

1 **The *abal/abaR* quorum sensing system effects pathogenicity in *Acinetobacter***
2 ***baumannii***

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17 **ABSTRACT**

18 *Acinetobacter baumannii* is a Gram-negative pathogen that has emerged as one of
19 the most troublesome pathogens for health care institutions globally. Bacterial
20 quorum sensing (QS) is a process of cell-to-cell communication that relies on the
21 production, secretion and detection of autoinducer (AI) signals to share information
22 about cell density and regulate gene expression accordingly. In this study, we

performed a comprehensive set of experiments show that deletion of quorum sensing genes showed differences in growth characteristics, morphology, biofilm formation and virulence, and increased susceptibility to some antimicrobials and exhibited motility defects. RNA-seq analysis indicated that genes involved in various aspects of energy production and conversion, Valine, leucine and isoleucine degradation and lipid transport and metabolism showed different expression.

IMPORTANCE Previous studies on bacterial quorum sensing mainly focused on biofilm formation and motility and antibiotic resistance. In this study, we focused on detecting the role of the *abal/abaR* QS system in the virulence of *A. baumannii*. Our work provides a new insight into *abal/abaR* quorum sensing system effects pathogenicity in *A. baumannii*. We propose that targeting the AHL synthase enzyme *abal* could provide an effective strategy for attenuating virulence. On the contrary, interdicting the autoinducer synthase–receptor *abaR* elicits unpredictable consequences, which may lead to enhanced bacterial virulence.

KEYWORDS: *A. baumannii*, quorum sensing, *abal/abaR*, virulence, transcriptome

INTRODUCTION

Acinetobacter baumannii is a Gram-negative pathogen that has emerged as one of the most troublesome pathogens for health care institutions globally. *A. baumannii* infections are increasingly difficult to treat because of multidrug-resistance in most strains causing infection in intensive care units (ICUs) (1). Virulence factors were used by bacteria that enable successful interaction with and subsequent adhesion and invasion of the human host (2). Previous studies have emphasized the importance of

45 iron acquisition, transports, cell-associated pili, lipopolysaccharides, outer membrane
 46 proteins such as *ompA*, *omp33*, *surA1* for virulence (3-5), but studies of quorum
 47 sensing effects pathogenicity in *A. baumannii* are limited. Bacterial quorum sensing
 48 (QS) is a process of cell-to-cell communication that relies on the production,
 49 secretion and detection of autoinducer (AIs) signals to share information about cell
 50 density and regulate gene expression accordingly (6). AIs are involved in the
 51 regulation of varied biological functions, including expression of virulence gene in
 52 *Vibrio cholera* (7), *Pseudomonas aeruginosa* PAO1 (8), *Staphylococcus aureus* (9),
 53 *Escherichia coli* (10) and other types of bacteria.
 54 *A. baumannii* presenting a typical quorum sensing (QS) system (*abal/abaR*) has been
 55 described(11). The *abal* gene encodes 183 amino acids, and this protein was
 56 predicted to function in signal transduction. The *abaR* gene encodes 238 amino
 57 acids, this protein is an autoinducer synthase–receptor (11). Previous studies on *A.*
 58 *baumannii* had focused on the role of quorum sensing systems in drug resistance,
 59 biofilm formation and motility (12, 13), but studies of quorum sensing effects
 60 pathogenicity in *A. baumannii* are poor.
 61 In this study, we used *A. baumannii* strain ATCC 17978 which has been the most
 62 frequently used model for scientific studies over the past two decades (2). A previous
 63 study isolated and characterized the autoinducer synthase *abal* from *Acinetobacter*
 64 *baumannii* M2, but failed to create an *abaR* deletion mutant for unknown reasons
 65 (14). To explore the role of the *abal/abaR* QS system in drug resistance, biofilm
 66 formation and virulence of *A. baumannii*, $\Delta abal$ and $\Delta abaR$ mutants of strain ATCC

17978 were created. We also made double mutant $\Delta abaIR$. The transcriptomes of WT, $\Delta abaI$, $\Delta abaR$ and $\Delta abaIR$ were determined by RNA-sequencing (RNA-seq).

RESULTS

The mutants showed differences in growth characteristics and morphology

To test the role of the *abal/abaR* QS system in *A. baumannii* growth curve, we determined by measuring the optical density (OD) of the culture over time. The growth of the $\Delta abaR$ and $\Delta abaIR$ mutants did not differ from that of the parent strain (Fig. 1A). The complemented strain $\Delta abaR$ (pME*abaR*) and overexpressed strains WT(pME*abal*), WT(pME*abaR*) also showed growth profiles similar to those of the wild type(Fig. 1A), suggesting that the gene *abaR* is not essential for *A. baumannii* growth. In contrast, $\Delta abaI$ mutant showed visibly slowed growth at the logarithmic phase. Growth of the $\Delta abaI$ mutant was partly rescued by expression of *abal* via the pME6032-derived plasmid pME*abal* (Fig. 1A). The empty vector pME6032, used as a control, did not affect the growth profile of *A. baumannii* ATCC 17978(Fig. 1A). These results demonstrated that *abal* affect the growth of *A. baumannii*. Subsequently, the morphology of the bacteria was observed by transmission electron microscopy. As shown in Figure 1B, WT was attached with extracellular secretions. $\Delta abaI$ mutant cell edges were transparent. $\Delta abaR$ mutant strains cytoplasmic density is lower. There was no obviously change in $\Delta abaIR$ mutant, but around the cell adhered partial secretions. Morphology of the $\Delta abaI$ mutant was partly rescued by expression of *abal* via the pME6032-derived plasmid pME*abal*. Morphology of the $\Delta abaR$ mutant was rescued by expression of *abaR* via the pME6032-derived plasmid pME*abaR*.

There was no significant difference between WT and overexpressed strain WT(pME*abal*). The overexpressed strain WT(pME*abaR*) attached a large number of extracellular secretions. The empty vector pME6032, used as a control, did not affect the morphology of *A. baumannii* ATCC 17978. These results indicated that QS is closely related to cell morphology and extracellular secretions.

Mutants showed increase susceptibility to antimicrobials

To determine whether deletion of quorum sensing genes changed in the drug resistance, the MICs of commonly used antibiotics for strains was determined. There was a decrease in the MICs of Kanamycin, Gentamicin, Penicillin, Streptomycin, Meropenem, Imipenem and Ampicillin for quorum sensing genes deletions compared to WT. Drug susceptibility of Δ *abal* and Δ *abaR* mutants were partly rescued by expression of *abal* and *abaR* via plasmid pME*abal* and pME*abaR* respectively. Overexpressed strain WT(pME*abal*) were more resistant in Cefepime and Cefperazone-Sulbactam. WT(pME*abaR*) were more resistant in Kanamycin, Streptomycin, Ceftizoxime, Cefepime, Cefperazone-Sulbactam and Paraxiline-tazobatan. The empty vector pME6032, used as a control, partly affect the drug susceptibility of *A. baumannii* ATCC 17978 (Table 4). These results indicated that QS affect strain resistance.

Screening of strains for AHLs production

To detect the effect of quorum sensing system on AHL of the strains, two different biosensor strains were used. As a result, no strains were found to produce AHLs based on the development of purple coloration in CV026 reporter strain (Fig. 2A to

C). $\Delta abal$, $\Delta abaR$ and $\Delta abalR$ were not observed to produce AHLs based on the development of green coloration in *A. tumefaciens* KYC55 reporter strain. AHLs production of $\Delta abal$ and $\Delta abaR$ mutants were rescued by expression of *abal* and *abaR* via plasmid pME*abal* and pME*abaR*, respectively. The empty vector pME6032, used as a control, did not affect the AHLs production of *A. baumannii* ATCC 17978 (Fig. 2D to F). These results indicate that *abal* and *abaR* both can affect AHLs production and *A. baumannii* may produce only long-chain signal molecules, but not short-chain AHLs.

Surface-associated motility relies on quorum sensing

To explore the role of quorum sensing in motility, we tested these strains surface motility phenotype on LB media supplemented with 0.3% agar. As a result, $\Delta abal$, $\Delta abaR$ and $\Delta abalR$ mutants compared with wild-type strain showed no obvious motility, motility of $\Delta abal$ mutants were not rescued by expression of *abal* via the plasmid pME*abal*, motility of $\Delta abaR$ mutants were partly rescued by expression of *abaR* via the plasmid pME*abaR*. The empty vector pME6032, used as a control, has an inhibitory effect on the motility of *A. baumannii* ATCC 17978. Overexpressed strain WT(pME*abaR*) compared with wild-type strain showed significantly increased motility. There was no significant difference between overexpressed strain WT(pME*abal*) and WT in the motility (Fig. 3A, B). These results indicated that quorum sensing system affects the motility of bacteria and *abaR* regulates bacterial motility.

Biofilm formation

To investigate the role of quorum sensing in biofilm formation on an abiotic surface,

we cultivated the strains mutants in 96-well plates for 24 h at 37°C. As a result, Filaments were formed in the culture medium of wild strain, mutant strains *ΔabaI*, *ΔabaR* had dot-like biofilm formation on the surface of liquid, *ΔabaIR* mutant strain had no biofilm on the liquid surface, there were dot-like biofilms on the liquid surface of *ΔabaI*(pME*abaI*) and *ΔabaR*(pME*abaR*) and they were connected into pieces. The biofilm on the liquid surface of the overexpressed strain WT(pME*abaI*) was lamellar, while the biofilm on the liquid surface of WT(pME*abaR*) was spot-like but thick (Fig. 4A). The absorbance of bacterial solution was detected, and the results were shown in the Figure 4B, there were significant difference between the absorbance of the parental strain and mutants *ΔabaI*, *ΔabaR*, however, for mutant *ΔabaIR* showed no difference. The absorbance of *ΔabaI* mutants were not rescued by expression of *abaI* via the plasmid pME*abaI*, absorbance of *ΔabaR* mutants were rescued by expression of *abaR* via the plasmid pME*abaR*. The absorbance of overexpressed strain WT(pME*abaR*) was significantly higher than that of wild strain. The biofilm forming ability of the strains were determined by crystal violet biofilm assay, and the differences between the wild-type and mutant strains were calculated. Compared with wild strains, the biofilm formation of all strains was significantly decreased, except for the overexpressed strain WT(pME*abaR*), which was significantly higher than that of wild strain (Fig. 4C). The results indicated that quorum sensing system affects the biofilm formation of bacteria.

Serum killing

Serum sensitivity has been involved in the toxic mechanisms of *A. baumannii*, to

elucidate the virulence of strains, we compared the serum sensitivity of mutants to WT. As shown in Fig 5 A, WT, *abaR* and WT(pME*abaR*) survived after incubation in serum, whereas Δ *abal*, Δ *abal*(pME*abal*) and Δ *abaIR* were entirely killed after 1 h at 37°C. The serum sensitivity of Δ *abal* mutants were not rescued by expression of *abal* via the plasmid pME*abal*, serum sensitivity of Δ *abaR* mutants were rescued by expression of *abaR* via the plasmid pME*abaR*. The empty vector pME6032, used as a control, did not affect the serum sensitivity of *A. baumannii* ATCC 17978. These results indicated that WT and Δ *abaR* were highly resistant to the killing action of serum, in contrast, Δ *abal* and Δ *abaIR* mutants were much more serum sensitive, showing a significant difference.

Quorum sensing plays a role in virulence in *G. mellonella* infection models

Quorum sensing controls the production of virulence factors in many bacterial species and is regarded as an attractive target to combat bacterial pathogenicity (15). To explore whether quorum-sensing genes are an important virulence factor determinant for *A. baumannii* in *G. mellonella*, we assessed the virulence of the quorum-sensing mutant strains compared to the isogenic parent strain ATCC 17978. Δ *abal* and Δ *abaIR* mutants were completely avirulent in this assay, while Δ *abaR* mutant remained fully virulent, killing *G. mellonella* larva as toxic as the wild type (Fig. 5B). Consistent with this finding, Laura Fernandez-Garcia found that injection of *G. mellonella* larvae with the *A. baumannii* ATCC 17978 strain caused higher mortality than injection with mutant *A. baumannii* ATCC 17978 Δ *abal* (16). The virulence of Δ *abal* mutant was not rescued by expression of *abal* via the plasmid

pME*abal*, virulence of Δ *abaR* mutant was rescued by expression of *abaR* via the plasmid pME*abaR*. The empty vector pME6032, used as a control, affect the virulence of *A. baumannii* ATCC 17978. The virulence of overexpressed strain WT(pME*abal*) and WT(pME*abaR*) were significantly reduced compared to the parent strain ATCC 17978. The results indicated that quorum sensing system plays a role in virulence in *G. mellonella* infection models.

Quorum sensing plays a role in virulence in mouse infection models

Whether these quorum-sensing genes of *A. baumannii* are important for virulence to a mammalian system is currently unknown. To evaluate the virulence of strains, we established a bacteremia model in mice by intraperitoneal injection of *A. baumannii*. In the experiments we analyzed the survival of infected mice with this model, found that a dose of approximately 1.8×10^8 CFU of Δ *abal* and Δ *abaIR* mutants were unable to cause lethality, but only one mouse (10/group) survived in the WT group, and all the mice in Δ *abaR* group died (date not shown) after 48 h. Subsequently, we used a dose of approximately 1.2×10^8 CFU of bacteria infected with 10 mice per group for survival studies. We observed that Δ *abal* and Δ *abaIR* mutants were unable to cause lethality; WT exhibited a low fatality rate, but Δ *abaR* and complemented strain Δ *abaR*(pME*abaR*) can cause more deaths (Fig. 6A). These results indicated that deletion of *abal* results in weaker toxicity in mouse models, while deletion of *abaR* results in enhanced virulence. To explore the virulence of mutants in host resistance against *A. baumannii* infection, the blood, lungs and spleens from BALB/C were collected at various time points after injected with 1.2×10^8 CFU of *A. baumannii*. We

analyzed bacterial burdens in the blood, lung and spleen of mice infected for 4 h, 24 h and 72 h. As a result, WT, $\Delta abaR$ mutant and complemented strain $\Delta abaR(pMEabaR)$ resulted in an increase in bacterial counts, $\Delta abal$ and $\Delta abalR$ mutants exhibited a remarkable reduction in the burden in blood, lung, and spleen at 4 h postinoculation. More specifically, as shown, $\Delta abal$ and $\Delta abalR$ mutants displayed a high serum clearance rate and resulted in a significant decrease in bacteremia at 4 h postinoculation. There were no differences at 24 h (Fig. 6B). The bacteria were completely eliminated at 72 hours (data not shown). These results indicated that quorum sensing system plays a role in virulence in mouse infection models.

Mutants causes differential gene expression in *A. baumannii* ATCC 17978

To identify transcriptional activity dependent on *abal/abaR* function, RNA-seq analysis was performed on *abal/abaR* mutants and WT strain. A total of 463 genes were classified as differentially expressed in mutants relative to WT. Compared with WT, in $\Delta abal$ mutant, a total of 159 protein-coding genes (out of 3848) were identified as differentially expressed by a log2-fold change greater than 1 or less than -1 ($P \leq 0.05$) (126 with increased expression, 33 with decreased expression). Deletion of *abaR* had a larger impact on the transcriptome of strain ATCC 17978, with the differential expression of 324 genes (211, 113 up down regulated). $\Delta abalR$ mutant had a total of 123 differentially expressed genes (79 genes with increased expression, 44 with decreased expression) (Fig. 7A to C) (Supplementary table). These results revealed that partial changes in gene expression occur with changes in

abal/abaR. To validate our RNA-seq analysis, quantitative reverse transcription qRT-PCR was used to validate the 10 upregulated genes (Fig. 7D). The results were consistent with the high-throughput sequencing data.

COGs annotation

To link transcriptional reprogramming by *abal/abaR* to function, differentially expressed genes were categorized into COGs (17, 18). The COG enrichment analysis identified that 7% of the genes belonging to the COG category [C] Energy production and conversion, were significantly repressed, and 10% of the genes were associated with the COG category [Q] Secondary metabolites biosynthesis, transport and catabolism, were highly regulated in Δ *abal* mutant. We observed a high proportion of genes with increased expression in Δ *abaR* mutant that encoded proteins involved in [I] Lipid transport and metabolism (21%), [Q] Secondary metabolites biosynthesis, transport and catabolism (18%), [G] Carbohydrate transport and metabolism (12%), [C] Energy production and conversion (11%) and [E] Amino acid transport and metabolism (10%), while a strong decrease in [J] Translation, ribosomal structure and biogenesis(24%). In Δ *abalR* mutant, 4% of the genes belonging to the COG category [C] Energy production and conversion, and [I] Lipid transport and metabolism were down-regulated, while 5% of the genes belonging to the COG category [G] Carbohydrate transport and metabolism were up-regulated (Fig. 8).

GO and KEGG pathways enrichment analysis of DEGs

The functions of the differentially expressed genes were annotated and classified gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway

enrichment analyses. The top 30 of significant GO terms were divided into two major categories—biological process and cellular component in $\Delta abaI$ mutant, as shown in Figure 9A. Among the biological processes, the DEGs were distributed to xenobiotic metabolic process, toxin metabolic/catabolic process, auxin metabolic /catabolic process, phenylacetate catabolic process and so on. In the cellular component field, DEGs were belonged to respiratory chain complex I, plasma membrane respiratory chain complex I, NADH dehydrogenase complex and respiratory chain. The top 30 significant GO terms were divided into three major categories—biological process, cellular component and molecular function in $\Delta abaR$ mutant, as shown in Figure 9C. Among the biological processes, the DEGs were distributed to ribosome assembly, translation, ribonucleoprotein complex assembly, organelle assembly, ribonucleoprotein complex subunit organization and peptide biosynthetic process. In the cellular component field, DEGs were belonged to cytosolic ribosome, ribosome, ribonucleoprotein complex, organelle part and cytosolic part. In molecular function, DEGs were responsible for structural constituent of ribosome, structural molecule activity and rRNA binding. The top 30 significant GO terms were divided into three major categories—biological process, cellular component and molecular function in $\Delta abaIR$ mutant, as shown in Figure 9E. Among the biological processes, the DEGs were distributed to response to metal ion, response to organonitrogen compound, cellular response to stress and anion transport. In the cellular component field, DEGs were belonged to outer membrane–bounded periplasmic space, periplasmic space, cell envelope and envelope. In molecular function, DEGs were responsible for copper

ion binding, cation/amino acid/organic acid/ organic anion transmembrane
transporter activity.

KEGG pathway enrichment suggested that DEGs of $\Delta abal$ mutant were significantly enriched in the pathways related to Phenylalanine metabolism, Oxidative phosphorylation, Benzoate degradation, Tryptophan metabolism, Arginine and proline metabolism, Fatty acid degradation and so on (Fig. 9 B). DEGs of $\Delta abaR$ mutant were mainly involved in the pathways related to Ribosome, Valine, leucine and isoleucine degradation, Propanoate metabolism, Pyruvate metabolism, Phenylalanine metabolism, Fatty acid degradation and so on (Fig. 9D). DEGs of $\Delta abaIR$ mutant were mainly involved in the pathways related to ABC transporters, Sulfur metabolism Nicotinate and nicotinamide metabolism and so on (Fig.9 F).

Given the different phenotypes of $\Delta abal$, $\Delta abaR$ and $\Delta abaIR$ mutants, the RNA-seq analysis revealed a subset of the genes that was most highly activated or suppressed by quorum sensing system, as shown in Figure 7B. We centralized our analysis on the gene subsets whose transcription was down in $\Delta abal$ and $\Delta abaR$ and $\Delta abaIR$ mutants, the quorum sensing gene (*abal* AUO97_RS06645) and nearby locus (AUO97_RS06600–06630) showed strongly reduced transcription. One study found that in *A. baumannii* M2 strain quorum sensing mediated by the *abal* is required for motility (19). We assessed the surface motility of the mutants, as shown in Figure 3. We observed that wild-type strain exhibited a robust surface motility phenotype and the mutants did not exhibit any signs of motility.

We mainly analyzed the gene expression of each group. Hemerythrin-like proteins

have an effect on oxidation-reduction regulation and antibiotic resistance (20).

AUO97_RS11650 (hemerythrin) was down-regulated in $\Delta abal$ mutant, and other antimicrobial resistance genes including AUO97_RS07490 (*mexK*), AUO97_RS07485 (*mexJ*), AUO97_RS07485 (efflux RND transporter periplasmic adaptor subunit) and AUO97_RS05665 (beta-lactamase domain protein), were down regulated. One gene, AUO97_RS16540 (*AdeA/AdeI* family multidrug efflux RND transporter periplasmic adaptor subunit) had 1.2-fold increased expression in $\Delta abaR$ mutant, while the expression of this gene was not changed in the $\Delta abaIR$ mutant. We then assessed the antimicrobial susceptibility of the mutants, as shown in Table 4, susceptibility of mutants towards a part of antimicrobials increased.

The *csu* operon is composed of 6 genes (*csuA/BABCDE*) and play a central role in initial bacterial attachment, and biofilm formation on abiotic surfaces (21). In $\Delta abal$ mutant, the *CsuA/BABCDE* chaperone-usher pili assembly system was showed high expression, except for the *CsuA* (AUO97_RS19210) gene. In $\Delta abaR$ mutant, *CsuA/B* (AUO97_RS19215), *CsuA* (AUO97_RS19210), *CsuB* (AUO97_RS19205) and *CsuC* (AUO97_RS19200) were highly expressed, whereas in the $\Delta abaIR$ mutant, only *CsuA/B* (AUO97_RS19215) was highly expressed. *CsuA/B*, which is predicted to form part of the type I pili rod that was up-regulated in all mutants. Of particular interest is their regulator genes *bfmR-bfmS*, which did not change in all mutants. Biofilm formation was observed on the liquid surface of the $\Delta abal$ and $\Delta abaR$ mutant (Fig. 4A). Previously study found that *CsuC* and *CsuE* are required in the early steps of biofilm formation (21). In some *A. baumannii* strains biofilms are not essential for

virulence (22). Apart from the *csu* operon, other genes controlled by quorum sensing that may have relations with biofilm formation. A1S_0644 (AUO97_RS08180), a hypothetical protein involved in biofilm formation was repressed in the $\Delta abaR$ mutant.

Secreted bacterial proteins can mediate serum resistance, a secreted serine protease which termed PKF is required for serum resistance and inhibits biofilm formation in *A. baumannii* (23). In $\Delta abaR$ mutant, PKF (AUO97_RS01525) was highly expressed, and no difference was observed in the $\Delta abal$ and $\Delta abalR$ mutants. We assessed the serum sensitivity test and the ability of mutant to form biofilms on abiotic surface. As shown in (Fig. 5A and Fig.4), WT and $\Delta abaR$ survived after incubation in serum, whereas $\Delta abal$ and $\Delta abalR$ were entirely killed after 1 h at 37°C. There was a remarkable decrease in the biofilm formation by $\Delta abaR$ mutant. Apart from this gene, other genes that may be associated with serum resistance and biofilm formation may be regulated by quorum sensing.

NADH is mainly involved in material and energy metabolism in cells, which is transferring energy to ATP synthesis through oxidative phosphorylation on the mitochondrial inner membrane (24, 25). In the respiratory chain of *A. baumannii*, there are 14 NADH-quinone oxidoreductase subunits involved in NADH dehydrogenase, which includes *NuoA-NuoN*. In $\Delta abal$ mutant, a subset of genes including AUO97_RS10980-11015 (*NuoG*, *NuoH*, *NuoI*, *NuoJ*, *NuoK*, *NuoL*, *NuoM* and *NuoN*) were all down-regulated (Fig. 10A). In $\Delta abaR$ mutant AUO97_RS11000 (*NuoK*) and AUO97_RS11015 (*NuoN*) were down-regulated, and there was no change in

331 *ΔabaIR* mutant. One study found that these genes are essential affect growth in LB
332 medium (26). We then assessed the growth characteristics and morphology of the
333 mutants, as shown in Figure 1A, 1B, *ΔabaI* mutant showed slightly slowed growth at
334 the logarithmic phase, the cytoplasm of the *ΔabaI* mutant appeared to be
335 transparent, and the cytoplasmic density of *ΔabaI* mutant is relatively low. These
336 genes play a significant role in mediating cell growth and energy metabolism in *A.*
337 *baumannii*. Apart from NADH dehydrogenase, other genes that may be associated
338 with cell growth and energy metabolism may be regulated by quorum sensing. In
339 *ΔabaI* mutant, a subset of genes involved in benzoate degradation (AUO97_RS17065-
340 17085) and tryptophan metabolism and limonene and pinene degradation were up-
341 regulated, this strain may utilize the beta-ketoadipate pathway and tryptophan for
342 energy supply (Fig. 10A).

343 The phenylacetic acid (PAA) catabolic pathway encoded by *paa* operon is a key route
344 in the catabolism of the Krebs cycle and this pathway is thought to contribute to
345 bacterial virulence (27, 28). The cluster is composed of 15 coding sequences (*paaZ*,
346 *paaA*, *paaB*, *paaC*, *paaD*, *paaE*, *paaF*, *paaG*, *paaH*, *paaI*, *paaK1*, *paaK2*, *paaX*, *paaY*
347 and *paaI*). In *ΔabaR* mutant, the *paa* operon was highly expressed (Fig. 10B). In *ΔabaI*
348 mutant, AUO97_RS14165 (*paaZ*), AUO97_RS14170 (*paaA*), AUO97_RS14175 (*paaB*),
349 AUO97_RS14180 (*paaC*), AUO97_RS14185 (*paaD*), AUO97_RS14190 (*paaE*),
350 AUO97_RS14195 (*paaF*), AUO97_RS14215 (*paaK1*) were highly expressed (Fig. 10A),
351 and the expression of this operon was not changed in the *ΔabaIR* mutant. Branched
352 chain amino acids (BCAAs), including leucine (Leu), isoleucine (Ile), and valine (Val), is

vital to both growth and virulence in bacteria (29, 30). In *ΔabaR* mutant, the Valine, leucine and isoleucine degradation pathway was up-regulated (Fig. 10B). The BCAAs serve as precursors for branched-chain fatty acids (BCFAs), which are predominant membrane fatty acids, the BCAAs are key co-regulators of virulence factors. In *ΔabaR* mutant, there are 27 genes involved in the propanoate metabolism pathway was up-regulated (Fig. 10B). In *Δabal* mutant, AUO97_RS14195, AUO97_RS16430, AUO97_RS06660, AUO97_RS18630 and AUO97_RS12705 involved in the propanoate metabolism pathway was up-regulated. In *ΔabaIR* mutant, AUO97_RS14380, AUO97_RS14375, AUO97_RS14370 involved in the propanoate metabolism pathway was up-regulated. Lipids play an important role in both the physiology and pathophysiology of living systems (31). Membrane phospholipids play a key role in the defense against antimicrobials, including host fatty acids (32-34). The COG enrichment analysis indicated that a large amount of genes with predicted functions in [I] Lipid transport and metabolism (21%), were up-regulated in *ΔabaR* mutant (Fig. 8). PAA, BCAAs and Lipid transport and metabolism may play a protective role against the host and serum. The K locus regulates the production of complex polysaccharides to protect against killing by host serum and enhance virulence in animal models of infection (35). In the K locus (O-glycosylation and wzy-dependent capsule synthesis locus) (AUO97_RS06870–06965), the gene AUO97_RS06875 (UDP-glucose 4-epimerase Gale) showed weakened transcription in the *Δabal* and *ΔabaIR* mutants by a 1.7-fold decrease and a 1.6-fold decrease, respectively, while there was no change in *ΔabaR* mutant. AUO97_RS13365 (*OmpA* family protein), a naturally

glycosylated protein in *A. baumannii* ATCC 17978, was expressed with a 1.8-fold increase in $\Delta abaR$ strain, and no difference in $\Delta abal$ and $\Delta abaIR$ mutants was observed. Ribosomal proteins (RPs) are well-known for their role in mediating protein synthesis and maintaining the stability of the ribosomal complex, which includes small and large subunits. There were 36 genes encoding for ribosomal proteins that exhibited reduced expression in $\Delta abaR$ mutant strain (Fig. 10B). 23 (L1-6, L9-13, L15-20, L22-23, L25, L28-29, L35) of them were associated with the large subunit while the remaining 13 (S2-8, S10-11, S14, S17-19) were associated with the small subunit. This change may enable *A. baumannii* to ‘fine-tune’ their proteomes to regulate the pathogenicity of bacteria. There was no change in $\Delta abal$ and $\Delta abaIR$ mutants. We assessed the virulence of the mutant in *G. mellonella* and mouse and serum sensitivity tests. As shown in Figure 5B and Figure 6 and Figure 5A, $\Delta abaR$ mutant enhances more virulence and serum resistance, while $\Delta abal$ and $\Delta abaIR$ mutants markedly attenuated the virulence of *A. baumannii*. The selected genes (*paaG*, *paaH*, *paaJ*, *paaK2*, *paaX*, *paaY* and *paal*) encode proteins in the PAA catabolic pathway, BCAAs, the capsule synthesis locus *GalE* and *OmpA* may contribute to virulence.

DISCUSSION

A. baumannii has become a very important hospital-acquired pathogen. Bacterial virulence is the prime determinant for the deterioration of an infected patient’s health. Quorum sensing (QS) is a cell-to-cell communication system utilized by bacteria to promote collective behaviors. Many bacteria use quorum sensing (QS) to

control virulence.

In the present study, we focused on detecting the role of the *abal/abaR* QS system in the virulence of *A. baumannii*. The mutant lacking *abal* is believed to be less virulent than wild-type strain. In contrast, *abaR* mutants were significantly more pathogenic than wild-type strain. This result was confirmed in our study by injection of *G. mellonella* larvae and a mouse model of infection and serum killing test. Our transcriptomic analysis results revealed that deletion of *abal* leads to the significant repression of energy production and conversion genes. The connection between energy metabolism and virulence has been reported in a multitude of bacteria. In *Vibrio cholerae*, the expression of virulence regulatory protein *ToxT* is affected by the NADH via respiration activity (36). In *Pseudomonas savastanoi*, *RhpR* directly regulate multiple metabolic pathways and phosphorylation to specifically control virulence (37). Therefore, *abal* may indirectly control bacterial virulence by inducing the differential expression of some key genes involved in NADH dehydrogenase in the respiratory chain. Deletion of *abaR* enhances more cytotoxicity and immune evasion. RNA-Seq analysis indicated that deletion of *abaR* leads to the significant overexpression of lipid transport and metabolism, carbohydrate transport and metabolism and amino acid transport and metabolism genes. Lipid metabolism plays a key role in the pathogenicity of some intracellular bacteria (38). It has been observed that lipids are the main carbon and energy source of *M. tuberculosis*, which switches from carbohydrate utilization to the fatty acid utilization pathway for the establishment of a successful infection(39). *A. baumannii* is a ubiquitous, facultative

intracellular bacterial pathogen (40). $\Delta abaR$ mutant may enhance lipid transport and metabolism to plays a protective role against the host. $\Delta abaIR$ mutant was slightly more pathogenic than $\Delta abaI$ mutants but less pathogenic than the $\Delta abaR$ mutants. This result was verified in our study by injection bacteria into *G. mellonella* larvae. Virulence through the intermediated phenylacetate catabolism pathway has been found in *A.baumannii*, and deletion of *paaE* attenuated *A. baumannii* virulence in mouse septicemia model (27). In *Burkholderia cenocepacia*, *paaA* and *paaE* insertional mutants showed reduced virulence, and interruption of *paaZ* and *paaF* slightly increased virulence in the *Caenorhabditis elegans* model of infection(41). Therefore, deletion of the *abaR* gene may indirectly enhance bacterial virulence via triggering the differential expression of a lot of key genes involved in the phenylacetate catabolism pathway. The selected genes (*paaG*, *paaH*, *paaJ*, *paaK2*, *paaX*, *paaY* and *paaI*) encode proteins in the PAA catabolic pathway that may contribute to virulence.

abal is a protein that synthesized acyl-homoserine lactones (AHLs), *abaR* is a LuxR homolog transcription factor/receptor for AHLs (42). In this study, only WT strain was observed to produce AHLs based on *A. tumefaciens* KYC55 reporter strains, while the green pigment was not observed in $\Delta abaI$, $\Delta abaR$ and $\Delta abaIR$ mutants. No purple pigment was observed in all strains based on *C. violaceum* CV026. In previous study, the absence of purple pigment may be attributed to low rate of the production of short chains homoserine lactone and fast degradation in the strains (43). Our transcriptomic analysis results revealed that deletion of *abaR* leads to the significant

repression of *abal*. Therefore, *abaR* may be a repressor such that repression is relieved when AHLs are bound. The results suggest that *abaR* generally represses its regulon of genes until it binds AHLs. When AHLs are bound, then repression is relieved. This may explain why deletion of *abal* is substantially different from deletion of *abaR*. When *abal* is mutated, then *abaR* still represses many different genes expression.

Interfering with quorum sensing is known as ‘quorum quenching’ and it will attenuate the virulence of the organisms (44). Many strategies for quorum-quenching have been proposed including targeting AHL synthase enzyme, the AHL binding receptor and the AHL itself (44). But previous studies on bacterial quorum quenching mainly focused on the influences on biofilm formation and motility and antibiotic resistance (12, 13). Our work provides a new insight into *abal/abaR* quorum sensing system effects pathogenicity in *A. baumannii*. We propose that targeting the AHL synthase enzyme *abal* could provide an effective strategy for attenuating virulence. On the contrary, interdicting the autoinducer synthase–receptor *abaR* elicits unpredictable consequences, which may lead to enhanced bacterial virulence.

MATERIALS AND METHODS

Bacterial strains, plasmids and culture conditions

Bacterial strains and plasmids used in this study are listed in Table 1. *A. baumannii* strains were grown in lysogeny broth (LB). Antibiotics were used at the following concentrations for *Escherichia coli*: kanamycin, 10 mg/L; ampicillin 25µg/mL and

tellurite, 6 mg/L. For *A. baumannii*: tellurite, 30 mg/L.

Strain construction

Strains $\Delta abal$, $\Delta abaR$, $\Delta abalR$ were unmarked deletion mutants created by a previous described method for acquiring marker-less deletions in *A. baumannii* with minor modifications (45). The primers used in this study are listed in Table 2. Briefly, the upstream and downstream homologous arms of the target gene were amplified and fused and then ligated into a tellurite-resistant suicide vector with the T4 ligase, pMO130-Tel^R (a generous gift from Addgene). The plasmid constructs were first introduced into *Escherichia coli* DH5 α and subsequently selected on LB agar containing 30 μ g/mL kanamycin. The kanamycin resistant colonies which carry a insertion of pMO130-Tel^R and a 2 kb amplicon corresponding to the size of the ligated upstream and downstream homologous arms of the target gene were tested by the corresponding designed primers. The resulting plasmids were used to transform into *E. coli* S17-1 and subsequently conjugate into *A. baumannii* ATCC 17978 via biparental conjugation. Exconjugants were selected on LB containing 30 μ g/mL tellurite and 25 μ g/mL ampicillin. *A. baumannii* ATCC17978 harboring the inserted pMO130-Tel^R-Gene-(Up/Down) construct was cultured in LB broth containing 10% sucrose and passaged seven days to select for stabilized deletion of gene and loss of the *sacB* gene by a second cross-over and allelic replacement. If the target gene has been deleted, PCR of genomic DNA from these bacteria would not produce any amplicon using a primer pair that anneals to the DNA that has been deleted. Mutants were complemented with the pME*abal* and pME*abaR* plasmids,

generated by cloning the *abal* and *abaR* genes and ligating into a shuttle plasmid vector with the T4 ligase, pME6032(46). Overexpressed strains were transformed by the pME*abal* and pME*abaR* plasmids. The complemented strains and Overexpressed strains were confirmed by PCR and restriction analysis of plasmids extracted from *A. baumannii* cells grown in LB medium containing 50 µg/ml tetracycline.

Growth curve measurement

A single colony of strain was inoculated into 2 ml of LB broth, and cultured with shaking (200 rpm) overnight at 37°C. The bacteria were collected by centrifugation at 4000rpm for 5min and suspended in sterile saline to turbidity comparable to a 0.5 McFarland standard. 20 µL was pipetted into a 96-well microtiter plate containing 180 µL of LB broth and incubated at 37°C. The OD₆₀₀ of cultures was measured at hourly intervals for up to 48 h to draw the growth curve. Tests were performed on eight individual biological replicates, in triplicates.

Transmission electron microscopy (TEM)

Bacterial cells (OD_{450nm} of 1.0) for SEM observation were harvested by centrifugation and washed three times with ddH₂O. Bacteria were prefixed with 2.5% glutaraldehyde in 0.1 M phosphate buffer (pH 7.4). Images were captured at 120 kv with a HITACHI H-7650 TEM.

Antimicrobial susceptibility

A. baumannii strains were cultured in LB liquid medium at 37°C with shaking overnight. Minimum inhibitory concentrations (MICs) for Kanamycin, Penicillin, Streptomycin, Meropenem, Imipenem, Ceftizoxime, Cefepime, Cefoperazone-

Sulbactam, Piperacillin-tazobactam, Ampicillin, Tetracycline and Spectinomycin were determined on 96-well plates by the broth microdilution protocols of the Clinical and Laboratory Standards Institute, and the results of MICs testing were interpreted according to the criteria of the CLSI 2013 guidelines. All experiments were carried out a minimum of three times.

Screening of AHL by *C. violaceum* CV026 and *A. tumefaciens* KYC55

A. baumannii can produce AHLs signal molecules with different chain lengths (43), it is essential to use biosensors that detect a broad range of AHLs. *C. violaceum* CV026 specific for short-chain AHLs (C4-C6 AHL molecules) and *A. tumefaciens* KYC55 specific for long-chain AHLs (C8-C14 AHL molecules) were utilized for screening AHLs producing bacterial strains. By the presence of short-chain AHLs, CV026 produces purple pigments. By the presence of long-chain AHLs, a green color is observed for *A. tumefaciens* KYC55 (43). Screening of the *A. baumannii* for production AHLs was carried out by agar plate diffusion assay with minor modifications (43, 47). Briefly, QS reporter strains were cultured in LB agar plates containing the antibiotics kanamycin 20 µg/mL for *C. violaceum* CV026, spectinomycin 50 µg/mL and tetracycline 4.5 µg/mL for *A. tumefaciens* KYC55. The plates were incubated at 28 °C for 24 h. 40 µg/mL of X-gal as a visualizing agent was incorporated into LB medium used for *A. tumefaciens* KYC55. For determining the production of Acyl homoserine signal molecules, *A. baumannii* and mutants and biosensor *C. violaceum* CV026 and *A. tumefaciens* KYC55 strain were inoculated side by side in a way that they had a 0.5 cm gap between them. *C. violaceum* CV026 and *A. tumefaciens* KYC55 were assessed

positive or negative according to the color changes in biosensor strain.

Surface motility assay

The motility test was performed according to the method as described previously with minor modifications (19). Briefly, the media used for surface motility assay was tryptone broth [10 g/liter tryptone (OXOID) and 5 g/liter NaCl] supplemented with 0.3% (wt/vol) Noble agar (BD). Plates were prepared and inoculated with bacteria from an overnight culture in LB agar (1.5%, wt/vol) plates at 37°C with a sterile toothpick. All assays were carried out in triplicate in a minimum of three independent experiments. After incubation at 30°C for 12–14 h, the zone of motility at the agar/Petri dish interface was observed.

Crystal violet biofilm assay

The biofilm forming ability test was performed in accordance with the method as described previously with minor modifications (48). Briefly, a few single colonies were suspended in sterile saline to turbidity comparable to a 0.5 McFarland standard. The suspension was under vortex movement for 1 min; 20 µL was pipetted into a 96-well microtiter plate containing 180 µL of LB broth and incubated for 24 h at 37°C. For crystal violet staining, the wells were rinsed with PBS to exclude loosely adherent cells and then stained for 30 min with 200 µl of 1% crystal violet. The wells were then rinsed with water and dried at room temperature. The amount of biofilm was quantitated by destaining the wells with 200 µl of 33% acetic acid and then measuring the optical density (OD) of the solution in a microplate spectrophotometer set at 595 nm. Tests were performed on ten individual biological

replicates, in triplicates. The differences between parent and mutant strains were calculated, and values returning a P value of <0.05 from a Student's t test were taken as significant.

Serum bactericidal assay

The serum resistance experiment was performed in accordance with the method as previously described with minor modifications (49). Briefly, 100 µl mid-log-phase *A. baumannii* culture (a bacterial titer of approximately 1×10^5 CFU) was mixed with 900 µl of either normal human serum or heat-inactivated serum (heated at 56°C for 30 min). The mixtures were incubated at 37°C, and aliquots of 100 µl were removed from the culture at 1 h for the determination of bacterial counts. The number of surviving CFU was determined by plating in triplicate. The results were expressed as percent survival, with 100% being the number of viable bacteria grown on Brain Heart Infusion agar plates.

Virulence in *Galleria mellonella*

Galleria mellonella has been known as a good model system to study *A. baumannii* pathogenesis (50). Survival of ATCC 17978 and mutants in *G. mellonella* was measured as previously described (50). An inoculum of 10^6 CFU bacteria was injected into *G. mellonella* larvae. The experiment was performed on ten individual biological replicates, in triplicate. Statistical analysis was carried out with GraphPad Prism 6 to produce Kaplan-Meier survival curves. The statistical significance of differences between parent and $\Delta abal$, $\Delta abaR$ and $\Delta abaIR$ mutant strains survival curves were calculated with a log rank test. P values of <0.05 were considered significant.

Murine model of pneumonia

8-10 week old BALB/C mice were obtained from Jilin University. Mice were kept in a sterile environment at Jilin University and maintained according to standard procedures. All research was conducted in complying with the institutional guidelines. The principles in the ARRIVE guidelines and the Basel declaration (<http://www.basel.declaration.org>) have been considered when planning the experiments. Models of pulmonary infection were performed as previously described (35). Briefly, infections were initiated by intraperitoneal injection of approximately 1.2×10^8 CFU of bacteria suspended in 100 μ l of PBS into groups of mice (10 mice per group for survival studies; 5 per group for analyses of bacterial counts).

Quantitative bacteriology

To assess bacterial burden, the lung and spleen were aseptically operated and homogenized in 1 ml sterile of PBS using tissue homogenizers. 100 μ l of the homogenates were cultured on Brain Heart Infusion agar plates to quantify the bacterial load of *A. baumannii* in the respective organs.

RNA sequencing and analysis

RNA was extracted from three biological replicates of each strain with a GeneMark Total RNA Purification Kit. RNA libraries were prepared and sequenced with Illumina HiSeq2000 at the Beijing Genomics Institute (BGI). Sequences were mapped to the ATCC 17978 genome (accession No.cp018664.1) using Bowtie2. Differentially expressed genes were identified using the DESeq2 package (Bioconductor). Genes were deemed as differentially expressed if they presented a log2-fold change greater

than 1 or less than -1 and P value (P-adj) was less than 0.05 in mutant strain compared to WT strain. Cluster of orthologous groups (COG) enrichment analysis was performed by dividing the percentage of genes up- or down-regulated for each category by the percentage of genes in that category across the whole genome (17, 51). Multiexperiment Viewer- version 4.9.0 was used to perform hierarchical clustering and heat map visualization(52). Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis, based on R software, were applied for the identification of pathways in which DEGs significantly enriched. The GO and KEGG pathway analysis of the DEGs was conducted through the ClusterProfiler package in R software (53). A P-value of <0.05 was considered to have statistical significance and to achieve significant enrichment. qRT-PCR was performed on the 7300 Plus Real-Time PCR System (Applied Biosystems) using a standard protocol from the FastStart Universal SYBR Green Master (Roche, Basel, Switzerland). Gene expression levels were quantified by using the $2^{-\Delta\Delta Ct}$ method with endogenous controls (16S). The Primers used for qRT-PCR assays are described in Table 3. All qRT-PCR assays were repeated 3×. The RNA-Seq data obtained in this study was submitted to Sequence Read Archive (SRA), BioProject ID PRJNA600672.

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Table 1 Bacterial strains and plasmids used in this study

Strain or plasmid	Relevant characteristics	Reference or source
<i>A. baumannii</i> strains		
ATCC		Ayush Kumar

17978(WT)		
<i>ΔabaI</i>	WT with deletion in <i>abaI</i> gene	This study
<i>ΔabaR</i>	WT with deletion in <i>abaR</i> gene	This study
<i>ΔabaIR</i>	WT with deletion in <i>abaI</i> and <i>abaR</i> genes	This study
<i>ΔabaI</i> (pME <i>abaI</i>)	<i>ΔabaI</i> harboring pME6032, containing the <i>abaI</i> gene	This study
<i>ΔabaR</i> (pME <i>abaR</i>)	<i>ΔabaR</i> harboring pME6032, containing the <i>abaR</i> gene	This study
WT(pME6032)	WT harboring pME6032, empty vector	This study
WT(pME <i>abaI</i>)	WT harboring pME6032, containing the <i>abaI</i> gene	This study
WT(pME <i>abaR</i>)	WT harboring pME6032, containing the <i>abaR</i> gene	This study
<i>E.coli</i> strains		
DH5α	F-φ 80 <i>lacZ</i> Δ M15 Δ (<i>lacZYA-argF</i>) U169 A1 <i>recA1 hsdR17(rk-,mk+)supE44λ-thi-1 gyrA96</i> <i>relA1 phoA</i>	Transgen
S17-1(ATCC47055)	Genotype: <i>recA pro hsdR RP4-2-Tc::Mu-Km::Tn7,Gm^S</i>	Biobw
<i>Chromobacterium violaceum</i>		
CV026	Detection of C4- and C6-HSLs	MingshengDong
<i>Agrobacterium tumefaciens</i>		

KYC55(pJZ372)	Detection of broad range of AHLs	MingyongZeng
(pJZ384)(pJZ410)		
R10(pCF218)	<i>Ptet-traR</i> , <i>Tc^R</i> , high AHL production strain	MingyongZeng
Plasmids		
pMO130-Tel ^R	Suicide plasmid, <i>xyIE⁺</i> , <i>sacB⁺</i> , <i>Km^R</i>	Addgene
pMO130-Tel ^R - <i>abal</i> -	pMO130-Tel ^R containing a 1 kb UP fragment (<i>abal</i>) and 1 kb DOWN fragment (<i>abal</i>)	This study
(Up/Down)		
pMO130-Tel ^R - <i>abaR</i> -	pMO130-Tel ^R containing a 1 kb UP fragment (<i>abaR</i>) and 1 kb DOWN fragment (<i>abaR</i>)	This study
(Up/Down)		
pME6032	shuttle plasmid for genetic complementation, <i>Tc^R</i>	Ke Lei Biological Technology Co.,Ltd
pME <i>abal</i>	pME6032 containing the <i>abal</i> gene (promoter and coding region)	This study
pME <i>abaR</i>	pME6032 containing the <i>abaR</i> gene (promoter and coding region)	This study

789 Table 2 Primer used in this study

primer name	sequence	product
<i>abaR</i> (SphI)up-F	TATGCATGCTTACGCCACTGACTAAGAG	1190bp

<i>abaR</i> (BamHI)up-R	GCTGGATCCCGATAAGAGACCACTAACCT	
<i>abaR</i> (BamHI)dw-F	TATGGATCCTTGAAGCGTAGGTCTAATCT	1136bp
<i>abaR</i> (PstI)dw-R	TATCTGCAGAAGGCGGTAAGTAAGAA	
<i>abal</i> (PstI)dw-F	TATCTGCAGCGCAACTACAGCCATACT	932bp
<i>abal</i> (NotI)dw-R	TATGCGGCCGCGCCTCTTACCGACTTACG	
<i>abal</i> -F	AAAGTTACCGCTACAGGG	435bp
<i>abal</i> -R	CACGATGGGCACGAAA	
<i>abaR</i> -F	TCCTCGGGTCCCAATA	310bp
<i>abaR</i> -R	TAAATCTACCGCATCAA	
<i>abal</i> (EcoRI)-F	CCGGAATTCCGGGTGGAAGCACTTGTAATGAA	654bp
<i>abal</i> (XhoI)-R	CCGCTCGAGCGGCTCATCTTGCTCGGTCATA	
<i>abaR</i> (EcoRI)-F	CCGGAATTCCGGCTACAAAAGCCCTAGCATT	808bp
<i>abaR</i> (XhoI)-R	CCGCTCGAGCGGAAGATTAGACCTACGCTTCA	
PME6032-F	CCTCATCAGTGCCAACATA	843bp
PME6032-R	CATACTCTGCGACATCGTA	

790 Table 3 Real-time quantitative PCR primers

qRT_PCR	sequence
AUO97_RS01130-F	CGCAACGCCATTACTA
AUO97_RS01130-R	TTGTTTATCGCATCCTG
AUO97_RS01135-F	TTGCTCCACCCACATA
AUO97_RS01135-R	TTGGCGTAACTTCACTT
AUO97_RS08710-F	ATGCCGAGTTTGCTTA

AUO97_RS08710-R	AACACGCTGTGAATCTTT
AUO97_RS13835-F	CGGTGCTTGATGTGCT
AUO97_RS13835-R	AAATGCGATAACGTGGA
AUO97_RS17125-F	GTCTACGCCGCTCTGT
AUO97_RS17125-R	AGGTTATTGAAGGTGGG
AUO97_RS17130-F	CCACATACGCCTTGCT
AUO97_RS17130-R	CCTCGGGAGATTCATT
AUO97_RS17135-F	TTTTGGGCATACTGACTTT
AUO97_RS17135-R	CTTCTGGACTCGGTAATGT
AUO97_RS17140-F	CCTTTGGTGCCGTAGA
AUO97_RS17140-R	ACCCGAACCTCACAGAC
AUO97_RS17145-F	GCGTTCCCAAGCCTCA
AUO97_RS17145-R	CTCGGTGATTACGATGGATG
AUO97_RS17160-F	CACCCAACCCACTGAA
AUO97_RS17160-R	AGCGTATGTGAGCCAAG
16S_qF	CAGCTCGTGTCGTGAGATGT
16S_qR	CGTAAGGGCCATGATGACTT

791 Table 4 MICs of antibiotics used in this study

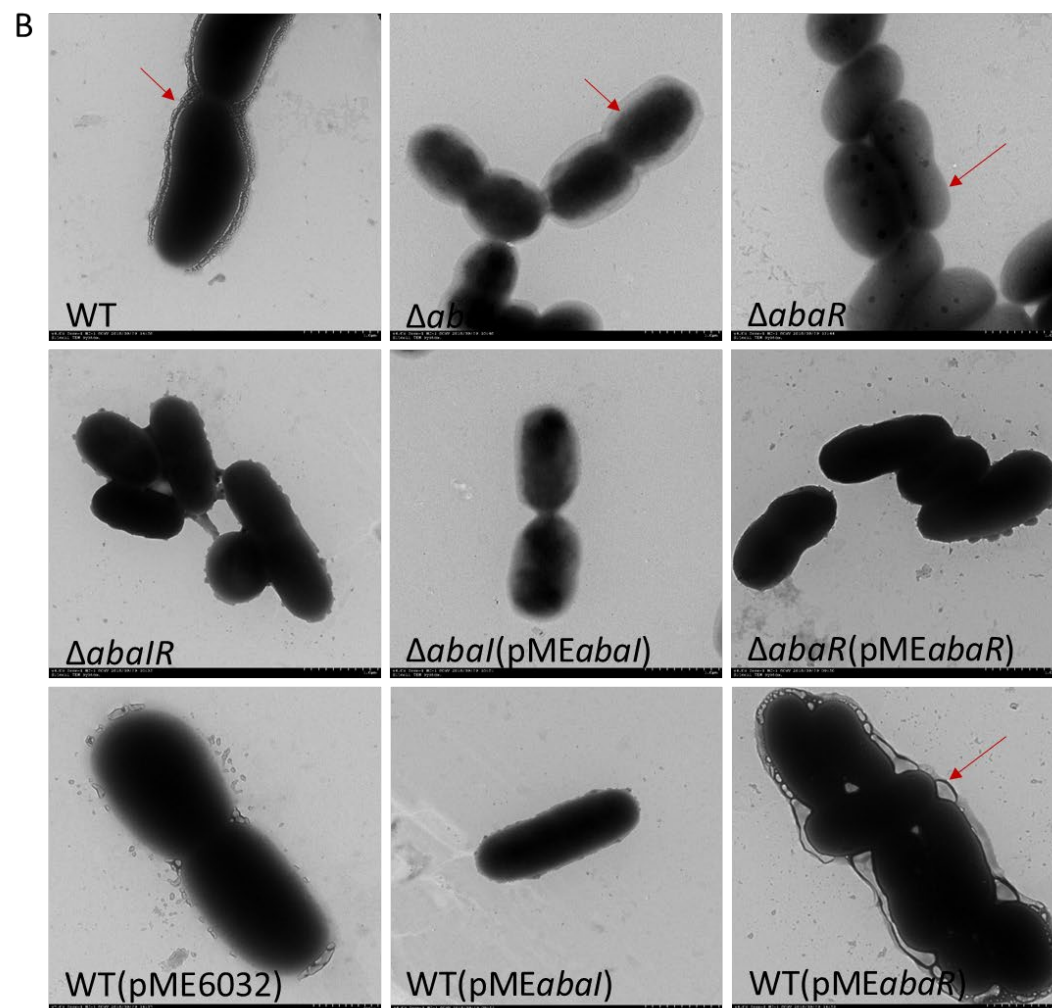
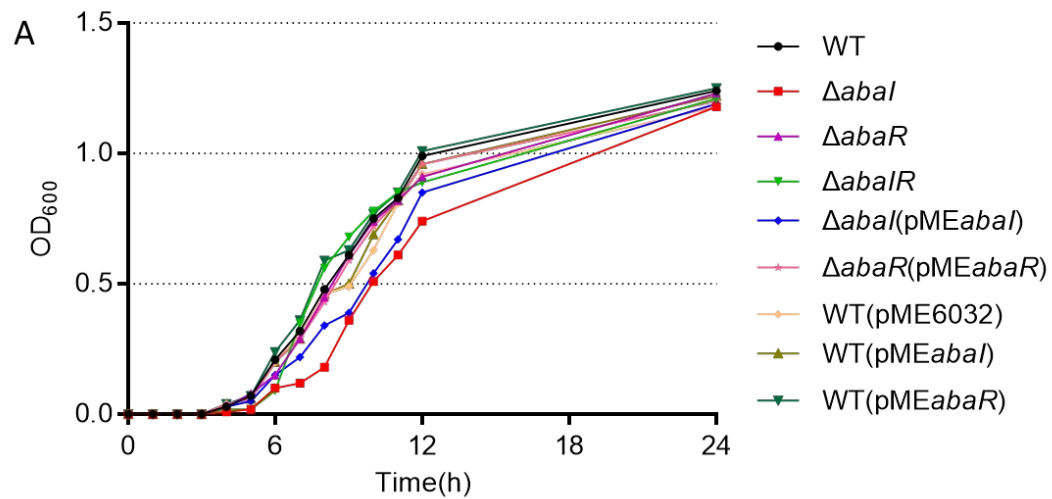
Antibiotic	MIC(μ g/ml)								
	Δa		Δa						
	Δa	<i>ba</i>	<i>baI</i>	$\Delta abal(p$	$\Delta abaR(p$	WT(pM	WT(WT(
	WT	<i>baI</i>	<i>R</i>	<i>R</i>	ME <i>abal</i>)	ME <i>abaR</i>)	E6032)	pME	pME

								<i>abal</i>	<i>aba</i>
)	R)
Kanamycin	8	2	4	4	4	8	8	8	16
				0.2					
Gentamicin	4	1	4	5	2	4	4	4	4
	12								
Penicillin	8	64	64	32	64	64	64	64	128
Streptomycin									
n	32	16	16	16	32	32	32	32	64
		0.2		0.2					
Meropenem	1	5	0.5	5	0.5	0.5	1	1	1
Imipenem	32	16	16	8	16	16	16	16	32
Ceftizoxime	8	8	8	8	8	8	8	8	16
Cefepime	2	8	8	2	8	8	8	8	8
Cefperazone									
-Sulbactam	2	8	2	2	8	4	2	4	4
Paraxiline-									
tazobatan	8	8	8	32	8	8	8	8	16
	>5	>5	12	>51				>51	>51
Vancomycin	12	12	8	2	>512	>512	>512	2	2
Ampicillin	64	32	64	32	32	32	32	32	64
Tetracycline	2	8	2	2	8	4	4	4	4

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in 64 64 64 64 64 64 64 64 64 64

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Figure 1. A) Growth curve analysis of *A.baumannii* and mutants in broth. B) Transmission electron microscope images of the targeted bacteria. Cells were observed with a HITACHI H-7650 TEM transmission electron microscope operated at 120 kv. Scale bar = 500 nm.

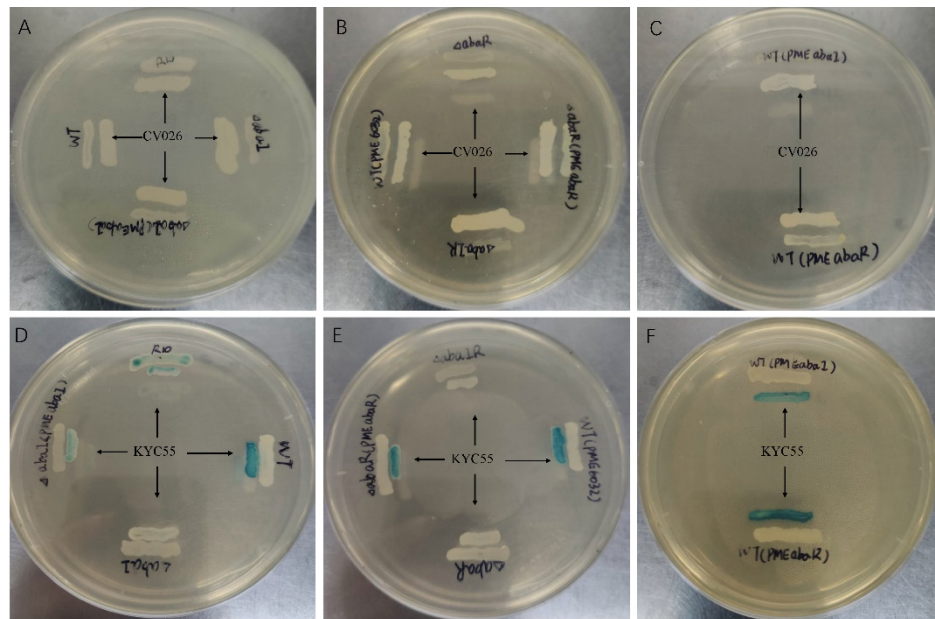


Figure 2. Screening of WT and mutants for AHLs production using agar-plate well diffusion assay with *C. violaceum* CV026 and *A. tumefaciens* KYC55 reporter strain.

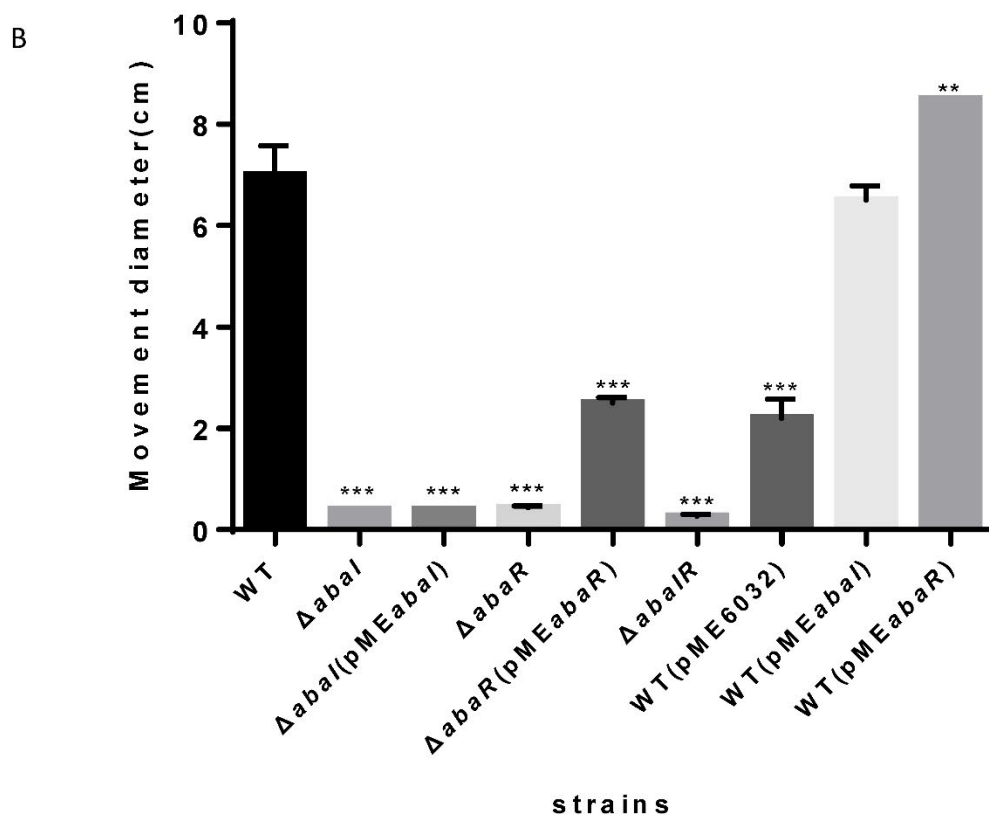
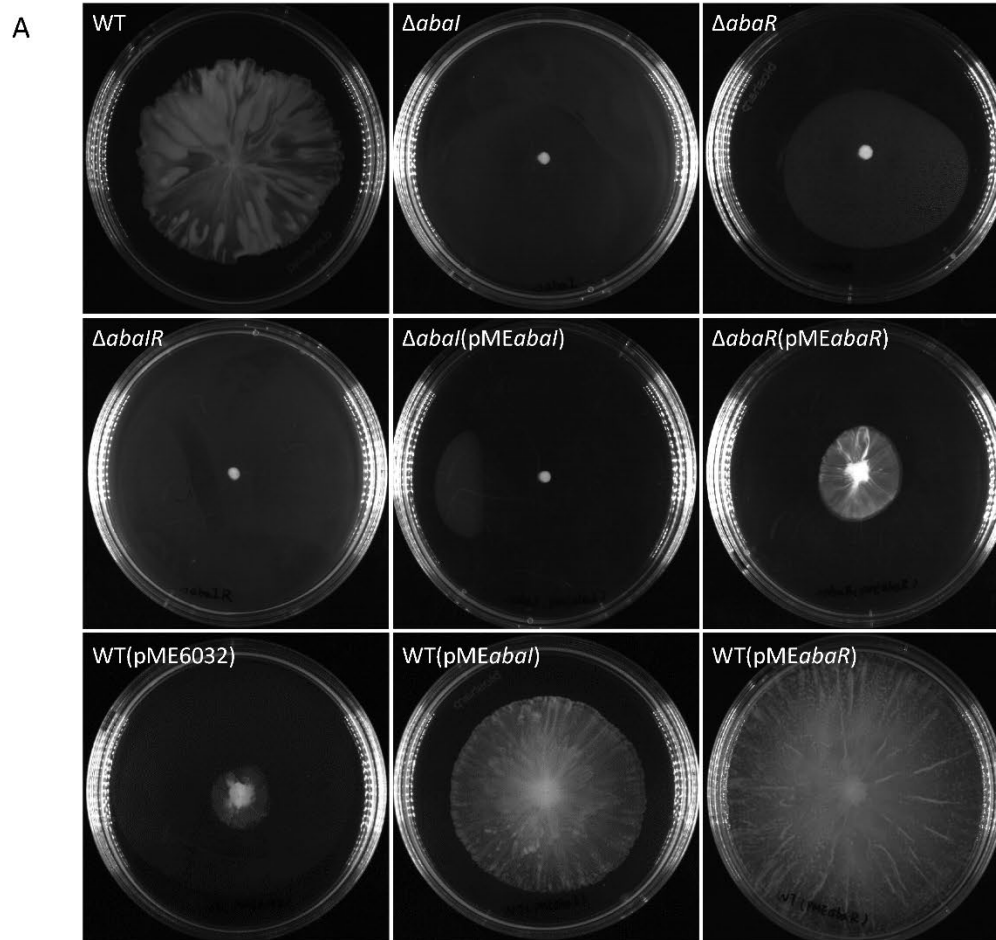


Figure 3. A) WT and mutants were inoculated on the surface of a semisolid agarose plate (0.3%) and incubated for 12–14 h at 30°C. *abaI*, *abaR*, and *abaIR* mutant strains demonstrated defects in surface-associated motility compared to the parental strain. B) The distance migrated (diameter) is shown for each strain and Error bars represent SD for three biological replicates.

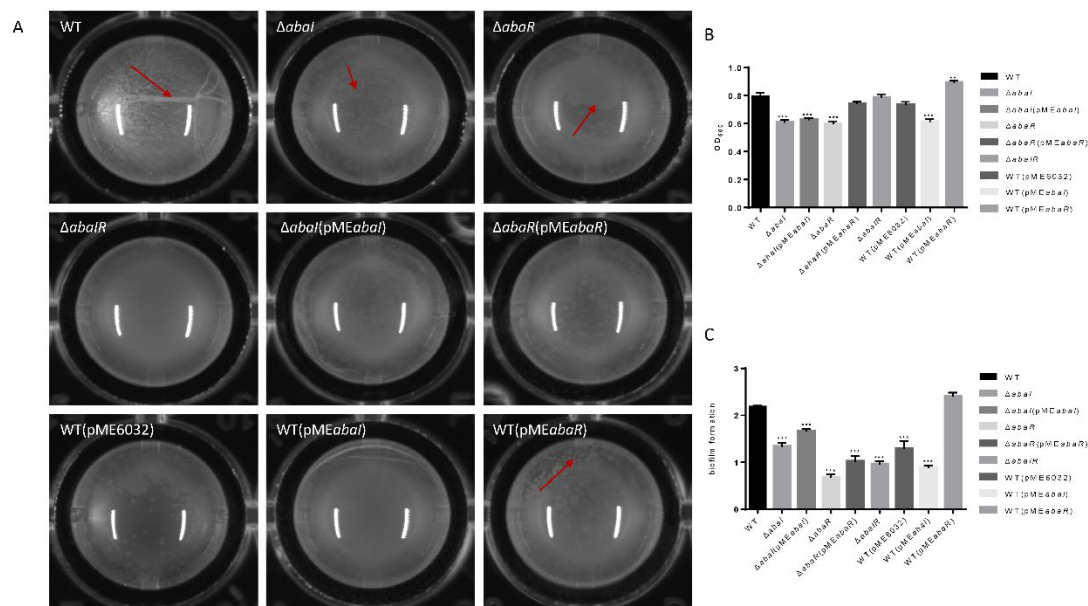


Figure 4. A) Visual changes in biofilm formation in 96-well plates for 24 h at 37°C, images were taken after 24 of growth. B) The absorbance of bacterial solution was detected by OD595. C) Biofilm formation on plastic at 37°C as determined by crystal violet staining. Markers show the OD595 compared with WT in individual biological replicates.

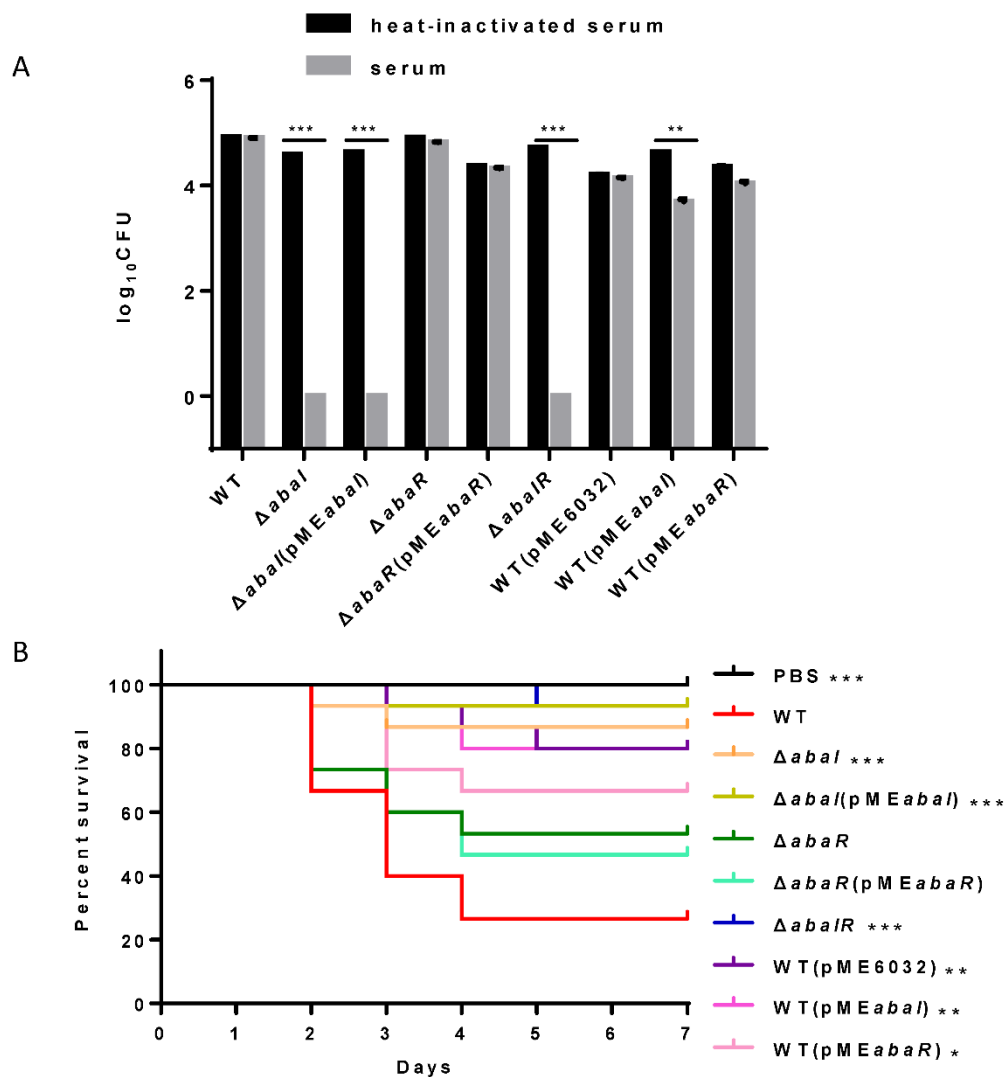


Figure 5. A) Sensitivity of strains to normal human serum (NHS). Viable bacterial counts were determined after 1 h of incubation at 37°C with rotation. Data are presented as percent survival, with 100% being the number of viable bacteria grown in heat-inactivated serum. All values are from triplicate samples and are representative of three independent experiments. B) Kaplan-Meier survival curve showing the virulence of PBS, WT and mutants in *G. mellonella*. The data show the percent survival (n=30) of *G. mellonella* after inoculation with 10^6 CFU of bacteria. Survival curves were compared using the log-rank (Mantel-Cox) test. *p < 0.05

822 **; $p < 0.005$; *** $p < 0.001$.

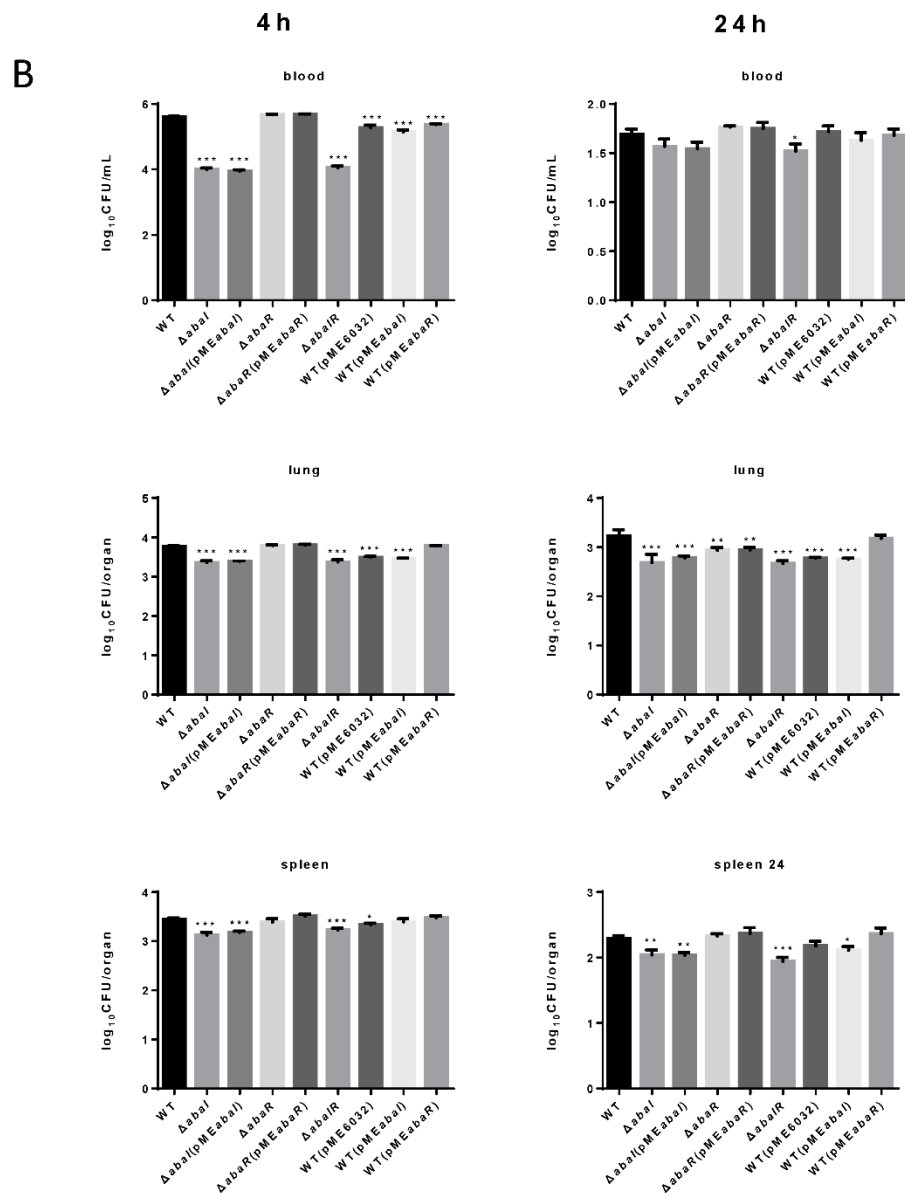
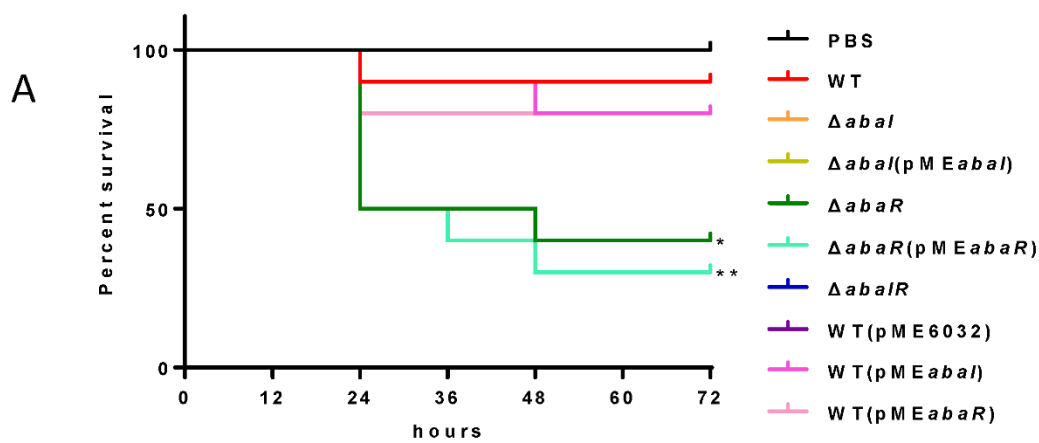


Figure 6. A) Kaplan-Meier survival curve of mouse inoculated with strains at a dose of 1.2×10^8 CFUs ($n=10$). Survival curves were compared using the log-rank (Mantel-Cox) test, $*p < 0.05$. B) *A. baumannii* bacterial burdens in the lungs, spleen, and blood. Bacterial burdens in the blood and respective organs were determined by quantitative bacteriology at 4 and 24 h postinoculation. An unpaired t test was used to validate the experimental data. $*p < 0.05$; $**p < 0.005$; $***p < 0.001$.

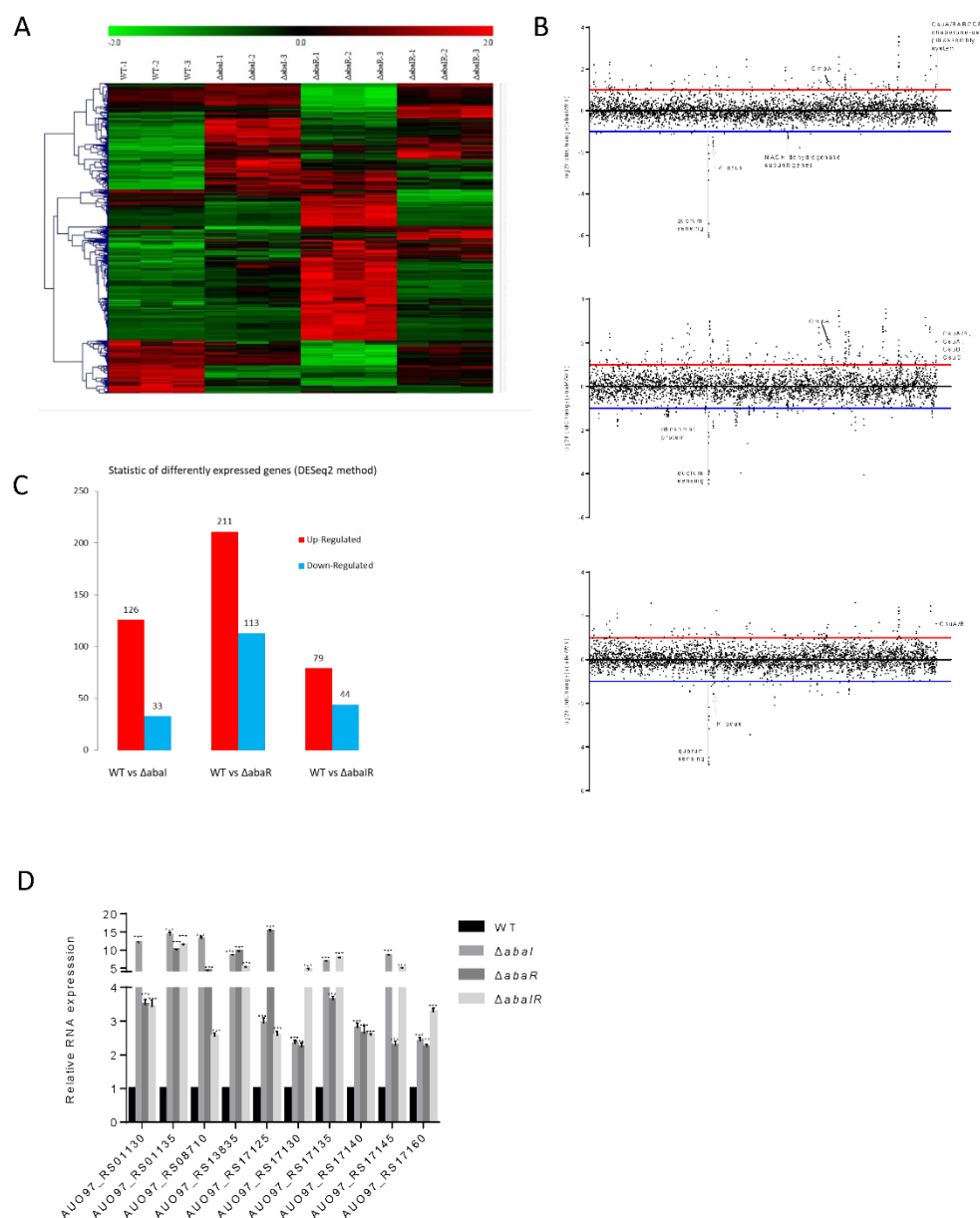


Figure 7. A) Heat map representation and hierarchical clustering of gene expression

changes. The x-coordinate represents the different experimental groups. Data represents differential gene expression profiles (PFKM) for genes listed along ordinate. Red indicates increased expression and green indicates decreased expression; color intensity indicates the magnitude of difference in expression according to horizontal scale at top. Black depicts genes with no significant difference in expression. B) The genome wide transcriptomic profile, genome-wide differential gene expression locus map, Plot of differential gene expression mutant compared with WT with respect to gene locus tag number. C) The vertical axis represents the number of significantly differentially expressed genes. The log₂-fold change in expression for each gene meeting the study threshold (log₂ fold change > 1, false discovery rate < 0.001). The number of significantly differentially expressed genes can be divided into the number of significantly up-regulated differentially expressed genes and the number of significantly down-regulated differentially expressed genes. D) Relative expression of 10 up-regulated genes, results are presented relative to WT which was normalized to 1. The results are expressed as mean ± SEM for at least 3 biological replicates. ***P < .001, t test.

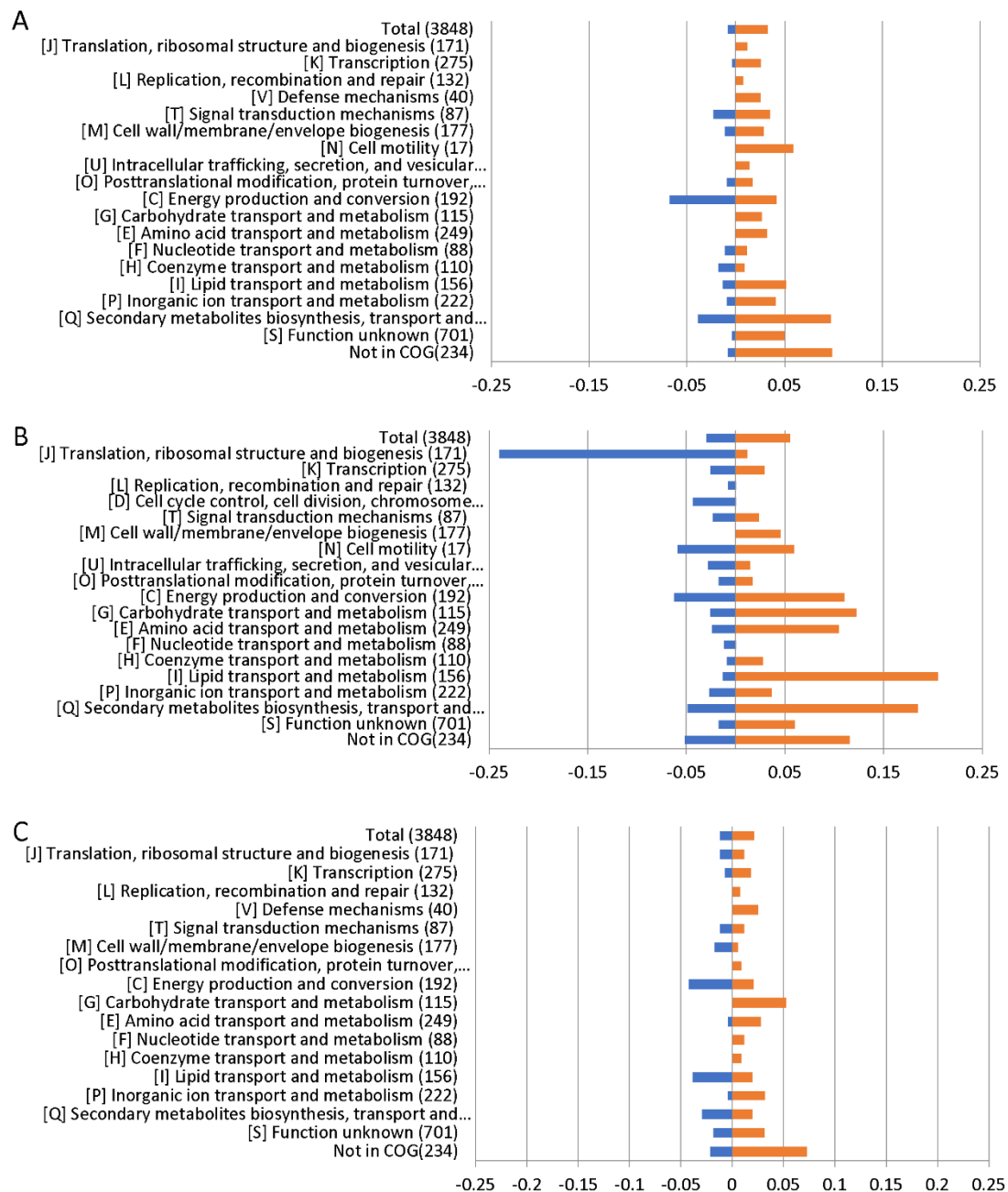


Figure 8. RNA-Seq results displayed by COG enrichment for differentially regulated genes. Cluster of orthologous groups (COG) enrichment analysis was performed by dividing the percentage of genes up- or down-regulated for each category by the percentage of genes in that category across the whole genome. Panels: A, $\Delta abal$; B, $\Delta abaR$; C, $\Delta abalR$.



Figure 9. A) Top 30 of GO enrichment of DEGs in *Δabal*. The shape of the point indicates the different ontology. The enrichment q value of each GO term was normalized as negative log10(q value) and is shown as a color gradient. The number of genes enriched in each GO term is represented by the size of the points. B) The significantly enriched KEGG pathway of DEGs in *Δabal*. The enrichment P adjustvalue of each pathway was shown as a color gradient. GeneRatio, number of differentially expressed genes/total number of genes in this KEGG pathway. The number of genes

enriched in each pathway is represented by the size of the points. C) Top 30 of GO enrichment of DEGs in *ΔabaR*. The shape of the point indicates the different ontology. The enrichment q value of each GO term was normalized as negative log₁₀(q value) and is shown as a color gradient. The number of genes enriched in each GO term is represented by the size of the points. D) The significantly enriched KEGG pathway of DEGs in *ΔabaR*. The enrichment P adjustvalue of each pathway was shown as a color gradient. GeneRatio, number of differentially expressed genes/total number of genes in this KEGG pathway. The number of genes enriched in each pathway is represented by the size of the points. E) Top 30 of GO enrichment of DEGs in *ΔabaIR*. The shape of the point indicates the different ontology. The enrichment q value of each GO term was normalized as negative log₁₀(q value) and is shown as a color gradient. The number of genes enriched in each GO term is represented by the size of the points. F) The significantly enriched KEGG pathway of DEGs in *ΔabaIR*. The enrichment P adjustvalue of each pathway was shown as a color gradient. GeneRatio, number of differentially expressed genes/total number of genes in this KEGG pathway. The number of genes enriched in each pathway is represented by the size of the points.

GeneID	log2FoldChange(Δ <i>abal</i> /WT)	Up-Down- Regulation(Δ <i>ab</i> <i>al</i> /WT)	Pvalu e	Product
AUO97_RS 06625	-6.0744	Down	0	acyl-CoA dehydrogenase
AUO97_RS 06615	-5.9747	Down	0	non-ribosomal peptide synthetase
AUO97_RS 06610	-5.88657	Down	0	outer membrane lipoprotein-sorting protein
AUO97_RS 06630	-5.44259	Down	0	acyl-CoA synthetase
AUO97_RS 06605	-3.3445	Down	1.1E- 107	hypothetical protein
AUO97_RS 06600	-2.88721	Down	4.97E- 78	alpha/beta hydrolase
AUO97_RS 06645	-2.30926	Down	1.64E- 07	GNAT family N- acetyltransferase
AUO97_RS 06620	-2.06687	Down	3.24E- 06	acyl carrier protein
AUO97_RS 11650	-1.78566	Down	1.77E- 32	hemerythrin

AUO97_RS	-1.71559	Down	1.47E-	UDP-glucose 4-
06875			59	epimerase GalE
AUO97_RS	-1.64711	Down	1.23E-	phosphopantetheine
06595			07	-protein transferase
AUO97_RS	-1.58854	Down	5.17E-	L-lactate permease
06865			94	
AUO97_RS	-1.50567	Down	7.58E-	alpha-hydroxy-acid
06855			53	oxidizing enzyme
AUO97_RS	-1.45419	Down	3.24E-	transcriptional
06860			26	regulator LldR
AUO97_RS	-1.33315	Down	9.15E-	NADH-quinone
11000			17	oxidoreductase subunit K
AUO97_RS	-1.28401	Down	1.16E-	D-lactate
06850			24	dehydrogenase
AUO97_RS	-1.27855	Down	4.17E-	NADH-quinone
11005			96	oxidoreductase subunit L
AUO97_RS	-1.27133	Down	2.73E-	NADH-quinone
10995			39	oxidoreductase subunit J
AUO97_RS	-1.25693	Down	1.91E-	NADH-quinone

11015			85	oxidoreductase
				subunit N
AUO97_RS	-1.25538	Down	4.49E-	NADH-quinone
10985			80	oxidoreductase
				subunit H
AUO97_RS	-1.21787	Down	3.2E-	NADH-quinone
11010			73	oxidoreductase
				subunit M
AUO97_RS	-1.14605	Down	7.24E-	NADH-quinone
10990			42	oxidoreductase
				subunit I
AUO97_RS	-1.14342	Down	7.7E-	oxygen-dependent
04545			49	coproporphyrinogen
				oxidase
AUO97_RS	-1.13713	Down	4.45E-	cytosine permease
15040			15	
AUO97_RS	-1.11951	Down	1.42E-	AcrB/AcrD/AcrF
07490			20	family protein
AUO97_RS	-1.11535	Down	3.08E-	isocitrate lyase
12255			46	
AUO97_RS	-1.11028	Down	3.71E-	hypothetical protein
04690			16	

AUO97_RS	-1.09799	Down	1.5E-	GGDEF domain-
03915			12	containing protein
AUO97_RS	-1.09371	Down	8.57E-	U32 family
00400			25	peptidase
AUO97_RS	-1.08569	Down	0.000	MBL fold metallo-
05665			189	hydrolase
AUO97_RS	-1.06889	Down	2.64E-	NADH-quinone
10980			57	oxidoreductase
				subunit NuoG
AUO97_RS	-1.06411	Down	1.08E-	efflux RND
07485			09	transporter
				periplasmic adaptor
				subunit
AUO97_RS	-1.02016	Down	7.07E-	DUF2147 domain-
05775			23	containing protein
AUO97_RS	1.001374	Up	1.2E-	putative DNA
04585			16	modification/repair
				radical SAM protein
AUO97_RS	1.011794	Up	0.005	TetR/AcrR family
11080			496	transcriptional
				regulator
AUO97_RS	1.013889	Up	1.31E-	heteromeric

01645			06	transposase
				endonuclease
				subunit TnsA
AUO97_RS	1.014466	Up	0.011	muconolactone
17070			544	delta-isomerase
AUO97_RS	1.025133	Up	1.34E-	Holliday junction
01845			12	branch migration
				protein RuvA
AUO97_RS	1.033632	Up	8.86E-	outer membrane
02620			13	lipoprotein carrier
				protein LolA
AUO97_RS	1.03403	Up	4.16E-	OmpA family protein
13365			23	
AUO97_RS	1.034741	Up	7.53E-	hypothetical protein
13625			10	
AUO97_RS	1.034749	Up	0.010	hypothetical protein
11050			909	
AUO97_RS	1.037826	Up	0.003	GlsB/YeaQ/YmgE
07280			311	family stress
				response membrane
				protein
AUO97_RS	1.042847	Up	2.75E-	SRPBCC domain-

12195			05	containing protein
AUO97_RS	1.043606	Up	0.009	GNAT family N-
05370			118	acetyltransferase
AUO97_RS	1.047928	Up	5.3E-	ImmA/IrrE family
16615			50	metallo-
				endopeptidase
AUO97_RS	1.052979	Up	2.83E-	phosphate ABC
01115			17	transporter,
				permease protein
				PstA
AUO97_RS	1.060287	Up	2.86E-	phenylacetate--CoA
14215			13	ligase
AUO97_RS	1.061309	Up	4.72E-	SPOR domain-
04650			18	containing protein
AUO97_RS	1.063226	Up	1.44E-	MacA family efflux
10110			20	pump subunit
AUO97_RS	1.065265	Up	2.54E-	toxin
03105			05	
AUO97_RS	1.066128	Up	4.92E-	hypothetical protein
16620			29	
AUO97_RS	1.07437	Up	1.36E-	VOC family protein
03210			05	

AUO97_RS	1.076757	Up	2.31E-	sulfurtransferase
17840			13	TusD
AUO97_RS	1.080796	Up	8.18E-	hypothetical protein
12700			05	
AUO97_RS	1.084479	Up	0.001	DUF4184 domain-
03445			824	containing protein
AUO97_RS	1.084642	Up	1.05E-	gamma-
12705			10	aminobutyraldehyde
				dehydrogenase
AUO97_RS	1.084666	Up	1.11E-	metal-dependent
11550			05	hydrolase
AUO97_RS	1.086385	Up	6.24E-	DUF541 domain-
01160			17	containing protein
AUO97_RS	1.089957	Up	5.57E-	transcriptional
15885			27	regulator
AUO97_RS	1.094631	Up	4.41E-	enoyl-CoA hydratase
06660			06	
AUO97_RS	1.100387	Up	3.94E-	proline/glycine
19180			07	betaine transporter
				ProP
AUO97_RS	1.100706	Up	0.002	PaaX family
00970			029	transcriptional

				regulator
AUO97_RS	1.108039	Up	2.06E-	hypothetical protein
13500			05	
AUO97_RS	1.109955	Up	5.76E-	membrane protein
01405			15	
AUO97_RS	1.111993	Up	0.000	3-oxoadipate CoA-
17085			72	transferase
AUO97_RS	1.125222	Up	2.47E-	type VI secretion
13980			07	system baseplate
				subunit TssE
AUO97_RS	1.130874	Up	1.28E-	LysR family
01255			29	transcriptional
				regulator
AUO97_RS	1.132006	Up	3.99E-	META domain-
12355			55	containing protein
AUO97_RS	1.135218	Up	1.36E-	universal stress
17615			07	protein
AUO97_RS	1.135699	Up	9.01E-	CoA transferase
16430			06	subunit A
AUO97_RS	1.136286	Up	1.71E-	FUSC family protein
09015			38	
AUO97_RS	1.14236	Up	7.91E-	DNA polymerase V

14475			09	
AUO97_RS	1.148054	Up	5.78E-	ABC transporter
02225			38	substrate-binding
				protein
AUO97_RS	1.151745	Up	1.11E-	hypothetical protein
01060			10	
AUO97_RS	1.153076	Up	4.64E-	hypothetical protein
16600			10	
AUO97_RS	1.154194	Up	1.2E-	enoyl-CoA hydratase
14195			05	
AUO97_RS	1.155982	Up	1.36E-	DNA-binding
00360			07	response regulator
AUO97_RS	1.156561	Up	4.43E-	DUF2726 domain-
06270			10	containing protein
AUO97_RS	1.165001	Up	4.24E-	aromatic amino acid
07670			11	transporter AroP
AUO97_RS	1.166185	Up	1.94E-	fumarylacetoacetase
07665			63	
AUO97_RS	1.168526	Up	1.13E-	haloacid
16010			32	dehalogenase
AUO97_RS	1.176465	Up	1E-07	SCPU domain-
19190				containing protein

AUO97_RS	1.188775	Up	4.99E-	fimbrial biogenesis
19195			16	outer membrane
				usher protein
AUO97_RS	1.189934	Up	0.005	hypothetical protein
00020			552	
AUO97_RS	1.202481	Up	1.73E-	TIGR01244 family
16300			45	phosphatase
AUO97_RS	1.204777	Up	0.005	hypothetical protein
07165			296	
AUO97_RS	1.204815	Up	0.003	RidA family protein
10250			704	
AUO97_RS	1.210701	Up	0.000	transcriptional
02595			229	regulator
AUO97_RS	1.211821	Up	1.5E-	acyl-CoA desaturase
07005			37	
AUO97_RS	1.212542	Up	1.27E-	sulfite exporter
16305			08	TauE/SafE family
				protein
AUO97_RS	1.214564	Up	2.84E-	Fe-S biogenesis
12115			32	protein NfuA
AUO97_RS	1.243207	Up	3.6E-	phosphate ABC
01120			18	transporter

				permease subunit
				PstC
AUO97_RS	1.246926	Up	2.2E-	phenylacetate-CoA
14190			06	oxygenase/reductas
				e subunit PaaK
AUO97_RS	1.253491	Up	1.81E-	allophanate
13840			20	hydrolase
AUO97_RS	1.264522	Up	4.69E-	PAAR domain-
16595			19	containing protein
AUO97_RS	1.274509	Up	0.000	SCPU domain-
19205			646	containing protein
AUO97_RS	1.27559	Up	4.91E-	molecular
19200			09	chaperone
AUO97_RS	1.276369	Up	8.02E-	hypothetical protein
00270			05	
AUO97_RS	1.307287	Up	1.03E-	hypothetical protein
04580			07	
AUO97_RS	1.309804	Up	9.99E-	phage major capsid
15625			06	protein
AUO97_RS	1.328101	Up	2.33E-	amino acid
12450			19	transporter
AUO97_RS	1.333536	Up	1.76E-	NADPH:quinone

05515			40	oxidoreductase
AUO97_RS	1.346309	Up	0.000	hypothetical protein
03405			218	
AUO97_RS	1.375679	Up	2.99E-	crotonase
12825			06	
AUO97_RS	1.376611	Up	0.000	DNA transfer protein
08885			394	p32
AUO97_RS	1.381641	Up	0.000	hypothetical protein
00265			74	
AUO97_RS	1.396496	Up	6.32E-	MBL fold metallo-
16295			27	hydrolase
AUO97_RS	1.398657	Up	7.72E-	hypothetical protein
00890			28	
AUO97_RS	1.410219	Up	9.19E-	hypothetical protein
04705			16	
AUO97_RS	1.454416	Up	1.2E-	flavin reductase
10870			26	
AUO97_RS	1.4574	Up	3.51E-	phenylacetate-CoA
14180			11	oxygenase subunit
				Paal
AUO97_RS	1.457907	Up	3.68E-	aldehyde
18630			75	dehydrogenase

AUO97_RS	1.458908	Up	1.83E-	aspartate
12715			09	aminotransferase family protein
AUO97_RS	1.468197	Up	3.65E-	catechol 1,2-
17075			14	dioxygenase
AUO97_RS	1.470222	Up	6.53E-	arginine N-
12720			08	succinyltransferase
AUO97_RS	1.484748	Up	1.28E-	deoxyguanosinetrip
01840			65	hosphate triphosphohydrolase
AUO97_RS	1.487037	Up	1.93E-	1,2-phenylacetyl-
14170			27	CoA epoxidase subunit A
AUO97_RS	1.493798	Up	1.05E-	hypothetical protein
05275			18	
AUO97_RS	1.496273	Up	1.16E-	3-oxoadipate CoA-
17080			05	transferase subunit A
AUO97_RS	1.534021	Up	1.12E-	1,2-phenylacetyl-
14175			19	CoA epoxidase subunit B
AUO97_RS	1.557012	Up	2.02E-	NAD-dependent

01145			49	aldehyde dehydrogenase
AUO97_RS	1.567974	Up	2.97E-	trehalose-
11225			14	phosphatase
AUO97_RS	1.607067	Up	3.22E-	DNA transfer protein
07745			31	p32
AUO97_RS	1.619212	Up	1.95E-	muconate
17065			10	cycloisomerase
AUO97_RS	1.628035	Up	6.97E-	phenylacetic acid
14165			17	degradation bifunctional protein PaaZ
AUO97_RS	1.660574	Up	6.92E-	C4-dicarboxylate
07095			08	ABC transporter
AUO97_RS	1.685455	Up	2.39E-	TetR/AcrR family
05520			30	transcriptional regulator
AUO97_RS	1.695967	Up	4.07E-	alcohol
18615			46	dehydrogenase
AUO97_RS	1.739369	Up	1.42E-	phenylacetate-CoA
14185			35	oxygenase subunit PaaJ

AUO97_RS	1.743263	Up	4E-17	taurine ABC
14725				transporter
				substrate-binding
				protein
AUO97_RS	1.744985	Up	1.2E-	MFS transporter
06395			73	
AUO97_RS	1.794527	Up	4.22E-	phosphonate ABC
01125			35	transporter
				substrate-binding
				protein
AUO97_RS	1.83163	Up	7.99E-	DNA-binding protein
00365			22	
AUO97_RS	1.910832	Up	7.76E-	LamB/YcsF family
13830			13	protein
AUO97_RS	1.926934	Up	5.8E-	methionine synthase
10865			205	
AUO97_RS	1.984749	Up	6.85E-	hypothetical protein
18900			17	
AUO97_RS	1.998418	Up	5.49E-	hypothetical protein
14470			06	
AUO97_RS	2.07496	Up	2.1E-	DUF1852 domain-
10860			191	containing protein

AUO97_RS	2.095124	Up	6.19E-	hypothetical protein
07050			12	
AUO97_RS	2.097862	Up	5.78E-	nuclear transport
17150			08	factor 2 family
				protein
AUO97_RS	2.116025	Up	7.01E-	EamA family
08715			29	transporter
AUO97_RS	2.141387	Up	5.07E-	SCPU domain-
19215			60	containing protein
AUO97_RS	2.147861	Up	7.66E-	amidase
17165			23	
AUO97_RS	2.174702	Up	4.1E-	hypothetical protein
03425			13	
AUO97_RS	2.205577	Up	1.57E-	RtcB family protein
00260			67	
AUO97_RS	2.216359	Up	6.67E-	aromatic amino acid
01130			33	transporter AroP
AUO97_RS	2.236657	Up	1.63E-	DUF1445 domain-
13835			29	containing protein
AUO97_RS	2.307109	Up	1.38E-	hypothetical protein
17155			08	
AUO97_RS	2.335458	Up	2.75E-	pyruvate

01135			62	decarboxylase
AUO97_RS	2.459453	Up	2.56E-	TetR/AcrR family
08710			34	transcriptional regulator
AUO97_RS	2.587926	Up	3.04E-	divalent metal
13825			24	cation transporter
AUO97_RS	2.644973	Up	3.5E-	hypothetical protein
18910			48	
AUO97_RS	2.673537	Up	8.63E-	flavin reductase
17125			24	
AUO97_RS	3.134825	Up	5.49E-	oxidoreductase
17130			24	
AUO97_RS	3.137551	Up	8.58E-	KR domain-
17135			27	containing protein
AUO97_RS	3.296468	Up	8.85E-	acyl-CoA
17160			48	dehydrogenase
AUO97_RS	3.302273	Up	5.99E-	aromatic-ring-
17140			17	hydroxylating dioxygenase subunit beta
AUO97_RS	3.557326	Up	8.79E-	aromatic ring-
17145			58	hydroxylating

dioxygenase subunit

alpha

891 Table 6 Differential expressed genes in $\Delta abaR$ strain

GeneID	log2FoldChange(Δ <i>abaR</i> /WT)	Up-Down- Regulation(Δa <i>baR</i> /WT)	Pvalu e	Product
AUO97_RS 00540	-1.46697	Down	7.01E -97	elongation factor Ts
AUO97_RS 00545	-1.23446	Down	6.5E- 101	30S ribosomal protein S2
AUO97_RS 01555	-1.25779	Down	7.5E- 12	sulfate ABC transporter substrate- binding protein
AUO97_RS 01560	-1.60798	Down	9.23E -07	alpha/beta hydrolase
AUO97_RS 01565	-1.80619	Down	3.15E -14	sulfate ABC transporter permease subunit CysT
AUO97_RS 01570	-1.51136	Down	1.53E -08	sulfate ABC transporter permease subunit CysW
AUO97_RS	-1.55706	Down	1.89E	sulfate ABC

01575			-17	transporter ATP-binding protein
AUO97_RS	-1.04633	Down	1.47E	phosphoribosylformylg
01835			-50	lycinamidine synthase
AUO97_RS	-1.24855	Down	7.89E	septum formation
02870			-07	inhibitor Maf
AUO97_RS	-1.006	Down	1.04E	translational GTPase
03165			-52	TypA
AUO97_RS	-1.02069	Down	2.64E	DUF934 domain-containing protein
03220			-08	
AUO97_RS	-1.00367	Down	7.42E	50S ribosomal protein
03975			-47	L13
AUO97_RS	-1.27941	Down	8.69E	EamA/RhaT family
04165			-08	transporter
AUO97_RS	-1.36319	Down	2.43E	50S ribosomal protein
04275			-55	L17
AUO97_RS	-1.26373	Down	9.25E	DNA-directed RNA
04280			-80	polymerase subunit alpha
AUO97_RS	-1.14133	Down	7.65E	30S ribosomal protein
04285			-54	S4
AUO97_RS	-1.09269	Down	1.17E	30S ribosomal protein

04290			-38	S11
AUO97_RS	-1.29326	Down	1.32E	preprotein translocase
04305			-74	subunit SecY
AUO97_RS	-1.09864	Down	1.39E	50S ribosomal protein
04310			-44	L15
AUO97_RS	-1.15251	Down	1.55E	30S ribosomal protein
04320			-40	S5
AUO97_RS	-1.14007	Down	2.33E	50S ribosomal protein
04325			-45	L18
AUO97_RS	-1.03587	Down	5.13E	50S ribosomal protein
04330			-39	L6
AUO97_RS	-1.12717	Down	1.21E	30S ribosomal protein
04335			-37	S8
AUO97_RS	-1.00921	Down	2.04E	30S ribosomal protein
04340			-22	S14
AUO97_RS	-1.04986	Down	2.5E-	50S ribosomal protein
04345			52	L5
AUO97_RS	-1.33542	Down	2.89E	30S ribosomal protein
04360			-22	S17
AUO97_RS	-1.38332	Down	9.06E	50S ribosomal protein
04365			-15	L29
AUO97_RS	-1.30303	Down	6.38E	50S ribosomal protein

04370			-42	L16
AUO97_RS	-1.38848	Down	3.29E	30S ribosomal protein
04375			-60	S3
AUO97_RS	-1.32586	Down	3.99E	50S ribosomal protein
04380			-40	L22
AUO97_RS	-1.2558	Down	3.56E	30S ribosomal protein
04385			-34	S19
AUO97_RS	-1.25482	Down	9.97E	50S ribosomal protein
04390			-55	L2
AUO97_RS	-1.33758	Down	3.92E	50S ribosomal protein
04395			-37	L23
AUO97_RS	-1.14341	Down	4.11E	50S ribosomal protein
04400			-43	L4
AUO97_RS	-1.19034	Down	3.39E	50S ribosomal protein
04405			-50	L3
AUO97_RS	-1.18708	Down	2.7E-	30S ribosomal protein
04410			30	S10
AUO97_RS	-1.0042	Down	1.6E-	flavohemoprotein
04430			53	
AUO97_RS	-1.16847	Down	2.27E	50S ribosomal protein
04805			-41	L19
AUO97_RS	-1.0155	Down	1.78E	MFS transporter

05405			-11	
AUO97_RS	-1.08048	Down	2.86E	ATP synthase epsilon
06420			-48	chain
AUO97_RS	-1.0439	Down	3.37E	ATP synthase subunit
06425			-50	beta
AUO97_RS	-1.19299	Down	3.17E	ATP synthase subunit
06430			-60	gamma
AUO97_RS	-1.00172	Down	5.3E-	ATP synthase subunit
06435			52	alpha
AUO97_RS	-1.3648	Down	3.66E	phosphopantetheine-
06595			-06	protein transferase
AUO97_RS	-2.11825	Down	8.13E	alpha/beta hydrolase
06600			-56	
AUO97_RS	-2.58786	Down	4.19E	hypothetical protein
06605			-97	
AUO97_RS	-4.02394	Down	0	outer membrane
06610				lipoprotein-sorting protein
AUO97_RS	-4.2825	Down	0	non-ribosomal peptide
06615				synthetase
AUO97_RS	-2.30484	Down	1.32E	acyl carrier protein
06620			-05	[Acinetobacter]

AUO97_RS	-4.46229	Down	0	acyl-CoA
06625				dehydrogenase
AUO97_RS	-3.82819	Down	0	acyl-CoA synthetase
06630				
AUO97_RS	-3.91695	Down	1.44E	LuxR family
06635			-13	transcriptional
				regulator
AUO97_RS	-1.18831	Down	0.010	GNAT family N-
06645			518	acetyltransferase
AUO97_RS	-1.57625	Down	9.75E	D-lactate
06850			-39	dehydrogenase
AUO97_RS	-1.66135	Down	2.76E	alpha-hydroxy-acid
06855			-57	oxidizing enzyme
AUO97_RS	-1.89372	Down	8E-42	transcriptional
06860				regulator LldR
AUO97_RS	-1.80838	Down	1.65E	L-lactate permease
06865			-24	[Acinetobacter]
AUO97_RS	-1.27639	Down	4.66E	dual-action HEIGH
07200			-18	metallo-peptidase
AUO97_RS	-1.0278	Down	0.000	hypothetical protein
08005			671	
AUO97_RS	-1.18969	Down	1.46E	ATP-binding protein

08095			-36	
AUO97_RS	-1.00682	Down	4.07E	hypothetical protein
08100			-06	
AUO97_RS	-1.50123	Down	4.68E	type VI secretion
08105			-08	protein
AUO97_RS	-1.6293	Down	3.47E	hypothetical protein
08110			-44	
AUO97_RS	-1.32724	Down	3.42E	type VI secretion
08115			-11	protein
AUO97_RS	-1.78941	Down	6.98E	hypothetical protein
08120			-25	
AUO97_RS	-1.63462	Down	1.71E	conjugal transfer
08125			-25	protein Trbl
AUO97_RS	-1.53505	Down	1E-14	hypothetical protein
08130				
AUO97_RS	-1.78221	Down	2.31E	conjugal transfer
08135			-11	protein
AUO97_RS	-1.63347	Down	2.54E	hypothetical protein
08175			-07	
AUO97_RS	-1.43919	Down	5.89E	hypothetical protein
08180			-15	
AUO97_RS	-1.2236	Down	5.97E	type IV pili twitching

08185			-15	motility protein PilT
AUO97_RS	-1.35697	Down	2.13E	hypothetical protein
08195			-17	
AUO97_RS	-1.00648	Down	0.000	hypothetical protein
08200			214	
AUO97_RS	-1.03879	Down	1.12E	hypothetical protein
08205			-06	
AUO97_RS	-1.0272	Down	1.39E	hypothetical protein
08345			-09	
AUO97_RS	-3.96826	Down	3.8E-	IS5 family transposase
08400			191	
AUO97_RS	-2.61617	Down	1.95E	DNA-binding protein
08775			-12	[Acinetobacter]
AUO97_RS	-1.19333	Down	1.89E	elongation factor Tu
08830			-65	
AUO97_RS	-1.12568	Down	8.29E	50S ribosomal protein
08850			-60	L11
AUO97_RS	-1.15414	Down	4.74E	50S ribosomal protein
08855			-68	L1
AUO97_RS	-1.25299	Down	6.63E	50S ribosomal protein
08860			-61	L10
AUO97_RS	-1.29006	Down	8.87E	50S ribosomal protein

08865			-84	L7/L12 [Acinetobacter]
AUO97_RS	-1.03148	Down	2.36E	DNA-directed RNA
08870			-50	polymerase subunit
				beta
AUO97_RS	-1.14418	Down	2.9E-	DNA-directed RNA
08875			73	polymerase subunit
				beta'
AUO97_RS	-1.04917	Down	4.83E	transcription
09110			-48	termination/antitermi
				nation protein NusA
AUO97_RS	-1.11845	Down	2.33E	translation initiation
09115			-57	factor IF-2
AUO97_RS	-1.02517	Down	3E-23	ribosome-binding
09120				factor A
AUO97_RS	-1.15939	Down	0.000	50S ribosomal protein
09675			133	L28 [Moraxellaceae]
AUO97_RS	-1.39769	Down	3.91E	50S ribosomal protein
10415			-09	L35
AUO97_RS	-1.23068	Down	1.37E	50S ribosomal protein
10420			-68	L20 [Acinetobacter]
AUO97_RS	-1.10035	Down	4.37E	NADH-quinone
11000			-14	oxidoreductase

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				subunit K
				[Acinetobacter]
AUO97_RS	-1.00922	Down	9.05E	NADH-quinone
11015			-51	oxidoreductase
				subunit N
AUO97_RS	-1.09784	Down	1.27E	MFS transporter
11215			-35	
AUO97_RS	-1.00307	Down	1.11E	50S ribosomal protein
11345			-16	L25
AUO97_RS	-1.12853	Down	2.42E	30S ribosomal protein
11530			-59	S7
AUO97_RS	-1.22746	Down	1.66E	elongation factor G
11535			-65	
AUO97_RS	-1.1171	Down	1.64E	malate:quinone
11840			-58	oxidoreductase
AUO97_RS	-1.05094	Down	0.008	Lrp/AsnC family
12710			596	transcriptional
				regulator
AUO97_RS	-1.23454	Down	0.000	transposase
13535			918	
AUO97_RS	-1.77276	Down	0.000	amino acid ABC
14515			107	transporter permease
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[Acinetobacter]				
AUO97_RS	-1.13951	Down	1.92E	ArtI protein
14525			-06	[Acinetobacter]
AUO97_RS	-1.41173	Down	1.07E	taurine ABC
14730			-09	transporter ATP-binding protein
AUO97_RS	-1.63502	Down	9.12E	taurine ABC
14735			-15	transporter permease
AUO97_RS	-2.01495	Down	7.36E	taurine dioxygenase
14740			-21	
AUO97_RS	-1.4971	Down	0.000	hypothetical protein
15190			116	
AUO97_RS	-4.0442	Down	0	trifunctional
15195				transcriptional
				regulator/proline
				dehydrogenase/L-
				glutamate gamma-
				semialdehyde
				dehydrogenase
AUO97_RS	-1.779	Down	1.1E-	sodium/proline
15205			174	symporter PutP
AUO97_RS	-1.43715	Down	4.91E	NAD(P)-dependent

16765			-05	alcohol dehydrogenase
AUO97_RS	-1.02093	Down	0.001	3-dehydroquinate
17945			295	dehydratase
AUO97_RS	-1.10603	Down	6.31E	protoheme IX
18980			-29	farnesyltransferase
AUO97_RS	-1.2489	Down	4.3E-	30S ribosomal protein
18985			72	S6
AUO97_RS	-1.16315	Down	5.79E	30S ribosomal protein
18990			-09	S18
AUO97_RS	-1.41125	Down	8.4E-	50S ribosomal protein
18995			118	L9
AUO97_RS	1.222331	Up	0.016	hypothetical protein
00020			824	
AUO97_RS	1.135363	Up	0.000	glycosyl transferase
00035			104	
AUO97_RS	1.1511	Up	5.99E	PIG-L family
00045			-08	deacetylase
AUO97_RS	1.098532	Up	7.5E-	acyl-CoA
00580			35	dehydrogenase
AUO97_RS	1.639534	Up	6.49E	alpha/beta hydrolase
00665			-71	
AUO97_RS	1.245914	Up	5.65E	hydrolase

00945			-06	
AUO97_RS	1.091104	Up	0.000	DUF466 domain-
00985			167	containing protein
AUO97_RS	1.196287	Up	1.09E	carbon starvation
00990			-52	protein A
AUO97_RS	2.419967	Up	6.12E	MFS transporter
01130			-42	
AUO97_RS	2.254064	Up	1.16E	ATP-dependent
01135			-83	protease
AUO97_RS	1.668297	Up	1.74E	NAD-dependent
01145			-90	aldehyde
				dehydrogenase
AUO97_RS	1.013324	Up	2.48E	hypothetical protein
01330			-20	
AUO97_RS	1.258765	Up	1.74E	PDZ domain-containing
01525			-42	protein
AUO97_RS	1.134019	Up	0.017	NIF3 1
01635			089	
AUO97_RS	1.056825	Up	5.66E	amidohydrolase
01855			-05	
AUO97_RS	1.096169	Up	2.03E	amino acid permease
02080			-37	

AUO97_RS	1.126299	Up	1.17E	glutamine
02905			-16	amidotransferase
AUO97_RS	1.25559	Up	7.25E	DUF1508 domain-
03090			-17	containing protein
AUO97_RS	1.492233	Up	1.04E	toxin
03105			-09	
AUO97_RS	1.158869	Up	6.14E	large conductance
03160			-24	mechanosensitive
				channel protein MscL
AUO97_RS	1.611018	Up	6.12E	VOC family protein
03210			-14	
AUO97_RS	1.156133	Up	1.9E-	acetyl/propionyl/meth
04000			16	ylcrotonyl-CoA
				carboxylase subunit
				alpha
AUO97_RS	1.052399	Up	4.02E	enoyl-CoA hydratase
04005			-05	
AUO97_RS	1.271182	Up	8.42E	acyl-CoA
04010			-15	dehydrogenase
AUO97_RS	1.648108	Up	9.91E	acetyl-CoA carboxylase
04015			-27	carboxyltransferase
				subunit

AUO97_RS	1.729121	Up	2.87E	KR domain-containing
04020			-19	protein
AUO97_RS	1.935767	Up	1.05E	DUF1446 domain-
04025			-53	containing protein
AUO97_RS	1.138211	Up	4.47E	hypothetical protein
04195			-65	
AUO97_RS	2.218472	Up	1.38E	hypothetical protein
04615			-19	
AUO97_RS	5.633865	Up	4.3E-	EamA/RhaT family
04620			106	transporter
AUO97_RS	1.264872	Up	2.7E-	hypothetical protein
04905			05	
AUO97_RS	1.231286	Up	4.4E-	LemA family protein
04915			31	
AUO97_RS	1.791924	Up	5.78E	hypothetical protein
05105			-67	
AUO97_RS	1.207876	Up	7.53E	sulfate permease
05140			-08	
AUO97_RS	1.821676	Up	9.5E-	EamA/RhaT family
05215			28	transporter
AUO97_RS	1.081392	Up	7.43E	hypothetical protein
05275			-10	

AUO97_RS	1.46563	Up	0.000	GNAT family N-
05370			574	acetyltransferase
AUO97_RS	1.02368	Up	2.04E	hydrolase
05440			-12	
AUO97_RS	1.550398	Up	9.3E-	NAD-dependent
05450			115	succinate-
				semialdehyde
				dehydrogenase
AUO97_RS	2.444237	Up	9.5E-	4-aminobutyrate--2-
05455			158	oxoglutarate
				transaminase
AUO97_RS	2.866641	Up	1.4E-	amino acid permease
05465			170	
AUO97_RS	1.227311	Up	1.59E	NADPH:quinone
05515			-21	oxidoreductase
AUO97_RS	1.298715	Up	6.71E	hypothetical protein
05545			-05	
AUO97_RS	2.370634	Up	1.4E-	cation acetate
05550			202	symporter
AUO97_RS	1.922574	Up	6.03E	DUF485 domain-
05555			-29	containing protein
				[Acinetobacter]

AUO97_RS	2.656199	Up	3.7E-	acetate--CoA ligase
05595			278	
AUO97_RS	1.336995	Up	2.19E	carbapenem
05635			-84	susceptibility porin
				CarO
AUO97_RS	1.641335	Up	2.51E	hypothetical protein
05805			-71	
AUO97_RS	1.057684	Up	5.68E	DUF2726 domain-
06270			-08	containing protein
AUO97_RS	1.175945	Up	0.014	DUF3861 domain-
06525			654	containing protein
AUO97_RS	1.175091	Up	4.65E	DoxX family protein
06550			-05	
AUO97_RS	2.333258	Up	6.99E	MFS transporter
06650			-28	
AUO97_RS	2.75065	Up	7.52E	enoyl-CoA
06655			-90	hydratase/isomerase
				family protein
AUO97_RS	2.947701	Up	1.15E	enoyl-CoA hydratase
06660			-61	
AUO97_RS	2.788771	Up	2.4E-	acyl-CoA
06665			101	dehydrogenase

AUO97_RS	2.99023	Up	6.78E	AMP-binding protein
06670			-31	
AUO97_RS	2.626672	Up	1.8E-	3-hydroxyisobutyrate
06675			101	dehydrogenase
AUO97_RS	2.412876	Up	5.5E-	methyImalonate-
06680			215	semialdehyde
				dehydrogenase
				(acylating)
AUO97_RS	1.738202	Up	2.05E	amino acid permease
06695			-58	
AUO97_RS	1.327951	Up	3.98E	RidA family protein
06700			-13	[Acinetobacter]
AUO97_RS	1.11741	Up	1.41E	alanine racemase
06705			-34	
AUO97_RS	1.417227	Up	3.65E	D-amino-acid
06710			-61	dehydrogenase
AUO97_RS	1.465739	Up	0.000	AsnC family
06715			52	transcriptional
				regulator
				[Acinetobacter]
AUO97_RS	1.075741	Up	0.002	sel1 repeat family
06785			995	protein

AUO97_RS	1.16987	Up	8.02E	DUF4126 domain-
06810			-09	containing protein
AUO97_RS	2.083996	Up	5.4E-	Fe/S-dependent 2-
06825			190	methylisocitrate
				dehydratase AcnD
AUO97_RS	2.154844	Up	7.5E-	2-methylcitrate
06830			125	synthase
AUO97_RS	2.034936	Up	2.1E-	methylisocitrate lyase
06835			108	
AUO97_RS	1.166137	Up	1.01E	GntR family
06840			-23	transcriptional
				regulator
AUO97_RS	1.277517	Up	0.012	hypothetical protein
07165			728	
AUO97_RS	1.067484	Up	0.004	GlsB/YeaQ/YmgE
07280			097	family stress response
				membrane protein
				[Acinetobacter]
AUO97_RS	1.453655	Up	7.14E	sodium-dependent
07430			-70	transporter
AUO97_RS	1.141851	Up	1.13E	PQQ-dependent sugar
07590			-09	dehydrogenase

AUO97_RS	1.903493	Up	1.1E-	4-
07645			213	hydroxyphenylpyruvat e dioxygenase
AUO97_RS	1.885403	Up	5.1E-	VOC family protein
07655			107	
AUO97_RS	1.644119	Up	1.7E-	maleylacetoacetate
07660			102	isomerase
AUO97_RS	1.732833	Up	6.8E-	fumarylacetoacetase
07665			139	
AUO97_RS	2.082498	Up	2.6E-	aromatic amino acid
07670			191	transporter AroP
AUO97_RS	1.109972	Up	2.23E	amino acid permease
07710			-40	
AUO97_RS	1.277428	Up	7.06E	imidazolonepropionas
07715			-54	e
AUO97_RS	1.392517	Up	2.47E	formimidoylglutamase
07720			-69	
AUO97_RS	1.165672	Up	1.52E	DUF885 domain-
07725			-07	containing protein
AUO97_RS	1.186045	Up	2.89E	hypothetical protein
07745			-16	
AUO97_RS	1.313813	Up	3.7E-	TetR/AcrR family

08710			08	transcriptional regulator
AUO97_RS	1.522507	Up	0.000	DNA transfer protein
08885			292	p32
AUO97_RS	1.441162	Up	1.05E	hypothetical protein
08925			-45	
AUO97_RS	1.990121	Up	9.89E	MerR family
09240			-17	transcriptional regulator
AUO97_RS	1.159549	Up	2.63E	hypothetical protein
09745			-05	
AUO97_RS	1.430921	Up	1.56E	phosphate
09845			-62	acetyltransferase
AUO97_RS	1.495476	Up	5.58E	acetate kinase
09850			-67	
AUO97_RS	1.130523	Up	6.26E	aconitate hydratase
10220			-63	AcnA
AUO97_RS	1.368536	Up	9.08E	hydroxypyruvate
10285			-22	isomerase
AUO97_RS	1.815771	Up	7.89E	acyl-CoA synthetase
10375			-80	
AUO97_RS	1.238882	Up	5.12E	acyl-CoA

10780			-22	dehydrogenase
AUO97_RS	1.219079	Up	1.81E	Ig-like domain
10915			-60	
AUO97_RS	1.547215	Up	0.000	hypothetical protein
11050			298	
AUO97_RS	1.277695	Up	2.06E	hypothetical protein
11055			-85	
AUO97_RS	1.046402	Up	3.48E	trehalose-6-phosphate
11220			-27	synthase
AUO97_RS	1.287005	Up	3.58E	threonylcarbamoyl-
11270			-12	AMP synthase
AUO97_RS	1.451916	Up	2.38E	metal-dependent
11550			-10	hydrolase
AUO97_RS	1.160465	Up	3.76E	gamma-
11750			-21	glutamyltransferase
				family protein
AUO97_RS	1.267775	Up	0.006	cupin domain-
11975			622	containing protein
				[Acinetobacter]
AUO97_RS	1.001019	Up	9.88E	amino acid transporter
12450			-12	
AUO97_RS	1.891923	Up	1E-13	hypothetical protein

12700				
AUO97_RS	1.395535	Up	2.52E	gamma-
12705			-22	aminobutyraldehyde
				dehydrogenase
AUO97_RS	2.700051	Up	1E-42	aspartate
12715				aminotransferase
				family protein
AUO97_RS	2.456076	Up	4.22E	arginine N-
12720			-24	succinyltransferase
AUO97_RS	1.332388	Up	1.17E	feruloyl-CoA synthase
12815			-05	
AUO97_RS	1.944957	Up	1E-12	crotonase
12825				
AUO97_RS	1.696962	Up	4.2E-	aromatic ring-
12850			09	hydroxylating
				dioxygenase subunit
				alpha
AUO97_RS	1.327513	Up	0.008	MFS transporter
12855			247	
AUO97_RS	1.063488	Up	0.004	hypothetical protein
13000			539	
AUO97_RS	1.167699	Up	0.003	hypothetical protein

13005			181	
AUO97_RS	1.254068	Up	0.011	hypothetical protein
13050			311	
AUO97_RS	1.816626	Up	1.1E-	OmpA family protein
13365			103	
AUO97_RS	1.28526	Up	2.37E	aromatic acid/H+
13440			-07	symport family MFS
				transporter
AUO97_RS	1.198891	Up	0.000	KR domain-containing
13450			264	protein
AUO97_RS	1.354883	Up	1.45E	benzoate 1,2-
13465			-13	dioxygenase large
				subunit
AUO97_RS	1.043153	Up	3.76E	Cu(I)-responsive
13485			-05	transcriptional
				regulator
				[Acinetobacter]
AUO97_RS	1.143059	Up	9.1E-	MFS transporter
13760			05	
AUO97_RS	3.234393	Up	6.8E-	divalent metal cation
13825			158	transporter
AUO97_RS	3.201213	Up	2.6E-	LamB/YcsF family

13830			131	protein
AUO97_RS	3.473384	Up	8.5E-	DUF1445 domain-
13835			107	containing protein
AUO97_RS	2.743149	Up	1.4E-	allophanate hydrolase
13840			134	
AUO97_RS	2.961316	Up	3.2E-	ATP-grasp domain-
13845			213	containing protein
AUO97_RS	1.08262	Up	2.65E	DUF333 domain-
14095			-11	containing protein
AUO97_RS	1.53906	Up	3.3E-	phenylacetic acid
14165			101	degradation
				bifunctional protein
				PaaZ
AUO97_RS	1.032446	Up	2.82E	1,2-phenylacetyl-CoA
14170			-49	epoxidase subunit A
AUO97_RS	1.3148	Up	1.55E	1,2-phenylacetyl-CoA
14175			-15	epoxidase subunit B
				[Acinetobacter]
AUO97_RS	1.499868	Up	1.65E	phenylacetate-CoA
14180			-67	oxygenase subunit Paal
AUO97_RS	1.536227	Up	1.89E	phenylacetate-CoA
14185			-33	oxygenase subunit

PaaJ [Acinetobacter]				
AUO97_RS	1.751782	Up	4.95E	phenylacetate-CoA
14190			-74	oxygenase/reductase
				subunit PaaK
AUO97_RS	1.762544	Up	1.76E	enoyl-CoA hydratase
14195			-44	
AUO97_RS	2.024242	Up	1.93E	2-(1,2-epoxy-1,2-
14200			-52	dihydrophenyl)acetyl-
				CoA isomerase
AUO97_RS	1.999641	Up	3.01E	3-hydroxyacyl-CoA
14205			-78	dehydrogenase
AUO97_RS	2.356772	Up	1.47E	3-oxoadipyl-CoA
14210			-86	thiolase
AUO97_RS	2.48519	Up	1E-99	phenylacetate--CoA
14215				ligase [Acinetobacter]
AUO97_RS	1.148118	Up	3.32E	phenylacetic acid
14220			-18	degradation operon
				negative regulatory
				protein PaaX
AUO97_RS	1.268769	Up	1.59E	carbonic anhydrase
14225			-07	
AUO97_RS	1.60666	Up	0.005	Paal family

14230			131	thioesterase
AUO97_RS	2.142704	Up	3.8E-	hypothetical protein
14350			210	
AUO97_RS	2.522866	Up	4.7E-	hydroxymethylglutaryl-
14360			198	CoA lyase
AUO97_RS	2.454808	Up	4.6E-	acetyl/propionyl/meth
14365			216	ylcrotonyl-CoA
				carboxylase subunit
				alpha
AUO97_RS	2.29445	Up	1E-	enoyl-CoA hydratase
14370			130	
AUO97_RS	2.072343	Up	2.5E-	methylcrotonoyl-CoA
14375			231	carboxylase subunit
				beta
AUO97_RS	1.70927	Up	3.3E-	isovaleryl-CoA
14380			142	dehydrogenase
				[Acinetobacter]
AUO97_RS	1.473479	Up	6.7E-	TetR/AcrR family
14385			88	transcriptional
				regulator
AUO97_RS	1.584436	Up	2.3E-	AMP-binding protein
14390			99	

AUO97_RS	1.860351	Up	2.77E	class I SAM-dependent
14395			-29	methyltransferase
AUO97_RS	1.850229	Up	2.47E	porin
14400			-24	
AUO97_RS	1.887777	Up	0.000	hypothetical protein
14470			657	
AUO97_RS	1.066247	Up	1.68E	LysE family
14480			-06	translocator
AUO97_RS	1.049086	Up	3.4E-	cytochrome ubiquinol
14690			28	oxidase subunit I
AUO97_RS	1.419848	Up	5.24E	peptide-methionine
14855			-21	(R)-S-oxide reductase
AUO97_RS	1.54179	Up	9.37E	amino acid ABC
14970			-77	transporter substrate-binding protein
AUO97_RS	1.38723	Up	7.4E-	amino acid ABC
14975			36	transporter permease
AUO97_RS	1.428635	Up	7.26E	amino acid ABC
14980			-24	transporter permease
AUO97_RS	1.5406	Up	2.68E	amino acid ABC
14985			-41	transporter ATP-binding protein

AUO97_RS	1.837935	Up	2.31E	hypothetical protein
15145			-06	
AUO97_RS	1.100482	Up	0.000	phage major capsid
15625			393	protein
AUO97_RS	1.402496	Up	3E-06	membrane protein
16085				
AUO97_RS	1.070249	Up	9.77E	helix-turn-helix
16245			-14	domain-containing
				protein
AUO97_RS	1.783306	Up	1.04E	lipoyl synthase
16250			-38	
AUO97_RS	2.613427	Up	5.1E-	thiamine
16255			147	pyrophosphate-
				dependent
				dehydrogenase E1
				component subunit
				alpha [Acinetobacter]
AUO97_RS	2.751704	Up	4.6E-	alpha-ketoacid
16260			128	dehydrogenase
				subunit beta
				[Acinetobacter]
AUO97_RS	2.709018	Up	3.3E-	pyruvate

16265			146	dehydrogenase complex dihydrolipoamide acetyltransferase
AUO97_RS	2.482195	Up	1.3E-	dihydrolipoyl
16270			103	dehydrogenase
AUO97_RS	2.532405	Up	7.87E	3-oxoacyl-ACP
16275			-35	reductase
AUO97_RS	2.044181	Up	8.99E	2,3-butanediol
16280			-68	dehydrogenase [Acinetobacter]
AUO97_RS	1.320639	Up	5.63E	sulfite exporter
16305			-11	TauE/SafE family protein
AUO97_RS	1.063217	Up	1.95E	MFS transporter
16380			-06	
AUO97_RS	2.547582	Up	1.8E-	acetyl-CoA C-
16415			236	acyltransferase
AUO97_RS	3.111344	Up	1.4E-	hypothetical protein
16420			138	
AUO97_RS	3.545127	Up	5E-	CoA transferase
16425			276	subunit B

AUO97_RS	3.355226	Up	2.2E-	CoA transferase
16430			212	subunit A
AUO97_RS	1.065725	Up	1.2E-	GntP family permease
16465			37	
AUO97_RS	1.220277	Up	2.06E	3-hydroxybutyrate
16470			-27	dehydrogenase
AUO97_RS	1.198637	Up	7.03E	AdeA/Adel family
16540			-05	multidrug efflux RND
				transporter
				periplasmic adaptor
				subunit
AUO97_RS	1.072523	Up	0.000	muconate
17065			169	cycloisomerase
AUO97_RS	1.183404	Up	0.000	flavin reductase
17125			615	
AUO97_RS	1.630775	Up	5.91E	oxidoreductase
17130			-05	
AUO97_RS	1.379569	Up	0.000	KR domain-containing
17135			479	protein
AUO97_RS	2.112924	Up	7.35E	aromatic-ring-
17140			-05	hydroxylating
				dioxygenase subunit

				beta
AUO97_RS	1.870779	Up	2.13E	aromatic ring-
17145			-11	hydroxylating
				dioxygenase subunit
				alpha
AUO97_RS	1.445298	Up	0.005	hypothetical protein
17155			927	
AUO97_RS	1.417474	Up	1.19E	acyl-CoA
17160			-07	dehydrogenase
AUO97_RS	1.037498	Up	0.006	protocatechuate 3,4-
17255			082	dioxygenase subunit
				alpha
AUO97_RS	1.339034	Up	0.016	4-
17265			976	carboxymuconolacton
				e decarboxylase
				[Acinetobacter]
AUO97_RS	1.117003	Up	0.000	aromatic acid/H+
17270			133	symport family MFS
				transporter
AUO97_RS	1.031416	Up	0.001	3-oxoadipate CoA-
17295			354	transferase subunit A
AUO97_RS	1.418298	Up	7.41E	hypothetical protein

17510			-19	
AUO97_RS	1.348617	Up	1.88E	univeal stress protein
17615			-12	
AUO97_RS	1.595015	Up	5.1E-	D-amino acid
17805			125	dehydrogenase
AUO97_RS	1.379384	Up	0.016	hypothetical protein
18020			194	
AUO97_RS	1.120939	Up	0.010	hypothetical protein
18065			31	
AUO97_RS	1.293585	Up	0.013	hypothetical protein
18165			585	
AUO97_RS	1.483132	Up	0.007	hypothetical protein
18270			185	
AUO97_RS	1.352626	Up	3.22E	RDD family protein
18455			-05	
AUO97_RS	3.165241	Up	2.2E-	alcohol dehydrogenase
18615			227	
AUO97_RS	2.790133	Up	6.7E-	aldehyde
18630			289	dehydrogenase
AUO97_RS	1.045856	Up	1.34E	ethanolamine
18635			-06	permease
AUO97_RS	1.168491	Up	0.000	ethanolamine

18640			154	ammonia-lyase
				subunit EutB
AUO97_RS	2.626809	Up	4.9E-	AMP-binding protein
18860			108	
AUO97_RS	2.497141	Up	1.3E-	butyryl-CoA
18865			129	dehydrogenase
AUO97_RS	2.711438	Up	1.4E-	3-hydroxyacyl-CoA
18870			155	dehydrogenase
AUO97_RS	1.091354	Up	0.000	hypothetical protein
19040			146	[Acinetobacter]
AUO97_RS	1.109533	Up	5.26E	molecular chaperone
19200			-07	
AUO97_RS	1.38997	Up	0.000	SCPU domain-
19205			595	containing protein
AUO97_RS	1.208871	Up	0.000	protein CsuA
19210			104	
AUO97_RS	2.042194	Up	3.42E	SCPU domain-
19215			-59	containing protein

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893 Table 7 Differential expressed genes in $\Delta abalR$ strain

GeneID	log2FoldChange(Δa	Up-Down-	Pvalue	Product
	<i>baIR</i> /WT)	Regulation(Δab		

<i>alR/WT)</i>				
AUO97_RS	-4.810564081	Down	0	acyl-CoA
06625				dehydrogenase
AUO97_RS	-4.798341091	Down	0	non-ribosomal
06615				peptide
				synthetase
AUO97_RS	-4.684191859	Down	0	outer membrane
06610				lipoprotein-
				sorting protein
AUO97_RS	-4.479849984	Down	0	acyl-CoA
06630				synthetase
AUO97_RS	-3.443053657	Down	0	membrane
08905				protein
AUO97_RS	-3.169896529	Down	1.77E-13	LuxR family
06635				transcriptional
				regulator
AUO97_RS	-2.775977102	Down	1.2E-108	hypothetical
06605				protein
AUO97_RS	-2.592760202	Down	1.05E-77	alpha/beta
06600				hydrolase
AUO97_RS	-2.580535991	Down	5.26E-09	GNAT family N-
06645				acetyltransferase

AUO97_RS	-2.187695047	Down	8.04E-07	acyl carrier
06620				protein
AUO97_RS	-2.092687691	Down	1.5E-128	NAD(P)(+)
10260				transhydrogenas
				e (Re/Si-specific)
				subunit alpha
AUO97_RS	-1.736715963	Down	1.03E-89	NAD(P)
10270				transhydrogenas
				e subunit beta
AUO97_RS	-1.715456717	Down	5.71E-10	NAD(P)
10265				transhydrogenas
				e subunit alpha
AUO97_RS	-1.610454816	Down	5.57E-10	SDR family
12875				NAD(P)-
				dependent
				oxidoreductase
AUO97_RS	-1.571786385	Down	1.63E-66	UDP-glucose 4-
06875				epimerase GalE
AUO97_RS	-1.571062479	Down	1.04E-66	isovaleryl-CoA
14380				dehydrogenase
AUO97_RS	-1.504167019	Down	1.89E-08	DUF2147
13765				domain-

				containing
				protein
AUO97_RS	-1.467640693	Down	7.99E-23	hypothetical
05565				protein
AUO97_RS	-1.450434646	Down	1.71E-06	esterase
12200				
AUO97_RS	-1.447421801	Down	2.09E-77	hypothetical
12630				protein
AUO97_RS	-1.418971886	Down	2.68E-07	DUF485 domain-
05555				containing
				protein
AUO97_RS	-1.416019051	Down	6.55E-44	AMP-binding
14390				protein
AUO97_RS	-1.363301003	Down	1.35E-64	methylcrotonoyl
14375				-CoA carboxylase
				subunit beta
AUO97_RS	-1.333055716	Down	3.01E-07	class I SAM-
14395				dependent
				methyltransferas
				e
gene2510	-1.254200121	Down	0.000113	#N/A
AUO97_RS	-1.221452269	Down	5.3E-91	histidine

07705				ammonia-lyase
AUO97_RS	-1.218989942	Down	6.02E-21	short-chain
06750				dehydrogenase
AUO97_RS	-1.216497945	Down	4E-69	acetyl-CoA
05160				hydrolase
AUO97_RS	-1.2055697	Down	7E-106	isocitrate lyase
12255				
AUO97_RS	-1.18255173	Down	1.22E-39	DUF2147
05775				domain-
				containing
				protein
AUO97_RS	-1.159218991	Down	1.38E-62	D-amino acid
12620				dehydrogenase
AUO97_RS	-1.15568351	Down	2.52E-33	hypothetical
10175				protein
AUO97_RS	-1.148829981	Down	0.008712	RNA-binding
09645				protein
AUO97_RS	-1.146164239	Down	6.59E-12	GntR family
06840				transcriptional
				regulator
AUO97_RS	-1.136579054	Down	3.51E-05	DUF1311
08910				domain-

				containing
				protein
AUO97_RS	-1.136034285	Down	3.57E-11	ribosome-
10590				associated
				translation
				inhibitor RaiA
AUO97_RS	-1.09534896	Down	1.37E-11	RidA family
12615				protein
AUO97_RS	-1.062020065	Down	2.24E-40	DegT/DnrJ/EryC1
06935				/StrS family
				aminotransferase
				e
AUO97_RS	-1.053989883	Down	0.001534	SRPBCC family
13875				protein
AUO97_RS	-1.027361924	Down	1.64E-13	enoyl-CoA
14370				hydratase
AUO97_RS	-1.01932917	Down	6.13E-84	malate synthase
15725				G
AUO97_RS	-1.012081007	Down	3.26E-22	acetate kinase
09850				
AUO97_RS	-1.007776244	Down	2.76E-26	RND transporter
07365				

AUO97_RS	-1.00310968	Down	1.46E-42	Ig-like domain
10915				
AUO97_RS	1.000516557	Up	3.19E-06	LysE family
14480				translocator
AUO97_RS	1.0133961	Up	8.83E-37	ferredoxin
07010				reductase
AUO97_RS	1.016484113	Up	3.04E-12	DUF541 domain-
01160				containing protein
AUO97_RS	1.022615214	Up	0.010216	hypothetical
14910				protein
AUO97_RS	1.027289495	Up	1.33E-12	DUF3108
04145				domain- containing protein
AUO97_RS	1.027636888	Up	0.000313	DUF2184
13145				domain- containing protein
AUO97_RS	1.050221533	Up	0.001537	transcriptional
02595				regulator
AUO97_RS	1.059975124	Up	0.000226	MFS transporter

17175				
AUO97_RS	1.065129674	Up	4.77E-12	phosphonate
01125				ABC transporter
				substrate-
				binding protein
AUO97_RS	1.083855153	Up	7.7E-06	XRE family
05210				transcriptional
				regulator
AUO97_RS	1.089851492	Up	5.25E-28	bacterioferritin
04890				
AUO97_RS	1.102335386	Up	2.83E-06	metal-
11550				dependent
				hydrolase
AUO97_RS	1.10618527	Up	0.00818	hypothetical
00265				protein
AUO97_RS	1.109814353	Up	1.46E-41	DUF1852
10860				domain-
				containing
				protein
AUO97_RS	1.111887863	Up	0.008051	hypothetical
13165				protein
AUO97_RS	1.117361686	Up	2.1E-12	adenosine

10765				deaminase
AUO97_RS	1.12070687	Up	0.001552	DUF2213
13135				domain- containing protein
AUO97_RS	1.121710543	Up	5.81E-05	arginine N- succinyltransferase
12720				se
AUO97_RS	1.122555825	Up	0.002472	EamA/RhaT family transporter
04620				
AUO97_RS	1.127777848	Up	0.001455	sulfonate ABC transporter substrate- binding protein
07060				
AUO97_RS	1.134673245	Up	0.009058	hypothetical protein
07165				
AUO97_RS	1.135437723	Up	5.34E-19	flavin reductase
10870				
AUO97_RS	1.145646353	Up	0.002439	outer membrane porin, OprD family
12860				

AUO97_RS	1.145856951	Up	1.85E-31	NADPH:quinone
05515				oxidoreductase
AUO97_RS	1.161085465	Up	1.95E-46	FUSC family
09015				protein
AUO97_RS	1.162966485	Up	0.001507	DUF1003
06745				domain-
				containing
				protein
AUO97_RS	1.16516071	Up	1.69E-06	aspartate
12715				aminotransferas
				e family protein
AUO97_RS	1.175348599	Up	6.55E-17	replication
05945				protein C
				[Proteobacteria]
AUO97_RS	1.187305046	Up	8.43E-06	hypothetical
11705				protein
AUO97_RS	1.19521274	Up	0.000815	hypothetical
13005				protein
AUO97_RS	1.197457681	Up	5.63E-15	hypothetical
07045				protein
AUO97_RS	1.200746597	Up	0.003007	DNA transfer
08880				protein p32

AUO97_RS	1.202220672	Up	0.000235	SfnB family
14960				sulfur
				acquisition
				oxidoreductase
AUO97_RS	1.206540056	Up	0.00495	stress-
18115				responsive
				nuclear
				envelope protein
AUO97_RS	1.211481854	Up	1.01E-39	LysR family
01255				transcriptional
				regulator
AUO97_RS	1.218264558	Up	9.15E-09	DUF1445
13835				domain-
				containing
				protein
AUO97_RS	1.273658088	Up	3.63E-49	acyl-CoA
07005				desaturase
AUO97_RS	1.274976219	Up	2.47E-25	HPP family
04575				protein
AUO97_RS	1.279002189	Up	0.001758	RidA family
10250				protein
AUO97_RS	1.290037253	Up	0.000228	hypothetical

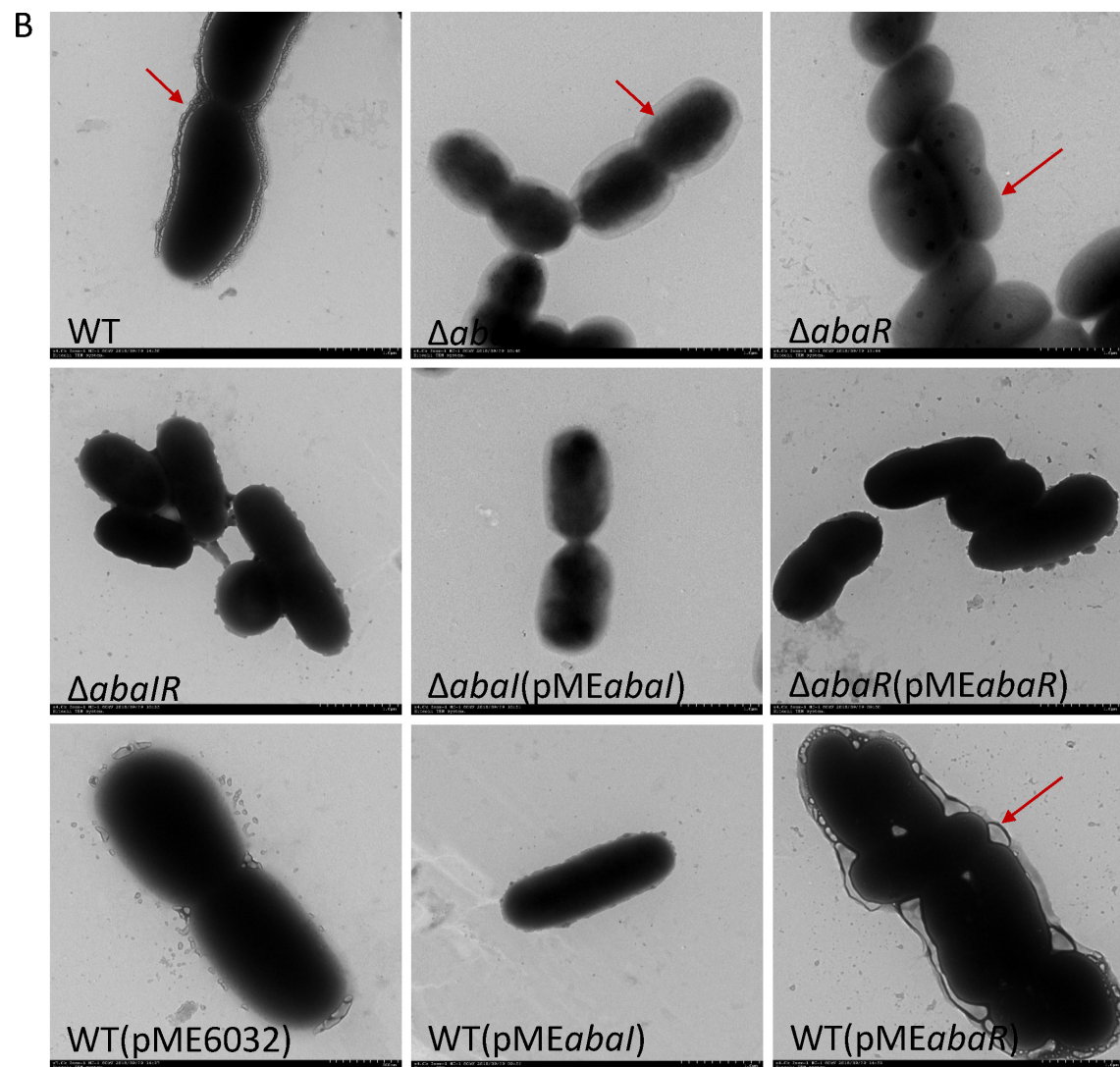
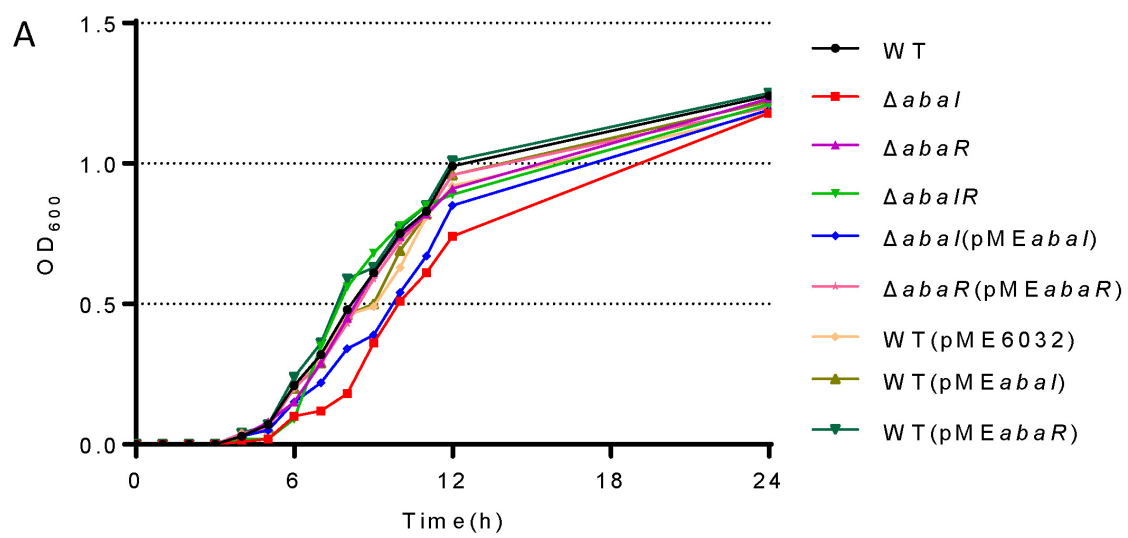
18125				protein
AUO97_RS	1.291462344	Up	6.13E-21	amino acid
12450				transporter
AUO97_RS	1.294967434	Up	1.56E-06	muconate
17065				cycloisomerase
AUO97_RS	1.311448775	Up	3.38E-06	phage major
15625				capsid protein
AUO97_RS	1.31494929	Up	0.000124	SMP-
16845				30/gluconolacto
				nase/LRE family
				protein
AUO97_RS	1.319981098	Up	2.03E-07	hypothetical
00195				protein
AUO97_RS	1.364315635	Up	2.3E-28	pyruvate
01135				decarboxylase
AUO97_RS	1.376815835	Up	4.79E-15	EamA/RhaT
05215				family
				transporter
AUO97_RS	1.390886913	Up	1.88E-28	MacA family
10110				efflux pump
				subunit
AUO97_RS	1.406842394	Up	6.74E-23	RtcB family

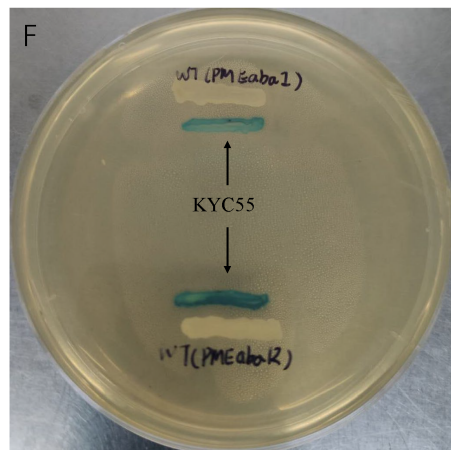
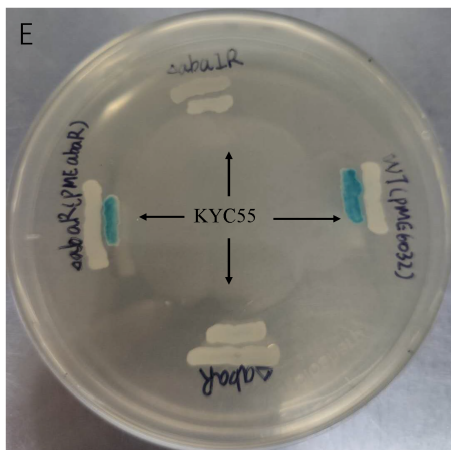
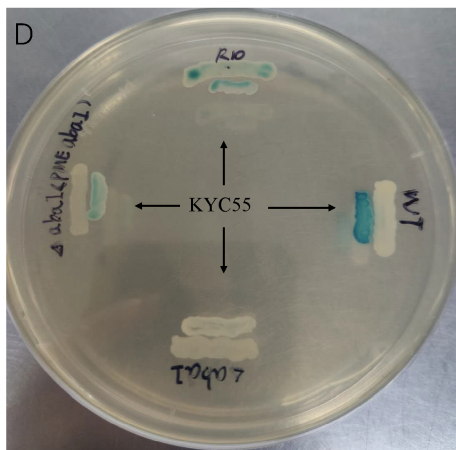
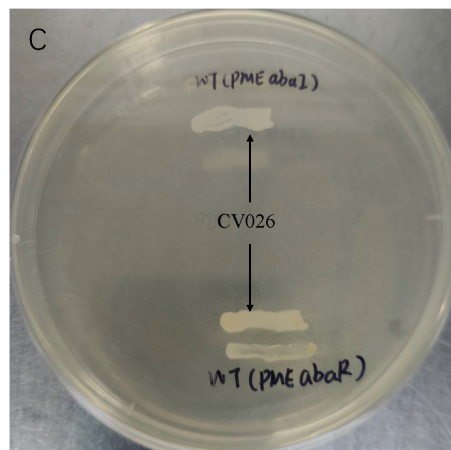
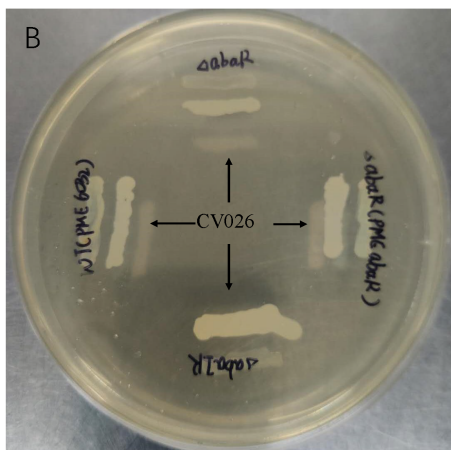
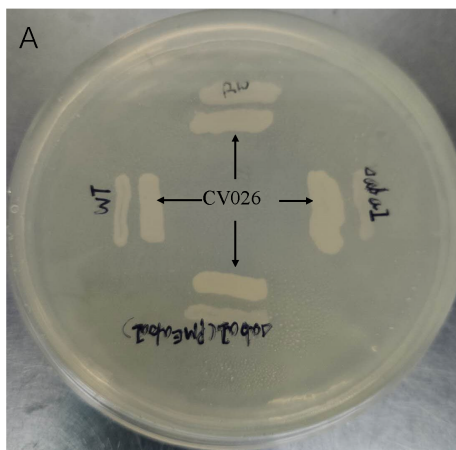
00260				protein
AUO97_RS	1.408770151	Up	1.15E-13	EamA family
08715				transporter
AUO97_RS	1.424467059	Up	5.57E-05	hypothetical
04705				protein
AUO97_RS	1.434908162	Up	6.18E-21	TetR/AcrR family
05520				transcriptional regulator
AUO97_RS	1.455698678	Up	1.21E-48	MFS transporter
06395				
AUO97_RS	1.463500264	Up	0.000157	hypothetical
13175				protein
AUO97_RS	1.482712098	Up	2.03E-06	flavin reductase
17125				
AUO97_RS	1.506892192	Up	0.0006	hypothetical
18270				protein
AUO97_RS	1.525928785	Up	8.33E-26	taurine ABC
14730				transporter ATP- binding protein
AUO97_RS	1.53094861	Up	9.1E-12	TetR/AcrR family
08710				transcriptional regulator

AUO97_RS	1.583794725	Up	5.9E-06	hypothetical
03405				protein
AUO97_RS	1.597978381	Up	8.73E-05	nuclear
17150				transport factor
				2 family protein
AUO97_RS	1.608502109	Up	0.000235	hypothetical
13235				protein
AUO97_RS	1.610222783	Up	5E-07	PaaX family
00970				transcriptional
				regulator
AUO97_RS	1.646501685	Up	1.18E-36	SCPU domain-
19215				containing
				protein
AUO97_RS	1.666892923	Up	8.55E-06	DNA transfer
08885				protein p32
AUO97_RS	1.69031736	Up	8.39E-36	sulfite exporter
16050				TauE/SafE family
				protein
AUO97_RS	1.762259496	Up	6.61E-20	aromatic amino
01130				acid transporter
				AroP
AUO97_RS	1.797926772	Up	5.12E-16	amidase

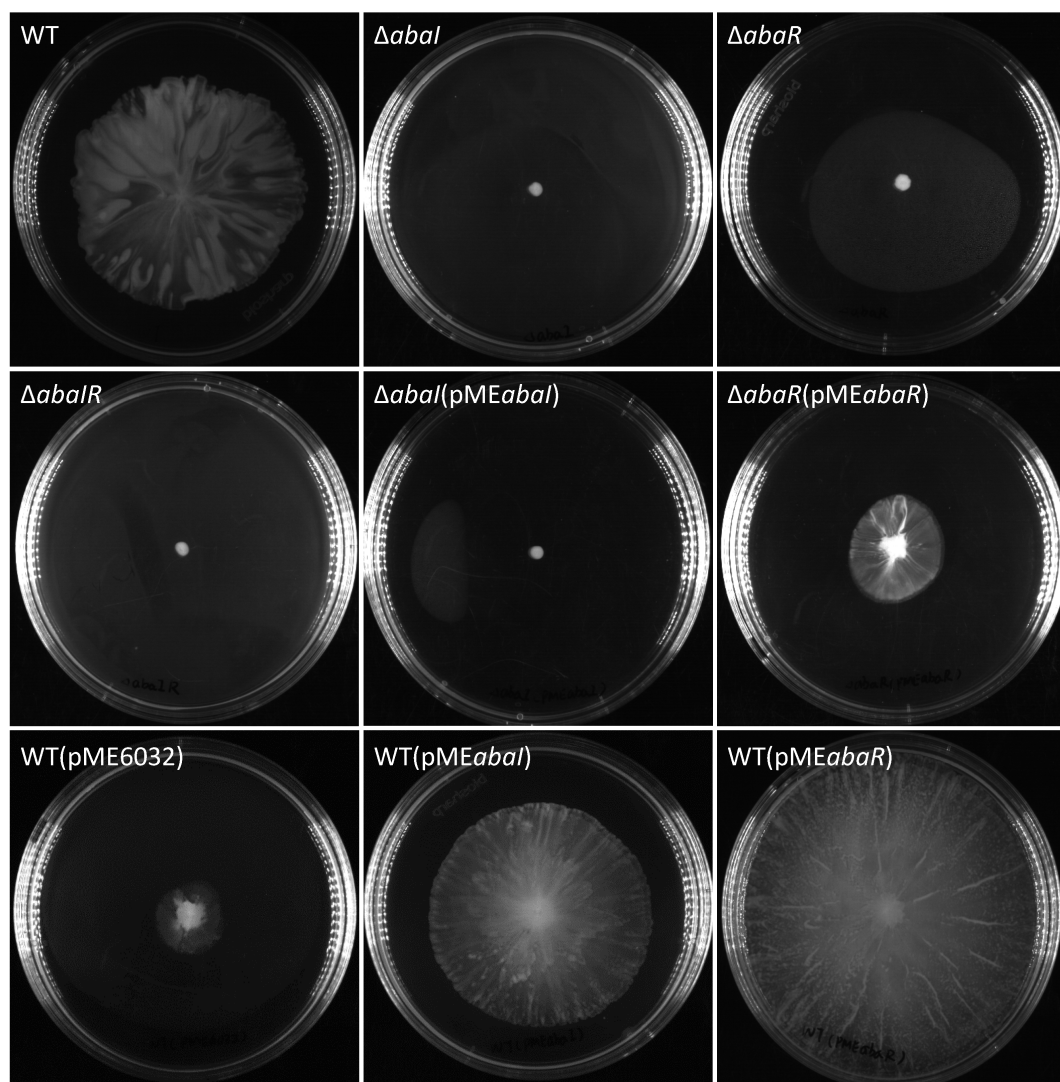
17165				
AUO97_RS	1.839119762	Up	2.78E-05	aromatic-ring-
17140				hydroxylating
				dioxygenase
				subunit beta
AUO97_RS	1.905157138	Up	5.15E-26	alpha/beta
01560				hydrolase
AUO97_RS	2.110174475	Up	2.41E-10	KR domain-
17135				containing
				protein
AUO97_RS	2.113312655	Up	9.47E-77	sulfate ABC
01555				transporter
				substrate-
				binding protein
AUO97_RS	2.203176565	Up	2.19E-10	oxidoreductase
17130				
AUO97_RS	2.210965901	Up	6.94E-18	hypothetical
18900				protein
AUO97_RS	2.239808823	Up	4.73E-22	acyl-CoA
17160				dehydrogenase
AUO97_RS	2.241276362	Up	6.25E-14	hypothetical
07050				protein

AUO97_RS 17145	2.394634424	Up	3.66E-18	aromatic ring- hydroxylating dioxygenase subunit alpha
AUO97_RS 18910	2.455858156	Up	5.07E-14	hypothetical protein
AUO97_RS 03425	2.581083497	Up	1.35E-17	hypothetical protein
AUO97_RS 14725	2.601467607	Up	6.94E-65	taurine ABC transporter substrate- binding protein

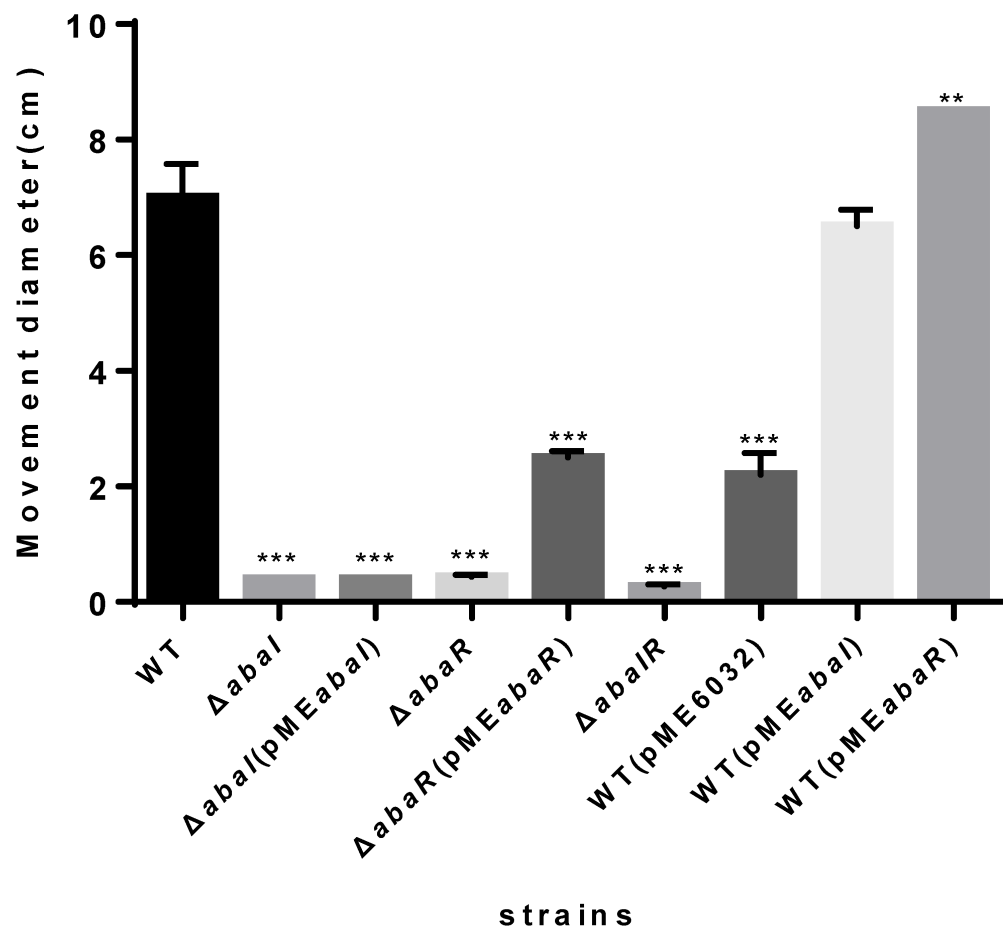




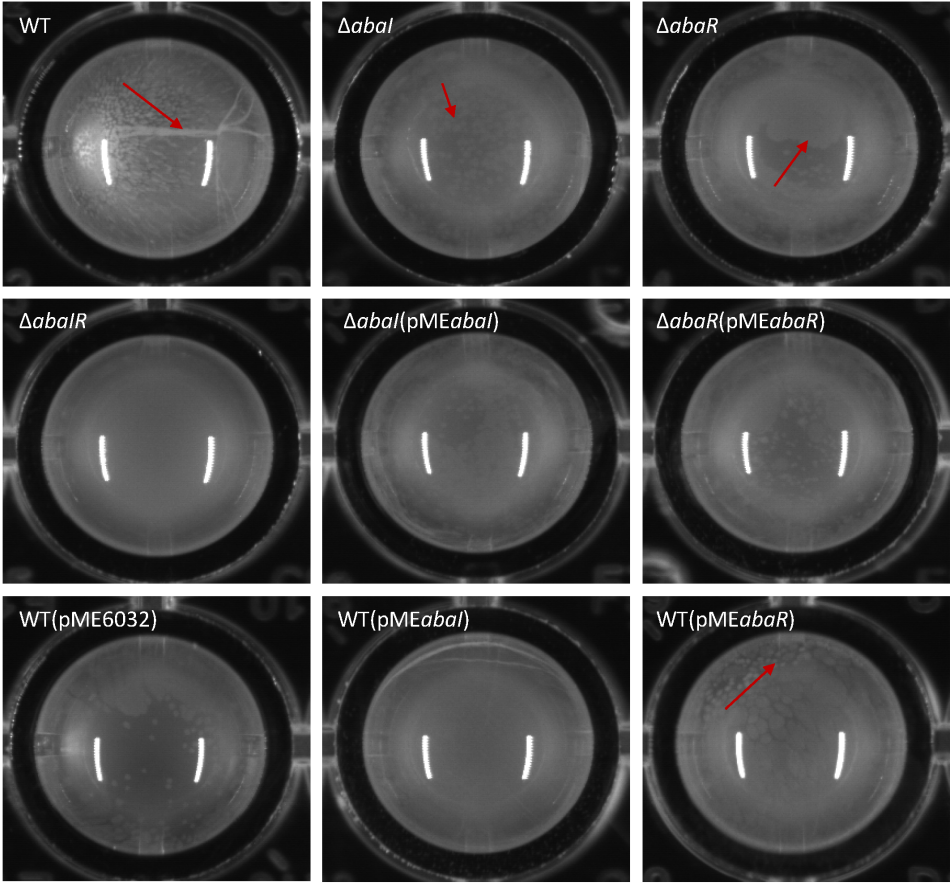
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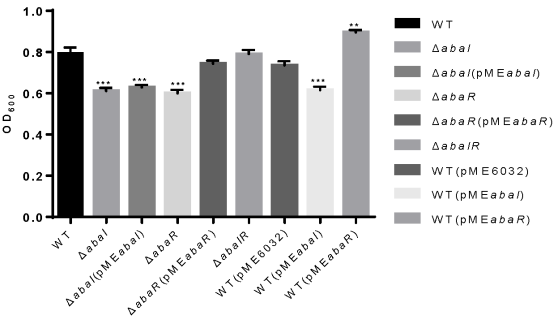
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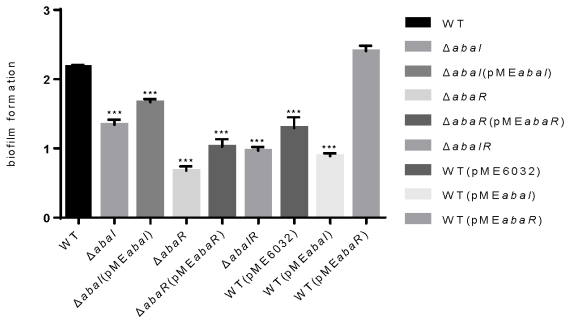
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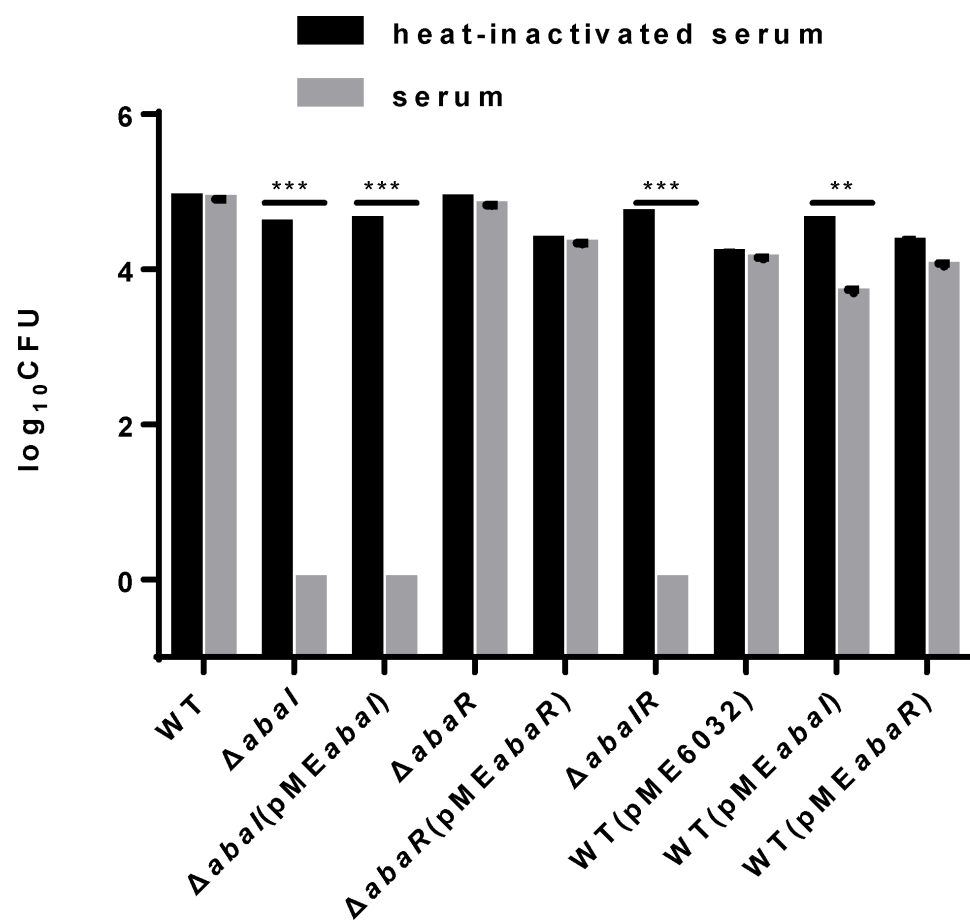
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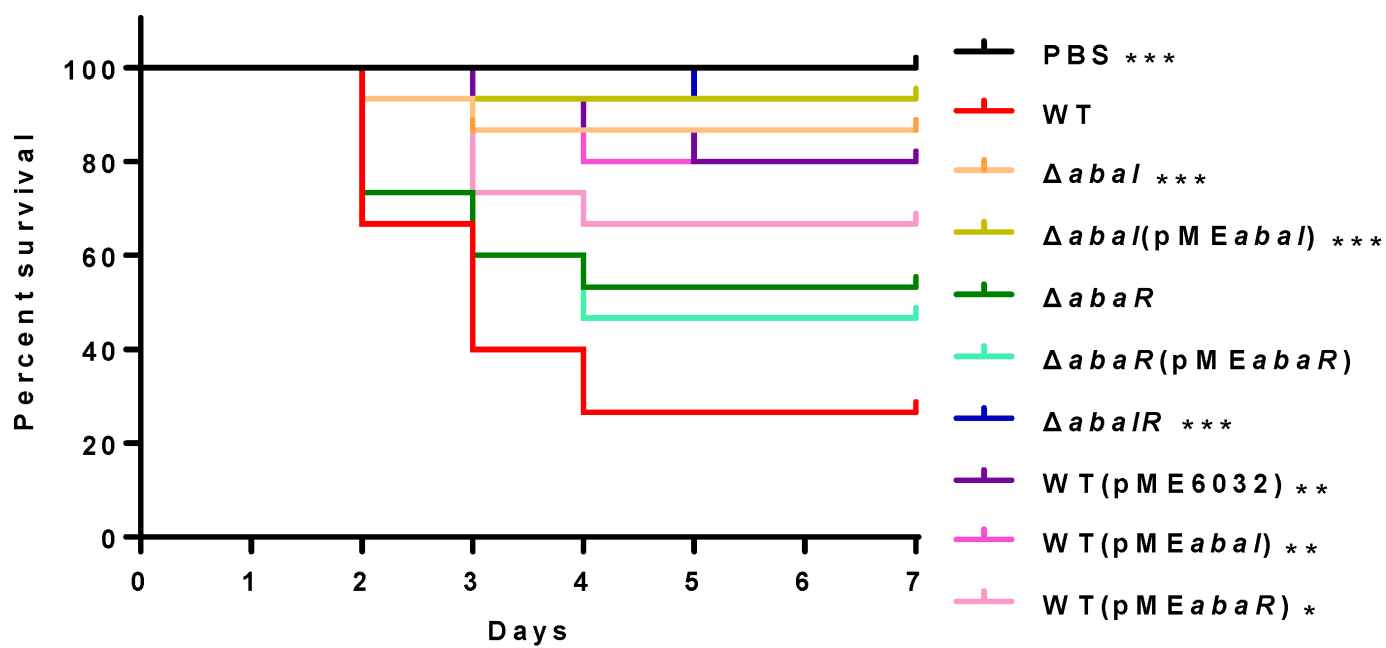
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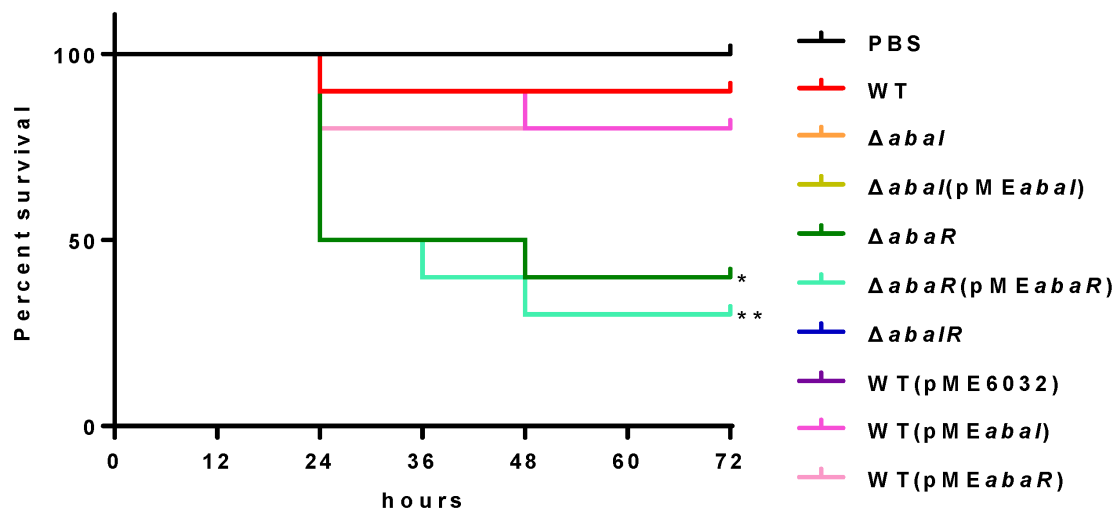
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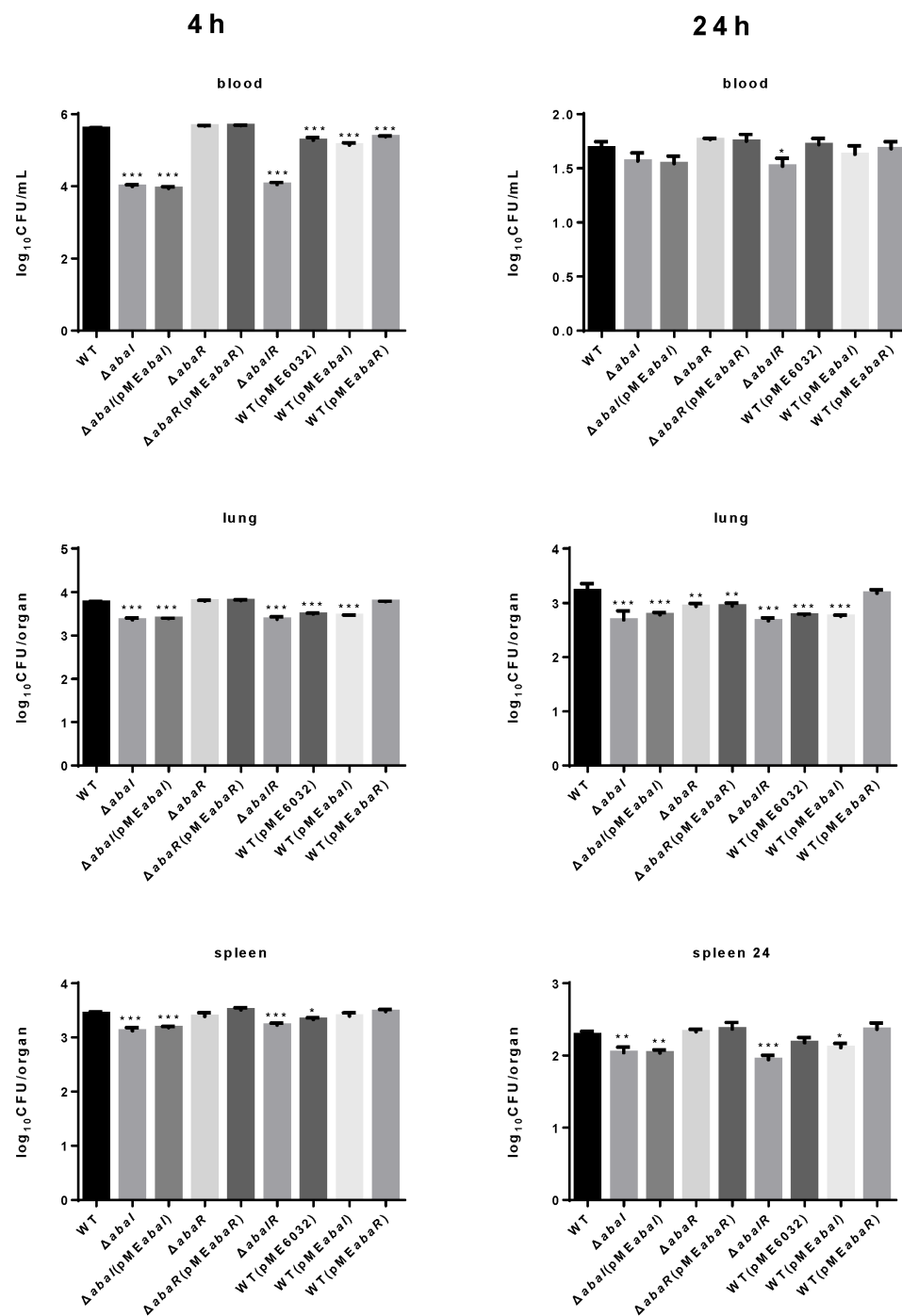
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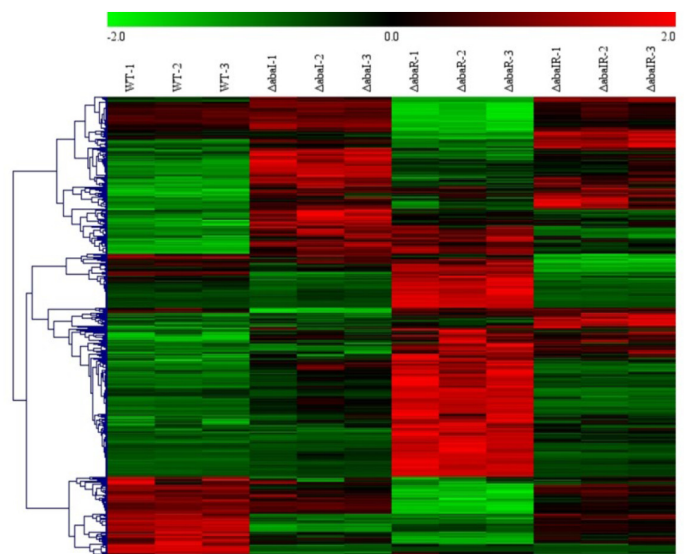
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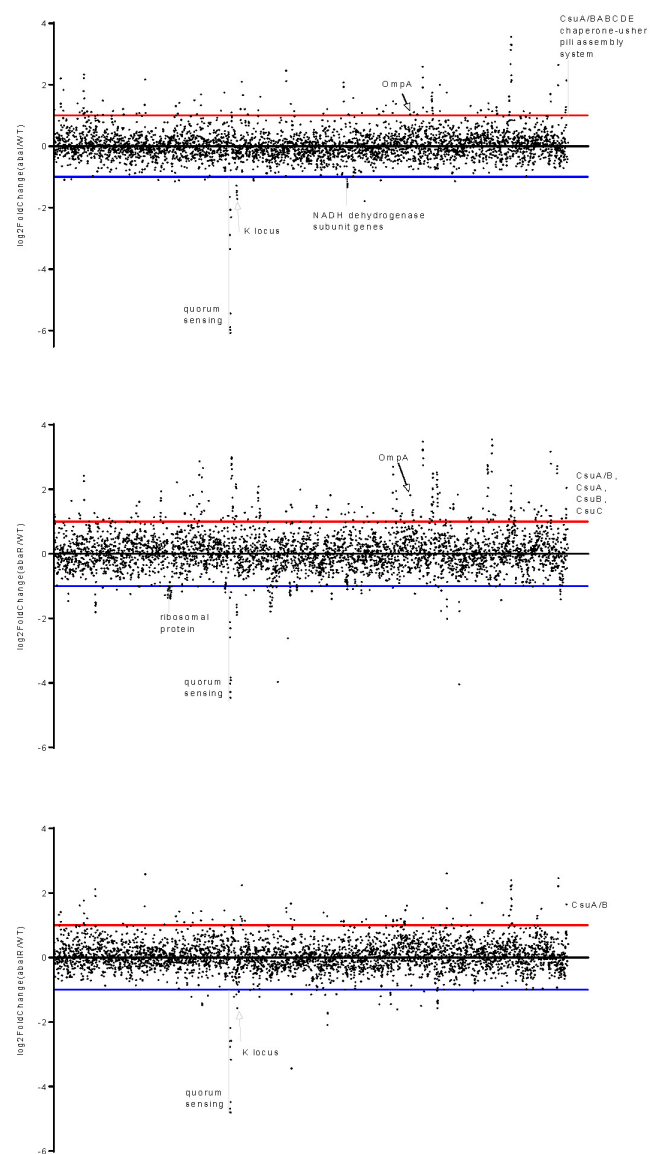
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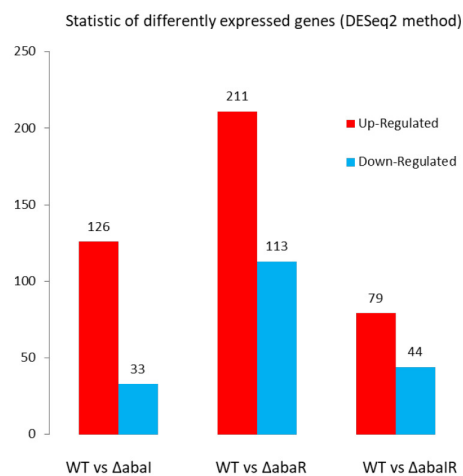
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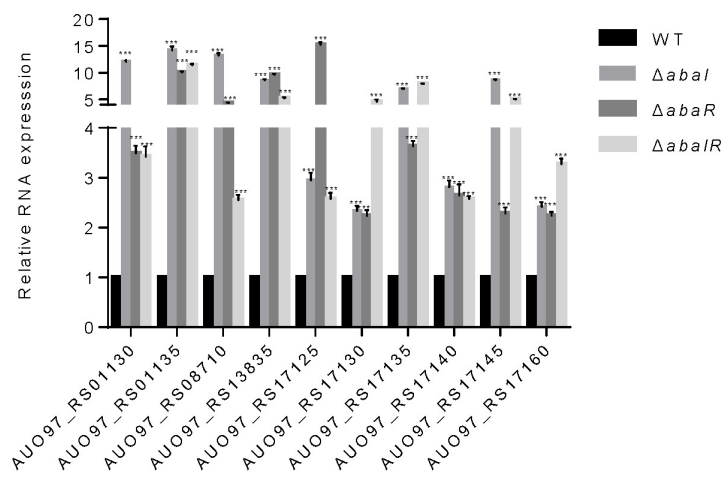
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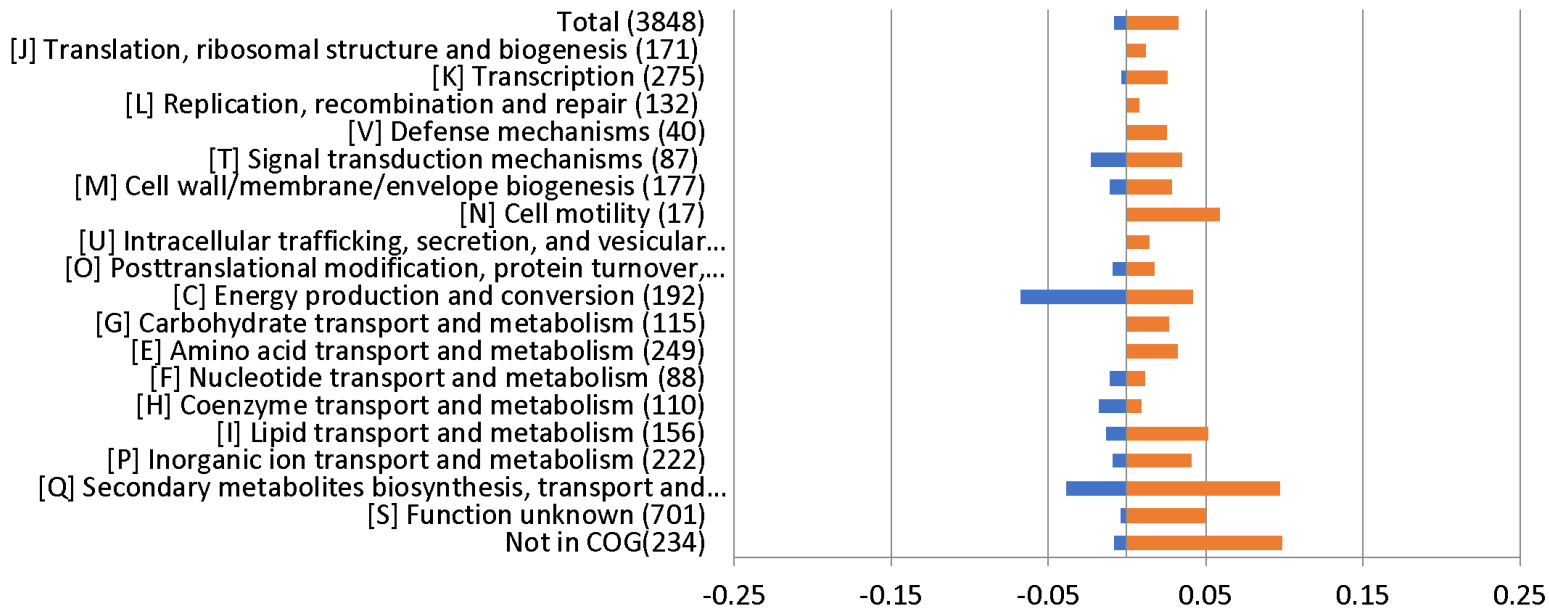
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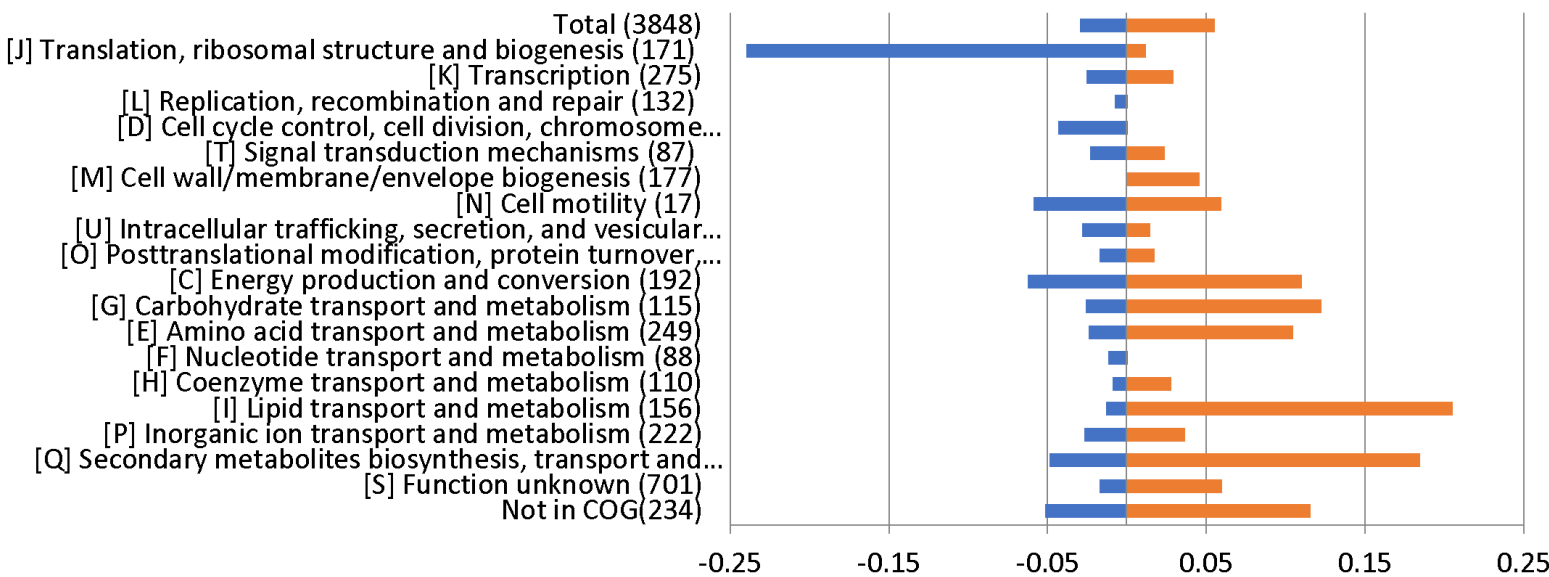
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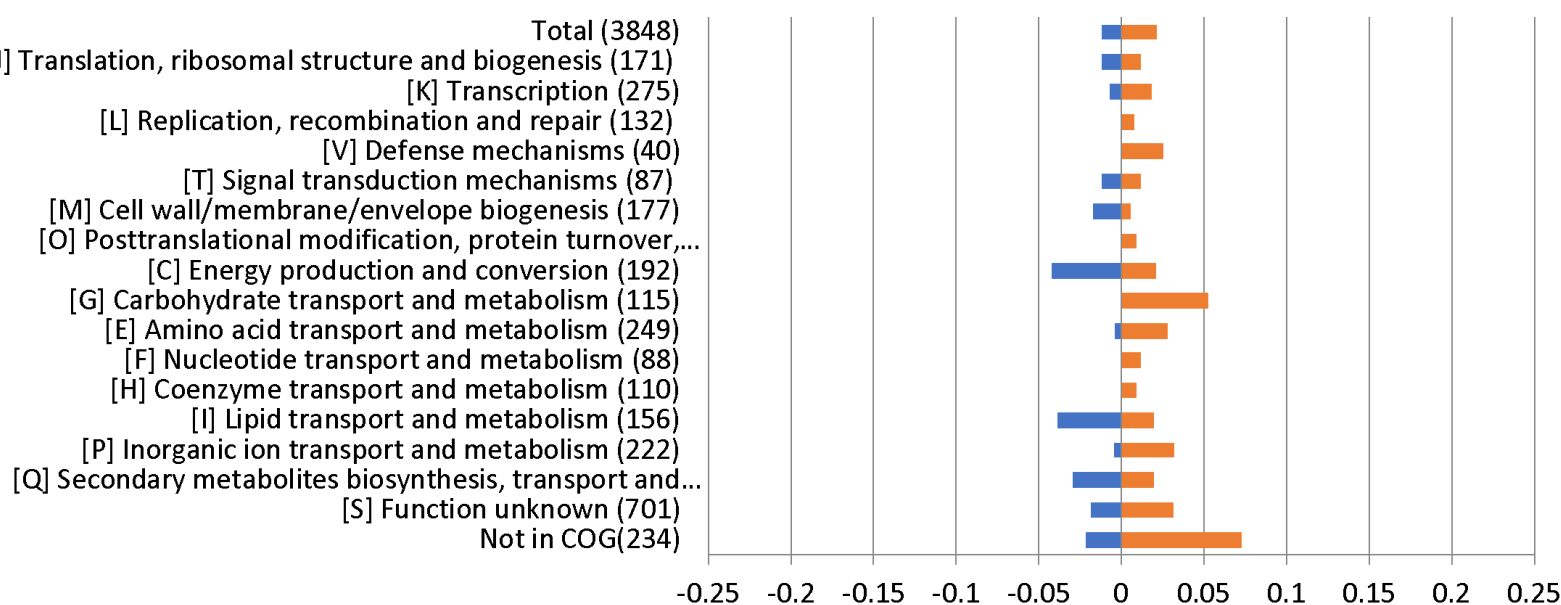
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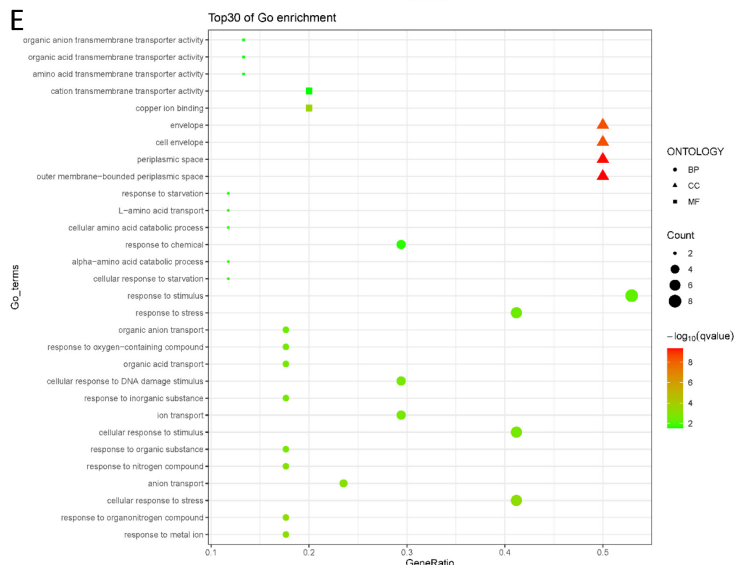
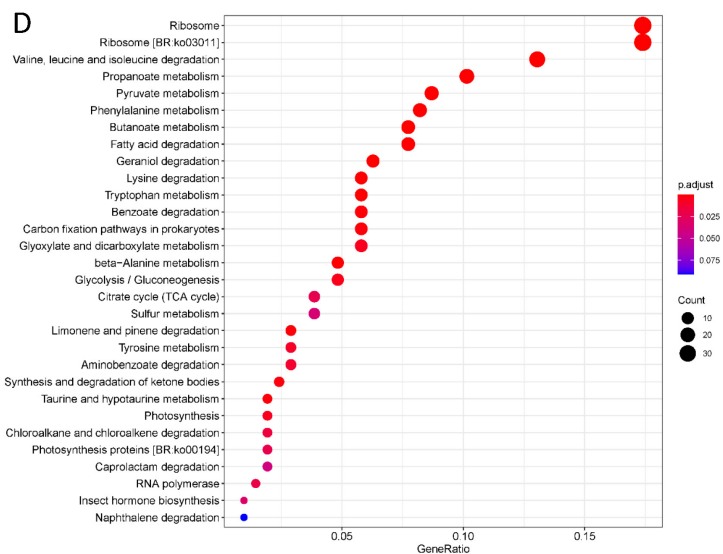
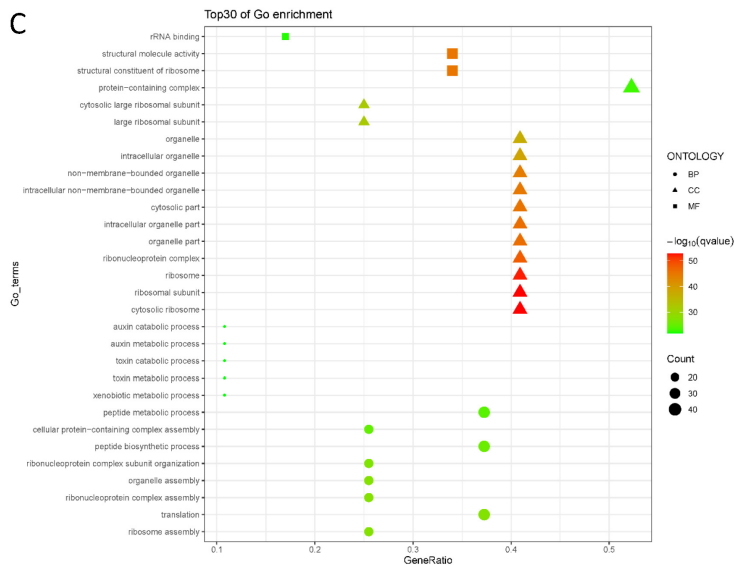
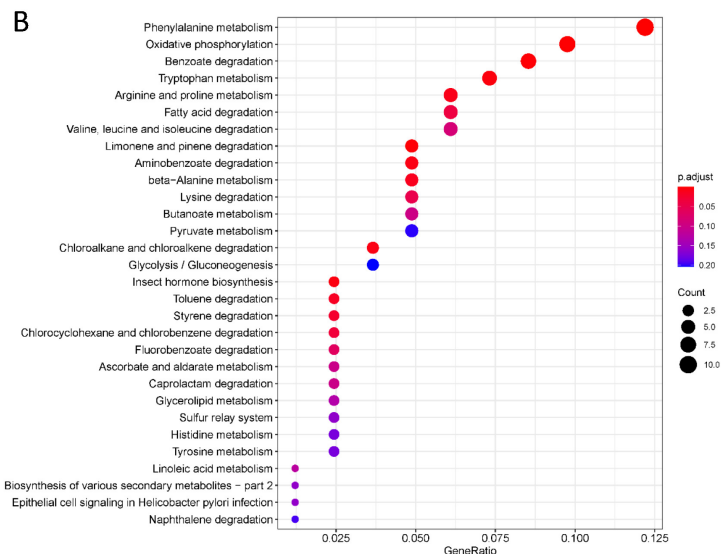
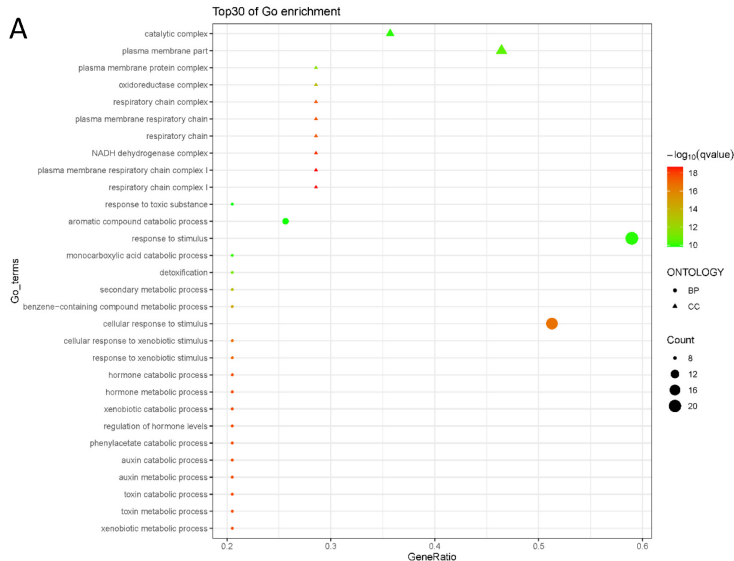


B



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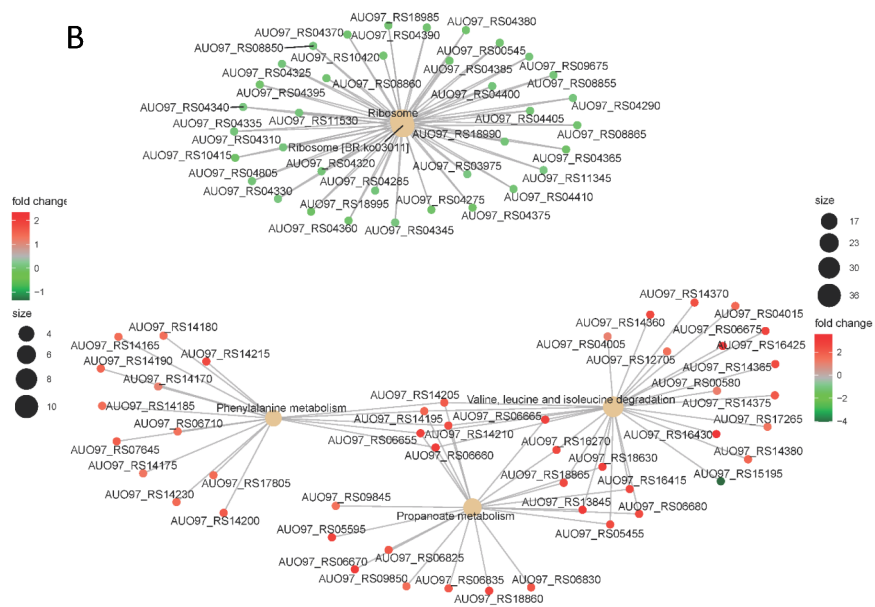




A



B



C



Table 4 Differential expressed genes in Δ abal strain

GeneID	log2FoldChange(Δ abal/WT)	Up-Down-Regulation(Δ abal/WT)	Pvalue	Product
AUO97_RS06625	-6.0744	Down	0	acyl-CoA dehydrogenase
AUO97_RS06615	-5.9747	Down	0	non-ribosomal peptide synthetase
AUO97_RS06610	-5.88657	Down	0	outer membrane lipoprotein-sorting protein
AUO97_RS06630	-5.44259	Down	0	acyl-CoA synthetase
AUO97_RS06605	-3.3445	Down	1.1E-107	hypothetical protein
AUO97_RS06600	-2.88721	Down	4.97E-78	alpha/beta hydrolase
AUO97_RS06645	-2.30926	Down	1.64E-07	GNAT family N-acetyltransferase
AUO97_RS06620	-2.06687	Down	3.24E-06	acyl carrier protein
AUO97_RS11650	-1.78566	Down	1.77E-32	hemerythrin
AUO97_RS06875	-1.71559	Down	1.47E-59	UDP-glucose 4-epimerase GalE
AUO97_RS06595	-1.64711	Down	1.23E-07	phosphopantetheine-protein transferase
AUO97_RS06865	-1.58854	Down	5.17E-94	L-lactate permease
AUO97_RS06855	-1.50567	Down	7.58E-53	alpha-hydroxy-acid oxidizing enzyme
AUO97_RS06860	-1.45419	Down	3.24E-26	transcriptional regulator LldR
AUO97_RS11000	-1.33315	Down	9.15E-17	NADH-quinone oxidoreductase subunit K
AUO97_RS06850	-1.28401	Down	1.16E-24	D-lactate dehydrogenase
AUO97_RS11005	-1.27855	Down	4.17E-96	NADH-quinone oxidoreductase subunit L
AUO97_RS10995	-1.27133	Down	2.73E-39	NADH-quinone oxidoreductase subunit J
AUO97_RS1	-1.25693	Down	1.91E-	NADH-quinone

1015			85	oxidoreductase subunit N
AUO97_RS1	-1.25538	Down	4.49E-	NADH-quinone
0985			80	oxidoreductase subunit H
AUO97_RS1	-1.21787	Down	3.2E-7	NADH-quinone
1010			3	oxidoreductase subunit M
AUO97_RS1	-1.14605	Down	7.24E-	NADH-quinone
0990			42	oxidoreductase subunit I
AUO97_RS0	-1.14342	Down	7.7E-4	oxygen-dependent coproporphyrinogen oxidase
4545			9	
AUO97_RS1	-1.13713	Down	4.45E-	cytosine permease
5040			15	
AUO97_RS0	-1.11951	Down	1.42E-	AcrB/AcrD/AcrF family protein
7490			20	
AUO97_RS1	-1.11535	Down	3.08E-	isocitrate lyase
2255			46	
AUO97_RS0	-1.11028	Down	3.71E-	hypothetical protein
4690			16	
AUO97_RS0	-1.09799	Down	1.5E-1	GGDEF
3915			2	domain-containing protein
AUO97_RS0	-1.09371	Down	8.57E-	U32 family peptidase
0400			25	
AUO97_RS0	-1.08569	Down	0.0001	MBL fold
5665			89	metallo-hydrolase
AUO97_RS1	-1.06889	Down	2.64E-	NADH-quinone
0980			57	oxidoreductase subunit NuoG
AUO97_RS0	-1.06411	Down	1.08E-	efflux RND
7485			09	transporter periplasmic adaptor subunit
AUO97_RS0	-1.02016	Down	7.07E-	DUF2147
5775			23	domain-containing protein
AUO97_RS0	1.001374	Up	1.2E-1	putative DNA
4585			6	modification/repair radical SAM protein
AUO97_RS1	1.011794	Up	0.0054	TetR/AcrR family
1080			96	transcriptional

				regulator
AUO97_RS0 1645	1.013889	Up	1.31E- 06	heteromeric transposase endonuclease subunit TnsA
AUO97_RS1 7070	1.014466	Up	0.0115 44	muconolactone delta-isomerase
AUO97_RS0 1845	1.025133	Up	1.34E- 12	Holliday junction branch migration protein RuvA
AUO97_RS0 2620	1.033632	Up	8.86E- 13	outer membrane lipoprotein carrier protein LolA
AUO97_RS1 3365	1.03403	Up	4.16E- 23	OmpA family protein
AUO97_RS1 3625	1.034741	Up	7.53E- 10	hypothetical protein
AUO97_RS1 1050	1.034749	Up	0.0109 09	hypothetical protein
AUO97_RS0 7280	1.037826	Up	0.0033 11	GlsB/YeaQ/YmgE family stress response membrane protein
AUO97_RS1 2195	1.042847	Up	2.75E- 05	SRPBCC domain-containing protein
AUO97_RS0 5370	1.043606	Up	0.0091 18	GNAT family N-acetyltransferase
AUO97_RS1 6615	1.047928	Up	5.3E-5 0	ImmA/IrrE family metallo-endopeptidas e
AUO97_RS0 1115	1.052979	Up	2.83E- 17	phosphate ABC transporter, permease protein PstA
AUO97_RS1 4215	1.060287	Up	2.86E- 13	phenylacetate--CoA ligase
AUO97_RS0 4650	1.061309	Up	4.72E- 18	SPOR domain-containing protein
AUO97_RS1 0110	1.063226	Up	1.44E- 20	MacA family efflux pump subunit
AUO97_RS0 3105	1.065265	Up	2.54E- 05	toxin
AUO97_RS1 6620	1.066128	Up	4.92E- 29	hypothetical protein

AUO97_RS0 3210	1.07437	Up	1.36E- 05	VOC family protein
AUO97_RS1 7840	1.076757	Up	2.31E- 13	sulfurtransferase TusD
AUO97_RS1 2700	1.080796	Up	8.18E- 05	hypothetical protein
AUO97_RS0 3445	1.084479	Up	0.0018 24	DUF4184 domain-containing protein
AUO97_RS1 2705	1.084642	Up	1.05E- 10	gamma-aminobutyral dehyde dehydrogenase
AUO97_RS1 1550	1.084666	Up	1.11E- 05	metal-dependent hydrolase
AUO97_RS0 1160	1.086385	Up	6.24E- 17	DUF541 domain-containing protein
AUO97_RS1 5885	1.089957	Up	5.57E- 27	transcriptional regulator
AUO97_RS0 6660	1.094631	Up	4.41E- 06	enoyl-CoA hydratase
AUO97_RS1 9180	1.100387	Up	3.94E- 07	proline/glycine betaine transporter ProP
AUO97_RS0 0970	1.100706	Up	0.0020 29	PaaX family transcriptional regulator
AUO97_RS1 3500	1.108039	Up	2.06E- 05	hypothetical protein
AUO97_RS0 1405	1.109955	Up	5.76E- 15	membrane protein
AUO97_RS1 7085	1.111993	Up	0.0007 2	3-oxoadipate CoA-transferase
AUO97_RS1 3980	1.125222	Up	2.47E- 07	type VI secretion system baseplate subunit TssE
AUO97_RS0 1255	1.130874	Up	1.28E- 29	LysR family transcriptional regulator
AUO97_RS1 2355	1.132006	Up	3.99E- 55	META domain-containing protein
AUO97_RS1 7615	1.135218	Up	1.36E- 07	universal stress protein

AUO97_RS1 6430	1.135699	Up	9.01E- 06	CoA transferase subunit A
AUO97_RS0 9015	1.136286	Up	1.71E- 38	FUSC family protein
AUO97_RS1 4475	1.14236	Up	7.91E- 09	DNA polymerase V
AUO97_RS0 2225	1.148054	Up	5.78E- 38	ABC transporter substrate-binding protein
AUO97_RS0 1060	1.151745	Up	1.11E- 10	hypothetical protein
AUO97_RS1 6600	1.153076	Up	4.64E- 10	hypothetical protein
AUO97_RS1 4195	1.154194	Up	1.2E-0 5	enoyl-CoA hydratase
AUO97_RS0 0360	1.155982	Up	1.36E- 07	DNA-binding response regulator
AUO97_RS0 6270	1.156561	Up	4.43E- 10	DUF2726 domain-containing protein
AUO97_RS0 7670	1.165001	Up	4.24E- 11	aromatic amino acid transporter AroP
AUO97_RS0 7665	1.166185	Up	1.94E- 63	fumarylacetoacetase
AUO97_RS1 6010	1.168526	Up	1.13E- 32	haloacid dehalogenase
AUO97_RS1 9190	1.176465	Up	1E-07	SCPU domain-containing protein
AUO97_RS1 9195	1.188775	Up	4.99E- 16	fimbrial biogenesis outer membrane usher protein
AUO97_RS0 0020	1.189934	Up	0.0055 52	hypothetical protein
AUO97_RS1 6300	1.202481	Up	1.73E- 45	TIGR01244 family phosphatase
AUO97_RS0 7165	1.204777	Up	0.0052 96	hypothetical protein
AUO97_RS1 0250	1.204815	Up	0.0037 04	RidA family protein
AUO97_RS0 2595	1.210701	Up	0.0002 29	transcriptional regulator
AUO97_RS0 7005	1.211821	Up	1.5E-3 7	acyl-CoA desaturase

AUO97_RS1 6305	1.212542	Up	1.27E- 08	sulfite exporter TauE/SafE family protein
AUO97_RS1 2115	1.214564	Up	2.84E- 32	Fe-S biogenesis protein NfuA
AUO97_RS0 1120	1.243207	Up	3.6E-1 8	phosphate ABC transporter permease subunit PstC
AUO97_RS1 4190	1.246926	Up	2.2E-0 6	phenylacetate-CoA oxygenase/reductase subunit PaaK
AUO97_RS1 3840	1.253491	Up	1.81E- 20	allophanate hydrolase
AUO97_RS1 6595	1.264522	Up	4.69E- 19	PAAR domain-containing protein
AUO97_RS1 9205	1.274509	Up	0.0006 46	SCPU domain-containing protein
AUO97_RS1 9200	1.27559	Up	4.91E- 09	molecular chaperone
AUO97_RS0 0270	1.276369	Up	8.02E- 05	hypothetical protein
AUO97_RS0 4580	1.307287	Up	1.03E- 07	hypothetical protein
AUO97_RS1 5625	1.309804	Up	9.99E- 06	phage major capsid protein
AUO97_RS1 2450	1.328101	Up	2.33E- 19	amino acid transporter
AUO97_RS0 5515	1.333536	Up	1.76E- 40	NADPH:quinone oxidoreductase
AUO97_RS0 3405	1.346309	Up	0.0002 18	hypothetical protein
AUO97_RS1 2825	1.375679	Up	2.99E- 06	crotonase
AUO97_RS0 8885	1.376611	Up	0.0003 94	DNA transfer protein p32
AUO97_RS0 0265	1.381641	Up	0.0007 4	hypothetical protein
AUO97_RS1 6295	1.396496	Up	6.32E- 27	MBL fold metallo-hydrolase
AUO97_RS0 0890	1.398657	Up	7.72E- 28	hypothetical protein
AUO97_RS0	1.410219	Up	9.19E-	hypothetical protein

4705			16	
AUO97_RS1	1.454416	Up	1.2E-2	flavin reductase
0870			6	
AUO97_RS1	1.4574	Up	3.51E-	phenylacetate-CoA
4180			11	oxygenase subunit PaaI
AUO97_RS1	1.457907	Up	3.68E-	aldehyde
8630			75	dehydrogenase
AUO97_RS1	1.458908	Up	1.83E-	aspartate
2715			09	aminotransferase family protein
AUO97_RS1	1.468197	Up	3.65E-	catechol
7075			14	1,2-dioxygenase
AUO97_RS1	1.470222	Up	6.53E-	arginine
2720			08	N-succinyltransferase
AUO97_RS0	1.484748	Up	1.28E-	deoxyguanosinetripho
1840			65	sphate triphosphohydrolase
AUO97_RS1	1.487037	Up	1.93E-	1,2-phenylacetyl-CoA
4170			27	epoxidase subunit A
AUO97_RS0	1.493798	Up	1.05E-	hypothetical protein
5275			18	
AUO97_RS1	1.496273	Up	1.16E-	3-oxoadipate
7080			05	CoA-transferase subunit A
AUO97_RS1	1.534021	Up	1.12E-	1,2-phenylacetyl-CoA
4175			19	epoxidase subunit B
AUO97_RS0	1.557012	Up	2.02E-	NAD-dependent
1145			49	aldehyde dehydrogenase
AUO97_RS1	1.567974	Up	2.97E-	trehalose-phosphatas
1225			14	e
AUO97_RS0	1.607067	Up	3.22E-	DNA transfer protein
7745			31	p32
AUO97_RS1	1.619212	Up	1.95E-	muconate
7065			10	cycloisomerase
AUO97_RS1	1.628035	Up	6.97E-	phenylacetic acid
4165			17	degradation bifunctional protein PaaZ
AUO97_RS0	1.660574	Up	6.92E-	C4-dicarboxylate ABC
7095			08	transporter
AUO97_RS0	1.685455	Up	2.39E-	TetR/AcrR family
5520			30	transcriptional

				regulator
AUO97_RS1 8615	1.695967	Up	4.07E- 46	alcohol dehydrogenase
AUO97_RS1 4185	1.739369	Up	1.42E- 35	phenylacetate-CoA oxygenase subunit PaaJ
AUO97_RS1 4725	1.743263	Up	4E-17	taurine ABC transporter substrate-binding protein
AUO97_RS0 6395	1.744985	Up	1.2E-7 3	MFS transporter
AUO97_RS0 1125	1.794527	Up	4.22E- 35	phosphonate ABC transporter substrate-binding protein
AUO97_RS0 0365	1.83163	Up	7.99E- 22	DNA-binding protein
AUO97_RS1 3830	1.910832	Up	7.76E- 13	LamB/YcsF family protein
AUO97_RS1 0865	1.926934	Up	5.8E-2 05	methionine synthase
AUO97_RS1 8900	1.984749	Up	6.85E- 17	hypothetical protein
AUO97_RS1 4470	1.998418	Up	5.49E- 06	hypothetical protein
AUO97_RS1 0860	2.07496	Up	2.1E-1 91	DUF1852 domain-containing protein
AUO97_RS0 7050	2.095124	Up	6.19E- 12	hypothetical protein
AUO97_RS1 7150	2.097862	Up	5.78E- 08	nuclear transport factor 2 family protein
AUO97_RS0 8715	2.116025	Up	7.01E- 29	EamA family transporter
AUO97_RS1 9215	2.141387	Up	5.07E- 60	SCPU domain-containing protein
AUO97_RS1 7165	2.147861	Up	7.66E- 23	amidase
AUO97_RS0 3425	2.174702	Up	4.1E-1 3	hypothetical protein
AUO97_RS0 0260	2.205577	Up	1.57E- 67	RtcB family protein

AUO97_RS0 1130	2.216359	Up	6.67E- 33	aromatic amino acid transporter AroP
AUO97_RS1 3835	2.236657	Up	1.63E- 29	DUF1445 domain-containing protein
AUO97_RS1 7155	2.307109	Up	1.38E- 08	hypothetical protein
AUO97_RS0 1135	2.335458	Up	2.75E- 62	pyruvate decarboxylase
AUO97_RS0 8710	2.459453	Up	2.56E- 34	TetR/AcrR family transcriptional regulator
AUO97_RS1 3825	2.587926	Up	3.04E- 24	divalent metal cation transporter
AUO97_RS1 8910	2.644973	Up	3.5E-4 8	hypothetical protein
AUO97_RS1 7125	2.673537	Up	8.63E- 24	flavin reductase
AUO97_RS1 7130	3.134825	Up	5.49E- 24	oxidoreductase
AUO97_RS1 7135	3.137551	Up	8.58E- 27	KR domain-containing protein
AUO97_RS1 7160	3.296468	Up	8.85E- 48	acyl-CoA dehydrogenase
AUO97_RS1 7140	3.302273	Up	5.99E- 17	aromatic-ring-hydroxy lating dioxygenase subunit beta
AUO97_RS1 7145	3.557326	Up	8.79E- 58	aromatic ring-hydroxylating dioxygenase subunit alpha

Table 5 Differential expressed genes in Δ abaR strain

GeneID	log2FoldChange(Δ abaR/WT)	Up-Down-Regulation(Δ abaR/WT)	Pvalue	Product
AUO97_RS 00540	-1.46697	Down	7.01E- 97	elongation factor Ts
AUO97_RS 00545	-1.23446	Down	6.5E- 101	30S ribosomal protein S2
AUO97_RS 01555	-1.25779	Down	7.5E- 12	sulfate ABC transporter substrate-binding protein
AUO97_RS 01560	-1.60798	Down	9.23E- 07	alpha/beta hydrolase
AUO97_RS 01565	-1.80619	Down	3.15E- 14	sulfate ABC transporter permease subunit CysT

AUO97_RS 01570	-1.51136	Down	1.53E -08	sulfate ABC transporter permease subunit CysW
AUO97_RS 01575	-1.55706	Down	1.89E -17	sulfate ABC transporter ATP-binding protein
AUO97_RS 01835	-1.04633	Down	1.47E -50	phosphoribosylformylglycine midine synthase
AUO97_RS 02870	-1.24855	Down	7.89E -07	septum formation inhibitor Maf
AUO97_RS 03165	-1.006	Down	1.04E -52	translational GTPase TypA
AUO97_RS 03220	-1.02069	Down	2.64E -08	DUF934 domain-containing protein
AUO97_RS 03975	-1.00367	Down	7.42E -47	50S ribosomal protein L13
AUO97_RS 04165	-1.27941	Down	8.69E -08	EamA/RhaT family transporter
AUO97_RS 04275	-1.36319	Down	2.43E -55	50S ribosomal protein L17
AUO97_RS 04280	-1.26373	Down	9.25E -80	DNA-directed RNA polymerase subunit alpha
AUO97_RS 04285	-1.14133	Down	7.65E -54	30S ribosomal protein S4
AUO97_RS 04290	-1.09269	Down	1.17E -38	30S ribosomal protein S11
AUO97_RS 04305	-1.29326	Down	1.32E -74	preprotein translocase subunit SecY
AUO97_RS 04310	-1.09864	Down	1.39E -44	50S ribosomal protein L15
AUO97_RS 04320	-1.15251	Down	1.55E -40	30S ribosomal protein S5
AUO97_RS 04325	-1.14007	Down	2.33E -45	50S ribosomal protein L18
AUO97_RS 04330	-1.03587	Down	5.13E -39	50S ribosomal protein L6
AUO97_RS 04335	-1.12717	Down	1.21E -37	30S ribosomal protein S8
AUO97_RS 04340	-1.00921	Down	2.04E -22	30S ribosomal protein S14
AUO97_RS 04345	-1.04986	Down	2.5E- 52	50S ribosomal protein L5
AUO97_RS 04360	-1.33542	Down	2.89E -22	30S ribosomal protein S17
AUO97_RS 04365	-1.38332	Down	9.06E -15	50S ribosomal protein L29

AUO97_RS 04370	-1.30303	Down	6.38E -42	50S ribosomal protein L16
AUO97_RS 04375	-1.38848	Down	3.29E -60	30S ribosomal protein S3
AUO97_RS 04380	-1.32586	Down	3.99E -40	50S ribosomal protein L22
AUO97_RS 04385	-1.2558	Down	3.56E -34	30S ribosomal protein S19
AUO97_RS 04390	-1.25482	Down	9.97E -55	50S ribosomal protein L2
AUO97_RS 04395	-1.33758	Down	3.92E -37	50S ribosomal protein L23
AUO97_RS 04400	-1.14341	Down	4.11E -43	50S ribosomal protein L4
AUO97_RS 04405	-1.19034	Down	3.39E -50	50S ribosomal protein L3
AUO97_RS 04410	-1.18708	Down	2.7E- 30	30S ribosomal protein S10
AUO97_RS 04430	-1.0042	Down	1.6E- 53	flavohepotein
AUO97_RS 04805	-1.16847	Down	2.27E -41	50S ribosomal protein L19
AUO97_RS 05405	-1.0155	Down	1.78E -11	MFS transporter
AUO97_RS 06420	-1.08048	Down	2.86E -48	ATP synthase epsilon chain
AUO97_RS 06425	-1.0439	Down	3.37E -50	ATP synthase subunit beta
AUO97_RS 06430	-1.19299	Down	3.17E -60	ATP synthase subunit gamma
AUO97_RS 06435	-1.00172	Down	5.3E- 52	ATP synthase subunit alpha
AUO97_RS 06595	-1.3648	Down	3.66E -06	phosphopantetheine-protein transferase
AUO97_RS 06600	-2.11825	Down	8.13E -56	alpha/beta hydrolase
AUO97_RS 06605	-2.58786	Down	4.19E -97	hypothetical protein
AUO97_RS 06610	-4.02394	Down	0	outer membrane lipoprotein-sorting protein
AUO97_RS 06615	-4.2825	Down	0	non-ribosomal peptide synthetase
AUO97_RS 06620	-2.30484	Down	1.32E -05	acyl carrier protein [Acinetobacter]

AUO97_RS 06625	-4.46229	Down	0	acyl-CoA dehydrogenase
AUO97_RS 06630	-3.82819	Down	0	acyl-CoA synthetase
AUO97_RS 06635	-3.91695	Down	1.44E -13	LuxR family transcriptional regulator
AUO97_RS 06645	-1.18831	Down	0.010 518	GNAT family N-acetyltransferase
AUO97_RS 06850	-1.57625	Down	9.75E -39	D-lactate dehydrogenase
AUO97_RS 06855	-1.66135	Down	2.76E -57	alpha-hydroxy-acid oxidizing enzyme
AUO97_RS 06860	-1.89372	Down	8E-42	transcriptional regulator LldR
AUO97_RS 06865	-1.80838	Down	1.65E -24	L-lactate permease [Acinetobacter]
AUO97_RS 07200	-1.27639	Down	4.66E -18	dual-action HEIGH metallo-peptidase
AUO97_RS 08005	-1.0278	Down	0.000 671	hypothetical protein
AUO97_RS 08095	-1.18969	Down	1.46E -36	ATP-binding protein
AUO97_RS 08100	-1.00682	Down	4.07E -06	hypothetical protein
AUO97_RS 08105	-1.50123	Down	4.68E -08	type VI secretion protein
AUO97_RS 08110	-1.6293	Down	3.47E -44	hypothetical protein
AUO97_RS 08115	-1.32724	Down	3.42E -11	type VI secretion protein
AUO97_RS 08120	-1.78941	Down	6.98E -25	hypothetical protein
AUO97_RS 08125	-1.63462	Down	1.71E -25	conjugal transfer protein TrbI
AUO97_RS 08130	-1.53505	Down	1E-14	hypothetical protein
AUO97_RS 08135	-1.78221	Down	2.31E -11	conjugal transfer protein
AUO97_RS 08175	-1.63347	Down	2.54E -07	hypothetical protein
AUO97_RS 08180	-1.43919	Down	5.89E -15	hypothetical protein
AUO97_RS 08185	-1.2236	Down	5.97E -15	type IV pili twitching motility protein PilT

AUO97_RS 08195	-1.35697	Down	2.13E -17	hypothetical protein
AUO97_RS 08200	-1.00648	Down	0.000 214	hypothetical protein
AUO97_RS 08205	-1.03879	Down	1.12E -06	hypothetical protein
AUO97_RS 08345	-1.0272	Down	1.39E -09	hypothetical protein
AUO97_RS 08400	-3.96826	Down	3.8E- 191	IS5 family transposase
AUO97_RS 08775	-2.61617	Down	1.95E -12	DNA-binding protein [Acinetobacter]
AUO97_RS 08830	-1.19333	Down	1.89E -65	elongation factor Tu
AUO97_RS 08850	-1.12568	Down	8.29E -60	50S ribosomal protein L11
AUO97_RS 08855	-1.15414	Down	4.74E -68	50S ribosomal protein L1
AUO97_RS 08860	-1.25299	Down	6.63E -61	50S ribosomal protein L10
AUO97_RS 08865	-1.29006	Down	8.87E -84	50S ribosomal protein L7/L12 [Acinetobacter]
AUO97_RS 08870	-1.03148	Down	2.36E -50	DNA-directed RNA polymerase subunit beta
AUO97_RS 08875	-1.14418	Down	2.9E- 73	DNA-directed RNA polymerase subunit beta'
AUO97_RS 09110	-1.04917	Down	4.83E -48	transcription termination/antitermination protein NusA
AUO97_RS 09115	-1.11845	Down	2.33E -57	translation initiation factor IF-2
AUO97_RS 09120	-1.02517	Down	3E-23	ribosome-binding factor A
AUO97_RS 09675	-1.15939	Down	0.000 133	50S ribosomal protein L28 [Moraxellaceae]
AUO97_RS 10415	-1.39769	Down	3.91E -09	50S ribosomal protein L35
AUO97_RS 10420	-1.23068	Down	1.37E -68	50S ribosomal protein L20 [Acinetobacter]
AUO97_RS 11000	-1.10035	Down	4.37E -14	NADH-quinone oxidoreductase subunit K [Acinetobacter]
AUO97_RS 11015	-1.00922	Down	9.05E -51	NADH-quinone oxidoreductase subunit N

AUO97_RS 11215	-1.09784	Down	1.27E -35	MFS transporter
AUO97_RS 11345	-1.00307	Down	1.11E -16	50S ribosomal protein L25
AUO97_RS 11530	-1.12853	Down	2.42E -59	30S ribosomal protein S7
AUO97_RS 11535	-1.22746	Down	1.66E -65	elongation factor G
AUO97_RS 11840	-1.1171	Down	1.64E -58	malate:quinone oxidoreductase
AUO97_RS 12710	-1.05094	Down	0.008 596	Lrp/AsnC family transcriptional regulator
AUO97_RS 13535	-1.23454	Down	0.000 918	transposase
AUO97_RS 14515	-1.77276	Down	0.000 107	amino acid ABC transporter permease [Acinetobacter]
AUO97_RS 14525	-1.13951	Down	1.92E -06	ArtI protein [Acinetobacter]
AUO97_RS 14730	-1.41173	Down	1.07E -09	taurine ABC transporter ATP-binding protein
AUO97_RS 14735	-1.63502	Down	9.12E -15	taurine ABC transporter permease
AUO97_RS 14740	-2.01495	Down	7.36E -21	taurine dioxygenase
AUO97_RS 15190	-1.4971	Down	0.000 116	hypothetical protein
AUO97_RS 15195	-4.0442	Down	0	trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase
AUO97_RS 15205	-1.779	Down	1.1E- 174	sodium/proline symporter PutP
AUO97_RS 16765	-1.43715	Down	4.91E -05	NAD(P)-dependent alcohol dehydrogenase
AUO97_RS 17945	-1.02093	Down	0.001 295	3-dehydroquinate dehydratase
AUO97_RS 18980	-1.10603	Down	6.31E -29	protoheme IX farnesyltransferase
AUO97_RS 18985	-1.2489	Down	4.3E- 72	30S ribosomal protein S6
AUO97_RS 18990	-1.16315	Down	5.79E -09	30S ribosomal protein S18
AUO97_RS	-1.41125	Down	8.4E-	50S ribosomal protein L9

18995			118	
AUO97_RS	1.222331	Up	0.016	hypothetical protein
00020			824	
AUO97_RS	1.135363	Up	0.000	glycosyl transferase
00035			104	
AUO97_RS	1.1511	Up	5.99E	PIG-L family deacetylase
00045			-08	
AUO97_RS	1.098532	Up	7.5E-	acyl-CoA dehydrogenase
00580			35	
AUO97_RS	1.639534	Up	6.49E	alpha/beta hydrolase
00665			-71	
AUO97_RS	1.245914	Up	5.65E	hydrolase
00945			-06	
AUO97_RS	1.091104	Up	0.000	DUF466 domain-containing
00985			167	protein
AUO97_RS	1.196287	Up	1.09E	carbon starvation protein A
00990			-52	
AUO97_RS	2.419967	Up	6.12E	MFS transporter
01130			-42	
AUO97_RS	2.254064	Up	1.16E	ATP-dependent protease
01135			-83	
AUO97_RS	1.668297	Up	1.74E	NAD-dependent aldehyde
01145			-90	dehydrogenase
AUO97_RS	1.013324	Up	2.48E	hypothetical protein
01330			-20	
AUO97_RS	1.258765	Up	1.74E	PDZ domain-containing
01525			-42	protein
AUO97_RS	1.134019	Up	0.017	NIF3 1
01635			089	
AUO97_RS	1.056825	Up	5.66E	amidohydrolase
01855			-05	
AUO97_RS	1.096169	Up	2.03E	amino acid permease
02080			-37	
AUO97_RS	1.126299	Up	1.17E	glutamine amidotransferase
02905			-16	
AUO97_RS	1.25559	Up	7.25E	DUF1508 domain-containing
03090			-17	protein
AUO97_RS	1.492233	Up	1.04E	toxin
03105			-09	
AUO97_RS	1.158869	Up	6.14E	large conductance
03160			-24	mechanosensitive channel
				protein MscL
AUO97_RS	1.611018	Up	6.12E	VOC family protein
03210			-14	

AUO97_RS 04000	1.156133	Up	1.9E- 16	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha
AUO97_RS 04005	1.052399	Up	4.02E- 05	enoyl-CoA hydratase
AUO97_RS 04010	1.271182	Up	8.42E- 15	acyl-CoA dehydrogenase
AUO97_RS 04015	1.648108	Up	9.91E- 27	acetyl-CoA carboxylase carboxyltransferase subunit
AUO97_RS 04020	1.729121	Up	2.87E- 19	KR domain-containing protein
AUO97_RS 04025	1.935767	Up	1.05E- 53	DUF1446 domain-containing protein
AUO97_RS 04195	1.138211	Up	4.47E- 65	hypothetical protein
AUO97_RS 04615	2.218472	Up	1.38E- 19	hypothetical protein
AUO97_RS 04620	5.633865	Up	4.3E- 106	EamA/RhaT family transporter
AUO97_RS 04905	1.264872	Up	2.7E- 05	hypothetical protein
AUO97_RS 04915	1.231286	Up	4.4E- 31	LemA family protein
AUO97_RS 05105	1.791924	Up	5.78E- 67	hypothetical protein
AUO97_RS 05140	1.207876	Up	7.53E- 08	sulfate permease
AUO97_RS 05215	1.821676	Up	9.5E- 28	EamA/RhaT family transporter
AUO97_RS 05275	1.081392	Up	7.43E- 10	hypothetical protein
AUO97_RS 05370	1.46563	Up	0.000 574	GNAT family N-acetyltransferase
AUO97_RS 05440	1.02368	Up	2.04E- 12	hydrolase
AUO97_RS 05450	1.550398	Up	9.3E- 115	NAD-dependent succinate-semialdehyde dehydrogenase
AUO97_RS 05455	2.444237	Up	9.5E- 158	4-aminobutyrate--2-oxoglutarate transaminase
AUO97_RS 05465	2.866641	Up	1.4E- 170	amino acid permease
AUO97_RS 05515	1.227311	Up	1.59E- 21	NADPH:quinone oxidoreductase

AUO97_RS 05545	1.298715	Up	6.71E -05	hypothetical protein
AUO97_RS 05550	2.370634	Up	1.4E- 202	cation acetate symporter
AUO97_RS 05555	1.922574	Up	6.03E -29	DUF485 domain-containing protein [Acinetobacter]
AUO97_RS 05595	2.656199	Up	3.7E- 278	acetate--CoA ligase
AUO97_RS 05635	1.336995	Up	2.19E -84	carbapenem susceptibility porin CarO
AUO97_RS 05805	1.641335	Up	2.51E -71	hypothetical protein
AUO97_RS 06270	1.057684	Up	5.68E -08	DUF2726 domain-containing protein
AUO97_RS 06525	1.175945	Up	0.014 654	DUF3861 domain-containing protein
AUO97_RS 06550	1.175091	Up	4.65E -05	DoxX family protein
AUO97_RS 06650	2.333258	Up	6.99E -28	MFS transporter
AUO97_RS 06655	2.75065	Up	7.52E -90	enoyl-CoA hydratase/isomerase family protein
AUO97_RS 06660	2.947701	Up	1.15E -61	enoyl-CoA hydratase
AUO97_RS 06665	2.788771	Up	2.4E- 101	acyl-CoA dehydrogenase
AUO97_RS 06670	2.99023	Up	6.78E -31	AMP-binding protein
AUO97_RS 06675	2.626672	Up	1.8E- 101	3-hydroxyisobutyrate dehydrogenase
AUO97_RS 06680	2.412876	Up	5.5E- 215	methylmalonate-semialdehy de dehydrogenase (acylating)
AUO97_RS 06695	1.738202	Up	2.05E -58	amino acid permease
AUO97_RS 06700	1.327951	Up	3.98E -13	RidA family protein [Acinetobacter]
AUO97_RS 06705	1.11741	Up	1.41E -34	alanine racemase
AUO97_RS 06710	1.417227	Up	3.65E -61	D-amino-acid dehydrogenase
AUO97_RS 06715	1.465739	Up	0.000 52	AsnC family transcriptional regulator [Acinetobacter]

AUO97_RS 06785	1.075741	Up	0.002 995	sel1 repeat family protein
AUO97_RS 06810	1.16987	Up	8.02E -09	DUF4126 domain-containing protein
AUO97_RS 06825	2.083996	Up	5.4E- 190	Fe/S-dependent 2-methylisocitrate dehydratase AcnD
AUO97_RS 06830	2.154844	Up	7.5E- 125	2-methylcitrate synthase
AUO97_RS 06835	2.034936	Up	2.1E- 108	methylisocitrate lyase
AUO97_RS 06840	1.166137	Up	1.01E -23	GntR family transcriptional regulator
AUO97_RS 07165	1.277517	Up	0.012 728	hypothetical protein
AUO97_RS 07280	1.067484	Up	0.004 097	GlsB/YeaQ/YmgE family stress response membrane protein [Acinetobacter]
AUO97_RS 07430	1.453655	Up	7.14E -70	sodium-dependent transporter
AUO97_RS 07590	1.141851	Up	1.13E -09	PQQ-dependent sugar dehydrogenase
AUO97_RS 07645	1.903493	Up	1.1E- 213	4-hydroxyphenylpyruvate dioxygenase
AUO97_RS 07655	1.885403	Up	5.1E- 107	VOC family protein
AUO97_RS 07660	1.644119	Up	1.7E- 102	maleylacetoacetate isomerase
AUO97_RS 07665	1.732833	Up	6.8E- 139	fumarylacetoacetase
AUO97_RS 07670	2.082498	Up	2.6E- 191	aromatic amino acid transporter AroP
AUO97_RS 07710	1.109972	Up	2.23E -40	amino acid permease
AUO97_RS 07715	1.277428	Up	7.06E -54	imidazolonepropionase
AUO97_RS 07720	1.392517	Up	2.47E -69	formimidoylglutamase
AUO97_RS 07725	1.165672	Up	1.52E -07	DUF885 domain-containing protein
AUO97_RS 07745	1.186045	Up	2.89E -16	hypothetical protein
AUO97_RS 08710	1.313813	Up	3.7E- 08	TetR/AcrR family transcriptional regulator

AUO97_RS 08885	1.522507	Up	0.000 292	DNA transfer protein p32
AUO97_RS 08925	1.441162	Up	1.05E -45	hypothetical protein
AUO97_RS 09240	1.990121	Up	9.89E -17	MerR family transcriptional regulator
AUO97_RS 09745	1.159549	Up	2.63E -05	hypothetical protein
AUO97_RS 09845	1.430921	Up	1.56E -62	phosphate acetyltransferase
AUO97_RS 09850	1.495476	Up	5.58E -67	acetate kinase
AUO97_RS 10220	1.130523	Up	6.26E -63	aconitate hydratase AcnA
AUO97_RS 10285	1.368536	Up	9.08E -22	hydroxypyruvate isomerase
AUO97_RS 10375	1.815771	Up	7.89E -80	acyl-CoA synthetase
AUO97_RS 10780	1.238882	Up	5.12E -22	acyl-CoA dehydrogenase
AUO97_RS 10915	1.219079	Up	1.81E -60	Ig-like domain
AUO97_RS 11050	1.547215	Up	0.000 298	hypothetical protein
AUO97_RS 11055	1.277695	Up	2.06E -85	hypothetical protein
AUO97_RS 11220	1.046402	Up	3.48E -27	trehalose-6-phosphate synthase
AUO97_RS 11270	1.287005	Up	3.58E -12	threonylcarbamoyl-AMP synthase
AUO97_RS 11550	1.451916	Up	2.38E -10	metal-dependent hydrolase
AUO97_RS 11750	1.160465	Up	3.76E -21	gamma-glutamyltransferase family protein
AUO97_RS 11975	1.267775	Up	0.006 622	cupin domain-containing protein [Acinetobacter]
AUO97_RS 12450	1.001019	Up	9.88E -12	amino acid transporter
AUO97_RS 12700	1.891923	Up	1E-13	hypothetical protein
AUO97_RS 12705	1.395535	Up	2.52E -22	gamma-aminobutyraldehyd e dehydrogenase
AUO97_RS 12715	2.700051	Up	1E-42	aspartate aminotransferase family protein

AUO97_RS 12720	2.456076	Up	4.22E-24	arginine N-succinyltransferase
AUO97_RS 12815	1.332388	Up	1.17E-05	feruloyl-CoA synthase
AUO97_RS 12825	1.944957	Up	1E-12	crotonase
AUO97_RS 12850	1.696962	Up	4.2E-09	aromatic ring-hydroxylating dioxygenase subunit alpha
AUO97_RS 12855	1.327513	Up	0.008247	MFS transporter
AUO97_RS 13000	1.063488	Up	0.004539	hypothetical protein
AUO97_RS 13005	1.167699	Up	0.003181	hypothetical protein
AUO97_RS 13050	1.254068	Up	0.011311	hypothetical protein
AUO97_RS 13365	1.816626	Up	1.1E-103	OmpA family protein
AUO97_RS 13440	1.28526	Up	2.37E-07	aromatic acid/H ⁺ symport family MFS transporter
AUO97_RS 13450	1.198891	Up	0.000264	KR domain-containing protein
AUO97_RS 13465	1.354883	Up	1.45E-13	benzoate 1,2-dioxygenase large subunit
AUO97_RS 13485	1.043153	Up	3.76E-05	Cu(I)-responsive transcriptional regulator [Acinetobacter]
AUO97_RS 13760	1.143059	Up	9.1E-05	MFS transporter
AUO97_RS 13825	3.234393	Up	6.8E-158	divalent metal cation transporter
AUO97_RS 13830	3.201213	Up	2.6E-131	LamB/YcsF family protein
AUO97_RS 13835	3.473384	Up	8.5E-107	DUF1445 domain-containing protein
AUO97_RS 13840	2.743149	Up	1.4E-134	allophanate hydrolase
AUO97_RS 13845	2.961316	Up	3.2E-213	ATP-grasp domain-containing protein
AUO97_RS 14095	1.08262	Up	2.65E-11	DUF333 domain-containing protein
AUO97_RS 14165	1.53906	Up	3.3E-101	phenylacetic acid degradation bifunctional protein PaaZ

AUO97_RS 14170	1.032446	Up	2.82E -49	1,2-phenylacetyl-CoA epoxidase subunit A
AUO97_RS 14175	1.3148	Up	1.55E -15	1,2-phenylacetyl-CoA epoxidase subunit B [Acinetobacter]
AUO97_RS 14180	1.499868	Up	1.65E -67	phenylacetate-CoA oxygenase subunit PaaI
AUO97_RS 14185	1.536227	Up	1.89E -33	phenylacetate-CoA oxygenase subunit PaaJ [Acinetobacter]
AUO97_RS 14190	1.751782	Up	4.95E -74	phenylacetate-CoA oxygenase/reductase subunit PaaK
AUO97_RS 14195	1.762544	Up	1.76E -44	enoyl-CoA hydratase
AUO97_RS 14200	2.024242	Up	1.93E -52	2-(1,2-epoxy-1,2-dihydrophe nyl)acetyl-CoA isomerase
AUO97_RS 14205	1.999641	Up	3.01E -78	3-hydroxyacyl-CoA dehydrogenase
AUO97_RS 14210	2.356772	Up	1.47E -86	3-oxoadipyl-CoA thiolase
AUO97_RS 14215	2.48519	Up	1E-99	phenylacetate--CoA ligase [Acinetobacter]
AUO97_RS 14220	1.148118	Up	3.32E -18	phenylacetic acid degradation operon negative regulatory protein PaaX
AUO97_RS 14225	1.268769	Up	1.59E -07	carbonic anhydrase
AUO97_RS 14230	1.60666	Up	0.005 131	Paal family thioesterase
AUO97_RS 14350	2.142704	Up	3.8E- 210	hypothetical protein
AUO97_RS 14360	2.522866	Up	4.7E- 198	hydroxymethylglutaryl-CoA lyase
AUO97_RS 14365	2.454808	Up	4.6E- 216	acetyl/propionyl/methylcro tonyl-CoA carboxylase subunit alpha
AUO97_RS 14370	2.29445	Up	1E-13 0	enoyl-CoA hydratase
AUO97_RS 14375	2.072343	Up	2.5E- 231	methylcrotonoyl-CoA carboxylase subunit beta
AUO97_RS 14380	1.70927	Up	3.3E- 142	isovaleryl-CoA dehydrogenase

				[Acinetobacter]	
AUO97_RS 14385	1.473479	Up	6.7E- 88	TetR/AcrR	family transcriptional regulator
AUO97_RS 14390	1.584436	Up	2.3E- 99	AMP-binding protein	
AUO97_RS 14395	1.860351	Up	2.77E- 29	class I	SAM-dependent methyltransferase
AUO97_RS 14400	1.850229	Up	2.47E- 24	porin	
AUO97_RS 14470	1.887777	Up	0.000 657	hypothetical protein	
AUO97_RS 14480	1.066247	Up	1.68E- 06	LysE family translocator	
AUO97_RS 14690	1.049086	Up	3.4E- 28	cytochrome	ubiquinol oxidase subunit I
AUO97_RS 14855	1.419848	Up	5.24E- 21	peptide-methionine (R)-S-oxide reductase	
AUO97_RS 14970	1.54179	Up	9.37E- 77	amino acid ABC transporter substrate-binding protein	
AUO97_RS 14975	1.38723	Up	7.4E- 36	amino acid ABC transporter permease	
AUO97_RS 14980	1.428635	Up	7.26E- 24	amino acid ABC transporter permease	
AUO97_RS 14985	1.5406	Up	2.68E- 41	amino acid ABC transporter ATP-binding protein	
AUO97_RS 15145	1.837935	Up	2.31E- 06	hypothetical protein	
AUO97_RS 15625	1.100482	Up	0.000 393	phage major capsid protein	
AUO97_RS 16085	1.402496	Up	3E-06	membrane protein	
AUO97_RS 16245	1.070249	Up	9.77E- 14	helix-turn-helix domain-containing protein	
AUO97_RS 16250	1.783306	Up	1.04E- 38	lipoyl synthase	
AUO97_RS 16255	2.613427	Up	5.1E- 147	thiamine	pyrophosphate-dependent dehydrogenase E1 component subunit alpha
AUO97_RS 16260	2.751704	Up	4.6E- 128	alpha-ketoacid dehydrogenase subunit beta	
				[Acinetobacter]	
AUO97_RS	2.709018	Up	3.3E-	pyruvate	dehydrogenase

16265			146	complex dihydrolipoamide acetyltransferase
AUO97_RS	2.482195	Up	1.3E-	dihydrolipoyl
16270			103	dehydrogenase
AUO97_RS	2.532405	Up	7.87E	3-oxoacyl-ACP reductase
16275			-35	
AUO97_RS	2.044181	Up	8.99E	2,3-butanediol
16280			-68	dehydrogenase [Acinetobacter]
AUO97_RS	1.320639	Up	5.63E	sulfite exporter TauE/SafE
16305			-11	family protein
AUO97_RS	1.063217	Up	1.95E	MFS transporter
16380			-06	
AUO97_RS	2.547582	Up	1.8E-	acetyl-CoA C-acyltransferase
16415			236	
AUO97_RS	3.111344	Up	1.4E-	hypothetical protein
16420			138	
AUO97_RS	3.545127	Up	5E-27	CoA transferase subunit B
16425			6	
AUO97_RS	3.355226	Up	2.2E-	CoA transferase subunit A
16430			212	
AUO97_RS	1.065725	Up	1.2E-	GntP family permease
16465			37	
AUO97_RS	1.220277	Up	2.06E	3-hydroxybutyrate
16470			-27	dehydrogenase
AUO97_RS	1.198637	Up	7.03E	AdeA/AdeI family multidrug
16540			-05	efflux RND transporter
				periplasmic adaptor subunit
AUO97_RS	1.072523	Up	0.000	muconate cycloisomerase
17065			169	
AUO97_RS	1.183404	Up	0.000	flavin reductase
17125			615	
AUO97_RS	1.630775	Up	5.91E	oxidoreductase
17130			-05	
AUO97_RS	1.379569	Up	0.000	KR domain-containing
17135			479	protein
AUO97_RS	2.112924	Up	7.35E	aromatic-ring-hydroxylating
17140			-05	dioxygenase subunit beta
AUO97_RS	1.870779	Up	2.13E	aromatic ring-hydroxylating
17145			-11	dioxygenase subunit alpha
AUO97_RS	1.445298	Up	0.005	hypothetical protein
17155			927	
AUO97_RS	1.417474	Up	1.19E	acyl-CoA dehydrogenase
17160			-07	

AUO97_RS 17255	1.037498	Up	0.006 082	protocatechuate 3,4-dioxygenase subunit alpha
AUO97_RS 17265	1.339034	Up	0.016 976	4-carboxymuconolactone decarboxylase [Acinetobacter]
AUO97_RS 17270	1.117003	Up	0.000 133	aromatic acid/H+ symport family MFS transporter
AUO97_RS 17295	1.031416	Up	0.001 354	3-oxoadipate CoA-transferase subunit A
AUO97_RS 17510	1.418298	Up	7.41E- -19	hypothetical protein
AUO97_RS 17615	1.348617	Up	1.88E- -12	univeal stress protein
AUO97_RS 17805	1.595015	Up	5.1E- 125	D-amino acid dehydrogenase
AUO97_RS 18020	1.379384	Up	0.016 194	hypothetical protein
AUO97_RS 18065	1.120939	Up	0.010 31	hypothetical protein
AUO97_RS 18165	1.293585	Up	0.013 585	hypothetical protein
AUO97_RS 18270	1.483132	Up	0.007 185	hypothetical protein
AUO97_RS 18455	1.352626	Up	3.22E- -05	RDD family protein
AUO97_RS 18615	3.165241	Up	2.2E- 227	alcohol dehydrogenase
AUO97_RS 18630	2.790133	Up	6.7E- 289	aldehyde dehydrogenase
AUO97_RS 18635	1.045856	Up	1.34E- -06	ethanolamine permease
AUO97_RS 18640	1.168491	Up	0.000 154	ethanolamine ammonia-lyase subunit EutB
AUO97_RS 18860	2.626809	Up	4.9E- 108	AMP-binding protein
AUO97_RS 18865	2.497141	Up	1.3E- 129	butyryl-CoA dehydrogenase
AUO97_RS 18870	2.711438	Up	1.4E- 155	3-hydroxyacyl-CoA dehydrogenase
AUO97_RS 19040	1.091354	Up	0.000 146	hypothetical protein [Acinetobacter]
AUO97_RS 19200	1.109533	Up	5.26E- -07	molecular chaperone

AUO97_RS 19205	1.38997	Up	0.000 595	SCPU protein	domain-containing
AUO97_RS 19210	1.208871	Up	0.000 104	protein CsuA	
AUO97_RS 19215	2.042194	Up	3.42E -59	SCPU protein	domain-containing

Table 6 Differential expressed genes in Δ abaIR strain

GeneID	log2FoldChange(Δ abaIR/WT)	Up-Down-Regulation(Δ abaIR/WT)	Pvalue	Product	
AUO97_RS 06625	-4.810564081	Down	0	acyl-CoA dehydrogenase	
AUO97_RS 06615	-4.798341091	Down	0	non-ribosomal peptide synthetase	
AUO97_RS 06610	-4.684191859	Down	0	outer membrane lipoprotein-sorting protein	
AUO97_RS 06630	-4.479849984	Down	0	acyl-CoA synthetase	
AUO97_RS 08905	-3.443053657	Down	0	membrane protein	
AUO97_RS 06635	-3.169896529	Down	1.77E-13	LuxR family transcriptional regulator	
AUO97_RS 06605	-2.775977102	Down	1.2E-108	hypothetical protein	
AUO97_RS 06600	-2.592760202	Down	1.05E-77	alpha/beta hydrolase	
AUO97_RS 06645	-2.580535991	Down	5.26E-09	GNAT family N-acetyltransferase	
AUO97_RS 06620	-2.187695047	Down	8.04E-07	acyl carrier protein	
AUO97_RS 10260	-2.092687691	Down	1.5E-128	NAD(P)(+) transhydrogenase (Re/Si-specific) subunit alpha	
AUO97_RS 10270	-1.736715963	Down	1.03E-89	NAD(P) transhydrogenase subunit beta	
AUO97_RS 10265	-1.715456717	Down	5.71E-10	NAD(P) transhydrogenase subunit alpha	
AUO97_RS 12875	-1.610454816	Down	5.57E-10	SDR family NAD(P)-dependent	

AUO97_RS 06875	-1.571786385	Down	1.63E-66	oxidoreductase UDP-glucose 4-epimerase GalE
AUO97_RS 14380	-1.571062479	Down	1.04E-66	isovaleryl-CoA dehydrogenase
AUO97_RS 13765	-1.504167019	Down	1.89E-08	DUF2147 domain-containing protein
AUO97_RS 05565	-1.467640693	Down	7.99E-23	hypothetical protein
AUO97_RS 12200	-1.450434646	Down	1.71E-06	esterase
AUO97_RS 12630	-1.447421801	Down	2.09E-77	hypothetical protein
AUO97_RS 05555	-1.418971886	Down	2.68E-07	DUF485 domain-containing protein
AUO97_RS 14390	-1.416019051	Down	6.55E-44	AMP-binding protein
AUO97_RS 14375	-1.363301003	Down	1.35E-64	methylcrotonoyl-Co A carboxylase subunit beta
AUO97_RS 14395	-1.333055716	Down	3.01E-07	class I SAM-dependent methyltransferase
gene2510	-1.254200121	Down	0.000113	#N/A
AUO97_RS 07705	-1.221452269	Down	5.3E-91	histidine ammonia-lyase
AUO97_RS 06750	-1.218989942	Down	6.02E-21	short-chain dehydrogenase
AUO97_RS 05160	-1.216497945	Down	4E-69	acetyl-CoA hydrolase
AUO97_RS 12255	-1.2055697	Down	7E-106	isocitrate lyase
AUO97_RS 05775	-1.18255173	Down	1.22E-39	DUF2147 domain-containing protein
AUO97_RS 12620	-1.159218991	Down	1.38E-62	D-amino acid dehydrogenase
AUO97_RS 10175	-1.15568351	Down	2.52E-33	hypothetical protein
AUO97_RS 09645	-1.148829981	Down	0.008712	RNA-binding protein
AUO97_RS	-1.146164239	Down	6.59E-12	GntR family

06840				transcriptional regulator
AUO97_RS	-1.136579054	Down	3.51E-05	DUF1311
08910				domain-containing protein
AUO97_RS	-1.136034285	Down	3.57E-11	ribosome-associated translation inhibitor
10590				RaiA
AUO97_RS	-1.09534896	Down	1.37E-11	RidA family protein
12615				
AUO97_RS	-1.062020065	Down	2.24E-40	DegT/DnrJ/EryC1/Str S family aminotransferase
06935				SRPBCC family protein
AUO97_RS	-1.053989883	Down	0.001534	enoyl-CoA hydratase
13875				
AUO97_RS	-1.027361924	Down	1.64E-13	malate synthase G
14370				
AUO97_RS	-1.01932917	Down	6.13E-84	acetate kinase
15725				
AUO97_RS	-1.012081007	Down	3.26E-22	RND transporter
09850				
AUO97_RS	-1.007776244	Down	2.76E-26	Ig-like domain
07365				
AUO97_RS	-1.00310968	Down	1.46E-42	LysE family translocator
10915				
AUO97_RS	1.000516557	Up	3.19E-06	ferredoxin reductase
14480				
AUO97_RS	1.0133961	Up	8.83E-37	DUF541
07010				domain-containing protein
AUO97_RS	1.016484113	Up	3.04E-12	hypothetical protein
01160				
AUO97_RS	1.022615214	Up	0.010216	DUF3108
14910				domain-containing protein
AUO97_RS	1.027289495	Up	1.33E-12	DUF2184
04145				domain-containing protein
AUO97_RS	1.027636888	Up	0.000313	transcriptional regulator
13145				
AUO97_RS	1.050221533	Up	0.001537	MFS transporter
02595				
AUO97_RS	1.059975124	Up	0.000226	
17175				

AUO97_RS 01125	1.065129674	Up	4.77E-12	phosphonate transporter substrate-binding protein	ABC
AUO97_RS 05210	1.083855153	Up	7.7E-06	XRE transcriptional regulator	family
AUO97_RS 04890	1.089851492	Up	5.25E-28	bacterioferritin	
AUO97_RS 11550	1.102335386	Up	2.83E-06	metal-dependent hydrolase	
AUO97_RS 00265	1.10618527	Up	0.00818	hypothetical protein	
AUO97_RS 10860	1.109814353	Up	1.46E-41	DUF1852 domain-containing protein	
AUO97_RS 13165	1.111887863	Up	0.008051	hypothetical protein	
AUO97_RS 10765	1.117361686	Up	2.1E-12	adenosine deaminase	
AUO97_RS 13135	1.12070687	Up	0.001552	DUF2213 domain-containing protein	
AUO97_RS 12720	1.121710543	Up	5.81E-05	arginine N-succinyltransferase	
AUO97_RS 04620	1.122555825	Up	0.002472	EamA/RhaT transporter	family
AUO97_RS 07060	1.127777848	Up	0.001455	sulfonate transporter substrate-binding protein	ABC
AUO97_RS 07165	1.134673245	Up	0.009058	hypothetical protein	
AUO97_RS 10870	1.135437723	Up	5.34E-19	flavin reductase	
AUO97_RS 12860	1.145646353	Up	0.002439	outer membrane porin, OprD family	
AUO97_RS 05515	1.145856951	Up	1.85E-31	NADPH:quinone oxidoreductase	
AUO97_RS 09015	1.161085465	Up	1.95E-46	FUSC family protein	
AUO97_RS 06745	1.162966485	Up	0.001507	DUF1003 domain-containing	

AUO97_RS 12715	1.16516071	Up	1.69E-06	protein aspartate aminotransferase family protein
AUO97_RS 05945	1.175348599	Up	6.55E-17	replication protein C [Proteobacteria]
AUO97_RS 11705	1.187305046	Up	8.43E-06	hypothetical protein
AUO97_RS 13005	1.19521274	Up	0.000815	hypothetical protein
AUO97_RS 07045	1.197457681	Up	5.63E-15	hypothetical protein
AUO97_RS 08880	1.200746597	Up	0.003007	DNA transfer protein p32
AUO97_RS 14960	1.202220672	Up	0.000235	SfnB family sulfur acquisition oxidoreductase
AUO97_RS 18115	1.206540056	Up	0.00495	stress-responsive nuclear envelope protein
AUO97_RS 01255	1.211481854	Up	1.01E-39	LysR family transcriptional regulator
AUO97_RS 13835	1.218264558	Up	9.15E-09	DUF1445 domain-containing protein
AUO97_RS 07005	1.273658088	Up	3.63E-49	acyl-CoA desaturase
AUO97_RS 04575	1.274976219	Up	2.47E-25	HPP family protein
AUO97_RS 10250	1.279002189	Up	0.001758	RidA family protein
AUO97_RS 18125	1.290037253	Up	0.000228	hypothetical protein
AUO97_RS 12450	1.291462344	Up	6.13E-21	amino acid transporter
AUO97_RS 17065	1.294967434	Up	1.56E-06	muconate cycloisomerase
AUO97_RS 15625	1.311448775	Up	3.38E-06	phage major capsid protein
AUO97_RS 16845	1.31494929	Up	0.000124	SMP-30/gluconolact onase/LRE family protein
AUO97_RS	1.319981098	Up	2.03E-07	hypothetical protein

00195					
AUO97_RS	1.364315635	Up	2.3E-28	pyruvate	
01135				decarboxylase	
AUO97_RS	1.376815835	Up	4.79E-15	EamA/RhaT	family
05215				transporter	
AUO97_RS	1.390886913	Up	1.88E-28	MacA	family efflux
10110				pump subunit	
AUO97_RS	1.406842394	Up	6.74E-23	RtcB	family protein
00260					
AUO97_RS	1.408770151	Up	1.15E-13	EamA	family
08715				transporter	
AUO97_RS	1.424467059	Up	5.57E-05	hypothetical protein	
04705					
AUO97_RS	1.434908162	Up	6.18E-21	TetR/AcrR	family
05520				transcriptional	
				regulator	
AUO97_RS	1.455698678	Up	1.21E-48	MFS	transporter
06395					
AUO97_RS	1.463500264	Up	0.000157	hypothetical protein	
13175					
AUO97_RS	1.482712098	Up	2.03E-06	flavin reductase	
17125					
AUO97_RS	1.506892192	Up	0.0006	hypothetical protein	
18270					
AUO97_RS	1.525928785	Up	8.33E-26	taurine	ABC
14730				transporter	
				ATP-binding protein	
AUO97_RS	1.53094861	Up	9.1E-12	TetR/AcrR	family
08710				transcriptional	
				regulator	
AUO97_RS	1.583794725	Up	5.9E-06	hypothetical protein	
03405					
AUO97_RS	1.597978381	Up	8.73E-05	nuclear	transport
17150				factor	2 family
				protein	
AUO97_RS	1.608502109	Up	0.000235	hypothetical protein	
13235					
AUO97_RS	1.610222783	Up	5E-07	PaaX	family
00970				transcriptional	
				regulator	
AUO97_RS	1.646501685	Up	1.18E-36	SCPU	
19215				domain-containing	
				protein	
AUO97_RS	1.666892923	Up	8.55E-06	DNA transfer protein	

08885					p32
AUO97_RS	1.69031736	Up	8.39E-36	sulfite exporter	
16050				TauE/SafE family	
				protein	
AUO97_RS	1.762259496	Up	6.61E-20	aromatic amino acid	
01130				transporter AroP	
AUO97_RS	1.797926772	Up	5.12E-16	amidase	
17165					
AUO97_RS	1.839119762	Up	2.78E-05	aromatic-ring-hydro	
17140				xylating dioxygenase	
				subunit beta	
AUO97_RS	1.905157138	Up	5.15E-26	alpha/beta	
01560				hydrolase	
AUO97_RS	2.110174475	Up	2.41E-10	KR	
17135				domain-containing	
				protein	
AUO97_RS	2.113312655	Up	9.47E-77	sulfate ABC	
01555				transporter	
				substrate-binding	
				protein	
AUO97_RS	2.203176565	Up	2.19E-10	oxidoreductase	
17130					
AUO97_RS	2.210965901	Up	6.94E-18	hypothetical protein	
18900					
AUO97_RS	2.239808823	Up	4.73E-22	acyl-CoA	
17160				dehydrogenase	
AUO97_RS	2.241276362	Up	6.25E-14	hypothetical protein	
07050					
AUO97_RS	2.394634424	Up	3.66E-18	aromatic	
17145				ring-hydroxylating	
				dioxygenase subunit	
				alpha	
AUO97_RS	2.455858156	Up	5.07E-14	hypothetical protein	
18910					
AUO97_RS	2.581083497	Up	1.35E-17	hypothetical protein	
03425					
AUO97_RS	2.601467607	Up	6.94E-65	taurine ABC	
14725				transporter	
				substrate-binding	
				protein	