA1	newcandsRNA1	-4.75
ABUW_RS03820		hypothetical protein	-4.56
ABUW_RS11825		LysE family translocator	-4.53
ABUW_RS10025		hypothetical protein	-4.46
ABUW_RS05725	bauD	ferric acinetobactin ABC transporter permease subunit BauD	-4.44
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-4.41
ABUW_RS10525		hypothetical protein	-4.33
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-4.25
ABUW_RS07500		hypothetical protein	-4.15
ABUW_RS01050		MFS transporter	-4.12
ABUW_RS03665		hypothetical protein	-4.04
ABUW_RS06350		hypothetical protein	-4.02
ABUW_RS17925		aldolase	-4.00
ABUW_RS15165		trehalose-6-phosphate synthase	-4.00
ABUW_RS12725		hypothetical protein	-3.97
ABUW_RS18450		D-amino acid dehydrogenase	-3.91
ABUW_RS10460		methyltransferase domain-containing protein	-3.82
ABUW_RS00895		hypothetical protein	-3.81
ABUW_RS14475		biliverdin-producing heme oxygenase	-3.78
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-3.77
ABUW_RS13110		LysE family transporter	-3.77
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-3.76
ABUW_RS12995		hypothetical protein	-3.75
ABUW_RS06610		hemin uptake protein HemP	-3.70
ABUW_RS14485		DUF560 domain-containing protein	-3.68
ABUW_RS07820		hypothetical protein	-3.68

ABUW_RS10070		transcriptional repressor	-3.64
ABUW_RS07960		spore coat protein U domain-containing protein	-3.63
ABUW_RS20230		hypothetical protein	-3.62
ABUW_RS16835	leuD	3-isopropylmalate dehydratase small subunit	-3.61
ABUW_RS18405		acyl-CoA dehydrogenase family protein	-3.61
ABUW_RS11885		hypothetical protein	-3.54
ABUW_RS15330		mechanosensitive ion channel	-3.42
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-3.34
ABUW_RS12970		hypothetical protein	-3.31
ABUW_RS18400		enoyl-CoA hydratase	-3.27
ABUW_RS11255		hypothetical protein	-3.26
sRNA21	sRNA21	sRNA21	-3.26
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-3.21
ABUW_RS08245		iron-containing redox enzyme family protein	-3.20
ABUW_RS06270		hypothetical protein	-3.17
ABUW_RS07170		NirD/YgiW/YdeI family stress tolerance protein	-3.17
ABUW_RS00260		DUF1328 domain-containing protein	-3.13
ABUW_RS18420		CoA-acylating methylmalonate-semialdehyde dehydrogenase	-3.12
ABUW_RS18435		amino acid permease	-3.12
ABUW_RS18415	mmsB	3-hydroxyisobutyrate dehydrogenase	-3.09
ABUW_RS16200		hypothetical protein	-3.06
ABUW_RS20475		hypothetical protein	-3.05
ABUW_RS14085		SRPBCC domain-containing protein	-3.04
ABUW_RS10530		PepSY domain-containing protein	-3.04
ABUW_RS20180		hypothetical protein	-3.03
ABUW_RS16840	leuC	3-isopropylmalate dehydratase large subunit	-3.02
ABUW_RS13105		hypothetical protein	-3.02
ABUW_RS07155		PIG-L family deacetylase	-3.01
sRNA101	sRNA101	sRNA101	-3.00
ABUW_RS14480		energy transducer TonB	-3.00
ABUW_RS12980		hypothetical protein	-2.94
ABUW_RS10615		(2Fe-2S)-binding protein	-2.90
ABUW_RS20235		hypothetical protein	-2.89
ABUW_RS11865		CinA family protein	-2.88
ABUW_RS18390		MHS family MFS transporter	-2.86
ABUW_RS16440		phosphatase PAP2 family protein	-2.85
ABUW_RS15570		substrate-binding domain-containing protein	-2.85
ABUW_RS14505		sigma-70 family RNA polymerase sigma factor	-2.84
ABUW_RS06435		hypothetical protein	-2.76
ABUW_RS11850		glucose 1-dehydrogenase	-2.74
ABUW_RS15160	otsB	trehalose-phosphatase	-2.74
ABUW_RS07825		rRNA pseudouridine synthase	-2.73
ABUW_RS11270		hypothetical protein	-2.71
sRNA42	sRNA42	sRNA42	-2.70
ABUW_RS07620		hypothetical protein	-2.66
ABUW_RS07160		class I SAM-dependent methyltransferase	-2.63
ABUW_RS07965		molecular chaperone	-2.60
ABUW_RS01615		hemerythrin domain-containing protein	-2.59
ABUW_RS10475		hypothetical protein	-2.56
ABUW_RS12405		DUF333 domain-containing protein	-2.54
ABUW_RS14395		hypothetical protein	-2.54
ABUW_RS07150		hypothetical protein	-2.53
ABUW_RS08540		hypothetical protein	-2.48
ABUW_RS14470		YbaN family protein	-2.47
ABUW_RS01760		hypothetical protein	-2.44
ABUW_RS15280		hypothetical protein	-2.40
ABUW_RS03180		VOC family protein	-2.37

ABUW_RS13505		acyl-CoA dehydrogenase family protein	-2.34
ABUW_RS11340		amino acid ABC transporter permease	-2.34
ABUW_RS16500		acetate kinase	-2.33
ABUW_RS20460		hypothetical protein	-2.33
ABUW_RS17400		serine hydrolase family protein	-2.32
ABUW_RS16505	pta	phosphate acetyltransferase	-2.32
ABUW_RS18535	prpB	methylisocitrate lyase	-2.30
ABUW_RS09185		alpha/beta hydrolase	-2.30
ABUW_RS18015		DUF2726 domain-containing protein	-2.27
ABUW_RS13005		hypothetical protein	-2.26
ABUW_RS15335		hypothetical protein	-2.25
ABUW_RS20295		hypothetical protein	-2.24
ABUW_RS13770		hypothetical protein	-2.24
ABUW_RS05820		DUF3015 family protein	-2.23
ABUW_RS14215		transketolase	-2.22
ABUW_RS08580		SOS response-associated peptidase family protein	-2.22
ABUW_RS10005		hypothetical protein	-2.22
ABUW_RS20155		hypothetical protein	-2.21
ABUW_RS10075		isochorismatase family protein	-2.20
ABUW_RS14460		DUF1275 domain-containing protein	-2.20
ABUW_RS10610		RraA family protein	-2.20
ABUW_RS03970		hypothetical protein	-2.19
ABUW_RS11880		hypothetical protein	-2.19
ABUW_RS00485		hypothetical protein	-2.17
ABUW_RS18530	prpC	2-methylcitrate synthase	-2.16
ABUW_RS01160	aqpZ	aquaporin Z	-2.16
ABUW_RS10125		transporter	-2.16
ABUW_RS09210		type 1 glutamine amidotransferase domain-containing protein	-2.15
ABUW_RS18395		enoyl-CoA hydratase/isomerase family protein	-2.14
ABUW_RS07860	hfq	RNA chaperone Hfq	-2.14
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	-2.14
ABUW_RS05715	basA	acinetobactin non-ribosomal peptide synthetase subunit BasA	-2.13
ABUW_RS18410		AMP-binding protein	-2.13
ABUW_RS12360	abaF	fosfomycin efflux MFS transporter AbaF	-2.13
ABUW_RS16445		glycosyltransferase family 1 protein	-2.11
ABUW_RS08055		hypothetical protein	-2.10
ABUW_RS14500		FecR domain-containing protein	-2.09
ABUW_RS01140		hypothetical protein	-2.07
ABUW_RS11335		amino acid ABC transporter permease	-2.05
ABUW_RS15290		NF038215 family lipoprotein	-2.05
ABUW_RS05710	bauF	acinetobactin utilization protein BauF	-2.05
sRNA96	sRNA96	sRNA96	-2.05
ABUW_RS08385	fumC	class II fumarate hydratase	-2.04
ABUW_RS20200		hypothetical protein	-2.04
ABUW_RS18100		TonB-dependent copper receptor	-2.04
ABUW_RS03105		MHS family MFS transporter	-2.04
ABUW_RS14210		transketolase	-2.02
ABUW_RS00710		TonB-dependent siderophore receptor	-1.99
ABUW_RS01215		DUF805 domain-containing protein	-1.99
ABUW_RS00920	betT	choline BCCT transporter BetT	-1.99
ABUW_RS01715		Glu/Leu/Phe/Val dehydrogenase	-1.98
ABUW_RS16435	iscX	Fe-S cluster assembly protein IscX	-1.98
ABUW_RS11425		tautomerase family protein	-1.95
ABUW_RS08390		hypothetical protein	-1.95
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.94
ABUW_RS16850		LysR family transcriptional regulator	-1.93
ABUW_RS11140		hypothetical protein	-1.93

ABUW_RS08045		hypothetical protein	-1.92
ABUW_RS01735	astB	N-succinylarginine dihydrolase	-1.90
ABUW_RS11070		helix-turn-helix transcriptional regulator	-1.89
ABUW_RS11935		methylcrotonoyl-CoA carboxylase	-1.88
ABUW_RS08710	ftsY	signal recognition particle-docking protein FtsY	-1.87
ABUW_RS10315		MBL fold metallo-hydrolase	-1.86
ABUW_RS08085		hypothetical protein	-1.85
ABUW_RS12175		DUF1330 domain-containing protein	-1.84
ABUW_RS00685		alpha/beta hydrolase	-1.84
ABUW_RS01510		bacterioferritin-associated ferredoxin	-1.82
ABUW_RS12730		3-hydroxyacyl-CoA dehydrogenase	-1.81
ABUW_RS03285		SRPBCC family protein	-1.80
ABUW_RS01730	astD	succinylglutamate-semialdehyde dehydrogenase	-1.79
ABUW_RS20505		hypothetical protein	-1.79
ABUW_RS14025		copper resistance protein NlpE	-1.78
ABUW_RS09615		alpha/beta hydrolase	-1.78
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-1.78
ABUW_RS08325		MoaD/ThiS family protein	-1.77
ABUW_RS18540		GntR family transcriptional regulator	-1.76
ABUW_RS17200		Na ⁺ /H ⁺ antiporter subunit C	-1.74
ABUW_RS11345		amino acid ABC transporter substrate-binding protein	-1.74
ABUW_RS08690		DUF2750 domain-containing protein	-1.74
ABUW_RS16845		DUF2061 domain-containing protein	-1.74
ABUW_RS15550		amidohydrolase	-1.72
ABUW_RS16430	ndk	nucleoside-diphosphate kinase	-1.72
ABUW_RS01670		superoxide dismutase family protein	-1.71
ABUW_RS17195		monovalent cation/H ⁺ antiporter subunit A	-1.71
ABUW_RS08670		hypothetical protein	-1.69
ABUW_RS13935		META and DUF4377 domain-containing protein	-1.69
ABUW_RS09290		cation:proton antiporter	-1.69
ABUW_RS02655		hypothetical protein	-1.69
ABUW_RS08320	moaA	GTP 3',8-cyclase MoaA	-1.69
ABUW_RS11945		acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	-1.69
ABUW_RS03160		glucose/quinolate/shikimate family membrane-bound PQQ-dependent dehydrogenase	-1.69
ABUW_RS14160		TonB-dependent siderophore receptor	-1.67
ABUW_RS05485		DUF2238 domain-containing protein	-1.67
ABUW_RS07430		GNAT family N-acetyltransferase	-1.67
ABUW_RS10890		DUF1049 domain-containing protein	-1.66
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.64
ABUW_RS07950		hypothetical protein	-1.64
ABUW_RS18185		F0F1 ATP synthase subunit B	-1.63
ABUW_RS01020		hydrolase	-1.61
ABUW_RS13250		OmpA family protein	-1.61
ABUW_RS09275		hydrolase	-1.59
ABUW_RS18150		glutathione peroxidase	-1.58
ABUW_RS19080		thermonuclease family protein	-1.56
ABUW_RS00765		M23 family metallopeptidase	-1.56
ABUW_RS07585		RDD family protein	-1.55
ABUW_RS18190	atpE	F0F1 ATP synthase subunit C	-1.54
ABUW_RS07065		M48 family metalloprotease	-1.54
ABUW_RS15260		LysE family transporter	-1.54
ABUW_RS08165		hypothetical protein	-1.53
ABUW_RS15855		organic hydroperoxide resistance protein	-1.53
ABUW_RS14550		DEAD/DEAH box helicase family protein	-1.53
ABUW_RS03230	mscL	large conductance mechanosensitive channel protein MscL	-1.52
ABUW_RS18620		oligosaccharide repeat unit polymerase	-1.52

ABUW_RS04510		diacylglycerol kinase	-1.52
ABUW_RS02650		hypothetical protein	-1.52
ABUW_RS00995		amino acid permease	-1.52
ABUW_RS13675		hypothetical protein	-1.51
ABUW_RS18610		sugar transferase	-1.51
ABUW_RS10690		phasin family protein	-1.51
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.51
ABUW_RS07855	miaA	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	-1.51
ABUW_RS12525		type VI secretion system tube protein Hcp	-1.50
ABUW_RS13985	ureG	urease accessory protein UreG	-1.50
ABUW_RS04665		amino acid permease	-1.50
ABUW_RS00370	hutC	histidine utilization repressor	-1.50
ABUW_RS12335		L-serine ammonia-lyase	-1.50
ABUW_RS08440		PAS domain-containing protein	-1.50
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-1.49
ABUW_RS09550		GNAT family N-acetyltransferase	-1.49
ABUW_RS06730		hypothetical protein	-1.48
ABUW_RS11625	cydB	cytochrome d ubiquinol oxidase subunit II	-1.47
ABUW_RS07425		sorbose dehydrogenase family protein	-1.47
ABUW_RS17460		hypothetical protein	-1.47
ABUW_RS12760		lauroyl acyltransferase	-1.46
ABUW_RS05420		SIMPL domain-containing protein	-1.46
ABUW_RS14220		MFS transporter	-1.46
ABUW_RS14240		galactose mutarotase	-1.46
ABUW_RS13045		NAD(P)-binding domain-containing protein	-1.45
ABUW_RS08705		hypothetical protein	-1.45
ABUW_RS16715		HdeD family acid-resistance protein	-1.44
ABUW_RS09270		antibiotic biosynthesis monooxygenase	-1.44
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-1.43
ABUW_RS00585		hypothetical protein	-1.42
ABUW_RS16465		alpha/beta hydrolase	-1.42
sRNA13	sRNA13	sRNA13	-1.41
ABUW_RS18475		ribonuclease E inhibitor RraB	-1.41
ABUW_RS12180		cytochrome b	-1.41
ABUW_RS07165		glycosyltransferase	-1.41
ABUW_RS20115		hypothetical protein	-1.40
ABUW_RS16950		DMT family transporter	-1.39
ABUW_RS08970		glucose/quinolate/shikimate family membrane-bound PQQ-dependent dehydrogenase	-1.39
ABUW_RS00110		sodium-dependent transporter	-1.39
ABUW_RS13980		HupE/UreJ family protein	-1.38
ABUW_RS16890		glutathione S-transferase family protein	-1.38
ABUW_RS17205		monovalent cation/H ⁺ antiporter subunit D	-1.38
ABUW_RS12785		GNAT family N-acetyltransferase	-1.38
ABUW_RS08170		serine hydrolase	-1.38
ABUW_RS12465	icmH	type IVB secretion system protein IcmH/DotU	-1.37
ABUW_RS00195		START domain-containing protein	-1.37
ABUW_RS06645		dicarboxylate/amino acid:cation symporter	-1.36
ABUW_RS06500		alpha/beta fold hydrolase	-1.36
ABUW_RS06715		sulfurtransferase TusA family protein	-1.35
ABUW_RS00690		DUF2147 domain-containing protein	-1.35
ABUW_RS14555		site-specific DNA-methyltransferase	-1.35
ABUW_RS10810		ABC transporter permease	-1.34
ABUW_RS13680		RHS repeat protein	-1.33
ABUW_RS01280		aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	-1.33
ABUW_RS00515		alpha/beta fold hydrolase	-1.33
ABUW_RS16895		YafY family transcriptional regulator	-1.33

ABUW_RS04930		NIF3 1	-1.33
ABUW_RS18095		hypothetical protein	-1.32
ABUW_RS14895		NAD ⁺ synthase	-1.32
ABUW_RS13000		hypothetical protein	-1.32
ABUW_RS01765		hypothetical protein	-1.31
ABUW_RS00865	acs	acetate--CoA ligase	-1.31
ABUW_RS08830		YnfA family protein	-1.31
ABUW_RS11330		amino acid ABC transporter ATP-binding protein	-1.30
ABUW_RS13990		urease accessory protein	-1.30
ABUW_RS01190		membrane protein	-1.30
ABUW_RS03500		DJ-1/Pfpl family protein	-1.30
ABUW_RS18865		hypothetical protein	-1.29
ABUW_RS02490		YfiR family protein	-1.29
ABUW_RS05330		DUF962 domain-containing protein	-1.29
ABUW_RS00870		cysteine hydrolase	-1.29
ABUW_RS01975		DUF853 domain-containing protein	-1.28
ABUW_RS08940	pcaC	4-carboxymuconolactone decarboxylase	-1.28
ABUW_RS10685		HU family DNA-binding protein	-1.27
ABUW_RS00025	cybC	cytochrome b562	-1.26
ABUW_RS13220		hypothetical protein	-1.26
ABUW_RS11910		hypothetical protein	-1.25
ABUW_RS17105		MerR family transcriptional regulator	-1.25
ABUW_RS19715		hypothetical protein	-1.25
ABUW_RS04830		CSLREA domain-containing protein	-1.25
ABUW_RS18615		glycosyltransferase family 4 protein	-1.24
ABUW_RS02295		malate dehydrogenase	-1.24
ABUW_RS05890		peptide MFS transporter	-1.23
ABUW_RS04285	odhB	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase	-1.23
ABUW_RS18740		YciK family oxidoreductase	-1.21
ABUW_RS05110		Paal family thioesterase	-1.20
ABUW_RS16475		NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-1.20
ABUW_RS06670		hypothetical protein	-1.19
ABUW_RS01490		TPM domain-containing protein	-1.19
ABUW_RS13360		hypothetical protein	-1.19
ABUW_RS14800	minE	cell division topological specificity factor MinE	-1.18
ABUW_RS05275	icd	NADP-dependent isocitrate dehydrogenase	-1.18
ABUW_RS00270		PQQ-dependent sugar dehydrogenase	-1.18
ABUW_RS16155		heavy metal translocating P-type ATPase	-1.18
ABUW_RS15470		ribonucleotide-diphosphate reductase subunit beta	-1.18
ABUW_RS08520		RNA-binding protein	-1.16
ABUW_RS11200		helix-turn-helix transcriptional regulator	-1.16
ABUW_RS16420	pilW	type IV pilus biogenesis/stability protein PilW	-1.15
ABUW_RS17220		Na ⁺ /H ⁺ antiporter subunit G	-1.14
ABUW_RS02765	oxa-23	carbapenem-hydrolyzing class D beta-lactamase OXA-23	-1.13
ABUW_RS04465		MFS transporter	-1.13
ABUW_RS18885	grpE	nucleotide exchange factor GrpE	-1.12
ABUW_RS07770		translocation/assembly module TamB domain-containing protein	-1.11
ABUW_RS11195		N-acetyltransferase	-1.11
ABUW_RS01485		TPM domain-containing protein	-1.11
ABUW_RS02660		3'-5' exonuclease	-1.11
ABUW_RS01370		hypothetical protein	-1.10
ABUW_RS01420	ponA	penicillin-binding protein PBP1a	-1.10
ABUW_RS09180		hypothetical protein	-1.10
ABUW_RS12460		hypothetical protein	-1.09
ABUW_RS15660		cation transporter	-1.09
ABUW_RS04325		neutral zinc metallopeptidase	-1.08

ABUW_RS15615	add	adenosine deaminase	-1.08
ABUW_RS05220		hypothetical protein	-1.07
ABUW_RS09260		sorbose dehydrogenase family protein	-1.07
ABUW_RS18605		acetyltransferase	-1.07
ABUW_RS08585		PQQ-dependent sugar dehydrogenase	-1.07
ABUW_RS14135		ABC transporter ATP-binding protein	-1.06
ABUW_RS08380		SDR family NAD(P)-dependent oxidoreductase	-1.06
ABUW_RS15880	polA	DNA polymerase I	-1.06
ABUW_RS07740		response regulator transcription factor	-1.06
ABUW_RS12470	tssK	type VI secretion system baseplate subunit TssK	-1.06
ABUW_RS18470		nuclear transport factor 2 family protein	-1.06
ABUW_RS04635	fdhD	formate dehydrogenase accessory sulfurtransferase FdhD	-1.05
ABUW_RS00475		hypothetical protein	-1.05
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.05
ABUW_RS13290		peptidoglycan DD-metalloendopeptidase family protein	-1.04
ABUW_RS01930		NAD(P)H-binding protein	-1.04
ABUW_RS14150		alpha/beta hydrolase	-1.04
ABUW_RS14870		EcsC family protein	-1.04
ABUW_RS03605	hchA	protein deglycase HchA	-1.04
ABUW_RS15255		dCTP deaminase	-1.03
ABUW_RS10815		Zn-dependent oligopeptidase	-1.02
ABUW_RS13195	ahpC	peroxiredoxin	-1.02
ABUW_RS05520		hypothetical protein	-1.01
ABUW_RS18525	acnD	Fe/S-dependent 2-methylisocitrate dehydratase AcnD	-1.01
ABUW_RS11725	yfcF	glutathione transferase	-1.00
ABUW_RS07765		outer membrane protein assembly factor	-1.00
ABUW_RS02675		hypothetical protein	-1.00

Table A3. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta adeS$ MEP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta adeS$ MEP vs WT MEP log2FC
sRNA92	sRNA92	sRNA92	4.43
sRNA48	sRNA48	sRNA48	4.20
ABUW_RS01510		bacterioferritin-associated ferredoxin	3.20
ABUW_RS11440	dapC	succinyl-diaminopimelate transaminase	2.96
ABUW_RS16540		TonB-dependent siderophore receptor	2.76
ABUW_RS14395		hypothetical protein	2.24
ABUW_RS20110		hypothetical protein	2.22
ABUW_RS03460		hypothetical protein	2.20
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	2.13
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	2.10
ABUW_RS01820		HPP family protein	2.07
ABUW_RS16655		energy transducer TonB	2.06
ABUW_RS17835		signal peptidase II	2.04
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	1.99
ABUW_RS17840		cation transporter	1.97
ABUW_RS20540		hypothetical protein	1.95
ABUW_RS18235		NAD-dependent malic enzyme	1.94
ABUW_RS17255		tRNA-Leu	1.93
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.91
ABUW_RS07730	kdpC	potassium-transporting ATPase subunit KdpC	1.90
ABUW_RS10700		Rrf2 family transcriptional regulator	1.90
ABUW_RS17685		ferrous iron transporter B	1.88
ABUW_RS03430		YdcF family protein	1.88
sRNA9	sRNA9	sRNA9	1.86

ABUW_RS10525		hypothetical protein	1.86
ABUW_RS15465		hypothetical protein	1.83
ABUW_RS08720		DUF2057 domain-containing protein	1.82
ABUW_RS02710		hypothetical protein	1.81
ABUW_RS11435	glnD	[protein-PII] uridylyltransferase	1.80
ABUW_RS10600		hypothetical protein	1.80
ABUW_RS07435		MFS transporter	1.77
ABUW_RS02020	rplV	50S ribosomal protein L22	1.74
ABUW_RS03530	mreD	rod shape-determining protein MreD	1.73
ABUW_RS00790		TonB-dependent siderophore receptor	1.71
ABUW_RS14610		hypothetical protein	1.70
ABUW_RS03465		alanine:cation symporter family protein	1.70
ABUW_RS01470		FAD-dependent oxidoreductase	1.69
ABUW_RS10715	iscA	iron-sulfur cluster assembly protein IscA	1.68
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	1.68
ABUW_RS10705		IscS subfamily cysteine desulfurase	1.66
ABUW_RS10720	hscB	Fe-S protein assembly co-chaperone HscB	1.65
ABUW_RS01995	rplC	50S ribosomal protein L3	1.65
ABUW_RS03220		uracil-xanthine permease	1.63
ABUW_RS13235	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	1.62
ABUW_RS17870	arsB	ACR3 family arsenite efflux transporter	1.62
ABUW_RS17690		ferrous iron transport protein A	1.62
ABUW_RS13945		RnfABCDGE type electron transport complex subunit B	1.61
ABUW_RS01990	rpsJ	30S ribosomal protein S10	1.61
ABUW_RS02015	rpsS	30S ribosomal protein S19	1.61
ABUW_RS18200		ATP synthase subunit I	1.60
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	1.59
ABUW_RS11115	putP	sodium/proline symporter PutP	1.59
ABUW_RS17215		monovalent cation/H ⁺ antiporter subunit F	1.59
ABUW_RS13745		TonB-dependent receptor	1.58
ABUW_RS17975		trimeric intracellular cation channel family protein	1.57
ABUW_RS02010	rplB	50S ribosomal protein L2	1.57
ABUW_RS18915		5-(carboxyamino)imidazole ribonucleotide synthase	1.56
ABUW_RS16770	gltP	glutamate/aspartate:proton symporter GltP	1.56
ABUW_RS02000	rplD	50S ribosomal protein L4	1.55
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	1.55
ABUW_RS07660	prmC	peptide chain release factor N(5)-glutamine methyltransferase	1.54
ABUW_RS04205		APC family permease	1.53
ABUW_RS19315	aadB	aminoglycoside nucleotidyltransferase ANT(2'')-Ia	1.53
ABUW_RS15225		tRNA-dihydrouridine synthase	1.53
ABUW_RS05430		aspartate aminotransferase family protein	1.52
ABUW_RS15010	ispE	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	1.52
ABUW_RS11080		DUF1275 domain-containing protein	1.52
ABUW_RS03525	mreC	rod shape-determining protein MreC	1.51
ABUW_RS03165		nitrite/sulfite reductase	1.51
ABUW_RS14380		YaeQ family protein	1.50
ABUW_RS01610		TSUP family transporter	1.50
ABUW_RS18195	atpB	F0F1 ATP synthase subunit A	1.49
ABUW_RS01350		amino acid permease	1.49
ABUW_RS16645		biopolymer transporter ExbD	1.49
ABUW_RS00150		pyrimidine permease	1.49
ABUW_RS02025	rpsC	30S ribosomal protein S3	1.48
ABUW_RS06655		alpha/beta hydrolase	1.47
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.46
ABUW_RS10225		TonB-dependent siderophore receptor	1.45

ABUW_RS16495		phosphogluconate dehydratase	1.44
ABUW_RS08035		TonB-dependent receptor	1.43
ABUW_RS17680		hypothetical protein	1.43
ABUW_RS07475	purD	phosphoribosylamine--glycine ligase	1.42
ABUW_RS02030	rplP	50S ribosomal protein L16	1.41
ABUW_RS17505	secE	preprotein translocase subunit SecE	1.41
ABUW_RS17510		tRNA-Trp	1.41
ABUW_RS01465	gltB	glutamate synthase large subunit	1.41
ABUW_RS16800	truA	tRNA pseudouridine(38-40) synthase TruA	1.40
ABUW_RS01580	rimM	ribosome maturation factor RimM	1.38
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.38
ABUW_RS07480	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.37
ABUW_RS16050		3'-5' exonuclease	1.37
sRNA96	sRNA96	sRNA96	1.36
ABUW_RS16490	eda	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2- dehydro-3-deoxy-phosphogluconate aldolase	1.36
ABUW_RS20525		hypothetical protein	1.36
ABUW_RS10380	aroC	chorismate synthase	1.36
ABUW_RS12800		O-methyltransferase	1.36
ABUW_RS14375		FKBP-type peptidyl-prolyl cis-trans isomerase	1.35
ABUW_RS06575		ferredoxin--NADP reductase	1.35
ABUW_RS17220		Na ⁺ /H ⁺ antiporter subunit G	1.33
ABUW_RS15035		ribose-phosphate pyrophosphokinase	1.33
ABUW_RS08680		aspartate aminotransferase family protein	1.32
ABUW_RS16995		TIGR03862 family flavoprotein	1.32
ABUW_RS03170		DUF934 domain-containing protein	1.32
ABUW_RS08750		DUF1449 family protein	1.32
ABUW_RS06095		ABC transporter permease	1.32
ABUW_RS05425		diaminobutyrte--2-oxoglutarate transaminase	1.31
ABUW_RS18685		carboxylating nicotinate-nucleotide diphosphorylase	1.31
ABUW_RS14200		inorganic phosphate transporter	1.31
ABUW_RS02080	rpsE	30S ribosomal protein S5	1.30
ABUW_RS13345		aspartate kinase	1.29
ABUW_RS11390	ychF	redox-regulated ATPase YchF	1.28
ABUW_RS06685		hydrolase	1.28
ABUW_RS19445		hypothetical protein	1.28
ABUW_RS02095	secY	preprotein translocase subunit SecY	1.28
ABUW_RS07560	cyoE	protoheme IX farnesyltransferase	1.27
ABUW_RS04280		2-oxoglutarate dehydrogenase E1 component	1.26
ABUW_RS02635	queA	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	1.26
ABUW_RS02145		membrane protein	1.25
ABUW_RS01200		helix-turn-helix transcriptional regulator	1.24
ABUW_RS13930		dioxygenase	1.24
ABUW_RS07545	rplI	50S ribosomal protein L9	1.24
ABUW_RS15430	ndhC	NADH-quinone oxidoreductase subunit A	1.24
ABUW_RS13860		cation transporter	1.24
ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	1.24
ABUW_RS16610		prolipoprotein diacylglycerol transferase	1.23
ABUW_RS15420	nuoC	NADH-quinone oxidoreductase subunit C/D	1.23
ABUW_RS17000		SAM-dependent methyltransferase	1.23
ABUW_RS17670	ftsW	putative lipid II flippase FtsW	1.23
ABUW_RS07655	prfA	peptide chain release factor 1	1.23
ABUW_RS14250		helix-turn-helix transcriptional regulator	1.23
ABUW_RS18180		F0F1 ATP synthase subunit delta	1.23

ABUW_RS14165	nfuA	Fe-S biogenesis protein NfuA	1.23
ABUW_RS04185	cobA	uroporphyrinogen-III C-methyltransferase	1.23
ABUW_RS17210		Na ⁺ /H ⁺ antiporter subunit E	1.23
ABUW_RS15425		NADH-quinone oxidoreductase subunit B	1.22
ABUW_RS17490	rplA	50S ribosomal protein L1	1.22
ABUW_RS16250		tRNA threonylcarbamoyladenosine dehydratase	1.22
ABUW_RS18920	purE	5-(carboxyamino)imidazole ribonucleotide mutase	1.22
ABUW_RS03210		amino acid permease	1.22
ABUW_RS15105		DUF177 domain-containing protein	1.22
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	1.22
ABUW_RS02370		TetR family transcriptional regulator	1.22
ABUW_RS17630		EamA family transporter	1.21
ABUW_RS12095		putative 2-aminoethylphosphonate ABC transporter substrate-binding protein	1.21
ABUW_RS13950	nth	endonuclease III	1.21
ABUW_RS14440		hypothetical protein	1.20
ABUW_RS02005	rplW	50S ribosomal protein L23	1.20
ABUW_RS04235		hypothetical protein	1.20
ABUW_RS00705	pyrE	orotate phosphoribosyltransferase	1.20
ABUW_RS02040	rpsQ	30S ribosomal protein S17	1.19
ABUW_RS03215		methyltransferase	1.19
ABUW_RS08235		PepSY domain-containing protein	1.19
ABUW_RS13015		hypothetical protein	1.19
ABUW_RS06080	rodA	rod shape-determining protein RodA	1.19
ABUW_RS03535		Maf-like protein	1.18
ABUW_RS15415	nuoE	NADH-quinone oxidoreductase subunit NuoE	1.18
ABUW_RS07565		cytochrome o ubiquinol oxidase subunit IV	1.18
ABUW_RS17865		arsenate reductase ArsC	1.18
ABUW_RS00965		DUF475 domain-containing protein	1.17
ABUW_RS15635		tRNA-Pro	1.17
ABUW_RS06100		ABC transporter ATP-binding protein	1.17
ABUW_RS03375	dapE	succinyl-diaminopimelate desuccinylase	1.17
ABUW_RS13375		NCS2 family permease	1.17
ABUW_RS02120	rpoA	DNA-directed RNA polymerase subunit alpha	1.16
ABUW_RS01220	hisH	imidazole glycerol phosphate synthase subunit HisH	1.16
ABUW_RS05460	pstC	phosphate ABC transporter permease subunit PstC	1.16
ABUW_RS17675		UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	1.16
ABUW_RS04805		phosphoribosylglycinamide formyltransferase	1.16
ABUW_RS05300		L-cystine transporter	1.15
ABUW_RS01905		magnesium transporter	1.15
ABUW_RS04275		succinate dehydrogenase iron-sulfur subunit	1.15
ABUW_RS16510		fumarate hydratase	1.15
ABUW_RS04265	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.14
ABUW_RS08755		Rieske (2Fe-2S) protein	1.14
ABUW_RS04545	ttcA	tRNA 2-thiocytidine(32) synthetase TtcA	1.14
ABUW_RS15410	nuoF	NADH-quinone oxidoreductase subunit NuoF	1.14
ABUW_RS04480		phosphoenolpyruvate carboxykinase (GTP)	1.14
ABUW_RS07575	cyoB	cytochrome o ubiquinol oxidase subunit I	1.13
ABUW_RS01585	trmD	tRNA (guanosine(37)-N1)-methyltransferase TrmD	1.13
ABUW_RS02060	rpsN	30S ribosomal protein S14	1.13
ABUW_RS11140		hypothetical protein	1.13
ABUW_RS06645		dicarboxylate/amino acid:cation symporter	1.12
ABUW_RS02070	rplF	50S ribosomal protein L6	1.12
ABUW_RS04450	folD	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	1.12

ABUW_RS02055	rplE	50S ribosomal protein L5	1.12
ABUW_RS12770		EamA family transporter	1.12
ABUW_RS18975	hpt	hypoxanthine phosphoribosyltransferase	1.11
ABUW_RS01800	glyQ	glycine--tRNA ligase subunit alpha	1.11
ABUW_RS05120		pyridoxal phosphate-dependent aminotransferase	1.11
ABUW_RS15400	nuoH	NADH-quinone oxidoreductase subunit NuoH	1.11
ABUW_RS04915	purL	phosphoribosylformylglycinamide synthase	1.11
ABUW_RS10885	pyrF	orotidine-5'-phosphate decarboxylase	1.10
ABUW_RS18675	murJ	murein biosynthesis integral membrane protein MurJ	1.10
ABUW_RS13020		helix-turn-helix transcriptional regulator	1.10
ABUW_RS07885		glutamine--tRNA ligase/YqeY domain fusion protein	1.10
ABUW_RS15045	pth	aminoacyl-tRNA hydrolase	1.10
ABUW_RS13720	argG	argininosuccinate synthase	1.10
ABUW_RS07570	cyoC	cytochrome o ubiquinol oxidase subunit III	1.09
ABUW_RS15390	nuoJ	NADH-quinone oxidoreductase subunit J	1.09
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.09
ABUW_RS11015		nucleotidyltransferase family protein	1.08
ABUW_RS11820		Lrp/AsnC family transcriptional regulator	1.08
ABUW_RS00035		ATP-binding cassette domain-containing protein	1.08
ABUW_RS15460		ribonucleoside-diphosphate reductase subunit alpha	1.08
ABUW_RS08760		adenosine kinase	1.08
ABUW_RS17995	mdtD	multidrug transporter subunit MdtD	1.08
ABUW_RS16625	thyA	thymidylate synthase	1.08
ABUW_RS11010	rsmG	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	1.07
ABUW_RS11020		phosphotransferase	1.07
ABUW_RS09595	adeR	efflux system response regulator transcription factor AdeR	1.07
ABUW_RS12790		ferredoxin family protein	1.07
ABUW_RS04385	carA	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	1.07
ABUW_RS18755	argA	amino-acid N-acetyltransferase	1.07
ABUW_RS17970		MFS transporter	1.07
ABUW_RS14170		rhomboid family intramembrane serine protease	1.06
ABUW_RS02085	rpmD	50S ribosomal protein L30	1.06
ABUW_RS07875		UDP-2,3-diacylglucosamine diphosphatase	1.06
ABUW_RS08465		phosphatidate cytidyltransferase	1.06
ABUW_RS05155		glyceraldehyde-3-phosphate dehydrogenase	1.05
ABUW_RS16795		asparaginase	1.05
ABUW_RS04455		methyltransferase	1.05
ABUW_RS11085		DUF2058 domain-containing protein	1.05
ABUW_RS16660	purU	formyltetrahydrofolate deformylase	1.05
ABUW_RS08400		hypothetical protein	1.05
ABUW_RS02115	rpsD	30S ribosomal protein S4	1.05
ABUW_RS07795		MFS transporter	1.05
ABUW_RS08885	kdsA	3-deoxy-8-phosphooctulonate synthase	1.05
ABUW_RS19005	yidC	membrane protein insertase YidC	1.05
ABUW_RS16630		dihydrofolate reductase	1.04
ABUW_RS07080	tsaD	tRNA (adenosine(37)-N6)- threonylcarbamoyltransferase complex transferase subunit TsaD	1.04
ABUW_RS00575		type VI secretion system tip protein VgrG	1.04
ABUW_RS15705		class I SAM-dependent methyltransferase	1.03
ABUW_RS08880		CTP synthase	1.03
ABUW_RS17055	Int	apolipoprotein N-acyltransferase	1.03
ABUW_RS17905		DDE-type integrase/transposase/recombinase	1.03

ABUW_RS03520		rod shape-determining protein	1.03
ABUW_RS07625		LLM class flavin-dependent oxidoreductase	1.02
ABUW_RS01940	plsB	glycerol-3-phosphate 1-O-acyltransferase PlsB	1.02
ABUW_RS16055	cysM	cysteine synthase CysM	1.02
ABUW_RS01175	hisF	imidazole glycerol phosphate synthase subunit HisF	1.02
ABUW_RS03225	typA	translational GTPase TypA	1.02
ABUW_RS11075	sstT	serine/threonine transporter SstT	1.02
ABUW_RS06090	queF	NADPH-dependent 7-cyano-7-deazaguanine reductase QueF	1.02
ABUW_RS02590		bestrophin	1.02
ABUW_RS13340	alaS	alanine--tRNA ligase	1.02
ABUW_RS01795		glycine--tRNA ligase subunit beta	1.02
ABUW_RS07550	rpsR	30S ribosomal protein S18	1.02
ABUW_RS16750		ATP-binding cassette domain-containing protein	1.01
ABUW_RS04240		YecA family protein	1.01
ABUW_RS08950	pcaG	protocatechuate 3,4-dioxygenase subunit alpha	1.01
ABUW_RS14435	mgo	malate dehydrogenase (quinone)	1.01
ABUW_RS11165	tkl	transketolase	1.01
ABUW_RS00770	aceE	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	1.01
ABUW_RS01305		TolC family protein	1.01
ABUW_RS11415		AziC family ABC transporter permease	1.01
ABUW_RS15050		aspartate 1-decarboxylase	1.00
ABUW_RS18175		F0F1 ATP synthase subunit alpha	1.00
ABUW_RS15405	nuoG	NADH-quinone oxidoreductase subunit NuoG	1.00
ABUW_RS01225	hisB	imidazoleglycerol-phosphate dehydratase HisB	1.00
ABUW_RS16295		EAL domain-containing protein	1.00
ABUW_RS18190	atpE	F0F1 ATP synthase subunit C	1.00

Gene	Gene Name	Function	$\Delta adeS$ MEP vs WT MEP log2FC
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	-7.45
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	-6.84
ABUW_RS09600	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	-6.77
ABUW_RS09605	adeB	multidrug efflux RND transporter permease subunit AdeB	-6.29
ABUW_RS09610	adeC	multidrug efflux RND transporter outer membrane channel subunit AdeC	-5.64
ABUW_RS12215		hypothetical protein	-5.39
ABUW_RS10115	antC	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.25
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-5.12
ABUW_RS10110	antB	anthranilate 1,2-dioxygenase small subunit	-5.01
ABUW_RS20235		hypothetical protein	-4.90
ABUW_RS12220		hypothetical protein	-4.77
ABUW_RS12230		hypothetical protein	-4.50
ABUW_RS19790		helix-turn-helix transcriptional regulator	-4.15
ABUW_RS12225		cold-shock protein	-3.91
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-3.77
ABUW_RS11675		malonate decarboxylase subunit delta	-3.75
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-3.72
ABUW_RS17065		hypothetical protein	-3.54
ABUW_RS04595		hypothetical protein	-3.43
ABUW_RS00380	hutU	urocanate hydratase	-3.33
ABUW_RS20230		hypothetical protein	-3.32
ABUW_RS10425		hypothetical protein	-3.10
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-2.98

ABUW_RS14740		bacteriohemerythrin	-2.91
ABUW_RS15175	bfr	bacterioferritin	-2.89
ABUW_RS07515		circularly permuted type 2 ATP-grasp protein	-2.84
ABUW_RS11305		TetR/AcrR family transcriptional regulator	-2.79
ABUW_RS12900		DUF4882 family protein	-2.77
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-2.75
ABUW_RS20180		hypothetical protein	-2.66
ABUW_RS13655		hypothetical protein	-2.64
ABUW_RS20315		hypothetical protein	-2.64
ABUW_RS00515		alpha/beta fold hydrolase	-2.60
ABUW_RS13005		hypothetical protein	-2.58
ABUW_RS12320	paaB	1,2-phenylacetyl-CoA epoxidase subunit B	-2.55
ABUW_RS13090		tRNA-Met	-2.54
ABUW_RS13085		transposase	-2.53
ABUW_RS11575	tauD	taurine dioxygenase	-2.47
ABUW_RS07520		alpha-E domain-containing protein	-2.42
ABUW_RS11275		cytosine permease	-2.41
ABUW_RS12745		DUF2147 domain-containing protein	-2.41
ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-2.39
ABUW_RS00660		HPF/RaiA family ribosome-associated protein	-2.36
ABUW_RS00385	hutH	histidine ammonia-lyase	-2.34
ABUW_RS09455		nicotinate phosphoribosyltransferase	-2.34
ABUW_RS00335		VOC family protein	-2.34
ABUW_RS12975		hypothetical protein	-2.33
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-2.32
ABUW_RS08590		universal stress protein	-2.32
ABUW_RS01495	pilA	pilin	-2.28
ABUW_RS07130		aspartate aminotransferase family protein	-2.22
ABUW_RS11780		transporter substrate-binding domain-containing protein	-2.21
ABUW_RS01445		type IV pilus secretin PilQ family protein	-2.20
ABUW_RS09300		amidohydrolase	-2.20
ABUW_RS05795	basI	acinetobactin biosynthesis phosphopantetheinyl transferase BasI	-2.19
ABUW_RS19040		zeta toxin family protein	-2.19
sRNA27	sRNA27	sRNA27	-2.18
ABUW_RS08535		hypothetical protein	-2.16
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	-2.15
ABUW_RS05750	basC	putative histamine N-monooxygenase	-2.14
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-2.13
ABUW_RS05685		hypothetical protein	-2.13
ABUW_RS13575		hypothetical protein	-2.10
ABUW_RS14685		VOC family protein	-2.08
ABUW_RS11425		tautomerase family protein	-2.08
ABUW_RS02525		hypothetical protein	-2.08
ABUW_RS11750		serine acetyltransferase	-2.07
ABUW_RS04995	cysW	sulfate ABC transporter permease subunit CysW	-2.07
ABUW_RS05790	basH	acinetobactin biosynthesis thioesterase BasH	-2.07
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	-2.06
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-2.05
ABUW_RS06320		hypothetical protein	-2.03
ABUW_RS07280		hypothetical protein	-2.03
ABUW_RS11360		SfnB family sulfur acquisition oxidoreductase	-2.03
ABUW_RS00800		YkgJ family cysteine cluster protein	-2.03
ABUW_RS13045		NAD(P)-binding domain-containing protein	-2.03
ABUW_RS02780		phage major tail tube protein	-2.03
ABUW_RS12325	paaA	1,2-phenylacetyl-CoA epoxidase subunit A	-2.03

ABUW_RS05230		hypothetical protein	-2.02
ABUW_RS00340	maiA	maleylacetoacetate isomerase	-2.01
ABUW_RS08700		hypothetical protein	-2.00
ABUW_RS15440		hypothetical protein	-1.99
ABUW_RS05000	cysT	sulfate ABC transporter permease subunit CysT	-1.99
ABUW_RS13380		hypothetical protein	-1.99
ABUW_RS00345	fahA	fumarylacetoacetase	-1.97
ABUW_RS15335		hypothetical protein	-1.96
ABUW_RS09525		DEAD/DEAH box helicase family protein	-1.96
ABUW_RS03180		VOC family protein	-1.96
ABUW_RS00405		DUF885 domain-containing protein	-1.96
ABUW_RS12315	paaC	phenylacetate-CoA oxygenase subunit PaaC	-1.96
ABUW_RS15615	add	adenosine deaminase	-1.95
ABUW_RS16890		glutathione S-transferase family protein	-1.95
ABUW_RS03310		YegP family protein	-1.95
ABUW_RS07135		CoA-acylating methylmalonate-semialdehyde dehydrogenase	-1.94
ABUW_RS12725		hypothetical protein	-1.93
ABUW_RS02785		phage tail sheath protein	-1.93
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-1.92
ABUW_RS07965		molecular chaperone	-1.92
ABUW_RS11355		SfnB family sulfur acquisition oxidoreductase	-1.92
ABUW_RS20485		hypothetical protein	-1.92
ABUW_RS07150		hypothetical protein	-1.88
ABUW_RS12330	paaZ	phenylacetic acid degradation bifunctional protein PaaZ	-1.86
ABUW_RS06280		hypothetical protein	-1.86
ABUW_RS13250		OmpA family protein	-1.86
ABUW_RS08095		universal stress protein	-1.86
ABUW_RS11785		amino acid ABC transporter ATP-binding protein	-1.86
ABUW_RS18520		hypothetical protein	-1.85
ABUW_RS01505	bfr	bacterioferritin	-1.84
ABUW_RS11370		methionine transporter	-1.84
ABUW_RS19235		hypothetical protein	-1.84
ABUW_RS00795		MBL fold metallo-hydrolase	-1.84
ABUW_RS02860		GPO family capsid scaffolding protein	-1.83
ABUW_RS15280		hypothetical protein	-1.83
ABUW_RS10835		energy transducer TonB	-1.83
ABUW_RS03605	hchA	protein deglycase HchA	-1.82
ABUW_RS16720		hypothetical protein	-1.81
ABUW_RS03365		radical SAM protein	-1.80
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-1.80
ABUW_RS03355		Hpt domain-containing protein	-1.78
ABUW_RS15495		hypothetical protein	-1.78
ABUW_RS02875		HAMP domain-containing histidine kinase	-1.78
sRNA75	sRNA75	sRNA75	-1.78
ABUW_RS19070		hypothetical protein	-1.78
ABUW_RS13450		GMC family oxidoreductase	-1.77
ABUW_RS09295		hypothetical protein	-1.77
ABUW_RS07960		spore coat protein U domain-containing protein	-1.77
ABUW_RS01440		pilus assembly protein PilP	-1.76
ABUW_RS02200		HAD-IB family hydrolase	-1.76
ABUW_RS08740		cytochrome ubiquinol oxidase subunit I	-1.76
ABUW_RS04600		hypothetical protein	-1.75
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-1.74
ABUW_RS11860		iron-containing redox enzyme family protein	-1.74
ABUW_RS01570		prepilin-type N-terminal cleavage/methylation domain-containing protein	-1.74
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	-1.72

ABUW_RS01565		prepilin-type N-terminal cleavage/methylation domain-containing protein	-1.71
ABUW_RS10005		hypothetical protein	-1.71
ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	-1.71
ABUW_RS19065		hypothetical protein	-1.71
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-1.71
ABUW_RS09960		hypothetical protein	-1.70
ABUW_RS03350		methyl-accepting chemotaxis protein	-1.70
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-1.69
ABUW_RS14485		DUF560 domain-containing protein	-1.68
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-1.68
ABUW_RS09550		GNAT family N-acetyltransferase	-1.68
ABUW_RS07970		fimbrial biogenesis outer membrane usher protein	-1.67
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	-1.67
ABUW_RS00895		hypothetical protein	-1.66
ABUW_RS19075		hypothetical protein	-1.65
ABUW_RS05480		BapA prefix-like domain-containing protein	-1.65
ABUW_RS05820		DUF3015 family protein	-1.65
ABUW_RS02625		LemA family protein	-1.63
ABUW_RS16965		SfnB family sulfur acquisition oxidoreductase	-1.63
ABUW_RS14030		isocitrate lyase	-1.63
ABUW_RS09275		hydrolase	-1.62
ABUW_RS05910		hypothetical protein	-1.62
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-1.60
ABUW_RS08725		cyd operon YbgE family protein	-1.60
ABUW_RS14175		arylsulfatase	-1.60
ABUW_RS09520		HD domain-containing protein	-1.59
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	-1.58
ABUW_RS16440		phosphatase PAP2 family protein	-1.58
ABUW_RS00415	murl	glutamate racemase	-1.58
ABUW_RS03090		peroxiredoxin	-1.58
ABUW_RS00260		DUF1328 domain-containing protein	-1.58
ABUW_RS05225		glycosyltransferase family 2 protein	-1.57
ABUW_RS17730		sigma-54-dependent Fis family transcriptional regulator	-1.57
ABUW_RS01560		VWA domain-containing protein	-1.57
ABUW_RS05540		LysR family transcriptional regulator	-1.57
ABUW_RS06500		alpha/beta fold hydrolase	-1.56
ABUW_RS17100		DnaJ domain-containing protein	-1.55
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.55
ABUW_RS08870		metal-dependent hydrolase	-1.55
ABUW_RS01435		type 4a pilus biogenesis protein PilO	-1.55
ABUW_RS16280		hypothetical protein	-1.54
ABUW_RS08540		hypothetical protein	-1.54
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.53
ABUW_RS05355	csy3	type I-F CRISPR-associated protein Csy3	-1.53
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.53
ABUW_RS11375		MetQ/NlpA family ABC transporter substrate-binding protein	-1.52
ABUW_RS05570		EAL domain-containing protein	-1.52
ABUW_RS12430		winged helix-turn-helix domain-containing protein	-1.52
ABUW_RS08695		hypothetical protein	-1.51
ABUW_RS14645	ggt	gamma-glutamyltransferase	-1.50
ABUW_RS13445		alpha/beta hydrolase	-1.49
ABUW_RS08240		TetR/AcrR family transcriptional regulator	-1.49
ABUW_RS09265		hypothetical protein	-1.49
ABUW_RS05825		DUF4105 domain-containing protein	-1.49
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	-1.48

ABUW_RS13760		RHS repeat protein	-1.47
ABUW_RS03345		purine-binding chemotaxis protein CheW	-1.46
ABUW_RS13280		CinA family protein	-1.45
ABUW_RS13755		RHS repeat-associated core domain-containing protein	-1.45
ABUW_RS19545		hypothetical protein	-1.45
ABUW_RS00370	hutC	histidine utilization repressor	-1.44
ABUW_RS04630		FdhF/YdeP family oxidoreductase	-1.44
ABUW_RS07980		glutathione S-transferase family protein	-1.44
ABUW_RS05340	cas3f	type I-F CRISPR-associated helicase Cas3	-1.44
ABUW_RS07985		SDR family NAD(P)-dependent oxidoreductase	-1.43
ABUW_RS01215		DUF805 domain-containing protein	-1.43
ABUW_RS09545		hypothetical protein	-1.43
ABUW_RS04355		metalloprotease	-1.43
ABUW_RS12760		lauroyl acyltransferase	-1.43
ABUW_RS08530		hypothetical protein	-1.43
ABUW_RS03360		hypothetical protein	-1.43
ABUW_RS15550		amidohydrolase	-1.43
ABUW_RS03585		PaaX family transcriptional regulator	-1.43
ABUW_RS12805		universal stress protein	-1.42
ABUW_RS09185		alpha/beta hydrolase	-1.42
ABUW_RS09260		sorbosone dehydrogenase family protein	-1.41
ABUW_RS07415		aspartate/glutamate racemase family protein	-1.41
ABUW_RS13390		SDR family NAD(P)-dependent oxidoreductase	-1.41
ABUW_RS13465		aromatic ring-hydroxylating dioxygenase subunit alpha	-1.40
ABUW_RS04990		sulfate ABC transporter ATP-binding protein	-1.39
ABUW_RS17150		polyphosphate--AMP phosphotransferase	-1.39
ABUW_RS19090		hypothetical protein	-1.39
ABUW_RS06560	yegQ	tRNA 5-hydroxyuridine modification protein YegQ	-1.38
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	-1.37
ABUW_RS16255	acnA	aconitate hydratase AcnA	-1.37
ABUW_RS02850		terminase	-1.37
ABUW_RS10615		(2Fe-2S)-binding protein	-1.36
ABUW_RS12635		sel1 repeat family protein	-1.36
ABUW_RS05345	csy1	type I-F CRISPR-associated protein Csy1	-1.35
ABUW_RS09290		cation:proton antiporter	-1.35
ABUW_RS04365		universal stress protein	-1.35
ABUW_RS17420		hypothetical protein	-1.35
ABUW_RS05220		hypothetical protein	-1.35
ABUW_RS19110		DUF2786 domain-containing protein	-1.34
ABUW_RS01615		hemerythrin domain-containing protein	-1.34
ABUW_RS12680		hypothetical protein	-1.33
ABUW_RS01425		pilus assembly protein PilM	-1.33
ABUW_RS11380		ATP-binding cassette domain-containing protein	-1.33
ABUW_RS04495		Ig-like domain repeat protein	-1.33
ABUW_RS05205		hypothetical protein	-1.32
ABUW_RS00410		HAD family hydrolase	-1.32
ABUW_RS05235		hypothetical protein	-1.32
ABUW_RS13815		hypothetical protein	-1.31
ABUW_RS13650		ATP-binding protein	-1.31
ABUW_RS12255		ATP-dependent helicase	-1.31
ABUW_RS07785		hypothetical protein	-1.30
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.30
ABUW_RS14715		PilT/PilU family type 4a pilus ATPase	-1.30
ABUW_RS00375		HutD family protein	-1.30
ABUW_RS09335		SMI1/KNR4 family protein	-1.30
ABUW_RS02520		dihydrolipoyl dehydrogenase	-1.29
ABUW_RS19080		thermonuclease family protein	-1.29

ABUW_RS17270	pilB	type IV-A pilus assembly ATPase PilB	-1.29
ABUW_RS15330		mechanosensitive ion channel	-1.28
ABUW_RS09280		LysR family transcriptional regulator	-1.28
ABUW_RS04910		deoxyguanosinetriphosphate triphosphohydrolase	-1.28
ABUW_RS15520		methionine synthase	-1.27
ABUW_RS12335		L-serine ammonia-lyase	-1.27
ABUW_RS18115		LysM peptidoglycan-binding domain-containing protein	-1.26
ABUW_RS13200		KTSC domain-containing protein	-1.26
ABUW_RS08390		hypothetical protein	-1.26
ABUW_RS10610		RraA family protein	-1.25
ABUW_RS05350	csy2	type I-F CRISPR-associated protein Csy2	-1.25
ABUW_RS02855		phage major capsid protein, P2 family	-1.25
ABUW_RS15165		trehalose-6-phosphate synthase	-1.25
ABUW_RS16715		HdeD family acid-resistance protein	-1.23
ABUW_RS03490		DUF1176 domain-containing protein	-1.23
ABUW_RS16285		TetR/AcrR family transcriptional regulator	-1.23
ABUW_RS11130		GrpB family protein	-1.23
ABUW_RS12830		TolC family protein	-1.23
ABUW_RS18765		sulfonate ABC transporter substrate-binding protein	-1.22
ABUW_RS09560		LysR family transcriptional regulator	-1.22
ABUW_RS11460	msrB	peptide-methionine (R)-S-oxide reductase MsrB	-1.21
ABUW_RS17275		type II secretion system F family protein	-1.21
ABUW_RS00395		imidazolonepropionase	-1.21
ABUW_RS18475		ribonuclease E inhibitor RraB	-1.21
ABUW_RS12520	tssE	type VI secretion system baseplate subunit TssE	-1.21
ABUW_RS12185		catalase family peroxidase	-1.20
ABUW_RS02715		BRCT domain-containing protein	-1.20
ABUW_RS13835		YraN family protein	-1.20
ABUW_RS09995		hypothetical protein	-1.20
ABUW_RS05215		hypothetical protein	-1.20
ABUW_RS11615		hypothetical protein	-1.19
ABUW_RS19060		hypothetical protein	-1.19
ABUW_RS08685		CBS domain-containing protein	-1.19
ABUW_RS11725	yfcF	glutathione transferase	-1.19
ABUW_RS11610		monooxygenase	-1.18
ABUW_RS06585		MgtC/SapB family protein	-1.17
ABUW_RS13220		hypothetical protein	-1.16
ABUW_RS16790		hypothetical protein	-1.16
ABUW_RS19100		hypothetical protein	-1.16
ABUW_RS18770	ssuD	FMNH2-dependent alkanesulfonate monooxygenase	-1.16
ABUW_RS11270		hypothetical protein	-1.15
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.15
ABUW_RS19085		H-NS histone family protein	-1.15
ABUW_RS16160		copper resistance protein CopC	-1.14
ABUW_RS05275	icd	NADP-dependent isocitrate dehydrogenase	-1.14
ABUW_RS15730		hypothetical protein	-1.14
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.13
ABUW_RS16960		acyl-CoA dehydrogenase family protein	-1.12
ABUW_RS05330		DUF962 domain-containing protein	-1.12
ABUW_RS04980	carO	ornithine uptake porin CarO type 3	-1.11
ABUW_RS10375		GGDEF domain-containing protein	-1.10
ABUW_RS14885		pirin family protein	-1.10
ABUW_RS00390		amino acid permease	-1.10
ABUW_RS11160		OsmC family protein	-1.09
ABUW_RS11950		hydroxymethylglutaryl-CoA lyase	-1.09
ABUW_RS11910		hypothetical protein	-1.08
ABUW_RS07975		spore coat protein U domain-containing protein	-1.08

ABUW_RS04345		hypothetical protein	-1.08
ABUW_RS19540		conjugal transfer protein TraF	-1.08
ABUW_RS04390		hypothetical protein	-1.07
ABUW_RS15715		gamma carbonic anhydrase family protein	-1.06
ABUW_RS05840	xdhA	xanthine dehydrogenase small subunit	-1.06
ABUW_RS07990		SDR family NAD(P)-dependent oxidoreductase	-1.06
ABUW_RS04895		amidohydrolase	-1.06
ABUW_RS09330		DUF2247 family protein	-1.06
ABUW_RS12715		serine hydrolase	-1.05
ABUW_RS10785		3'(2'),5'-bisphosphate nucleotidase CysQ	-1.05
ABUW_RS18705		acyl-CoA desaturase	-1.04
ABUW_RS16085		SDR family NAD(P)-dependent oxidoreductase	-1.03
ABUW_RS01665	yccS	TIGR01666 family membrane protein	-1.03
ABUW_RS14870		EcsC family protein	-1.03
ABUW_RS08440		PAS domain-containing protein	-1.03
ABUW_RS15055		GDYXXLY domain-containing protein	-1.02
ABUW_RS10015		phospholipase D family protein	-1.02
ABUW_RS13125		GFA family protein	-1.01
ABUW_RS08315		molybdopterin-dependent oxidoreductase	-1.00
ABUW_RS11455		glutathione peroxidase	-1.00
ABUW_RS18560	lldR	transcriptional regulator LldR	-1.00
ABUW_RS18820		NAD(P)H-dependent oxidoreductase	-1.00
ABUW_RS17640		hypothetical protein	-1.00

Table A4. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta adeS$ LSP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta adeS$ LSP vs WT LSP log2FC
ABUW_RS20020		TniB family NTP-binding protein	6.59
ABUW_RS19340		hypothetical protein	6.52
ABUW_RS19240		hypothetical protein	6.05
ABUW_RS20015		Mu transposase C-terminal domain-containing protein	5.92
ABUW_RS19125		hypothetical protein	5.65
ABUW_RS19355		hypothetical protein	5.56
ABUW_RS19130		SAM-dependent DNA methyltransferase	5.46
ABUW_RS10215		hypothetical protein	5.15
ABUW_RS19235		hypothetical protein	4.94
ABUW_RS19345		molecular chaperone DnaJ	4.93
ABUW_RS19360		hypothetical protein	4.74
ABUW_RS19135		hypothetical protein	4.54
ABUW_RS02145		membrane protein	4.47
ABUW_RS03860		hypothetical protein	4.46
ABUW_RS19175		hypothetical protein	4.24
ABUW_RS19220		hypothetical protein	4.12
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	4.02
ABUW_RS09970		molecular chaperone	3.98
ABUW_RS19350		hypothetical protein	3.97
ABUW_RS19030		replication initiation protein	3.96
ABUW_RS10120		AraC family transcriptional regulator	3.95
ABUW_RS19225		hypothetical protein	3.87
ABUW_RS19195		hypothetical protein	3.83
ABUW_RS19900		glutathione S-transferase	3.80
ABUW_RS19165		toxic anion resistance protein	3.58
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	3.55
ABUW_RS19150		hypothetical protein	3.55
ABUW_RS14535		hypothetical protein	3.29

ABUW_RS11310		1-acyl-sn-glycerol-3-phosphate acyltransferase	3.22
ABUW_RS19370		hypothetical protein	3.18
ABUW_RS09965		type 1 fimbrial protein	3.17
ABUW_RS20385		hypothetical protein	3.15
ABUW_RS10210		hypothetical protein	3.14
ABUW_RS15150	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	3.06
ABUW_RS19230		hypothetical protein	3.04
ABUW_RS09030		MFS transporter	3.04
ABUW_RS19365		hypothetical protein	3.01
ABUW_RS19155		hypothetical protein	2.91
ABUW_RS03460		hypothetical protein	2.88
ABUW_RS01100		hypothetical protein	2.83
ABUW_RS02690		hypothetical protein	2.80
ABUW_RS15145		8-amino-7-oxononanoate synthase	2.80
ABUW_RS01305		TolC family protein	2.78
ABUW_RS19170		hypothetical protein	2.77
ABUW_RS05450		amino acid permease	2.73
ABUW_RS08270	aroQ	type II 3-dehydroquinate dehydratase	2.73
ABUW_RS12960		DUF2280 domain-containing protein	2.73
ABUW_RS13905		hypothetical protein	2.72
ABUW_RS19145		ParB/RepB/Spo0J family partition protein	2.68
ABUW_RS04730		ChbG/HpnK family deacetylase	2.66
ABUW_RS12350		APC family permease	2.65
ABUW_RS08495	fabZ	3-hydroxyacyl-ACP dehydratase FabZ	2.65
ABUW_RS15140	bioC	malonyl-ACP O-methyltransferase BioC	2.65
ABUW_RS11715		CidA/LrgA family protein	2.64
ABUW_RS11530		metalloregulator ArsR/SmtB family transcription factor	2.63
ABUW_RS11535	arsC	arsenate reductase (glutaredoxin)	2.61
ABUW_RS09295		hypothetical protein	2.61
ABUW_RS12620		hypothetical protein	2.60
ABUW_RS16230		tyrosine-type recombinase/integrase	2.60
ABUW_RS11400		Crp/Fnr family transcriptional regulator	2.54
ABUW_RS11290		integrase family protein	2.53
ABUW_RS18520		hypothetical protein	2.53
ABUW_RS00925	omp33-36	porin Omp33-36	2.51
ABUW_RS08560		amino acid permease	2.50
ABUW_RS19660	rnpB	RNase P RNA component class A	2.44
ABUW_RS19140		ParA family protein	2.43
ABUW_RS09655		hypothetical protein	2.40
ABUW_RS12010		enoyl-CoA hydratase	2.38
ABUW_RS19190		hypothetical protein	2.34
ABUW_RS19520	traW	type-F conjugative transfer system protein TraW	2.33
ABUW_RS08395		hypothetical protein	2.33
ABUW_RS19205		hypothetical protein	2.32
ABUW_RS11650	madL	malonate transporter subunit MadL	2.31
ABUW_RS20105		hypothetical protein	2.30
ABUW_RS08555	kynU	kynureninase	2.30
ABUW_RS05140	uvrB	excinuclease ABC subunit UvrB	2.30
ABUW_RS10175		LysR family transcriptional regulator	2.29
ABUW_RS06110		hypothetical protein	2.28
ABUW_RS18480		RluA family pseudouridine synthase	2.27
sRNA58	sRNA58	sRNA58	2.26
ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	2.25
ABUW_RS12060		acyl-CoA dehydrogenase family protein	2.24
ABUW_RS08020		hypothetical protein	2.23
ABUW_RS10495		porin	2.22

ABUW_RS11305		TetR/AcrR family transcriptional regulator	2.21
ABUW_RS11325		hypothetical protein	2.21
ABUW_RS16775		endonuclease/exonuclease/phosphatase family protein	2.20
ABUW_RS07670		aliphatic sulfonate ABC transporter substrate-binding protein	2.20
ABUW_RS17915		ATP-binding protein	2.18
ABUW_RS17835		signal peptidase II	2.17
ABUW_RS12095		putative 2-aminoethylphosphonate ABC transporter substrate-binding protein	2.16
ABUW_RS02985		hypothetical protein	2.15
ABUW_RS04035		1-acyl-sn-glycerol-3-phosphate acyltransferase	2.15
ABUW_RS07410		GNAT family N-acetyltransferase	2.14
ABUW_RS19015	rnpA	ribonuclease P protein component	2.13
ABUW_RS05380		RluA family pseudouridine synthase	2.13
ABUW_RS09375		SMP-30/gluconolactonase/LRE family protein	2.13
ABUW_RS08500	lpxA	acyl-ACP--UDP-N-acetylglucosamine O-acyltransferase	2.13
ABUW_RS14385	dctA	C4-dicarboxylate transporter DctA	2.12
ABUW_RS09240		SDR family oxidoreductase	2.12
ABUW_RS12955	terL	phage terminase large subunit	2.10
ABUW_RS13080		LexA family transcriptional regulator	2.10
ABUW_RS19120		hypothetical protein	2.09
ABUW_RS13845		hypothetical protein	2.09
ABUW_RS15135	bioD	ATP-dependent dethiobiotin synthetase BioD	2.07
ABUW_RS19185		hypothetical protein	2.07
ABUW_RS05660	yddG	aromatic amino acid DMT transporter YddG	2.04
ABUW_RS09490		hypothetical protein	2.04
ABUW_RS03330		hypothetical protein	2.00
ABUW_RS16335		MacA family efflux pump subunit	1.99
ABUW_RS09085	feaR	transcriptional regulator FeaR	1.98
ABUW_RS01600		lipase secretion chaperone	1.97
ABUW_RS09485		DHA2 family efflux MFS transporter permease subunit	1.97
ABUW_RS06830		helix-turn-helix domain-containing protein	1.97
ABUW_RS08265	accB	acetyl-CoA carboxylase biotin carboxyl carrier protein	1.96
ABUW_RS10320		sigma-54-dependent Fis family transcriptional regulator	1.96
ABUW_RS10540		sulfite exporter TauE/SafE family protein	1.96
ABUW_RS03850		hypothetical protein	1.95
ABUW_RS00415	murl	glutamate racemase	1.95
ABUW_RS02790		phage tail protein	1.95
ABUW_RS19510		hypothetical protein	1.95
ABUW_RS18515		hypothetical protein	1.94
sRNA54	sRNA54	sRNA54	1.94
ABUW_RS19020	rpmH	50S ribosomal protein L34	1.92
ABUW_RS01920		ComF family protein	1.92
ABUW_RS07100		protein kinase	1.91
ABUW_RS12965		transposase	1.91
ABUW_RS10865		cell division protein ZapE	1.90
ABUW_RS19375		type IV secretion system DNA-binding domain-containing protein	1.90
ABUW_RS20110		hypothetical protein	1.89
ABUW_RS09480		HlyD family secretion protein	1.88
ABUW_RS16350		enoyl-ACP reductase	1.88
ABUW_RS09150		hypothetical protein	1.88
ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	1.83
ABUW_RS04030		patatin-like phospholipase family protein	1.83
ABUW_RS07715		2-amino-4-hydroxy-6-hydroxymethylhydropteridine diphosphokinase	1.83
ABUW_RS12090		ATP-binding cassette domain-containing protein	1.82
ABUW_RS15705		class I SAM-dependent methyltransferase	1.82

ABUW_RS10485		YARHG domain-containing protein	1.82
ABUW_RS19705		hypothetical protein	1.81
ABUW_RS14145		carbonic anhydrase	1.80
ABUW_RS11525	arsB	ACR3 family arsenite efflux transporter	1.80
ABUW_RS04360		MGMT family protein	1.80
ABUW_RS00985		AzIC family ABC transporter permease	1.80
ABUW_RS11350		glutathione S-transferase	1.79
ABUW_RS01435		type 4a pilus biogenesis protein PilO	1.78
ABUW_RS10100		LysR family transcriptional regulator	1.77
ABUW_RS19505	traC	type IV secretion system protein TraC	1.76
ABUW_RS11220	bioB	biotin synthase BioB	1.75
ABUW_RS00410		HAD family hydrolase	1.75
ABUW_RS17855	arsC	arsenate reductase (glutaredoxin)	1.75
ABUW_RS08260	accC	acetyl-CoA carboxylase biotin carboxylase subunit	1.75
ABUW_RS07445		dicarboxylate/amino acid:cation symporter	1.75
ABUW_RS11770		LysR family transcriptional regulator	1.74
ABUW_RS12055		CoA transferase	1.72
ABUW_RS11065		TetR/AcrR family transcriptional regulator	1.71
ABUW_RS06575		ferredoxin--NADP reductase	1.71
ABUW_RS07370		DUF1365 domain-containing protein	1.71
ABUW_RS18720		TetR/AcrR family transcriptional regulator	1.70
ABUW_RS08655	brnQ	branched-chain amino acid transport system II carrier protein	1.70
ABUW_RS05900		chorismate lyase	1.70
ABUW_RS18130		DMT family transporter	1.70
ABUW_RS19490		DsbC family protein	1.69
ABUW_RS11445		LysE family translocator	1.69
ABUW_RS02310		2OG-Fe(II) oxygenase	1.69
ABUW_RS18365		acyl-CoA dehydrogenase	1.69
ABUW_RS19690		hypothetical protein	1.68
ABUW_RS10465		cell envelope integrity protein TolA	1.67
ABUW_RS09000		LysR family transcriptional regulator	1.67
ABUW_RS02965		RcnB family protein	1.66
ABUW_RS07400		chalcone isomerase family protein	1.65
ABUW_RS09640		outer membrane protein transport protein	1.65
ABUW_RS15750		C39 family peptidase	1.65
ABUW_RS10480		GFA family protein	1.65
ABUW_RS10200		LysR family transcriptional regulator	1.65
ABUW_RS13415		SDR family NAD(P)-dependent oxidoreductase	1.65
ABUW_RS10490		HIT family protein	1.64
ABUW_RS06850		hypothetical protein	1.64
ABUW_RS00885	msuE	FMN reductase	1.63
ABUW_RS17425		hypothetical protein	1.63
ABUW_RS14875		beta-ketoacyl-ACP synthase II	1.62
ABUW_RS13395		metal-dependent hydrolase	1.61
ABUW_RS18135		TetR/AcrR family transcriptional regulator	1.61
ABUW_RS08975		hypothetical protein	1.61
ABUW_RS07835		type II toxin-antitoxin system RelB/DinJ family antitoxin	1.60
ABUW_RS05650		hypothetical protein	1.59
ABUW_RS01425		pilus assembly protein PilM	1.58
ABUW_RS12085		putative 2-aminoethylphosphonate ABC transporter permease subunit	1.58
ABUW_RS13565		AraC family transcriptional regulator	1.57
ABUW_RS11655	mdcH	malonate decarboxylase subunit epsilon	1.56
ABUW_RS19405		hypothetical protein	1.55
ABUW_RS13060		LysE family translocator	1.55
ABUW_RS13915		5-formyltetrahydrofolate cyclo-ligase	1.55

ABUW_RS17025	murl	glutamate racemase	1.54
ABUW_RS01300		hypothetical protein	1.54
ABUW_RS14075	lysS	lysine--tRNA ligase	1.54
ABUW_RS05375		isochorismatase	1.53
ABUW_RS04575		non-ribosomal peptide synthetase	1.52
ABUW_RS05240		deoxyribodipyrimidine photo-lyase	1.51
ABUW_RS08410		hypothetical protein	1.51
ABUW_RS10870		AraC family transcriptional regulator	1.51
ABUW_RS00635		ion channel protein Tsx	1.50
ABUW_RS02930		hypothetical protein	1.50
ABUW_RS07540	dnaB	replicative DNA helicase	1.50
ABUW_RS11215	queG	tRNA epoxyqueuosine(34) reductase QueG	1.50
ABUW_RS07775		hypothetical protein	1.49
ABUW_RS12355		aldehyde dehydrogenase (NADP(+))	1.48
ABUW_RS07405		nuclear transport factor 2 family protein	1.48
ABUW_RS12585		NAD(P)H-dependent oxidoreductase	1.48
ABUW_RS07875		UDP-2,3-diacylglycerol diphosphatase	1.48
ABUW_RS00100		glutathione S-transferase family protein	1.47
ABUW_RS03585		PaaX family transcriptional regulator	1.47
ABUW_RS08635		alpha/beta fold hydrolase	1.46
ABUW_RS09250		metal-dependent hydrolase	1.46
ABUW_RS04555		transglycosylase SLT domain-containing protein	1.43
ABUW_RS18035		DUF2938 domain-containing protein	1.42
ABUW_RS12740		exo-alpha-sialidase	1.42
ABUW_RS10470		hypothetical protein	1.42
ABUW_RS14035		LysR family transcriptional regulator	1.41
ABUW_RS19065		hypothetical protein	1.40
ABUW_RS19575		hypothetical protein	1.40
ABUW_RS08525		HAD-IA family hydrolase	1.39
ABUW_RS10910		SRPBCC family protein	1.38
ABUW_RS10410		YcgL domain-containing protein	1.38
ABUW_RS15760		chorismate-binding protein	1.37
ABUW_RS18680	ampD	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD	1.36
ABUW_RS19570		Y-family DNA polymerase	1.35
ABUW_RS02480		OmpA family protein	1.35
ABUW_RS05155		glyceraldehyde-3-phosphate dehydrogenase	1.35
ABUW_RS06585		MgtC/SapB family protein	1.35
ABUW_RS13640		amino acid permease	1.34
ABUW_RS06845		hypothetical protein	1.34
ABUW_RS07270	csuD	Csu fimbrial usher CsuD	1.33
ABUW_RS03440		Sdpl family protein	1.32
ABUW_RS19620		DIP1984 family protein	1.32
ABUW_RS12580		helix-turn-helix transcriptional regulator	1.31
ABUW_RS05510		gamma carbonic anhydrase family protein	1.28
ABUW_RS09620		NAD(P)/FAD-dependent oxidoreductase	1.28
ABUW_RS04390		hypothetical protein	1.27
ABUW_RS13530		FadR family transcriptional regulator	1.27
ABUW_RS19600		sel1 repeat family protein	1.27
ABUW_RS08460	uppS	di-trans,poly-cis-decaprenylcistransferase	1.25
ABUW_RS11060		cupin domain-containing protein	1.25
ABUW_RS16520		DUF2846 domain-containing protein	1.24
ABUW_RS05880		aminodeoxychorismate/antranilate synthase component II	1.24
ABUW_RS01665	yccS	TIGR01666 family membrane protein	1.23
ABUW_RS10575		2'-5' RNA ligase family protein	1.23
ABUW_RS01210		3'-5' exonuclease domain-containing protein 2	1.23
ABUW_RS11260		LysR family transcriptional regulator	1.22
ABUW_RS11055	maf	septum formation protein Maf	1.21

ABUW_RS17705		homoserine dehydrogenase	1.21
ABUW_RS10930		6-carboxytetrahydropterin synthase	1.21
ABUW_RS01310		efflux RND transporter periplasmic adaptor subunit	1.20
ABUW_RS09650		helix-turn-helix transcriptional regulator	1.20
ABUW_RS08135	leuE	leucine efflux protein LeuE	1.19
ABUW_RS00565		glutamate--cysteine ligase	1.18
ABUW_RS16625	thyA	thymidylate synthase	1.18
ABUW_RS09105		penicillin acylase family protein	1.17
ABUW_RS14010	ureA	urease subunit gamma	1.17
ABUW_RS18265		DUF3861 domain-containing protein	1.16
ABUW_RS10555		histidine-type phosphatase	1.15
ABUW_RS11595		hypothetical protein	1.15
ABUW_RS19550		conjugal transfer protein TraH	1.15
ABUW_RS02485		diguanylate cyclase	1.14
ABUW_RS03190		GspH/FimT family pseudopilin	1.13
ABUW_RS00875		winged helix-turn-helix transcriptional regulator	1.13
ABUW_RS19100		hypothetical protein	1.13
ABUW_RS02935		hypothetical protein	1.13
ABUW_RS08760		adenosine kinase	1.13
ABUW_RS13560		DMT family transporter	1.12
ABUW_RS08400		hypothetical protein	1.12
ABUW_RS19055		hypothetical protein	1.12
ABUW_RS09160		dihydroxy-acid dehydratase	1.12
ABUW_RS18485		DUF1003 domain-containing protein	1.12
ABUW_RS17565	gspN	type II secretion system protein N	1.11
ABUW_RS10430		HRDC domain-containing protein	1.11
ABUW_RS06825		hypothetical protein	1.11
ABUW_RS02165		hypothetical protein	1.11
ABUW_RS12670	mumR	LysR family transcriptional regulator MumR	1.10
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.10
ABUW_RS04560	greB	transcription elongation factor GreB	1.09
ABUW_RS04880	tolR	protein TolR	1.09
ABUW_RS01705		hypothetical protein	1.08
ABUW_RS11410		hypothetical protein	1.07
ABUW_RS08060		hypothetical protein	1.07
ABUW_RS17310	recN	DNA repair protein RecN	1.06
ABUW_RS17910		heteromeric transposase endonuclease subunit TnsA	1.06
ABUW_RS10545		3-deoxy-7-phosphoheptulonate synthase	1.06
ABUW_RS05705		PAS domain-containing protein	1.06
ABUW_RS12860		cysteine--tRNA ligase	1.06
ABUW_RS14670		FAD-dependent oxidoreductase	1.05
ABUW_RS15895	tilS	tRNA lysidine(34) synthetase TilS	1.05
ABUW_RS11720		LysR family transcriptional regulator	1.05
ABUW_RS07605	pgaB	poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB	1.04
ABUW_RS14880	hemJ	protoporphyrinogen oxidase HemJ	1.04
ABUW_RS07790		ion transporter	1.04
ABUW_RS08750		DUF1449 family protein	1.03
ABUW_RS01965		Rrf2 family transcriptional regulator	1.02
ABUW_RS15480		PhzF family isomerase	1.02
ABUW_RS00930		GGDEF domain-containing protein	1.02
ABUW_RS07840		pseudouridylate synthase	1.02
ABUW_RS02555		YajQ family cyclic di-GMP-binding protein	1.01
ABUW_RS05870		TonB-dependent receptor	1.01
ABUW_RS12590	uca	urea carboxylase	1.01
ABUW_RS02220		YcxB family protein	1.00
ABUW_RS09660		replication initiation factor domain-containing protein	1.00

ABUW_RS13545	gudD	glucarate dehydratase	1.00

Gene	Gene Name	Function	$\Delta adeS$ LSP vs WT LSP log2FC
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	-7.23
ABUW_RS15580	tcuA	FAD-dependent tricarballoylate dehydrogenase TcuA	-6.79
ABUW_RS11870		hypothetical protein	-6.71
ABUW_RS15585	tcuB	tricarballoylate utilization 4Fe-4S protein TcuB	-6.71
ABUW_RS11875		hypothetical protein	-6.54
ABUW_RS08050		hypothetical protein	-5.59
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-5.19
ABUW_RS10585		acetyltransferase	-5.03
ABUW_RS10640		siderophore biosynthesis protein	-4.85
ABUW_RS15565		MFS transporter	-4.75
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-4.67
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-4.67
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-4.51
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-4.51
ABUW_RS05750	basC	putative histamine N-monooxygenase	-4.46
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-4.41
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-4.32
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-4.31
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-4.29
ABUW_RS07500		hypothetical protein	-4.27
ABUW_RS11855	katE	catalase HPII	-4.27
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-4.26
ABUW_RS18440		RidA family protein	-4.24
ABUW_RS11860		iron-containing redox enzyme family protein	-4.08
ABUW_RS17925		aldolase	-4.08
ABUW_RS16200		hypothetical protein	-3.88
ABUW_RS18445	alr	alanine racemase	-3.84
ABUW_RS13040		hypothetical protein	-3.84
ABUW_RS13010		DUF4142 domain-containing protein	-3.83
ABUW_RS20145		hypothetical protein	-3.81
ABUW_RS11825		LysE family translocator	-3.77
ABUW_RS03995		tRNA-Arg	-3.73
ABUW_RS14485		DUF560 domain-containing protein	-3.68
ABUW_RS15165		trehalose-6-phosphate synthase	-3.65
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-3.63
ABUW_RS01050		MFS transporter	-3.61
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-3.57
ABUW_RS18450		D-amino acid dehydrogenase	-3.50
ABUW_RS15570		substrate-binding domain-containing protein	-3.50
ABUW_RS14475		biliverdin-producing heme oxygenase	-3.48
ABUW_RS20235		hypothetical protein	-3.39
ABUW_RS01495	pilA	pilin	-3.32
ABUW_RS00895		hypothetical protein	-3.26
ABUW_RS05730	bauC	ferric acinetobactin ABC transporter permease subunit BauC	-3.26
ABUW_RS06610		hemin uptake protein HemP	-3.23
ABUW_RS10525		hypothetical protein	-3.23
ABUW_RS12975		hypothetical protein	-3.17
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-3.15
ABUW_RS11850		glucose 1-dehydrogenase	-3.15
ABUW_RS12725		hypothetical protein	-3.11
ABUW_RS15330		mechanosensitive ion channel	-3.10

ABUW_RS07960		spore coat protein U domain-containing protein	-3.10
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-3.09
ABUW_RS07155		PIG-L family deacetylase	-3.09
ABUW_RS15335		hypothetical protein	-3.07
ABUW_RS07170		NirD/YgiW/YdeI family stress tolerance protein	-2.90
ABUW_RS07145		DUF2171 domain-containing protein	-2.84
ABUW_RS14470		YbaN family protein	-2.83
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-2.82
ABUW_RS09210		type 1 glutamine amidotransferase domain-containing protein	-2.81
ABUW_RS07160		class I SAM-dependent methyltransferase	-2.79
ABUW_RS00260		DUF1328 domain-containing protein	-2.76
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-2.75
ABUW_RS08580		SOS response-associated peptidase family protein	-2.71
ABUW_RS10010		hypothetical protein	-2.70
ABUW_RS15160	otsB	trehalose-phosphatase	-2.70
ABUW_RS14480		energy transducer TonB	-2.64
ABUW_RS05725	bauD	ferric acinetobactin ABC transporter permease subunit BauD	-2.63
sRNA65	sRNA65	sRNA65	-2.54
ABUW_RS20475		hypothetical protein	-2.48
ABUW_RS20295		hypothetical protein	-2.48
newcandsRNA1	newcandsRNA1	newcandsRNA1	-2.47
ABUW_RS10025		hypothetical protein	-2.46
ABUW_RS10530		PepSY domain-containing protein	-2.42
ABUW_RS11885		hypothetical protein	-2.37
ABUW_RS01005	gabT	4-aminobutyrate--2-oxoglutarate transaminase	-2.28
ABUW_RS10475		hypothetical protein	-2.27
ABUW_RS01160	aqpZ	aquaporin Z	-2.25
ABUW_RS01140		hypothetical protein	-2.25
ABUW_RS11270		hypothetical protein	-2.23
ABUW_RS17400		serine hydrolase family protein	-2.20
ABUW_RS13005		hypothetical protein	-2.19
ABUW_RS16440		phosphatase PAP2 family protein	-2.17
ABUW_RS20180		hypothetical protein	-2.15
ABUW_RS00485		hypothetical protein	-2.14
sRNA104	sRNA104	sRNA104	-2.12
ABUW_RS16500		acetate kinase	-2.12
ABUW_RS20200		hypothetical protein	-2.10
ABUW_RS01510		bacterioferritin-associated ferredoxin	-2.09
ABUW_RS11935		methylcrotonoyl-CoA carboxylase	-2.07
ABUW_RS03180		VOC family protein	-2.07
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-2.07
ABUW_RS16505	pta	phosphate acetyltransferase	-2.04
ABUW_RS10070		transcriptional repressor	-2.04
ABUW_RS17460		hypothetical protein	-2.04
ABUW_RS05710	bauF	acinetobactin utilization protein BauF	-2.02
ABUW_RS07965		molecular chaperone	-2.02
ABUW_RS15280		hypothetical protein	-2.00
sRNA13	sRNA13	sRNA13	-1.99
ABUW_RS01760		hypothetical protein	-1.98
ABUW_RS11140		hypothetical protein	-1.96
ABUW_RS14395		hypothetical protein	-1.94
ABUW_RS16445		glycosyltransferase family 1 protein	-1.94
ABUW_RS09185		alpha/beta hydrolase	-1.91
ABUW_RS08045		hypothetical protein	-1.90
ABUW_RS07950		hypothetical protein	-1.89
ABUW_RS01615		hemerythrin domain-containing protein	-1.87

ABUW_RS07620		hypothetical protein	-1.87
ABUW_RS11945		acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	-1.86
ABUW_RS16845		DUF2061 domain-containing protein	-1.85
ABUW_RS11940		enoyl-CoA hydratase/isomerase family protein	-1.85
ABUW_RS18740		YciK family oxidoreductase	-1.84
ABUW_RS00115		methionine/alanine import family NSS transporter small subunit	-1.83
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-1.81
ABUW_RS01215		DUF805 domain-containing protein	-1.80
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	-1.77
ABUW_RS08390		hypothetical protein	-1.75
ABUW_RS00995		amino acid permease	-1.75
ABUW_RS16840	leuC	3-isopropylmalate dehydratase large subunit	-1.75
ABUW_RS20155		hypothetical protein	-1.72
ABUW_RS15290		NF038215 family lipoprotein	-1.71
ABUW_RS18045		transglycosylase SLT domain-containing protein	-1.70
ABUW_RS11625	cydB	cytochrome d ubiquinol oxidase subunit II	-1.70
ABUW_RS10075		isochorismatase family protein	-1.69
ABUW_RS16835	leuD	3-isopropylmalate dehydratase small subunit	-1.68
ABUW_RS20115		hypothetical protein	-1.67
ABUW_RS14505		sigma-70 family RNA polymerase sigma factor	-1.66
ABUW_RS08690		DUF2750 domain-containing protein	-1.63
ABUW_RS13250		OmpA family protein	-1.61
ABUW_RS17105		MerR family transcriptional regulator	-1.61
ABUW_RS17930		dihydrodipicolinate synthase family protein	-1.60
ABUW_RS07425		sorbose dehydrogenase family protein	-1.59
ABUW_RS16255	acnA	aconitate hydratase AcnA	-1.59
ABUW_RS16155		heavy metal translocating P-type ATPase	-1.57
ABUW_RS08385	fumC	class II fumarate hydratase	-1.57
ABUW_RS15260		LysE family transporter	-1.55
ABUW_RS20505		hypothetical protein	-1.54
ABUW_RS06905		hypothetical protein	-1.54
ABUW_RS16850		LysR family transcriptional regulator	-1.54
ABUW_RS02655		hypothetical protein	-1.52
ABUW_RS11515		chromate transporter	-1.51
ABUW_RS05715	basA	acinetobactin non-ribosomal peptide synthetase subunit BasA	-1.48
ABUW_RS07150		hypothetical protein	-1.48
ABUW_RS07430		GNAT family N-acetyltransferase	-1.47
ABUW_RS10130		flavin reductase family protein	-1.47
ABUW_RS02650		hypothetical protein	-1.46
ABUW_RS07855	miaA	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	-1.45
ABUW_RS08440		PAS domain-containing protein	-1.45
ABUW_RS01670		superoxide dismutase family protein	-1.44
ABUW_RS00195		START domain-containing protein	-1.43
ABUW_RS01765		hypothetical protein	-1.42
ABUW_RS07065		M48 family metalloprotease	-1.42
ABUW_RS12915		fibronectin type III domain-containing protein	-1.42
ABUW_RS18470		nuclear transport factor 2 family protein	-1.42
ABUW_RS00685		alpha/beta hydrolase	-1.41
ABUW_RS16950		DMT family transporter	-1.41
ABUW_RS15550		amidohydrolase	-1.41
ABUW_RS15880	polA	DNA polymerase I	-1.40
ABUW_RS07860	hfq	RNA chaperone Hfq	-1.39
ABUW_RS03500		DJ-1/Pfpl family protein	-1.39
ABUW_RS06670		hypothetical protein	-1.39
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.39
ABUW_RS07585		RDD family protein	-1.39
ABUW_RS16715		HdeD family acid-resistance protein	-1.37

ABUW_RS01975		DUF853 domain-containing protein	-1.36
ABUW_RS09585		hypothetical protein	-1.36
ABUW_RS01020		hydrolase	-1.35
ABUW_RS03310		YegP family protein	-1.35
ABUW_RS14850	tuf	elongation factor Tu	-1.35
ABUW_RS10890		DUF1049 domain-containing protein	-1.35
ABUW_RS14210		transketolase	-1.34
ABUW_RS00515		alpha/beta fold hydrolase	-1.34
ABUW_RS15855		organic hydroperoxide resistance protein	-1.33
ABUW_RS13980		HupE/UreJ family protein	-1.33
ABUW_RS11425		tautomerase family protein	-1.33
ABUW_RS16420	pilW	type IV pilus biogenesis/stability protein PilW	-1.32
ABUW_RS05220		hypothetical protein	-1.32
ABUW_RS17145		hypothetical protein	-1.31
ABUW_RS01930		NAD(P)H-binding protein	-1.29
ABUW_RS02665	ssb	single-stranded DNA-binding protein	-1.28
ABUW_RS00690		DUF2147 domain-containing protein	-1.28
ABUW_RS04285	odhB	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase	-1.28
ABUW_RS08380		SDR family NAD(P)-dependent oxidoreductase	-1.28
ABUW_RS14025		copper resistance protein NlpE	-1.25
ABUW_RS16080	rsfS	ribosome silencing factor	-1.25
ABUW_RS00545		pyridoxal phosphate-dependent aminotransferase	-1.24
ABUW_RS11200		helix-turn-helix transcriptional regulator	-1.23
ABUW_RS18475		ribonuclease E inhibitor RraB	-1.23
ABUW_RS12465	icmH	type IVB secretion system protein IcmH/DotU	-1.22
ABUW_RS08405		D-amino acid dehydrogenase	-1.22
ABUW_RS00015	recF	DNA replication/repair protein RecF	-1.21
ABUW_RS15615	add	adenosine deaminase	-1.21
ABUW_RS13680		RHS repeat protein	-1.20
ABUW_RS06710	rpoH	RNA polymerase sigma factor RpoH	-1.20
ABUW_RS14675		TIGR01777 family oxidoreductase	-1.18
ABUW_RS14760		phosphomannomutase/phosphoglucomutase	-1.17
ABUW_RS18865		hypothetical protein	-1.17
ABUW_RS02765	oxa-23	carbapenem-hydrolyzing class D beta-lactamase OXA-23	-1.16
ABUW_RS02660		3'-5' exonuclease	-1.16
ABUW_RS11615		hypothetical protein	-1.15
ABUW_RS08520		RNA-binding protein	-1.15
ABUW_RS08700		hypothetical protein	-1.15
ABUW_RS12605		glutathione-dependent formaldehyde dehydrogenase	-1.15
ABUW_RS18885	grpE	nucleotide exchange factor GrpE	-1.14
ABUW_RS08830		YnfA family protein	-1.13
ABUW_RS09080		flavin reductase family protein	-1.12
ABUW_RS11160		OsmC family protein	-1.11
ABUW_RS15660		cation transporter	-1.11
ABUW_RS16425	rlmN	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN	-1.10
ABUW_RS17100		DnaJ domain-containing protein	-1.10
ABUW_RS05805		murein L,D-transpeptidase	-1.09
ABUW_RS16680	rpmG	50S ribosomal protein L33	-1.09
ABUW_RS03550		wax ester/triacylglycerol synthase family O-acyltransferase	-1.09
ABUW_RS13990		urease accessory protein	-1.09
ABUW_RS00025	cybC	cytochrome b562	-1.08
ABUW_RS12460		hypothetical protein	-1.07
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.07
ABUW_RS17220		Na ⁺ /H ⁺ antiporter subunit G	-1.07
ABUW_RS08435	glnG	nitrogen regulation protein NR(I)	-1.06
ABUW_RS04630		FdhF/YdeP family oxidoreductase	-1.06

ABUW_RS08425	argF	ornithine carbamoyltransferase	-1.05
ABUW_RS06645		dicarboxylate/amino acid:cation symporter	-1.03
ABUW_RS14030		isocitrate lyase	-1.02
ABUW_RS10275	chrA	chromate efflux transporter	-1.00
ABUW_RS00525	phoB	phosphate regulon transcriptional regulator PhoB	-1.00
ABUW_RS05890		peptide MFS transporter	-1.00

Table A5. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta baeR$ MEP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta baeR$ MEP vs WT MEP log2FC
newcandsRNA1	newcandsRNA1	newcandsRNA1	4.05
sRNA2	sRNA2	sRNA2	3.47
ABUW_RS11230		hypothetical protein	3.47
ABUW_RS10220		aspartate ammonia-lyase	3.30
ABUW_RS01510		bacterioferritin-associated ferredoxin	2.91
ABUW_RS16540		TonB-dependent siderophore receptor	2.69
ABUW_RS05285		hypothetical protein	2.66
ABUW_RS10595		PepSY domain-containing protein	2.52
ABUW_RS11620		cytochrome ubiquinol oxidase subunit I	2.41
ABUW_RS20540		hypothetical protein	2.40
ABUW_RS10590		hypothetical protein	2.36
ABUW_RS11625	cydB	cytochrome d ubiquinol oxidase subunit II	2.35
ABUW_RS10070		transcriptional repressor	2.33
ABUW_RS10170		hypothetical protein	2.32
ABUW_RS10600		hypothetical protein	2.31
ABUW_RS20550		hypothetical protein	2.29
ABUW_RS10530		PepSY domain-containing protein	2.27
ABUW_RS09650		helix-turn-helix transcriptional regulator	2.22
sRNA72	sRNA72	sRNA72	2.20
ABUW_RS06655		alpha/beta hydrolase	2.14
ABUW_RS18515		hypothetical protein	2.11
ABUW_RS18095		hypothetical protein	2.10
ABUW_RS08055		hypothetical protein	2.10
ABUW_RS03435		PepSY domain-containing protein	2.09
ABUW_RS11440	dapC	succinylidiaminopimelate transaminase	2.08
ABUW_RS07805		DUF4198 domain-containing protein	2.05
ABUW_RS10535		hypothetical protein	2.05
ABUW_RS03465		alanine:cation symporter family protein	2.04
ABUW_RS14110		SPOR domain-containing protein	2.00
ABUW_RS09535		hypothetical protein	1.98
ABUW_RS18895		matrixin family metalloprotease	1.97
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	1.97
ABUW_RS10215		hypothetical protein	1.92
ABUW_RS13405		TetR/AcrR family transcriptional regulator	1.90
ABUW_RS00200		MFS transporter	1.90
ABUW_RS11255		hypothetical protein	1.90
ABUW_RS01095		helix-turn-helix transcriptional regulator	1.89
ABUW_RS11290		integrase family protein	1.88
ABUW_RS07145		DUF2171 domain-containing protein	1.85
ABUW_RS14160		TonB-dependent siderophore receptor	1.83
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	1.82
ABUW_RS16655		energy transducer TonB	1.82
ABUW_RS15855		organic hydroperoxide resistance protein	1.82
ABUW_RS08975		hypothetical protein	1.82

ABUW_RS00205	dkgB	2,5-didehydrogluconate reductase DkgB	1.81
ABUW_RS07020		hypothetical protein	1.81
ABUW_RS17840		cation transporter	1.81
ABUW_RS03430		YdcF family protein	1.81
ABUW_RS01120		AraC family transcriptional regulator	1.81
ABUW_RS09670		hypothetical protein	1.80
ABUW_RS12775		Lrp/AsnC family transcriptional regulator	1.80
ABUW_RS12885		hypothetical protein	1.79
ABUW_RS08670		hypothetical protein	1.79
ABUW_RS08605		hypothetical protein	1.77
ABUW_RS08035		TonB-dependent receptor	1.77
ABUW_RS15270		5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	1.77
ABUW_RS03295		alkylphosphonate utilization protein	1.76
ABUW_RS13745		TonB-dependent receptor	1.76
ABUW_RS08065		N-acetyltransferase	1.76
ABUW_RS18720		TetR/AcrR family transcriptional regulator	1.75
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	1.75
ABUW_RS19625		hypothetical protein	1.74
ABUW_RS05410		DUF4442 domain-containing protein	1.74
ABUW_RS06255		hypothetical protein	1.72
ABUW_RS08395		hypothetical protein	1.72
ABUW_RS00790		TonB-dependent siderophore receptor	1.72
ABUW_RS08110		RDD family protein	1.70
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	1.70
ABUW_RS08060		hypothetical protein	1.69
ABUW_RS02955		phospholipase D family protein	1.68
ABUW_RS10470		hypothetical protein	1.67
ABUW_RS17570		H-NS histone family protein	1.67
ABUW_RS19865		hypothetical protein	1.67
ABUW_RS18030		helix-turn-helix domain-containing protein	1.67
ABUW_RS09960		hypothetical protein	1.66
ABUW_RS13765		hypothetical protein	1.66
ABUW_RS12405		DUF333 domain-containing protein	1.65
ABUW_RS13865		MerR family transcriptional regulator	1.65
ABUW_RS16845		DUF2061 domain-containing protein	1.65
ABUW_RS10650		hypothetical protein	1.65
ABUW_RS01655		hypothetical protein	1.64
ABUW_RS08025		hypothetical protein	1.64
ABUW_RS00585		hypothetical protein	1.64
ABUW_RS03110		hemolysin III family protein	1.64
ABUW_RS18505		DUF4844 domain-containing protein	1.63
ABUW_RS18085		TetR family transcriptional regulator	1.62
ABUW_RS11085		DUF2058 domain-containing protein	1.62
ABUW_RS20205		hypothetical protein	1.61
ABUW_RS07435		MFS transporter	1.60
ABUW_RS09205		MerR family transcriptional regulator	1.60
ABUW_RS11410		hypothetical protein	1.60
ABUW_RS16645		biopolymer transporter ExbD	1.59
ABUW_RS09345		hypothetical protein	1.56
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.56
ABUW_RS17685		ferrous iron transporter B	1.55
ABUW_RS00710		TonB-dependent siderophore receptor	1.55
ABUW_RS19600		sel1 repeat family protein	1.54
ABUW_RS10695		hypothetical protein	1.54
ABUW_RS11555		LysR family transcriptional regulator	1.54

ABUW_RS08400		hypothetical protein	1.53
ABUW_RS12890		hypothetical protein	1.53
ABUW_RS08715		nitroreductase family protein	1.53
ABUW_RS08615		PEGA domain-containing protein	1.52
ABUW_RS09540		endonuclease/exonuclease/phosphatase family protein	1.51
ABUW_RS13910		hypothetical protein	1.51
ABUW_RS02555		YajQ family cyclic di-GMP-binding protein	1.50
ABUW_RS07440		TetR/AcrR family transcriptional regulator	1.50
ABUW_RS06825		hypothetical protein	1.49
ABUW_RS06475		DUF4760 domain-containing protein	1.49
ABUW_RS09665		hypothetical protein	1.49
ABUW_RS11155		polyisoprenoid-binding protein	1.49
ABUW_RS08550		Lrp/AsnC family transcriptional regulator	1.49
ABUW_RS09645		hypothetical protein	1.48
ABUW_RS09695		hypothetical protein	1.48
ABUW_RS08765		TonB-dependent siderophore receptor	1.48
ABUW_RS17865		arsenate reductase ArsC	1.47
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	1.46
ABUW_RS07355		lipocalin family protein	1.46
ABUW_RS08545		GNAT family N-acetyltransferase	1.46
ABUW_RS08645		hypothetical protein	1.45
ABUW_RS20110		hypothetical protein	1.45
ABUW_RS07880		peptidyl-prolyl cis-trans isomerase	1.44
ABUW_RS08205		lactonase family protein	1.44
ABUW_RS17690		ferrous iron transport protein A	1.43
ABUW_RS14145		carbonic anhydrase	1.43
ABUW_RS10645	ybaK	Cys-tRNA(Pro) deacylase	1.43
ABUW_RS13585		hypothetical protein	1.43
ABUW_RS18235		NAD-dependent malic enzyme	1.43
ABUW_RS10200		LysR family transcriptional regulator	1.42
ABUW_RS07225		SRPBCC family protein	1.42
ABUW_RS06830		helix-turn-helix domain-containing protein	1.42
ABUW_RS10605	bfnH	TonB-dependent receptor	1.42
ABUW_RS09410		TetR/AcrR family transcriptional regulator	1.41
ABUW_RS05680		hypothetical protein	1.41
ABUW_RS09660		replication initiation factor domain-containing protein	1.41
ABUW_RS01785		DUF262 domain-containing protein	1.41
ABUW_RS13100		exodeoxyribonuclease VII small subunit	1.40
ABUW_RS10320		sigma-54-dependent Fis family transcriptional regulator	1.40
ABUW_RS03005		acyl-CoA desaturase	1.40
ABUW_RS12990		hypothetical protein	1.40
ABUW_RS09625		TetR/AcrR family transcriptional regulator	1.39
ABUW_RS11120		Lrp/AsnC ligand binding domain-containing protein	1.39
ABUW_RS06275		hypothetical protein	1.39
ABUW_RS19620		DIP1984 family protein	1.39
ABUW_RS11320		Lrp/AsnC family transcriptional regulator	1.39
ABUW_RS10430		HRDC domain-containing protein	1.38
ABUW_RS11265		DMT family transporter	1.38
ABUW_RS08310		NTP transferase domain-containing protein	1.37
ABUW_RS08255		hypothetical protein	1.37
ABUW_RS08420		protein tyrosine phosphatase family protein	1.36
ABUW_RS19385		hypothetical protein	1.36
ABUW_RS15085	acpP	acyl carrier protein	1.36
ABUW_RS01530	gmk	guanylate kinase	1.35

ABUW_RS18140		MFS transporter	1.35
ABUW_RS08610		MarR family transcriptional regulator	1.34
ABUW_RS01705		hypothetical protein	1.34
ABUW_RS03915		Arc family DNA-binding protein	1.34
ABUW_RS13870		hypothetical protein	1.34
ABUW_RS09470		LuxR family transcriptional regulator	1.34
ABUW_RS15795		RNA polymerase factor sigma-54	1.34
ABUW_RS16770	gltP	glutamate/aspartate:proton symporter GltP	1.33
ABUW_RS13860		cation transporter	1.33
ABUW_RS18975	hpt	hypoxanthine phosphoribosyltransferase	1.33
ABUW_RS09690		zonular occludens toxin	1.33
ABUW_RS11315		YebC/PmpR family DNA-binding transcriptional regulator	1.33
sRNA96	sRNA96	sRNA96	1.33
ABUW_RS11615		hypothetical protein	1.33
ABUW_RS17900		TniB family NTP-binding protein	1.32
ABUW_RS02480		OmpA family protein	1.31
ABUW_RS06250		hypothetical protein	1.31
ABUW_RS07775		hypothetical protein	1.31
ABUW_RS08710	ftsY	signal recognition particle-docking protein FtsY	1.30
ABUW_RS11820		Lrp/AsnC family transcriptional regulator	1.30
ABUW_RS05670		type II toxin-antitoxin system Phd/YefM family antitoxin	1.29
sRNA42	sRNA42	sRNA42	1.29
ABUW_RS05255		D-alanyl-D-alanine carboxypeptidase PBP6B	1.29
ABUW_RS00590		hypothetical protein	1.29
ABUW_RS17410		hypothetical protein	1.29
ABUW_RS02530		TIGR01244 family phosphatase	1.29
ABUW_RS10685		HU family DNA-binding protein	1.28
ABUW_RS15860	gspE	type II secretion system ATPase GspE	1.28
ABUW_RS07200	gltS	sodium/glutamate symporter	1.28
ABUW_RS08575		SulP family inorganic anion transporter	1.28
ABUW_RS08240		TetR/AcrR family transcriptional regulator	1.28
ABUW_RS05240		deoxyribodipyrimidine photo-lyase	1.27
ABUW_RS12585		NAD(P)H-dependent oxidoreductase	1.27
sRNA69	sRNA69	sRNA69	1.26
ABUW_RS11115	putP	sodium/proline symporter PutP	1.26
ABUW_RS10300		hypothetical protein	1.26
ABUW_RS11160		OsmC family protein	1.25
ABUW_RS12700		hypothetical protein	1.25
ABUW_RS17400		serine hydrolase family protein	1.25
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	1.25
ABUW_RS17985		TerC family protein	1.24
ABUW_RS17300		pyrimidine/purine nucleoside phosphorylase	1.24
ABUW_RS19230		hypothetical protein	1.24
ABUW_RS10870		AraC family transcriptional regulator	1.23
ABUW_RS19995		hypothetical protein	1.23
ABUW_RS17910		heteromeric transposase endonuclease subunit TnsA	1.23
ABUW_RS07625		LLM class flavin-dependent oxidoreductase	1.22
ABUW_RS01325		hypothetical protein	1.22
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	1.22
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	1.22
ABUW_RS01290		hypothetical protein	1.21
ABUW_RS02590		bestrophin	1.21
ABUW_RS10465		cell envelope integrity protein TolA	1.20
ABUW_RS19375		type IV secretion system DNA-binding domain-containing protein	1.20

ABUW_RS02370		TetR family transcriptional regulator	1.20
ABUW_RS11405		hypothetical protein	1.20
ABUW_RS05040		Do family serine endopeptidase	1.20
ABUW_RS00695		arsenate reductase	1.19
ABUW_RS07295	proP	glycine betaine/L-proline transporter ProP	1.19
ABUW_RS04090		hypothetical protein	1.19
ABUW_RS20495		hypothetical protein	1.18
ABUW_RS04235		hypothetical protein	1.18
ABUW_RS06015		MFS transporter	1.18
ABUW_RS14090		rubredoxin	1.17
ABUW_RS10420		hypothetical protein	1.17
ABUW_RS04465		MFS transporter	1.16
ABUW_RS08415	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.16
ABUW_RS13020		helix-turn-helix transcriptional regulator	1.16
ABUW_RS03980		hypothetical protein	1.16
ABUW_RS03235		gamma-glutamylcyclotransferase	1.16
ABUW_RS14965	smpB	SsrA-binding protein SmpB	1.16
ABUW_RS11180		hypothetical protein	1.16
ABUW_RS14375		FKBP-type peptidyl-prolyl cis-trans isomerase	1.16
ABUW_RS11285		LysR family transcriptional regulator	1.15
ABUW_RS03850		hypothetical protein	1.15
ABUW_RS05890		peptide MFS transporter	1.14
ABUW_RS02550		DUF4442 domain-containing protein	1.14
ABUW_RS12205		LysR family transcriptional regulator	1.14
ABUW_RS05555	gloA	lactoylglutathione lyase	1.14
ABUW_RS10675		AraC family transcriptional regulator	1.14
ABUW_RS04240		YecA family protein	1.14
ABUW_RS11140		hypothetical protein	1.13
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	1.13
ABUW_RS07470		hypothetical protein	1.13
ABUW_RS09595	adeR	efflux system response regulator transcription factor AdeR	1.12
ABUW_RS10680		SurA N-terminal domain-containing protein	1.12
ABUW_RS16880	hcaR	DNA-binding transcriptional regulator HcaR	1.12
ABUW_RS16660	purU	formyltetrahydrofolate deformylase	1.11
ABUW_RS14025		copper resistance protein NlpE	1.11
ABUW_RS10935	gspK	type II secretion system minor pseudopilin GspK	1.11
ABUW_RS07890		glutamine amidotransferase	1.10
ABUW_RS14170		rhomboid family intramembrane serine protease	1.09
ABUW_RS01410		hypothetical protein	1.09
ABUW_RS08705		hypothetical protein	1.09
ABUW_RS10885	pyrF	orotidine-5'-phosphate decarboxylase	1.09
ABUW_RS13245		DUF2520 domain-containing protein	1.09
ABUW_RS05520		hypothetical protein	1.08
ABUW_RS14810	rhtC	threonine export protein RhtC	1.08
ABUW_RS08505		tetratricopeptide repeat protein	1.08
ABUW_RS11010	rsmG	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	1.08
ABUW_RS10750		hypothetical protein	1.07
ABUW_RS12100		UTRA domain-containing protein	1.06
ABUW_RS01270		bifunctional SulP family inorganic anion transporter/carbonic anhydrase	1.06
ABUW_RS17905		DDE-type integrase/transposase/recombinase	1.06
ABUW_RS18135		TetR/AcrR family transcriptional regulator	1.06
ABUW_RS05940		superoxide dismutase	1.06
ABUW_RS02260		hypothetical protein	1.06

ABUW_RS08650		heme-binding protein	1.06
ABUW_RS11220	bioB	biotin synthase BioB	1.06
ABUW_RS17815		hypothetical protein	1.05
ABUW_RS09000		LysR family transcriptional regulator	1.05
ABUW_RS16350		enoyl-ACP reductase	1.05
ABUW_RS18460		DUF1624 domain-containing protein	1.04
ABUW_RS05390		AI-2E family transporter	1.04
ABUW_RS17695	xerD	site-specific tyrosine recombinase XerD	1.04
ABUW_RS09145		LysR family transcriptional regulator	1.04
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.04
ABUW_RS12935		hypothetical protein	1.04
ABUW_RS12390		GntR family transcriptional regulator	1.03
ABUW_RS10775	rpsT	30S ribosomal protein S20	1.03
ABUW_RS10205		LysR family transcriptional regulator	1.03
ABUW_RS07350		heavy metal sensor histidine kinase	1.03
ABUW_RS08565		alpha/beta hydrolase	1.03
ABUW_RS07215		aldo/keto reductase	1.02
ABUW_RS04550		SCP2 sterol-binding domain-containing protein	1.02
ABUW_RS03010		META domain-containing protein	1.01
ABUW_RS14720	fur	ferric iron uptake transcriptional regulator	1.01
ABUW_RS18295		DedA family protein	1.00
ABUW_RS00105		TIGR04219 family outer membrane beta-barrel protein	1.00
ABUW_RS14680		ABZJ_00895 family protein	1.00
ABUW_RS04200		flavodoxin family protein	1.00

Gene	Gene Name	Function	Δ baeR MEP vs WT MEP log2FC
ABUW_RS02995		response regulator	-14.24
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	-7.74
ABUW_RS10115	antC	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.77
ABUW_RS10110	antB	anthranilate 1,2-dioxygenase small subunit	-5.47
ABUW_RS01005	gabT	4-aminobutyrate--2-oxoglutarate transaminase	-4.21
ABUW_RS00380	hutU	urocanate hydratase	-4.16
ABUW_RS01010		NAD-dependent succinate-semialdehyde dehydrogenase	-3.46
ABUW_RS09115	pcaF	3-oxoadipyl-CoA thiolase	-3.04
ABUW_RS12300		enoyl-CoA hydratase/isomerase family protein	-2.89
ABUW_RS15525		DUF1852 domain-containing protein	-2.86
ABUW_RS17065		hypothetical protein	-2.85
ABUW_RS12295		2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	-2.85
ABUW_RS15515		flavin reductase	-2.84
ABUW_RS15520		methionine synthase	-2.82
ABUW_RS13600		aspartate aminotransferase family protein	-2.71
ABUW_RS00385	hutH	histidine ammonia-lyase	-2.65
sRNA6	sRNA6	sRNA6	-2.61
ABUW_RS18550	dld	D-lactate dehydrogenase	-2.61
ABUW_RS00340	maiA	maleylacetoacetate isomerase	-2.53
ABUW_RS01870		DEAD/DEAH box helicase	-2.50
ABUW_RS00995		amino acid permease	-2.49
ABUW_RS18555	lldD	FMN-dependent L-lactate dehydrogenase LldD	-2.48
ABUW_RS00335		VOC family protein	-2.45
ABUW_RS11940		enoyl-CoA hydratase/isomerase family protein	-2.42
ABUW_RS13595	astA	arginine N-succinyltransferase	-2.42
ABUW_RS03655		hypothetical protein	-2.40
ABUW_RS02785		phage tail sheath protein	-2.40
ABUW_RS10350		alpha-ketoacid dehydrogenase subunit beta	-2.39

ABUW_RS07135		CoA-acylating methylmalonate-semialdehyde dehydrogenase	-2.39
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-2.36
ABUW_RS13445		alpha/beta hydrolase	-2.36
ABUW_RS12310	paaJ	phenylacetate-CoA oxygenase subunit PaaJ	-2.34
ABUW_RS11935		methylcrotonoyl-CoA carboxylase	-2.29
ABUW_RS00390		amino acid permease	-2.27
ABUW_RS09970		molecular chaperone	-2.26
ABUW_RS18560	lIdR	transcriptional regulator LIdR	-2.26
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-2.16
ABUW_RS09500		TolC family protein	-2.14
ABUW_RS00345	fahA	fumarylacetoacetase	-2.12
ABUW_RS02860		GPO family capsid scaffolding protein	-2.11
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-2.11
ABUW_RS09975		fimbrial biogenesis outer membrane usher protein	-2.11
ABUW_RS00395		imidazolonepropionase	-2.11
ABUW_RS11760		cysteine desulfurase	-2.09
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-2.07
ABUW_RS13330		ATP phosphoribosyltransferase regulatory subunit	-2.05
sRNA88	sRNA88	sRNA88	-2.04
ABUW_RS07130		aspartate aminotransferase family protein	-2.03
ABUW_RS10345		2-oxo acid dehydrogenase subunit E2	-2.02
ABUW_RS05230		hypothetical protein	-1.97
ABUW_RS00800		YkgJ family cysteine cluster protein	-1.96
ABUW_RS11755		hypothetical protein	-1.95
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	-1.93
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	-1.93
ABUW_RS14430	betA	choline dehydrogenase	-1.92
ABUW_RS00370	hutC	histidine utilization repressor	-1.92
ABUW_RS11945		acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	-1.91
ABUW_RS06865		hypothetical protein	-1.89
ABUW_RS12305	paaK	phenylacetate-CoA oxygenase/reductase subunit PaaK	-1.87
ABUW_RS00400	hutG	formimidoylglutamase	-1.86
ABUW_RS08725		cyd operon YbgE family protein	-1.84
ABUW_RS18565	lIdP	L-lactate permease	-1.82
ABUW_RS15175	bfr	bacterioferritin	-1.82
ABUW_RS18945		TerC family protein	-1.82
ABUW_RS09505		hypothetical protein	-1.82
ABUW_RS16505	pta	phosphate acetyltransferase	-1.81
ABUW_RS14030		isocitrate lyase	-1.81
ABUW_RS12290		3-hydroxyacyl-CoA dehydrogenase	-1.79
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-1.77
ABUW_RS13115		hypothetical protein	-1.76
ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-1.74
ABUW_RS16890		glutathione S-transferase family protein	-1.71
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	-1.71
ABUW_RS19270		trimethoprim-resistant dihydrofolate reductase DfrA7	-1.71
ABUW_RS12520	tssE	type VI secretion system baseplate subunit TssE	-1.70
ABUW_RS07630		hypothetical protein	-1.70
ABUW_RS16440		phosphatase PAP2 family protein	-1.69
ABUW_RS16915		Rne/Rng family ribonuclease	-1.69
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	-1.68
ABUW_RS00405		DUF885 domain-containing protein	-1.68
ABUW_RS13465		aromatic ring-hydroxylating dioxygenase subunit alpha	-1.68
ABUW_RS00375		HutD family protein	-1.67
ABUW_RS12320	paaB	1,2-phenylacetyl-CoA epoxidase subunit B	-1.66

ABUW_RS13435		NAD(P)/FAD-dependent oxidoreductase	-1.66
ABUW_RS09485		DHA2 family efflux MFS transporter permease subunit	-1.64
ABUW_RS07900		ethanolamine ammonia-lyase subunit EutB	-1.62
ABUW_RS19265		quaternary ammonium compound efflux SMR transporter QacE delta 1	-1.60
ABUW_RS02855		phage major capsid protein, P2 family	-1.59
ABUW_RS11670		biotin-independent malonate decarboxylase subunit beta	-1.59
ABUW_RS03605	hchA	protein deglycase HchA	-1.58
ABUW_RS02395		enoyl-CoA hydratase/isomerase family protein	-1.58
ABUW_RS03180		VOC family protein	-1.57
ABUW_RS12315	paaC	phenylacetate-CoA oxygenase subunit PaaC	-1.56
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.56
ABUW_RS18530	prpC	2-methylcitrate synthase	-1.55
ABUW_RS02845		head completion/stabilization protein	-1.53
ABUW_RS06300	terL	phage terminase large subunit	-1.53
ABUW_RS02390		acyl-CoA dehydrogenase family protein	-1.53
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	-1.52
sRNA87	sRNA87	sRNA87	-1.51
ABUW_RS02840		tail protein X	-1.50
ABUW_RS01990	rpsJ	30S ribosomal protein S10	-1.49
ABUW_RS15615	add	adenosine deaminase	-1.49
ABUW_RS05220		hypothetical protein	-1.49
ABUW_RS15630		tRNA-Arg	-1.48
ABUW_RS16500		acetate kinase	-1.48
ABUW_RS00935	uvrA	excinuclease ABC subunit UvrA	-1.46
ABUW_RS04495		Ig-like domain repeat protein	-1.46
ABUW_RS04555		transglycosylase SLT domain-containing protein	-1.45
ABUW_RS05750	basC	putative histamine N-monooxygenase	-1.44
ABUW_RS10820		ABC transporter substrate-binding protein	-1.44
ABUW_RS07270	csuD	Csu fimbrial usher CsuD	-1.44
ABUW_RS15570		substrate-binding domain-containing protein	-1.43
ABUW_RS18965	guaD	guanine deaminase	-1.42
ABUW_RS00245	mutY	A/G-specific adenine glycosylase	-1.42
ABUW_RS02780		phage major tail tube protein	-1.41
ABUW_RS07505	mnmG	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	-1.41
ABUW_RS05225		glycosyltransferase family 2 protein	-1.41
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.40
ABUW_RS11950		hydroxymethylglutaryl-CoA lyase	-1.40
ABUW_RS00605		hypothetical protein	-1.39
ABUW_RS15165		trehalose-6-phosphate synthase	-1.39
ABUW_RS13450		GMC family oxidoreductase	-1.39
ABUW_RS13260		aspartate carbamoyltransferase catalytic subunit	-1.38
ABUW_RS11360		SfnB family sulfur acquisition oxidoreductase	-1.38
ABUW_RS06560	yegQ	tRNA 5-hydroxyuridine modification protein YegQ	-1.38
ABUW_RS14280		aldehyde dehydrogenase	-1.36
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.36
ABUW_RS18960		aromatic ring-hydroxylating dioxygenase subunit alpha	-1.35
ABUW_RS16445		glycosyltransferase family 1 protein	-1.34
ABUW_RS01360		tRNA-Ala	-1.33
ABUW_RS18770	ssuD	FMNH2-dependent alkanesulfonate monooxygenase	-1.33
ABUW_RS01000		PLP-dependent aminotransferase family protein	-1.33
ABUW_RS02850		terminase	-1.32
ABUW_RS13685		type VI secretion system tip protein VgrG	-1.32
ABUW_RS17475	rpoB	DNA-directed RNA polymerase subunit beta	-1.31
ABUW_RS08440		PAS domain-containing protein	-1.30
ABUW_RS08190	plc1	phospholipase C, phosphocholine-specific	-1.29

ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	-1.28
ABUW_RS16895		YafY family transcriptional regulator	-1.27
ABUW_RS03135		enoyl-CoA hydratase/isomerase family protein	-1.27
ABUW_RS18765		sulfonate ABC transporter substrate-binding protein	-1.27
ABUW_RS17385	fadB	fatty acid oxidation complex subunit alpha FadB	-1.25
ABUW_RS12795		hypothetical protein	-1.24
ABUW_RS12830		TolC family protein	-1.24
ABUW_RS15170		MFS transporter	-1.24
ABUW_RS11370		methionine transporter	-1.23
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.23
ABUW_RS04990		sulfate ABC transporter ATP-binding protein	-1.22
ABUW_RS14525		OprD family outer membrane porin	-1.22
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.21
ABUW_RS13390		SDR family NAD(P)-dependent oxidoreductase	-1.21
ABUW_RS06785		YqaJ viral recombinase family protein	-1.21
ABUW_RS11920		AMP-binding protein	-1.21
ABUW_RS20115		hypothetical protein	-1.21
ABUW_RS12915		fibronectin type III domain-containing protein	-1.21
ABUW_RS09495		GH3 auxin-responsive promoter family protein	-1.20
ABUW_RS01280		aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	-1.20
ABUW_RS14205	metH	methionine synthase	-1.19
ABUW_RS14180		formylglycine-generating enzyme family protein	-1.18
ABUW_RS02060	rpsN	30S ribosomal protein S14	-1.18
ABUW_RS00270		PQQ-dependent sugar dehydrogenase	-1.18
ABUW_RS14550		DEAD/DEAH box helicase family protein	-1.17
ABUW_RS00155	ppc	phosphoenolpyruvate carboxylase	-1.17
ABUW_RS16255	acnA	aconitate hydratase AcnA	-1.16
ABUW_RS02055	rplE	50S ribosomal protein L5	-1.15
ABUW_RS02385		acetyl-CoA carboxylase carboxyltransferase subunit	-1.14
ABUW_RS05205		hypothetical protein	-1.13
ABUW_RS05540		LysR family transcriptional regulator	-1.13
ABUW_RS15475		hypothetical protein	-1.13
ABUW_RS04905	ruvA	Holliday junction branch migration protein RuvA	-1.13
ABUW_RS11850		glucose 1-dehydrogenase	-1.13
ABUW_RS11700		FMN-binding negative transcriptional regulator	-1.12
ABUW_RS01245		GNAT family acetyltransferase	-1.12
ABUW_RS15415	nuoE	NADH-quinone oxidoreductase subunit NuoE	-1.12
ABUW_RS04910		deoxyguanosinetriphosphate triphosphohydrolase	-1.11
ABUW_RS12335		L-serine ammonia-lyase	-1.10
ABUW_RS14885		pirin family protein	-1.09
ABUW_RS01845	aroE	shikimate dehydrogenase	-1.09
ABUW_RS11375		MetQ/NlpA family ABC transporter substrate-binding protein	-1.09
ABUW_RS07985		SDR family NAD(P)-dependent oxidoreductase	-1.09
ABUW_RS05840	xdhA	xanthine dehydrogenase small subunit	-1.08
ABUW_RS05845	xdhB	xanthine dehydrogenase molybdopterin binding subunit	-1.08
sRNA89	sRNA89	sRNA89	-1.07
ABUW_RS19930	ssrA	transfer-messenger RNA	-1.07
ABUW_RS18955		glutathionylspermidine synthase family protein	-1.07
ABUW_RS17165		hypothetical protein	-1.07
ABUW_RS17125		EstA family serine hydrolase	-1.05
ABUW_RS03635		hypothetical protein	-1.05
ABUW_RS15045	pth	aminoacyl-tRNA hydrolase	-1.04
ABUW_RS13570		coniferyl aldehyde dehydrogenase	-1.04
ABUW_RS18160		F0F1 ATP synthase subunit epsilon	-1.04
ABUW_RS04670		hypothetical protein	-1.04

ABUW_RS18780		ATP-binding cassette domain-containing protein	-1.03
ABUW_RS17235	nusA	transcription termination/antitermination protein NusA	-1.03
ABUW_RS05865	trpD	anthranilate phosphoribosyltransferase	-1.02
ABUW_RS11485		RNA methyltransferase	-1.02
ABUW_RS00225		NAD(P)-dependent alcohol dehydrogenase	-1.02
ABUW_RS02050	rplX	50S ribosomal protein L24	-1.02
ABUW_RS14015		urease accessory protein UreD	-1.01
ABUW_RS11815		hypothetical protein	-1.01
ABUW_RS02085	rpmD	50S ribosomal protein L30	-1.01
ABUW_RS18470		nuclear transport factor 2 family protein	-1.00
ABUW_RS13340	alaS	alanine--tRNA ligase	-1.00

Table A5. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta baeR$ LSP. blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta baeR$ LSP vs WT LSP log2FC
ABUW_RS02995	<i>baeR</i>	response regulator	-13.63
ABUW_RS07640		hypothetical protein	-1.25

Table A6. Overview of genes that are differentially expressed as identified through RNA-seq analysis in $\Delta baeS$ MEP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	$\Delta baeS$ MEP vs WT MEP log2FC
sRNA84	sRNA84	sRNA84	4.94
ABUW_RS19905	ssrS	6S RNA	4.68
ABUW_RS17840		cation transporter	4.05
ABUW_RS17830		ISL3-like element IS _{Ppu12} family transposase	3.78
ABUW_RS13860		cation transporter	3.57
ABUW_RS17835		signal peptidase II	3.25
ABUW_RS09655		hypothetical protein	3.21
sRNA24	sRNA24	sRNA24	3.15
sRNA1	sRNA1	sRNA1	3.07
sRNA2	sRNA2	sRNA2	2.98
ABUW_RS07110		tRNA-Trp	2.91
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	2.78
ABUW_RS01510		bacterioferritin-associated ferredoxin	2.71
sRNA42	sRNA42	sRNA42	2.66
sRNA96	sRNA96	sRNA96	2.51
ABUW_RS09675		hypothetical protein	2.45
ABUW_RS07005		acyltransferase	2.39
ABUW_RS11440	dapC	succinyldiaminopimelate transaminase	2.31
sRNA100	sRNA100	sRNA100	2.23
sRNA15	sRNA15	sRNA15	2.18
ABUW_RS00585		hypothetical protein	2.17
ABUW_RS16540		TonB-dependent siderophore receptor	2.12
ABUW_RS19445		hypothetical protein	2.04
ABUW_RS09660		replication initiation factor domain-containing protein	2.00
ABUW_RS02140		succinate dehydrogenase assembly factor 2	1.96
ABUW_RS03465		alanine:cation symporter family protein	1.81
ABUW_RS07445		dicarboxylate/amino acid:cation symporter	1.78
ABUW_RS11115	putP	sodium/proline symporter PutP	1.75
ABUW_RS01470		FAD-dependent oxidoreductase	1.72
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	1.71
ABUW_RS20110		hypothetical protein	1.70

ABUW_RS18235		NAD-dependent malic enzyme	1.68
sRNA90	sRNA90	sRNA90	1.60
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	1.59
ABUW_RS10775	rpsT	30S ribosomal protein S20	1.57
ABUW_RS05670		type II toxin-antitoxin system Phd/YefM family antitoxin	1.51
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.50
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	1.50
ABUW_RS16645		biopolymer transporter ExbD	1.48
ABUW_RS13485	mhpT	3-(3-hydroxy-phenyl)propionate transporter MhpT	1.46
ABUW_RS08720		DUF2057 domain-containing protein	1.46
ABUW_RS11140		hypothetical protein	1.44
ABUW_RS11230		hypothetical protein	1.43
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	1.43
ABUW_RS13490		p-hydroxycinnamoyl CoA hydratase/lyase	1.42
ABUW_RS00045		hypothetical protein	1.39
ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	1.36
ABUW_RS08035		TonB-dependent receptor	1.35
ABUW_RS09665		hypothetical protein	1.35
ABUW_RS18095		hypothetical protein	1.34
ABUW_RS05565	rpmE	50S ribosomal protein L31	1.34
ABUW_RS09355		MFS transporter	1.34
ABUW_RS11315		YebC/PmpR family DNA-binding transcriptional regulator	1.34
ABUW_RS02370		TetR family transcriptional regulator	1.33
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	1.32
ABUW_RS13745		TonB-dependent receptor	1.31
ABUW_RS08255		hypothetical protein	1.30
ABUW_RS09650		helix-turn-helix transcriptional regulator	1.30
ABUW_RS08680		aspartate aminotransferase family protein	1.30
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.29
sRNA63	sRNA63	sRNA63	1.28
ABUW_RS16655		energy transducer TonB	1.26
ABUW_RS17685		ferrous iron transporter B	1.25
ABUW_RS07565		cytochrome o ubiquinol oxidase subunit IV	1.24
ABUW_RS05320		hypothetical protein	1.23
ABUW_RS01465	gltB	glutamate synthase large subunit	1.22
ABUW_RS08000		Lrp/AsnC family transcriptional regulator	1.22
ABUW_RS00965		DUF475 domain-containing protein	1.20
ABUW_RS01325		hypothetical protein	1.20
ABUW_RS07730	kdpC	potassium-transporting ATPase subunit KdpC	1.20
ABUW_RS13020		helix-turn-helix transcriptional regulator	1.19
ABUW_RS17120	rpsO	30S ribosomal protein S15	1.19
ABUW_RS17300		pyrimidine/purine nucleoside phosphorylase	1.18
ABUW_RS00705	pyrE	orotate phosphoribosyltransferase	1.18
ABUW_RS14765	dut	dUTP diphosphatase	1.17
ABUW_RS17850		universal stress protein	1.16
ABUW_RS04380	carB	carbamoyl-phosphate synthase large subunit	1.15
ABUW_RS07880		peptidyl-prolyl cis-trans isomerase	1.15
ABUW_RS00190	dapB	4-hydroxy-tetrahydronicotinate reductase	1.14
ABUW_RS06655		alpha/beta hydrolase	1.13
ABUW_RS11820		Lrp/AsnC family transcriptional regulator	1.13
ABUW_RS08645		hypothetical protein	1.12
ABUW_RS09160		dihydroxy-acid dehydratase	1.12
ABUW_RS06105		site-specific integrase	1.12
ABUW_RS17225		ribosome-binding factor A	1.11
ABUW_RS11015		nucleotidyltransferase family protein	1.10

ABUW_RS12770		EamA family transporter	1.10
ABUW_RS08890	eno	phosphopyruvate hydratase	1.10
ABUW_RS14510		LysR family transcriptional regulator	1.09
ABUW_RS07475	purD	phosphoribosylamine--glycine ligase	1.07
ABUW_RS14705		YggS family pyridoxal phosphate-dependent enzyme	1.06
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.05
ABUW_RS13940	gdhA	NADP-specific glutamate dehydrogenase	1.04
ABUW_RS04860		NF038105 family protein	1.03
ABUW_RS04015		MmcQ/YjbR family DNA-binding protein	1.01
ABUW_RS13535		aldehyde dehydrogenase (NADP(+))	1.01
ABUW_RS04235		hypothetical protein	1.01
ABUW_RS15360		cold shock domain-containing protein	1.00

Gene	Gene Name	Function	Δ baeS MEP vs WT MEP log2FC
ABUW_RS02990	baeS	sensor histidine kinase efflux regulator BaeS	-12.89
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	-6.80
ABUW_RS10115	antC	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.58
ABUW_RS10110	antB	anthranilate 1,2-dioxygenase small subunit	-5.54
ABUW_RS20235		hypothetical protein	-4.16
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-3.63
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-3.33
ABUW_RS07260	csuB	Csu fimbrial biogenesis protein CsuB	-3.31
ABUW_RS07255	csuA	Csu fimbrial biogenesis protein CsuA	-3.23
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-3.10
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-2.92
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	-2.80
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-2.67
ABUW_RS15565		MFS transporter	-2.59
ABUW_RS19040		zeta toxin family protein	-2.58
ABUW_RS20485		hypothetical protein	-2.48
ABUW_RS11870		hypothetical protein	-2.47
ABUW_RS08725		cyd operon YbgE family protein	-2.46
ABUW_RS02840		tail protein X	-2.46
ABUW_RS13055		cold-shock protein	-2.43
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-2.39
ABUW_RS12725		hypothetical protein	-2.38
ABUW_RS09970		molecular chaperone	-2.36
ABUW_RS02860		GPO family capsid scaffolding protein	-2.30
ABUW_RS02785		phage tail sheath protein	-2.29
ABUW_RS11895		hypothetical protein	-2.28
ABUW_RS03380		entericidin A/B family lipoprotein	-2.26
sRNA31	sRNA31	sRNA31	-2.23
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-2.22
ABUW_RS12975		hypothetical protein	-2.22
sRNA86	sRNA86	sRNA86	-2.21
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-2.20
ABUW_RS07500		hypothetical protein	-2.18
ABUW_RS07520		alpha-E domain-containing protein	-2.18
ABUW_RS07270	csuD	Csu fimbrial usher CsuD	-2.17
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-2.16
ABUW_RS20315		hypothetical protein	-2.15
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	-2.14
ABUW_RS05795	basI	acinetobactin biosynthesis phosphopantetheinyl transferase BasI	-2.12

ABUW_RS14490		transferrin-binding protein-like solute binding protein	-2.11
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	-2.11
ABUW_RS17515	tuf	elongation factor Tu	-2.10
ABUW_RS11370		methionine transporter	-2.10
ABUW_RS02995		response regulator	-2.10
ABUW_RS01140		hypothetical protein	-2.09
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-2.08
ABUW_RS04995	cysW	sulfate ABC transporter permease subunit CysW	-2.07
ABUW_RS07250	csuAB	Csu fimbrial major subunit CsuAB	-2.04
ABUW_RS07265	csuC	Csu fimbrial biogenesis chaperone CsuC	-2.02
ABUW_RS01750		hypothetical protein	-1.99
ABUW_RS15160	otsB	trehalose-phosphatase	-1.99
ABUW_RS10010		hypothetical protein	-1.99
ABUW_RS07965		molecular chaperone	-1.97
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-1.97
ABUW_RS00340	maiA	maleylacetoacetate isomerase	-1.94
ABUW_RS06780		hypothetical protein	-1.94
ABUW_RS11575	tauD	taurine dioxygenase	-1.93
ABUW_RS02780		phage major tail tube protein	-1.93
ABUW_RS09700		hypothetical protein	-1.90
ABUW_RS09975		fimbrial biogenesis outer membrane usher protein	-1.88
ABUW_RS01615		hemerythrin domain-containing protein	-1.88
ABUW_RS09985		DUF4882 family protein	-1.88
ABUW_RS02845		head completion/stabilization protein	-1.86
ABUW_RS02850		terminase	-1.85
ABUW_RS12745		DUF2147 domain-containing protein	-1.84
ABUW_RS05000	cysT	sulfate ABC transporter permease subunit CysT	-1.84
ABUW_RS11380		ATP-binding cassette domain-containing protein	-1.81
ABUW_RS11425		tautomerase family protein	-1.79
sRNA76	sRNA76	sRNA76	-1.78
ABUW_RS05750	basC	putative histamine N-monooxygenase	-1.76
ABUW_RS18770	ssuD	FMNH2-dependent alkanesulfonate monooxygenase	-1.76
ABUW_RS19065		hypothetical protein	-1.76
ABUW_RS03605	hchA	protein deglycase HchA	-1.75
ABUW_RS20115		hypothetical protein	-1.75
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-1.73
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-1.73
ABUW_RS07960		spore coat protein U domain-containing protein	-1.72
ABUW_RS08590		universal stress protein	-1.71
ABUW_RS12520	tssE	type VI secretion system baseplate subunit TssE	-1.70
ABUW_RS07135		CoA-acylating methylmalonate-semialdehyde dehydrogenase	-1.69
ABUW_RS19690		hypothetical protein	-1.67
ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-1.66
ABUW_RS05230		hypothetical protein	-1.65
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-1.65
ABUW_RS20105		hypothetical protein	-1.65
ABUW_RS13250		OmpA family protein	-1.59
ABUW_RS06730		hypothetical protein	-1.59
ABUW_RS11780		transporter substrate-binding domain-containing protein	-1.55
ABUW_RS10615		(2Fe-2S)-binding protein	-1.55
ABUW_RS05225		glycosyltransferase family 2 protein	-1.55
ABUW_RS16255	acnA	aconitate hydratase AcnA	-1.53
ABUW_RS15330		mechanosensitive ion channel	-1.53
ABUW_RS00385	hutH	histidine ammonia-lyase	-1.51
ABUW_RS00395		imidazolonepropionase	-1.51
ABUW_RS05790	basH	acinetobactin biosynthesis thioesterase BasH	-1.51

ABUW_RS02675		hypothetical protein	-1.50
ABUW_RS11375		MetQ/NlpA family ABC transporter substrate-binding protein	-1.48
ABUW_RS01745		hypothetical protein	-1.48
ABUW_RS05540		LysR family transcriptional regulator	-1.47
ABUW_RS00515		alpha/beta fold hydrolase	-1.46
ABUW_RS13115		hypothetical protein	-1.46
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.45
ABUW_RS00800		YkgJ family cysteine cluster protein	-1.44
ABUW_RS11760		cysteine desulfurase	-1.44
ABUW_RS05220		hypothetical protein	-1.43
ABUW_RS07130		aspartate aminotransferase family protein	-1.42
ABUW_RS13045		NAD(P)-binding domain-containing protein	-1.39
ABUW_RS06135		hypothetical protein	-1.39
ABUW_RS00370	hutC	histidine utilization repressor	-1.39
ABUW_RS11360		SfnB family sulfur acquisition oxidoreductase	-1.38
ABUW_RS03310		YegP family protein	-1.37
ABUW_RS13005		hypothetical protein	-1.36
ABUW_RS18630		oligosaccharide flippase family protein	-1.36
ABUW_RS10835		energy transducer TonB	-1.35
ABUW_RS05570		EAL domain-containing protein	-1.35
ABUW_RS19580		hypothetical protein	-1.35
ABUW_RS18765		sulfonate ABC transporter substrate-binding protein	-1.35
ABUW_RS05685		hypothetical protein	-1.35
ABUW_RS10610		RraA family protein	-1.35
ABUW_RS01215		DUF805 domain-containing protein	-1.34
ABUW_RS10820		ABC transporter substrate-binding protein	-1.34
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	-1.34
ABUW_RS13935		META and DUF4377 domain-containing protein	-1.34
ABUW_RS17420		hypothetical protein	-1.33
ABUW_RS04980	carO	ornithine uptake porin CarO type 3	-1.33
ABUW_RS02205		hypothetical protein	-1.32
ABUW_RS00405		DUF885 domain-containing protein	-1.32
ABUW_RS09995		hypothetical protein	-1.32
ABUW_RS10815		Zn-dependent oligopeptidase	-1.31
ABUW_RS00390		amino acid permease	-1.31
ABUW_RS03205		RtcB family protein	-1.31
ABUW_RS15175	bfr	bacterioferritin	-1.30
ABUW_RS16720		hypothetical protein	-1.29
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	-1.28
ABUW_RS03180		VOC family protein	-1.28
ABUW_RS05420		SIMPL domain-containing protein	-1.28
ABUW_RS10580		HAD family hydrolase	-1.27
ABUW_RS19085		H-NS histone family protein	-1.25
ABUW_RS05995		acyl-CoA dehydrogenase	-1.23
ABUW_RS02525		hypothetical protein	-1.23
ABUW_RS16440		phosphatase PAP2 family protein	-1.22
ABUW_RS04495		Ig-like domain repeat protein	-1.22
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	-1.21
ABUW_RS05340	cas3f	type I-F CRISPR-associated helicase Cas3	-1.21
ABUW_RS15615	add	adenosine deaminase	-1.20
ABUW_RS18945		TerC family protein	-1.20
ABUW_RS05875		M1 family metalloproteinase	-1.18
ABUW_RS04990		sulfate ABC transporter ATP-binding protein	-1.18
ABUW_RS16715		HdeD family acid-resistance protein	-1.16
ABUW_RS14030		isocitrate lyase	-1.16
ABUW_RS15055		GDYXXLY domain-containing protein	-1.16
ABUW_RS13450		GMC family oxidoreductase	-1.16

ABUW_RS16080	rsfS	ribosome silencing factor	-1.15
ABUW_RS19100		hypothetical protein	-1.15
ABUW_RS02855		phage major capsid protein, P2 family	-1.14
ABUW_RS09290		cation:proton antiporter	-1.14
ABUW_RS16160		copper resistance protein CopC	-1.14
ABUW_RS01345		hypothetical protein	-1.14
ABUW_RS07415		aspartate/glutamate racemase family protein	-1.12
ABUW_RS10840		MotA/TolQ/ExbB proton channel family protein	-1.12
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.11
ABUW_RS08700		hypothetical protein	-1.10
ABUW_RS18625		hypothetical protein	-1.10
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	-1.09
ABUW_RS00545		pyridoxal phosphate-dependent aminotransferase	-1.09
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.08
ABUW_RS04740		ABC transporter permease	-1.08
ABUW_RS13125		GFA family protein	-1.08
ABUW_RS08190	plc1	phospholipase C, phosphocholine-specific	-1.07
ABUW_RS16085		SDR family NAD(P)-dependent oxidoreductase	-1.06
ABUW_RS06785		YqaJ viral recombinase family protein	-1.05
ABUW_RS01765		hypothetical protein	-1.05
ABUW_RS12515	tssF	type VI secretion system baseplate subunit TssF	-1.04
ABUW_RS02660		3'-5' exonuclease	-1.04
ABUW_RS17100		DnaJ domain-containing protein	-1.04
ABUW_RS15045	pth	aminoacyl-tRNA hydrolase	-1.03
ABUW_RS19105		hypothetical protein	-1.02
ABUW_RS05360	cas6f	type I-F CRISPR-associated endoribonuclease Cas6/Csy4	-1.02
ABUW_RS08440		PAS domain-containing protein	-1.01
ABUW_RS00685		alpha/beta hydrolase	-1.01
ABUW_RS08390		hypothetical protein	-1.01
ABUW_RS09550		GNAT family N-acetyltransferase	-1.01

Table A6. Overview of genes that are differentially expressed as identified through RNA-seq analysis in *ΔbaeS* LSP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	<i>ΔbaeS</i> LSP vs WT LSP log2FC
sRNA84	sRNA84	sRNA84	8.05
ABUW_RS19905	ssrS	6S RNA	8.02
ABUW_RS07105		tRNA-Leu	7.25
ABUW_RS07110		tRNA-Trp	7.10
ABUW_RS09970		molecular chaperone	6.95
sRNA77	sRNA77	sRNA77	6.76
ABUW_RS12755		TetR/AcrR family transcriptional regulator	6.66
ABUW_RS09965		type 1 fimbrial protein	6.08
ABUW_RS08150	aceI	chlorhexidine efflux PACE transporter AceI	6.02
ABUW_RS15030		tRNA-Gln	6.01
ABUW_RS19340		hypothetical protein	5.64
ABUW_RS19240		hypothetical protein	5.58
sRNA81	sRNA81	sRNA81	5.56
ABUW_RS15025		tRNA-Gln	5.54
ABUW_RS06940		hypothetical protein	5.47
ABUW_RS19125		hypothetical protein	5.42
ABUW_RS09655		hypothetical protein	5.37
ABUW_RS14535		hypothetical protein	5.21
sRNA100	sRNA100	sRNA100	5.18
sRNA62	sRNA62	sRNA62	4.92
ABUW_RS19235		hypothetical protein	4.85

ABUW_RS19355		hypothetical protein	4.84
ABUW_RS10215		hypothetical protein	4.78
ABUW_RS13265		hypothetical protein	4.73
ABUW_RS03860		hypothetical protein	4.71
ABUW_RS19135		hypothetical protein	4.64
ABUW_RS19130		SAM-dependent DNA methyltransferase	4.63
ABUW_RS02145		membrane protein	4.58
ABUW_RS12415		hypothetical protein	4.44
ABUW_RS05380		RluA family pseudouridine synthase	4.43
sRNA46	sRNA46	sRNA46	4.31
sRNA1	sRNA1	sRNA1	4.21
ABUW_RS01045		tRNA-Thr	4.19
sRNA24	sRNA24	sRNA24	4.17
ABUW_RS19120		hypothetical protein	4.15
ABUW_RS12675		hypothetical protein	4.08
ABUW_RS15510		TetR/AcrR family transcriptional regulator	4.01
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	3.99
ABUW_RS07925		iron-containing alcohol dehydrogenase	3.99
ABUW_RS19220		hypothetical protein	3.98
sRNA4	sRNA4	sRNA4	3.95
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	3.91
ABUW_RS20105		hypothetical protein	3.91
ABUW_RS10120		AraC family transcriptional regulator	3.83
ABUW_RS15625		tRNA-His	3.83
ABUW_RS19345		molecular chaperone DnaJ	3.81
ABUW_RS05140	uvrB	excinuclease ABC subunit UvrB	3.81
ABUW_RS06815		hypothetical protein	3.80
ABUW_RS04760		hypothetical protein	3.78
ABUW_RS04445		tRNA-Cys	3.77
ABUW_RS03685		hypothetical protein	3.73
ABUW_RS19020	rpmH	50S ribosomal protein L34	3.71
ABUW_RS15665		copper resistance protein B	3.70
ABUW_RS19360		hypothetical protein	3.69
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	3.67
ABUW_RS11310		1-acyl-sn-glycerol-3-phosphate acyltransferase	3.67
ABUW_RS19930	ssrA	transfer-messenger RNA	3.67
ABUW_RS19660	rnpB	RNase P RNA component class A	3.67
sRNA89	sRNA89	sRNA89	3.67
ABUW_RS20015		Mu transposase C-terminal domain-containing protein	3.66
ABUW_RS05010		sulfate ABC transporter substrate-binding protein	3.56
ABUW_RS09975		fimbrial biogenesis outer membrane usher protein	3.53
ABUW_RS01430		PilN domain-containing protein	3.49
ABUW_RS15525		DUF1852 domain-containing protein	3.49
ABUW_RS08560		amino acid permease	3.49
sRNA88	sRNA88	sRNA88	3.48
ABUW_RS19900		glutathione S-transferase	3.48
ABUW_RS01305		TolC family protein	3.44
ABUW_RS17915		ATP-binding protein	3.44
ABUW_RS12350		APC family permease	3.41
ABUW_RS19015	rnpA	ribonuclease P protein component	3.40
ABUW_RS04720		GtrA family protein	3.37
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	3.32
sRNA93	sRNA93	sRNA93	3.32
ABUW_RS17835		signal peptidase II	3.31
ABUW_RS04625		glycerate kinase	3.30

ABUW_RS10100		LysR family transcriptional regulator	3.29
ABUW_RS19295		APH(6)-I family aminoglycoside O-phosphotransferase	3.28
ABUW_RS01425		pilus assembly protein PilM	3.28
ABUW_RS01540		GspH/FimT family pseudopilin	3.26
ABUW_RS19350		hypothetical protein	3.24
ABUW_RS09030		MFS transporter	3.21
ABUW_RS00800		YkgJ family cysteine cluster protein	3.21
ABUW_RS20020		TniB family NTP-binding protein	3.20
ABUW_RS11530		metalloregulator ArsR/SmtB family transcription factor	3.20
ABUW_RS17360		thioesterase family protein	3.19
ABUW_RS06325		hypothetical protein	3.17
ABUW_RS12960		DUF2280 domain-containing protein	3.16
ABUW_RS00795		MBL fold metallo-hydrolase	3.14
sRNA15	sRNA15	sRNA15	3.13
ABUW_RS17840		cation transporter	3.10
ABUW_RS16860		RNA pyrophosphohydrolase	3.10
ABUW_RS19300	aph(3'')-Ib	aminoglycoside O-phosphotransferase APH(3'')-Ib	3.09
ABUW_RS01440		pilus assembly protein PilP	3.06
ABUW_RS05375		isochorismatase	3.05
ABUW_RS09050		hypothetical protein	3.02
ABUW_RS12095		putative 2-aminoethylphosphonate ABC transporter substrate-binding protein	3.01
ABUW_RS01545	pilV	type IV pilus modification protein PilV	3.00
ABUW_RS05005		alpha/beta hydrolase	2.99
ABUW_RS19030		replication initiation protein	2.97
ABUW_RS00985		AzIC family ABC transporter permease	2.97
ABUW_RS19195		hypothetical protein	2.97
ABUW_RS06110		hypothetical protein	2.96
ABUW_RS19255		GNAT family N-acetyltransferase	2.95
ABUW_RS02690		hypothetical protein	2.95
ABUW_RS09660		replication initiation factor domain-containing protein	2.95
ABUW_RS02785		phage tail sheath protein	2.94
ABUW_RS16315		DUF4124 domain-containing protein	2.94
ABUW_RS17250		tRNA-Met	2.93
ABUW_RS15520		methionine synthase	2.91
ABUW_RS09465		methylenetetrahydrofolate reductase C-terminal domain-containing protein	2.91
ABUW_RS15630		tRNA-Arg	2.88
ABUW_RS07435		MFS transporter	2.88
ABUW_RS17525		tRNA-Gly	2.88
ABUW_RS02810		phage baseplate assembly protein V	2.86
ABUW_RS03345		purine-binding chemotaxis protein CheW	2.86
ABUW_RS14445		homocysteine S-methyltransferase family protein	2.85
ABUW_RS18480		RluA family pseudouridine synthase	2.85
ABUW_RS11925		TetR/AcrR family transcriptional regulator	2.84
ABUW_RS01495	pilA	pilin	2.84
ABUW_RS09485		DHA2 family efflux MFS transporter permease subunit	2.83
ABUW_RS17255		tRNA-Leu	2.82
ABUW_RS04730		ChbG/HpnK family deacetylase	2.82
ABUW_RS11275		cytosine permease	2.82
ABUW_RS17440		outer membrane beta-barrel protein	2.82
ABUW_RS15950	rplT	50S ribosomal protein L20	2.81
ABUW_RS15955	rplM	50S ribosomal protein L35	2.77
ABUW_RS20430		hypothetical protein	2.77
ABUW_RS03530	mreD	rod shape-determining protein MreD	2.75

ABUW_RS09150		hypothetical protein	2.75
sRNA9	sRNA9	sRNA9	2.74
ABUW_RS12355		aldehyde dehydrogenase (NADP(+))	2.74
sRNA60	sRNA60	sRNA60	2.71
ABUW_RS03655		hypothetical protein	2.70
ABUW_RS18360		acyl carrier protein	2.69
ABUW_RS18950		hypothetical protein	2.69
ABUW_RS13565		AraC family transcriptional regulator	2.69
ABUW_RS04395		DOMON-like domain-containing protein	2.67
ABUW_RS11715		CidA/LrgA family protein	2.67
ABUW_RS18115		LysM peptidoglycan-binding domain-containing protein	2.66
ABUW_RS13460		MFS transporter	2.66
ABUW_RS14710		type IV pilus twitching motility protein PilT	2.65
ABUW_RS06195		hypothetical protein	2.65
ABUW_RS03525	mreC	rod shape-determining protein MreC	2.65
ABUW_RS17535		tRNA-Thr	2.64
ABUW_RS16775		endonuclease/exonuclease/phosphatase family protein	2.64
ABUW_RS14740		bacteriohemerythrin	2.63
ABUW_RS15705		class I SAM-dependent methyltransferase	2.63
ABUW_RS12285	pcaF	3-oxoadipyl-CoA thiolase	2.62
ABUW_RS18370		fatty acyl-AMP ligase	2.62
ABUW_RS08725		cyd operon YbgE family protein	2.61
ABUW_RS18565	lldP	L-lactate permease	2.59
ABUW_RS18365		acyl-CoA dehydrogenase	2.59
ABUW_RS01710		amino acid permease	2.58
ABUW_RS09295		hypothetical protein	2.58
ABUW_RS12650		5-oxoprolinase/urea amidolyase family protein	2.58
ABUW_RS12010		enoyl-CoA hydratase	2.57
ABUW_RS19690		hypothetical protein	2.57
ABUW_RS01435		type 4a pilus biogenesis protein PilO	2.56
ABUW_RS02735		ogr/Delta-like zinc finger family protein	2.55
ABUW_RS12090		ATP-binding cassette domain-containing protein	2.54
ABUW_RS07905	eat	ethanolamine permease	2.54
ABUW_RS11325		hypothetical protein	2.54
ABUW_RS03690		GntR family transcriptional regulator	2.53
ABUW_RS19010	yidD	membrane protein insertion efficiency factor YidD	2.53
ABUW_RS20110		hypothetical protein	2.52
ABUW_RS16230		tyrosine-type recombinase/integrase	2.52
ABUW_RS09045		acyl-CoA dehydrogenase family protein	2.51
ABUW_RS18190	atpE	F0F1 ATP synthase subunit C	2.51
ABUW_RS13905		hypothetical protein	2.51
ABUW_RS19370		hypothetical protein	2.51
ABUW_RS05150	rarD	EamA family transporter RarD	2.50
ABUW_RS00320		DUF523 domain-containing protein	2.50
ABUW_RS14265		MFS transporter	2.50
ABUW_RS14320		SDR family oxidoreductase	2.47
ABUW_RS13025		MFS transporter	2.47
ABUW_RS03665		hypothetical protein	2.46
ABUW_RS16495		phosphogluconate dehydratase	2.45
ABUW_RS03460		hypothetical protein	2.44
ABUW_RS19305		ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2	2.43
ABUW_RS06190		hypothetical protein	2.43
ABUW_RS17445		TRAP transporter large permease subunit	2.43
ABUW_RS09565		SDR family NAD(P)-dependent oxidoreductase	2.43
ABUW_RS15920		hypothetical protein	2.43

sRNA54	sRNA54	sRNA54	2.43
ABUW_RS05000	cysT	sulfate ABC transporter permease subunit CysT	2.41
ABUW_RS19520	traW	type-F conjugative transfer system protein TraW	2.41
ABUW_RS16810	infA	translation initiation factor IF-1	2.41
ABUW_RS06835		hypothetical protein	2.41
ABUW_RS10210		hypothetical protein	2.40
ABUW_RS01400	murF	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	2.39
ABUW_RS07370		DUF1365 domain-containing protein	2.38
ABUW_RS00315		MATE family efflux transporter	2.37
ABUW_RS12940		DUF2158 domain-containing protein	2.37
ABUW_RS06820		hypothetical protein	2.37
ABUW_RS09390		DMT family transporter	2.37
sRNA49	sRNA49	sRNA49	2.36
ABUW_RS18300		LysE family transporter	2.36
ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	2.35
ABUW_RS02620	tgt	tRNA guanosine(34) transglycosylase Tgt	2.35
ABUW_RS06830		helix-turn-helix domain-containing protein	2.35
ABUW_RS06160		hypothetical protein	2.33
ABUW_RS15670		copper resistance system multicopper oxidase	2.33
ABUW_RS00925	omp33-36	porin Omp33-36	2.32
ABUW_RS12265		Paal family thioesterase	2.32
ABUW_RS08555	kynU	kynureninase	2.31
ABUW_RS07055		hypothetical protein	2.31
ABUW_RS09650		helix-turn-helix transcriptional regulator	2.30
ABUW_RS06560	yegQ	tRNA 5-hydroxyuridine modification protein YegQ	2.30
ABUW_RS05660	yddG	aromatic amino acid DMT transporter YddG	2.30
ABUW_RS14330		hypothetical protein	2.28
ABUW_RS09040		amidase	2.28
ABUW_RS00390		amino acid permease	2.28
ABUW_RS09600	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	2.28
ABUW_RS18195	atpB	FOF1 ATP synthase subunit A	2.27
ABUW_RS18120	dprA	DNA-processing protein DprA	2.27
ABUW_RS08100		hypothetical protein	2.26
ABUW_RS03330		hypothetical protein	2.26
ABUW_RS12085		putative 2-aminoethylphosphonate ABC transporter permease subunit	2.25
ABUW_RS12655		putative hydro-lyase	2.25
ABUW_RS12290		3-hydroxyacyl-CoA dehydrogenase	2.24
ABUW_RS16490	eda	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase	2.24
ABUW_RS04035		1-acyl-sn-glycerol-3-phosphate acyltransferase	2.23
ABUW_RS11240		fimbria/pilus periplasmic chaperone	2.23
ABUW_RS06285		hypothetical protein	2.23
ABUW_RS12015		SDR family oxidoreductase	2.23
ABUW_RS01550		PiW family protein	2.22
ABUW_RS02310		2OG-Fe(II) oxygenase	2.22
ABUW_RS18200		ATP synthase subunit I	2.22
ABUW_RS00285		hypothetical protein	2.21
ABUW_RS07545	rplI	50S ribosomal protein L9	2.20
ABUW_RS11525	arsB	ACR3 family arsenite efflux transporter	2.20
ABUW_RS12295		2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	2.19
ABUW_RS00885	msuE	FMN reductase	2.19
ABUW_RS14255		glutaminase	2.19
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	2.17
ABUW_RS19260	sul1	sulfonamide-resistant dihydropteroate synthase Sul1	2.17

ABUW_RS17530		tRNA-Tyr	2.16
ABUW_RS01555		hypothetical protein	2.16
ABUW_RS18685		carboxylating nicotinate-nucleotide diphosphorylase	2.16
ABUW_RS17855	arsC	arsenate reductase (glutaredoxin)	2.16
ABUW_RS19165		toxic anion resistance protein	2.16
ABUW_RS11305		TetR/AcrR family transcriptional regulator	2.16
ABUW_RS11950		hydroxymethylglutaryl-CoA lyase	2.15
ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	2.15
ABUW_RS12280	paaF	phenylacetate--CoA ligase	2.13
ABUW_RS02590		bestrophin	2.12
ABUW_RS19140		ParA family protein	2.12
ABUW_RS15515		flavin reductase	2.12
ABUW_RS17975		trimeric intracellular cation channel family protein	2.12
ABUW_RS09365		SLC13 family permease	2.12
ABUW_RS12665		divalent metal cation transporter	2.11
ABUW_RS19310		CmlA family chloramphenicol efflux MFS transporter	2.11
ABUW_RS12955	terL	phage terminase large subunit	2.11
ABUW_RS06840		ribbon-helix-helix protein, CopG family	2.11
ABUW_RS19225		hypothetical protein	2.11
ABUW_RS18030		helix-turn-helix domain-containing protein	2.11
ABUW_RS00385	hutH	histidine ammonia-lyase	2.10
ABUW_RS01375		sulfate ABC transporter substrate-binding protein	2.10
ABUW_RS12060		acyl-CoA dehydrogenase family protein	2.10
ABUW_RS09060		aromatic ring-hydroxylating dioxygenase subunit alpha	2.08
sRNA61	sRNA61	sRNA61	2.08
ABUW_RS02265		energy transducer TonB	2.07
ABUW_RS10270		GntR family transcriptional regulator	2.07
ABUW_RS00905		DUF485 domain-containing protein	2.06
ABUW_RS20385		hypothetical protein	2.06
ABUW_RS16995		TIGR03862 family flavoprotein	2.06
sRNA37	sRNA37	sRNA37	2.06
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	2.05
ABUW_RS09480		HlyD family secretion protein	2.05
ABUW_RS00730	murC	UDP-N-acetylmuramate--L-alanine ligase	2.05
ABUW_RS17275		type II secretion system F family protein	2.05
ABUW_RS06330		hypothetical protein	2.04
ABUW_RS11770		LysR family transcriptional regulator	2.03
ABUW_RS16820		hypothetical protein	2.03
ABUW_RS11590	tauA	taurine ABC transporter substrate-binding protein	2.03
ABUW_RS15710	tsaB	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	2.03
ABUW_RS12965		transposase	2.03
ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	2.03
ABUW_RS04030		patatin-like phospholipase family protein	2.03
ABUW_RS04580		hypothetical protein	2.02
ABUW_RS12620		hypothetical protein	2.02
ABUW_RS12410	soxR	redox-sensitive transcriptional activator SoxR	2.01
ABUW_RS00455	thiL	thiamine-phosphate kinase	2.00
ABUW_RS09575		alpha/beta fold hydrolase	2.00
ABUW_RS03350		methyl-accepting chemotaxis protein	2.00
ABUW_RS12005		acyl-CoA dehydrogenase family protein	2.00
ABUW_RS07715		2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase	1.99

ABUW_RS12825		type I secretion system permease/ATPase	1.99
ABUW_RS01870		DEAD/DEAH box helicase	1.99
ABUW_RS09240		SDR family oxidoreductase	1.99
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.99
ABUW_RS19230		hypothetical protein	1.99
ABUW_RS03045		DUF2804 domain-containing protein	1.98
ABUW_RS14325		aromatic ring-hydroxylating dioxygenase subunit alpha	1.98
ABUW_RS00380	hutU	urocanate hydratase	1.97
ABUW_RS02815		phage virion morphogenesis protein	1.97
ABUW_RS12140		cytosine permease	1.97
ABUW_RS10175		LysR family transcriptional regulator	1.97
ABUW_RS17365	uvrC	excinuclease ABC subunit UvrC	1.97
ABUW_RS16520		DUF2846 domain-containing protein	1.95
ABUW_RS11930		isovaleryl-CoA dehydrogenase	1.94
ABUW_RS00400	hutG	formimidoylglutamase	1.94
ABUW_RS02935		hypothetical protein	1.94
ABUW_RS13340	alaS	alanine--tRNA ligase	1.94
ABUW_RS00575		type VI secretion system tip protein VgrG	1.93
ABUW_RS17295	rlmB	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	1.93
ABUW_RS15680		HAD family hydrolase	1.93
ABUW_RS17630		EamA family transporter	1.93
ABUW_RS07875		UDP-2,3-diacylglucosamine diphosphatase	1.92
ABUW_RS00395		imidazolonepropionase	1.92
ABUW_RS01445		type IV pilus secretin PilQ family protein	1.92
ABUW_RS18555	lldD	FMN-dependent L-lactate dehydrogenase LldD	1.92
ABUW_RS10995		MotA/TolQ/ExbB proton channel family protein	1.91
ABUW_RS01920		ComF family protein	1.91
ABUW_RS14180		formylglycine-generating enzyme family protein	1.91
ABUW_RS06845		hypothetical protein	1.90
ABUW_RS06155		hypothetical protein	1.89
ABUW_RS05900		chorismate lyase	1.89
ABUW_RS06850		hypothetical protein	1.89
ABUW_RS01600		lipase secretion chaperone	1.88
ABUW_RS11445		LysE family translocator	1.88
ABUW_RS15750		C39 family peptidase	1.87
ABUW_RS06205		AAA family ATPase	1.87
ABUW_RS18955		glutathionylspermidine synthase family protein	1.87
ABUW_RS13610		gamma-aminobutyraldehyde dehydrogenase	1.85
ABUW_RS18355		non-ribosomal peptide synthetase	1.85
ABUW_RS06530		ABC transporter substrate-binding protein	1.85
ABUW_RS05080	recO	DNA repair protein RecO	1.84
ABUW_RS04555		transglycosylase SLT domain-containing protein	1.84
ABUW_RS10265		fumarate reductase/succinate dehydrogenase flavoprotein subunit	1.83
ABUW_RS07670		aliphatic sulfonate ABC transporter substrate-binding protein	1.83
ABUW_RS01060		DMT family transporter	1.83
ABUW_RS11700		FMN-binding negative transcriptional regulator	1.83
ABUW_RS18175		F0F1 ATP synthase subunit alpha	1.83
ABUW_RS17730		sigma-54-dependent Fis family transcriptional regulator	1.83
ABUW_RS18180		F0F1 ATP synthase subunit delta	1.82
ABUW_RS15170		MFS transporter	1.82
ABUW_RS03355		Hpt domain-containing protein	1.82
ABUW_RS07045	purF	amidophosphoribosyltransferase	1.82
ABUW_RS19145		ParB/RepB/Spo0J family partition protein	1.81

ABUW_RS04575		non-ribosomal peptide synthetase	1.81
ABUW_RS16790		hypothetical protein	1.81
ABUW_RS06525	adeL	multidrug efflux transcriptional repressor AdeL	1.80
ABUW_RS17565	gspN	type II secretion system protein N	1.80
ABUW_RS18185		F0F1 ATP synthase subunit B	1.79
ABUW_RS15315		1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase	1.79
ABUW_RS19635		protein rep	1.79
ABUW_RS05290		YbfB/YjiJ family MFS transporter	1.79
ABUW_RS18550	dld	D-lactate dehydrogenase	1.79
ABUW_RS11940		enoyl-CoA hydratase/isomerase family protein	1.78
ABUW_RS13080		LexA family transcriptional regulator	1.78
ABUW_RS01350		amino acid permease	1.77
ABUW_RS01100		hypothetical protein	1.77
ABUW_RS13925	rlmH	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	1.77
ABUW_RS09495		GH3 auxin-responsive promoter family protein	1.76
ABUW_RS14010	ureA	urease subunit gamma	1.76
ABUW_RS02845		head completion/stabilization protein	1.75
ABUW_RS02420	rpsI	30S ribosomal protein S9	1.75
ABUW_RS02855		phage major capsid protein, P2 family	1.75
ABUW_RS03205		RtcB family protein	1.75
ABUW_RS07685		acyl-CoA dehydrogenase family protein	1.75
ABUW_RS19470	traL	type IV conjugative transfer system protein TraL	1.75
ABUW_RS02595	radC	DNA repair protein RadC	1.75
ABUW_RS02565		bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC	1.74
ABUW_RS01270		bifunctional SulP family inorganic anion transporter/carbonic anhydrase	1.74
ABUW_RS01265		RNA-binding transcriptional accessory protein	1.74
ABUW_RS09220		Rrf2 family transcriptional regulator	1.74
ABUW_RS01405		phospho-N-acetylmuramoyl-pentapeptide-transferase	1.73
ABUW_RS09490		hypothetical protein	1.73
ABUW_RS14365	pgaC	poly-beta-1,6 N-acetyl-D-glucosamine synthase	1.73
ABUW_RS18560	lldR	transcriptional regulator LldR	1.73
ABUW_RS00635		ion channel protein Tsx	1.72
ABUW_RS18485		DUF1003 domain-containing protein	1.72
ABUW_RS14385	dctA	C4-dicarboxylate transporter DctA	1.72
ABUW_RS09300		amidohydrolase	1.72
ABUW_RS17330		DUF1656 domain-containing protein	1.71
ABUW_RS12885		hypothetical protein	1.71
ABUW_RS01310		efflux RND transporter periplasmic adaptor subunit	1.71
ABUW_RS18455		Lrp/AsnC ligand binding domain-containing protein	1.71
ABUW_RS16270		hypothetical protein	1.71
ABUW_RS18170	atpG	F0F1 ATP synthase subunit gamma	1.70
ABUW_RS17000		SAM-dependent methyltransferase	1.69
ABUW_RS04265	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.69
ABUW_RS12055		CoA transferase	1.69
ABUW_RS12380		FAD-binding oxidoreductase	1.68
ABUW_RS02150		hypothetical protein	1.68
ABUW_RS02395		enoyl-CoA hydratase/isomerase family protein	1.68
ABUW_RS11290		integrase family protein	1.68
ABUW_RS18165	atpD	F0F1 ATP synthase subunit beta	1.67
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	1.67
ABUW_RS00240		M23 family metalloproteinase	1.67

ABUW_RS00630	hpxO	FAD-dependent urate hydroxylase HpxO	1.67
ABUW_RS00035		ATP-binding cassette domain-containing protein	1.67
ABUW_RS12660		LamB/YcsF family protein	1.67
ABUW_RS17560		general secretion pathway protein	1.66
ABUW_RS07505	mnmG	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	1.65
ABUW_RS03215		methyltransferase	1.65
ABUW_RS07800		membrane protein	1.65
ABUW_RS16260		TatD family hydrolase	1.65
ABUW_RS11935		methylcrotonoyl-CoA carboxylase	1.65
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.65
ABUW_RS03165		nitrite/sulfite reductase	1.65
ABUW_RS12830		TolC family protein	1.65
ABUW_RS18035		DUF2938 domain-containing protein	1.64
ABUW_RS03705		hypothetical protein	1.64
ABUW_RS11260		LysR family transcriptional regulator	1.64
ABUW_RS12590	uca	urea carboxylase	1.64
ABUW_RS15150	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	1.63
ABUW_RS04480		phosphoenolpyruvate carboxykinase (GTP)	1.63
ABUW_RS02375		DUF1446 domain-containing protein	1.63
ABUW_RS18680	ampD	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD	1.63
ABUW_RS19005	yidC	membrane protein insertase YidC	1.63
ABUW_RS03585		PaaX family transcriptional regulator	1.63
ABUW_RS17810		ATP-binding protein	1.63
ABUW_RS05870		TonB-dependent receptor	1.63
ABUW_RS02580		septation protein IspZ	1.63
ABUW_RS07785		hypothetical protein	1.62
ABUW_RS01210		3'-5' exonuclease domain-containing protein 2	1.62
ABUW_RS02370		TetR family transcriptional regulator	1.62
ABUW_RS13940	gdhA	NADP-specific glutamate dehydrogenase	1.62
ABUW_RS05890		peptide MFS transporter	1.62
ABUW_RS13590		amino acid permease	1.62
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.62
ABUW_RS03465		alanine:cation symporter family protein	1.61
ABUW_RS17260	secG	preprotein translocase subunit SecG	1.61
ABUW_RS15355		excalibur calcium-binding domain-containing protein	1.60
ABUW_RS15600		acyl-CoA dehydrogenase	1.59
ABUW_RS11650	madL	malonate transporter subunit MadL	1.59
ABUW_RS18425		LysR family transcriptional regulator	1.59
ABUW_RS13800		ABC transporter substrate-binding protein	1.59
ABUW_RS09070		SDR family oxidoreductase	1.58
ABUW_RS00725	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	1.58
ABUW_RS04145		site-specific recombinase	1.58
ABUW_RS17675		UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	1.58
ABUW_RS02780		phage major tail tube protein	1.58
ABUW_RS14655		EmrA/EmrK family multidrug efflux transporter periplasmic adaptor subunit	1.58
ABUW_RS20545		zinc ribbon-containing protein	1.58
ABUW_RS11995		3-oxoacid CoA-transferase subunit A	1.58
ABUW_RS04260	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.58
ABUW_RS17405		MerR family transcriptional regulator	1.58
ABUW_RS11595		hypothetical protein	1.57
ABUW_RS14785		hypothetical protein	1.57

ABUW_RS11690		MFS transporter	1.57
ABUW_RS15305		MFS transporter	1.56
ABUW_RS11215	queG	tRNA epoxyqueuosine(34) reductase QueG	1.55
ABUW_RS03220		uracil-xanthine permease	1.55
ABUW_RS18160		F0F1 ATP synthase subunit epsilon	1.55
ABUW_RS19205		hypothetical protein	1.55
ABUW_RS00850		16S rRNA (uracil(1498)-N(3))-methyltransferase	1.55
ABUW_RS09985		DUF4882 family protein	1.54
ABUW_RS06070		septal ring lytic transglycosylase RlpA family protein	1.54
ABUW_RS13235	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	1.54
ABUW_RS16575		hypothetical protein	1.54
ABUW_RS02865		terminase family protein	1.54
ABUW_RS09980		type 1 fimbrial protein	1.53
ABUW_RS07600	pgaA	poly-beta-1,6 N-acetyl-D-glucosamine exporter porin PgaA	1.53
ABUW_RS09245		acetoacetate decarboxylase family protein	1.53
ABUW_RS17315		YqgE/AlgH family protein	1.53
ABUW_RS06535	hisQ	histidine ABC transporter permease HisQ	1.53
ABUW_RS16240		hypothetical protein	1.52
ABUW_RS14175		arylsulfatase	1.52
ABUW_RS19375		type IV secretion system DNA-binding domain-containing protein	1.52
ABUW_RS14080		esterase	1.52
ABUW_RS10870		AraC family transcriptional regulator	1.52
ABUW_RS14650		DHA2 family efflux MFS transporter permease subunit	1.51
ABUW_RS13545	gudD	glucarate dehydratase	1.51
ABUW_RS01065		hypothetical protein	1.51
ABUW_RS02000	rplD	50S ribosomal protein L4	1.51
ABUW_RS19170		hypothetical protein	1.51
ABUW_RS04620		TetR/AcrR family transcriptional regulator	1.50
ABUW_RS12670	mumR	LysR family transcriptional regulator MumR	1.50
ABUW_RS04880	tolR	protein TolR	1.50
ABUW_RS08465		phosphatidate cytidyltransferase	1.49
ABUW_RS08295	nirB	nitrite reductase large subunit	1.49
ABUW_RS12270		carbonic anhydrase	1.48
ABUW_RS06520	adeF	multidrug efflux RND transporter periplasmic adaptor subunit AdeF	1.48
ABUW_RS00980		AzID domain-containing protein	1.48
ABUW_RS02965		RcnB family protein	1.48
ABUW_RS12750		MFS transporter	1.47
ABUW_RS18520		hypothetical protein	1.47
ABUW_RS17320	ruvX	Holliday junction resolvase RuvX	1.47
ABUW_RS04450	folD	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	1.47
ABUW_RS18870		hypothetical protein	1.47
sRNA76	sRNA76	sRNA76	1.47
ABUW_RS16885		DUF1345 domain-containing protein	1.47
ABUW_RS16485		permease	1.46
ABUW_RS02605	secF	protein translocase subunit SecF	1.46
ABUW_RS16625	thyA	thymidylate synthase	1.46
ABUW_RS09570		SDR family NAD(P)-dependent oxidoreductase	1.45
ABUW_RS19550		conjugal transfer protein TraH	1.45
ABUW_RS00355		hypothetical protein	1.45
ABUW_RS02940	aspS	aspartate--tRNA ligase	1.44
ABUW_RS03335	pilG	twitching motility response regulator PilG	1.44
ABUW_RS12770		EamA family transporter	1.44

ABUW_RS15035		ribose-phosphate pyrophosphokinase	1.43
ABUW_RS06360		hypothetical protein	1.43
ABUW_RS17650		NUDIX domain-containing protein	1.43
ABUW_RS18375	abaR	LuxR family transcriptional regulator AbaR	1.43
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	1.42
ABUW_RS03590		undecaprenyl-diphosphate phosphatase	1.42
ABUW_RS13485	mhpT	3-(3-hydroxy-phenyl)propionate transporter MhpT	1.42
ABUW_RS16620		hypothetical protein	1.42
ABUW_RS04150		polyprenyl synthetase family protein	1.42
ABUW_RS14520		MFS transporter	1.41
ABUW_RS02355		GFA family protein	1.41
ABUW_RS02860		GPO family capsid scaffolding protein	1.41
ABUW_RS14075	lysS	lysine--tRNA ligase	1.41
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	1.41
ABUW_RS09345		hypothetical protein	1.40
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	1.40
ABUW_RS10480		GFA family protein	1.40
ABUW_RS12645		ATP-grasp domain-containing protein	1.40
ABUW_RS10495		porin	1.40
ABUW_RS00880	sfnG	dimethyl sulfone monooxygenase SfnG	1.40
ABUW_RS16720		hypothetical protein	1.40
ABUW_RS05705		PAS domain-containing protein	1.39
ABUW_RS11915		class I SAM-dependent methyltransferase	1.39
ABUW_RS14640		tyrosine-type recombinase/integrase	1.39
ABUW_RS11920		AMP-binding protein	1.39
ABUW_RS11735		LysR family transcriptional regulator	1.38
ABUW_RS15285	metG	methionine--tRNA ligase	1.38
ABUW_RS01080		AraC family transcriptional regulator	1.38
ABUW_RS16475		NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1.38
ABUW_RS10835		energy transducer TonB	1.38
ABUW_RS02380		SDR family oxidoreductase	1.37
ABUW_RS19505	traC	type IV secretion system protein TraC	1.37
ABUW_RS04255	gltA	citrate (Si)-synthase	1.37
ABUW_RS15960	nreB	nickel resistance MFS transporter NreB	1.37
ABUW_RS01315		CusA/CzcA family heavy metal efflux RND transporter	1.37
ABUW_RS06585		MgtC/SapB family protein	1.37
ABUW_RS09360		amidohydrolase family protein	1.37
ABUW_RS10575		2'-5' RNA ligase family protein	1.37
ABUW_RS02140		succinate dehydrogenase assembly factor 2	1.37
ABUW_RS16100		Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha	1.37
ABUW_RS13295		GNAT family N-acetyltransferase	1.37
ABUW_RS15445	bfmS	sensor histidine kinase BfmS	1.36
ABUW_RS04135	adel	multidrug efflux RND transporter periplasmic adaptor subunit Adel	1.36
ABUW_RS08280		ABC transporter substrate-binding protein	1.36
ABUW_RS15200		sulfite exporter TauE/SafE family protein	1.35
ABUW_RS02220		YcxB family protein	1.35
ABUW_RS06080	rodA	rod shape-determining protein RodA	1.35
ABUW_RS11055	maf	septum formation protein Maf	1.35
ABUW_RS16555		homoserine O-acetyltransferase	1.34
ABUW_RS14645	ggt	gamma-glutamyltransferase	1.34
ABUW_RS12025		3-oxoadipyl-CoA thiolase	1.34
ABUW_RS10910		SRPBCC family protein	1.34
ABUW_RS00150		pyrimidine permease	1.34
ABUW_RS12735		DUF1826 domain-containing protein	1.34

ABUW_RS13430		AraC family transcriptional regulator	1.33
ABUW_RS02930		hypothetical protein	1.33
ABUW_RS16910		hypothetical protein	1.33
ABUW_RS15530		LysR family transcriptional regulator	1.33
ABUW_RS16460		class I SAM-dependent methyltransferase	1.33
ABUW_RS13640		amino acid permease	1.33
ABUW_RS14280		aldehyde dehydrogenase	1.33
ABUW_RS17215		monovalent cation/H ⁺ antiporter subunit F	1.33
ABUW_RS03830		hypothetical protein	1.33
ABUW_RS14525		OprD family outer membrane porin	1.32
ABUW_RS11565		NCS1 family nucleobase:cation symporter-1	1.32
ABUW_RS04615		SDR family oxidoreductase	1.32
ABUW_RS01290		hypothetical protein	1.32
ABUW_RS05020	mltG	endolytic transglycosylase MltG	1.32
ABUW_RS11570		aspartate/glutamate racemase family protein	1.32
ABUW_RS08130		Lrp/AsnC family transcriptional regulator	1.31
ABUW_RS08025		hypothetical protein	1.31
ABUW_RS07660	prmC	peptide chain release factor N(5)-glutamine methyltransferase	1.31
ABUW_RS10775	rpsT	30S ribosomal protein S20	1.31
ABUW_RS11740		SDR family oxidoreductase	1.31
ABUW_RS08530		hypothetical protein	1.31
ABUW_RS00600		SH3 domain-containing protein	1.31
ABUW_RS13495		aldehyde dehydrogenase	1.30
ABUW_RS11705		PLP-dependent aminotransferase family protein	1.30
ABUW_RS01300		hypothetical protein	1.30
ABUW_RS02685		toprim domain-containing protein	1.30
ABUW_RS04820	hda	DnaA regulatory inactivator Hda	1.30
ABUW_RS01660	craA	MFS transporter	1.29
ABUW_RS10470		hypothetical protein	1.29
ABUW_RS07540	dnaB	replicative DNA helicase	1.29
ABUW_RS16250		tRNA threonylcarbamoyladenosine dehydratase	1.29
ABUW_RS17665	gluQRS	tRNA glutamyl-Q(34) synthetase GluQRS	1.29
ABUW_RS19610		BrnA antitoxin family protein	1.28
ABUW_RS02080	rpsE	30S ribosomal protein S5	1.28
ABUW_RS00715		DUF1737 domain-containing protein	1.28
ABUW_RS01390	ftsI	penicillin-binding protein PBP3	1.28
ABUW_RS03800		terminase family protein	1.27
ABUW_RS03535		Maf-like protein	1.27
ABUW_RS05825		DUF4105 domain-containing protein	1.27
ABUW_RS11060		cupin domain-containing protein	1.26
ABUW_RS17625		TolC family outer membrane protein	1.26
ABUW_RS08925		3-carboxy-cis,cis-muconate cycloisomerase	1.25
ABUW_RS02295		malate dehydrogenase	1.25
ABUW_RS06995	terL	phage terminase large subunit	1.25
ABUW_RS07460		ABC transporter permease	1.25
ABUW_RS01395		UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	1.25
ABUW_RS04775		lipoprotein-releasing ABC transporter permease subunit	1.24
ABUW_RS12580		helix-turn-helix transcriptional regulator	1.24
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	1.24
ABUW_RS04270		succinate dehydrogenase flavoprotein subunit	1.23
ABUW_RS08270	aroQ	type II 3-dehydroquinate dehydratase	1.23
ABUW_RS12425		GNAT family N-acetyltransferase	1.23
ABUW_RS07935		5-carboxymethyl-2-hydroxymuconate Delta-isomerase	1.23
ABUW_RS08355		DMT family transporter	1.23

ABUW_RS17335		FUSC family protein	1.23
ABUW_RS07040		CvpA family protein	1.22
ABUW_RS03320		efflux RND transporter permease subunit	1.22
ABUW_RS01685		endonuclease	1.22
ABUW_RS16990		GFA family protein	1.21
ABUW_RS02610	secD	protein translocase subunit SecD	1.21
ABUW_RS06300	terL	phage terminase large subunit	1.21
ABUW_RS11810		response regulator	1.21
ABUW_RS17790	nrdR	transcriptional repressor NrdR	1.20
ABUW_RS19715		hypothetical protein	1.20
ABUW_RS19265		quaternary ammonium compound efflux SMR transporter QacE delta 1	1.20
ABUW_RS00245	mutY	A/G-specific adenine glycosylase	1.20
sRNA97	sRNA97	sRNA97	1.20
ABUW_RS05245		peptidylprolyl isomerase	1.19
ABUW_RS01755		S8 family serine peptidase	1.19
ABUW_RS16095		NAD(P) transhydrogenase subunit alpha	1.19
ABUW_RS14765	dut	dUTP diphosphatase	1.19
ABUW_RS15980	thrS	threonine--tRNA ligase	1.19
ABUW_RS15350	gigC	LysR family transcriptional regulator GigC	1.18
ABUW_RS00415	murI	glutamate racemase	1.18
ABUW_RS13720	argG	argininosuccinate synthase	1.18
ABUW_RS00740		cell division protein FtsQ/DivIB	1.18
ABUW_RS17820		SulP family inorganic anion transporter	1.18
ABUW_RS00270		PQQ-dependent sugar dehydrogenase	1.17
ABUW_RS07840		pseudouridylate synthase	1.17
ABUW_RS17850		universal stress protein	1.17
ABUW_RS01465	gltB	glutamate synthase large subunit	1.16
ABUW_RS14360	pgaD	poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD	1.16
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.16
ABUW_RS08655	brnQ	branched-chain amino acid transport system II carrier protein	1.16
ABUW_RS05810		uroporphyrinogen decarboxylase	1.16
ABUW_RS02115	rpsD	30S ribosomal protein S4	1.15
ABUW_RS02615	yajC	preprotein translocase subunit YajC	1.15
ABUW_RS01990	rpsJ	30S ribosomal protein S10	1.15
ABUW_RS07100		protein kinase	1.15
ABUW_RS06615		thiamine phosphate synthase	1.15
ABUW_RS05040		Do family serine endopeptidase	1.15
ABUW_RS16195		hypothetical protein	1.15
ABUW_RS09255		NADH:flavin oxidoreductase/NADH oxidase family protein	1.15
ABUW_RS05535		peptidoglycan DD-metalloendopeptidase family protein	1.14
ABUW_RS01205	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1.14
ABUW_RS07405		nuclear transport factor 2 family protein	1.14
ABUW_RS12850		HAD-IIIa family hydrolase	1.14
ABUW_RS12135		hypothetical protein	1.14
ABUW_RS07550	rpsR	30S ribosomal protein S18	1.14
ABUW_RS09105		penicillin acylase family protein	1.14
ABUW_RS02360		DUF4256 domain-containing protein	1.14
ABUW_RS02450		LrgB family protein	1.13
ABUW_RS17725		PAS domain-containing sensor histidine kinase	1.13
ABUW_RS04140		phosphatase PAP2 family protein	1.13
ABUW_RS00375		HutD family protein	1.13

ABUW_RS16980		HopJ type III effector protein	1.12
ABUW_RS03250		DNA-3-methyladenine glycosylase	1.12
ABUW_RS06600		response regulator transcription factor	1.12
ABUW_RS14780		acyltransferase	1.11
ABUW_RS02135		acyl-CoA dehydrogenase family protein	1.11
ABUW_RS17615		oxidative damage protection protein	1.11
ABUW_RS02060	rpsN	30S ribosomal protein S14	1.10
ABUW_RS10660		acyl-CoA dehydrogenase family protein	1.10
ABUW_RS03900		DUF4236 domain-containing protein	1.10
ABUW_RS18205		zinc ABC transporter substrate-binding protein	1.10
ABUW_RS04130	adeJ	multidrug efflux RND transporter permease subunit AdeJ	1.10
ABUW_RS17870	arsB	ACR3 family arsenite efflux transporter	1.09
ABUW_RS11720		LysR family transcriptional regulator	1.09
ABUW_RS03190		GspH/FimT family pseudopilin	1.09
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	1.09
ABUW_RS00180	dnaJ	molecular chaperone DnaJ	1.09
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.09
ABUW_RS12450		LysR family transcriptional regulator	1.09
ABUW_RS13375		NCS2 family permease	1.08
ABUW_RS06125		hypothetical protein	1.08
ABUW_RS07665		ABC transporter permease	1.08
ABUW_RS01965		Rrf2 family transcriptional regulator	1.08
ABUW_RS00040		RND transporter	1.08
ABUW_RS10560		histidine phosphatase family protein	1.08
ABUW_RS15780	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.08
ABUW_RS09160		dihydroxy-acid dehydratase	1.08
ABUW_RS12275	paaX	phenylacetic acid degradation operon negative regulatory protein PaaX	1.08
ABUW_RS05840	xdhA	xanthine dehydrogenase small subunit	1.07
ABUW_RS18350		outer membrane lipoprotein-sorting protein	1.07
ABUW_RS05645		ethanolamine utilization protein EutQ	1.07
ABUW_RS18655		low molecular weight phosphotyrosine protein phosphatase	1.07
ABUW_RS08215	murB	UDP-N-acetylmuramate dehydrogenase	1.06
ABUW_RS03075		SPOR domain-containing protein	1.06
ABUW_RS01805		tetracycline resistance MFS efflux pump	1.06
ABUW_RS18135		TetR/AcrR family transcriptional regulator	1.06
ABUW_RS02170		YheV family putative metal-binding protein	1.06
ABUW_RS08460	uppS	di-trans,poly-cis-decaprenylcistransferase	1.06
ABUW_RS02105	rpsM	30S ribosomal protein S13	1.05
ABUW_RS07200	gltS	sodium/glutamate symporter	1.05
ABUW_RS05145		lipocalin family protein	1.05
ABUW_RS16630		dihydrofolate reductase	1.05
ABUW_RS18265		DUF3861 domain-containing protein	1.05
ABUW_RS10915	tadA	tRNA adenosine(34) deaminase TadA	1.05
ABUW_RS11015		nucleotidyltransferase family protein	1.04
ABUW_RS19570		Y-family DNA polymerase	1.04
ABUW_RS00840		alkene reductase	1.04
ABUW_RS16595	alp2	DUF839 domain-containing protein	1.04
ABUW_RS18855		peptidyl-prolyl cis-trans isomerase	1.04
ABUW_RS05045		acyl-CoA thioesterase	1.04
ABUW_RS13335	gap	type I glyceraldehyde-3-phosphate dehydrogenase	1.04
ABUW_RS00450		phosphatidylglycerophosphatase A	1.03
ABUW_RS03040		DUF1543 domain-containing protein	1.02
ABUW_RS15480		PhzF family isomerase	1.02
ABUW_RS04645		4-phosphoerythronate dehydrogenase	1.02

ABUW_RS05060		DUF4845 domain-containing protein	1.02
ABUW_RS07775		hypothetical protein	1.01
ABUW_RS07970		fimbrial biogenesis outer membrane usher protein	1.01
ABUW_RS16535		trigger factor	1.00
ABUW_RS03390		YbaN family protein	1.00
ABUW_RS18615		glycosyltransferase family 4 protein	1.00

Gene	Gene Name	Function	$\Delta baeS$ LSP vs WT LSP log2FC
ABUW_RS02990	baeS	sensor histidine kinase efflux regulator BaeS	-11.51
ABUW_RS10640		siderophore biosynthesis protein	-7.78
ABUW_RS15580	tcuA	FAD-dependent tricarballoylate dehydrogenase TcuA	-7.21
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-7.07
ABUW_RS15585	tcuB	tricarballoylate utilization 4Fe-4S protein TcuB	-6.94
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-6.58
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-6.42
ABUW_RS10585		acetyltransferase	-6.38
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.92
ABUW_RS15565		MFS transporter	-5.75
ABUW_RS10525		hypothetical protein	-5.32
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-5.31
ABUW_RS08050		hypothetical protein	-5.07
ABUW_RS11870		hypothetical protein	-5.01
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-4.97
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-4.90
ABUW_RS05750	basC	putative histamine N-monooxygenase	-4.47
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-4.47
ABUW_RS06610		hemin uptake protein HemP	-4.39
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-4.35
ABUW_RS11875		hypothetical protein	-4.35
ABUW_RS13040		hypothetical protein	-4.30
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-4.24
ABUW_RS10520		TonB-dependent siderophore receptor	-4.23
ABUW_RS05730	bauC	ferric acinetobactin ABC transporter permease subunit BauC	-4.06
ABUW_RS14480		energy transducer TonB	-4.05
ABUW_RS20145		hypothetical protein	-4.01
ABUW_RS00895		hypothetical protein	-3.92
ABUW_RS10530		PepSY domain-containing protein	-3.91
ABUW_RS01050		MFS transporter	-3.86
ABUW_RS16845		DUF2061 domain-containing protein	-3.84
ABUW_RS07500		hypothetical protein	-3.80
ABUW_RS01745		hypothetical protein	-3.63
ABUW_RS05710	bauF	acinetobactin utilization protein BauF	-3.63
ABUW_RS17925		aldolase	-3.62
ABUW_RS13010		DUF4142 domain-containing protein	-3.62
ABUW_RS12975		hypothetical protein	-3.62
ABUW_RS09210		type 1 glutamine amidotransferase domain-containing protein	-3.61
ABUW_RS20200		hypothetical protein	-3.57
ABUW_RS14485		DUF560 domain-containing protein	-3.57
ABUW_RS11860		iron-containing redox enzyme family protein	-3.56
ABUW_RS15570		substrate-binding domain-containing protein	-3.56
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-3.55
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-3.55
ABUW_RS15335		hypothetical protein	-3.52
ABUW_RS10010		hypothetical protein	-3.50

ABUW_RS11345		amino acid ABC transporter substrate-binding protein	-3.45
ABUW_RS08590		universal stress protein	-3.41
ABUW_RS03310		YegP family protein	-3.35
ABUW_RS01510		bacterioferritin-associated ferredoxin	-3.29
ABUW_RS11855	katE	catalase HPII	-3.24
ABUW_RS00710		TonB-dependent siderophore receptor	-3.20
ABUW_RS15330		mechanosensitive ion channel	-3.17
ABUW_RS11270		hypothetical protein	-3.17
ABUW_RS10070		transcriptional repressor	-3.16
ABUW_RS17400		serine hydrolase family protein	-3.12
ABUW_RS00115		methionine/alanine import family NSS transporter small subunit	-3.09
ABUW_RS18750		RcnB family protein	-3.08
ABUW_RS00660		HPF/RaiA family ribosome-associated protein	-3.07
ABUW_RS07145		DUF2171 domain-containing protein	-3.06
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-3.05
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-3.05
ABUW_RS07805		DUF4198 domain-containing protein	-3.03
ABUW_RS03760		DUF968 domain-containing protein	-2.96
ABUW_RS07620		hypothetical protein	-2.94
ABUW_RS06730		hypothetical protein	-2.93
ABUW_RS05420		SIMPL domain-containing protein	-2.90
ABUW_RS20505		hypothetical protein	-2.87
ABUW_RS08700		hypothetical protein	-2.86
ABUW_RS08390		hypothetical protein	-2.84
ABUW_RS14475		biliverdin-producing heme oxygenase	-2.83
ABUW_RS18865		hypothetical protein	-2.82
ABUW_RS17460		hypothetical protein	-2.79
ABUW_RS10890		DUF1049 domain-containing protein	-2.78
ABUW_RS02205		hypothetical protein	-2.76
ABUW_RS14505		sigma-70 family RNA polymerase sigma factor	-2.76
ABUW_RS15280		hypothetical protein	-2.73
ABUW_RS19580		hypothetical protein	-2.70
ABUW_RS01370		hypothetical protein	-2.69
ABUW_RS11160		OsmC family protein	-2.65
ABUW_RS20295		hypothetical protein	-2.64
ABUW_RS01615		hemerythrin domain-containing protein	-2.62
ABUW_RS16080	rsfS	ribosome silencing factor	-2.57
ABUW_RS13105		hypothetical protein	-2.56
ABUW_RS03005		acyl-CoA desaturase	-2.55
ABUW_RS17680		hypothetical protein	-2.55
ABUW_RS17645	thiC	phosphomethylpyrimidine synthase ThiC	-2.54
ABUW_RS20135		hypothetical protein	-2.53
ABUW_RS01760		hypothetical protein	-2.52
ABUW_RS16815		DUF1311 domain-containing protein	-2.51
ABUW_RS02875		HAMP domain-containing histidine kinase	-2.51
ABUW_RS05725	bauD	ferric acinetobactin ABC transporter permease subunit BauD	-2.50
ABUW_RS12900		DUF4882 family protein	-2.47
ABUW_RS03435		PepSY domain-containing protein	-2.44
ABUW_RS14870		EcsC family protein	-2.44
ABUW_RS07430		GNAT family N-acetyltransferase	-2.43
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-2.41
ABUW_RS16255	acnA	aconitate hydratase AcnA	-2.41
ABUW_RS10850		biopolymer transporter ExbD	-2.40
ABUW_RS15790	raiA	ribosome-associated translation inhibitor RaiA	-2.40
ABUW_RS15290		NF038215 family lipoprotein	-2.39
ABUW_RS11265		DMT family transporter	-2.39
ABUW_RS11850		glucose 1-dehydrogenase	-2.37

ABUW_RS11425		tautomerase family protein	-2.36
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	-2.35
ABUW_RS08715		nitroreductase family protein	-2.35
ABUW_RS02650		hypothetical protein	-2.35
sRNA13	sRNA13	sRNA13	-2.31
ABUW_RS00485		hypothetical protein	-2.31
ABUW_RS10125		transporter	-2.29
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-2.29
ABUW_RS08690		DUF2750 domain-containing protein	-2.29
ABUW_RS06975		hypothetical protein	-2.28
ABUW_RS07855	miaA	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	-2.27
ABUW_RS15160	otsB	trehalose-phosphatase	-2.27
ABUW_RS13365		cytochrome b	-2.26
ABUW_RS13005		hypothetical protein	-2.26
ABUW_RS05940		superoxide dismutase	-2.26
ABUW_RS08195		acyl-CoA thioesterase	-2.22
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-2.21
ABUW_RS10895		integration host factor subunit beta	-2.18
ABUW_RS10075		isochorismatase family protein	-2.16
ABUW_RS12795		hypothetical protein	-2.16
ABUW_RS15165		trehalose-6-phosphate synthase	-2.15
ABUW_RS01690		hypothetical protein	-2.14
ABUW_RS04365		universal stress protein	-2.14
ABUW_RS19720	bap	Ig-like domain-containing protein	-2.13
ABUW_RS12465	icmH	type IVB secretion system protein IcmH/DotU	-2.13
ABUW_RS13680		RHS repeat protein	-2.11
ABUW_RS07425		sorbose dehydrogenase family protein	-2.10
ABUW_RS00025	cybC	cytochrome b562	-2.10
ABUW_RS00690		DUF2147 domain-containing protein	-2.08
ABUW_RS11150		lecithin retinol acyltransferase family protein	-2.08
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	-2.08
ABUW_RS11615		hypothetical protein	-2.07
ABUW_RS01765		hypothetical protein	-2.07
ABUW_RS08380		SDR family NAD(P)-dependent oxidoreductase	-2.06
ABUW_RS15230		hypothetical protein	-2.06
ABUW_RS01895		ABC transporter substrate-binding protein	-2.06
ABUW_RS03920		Arc family DNA-binding protein	-2.05
ABUW_RS02995		response regulator	-2.05
ABUW_RS03380		entericidin A/B family lipoprotein	-2.04
ABUW_RS03155		carbohydrate porin	-2.04
ABUW_RS18875		MBL fold metallo-hydrolase	-2.04
ABUW_RS10475		hypothetical protein	-2.04
ABUW_RS07170		NirD/YgiW/YdeI family stress tolerance protein	-2.01
ABUW_RS15055		GDYXXLXY domain-containing protein	-1.99
ABUW_RS14730		RnfH family protein	-1.99
ABUW_RS02765	oxa-23	carbapenem-hydrolyzing class D beta-lactamase OXA-23	-1.99
ABUW_RS16640	msrA	peptide-methionine (S)-S-oxide reductase MsrA	-1.99
ABUW_RS16155		heavy metal translocating P-type ATPase	-1.98
ABUW_RS12725		hypothetical protein	-1.97
ABUW_RS17105		MerR family transcriptional regulator	-1.97
ABUW_RS08770		insulinase family protein	-1.96
ABUW_RS00825		putative porin	-1.95
ABUW_RS08095		universal stress protein	-1.95
ABUW_RS16680	rpmG	50S ribosomal protein L33	-1.94
ABUW_RS02270	ybeY	rRNA maturation RNase YbeY	-1.93
ABUW_RS18440		RidA family protein	-1.93
ABUW_RS13450		GMC family oxidoreductase	-1.93

ABUW_RS05330		DUF962 domain-containing protein	-1.92
ABUW_RS00515		alpha/beta fold hydrolase	-1.92
ABUW_RS06655		alpha/beta hydrolase	-1.92
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.92
ABUW_RS17190		AAA family ATPase	-1.91
ABUW_RS13675		hypothetical protein	-1.90
ABUW_RS08825	clpA	ATP-dependent Clp protease ATP-binding subunit ClpA	-1.90
ABUW_RS01020		hydrolase	-1.89
ABUW_RS01295		hypothetical protein	-1.89
ABUW_RS04960		hypothetical protein	-1.88
ABUW_RS14030		isocitrate lyase	-1.87
ABUW_RS11885		hypothetical protein	-1.87
ABUW_RS18740		YciK family oxidoreductase	-1.86
ABUW_RS02260		hypothetical protein	-1.86
ABUW_RS09275		hydrolase	-1.85
ABUW_RS06900		hypothetical protein	-1.84
ABUW_RS00490		hypothetical protein	-1.84
ABUW_RS12805		universal stress protein	-1.84
ABUW_RS00300		4-hydroxy-tetrahydronicotinate synthase	-1.84
ABUW_RS05425		diaminobutyrate--2-oxoglutarate transaminase	-1.83
ABUW_RS04295	sucC	ADP-forming succinate--CoA ligase subunit beta	-1.83
ABUW_RS07225		SRPBCC family protein	-1.83
ABUW_RS10845		biopolymer transporter ExbD	-1.82
ABUW_RS10095	modA	molybdate ABC transporter substrate-binding protein	-1.82
ABUW_RS05130		diguanylate cyclase	-1.82
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.81
ABUW_RS01645		antibiotic biosynthesis monooxygenase	-1.81
ABUW_RS00015	recF	DNA replication/repair protein RecF	-1.80
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.79
ABUW_RS02475		metallophosphoesterase	-1.79
ABUW_RS01640		hypothetical protein	-1.79
ABUW_RS09540		endonuclease/exonuclease/phosphatase family protein	-1.78
ABUW_RS11145		phosphodiester glycosidase family protein	-1.78
ABUW_RS01320		cation transporter	-1.78
ABUW_RS03890		DUF4258 domain-containing protein	-1.77
ABUW_RS04300	sucD	succinate--CoA ligase subunit alpha	-1.76
ABUW_RS01975		DUF853 domain-containing protein	-1.76
ABUW_RS17640		hypothetical protein	-1.76
ABUW_RS07860	hfq	RNA chaperone Hfq	-1.75
ABUW_RS08165		hypothetical protein	-1.75
ABUW_RS07585		RDD family protein	-1.75
ABUW_RS18050	cysK	cysteine synthase A	-1.74
ABUW_RS16745		SlyX family protein	-1.74
ABUW_RS00020	gyrB	DNA topoisomerase (ATP-hydrolyzing) subunit B	-1.73
ABUW_RS14155		hypothetical protein	-1.73
ABUW_RS08075		OmpW family protein	-1.72
ABUW_RS10615		(2Fe-2S)-binding protein	-1.72
ABUW_RS08040		mechanosensitive ion channel	-1.72
ABUW_RS03500		DJ-1/Pfpl family protein	-1.71
ABUW_RS02240		YihY family inner membrane protein	-1.71
ABUW_RS06710	rpoH	RNA polymerase sigma factor RpoH	-1.71
ABUW_RS19085		H-NS histone family protein	-1.71
ABUW_RS16850		LysR family transcriptional regulator	-1.71
ABUW_RS07870	nfsB	oxygen-insensitive NAD(P)H nitroreductase	-1.71
ABUW_RS06905		hypothetical protein	-1.70
ABUW_RS07950		hypothetical protein	-1.70
ABUW_RS18815		peptidylprolyl isomerase	-1.70

ABUW_RS17395		hypothetical protein	-1.70
ABUW_RS11070		helix-turn-helix transcriptional regulator	-1.69
ABUW_RS09585		hypothetical protein	-1.69
ABUW_RS08385	fumC	class II fumarate hydratase	-1.68
ABUW_RS05805		murein L,D-transpeptidase	-1.68
ABUW_RS15365	upp	uracil phosphoribosyltransferase	-1.67
ABUW_RS07220		SDR family oxidoreductase	-1.67
ABUW_RS01930		NAD(P)H-binding protein	-1.67
ABUW_RS17145		hypothetical protein	-1.67
ABUW_RS02655		hypothetical protein	-1.66
ABUW_RS14025		copper resistance protein NlpE	-1.66
ABUW_RS08820	clpS	ATP-dependent Clp protease adapter ClpS	-1.66
ABUW_RS12545		hypothetical protein	-1.65
ABUW_RS16695		hypothetical protein	-1.65
ABUW_RS14160		TonB-dependent siderophore receptor	-1.65
ABUW_RS02970		phosphate-starvation-inducible PsiE family protein	-1.65
ABUW_RS09185		alpha/beta hydrolase	-1.64
ABUW_RS04865	pal	peptidoglycan-associated lipoprotein Pal	-1.64
ABUW_RS01480		LemA family protein	-1.64
ABUW_RS04950		peroxiredoxin	-1.63
ABUW_RS00195		START domain-containing protein	-1.63
ABUW_RS03195		OmpA family protein	-1.62
ABUW_RS13210		DUF1653 domain-containing protein	-1.62
ABUW_RS13985	ureG	urease accessory protein UreG	-1.61
ABUW_RS03970		hypothetical protein	-1.60
ABUW_RS16675	rpmB	50S ribosomal protein L28	-1.60
ABUW_RS15260		LysE family transporter	-1.60
ABUW_RS05135		hypothetical protein	-1.60
ABUW_RS08775		phospholipase A	-1.59
ABUW_RS03145		AraC family transcriptional regulator	-1.59
ABUW_RS12460		hypothetical protein	-1.59
ABUW_RS05260		M61 family metallopeptidase	-1.58
ABUW_RS02715		BRCT domain-containing protein	-1.58
ABUW_RS06670		hypothetical protein	-1.58
ABUW_RS08705		hypothetical protein	-1.58
ABUW_RS15655		multidrug efflux SMR transporter	-1.58
ABUW_RS09270		antibiotic biosynthesis monooxygenase	-1.57
ABUW_RS00555		hypothetical protein	-1.57
ABUW_RS03550		wax ester/triacylglycerol synthase family O-acyltransferase	-1.57
ABUW_RS01015		LysR family transcriptional regulator	-1.56
ABUW_RS14805		PA4642 family protein	-1.56
ABUW_RS08840		alpha/beta hydrolase	-1.54
ABUW_RS03180		VOC family protein	-1.54
ABUW_RS03895		helix-turn-helix domain-containing protein	-1.54
ABUW_RS01490		TPM domain-containing protein	-1.54
ABUW_RS08425	argF	ornithine carbamoyltransferase	-1.53
ABUW_RS14550		DEAD/DEAH box helicase family protein	-1.53
ABUW_RS14215		transketolase	-1.52
ABUW_RS10860		malate synthase G	-1.52
ABUW_RS09180		hypothetical protein	-1.50
ABUW_RS06250		hypothetical protein	-1.50
ABUW_RS05430		aspartate aminotransferase family protein	-1.50
ABUW_RS13205		O-methyltransferase	-1.50
ABUW_RS08580		SOS response-associated peptidase family protein	-1.49
ABUW_RS02535		alpha/beta hydrolase	-1.49
ABUW_RS16305	ilvN	acetolactate synthase small subunit	-1.49
ABUW_RS00295		hypothetical protein	-1.49

ABUW_RS12470	tssK	type VI secretion system baseplate subunit TssK	-1.48
ABUW_RS10510		DUF2797 domain-containing protein	-1.48
ABUW_RS11200		helix-turn-helix transcriptional regulator	-1.48
ABUW_RS15855		organic hydroperoxide resistance protein	-1.48
ABUW_RS13275		hypothetical protein	-1.47
ABUW_RS06400		ORF6N domain-containing protein	-1.47
ABUW_RS06000	lipA	lipoyl synthase	-1.46
ABUW_RS04515		MBL fold metallo-hydrolase	-1.46
ABUW_RS08430	adeN	multidrug efflux transcriptional repressor AdeN	-1.46
ABUW_RS03445	yccS	TIGR01666 family membrane protein	-1.45
ABUW_RS10690		phasin family protein	-1.44
ABUW_RS14720	fur	ferric iron uptake transcriptional regulator	-1.44
ABUW_RS00475		hypothetical protein	-1.43
ABUW_RS06280		hypothetical protein	-1.43
ABUW_RS02275		PhoH family protein	-1.43
ABUW_RS14810	rhtC	threonine export protein RhtC	-1.42
ABUW_RS05315		DUF3144 domain-containing protein	-1.42
ABUW_RS13250		OmpA family protein	-1.42
ABUW_RS13885	pepP	Xaa-Pro aminopeptidase	-1.41
ABUW_RS11625	cydB	cytochrome d ubiquinol oxidase subunit II	-1.41
ABUW_RS08585		PQQ-dependent sugar dehydrogenase	-1.41
ABUW_RS18150		glutathione peroxidase	-1.41
ABUW_RS04490		metallophosphoesterase	-1.41
ABUW_RS14555		site-specific DNA-methyltransferase	-1.40
ABUW_RS02985		hypothetical protein	-1.40
ABUW_RS07590	ppsA	phosphoenolpyruvate synthase	-1.39
ABUW_RS17930		dihydrodipicolinate synthase family protein	-1.39
ABUW_RS18475		ribonuclease E inhibitor RraB	-1.38
ABUW_RS16355		Bax inhibitor-1/YccA family protein	-1.38
ABUW_RS05205		hypothetical protein	-1.38
ABUW_RS01215		DUF805 domain-containing protein	-1.37
ABUW_RS13990		urease accessory protein	-1.37
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-1.37
ABUW_RS00030		VTT domain-containing protein	-1.36
ABUW_RS18275		aminoglycoside nucleotidyltransferase ANT(3'')-IIa	-1.36
ABUW_RS04380	carB	carbamoyl-phosphate synthase large subunit	-1.36
ABUW_RS04090		hypothetical protein	-1.36
ABUW_RS08710	ftsY	signal recognition particle-docking protein FtsY	-1.36
ABUW_RS16855		HAD-IB family hydrolase	-1.35
ABUW_RS10610		RraA family protein	-1.35
ABUW_RS01475		metal-dependent hydrolase	-1.35
ABUW_RS02540	trxC	thioredoxin TrxC	-1.35
sRNA18	sRNA18	sRNA18	-1.35
ABUW_RS13280		CinA family protein	-1.35
ABUW_RS17100		DnaJ domain-containing protein	-1.35
ABUW_RS13225		glutathione S-transferase N-terminal domain-containing protein	-1.35
ABUW_RS01025		pirin family protein	-1.34
ABUW_RS02660		3'-5' exonuclease	-1.34
ABUW_RS02300		DUF2789 domain-containing protein	-1.34
ABUW_RS08200		iron-containing alcohol dehydrogenase	-1.33
ABUW_RS03230	mscL	large conductance mechanosensitive channel protein MscL	-1.33
ABUW_RS18670		FKBP-type peptidyl-prolyl cis-trans isomerase	-1.33
ABUW_RS04965	queC	7-cyano-7-deazaguanine synthase QueC	-1.33
ABUW_RS08440		PAS domain-containing protein	-1.33
ABUW_RS14815		DNA translocase FtsK	-1.32
ABUW_RS11440	dapC	succinyl-diaminopimelate transaminase	-1.32
ABUW_RS06620		tetratricopeptide repeat protein	-1.32

ABUW_RS07765		outer membrane protein assembly factor	-1.31
ABUW_RS15215	ffh	signal recognition particle protein	-1.31
ABUW_RS16375	grxC	glutaredoxin 3	-1.30
ABUW_RS02975		acyl-CoA dehydrogenase C-terminal domain-containing protein	-1.30
ABUW_RS11725	yfcF	glutathione transferase	-1.29
ABUW_RS16325		hypothetical protein	-1.29
ABUW_RS08435	glnG	nitrogen regulation protein NR(I)	-1.29
ABUW_RS20125		hypothetical protein	-1.29
ABUW_RS05095		SDR family oxidoreductase	-1.28
ABUW_RS13200		KTSC domain-containing protein	-1.28
ABUW_RS07755	coq7	2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinone monooxygenase	-1.28
ABUW_RS11835		hypothetical protein	-1.28
ABUW_RS06680		MBL fold metallo-hydrolase	-1.28
ABUW_RS02325		hypothetical protein	-1.28
ABUW_RS11155		polyisoprenoid-binding protein	-1.27
ABUW_RS14300		cupin domain-containing protein	-1.27
ABUW_RS09020		SDR family oxidoreductase	-1.26
ABUW_RS10605	bfnH	TonB-dependent receptor	-1.26
ABUW_RS04095		valine--tRNA ligase	-1.26
ABUW_RS12915		fibronectin type III domain-containing protein	-1.26
ABUW_RS14210		transketolase	-1.26
ABUW_RS17410		hypothetical protein	-1.25
ABUW_RS14680		ABZJ_00895 family protein	-1.25
ABUW_RS19625		hypothetical protein	-1.25
ABUW_RS03630		hypothetical protein	-1.24
ABUW_RS10015		phospholipase D family protein	-1.24
ABUW_RS04935		enoyl-CoA hydratase/isomerase family protein	-1.24
ABUW_RS04385	carA	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	-1.24
ABUW_RS18245		SPOR domain-containing protein	-1.23
ABUW_RS01485		TPM domain-containing protein	-1.22
ABUW_RS14590		hypothetical protein	-1.21
ABUW_RS02920		glycosyltransferase family 25 protein	-1.21
ABUW_RS17450		alpha/beta fold hydrolase	-1.21
ABUW_RS03910		hypothetical protein	-1.21
ABUW_RS15730		hypothetical protein	-1.20
ABUW_RS15255		dCTP deaminase	-1.20
ABUW_RS18820		NAD(P)H-dependent oxidoreductase	-1.19
ABUW_RS01260	ompR	two-component system response regulator OmpR	-1.19
ABUW_RS05830		class C extended-spectrum beta-lactamase ADC-11	-1.19
ABUW_RS09550		GNAT family N-acetyltransferase	-1.19
ABUW_RS06650		acyl-CoA dehydrogenase family protein	-1.19
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.18
ABUW_RS16715		HdeD family acid-resistance protein	-1.18
ABUW_RS16425	rlmN	23S rRNA (adenine(2503)-C(2))-methyltransferase RlmN	-1.18
ABUW_RS06420		tape measure protein	-1.18
ABUW_RS00685		alpha/beta hydrolase	-1.17
ABUW_RS03065		acetyl-CoA carboxylase carboxyltransferase subunit beta	-1.17
ABUW_RS00890		response regulator transcription factor	-1.17
ABUW_RS14170		rhomboid family intramembrane serine protease	-1.17
ABUW_RS17340		transcriptional regulator	-1.17
ABUW_RS17155		hypothetical protein	-1.17
ABUW_RS16445		glycosyltransferase family 1 protein	-1.17
ABUW_RS05520		hypothetical protein	-1.17
ABUW_RS08090		ABC-F family ATP-binding cassette domain-containing protein	-1.16
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	-1.16
ABUW_RS01950		dicarboxylate/amino acid:cation symporter	-1.15
ABUW_RS08485		OmpH family outer membrane protein	-1.15

ABUW_RS08995	pcaU	IcIR family transcriptional regulator PcaU	-1.15
ABUW_RS01945		acyl-CoA thioesterase II	-1.15
ABUW_RS17985		TerC family protein	-1.15
ABUW_RS10580		HAD family hydrolase	-1.15
ABUW_RS05070	era	GTPase Era	-1.14
ABUW_RS15825		VacJ family lipoprotein	-1.14
ABUW_RS18790		5'-nucleosidase	-1.14
ABUW_RS05310		insulinase family protein	-1.14
ABUW_RS07675		AraC family transcriptional regulator	-1.14
ABUW_RS13245		DUF2520 domain-containing protein	-1.14
ABUW_RS16465		alpha/beta hydrolase	-1.13
ABUW_RS16360	orn	oligoribonuclease	-1.13
ABUW_RS18110		peptide deformylase	-1.13
ABUW_RS07700		HesA/MoeB/ThiF family protein	-1.13
ABUW_RS15880	polA	DNA polymerase I	-1.12
ABUW_RS09680		hypothetical protein	-1.12
ABUW_RS15660		cation transporter	-1.12
ABUW_RS04020		SPFH/Band 7/PHB domain protein	-1.12
ABUW_RS16075		TIM barrel protein	-1.12
ABUW_RS01910		TIGR00730 family Rossmann fold protein	-1.12
ABUW_RS09290		cation:proton antiporter	-1.12
ABUW_RS12065		MFS transporter	-1.11
ABUW_RS12475	tssA	type VI secretion system protein TssA	-1.11
ABUW_RS03915		Arc family DNA-binding protein	-1.11
ABUW_RS02255		DUF3108 domain-containing protein	-1.11
ABUW_RS01705		hypothetical protein	-1.10
ABUW_RS15715		gamma carbonic anhydrase family protein	-1.10
ABUW_RS06550	abeS	multidrug efflux SMR transporter AbeS	-1.10
ABUW_RS06625	mrcB	penicillin-binding protein 1B	-1.10
ABUW_RS03010		META domain-containing protein	-1.10
sRNA17	sRNA17	sRNA17	-1.10
ABUW_RS16440		phosphatase PAP2 family protein	-1.09
ABUW_RS04985	cbl	CysB family HTH-type transcriptional regulator	-1.09
ABUW_RS18235		NAD-dependent malic enzyme	-1.09
ABUW_RS07595		kinase/pyrophosphorylase	-1.09
ABUW_RS02490		YfiR family protein	-1.09
ABUW_RS08660	map	type I methionyl aminopeptidase	-1.09
ABUW_RS02545		acyl-CoA thioesterase	-1.09
ABUW_RS02915		hypothetical protein	-1.09
ABUW_RS05695		pirin family protein	-1.08
ABUW_RS00870		cysteine hydrolase	-1.08
ABUW_RS13870		hypothetical protein	-1.08
ABUW_RS14900		hypothetical protein	-1.08
ABUW_RS00560		DUF924 domain-containing protein	-1.08
ABUW_RS05305		PhzF family phenazine biosynthesis protein	-1.08
ABUW_RS12880		hypothetical protein	-1.07
ABUW_RS05485		DUF2238 domain-containing protein	-1.07
ABUW_RS16970		ABC transporter	-1.07
ABUW_RS16565		sel1 repeat family protein	-1.07
ABUW_RS13240		glutathione S-transferase	-1.07
ABUW_RS04215		hypothetical protein	-1.07
ABUW_RS06970		hypothetical protein	-1.07
ABUW_RS01190		membrane protein	-1.07
ABUW_RS08875		hypothetical protein	-1.07
ABUW_RS12610		SRPBCC family protein	-1.06
ABUW_RS02180	rnR	ribonuclease R	-1.06
ABUW_RS15275	apbC	iron-sulfur cluster carrier protein ApbC	-1.06

ABUW_RS03595		AraC family transcriptional regulator	-1.05
ABUW_RS01650		NAD(P)H-dependent oxidoreductase	-1.05
ABUW_RS15090	fabG	3-oxoacyl-ACP reductase FabG	-1.05
ABUW_RS10770		nucleoside-diphosphate sugar epimerase	-1.05
ABUW_RS10655		AarF/ABC1/UbiB kinase family protein	-1.05
ABUW_RS05985		peptidase C39	-1.04
ABUW_RS18645	tvbB	Vi polysaccharide biosynthesis UDP-N-acetylglucosamine C-6 dehydrogenase TvB	-1.04
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.04
ABUW_RS17160	ubiE	bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polypropenyl-1,4-benzoquinol methylase UbiE	-1.03
ABUW_RS00920	betT	choline BCCT transporter BetT	-1.03
ABUW_RS01420	ponA	penicillin-binding protein PBP1a	-1.03
ABUW_RS00945		zinc-binding dehydrogenase	-1.02
ABUW_RS14675		TIGR01777 family oxidoreductase	-1.02
ABUW_RS00770	aceE	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	-1.01
ABUW_RS07065		M48 family metalloprotease	-1.01
ABUW_RS15360		cold shock domain-containing protein	-1.01
ABUW_RS12745		DUF2147 domain-containing protein	-1.00
ABUW_RS04250		DUF1289 domain-containing protein	-1.00
ABUW_RS14115	ppk1	polyphosphate kinase 1	-1.00
ABUW_RS07345		heavy metal response regulator transcription factor	-1.00

Table A7. Overview of genes that are differentially expressed as identified through RNA-seq analysis in *ΔgacA* MEP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	<i>ΔgacA</i> MEP vs WT MEP log2FC
sRNA92	sRNA92	sRNA92	6.10
ABUW_RS09120		CoA transferase subunit B	6.09
ABUW_RS11825		LysE family translocator	5.93
ABUW_RS10185		CoA transferase subunit B	5.34
ABUW_RS10190		short-chain fatty acid transporter	5.14
ABUW_RS11715		CidA/LrgA family protein	4.92
sRNA94	sRNA94	sRNA94	4.72
ABUW_RS10180		CoA transferase subunit A	4.57
ABUW_RS13600		aspartate aminotransferase family protein	4.55
ABUW_RS09140		muconate cycloisomerase	4.34
ABUW_RS10195		thiolase family protein	4.19
ABUW_RS09130	catA	catechol 1,2-dioxygenase	3.91
ABUW_RS09135	catC	muconolactone Delta-isomerase	3.84
ABUW_RS10160		3-hydroxybutyrate dehydrogenase	3.77
ABUW_RS10165		GntP family permease	3.67
ABUW_RS18435		amino acid permease	3.66
ABUW_RS13855		amino acid transporter	3.64
ABUW_RS11710		LrgB family protein	3.61
ABUW_RS10150		MFS transporter	3.51
ABUW_RS03465		alanine:cation symporter family protein	3.50
ABUW_RS13595	astA	arginine N-succinyltransferase	3.40
ABUW_RS11475		type II asparaginase	3.36
ABUW_RS18235		NAD-dependent malic enzyme	3.36
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	3.33
ABUW_RS10110	antB	anthranilate 1,2-dioxygenase small subunit	3.21
sRNA96	sRNA96	sRNA96	3.19
ABUW_RS07110		tRNA-Trp	3.18
ABUW_RS08125		benzoate/H(+) symporter BenE family transporter	3.14
ABUW_RS10115	antC	anthranilate 1,2-dioxygenase electron transfer component AntC	3.05

ABUW_RS18450		D-amino acid dehydrogenase	2.99
ABUW_RS16770	gltP	glutamate/aspartate:proton symporter GltP	2.98
ABUW_RS11440	dapC	succinyldiaminopimelate transaminase	2.95
ABUW_RS10775	rpsT	30S ribosomal protein S20	2.95
sRNA24	sRNA24	sRNA24	2.95
ABUW_RS13860		cation transporter	2.93
ABUW_RS03460		hypothetical protein	2.87
ABUW_RS10355		thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha	2.85
ABUW_RS09110	pcaD	3-oxoadipate enol-lactonase	2.82
ABUW_RS01235		tRNA-Phe	2.80
ABUW_RS05565	rpmE	50S ribosomal protein L31	2.80
ABUW_RS01710		amino acid permease	2.77
ABUW_RS06595		NirD/YgiW/Ydel family stress tolerance protein	2.76
ABUW_RS18440		RidA family protein	2.73
ABUW_RS10350		alpha-ketoacid dehydrogenase subunit beta	2.70
sRNA1	sRNA1	sRNA1	2.69
sRNA81	sRNA81	sRNA81	2.67
ABUW_RS10340	lpdA	dihydrolipoyl dehydrogenase	2.65
ABUW_RS13520		Paal family thioesterase	2.64
ABUW_RS09115	pcaF	3-oxoadipyl-CoA thiolase	2.63
ABUW_RS10120		AraC family transcriptional regulator	2.62
ABUW_RS10345		2-oxo acid dehydrogenase subunit E2	2.61
sRNA84	sRNA84	sRNA84	2.59
ABUW_RS01740	astE	succinylglutamate desuccinylase	2.56
ABUW_RS13745		TonB-dependent receptor	2.50
ABUW_RS18100		TonB-dependent copper receptor	2.50
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	2.49
ABUW_RS17840		cation transporter	2.49
ABUW_RS11140		hypothetical protein	2.49
ABUW_RS00705	pyrE	orotate phosphoribosyltransferase	2.48
ABUW_RS19905	ssrS	6S RNA	2.47
ABUW_RS16810	infA	translation initiation factor IF-1	2.45
ABUW_RS05445		alpha-keto acid decarboxylase family protein	2.44
ABUW_RS09355		MFS transporter	2.42
ABUW_RS08720		DUF2057 domain-containing protein	2.42
ABUW_RS03430		YdcF family protein	2.39
ABUW_RS20110		hypothetical protein	2.38
ABUW_RS18445	alr	alanine racemase	2.37
ABUW_RS01350		amino acid permease	2.37
ABUW_RS11115	putP	sodium/proline symporter PutP	2.37
ABUW_RS07640		hypothetical protein	2.34
ABUW_RS07105		tRNA-Leu	2.33
ABUW_RS05660	yddG	aromatic amino acid DMT transporter YddG	2.32
ABUW_RS13515		DUF3237 domain-containing protein	2.31
ABUW_RS15950	rplT	50S ribosomal protein L20	2.31
ABUW_RS04505	groL	chaperonin GroEL	2.31
ABUW_RS08715		nitroreductase family protein	2.31
ABUW_RS06195		hypothetical protein	2.30
ABUW_RS13590		amino acid permease	2.29
ABUW_RS09575		alpha/beta fold hydrolase	2.29
ABUW_RS15030		tRNA-Gln	2.28
ABUW_RS15025		tRNA-Gln	2.28
ABUW_RS16540		TonB-dependent siderophore receptor	2.27
ABUW_RS08890	eno	phosphopyruvate hydratase	2.27
ABUW_RS14650		DHA2 family efflux MFS transporter permease subunit	2.26
ABUW_RS17330		DUF1656 domain-containing protein	2.26

ABUW_RS09365		SLC13 family permease	2.26
ABUW_RS13510		OprD family porin	2.25
ABUW_RS00770	aceE	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	2.24
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	2.24
ABUW_RS01820		HPP family protein	2.22
ABUW_RS01735	astB	N-succinylarginine dihydrolase	2.20
ABUW_RS02545		acyl-CoA thioesterase	2.17
ABUW_RS00350		amino acid permease	2.17
ABUW_RS11170		methionine adenosyltransferase	2.16
ABUW_RS04545	ttcA	tRNA 2-thiocytidine(32) synthetase TtcA	2.16
ABUW_RS07565		cytochrome o ubiquinol oxidase subunit IV	2.15
sRNA6	sRNA6	sRNA6	2.15
ABUW_RS17975		trimeric intracellular cation channel family protein	2.14
ABUW_RS01510		bacterioferritin-associated ferredoxin	2.14
ABUW_RS02635	queA	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	2.11
ABUW_RS01470		FAD-dependent oxidoreductase	2.10
ABUW_RS00150		pyrimidine permease	2.10
ABUW_RS10710	iscU	Fe-S cluster assembly scaffold IscU	2.09
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	2.09
ABUW_RS00965		DUF475 domain-containing protein	2.09
ABUW_RS17510		tRNA-Trp	2.08
ABUW_RS05670		type II toxin-antitoxin system Phd/YefM family antitoxin	2.07
ABUW_RS14165	nfuA	Fe-S biogenesis protein NfuA	2.06
ABUW_RS13490		p-hydroxycinnamoyl CoA hydratase/lyase	2.05
ABUW_RS17645	thiC	phosphomethylpyrimidine synthase ThiC	2.04
ABUW_RS18975	hpt	hypoxanthine phosphoribosyltransferase	2.03
ABUW_RS06575		ferredoxin--NADP reductase	2.02
ABUW_RS05835	folE	GTP cyclohydrolase I FolE	2.02
ABUW_RS01195		DMT family transporter	2.02
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	2.01
ABUW_RS18035		DUF2938 domain-containing protein	2.01
ABUW_RS08355		DMT family transporter	2.01
ABUW_RS17120	rpsO	30S ribosomal protein S15	2.01
ABUW_RS13525		tannase/feruloyl esterase family alpha/beta hydrolase	2.00
ABUW_RS13495		aldehyde dehydrogenase	2.00
ABUW_RS15955	rpml	50S ribosomal protein L35	1.98
ABUW_RS06685		hydrolase	1.98
ABUW_RS02000	rplD	50S ribosomal protein L4	1.97
ABUW_RS18430		amino acid permease	1.97
ABUW_RS05120		pyridoxal phosphate-dependent aminotransferase	1.97
ABUW_RS18030		helix-turn-helix domain-containing protein	1.97
ABUW_RS11315		YebC/PmpR family DNA-binding transcriptional regulator	1.97
ABUW_RS10380	aroC	chorismate synthase	1.97
ABUW_RS05155		glyceraldehyde-3-phosphate dehydrogenase	1.97
ABUW_RS09620		NAD(P)/FAD-dependent oxidoreductase	1.96
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.96
ABUW_RS07545	rplI	50S ribosomal protein L9	1.95
ABUW_RS14765	dut	dUTP diphosphatase	1.94
ABUW_RS08680		aspartate aminotransferase family protein	1.94
sRNA37	sRNA37	sRNA37	1.94
ABUW_RS10140		SDR family oxidoreductase	1.93
ABUW_RS14435	mgo	malate dehydrogenase (quinone)	1.93
ABUW_RS14915		NAD-dependent succinate-semialdehyde dehydrogenase	1.93
ABUW_RS13235	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	1.92
ABUW_RS18915		5-(carboxyamino)imidazole ribonucleotide synthase	1.92

ABUW_RS19255		GNAT family N-acetyltransferase	1.92
ABUW_RS17430	htpG	molecular chaperone HtpG	1.91
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	1.91
ABUW_RS10225		TonB-dependent siderophore receptor	1.91
ABUW_RS09360		amidohydrolase family protein	1.91
ABUW_RS09090	tynA	primary-amine oxidase	1.90
ABUW_RS07445		dicarboxylate/amino acid:cation symporter	1.89
ABUW_RS17300		pyrimidine/purine nucleoside phosphorylase	1.89
ABUW_RS07475	purD	phosphoribosylamine--glycine ligase	1.89
ABUW_RS07045	purF	amidophosphoribosyltransferase	1.88
ABUW_RS13360		hypothetical protein	1.88
ABUW_RS08560		amino acid permease	1.87
ABUW_RS17835		signal peptidase II	1.87
ABUW_RS01575	rpsP	30S ribosomal protein S16	1.86
ABUW_RS04915	purL	phosphoribosylformylglycinamide synthase	1.86
ABUW_RS12800		O-methyltransferase	1.86
ABUW_RS07625		LLM class flavin-dependent oxidoreductase	1.85
ABUW_RS00055	erpA	iron-sulfur cluster insertion protein ErpA	1.85
ABUW_RS14395		hypothetical protein	1.85
sRNA101	sRNA101	sRNA101	1.84
ABUW_RS04300	sucD	succinate--CoA ligase subunit alpha	1.84
ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	1.83
ABUW_RS01175	hisF	imidazole glycerol phosphate synthase subunit HisF	1.83
ABUW_RS02015	rpsS	30S ribosomal protein S19	1.83
ABUW_RS11015		nucleotidyltransferase family protein	1.82
ABUW_RS03375	dapE	succinyl-diaminopimelate desuccinylase	1.82
ABUW_RS10540		sulfite exporter TauE/SafE family protein	1.82
ABUW_RS13375		NCS2 family permease	1.82
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	1.82
ABUW_RS16510		fumarate hydratase	1.82
ABUW_RS06040		elongation factor Ts	1.82
ABUW_RS06505		serine hydroxymethyltransferase	1.82
ABUW_RS00325	hppD	4-hydroxyphenylpyruvate dioxygenase	1.81
ABUW_RS18675	murJ	murein biosynthesis integral membrane protein MurJ	1.81
ABUW_RS03220		uracil-xanthine permease	1.80
ABUW_RS14200		inorganic phosphate transporter	1.80
ABUW_RS15295		LysE family translocator	1.79
ABUW_RS11400		Crp/Fnr family transcriptional regulator	1.79
ABUW_RS18700	rph	ribonuclease PH	1.79
ABUW_RS17490	rplA	50S ribosomal protein L1	1.79
ABUW_RS14245		MFS transporter	1.78
ABUW_RS07880		peptidyl-prolyl cis-trans isomerase	1.78
ABUW_RS04450	folD	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	1.78
ABUW_RS08885	kdsA	3-deoxy-8-phosphooctulonate synthase	1.78
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	1.78
ABUW_RS08150	acel	chlorhexidine efflux PACE transporter Acel	1.78
ABUW_RS01025		pirin family protein	1.78
ABUW_RS17670	ftsW	putative lipid II flippase FtsW	1.77
ABUW_RS13345		aspartate kinase	1.77
ABUW_RS09065		aromatic-ring-hydroxylating dioxygenase subunit beta	1.77
ABUW_RS06025		OmpW family protein	1.77
ABUW_RS05430		aspartate aminotransferase family protein	1.77
ABUW_RS16430	ndk	nucleoside-diphosphate kinase	1.77
ABUW_RS07795		MFS transporter	1.77
ABUW_RS11820		Lrp/AsnC family transcriptional regulator	1.76
ABUW_RS13485	mhpT	3-(3-hydroxy-phenyl)propionate transporter MhpT	1.76

ABUW_RS17090		Hsp33 family molecular chaperone HslO	1.76
ABUW_RS02140		succinate dehydrogenase assembly factor 2	1.75
ABUW_RS00995		amino acid permease	1.75
ABUW_RS13460		MFS transporter	1.75
ABUW_RS04975	dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	1.75
ABUW_RS08880		CTP synthase	1.75
ABUW_RS18870		hypothetical protein	1.74
ABUW_RS01730	astD	succinylglutamate-semialdehyde dehydrogenase	1.73
ABUW_RS11080		DUF1275 domain-containing protein	1.73
sRNA42	sRNA42	sRNA42	1.73
ABUW_RS10920		enoyl-CoA hydratase/isomerase family protein	1.72
ABUW_RS19445		hypothetical protein	1.72
ABUW_RS15270		5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	1.71
ABUW_RS00480	serB	phosphoserine phosphatase SerB	1.71
ABUW_RS06005	sthA	Si-specific NAD(P)(+) transhydrogenase	1.71
ABUW_RS15390	nuoJ	NADH-quinone oxidoreductase subunit J	1.71
ABUW_RS07655	prfA	peptide chain release factor 1	1.71
ABUW_RS10360	lipA	lipoyl synthase	1.70
ABUW_RS03170		DUF934 domain-containing protein	1.70
ABUW_RS16435	iscX	Fe-S cluster assembly protein IscX	1.70
ABUW_RS08555	kynU	kynureninase	1.70
ABUW_RS10155		AraC family transcriptional regulator	1.69
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.69
ABUW_RS01865		inositol monophosphatase	1.68
ABUW_RS04650	genX	EF-P lysine aminoacylase GenX	1.68
ABUW_RS17685		ferrous iron transporter B	1.68
ABUW_RS08760		adenosine kinase	1.67
ABUW_RS14705		YggS family pyridoxal phosphate-dependent enzyme	1.67
ABUW_RS15685	rpe	ribose-phosphate 3-epimerase	1.67
ABUW_RS09075		oxidoreductase	1.66
ABUW_RS04810	purM	phosphoribosylformylglycinamide cyclo-ligase	1.66
ABUW_RS09635		hypothetical protein	1.66
ABUW_RS13955	adk	adenylate kinase	1.66
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.66
ABUW_RS10715	iscA	iron-sulfur cluster assembly protein IscA	1.66
ABUW_RS07460		ABC transporter permease	1.65
ABUW_RS02250		xanthine phosphoribosyltransferase	1.64
ABUW_RS01715		Glu/Leu/Phe/Val dehydrogenase	1.64
ABUW_RS09150		hypothetical protein	1.63
ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	1.63
ABUW_RS13455		OprD family outer membrane porin	1.63
ABUW_RS04295	sucC	ADP-forming succinate--CoA ligase subunit beta	1.62
ABUW_RS02420	rpsI	30S ribosomal protein S9	1.61
ABUW_RS13505		acyl-CoA dehydrogenase family protein	1.61
ABUW_RS05300		L-cystine transporter	1.61
ABUW_RS14930		BCCT family carnitine transporter	1.60
ABUW_RS09085	feaR	transcriptional regulator FeaR	1.60
ABUW_RS12140		cytosine permease	1.60
ABUW_RS02010	rplB	50S ribosomal protein L2	1.60
ABUW_RS07660	prmC	peptide chain release factor N(5)-glutamine methyltransferase	1.60
ABUW_RS11005		ParA family protein	1.59
ABUW_RS06105		site-specific integrase	1.59
ABUW_RS16360	orn	oligoribonuclease	1.59
ABUW_RS11035		fructose-bisphosphate aldolase class II	1.59
ABUW_RS17050		CBS domain-containing protein	1.59
ABUW_RS17850		universal stress protein	1.59

ABUW_RS09095		hypothetical protein	1.59
ABUW_RS18240		arginine--tRNA ligase	1.58
ABUW_RS12350		APC family permease	1.58
ABUW_RS16275		peptide chain release factor 3	1.58
ABUW_RS18685		carboxylating nicotinate-nucleotide diphosphorylase	1.57
ABUW_RS03555		phosphoadenylyl-sulfate reductase	1.57
ABUW_RS14440		hypothetical protein	1.57
ABUW_RS04375	greA	transcription elongation factor GreA	1.57
ABUW_RS08710	ftsY	signal recognition particle-docking protein FtsY	1.57
ABUW_RS17870	arsB	ACR3 family arsenite efflux transporter	1.57
ABUW_RS15640	nadA	quinolinate synthase NadA	1.56
ABUW_RS07470		hypothetical protein	1.56
sRNA102	sRNA102	sRNA102	1.56
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	1.56
ABUW_RS07630		hypothetical protein	1.55
ABUW_RS13325		adenylosuccinate synthase	1.55
ABUW_RS08160		3-oxoacyl-ACP reductase	1.55
ABUW_RS06330		hypothetical protein	1.55
ABUW_RS07230		ATP-binding protein	1.54
ABUW_RS13720	argG	argininosuccinate synthase	1.54
ABUW_RS00190	dapB	4-hydroxy-tetrahydronicotinate reductase	1.54
ABUW_RS01050		MFS transporter	1.54
ABUW_RS10705		IscS subfamily cysteine desulfurase	1.53
ABUW_RS14515		dihydrodipicolinate synthase family protein	1.53
ABUW_RS11205	ruvC	crossover junction endodeoxyribonuclease RuvC	1.53
ABUW_RS01135		potassium transporter Kup	1.53
ABUW_RS04035		1-acyl-sn-glycerol-3-phosphate acyltransferase	1.53
ABUW_RS13255		aspartate carbamoyltransferase	1.53
ABUW_RS05500	mnmA	tRNA 2-thiouridine(34) synthase MnmA	1.52
sRNA15	sRNA15	sRNA15	1.52
ABUW_RS08000		Lrp/AsnC family transcriptional regulator	1.51
ABUW_RS04275		succinate dehydrogenase iron-sulfur subunit	1.51
ABUW_RS01630	serA	phosphoglycerate dehydrogenase	1.51
ABUW_RS01655		hypothetical protein	1.50
ABUW_RS01720		aspartate aminotransferase family protein	1.50
ABUW_RS18315		SirB2 family protein	1.50
ABUW_RS04285	odhB	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase	1.50
ABUW_RS17740		2,3-bisphosphoglycerate-independent phosphoglycerate mutase	1.50
ABUW_RS17225		ribosome-binding factor A	1.50
ABUW_RS15645	argJ	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ	1.50
ABUW_RS01205	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1.50
ABUW_RS04380	carB	carbamoyl-phosphate synthase large subunit	1.49
ABUW_RS18990	dmeF	CDF family Co(II)/Ni(II) efflux transporter DmeF	1.49
ABUW_RS14325		aromatic ring-hydroxylating dioxygenase subunit alpha	1.49
ABUW_RS07550	rpsR	30S ribosomal protein S18	1.49
ABUW_RS13400		pirin family protein	1.49
ABUW_RS08810		N-acetyl-gamma-glutamyl-phosphate reductase	1.49
ABUW_RS15400	nuoH	NADH-quinone oxidoreductase subunit NuoH	1.49
ABUW_RS13020		helix-turn-helix transcriptional regulator	1.49
ABUW_RS11020		phosphotransferase	1.48
ABUW_RS12935		hypothetical protein	1.48
ABUW_RS11000		ParB/RepB/Spo0J family partition protein	1.48
ABUW_RS16490	eda	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase	1.48

ABUW_RS10885	pyrF	orotidine-5'-phosphate decarboxylase	1.47
ABUW_RS16535		trigger factor	1.47
ABUW_RS08455	frr	ribosome recycling factor	1.47
ABUW_RS01200		helix-turn-helix transcriptional regulator	1.47
ABUW_RS12135		hypothetical protein	1.46
ABUW_RS14910		oxidoreductase	1.46
ABUW_RS17505	secE	preprotein translocase subunit SecE	1.46
ABUW_RS01610		TSUP family transporter	1.46
ABUW_RS11490	cysE	serine O-acetyltransferase	1.46
ABUW_RS10385	prmB	50S ribosomal protein L3 N(5)-glutamine methyltransferase	1.46
ABUW_RS15380	nuoL	NADH-quinone oxidoreductase subunit L	1.46
ABUW_RS05255		D-alanyl-D-alanine carboxypeptidase PBP6B	1.46
ABUW_RS18795		TDT family transporter	1.46
ABUW_RS18280	guaA	glutamine-hydrolyzing GMP synthase	1.46
ABUW_RS09390		DMT family transporter	1.45
ABUW_RS05385	rapA	RNA polymerase-associated protein RapA	1.45
ABUW_RS07845	tsaE	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	1.45
ABUW_RS07435		MFS transporter	1.45
ABUW_RS00200		MFS transporter	1.44
ABUW_RS13950	nth	endonuclease III	1.44
ABUW_RS08755		Rieske (2Fe-2S) protein	1.44
ABUW_RS15370	nuoN	NADH-quinone oxidoreductase subunit NuoN	1.44
ABUW_RS15180	ligA	NAD-dependent DNA ligase LigA	1.43
ABUW_RS10915	tadA	tRNA adenosine(34) deaminase TadA	1.43
ABUW_RS11085		DUF2058 domain-containing protein	1.43
ABUW_RS15430	ndhC	NADH-quinone oxidoreductase subunit A	1.43
ABUW_RS11165	tkt	transketolase	1.43
ABUW_RS15885		YggT family protein	1.42
ABUW_RS18920	purE	5-(carboxyamino)imidazole ribonucleotide mutase	1.42
ABUW_RS08790	ilvA	threonine ammonia-lyase, biosynthetic	1.42
ABUW_RS04165	rpmA	50S ribosomal protein L27	1.42
ABUW_RS07480	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.42
ABUW_RS00290	purC	phosphoribosylaminoimidazolesuccinocarboxamide synthase	1.42
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	1.42
ABUW_RS15035		ribose-phosphate pyrophosphokinase	1.41
ABUW_RS07200	gltS	sodium/glutamate symporter	1.41
ABUW_RS08905		2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	1.41
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.41
ABUW_RS14920		Rieske 2Fe-2S domain-containing protein	1.41
ABUW_RS17325		HlyD family secretion protein	1.41
ABUW_RS05560		bile acid:sodium symporter	1.41
ABUW_RS06030	map	type I methionyl aminopeptidase	1.40
ABUW_RS14305		MFS transporter	1.40
ABUW_RS04480		phosphoenolpyruvate carboxykinase (GTP)	1.40
ABUW_RS13500		AMP-binding protein	1.39
ABUW_RS02370		TetR family transcriptional regulator	1.39
ABUW_RS03560	thrH	bifunctional phosphoserine phosphatase/homoserine phosphotransferase ThrH	1.39
ABUW_RS14925		alpha/beta hydrolase	1.39
ABUW_RS01585	trmD	tRNA (guanosine(37)-N1)-methyltransferase TrmD	1.39
ABUW_RS07555	rpsF	30S ribosomal protein S6	1.39
ABUW_RS14400		acyl-CoA thioesterase	1.38
ABUW_RS08035		TonB-dependent receptor	1.38
ABUW_RS11045		phosphoglycerate kinase	1.38
ABUW_RS01635		FAD-binding oxidoreductase	1.38
ABUW_RS07075	rpsU	30S ribosomal protein S21	1.38

ABUW_RS07210		LysR family transcriptional regulator	1.38
ABUW_RS17880	trxB	thioredoxin-disulfide reductase	1.37
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.37
ABUW_RS03225	typA	translational GTPase TypA	1.37
ABUW_RS05265		NADP-dependent isocitrate dehydrogenase	1.37
ABUW_RS13535		aldehyde dehydrogenase (NADP(+))	1.37
ABUW_RS10505		hypothetical protein	1.37
ABUW_RS07575	cyoB	cytochrome o ubiquinol oxidase subunit I	1.36
ABUW_RS07060		D-glycerate dehydrogenase	1.36
ABUW_RS05425		diaminobutyrate--2-oxoglutarate transaminase	1.36
ABUW_RS16405	hisS	histidine--tRNA ligase	1.36
ABUW_RS15105		DUF177 domain-containing protein	1.36
ABUW_RS15255		dCTP deaminase	1.36
ABUW_RS02115	rpsD	30S ribosomal protein S4	1.36
ABUW_RS13630		APC family permease	1.36
ABUW_RS02080	rpsE	30S ribosomal protein S5	1.35
ABUW_RS12355		aldehyde dehydrogenase (NADP(+))	1.35
ABUW_RS09615		alpha/beta hydrolase	1.35
ABUW_RS11390	ychF	redox-regulated ATPase YchF	1.35
ABUW_RS13165		1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	1.35
ABUW_RS10230		MFS transporter	1.35
ABUW_RS05490	purB	adenylosuccinate lyase	1.35
ABUW_RS01725	astA	arginine N-succinyltransferase	1.35
ABUW_RS13945		RnfABCDGE type electron transport complex subunit B	1.34
ABUW_RS03165		nitrite/sulfite reductase	1.34
ABUW_RS05015	pabC	aminodeoxychorismate lyase	1.34
ABUW_RS00830	prfB	peptide chain release factor 2	1.34
ABUW_RS04260	sdhC	succinate dehydrogenase, cytochrome b556 subunit	1.33
ABUW_RS17865		arsenate reductase ArsC	1.33
ABUW_RS16495		phosphogluconate dehydratase	1.33
ABUW_RS17445		TRAP transporter large permease subunit	1.33
ABUW_RS15425		NADH-quinone oxidoreductase subunit B	1.33
ABUW_RS04290	lpdA	dihydrolipoyl dehydrogenase	1.33
ABUW_RS07870	nfsB	oxygen-insensitive NAD(P)H nitroreductase	1.33
ABUW_RS14075	lysS	lysine--tRNA ligase	1.33
ABUW_RS04680	dapF	diaminopimelate epimerase	1.32
ABUW_RS02145		membrane protein	1.32
ABUW_RS08345		helix-turn-helix transcriptional regulator	1.32
ABUW_RS07885		glutamine--tRNA ligase/YqeY domain fusion protein	1.32
ABUW_RS01220	hisH	imidazole glycerol phosphate synthase subunit HisH	1.32
ABUW_RS13930		dioxygenase	1.32
sRNA13	sRNA13	sRNA13	1.32
ABUW_RS04265	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.31
ABUW_RS02295		malate dehydrogenase	1.31
ABUW_RS16655		energy transducer TonB	1.31
ABUW_RS16645		biopolymer transporter ExbD	1.31
ABUW_RS10900	rpsA	30S ribosomal protein S1	1.31
ABUW_RS01465	gltB	glutamate synthase large subunit	1.30
ABUW_RS00070		tyrosine--tRNA ligase	1.30
ABUW_RS01285	ettA	energy-dependent translational throttle protein EttA	1.30
ABUW_RS14850	tuf	elongation factor Tu	1.30
ABUW_RS04010		polyprenyl synthetase family protein	1.30
ABUW_RS12145		aldehyde dehydrogenase	1.30
ABUW_RS18460		DUF1624 domain-containing protein	1.30
ABUW_RS15710	tsaB	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	1.29

ABUW_RS07695		flavin reductase family protein	1.29
ABUW_RS08445	rimO	30S ribosomal protein S12 methylthiotransferase RimO	1.29
ABUW_RS10280		NAD(P)H-dependent oxidoreductase	1.29
ABUW_RS13370		adenosine deaminase	1.28
ABUW_RS00805	guaB	IMP dehydrogenase	1.28
ABUW_RS13640		amino acid permease	1.28
ABUW_RS10450		O-succinylhomoserine sulfhydrylase	1.28
ABUW_RS15775		ATP phosphoribosyltransferase	1.28
ABUW_RS18130		DMT family transporter	1.28
ABUW_RS09630		FAD-binding oxidoreductase	1.28
ABUW_RS12770		EamA family transporter	1.28
ABUW_RS07780		bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	1.28
ABUW_RS12860		cysteine--tRNA ligase	1.28
ABUW_RS04270		succinate dehydrogenase flavoprotein subunit	1.27
ABUW_RS05695		pirin family protein	1.27
ABUW_RS16610		prolipoprotein diacylglycerol transferase	1.27
ABUW_RS01325		hypothetical protein	1.27
ABUW_RS04780	lolD	lipoprotein-releasing ABC transporter ATP-binding protein LolD	1.27
ABUW_RS08300	nirD	nitrite reductase small subunit NirD	1.27
ABUW_RS15840		carbon-nitrogen hydrolase family protein	1.27
ABUW_RS05940		superoxide dismutase	1.26
ABUW_RS12450		LysR family transcriptional regulator	1.26
ABUW_RS04280		2-oxoglutarate dehydrogenase E1 component	1.26
ABUW_RS01795		glycine--tRNA ligase subunit beta	1.26
ABUW_RS18245		SPOR domain-containing protein	1.26
ABUW_RS15910	trxA	thioredoxin	1.26
ABUW_RS15920		hypothetical protein	1.26
ABUW_RS18720		TetR/AcrR family transcriptional regulator	1.26
ABUW_RS13925	rlmH	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	1.26
ABUW_RS15420	nuoC	NADH-quinone oxidoreductase subunit C/D	1.26
ABUW_RS03915		Arc family DNA-binding protein	1.26
ABUW_RS04015		MmcQ/YjbR family DNA-binding protein	1.26
ABUW_RS15385	nuoK	NADH-quinone oxidoreductase subunit NuoK	1.26
ABUW_RS16350		enoyl-ACP reductase	1.25
ABUW_RS17955		hypothetical protein	1.25
ABUW_RS10975	kdsB	3-deoxy-manno-octulosonate cytidyltransferase	1.25
ABUW_RS17295	rlmB	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	1.25
ABUW_RS17055	Int	apolipoprotein N-acyltransferase	1.25
ABUW_RS15960	nreB	nickel resistance MFS transporter NreB	1.25
ABUW_RS15375	nuoM	NADH-quinone oxidoreductase subunit M	1.25
ABUW_RS07080	tsaD	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	1.25
ABUW_RS14150		alpha/beta hydrolase	1.25
ABUW_RS03210		amino acid permease	1.24
ABUW_RS11410		hypothetical protein	1.24
ABUW_RS16995		TIGR03862 family flavoprotein	1.24
ABUW_RS02310		2OG-Fe(II) oxygenase	1.23
ABUW_RS14510		LysR family transcriptional regulator	1.23
ABUW_RS19385		hypothetical protein	1.23
ABUW_RS04655		Tim44 domain-containing protein	1.23
ABUW_RS15225		tRNA-dihydrouridine synthase	1.23
ABUW_RS15050		aspartate 1-decarboxylase	1.23
ABUW_RS01270		bifunctional SulP family inorganic anion transporter/carbonic anhydrase	1.22
ABUW_RS00790		TonB-dependent siderophore receptor	1.22

ABUW_RS08185		DNA polymerase III subunit gamma/tau	1.22
ABUW_RS14145		carbonic anhydrase	1.22
ABUW_RS03525	mreC	rod shape-determining protein MreC	1.21
ABUW_RS12790		ferredoxin family protein	1.21
ABUW_RS16660	purU	formyltetrahydrofolate deformylase	1.21
ABUW_RS00855		mechanosensitive ion channel family protein	1.21
ABUW_RS18755	argA	amino-acid N-acetyltransferase	1.21
ABUW_RS07730	kdpC	potassium-transporting ATPase subunit KdpC	1.21
ABUW_RS09570		SDR family NAD(P)-dependent oxidoreductase	1.20
ABUW_RS05040		Do family serine endopeptidase	1.20
ABUW_RS14045		CitMHS family transporter	1.20
ABUW_RS09465		methylenetetrahydrofolate reductase C-terminal domain-containing protein	1.20
ABUW_RS17705		homoserine dehydrogenase	1.20
ABUW_RS02125	rplQ	50S ribosomal protein L17	1.20
ABUW_RS15125	scpB	SMC-Scp complex subunit ScpB	1.19
ABUW_RS19005	yidC	membrane protein insertase YidC	1.19
ABUW_RS05495	hflD	high frequency lysogenization protein HflD	1.19
ABUW_RS07055		hypothetical protein	1.19
ABUW_RS04190		tRNA (cytidine(34)-2'-O)-methyltransferase	1.19
ABUW_RS14960	coaD	pantetheine-phosphate adenyltransferase	1.19
ABUW_RS05880		aminodeoxychorismate/anthranilate synthase component II	1.19
ABUW_RS15115		threonylcarbamoyl-AMP synthase	1.19
ABUW_RS02955		phospholipase D family protein	1.18
ABUW_RS03240		peptidylprolyl isomerase	1.18
ABUW_RS02110	rpsK	30S ribosomal protein S11	1.18
ABUW_RS07040		CvpA family protein	1.18
ABUW_RS06080	rodA	rod shape-determining protein RodA	1.18
ABUW_RS15345		ferredoxin--NADP reductase	1.18
ABUW_RS14855	fusA	elongation factor G	1.18
ABUW_RS02025	rpsC	30S ribosomal protein S3	1.18
ABUW_RS15100	rpmF	50S ribosomal protein L32	1.18
ABUW_RS11430	purT	formate-dependent phosphoribosylglycinamide formyltransferase	1.17
ABUW_RS04805		phosphoribosylglycinamide formyltransferase	1.17
ABUW_RS03280		folate-binding protein YgfZ	1.17
ABUW_RS05085	pdxJ	pyridoxine 5'-phosphate synthase	1.17
ABUW_RS04960		hypothetical protein	1.17
ABUW_RS08575		SulP family inorganic anion transporter	1.17
ABUW_RS04095		valine--tRNA ligase	1.17
ABUW_RS10650		hypothetical protein	1.17
ABUW_RS17945	ppa	inorganic diphosphatase	1.17
ABUW_RS14820	trxB	thioredoxin-disulfide reductase	1.17
ABUW_RS16055	cysM	cysteine synthase CysM	1.17
ABUW_RS03505	gatB	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	1.16
ABUW_RS00460	nusB	transcription antitermination factor NusB	1.16
ABUW_RS17675		UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	1.16
ABUW_RS15410	nuoF	NADH-quinone oxidoreductase subunit NuoF	1.16
ABUW_RS04180	serS	serine--tRNA ligase	1.16
ABUW_RS14390		GTP-binding protein	1.15
ABUW_RS04315	trpS	tryptophan--tRNA ligase	1.15
ABUW_RS13540	kdgD	5-dehydro-4-deoxyglucarate dehydratase	1.15
ABUW_RS17970		MFS transporter	1.15
ABUW_RS05970		16S rRNA (uracil(1498)-N(3))-methyltransferase	1.15
ABUW_RS19805		helix-turn-helix transcriptional regulator	1.15
ABUW_RS15040	rplY	50S ribosomal protein L25	1.15
ABUW_RS15545		AraC family transcriptional regulator	1.15

ABUW_RS01745		hypothetical protein	1.15
ABUW_RS11215	queG	tRNA epoxyqueuosine(34) reductase QueG	1.15
ABUW_RS01940	plsB	glycerol-3-phosphate 1-O-acyltransferase PlsB	1.14
ABUW_RS09160		dihydroxy-acid dehydratase	1.14
ABUW_RS11740		SDR family oxidoreductase	1.14
ABUW_RS00120	rsmB	16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB	1.14
ABUW_RS08995	pcaU	IcIR family transcriptional regulator PcaU	1.14
ABUW_RS06695		thiazole synthase	1.14
ABUW_RS12055		CoA transferase	1.14
ABUW_RS17045	tusA	sulfurtransferase TusA	1.14
ABUW_RS01995	rplC	50S ribosomal protein L3	1.14
ABUW_RS07570	cyoC	cytochrome o ubiquinol oxidase subunit III	1.14
ABUW_RS13335	gap	type I glyceraldehyde-3-phosphate dehydrogenase	1.13
ABUW_RS15765		histidinol-phosphate transaminase	1.13
ABUW_RS00235		hypothetical protein	1.13
ABUW_RS14275		thiamine pyrophosphate-binding protein	1.13
ABUW_RS14105		hydrogen peroxide-inducible genes activator	1.13
ABUW_RS10510		DUF2797 domain-containing protein	1.13
ABUW_RS16570	rdgB	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	1.13
ABUW_RS04690		LysE family translocator	1.13
ABUW_RS15855		organic hydroperoxide resistance protein	1.13
ABUW_RS11075	sstT	serine/threonine transporter SstT	1.13
ABUW_RS19000	mnME	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnME	1.13
ABUW_RS13545	gudD	glucarate dehydratase	1.13
ABUW_RS16750		ATP-binding cassette domain-containing protein	1.13
ABUW_RS14310		FAD-dependent oxidoreductase	1.12
ABUW_RS05190	dusB	tRNA dihydrouridine synthase DusB	1.12
ABUW_RS06525	adeL	multidrug efflux transcriptional repressor AdeL	1.12
ABUW_RS18380		DUF4902 domain-containing protein	1.12
ABUW_RS10740		HIT domain-containing protein	1.12
ABUW_RS04385	carA	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	1.12
ABUW_RS17710		threonine synthase	1.12
ABUW_RS17995	mdtD	multidrug transporter subunit MdtD	1.12
ABUW_RS16880	hcaR	DNA-binding transcriptional regulator HcaR	1.12
ABUW_RS02075	rplR	50S ribosomal protein L18	1.11
ABUW_RS06090	queF	NADPH-dependent 7-cyano-7-deazaguanine reductase QueF	1.11
ABUW_RS08235		PepSY domain-containing protein	1.11
ABUW_RS18195	atpB	F ₀ F ₁ ATP synthase subunit A	1.11
ABUW_RS04645		4-phosphoerythronate dehydrogenase	1.11
ABUW_RS02215		nitroreductase family protein	1.11
ABUW_RS00925	omp33-36	porin Omp33-36	1.11
ABUW_RS00510	psd	phosphatidylserine decarboxylase	1.11
ABUW_RS13900		cell division protein ZapA	1.11
ABUW_RS07815		DUF441 domain-containing protein	1.11
ABUW_RS04700		electron transfer flavoprotein subunit beta/FixA family protein	1.11
ABUW_RS03530	mreD	rod shape-determining protein MreD	1.11
ABUW_RS06035	rpsB	30S ribosomal protein S2	1.10
ABUW_RS16115		MFS transporter	1.10
ABUW_RS01180		homoserine kinase	1.10
ABUW_RS04500		co-chaperone GroES	1.10
ABUW_RS04235		hypothetical protein	1.10
ABUW_RS05090		tRNA-(ms[2]io[6]A)-hydroxylase	1.10
ABUW_RS07035		quinone-dependent dihydroorotate dehydrogenase	1.10
ABUW_RS11990		3-oxoacid CoA-transferase subunit B	1.10
ABUW_RS10950		type II secretion system protein	1.10

ABUW_RS06645		dicarboxylate/amino acid:cation symporter	1.10
ABUW_RS01265		RNA-binding transcriptional accessory protein	1.10
ABUW_RS09595	adeR	efflux system response regulator transcription factor AdeR	1.10
ABUW_RS01405		phospho-N-acetylmuramoyl-pentapeptide-transferase	1.10
ABUW_RS17415		DsbA family oxidoreductase	1.10
ABUW_RS09145		LysR family transcriptional regulator	1.09
ABUW_RS17950		MAPEG family protein	1.09
ABUW_RS14800	minE	cell division topological specificity factor MinE	1.09
ABUW_RS01530	gmk	guanylate kinase	1.09
ABUW_RS08620		PTS transporter subunit EIIC	1.09
ABUW_RS02060	rpsN	30S ribosomal protein S14	1.09
ABUW_RS04205		APC family permease	1.09
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	1.08
ABUW_RS13315		M48 family metalloproteinase	1.08
ABUW_RS08400		hypothetical protein	1.08
ABUW_RS00045		hypothetical protein	1.08
ABUW_RS17690		ferrous iron transport protein A	1.08
ABUW_RS05985		peptidase C39	1.08
ABUW_RS10135		hypothetical protein	1.08
ABUW_RS01590	rplS	50S ribosomal protein L19	1.07
ABUW_RS17495	rplK	50S ribosomal protein L11	1.07
ABUW_RS17875	arsH	arsenical resistance protein ArsH	1.07
ABUW_RS15415	nuoE	NADH-quinone oxidoreductase subunit NuoE	1.07
ABUW_RS08505		tetratricopeptide repeat protein	1.07
ABUW_RS08415	ispF	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	1.07
ABUW_RS05035	nadB	L-aspartate oxidase	1.07
ABUW_RS17355	pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	1.07
ABUW_RS17365	uvrC	excinuclease ABC subunit UvrC	1.06
ABUW_RS20125		hypothetical protein	1.06
ABUW_RS04705		FAD-binding protein	1.06
ABUW_RS16395	bamB	outer membrane protein assembly factor BamB	1.06
sRNA91	sRNA91	sRNA91	1.06
ABUW_RS09665		hypothetical protein	1.06
ABUW_RS18680	ampD	1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD	1.06
ABUW_RS17620	phoU	phosphate signaling complex protein PhoU	1.05
ABUW_RS14210		transketolase	1.05
ABUW_RS01945		acyl-CoA thioesterase II	1.05
ABUW_RS05855		Smr/MutS family protein	1.05
ABUW_RS18885	grpE	nucleotide exchange factor GrpE	1.05
ABUW_RS11975		Paal family thioesterase	1.04
ABUW_RS01500		O-antigen ligase family protein	1.04
ABUW_RS00730	murC	UDP-N-acetylmuramate--L-alanine ligase	1.04
ABUW_RS14365	pgaC	poly-beta-1,6 N-acetyl-D-glucosamine synthase	1.04
ABUW_RS13550		MFS transporter	1.04
ABUW_RS05895	glnA	type I glutamate--ammonia ligase	1.04
ABUW_RS18355		non-ribosomal peptide synthetase	1.04
ABUW_RS07580	cyoA	ubiquinol oxidase subunit II	1.03
ABUW_RS17290		DMT family transporter	1.03
ABUW_RS08215	murB	UDP-N-acetylmuramate dehydrogenase	1.03
ABUW_RS12100		UTRA domain-containing protein	1.03
ABUW_RS00635		ion channel protein Tsx	1.03
ABUW_RS07560	cyoE	protoheme IX farnesyltransferase	1.03
ABUW_RS18220	znuB	zinc ABC transporter permease subunit ZnuB	1.03
ABUW_RS01055		LysR family transcriptional regulator	1.03
ABUW_RS14285		aspartate dehydrogenase	1.03
ABUW_RS14065	cysD	sulfate adenyltransferase subunit CysD	1.02

ABUW_RS16805		AraC family transcriptional regulator	1.02
ABUW_RS05320		hypothetical protein	1.02
ABUW_RS15890		pyrroline-5-carboxylate reductase	1.02
ABUW_RS13340	alaS	alanine--tRNA ligase	1.02
ABUW_RS16800	truA	tRNA pseudouridine(38-40) synthase TruA	1.02
ABUW_RS16485		permease	1.02
ABUW_RS06095		ABC transporter permease	1.02
ABUW_RS08945	pcaH	protocatechuate 3,4-dioxygenase subunit beta	1.02
ABUW_RS09070		SDR family oxidoreductase	1.02
ABUW_RS15540		fatty acid desaturase	1.01
ABUW_RS07650		type 1 glutamine amidotransferase domain-containing protein	1.01
ABUW_RS02320	pssA	CDP-diacylglycerol--serine O-phosphatidyltransferase	1.01
ABUW_RS15705		class I SAM-dependent methyltransferase	1.01
ABUW_RS11480	dnaE	DNA polymerase III subunit alpha	1.01
ABUW_RS15360		cold shock domain-containing protein	1.01
ABUW_RS14880	hemJ	protoporphyrinogen oxidase HemJ	1.01
ABUW_RS02605	secF	protein translocase subunit SecF	1.01
ABUW_RS12050		IclR family transcriptional regulator	1.01
ABUW_RS09580		AraC family transcriptional regulator	1.01
ABUW_RS11220	bioB	biotin synthase BioB	1.01
ABUW_RS16575		hypothetical protein	1.01
ABUW_RS16250		tRNA threonylcarbamoyladenosine dehydratase	1.01
ABUW_RS09105		penicillin acylase family protein	1.01
ABUW_RS17025	murl	glutamate racemase	1.01
ABUW_RS08675	grxD	Grx4 family monothiol glutaredoxin	1.01
ABUW_RS03535		Maf-like protein	1.00
ABUW_RS07505	mnmg	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	1.00
ABUW_RS01800	glyQ	glycine--tRNA ligase subunit alpha	1.00
ABUW_RS11285		LysR family transcriptional regulator	1.00
ABUW_RS16410	ispG	flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	1.00
ABUW_RS08360		TusE/DsrC/DsvC family sulfur relay protein	1.00
ABUW_RS10410		YcgL domain-containing protein	1.00
ABUW_RS16390	der	ribosome biogenesis GTPase Der	1.00
ABUW_RS07855	miaA	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	1.00
ABUW_RS17010		MBL fold metallo-hydrolase	1.00
ABUW_RS08750		DUF1449 family protein	1.00

Gene	Gene Name	Function	Δ gacA MEP vs WT MEP log2FC
ABUW_RS01495	pilA	pilin	-7.52
ABUW_RS12745		DUF2147 domain-containing protein	-6.25
sRNA29	sRNA29	sRNA29	-6.00
sRNA97	sRNA97	sRNA97	-5.99
ABUW_RS07180		hypothetical protein	-5.56
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-5.44
sRNA64	sRNA64	sRNA64	-5.25
ABUW_RS20520		hypothetical protein	-5.24
sRNA99	sRNA99	sRNA99	-5.22
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-5.19
ABUW_RS12225		cold-shock protein	-4.90
ABUW_RS13655		hypothetical protein	-4.90
ABUW_RS08535		hypothetical protein	-4.65
ABUW_RS00905		DUF485 domain-containing protein	-4.59
ABUW_RS07255	csuA	Csu fimbrial biogenesis protein CsuA	-4.54
ABUW_RS12215		hypothetical protein	-4.53

ABUW_RS11425		tautomerase family protein	-4.52
ABUW_RS01215		DUF805 domain-containing protein	-4.48
ABUW_RS14740		bacteriohemerythrin	-4.42
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-4.38
ABUW_RS04595		hypothetical protein	-4.37
ABUW_RS04600		hypothetical protein	-4.34
ABUW_RS20230		hypothetical protein	-4.22
ABUW_RS20535		hypothetical protein	-4.22
ABUW_RS14080		esterase	-4.18
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-4.15
ABUW_RS10425		hypothetical protein	-4.13
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-4.07
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-3.98
ABUW_RS01445		type IV pilus secretin PilQ family protein	-3.96
ABUW_RS13055		cold-shock protein	-3.91
ABUW_RS07260	csuB	Csu fimbrial biogenesis protein CsuB	-3.88
ABUW_RS01435		type 4a pilus biogenesis protein PilO	-3.78
ABUW_RS12220		hypothetical protein	-3.78
ABUW_RS03355		Hpt domain-containing protein	-3.77
ABUW_RS11305		TetR/AcrR family transcriptional regulator	-3.73
ABUW_RS10465		cell envelope integrity protein TolA	-3.72
sRNA75	sRNA75	sRNA75	-3.70
ABUW_RS02525		hypothetical protein	-3.68
ABUW_RS07800		membrane protein	-3.62
ABUW_RS12230		hypothetical protein	-3.60
ABUW_RS00800		YkgJ family cysteine cluster protein	-3.58
ABUW_RS01565		prepilin-type N-terminal cleavage/methylation domain-containing protein	-3.56
ABUW_RS07280		hypothetical protein	-3.56
ABUW_RS20485		hypothetical protein	-3.54
ABUW_RS20145		hypothetical protein	-3.53
ABUW_RS09310		TetR/AcrR family transcriptional regulator	-3.50
ABUW_RS05795	basI	acinetobactin biosynthesis phosphopantetheinyl transferase BasI	-3.49
ABUW_RS13575		hypothetical protein	-3.46
ABUW_RS16290		TetR/AcrR family transcriptional regulator	-3.46
ABUW_RS19040		zeta toxin family protein	-3.45
ABUW_RS01100		hypothetical protein	-3.44
ABUW_RS11895		hypothetical protein	-3.42
ABUW_RS09960		hypothetical protein	-3.40
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-3.40
ABUW_RS05820		DUF3015 family protein	-3.39
ABUW_RS01540		GspH/FimT family pseudopilin	-3.39
sRNA85	sRNA85	sRNA85	-3.35
ABUW_RS03345		purine-binding chemotaxis protein CheW	-3.33
ABUW_RS03350		methyl-accepting chemotaxis protein	-3.32
ABUW_RS03380		entericidin A/B family lipoprotein	-3.31
ABUW_RS00910		cation acetate symporter	-3.31
ABUW_RS01440		pilus assembly protein PilP	-3.30
ABUW_RS09350		DUF2314 domain-containing protein	-3.28
ABUW_RS05685		hypothetical protein	-3.28
ABUW_RS13775		hypothetical protein	-3.28
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-3.27
ABUW_RS01250		acetyl-CoA hydrolase/transferase family protein	-3.26
ABUW_RS01560		VWA domain-containing protein	-3.26
ABUW_RS13750		hypothetical protein	-3.24
ABUW_RS13005		hypothetical protein	-3.23

ABUW_RS19175		hypothetical protein	-3.22
ABUW_RS03310		YegP family protein	-3.22
sRNA61	sRNA61	sRNA61	-3.21
ABUW_RS12325	paaA	1,2-phenylacetyl-CoA epoxidase subunit A	-3.20
ABUW_RS00895		hypothetical protein	-3.18
ABUW_RS01750		hypothetical protein	-3.18
ABUW_RS07980		glutathione S-transferase family protein	-3.17
sRNA87	sRNA87	sRNA87	-3.16
ABUW_RS04495		Ig-like domain repeat protein	-3.15
ABUW_RS17720		response regulator	-3.14
ABUW_RS14715		PilT/PilU family type 4a pilus ATPase	-3.12
ABUW_RS12975		hypothetical protein	-3.11
ABUW_RS02595	radC	DNA repair protein RadC	-3.11
ABUW_RS09985		DUF4882 family protein	-3.10
ABUW_RS01550		PilW family protein	-3.10
ABUW_RS01570		prepilin-type N-terminal cleavage/methylation domain-containing protein	-3.10
ABUW_RS00515		alpha/beta fold hydrolase	-3.08
ABUW_RS09545		hypothetical protein	-3.08
ABUW_RS01615		hemerythrin domain-containing protein	-3.05
ABUW_RS15455		hypothetical protein	-3.04
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-3.04
ABUW_RS17730		sigma-54-dependent Fis family transcriptional regulator	-3.01
ABUW_RS06235		hypothetical protein	-3.01
ABUW_RS07965		molecular chaperone	-3.01
ABUW_RS20235		hypothetical protein	-2.98
ABUW_RS14710		type IV pilus twitching motility protein PilT	-2.96
ABUW_RS07410		GNAT family N-acetyltransferase	-2.94
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	-2.93
ABUW_RS00795		MBL fold metallo-hydrolase	-2.90
ABUW_RS12725		hypothetical protein	-2.89
ABUW_RS03360		hypothetical protein	-2.88
ABUW_RS06780		hypothetical protein	-2.88
ABUW_RS05480		BapA prefix-like domain-containing protein	-2.88
ABUW_RS12320	paaB	1,2-phenylacetyl-CoA epoxidase subunit B	-2.87
ABUW_RS09525		DEAD/DEAH box helicase family protein	-2.87
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-2.84
ABUW_RS05570		EAL domain-containing protein	-2.84
ABUW_RS04365		universal stress protein	-2.83
sRNA27	sRNA27	sRNA27	-2.83
ABUW_RS15510		TetR/AcrR family transcriptional regulator	-2.83
ABUW_RS11865		CinA family protein	-2.83
ABUW_RS08695		hypothetical protein	-2.82
ABUW_RS09550		GNAT family N-acetyltransferase	-2.81
ABUW_RS17275		type II secretion system F family protein	-2.81
ABUW_RS19460		hypothetical protein	-2.81
ABUW_RS15500		hypothetical protein	-2.81
ABUW_RS20515		hypothetical protein	-2.80
ABUW_RS06320		hypothetical protein	-2.80
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-2.79
ABUW_RS12900		DUF4882 family protein	-2.79
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-2.79
ABUW_RS01430		PilN domain-containing protein	-2.79
ABUW_RS13380		hypothetical protein	-2.79
ABUW_RS03905		hypothetical protein	-2.76
ABUW_RS17100		DnaJ domain-containing protein	-2.76

ABUW_RS03795		DUF2280 domain-containing protein	-2.75
ABUW_RS17380		hypothetical protein	-2.73
ABUW_RS05235		hypothetical protein	-2.73
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-2.70
ABUW_RS19900		glutathione S-transferase	-2.70
ABUW_RS07265	csuC	Csu fimbrial biogenesis chaperone CsuC	-2.68
ABUW_RS02810		phage baseplate assembly protein V	-2.68
ABUW_RS13040		hypothetical protein	-2.67
ABUW_RS11755		hypothetical protein	-2.66
ABUW_RS16720		hypothetical protein	-2.65
ABUW_RS06315		hypothetical protein	-2.64
ABUW_RS03365		radical SAM protein	-2.63
ABUW_RS05825		DUF4105 domain-containing protein	-2.62
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-2.62
ABUW_RS15495		hypothetical protein	-2.61
ABUW_RS02200		HAD-IB family hydrolase	-2.61
ABUW_RS07305		TetR/AcrR family transcriptional regulator	-2.61
ABUW_RS15280		hypothetical protein	-2.60
ABUW_RS15160	otsB	trehalose-phosphatase	-2.59
ABUW_RS07520		alpha-E domain-containing protein	-2.58
ABUW_RS10005		hypothetical protein	-2.57
ABUW_RS00660		HPF/RaiA family ribosome-associated protein	-2.56
ABUW_RS13580		DUF4265 domain-containing protein	-2.56
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-2.55
ABUW_RS19180		hypothetical protein	-2.55
ABUW_RS07270	csuD	Csu fimbrial usher CsuD	-2.54
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	-2.53
ABUW_RS18520		hypothetical protein	-2.53
ABUW_RS10835		energy transducer TonB	-2.53
ABUW_RS12315	paaC	phenylacetate-CoA oxygenase subunit PaaC	-2.53
ABUW_RS12635		sel1 repeat family protein	-2.52
ABUW_RS12520	tssE	type VI secretion system baseplate subunit TssE	-2.52
ABUW_RS11945		acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	-2.52
ABUW_RS06285		hypothetical protein	-2.52
ABUW_RS06250		hypothetical protein	-2.51
ABUW_RS05215		hypothetical protein	-2.50
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-2.49
ABUW_RS12330	paaZ	phenylacetic acid degradation bifunctional protein PaaZ	-2.49
ABUW_RS03490		DUF1176 domain-containing protein	-2.48
ABUW_RS03850		hypothetical protein	-2.48
ABUW_RS02860		GPO family capsid scaffolding protein	-2.47
ABUW_RS13755		RHS repeat-associated core domain-containing protein	-2.47
ABUW_RS02850		terminase	-2.46
ABUW_RS14030		isocitrate lyase	-2.46
ABUW_RS19100		hypothetical protein	-2.45
ABUW_RS19065		hypothetical protein	-2.45
ABUW_RS14685		VOC family protein	-2.44
ABUW_RS01545	pilV	type IV pilus modification protein PilV	-2.44
ABUW_RS03785		hypothetical protein	-2.44
ABUW_RS11615		hypothetical protein	-2.44
ABUW_RS09700		hypothetical protein	-2.43
ABUW_RS01555		hypothetical protein	-2.43
ABUW_RS07515		circularly permuted type 2 ATP-grasp protein	-2.42
ABUW_RS18120	dprA	DNA-processing protein DprA	-2.41
sRNA31	sRNA31	sRNA31	-2.41
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-2.41
ABUW_RS12310	paaJ	phenylacetate-CoA oxygenase subunit PaaJ	-2.41

ABUW_RS07820		hypothetical protein	-2.41
ABUW_RS16285		TetR/AcrR family transcriptional regulator	-2.41
ABUW_RS03605	hchA	protein deglycase HchA	-2.41
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-2.40
ABUW_RS01345		hypothetical protein	-2.39
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-2.38
ABUW_RS10640		siderophore biosynthesis protein	-2.38
ABUW_RS07250	csuAB	Csu fimbrial major subunit CsuAB	-2.38
ABUW_RS05340	cas3f	type I-F CRISPR-associated helicase Cas3	-2.38
ABUW_RS05350	csy2	type I-F CRISPR-associated protein Csy2	-2.37
ABUW_RS11870		hypothetical protein	-2.37
ABUW_RS10615		(2Fe-2S)-binding protein	-2.37
ABUW_RS19585		hypothetical protein	-2.36
ABUW_RS01425		pilus assembly protein PilM	-2.36
ABUW_RS13070		hypothetical protein	-2.35
ABUW_RS09490		hypothetical protein	-2.34
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-2.34
ABUW_RS17420		hypothetical protein	-2.33
ABUW_RS13050		hypothetical protein	-2.33
ABUW_RS03180		VOC family protein	-2.33
ABUW_RS12960		DUF2280 domain-containing protein	-2.32
ABUW_RS05230		hypothetical protein	-2.32
ABUW_RS19705		hypothetical protein	-2.32
ABUW_RS16500		acetate kinase	-2.31
ABUW_RS13815		hypothetical protein	-2.30
ABUW_RS10025		hypothetical protein	-2.30
ABUW_RS16505	pta	phosphate acetyltransferase	-2.28
ABUW_RS00285		hypothetical protein	-2.27
ABUW_RS05790	basH	acinetobactin biosynthesis thioesterase BasH	-2.27
ABUW_RS20550		hypothetical protein	-2.26
ABUW_RS02845		head completion/stabilization protein	-2.25
ABUW_RS16790		hypothetical protein	-2.25
ABUW_RS00600		SH3 domain-containing protein	-2.25
ABUW_RS16255	acnA	aconitate hydratase AcnA	-2.24
ABUW_RS09315		hypothetical protein	-2.24
ABUW_RS18115		LysM peptidoglycan-binding domain-containing protein	-2.24
ABUW_RS04355		metalloprotease	-2.23
ABUW_RS09335		SMI1/KNR4 family protein	-2.23
ABUW_RS02785		phage tail sheath protein	-2.21
ABUW_RS10815		Zn-dependent oligopeptidase	-2.21
ABUW_RS19070		hypothetical protein	-2.21
sRNA65	sRNA65	sRNA65	-2.20
ABUW_RS19580		hypothetical protein	-2.20
ABUW_RS12255		ATP-dependent helicase	-2.20
ABUW_RS08590		universal stress protein	-2.20
ABUW_RS05115		GFA family protein	-2.20
ABUW_RS05540		LysR family transcriptional regulator	-2.20
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-2.19
ABUW_RS05910		hypothetical protein	-2.19
ABUW_RS04425		hypothetical protein	-2.19
ABUW_RS05750	basC	putative histamine N-monooxygenase	-2.19
ABUW_RS00405		DUF885 domain-containing protein	-2.18
ABUW_RS09290		cation:proton antiporter	-2.17
ABUW_RS08530		hypothetical protein	-2.16
ABUW_RS18955		glutathionylspermidine synthase family protein	-2.16
ABUW_RS06115		hypothetical protein	-2.16

ABUW_RS02625		LemA family protein	-2.15
ABUW_RS04580		hypothetical protein	-2.15
ABUW_RS05730	bauC	ferric acinetobactin ABC transporter permease subunit BauC	-2.15
ABUW_RS15440		hypothetical protein	-2.15
ABUW_RS15055		GDYXXLXY domain-containing protein	-2.15
ABUW_RS03585		PaaX family transcriptional regulator	-2.15
ABUW_RS14645	ggt	gamma-glutamyltransferase	-2.14
ABUW_RS13250		OmpA family protein	-2.14
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	-2.14
ABUW_RS05485		DUF2238 domain-containing protein	-2.14
ABUW_RS20545		zinc ribbon-containing protein	-2.13
ABUW_RS15505		hypothetical protein	-2.13
ABUW_RS19105		hypothetical protein	-2.13
ABUW_RS02735		ogr/Delta-like zinc finger family protein	-2.13
ABUW_RS11935		methylocrotonoyl-CoA carboxylase	-2.12
ABUW_RS15330		mechanosensitive ion channel	-2.10
ABUW_RS11940		enoyl-CoA hydratase/isomerase family protein	-2.10
ABUW_RS10820		ABC transporter substrate-binding protein	-2.10
ABUW_RS01665	yccS	TIGR01666 family membrane protein	-2.09
ABUW_RS09295		hypothetical protein	-2.09
ABUW_RS15615	add	adenosine deaminase	-2.08
ABUW_RS13450		GMC family oxidoreductase	-2.08
ABUW_RS18950		hypothetical protein	-2.07
ABUW_RS17150		polyphosphate--AMP phosphotransferase	-2.07
ABUW_RS00415	murl	glutamate racemase	-2.07
ABUW_RS11455		glutathione peroxidase	-2.07
ABUW_RS11930		isovaleryl-CoA dehydrogenase	-2.06
ABUW_RS10840		MotA/TolQ/ExbB proton channel family protein	-2.06
ABUW_RS20315		hypothetical protein	-2.05
ABUW_RS09500		TolC family protein	-2.04
ABUW_RS13585		hypothetical protein	-2.04
ABUW_RS12630		hypothetical protein	-2.04
ABUW_RS12680		hypothetical protein	-2.04
ABUW_RS07310		DMT family transporter	-2.04
ABUW_RS08700		hypothetical protein	-2.04
ABUW_RS16715		HdeD family acid-resistance protein	-2.03
ABUW_RS12980		hypothetical protein	-2.03
ABUW_RS07175		BLUF domain-containing protein	-2.03
ABUW_RS15335		hypothetical protein	-2.03
ABUW_RS07985		SDR family NAD(P)-dependent oxidoreductase	-2.02
ABUW_RS03610		AlpA family phage regulatory protein	-2.02
ABUW_RS04515		MBL fold metallo-hydrolase	-2.02
ABUW_RS06585		MgtC/SapB family protein	-2.01
ABUW_RS12830		TolC family protein	-2.00
ABUW_RS11880		hypothetical protein	-1.98
ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	-1.98
ABUW_RS09275		hydrolase	-1.96
ABUW_RS12540		hypothetical protein	-1.96
ABUW_RS08725		cyd operon YbgE family protein	-1.96
ABUW_RS09520		HD domain-containing protein	-1.95
ABUW_RS11270		hypothetical protein	-1.94
ABUW_RS13105		hypothetical protein	-1.94
ABUW_RS09975		fimbrial biogenesis outer membrane usher protein	-1.94
ABUW_RS16315		DUF4124 domain-containing protein	-1.93
sRNA8	sRNA8	sRNA8	-1.92
ABUW_RS03970		hypothetical protein	-1.90
ABUW_RS19085		H-NS histone family protein	-1.89

ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-1.89
ABUW_RS17270	pilB	type IV-A pilus assembly ATPase PilB	-1.88
ABUW_RS12880		hypothetical protein	-1.88
ABUW_RS11130		GrpB family protein	-1.88
ABUW_RS11235		type 1 fimbrial protein	-1.88
ABUW_RS05875		M1 family metallopeptidase	-1.88
ABUW_RS18015		DUF2726 domain-containing protein	-1.88
ABUW_RS12185		catalase family peroxidase	-1.87
ABUW_RS10610		RraA family protein	-1.87
ABUW_RS15550		amidohydrolase	-1.87
ABUW_RS02390		acyl-CoA dehydrogenase family protein	-1.86
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	-1.86
ABUW_RS07170		NirD/YgiW/YdeI family stress tolerance protein	-1.86
ABUW_RS03620		hypothetical protein	-1.86
ABUW_RS19110		DUF2786 domain-containing protein	-1.85
ABUW_RS03975		hypothetical protein	-1.85
ABUW_RS05225		glycosyltransferase family 2 protein	-1.85
ABUW_RS19075		hypothetical protein	-1.85
ABUW_RS13685		type VI secretion system tip protein VgrG	-1.85
ABUW_RS05525		hypothetical protein	-1.85
ABUW_RS10010		hypothetical protein	-1.85
ABUW_RS10845		biopolymer transporter ExbD	-1.85
ABUW_RS06280		hypothetical protein	-1.83
ABUW_RS14630		hypothetical protein	-1.83
ABUW_RS09995		hypothetical protein	-1.83
ABUW_RS13770		hypothetical protein	-1.83
ABUW_RS07415		aspartate/glutamate racemase family protein	-1.82
ABUW_RS05205		hypothetical protein	-1.82
ABUW_RS08585		PQQ-dependent sugar dehydrogenase	-1.82
ABUW_RS04635	fdhD	formate dehydrogenase accessory sulfurtransferase FdhD	-1.81
ABUW_RS18630		oligosaccharide flippase family protein	-1.81
ABUW_RS02630		hypothetical protein	-1.81
ABUW_RS13680		RHS repeat protein	-1.81
ABUW_RS05220		hypothetical protein	-1.81
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	-1.81
ABUW_RS16890		glutathione S-transferase family protein	-1.80
ABUW_RS02840		tail protein X	-1.80
ABUW_RS13045		NAD(P)-binding domain-containing protein	-1.80
ABUW_RS19575		hypothetical protein	-1.79
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.79
ABUW_RS13760		RHS repeat protein	-1.79
ABUW_RS07125		LysR family transcriptional regulator	-1.78
ABUW_RS02300		DUF2789 domain-containing protein	-1.78
ABUW_RS02715		BRCT domain-containing protein	-1.78
ABUW_RS12515	tssF	type VI secretion system baseplate subunit TssF	-1.77
ABUW_RS11950		hydroxymethylglutaryl-CoA lyase	-1.77
ABUW_RS08745		hypothetical protein	-1.77
ABUW_RS10070		transcriptional repressor	-1.76
ABUW_RS09330		DUF2247 family protein	-1.76
ABUW_RS19515	lepB	signal peptidase I	-1.76
ABUW_RS14485		DUF560 domain-containing protein	-1.75
ABUW_RS07400		chalcone isomerase family protein	-1.75
ABUW_RS12620		hypothetical protein	-1.75
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.74
ABUW_RS18625		hypothetical protein	-1.74
ABUW_RS00410		HAD family hydrolase	-1.73
ABUW_RS12305	paaK	phenylacetate-CoA oxygenase/reductase subunit PaaK	-1.73

ABUW_RS18490		SDR family NAD(P)-dependent oxidoreductase	-1.73
ABUW_RS08740		cytochrome ubiquinol oxidase subunit I	-1.73
ABUW_RS12740		exo-alpha-sialidase	-1.73
ABUW_RS04730		ChbG/HpnK family deacetylase	-1.72
ABUW_RS04630		FdhF/YdeP family oxidoreductase	-1.72
ABUW_RS11225		hypothetical protein	-1.71
ABUW_RS20180		hypothetical protein	-1.71
ABUW_RS00380	hutU	urocanate hydratase	-1.71
ABUW_RS10770		nucleoside-diphosphate sugar epimerase	-1.71
ABUW_RS07970		fimbrial biogenesis outer membrane usher protein	-1.71
ABUW_RS04155		hypothetical protein	-1.71
ABUW_RS03330		hypothetical protein	-1.70
ABUW_RS05355	csy3	type I-F CRISPR-associated protein Csy3	-1.70
ABUW_RS07500		hypothetical protein	-1.70
ABUW_RS19690		hypothetical protein	-1.69
ABUW_RS05345	csy1	type I-F CRISPR-associated protein Csy1	-1.69
ABUW_RS03500		DJ-1/Pfpl family protein	-1.69
sRNA28	sRNA28	sRNA28	-1.68
ABUW_RS09270		antibiotic biosynthesis monooxygenase	-1.68
ABUW_RS04540		lytic transglycosylase domain-containing protein	-1.68
ABUW_RS20460		hypothetical protein	-1.68
ABUW_RS00595		DUF1311 domain-containing protein	-1.67
ABUW_RS19045		DUF1173 domain-containing protein	-1.67
ABUW_RS11300		hypothetical protein	-1.67
ABUW_RS03910		hypothetical protein	-1.66
ABUW_RS00685		alpha/beta hydrolase	-1.66
ABUW_RS15355		excalibur calcium-binding domain-containing protein	-1.66
ABUW_RS19170		hypothetical protein	-1.66
ABUW_RS10855		hypothetical protein	-1.66
ABUW_RS07325		MCE family protein	-1.65
ABUW_RS15530		LysR family transcriptional regulator	-1.65
ABUW_RS08540		hypothetical protein	-1.65
ABUW_RS20115		hypothetical protein	-1.64
ABUW_RS00915		hypothetical protein	-1.64
ABUW_RS13115		hypothetical protein	-1.64
ABUW_RS13065		N-acetylmuramidase	-1.63
ABUW_RS05360	cas6f	type I-F CRISPR-associated endoribonuclease Cas6/Csy4	-1.63
ABUW_RS07960		spore coat protein U domain-containing protein	-1.63
ABUW_RS18620		oligosaccharide repeat unit polymerase	-1.62
ABUW_RS01060		DMT family transporter	-1.62
ABUW_RS01160	aqpZ	aquaporin Z	-1.62
ABUW_RS13650		ATP-binding protein	-1.62
ABUW_RS02780		phage major tail tube protein	-1.62
ABUW_RS08685		CBS domain-containing protein	-1.62
ABUW_RS06295		DUF2280 domain-containing protein	-1.61
ABUW_RS03655		hypothetical protein	-1.61
ABUW_RS12890		hypothetical protein	-1.61
ABUW_RS00260		DUF1328 domain-containing protein	-1.60
ABUW_RS19545		hypothetical protein	-1.60
ABUW_RS12965		transposase	-1.60
ABUW_RS08045		hypothetical protein	-1.60
ABUW_RS20270		hypothetical protein	-1.60
ABUW_RS04980	carO	ornithine uptake porin CarO type 3	-1.60
ABUW_RS09325		hypothetical protein	-1.60
ABUW_RS18470		nuclear transport factor 2 family protein	-1.59
ABUW_RS00370	hutC	histidine utilization repressor	-1.59
ABUW_RS08440		PAS domain-containing protein	-1.58

sRNA100	sRNA100	sRNA100	-1.58
ABUW_RS01840		hypothetical protein	-1.58
ABUW_RS19080		thermonuclease family protein	-1.58
ABUW_RS13835		YraN family protein	-1.58
ABUW_RS11725	yfcF	glutathione transferase	-1.57
ABUW_RS11760		cysteine desulfurase	-1.57
ABUW_RS03835		hypothetical protein	-1.57
ABUW_RS19620		DIP1984 family protein	-1.56
ABUW_RS15790	raiA	ribosome-associated translation inhibitor RaiA	-1.56
ABUW_RS09345		hypothetical protein	-1.56
ABUW_RS16895		YafY family transcriptional regulator	-1.56
ABUW_RS12485		PAAR domain-containing protein	-1.55
ABUW_RS03340		response regulator	-1.55
ABUW_RS09185		alpha/beta hydrolase	-1.55
ABUW_RS12715		serine hydrolase	-1.55
ABUW_RS04785		DNA internalization-related competence protein ComEC/Rec2	-1.54
ABUW_RS14885		pirin family protein	-1.54
ABUW_RS02445		DUF2147 domain-containing protein	-1.54
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.54
ABUW_RS19560		transglycosylase SLT domain-containing protein	-1.54
ABUW_RS10825		ABC transporter substrate-binding protein	-1.53
ABUW_RS03745		hypothetical protein	-1.53
ABUW_RS11910		hypothetical protein	-1.52
ABUW_RS17455		DUF4442 domain-containing protein	-1.52
ABUW_RS15290		NF038215 family lipoprotein	-1.52
ABUW_RS02205		hypothetical protein	-1.52
ABUW_RS11860		iron-containing redox enzyme family protein	-1.52
ABUW_RS12625		hypothetical protein	-1.51
ABUW_RS12335		L-serine ammonia-lyase	-1.51
ABUW_RS00365		acyltransferase	-1.51
ABUW_RS01480		LemA family protein	-1.51
ABUW_RS12685		hypothetical protein	-1.50
ABUW_RS14015		urease accessory protein UreD	-1.50
ABUW_RS01485		TPM domain-containing protein	-1.50
ABUW_RS12720		GNAT family N-acetyltransferase	-1.50
ABUW_RS00375		HutD family protein	-1.49
ABUW_RS02875		HAMP domain-containing histidine kinase	-1.49
ABUW_RS08095		universal stress protein	-1.49
ABUW_RS12760		lauroyl acyltransferase	-1.48
ABUW_RS18825		ankyrin repeat domain-containing protein	-1.48
ABUW_RS12180		cytochrome b	-1.47
ABUW_RS17175		FAD-dependent monooxygenase	-1.47
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-1.47
ABUW_RS10375		GGDEF domain-containing protein	-1.47
ABUW_RS01280		aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	-1.47
ABUW_RS04895		amidohydrolase	-1.47
ABUW_RS04090		hypothetical protein	-1.47
ABUW_RS17280		prepilin peptidase	-1.46
ABUW_RS01105		hypothetical protein	-1.46
ABUW_RS01150		LysE family translocator	-1.46
ABUW_RS11920		AMP-binding protein	-1.46
ABUW_RS16025		ComEA family DNA-binding protein	-1.46
ABUW_RS15060		DUF2157 domain-containing protein	-1.45
ABUW_RS02745		phage tail protein	-1.45
ABUW_RS12425		GNAT family N-acetyltransferase	-1.45
ABUW_RS14690		OsmC family protein	-1.45

ABUW_RS12430		winged helix-turn-helix domain-containing protein	-1.44
ABUW_RS06275		hypothetical protein	-1.44
ABUW_RS09560		LysR family transcriptional regulator	-1.44
ABUW_RS12805		universal stress protein	-1.43
ABUW_RS16280		hypothetical protein	-1.43
ABUW_RS12505		hypothetical protein	-1.42
ABUW_RS07995		chorismate mutase	-1.42
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.42
ABUW_RS10015		phospholipase D family protein	-1.41
ABUW_RS16475		NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-1.41
sRNA69	sRNA69	sRNA69	-1.40
ABUW_RS10580		HAD family hydrolase	-1.40
ABUW_RS00645	uraH	hydroxyisourate hydrolase	-1.40
ABUW_RS05575		hypothetical protein	-1.40
ABUW_RS00650	uraD	2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase	-1.40
ABUW_RS06135		hypothetical protein	-1.39
ABUW_RS02520		dihydrolipoyl dehydrogenase	-1.39
ABUW_RS18255		OsmC family protein	-1.39
ABUW_RS17065		hypothetical protein	-1.39
ABUW_RS14460		DUF1275 domain-containing protein	-1.39
ABUW_RS09265		hypothetical protein	-1.38
ABUW_RS10940	gspJ	type II secretion system minor pseudopilin GspJ	-1.38
sRNA18	sRNA18	sRNA18	-1.38
ABUW_RS07790		ion transporter	-1.38
ABUW_RS12825		type I secretion system permease/ATPase	-1.38
ABUW_RS08200		iron-containing alcohol dehydrogenase	-1.37
ABUW_RS13200		KTSC domain-containing protein	-1.37
ABUW_RS04910		deoxyguanosinetriphosphate triphosphohydrolase	-1.37
ABUW_RS10810		ABC transporter permease	-1.36
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	-1.36
ABUW_RS12490		OmpA family protein	-1.36
ABUW_RS03855		hypothetical protein	-1.36
ABUW_RS07975		spore coat protein U domain-containing protein	-1.36
ABUW_RS03485		DUF4850 domain-containing protein	-1.35
ABUW_RS13220		hypothetical protein	-1.35
ABUW_RS14595		single-stranded DNA-binding protein	-1.34
ABUW_RS19890		hypothetical protein	-1.34
ABUW_RS10315		MBL fold metallo-hydrolase	-1.34
ABUW_RS16030	mazG	nucleoside triphosphate pyrophosphohydrolase	-1.33
ABUW_RS08870		metal-dependent hydrolase	-1.33
ABUW_RS06240		hypothetical protein	-1.33
ABUW_RS07620		hypothetical protein	-1.33
ABUW_RS01070		hypothetical protein	-1.33
ABUW_RS13320		hypothetical protein	-1.32
ABUW_RS03190		GspH/FimT family pseudopilin	-1.32
ABUW_RS06900		hypothetical protein	-1.31
ABUW_RS16160		copper resistance protein CopC	-1.31
ABUW_RS16085		SDR family NAD(P)-dependent oxidoreductase	-1.31
ABUW_RS07615	pgaD	poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD	-1.31
ABUW_RS07330		membrane integrity-associated transporter subunit PqiC	-1.30
ABUW_RS02720		hypothetical protein	-1.30
ABUW_RS14555		site-specific DNA-methyltransferase	-1.30
ABUW_RS11785		amino acid ABC transporter ATP-binding protein	-1.30
ABUW_RS00385	hutH	histidine ammonia-lyase	-1.30
ABUW_RS13385		NAD(P)/FAD-dependent oxidoreductase	-1.30
ABUW_RS09585		hypothetical protein	-1.29
ABUW_RS07990		SDR family NAD(P)-dependent oxidoreductase	-1.29

ABUW_RS05420		SIMPL domain-containing protein	-1.29
ABUW_RS01765		hypothetical protein	-1.29
ABUW_RS16210		hypothetical protein	-1.29
ABUW_RS16440		phosphatase PAP2 family protein	-1.29
ABUW_RS01125		GNAT family N-acetyltransferase	-1.28
ABUW_RS18895		matrixin family metalloprotease	-1.28
ABUW_RS05195		nitronate monooxygenase	-1.28
ABUW_RS04685		alpha/beta fold hydrolase	-1.27
ABUW_RS05715	basA	acinetobactin non-ribosomal peptide synthetase subunit BasA	-1.27
ABUW_RS08390		hypothetical protein	-1.27
ABUW_RS10800		ABC transporter ATP-binding protein	-1.26
ABUW_RS05710	bauF	acinetobactin utilization protein BauF	-1.26
ABUW_RS17095		LysE family translocator	-1.26
ABUW_RS04740		ABC transporter permease	-1.26
ABUW_RS19090		hypothetical protein	-1.24
ABUW_RS10850		biopolymer transporter ExbD	-1.24
ABUW_RS11370		methionine transporter	-1.24
ABUW_RS07395		response regulator transcription factor	-1.24
ABUW_RS07315		paraquat-inducible protein A	-1.23
ABUW_RS09180		hypothetical protein	-1.23
ABUW_RS15175	bfr	bacterioferritin	-1.23
ABUW_RS13280		CinA family protein	-1.23
ABUW_RS04020		SPFH/Band 7/PHB domain protein	-1.23
ABUW_RS08315		molybdopterin-dependent oxidoreductase	-1.22
ABUW_RS08190	plc1	phospholipase C, phosphocholine-specific	-1.22
ABUW_RS10805		ABC transporter permease	-1.22
ABUW_RS06345		hypothetical protein	-1.22
ABUW_RS03150		CoA transferase	-1.22
ABUW_RS06670		hypothetical protein	-1.22
ABUW_RS11375		MetQ/NlpA family ABC transporter substrate-binding protein	-1.21
ABUW_RS03335	pilG	twitching motility response regulator PilG	-1.21
ABUW_RS18995		metal/formaldehyde-sensitive transcriptional repressor	-1.21
ABUW_RS17655	cpdA	3',5'-cyclic-AMP phosphodiesterase	-1.21
ABUW_RS13820	nudC	NAD(+) diphosphatase	-1.20
sRNA76	sRNA76	sRNA76	-1.20
ABUW_RS19535	traN	conjugal transfer protein TraN	-1.20
ABUW_RS11350		glutathione S-transferase	-1.20
ABUW_RS17640		hypothetical protein	-1.20
ABUW_RS00040		RND transporter	-1.20
ABUW_RS17060		tRNA-binding protein	-1.19
ABUW_RS11690		MFS transporter	-1.19
ABUW_RS11780		transporter substrate-binding domain-containing protein	-1.19
ABUW_RS07320		paraquat-inducible protein A	-1.19
ABUW_RS05995		acyl-CoA dehydrogenase	-1.19
ABUW_RS05125		hypothetical protein	-1.19
ABUW_RS07425		sorbose dehydrogenase family protein	-1.18
ABUW_RS12690		RHS domain-containing protein	-1.17
ABUW_RS01020		hydrolase	-1.17
ABUW_RS10075		isochorismatase family protein	-1.17
ABUW_RS19395		hypothetical protein	-1.17
ABUW_RS03080		dual specificity protein phosphatase family protein	-1.17
ABUW_RS14760		phosphomannomutase/phosphoglucomutase	-1.16
ABUW_RS09260		sorbose dehydrogenase family protein	-1.16
ABUW_RS01490		TPM domain-containing protein	-1.15
ABUW_RS00590		hypothetical protein	-1.15
ABUW_RS08090		ABC-F family ATP-binding cassette domain-containing protein	-1.15
ABUW_RS09280		LysR family transcriptional regulator	-1.15

ABUW_RS02970		phosphate-starvation-inducible PsiE family protein	-1.15
ABUW_RS11405		hypothetical protein	-1.15
ABUW_RS14240		galactose mutarotase	-1.14
ABUW_RS10555		histidine-type phosphatase	-1.14
sRNA72	sRNA72	sRNA72	-1.14
ABUW_RS07920		alpha/beta hydrolase	-1.14
ABUW_RS18865		hypothetical protein	-1.14
ABUW_RS03085		MBL fold metallo-hydrolase	-1.14
ABUW_RS16305	ilvN	acetolactate synthase small subunit	-1.13
ABUW_RS02560		sulfurtransferase	-1.13
ABUW_RS03630		hypothetical protein	-1.13
ABUW_RS18740		YciK family oxidoreductase	-1.13
ABUW_RS18710		ferredoxin reductase	-1.13
ABUW_RS12555		ABC transporter ATP-binding protein	-1.13
ABUW_RS02730		TraR/DksA C4-type zinc finger protein	-1.13
ABUW_RS07805		DUF4198 domain-containing protein	-1.12
ABUW_RS15730		hypothetical protein	-1.12
ABUW_RS01975		DUF853 domain-containing protein	-1.12
ABUW_RS09010		phosphotransferase family protein	-1.12
ABUW_RS07830		GNAT family N-acetyltransferase	-1.12
ABUW_RS04815	perM	AI-2E family transporter	-1.11
ABUW_RS10420		hypothetical protein	-1.11
ABUW_RS18585		UDP-glucose/GDP-mannose dehydrogenase family protein	-1.11
ABUW_RS06180		hypothetical protein	-1.10
ABUW_RS15515		flavin reductase	-1.10
ABUW_RS19540		conjugal transfer protein TraF	-1.10
ABUW_RS18945		TerC family protein	-1.09
ABUW_RS12820		HlyD family type I secretion periplasmic adaptor subunit	-1.09
ABUW_RS02855		phage major capsid protein, P2 family	-1.09
ABUW_RS08550		Lrp/AsnC family transcriptional regulator	-1.09
ABUW_RS18475		ribonuclease E inhibitor RraB	-1.08
ABUW_RS08615		PEGA domain-containing protein	-1.08
ABUW_RS04905	ruvA	Holliday junction branch migration protein RuvA	-1.08
ABUW_RS04115		YbjQ family protein	-1.07
ABUW_RS09020		SDR family oxidoreductase	-1.07
ABUW_RS13570		coniferyl aldehyde dehydrogenase	-1.07
ABUW_RS01790		hypothetical protein	-1.07
ABUW_RS14430	betA	choline dehydrogenase	-1.07
ABUW_RS14870		EcsC family protein	-1.06
ABUW_RS01065		hypothetical protein	-1.06
ABUW_RS15660		cation transporter	-1.06
ABUW_RS13355	rnhB	ribonuclease HII	-1.06
ABUW_RS12700		hypothetical protein	-1.05
ABUW_RS11850		glucose 1-dehydrogenase	-1.05
ABUW_RS01245		GNAT family acetyltransferase	-1.05
ABUW_RS11545		amidohydrolase	-1.05
ABUW_RS14550		DEAD/DEAH box helicase family protein	-1.04
ABUW_RS04485		NAD(+)/NADH kinase	-1.04
ABUW_RS18615		glycosyltransferase family 4 protein	-1.04
ABUW_RS12245		hypothetical protein	-1.04
ABUW_RS16185		hypothetical protein	-1.04
ABUW_RS03370		alpha/beta fold hydrolase	-1.04
ABUW_RS09235		AraC family transcriptional regulator	-1.03
ABUW_RS18610		sugar transferase	-1.03
ABUW_RS15965		DedA family protein	-1.03
ABUW_RS16180		hypothetical protein	-1.03
ABUW_RS10880		lysine exporter LysO family protein	-1.03

ABUW_RS06975		hypothetical protein	-1.03
ABUW_RS12765		EAL domain-containing protein	-1.02
ABUW_RS16080	rsfS	ribosome silencing factor	-1.02
ABUW_RS12460		hypothetical protein	-1.02
ABUW_RS17815		hypothetical protein	-1.02
ABUW_RS17190		AAA family ATPase	-1.02
ABUW_RS01410		hypothetical protein	-1.02
ABUW_RS04110		nuclear transport factor 2 family protein	-1.01
ABUW_RS15745		hypothetical protein	-1.01
ABUW_RS11065		TetR/AcrR family transcriptional regulator	-1.01
ABUW_RS00545		pyridoxal phosphate-dependent aminotransferase	-1.01
ABUW_RS15165		trehalose-6-phosphate synthase	-1.00
ABUW_RS00665		ankyrin repeat domain-containing protein	-1.00

Table A8. Overview of genes that are differentially expressed as identified through RNA-seq analysis in *ΔgacA* LSP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	<i>ΔgacA</i> LSP vs WT LSP log2FC
ABUW_RS19295		APH(6)-I family aminoglycoside O-phosphotransferase	6.51
ABUW_RS01355		tRNA-Glu	6.32
ABUW_RS19300	aph(3'')-Ib	aminoglycoside O-phosphotransferase APH(3'')-Ib	6.31
ABUW_RS19305		ANT(3'')-Ia family aminoglycoside nucleotidyltransferase AadA2	6.23
sRNA26	sRNA26	sRNA26	6.20
ABUW_RS06940		hypothetical protein	6.11
ABUW_RS07110		tRNA-Trp	5.89
ABUW_RS12755		TetR/AcrR family transcriptional regulator	5.62
ABUW_RS06215		hypothetical protein	5.59
ABUW_RS01305		TolC family protein	5.55
ABUW_RS07105		tRNA-Leu	5.53
sRNA81	sRNA81	sRNA81	5.39
ABUW_RS19240		hypothetical protein	5.36
ABUW_RS02145		membrane protein	5.33
ABUW_RS19310		CmlA family chloramphenicol efflux MFS transporter	5.27
ABUW_RS08015		hypothetical protein	5.25
ABUW_RS11765		LysE family translocator	5.21
ABUW_RS19255		GNAT family N-acetyltransferase	5.08
ABUW_RS03860		hypothetical protein	5.06
ABUW_RS20020		TniB family NTP-binding protein	5.01
ABUW_RS19130		SAM-dependent DNA methyltransferase	4.86
ABUW_RS19125		hypothetical protein	4.85
ABUW_RS10540		sulfite exporter TauE/SafE family protein	4.81
sRNA53	sRNA53	sRNA53	4.74
sRNA84	sRNA84	sRNA84	4.62
ABUW_RS19905	ssrS	6S RNA	4.59
ABUW_RS09380		MFS transporter	4.41
ABUW_RS01250		acetyl-CoA hydrolase/transferase family protein	4.39
ABUW_RS17835		signal peptidase II	4.36
ABUW_RS19340		hypothetical protein	4.34
sRNA95	sRNA95	sRNA95	4.26
ABUW_RS19635		protein rep	4.23
ABUW_RS19235		hypothetical protein	4.13
ABUW_RS01870		DEAD/DEAH box helicase	4.03
ABUW_RS16340		MacB family efflux pump subunit	4.03
ABUW_RS19355		hypothetical protein	4.02

ABUW_RS10215		hypothetical protein	4.00
ABUW_RS09375		SMP-30/gluconolactonase/LRE family protein	3.98
sRNA24	sRNA24	sRNA24	3.94
ABUW_RS04265	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	3.88
ABUW_RS11925		TetR/AcrR family transcriptional regulator	3.88
ABUW_RS15200		sulfite exporter TauE/SafE family protein	3.85
ABUW_RS19370		hypothetical protein	3.81
ABUW_RS14440		hypothetical protein	3.79
sRNA37	sRNA37	sRNA37	3.75
ABUW_RS19930	ssrA	transfer-messenger RNA	3.75
sRNA89	sRNA89	sRNA89	3.74
ABUW_RS17840		cation transporter	3.73
ABUW_RS04260	sdhC	succinate dehydrogenase, cytochrome b556 subunit	3.73
ABUW_RS04555		transglycosylase SLT domain-containing protein	3.67
ABUW_RS15705		class I SAM-dependent methyltransferase	3.62
sRNA77	sRNA77	sRNA77	3.61
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	3.57
ABUW_RS04395		DOMON-like domain-containing protein	3.56
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	3.55
ABUW_RS16345	adeC	AdeC/AdeK/OprM family multidrug efflux complex outer membrane factor	3.55
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	3.53
ABUW_RS20015		Mu transposase C-terminal domain-containing protein	3.49
ABUW_RS19015	rnpA	ribonuclease P protein component	3.47
ABUW_RS17245		tRNA-Met	3.45
ABUW_RS15025		tRNA-Gln	3.45
ABUW_RS19315	aadB	aminoglycoside nucleotidyltransferase ANT(2'')-Ia	3.42
ABUW_RS19660	rnpB	RNase P RNA component class A	3.42
sRNA88	sRNA88	sRNA88	3.39
ABUW_RS05010		sulfate ABC transporter substrate-binding protein	3.38
ABUW_RS15710	tsaB	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	3.35
ABUW_RS14535		hypothetical protein	3.34
sRNA92	sRNA92	sRNA92	3.33
ABUW_RS01315		CusA/CzcA family heavy metal efflux RND transporter	3.32
ABUW_RS13375		NCS2 family permease	3.30
ABUW_RS13640		amino acid permease	3.29
ABUW_RS19220		hypothetical protein	3.29
ABUW_RS19350		hypothetical protein	3.28
ABUW_RS12300		enoyl-CoA hydratase/isomerase family protein	3.26
ABUW_RS17630		EamA family transporter	3.24
ABUW_RS18200		ATP synthase subunit I	3.19
ABUW_RS19360		hypothetical protein	3.19
ABUW_RS06920		head-tail connector protein	3.18
ABUW_RS16230		tyrosine-type recombinase/integrase	3.17
ABUW_RS01310		efflux RND transporter periplasmic adaptor subunit	3.16
ABUW_RS16335		MacA family efflux pump subunit	3.15
ABUW_RS04135	adel	multidrug efflux RND transporter periplasmic adaptor subunit Adel	3.14
ABUW_RS19260	sul1	sulfonamide-resistant dihydropteroate synthase Sul1	3.12
ABUW_RS18190	atpE	F0F1 ATP synthase subunit C	3.11
sRNA1	sRNA1	sRNA1	3.08
ABUW_RS16095		NAD(P) transhydrogenase subunit alpha	3.07
ABUW_RS19030		replication initiation protein	3.06
ABUW_RS15380	nuoL	NADH-quinone oxidoreductase subunit L	3.06
ABUW_RS05000	cysT	sulfate ABC transporter permease subunit CysT	3.01
ABUW_RS17330		DUF1656 domain-containing protein	3.01

ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	3.00
ABUW_RS16625	thyA	thymidylate synthase	2.97
ABUW_RS11170		methionine adenosyltransferase	2.93
ABUW_RS12295		2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	2.93
ABUW_RS19275		aminoglycoside N-acetyltransferase AAC(6')-Ib3	2.92
ABUW_RS18020		YgiQ family radical SAM protein	2.91
ABUW_RS19270		trimethoprim-resistant dihydrofolate reductase DfrA7	2.90
ABUW_RS16100		Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha	2.90
ABUW_RS04130	adeJ	multidrug efflux RND transporter permease subunit AdeJ	2.90
ABUW_RS02985		hypothetical protein	2.88
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	2.88
ABUW_RS09685		DUF2523 domain-containing protein	2.88
ABUW_RS13860		cation transporter	2.86
ABUW_RS14325		aromatic ring-hydroxylating dioxygenase subunit alpha	2.84
ABUW_RS16810	infA	translation initiation factor IF-1	2.84
ABUW_RS18280	guaA	glutamine-hydrolyzing GMP synthase	2.82
ABUW_RS04270		succinate dehydrogenase flavoprotein subunit	2.81
ABUW_RS09970		molecular chaperone	2.81
ABUW_RS11650	madL	malonate transporter subunit MadL	2.80
ABUW_RS17295	rlmB	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	2.80
ABUW_RS07685		acyl-CoA dehydrogenase family protein	2.79
ABUW_RS00315		MATE family efflux transporter	2.78
ABUW_RS00640		purine permease	2.76
ABUW_RS08465		phosphatidate cytidyltransferase	2.76
ABUW_RS18030		helix-turn-helix domain-containing protein	2.75
ABUW_RS20105		hypothetical protein	2.75
ABUW_RS00635		ion channel protein Tsx	2.75
ABUW_RS13565		AraC family transcriptional regulator	2.74
ABUW_RS19140		ParA family protein	2.73
ABUW_RS04400	yhbY	ribosome assembly RNA-binding protein YhbY	2.73
ABUW_RS00985		AzIC family ABC transporter permease	2.73
ABUW_RS14410		choline transporter	2.72
ABUW_RS19345		molecular chaperone DnaJ	2.72
ABUW_RS12285	pcaF	3-oxoadipyl-CoA thiolase	2.72
ABUW_RS18185		F0F1 ATP synthase subunit B	2.71
ABUW_RS16630		dihydrofolate reductase	2.70
ABUW_RS08760		adenosine kinase	2.69
ABUW_RS15170		MFS transporter	2.69
ABUW_RS02295		malate dehydrogenase	2.67
ABUW_RS02000	rplD	50S ribosomal protein L4	2.66
ABUW_RS05500	mnmA	tRNA 2-thiouridine(34) synthase MnmA	2.65
ABUW_RS07660	prmC	peptide chain release factor N(5)-glutamine methyltransferase	2.63
ABUW_RS02635	queA	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	2.63
ABUW_RS00320		DUF523 domain-containing protein	2.63
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	2.63
ABUW_RS14445		homocysteine S-methyltransferase family protein	2.62
ABUW_RS12770		EamA family transporter	2.61
ABUW_RS05150	rarD	EamA family transporter RarD	2.61
ABUW_RS11390	ychF	redox-regulated ATPase YchF	2.59
sRNA55	sRNA55	sRNA55	2.59
ABUW_RS12140		cytosine permease	2.59
ABUW_RS09420		dihydroxy-acid dehydratase family protein	2.58
ABUW_RS10170		hypothetical protein	2.57
ABUW_RS05005		alpha/beta hydrolase	2.57
ABUW_RS00835		helix-turn-helix transcriptional regulator	2.57

ABUW_RS12055		CoA transferase	2.57
ABUW_RS03040		DUF1543 domain-containing protein	2.55
ABUW_RS06850		hypothetical protein	2.54
ABUW_RS16090		NAD(P)(+) transhydrogenase (Re/Si-specific) subunit beta	2.53
ABUW_RS07795		MFS transporter	2.52
ABUW_RS11530		metalloregulator ArsR/SmtB family transcription factor	2.51
ABUW_RS18435		amino acid permease	2.51
ABUW_RS11310		1-acyl-sn-glycerol-3-phosphate acyltransferase	2.51
ABUW_RS17820		SulP family inorganic anion transporter	2.50
ABUW_RS12290		3-hydroxyacyl-CoA dehydrogenase	2.50
ABUW_RS17525		tRNA-Gly	2.49
ABUW_RS12310	paaJ	phenylacetate-CoA oxygenase subunit PaaJ	2.49
ABUW_RS10480		GFA family protein	2.49
ABUW_RS06485		tRNA-Arg	2.48
ABUW_RS16275		peptide chain release factor 3	2.47
sRNA61	sRNA61	sRNA61	2.47
ABUW_RS15390	nuoJ	NADH-quinone oxidoreductase subunit J	2.46
ABUW_RS15465		hypothetical protein	2.45
ABUW_RS05170	cgtA	Obg family GTPase CgtA	2.44
ABUW_RS03205		RtcB family protein	2.43
ABUW_RS16620		hypothetical protein	2.43
ABUW_RS14320		SDR family oxidoreductase	2.42
ABUW_RS04140		phosphatase PAP2 family protein	2.42
ABUW_RS02115	rpsD	30S ribosomal protein S4	2.42
ABUW_RS18535	prpB	methylosuccinate lyase	2.41
ABUW_RS05665		DMT family transporter	2.40
ABUW_RS12355		aldehyde dehydrogenase (NADP(+))	2.40
ABUW_RS17675		UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	2.39
ABUW_RS05835	folE	GTP cyclohydrolase I FolE	2.39
ABUW_RS04970	queE	7-carboxy-7-deazaquinine synthase QueE	2.38
ABUW_RS03185		thiolase family protein	2.38
ABUW_RS08740		cytochrome ubiquinol oxidase subunit I	2.37
ABUW_RS09220		Rrf2 family transcriptional regulator	2.37
ABUW_RS13835		YraN family protein	2.37
ABUW_RS10120		AraC family transcriptional regulator	2.37
ABUW_RS01465	gltB	glutamate synthase large subunit	2.36
ABUW_RS05560		bile acid:sodium symporter	2.36
ABUW_RS06195		hypothetical protein	2.36
ABUW_RS14365	pgaC	poly-beta-1,6 N-acetyl-D-glucosamine synthase	2.36
ABUW_RS12850		HAD-IIIa family hydrolase	2.35
ABUW_RS15375	nuoM	NADH-quinone oxidoreductase subunit M	2.35
ABUW_RS15760		chorismate-binding protein	2.35
ABUW_RS02945		DUF4184 family protein	2.34
ABUW_RS08880		CTP synthase	2.34
ABUW_RS15750		C39 family peptidase	2.34
ABUW_RS12060		acyl-CoA dehydrogenase family protein	2.34
ABUW_RS17975		trimeric intracellular cation channel family protein	2.34
ABUW_RS05380		RluA family pseudouridine synthase	2.34
ABUW_RS00925	omp33-36	porin Omp33-36	2.34
ABUW_RS15400	nuoH	NADH-quinone oxidoreductase subunit NuoH	2.33
ABUW_RS03525	mreC	rod shape-determining protein MreC	2.33
ABUW_RS06820		hypothetical protein	2.32
ABUW_RS14405		MarC family protein	2.32
ABUW_RS05980		adenosylhomocysteinase	2.32
ABUW_RS00755		UDP-3-O-acyl-N-acetylglucosamine deacetylase	2.31
ABUW_RS15770	hisD	histidinol dehydrogenase	2.31

ABUW_RS01585	trmD	tRNA (guanosine(37)-N1)-methyltransferase TrmD	2.31
ABUW_RS11400		Crp/Fnr family transcriptional regulator	2.31
ABUW_RS16575		hypothetical protein	2.30
ABUW_RS05915		hypothetical protein	2.30
ABUW_RS06810		hypothetical protein	2.29
ABUW_RS16405	hisS	histidine--tRNA ligase	2.29
ABUW_RS01425		pilus assembly protein PilM	2.29
ABUW_RS03840		hypothetical protein	2.29
ABUW_RS04450	folD	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	2.29
ABUW_RS00785		TMEM165/GDT1 family protein	2.29
ABUW_RS03530	mreD	rod shape-determining protein MreD	2.29
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	2.28
ABUW_RS00350		amino acid permease	2.28
ABUW_RS09485		DHA2 family efflux MFS transporter permease subunit	2.28
ABUW_RS06695		thiazole synthase	2.28
ABUW_RS04720		GtrA family protein	2.27
ABUW_RS13325		adenylosuccinate synthase	2.27
ABUW_RS06080	rodA	rod shape-determining protein RodA	2.27
ABUW_RS15425		NADH-quinone oxidoreductase subunit B	2.27
ABUW_RS05975	metF	methylenetetrahydrofolate reductase [NAD(P)H]	2.26
ABUW_RS17870	arsB	ACR3 family arsenite efflux transporter	2.26
ABUW_RS01805		tetracycline resistance MFS efflux pump	2.26
ABUW_RS08215	murB	UDP-N-acetylmuramate dehydrogenase	2.26
ABUW_RS16770	gltP	glutamate/aspartate:proton symporter GltP	2.26
ABUW_RS13555	garD	galactarate dehydratase	2.26
ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	2.25
ABUW_RS10380	aroC	chorismate synthase	2.24
ABUW_RS11325		hypothetical protein	2.24
ABUW_RS12385		4-hydroxyproline epimerase	2.24
ABUW_RS07560	cyoE	protoheme IX farnesyltransferase	2.24
ABUW_RS17290		DMT family transporter	2.23
ABUW_RS15520		methionine synthase	2.23
ABUW_RS12330	paaZ	phenylacetic acid degradation bifunctional protein PaaZ	2.23
ABUW_RS19120		hypothetical protein	2.23
ABUW_RS08130		Lrp/AsnC family transcriptional regulator	2.23
ABUW_RS07505	mnmg	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	2.23
ABUW_RS16260		TatD family hydrolase	2.23
ABUW_RS19020	rpmH	50S ribosomal protein L34	2.22
ABUW_RS12015		SDR family oxidoreductase	2.22
ABUW_RS01000		PLP-dependent aminotransferase family protein	2.22
sRNA102	sRNA102	sRNA102	2.22
ABUW_RS15935	pheS	phenylalanine--tRNA ligase subunit alpha	2.22
ABUW_RS20430		hypothetical protein	2.22
ABUW_RS11580	tauC	taurine ABC transporter permease TauC	2.21
ABUW_RS15295		LysE family translocator	2.21
ABUW_RS15665		copper resistance protein B	2.20
ABUW_RS17115	pnp	polyribonucleotide nucleotidyltransferase	2.20
ABUW_RS17710		threonine synthase	2.20
ABUW_RS15950	rplT	50S ribosomal protein L20	2.20
ABUW_RS02110	rpsK	30S ribosomal protein S11	2.20
ABUW_RS08460	uppS	di-trans,poly-cis-decaprenylcistransferase	2.19
ABUW_RS02235		DMT family transporter	2.19
ABUW_RS17445		TRAP transporter large permease subunit	2.19
ABUW_RS08560		amino acid permease	2.19
ABUW_RS15385	nuoK	NADH-quinone oxidoreductase subunit NuoK	2.19

ABUW_RS12350		APC family permease	2.19
ABUW_RS04975	dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	2.18
ABUW_RS13720	argG	argininosuccinate synthase	2.18
ABUW_RS05505		NUDIX hydrolase	2.17
ABUW_RS13340	alaS	alanine--tRNA ligase	2.17
ABUW_RS05970		16S rRNA (uracil(1498)-N(3))-methyltransferase	2.17
ABUW_RS16390	der	ribosome biogenesis GTPase Der	2.17
ABUW_RS07715		2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase	2.16
ABUW_RS06490		hypothetical protein	2.16
ABUW_RS18035		DUF2938 domain-containing protein	2.15
ABUW_RS17255		tRNA-Leu	2.15
ABUW_RS01380	rsmH	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	2.15
ABUW_RS16995		TIGR03862 family flavoprotein	2.14
ABUW_RS06615		thiamine phosphate synthase	2.14
ABUW_RS03955		hypothetical protein	2.14
ABUW_RS03130		hypothetical protein	2.14
ABUW_RS14360	pgaD	poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD	2.13
ABUW_RS15130	rluB	23S rRNA pseudouridine(2605) synthase RluB	2.13
ABUW_RS14075	lysS	lysine--tRNA ligase	2.13
ABUW_RS07580	cyoA	ubiquinol oxidase subunit II	2.13
ABUW_RS03220		uracil-xanthine permease	2.12
ABUW_RS03960		hypothetical protein	2.12
ABUW_RS15495		hypothetical protein	2.12
ABUW_RS19010	yidD	membrane protein insertion efficiency factor YidD	2.11
ABUW_RS02080	rpsE	30S ribosomal protein S5	2.11
ABUW_RS11780		transporter substrate-binding domain-containing protein	2.11
ABUW_RS18915		5-(carboxyamino)imidazole ribonucleotide synthase	2.10
ABUW_RS17505	secE	preprotein translocase subunit SecE	2.10
ABUW_RS12965		transposase	2.10
ABUW_RS09390		DMT family transporter	2.10
ABUW_RS18920	purE	5-(carboxyamino)imidazole ribonucleotide mutase	2.10
ABUW_RS08885	kdsA	3-deoxy-8-phosphooctulonate synthase	2.10
ABUW_RS06560	yegQ	tRNA 5-hydroxyuridine modification protein YegQ	2.10
ABUW_RS07555	rpsF	30S ribosomal protein S6	2.09
ABUW_RS15430	ndhC	NADH-quinone oxidoreductase subunit A	2.09
ABUW_RS07905	eat	ethanolamine permease	2.09
ABUW_RS19005	yidC	membrane protein insertase YidC	2.09
ABUW_RS11475		type II asparaginase	2.09
ABUW_RS05155		glyceraldehyde-3-phosphate dehydrogenase	2.08
ABUW_RS06205		AAA family ATPase	2.08
ABUW_RS15135	bioD	ATP-dependent dethiobiotin synthetase BioD	2.08
ABUW_RS00310		bile acid:sodium symporter family protein	2.08
ABUW_RS04480		phosphoenolpyruvate carboxykinase (GTP)	2.07
ABUW_RS19365		hypothetical protein	2.07
ABUW_RS14670		FAD-dependent oxidoreductase	2.07
ABUW_RS15985		acyl-CoA synthetase	2.06
ABUW_RS00245	mutY	A/G-specific adenine glycosylase	2.05
ABUW_RS07670		aliphatic sulfonate ABC transporter substrate-binding protein	2.05
ABUW_RS12305	paaK	phenylacetate-CoA oxygenase/reductase subunit PaaK	2.05
ABUW_RS08725		cyd operon YbgE family protein	2.05
ABUW_RS19470	traL	type IV conjugative transfer system protein TraL	2.05
ABUW_RS17240	rimP	ribosome maturation factor RimP	2.05
ABUW_RS13025		MFS transporter	2.04
ABUW_RS18180		F0F1 ATP synthase subunit delta	2.04

ABUW_RS17520		tRNA-Thr	2.04
ABUW_RS19500	traV	type IV conjugative transfer system lipoprotein TraV	2.03
ABUW_RS15895	tilS	tRNA lysidine(34) synthetase TilS	2.03
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	2.03
ABUW_RS12095		putative 2-aminoethylphosphonate ABC transporter substrate-binding protein	2.03
ABUW_RS00730	murC	UDP-N-acetylmuramate--L-alanine ligase	2.03
ABUW_RS03175		quaternary ammonium transporter	2.03
ABUW_RS05085	pdxJ	pyridoxine 5'-phosphate synthase	2.02
ABUW_RS02690		hypothetical protein	2.02
ABUW_RS18540		GntR family transcriptional regulator	2.02
ABUW_RS11585		ATP-binding cassette domain-containing protein	2.02
ABUW_RS07370		DUF1365 domain-containing protein	2.02
ABUW_RS09565		SDR family NAD(P)-dependent oxidoreductase	2.02
ABUW_RS11660		malonate decarboxylase holo-ACP synthase	2.02
ABUW_RS09965		type 1 fimbrial protein	2.01
ABUW_RS16010	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	2.01
ABUW_RS03020		cob(I)yrinic acid a,c-diamide adenosyltransferase	2.01
ABUW_RS05525		hypothetical protein	2.00
ABUW_RS10435	recR	recombination protein RecR	2.00
ABUW_RS17575		acyl-CoA thioesterase	2.00
ABUW_RS09425		fumarylacetoacetate hydrolase family protein	2.00
ABUW_RS03125		patatin family protein	1.99
ABUW_RS05120		pyridoxal phosphate-dependent aminotransferase	1.99
ABUW_RS08125		benzoate/H(+) symporter BenE family transporter	1.99
sRNA15	sRNA15	sRNA15	1.98
ABUW_RS11655	mdcH	malonate decarboxylase subunit epsilon	1.98
ABUW_RS18345		hypothetical protein	1.98
ABUW_RS14995		glutamyl-tRNA reductase	1.98
ABUW_RS11525	arsB	ACR3 family arsenite efflux transporter	1.97
ABUW_RS12005		acyl-CoA dehydrogenase family protein	1.97
ABUW_RS10165		GntP family permease	1.97
ABUW_RS14850	tuf	elongation factor Tu	1.96
ABUW_RS15525		DUF1852 domain-containing protein	1.96
ABUW_RS12860		cysteine--tRNA ligase	1.96
ABUW_RS15370	nuoN	NADH-quinone oxidoreductase subunit NuoN	1.96
ABUW_RS01300		hypothetical protein	1.95
ABUW_RS14010	ureA	urease subunit gamma	1.95
ABUW_RS14880	hemJ	protoporphyrinogen oxidase HemJ	1.95
ABUW_RS16535		trigger factor	1.95
ABUW_RS00455	thiL	thiamine-phosphate kinase	1.95
ABUW_RS19265		quaternary ammonium compound efflux SMR transporter QacE delta 1	1.95
ABUW_RS03800		terminase family protein	1.95
ABUW_RS17475	rpoB	DNA-directed RNA polymerase subunit beta	1.94
ABUW_RS16055	cysM	cysteine synthase CysM	1.93
ABUW_RS01375		sulfate ABC transporter substrate-binding protein	1.93
ABUW_RS12085		putative 2-aminoethylphosphonate ABC transporter permease subunit	1.93
ABUW_RS11020		phosphotransferase	1.93
ABUW_RS11015		nucleotidyltransferase family protein	1.93
ABUW_RS10910		SRPBCC family protein	1.93
ABUW_RS11785		amino acid ABC transporter ATP-binding protein	1.92
ABUW_RS15035		ribose-phosphate pyrophosphokinase	1.92
ABUW_RS18170	atpG	F0F1 ATP synthase subunit gamma	1.92
ABUW_RS08210		low molecular weight phosphotyrosine protein phosphatase	1.92
ABUW_RS13255		aspartate carbamoyltransferase	1.91

ABUW_RS03035	trpB	tryptophan synthase subunit beta	1.91
ABUW_RS02600	coaBC	bifunctional phosphopantothienoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC	1.91
ABUW_RS07080	tsaD	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	1.90
ABUW_RS00805	guaB	IMP dehydrogenase	1.90
ABUW_RS17000		SAM-dependent methyltransferase	1.90
ABUW_RS01800	glyQ	glycine--tRNA ligase subunit alpha	1.90
ABUW_RS02395		enoyl-CoA hydratase/isomerase family protein	1.90
ABUW_RS01575	rpsP	30S ribosomal protein S16	1.89
ABUW_RS02930		hypothetical protein	1.89
ABUW_RS16485		permease	1.89
ABUW_RS05045		acyl-CoA thioesterase	1.89
ABUW_RS13260		aspartate carbamoyltransferase catalytic subunit	1.89
ABUW_RS15065	ribB	3,4-dihydroxy-2-butanone-4-phosphate synthase	1.89
ABUW_RS04275		succinate dehydrogenase iron-sulfur subunit	1.89
ABUW_RS15900		acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.89
ABUW_RS06110		hypothetical protein	1.89
ABUW_RS10230		MFS transporter	1.88
ABUW_RS02570		hypothetical protein	1.88
ABUW_RS14650		DHA2 family efflux MFS transporter permease subunit	1.88
ABUW_RS00065		anhydro-N-acetylmuramic acid kinase	1.88
ABUW_RS08890	eno	phosphopyruvate hydratase	1.88
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	1.87
ABUW_RS03695		AAA family ATPase	1.87
ABUW_RS18195	atpB	F0F1 ATP synthase subunit A	1.87
ABUW_RS05050	lepA	elongation factor 4	1.87
ABUW_RS03900		DUF4236 domain-containing protein	1.87
ABUW_RS07640		hypothetical protein	1.87
ABUW_RS18355		non-ribosomal peptide synthetase	1.87
ABUW_RS05090		tRNA-(ms[2]io[6]A)-hydroxylase	1.86
ABUW_RS02070	rplF	50S ribosomal protein L6	1.86
ABUW_RS06040		elongation factor Ts	1.86
ABUW_RS12750		MFS transporter	1.86
ABUW_RS16510		fumarate hydratase	1.85
ABUW_RS07680		3-hydroxyacyl-CoA dehydrogenase	1.85
ABUW_RS06525	adeL	multidrug efflux transcriptional repressor AdeL	1.84
ABUW_RS01660	craA	MFS transporter	1.84
ABUW_RS09480		HlyD family secretion protein	1.84
ABUW_RS04880	tolR	protein TolR	1.83
ABUW_RS02060	rpsN	30S ribosomal protein S14	1.83
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.83
ABUW_RS03690		GntR family transcriptional regulator	1.83
ABUW_RS19145		ParB/RepB/Spo0J family partition protein	1.83
ABUW_RS05865	trpD	anthranilate phosphoribosyltransferase	1.82
ABUW_RS08555	kynU	kynureninase	1.82
ABUW_RS17810		ATP-binding protein	1.82
ABUW_RS08790	ilvA	threonine ammonia-lyase, biosynthetic	1.82
ABUW_RS05175		glutamate 5-kinase	1.81
ABUW_RS01580	rimM	ribosome maturation factor RimM	1.81
ABUW_RS01965		Rrf2 family transcriptional regulator	1.81
ABUW_RS15420	nuoC	NADH-quinone oxidoreductase subunit C/D	1.81
ABUW_RS02165		hypothetical protein	1.80
ABUW_RS14610		hypothetical protein	1.80
ABUW_RS16410	ispG	flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl- diphosphate synthase	1.80

ABUW_RS07445		dicarboxylate/amino acid:cation symporter	1.80
ABUW_RS12365		AraC family transcriptional regulator	1.79
ABUW_RS18175		F0F1 ATP synthase subunit alpha	1.79
ABUW_RS04035		1-acyl-sn-glycerol-3-phosphate acyltransferase	1.79
ABUW_RS04645		4-phosphoerythronate dehydrogenase	1.79
ABUW_RS00965		DUF475 domain-containing protein	1.79
ABUW_RS15775		ATP phosphoribosyltransferase	1.79
ABUW_RS14255		glutaminase	1.79
ABUW_RS11135	trmA	tRNA (uridine(54)-C5)-methyltransferase TrmA	1.78
ABUW_RS14310		FAD-dependent oxidoreductase	1.78
ABUW_RS17375	lpxO	lipid A hydroxylase LpxO	1.78
ABUW_RS11060		cupin domain-containing protein	1.78
ABUW_RS11750		serine acetyltransferase	1.78
ABUW_RS15410	nuoF	NADH-quinone oxidoreductase subunit NuoF	1.78
ABUW_RS12090		ATP-binding cassette domain-containing protein	1.78
ABUW_RS10995		MotA/TolQ/ExbB proton channel family protein	1.77
ABUW_RS02960		hypothetical protein	1.76
ABUW_RS17670	ftsW	putative lipid II flippase FtsW	1.76
ABUW_RS05080	recO	DNA repair protein RecO	1.75
ABUW_RS02075	rplR	50S ribosomal protein L18	1.75
ABUW_RS00725	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	1.75
ABUW_RS11485		RNA methyltransferase	1.75
ABUW_RS04375	greA	transcription elongation factor GreA	1.74
ABUW_RS15285	metG	methionine--tRNA ligase	1.74
ABUW_RS10100		LysR family transcriptional regulator	1.74
ABUW_RS12320	paaB	1,2-phenylacetyl-CoA epoxidase subunit B	1.74
ABUW_RS02095	secY	preprotein translocase subunit SecY	1.74
ABUW_RS02015	rpsS	30S ribosomal protein S19	1.73
ABUW_RS11690		MFS transporter	1.73
ABUW_RS09465		methylenetetrahydrofolate reductase C-terminal domain-containing protein	1.73
ABUW_RS07540	dnaB	replicative DNA helicase	1.73
ABUW_RS03830		hypothetical protein	1.73
ABUW_RS02090	rplO	50S ribosomal protein L15	1.73
ABUW_RS11215	queG	tRNA epoxyqueuosine(34) reductase QueG	1.72
ABUW_RS14855	fusA	elongation factor G	1.72
ABUW_RS04810	purM	phosphoribosylformylglycinamide cyclo-ligase	1.71
ABUW_RS10305		sulfite exporter TauE/SafE family protein	1.71
ABUW_RS12080		TIGR03364 family FAD-dependent oxidoreductase	1.71
ABUW_RS08935		MFS transporter	1.71
ABUW_RS07655	prfA	peptide chain release factor 1	1.70
ABUW_RS11090		ABC transporter ATP-binding protein	1.70
ABUW_RS18370		fatty acyl-AMP ligase	1.70
ABUW_RS13165		1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	1.70
ABUW_RS10295		EamA family transporter	1.70
ABUW_RS02310		2OG-Fe(II) oxygenase	1.70
ABUW_RS13330		ATP phosphoribosyltransferase regulatory subunit	1.70
ABUW_RS17335		FUSC family protein	1.69
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.69
ABUW_RS04650	genX	EF-P lysine aminoacylase GenX	1.69
ABUW_RS15395	nuoI	NADH-quinone oxidoreductase subunit NuoI	1.69
sRNA46	sRNA46	sRNA46	1.68
ABUW_RS13535		aldehyde dehydrogenase (NADP(+))	1.68
ABUW_RS19230		hypothetical protein	1.68
ABUW_RS13395		metal-dependent hydrolase	1.68
ABUW_RS13840	rsml	16S rRNA (cytidine(1402)-2'-O)-methyltransferase	1.68

ABUW_RS14280		aldehyde dehydrogenase	1.67
ABUW_RS05495	hflD	high frequency lysogenization protein HflD	1.67
ABUW_RS07210		LysR family transcriptional regulator	1.67
ABUW_RS17795		ammonium transporter	1.67
ABUW_RS02010	rplB	50S ribosomal protein L2	1.67
ABUW_RS17950		MAPEG family protein	1.66
ABUW_RS04255	gltA	citrate (Si)-synthase	1.66
ABUW_RS08905		2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	1.66
ABUW_RS15955	rpml	50S ribosomal protein L35	1.66
ABUW_RS15140	bioC	malonyl-ACP O-methyltransferase BioC	1.65
ABUW_RS14660		thioesterase family protein	1.65
ABUW_RS00240		M23 family metalloproteinase	1.65
ABUW_RS10370		iron-containing redox enzyme family protein	1.65
ABUW_RS13235	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	1.65
ABUW_RS15780	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.64
ABUW_RS03725		hypothetical protein	1.64
ABUW_RS01470		FAD-dependent oxidoreductase	1.64
ABUW_RS02580		septation protein IspZ	1.64
ABUW_RS00830	prfB	peptide chain release factor 2	1.63
ABUW_RS19505	traC	type IV secretion system protein TraC	1.63
ABUW_RS15110		elongation factor P hydroxylase	1.63
ABUW_RS13940	gdhA	NADP-specific glutamate dehydrogenase	1.63
ABUW_RS11665	mdcE	biotin-independent malonate decarboxylase subunit gamma	1.63
ABUW_RS03465		alanine:cation symporter family protein	1.63
ABUW_RS00060		alpha/beta fold hydrolase	1.63
ABUW_RS02220		YcxB family protein	1.63
ABUW_RS11095		MaoC family dehydratase	1.63
ABUW_RS16270		hypothetical protein	1.62
ABUW_RS00840		alkene reductase	1.62
ABUW_RS16235	dusA	tRNA dihydrouridine(20/20a) synthase DusA	1.62
ABUW_RS08180	amvA	multidrug efflux MFS transporter AmvA	1.62
ABUW_RS01430		PilN domain-containing protein	1.62
ABUW_RS04775		lipoprotein-releasing ABC transporter permease subunit	1.61
ABUW_RS13790		ABC transporter permease	1.61
ABUW_RS04660	radA	DNA repair protein RadA	1.61
ABUW_RS05670		type II toxin-antitoxin system Phd/YefM family antitoxin	1.61
ABUW_RS15415	nuoE	NADH-quinone oxidoreductase subunit NuoE	1.60
ABUW_RS09570		SDR family NAD(P)-dependent oxidoreductase	1.60
ABUW_RS14205	methH	methionine synthase	1.59
ABUW_RS18165	atpD	F0F1 ATP synthase subunit beta	1.59
ABUW_RS08375	tusD	sulfurtransferase complex subunit TusD	1.58
ABUW_RS07565		cytochrome o ubiquinol oxidase subunit IV	1.58
ABUW_RS02615	yajC	preprotein translocase subunit YajC	1.58
ABUW_RS01795		glycine--tRNA ligase subunit beta	1.58
ABUW_RS17225		ribosome-binding factor A	1.57
ABUW_RS01205	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1.57
ABUW_RS02610	secD	protein translocase subunit SecD	1.57
ABUW_RS05635		FAD-dependent oxidoreductase	1.57
ABUW_RS16480		gluconokinase	1.57
ABUW_RS15860	gspE	type II secretion system ATPase GspE	1.57
ABUW_RS09695		hypothetical protein	1.57
ABUW_RS19000	mnme	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase Mnme	1.57
ABUW_RS07575	cyoB	cytochrome o ubiquinol oxidase subunit I	1.57
ABUW_RS06190		hypothetical protein	1.56

ABUW_RS03505	gatB	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	1.56
ABUW_RS14285		aspartate dehydrogenase	1.56
ABUW_RS17610	argH	argininosuccinate lyase	1.56
ABUW_RS00800		YkgJ family cysteine cluster protein	1.56
ABUW_RS17010		MBL fold metallo-hydrolase	1.56
ABUW_RS12550		ABC transporter permease	1.56
ABUW_RS16015	folK	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	1.55
ABUW_RS10565	cobT	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase	1.55
ABUW_RS02055	rplE	50S ribosomal protein L5	1.55
ABUW_RS01265		RNA-binding transcriptional accessory protein	1.55
ABUW_RS06160		hypothetical protein	1.55
ABUW_RS03435		PepSY domain-containing protein	1.55
ABUW_RS04455		methyltransferase	1.54
ABUW_RS03215		methyltransferase	1.54
ABUW_RS17490	rplA	50S ribosomal protein L1	1.54
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.54
ABUW_RS01400	murF	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	1.54
ABUW_RS14070		capsule assembly Wzi family protein	1.54
ABUW_RS00480	serB	phosphoserine phosphatase SerB	1.54
ABUW_RS19805		helix-turn-helix transcriptional regulator	1.53
ABUW_RS11490	cysE	serine O-acetyltransferase	1.53
ABUW_RS02120	rpoA	DNA-directed RNA polymerase subunit alpha	1.53
ABUW_RS10385	prnB	50S ribosomal protein L3 N(5)-glutamine methyltransferase	1.52
ABUW_RS10505		hypothetical protein	1.52
ABUW_RS14525		OprD family outer membrane porin	1.52
ABUW_RS01145		DNA/RNA non-specific endonuclease	1.52
ABUW_RS14385	dctA	C4-dicarboxylate transporter DctA	1.51
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	1.51
ABUW_RS01995	rplC	50S ribosomal protein L3	1.51
ABUW_RS11075	sstT	serine/threonine transporter SstT	1.51
ABUW_RS02480		OmpA family protein	1.50
ABUW_RS04575		non-ribosomal peptide synthetase	1.50
ABUW_RS17915		ATP-binding protein	1.50
ABUW_RS02565		bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC	1.50
ABUW_RS19385		hypothetical protein	1.49
ABUW_RS17470	rpoC	DNA-directed RNA polymerase subunit beta'	1.49
ABUW_RS07835		type II toxin-antitoxin system RelB/DinJ family antitoxin	1.49
ABUW_RS05645		ethanolamine utilization protein EutQ	1.49
ABUW_RS16395	bamB	outer membrane protein assembly factor BamB	1.49
ABUW_RS02105	rpsM	30S ribosomal protein S13	1.48
ABUW_RS19485		conjugal transfer protein TraB	1.48
ABUW_RS12955	terL	phage terminase large subunit	1.48
ABUW_RS16490	eda	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase	1.48
ABUW_RS17885		NAD(P)/FAD-dependent oxidoreductase	1.48
ABUW_RS08295	nirB	nitrite reductase large subunit	1.47
ABUW_RS19205		hypothetical protein	1.47
ABUW_RS16105		DMT family transporter	1.47
ABUW_RS02065	rpsH	30S ribosomal protein S8	1.47
ABUW_RS01820		HPP family protein	1.47
ABUW_RS15145		8-amino-7-oxononanoate synthase	1.47

ABUW_RS06495		DUF3820 family protein	1.47
ABUW_RS17725		PAS domain-containing sensor histidine kinase	1.47
ABUW_RS16860		RNA pyrophosphohydrolase	1.47
ABUW_RS15480		PhzF family isomerase	1.46
ABUW_RS00070		tyrosine--tRNA ligase	1.46
ABUW_RS01195		DMT family transporter	1.46
ABUW_RS04030		patatin-like phospholipase family protein	1.46
ABUW_RS18745		RcnB family protein	1.46
ABUW_RS15965		DedA family protein	1.46
ABUW_RS18365		acyl-CoA dehydrogenase	1.45
ABUW_RS17540	trpE	anthranilate synthase component I	1.45
ABUW_RS14345		hypothetical protein	1.45
ABUW_RS15405	nuoG	NADH-quinone oxidoreductase subunit NuoG	1.45
ABUW_RS06845		hypothetical protein	1.45
ABUW_RS09665		hypothetical protein	1.45
ABUW_RS00150		pyrimidine permease	1.45
ABUW_RS19525		TraU family protein	1.45
ABUW_RS08310		NTP transferase domain-containing protein	1.45
ABUW_RS17740		2,3-bisphosphoglycerate-independent phosphoglycerate mutase	1.45
ABUW_RS04625		glycerate kinase	1.45
ABUW_RS07460		ABC transporter permease	1.44
ABUW_RS17500	nusG	transcription termination/antitermination protein NusG	1.44
ABUW_RS12190		MFS transporter	1.44
ABUW_RS01180		homoserine kinase	1.43
ABUW_RS01200		helix-turn-helix transcriptional regulator	1.43
ABUW_RS06360		hypothetical protein	1.43
ABUW_RS15980	thrS	threonine--tRNA ligase	1.43
ABUW_RS04055		DNA-binding response regulator PmrA	1.43
ABUW_RS01855	ribA	GTP cyclohydrolase II	1.42
ABUW_RS11815		hypothetical protein	1.42
ABUW_RS10950		type II secretion system protein	1.42
ABUW_RS18770	ssuD	FMNH ₂ -dependent alkanesulfonate monooxygenase	1.42
ABUW_RS13795	yejB	microcin C ABC transporter permease YejB	1.42
ABUW_RS16750		ATP-binding cassette domain-containing protein	1.42
ABUW_RS02620	tgt	tRNA guanosine(34) transglycosylase Tgt	1.41
ABUW_RS08445	rimO	30S ribosomal protein S12 methyltransferase RimO	1.41
ABUW_RS16020	pcnB	polynucleotide adenyllyltransferase PcnB	1.41
ABUW_RS02485		diguanylate cyclase	1.41
ABUW_RS07610	pgaC	poly-beta-1,6 N-acetyl-D-glucosamine synthase	1.41
ABUW_RS07775		hypothetical protein	1.41
ABUW_RS06705		DUF423 domain-containing protein	1.40
ABUW_RS08470		1-deoxy-D-xylulose-5-phosphate reductoisomerase	1.40
ABUW_RS14765	dut	dUTP diphosphatase	1.40
ABUW_RS00900		hybrid sensor histidine kinase/response regulator	1.40
ABUW_RS00705	pyrE	orotate phosphoribosyltransferase	1.40
ABUW_RS09600	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	1.40
ABUW_RS07200	gltS	sodium/glutamate symporter	1.40
ABUW_RS11260		LysR family transcriptional regulator	1.40
ABUW_RS08060		hypothetical protein	1.39
ABUW_RS09580		AraC family transcriptional regulator	1.39
ABUW_RS08750		DUF1449 family protein	1.39
ABUW_RS14315		VOC family protein	1.38
ABUW_RS05055	lepB	signal peptidase I	1.38
ABUW_RS02935		hypothetical protein	1.38
ABUW_RS04545	ttcA	tRNA 2-thiocytidine(32) synthetase TtcA	1.38

ABUW_RS02320	pssA	CDP-diacylglycerol--serine O-phosphatidyltransferase	1.38
ABUW_RS02370		TetR family transcriptional regulator	1.38
ABUW_RS01630	serA	phosphoglycerate dehydrogenase	1.37
ABUW_RS16555		homoserine O-acetyltransferase	1.37
ABUW_RS18555	lldD	FMN-dependent L-lactate dehydrogenase LldD	1.37
ABUW_RS14420	betI	transcriptional regulator BetI	1.37
ABUW_RS17205		monovalent cation/H ⁺ antiporter subunit D	1.37
ABUW_RS15125	scpB	SMC-Scp complex subunit ScpB	1.37
ABUW_RS15610		zinc-binding dehydrogenase	1.37
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	1.37
ABUW_RS13355	rnhB	ribonuclease HII	1.37
ABUW_RS17360		thioesterase family protein	1.36
ABUW_RS11980		MFS transporter	1.36
ABUW_RS17580		hypothetical protein	1.36
ABUW_RS03070	folC	bifunctional tetrahydrofolate synthase/dihydrofolate synthase	1.36
ABUW_RS10085		ATP-binding cassette domain-containing protein	1.36
ABUW_RS12590	uca	urea carboxylase	1.36
ABUW_RS17970		MFS transporter	1.36
ABUW_RS19280		class A extended-spectrum beta-lactamase GES-11	1.36
ABUW_RS17875	arsH	arsenical resistance protein ArsH	1.36
ABUW_RS01860	dxs	1-deoxy-D-xylulose-5-phosphate synthase	1.36
ABUW_RS16050		3'-5' exonuclease	1.36
ABUW_RS14430	betA	choline dehydrogenase	1.35
ABUW_RS06045		DUF3465 domain-containing protein	1.35
ABUW_RS04915	purL	phosphoribosylformylglycinamide synthase	1.34
ABUW_RS01060		DMT family transporter	1.34
ABUW_RS17705		homoserine dehydrogenase	1.34
ABUW_RS08475	rseP	RIP metalloprotease RseP	1.34
ABUW_RS18685		carboxylating nicotinate-nucleotide diphosphorylase	1.34
ABUW_RS12105	pobA	4-hydroxybenzoate 3-monooxygenase	1.34
ABUW_RS02420	rpsI	30S ribosomal protein S9	1.34
ABUW_RS10755		Dyp-type peroxidase	1.33
ABUW_RS18160		F0F1 ATP synthase subunit epsilon	1.33
ABUW_RS14245		MFS transporter	1.33
ABUW_RS02125	rplQ	50S ribosomal protein L17	1.33
ABUW_RS03510	gatA	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatA	1.33
ABUW_RS08235		PepSY domain-containing protein	1.33
ABUW_RS00035		ATP-binding cassette domain-containing protein	1.33
ABUW_RS03590		undecaprenyl-diphosphate phosphatase	1.32
ABUW_RS02045	rplN	50S ribosomal protein L14	1.32
ABUW_RS08925		3-carboxy-cis,cis-muconate cycloisomerase	1.32
ABUW_RS02085	rpmD	50S ribosomal protein L30	1.32
ABUW_RS04525		multidrug efflux RND transporter permease subunit	1.32
ABUW_RS14930		BCCT family carnitine transporter	1.32
ABUW_RS11420	ygaH	L-valine transporter subunit YgaH	1.32
ABUW_RS18350		outer membrane lipoprotein-sorting protein	1.31
ABUW_RS06505		serine hydroxymethyltransferase	1.31
ABUW_RS05880		aminodeoxychorismate/anthranilate synthase component II	1.31
ABUW_RS04180	serS	serine--tRNA ligase	1.31
ABUW_RS03045		DUF2804 domain-containing protein	1.30
ABUW_RS13390		SDR family NAD(P)-dependent oxidoreductase	1.30
ABUW_RS01390	ftsI	penicillin-binding protein PBP3	1.30
ABUW_RS16570	rdgB	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	1.30
ABUW_RS14275		thiamine pyrophosphate-binding protein	1.30

ABUW_RS18935		low temperature requirement protein A	1.29
ABUW_RS14435	mgo	malate dehydrogenase (quinone)	1.29
ABUW_RS05190	dusB	tRNA dihydrouridine synthase DusB	1.29
ABUW_RS04675	lysA	diaminopimelate decarboxylase	1.29
ABUW_RS05565	rpmE	50S ribosomal protein L31	1.29
ABUW_RS11290		integrase family protein	1.29
ABUW_RS06700	thiS	sulfur carrier protein ThiS	1.29
ABUW_RS08945	pcaH	protocatechuate 3,4-dioxygenase subunit beta	1.29
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.29
ABUW_RS07360		acyl-CoA desaturase	1.28
ABUW_RS08355		DMT family transporter	1.28
ABUW_RS17260	secG	preprotein translocase subunit SecG	1.28
ABUW_RS06030	map	type I methionyl aminopeptidase	1.28
ABUW_RS17880	trxB	thioredoxin-disulfide reductase	1.28
ABUW_RS11080		DUF1275 domain-containing protein	1.27
ABUW_RS12990		hypothetical protein	1.27
ABUW_RS08500	lpxA	acyl-ACP--UDP-N-acetylglucosamine O-acyltransferase	1.27
ABUW_RS17790	nrdR	transcriptional repressor NrdR	1.27
ABUW_RS02170		YheV family putative metal-binding protein	1.27
ABUW_RS08300	nirD	nitrite reductase small subunit NirD	1.26
ABUW_RS01350		amino acid permease	1.26
ABUW_RS05015	pabC	aminodeoxychorismate lyase	1.26
ABUW_RS00510	psd	phosphatidylserine decarboxylase	1.26
ABUW_RS19615	znuD2	TonB-dependent receptor ZnuD2	1.26
ABUW_RS04385	carA	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	1.26
ABUW_RS00780		hypothetical protein	1.26
ABUW_RS09160		dihydroxy-acid dehydratase	1.26
ABUW_RS04770		EamA family transporter	1.25
ABUW_RS07545	rplI	50S ribosomal protein L9	1.25
ABUW_RS17565	gspN	type II secretion system protein N	1.25
ABUW_RS04420		hypothetical protein	1.25
ABUW_RS06070		septal ring lytic transglycosylase RlpA family protein	1.25
ABUW_RS06035	rpsB	30S ribosomal protein S2	1.25
ABUW_RS09215		FAD-dependent oxidoreductase	1.25
ABUW_RS14095		FAD-dependent oxidoreductase	1.25
ABUW_RS15765		histidinol-phosphate transaminase	1.25
ABUW_RS06515	adeG	multidrug efflux RND transporter permease subunit AdeG	1.24
ABUW_RS02380		SDR family oxidoreductase	1.24
ABUW_RS14935		tartrate dehydrogenase	1.24
ABUW_RS14875		beta-ketoacyl-ACP synthase II	1.24
ABUW_RS19375		type IV secretion system DNA-binding domain-containing protein	1.24
ABUW_RS16070		NAD(P)-dependent oxidoreductase	1.23
ABUW_RS14655		EmrA/EmrK family multidrug efflux transporter periplasmic adaptor subunit	1.23
ABUW_RS04150		polyprenyl synthetase family protein	1.23
ABUW_RS01405		phospho-N-acetylmuramoyl-pentapeptide-transferase	1.23
ABUW_RS05705		PAS domain-containing protein	1.23
ABUW_RS11770		LysR family transcriptional regulator	1.23
ABUW_RS17590		uroporphyrinogen-III synthase	1.23
ABUW_RS10205		LysR family transcriptional regulator	1.23
ABUW_RS08630	ptsP	phosphoenolpyruvate--protein phosphotransferase	1.23
ABUW_RS16870	katG	catalase/peroxidase HPI	1.23
ABUW_RS12135		hypothetical protein	1.23
ABUW_RS15960	nreB	nickel resistance MFS transporter NreB	1.22
ABUW_RS15930	pheT	phenylalanine--tRNA ligase subunit beta	1.22
ABUW_RS13545	gudD	glucarate dehydratase	1.22

ABUW_RS18695	plc2	phospholipase C, phosphocholine-specific	1.22
ABUW_RS08950	pcaG	protocatechuate 3,4-dioxygenase subunit alpha	1.21
ABUW_RS00720	gshB	glutathione synthase	1.21
ABUW_RS06740		NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1.21
ABUW_RS17415		DsbA family oxidoreductase	1.21
ABUW_RS00400	hutG	formimidoylglutamase	1.21
ABUW_RS13560		DMT family transporter	1.21
ABUW_RS12855		KpsF/GutQ family sugar-phosphate isomerase	1.20
ABUW_RS16665		TetR/AcrR family transcriptional regulator	1.20
ABUW_RS16660	purU	formyltetrahydrofolate deformylase	1.20
ABUW_RS16250		tRNA threonylcarbamoyladenosine dehydratase	1.20
ABUW_RS18140		MFS transporter	1.20
ABUW_RS09405		MFS transporter	1.20
ABUW_RS13830		BON domain-containing protein	1.19
ABUW_RS07630		hypothetical protein	1.19
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	1.19
ABUW_RS00880	sfnG	dimethyl sulfone monooxygenase SfnG	1.19
ABUW_RS00005	dnaA	chromosomal replication initiator protein DnaA	1.19
ABUW_RS18715		TetR family transcriptional regulator	1.19
ABUW_RS18560	lIdR	transcriptional regulator LIdR	1.18
ABUW_RS10470		hypothetical protein	1.18
ABUW_RS04010		polyprenyl synthetase family protein	1.18
ABUW_RS17850		universal stress protein	1.18
ABUW_RS01185		DUF1294 domain-containing protein	1.18
ABUW_RS04900	ruvB	Holliday junction branch migration DNA helicase RuvB	1.18
ABUW_RS10775	rpsT	30S ribosomal protein S20	1.17
ABUW_RS18240		arginine--tRNA ligase	1.17
ABUW_RS17745	lptG	LPS export ABC transporter permease LptG	1.17
ABUW_RS01620		EamA family transporter	1.17
ABUW_RS18525	acnD	Fe/S-dependent 2-methylisocitrate dehydratase AcnD	1.17
ABUW_RS11065		TetR/AcrR family transcriptional regulator	1.17
ABUW_RS17865		arsenate reductase ArsC	1.17
ABUW_RS13335	gap	type I glyceraldehyde-3-phosphate dehydrogenase	1.16
ABUW_RS15685	rpe	ribulose-phosphate 3-epimerase	1.15
ABUW_RS11820		Lrp/AsnC family transcriptional regulator	1.15
ABUW_RS18960		aromatic ring-hydroxylating dioxygenase subunit alpha	1.15
ABUW_RS01165		AraC family transcriptional regulator	1.15
ABUW_RS12660		LamB/YcsF family protein	1.15
ABUW_RS07875		UDP-2,3-diacylglucosamine diphosphatase	1.15
ABUW_RS12640		chloride channel protein	1.14
ABUW_RS16455	nagZ	beta-N-acetylhexosaminidase	1.14
ABUW_RS03210		amino acid permease	1.14
ABUW_RS13925	rlmH	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	1.14
ABUW_RS15670		copper resistance system multicopper oxidase	1.14
ABUW_RS02225		fumarylacetoacetate hydrolase family protein	1.14
ABUW_RS16495		phosphogluconate dehydratase	1.14
ABUW_RS14565		helicase	1.14
ABUW_RS15350	gigC	LysR family transcriptional regulator GigC	1.14
ABUW_RS05490	purB	adenylosuccinate lyase	1.13
ABUW_RS14060	cysN	sulfate adenylyltransferase subunit CysN	1.13
ABUW_RS20285		hypothetical protein	1.13
ABUW_RS06300	terL	phage terminase large subunit	1.13
ABUW_RS14415		BCCT family transporter	1.12
ABUW_RS03640		hypothetical protein	1.12
ABUW_RS02280	miaB	tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB	1.11

ABUW_RS01610		TSUP family transporter	1.11
ABUW_RS14035		LysR family transcriptional regulator	1.11
ABUW_RS17785	ribD	bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD	1.11
ABUW_RS08810		N-acetyl-gamma-glutamyl-phosphate reductase	1.10
ABUW_RS15680		HAD family hydrolase	1.10
ABUW_RS04710	gyrA	DNA gyrase subunit A	1.10
ABUW_RS00225		NAD(P)-dependent alcohol dehydrogenase	1.10
ABUW_RS17825		universal stress protein	1.10
ABUW_RS13955	adk	adenylate kinase	1.09
ABUW_RS04290	lpdA	dihydrolipoyl dehydrogenase	1.09
ABUW_RS07780		bifunctional aconitate hydratase 2/2-methylisocitrate hydratase	1.09
ABUW_RS01885	mleA	lipid asymmetry maintenance ABC transporter permease subunit MleA	1.08
ABUW_RS01285	ettA	energy-dependent translational throttle protein EttA	1.08
ABUW_RS01500		O-antigen ligase family protein	1.07
ABUW_RS10865		cell division protein ZapE	1.07
ABUW_RS19570		Y-family DNA polymerase	1.07
ABUW_RS08280		ABC transporter substrate-binding protein	1.07
ABUW_RS08980		YeeE/YedE family protein	1.07
ABUW_RS16725	topA	type I DNA topoisomerase	1.07
ABUW_RS04470	glpK	glycerol kinase GlpK	1.07
ABUW_RS16400		tetratricopeptide repeat protein	1.06
ABUW_RS01135		potassium transporter Kup	1.06
ABUW_RS05460	pstC	phosphate ABC transporter permease subunit PstC	1.06
ABUW_RS10760		glutathione S-transferase N-terminal domain-containing protein	1.06
ABUW_RS18675	murJ	murein biosynthesis integral membrane protein MurJ	1.06
ABUW_RS06745		histidine phosphatase family protein	1.05
ABUW_RS17300		pyrimidine/purine nucleoside phosphorylase	1.05
ABUW_RS06565		PLP-dependent aminotransferase family protein	1.05
ABUW_RS17130	recD	exodeoxyribonuclease V subunit alpha	1.05
ABUW_RS18130		DMT family transporter	1.05
ABUW_RS02440		symmetrical bis(5'-nucleosyl)-tetraphosphatase	1.05
ABUW_RS10245		ABC transporter ATP-binding protein	1.05
ABUW_RS14695		exonuclease SbcCD subunit D	1.04
ABUW_RS12400		dihydrodipicolinate synthase family protein	1.04
ABUW_RS00010		DNA polymerase III subunit beta	1.04
ABUW_RS06305		DUF4055 domain-containing protein	1.04
ABUW_RS10935	gspK	type II secretion system minor pseudopilin GspK	1.04
ABUW_RS18430		amino acid permease	1.04
ABUW_RS10560		histidine phosphatase family protein	1.04
ABUW_RS16700		ASCH domain-containing protein	1.03
ABUW_RS03075		SPOR domain-containing protein	1.03
ABUW_RS16610		prolipoprotein diacylglycerol transferase	1.03
ABUW_RS10050	pqqC	pyrroloquinoline-quinone synthase PqqC	1.02
ABUW_RS05810		uroporphyrinogen decarboxylase	1.02
ABUW_RS06335		hypothetical protein	1.01
ABUW_RS02855		phage major capsid protein, P2 family	1.01
ABUW_RS05855		Smr/MutS family protein	1.00
ABUW_RS00360	zigA	zinc metallochaperone GTPase ZigA	1.00
ABUW_RS17955		hypothetical protein	1.00
ABUW_RS08455	frr	ribosome recycling factor	1.00
ABUW_RS10805		ABC transporter permease	1.00

Gene	Gene Name	Function	Δ gacA LSP vs WT LSP log2FC
sRNA97	sRNA97	sRNA97	-9.75
ABUW_RS11870		hypothetical protein	-8.37
ABUW_RS08050		hypothetical protein	-7.85
sRNA106	sRNA106	sRNA106	-7.74
ABUW_RS11875		hypothetical protein	-7.71
ABUW_RS07500		hypothetical protein	-7.13
ABUW_RS12975		hypothetical protein	-7.05
ABUW_RS20235		hypothetical protein	-6.95
ABUW_RS10640		siderophore biosynthesis protein	-6.90
ABUW_RS15585	tcuB	tricarballate utilization 4Fe-4S protein TcuB	-6.84
ABUW_RS13040		hypothetical protein	-6.73
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-6.58
ABUW_RS18865		hypothetical protein	-6.39
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-6.32
ABUW_RS15580	tcuA	FAD-dependent tricarballate dehydrogenase TcuA	-6.16
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-5.97
ABUW_RS01615		hemerythrin domain-containing protein	-5.84
sRNA99	sRNA99	sRNA99	-5.80
ABUW_RS03310		YegP family protein	-5.80
ABUW_RS09210		type 1 glutamine amidotransferase domain-containing protein	-5.72
ABUW_RS11855	katE	catalase HP11	-5.70
ABUW_RS13010		DUF4142 domain-containing protein	-5.68
ABUW_RS04155		hypothetical protein	-5.68
ABUW_RS15335		hypothetical protein	-5.66
ABUW_RS03380		entericidin A/B family lipoprotein	-5.63
ABUW_RS15565		MFS transporter	-5.61
ABUW_RS17720		response regulator	-5.52
newcandsRNA1	newcandsRNA1	newcandsRNA1	-5.52
ABUW_RS11425		tautomerase family protein	-5.41
ABUW_RS08580		SOS response-associated peptidase family protein	-5.40
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-5.36
ABUW_RS07280		hypothetical protein	-5.33
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-5.24
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.12
ABUW_RS11860		iron-containing redox enzyme family protein	-5.11
ABUW_RS10585		acetyltransferase	-4.98
ABUW_RS19460		hypothetical protein	-4.98
ABUW_RS05750	basC	putative histamine N-monooxygenase	-4.93
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-4.87
ABUW_RS20295		hypothetical protein	-4.79
ABUW_RS07170		NirD/YgiW/Ydel family stress tolerance protein	-4.78
ABUW_RS06115		hypothetical protein	-4.75
ABUW_RS11345		amino acid ABC transporter substrate-binding protein	-4.73
ABUW_RS12725		hypothetical protein	-4.67
ABUW_RS13520		Paal family thioesterase	-4.67
ABUW_RS06930		hypothetical protein	-4.58
ABUW_RS15330		mechanosensitive ion channel	-4.54
ABUW_RS13005		hypothetical protein	-4.49
ABUW_RS20200		hypothetical protein	-4.49
ABUW_RS15165		trehalose-6-phosphate synthase	-4.48
ABUW_RS15280		hypothetical protein	-4.42
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-4.39
ABUW_RS00660		HPF/RaiA family ribosome-associated protein	-4.39

ABUW_RS07145		DUF2171 domain-containing protein	-4.35
ABUW_RS08590		universal stress protein	-4.30
ABUW_RS16845		DUF2061 domain-containing protein	-4.27
ABUW_RS17460		hypothetical protein	-4.27
ABUW_RS20505		hypothetical protein	-4.26
ABUW_RS10025		hypothetical protein	-4.22
ABUW_RS01760		hypothetical protein	-4.20
sRNA21	sRNA21	sRNA21	-4.20
ABUW_RS09545		hypothetical protein	-4.19
ABUW_RS07620		hypothetical protein	-4.17
sRNA2	sRNA2	sRNA2	-4.12
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-4.11
ABUW_RS10070		transcriptional repressor	-4.11
ABUW_RS08700		hypothetical protein	-4.10
ABUW_RS20155		hypothetical protein	-4.07
ABUW_RS20145		hypothetical protein	-4.06
ABUW_RS16255	acnA	aconitate hydratase AcnA	-4.06
ABUW_RS11270		hypothetical protein	-4.05
ABUW_RS03180		VOC family protein	-4.05
ABUW_RS06610		hemin uptake protein HemP	-4.02
ABUW_RS12900		DUF4882 family protein	-4.01
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-4.00
ABUW_RS13250		OmpA family protein	-3.99
ABUW_RS00260		DUF1328 domain-containing protein	-3.98
ABUW_RS08390		hypothetical protein	-3.96
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-3.91
ABUW_RS10460		methyltransferase domain-containing protein	-3.91
ABUW_RS16975		type B 50S ribosomal protein L31	-3.91
ABUW_RS10010		hypothetical protein	-3.90
ABUW_RS17925		aldolase	-3.89
ABUW_RS12225		cold-shock protein	-3.88
ABUW_RS07960		spore coat protein U domain-containing protein	-3.86
ABUW_RS00895		hypothetical protein	-3.80
ABUW_RS16080	rsfS	ribosome silencing factor	-3.79
ABUW_RS00690		DUF2147 domain-containing protein	-3.77
ABUW_RS05795	basI	acinetobactin biosynthesis phosphopantetheinyl transferase BasI	-3.75
ABUW_RS20180		hypothetical protein	-3.74
ABUW_RS15160	otsB	trehalose-phosphatase	-3.72
ABUW_RS01140		hypothetical protein	-3.71
sRNA100	sRNA100	sRNA100	-3.70
ABUW_RS12680		hypothetical protein	-3.69
ABUW_RS01150		LysE family translocator	-3.63
ABUW_RS15855		organic hydroperoxide resistance protein	-3.62
ABUW_RS11885		hypothetical protein	-3.61
ABUW_RS09960		hypothetical protein	-3.60
ABUW_RS16835	leuD	3-isopropylmalate dehydratase small subunit	-3.56
sRNA104	sRNA104	sRNA104	-3.55
ABUW_RS19800	pqqA	pyrroloquinoline quinone precursor peptide PqqA	-3.54
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-3.54
ABUW_RS08535		hypothetical protein	-3.52
ABUW_RS01495	pilA	pilin	-3.52
ABUW_RS20475		hypothetical protein	-3.49
ABUW_RS11160		OsmC family protein	-3.46
ABUW_RS12745		DUF2147 domain-containing protein	-3.46
ABUW_RS13105		hypothetical protein	-3.45

ABUW_RS08045		hypothetical protein	-3.44
ABUW_RS15440		hypothetical protein	-3.44
ABUW_RS02300		DUF2789 domain-containing protein	-3.43
ABUW_RS08540		hypothetical protein	-3.42
ABUW_RS11850		glucose 1-dehydrogenase	-3.40
ABUW_RS05710	bauF	acinetobactin utilization protein BauF	-3.38
ABUW_RS19580		hypothetical protein	-3.36
ABUW_RS08085		hypothetical protein	-3.36
ABUW_RS13680		RHS repeat protein	-3.34
ABUW_RS02875		HAMP domain-containing histidine kinase	-3.34
ABUW_RS03760		DUF968 domain-containing protein	-3.33
ABUW_RS14025		copper resistance protein NlpE	-3.31
ABUW_RS13445		alpha/beta hydrolase	-3.31
ABUW_RS14480		energy transducer TonB	-3.30
ABUW_RS15290		NF038215 family lipoprotein	-3.30
ABUW_RS13200		KTSC domain-containing protein	-3.29
ABUW_RS01370		hypothetical protein	-3.29
ABUW_RS07965		molecular chaperone	-3.26
ABUW_RS07820		hypothetical protein	-3.26
ABUW_RS12635		sel1 repeat family protein	-3.26
sRNA65	sRNA65	sRNA65	-3.23
ABUW_RS10315		MBL fold metallo-hydrolase	-3.16
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-3.12
ABUW_RS09550		GNAT family N-acetyltransferase	-3.07
ABUW_RS17640		hypothetical protein	-3.04
ABUW_RS04600		hypothetical protein	-3.03
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-3.03
ABUW_RS01215		DUF805 domain-containing protein	-3.03
ABUW_RS02325		hypothetical protein	-3.03
ABUW_RS07950		hypothetical protein	-3.02
ABUW_RS06275		hypothetical protein	-3.00
ABUW_RS04365		universal stress protein	-2.97
ABUW_RS12980		hypothetical protein	-2.97
ABUW_RS07155		PIG-L family deacetylase	-2.97
ABUW_RS10075		isochorismatase family protein	-2.97
ABUW_RS14485		DUF560 domain-containing protein	-2.97
ABUW_RS08585		PQQ-dependent sugar dehydrogenase	-2.95
ABUW_RS06780		hypothetical protein	-2.95
ABUW_RS18475		ribonuclease E inhibitor RraB	-2.95
ABUW_RS17105		MerR family transcriptional regulator	-2.93
ABUW_RS01745		hypothetical protein	-2.93
ABUW_RS01050		MFS transporter	-2.92
ABUW_RS15455		hypothetical protein	-2.92
ABUW_RS18400		enoyl-CoA hydratase	-2.91
ABUW_RS11895		hypothetical protein	-2.88
ABUW_RS18470		nuclear transport factor 2 family protein	-2.85
ABUW_RS07515		circularly permuted type 2 ATP-grasp protein	-2.85
ABUW_RS18045		transglycosylase SLT domain-containing protein	-2.85
ABUW_RS17100		DnaJ domain-containing protein	-2.84
ABUW_RS15790	raiA	ribosome-associated translation inhibitor RaiA	-2.83
ABUW_RS13115		hypothetical protein	-2.81
ABUW_RS03285		SRPBCC family protein	-2.79
ABUW_RS15570		substrate-binding domain-containing protein	-2.78
ABUW_RS17930		dihydrodipicolinate synthase family protein	-2.78
ABUW_RS06270		hypothetical protein	-2.78
ABUW_RS20115		hypothetical protein	-2.78

ABUW_RS14685		VOC family protein	-2.75
sRNA27	sRNA27	sRNA27	-2.74
ABUW_RS01020		hydrolase	-2.73
ABUW_RS09520		HD domain-containing protein	-2.73
ABUW_RS16840	leuC	3-isopropylmalate dehydratase large subunit	-2.72
ABUW_RS17395		hypothetical protein	-2.72
ABUW_RS17145		hypothetical protein	-2.68
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-2.68
ABUW_RS16715		HdeD family acid-resistance protein	-2.67
ABUW_RS07520		alpha-E domain-containing protein	-2.65
ABUW_RS07860	hfq	RNA chaperone Hfq	-2.64
ABUW_RS10475		hypothetical protein	-2.61
ABUW_RS11150		lecithin retinol acyltransferase family protein	-2.61
ABUW_RS03905		hypothetical protein	-2.60
ABUW_RS20315		hypothetical protein	-2.60
ABUW_RS05220		hypothetical protein	-2.58
ABUW_RS01480		LemA family protein	-2.58
ABUW_RS15615	add	adenosine deaminase	-2.57
ABUW_RS18995		metal/formaldehyde-sensitive transcriptional repressor	-2.56
ABUW_RS08650		heme-binding protein	-2.55
ABUW_RS20445		hypothetical protein	-2.55
ABUW_RS08380		SDR family NAD(P)-dependent oxidoreductase	-2.54
sRNA90	sRNA90	sRNA90	-2.54
ABUW_RS08440		PAS domain-containing protein	-2.53
ABUW_RS20550		hypothetical protein	-2.53
ABUW_RS12610		SRPBCC family protein	-2.52
ABUW_RS16160		copper resistance protein CopC	-2.52
ABUW_RS12465	icmH	type IVB secretion system protein IcmH/DotU	-2.51
ABUW_RS09095		hypothetical protein	-2.50
ABUW_RS01765		hypothetical protein	-2.50
ABUW_RS18905		hypothetical protein	-2.49
ABUW_RS14085		SRPBCC domain-containing protein	-2.49
ABUW_RS10895		integration host factor subunit beta	-2.49
ABUW_RS15230		hypothetical protein	-2.49
ABUW_RS00115		methionine/alanine import family NSS transporter small subunit	-2.48
ABUW_RS07160		class I SAM-dependent methyltransferase	-2.47
ABUW_RS10005		hypothetical protein	-2.47
ABUW_RS05420		SIMPL domain-containing protein	-2.46
ABUW_RS03890		DUF4258 domain-containing protein	-2.46
ABUW_RS07440		TetR/AcrR family transcriptional regulator	-2.45
ABUW_RS19335		hypothetical protein	-2.45
ABUW_RS17400		serine hydrolase family protein	-2.45
ABUW_RS14475		biliverdin-producing heme oxygenase	-2.43
ABUW_RS04570		SgcJ/EcaC family oxidoreductase	-2.43
ABUW_RS00015	recF	DNA replication/repair protein RecF	-2.42
ABUW_RS08875		hypothetical protein	-2.41
ABUW_RS07085		hypothetical protein	-2.40
ABUW_RS08040		mechanosensitive ion channel	-2.40
ABUW_RS03995		tRNA-Arg	-2.40
ABUW_RS04935		enoyl-CoA hydratase/isomerase family protein	-2.39
ABUW_RS10520		TonB-dependent siderophore receptor	-2.39
ABUW_RS15550		amidohydrolase	-2.39
ABUW_RS10890		DUF1049 domain-containing protein	-2.38
ABUW_RS07430		GNAT family N-acetyltransferase	-2.37
ABUW_RS17455		DUF4442 domain-containing protein	-2.37

ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-2.36
ABUW_RS05820		DUF3015 family protein	-2.35
ABUW_RS08095		universal stress protein	-2.35
ABUW_RS20545		zinc ribbon-containing protein	-2.34
ABUW_RS11155		polyisoprenoid-binding protein	-2.34
ABUW_RS12540		hypothetical protein	-2.33
ABUW_RS07855	miaA	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	-2.32
ABUW_RS10360	lipA	lipoyl synthase	-2.31
ABUW_RS15300		TetR/AcrR family transcriptional regulator	-2.31
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-2.31
ABUW_RS02660		3'-5' exonuclease	-2.30
ABUW_RS01120		AraC family transcriptional regulator	-2.30
ABUW_RS11725	yfcF	glutathione transferase	-2.29
ABUW_RS01345		hypothetical protein	-2.29
ABUW_RS01510		bacterioferritin-associated ferredoxin	-2.29
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-2.29
ABUW_RS01640		hypothetical protein	-2.28
ABUW_RS16030	mazG	nucleoside triphosphate pyrophosphohydrolase	-2.27
ABUW_RS16285		TetR/AcrR family transcriptional regulator	-2.27
ABUW_RS14775		OmpA family protein	-2.26
ABUW_RS16815		DUF1311 domain-containing protein	-2.26
ABUW_RS12585		NAD(P)H-dependent oxidoreductase	-2.25
ABUW_RS14155		hypothetical protein	-2.25
ABUW_RS14505		sigma-70 family RNA polymerase sigma factor	-2.25
ABUW_RS04515		MBL fold metallo-hydrolase	-2.24
ABUW_RS16445		glycosyltransferase family 1 protein	-2.24
ABUW_RS08820	clpS	ATP-dependent Clp protease adapter ClpS	-2.24
ABUW_RS06730		hypothetical protein	-2.24
ABUW_RS13985	ureG	urease accessory protein UreG	-2.24
ABUW_RS02655		hypothetical protein	-2.23
ABUW_RS05205		hypothetical protein	-2.23
ABUW_RS09540		endonuclease/exonuclease/phosphatase family protein	-2.22
ABUW_RS07175		BLUF domain-containing protein	-2.21
ABUW_RS12805		universal stress protein	-2.21
ABUW_RS05685		hypothetical protein	-2.21
ABUW_RS10095	modA	molybdate ABC transporter substrate-binding protein	-2.20
ABUW_RS05125		hypothetical protein	-2.20
ABUW_RS05730	bauC	ferric acinetobactin ABC transporter permease subunit BauC	-2.20
ABUW_RS17800	glnK	P-II family nitrogen regulator	-2.20
ABUW_RS02205		hypothetical protein	-2.20
ABUW_RS11405		hypothetical protein	-2.19
ABUW_RS13910		hypothetical protein	-2.19
ABUW_RS01160	aqpZ	aquaporin Z	-2.18
ABUW_RS16085		SDR family NAD(P)-dependent oxidoreductase	-2.17
ABUW_RS14495		TonB-dependent receptor	-2.17
ABUW_RS01005	gabT	4-aminobutyrate--2-oxoglutarate transaminase	-2.17
ABUW_RS11070		helix-turn-helix transcriptional regulator	-2.15
ABUW_RS11455		glutathione peroxidase	-2.15
ABUW_RS12910		right-handed parallel beta-helix repeat-containing protein	-2.14
ABUW_RS02410		ClpXP protease specificity-enhancing factor	-2.14
ABUW_RS10525		hypothetical protein	-2.13
ABUW_RS02270	ybeY	rRNA maturation RNase YbeY	-2.13
ABUW_RS17465		hypothetical protein	-2.13
ABUW_RS07425		sorbose dehydrogenase family protein	-2.13
ABUW_RS00870		cysteine hydrolase	-2.12

ABUW_RS15925		integration host factor subunit alpha	-2.12
ABUW_RS00665		ankyrin repeat domain-containing protein	-2.11
ABUW_RS10445		hypothetical protein	-2.10
ABUW_RS13100		exodeoxyribonuclease VII small subunit	-2.10
ABUW_RS10015		phospholipase D family protein	-2.10
ABUW_RS17410		hypothetical protein	-2.10
ABUW_RS07125		LysR family transcriptional regulator	-2.09
ABUW_RS14630		hypothetical protein	-2.09
ABUW_RS16440		phosphatase PAP2 family protein	-2.09
ABUW_RS04950		peroxiredoxin	-2.09
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-2.08
ABUW_RS20420		hypothetical protein	-2.08
sRNA72	sRNA72	sRNA72	-2.08
sRNA28	sRNA28	sRNA28	-2.07
ABUW_RS12460		hypothetical protein	-2.06
ABUW_RS08055		hypothetical protein	-2.06
ABUW_RS18740		YciK family oxidoreductase	-2.06
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	-2.05
ABUW_RS18885	grpE	nucleotide exchange factor GrpE	-2.05
ABUW_RS06255		hypothetical protein	-2.04
ABUW_RS06315		hypothetical protein	-2.04
ABUW_RS01125		GNAT family N-acetyltransferase	-2.04
ABUW_RS18485		DUF1003 domain-containing protein	-2.02
ABUW_RS00545		pyridoxal phosphate-dependent aminotransferase	-2.01
ABUW_RS08685		CBS domain-containing protein	-1.99
ABUW_RS12245		hypothetical protein	-1.99
ABUW_RS04980	carO	ornithine uptake porin CarO type 3	-1.99
ABUW_RS12890		hypothetical protein	-1.99
ABUW_RS06265		hypothetical protein	-1.98
ABUW_RS18405		acyl-CoA dehydrogenase family protein	-1.97
ABUW_RS06905		hypothetical protein	-1.97
ABUW_RS08395		hypothetical protein	-1.97
ABUW_RS05570		EAL domain-containing protein	-1.97
ABUW_RS10530		PepSY domain-containing protein	-1.97
ABUW_RS05180		HAD-IB family hydrolase	-1.97
ABUW_RS06655		alpha/beta hydrolase	-1.96
ABUW_RS03970		hypothetical protein	-1.96
ABUW_RS05485		DUF2238 domain-containing protein	-1.95
ABUW_RS13750		hypothetical protein	-1.94
ABUW_RS05130		diguanylate cyclase	-1.94
ABUW_RS10840		MotA/TolQ/ExbB proton channel family protein	-1.94
ABUW_RS12200		CoA transferase	-1.93
ABUW_RS05680		hypothetical protein	-1.93
ABUW_RS11835		hypothetical protein	-1.93
ABUW_RS03620		hypothetical protein	-1.93
ABUW_RS18820		NAD(P)H-dependent oxidoreductase	-1.93
ABUW_RS03610		AlpA family phage regulatory protein	-1.92
ABUW_RS11180		hypothetical protein	-1.92
ABUW_RS05675		TetR/AcrR family transcriptional regulator	-1.91
ABUW_RS13935		META and DUF4377 domain-containing protein	-1.91
ABUW_RS00710		TonB-dependent siderophore receptor	-1.91
ABUW_RS07450		hypothetical protein	-1.91
ABUW_RS12525		type VI secretion system tube protein Hcp	-1.90
ABUW_RS02745		phage tail protein	-1.89
ABUW_RS08690		DUF2750 domain-containing protein	-1.89
ABUW_RS17070	gspG	type II secretion system major pseudopilin GspG	-1.88
ABUW_RS06670		hypothetical protein	-1.88

ABUW_RS01490		TPM domain-containing protein	-1.88
ABUW_RS01110		helix-turn-helix transcriptional regulator	-1.88
ABUW_RS19585		hypothetical protein	-1.88
ABUW_RS03050		metal-dependent hydrolase	-1.87
ABUW_RS11265		DMT family transporter	-1.87
ABUW_RS03910		hypothetical protein	-1.87
ABUW_RS16210		hypothetical protein	-1.87
ABUW_RS01485		TPM domain-containing protein	-1.86
ABUW_RS05110		Paal family thioesterase	-1.85
ABUW_RS13775		hypothetical protein	-1.85
ABUW_RS05350	csy2	type I-F CRISPR-associated protein Csy2	-1.85
ABUW_RS05325		CYTH and CHAD domain-containing protein	-1.85
ABUW_RS02650		hypothetical protein	-1.85
ABUW_RS14830		arginyltransferase	-1.84
sRNA87	sRNA87	sRNA87	-1.84
ABUW_RS09525		DEAD/DEAH box helicase family protein	-1.84
ABUW_RS18670		FKBP-type peptidyl-prolyl cis-trans isomerase	-1.84
ABUW_RS09180		hypothetical protein	-1.84
ABUW_RS09585		hypothetical protein	-1.84
ABUW_RS19080		thermonuclease family protein	-1.84
ABUW_RS18815		peptidylprolyl isomerase	-1.84
ABUW_RS09185		alpha/beta hydrolase	-1.84
ABUW_RS04860		NF038105 family protein	-1.83
ABUW_RS13870		hypothetical protein	-1.83
ABUW_RS17420		hypothetical protein	-1.83
ABUW_RS08895		DUF421 domain-containing protein	-1.82
ABUW_RS00685		alpha/beta hydrolase	-1.82
ABUW_RS00560		DUF924 domain-containing protein	-1.82
ABUW_RS10375		GGDEF domain-containing protein	-1.81
ABUW_RS10845		biopolymer transporter ExbD	-1.80
ABUW_RS08795	rpiA	ribose-5-phosphate isomerase RpiA	-1.80
ABUW_RS00515		alpha/beta fold hydrolase	-1.80
ABUW_RS02585		PHP domain-containing protein	-1.80
ABUW_RS06420		tape measure protein	-1.80
ABUW_RS13450		GMC family oxidoreductase	-1.80
ABUW_RS06975		hypothetical protein	-1.79
ABUW_RS08660	map	type I methionyl aminopeptidase	-1.79
ABUW_RS03500		DJ-1/Pfpl family protein	-1.79
ABUW_RS09025		OprD family outer membrane porin	-1.79
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-1.79
ABUW_RS18890	dnaK	molecular chaperone DnaK	-1.79
ABUW_RS05355	csy3	type I-F CRISPR-associated protein Csy3	-1.78
ABUW_RS01105		hypothetical protein	-1.78
ABUW_RS08000		Lrp/AsnC family transcriptional regulator	-1.78
ABUW_RS08870		metal-dependent hydrolase	-1.77
ABUW_RS14760		phosphomannomutase/phosphoglucomutase	-1.77
ABUW_RS09560		LysR family transcriptional regulator	-1.76
ABUW_RS13280		CinA family protein	-1.76
ABUW_RS17190		AAA family ATPase	-1.76
ABUW_RS03090		peroxiredoxin	-1.75
ABUW_RS01975		DUF853 domain-containing protein	-1.74
ABUW_RS14805		PA4642 family protein	-1.74
ABUW_RS02305		hypothetical protein	-1.74
ABUW_RS08075		OmpW family protein	-1.74
ABUW_RS13275		hypothetical protein	-1.73
ABUW_RS14720	fur	ferric iron uptake transcriptional regulator	-1.73
ABUW_RS08430	adeN	multidrug efflux transcriptional repressor AdeN	-1.73

ABUW_RS16465		alpha/beta hydrolase	-1.73
ABUW_RS05790	basH	acinetobactin biosynthesis thioesterase BasH	-1.73
ABUW_RS17380		hypothetical protein	-1.73
ABUW_RS15730		hypothetical protein	-1.72
ABUW_RS16640	msrA	peptide-methionine (S)-S-oxide reductase MsrA	-1.72
ABUW_RS06240		hypothetical protein	-1.72
ABUW_RS16155		heavy metal translocating P-type ATPase	-1.72
ABUW_RS07805		DUF4198 domain-containing protein	-1.72
ABUW_RS10155		AraC family transcriptional regulator	-1.71
ABUW_RS19565		hypothetical protein	-1.71
ABUW_RS06680		MBL fold metallo-hydrolase	-1.71
ABUW_RS06400		ORF6N domain-containing protein	-1.70
ABUW_RS11465		pyridoxal phosphate-dependent aminotransferase	-1.70
ABUW_RS02535		alpha/beta hydrolase	-1.69
ABUW_RS07955	pepN	aminopeptidase N	-1.69
ABUW_RS03155		carbohydrate porin	-1.68
ABUW_RS08695		hypothetical protein	-1.68
ABUW_RS01295		hypothetical protein	-1.67
ABUW_RS08255		hypothetical protein	-1.67
ABUW_RS10490		HIT family protein	-1.66
ABUW_RS13675		hypothetical protein	-1.66
ABUW_RS14600		DUF927 domain-containing protein	-1.66
ABUW_RS07150		hypothetical protein	-1.66
ABUW_RS07830		GNAT family N-acetyltransferase	-1.66
ABUW_RS02560		sulfurtransferase	-1.66
ABUW_RS18150		glutathione peroxidase	-1.65
ABUW_RS02915		hypothetical protein	-1.65
ABUW_RS06710	rpoH	RNA polymerase sigma factor RpoH	-1.65
ABUW_RS04350		CapA family protein	-1.64
ABUW_RS06405		hypothetical protein	-1.64
ABUW_RS04630		FdhF/YdeP family oxidoreductase	-1.63
ABUW_RS13685		type VI secretion system tip protein VgrG	-1.63
ABUW_RS06900		hypothetical protein	-1.63
ABUW_RS08240		TetR/AcrR family transcriptional regulator	-1.62
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.62
ABUW_RS07980		glutathione S-transferase family protein	-1.62
ABUW_RS14690		OsmC family protein	-1.62
ABUW_RS05965		EAL domain-containing protein	-1.61
ABUW_RS14590		hypothetical protein	-1.61
ABUW_RS03005		acyl-CoA desaturase	-1.61
ABUW_RS04310		hypothetical protein	-1.60
ABUW_RS09265		hypothetical protein	-1.60
ABUW_RS17730		sigma-54-dependent Fis family transcriptional regulator	-1.59
ABUW_RS00285		hypothetical protein	-1.59
ABUW_RS01015		LysR family transcriptional regulator	-1.59
ABUW_RS04750		TolC family protein	-1.59
ABUW_RS19995		hypothetical protein	-1.59
ABUW_RS01690		hypothetical protein	-1.58
ABUW_RS13765		hypothetical protein	-1.58
ABUW_RS18255		OsmC family protein	-1.58
ABUW_RS16240		hypothetical protein	-1.58
ABUW_RS08325		MoaD/ThiS family protein	-1.58
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.58
ABUW_RS18010		RidA family protein	-1.57
ABUW_RS09330		DUF2247 family protein	-1.57
ABUW_RS10125		transporter	-1.56
ABUW_RS17805		accessory factor UbiK family protein	-1.56

ABUW_RS10685		HU family DNA-binding protein	-1.56
ABUW_RS08705		hypothetical protein	-1.56
ABUW_RS01670		superoxide dismutase family protein	-1.56
ABUW_RS02970		phosphate-starvation-inducible PsiE family protein	-1.55
ABUW_RS11495		hypothetical protein	-1.55
ABUW_RS01245		GNAT family acetyltransferase	-1.55
ABUW_RS16675	rpmB	50S ribosomal protein L28	-1.55
ABUW_RS10770		nucleoside-diphosphate sugar epimerase	-1.54
ABUW_RS19450		hypothetical protein	-1.54
ABUW_RS07825		rRNA pseudouridine synthase	-1.54
ABUW_RS09290		cation:proton antiporter	-1.54
ABUW_RS13065		N-acetylmuramidase	-1.54
ABUW_RS04355		metalloprotease	-1.53
ABUW_RS02540	trxC	thioredoxin TrxC	-1.53
ABUW_RS03915		Arc family DNA-binding protein	-1.53
ABUW_RS03895		helix-turn-helix domain-containing protein	-1.52
ABUW_RS14810	rhtC	threonine export protein RhtC	-1.52
ABUW_RS09260		sorbose dehydrogenase family protein	-1.51
ABUW_RS10660		acyl-CoA dehydrogenase family protein	-1.51
ABUW_RS06500		alpha/beta fold hydrolase	-1.51
ABUW_RS14900		hypothetical protein	-1.51
ABUW_RS00195		START domain-containing protein	-1.51
ABUW_RS00825		putative porin	-1.51
ABUW_RS02475		metallophosphoesterase	-1.51
ABUW_RS00030		VTT domain-containing protein	-1.50
ABUW_RS17430	htpG	molecular chaperone HtpG	-1.50
ABUW_RS07065		M48 family metalloprotease	-1.50
ABUW_RS07585		RDD family protein	-1.50
ABUW_RS17770		hypothetical protein	-1.50
ABUW_RS17645	thiC	phosphomethylpyrimidine synthase ThiC	-1.50
ABUW_RS18145		helix-turn-helix domain-containing protein	-1.49
ABUW_RS06250		hypothetical protein	-1.49
ABUW_RS14550		DEAD/DEAH box helicase family protein	-1.48
ABUW_RS01595		triacylglycerol lipase	-1.48
ABUW_RS03445	yccS	TIGR01666 family membrane protein	-1.48
ABUW_RS16185		hypothetical protein	-1.48
ABUW_RS02665	ssb	single-stranded DNA-binding protein	-1.47
ABUW_RS13195	ahpC	peroxiredoxin	-1.47
ABUW_RS10365		transcriptional regulator	-1.47
ABUW_RS14120	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	-1.45
ABUW_RS06000	lipA	lipoyl synthase	-1.45
ABUW_RS14140		arylesterase	-1.45
ABUW_RS19560		transglycosylase SLT domain-containing protein	-1.45
ABUW_RS04500		co-chaperone GroES	-1.45
ABUW_RS13760		RHS repeat protein	-1.43
ABUW_RS12440		nucleoside deaminase	-1.43
ABUW_RS05520		hypothetical protein	-1.43
ABUW_RS16880	hcaR	DNA-binding transcriptional regulator HcaR	-1.43
ABUW_RS00025	cybC	cytochrome b562	-1.43
ABUW_RS05805		murein L,D-transpeptidase	-1.43
ABUW_RS11185		FxA family protein	-1.43
ABUW_RS08610		MarR family transcriptional regulator	-1.43
ABUW_RS12255		ATP-dependent helicase	-1.43
ABUW_RS14555		site-specific DNA-methyltransferase	-1.43
ABUW_RS00865	acs	acetate--CoA ligase	-1.43
ABUW_RS10615		(2Fe-2S)-binding protein	-1.42

ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.42
ABUW_RS14755	argB	acetylglutamate kinase	-1.42
ABUW_RS10940	gspJ	type II secretion system minor pseudopilin GspJ	-1.42
ABUW_RS05195		nitronate monooxygenase	-1.42
ABUW_RS17450		alpha/beta fold hydrolase	-1.42
ABUW_RS16890		glutathione S-transferase family protein	-1.41
ABUW_RS11330		amino acid ABC transporter ATP-binding protein	-1.41
ABUW_RS16035		SDR family oxidoreductase	-1.41
ABUW_RS19085		H-NS histone family protein	-1.41
ABUW_RS11615		hypothetical protein	-1.41
ABUW_RS01525	rpoZ	DNA-directed RNA polymerase subunit omega	-1.40
ABUW_RS05095		SDR family oxidoreductase	-1.40
ABUW_RS00045		hypothetical protein	-1.40
ABUW_RS09275		hydrolase	-1.40
ABUW_RS10000		catalase family protein	-1.40
ABUW_RS08530		hypothetical protein	-1.40
ABUW_RS13525		tannase/feruloyl esterase family alpha/beta hydrolase	-1.40
ABUW_RS19540		conjugal transfer protein TraF	-1.39
ABUW_RS05940		superoxide dismutase	-1.39
ABUW_RS07765		outer membrane protein assembly factor	-1.39
ABUW_RS00110		sodium-dependent transporter	-1.38
ABUW_RS16550	leuA	2-isopropylmalate synthase	-1.38
ABUW_RS18720		TetR/AcrR family transcriptional regulator	-1.38
ABUW_RS13220		hypothetical protein	-1.38
ABUW_RS17900		TniB family NTP-binding protein	-1.38
ABUW_RS17340		transcriptional regulator	-1.38
ABUW_RS00915		hypothetical protein	-1.38
ABUW_RS13365		cytochrome b	-1.37
ABUW_RS12545		hypothetical protein	-1.37
ABUW_RS04960		hypothetical protein	-1.37
ABUW_RS05480		BapA prefix-like domain-containing protein	-1.36
ABUW_RS18050	cysK	cysteine synthase A	-1.36
ABUW_RS08765		TonB-dependent siderophore receptor	-1.36
ABUW_RS14240		galactose mutarotase	-1.36
ABUW_RS08385	fumC	class II fumarate hydratase	-1.36
ABUW_RS04815	perM	AI-2E family transporter	-1.36
ABUW_RS09020		SDR family oxidoreductase	-1.36
ABUW_RS03485		DUF4850 domain-containing protein	-1.36
ABUW_RS19105		hypothetical protein	-1.35
ABUW_RS17570		H-NS histone family protein	-1.35
ABUW_RS02130		NAD(P)/FAD-dependent oxidoreductase	-1.35
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.35
ABUW_RS13225		glutathione S-transferase N-terminal domain-containing protein	-1.35
ABUW_RS09205		MerR family transcriptional regulator	-1.34
ABUW_RS13000		hypothetical protein	-1.34
ABUW_RS15870		mechanosensitive ion channel family protein	-1.34
ABUW_RS10850		biopolymer transporter ExbD	-1.34
ABUW_RS10815		Zn-dependent oligopeptidase	-1.33
ABUW_RS13650		ATP-binding protein	-1.33
ABUW_RS07395		response regulator transcription factor	-1.33
ABUW_RS03490		DUF1176 domain-containing protein	-1.33
ABUW_RS03270		sel1 repeat family protein	-1.32
ABUW_RS08435	glnG	nitrogen regulation protein NR(I)	-1.32
ABUW_RS03550		wax ester/triacylglycerol synthase family O-acyltransferase	-1.31
ABUW_RS16695		hypothetical protein	-1.31

ABUW_RS04910		deoxyguanosinetriphosphate triphosphohydrolase	-1.31
ABUW_RS00490		hypothetical protein	-1.31
ABUW_RS00645	uraH	hydroxyisourate hydrolase	-1.30
ABUW_RS12475	tssA	type VI secretion system protein TssA	-1.30
ABUW_RS02405		hypothetical protein	-1.30
ABUW_RS08195		acyl-CoA thioesterase	-1.30
ABUW_RS02275		PhoH family protein	-1.30
ABUW_RS02765	oxa-23	carbapenem-hydrolyzing class D beta-lactamase OXA-23	-1.28
	sRNA18	sRNA18	-1.28
ABUW_RS09350		DUF2314 domain-containing protein	-1.28
ABUW_RS13755		RHS repeat-associated core domain-containing protein	-1.28
ABUW_RS03365		radical SAM protein	-1.28
ABUW_RS16680	rpmG	50S ribosomal protein L33	-1.28
ABUW_RS09645		hypothetical protein	-1.27
ABUW_RS03145		AraC family transcriptional regulator	-1.27
ABUW_RS09155		FadR family transcriptional regulator	-1.25
ABUW_RS13240		glutathione S-transferase	-1.25
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.25
ABUW_RS08420		protein tyrosine phosphatase family protein	-1.25
ABUW_RS02520		dihydrolipoyl dehydrogenase	-1.25
ABUW_RS07250	csuAB	Csu fimbrial major subunit CsuAB	-1.25
ABUW_RS08520		RNA-binding protein	-1.25
ABUW_RS04225		DUF493 domain-containing protein	-1.24
ABUW_RS04090		hypothetical protein	-1.24
ABUW_RS20305		hypothetical protein	-1.24
ABUW_RS14030		isocitrate lyase	-1.24
ABUW_RS00180	dnaJ	molecular chaperone DnaJ	-1.24
ABUW_RS03925		KilA-N domain-containing protein	-1.23
ABUW_RS10945	gspl	type II secretion system minor pseudopilin Gspl	-1.23
ABUW_RS00680		GGDEF domain-containing protein	-1.23
ABUW_RS04835		DUF3106 domain-containing protein	-1.23
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-1.23
ABUW_RS06620		tetratricopeptide repeat protein	-1.23
ABUW_RS08720		DUF2057 domain-containing protein	-1.22
ABUW_RS15720		CoA pyrophosphatase	-1.22
ABUW_RS04955		diphthine--ammonia ligase	-1.22
ABUW_RS10330		2,3-butanediol dehydrogenase	-1.22
ABUW_RS05260		M61 family metalloproteinase	-1.22
ABUW_RS17815		hypothetical protein	-1.22
ABUW_RS08200		iron-containing alcohol dehydrogenase	-1.21
ABUW_RS10390	trpB	tryptophan synthase subunit beta	-1.21
ABUW_RS14940		LysR family transcriptional regulator	-1.20
ABUW_RS13815		hypothetical protein	-1.20
ABUW_RS16850		LysR family transcriptional regulator	-1.20
ABUW_RS09335		SMI1/KNR4 family protein	-1.20
ABUW_RS15365	upp	uracil phosphoribosyltransferase	-1.19
ABUW_RS12470	tssK	type VI secretion system baseplate subunit TssK	-1.18
ABUW_RS15945		hypothetical protein	-1.18
ABUW_RS01700		class I SAM-dependent methyltransferase	-1.18
ABUW_RS01985		type 1 glutamine amidotransferase	-1.17
ABUW_RS12840	lptA	lipopolysaccharide transport periplasmic protein LptA	-1.17
ABUW_RS10655		AarF/ABC1/UbiB kinase family protein	-1.16
ABUW_RS18575	galE	UDP-glucose 4-epimerase GalE	-1.16
ABUW_RS18125		threonylcarbamoyl-AMP synthase	-1.16
ABUW_RS12715		serine hydrolase	-1.16
ABUW_RS12130		NAD-dependent succinate-semialdehyde dehydrogenase	-1.15

ABUW_RS15075		hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	-1.15
ABUW_RS00020	gyrB	DNA topoisomerase (ATP-hydrolyzing) subunit B	-1.15
ABUW_RS00940		TetR/AcrR family transcriptional regulator	-1.15
ABUW_RS01930		NAD(P)H-binding protein	-1.15
ABUW_RS01695		hypothetical protein	-1.15
ABUW_RS12445		ankyrin repeat domain-containing protein	-1.14
ABUW_RS05995		acyl-CoA dehydrogenase	-1.14
ABUW_RS02260		hypothetical protein	-1.14
ABUW_RS04115		YbjQ family protein	-1.14
ABUW_RS06685		hydrolase	-1.13
ABUW_RS08675	grxD	Grx4 family monothiol glutaredoxin	-1.13
ABUW_RS17715	pbpG	D-alanyl-D-alanine endopeptidase PBP7/8	-1.13
ABUW_RS16745		SlyX family protein	-1.13
ABUW_RS17605		histidine kinase	-1.13
ABUW_RS05225		glycosyltransferase family 2 protein	-1.13
ABUW_RS00960	tenA	thiaminase II	-1.12
ABUW_RS15000		tetratricopeptide repeat protein	-1.12
ABUW_RS02920		glycosyltransferase family 25 protein	-1.12
ABUW_RS18785		TetR/AcrR family transcriptional regulator	-1.12
ABUW_RS18000		glycoside hydrolase family 25 protein	-1.12
ABUW_RS04745		HlyD family secretion protein	-1.11
ABUW_RS05425		diaminobutyrate--2-oxoglutarate transaminase	-1.11
ABUW_RS02240		YihY family inner membrane protein	-1.11
ABUW_RS00500	pncB	nicotinate phosphoribosyltransferase	-1.11
ABUW_RS05330		DUF962 domain-containing protein	-1.10
ABUW_RS08775		phospholipase A	-1.10
ABUW_RS06650		acyl-CoA dehydrogenase family protein	-1.10
ABUW_RS00770	aceE	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	-1.10
ABUW_RS19090		hypothetical protein	-1.09
ABUW_RS03100		hypothetical protein	-1.09
ABUW_RS10580		HAD family hydrolase	-1.09
ABUW_RS07970		fimbrial biogenesis outer membrane usher protein	-1.09
ABUW_RS19465		hypothetical protein	-1.09
ABUW_RS15005	lolB	outer membrane lipoprotein LolB	-1.08
ABUW_RS05360	cas6f	type I-F CRISPR-associated endoribonuclease Cas6/Csy4	-1.08
ABUW_RS11460	msrB	peptide-methionine (R)-S-oxide reductase MsrB	-1.08
ABUW_RS12170		GntR family transcriptional regulator	-1.08
ABUW_RS03385		DUF1853 family protein	-1.07
ABUW_RS08825	clpA	ATP-dependent Clp protease ATP-binding subunit ClpA	-1.06
ABUW_RS10020		uracil-DNA glycosylase family protein	-1.06
ABUW_RS18985		DsbC family protein	-1.06
ABUW_RS16635		DUF4105 domain-containing protein	-1.06
ABUW_RS18490		SDR family NAD(P)-dependent oxidoreductase	-1.05
ABUW_RS11190		OXA-51 family carbapenem-hydrolyzing class D beta-lactamase OXA-69	-1.05
ABUW_RS15055		GDYXXLXY domain-containing protein	-1.05
ABUW_RS04110		nuclear transport factor 2 family protein	-1.05
ABUW_RS04870	tolB	Tol-Pal system beta propeller repeat protein TolB	-1.04
ABUW_RS13310		NADP(H)-dependent aldo-keto reductase	-1.04
ABUW_RS04920		multidrug efflux MFS transporter	-1.04
ABUW_RS11040		hypothetical protein	-1.04
ABUW_RS14965	smpB	SsrA-binding protein SmpB	-1.04
ABUW_RS12490		OmpA family protein	-1.04
ABUW_RS06970		hypothetical protein	-1.04
ABUW_RS14990		DNA primase	-1.03

ABUW_RS05910		hypothetical protein	-1.03
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	-1.03
ABUW_RS12705		RHS domain-containing protein	-1.03
ABUW_RS09035		winged helix-turn-helix transcriptional regulator	-1.03
ABUW_RS05830		class C extended-spectrum beta-lactamase ADC-11	-1.02
ABUW_RS14870		EcsC family protein	-1.02
ABUW_RS03080		dual specificity protein phosphatase family protein	-1.01
ABUW_RS19625		hypothetical protein	-1.01
ABUW_RS08840		alpha/beta hydrolase	-1.01
ABUW_RS11285		LysR family transcriptional regulator	-1.00
ABUW_RS03195		OmpA family protein	-1.00
ABUW_RS15575		LysR family transcriptional regulator	-1.00

Table A9. Overview of genes that are differentially expressed as identified through RNA-seq analysis in *ΔgacS* MEP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	<i>ΔgacS</i> MEP vs WT MEP log2FC
sRNA84	sRNA84	sRNA84	5.01
ABUW_RS19905	ssrS	6S RNA	4.75
ABUW_RS09120		CoA transferase subunit B	4.66
ABUW_RS11470		dicarboxylate/amino acid:cation symporter	4.57
sRNA92	sRNA92	sRNA92	4.50
ABUW_RS09655		hypothetical protein	4.43
ABUW_RS09675		hypothetical protein	4.31
sRNA96	sRNA96	sRNA96	4.11
ABUW_RS01510		bacterioferritin-associated ferredoxin	4.05
ABUW_RS07110		tRNA-Trp	4.03
ABUW_RS18100		TonB-dependent copper receptor	3.92
ABUW_RS11715		CidA/LrgA family protein	3.90
ABUW_RS09670		hypothetical protein	3.75
ABUW_RS16540		TonB-dependent siderophore receptor	3.73
ABUW_RS16925		tRNA-Lys	3.71
ABUW_RS07105		tRNA-Leu	3.67
ABUW_RS11825		LysE family translocator	3.56
ABUW_RS11475		type II asparaginase	3.53
ABUW_RS17840		cation transporter	3.49
sRNA24	sRNA24	sRNA24	3.48
ABUW_RS13745		TonB-dependent receptor	3.46
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	3.42
sRNA81	sRNA81	sRNA81	3.41
sRNA1	sRNA1	sRNA1	3.39
ABUW_RS13860		cation transporter	3.38
ABUW_RS17835		signal peptidase II	3.36
ABUW_RS16770	gltP	glutamate/aspartate:proton symporter GltP	3.27
sRNA42	sRNA42	sRNA42	3.10
ABUW_RS04445		tRNA-Cys	3.07
ABUW_RS03465		alanine:cation symporter family protein	3.05
ABUW_RS10185		CoA transferase subunit B	3.05
ABUW_RS18235		NAD-dependent malic enzyme	3.01
ABUW_RS07115		tRNA-Leu	2.96
ABUW_RS11295		tRNA-Ile	2.92
ABUW_RS11440	dapC	succinyldiaminopimelate transaminase	2.88
ABUW_RS02640		tRNA-Leu	2.85
ABUW_RS03460		hypothetical protein	2.78
ABUW_RS11710		LrgB family protein	2.76
ABUW_RS10180		CoA transferase subunit A	2.75

ABUW_RS10160		3-hydroxybutyrate dehydrogenase	2.72
ABUW_RS09660		replication initiation factor domain-containing protein	2.72
ABUW_RS10190		short-chain fatty acid transporter	2.69
ABUW_RS07485	fis	DNA-binding transcriptional regulator Fis	2.67
ABUW_RS18095		hypothetical protein	2.66
ABUW_RS10195		thiolase family protein	2.65
ABUW_RS08035		TonB-dependent receptor	2.65
ABUW_RS00710		TonB-dependent siderophore receptor	2.63
ABUW_RS10220		aspartate ammonia-lyase	2.60
ABUW_RS20110		hypothetical protein	2.54
sRNA15	sRNA15	sRNA15	2.53
ABUW_RS10165		GntP family permease	2.53
ABUW_RS11140		hypothetical protein	2.52
sRNA77	sRNA77	sRNA77	2.51
ABUW_RS00790		TonB-dependent siderophore receptor	2.51
ABUW_RS16645		biopolymer transporter ExbD	2.49
ABUW_RS10520		TonB-dependent siderophore receptor	2.47
ABUW_RS15030		tRNA-Gln	2.45
ABUW_RS10525		hypothetical protein	2.45
ABUW_RS05660	yddG	aromatic amino acid DMT transporter YddG	2.43
ABUW_RS10775	rpsT	30S ribosomal protein S20	2.43
ABUW_RS14160		TonB-dependent siderophore receptor	2.41
ABUW_RS17250		tRNA-Met	2.38
ABUW_RS16655		energy transducer TonB	2.37
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	2.36
ABUW_RS01740	astE	succinylglutamate desuccinylase	2.36
ABUW_RS13520		Paal family thioesterase	2.34
ABUW_RS18435		amino acid permease	2.33
ABUW_RS01350		amino acid permease	2.31
ABUW_RS00770	aceE	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	2.30
ABUW_RS15025		tRNA-Gln	2.28
ABUW_RS10600		hypothetical protein	2.28
ABUW_RS09665		hypothetical protein	2.25
ABUW_RS17685		ferrous iron transporter B	2.22
ABUW_RS10530		PepSY domain-containing protein	2.19
ABUW_RS13235	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	2.19
ABUW_RS02140		succinate dehydrogenase assembly factor 2	2.19
ABUW_RS09635		hypothetical protein	2.18
ABUW_RS01045		tRNA-Thr	2.14
ABUW_RS11115	putP	sodium/proline symporter PutP	2.12
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	2.10
ABUW_RS02000	rplD	50S ribosomal protein L4	2.10
ABUW_RS14395		hypothetical protein	2.10
ABUW_RS08150	acel	chlorhexidine efflux PACE transporter AceI	2.09
ABUW_RS03430		YdcF family protein	2.08
sRNA102	sRNA102	sRNA102	2.08
ABUW_RS14435	mgo	malate dehydrogenase (quinone)	2.06
ABUW_RS06195		hypothetical protein	2.05
ABUW_RS07565		cytochrome o ubiquinol oxidase subunit IV	2.02
ABUW_RS11315		YebC/PmpR family DNA-binding transcriptional regulator	2.02
ABUW_RS16810	infA	translation initiation factor IF-1	1.99
ABUW_RS10710	iscU	Fe-S cluster assembly scaffold IscU	1.99
ABUW_RS17330		DUF1656 domain-containing protein	1.98
ABUW_RS17255		tRNA-Leu	1.98
ABUW_RS07445		dicarboxylate/amino acid:cation symporter	1.98

ABUW_RS13515		DUF3237 domain-containing protein	1.97
ABUW_RS13490		p-hydroxycinnamoyl CoA hydratase/lyase	1.97
ABUW_RS19715		hypothetical protein	1.96
ABUW_RS04285	odhB	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase	1.95
ABUW_RS08890	eno	phosphopyruvate hydratase	1.95
ABUW_RS19445		hypothetical protein	1.94
ABUW_RS07545	rplI	50S ribosomal protein L9	1.94
ABUW_RS01735	astB	N-succinylarginine dihydrolase	1.93
ABUW_RS13510		OprD family porin	1.92
ABUW_RS17505	secE	preprotein translocase subunit SecE	1.92
ABUW_RS01235		tRNA-Phe	1.91
ABUW_RS05565	rpmE	50S ribosomal protein L31	1.90
ABUW_RS02015	rpsS	30S ribosomal protein S19	1.90
ABUW_RS04300	sucD	succinate--CoA ligase subunit alpha	1.90
ABUW_RS17510		tRNA-Trp	1.90
ABUW_RS17690		ferrous iron transport protein A	1.88
ABUW_RS20465		hypothetical protein	1.88
ABUW_RS17680		hypothetical protein	1.87
ABUW_RS10715	iscA	iron-sulfur cluster assembly protein IscA	1.86
ABUW_RS07475	purD	phosphoribosylamine--glycine ligase	1.85
ABUW_RS08720		DUF2057 domain-containing protein	1.85
ABUW_RS18105		DUF2946 family protein	1.85
ABUW_RS14380		YaeQ family protein	1.83
ABUW_RS08765		TonB-dependent siderophore receptor	1.83
ABUW_RS12140		cytosine permease	1.83
ABUW_RS18430		amino acid permease	1.83
ABUW_RS14500		FecR domain-containing protein	1.83
ABUW_RS18915		5-(carboxyamino)imidazole ribonucleotide synthase	1.83
ABUW_RS14610		hypothetical protein	1.83
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	1.82
ABUW_RS05430		aspartate aminotransferase family protein	1.82
ABUW_RS10225		TonB-dependent siderophore receptor	1.82
ABUW_RS13495		aldehyde dehydrogenase	1.81
ABUW_RS17870	arsB	ACR3 family arsenite efflux transporter	1.81
sRNA46	sRNA46	sRNA46	1.81
ABUW_RS15855		organic hydroperoxide resistance protein	1.80
ABUW_RS08070		TonB-dependent siderophore receptor	1.80
ABUW_RS00150		pyrimidine permease	1.80
ABUW_RS06575		ferredoxin--NADP reductase	1.80
ABUW_RS18450		D-amino acid dehydrogenase	1.80
ABUW_RS02420	rpsI	30S ribosomal protein S9	1.79
ABUW_RS04380	carB	carbamoyl-phosphate synthase large subunit	1.79
ABUW_RS13855		amino acid transporter	1.78
ABUW_RS13345		aspartate kinase	1.78
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.78
ABUW_RS02635	queA	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	1.78
ABUW_RS06655		alpha/beta hydrolase	1.77
ABUW_RS07625		LLM class flavin-dependent oxidoreductase	1.76
ABUW_RS04280		2-oxoglutarate dehydrogenase E1 component	1.76
ABUW_RS16430	ndk	nucleoside-diphosphate kinase	1.76
ABUW_RS04545	ttcA	tRNA 2-thiocytidine(32) synthetase TtcA	1.76
ABUW_RS01820		HPP family protein	1.75
ABUW_RS13020		helix-turn-helix transcriptional regulator	1.73
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	1.73
ABUW_RS00705	pyrE	orotate phosphoribosyltransferase	1.72

ABUW_RS10595		PepSY domain-containing protein	1.72
ABUW_RS17975		trimeric intracellular cation channel family protein	1.72
ABUW_RS01470		FAD-dependent oxidoreductase	1.72
ABUW_RS04290	lpdA	dihydrolipoyl dehydrogenase	1.71
sRNA37	sRNA37	sRNA37	1.71
ABUW_RS20225		alpha/beta hydrolase	1.71
ABUW_RS14650		DHA2 family efflux MFS transporter permease subunit	1.70
ABUW_RS03435		PepSY domain-containing protein	1.70
ABUW_RS14165	nfuA	Fe-S biogenesis protein NfuA	1.69
ABUW_RS17430	htpG	molecular chaperone HtpG	1.68
ABUW_RS06025		OmpW family protein	1.68
sRNA101	sRNA101	sRNA101	1.67
ABUW_RS01730	astD	succinylglutamate-semialdehyde dehydrogenase	1.67
ABUW_RS09065		aromatic-ring-hydroxylating dioxygenase subunit beta	1.67
ABUW_RS15950	rplT	50S ribosomal protein L20	1.67
ABUW_RS03220		uracil-xanthine permease	1.67
ABUW_RS08880		CTP synthase	1.66
ABUW_RS13610		gamma-aminobutyraldehyde dehydrogenase	1.66
ABUW_RS10705		IscS subfamily cysteine desulfurase	1.66
ABUW_RS04505	groL	chaperonin GroEL	1.65
ABUW_RS04450	folD	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	1.65
sRNA90	sRNA90	sRNA90	1.65
ABUW_RS11015		nucleotidyltransferase family protein	1.65
ABUW_RS01360		tRNA-Ala	1.65
ABUW_RS00350		amino acid permease	1.65
ABUW_RS07435		MFS transporter	1.65
ABUW_RS12350		APC family permease	1.64
ABUW_RS08885	kdsA	3-deoxy-8-phosphooctulonate synthase	1.64
ABUW_RS08670		hypothetical protein	1.63
ABUW_RS17645	thiC	phosphomethylpyrimidine synthase ThiC	1.63
ABUW_RS11820		Lrp/AsnC family transcriptional regulator	1.63
ABUW_RS18975	hpt	hypoxanthine phosphoribosyltransferase	1.63
ABUW_RS18900		matrixin family metalloprotease	1.63
ABUW_RS20220		flavin reductase family protein	1.62
ABUW_RS03165		nitrite/sulfite reductase	1.62
ABUW_RS16510		fumarate hydratase	1.62
ABUW_RS03170		DUF934 domain-containing protein	1.62
ABUW_RS08115	mgtA	magnesium-translocating P-type ATPase	1.62
ABUW_RS10605	bfnH	TonB-dependent receptor	1.61
ABUW_RS02370		TetR family transcriptional regulator	1.61
ABUW_RS10915	tadA	tRNA adenosine(34) deaminase TadA	1.61
ABUW_RS02010	rplB	50S ribosomal protein L2	1.61
ABUW_RS01590	rplS	50S ribosomal protein L19	1.61
ABUW_RS00965		DUF475 domain-containing protein	1.61
ABUW_RS10535		hypothetical protein	1.60
ABUW_RS06105		site-specific integrase	1.60
ABUW_RS03535		Maf-like protein	1.60
ABUW_RS04375	greA	transcription elongation factor GreA	1.60
ABUW_RS02080	rpsE	30S ribosomal protein S5	1.59
ABUW_RS12355		aldehyde dehydrogenase (NADP(+))	1.59
ABUW_RS12800		O-methyltransferase	1.59
ABUW_RS08680		aspartate aminotransferase family protein	1.58
ABUW_RS07640		hypothetical protein	1.58
ABUW_RS17120	rpsO	30S ribosomal protein S15	1.58

ABUW_RS13720	argG	argininosuccinate synthase	1.57
ABUW_RS09630		FAD-binding oxidoreductase	1.57
ABUW_RS04295	sucC	ADP-forming succinate--CoA ligase subunit beta	1.57
ABUW_RS06685		hydrolase	1.56
ABUW_RS16490	eda	bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase	1.56
ABUW_RS14200		inorganic phosphate transporter	1.56
ABUW_RS07925		iron-containing alcohol dehydrogenase	1.56
ABUW_RS02090	rplO	50S ribosomal protein L15	1.56
ABUW_RS10725	hscA	Fe-S protein assembly chaperone HscA	1.56
ABUW_RS01195		DMT family transporter	1.55
ABUW_RS09620		NAD(P)/FAD-dependent oxidoreductase	1.55
ABUW_RS16275		peptide chain release factor 3	1.55
ABUW_RS01990	rpsJ	30S ribosomal protein S10	1.54
ABUW_RS15920		hypothetical protein	1.54
ABUW_RS09150		hypothetical protein	1.54
ABUW_RS11390	ychF	redox-regulated ATPase YchF	1.54
ABUW_RS01720		aspartate aminotransferase family protein	1.53
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.53
ABUW_RS01575	rpsP	30S ribosomal protein S16	1.53
ABUW_RS13360		hypothetical protein	1.52
ABUW_RS03530	mreD	rod shape-determining protein MreD	1.52
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	1.51
ABUW_RS07045	purF	amidophosphoribosyltransferase	1.51
ABUW_RS04915	purL	phosphoribosylformylglycinamide synthase	1.51
ABUW_RS07480	purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	1.51
ABUW_RS01725	astA	arginine N-succinyltransferase	1.51
ABUW_RS14765	dut	dUTP diphosphatase	1.50
ABUW_RS05670		type II toxin-antitoxin system Phd/YefM family antitoxin	1.50
ABUW_RS04275		succinate dehydrogenase iron-sulfur subunit	1.49
ABUW_RS08755		Rieske (2Fe-2S) protein	1.49
sRNA54	sRNA54	sRNA54	1.49
ABUW_RS10380	aroC	chorismate synthase	1.49
ABUW_RS08945	pcaH	protocatechuate 3,4-dioxygenase subunit beta	1.49
ABUW_RS17490	rplA	50S ribosomal protein L1	1.48
ABUW_RS03525	mreC	rod shape-determining protein MreC	1.48
ABUW_RS02060	rpsN	30S ribosomal protein S14	1.48
ABUW_RS17225		ribosome-binding factor A	1.48
ABUW_RS07005		acyltransferase	1.48
ABUW_RS07630		hypothetical protein	1.47
ABUW_RS18440		RidA family protein	1.47
ABUW_RS13375		NCS2 family permease	1.47
ABUW_RS02020	rplV	50S ribosomal protein L22	1.46
ABUW_RS02115	rpsD	30S ribosomal protein S4	1.46
ABUW_RS04385	carA	glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit	1.46
ABUW_RS07880		peptidyl-prolyl cis-trans isomerase	1.46
ABUW_RS14440		hypothetical protein	1.45
ABUW_RS08760		adenosine kinase	1.44
ABUW_RS06505		serine hydroxymethyltransferase	1.44
ABUW_RS07460		ABC transporter permease	1.44
ABUW_RS05300		L-cystine transporter	1.44
ABUW_RS10505		hypothetical protein	1.44
ABUW_RS17880	trxB	thioredoxin-disulfide reductase	1.44

ABUW_RS08000		Lrp/AsnC family transcriptional regulator	1.44
ABUW_RS14915		NAD-dependent succinate-semialdehyde dehydrogenase	1.43
ABUW_RS01710		amino acid permease	1.43
ABUW_RS07845	tsaE	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE	1.42
ABUW_RS05155		glyceraldehyde-3-phosphate dehydrogenase	1.42
ABUW_RS13535		aldehyde dehydrogenase (NADP(+))	1.42
ABUW_RS18920	purE	5-(carboxyamino)imidazole ribonucleotide mutase	1.41
ABUW_RS18685		carboxylating nicotinate-nucleotide diphosphorylase	1.41
ABUW_RS04235		hypothetical protein	1.41
ABUW_RS17300		pyrimidine/purine nucleoside phosphorylase	1.41
ABUW_RS19020	rpmH	50S ribosomal protein L34	1.41
ABUW_RS13485	mhpT	3-(3-hydroxy-phenyl)propionate transporter MhpT	1.41
ABUW_RS05500	mnmA	tRNA 2-thiouridine(34) synthase MnmA	1.41
ABUW_RS13525		tannase/feruloyl esterase family alpha/beta hydrolase	1.41
ABUW_RS04810	purM	phosphoribosylformylglycinamide cyclo-ligase	1.41
ABUW_RS02025	rpsC	30S ribosomal protein S3	1.40
ABUW_RS01175	hisF	imidazole glycerol phosphate synthase subunit HisF	1.40
ABUW_RS17635		TetR/AcrR family transcriptional regulator	1.40
ABUW_RS11170		methionine adenosyltransferase	1.40
ABUW_RS10920		enoyl-CoA hydratase/isomerase family protein	1.40
ABUW_RS11020		phosphotransferase	1.40
ABUW_RS06095		ABC transporter permease	1.40
ABUW_RS15105		DUF177 domain-containing protein	1.39
ABUW_RS10385	prmB	50S ribosomal protein L3 N(5)-glutamine methyltransferase	1.39
ABUW_RS07655	prfA	peptide chain release factor 1	1.39
ABUW_RS01325		hypothetical protein	1.39
ABUW_RS11070		helix-turn-helix transcriptional regulator	1.38
ABUW_RS12145		aldehyde dehydrogenase	1.38
ABUW_RS08125		benzoate/H(+) symporter BenE family transporter	1.38
ABUW_RS11080		DUF1275 domain-containing protein	1.38
ABUW_RS15035		ribose-phosphate pyrophosphokinase	1.37
ABUW_RS04205		APC family permease	1.37
ABUW_RS04270		succinate dehydrogenase flavoprotein subunit	1.36
ABUW_RS07660	prmC	peptide chain release factor N(5)-glutamine methyltransferase	1.36
ABUW_RS05120		pyridoxal phosphate-dependent aminotransferase	1.36
ABUW_RS18990	dmeF	CDF family Co(II)/Ni(II) efflux transporter DmeF	1.36
ABUW_RS14505		sigma-70 family RNA polymerase sigma factor	1.36
ABUW_RS11230		hypothetical protein	1.36
ABUW_RS01200		helix-turn-helix transcriptional regulator	1.35
ABUW_RS16535		trigger factor	1.35
ABUW_RS01995	rplC	50S ribosomal protein L3	1.35
ABUW_RS08355		DMT family transporter	1.35
ABUW_RS01795		glycine--tRNA ligase subunit beta	1.35
ABUW_RS07195		alpha/beta fold hydrolase	1.35
ABUW_RS11005		ParA family protein	1.35
ABUW_RS09075		oxidoreductase	1.34
ABUW_RS05425		diaminobutyrate--2-oxoglutarate transaminase	1.34
ABUW_RS15400	nuoH	NADH-quinone oxidoreductase subunit NuoH	1.34
ABUW_RS12135		hypothetical protein	1.34
ABUW_RS06040		elongation factor Ts	1.34
ABUW_RS15295		LysE family translocator	1.32

ABUW_RS15390	nuoJ	NADH-quinone oxidoreductase subunit J	1.32
ABUW_RS02075	rplR	50S ribosomal protein L18	1.32
ABUW_RS08160		3-oxoacyl-ACP reductase	1.32
ABUW_RS15225		tRNA-dihydrouridine synthase	1.32
ABUW_RS18675	murJ	murein biosynthesis integral membrane protein MurJ	1.32
ABUW_RS02545		acyl-CoA thioesterase	1.31
ABUW_RS02095	secY	preprotein translocase subunit SecY	1.31
ABUW_RS15380	nuoL	NADH-quinone oxidoreductase subunit L	1.31
ABUW_RS08555	kynU	kynureninase	1.31
ABUW_RS18280	guaA	glutamine-hydrolyzing GMP synthase	1.31
ABUW_RS11205	ruvC	crossover junction endodeoxyribonuclease RuvC	1.31
ABUW_RS16495		phosphogluconate dehydratase	1.31
ABUW_RS02250		xanthine phosphoribosyltransferase	1.31
ABUW_RS13540	kdgD	5-dehydro-4-deoxyglucarate dehydratase	1.31
ABUW_RS02085	rpmD	50S ribosomal protein L30	1.31
ABUW_RS01270		bifunctional SulP family inorganic anion transporter/carbonic anhydrase	1.31
ABUW_RS00200		MFS transporter	1.30
ABUW_RS01465	gltB	glutamate synthase large subunit	1.30
ABUW_RS07570	cyoC	cytochrome o ubiquinol oxidase subunit III	1.30
ABUW_RS04180	serS	serine--tRNA ligase	1.30
ABUW_RS04480		phosphoenolpyruvate carboxykinase (GTP)	1.30
ABUW_RS16660	purU	formyltetrahydrofolate deformylase	1.30
ABUW_RS04805		phosphoribosylglycinamide formyltransferase	1.30
ABUW_RS18240		arginine--tRNA ligase	1.29
ABUW_RS11740		SDR family oxidoreductase	1.29
ABUW_RS11045		phosphoglycerate kinase	1.29
ABUW_RS09090	tynA	primary-amine oxidase	1.29
ABUW_RS11000		ParB/RepB/Spo0J family partition protein	1.29
ABUW_RS15370	nuoN	NADH-quinone oxidoreductase subunit NuoN	1.29
ABUW_RS13505		acyl-CoA dehydrogenase family protein	1.29
ABUW_RS03375	dapE	succinyl-diaminopimelate desuccinylase	1.28
ABUW_RS09650		helix-turn-helix transcriptional regulator	1.28
ABUW_RS14850	tuf	elongation factor Tu	1.27
ABUW_RS04265	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.27
ABUW_RS00830	prfB	peptide chain release factor 2	1.27
ABUW_RS12150		LLM class flavin-dependent oxidoreductase	1.27
ABUW_RS01135		potassium transporter Kup	1.27
ABUW_RS18190	atpE	FOF1 ATP synthase subunit C	1.27
ABUW_RS08455	frr	ribosome recycling factor	1.27
ABUW_RS20205		hypothetical protein	1.27
ABUW_RS02030	rplP	50S ribosomal protein L16	1.27
ABUW_RS11165	tkt	transketolase	1.26
ABUW_RS18795		TDT family transporter	1.26
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	1.26
ABUW_RS01585	trmD	tRNA (guanosine(37)-N1)-methyltransferase TrmD	1.26
ABUW_RS15425		NADH-quinone oxidoreductase subunit B	1.26
ABUW_RS13615		nuclear transport factor 2 family protein	1.26
ABUW_RS02125	rplQ	50S ribosomal protein L17	1.25
ABUW_RS17445		TRAP transporter large permease subunit	1.25
ABUW_RS03555		phosphoadenylyl-sulfate reductase	1.25
ABUW_RS15385	nuoK	NADH-quinone oxidoreductase subunit NuoK	1.25
ABUW_RS20525		hypothetical protein	1.24
ABUW_RS17865		arsenate reductase ArsC	1.24
ABUW_RS15430	ndhC	NADH-quinone oxidoreductase subunit A	1.24
ABUW_RS17850		universal stress protein	1.24

ABUW_RS09465		methylenetetrahydrofolate reductase C-terminal domain-containing protein	1.24
ABUW_RS17630		EamA family transporter	1.24
ABUW_RS09060		aromatic ring-hydroxylating dioxygenase subunit alpha	1.24
ABUW_RS15420	nuoC	NADH-quinone oxidoreductase subunit C/D	1.23
ABUW_RS16800	truA	tRNA pseudouridine(38-40) synthase TruA	1.23
ABUW_RS11770		LysR family transcriptional regulator	1.23
ABUW_RS14375		FKBP-type peptidyl-prolyl cis-trans isomerase	1.23
ABUW_RS04650	genX	EF-P lysine aminoacylase GenX	1.23
ABUW_RS09470		LuxR family transcriptional regulator	1.23
ABUW_RS07795		MFS transporter	1.22
ABUW_RS15955	rpml	50S ribosomal protein L35	1.22
ABUW_RS13925	rlmH	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	1.22
ABUW_RS07815		DUF441 domain-containing protein	1.22
ABUW_RS00480	serB	phosphoserine phosphatase SerB	1.21
ABUW_RS01050		MFS transporter	1.21
ABUW_RS09355		MFS transporter	1.21
ABUW_RS13550		MFS transporter	1.21
ABUW_RS08560		amino acid permease	1.21
ABUW_RS15775		ATP phosphoribosyltransferase	1.20
ABUW_RS17670	ftsW	putative lipid II flippase FtsW	1.20
ABUW_RS07885		glutamine--tRNA ligase/YqeY domain fusion protein	1.20
ABUW_RS03210		amino acid permease	1.20
ABUW_RS08120		MgtC/SapB family protein	1.19
ABUW_RS08715		nitroreductase family protein	1.19
ABUW_RS08645		hypothetical protein	1.19
ABUW_RS15270		5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	1.19
ABUW_RS08675	grxD	Grx4 family monothiol glutaredoxin	1.19
ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	1.19
ABUW_RS00070		tyrosine--tRNA ligase	1.19
ABUW_RS05385	rapA	RNA polymerase-associated protein RapA	1.18
ABUW_RS17325		HlyD family secretion protein	1.18
ABUW_RS17740		2,3-bisphosphoglycerate-independent phosphoglycerate mutase	1.17
ABUW_RS16995		TIGR03862 family flavoprotein	1.17
ABUW_RS14210		transketolase	1.17
ABUW_RS04165	rpmA	50S ribosomal protein L27	1.17
ABUW_RS17035		electron transfer flavoprotein-ubiquinone oxidoreductase	1.17
ABUW_RS17615		oxidative damage protection protein	1.17
ABUW_RS14920		Rieske 2Fe-2S domain-containing protein	1.17
ABUW_RS14880	hemJ	protoporphyrinogen oxidase HemJ	1.17
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.16
ABUW_RS01655		hypothetical protein	1.16
ABUW_RS13950	nth	endonuclease III	1.16
ABUW_RS00190	dapB	4-hydroxy-tetrahydrodipicolinate reductase	1.16
ABUW_RS15415	nuoE	NADH-quinone oxidoreductase subunit NuoE	1.16
ABUW_RS15840		carbon-nitrogen hydrolase family protein	1.16
ABUW_RS07070		GatB/YqeY domain-containing protein	1.15
ABUW_RS04015		MmcQ/YjbR family DNA-binding protein	1.15
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	1.15
ABUW_RS14910		oxidoreductase	1.15
ABUW_RS14075	lysS	lysine--tRNA ligase	1.15
ABUW_RS04095		valine--tRNA ligase	1.15

ABUW_RS12025		3-oxoadipyl-CoA thiolase	1.15
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	1.15
ABUW_RS00715		DUF1737 domain-containing protein	1.14
ABUW_RS07575	cyoB	cytochrome o ubiquinol oxidase subunit I	1.14
ABUW_RS14515		dihydrodipicolinate synthase family protein	1.14
ABUW_RS00730	murC	UDP-N-acetylmuramate--L-alanine ligase	1.14
ABUW_RS11215	queG	tRNA epoxyqueuosine(34) reductase QueG	1.14
ABUW_RS11085		DUF2058 domain-containing protein	1.14
ABUW_RS04315	trpS	tryptophan--tRNA ligase	1.13
ABUW_RS00055	erpA	iron-sulfur cluster insertion protein ErpA	1.13
ABUW_RS04190		tRNA (cytidine(34)-2'-O)-methyltransferase	1.13
ABUW_RS02040	rpsQ	30S ribosomal protein S17	1.13
ABUW_RS08400		hypothetical protein	1.13
ABUW_RS01610		TSUP family transporter	1.13
ABUW_RS13500		AMP-binding protein	1.13
ABUW_RS16115		MFS transporter	1.13
ABUW_RS13255		aspartate carbamoyltransferase	1.13
ABUW_RS18035		DUF2938 domain-containing protein	1.12
ABUW_RS13930		dioxygenase	1.12
ABUW_RS00290	purC	phosphoribosylaminoimidazolesuccinocarboxamide synthase	1.12
ABUW_RS08025		hypothetical protein	1.12
ABUW_RS17090		Hsp33 family molecular chaperone HsIO	1.12
ABUW_RS17905		DDE-type integrase/transposase/recombinase	1.11
ABUW_RS08960		right-handed parallel beta-helix repeat-containing protein	1.11
ABUW_RS02685		toprim domain-containing protein	1.11
ABUW_RS11490	cysE	serine O-acetyltransferase	1.11
ABUW_RS08750		DUF1449 family protein	1.11
ABUW_RS08935		MFS transporter	1.11
ABUW_RS14275		thiamine pyrophosphate-binding protein	1.11
ABUW_RS01530	gmk	guanylate kinase	1.11
ABUW_RS08965		carbohydrate porin	1.11
ABUW_RS07550	rpsR	30S ribosomal protein S18	1.11
ABUW_RS08575		SulP family inorganic anion transporter	1.11
ABUW_RS10885	pyrF	orotidine-5'-phosphate decarboxylase	1.10
ABUW_RS15410	nuoF	NADH-quinone oxidoreductase subunit NuoF	1.10
ABUW_RS15255		dCTP deaminase	1.10
ABUW_RS04010		polyprenyl synthetase family protein	1.10
ABUW_RS06090	queF	NADPH-dependent 7-cyano-7-deazaguanine reductase QueF	1.10
ABUW_RS14855	fusA	elongation factor G	1.10
ABUW_RS05970		16S rRNA (uracil(1498)-N(3))-methyltransferase	1.09
ABUW_RS07215		aldo/keto reductase	1.09
ABUW_RS17000		SAM-dependent methyltransferase	1.09
ABUW_RS00205	dkgB	2,5-didehydrogluconate reductase DkgB	1.09
ABUW_RS17910		heteromeric transposase endonuclease subunit TnsA	1.09
ABUW_RS02550		DUF4442 domain-containing protein	1.09
ABUW_RS07040		CvpA family protein	1.09
ABUW_RS07725	kdpB	potassium-transporting ATPase subunit KdpB	1.08
ABUW_RS05985		peptidase C39	1.08
ABUW_RS03225	typA	translational GTPase TypA	1.08
ABUW_RS11035		fructose-bisphosphate aldolase class II	1.07
ABUW_RS04185	cobA	uroporphyrinogen-III C-methyltransferase	1.07
ABUW_RS12770		EamA family transporter	1.07
ABUW_RS11010	rsmG	16S rRNA (guanine(527)-N(7))-methyltransferase RsmG	1.07

ABUW_RS00735		D-alanine--D-alanine ligase	1.07
ABUW_RS12790		ferredoxin family protein	1.07
ABUW_RS00805	guaB	IMP dehydrogenase	1.07
ABUW_RS07075	rpsU	30S ribosomal protein S21	1.07
ABUW_RS15125	scpB	SMC-Scp complex subunit ScpB	1.06
ABUW_RS18460		DUF1624 domain-containing protein	1.06
ABUW_RS15360		cold shock domain-containing protein	1.06
ABUW_RS14250		helix-turn-helix transcriptional regulator	1.06
ABUW_RS16880	hcaR	DNA-binding transcriptional regulator HcaR	1.06
ABUW_RS17855	arsC	arsenate reductase (glutaredoxin)	1.05
ABUW_RS00495		D-tyrosyl-tRNA(Tyr) deacylase	1.05
ABUW_RS04625		glycerate kinase	1.05
ABUW_RS16610		prolipoprotein diacylglycerol transferase	1.05
ABUW_RS15050		aspartate 1-decarboxylase	1.05
ABUW_RS07560	cyoE	protoheme IX farnesyltransferase	1.05
ABUW_RS10740		HIT domain-containing protein	1.05
ABUW_RS18140		MFS transporter	1.05
ABUW_RS11410		hypothetical protein	1.05
ABUW_RS07080	tsaD	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	1.05
ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	1.05
ABUW_RS07440		TetR/AcrR family transcriptional regulator	1.04
ABUW_RS14170		rhomboid family intramembrane serine protease	1.04
ABUW_RS03505	gatB	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	1.04
ABUW_RS17945	ppa	inorganic diphosphatase	1.04
ABUW_RS04500		co-chaperone GroES	1.04
ABUW_RS14705		YggS family pyridoxal phosphate-dependent enzyme	1.04
ABUW_RS00855		mechanosensitive ion channel family protein	1.04
ABUW_RS04680	dapF	diaminopimelate epimerase	1.04
ABUW_RS15180	ligA	NAD-dependent DNA ligase LigA	1.04
ABUW_RS15645	argJ	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ	1.03
ABUW_RS00635		ion channel protein Tsx	1.03
ABUW_RS12450		LysR family transcriptional regulator	1.03
ABUW_RS16390	der	ribosome biogenesis GTPase Der	1.03
ABUW_RS06005	sthA	Si-specific NAD(P)(+) transhydrogenase	1.03
ABUW_RS07060		D-glycerate dehydrogenase	1.03
ABUW_RS01800	glyQ	glycine--tRNA ligase subunit alpha	1.03
ABUW_RS08620		PTS transporter subunit EIIC	1.03
ABUW_RS13545	gudD	glucarate dehydratase	1.03
ABUW_RS00585		hypothetical protein	1.02
ABUW_RS15305		MFS transporter	1.02
ABUW_RS20530		hypothetical protein	1.02
ABUW_RS12935		hypothetical protein	1.02
ABUW_RS01265		RNA-binding transcriptional accessory protein	1.02
ABUW_RS15760		chorismate-binding protein	1.02
ABUW_RS12860		cysteine--tRNA ligase	1.02
ABUW_RS17900		TniB family NTP-binding protein	1.02
ABUW_RS04645		4-phosphoerythronate dehydrogenase	1.02
ABUW_RS07035		quinone-dependent dihydroorotate dehydrogenase	1.01
ABUW_RS02605	secF	protein translocase subunit SecF	1.01
ABUW_RS06030	map	type I methionyl aminopeptidase	1.01
ABUW_RS05490	purB	adenylosuccinate lyase	1.01
ABUW_RS06080	rodA	rod shape-determining protein RodA	1.01
ABUW_RS17375	lpxO	lipid A hydroxylase LpxO	1.01

ABUW_RS13340	alaS	alanine--tRNA ligase	1.01
ABUW_RS19000	mnme	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnME	1.01
ABUW_RS16405	hisS	histidine--tRNA ligase	1.01
ABUW_RS03830		hypothetical protein	1.01
ABUW_RS01365		glutamate--tRNA ligase	1.00
ABUW_RS17675		UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	1.00
ABUW_RS02055	rplE	50S ribosomal protein L5	1.00
ABUW_RS17480	rplL	50S ribosomal protein L7/L12	1.00
ABUW_RS02045	rplN	50S ribosomal protein L14	1.00
ABUW_RS17955		hypothetical protein	1.00
ABUW_RS04975	dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	1.00
ABUW_RS15640	nadA	quinolinate synthase NadA	1.00
ABUW_RS15085	acpP	acyl carrier protein	1.00
ABUW_RS03120		GNAT family N-acetyltransferase	1.00

Gene	Gene Name	Function	Δ gacS MEP vs WT MEP log2FC
ABUW_RS16060		response regulator	-10.15
sRNA99	sRNA99	sRNA99	-7.56
ABUW_RS10105	antA	anthranilate 1,2-dioxygenase large subunit	-6.80
sRNA29	sRNA29	sRNA29	-6.57
ABUW_RS07180		hypothetical protein	-5.81
ABUW_RS10110	antB	anthranilate 1,2-dioxygenase small subunit	-5.61
ABUW_RS10115	antC	anthranilate 1,2-dioxygenase electron transfer component AntC	-5.17
ABUW_RS12210		TetR/AcrR family transcriptional regulator	-4.88
ABUW_RS01495	pilA	pilin	-4.42
ABUW_RS00905		DUF485 domain-containing protein	-4.25
ABUW_RS07260	csuB	Csu fimbrial biogenesis protein CsuB	-3.99
sRNA97	sRNA97	sRNA97	-3.93
ABUW_RS13655		hypothetical protein	-3.76
ABUW_RS12745		DUF2147 domain-containing protein	-3.76
ABUW_RS00910		cation acetate symporter	-3.73
ABUW_RS14080		esterase	-3.62
ABUW_RS01250		acetyl-CoA hydrolase/transferase family protein	-3.61
ABUW_RS20235		hypothetical protein	-3.59
ABUW_RS11425		tautomerase family protein	-3.59
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	-3.58
ABUW_RS07255	csuA	Csu fimbrial biogenesis protein CsuA	-3.58
ABUW_RS12215		hypothetical protein	-3.51
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-3.51
ABUW_RS01215		DUF805 domain-containing protein	-3.48
ABUW_RS04595		hypothetical protein	-3.43
ABUW_RS00895		hypothetical protein	-3.41
ABUW_RS02525		hypothetical protein	-3.37
ABUW_RS19040		zeta toxin family protein	-3.28
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-3.23
ABUW_RS09700		hypothetical protein	-3.20
ABUW_RS12325	paaA	1,2-phenylacetyl-CoA epoxidase subunit A	-3.18
ABUW_RS13055		cold-shock protein	-3.17
ABUW_RS15500		hypothetical protein	-3.15
ABUW_RS11895		hypothetical protein	-3.12
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	-3.11
ABUW_RS00515		alpha/beta fold hydrolase	-3.10
ABUW_RS12975		hypothetical protein	-3.08
ABUW_RS01750		hypothetical protein	-3.06

ABUW_RS01445		type IV pilus secretin PilQ family protein	-3.04
ABUW_RS12220		hypothetical protein	-3.02
ABUW_RS17065		hypothetical protein	-3.00
ABUW_RS08725		cyd operon YbgE family protein	-2.98
ABUW_RS15280		hypothetical protein	-2.98
ABUW_RS11305		TetR/AcrR family transcriptional regulator	-2.97
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-2.94
ABUW_RS20535		hypothetical protein	-2.93
ABUW_RS12320	paaB	1,2-phenylacetyl-CoA epoxidase subunit B	-2.93
ABUW_RS00800		YkgJ family cysteine cluster protein	-2.91
ABUW_RS20230		hypothetical protein	-2.90
ABUW_RS15160	otsB	trehalose-phosphatase	-2.90
ABUW_RS14740		bacteriohemerythrin	-2.88
ABUW_RS20485		hypothetical protein	-2.86
ABUW_RS05820		DUF3015 family protein	-2.83
ABUW_RS12230		hypothetical protein	-2.82
ABUW_RS01615		hemerythrin domain-containing protein	-2.81
ABUW_RS15175	bfr	bacterioferritin	-2.79
ABUW_RS03355		Hpt domain-containing protein	-2.78
ABUW_RS05685		hypothetical protein	-2.75
ABUW_RS08535		hypothetical protein	-2.74
ABUW_RS03310		YegP family protein	-2.73
ABUW_RS14030		isocitrate lyase	-2.72
ABUW_RS07250	csuAB	Csu fimbrial major subunit CsuAB	-2.70
ABUW_RS12725		hypothetical protein	-2.68
ABUW_RS12310	paaJ	phenylacetate-CoA oxygenase subunit PaaJ	-2.64
ABUW_RS03350		methyl-accepting chemotaxis protein	-2.64
ABUW_RS04495		Ig-like domain repeat protein	-2.63
sRNA75	sRNA75	sRNA75	-2.63
ABUW_RS01440		pilus assembly protein PilP	-2.59
ABUW_RS05570		EAL domain-containing protein	-2.55
ABUW_RS15495		hypothetical protein	-2.54
ABUW_RS08740		cytochrome ubiquinol oxidase subunit I	-2.54
ABUW_RS15565		MFS transporter	-2.53
ABUW_RS09985		DUF4882 family protein	-2.53
ABUW_RS13775		hypothetical protein	-2.53
ABUW_RS03345		purine-binding chemotaxis protein CheW	-2.52
ABUW_RS12315	paaC	phenylacetate-CoA oxygenase subunit PaaC	-2.52
ABUW_RS16500		acetate kinase	-2.51
ABUW_RS00795		MBL fold metallo-hydrolase	-2.50
ABUW_RS10425		hypothetical protein	-2.50
ABUW_RS09545		hypothetical protein	-2.49
ABUW_RS11870		hypothetical protein	-2.48
ABUW_RS07520		alpha-E domain-containing protein	-2.48
ABUW_RS07265	csuC	Csu fimbrial biogenesis chaperone CsuC	-2.45
ABUW_RS08590		universal stress protein	-2.45
ABUW_RS11755		hypothetical protein	-2.45
ABUW_RS14715		PilT/PilU family type 4a pilus ATPase	-2.44
ABUW_RS17730		sigma-54-dependent Fis family transcriptional regulator	-2.40
ABUW_RS01435		type 4a pilus biogenesis protein PilO	-2.39
ABUW_RS07270	csuD	Csu fimbrial usher CsuD	-2.38
ABUW_RS12330	paaZ	phenylacetic acid degradation bifunctional protein PaaZ	-2.37
ABUW_RS17100		DnaJ domain-containing protein	-2.37
ABUW_RS06250		hypothetical protein	-2.37
ABUW_RS16505	pta	phosphate acetyltransferase	-2.36
ABUW_RS12900		DUF4882 family protein	-2.36

ABUW_RS01565		prepilin-type N-terminal cleavage/methylation domain-containing protein	-2.35
ABUW_RS14645	ggt	gamma-glutamyltransferase	-2.35
ABUW_RS08745		hypothetical protein	-2.34
ABUW_RS16720		hypothetical protein	-2.34
ABUW_RS10465		cell envelope integrity protein TolA	-2.32
ABUW_RS03180		VOC family protein	-2.32
ABUW_RS09270		antibiotic biosynthesis monooxygenase	-2.32
ABUW_RS07965		molecular chaperone	-2.31
ABUW_RS01100		hypothetical protein	-2.29
ABUW_RS10835		energy transducer TonB	-2.29
ABUW_RS03365		radical SAM protein	-2.29
ABUW_RS00380	hutU	urocanate hydratase	-2.28
ABUW_RS03605	hchA	protein deglycase HchA	-2.28
ABUW_RS13250		OmpA family protein	-2.28
ABUW_RS11775		cysteine ABC transporter substrate-binding protein	-2.27
ABUW_RS17420		hypothetical protein	-2.26
ABUW_RS15615	add	adenosine deaminase	-2.25
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	-2.25
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-2.24
ABUW_RS13005		hypothetical protein	-2.23
ABUW_RS09525		DEAD/DEAH box helicase family protein	-2.23
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-2.22
ABUW_RS07515		circularly permuted type 2 ATP-grasp protein	-2.22
ABUW_RS11780		transporter substrate-binding domain-containing protein	-2.21
ABUW_RS03360		hypothetical protein	-2.20
sRNA61	sRNA61	sRNA61	-2.19
ABUW_RS01570		prepilin-type N-terminal cleavage/methylation domain-containing protein	-2.18
ABUW_RS02595	radC	DNA repair protein RadC	-2.18
ABUW_RS02860		GPO family capsid scaffolding protein	-2.17
ABUW_RS00660		HPF/RaiA family ribosome-associated protein	-2.17
ABUW_RS04590		hypothetical protein	-2.16
ABUW_RS18520		hypothetical protein	-2.16
ABUW_RS15335		hypothetical protein	-2.16
ABUW_RS11615		hypothetical protein	-2.15
ABUW_RS11365		LLM class flavin-dependent oxidoreductase	-2.14
ABUW_RS15330		mechanosensitive ion channel	-2.14
ABUW_RS07500		hypothetical protein	-2.13
ABUW_RS05480		BapA prefix-like domain-containing protein	-2.12
ABUW_RS14710		type IV pilus twitching motility protein PilT	-2.12
ABUW_RS13380		hypothetical protein	-2.12
ABUW_RS17440		outer membrane beta-barrel protein	-2.11
ABUW_RS05825		DUF4105 domain-containing protein	-2.10
ABUW_RS09550		GNAT family N-acetyltransferase	-2.10
ABUW_RS01430		PilN domain-containing protein	-2.10
ABUW_RS10010		hypothetical protein	-2.09
ABUW_RS06320		hypothetical protein	-2.09
ABUW_RS16790		hypothetical protein	-2.08
ABUW_RS01560		VWA domain-containing protein	-2.08
ABUW_RS05540		LysR family transcriptional regulator	-2.06
ABUW_RS02780		phage major tail tube protein	-2.06
ABUW_RS13040		hypothetical protein	-2.06
ABUW_RS02785		phage tail sheath protein	-2.05
ABUW_RS20145		hypothetical protein	-2.05
ABUW_RS13575		hypothetical protein	-2.05
ABUW_RS09275		hydrolase	-2.04

ABUW_RS18015		DUF2726 domain-containing protein	-2.04
ABUW_RS04355		metalloprotease	-2.03
ABUW_RS07980		glutathione S-transferase family protein	-2.03
ABUW_RS04365		universal stress protein	-2.02
ABUW_RS05215		hypothetical protein	-2.02
ABUW_RS03490		DUF1176 domain-containing protein	-2.01
ABUW_RS03585		PaaX family transcriptional regulator	-2.01
ABUW_RS02625		LemA family protein	-2.00
ABUW_RS03785		hypothetical protein	-2.00
ABUW_RS19580		hypothetical protein	-1.99
ABUW_RS04995	cysW	sulfate ABC transporter permease subunit CysW	-1.98
ABUW_RS07415		aspartate/glutamate racemase family protein	-1.98
ABUW_RS11270		hypothetical protein	-1.98
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.98
ABUW_RS00405		DUF885 domain-containing protein	-1.98
ABUW_RS10580		HAD family hydrolase	-1.98
ABUW_RS16255	acnA	aconitate hydratase AcnA	-1.98
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	-1.96
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	-1.96
ABUW_RS07410		GNAT family N-acetyltransferase	-1.96
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.95
ABUW_RS11370		methionine transporter	-1.94
ABUW_RS19460		hypothetical protein	-1.94
ABUW_RS17150		polyphosphate--AMP phosphotransferase	-1.94
ABUW_RS06315		hypothetical protein	-1.92
ABUW_RS13450		GMC family oxidoreductase	-1.92
ABUW_RS05000	cysT	sulfate ABC transporter permease subunit CysT	-1.92
ABUW_RS05235		hypothetical protein	-1.91
ABUW_RS11575	tauD	taurine dioxygenase	-1.91
ABUW_RS02840		tail protein X	-1.91
ABUW_RS09290		cation:proton antiporter	-1.91
ABUW_RS09960		hypothetical protein	-1.90
ABUW_RS15440		hypothetical protein	-1.90
ABUW_RS13045		NAD(P)-binding domain-containing protein	-1.89
ABUW_RS19065		hypothetical protein	-1.89
ABUW_RS07280		hypothetical protein	-1.88
ABUW_RS05910		hypothetical protein	-1.88
ABUW_RS01425		pilus assembly protein PilM	-1.88
ABUW_RS09185		alpha/beta hydrolase	-1.87
ABUW_RS05340	cas3f	type I-F CRISPR-associated helicase Cas3	-1.87
ABUW_RS09295		hypothetical protein	-1.87
ABUW_RS12185		catalase family peroxidase	-1.87
ABUW_RS12520	tssE	type VI secretion system baseplate subunit TssE	-1.86
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-1.86
ABUW_RS02200		HAD-IB family hydrolase	-1.86
ABUW_RS05230		hypothetical protein	-1.85
ABUW_RS05005		alpha/beta hydrolase	-1.85
ABUW_RS19100		hypothetical protein	-1.83
ABUW_RS13685		type VI secretion system tip protein VgrG	-1.82
ABUW_RS17275		type II secretion system F family protein	-1.82
ABUW_RS07170		NirD/YgiW/YdeI family stress tolerance protein	-1.82
ABUW_RS07310		DMT family transporter	-1.81
ABUW_RS00415	murl	glutamate racemase	-1.81
ABUW_RS02845		head completion/stabilization protein	-1.81
ABUW_RS11785		amino acid ABC transporter ATP-binding protein	-1.81
ABUW_RS09350		DUF2314 domain-containing protein	-1.80
ABUW_RS08700		hypothetical protein	-1.80

ABUW_RS07985		SDR family NAD(P)-dependent oxidoreductase	-1.80
ABUW_RS13750		hypothetical protein	-1.80
ABUW_RS09520		HD domain-containing protein	-1.79
ABUW_RS15055		GDYXXLY domain-containing protein	-1.79
ABUW_RS18115		LysM peptidoglycan-binding domain-containing protein	-1.78
ABUW_RS05875		M1 family metalloproteinase	-1.77
ABUW_RS19085		H-NS histone family protein	-1.76
ABUW_RS10815		Zn-dependent oligopeptidase	-1.75
ABUW_RS07990		SDR family NAD(P)-dependent oxidoreductase	-1.75
ABUW_RS05350	csy2	type I-F CRISPR-associated protein Csy2	-1.75
ABUW_RS13815		hypothetical protein	-1.74
ABUW_RS02715		BRCT domain-containing protein	-1.74
ABUW_RS10770		nucleoside-diphosphate sugar epimerase	-1.73
ABUW_RS03380		entericidin A/B family lipoprotein	-1.72
ABUW_RS06560	yegQ	tRNA 5-hydroxyuridine modification protein YegQ	-1.72
ABUW_RS00600		SH3 domain-containing protein	-1.71
ABUW_RS01540		GspH/FimT family pseudopilin	-1.71
ABUW_RS17380		hypothetical protein	-1.71
ABUW_RS01480		LemA family protein	-1.69
ABUW_RS05795	basI	acinetobactin biosynthesis phosphopantetheinyl transferase BasI	-1.69
ABUW_RS19105		hypothetical protein	-1.68
ABUW_RS02735		ogr/Delta-like zinc finger family protein	-1.67
ABUW_RS00370	hutC	histidine utilization repressor	-1.67
ABUW_RS18120	dprA	DNA-processing protein DprA	-1.67
ABUW_RS05345	csy1	type I-F CRISPR-associated protein Csy1	-1.66
ABUW_RS10820		ABC transporter substrate-binding protein	-1.66
ABUW_RS05225		glycosyltransferase family 2 protein	-1.66
ABUW_RS01665	yccS	TIGR01666 family membrane protein	-1.65
ABUW_RS04910		deoxyguanosinetriphosphate triphosphohydrolase	-1.65
ABUW_RS18490		SDR family NAD(P)-dependent oxidoreductase	-1.64
ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	-1.64
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-1.64
ABUW_RS09995		hypothetical protein	-1.64
ABUW_RS12305	paak	phenylacetate-CoA oxygenase/reductase subunit Paak	-1.64
ABUW_RS00385	hutH	histidine ammonia-lyase	-1.63
ABUW_RS12880		hypothetical protein	-1.63
ABUW_RS13105		hypothetical protein	-1.63
ABUW_RS05360	cas6f	type I-F CRISPR-associated endoribonuclease Cas6/Csy4	-1.62
ABUW_RS05205		hypothetical protein	-1.62
ABUW_RS13755		RHS repeat-associated core domain-containing protein	-1.62
ABUW_RS15505		hypothetical protein	-1.62
ABUW_RS18950		hypothetical protein	-1.61
ABUW_RS15550		amidohydrolase	-1.61
ABUW_RS19070		hypothetical protein	-1.60
ABUW_RS11375		MetQ/NlpA family ABC transporter substrate-binding protein	-1.60
ABUW_RS12760		lauroyl acyltransferase	-1.59
ABUW_RS19430		hypothetical protein	-1.59
ABUW_RS04980	carO	ornithine uptake porin CarO type 3	-1.59
ABUW_RS11380		ATP-binding cassette domain-containing protein	-1.58
ABUW_RS05485		DUF2238 domain-containing protein	-1.58
ABUW_RS07960		spore coat protein U domain-containing protein	-1.58
ABUW_RS03975		hypothetical protein	-1.57
ABUW_RS02875		HAMP domain-containing histidine kinase	-1.57
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.57
ABUW_RS03850		hypothetical protein	-1.57
ABUW_RS18765		sulfonate ABC transporter substrate-binding protein	-1.57

ABUW_RS19705		hypothetical protein	-1.57
ABUW_RS09975		fimbrial biogenesis outer membrane usher protein	-1.56
ABUW_RS16440		phosphatase PAP2 family protein	-1.56
ABUW_RS12255		ATP-dependent helicase	-1.55
ABUW_RS00410		HAD family hydrolase	-1.54
sRNA27	sRNA27	sRNA27	-1.54
ABUW_RS03500		DJ-1/Pfpl family protein	-1.54
ABUW_RS11860		iron-containing redox enzyme family protein	-1.54
ABUW_RS05355	csy3	type I-F CRISPR-associated protein Csy3	-1.54
ABUW_RS11360		SfnB family sulfur acquisition oxidoreductase	-1.53
ABUW_RS19585		hypothetical protein	-1.53
ABUW_RS05220		hypothetical protein	-1.53
ABUW_RS06585		MgtC/SapB family protein	-1.53
ABUW_RS02850		terminase	-1.53
ABUW_RS01345		hypothetical protein	-1.53
ABUW_RS12430		winged helix-turn-helix domain-containing protein	-1.53
ABUW_RS13280		CinA family protein	-1.52
ABUW_RS02520		dihydrolipoyl dehydrogenase	-1.52
ABUW_RS01485		TPM domain-containing protein	-1.52
ABUW_RS15355		excalibur calcium-binding domain-containing protein	-1.51
ABUW_RS13680		RHS repeat protein	-1.51
ABUW_RS04630		FdhF/YdeP family oxidoreductase	-1.51
ABUW_RS13760		RHS repeat protein	-1.51
ABUW_RS19080		thermonuclease family protein	-1.51
ABUW_RS01505	bfr	bacterioferritin	-1.51
ABUW_RS13650		ATP-binding protein	-1.50
ABUW_RS12805		universal stress protein	-1.49
ABUW_RS11910		hypothetical protein	-1.49
ABUW_RS03905		hypothetical protein	-1.49
ABUW_RS03090		peroxiredoxin	-1.48
ABUW_RS01550		PilW family protein	-1.48
ABUW_RS11945		acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha	-1.47
ABUW_RS08440		PAS domain-containing protein	-1.47
ABUW_RS18955		glutathionylspermidine synthase family protein	-1.47
ABUW_RS12630		hypothetical protein	-1.47
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	-1.47
ABUW_RS11920		AMP-binding protein	-1.46
ABUW_RS13585		hypothetical protein	-1.46
ABUW_RS11760		cysteine desulfurase	-1.46
ABUW_RS19045		DUF1173 domain-containing protein	-1.46
ABUW_RS01280		aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme	-1.45
ABUW_RS18560	lIdR	transcriptional regulator LldR	-1.45
ABUW_RS08530		hypothetical protein	-1.45
ABUW_RS07135		CoA-acylating methylmalonate-semialdehyde dehydrogenase	-1.45
ABUW_RS03330		hypothetical protein	-1.45
ABUW_RS19180		hypothetical protein	-1.44
ABUW_RS17270	pilB	type IV-A pilus assembly ATPase PilB	-1.44
ABUW_RS04020		SPFH/Band 7/PHB domain protein	-1.44
ABUW_RS00285		hypothetical protein	-1.44
ABUW_RS18625		hypothetical protein	-1.43
ABUW_RS02630		hypothetical protein	-1.43
ABUW_RS10840		MotA/TolQ/ExbB proton channel family protein	-1.43
ABUW_RS04515		MBL fold metallo-hydrolase	-1.43
ABUW_RS00485		hypothetical protein	-1.43
ABUW_RS15060		DUF2157 domain-containing protein	-1.43
ABUW_RS14630		hypothetical protein	-1.42

ABUW_RS16715		HdeD family acid-resistance protein	-1.42
ABUW_RS16890		glutathione S-transferase family protein	-1.42
ABUW_RS09335		SMI1/KNR4 family protein	-1.42
ABUW_RS14870		EcsC family protein	-1.41
ABUW_RS08095		universal stress protein	-1.41
ABUW_RS16305	ilvN	acetolactate synthase small subunit	-1.41
ABUW_RS18820		NAD(P)H-dependent oxidoreductase	-1.41
ABUW_RS03920		Arc family DNA-binding protein	-1.41
ABUW_RS07400		chalcone isomerase family protein	-1.40
ABUW_RS02445		DUF2147 domain-containing protein	-1.40
ABUW_RS03970		hypothetical protein	-1.40
ABUW_RS08695		hypothetical protein	-1.39
ABUW_RS12830		TolC family protein	-1.39
ABUW_RS09280		LysR family transcriptional regulator	-1.39
ABUW_RS10005		hypothetical protein	-1.39
ABUW_RS18630		oligosaccharide flippase family protein	-1.39
ABUW_RS05420		SIMPL domain-containing protein	-1.38
ABUW_RS11130		GrpB family protein	-1.38
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-1.38
ABUW_RS05525		hypothetical protein	-1.38
ABUW_RS16475		NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	-1.38
ABUW_RS06730		hypothetical protein	-1.38
ABUW_RS14685		VOC family protein	-1.37
ABUW_RS20115		hypothetical protein	-1.37
ABUW_RS19545		hypothetical protein	-1.36
ABUW_RS18475		ribonuclease E inhibitor RraB	-1.36
ABUW_RS06295		DUF2280 domain-containing protein	-1.36
ABUW_RS07970		fimbrial biogenesis outer membrane usher protein	-1.36
ABUW_RS19110		DUF2786 domain-containing protein	-1.36
ABUW_RS11235		type 1 fimbrial protein	-1.36
ABUW_RS11405		hypothetical protein	-1.36
ABUW_RS00685		alpha/beta hydrolase	-1.36
ABUW_RS01840		hypothetical protein	-1.36
ABUW_RS16895		YafY family transcriptional regulator	-1.36
ABUW_RS07800		membrane protein	-1.35
ABUW_RS18255		OsmC family protein	-1.35
ABUW_RS10015		phospholipase D family protein	-1.35
ABUW_RS18945		TerC family protein	-1.34
ABUW_RS01160	aqpZ	aquaporin Z	-1.34
ABUW_RS19575		hypothetical protein	-1.34
ABUW_RS15790	raiA	ribosome-associated translation inhibitor RaiA	-1.34
ABUW_RS19090		hypothetical protein	-1.34
ABUW_RS13125		GFA family protein	-1.34
ABUW_RS13835		YraN family protein	-1.33
ABUW_RS17105		MerR family transcriptional regulator	-1.33
ABUW_RS03340		response regulator	-1.33
ABUW_RS08685		CBS domain-containing protein	-1.33
ABUW_RS06280		hypothetical protein	-1.33
ABUW_RS08585		PQQ-dependent sugar dehydrogenase	-1.32
ABUW_RS08045		hypothetical protein	-1.32
ABUW_RS11160		OsmC family protein	-1.32
ABUW_RS03285		SRPBCC family protein	-1.32
ABUW_RS11725	yfcF	glutathione transferase	-1.31
ABUW_RS00250		HIT family protein	-1.31
ABUW_RS16315		DUF4124 domain-containing protein	-1.31
ABUW_RS10845		biopolymer transporter ExbD	-1.30

ABUW_RS13220		hypothetical protein	-1.29
ABUW_RS14690		OsmC family protein	-1.29
ABUW_RS08200		iron-containing alcohol dehydrogenase	-1.29
ABUW_RS17175		FAD-dependent monooxygenase	-1.29
ABUW_RS15165		trehalose-6-phosphate synthase	-1.29
ABUW_RS04990		sulfate ABC transporter ATP-binding protein	-1.28
ABUW_RS10785		3'(2'),5'-bisphosphate nucleotidase CysQ	-1.28
ABUW_RS16210		hypothetical protein	-1.28
ABUW_RS07975		spore coat protein U domain-containing protein	-1.28
ABUW_RS12685		hypothetical protein	-1.28
ABUW_RS17455		DUF4442 domain-containing protein	-1.28
ABUW_RS18565	lldP	L-lactate permease	-1.27
ABUW_RS18620		oligosaccharide repeat unit polymerase	-1.27
ABUW_RS13200		KTSC domain-containing protein	-1.27
ABUW_RS07620		hypothetical protein	-1.26
sRNA76	sRNA76	sRNA76	-1.26
ABUW_RS01555		hypothetical protein	-1.26
ABUW_RS05790	basH	acinetobactin biosynthesis thioesterase BasH	-1.26
ABUW_RS00645	uraH	hydroxyisourate hydrolase	-1.26
ABUW_RS17640		hypothetical protein	-1.25
ABUW_RS04635	fdhD	formate dehydrogenase accessory sulfurtransferase FdhD	-1.25
ABUW_RS19620		DIP1984 family protein	-1.25
ABUW_RS01765		hypothetical protein	-1.25
ABUW_RS19530	trbC	type-F conjugative transfer system pilin assembly protein TrbC	-1.24
ABUW_RS01020		hydrolase	-1.24
ABUW_RS00375		HutD family protein	-1.24
ABUW_RS07125		LysR family transcriptional regulator	-1.24
ABUW_RS10375		GGDEF domain-containing protein	-1.23
ABUW_RS03910		hypothetical protein	-1.23
ABUW_RS04785		DNA internalization-related competence protein ComEC/Rec2	-1.23
ABUW_RS13070		hypothetical protein	-1.23
ABUW_RS04485		NAD(+)/NADH kinase	-1.23
ABUW_RS17190		AAA family ATPase	-1.23
ABUW_RS11265		DMT family transporter	-1.23
ABUW_RS12635		sel1 repeat family protein	-1.23
ABUW_RS09330		DUF2247 family protein	-1.23
ABUW_RS07325		MCE family protein	-1.22
ABUW_RS10825		ABC transporter substrate-binding protein	-1.22
ABUW_RS10860		malate synthase G	-1.22
ABUW_RS16160		copper resistance protein CopC	-1.22
ABUW_RS08390		hypothetical protein	-1.21
ABUW_RS03485		DUF4850 domain-containing protein	-1.21
ABUW_RS04895		amidohydrolase	-1.20
ABUW_RS04540		lytic transglycosylase domain-containing protein	-1.20
ABUW_RS05195		nitronate monooxygenase	-1.20
ABUW_RS16285		TetR/AcrR family transcriptional regulator	-1.20
ABUW_RS08090		ABC-F family ATP-binding cassette domain-containing protein	-1.20
ABUW_RS17435		DUF1311 domain-containing protein	-1.19
ABUW_RS19075		hypothetical protein	-1.19
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-1.19
ABUW_RS10485		YARHG domain-containing protein	-1.18
ABUW_RS09260		sorbose dehydrogenase family protein	-1.18
ABUW_RS14240		galactose mutarotase	-1.18
ABUW_RS16080	rfsS	ribosome silencing factor	-1.17
ABUW_RS05575		hypothetical protein	-1.16
ABUW_RS07130		aspartate aminotransferase family protein	-1.16
ABUW_RS10805		ABC transporter permease	-1.16

ABUW_RS14885		pirin family protein	-1.16
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.16
ABUW_RS18770	ssuD	FMNH2-dependent alkanesulfonate monooxygenase	-1.16
ABUW_RS13115		hypothetical protein	-1.15
ABUW_RS07995		chorismate mutase	-1.15
ABUW_RS01060		DMT family transporter	-1.15
ABUW_RS00365		acyltransferase	-1.15
ABUW_RS18250		glutathione S-transferase	-1.15
ABUW_RS19060		hypothetical protein	-1.14
ABUW_RS00915		hypothetical protein	-1.14
ABUW_RS07405		nuclear transport factor 2 family protein	-1.14
ABUW_RS15680		HAD family hydrolase	-1.14
ABUW_RS11455		glutathione peroxidase	-1.13
ABUW_RS01760		hypothetical protein	-1.13
ABUW_RS16280		hypothetical protein	-1.13
ABUW_RS09265		hypothetical protein	-1.13
ABUW_RS01370		hypothetical protein	-1.13
ABUW_RS18585		UDP-glucose/GDP-mannose dehydrogenase family protein	-1.12
ABUW_RS18580	pgi	glucose-6-phosphate isomerase	-1.12
ABUW_RS07425		sorbose dehydrogenase family protein	-1.12
ABUW_RS15530		LysR family transcriptional regulator	-1.12
ABUW_RS18610		sugar transferase	-1.10
ABUW_RS05995		acyl-CoA dehydrogenase	-1.10
ABUW_RS18230		Dyp-type peroxidase	-1.10
ABUW_RS18740		YciK family oxidoreductase	-1.10
ABUW_RS01490		TPM domain-containing protein	-1.09
ABUW_RS12515	tssF	type VI secretion system baseplate subunit TssF	-1.09
ABUW_RS12425		GNAT family N-acetyltransferase	-1.09
ABUW_RS08315		molybdopterin-dependent oxidoreductase	-1.09
ABUW_RS12535	tssB	type VI secretion system contractile sheath small subunit	-1.08
ABUW_RS18550	dld	D-lactate dehydrogenase	-1.08
ABUW_RS19560		transglycosylase SLT domain-containing protein	-1.08
ABUW_RS04215		hypothetical protein	-1.08
ABUW_RS12180		cytochrome b	-1.07
ABUW_RS10880		lysine exporter LysO family protein	-1.07
ABUW_RS12740		exo-alpha-sialidase	-1.07
ABUW_RS02730		TraR/DksA C4-type zinc finger protein	-1.07
ABUW_RS04685		alpha/beta fold hydrolase	-1.06
ABUW_RS16025		ComEA family DNA-binding protein	-1.06
ABUW_RS17280		prepilin peptidase	-1.06
ABUW_RS10800		ABC transporter ATP-binding protein	-1.06
ABUW_RS18470		nuclear transport factor 2 family protein	-1.06
ABUW_RS08190	plc1	phospholipase C, phosphocholine-specific	-1.05
ABUW_RS15970		glutathione S-transferase N-terminal domain-containing protein	-1.05
ABUW_RS18615		glycosyltransferase family 4 protein	-1.05
ABUW_RS04740		ABC transporter permease	-1.05
ABUW_RS02205		hypothetical protein	-1.04
ABUW_RS01125		GNAT family N-acetyltransferase	-1.04
ABUW_RS03335	pilG	twitching motility response regulator PilG	-1.04
ABUW_RS03150		CoA transferase	-1.03
ABUW_RS10810		ABC transporter permease	-1.03
ABUW_RS02390		acyl-CoA dehydrogenase family protein	-1.03
ABUW_RS13820	nudC	NAD(+) diphosphatase	-1.03
ABUW_RS12715		serine hydrolase	-1.03
ABUW_RS17815		hypothetical protein	-1.03
ABUW_RS03085		MBL fold metallo-hydrolase	-1.03
ABUW_RS09695		hypothetical protein	-1.03

ABUW_RS05310		insulinase family protein	-1.03
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	-1.03
ABUW_RS08690		DUF2750 domain-containing protein	-1.02
ABUW_RS00610		esterase	-1.02
ABUW_RS07330		membrane integrity-associated transporter subunit PqiC	-1.02
ABUW_RS17655	cpdA	3',5'-cyclic-AMP phosphodiesterase	-1.02
ABUW_RS17060		tRNA-binding protein	-1.02
ABUW_RS10255		ABC transporter substrate-binding protein	-1.02
ABUW_RS00665		ankyrin repeat domain-containing protein	-1.01
ABUW_RS12335		L-serine ammonia-lyase	-1.01
ABUW_RS09690		zonular occludens toxin	-1.01
ABUW_RS00395		imidazolonepropionase	-1.01
ABUW_RS02855		phage major capsid protein, P2 family	-1.01
ABUW_RS19480		type-F conjugative transfer system secretin TraK	-1.01
ABUW_RS02270	ybeY	rRNA maturation RNase YbeY	-1.01
ABUW_RS12625		hypothetical protein	-1.00
ABUW_RS09560		LysR family transcriptional regulator	-1.00
sRNA65	sRNA65	sRNA65	-1.00

Table A10. Overview of genes that are differentially expressed as identified through RNA-seq analysis in *ΔgacS* LSP. Red color indicated as upregulated and blue color indicated as downregulated.

Gene	Gene Name	Function	<i>ΔgacS</i> LSP vs WT LSP log2FC
ABUW_RS19240		hypothetical protein	7.66
ABUW_RS11925		TetR/AcrR family transcriptional regulator	7.29
ABUW_RS19235		hypothetical protein	7.09
ABUW_RS15030		tRNA-Gln	6.76
ABUW_RS19340		hypothetical protein	6.70
sRNA84	sRNA84	sRNA84	6.56
ABUW_RS19905	ssrS	6S RNA	6.53
ABUW_RS19125		hypothetical protein	6.36
ABUW_RS07105		tRNA-Leu	6.15
ABUW_RS08150	acel	chlorhexidine efflux PACE transporter Acel	6.00
ABUW_RS12755		TetR/AcrR family transcriptional regulator	5.98
ABUW_RS14535		hypothetical protein	5.93
ABUW_RS03965		hypothetical protein	5.92
ABUW_RS19415		IS30-like element ISAbA125 family transposase	5.88
ABUW_RS10215		hypothetical protein	5.87
ABUW_RS14335		non-heme iron oxygenase ferredoxin subunit	5.73
ABUW_RS03795		DUF2280 domain-containing protein	5.70
ABUW_RS06940		hypothetical protein	5.61
ABUW_RS01355		tRNA-Glu	5.59
ABUW_RS19355		hypothetical protein	5.52
sRNA53	sRNA53	sRNA53	5.45
sRNA81	sRNA81	sRNA81	5.44
ABUW_RS19130		SAM-dependent DNA methyltransferase	5.36
ABUW_RS07110		tRNA-Trp	5.35
sRNA4	sRNA4	sRNA4	5.18
ABUW_RS03860		hypothetical protein	5.14
ABUW_RS01090		carboxymuconolactone decarboxylase family protein	4.97
ABUW_RS13905		hypothetical protein	4.96
ABUW_RS19345		molecular chaperone DnaJ	4.91
sRNA1	sRNA1	sRNA1	4.87
sRNA24	sRNA24	sRNA24	4.87
ABUW_RS09040		amidase	4.85
ABUW_RS14330		hypothetical protein	4.83

sRNA77	sRNA77	sRNA77	4.80
ABUW_RS19020	rpmH	50S ribosomal protein L34	4.76
ABUW_RS13565		AraC family transcriptional regulator	4.73
ABUW_RS09655		hypothetical protein	4.68
ABUW_RS09310		TetR/AcrR family transcriptional regulator	4.67
ABUW_RS01305		TolC family protein	4.58
ABUW_RS12415		hypothetical protein	4.56
ABUW_RS19135		hypothetical protein	4.52
ABUW_RS11310		1-acyl-sn-glycerol-3-phosphate acyltransferase	4.52
ABUW_RS12675		hypothetical protein	4.48
ABUW_RS10120		AraC family transcriptional regulator	4.46
ABUW_RS11920		AMP-binding protein	4.46
ABUW_RS15025		tRNA-Gln	4.40
ABUW_RS13090		tRNA-Met	4.35
ABUW_RS09030		MFS transporter	4.35
ABUW_RS19360		hypothetical protein	4.32
ABUW_RS16860		RNA pyrophosphohydrolase	4.26
ABUW_RS19370		hypothetical protein	4.24
ABUW_RS14325		aromatic ring-hydroxylating dioxygenase subunit alpha	4.21
ABUW_RS01870		DEAD/DEAH box helicase	4.20
ABUW_RS01045		tRNA-Thr	4.08
sRNA92	sRNA92	sRNA92	4.08
ABUW_RS04035		1-acyl-sn-glycerol-3-phosphate acyltransferase	4.04
ABUW_RS02690		hypothetical protein	4.00
ABUW_RS19015	rnpA	ribonuclease P protein component	3.97
ABUW_RS20075		transposase domain-containing protein	3.95
ABUW_RS10100		LysR family transcriptional regulator	3.90
ABUW_RS01775		EamA family transporter	3.88
ABUW_RS04395		DOMON-like domain-containing protein	3.87
ABUW_RS13085		transposase	3.86
ABUW_RS02145		membrane protein	3.82
ABUW_RS01250		acetyl-CoA hydrolase/transferase family protein	3.82
ABUW_RS04555		transglycosylase SLT domain-containing protein	3.81
ABUW_RS16810	infA	translation initiation factor IF-1	3.79
sRNA60	sRNA60	sRNA60	3.77
ABUW_RS19350		hypothetical protein	3.74
ABUW_RS11305		TetR/AcrR family transcriptional regulator	3.65
sRNA46	sRNA46	sRNA46	3.64
ABUW_RS00985		AziC family ABC transporter permease	3.62
ABUW_RS20015		Mu transposase C-terminal domain-containing protein	3.60
ABUW_RS10480		GFA family protein	3.59
ABUW_RS09050		hypothetical protein	3.55
ABUW_RS02810		phage baseplate assembly protein V	3.52
ABUW_RS01425		pilus assembly protein PilM	3.48
ABUW_RS04400	yhbY	ribosome assembly RNA-binding protein YhbY	3.43
ABUW_RS17250		tRNA-Met	3.43
ABUW_RS15710	tsaB	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB	3.42
ABUW_RS11735		LysR family transcriptional regulator	3.38
ABUW_RS09055		nuclear transport factor 2 family protein	3.36
ABUW_RS11530		metalloregulator ArsR/SmtB family transcription factor	3.34
sRNA37	sRNA37	sRNA37	3.32
ABUW_RS13265		hypothetical protein	3.31
ABUW_RS19030		replication initiation protein	3.30
ABUW_RS19220		hypothetical protein	3.30
ABUW_RS20270		hypothetical protein	3.29
ABUW_RS14320		SDR family oxidoreductase	3.28

ABUW_RS17255		tRNA-Leu	3.28
ABUW_RS18015		DUF2726 domain-containing protein	3.20
ABUW_RS17630		EamA family transporter	3.19
ABUW_RS06595		NirD/YgiW/YdeI family stress tolerance protein	3.16
ABUW_RS11295		tRNA-Ile	3.14
ABUW_RS12410	soxR	redox-sensitive transcriptional activator SoxR	3.13
ABUW_RS19660	rnpB	RNase P RNA component class A	3.13
sRNA88	sRNA88	sRNA88	3.13
ABUW_RS12095		putative 2-aminoethylphosphonate ABC transporter substrate-binding protein	3.11
ABUW_RS17915		ATP-binding protein	3.11
ABUW_RS08100		hypothetical protein	3.10
ABUW_RS01310		efflux RND transporter periplasmic adaptor subunit	3.08
ABUW_RS17245		tRNA-Met	3.05
ABUW_RS01445		type IV pilus secretin PilQ family protein	3.02
ABUW_RS14445		homocysteine S-methyltransferase family protein	3.01
ABUW_RS11240		fimbria/pilus periplasmic chaperone	3.00
ABUW_RS10210		hypothetical protein	2.99
ABUW_RS19140		ParA family protein	2.98
ABUW_RS12385		4-hydroxyproline epimerase	2.97
ABUW_RS15525		DUF1852 domain-containing protein	2.95
ABUW_RS01600		lipase secretion chaperone	2.95
ABUW_RS12960		DUF2280 domain-containing protein	2.94
ABUW_RS04625		glycerate kinase	2.90
ABUW_RS19925		single-stranded DNA-binding protein	2.89
sRNA49	sRNA49	sRNA49	2.88
ABUW_RS06555		YfhL family 4Fe-4S dicluster ferredoxin	2.88
ABUW_RS15200		sulfite exporter TauE/SafE family protein	2.88
ABUW_RS19120		hypothetical protein	2.86
ABUW_RS08010		hypothetical protein	2.86
ABUW_RS12720		GNAT family N-acetyltransferase	2.86
ABUW_RS14110		SPOR domain-containing protein	2.85
ABUW_RS11325		hypothetical protein	2.85
sRNA15	sRNA15	sRNA15	2.84
ABUW_RS02815		phage virion morphogenesis protein	2.83
ABUW_RS04560	greB	transcription elongation factor GreB	2.83
ABUW_RS03330		hypothetical protein	2.81
ABUW_RS02370		TetR family transcriptional regulator	2.81
ABUW_RS06110		hypothetical protein	2.79
ABUW_RS04445		tRNA-Cys	2.79
ABUW_RS11275		cytosine permease	2.78
ABUW_RS05290		YbfB/YjiJ family MFS transporter	2.78
ABUW_RS16620		hypothetical protein	2.76
ABUW_RS13150	benA	benzoate 1,2-dioxygenase large subunit	2.76
ABUW_RS15355		excalibur calcium-binding domain-containing protein	2.75
ABUW_RS17240	rimP	ribosome maturation factor RimP	2.75
ABUW_RS07670		aliphatic sulfonate ABC transporter substrate-binding protein	2.75
ABUW_RS11765		LysE family translocator	2.75
ABUW_RS07835		type II toxin-antitoxin system RelB/DinJ family antitoxin	2.73
ABUW_RS09060		aromatic ring-hydroxylating dioxygenase subunit alpha	2.72
ABUW_RS15705		class I SAM-dependent methyltransferase	2.72
ABUW_RS13155	benB	benzoate 1,2-dioxygenase small subunit	2.71
ABUW_RS14080		esterase	2.71
ABUW_RS19010	yidD	membrane protein insertion efficiency factor YidD	2.71
ABUW_RS17855	arsC	arsenate reductase (glutaredoxin)	2.71
ABUW_RS09500		TolC family protein	2.70
ABUW_RS18200		ATP synthase subunit I	2.68

ABUW_RS12970		hypothetical protein	2.67
ABUW_RS11280		PACE efflux transporter	2.67
ABUW_RS03460		hypothetical protein	2.66
sRNA61	sRNA61	sRNA61	2.65
ABUW_RS12365		AraC family transcriptional regulator	2.65
ABUW_RS19715		hypothetical protein	2.64
ABUW_RS18020		YgiQ family radical SAM protein	2.63
ABUW_RS11690		MFS transporter	2.62
sRNA102	sRNA102	sRNA102	2.62
ABUW_RS12090		ATP-binding cassette domain-containing protein	2.59
ABUW_RS16575		hypothetical protein	2.59
ABUW_RS09045		acyl-CoA dehydrogenase family protein	2.58
ABUW_RS00635		ion channel protein Tsx	2.56
ABUW_RS17835		signal peptidase II	2.56
ABUW_RS17635		TetR/AcrR family transcriptional regulator	2.54
ABUW_RS00315		MATE family efflux transporter	2.54
ABUW_RS19900		glutathione S-transferase	2.54
ABUW_RS03205		RtcB family protein	2.53
ABUW_RS15520		methionine synthase	2.52
ABUW_RS12055		CoA transferase	2.52
ABUW_RS09565		SDR family NAD(P)-dependent oxidoreductase	2.51
ABUW_RS12015		SDR family oxidoreductase	2.51
ABUW_RS17535		tRNA-Thr	2.51
ABUW_RS00420		hypothetical protein	2.49
ABUW_RS12350		APC family permease	2.49
ABUW_RS08735	cydB	cytochrome d ubiquinol oxidase subunit II	2.48
ABUW_RS00245	mutY	A/G-specific adenine glycosylase	2.48
ABUW_RS01300		hypothetical protein	2.48
ABUW_RS02185		tRNA-Ser	2.47
ABUW_RS00905		DUF485 domain-containing protein	2.46
ABUW_RS09965		type 1 fimbrial protein	2.46
ABUW_RS14255		glutaminase	2.45
ABUW_RS17295	rlmB	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	2.44
ABUW_RS06285		hypothetical protein	2.44
ABUW_RS06045		DUF3465 domain-containing protein	2.42
ABUW_RS19165		toxic anion resistance protein	2.42
ABUW_RS00320		DUF523 domain-containing protein	2.42
ABUW_RS10910		SRPBCC family protein	2.41
ABUW_RS00925	omp33-36	porin Omp33-36	2.41
ABUW_RS02140		succinate dehydrogenase assembly factor 2	2.41
ABUW_RS04580		hypothetical protein	2.39
ABUW_RS07915		transcriptional regulator	2.39
ABUW_RS08130		Lrp/AsnC family transcriptional regulator	2.39
ABUW_RS16625	thyA	thymidylate synthase	2.39
ABUW_RS01315		CusA/CzcA family heavy metal efflux RND transporter	2.38
ABUW_RS16230		tyrosine-type recombinase/integrase	2.38
ABUW_RS05835	folE	GTP cyclohydrolase I FolE	2.37
ABUW_RS10495		porin	2.36
ABUW_RS19190		hypothetical protein	2.36
ABUW_RS10270		GntR family transcriptional regulator	2.36
ABUW_RS03685		hypothetical protein	2.35
ABUW_RS16290		TetR/AcrR family transcriptional regulator	2.34
ABUW_RS06920		head-tail connector protein	2.34
ABUW_RS07370		DUF1365 domain-containing protein	2.33
ABUW_RS02960		hypothetical protein	2.33
ABUW_RS13175		aromatic acid/H ⁺ symport family MFS transporter	2.32
ABUW_RS10540		sulfite exporter TauE/SafE family protein	2.32

ABUW_RS13640		amino acid permease	2.31
ABUW_RS11475		type II asparaginase	2.30
ABUW_RS14315		VOC family protein	2.30
ABUW_RS08560		amino acid permease	2.29
ABUW_RS01540		GspH/FimT family pseudopilin	2.29
ABUW_RS02310		2OG-Fe(II) oxygenase	2.28
ABUW_RS13845		hypothetical protein	2.27
ABUW_RS03215		methyltransferase	2.27
ABUW_RS12990		hypothetical protein	2.27
sRNA105	sRNA105	sRNA105	2.27
ABUW_RS01545	pilV	type IV pilus modification protein PilV	2.27
ABUW_RS19145		ParB/RepB/Spo0J family partition protein	2.26
ABUW_RS12965		transposase	2.26
ABUW_RS13180		OprD family outer membrane porin	2.26
ABUW_RS16775		endonuclease/exonuclease/phosphatase family protein	2.25
ABUW_RS03150		CoA transferase	2.24
ABUW_RS14710		type IV pilus twitching motility protein PilT	2.24
ABUW_RS11650	madL	malonate transporter subunit MadL	2.24
ABUW_RS07785		hypothetical protein	2.23
sRNA54	sRNA54	sRNA54	2.23
ABUW_RS09660		replication initiation factor domain-containing protein	2.22
ABUW_RS11170		methionine adenosyltransferase	2.22
ABUW_RS11595		hypothetical protein	2.21
ABUW_RS10175		LysR family transcriptional regulator	2.20
ABUW_RS08025		hypothetical protein	2.20
ABUW_RS04520		glycerophosphodiester phosphodiesterase	2.20
ABUW_RS05380		RluA family pseudouridine synthase	2.19
ABUW_RS11975		Paal family thioesterase	2.19
ABUW_RS18030		helix-turn-helix domain-containing protein	2.19
ABUW_RS20280		hypothetical protein	2.18
ABUW_RS09600	adeA	multidrug efflux RND transporter periplasmic adaptor subunit AdeA	2.18
ABUW_RS17820		SulP family inorganic anion transporter	2.18
ABUW_RS17525		tRNA-Gly	2.17
ABUW_RS19115		hypothetical protein	2.17
ABUW_RS08760		adenosine kinase	2.17
ABUW_RS05660	yddG	aromatic amino acid DMT transporter YddG	2.16
ABUW_RS13925	rlmH	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH	2.16
ABUW_RS17000		SAM-dependent methyltransferase	2.16
ABUW_RS05010		sulfate ABC transporter substrate-binding protein	2.14
ABUW_RS19365		hypothetical protein	2.14
sRNA3	sRNA3	sRNA3	2.14
ABUW_RS09570		SDR family NAD(P)-dependent oxidoreductase	2.13
ABUW_RS17830		ISL3-like element ISPPu12 family transposase	2.13
ABUW_RS00785		TMEM165/GDT1 family protein	2.13
sRNA38	sRNA38	sRNA38	2.13
ABUW_RS13460		MFS transporter	2.12
ABUW_RS03185		thiolase family protein	2.12
ABUW_RS01805		tetracycline resistance MFS efflux pump	2.12
ABUW_RS14465		hypothetical protein	2.11
ABUW_RS16925		tRNA-Lys	2.11
ABUW_RS20105		hypothetical protein	2.11
ABUW_RS15170		MFS transporter	2.11
ABUW_RS12005		acyl-CoA dehydrogenase family protein	2.11
ABUW_RS05500	mnmA	tRNA 2-thiouridine(34) synthase MnmA	2.11
ABUW_RS02595	radC	DNA repair protein RadC	2.11
ABUW_RS09140		muconate cycloisomerase	2.11
ABUW_RS11065		TetR/AcrR family transcriptional regulator	2.11

ABUW_RS12010		enoyl-CoA hydratase	2.10
ABUW_RS18370		fatty acyl-AMP ligase	2.10
ABUW_RS20335		hypothetical protein	2.10
ABUW_RS05705		PAS domain-containing protein	2.09
ABUW_RS19195		hypothetical protein	2.09
ABUW_RS07600	pgaA	poly-beta-1,6 N-acetyl-D-glucosamine exporter porin PgaA	2.09
ABUW_RS09480		HlyD family secretion protein	2.09
ABUW_RS18300		LysE family transporter	2.09
ABUW_RS03800		terminase family protein	2.09
ABUW_RS07900		ethanolamine ammonia-lyase subunit EutB	2.08
ABUW_RS11400		Crp/Fnr family transcriptional regulator	2.08
ABUW_RS12955	terL	phage terminase large subunit	2.07
ABUW_RS16595	alp2	DUF839 domain-containing protein	2.07
ABUW_RS00380	hutU	urocanate hydratase	2.07
ABUW_RS16430	ndk	nucleoside-diphosphate kinase	2.06
ABUW_RS05980		adenosylhomocysteinase	2.05
ABUW_RS08460	uppS	di-trans,poly-cis-decaprenylcistransferase	2.05
ABUW_RS06490		hypothetical protein	2.05
ABUW_RS00370	hutC	histidine utilization repressor	2.05
ABUW_RS01685		endonuclease	2.05
ABUW_RS17115	pnp	polyribonucleotide nucleotidyltransferase	2.04
ABUW_RS02735		ogr/Delta-like zinc finger family protein	2.04
ABUW_RS09300		amidohydrolase	2.03
ABUW_RS16820		hypothetical protein	2.03
ABUW_RS00040		RND transporter	2.03
ABUW_RS18900		matrixin family metalloprotease	2.03
ABUW_RS06365		hypothetical protein	2.03
ABUW_RS03290		DUF488 domain-containing protein	2.03
sRNA9	sRNA9	sRNA9	2.03
ABUW_RS17840		cation transporter	2.02
ABUW_RS05900		chorismate lyase	2.01
ABUW_RS17445		TRAP transporter large permease subunit	2.01
ABUW_RS09070		SDR family oxidoreductase	2.01
ABUW_RS05170	cgtA	Obg family GTPase CgtA	2.01
ABUW_RS03960		hypothetical protein	2.01
ABUW_RS12140		cytosine permease	2.01
ABUW_RS11930		isovaleryl-CoA dehydrogenase	2.01
ABUW_RS13605		Lrp/AsnC family transcriptional regulator	2.01
ABUW_RS02635	queA	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA	2.00
ABUW_RS07505	mnmg	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG	2.00
sRNA93	sRNA93	sRNA93	2.00
ABUW_RS19405		hypothetical protein	2.00
ABUW_RS04260	sdhC	succinate dehydrogenase, cytochrome b556 subunit	2.00
ABUW_RS13165		1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	1.99
ABUW_RS01360		tRNA-Ala	1.99
ABUW_RS05155		glyceraldehyde-3-phosphate dehydrogenase	1.99
ABUW_RS11390	ychF	redox-regulated ATPase YchF	1.99
ABUW_RS00795		MBL fold metallo-hydrolase	1.98
ABUW_RS02965		RcnB family protein	1.98
ABUW_RS15605		LysR family transcriptional regulator	1.98
ABUW_RS14075	lysS	lysine--tRNA ligase	1.98
ABUW_RS04030		patatin-like phospholipase family protein	1.98
ABUW_RS19375		type IV secretion system DNA-binding domain-containing protein	1.97
ABUW_RS11795		amino acid ABC transporter permease	1.97
ABUW_RS05150	rarD	EamA family transporter RarD	1.97

ABUW_RS15760		chorismate-binding protein	1.97
ABUW_RS03820		hypothetical protein	1.97
ABUW_RS13080		LexA family transcriptional regulator	1.96
ABUW_RS13235	trmB	tRNA (guanosine(46)-N7)-methyltransferase TrmB	1.96
ABUW_RS02395		enoyl-CoA hydratase/isomerase family protein	1.96
ABUW_RS17505	secE	preprotein translocase subunit SecE	1.96
ABUW_RS15670		copper resistance system multicopper oxidase	1.96
ABUW_RS10775	rpsT	30S ribosomal protein S20	1.95
ABUW_RS09575		alpha/beta fold hydrolase	1.95
ABUW_RS07420	yddG	aromatic amino acid DMT transporter YddG	1.95
ABUW_RS04140		phosphatase PAP2 family protein	1.94
ABUW_RS14310		FAD-dependent oxidoreductase	1.94
ABUW_RS18950		hypothetical protein	1.94
ABUW_RS01920		ComF family protein	1.94
ABUW_RS19230		hypothetical protein	1.93
ABUW_RS07275	csuE	Csu fimbrial tip adhesin CsuE	1.93
ABUW_RS16315		DUF4124 domain-containing protein	1.93
ABUW_RS14410		choline transporter	1.93
ABUW_RS17810		ATP-binding protein	1.93
ABUW_RS18375	abaR	LuxR family transcriptional regulator AbaR	1.93
ABUW_RS14610		hypothetical protein	1.92
ABUW_RS16105		DMT family transporter	1.92
ABUW_RS12060		acyl-CoA dehydrogenase family protein	1.91
ABUW_RS01625		EamA family transporter	1.91
ABUW_RS08280		ABC transporter substrate-binding protein	1.91
ABUW_RS13480		MarR family transcriptional regulator	1.90
ABUW_RS02295		malate dehydrogenase	1.90
ABUW_RS06720		cold-shock protein	1.89
ABUW_RS19930	ssrA	transfer-messenger RNA	1.89
sRNA89	sRNA89	sRNA89	1.89
ABUW_RS07800		membrane protein	1.89
ABUW_RS04970	queE	7-carboxy-7-deazaguanine synthase QueE	1.88
ABUW_RS01380	rsmH	16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH	1.88
ABUW_RS09150		hypothetical protein	1.88
ABUW_RS16520		DUF2846 domain-containing protein	1.87
ABUW_RS03220		uracil-xanthine permease	1.87
ABUW_RS19570		Y-family DNA polymerase	1.86
ABUW_RS01660	craA	MFS transporter	1.86
ABUW_RS03045		DUF2804 domain-containing protein	1.86
ABUW_RS05525		hypothetical protein	1.86
ABUW_RS02420	rpsI	30S ribosomal protein S9	1.86
ABUW_RS15750		C39 family peptidase	1.86
ABUW_RS15465		hypothetical protein	1.85
ABUW_RS16995		TIGR03862 family flavoprotein	1.85
ABUW_RS16535		trigger factor	1.85
ABUW_RS02360		DUF4256 domain-containing protein	1.85
ABUW_RS14520		MFS transporter	1.85
ABUW_RS15285	metG	methionine--tRNA ligase	1.84
ABUW_RS10505		hypothetical protein	1.84
ABUW_RS01820		HPP family protein	1.84
ABUW_RS03525	mreC	rod shape-determining protein MreC	1.84
ABUW_RS18585		UDP-glucose/GDP-mannose dehydrogenase family protein	1.84
ABUW_RS04880	tolR	protein TolR	1.83
ABUW_RS00630	hpxO	FAD-dependent urate hydroxylase HpxO	1.82
ABUW_RS08465		phosphatidate cytidyltransferase	1.82
ABUW_RS09485		DHA2 family efflux MFS transporter permease subunit	1.82
ABUW_RS10385	prmB	50S ribosomal protein L3 N(5)-glutamine methyltransferase	1.82

ABUW_RS09390		DMT family transporter	1.82
ABUW_RS15630		tRNA-Arg	1.82
ABUW_RS05915		hypothetical protein	1.82
ABUW_RS19635		protein rep	1.82
ABUW_RS19060		hypothetical protein	1.81
ABUW_RS11565		NCS1 family nucleobase:cation symporter-1	1.81
ABUW_RS04265	sdhD	succinate dehydrogenase, hydrophobic membrane anchor protein	1.81
ABUW_RS14525		OprD family outer membrane porin	1.80
ABUW_RS04645		4-phosphoerythronate dehydrogenase	1.80
ABUW_RS02790		phage tail protein	1.80
ABUW_RS12165		amino acid synthesis family protein	1.80
ABUW_RS14175		arylsulfatase	1.80
ABUW_RS07690		AMP-binding protein	1.79
ABUW_RS01375		sulfate ABC transporter substrate-binding protein	1.79
ABUW_RS11570		aspartate/glutamate racemase family protein	1.78
ABUW_RS00385	hutH	histidine ammonia-lyase	1.78
ABUW_RS12860		cysteine--tRNA ligase	1.78
ABUW_RS16780	asd	aspartate-semialdehyde dehydrogenase	1.78
ABUW_RS13025		MFS transporter	1.78
ABUW_RS07875		UDP-2,3-diacylglucosamine diphosphatase	1.78
ABUW_RS03530	mreD	rod shape-determining protein MreD	1.77
ABUW_RS07795		MFS transporter	1.77
ABUW_RS02220		YcxB family protein	1.77
ABUW_RS05285		hypothetical protein	1.77
ABUW_RS09130	catA	catechol 1,2-dioxygenase	1.77
ABUW_RS01850	hemF	oxygen-dependent coproporphyrinogen oxidase	1.76
ABUW_RS09105		penicillin acylase family protein	1.76
ABUW_RS19505	traC	type IV secretion system protein TraC	1.76
ABUW_RS09295		hypothetical protein	1.76
ABUW_RS17675		UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase	1.76
ABUW_RS01580	rimM	ribosome maturation factor RimM	1.75
ABUW_RS13340	alaS	alanine--tRNA ligase	1.75
ABUW_RS08725		cyd operon YbgE family protein	1.75
sRNA71	sRNA71	sRNA71	1.75
ABUW_RS20110		hypothetical protein	1.75
ABUW_RS10165		GntP family permease	1.75
ABUW_RS00405		DUF885 domain-containing protein	1.74
ABUW_RS00285		hypothetical protein	1.74
ABUW_RS19205		hypothetical protein	1.74
ABUW_RS08740		cytochrome ubiquinol oxidase subunit I	1.74
ABUW_RS05505		NUDIX hydrolase	1.73
ABUW_RS17845	cadR	Cd(II)/Pb(II)-responsive transcriptional regulator	1.73
ABUW_RS02935		hypothetical protein	1.73
ABUW_RS13720	argG	argininosuccinate synthase	1.73
ABUW_RS18685		carboxylating nicotinate-nucleotide diphosphorylase	1.72
ABUW_RS02930		hypothetical protein	1.72
ABUW_RS15770	hisD	histidinol dehydrogenase	1.72
ABUW_RS18520		hypothetical protein	1.72
ABUW_RS00955		GlpM family protein	1.72
ABUW_RS06330		hypothetical protein	1.71
ABUW_RS13415		SDR family NAD(P)-dependent oxidoreductase	1.71
ABUW_RS01755		S8 family serine peptidase	1.70
ABUW_RS08605		hypothetical protein	1.70
ABUW_RS06600		response regulator transcription factor	1.70
ABUW_RS13770		hypothetical protein	1.70
ABUW_RS19470	traL	type IV conjugative transfer system protein TraL	1.70
ABUW_RS15895	tilS	tRNA lysidine(34) synthetase TilS	1.69

ABUW_RS04755	serC	3-phosphoserine/phosphohydroxythreonine transaminase	1.69
ABUW_RS05810		uroporphyrinogen decarboxylase	1.69
ABUW_RS06590	tadA	Flp pilus assembly complex ATPase component TadA	1.69
ABUW_RS12590	uca	urea carboxylase	1.69
ABUW_RS12950		DUF1073 domain-containing protein	1.69
ABUW_RS17530		tRNA-Tyr	1.69
ABUW_RS20530		hypothetical protein	1.68
ABUW_RS15955	rpml	50S ribosomal protein L35	1.68
ABUW_RS18425		LysR family transcriptional regulator	1.68
ABUW_RS15905	ppx	exopolyphosphatase	1.68
ABUW_RS05335	cas1f	type I-F CRISPR-associated endonuclease Cas1	1.68
ABUW_RS03830		hypothetical protein	1.68
ABUW_RS17475	rpoB	DNA-directed RNA polymerase subunit beta	1.67
ABUW_RS16460		class I SAM-dependent methyltransferase	1.67
ABUW_RS10320		sigma-54-dependent Fis family transcriptional regulator	1.67
ABUW_RS08555	kynU	kynureninase	1.67
ABUW_RS10435	recR	recombination protein RecR	1.67
ABUW_RS08210		low molecular weight phosphotyrosine protein phosphatase	1.67
ABUW_RS09065		aromatic-ring-hydroxylating dioxygenase subunit beta	1.67
ABUW_RS20120		hypothetical protein	1.66
ABUW_RS02565		bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC	1.66
ABUW_RS09490		hypothetical protein	1.66
ABUW_RS13355	rnhB	ribonuclease HII	1.66
ABUW_RS02425	rplM	50S ribosomal protein L13	1.66
ABUW_RS11810		response regulator	1.66
ABUW_RS16985	crcB	fluoride efflux transporter CrcB	1.66
ABUW_RS07365		FAD-dependent oxidoreductase	1.65
ABUW_RS12735		DUF1826 domain-containing protein	1.65
ABUW_RS08020		hypothetical protein	1.65
ABUW_RS08120		MgtC/SapB family protein	1.65
ABUW_RS04480		phosphoenolpyruvate carboxykinase (GTP)	1.65
ABUW_RS03190		GspH/FimT family pseudopilin	1.65
ABUW_RS00375		HutD family protein	1.65
ABUW_RS12770		EamA family transporter	1.65
ABUW_RS07905	eat	ethanolamine permease	1.64
ABUW_RS12085		putative 2-aminoethylphosphonate ABC transporter permease subunit	1.64
ABUW_RS07935		5-carboxymethyl-2-hydroxymuconate Delta-isomerase	1.64
ABUW_RS17360		thioesterase family protein	1.64
ABUW_RS16390	der	ribosome biogenesis GTPase Der	1.63
ABUW_RS14385	dctA	C4-dicarboxylate transporter DctA	1.63
ABUW_RS05975	metF	methylenetetrahydrofolate reductase [NAD(P)H]	1.63
ABUW_RS03655		hypothetical protein	1.62
ABUW_RS04255	gltA	citrate (Si)-synthase	1.62
ABUW_RS15665		copper resistance protein B	1.62
ABUW_RS00350		amino acid permease	1.61
ABUW_RS11215	queG	tRNA epoxyqueuosine(34) reductase QueG	1.61
ABUW_RS06080	rodA	rod shape-determining protein RodA	1.61
ABUW_RS06575		ferredoxin--NADP reductase	1.61
ABUW_RS16250		tRNA threonylcarbamoyladenosine dehydratase	1.60
ABUW_RS10575		2'-5' RNA ligase family protein	1.60
ABUW_RS04450	folD	bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD	1.60
sRNA63	sRNA63	sRNA63	1.59
ABUW_RS07000		hypothetical protein	1.59

ABUW_RS10470		hypothetical protein	1.59
ABUW_RS11060		cupin domain-containing protein	1.59
ABUW_RS10265		fumarate reductase/succinate dehydrogenase flavoprotein subunit	1.58
ABUW_RS15130	rluB	23S rRNA pseudouridine(2605) synthase RluB	1.58
ABUW_RS13430		AraC family transcriptional regulator	1.58
ABUW_RS05050	lepA	elongation factor 4	1.58
ABUW_RS16275		peptide chain release factor 3	1.58
ABUW_RS14440		hypothetical protein	1.58
ABUW_RS07680		3-hydroxyacyl-CoA dehydrogenase	1.58
ABUW_RS07080	tsaD	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD	1.57
ABUW_RS06535	hisQ	histidine ABC transporter permease HisQ	1.57
ABUW_RS16070		NAD(P)-dependent oxidoreductase	1.57
ABUW_RS13795	yejB	microcin C ABC transporter permease YejB	1.57
ABUW_RS13590		amino acid permease	1.57
ABUW_RS04135	adel	multidrug efflux RND transporter periplasmic adaptor subunit Adel	1.57
ABUW_RS06850		hypothetical protein	1.56
ABUW_RS08270	aroQ	type II 3-dehydroquinate dehydratase	1.56
ABUW_RS09345		hypothetical protein	1.56
ABUW_RS06070		septal ring lytic transglycosylase RlpA family protein	1.55
ABUW_RS09985		DUF4882 family protein	1.55
ABUW_RS05045		acyl-CoA thioesterase	1.55
ABUW_RS13840	rsml	16S rRNA (cytidine(1402)-2'-O)-methyltransferase	1.55
ABUW_RS08235		PepSY domain-containing protein	1.54
ABUW_RS08730	cydX	cytochrome bd-I oxidase subunit CydX	1.54
ABUW_RS05650		hypothetical protein	1.54
ABUW_RS15110		elongation factor P hydroxylase	1.54
ABUW_RS04975	dapD	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	1.54
ABUW_RS03825		hypothetical protein	1.54
ABUW_RS13375		NCS2 family permease	1.53
ABUW_RS13545	gudD	glucarate dehydratase	1.53
ABUW_RS17615		oxidative damage protection protein	1.52
ABUW_RS11550		hydrolase	1.52
ABUW_RS11980		MFS transporter	1.52
ABUW_RS18280	guaA	glutamine-hydrolyzing GMP synthase	1.51
ABUW_RS13940	gdhA	NADP-specific glutamate dehydrogenase	1.51
ABUW_RS05375		isochorismatase	1.51
ABUW_RS09220		Rrf2 family transcriptional regulator	1.51
ABUW_RS06845		hypothetical protein	1.51
ABUW_RS07715		2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	1.51
ABUW_RS19615	znuD2	TonB-dependent receptor ZnuD2	1.51
ABUW_RS02570		hypothetical protein	1.51
ABUW_RS09160		dihydroxy-acid dehydratase	1.51
ABUW_RS04575		non-ribosomal peptide synthetase	1.50
ABUW_RS00065		anhydro-N-acetylmuramic acid kinase	1.50
ABUW_RS17330		DUF1656 domain-containing protein	1.50
ABUW_RS00240		M23 family metalloproteinase	1.50
ABUW_RS19005	yidC	membrane protein insertase YidC	1.50
ABUW_RS01115		NAD(P)H-dependent oxidoreductase	1.50
ABUW_RS18960		aromatic ring-hydroxylating dioxygenase subunit alpha	1.50
ABUW_RS07865		DMT family transporter	1.49
ABUW_RS18205		zinc ABC transporter substrate-binding protein	1.49
ABUW_RS15625		tRNA-His	1.49
ABUW_RS11445		LysE family translocator	1.49
ABUW_RS16630		dihydrofolate reductase	1.49
ABUW_RS05865	trpD	anthranilate phosphoribosyltransferase	1.49

ABUW_RS18455		Lrp/AsnC ligand binding domain-containing protein	1.49
ABUW_RS14365	pgaC	poly-beta-1,6 N-acetyl-D-glucosamine synthase	1.48
ABUW_RS18355		non-ribosomal peptide synthetase	1.48
ABUW_RS03125		patatin family protein	1.48
ABUW_RS18855		peptidyl-prolyl cis-trans isomerase	1.48
ABUW_RS18695	plc2	phospholipase C, phosphocholine-specific	1.48
ABUW_RS00885	msuE	FMN reductase	1.48
ABUW_RS17575		acyl-CoA thioesterase	1.47
ABUW_RS15125	scpB	SMC-Scp complex subunit ScpB	1.47
ABUW_RS17695	xerD	site-specific tyrosine recombinase XerD	1.47
ABUW_RS02580		septation protein IspZ	1.46
ABUW_RS14230		LysR family transcriptional regulator	1.46
ABUW_RS08655	brnQ	branched-chain amino acid transport system II carrier protein	1.45
ABUW_RS02800		baseplate J/gp47 family protein	1.45
ABUW_RS05410		DUF4442 domain-containing protein	1.45
ABUW_RS09590	adeS	two-component sensor histidine kinase AdeS	1.45
ABUW_RS01095		helix-turn-helix transcriptional regulator	1.45
ABUW_RS11740		SDR family oxidoreductase	1.44
ABUW_RS13260		aspartate carbamoyltransferase catalytic subunit	1.44
ABUW_RS08570		S8 family peptidase	1.44
ABUW_RS15035		ribose-phosphate pyrophosphokinase	1.44
ABUW_RS10995		MotA/TolQ/ExbB proton channel family protein	1.44
ABUW_RS02865		terminase family protein	1.43
ABUW_RS08180	amvA	multidrug efflux MFS transporter AmvA	1.43
ABUW_RS08220		YdcF family protein	1.43
ABUW_RS01575	rpsP	30S ribosomal protein S16	1.43
ABUW_RS14995		glutamyl-tRNA reductase	1.43
ABUW_RS15900		acetyl-CoA carboxylase carboxyltransferase subunit alpha	1.42
sRNA75	sRNA75	sRNA75	1.41
ABUW_RS01350		amino acid permease	1.41
ABUW_RS15920		hypothetical protein	1.41
ABUW_RS13390		SDR family NAD(P)-dependent oxidoreductase	1.41
ABUW_RS08215	murB	UDP-N-acetylmuramate dehydrogenase	1.41
ABUW_RS04545	ttcA	tRNA 2-thiocytidine(32) synthetase TtcA	1.41
ABUW_RS16790		hypothetical protein	1.40
ABUW_RS11985		hypothetical protein	1.40
ABUW_RS10380	aroC	chorismate synthase	1.40
ABUW_RS00755		UDP-3-O-acyl-N-acetylglucosamine deacetylase	1.40
ABUW_RS14655		EmrA/EmrK family multidrug efflux transporter periplasmic adaptor subunit	1.40
ABUW_RS14405		MarC family protein	1.40
ABUW_RS13335	gap	type I glyceraldehyde-3-phosphate dehydrogenase	1.40
ABUW_RS10305		sulfite exporter TauE/SafE family protein	1.39
ABUW_RS06995	terL	phage terminase large subunit	1.39
ABUW_RS08420		protein tyrosine phosphatase family protein	1.39
ABUW_RS11915		class I SAM-dependent methyltransferase	1.39
ABUW_RS16910		hypothetical protein	1.39
ABUW_RS07235		FadR family transcriptional regulator	1.39
ABUW_RS14750		GNAT family N-acetyltransferase	1.39
ABUW_RS05870		TonB-dependent receptor	1.38
ABUW_RS12395		EamA family transporter	1.38
ABUW_RS17335		FUSC family protein	1.38
ABUW_RS13635		FAD-binding oxidoreductase	1.38
ABUW_RS06360		hypothetical protein	1.38
ABUW_RS04245		rhodanese-related sulfurtransferase	1.38
ABUW_RS15950	rplT	50S ribosomal protein L20	1.38
ABUW_RS00410		HAD family hydrolase	1.38

ABUW_RS17540	trpE	anthranilate synthase component I	1.37
ABUW_RS18190	atpE	F0F1 ATP synthase subunit C	1.37
ABUW_RS11815		hypothetical protein	1.37
ABUW_RS18025		esterase-like activity of phytase family protein	1.37
ABUW_RS05080	recO	DNA repair protein RecO	1.36
ABUW_RS04375	greA	transcription elongation factor GreA	1.36
sRNA76	sRNA76	sRNA76	1.36
ABUW_RS10065		bifunctional metallophosphatase/5'-nucleotidase	1.36
ABUW_RS16065		crotonase/enoyl-CoA hydratase family protein	1.36
ABUW_RS00740		cell division protein FtsQ/DivIB	1.35
ABUW_RS05815		DUF817 family protein	1.35
ABUW_RS11075	sstT	serine/threonine transporter SstT	1.35
ABUW_RS11015		nucleotidyltransferase family protein	1.35
ABUW_RS12750		MFS transporter	1.34
ABUW_RS14035		LysR family transcriptional regulator	1.34
ABUW_RS20205		hypothetical protein	1.34
ABUW_RS01465	gltB	glutamate synthase large subunit	1.34
ABUW_RS06840		ribbon-helix-helix protein, CopG family	1.34
sRNA42	sRNA42	sRNA42	1.34
ABUW_RS05970		16S rRNA (uracil(1498)-N(3))-methyltransferase	1.34
ABUW_RS16770	gltP	glutamate/aspartate:proton symporter GltP	1.34
ABUW_RS13555	garD	galactarate dehydratase	1.34
ABUW_RS15475		hypothetical protein	1.34
ABUW_RS04130	adeJ	multidrug efflux RND transporter permease subunit AdeJ	1.33
ABUW_RS17260	secG	preprotein translocase subunit SecG	1.33
ABUW_RS19000	mnmeE	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmeE	1.33
ABUW_RS11020		phosphotransferase	1.33
ABUW_RS17650		NUDIX domain-containing protein	1.33
ABUW_RS17975		trimeric intracellular cation channel family protein	1.33
ABUW_RS10550		adenosylcobinamide-GDP ribazoletransferase	1.32
ABUW_RS17565	gspN	type II secretion system protein N	1.32
ABUW_RS16235	dusA	tRNA dihydrouridine(20/20a) synthase DusA	1.32
ABUW_RS06560	yegQ	tRNA 5-hydroxyuridine modification protein YegQ	1.32
ABUW_RS17275		type II secretion system F family protein	1.31
ABUW_RS01195		DMT family transporter	1.31
ABUW_RS06020		MFS transporter	1.31
ABUW_RS09510		acid phosphatase	1.31
ABUW_RS18115		LysM peptidoglycan-binding domain-containing protein	1.31
ABUW_RS04270		succinate dehydrogenase flavoprotein subunit	1.30
ABUW_RS06305		DUF4055 domain-containing protein	1.30
ABUW_RS12875		site-specific integrase	1.30
ABUW_RS14070		capsule assembly Wzi family protein	1.30
ABUW_RS16570	rdgB	RdgB/HAM1 family non-canonical purine NTP pyrophosphatase	1.29
ABUW_RS14270		hypothetical protein	1.29
ABUW_RS02575		hypothetical protein	1.29
ABUW_RS00400	hutG	formimidoylglutamase	1.29
ABUW_RS20165		hypothetical protein	1.29
ABUW_RS13230		ExeM/NucH family extracellular endonuclease	1.29
ABUW_RS07405		nuclear transport factor 2 family protein	1.28
ABUW_RS15935	pheS	phenylalanine--tRNA ligase subunit alpha	1.28
ABUW_RS02620	tgt	tRNA guanosine(34) transglycosylase Tgt	1.27
ABUW_RS07660	prmC	peptide chain release factor N(5)-glutamine methyltransferase	1.27
ABUW_RS17610	argH	argininosuccinate lyase	1.27
ABUW_RS15340		hypothetical protein	1.27
ABUW_RS10950		type II secretion system protein	1.27
ABUW_RS17940		OprD family outer membrane porin	1.26

ABUW_RS11055	maf	septum formation protein Maf	1.26
ABUW_RS07840		pseudouridylate synthase	1.26
ABUW_RS14010	ureA	urease subunit gamma	1.26
ABUW_RS02855		phage major capsid protein, P2 family	1.26
ABUW_RS14650		DHA2 family efflux MFS transporter permease subunit	1.26
ABUW_RS06300	terL	phage terminase large subunit	1.26
ABUW_RS08470		1-deoxy-D-xylulose-5-phosphate reductoisomerase	1.25
ABUW_RS05055	lepB	signal peptidase I	1.25
ABUW_RS19550		conjugal transfer protein TraH	1.25
ABUW_RS08880		CTP synthase	1.25
ABUW_RS04850		RNA methyltransferase	1.24
ABUW_RS12420		epoxyqueuosine reductase QueH	1.24
ABUW_RS13490		p-hydroxycinnamoyl CoA hydratase/lyase	1.24
ABUW_RS01965		Rrf2 family transcriptional regulator	1.24
ABUW_RS15560		LysR family transcriptional regulator	1.24
ABUW_RS15315		1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase	1.24
ABUW_RS15680		HAD family hydrolase	1.24
ABUW_RS18345		hypothetical protein	1.23
ABUW_RS00495		D-tyrosyl-tRNA(Tyr) deacylase	1.23
ABUW_RS11125	putA	trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	1.23
ABUW_RS02265		energy transducer TonB	1.23
ABUW_RS02485		diguanylate cyclase	1.23
ABUW_RS10965		PilZ domain-containing protein	1.23
ABUW_RS07720	kdpA	potassium-transporting ATPase subunit KdpA	1.23
ABUW_RS16755		LysE family translocator	1.23
ABUW_RS12425		GNAT family N-acetyltransferase	1.22
ABUW_RS12855		KpsF/GutQ family sugar-phosphate isomerase	1.22
ABUW_RS00725	murG	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	1.22
ABUW_RS11955		LysR family transcriptional regulator	1.21
ABUW_RS01065		hypothetical protein	1.21
ABUW_RS16600	phoX	PhoX family phosphatase	1.21
ABUW_RS15530		LysR family transcriptional regulator	1.21
ABUW_RS09075		oxidoreductase	1.21
ABUW_RS11250		fimbrial protein	1.21
ABUW_RS06530		ABC transporter substrate-binding protein	1.21
ABUW_RS06695		thiazole synthase	1.21
ABUW_RS15150	bioA	adenosylmethionine--8-amino-7-oxononanoate transaminase	1.21
ABUW_RS01060		DMT family transporter	1.21
ABUW_RS07665		ABC transporter permease	1.20
ABUW_RS20425		hypothetical protein	1.20
ABUW_RS04150		polyprenyl synthetase family protein	1.20
ABUW_RS02045	rplN	50S ribosomal protein L14	1.20
ABUW_RS18225		LysE family transporter	1.20
ABUW_RS06065		DUF962 domain-containing protein	1.20
ABUW_RS10295		EamA family transporter	1.20
ABUW_RS07540	dnaB	replicative DNA helicase	1.20
ABUW_RS00850		16S rRNA (uracil(1498)-N(3))-methyltransferase	1.19
ABUW_RS00035		ATP-binding cassette domain-containing protein	1.19
ABUW_RS09405		MFS transporter	1.19
ABUW_RS01855	ribA	GTP cyclohydrolase II	1.19
ABUW_RS13535		aldehyde dehydrogenase (NADP(+))	1.19
ABUW_RS11260		LysR family transcriptional regulator	1.19
ABUW_RS02860		GPO family capsid scaffolding protein	1.19
ABUW_RS02165		hypothetical protein	1.19
ABUW_RS02385		acetyl-CoA carboxylase carboxyltransferase subunit	1.19

ABUW_RS18955		glutathionylspermidine synthase family protein	1.19
ABUW_RS06055		AzIC family ABC transporter permease	1.18
ABUW_RS12550		ABC transporter permease	1.18
ABUW_RS16485		permease	1.18
ABUW_RS15780	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1.18
ABUW_RS14435	mgo	malate dehydrogenase (quinone)	1.18
ABUW_RS02235		DMT family transporter	1.18
ABUW_RS14880	hemJ	protoporphyrinogen oxidase HemJ	1.18
ABUW_RS05580	epmB	EF-P beta-lysylation protein EpmB	1.18
ABUW_RS00695		arsenate reductase	1.17
ABUW_RS05175		glutamate 5-kinase	1.16
ABUW_RS15610		zinc-binding dehydrogenase	1.16
ABUW_RS10645	ybaK	Cys-tRNA(Pro) deacylase	1.16
ABUW_RS13560		DMT family transporter	1.15
ABUW_RS11040		hypothetical protein	1.15
ABUW_RS07685		acyl-CoA dehydrogenase family protein	1.15
ABUW_RS05530	surE	5'/3'-nucleotidase SurE	1.15
ABUW_RS04235		hypothetical protein	1.15
ABUW_RS07175		BLUF domain-containing protein	1.14
ABUW_RS12660		LamB/YcsF family protein	1.14
ABUW_RS03035	trpB	tryptophan synthase subunit beta	1.14
ABUW_RS01265		RNA-binding transcriptional accessory protein	1.14
ABUW_RS00425		DNA cytosine methyltransferase	1.14
ABUW_RS14380		YaeQ family protein	1.13
ABUW_RS04765		Yail/YqxJ family protein	1.13
ABUW_RS16540		TonB-dependent siderophore receptor	1.13
ABUW_RS17290		DMT family transporter	1.13
ABUW_RS08295	nirB	nitrite reductase large subunit	1.13
ABUW_RS18990	dmeF	CDF family Co(II)/Ni(II) efflux transporter DmeF	1.13
ABUW_RS14015		urease accessory protein UreD	1.12
ABUW_RS16365	rsgA	ribosome small subunit-dependent GTPase A	1.12
ABUW_RS01000		PLP-dependent aminotransferase family protein	1.12
ABUW_RS16730		hypothetical protein	1.12
ABUW_RS08115	mgtA	magnesium-translocating P-type ATPase	1.12
ABUW_RS19390		hypothetical protein	1.12
ABUW_RS05120		pyridoxal phosphate-dependent aminotransferase	1.12
ABUW_RS04435	alp1	alkaline phosphatase D family protein	1.12
ABUW_RS14245		MFS transporter	1.12
ABUW_RS15445	bfmS	sensor histidine kinase BfmS	1.11
ABUW_RS03030		phosphoribosylanthranilate isomerase	1.11
ABUW_RS14205	methH	methionine synthase	1.11
ABUW_RS17125		EstA family serine hydrolase	1.11
ABUW_RS02135		acyl-CoA dehydrogenase family protein	1.11
ABUW_RS13145		LysR family transcriptional regulator	1.11
ABUW_RS10915	tadA	tRNA adenosine(34) deaminase TadA	1.10
ABUW_RS18600		DegT/DnrJ/EryC1/StrS aminotransferase family protein	1.10
ABUW_RS13020		helix-turn-helix transcriptional regulator	1.10
ABUW_RS18240		arginine--tRNA ligase	1.10
ABUW_RS11770		LysR family transcriptional regulator	1.10
ABUW_RS17850		universal stress protein	1.10
ABUW_RS08035		TonB-dependent receptor	1.10
ABUW_RS06945		carbohydrate-binding protein	1.10
ABUW_RS10560		histidine phosphatase family protein	1.10
ABUW_RS15960	nreB	nickel resistance MFS transporter NreB	1.09
ABUW_RS01610		TSUP family transporter	1.09
ABUW_RS12850		HAD-IIIa family hydrolase	1.09
ABUW_RS03480	sbmA	peptide antibiotic transporter SbmA	1.09

ABUW_RS16750		ATP-binding cassette domain-containing protein	1.09
ABUW_RS17860		metalloregulator ArsR/SmtB family transcription factor	1.08
ABUW_RS10930		6-carboxytetrahydropterin synthase	1.08
ABUW_RS12670	mumR	LysR family transcriptional regulator MumR	1.08
ABUW_RS00355		hypothetical protein	1.08
ABUW_RS04810	purM	phosphoribosylformylglycinamide cyclo-ligase	1.08
ABUW_RS18380		DUF4902 domain-containing protein	1.08
ABUW_RS01200		helix-turn-helix transcriptional regulator	1.08
ABUW_RS01800	glyQ	glycine--tRNA ligase subunit alpha	1.08
ABUW_RS12135		hypothetical protein	1.07
ABUW_RS17625		TolC family outer membrane protein	1.07
ABUW_RS12390		GntR family transcriptional regulator	1.07
ABUW_RS00990		helix-turn-helix transcriptional regulator	1.07
ABUW_RS02445		DUF2147 domain-containing protein	1.07
ABUW_RS01530	gmk	guanylate kinase	1.07
ABUW_RS16025		ComEA family DNA-binding protein	1.06
ABUW_RS04075		LysR family transcriptional regulator	1.06
ABUW_RS18775	ssuC	aliphatic sulfonate ABC transporter permease SsuC	1.06
ABUW_RS16015	folK	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphokinase	1.06
ABUW_RS13485	mhpT	3-(3-hydroxy-phenyl)propionate transporter MhpT	1.06
ABUW_RS07490		zinc-ribbon and DUF3426 domain-containing protein	1.05
ABUW_RS14180		formylglycine-generating enzyme family protein	1.04
ABUW_RS06705		DUF423 domain-containing protein	1.04
ABUW_RS10825		ABC transporter substrate-binding protein	1.04
ABUW_RS00455	thiL	thiamine-phosphate kinase	1.04
ABUW_RS00360	zigA	zinc metallochaperone GTPase ZigA	1.04
ABUW_RS14695		exonuclease SbcCD subunit D	1.04
ABUW_RS04650	genX	EF-P lysine aminoacylase GenX	1.03
ABUW_RS14095		FAD-dependent oxidoreductase	1.03
ABUW_RS14670		FAD-dependent oxidoreductase	1.03
ABUW_RS12690		RHS domain-containing protein	1.02
ABUW_RS00720	gshB	glutathione synthase	1.02
ABUW_RS04715		glycosyltransferase family 39 protein	1.02
ABUW_RS16885		DUF1345 domain-containing protein	1.01
ABUW_RS11720		LysR family transcriptional regulator	1.01
ABUW_RS13860		cation transporter	1.01
ABUW_RS11500		alpha/beta fold hydrolase	1.01
ABUW_RS06700	thiS	sulfur carrier protein ThiS	1.01
ABUW_RS03040		DUF1543 domain-containing protein	1.01
ABUW_RS16660	purU	formyltetrahydrofolate deformylase	1.01
ABUW_RS16555		homoserine O-acetyltransferase	1.01
ABUW_RS04080		AEC family transporter	1.00
ABUW_RS17950		MAPEG family protein	1.00
ABUW_RS15210		pantothenate kinase	1.00
ABUW_RS16055	cysM	cysteine synthase CysM	1.00
ABUW_RS11410		hypothetical protein	1.00
ABUW_RS04370		CatB-related O-acetyltransferase	1.00

Gene	Gene Name	Function	Δ gacS LSP vs WT LSP log2FC
ABUW_RS16060		response regulator	-9.50
ABUW_RS08050		hypothetical protein	-9.16
ABUW_RS11870		hypothetical protein	-8.61
ABUW_RS11875		hypothetical protein	-8.14
ABUW_RS12975		hypothetical protein	-7.77

ABUW_RS13010		DUF4142 domain-containing protein	-7.00
ABUW_RS10640		siderophore biosynthesis protein	-6.60
ABUW_RS10635		SidA/lucD/PvdA family monooxygenase	-6.13
ABUW_RS13040		hypothetical protein	-6.10
sRNA97	sRNA97	sRNA97	-5.97
ABUW_RS11855	katE	catalase HP11	-5.89
ABUW_RS15585	tcuB	tricarballate utilization 4Fe-4S protein TcuB	-5.72
ABUW_RS07500		hypothetical protein	-5.60
sRNA99	sRNA99	sRNA99	-5.59
ABUW_RS05765	basF	acinetobactin biosynthesis bifunctional isochorismatase/aryl carrier protein BasF	-5.57
ABUW_RS15565		MFS transporter	-5.48
ABUW_RS05760	basE	(2,3-dihydroxybenzoyl)adenylate synthase BasE	-5.43
ABUW_RS05755	basD	acinetobactin non-ribosomal peptide synthetase subunit BasD	-5.27
ABUW_RS15330		mechanosensitive ion channel	-5.26
ABUW_RS15580	tcuA	FAD-dependent tricarballate dehydrogenase TcuA	-5.21
ABUW_RS11860		iron-containing redox enzyme family protein	-5.17
ABUW_RS07145		DUF2171 domain-containing protein	-5.10
sRNA106	sRNA106	sRNA106	-5.01
ABUW_RS11270		hypothetical protein	-4.98
ABUW_RS10010		hypothetical protein	-4.89
ABUW_RS16835	leuD	3-isopropylmalate dehydratase small subunit	-4.88
sRNA2	sRNA2	sRNA2	-4.88
ABUW_RS11345		amino acid ABC transporter substrate-binding protein	-4.80
newcandsRNA1	newcandsRNA1	newcandsRNA1	-4.76
ABUW_RS10625		siderophore achromobactin biosynthesis protein AcsC	-4.52
ABUW_RS09210		type 1 glutamine amidotransferase domain-containing protein	-4.43
ABUW_RS16845		DUF2061 domain-containing protein	-4.34
ABUW_RS10630		DHA2 family efflux MFS transporter permease subunit	-4.33
ABUW_RS20145		hypothetical protein	-4.23
ABUW_RS05770	basG	acinetobactin biosynthesis histidine decarboxylase BasG	-4.20
ABUW_RS05720	basB	acinetobactin non-ribosomal peptide synthetase subunit BasB	-4.18
ABUW_RS15335		hypothetical protein	-4.17
ABUW_RS06610		hemin uptake protein HemP	-4.08
ABUW_RS12725		hypothetical protein	-4.06
ABUW_RS15160	otsB	trehalose-phosphatase	-4.02
ABUW_RS01745		hypothetical protein	-3.93
ABUW_RS00895		hypothetical protein	-3.93
ABUW_RS15165		trehalose-6-phosphate synthase	-3.90
ABUW_RS10620		lucA/lucC family siderophore biosynthesis protein	-3.84
ABUW_RS12900		DUF4882 family protein	-3.79
ABUW_RS01615		hemerythrin domain-containing protein	-3.72
ABUW_RS17925		aldolase	-3.69
ABUW_RS10460		methyltransferase domain-containing protein	-3.66
ABUW_RS03310		YegP family protein	-3.66
ABUW_RS16840	leuC	3-isopropylmalate dehydratase large subunit	-3.63
ABUW_RS05750	basC	putative histamine N-monooxygenase	-3.60
ABUW_RS05735	bauE	ferric acinetobactin ABC transporter ATP-binding protein BauE	-3.56
ABUW_RS16255	acnA	aconitate hydratase AcnA	-3.52
ABUW_RS20200		hypothetical protein	-3.49
ABUW_RS10525		hypothetical protein	-3.48
ABUW_RS09435		SDR family oxidoreductase	-3.42
ABUW_RS05710	bauF	acinetobactin utilization protein BauF	-3.41
ABUW_RS18475		ribonuclease E inhibitor RraB	-3.40
ABUW_RS07620		hypothetical protein	-3.38
ABUW_RS08690		DUF2750 domain-containing protein	-3.37
ABUW_RS17400		serine hydrolase family protein	-3.37

ABUW_RS05730	bauC	ferric acinetobactin ABC transporter permease subunit BauC	-3.35
ABUW_RS11960		indolepyruvate ferredoxin oxidoreductase family protein	-3.33
ABUW_RS01050		MFS transporter	-3.32
ABUW_RS01760		hypothetical protein	-3.32
ABUW_RS05800	basJ	acinetobactin biosynthesis isochorismate synthase BasJ	-3.25
ABUW_RS08390		hypothetical protein	-3.25
ABUW_RS11465		pyridoxal phosphate-dependent aminotransferase	-3.23
ABUW_RS06730		hypothetical protein	-3.22
ABUW_RS07170		NirD/YgiW/YdeI family stress tolerance protein	-3.20
ABUW_RS10070		transcriptional repressor	-3.20
ABUW_RS11265		DMT family transporter	-3.20
ABUW_RS08590		universal stress protein	-3.20
ABUW_RS15790	raiA	ribosome-associated translation inhibitor RaiA	-3.19
ABUW_RS10025		hypothetical protein	-3.17
ABUW_RS11425		tautomerase family protein	-3.15
ABUW_RS07450		hypothetical protein	-3.10
ABUW_RS02875		HAMP domain-containing histidine kinase	-3.10
ABUW_RS14490		transferrin-binding protein-like solute binding protein	-3.09
ABUW_RS08580		SOS response-associated peptidase family protein	-3.02
ABUW_RS15280		hypothetical protein	-3.01
ABUW_RS05725	bauD	ferric acinetobactin ABC transporter permease subunit BauD	-2.96
ABUW_RS13105		hypothetical protein	-2.93
ABUW_RS10730	fdx	ISC system 2Fe-2S type ferredoxin	-2.92
ABUW_RS15570		substrate-binding domain-containing protein	-2.90
ABUW_RS05740	bauB	siderophore-binding periplasmic lipoprotein BauB	-2.88
ABUW_RS17105		MerR family transcriptional regulator	-2.86
ABUW_RS13250		OmpA family protein	-2.83
ABUW_RS13675		hypothetical protein	-2.83
ABUW_RS00660		HPF/RaiA family ribosome-associated protein	-2.83
ABUW_RS17680		hypothetical protein	-2.82
ABUW_RS03890		DUF4258 domain-containing protein	-2.79
ABUW_RS14025		copper resistance protein NlpE	-2.78
ABUW_RS01765		hypothetical protein	-2.77
ABUW_RS11160		OsmC family protein	-2.76
ABUW_RS10890		DUF1049 domain-containing protein	-2.76
ABUW_RS09440		MFS transporter	-2.76
ABUW_RS13680		RHS repeat protein	-2.73
ABUW_RS05785	barB	acinetobactin export ABC transporter permease/ATP-binding subunit BarB	-2.70
ABUW_RS18440		RidA family protein	-2.70
ABUW_RS07155		PIG-L family deacetylase	-2.68
ABUW_RS17395		hypothetical protein	-2.67
ABUW_RS10475		hypothetical protein	-2.65
ABUW_RS11150		lecithin retinol acyltransferase family protein	-2.65
ABUW_RS04365		universal stress protein	-2.64
ABUW_RS17460		hypothetical protein	-2.64
ABUW_RS11885		hypothetical protein	-2.64
ABUW_RS00690		DUF2147 domain-containing protein	-2.63
ABUW_RS12805		universal stress protein	-2.61
ABUW_RS01975		DUF853 domain-containing protein	-2.60
ABUW_RS11335		amino acid ABC transporter permease	-2.58
ABUW_RS10520		TonB-dependent siderophore receptor	-2.58
ABUW_RS00115		methionine/alanine import family NSS transporter small subunit	-2.55
ABUW_RS07855	miaA	tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA	-2.53
ABUW_RS07820		hypothetical protein	-2.52
ABUW_RS08075		OmpW family protein	-2.51
ABUW_RS18445	alr	alanine racemase	-2.50
sRNA104	sRNA104	sRNA104	-2.49

ABUW_RS14775		OmpA family protein	-2.49
ABUW_RS13005		hypothetical protein	-2.48
ABUW_RS18400		enoyl-CoA hydratase	-2.48
ABUW_RS12465	icmH	type IVB secretion system protein IcmH/DotU	-2.47
ABUW_RS07960		spore coat protein U domain-containing protein	-2.47
ABUW_RS11850		glucose 1-dehydrogenase	-2.47
ABUW_RS10895		integration host factor subunit beta	-2.44
ABUW_RS01160	aqpZ	aquaporin Z	-2.44
ABUW_RS14215		transketolase	-2.43
ABUW_RS11340		amino acid ABC transporter permease	-2.43
ABUW_RS19580		hypothetical protein	-2.42
ABUW_RS16465		alpha/beta hydrolase	-2.41
ABUW_RS09415		aldehyde dehydrogenase (NADP(+))	-2.38
ABUW_RS06900		hypothetical protein	-2.37
ABUW_RS06905		hypothetical protein	-2.37
ABUW_RS01490		TPM domain-containing protein	-2.36
ABUW_RS10725	hscA	Fe-S protein assembly chaperone HscA	-2.36
ABUW_RS07160		class I SAM-dependent methyltransferase	-2.35
ABUW_RS08040		mechanosensitive ion channel	-2.33
ABUW_RS10075		isochorismatase family protein	-2.32
ABUW_RS01825		PspC domain-containing protein	-2.32
ABUW_RS17190		AAA family ATPase	-2.32
ABUW_RS20155		hypothetical protein	-2.31
ABUW_RS20295		hypothetical protein	-2.30
ABUW_RS05420		SIMPL domain-containing protein	-2.29
sRNA13	sRNA13	sRNA13	-2.29
ABUW_RS18980		GlsB/YeaQ/YmgE family stress response membrane protein	-2.29
ABUW_RS08700		hypothetical protein	-2.28
ABUW_RS05325		CYTH and CHAD domain-containing protein	-2.28
ABUW_RS19085		H-NS histone family protein	-2.28
ABUW_RS01370		hypothetical protein	-2.27
ABUW_RS07805		DUF4198 domain-containing protein	-2.26
ABUW_RS15080	lysM	peptidoglycan-binding protein LysM	-2.26
ABUW_RS18865		hypothetical protein	-2.26
ABUW_RS02205		hypothetical protein	-2.26
ABUW_RS10705		IscS subfamily cysteine desulfurase	-2.25
ABUW_RS03180		VOC family protein	-2.25
ABUW_RS09445		NAD(P)-dependent oxidoreductase	-2.24
ABUW_RS19720	bap	Ig-like domain-containing protein	-2.22
ABUW_RS13110		LysE family transporter	-2.22
ABUW_RS11835		hypothetical protein	-2.22
ABUW_RS07425		sorbose dehydrogenase family protein	-2.21
ABUW_RS02270	ybeY	rRNA maturation RNase YbeY	-2.20
ABUW_RS17410		hypothetical protein	-2.20
ABUW_RS00325	hppD	4-hydroxyphenylpyruvate dioxygenase	-2.19
ABUW_RS01970		flavohemoprotein	-2.19
ABUW_RS02650		hypothetical protein	-2.18
ABUW_RS18740		YciK family oxidoreductase	-2.18
ABUW_RS07430		GNAT family N-acetyltransferase	-2.18
ABUW_RS16080	rsfS	ribosome silencing factor	-2.17
ABUW_RS15230		hypothetical protein	-2.16
ABUW_RS04960		hypothetical protein	-2.16
ABUW_RS08245		iron-containing redox enzyme family protein	-2.12
ABUW_RS18890	dnaK	molecular chaperone DnaK	-2.12
ABUW_RS16690		hypothetical protein	-2.11
ABUW_RS16200		hypothetical protein	-2.10
ABUW_RS08380		SDR family NAD(P)-dependent oxidoreductase	-2.09

ABUW_RS03380		entericidin A/B family lipoprotein	-2.08
ABUW_RS11185		FxsA family protein	-2.08
ABUW_RS10720	hscB	Fe-S protein assembly co-chaperone HscB	-2.07
ABUW_RS00545		pyridoxal phosphate-dependent aminotransferase	-2.06
ABUW_RS02655		hypothetical protein	-2.06
ABUW_RS16035		SDR family oxidoreductase	-2.06
ABUW_RS16975		type B 50S ribosomal protein L31	-2.06
ABUW_RS05780	barA	acinetobactin export ABC transporter permease/ATP-binding subunit BarA	-2.05
ABUW_RS18405		acyl-CoA dehydrogenase family protein	-2.05
ABUW_RS09420		dihydroxy-acid dehydratase family protein	-2.04
ABUW_RS17145		hypothetical protein	-2.03
ABUW_RS08825	clpA	ATP-dependent Clp protease ATP-binding subunit ClpA	-2.01
sRNA100	sRNA100	sRNA100	-2.00
ABUW_RS08585		PQQ-dependent sugar dehydrogenase	-2.00
ABUW_RS10125		transporter	-1.99
ABUW_RS14475		biliverdin-producing heme oxygenase	-1.99
ABUW_RS16155		heavy metal translocating P-type ATPase	-1.99
ABUW_RS02920		glycosyltransferase family 25 protein	-1.99
ABUW_RS08325		MoaD/ThiS family protein	-1.98
ABUW_RS17800	glnK	P-II family nitrogen regulator	-1.98
ABUW_RS19460		hypothetical protein	-1.98
ABUW_RS06670		hypothetical protein	-1.97
ABUW_RS03005		acyl-CoA desaturase	-1.97
ABUW_RS02035	rpmC	50S ribosomal protein L29	-1.97
ABUW_RS00865	acs	acetate--CoA ligase	-1.97
ABUW_RS13685		type VI secretion system tip protein VgrG	-1.97
ABUW_RS00710		TonB-dependent siderophore receptor	-1.96
ABUW_RS03970		hypothetical protein	-1.96
ABUW_RS04815	perM	AI-2E family transporter	-1.95
ABUW_RS01140		hypothetical protein	-1.94
ABUW_RS18820		NAD(P)H-dependent oxidoreductase	-1.94
ABUW_RS13650		ATP-binding protein	-1.93
ABUW_RS04570		SgcJ/EcaC family oxidoreductase	-1.93
ABUW_RS10530		PepSY domain-containing protein	-1.92
ABUW_RS15440		hypothetical protein	-1.92
ABUW_RS03500		DJ-1/Pfpl family protein	-1.92
ABUW_RS15755		hypothetical protein	-1.91
ABUW_RS08770		insulinase family protein	-1.91
ABUW_RS01895		ABC transporter substrate-binding protein	-1.91
ABUW_RS17640		hypothetical protein	-1.90
ABUW_RS11330		amino acid ABC transporter ATP-binding protein	-1.90
ABUW_RS04500		co-chaperone GroES	-1.89
ABUW_RS16695		hypothetical protein	-1.89
ABUW_RS16550	leuA	2-isopropylmalate synthase	-1.89
ABUW_RS11455		glutathione peroxidase	-1.88
ABUW_RS13225		glutathione S-transferase N-terminal domain-containing protein	-1.88
ABUW_RS19080		thermonuclease family protein	-1.88
ABUW_RS05210	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.87
ABUW_RS00825		putative porin	-1.85
ABUW_RS10095	modA	molybdate ABC transporter substrate-binding protein	-1.85
ABUW_RS13200		KTSC domain-containing protein	-1.85
ABUW_RS08685		CBS domain-containing protein	-1.84
ABUW_RS17645	thiC	phosphomethylpyrimidine synthase ThiC	-1.84
ABUW_RS14030		isocitrate lyase	-1.84
ABUW_RS03145		AraC family transcriptional regulator	-1.83
ABUW_RS00025	cybC	cytochrome b562	-1.83
ABUW_RS04350		CapA family protein	-1.82

ABUW_RS16815		DUF1311 domain-containing protein	-1.82
ABUW_RS08875		hypothetical protein	-1.82
ABUW_RS13990		urease accessory protein	-1.82
ABUW_RS14870		EcsC family protein	-1.81
ABUW_RS11685	mdcA	malonate decarboxylase subunit alpha	-1.81
ABUW_RS15615	add	adenosine deaminase	-1.80
ABUW_RS05220		hypothetical protein	-1.79
ABUW_RS14485		DUF560 domain-containing protein	-1.79
ABUW_RS13285	clpB	ATP-dependent chaperone ClpB	-1.79
ABUW_RS08055		hypothetical protein	-1.79
ABUW_RS09670		hypothetical protein	-1.79
ABUW_RS13985	ureG	urease accessory protein UreG	-1.78
ABUW_RS09540		endonuclease/exonuclease/phosphatase family protein	-1.78
ABUW_RS00515		alpha/beta fold hydrolase	-1.78
ABUW_RS01510		bacterioferritin-associated ferredoxin	-1.78
ABUW_RS01005	gabT	4-aminobutyrate--2-oxoglutarate transaminase	-1.78
ABUW_RS14550		DEAD/DEAH box helicase family protein	-1.77
ABUW_RS05940		superoxide dismutase	-1.77
ABUW_RS11865		CinA family protein	-1.76
ABUW_RS01015		LysR family transcriptional regulator	-1.76
ABUW_RS06435		hypothetical protein	-1.76
ABUW_RS09185		alpha/beta hydrolase	-1.76
ABUW_RS01150		LysE family translocator	-1.76
ABUW_RS10330		2,3-butanediol dehydrogenase	-1.76
ABUW_RS19585		hypothetical protein	-1.75
ABUW_RS14505		sigma-70 family RNA polymerase sigma factor	-1.75
ABUW_RS04950		peroxiredoxin	-1.75
ABUW_RS16715		HdeD family acid-resistance protein	-1.75
ABUW_RS18905		hypothetical protein	-1.75
ABUW_RS04225		DUF493 domain-containing protein	-1.75
ABUW_RS16085		SDR family NAD(P)-dependent oxidoreductase	-1.74
ABUW_RS15855		organic hydroperoxide resistance protein	-1.74
ABUW_RS06775		hypothetical protein	-1.74
ABUW_RS18885	grpE	nucleotide exchange factor GrpE	-1.74
ABUW_RS02325		hypothetical protein	-1.72
ABUW_RS01690		hypothetical protein	-1.72
ABUW_RS20135		hypothetical protein	-1.72
ABUW_RS14760		phosphomannomutase/phosphoglucomutase	-1.72
ABUW_RS05260		M61 family metallopeptidase	-1.72
ABUW_RS12795		hypothetical protein	-1.71
ABUW_RS08440		PAS domain-containing protein	-1.71
ABUW_RS15055		GDYXXLXY domain-containing protein	-1.71
ABUW_RS02660		3'-5' exonuclease	-1.70
ABUW_RS08260	accC	acetyl-CoA carboxylase biotin carboxylase subunit	-1.70
ABUW_RS13130	cueR	Cu(I)-responsive transcriptional regulator	-1.70
ABUW_RS11460	msrB	peptide-methionine (R)-S-oxide reductase MsrB	-1.69
ABUW_RS18670		FKBP-type peptidyl-prolyl cis-trans isomerase	-1.69
ABUW_RS00870		cysteine hydrolase	-1.69
ABUW_RS02240		YihY family inner membrane protein	-1.68
ABUW_RS01480		LemA family protein	-1.68
ABUW_RS09425		fumarylacetoacetate hydrolase family protein	-1.68
ABUW_RS13100		exodeoxyribonuclease VII small subunit	-1.68
ABUW_RS17900		TniB family NTP-binding protein	-1.67
ABUW_RS13280		CinA family protein	-1.67
ABUW_RS05570		EAL domain-containing protein	-1.65
ABUW_RS10005		hypothetical protein	-1.65
ABUW_RS06780		hypothetical protein	-1.65

ABUW_RS14840		metal-dependent hydrolase	-1.64
ABUW_RS10715	iscA	iron-sulfur cluster assembly protein IscA	-1.64
ABUW_RS16160		copper resistance protein CopC	-1.64
ABUW_RS12460		hypothetical protein	-1.64
ABUW_RS12730		3-hydroxyacyl-CoA dehydrogenase	-1.64
ABUW_RS14590		hypothetical protein	-1.63
ABUW_RS11440	dapC	succinyl/diaminopimelate transaminase	-1.63
ABUW_RS14210		transketolase	-1.63
ABUW_RS07860	hfq	RNA chaperone Hfq	-1.63
ABUW_RS16440		phosphatase PAP2 family protein	-1.63
ABUW_RS18580	pgi	glucose-6-phosphate isomerase	-1.63
ABUW_RS03925		KilA-N domain-containing protein	-1.62
ABUW_RS00015	recF	DNA replication/repair protein RecF	-1.62
ABUW_RS10710	iscU	Fe-S cluster assembly scaffold IscU	-1.62
ABUW_RS00775		2-oxo acid dehydrogenase subunit E2	-1.62
ABUW_RS12200		CoA transferase	-1.62
ABUW_RS04655		Tim44 domain-containing protein	-1.62
ABUW_RS06635		YeaC family protein	-1.61
ABUW_RS05130		diguanylate cyclase	-1.61
ABUW_RS01215		DUF805 domain-containing protein	-1.61
ABUW_RS01645		antibiotic biosynthesis monooxygenase	-1.61
ABUW_RS04300	sucD	succinate--CoA ligase subunit alpha	-1.61
ABUW_RS03285		SRPBCC family protein	-1.60
ABUW_RS10655		AarF/ABC1/UbiB kinase family protein	-1.60
ABUW_RS02535		alpha/beta hydrolase	-1.60
sRNA65	sRNA65	sRNA65	-1.60
ABUW_RS03435		PepSY domain-containing protein	-1.59
ABUW_RS16655		energy transducer TonB	-1.59
ABUW_RS12885		hypothetical protein	-1.59
ABUW_RS00940		TetR/AcrR family transcriptional regulator	-1.58
ABUW_RS18050	cysK	cysteine synthase A	-1.58
ABUW_RS03895		helix-turn-helix domain-containing protein	-1.58
ABUW_RS12245		hypothetical protein	-1.58
ABUW_RS03445	yccS	TIGR01666 family membrane protein	-1.58
ABUW_RS08385	fumC	class II fumarate hydratase	-1.58
ABUW_RS18815		peptidylprolyl isomerase	-1.58
ABUW_RS11575	tauD	taurine dioxygenase	-1.58
ABUW_RS04170	lolA	outer membrane lipoprotein chaperone LolA	-1.58
ABUW_RS00300		4-hydroxy-tetrahydrodipicolinate synthase	-1.57
ABUW_RS14910		oxidoreductase	-1.57
ABUW_RS07955	pepN	aminopeptidase N	-1.57
ABUW_RS05195		nitronate monooxygenase	-1.57
ABUW_RS08820	clpS	ATP-dependent Clp protease adapter ClpS	-1.57
ABUW_RS08540		hypothetical protein	-1.57
ABUW_RS14805		PA4642 family protein	-1.57
ABUW_RS00295		hypothetical protein	-1.56
ABUW_RS18470		nuclear transport factor 2 family protein	-1.56
ABUW_RS09265		hypothetical protein	-1.56
ABUW_RS12610		SRPBCC family protein	-1.56
ABUW_RS08520		RNA-binding protein	-1.56
ABUW_RS02540	trxC	thioredoxin TrxC	-1.56
ABUW_RS01640		hypothetical protein	-1.56
ABUW_RS05205		hypothetical protein	-1.55
ABUW_RS00945		zinc-binding dehydrogenase	-1.55
ABUW_RS06710	rpoH	RNA polymerase sigma factor RpoH	-1.55
ABUW_RS09180		hypothetical protein	-1.54
ABUW_RS09285		PQQ-dependent sugar dehydrogenase	-1.54

ABUW_RS10490		HIT family protein	-1.54
ABUW_RS16640	msrA	peptide-methionine (S)-S-oxide reductase MsrA	-1.54
ABUW_RS10770		nucleoside-diphosphate sugar epimerase	-1.54
ABUW_RS11625	cydB	cytochrome d ubiquinol oxidase subunit II	-1.53
ABUW_RS13095		exodeoxyribonuclease VII large subunit	-1.53
ABUW_RS13365		cytochrome b	-1.53
ABUW_RS04490		metallophosphoesterase	-1.53
ABUW_RS03050		metal-dependent hydrolase	-1.53
ABUW_RS07085		hypothetical protein	-1.53
ABUW_RS10485		YARHG domain-containing protein	-1.52
ABUW_RS11730	yghU	glutathione-dependent disulfide-bond oxidoreductase	-1.52
ABUW_RS09290		cation:proton antiporter	-1.52
ABUW_RS03155		carbohydrate porin	-1.52
ABUW_RS02255		DUF3108 domain-containing protein	-1.51
ABUW_RS07225		SRPBCC family protein	-1.51
ABUW_RS11155		polyisoprenoid-binding protein	-1.51
ABUW_RS12530	tssC	type VI secretion system contractile sheath large subunit	-1.50
ABUW_RS12185		catalase family peroxidase	-1.50
ABUW_RS02665	ssb	single-stranded DNA-binding protein	-1.50
ABUW_RS06570		PhzF family phenazine biosynthesis protein	-1.50
ABUW_RS10845		biopolymer transporter ExbD	-1.50
ABUW_RS01485		TPM domain-containing protein	-1.50
ABUW_RS02670		hypothetical protein	-1.50
ABUW_RS09270		antibiotic biosynthesis monooxygenase	-1.50
ABUW_RS07220		SDR family oxidoreductase	-1.50
ABUW_RS05135		hypothetical protein	-1.49
ABUW_RS15870		mechanosensitive ion channel family protein	-1.48
ABUW_RS14155		hypothetical protein	-1.48
ABUW_RS03260		NADH:flavin oxidoreductase/NADH oxidase	-1.47
ABUW_RS03090		peroxiredoxin	-1.47
ABUW_RS06655		alpha/beta hydrolase	-1.46
ABUW_RS08840		alpha/beta hydrolase	-1.45
ABUW_RS07455	gloB	hydroxyacylglutathione hydrolase	-1.45
ABUW_RS02275		PhoH family protein	-1.45
ABUW_RS02180	rnr	ribonuclease R	-1.45
ABUW_RS17715	pbpG	D-alanyl-D-alanine endopeptidase PBP7/8	-1.45
ABUW_RS00020	gyrB	DNA topoisomerase (ATP-hydrolyzing) subunit B	-1.44
ABUW_RS12125		carboxymuconolactone decarboxylase family protein	-1.44
ABUW_RS13220		hypothetical protein	-1.44
ABUW_RS08430	adeN	multidrug efflux transcriptional repressor AdeN	-1.44
ABUW_RS06760		hypothetical protein	-1.44
ABUW_RS15290		NF038215 family lipoprotein	-1.44
ABUW_RS10015		phospholipase D family protein	-1.44
ABUW_RS16305	ilvN	acetolactate synthase small subunit	-1.43
ABUW_RS14555		site-specific DNA-methyltransferase	-1.43
ABUW_RS04090		hypothetical protein	-1.43
ABUW_RS05820		DUF3015 family protein	-1.43
ABUW_RS11435	glnD	[protein-Pil] uridylyltransferase	-1.43
ABUW_RS04865	pal	peptidoglycan-associated lipoprotein Pal	-1.42
ABUW_RS07765		outer membrane protein assembly factor	-1.41
ABUW_RS04295	sucC	ADP-forming succinate--CoA ligase subunit beta	-1.41
ABUW_RS18230		Dyp-type peroxidase	-1.41
ABUW_RS16740		zinc-binding alcohol dehydrogenase family protein	-1.41
ABUW_RS01670		superoxide dismutase family protein	-1.40
ABUW_RS05425		diaminobutyrate--2-oxoglutarate transaminase	-1.39
ABUW_RS08200		iron-containing alcohol dehydrogenase	-1.39
ABUW_RS10600		hypothetical protein	-1.38

ABUW_RS14730		RnfH family protein	-1.38
ABUW_RS08705		hypothetical protein	-1.38
ABUW_RS00810	glmM	phosphoglucosamine mutase	-1.38
ABUW_RS10135		hypothetical protein	-1.37
ABUW_RS05695		pirin family protein	-1.37
ABUW_RS05070	era	GTPase Era	-1.37
ABUW_RS06400		ORF6N domain-containing protein	-1.37
ABUW_RS11450		AraC family transcriptional regulator	-1.37
ABUW_RS04325		neutral zinc metalloproteinase	-1.37
ABUW_RS14570		hypothetical protein	-1.36
ABUW_RS05305		PhzF family phenazine biosynthesis protein	-1.36
ABUW_RS02300		DUF2789 domain-containing protein	-1.36
ABUW_RS12525		type VI secretion system tube protein Hcp	-1.36
ABUW_RS09555		alpha/beta hydrolase	-1.36
ABUW_RS13405		TetR/AcrR family transcriptional regulator	-1.36
ABUW_RS14055		DUF2239 family protein	-1.36
ABUW_RS02410		ClpXP protease specificity-enhancing factor	-1.36
ABUW_RS18055		GNAT family N-acetyltransferase	-1.36
ABUW_RS09020		SDR family oxidoreductase	-1.36
ABUW_RS00490		hypothetical protein	-1.36
ABUW_RS11680		triphosphoribosyl-dephospho-CoA synthase	-1.35
ABUW_RS02765	oxa-23	carbapenem-hydrolyzing class D beta-lactamase OXA-23	-1.35
ABUW_RS16890		glutathione S-transferase family protein	-1.35
ABUW_RS07755	coq7	2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinone monooxygenase	-1.34
ABUW_RS12470	tssK	type VI secretion system baseplate subunit TssK	-1.34
ABUW_RS00555		hypothetical protein	-1.34
ABUW_RS15090	fabG	3-oxoacyl-ACP reductase FabG	-1.34
ABUW_RS10690		phasin family protein	-1.33
ABUW_RS04745		HlyD family secretion protein	-1.33
ABUW_RS05475	sohB	protease SohB	-1.33
ABUW_RS04965	queC	7-cyano-7-deazaguanine synthase QueC	-1.33
ABUW_RS02915		hypothetical protein	-1.33
ABUW_RS01320		cation transporter	-1.32
ABUW_RS05430		aspartate aminotransferase family protein	-1.32
ABUW_RS06000	lipA	lipoyl synthase	-1.32
ABUW_RS10580		HAD family hydrolase	-1.32
ABUW_RS03770		RelA/SpoT domain-containing protein	-1.32
ABUW_RS06425		hypothetical protein	-1.31
ABUW_RS02475		metallophosphoesterase	-1.31
ABUW_RS07585		RDD family protein	-1.31
ABUW_RS10595		PepSY domain-containing protein	-1.31
ABUW_RS06770		hypothetical protein	-1.31
ABUW_RS16680	rpmG	50S ribosomal protein L33	-1.31
ABUW_RS07050		M48 family metalloprotease	-1.31
ABUW_RS04215		hypothetical protein	-1.31
ABUW_RS08095		universal stress protein	-1.30
ABUW_RS12475	tssA	type VI secretion system protein TssA	-1.30
ABUW_RS08195		acyl-CoA thioesterase	-1.30
ABUW_RS01890		outer membrane lipid asymmetry maintenance protein MlaD	-1.30
ABUW_RS01910		TIGR00730 family Rossmann fold protein	-1.30
ABUW_RS10060	ppk1	polyphosphate kinase 1	-1.29
ABUW_RS07965		molecular chaperone	-1.29
ABUW_RS14140		arylesterase	-1.28
ABUW_RS06250		hypothetical protein	-1.27
ABUW_RS08775		phospholipase A	-1.27
ABUW_RS08715		nitroreductase family protein	-1.27
ABUW_RS16355		Bax inhibitor-1/YccA family protein	-1.26

ABUW_RS00960	tenA	thiaminase II	-1.26
ABUW_RS06240		hypothetical protein	-1.26
ABUW_RS01020		hydrolase	-1.25
ABUW_RS15550		amidohydrolase	-1.25
ABUW_RS13000		hypothetical protein	-1.25
ABUW_RS00110		sodium-dependent transporter	-1.25
ABUW_RS01295		hypothetical protein	-1.25
ABUW_RS08435	glnG	nitrogen regulation protein NR(I)	-1.25
ABUW_RS03615		hypothetical protein	-1.25
ABUW_RS19540		conjugal transfer protein TraF	-1.25
ABUW_RS06765		hypothetical protein	-1.24
ABUW_RS00205	dkgB	2,5-didehydrogluconate reductase DkgB	-1.24
ABUW_RS09550		GNAT family N-acetyltransferase	-1.24
ABUW_RS02130		NAD(P)/FAD-dependent oxidoreductase	-1.23
ABUW_RS12880		hypothetical protein	-1.22
ABUW_RS16825	leuB	3-isopropylmalate dehydrogenase	-1.22
ABUW_RS05745	bauA	TonB-dependent ferric acinetobactin receptor BauA	-1.22
ABUW_RS18255		OsmC family protein	-1.21
ABUW_RS05805		murein L,D-transpeptidase	-1.21
ABUW_RS08405		D-amino acid dehydrogenase	-1.21
ABUW_RS18320		BolA family transcriptional regulator	-1.21
ABUW_RS17450		alpha/beta fold hydrolase	-1.20
ABUW_RS13450		GMC family oxidoreductase	-1.20
ABUW_RS01040		GFA family protein	-1.19
ABUW_RS01635		FAD-binding oxidoreductase	-1.19
ABUW_RS17985		TerC family protein	-1.19
ABUW_RS05330		DUF962 domain-containing protein	-1.19
ABUW_RS08155		acetyl-CoA C-acetyltransferase	-1.19
ABUW_RS09585		hypothetical protein	-1.19
ABUW_RS10840		MotA/TolQ/ExbB proton channel family protein	-1.19
ABUW_RS04505	groL	chaperonin GroEL	-1.19
ABUW_RS15260		LysE family transporter	-1.18
ABUW_RS13865		MerR family transcriptional regulator	-1.18
ABUW_RS03550		wax ester/triacylglycerol synthase family O-acyltransferase	-1.18
ABUW_RS17110		magnesium transporter CorA family protein	-1.18
ABUW_RS19565		hypothetical protein	-1.17
ABUW_RS05350	csy2	type I-F CRISPR-associated protein Csy2	-1.17
ABUW_RS13980		HupE/UreJ family protein	-1.17
ABUW_RS18705		acyl-CoA desaturase	-1.17
ABUW_RS17090		Hsp33 family molecular chaperone HsIO	-1.17
ABUW_RS08340		molybdopterin molybdotransferase MoeA	-1.16
ABUW_RS10375		GGDEF domain-containing protein	-1.16
ABUW_RS03915		Arc family DNA-binding protein	-1.16
ABUW_RS05360	cas6f	type I-F CRISPR-associated endoribonuclease Cas6/Csy4	-1.16
ABUW_RS09525		DEAD/DEAH box helicase family protein	-1.16
ABUW_RS16650		MotA/TolQ/ExbB proton channel family protein	-1.16
ABUW_RS17895		TniQ family protein	-1.15
ABUW_RS01950		dicarboxylate/amino acid:cation symporter	-1.15
ABUW_RS06630		NAD(+) kinase	-1.15
ABUW_RS14990		DNA primase	-1.15
ABUW_RS14900		hypothetical protein	-1.15
ABUW_RS02405		hypothetical protein	-1.15
ABUW_RS08335		bifunctional molybdenum cofactor biosynthesis protein MoaC/MoaB	-1.15
ABUW_RS07705		AarF/ABC1/UbiB kinase family protein	-1.14
ABUW_RS16675	rpmB	50S ribosomal protein L28	-1.14
ABUW_RS06970		hypothetical protein	-1.14
ABUW_RS10510		DUF2797 domain-containing protein	-1.13

ABUW_RS02715		BRCT domain-containing protein	-1.13
ABUW_RS05545		ATP-binding protein	-1.13
ABUW_RS10390	trpB	tryptophan synthase subunit beta	-1.13
ABUW_RS04980	carO	ornithine uptake porin CarO type 3	-1.13
ABUW_RS07380		DUF1295 domain-containing protein	-1.13
ABUW_RS04705		FAD-binding protein	-1.13
ABUW_RS00030		VTT domain-containing protein	-1.12
ABUW_RS00935	uvrA	excinuclease ABC subunit UvrA	-1.12
ABUW_RS16850		LysR family transcriptional regulator	-1.12
ABUW_RS11145		phosphodiester glycosidase family protein	-1.12
ABUW_RS02545		acyl-CoA thioesterase	-1.12
ABUW_RS05095		SDR family oxidoreductase	-1.12
ABUW_RS05355	csy3	type I-F CRISPR-associated protein Csy3	-1.12
ABUW_RS18725		thiol:disulfide interchange protein DsbA/DsbL	-1.12
ABUW_RS03010		META domain-containing protein	-1.11
ABUW_RS18995		metal/formaldehyde-sensitive transcriptional repressor	-1.10
ABUW_RS04515		MBL fold metallo-hydrolase	-1.10
ABUW_RS05395	fabR	HTH-type transcriptional repressor FabR	-1.10
ABUW_RS04410	ftsH	ATP-dependent zinc metalloprotease FtsH	-1.10
ABUW_RS04985	cbl	CysB family HTH-type transcriptional regulator	-1.09
ABUW_RS17905		DDE-type integrase/transposase/recombinase	-1.09
ABUW_RS15940		hypothetical protein	-1.09
ABUW_RS03245	mutM	bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase	-1.09
ABUW_RS18150		glutathione peroxidase	-1.08
ABUW_RS05310		insulinase family protein	-1.08
ABUW_RS15730		hypothetical protein	-1.08
ABUW_RS04870	tolB	Tol-Pal system beta propeller repeat protein TolB	-1.08
ABUW_RS05955		multifunctional CCA addition/repair protein	-1.08
ABUW_RS00560		DUF924 domain-containing protein	-1.08
ABUW_RS04475	glpD	glycerol-3-phosphate dehydrogenase	-1.08
ABUW_RS19995		hypothetical protein	-1.07
ABUW_RS04175		DUF3298 domain-containing protein	-1.07
ABUW_RS16895		YafY family transcriptional regulator	-1.07
ABUW_RS09410		TetR/AcrR family transcriptional regulator	-1.07
ABUW_RS18525	acnD	Fe/S-dependent 2-methylisocitrate dehydratase AcnD	-1.07
ABUW_RS18245		SPOR domain-containing protein	-1.07
ABUW_RS10860		malate synthase G	-1.06
ABUW_RS13870		hypothetical protein	-1.06
ABUW_RS03195		OmpA family protein	-1.06
ABUW_RS05485		DUF2238 domain-containing protein	-1.06
ABUW_RS18875		MBL fold metallo-hydrolase	-1.06
ABUW_RS04210		iron-containing alcohol dehydrogenase	-1.06
ABUW_RS16970		ABC transporter	-1.05
ABUW_RS02980		acyl-CoA dehydrogenase C-terminal domain-containing protein	-1.05
ABUW_RS02285		lytic transglycosylase domain-containing protein	-1.05
ABUW_RS08660	map	type I methionyl aminopeptidase	-1.05
ABUW_RS18640	wecB	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	-1.04
ABUW_RS00665		ankyrin repeat domain-containing protein	-1.04
ABUW_RS13310		NADP(H)-dependent aldo-keto reductase	-1.04
ABUW_RS04920		multidrug efflux MFS transporter	-1.04
ABUW_RS16950		DMT family transporter	-1.04
ABUW_RS11110		NAD-dependent deacylase	-1.04
ABUW_RS19620		DIP1984 family protein	-1.03
ABUW_RS00890		response regulator transcription factor	-1.03
ABUW_RS12130		NAD-dependent succinate-semialdehyde dehydrogenase	-1.03
ABUW_RS05910		hypothetical protein	-1.02

ABUW_RS16805		AraC family transcriptional regulator	-1.02
ABUW_RS16375	grxC	glutaredoxin 3	-1.02
ABUW_RS02995		response regulator	-1.02
ABUW_RS15365	upp	uracil phosphoribosyltransferase	-1.02
ABUW_RS14720	fur	ferric iron uptake transcriptional regulator	-1.01
ABUW_RS05385	rapA	RNA polymerase-associated protein RapA	-1.01
ABUW_RS03570		NAD(P)H-dependent oxidoreductase	-1.01
ABUW_RS14620		hypothetical protein	-1.01
ABUW_RS13275		hypothetical protein	-1.01
ABUW_RS19090		hypothetical protein	-1.01
ABUW_RS07090		ATP-binding protein	-1.00
ABUW_RS00170		efflux RND transporter permease subunit	-1.00
ABUW_RS16265		DUF3298 domain-containing protein	-1.00
ABUW_RS03910		hypothetical protein	-1.00
ABUW_RS18635	wecC	UDP-N-acetyl-D-mannosamine dehydrogenase	-1.00
ABUW_RS04310		hypothetical protein	-1.00
ABUW_RS06620		tetratricopeptide repeat protein	-1.00
ABUW_RS03730		hypothetical protein	-1.00