

1 The *abaI/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

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

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

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

38 **INTRODUCTION**

39 *Acinetobacter baumannii* is a Gram-negative pathogen that has emerged as one of  
40 the most troublesome pathogens for health care institutions globally. *A. baumannii*  
41 infections are increasingly difficult to treat because of multidrug-resistance in most  
42 strains causing infection in intensive care units (ICUs) (1). Virulence factors were used  
43 by bacteria that enable successful interaction with and subsequent adhesion and  
44 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 (*abaI/abaR*) has been

55 described(11). The *abaI* 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 *abaI* from *Acinetobacter*

64 *baumannii* M2, but failed to create an *abaR* deletion mutant for unknown reasons

65 (14). To explore the role of the *abaI/abaR* QS system in drug resistance, biofilm

66 formation and virulence of *A. baumannii*,  $\Delta$ *abaI* and  $\Delta$ *abaR* mutants of strain ATCC

67 17978 were created. We also made double mutant  $\Delta abalR$ . The transcriptomes of

68 WT,  $\Delta abal$ ,  $\Delta abaR$  and  $\Delta abalR$  were determined by RNA-sequencing (RNA-seq).

69 **RESULTS**

70 **The mutants showed differences in growth characteristics and morphology**

71 To test the role of the  $abal/abaR$  QS system in *A. baumannii* growth curve, we

72 determined by measuring the optical density (OD) of the culture over time. The

73 growth of the  $\Delta abaR$  and  $\Delta abalR$  mutants did not differ from that of the parent strain

74 (Fig. 1A). The complemented strain  $\Delta abaR$ (pME $abaR$ ) and overexpressed strains

75 WT(pME $abal$ ), WT(pME $abaR$ ) also showed growth profiles similar to those of the

76 wild type(Fig. 1A), suggesting that the gene  $abaR$  is not essential for *A. baumannii*

77 growth. In contrast,  $\Delta abal$  mutant showed visibly slowed growth at the logarithmic

78 phase. Growth of the  $\Delta abal$  mutant was partly rescued by expression of  $abal$  via the

79 pME6032-derived plasmid pME $abal$  (Fig. 1A). The empty vector pME6032, used as a

80 control, did not affect the growth profile of *A. baumannii* ATCC 17978(Fig. 1A). These

81 results demonstrated that  $abal$  affect the growth of *A. baumannii*. Subsequently, the

82 morphology of the bacteria was observed by transmission electron microscopy. As

83 shown in Figure 1B, WT was attached with extracellular secretions.  $\Delta abal$  mutant cell

84 edges were transparent.  $\Delta abaR$  mutant strains cytoplasmic density is lower. There

85 was no obviously change in  $\Delta abalR$  mutant, but around the cell adhered partial

86 secretions. Morphology of the  $\Delta abal$  mutant was partly rescued by expression of

87  $abal$  via the pME6032-derived plasmid pME $abal$ . Morphology of the  $\Delta abaR$  mutant

88 was rescued by expression of  $abaR$  via the pME6032-derived plasmid pME $abaR$ .

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

94 **Mutants showed increase susceptibility to antimicrobials**

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

107 **Screening of strains for AHLs production**

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

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

119 **Surface-associated motility relies on quorum sensing**

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

131 **Biofilm formation**

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

133 we cultivated the strains mutants in 96-well plates for 24 h at 37°C. As a result,  
134 Filaments were formed in the culture medium of wild strain, mutant strains  $\Delta abal$ ,  
135  $\Delta abaR$  had dot-like biofilm formation on the surface of liquid,  $\Delta abaR$  mutant strain  
136 had no biofilm on the liquid surface, there were dot-like biofilms on the liquid surface  
137 of  $\Delta abal$ (pME $abal$ ) and  $\Delta abaR$ (pME $abaR$ )and they were connected into pieces. The  
138 biofilm on the liquid surface of the overexpressed strain WT(pME $abal$ ) was lamellar,  
139 while the biofilm on the liquid surface of WT(pME $abaR$ ) was spot-like but thick (Fig.  
140 4A). The absorbance of bacterial solution was detected, and the results were shown  
141 in the Figure 4B, there were significant difference between the absorbance of the  
142 parental strain and mutants  $\Delta abal$ ,  $\Delta abaR$ , however, for mutant  $\Delta abaR$  showed no  
143 difference. The absorbance of  $\Delta abal$  mutants were not rescued by expression of  $abal$   
144 via the plasmid pME $abal$ , absorbance of  $\Delta abaR$  mutants were rescued by expression  
145 of  $abaR$  via the plasmid pME $abaR$ . The absorbance of overexpressed strain  
146 WT(pME $abaR$ ) was significantly higher than that of wild strain. The biofilm forming  
147 ability of the strains were determined by crystal violet biofilm assay, and the  
148 differences between the wild-type and mutant strains were calculated. Compared  
149 with wild strains, the biofilm formation of all strains was significantly decreased,  
150 except for the overexpressed strain WT(pME $abaR$ ), which was significantly higher  
151 than that of wild strain (Fig. 4C). The results indicated that quorum sensing system  
152 affects the biofilm formation of bacteria.

153 **Serum killing**

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

155 elucidate the virulence of strains, we compared the serum sensitivity of mutants to  
156 WT. As shown in Fig 5 A, WT, *abaR* and WT(pME*abaR*) survived after incubation in  
157 serum, whereas  $\Delta$ *abaI*,  $\Delta$ *abaI*(pME*abaI*) and  $\Delta$ *abaI*R were entirely killed after 1 h at  
158 37°C. The serum sensitivity of  $\Delta$ *abaI* mutants were not rescued by expression of *abaI*  
159 via the plasmid pME*abaI*, serum sensitivity of  $\Delta$ *abaI*R mutants were rescued by  
160 expression of *abaR* via the plasmid pME*abaR*. The empty vector pME6032, used as a  
161 control, did not affect the serum sensitivity of *A. baumannii* ATCC 17978. These  
162 results indicated that WT and  $\Delta$ *abaR* were highly resistant to the killing action of  
163 serum, in contrast,  $\Delta$ *abaI* and  $\Delta$ *abaI*R mutants were much more serum sensitive,  
164 showing a significant difference.

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

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

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

183 **Quorum sensing plays a role in virulence in mouse infection models**

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

199 analyzed bacterial burdens in the blood, lung and spleen of mice infected for 4 h, 24  
200 h and 72 h. As a result, WT,  $\Delta abaR$  mutant and complemented strain  
201  $\Delta abaR(pMEabaR)$  resulted in an increase in bacterial counts,  $\Delta abal$  and  $\Delta abalR$   
202 mutants exhibited a remarkable reduction in the burden in blood, lung, and spleen at  
203 4 h postinoculation. More specifically, as shown,  $\Delta abal$  and  $\Delta abalR$  mutants  
204 displayed a high serum clearance rate and resulted in a significant decrease in  
205 bacteremia at 4 h postinoculation. There were no differences at 24 h (Fig. 6B). The  
206 bacteria were completely eliminated at 72 hours (data not shown). These results  
207 indicated that quorum sensing system plays a role in virulence in mouse infection  
208 models.

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

210 To identify transcriptional activity dependent on *abal/abaR* function, RNA-seq  
211 analysis was performed on *abal/abaR* mutants and WT strain. A total of 463 genes  
212 were classified as differentially expressed in mutants relative to WT. Compared with  
213 WT, in  $\Delta abal$  mutant, a total of 159 protein-coding genes (out of 3848) were  
214 identified as differentially expressed by a log2-fold change greater than 1 or less than  
215 -1 ( $P \leq 0.05$ ) (126 with increased expression, 33 with decreased expression).  
216 Deletion of *abaR* had a larger impact on the transcriptome of strain ATCC 17978, with  
217 the differential expression of 324 genes (211, 113 up down regulated).  $\Delta abalR$   
218 mutant had a total of 123 differentially expressed genes (79 genes with increased  
219 expression, 44 with decreased expression) (Fig. 7A to C) (Supplementary table).  
220 These results revealed that partial changes in gene expression occur with changes in

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

224 **COGs annotation**

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

240 **GO and KEGG pathways enrichment analysis of DEGs**

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

243 enrichment analyses. The top 30 of significant GO terms were divided into two major  
244 categories—biological process and cellular component in  $\Delta abal$  mutant, as shown in  
245 Figure 9A. Among the biological processes, the DEGs were distributed to xenobiotic  
246 metabolic process, toxin metabolic/catabolic process, auxin metabolic /catabolic  
247 process, phenylacetate catabolic process and so on. In the cellular component field,  
248 DEGs were belonged to respiratory chain complex I, plasma membrane respiratory  
249 chain complex I, NADH dehydrogenase complex and respiratory chain. The top 30  
250 significant GO terms were divided into three major categories—biological process,  
251 cellular component and molecular function in  $\Delta abalR$  mutant, as shown in Figure 9C.  
252 Among the biological processes, the DEGs were distributed to ribosome assembly,  
253 translation, ribonucleoprotein complex assembly, organelle assembly,  
254 ribonucleoprotein complex subunit organization and peptide biosynthetic process. In  
255 the cellular component field, DEGs were belonged to cytosolic ribosome, ribosome,  
256 ribonucleoprotein complex, organelle part and cytosolic part. In molecular function,  
257 DEGs were responsible for structural constituent of ribosome, structural molecule  
258 activity and rRNA binding. The top 30 significant GO terms were divided into three  
259 major categories—biological process, cellular component and molecular function in  
260  $\Delta abalR$  mutant, as shown in Figure 9E. Among the biological processes, the DEGs  
261 were distributed to response to metal ion, response to organonitrogen compound,  
262 cellular response to stress and anion transport. In the cellular component field, DEGs  
263 were belonged to outer membrane–bounded periplasmic space, periplasmic space,  
264 cell envelope and envelope. In molecular function, DEGs were responsible for copper

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

267 KEGG pathway enrichment suggested that DEGs of  $\Delta abal$  mutant were significantly  
268 enriched in the pathways related to Phenylalanine metabolism, Oxidative  
269 phosphorylation, Benzoate degradation, Tryptophan metabolism, Arginine and  
270 proline metabolism, Fatty acid degradation and so on (Fig. 9 B). DEGs of  $\Delta abaR$   
271 mutant were mainly involved in the pathways related to Ribosome, Valine, leucine  
272 and isoleucine degradation, Propanoate metabolism, Pyruvate metabolism,  
273 Phenylalanine metabolism, Fatty acid degradation and so on (Fig. 9D). DEGs of  
274  $\Delta abalR$  mutant were mainly involved in the pathways related to ABC transporters,  
275 Sulfur metabolism Nicotinate and nicotinamide metabolism and so on (Fig.9 F).  
276 Given the different phenotypes of  $\Delta abal$ ,  $\Delta abaR$  and  $\Delta abalR$  mutants, the RNA-seq  
277 analysis revealed a subset of the genes that was most highly activated or suppressed  
278 by quorum sensing system, as shown in Figure 7B. We centralized our analysis on  
279 the gene subsets whose transcription was down in  $\Delta abal$  and  $\Delta abaR$  and  $\Delta abalR$   
280 mutants, the quorum sensing gene (*abal* AUO97\_RS06645) and nearby locus  
281 (AUO97\_RS06600–06630) showed strongly reduced transcription. One study found  
282 that in *A. baumannii* M2 strain quorum sensing mediated by the *abal* is required for  
283 motility (19). We assessed the surface motility of the mutants, as shown in Figure 3.  
284 We observed that wild-type strain exhibited a robust surface motility phenotype and  
285 the mutants did not exhibit any signs of motility.  
286 We mainly analyzed the gene expression of each group. Hemerythrin-like proteins

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

288 AUO97\_RS11650 (hemerythrin) was down-regulated in  $\Delta abal$  mutant, and other

289 antimicrobial resistance genes including AUO97\_RS07490 (*mexK*), AUO97\_RS07485

290 (*mexJ*), AUO97\_RS07485 (efflux RND transporter periplasmic adaptor subunit) and

291 AUO97\_RS05665 (beta-lactamase domain protein), were down regulated. One gene,

292 AUO97\_RS16540 (*AdeA/AdeI* family multidrug efflux RND transporter periplasmic

293 adaptor subunit) had 1.2-fold increased expression in  $\Delta abaR$  mutant, while the

294 expression of this gene was not changed in the  $\Delta abalR$  mutant. We then assessed the

295 antimicrobial susceptibility of the mutants, as shown in Table 4, susceptibility of

296 mutants towards a part of antimicrobials increased.

297 The *csu* operon is composed of 6 genes (*csuA/BABCDE*) and play a central role in

298 initial bacterial attachment, and biofilm formation on abiotic surfaces (21). In  $\Delta abal$

299 mutant, the *CsuA/BABCDE* chaperone-usher pili assembly system was showed high

300 expression, except for the *CsuA* (AUO97\_RS19210) gene. In  $\Delta abaR$  mutant, *CsuA/B*

301 (AUO97\_RS19215), *CsuA* (AUO97\_RS19210), *CsuB* (AUO97\_RS19205) and *CsuC*

302 (AUO97\_RS19200) were highly expressed, whereas in the  $\Delta abalR$  mutant, only

303 *CsuA/B* (AUO97\_RS19215) was highly expressed. *CsuA/B*, which is predicted to form

304 part of the type I pili rod that was up-regulated in all mutants. Of particular interest is

305 their regulator genes *bfmR-bfmS*, which did not change in all mutants. Biofilm

306 formation was observed on the liquid surface of the  $\Delta abal$  and  $\Delta abaR$  mutant (Fig.

307 4A). Previously study found that *CsuC* and *CsuE* are required in the early steps of

308 biofilm formation (21). In some *A. baumannii* strains biofilms are not essential for

309 virulence (22). Apart from the *csu* operon, other genes controlled by quorum sensing  
310 that may have relations with biofilm formation. A1S\_0644 (AUO97\_RS08180), a  
311 hypothetical protein involved in biofilm formation was repressed in the *ΔabaR*  
312 mutant.

313 Secreted bacterial proteins can mediate serum resistance, a secreted serine protease  
314 which termed PKF is required for serum resistance and inhibits biofilm formation in  
315 *A. baumannii* (23). In *ΔabaR* mutant, PKF (AUO97\_RS01525) was highly expressed,  
316 and no difference was observed in the *ΔabaI* and *ΔabaIR* mutants. We assessed the  
317 serum sensitivity test and the ability of mutant to form biofilms on abiotic surface. As  
318 shown in (Fig. 5A and Fig.4), WT and *ΔabaR* survived after incubation in serum,  
319 whereas *ΔabaI* and *ΔabaIR* were entirely killed after 1 h at 37°C. There was a  
320 remarkable decrease in the biofilm formation by *ΔabaR* mutant. Apart from this  
321 gene, other genes that may be associated with serum resistance and biofilm  
322 formation may be regulated by quorum sensing.

323 NADH is mainly involved in material and energy metabolism in cells, which is  
324 transferring energy to ATP synthesis through oxidative phosphorylation on the  
325 mitochondrial inner membrane (24, 25). In the respiratory chain of *A. baumannii*,  
326 there are 14 NADH-quinone oxidoreductase subunits involved in NADH  
327 dehydrogenase, which includes *NuoA-NuoN*. In *ΔabaI* mutant, a subset of genes  
328 including AUO97\_RS10980 -11015 (*NuoG, NuoH, Nuol, NuoJ, NouK, NuoL, NuoM* and  
329 *NuoN*) were all down-regulated (Fig. 10A). In *ΔabaR* mutant AUO97\_RS11000 (*NouK*  
330 and AUO97\_RS11015 (*NuoN*) were down-regulated, and there was no change in

331  $\Delta abalR$  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,  $\Delta abal$  mutant showed slightly slowed growth at  
334 the logarithmic phase, the cytoplasm of the  $\Delta abal$  mutant appeared to be  
335 transparent, and the cytoplasmic density of  $\Delta abal$  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  $\Delta abal$  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*, *paaJ*, *paaK1*, *paaK2*, *paaX*, *paaY*  
347 and *paaI*). In  $\Delta abalR$  mutant, the *paa* operon was highly expressed (Fig. 10B). In  $\Delta abal$   
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  $\Delta abalR$  mutant. Branched  
352 chain amino acids (BCAAs), including leucine (Leu), isoleucine (Ile), and valine (Val), is

353 vital to both growth and virulence in bacteria (29, 30). In  $\Delta abaR$  mutant, the Valine,  
354 leucine and isoleucine degradation pathway was up-regulated (Fig. 10B). The BCAAs  
355 serve as precursors for branched-chain fatty acids (BCFAs), which are predominant  
356 membrane fatty acids, the BCAAs are key co-regulators of virulence factors. In  $\Delta abaR$   
357 mutant, there are 27 genes involved in the propanoate metabolism pathway was up-  
358 regulated (Fig. 10B). In  $\Delta abal$  mutant, AUO97\_RS14195, AUO97\_RS16430,  
359 AUO97\_RS06660, AUO97\_RS18630 and AUO97\_RS12705 involved in the propanoate  
360 metabolism pathway was up-regulated. In  $\Delta abalR$  mutant, AUO97\_RS14380,  
361 AUO97\_RS14375, AUO97\_RS14370 involved in the propanoate metabolism pathway  
362 was up-regulated. Lipids play an important role in both the physiology and  
363 pathophysiology of living systems (31). Membrane phospholipids play a key role in  
364 the defense against antimicrobials, including host fatty acids (32-34). The COG  
365 enrichment analysis indicated that a large amount of genes with predicted functions  
366 in [I] Lipid transport and metabolism (21%), were up-regulated in  $\Delta abaR$  mutant (Fig.  
367 8). PAA, BCAAs and Lipid transport and metabolism may play a protective role against  
368 the host and serum. The K locus regulates the production of complex polysaccharides  
369 to protect against killing by host serum and enhance virulence in animal models of  
370 infection (35). In the K locus (O-glycosylation and wzy-dependent capsule synthesis  
371 locus) (AUO97\_RS06870–06965), the gene AUO97\_RS06875 (UDP-glucose 4-  
372 epimerase GalE) showed weakened transcription in the  $\Delta abal$  and  $\Delta abalR$  mutants  
373 by a 1.7-fold decrease and a 1.6-fold decrease, respectively, while there was no  
374 change in  $\Delta abaR$  mutant. AUO97\_RS13365 (*OmpA* family protein), a naturally

375 glycosylated protein in *A. baumannii* ATCC 17978, was expressed with a 1.8-fold  
376 increase in  $\Delta abaR$  strain, and no difference in  $\Delta abal$  and  $\Delta abalR$  mutants was  
377 observed. Ribosomal proteins (RPs) are well-known for their role in mediating  
378 protein synthesis and maintaining the stability of the ribosomal complex, which  
379 includes small and large subunits. There were 36 genes encoding for ribosomal  
380 proteins that exhibited reduced expression in  $\Delta abaR$  mutant strain (Fig. 10B). 23 (L1-  
381 6, L9-13, L15-20, L22-23, L25, L28-29, L35) of them were associated with the large  
382 subunit while the remaining 13 (S2-8, S10-11, S14, S17-19) were associated with the  
383 small subunit. This change may enable *A. baumannii* to 'fine-tune' their proteomes  
384 to regulate the pathogenicity of bacteria. There was no change in  $\Delta abal$  and  $\Delta abalR$   
385 mutants. We assessed the virulence of the mutant in *G. mellonella* and mouse and  
386 serum sensitivity tests. As shown in Figure 5B and Figure 6 and Figure 5A,  $\Delta abaR$   
387 mutant enhances more virulence and serum resistance, while  $\Delta abal$  and  $\Delta abalR$   
388 mutants markedly attenuated the virulence of *A. baumannii*. The selected genes  
389 (*paaG*, *paaH*, *paaJ*, *paaK2*, *paaX*, *paaY* and *paaI*) encode proteins in the PAA  
390 catabolic pathway, BCAAs, the capsule synthesis locus *GalE* and *OmpA* may  
391 contribute to virulence.

## 392 **DISCUSSION**

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

397 control virulence.

398 In the present study, we focused on detecting the role of the *abaI/abaR* QS system in

399 the virulence of *A. baumannii*. The mutant lacking *abaI* is believed to be less virulent

400 than wild-type strain. In contrast, *abaR* mutants were significantly more pathogenic

401 than wild-type strain. This result was confirmed in our study by injection of *G.*

402 *mellonella* larvae and a mouse model of infection and serum killing test. Our

403 transcriptomic analysis results revealed that deletion of *abaI* leads to the significant

404 repression of energy production and conversion genes. The connection between

405 energy metabolism and virulence has been reported in a multitude of bacteria. In

406 *Vibrio cholerae*, the expression of virulence regulatory protein *ToxT* is affected by the

407 NADH via respiration activity (36). In *Pseudomonas savastanoi*, *RhpR* directly regulate

408 multiple metabolic pathways and phosphorylation to specifically control virulence

409 (37). Therefore, *abaI* may indirectly control bacterial virulence by inducing the

410 differential expression of some key genes involved in NADH dehydrogenase in the

411 respiratory chain. Deletion of *abaR* enhances more cytotoxicity and immune evasion.

412 RNA-Seq analysis indicated that deletion of *abaR* leads to the significant

413 overexpression of lipid transport and metabolism, carbohydrate transport and

414 metabolism and amino acid transport and metabolism genes. Lipid metabolism plays

415 a key role in the pathogenicity of some intracellular bacteria (38). It has been

416 observed that lipids are the main carbon and energy source of *M. tuberculosis*, which

417 switches from carbohydrate utilization to the fatty acid utilization pathway for the

418 establishment of a successful infection(39). *A. baumannii* is a ubiquitous, facultative

419 intracellular bacterial pathogen (40).  $\Delta abaR$  mutant may enhance lipid transport and  
420 metabolism to plays a protective role against the host.  $\Delta abaR$  mutant was slightly  
421 more pathogenic than  $\Delta abal$  mutants but less pathogenic than the  $\Delta abaR$  mutants.  
422 This result was verified in our study by injection bacteria into *G. mellonella* larvae.  
423 Virulence through the intermediated phenylacetate catabolism pathway has been  
424 found in *A.baumannii*, and deletion of *paaE* attenuated *A. baumannii* virulence in  
425 mouse septicemia model (27). In *Burkholderia cenocepacia*, *paaA* and *paaE*  
426 insertional mutants showed reduced virulence, and interruption of *paaZ* and *paaF*  
427 slightly increased virulence in the *Caenorhabditis elegans* model of infection(41).  
428 Therefore, deletion of the *abaR* gene may indirectly enhance bacterial virulence via  
429 triggering the differential expression of a lot of key genes involved in the  
430 phenylacetate catabolism pathway. The selected genes (*paaG*, *paaH*, *paaJ*, *paaK2*,  
431 *paaX*,*paaY* and *paaI*) encode proteins in the PAA catabolic pathway that may  
432 contribute to virulence.  
433 *abal* is a protein that synthesized acyl-homoserine lactones (AHLs), *abaR* is a LuxR  
434 homolog transcription factor/receptor for AHLs (42). In this study, only WT strain was  
435 observed to produce AHLs based on *A. tumefaciens* KYC55 reporter strains, while the  
436 green pigment was not observed in  $\Delta abal$ ,  $\Delta abaR$  and  $\Delta abaR$  mutants. No purple  
437 pigment was observed in all strains based on *C. violaceum* CV026. In previous study,  
438 the absence of purple pigment may be attributed to low rate of the production of  
439 short chains homoserine lactone and fast degradation in the strains (43). Our  
440 transcriptomic analysis results revealed that deletion of *abaR* leads to the significant

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

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

458 **MATERIALS AND METHODS**

459 **Bacterial strains, plasmids and culture conditions**

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

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

464 **Strain construction**

465 Strains  $\Delta abal$ ,  $\Delta abaR$ ,  $\Delta abalR$  were unmarked deletion mutants created by a previous

466 described method for acquiring marker-less deletions in *A. baumannii* with minor

467 modifications (45). The primers used in this study are listed in Table 2. Briefly, the

468 upstream and downstream homologous arms of the target gene were amplified and

469 fused and then ligated into a tellurite-resistant suicide vector with the T4 ligase,

470 pMO130-Tel<sup>R</sup> (a generous gift from Addgene). The plasmid constructs were first

471 introduced into *Escherichia coli* DH5 $\alpha$  and subsequently selected on LB agar

472 containing 30  $\mu$ g/mL kanamycin. The kanamycin resistant colonies which carry a

473 insertion of pMO130-Tel<sup>R</sup> and a 2 kb amplimer corresponding to the size of the

474 ligated upstream and downstream homologous arms of the target gene were tested

475 by the corresponding designed primers. The resulting plasmids were used to

476 transform into *E.coli* S17-1 and subsequently conjugate into *A. baumannii* ATCC

477 17978 via biparental conjugation. Exconjugants were selected on LB containing 30

478  $\mu$ g/mL tellurite and 25  $\mu$ g/mL ampicillin. *A. baumannii* ATCC17978 harboring the

479 inserted pMO130-Tel<sup>R</sup>-Gene-(Up/Down) construct was cultured in LB broth

480 containing 10% sucrose and passaged seven days to select for stabilized deletion of

481 gene and loss of the *sacB* gene by a second cross-over and allelic replacement. If the

482 target gene has been deleted, PCR of genomic DNA from these bacteria would not

483 produce any amplimer using a primer pair that anneals to the DNA that has been

484 deleted. Mutants were complemented with the pME $abal$  and pME $abaR$  plasmids,

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

490 **Growth curve measurement**

491 A single colony of strain was inoculated into 2 ml of LB broth, and cultured with  
492 shaking (200 rpm) overnight at 37°C. The bacteria were collected by centrifugation at  
493 4000rpm for 5min and suspended in sterile saline to turbidity comparable to a 0.5  
494 McFarland standard. 20 µL was pipetted into a 96-well microtiter plate containing  
495 180 µL of LB broth and incubated at 37°C. The OD<sub>600</sub> of cultures was measured at  
496 hourly intervals for up to 48 h to draw the growth curve. Tests were performed on  
497 eight individual biological replicates, in triplicates.

498 **Transmission electron microscopy (TEM)**

499 Bacterial cells (OD450nm of 1.0) for SEM observation were harvested by  
500 centrifugation and washed three times with ddH<sub>2</sub>O. Bacteria were prefixed with 2.5%  
501 glutaraldehyde in 0.1 M phosphate buffer (pH 7.4). Images were captured at 120 kv  
502 with a HITACHI H-7650 TEM.

503 **Antimicrobial susceptibility**

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

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

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

513 *A. baumannii* can produce AHLs signal molecules with different chain lengths (43), it  
514 is essential to use biosensors that detect a broad range of AHLs. *C. violaceum* CV026  
515 specific for short-chain AHLs (C4-C6 AHL molecules) and *A. tumefaciens* KYC55  
516 specific for long-chain AHLs (C8-C14 AHL molecules) were utilized for screening AHLs  
517 producing bacterial strains. By the presence of short-chain AHLs, CV026 produces  
518 purple pigments. By the presence of long-chain AHLs, a green color is observed for *A.*  
519 *tumefaciens* KYC55 (43). Screening of the *A. baumannii* for production AHLs was  
520 carried out by agar plate diffusion assay with minor modifications (43, 47). Briefly, QS  
521 reporter strains were cultured in LB agar plates containing the antibiotics kanamycin  
522 20 µg/mL for *C. violaceum* CV026, spectinomycin 50 µg/mL and tetracycline 4.5  
523 µg/mL for *A. tumefaciens* KYC55. The plates were incubated at 28 °C for 24 h. 40  
524 µg/mL of X-gal as a visualizing agent was incorporated into LB medium used for *A.*  
525 *tumefaciens* KYC55. For determining the production of Acyl homoserine signal  
526 molecules, *A. baumannii* and mutants and biosensor *C. violaceum* CV026 and *A.*  
527 *tumefaciens* KYC55 strain were inoculated side by side in a way that they had a 0.5  
528 cm gap between them. *C. violaceum* CV026 and *A. tumefaciens* KYC55 were assessed

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

530 **Surface motility assay**

531 The motility test was performed according to the method as described previously

532 with minor modifications (19). Briefly, the media used for surface motility assay was

533 tryptone broth [10 g/liter tryptone (OXOID) and 5 g/liter NaCl] supplemented with

534 0.3% (wt/vol) Noble agar (BD). Plates were prepared and inoculated with bacteria

535 from an overnight culture in LB agar (1.5%, wt/vol) plates at 37°C with a sterile

536 toothpick. All assays were carried out in triplicate in a minimum of three

537 independent experiments. After incubation at 30°C for 12–14 h, the zone of motility

538 at the agar/Petri dish interface was observed.

539 **Crystal violet biofilm assay**

540 The biofilm forming ability test was performed in accordance with the method as

541 described previously with minor modifications (48). Briefly, a few single colonies

542 were suspended in sterile saline to turbidity comparable to a 0.5 McFarland

543 standard. The suspension was under vortex movement for 1 min; 20 µL was pipetted

544 into a 96-well microtiter plate containing 180 µL of LB broth and incubated for 24 h at

545 37°C. For crystal violet staining, the wells were rinsed with PBS to exclude loosely

546 adherent cells and then stained for 30 min with 200 µL of 1% crystal violet. The wells

547 were then rinsed with water and dried at room temperature. The amount of biofilm

548 was quantitated by destaining the wells with 200 µL of 33% acetic acid and then

549 measuring the optical density (OD) of the solution in a microplate

550 spectrophotometer set at 595 nm. Tests were performed on ten individual biological

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

554 **Serum bactericidal assay**

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

564 **Virulence in *Galleria mellonella***

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

573 **Murine model of pneumonia**

574 8-10 week old BALB/C mice were obtained from Jilin University. Mice were kept in a  
575 sterile environment at Jilin University and maintained according to standard  
576 procedures. All research was conducted in complying with the institutional  
577 guidelines. The principles in the ARRIVE guidelines and the Basel declaration  
578 (<http://www.basel.declaration.org>) have been considered when planning the  
579 experiments. Models of pulmonary infection were performed as previously described  
580 (35). Briefly, infections were initiated by intraperitoneal injection of approximately  
581  $1.2 \times 10^8$  CFU of bacteria suspended in 100  $\mu$ l of PBS into groups of mice (10 mice per  
582 group for survival studies; 5 per group for analyses of bacterial counts).

583 **Quantitative bacteriology**

584 To assess bacterial burden, the lung and spleen were aseptically operated and  
585 homogenized in 1 ml sterile of PBS using tissue homogenizers. 100  $\mu$ l of the  
586 homogenates were cultured on Brain Heart Infusion agar plates to quantify the  
587 bacterial load of *A. baumannii* in the respective organs. **RNA sequencing and**  
588 **analysis**

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

595 than 1 or less than -1 and P value (P-adj) was less than 0.05 in mutant strain  
596 compared to WT strain. Cluster of orthologous groups (COG) enrichment analysis was  
597 performed by dividing the percentage of genes up- or down-regulated for each  
598 category by the percentage of genes in that category across the whole genome (17,  
599 51). Multiexperiment Viewer- version 4.9.0 was used to perform hierarchical  
600 clustering and heat map visualization(52). Gene Ontology (GO) and Kyoto  
601 Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis, based on  
602 R software, were applied for the identification of pathways in which DEGs  
603 significantly enriched. The GO and KEGG pathway analysis of the DEGs was  
604 conducted through the ClusterProfiler package in R software (53). A P-value of <0.05  
605 was considered to have statistical significance and to achieve significant enrichment.  
606 qRT-PCR was performed on the 7300 Plus Real-Time PCR System (Applied  
607 Biosystems) using a standard protocol from the FastStart Universal SYBR Green  
608 Master (Roche, Basel, Switzerland). Gene expression levels were quantified by using  
609 the  $2^{-\Delta\Delta Ct}$  method with endogenous controls (16S). The Primers used for qRT-PCR  
610 assays are described in Table 3. All qRT-PCR assays were repeated 3x. The RNA-Seq  
611 data obtained in this study was submitted to Sequence Read Archive (SRA),  
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788 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)

$\Delta abal$	WT with deletion in <i>abal</i> gene	This study
$\Delta abaR$	WT with deletion in <i>abaR</i> gene	This study
$\Delta abalR$	WT with deletion in <i>abal</i> and <i>abaR</i> genes	This study
$\Delta abal$ (pMEaba	$\Delta abal$ harboring pME6032, containing the <i>abal</i>	This study
I)	gene	
$\Delta abaR$ (pMEab	$\Delta abaR$ harboring pME6032, containing the	This study
<i>aR</i> )	<i>abaR</i> gene	
WT(pME6032)	WT harboring pME6032, empty vector	This study
WT(pMEabal)	WT harboring pME6032, containing the <i>abal</i>	This study
	gene	
WT(pMEabaR)	WT harboring pME6032, containing the <i>abaR</i>	This study
	gene	

*E.coli* strains

DH5 $\alpha$	F- $\phi$ 80/ <i>lacZ</i> $\Delta$ M15 $\Delta$ ( <i>lacZYA-argF</i> ) U169 A1	Transgen
	<i>recA1 hsdR17(rk-,mk+)supE44λ-thi-1 gyrA96</i>	
	<i>relA1 phoA</i>	
S17-	Genotype: <i>recA pro hsdR RP4-2-Tc::Mu-1(ATCC47055) Km::Tn7,Gm<sup>S</sup></i>	Biobw

*Chromobacterium violaceum*

CV026	Detection of C4- and C6-HSLs	MingshengDong
	<i>Agrobacterium tumefaciens</i>	

---

KYC55(pJZ372)	Detection of broad range of AHLs	MingyongZeng
(pJZ384)(pJZ41		
0)		
R10(pCF218) <i>Ptet-traR, Tc<sup>R</sup>, high AHL production strain</i>		
		MingyongZeng
Plasmids		
pMO130-Tel <sup>R</sup>	Suicide plasmid, <i>xy/E<sup>+</sup>, sacB<sup>+</sup>, Km<sup>R</sup></i>	Addgene
pMO130-Tel <sup>R-</sup>	pMO130-Tel <sup>R</sup> containing a 1 kb UP fragment	This study
<i>abaI-</i>	( <i>abaI</i> ) and 1 kb DOWN fragment ( <i>abaI</i> )	
(Up/Down)		
pMO130-Tel <sup>R-</sup>	pMO130-Tel <sup>R</sup> containing a 1 kb UP fragment	This study
<i>abaR-</i>	( <i>abaR</i> ) and 1 kb DOWN fragment ( <i>abaR</i> )	
(Up/Down)		
pME6032	shuttle plasmid for genetic complementation,	Ke Lei Biological
	<i>Tc<sup>R</sup></i>	Technology
		Co.,Ltd
pME <i>abaI</i>	pME6032 containing the <i>abaI</i> gene (promoter	This study
	and coding region)	
pME <i>abaR</i>	pME6032 containing the <i>abaR</i> gene (promoter	This study
	and coding region)	

---

789 Table 2 Primer used in this study

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

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<i>abaR</i> (BamHI)up-R	GCTGGATCCCGATAAGAGACCACTAACCT	
<i>abaR</i> (BamHI)dw-F	TATGGATCCTTGAAGCGTAGGTCTAATCT	1136bp
<i>abaR</i> (PstI)dw-R	TATCTGCAGAAGGCGGTAAGTAAAGAA	
<i>abal</i> (PstI)dw-F	TATCTGCAGCGCAACTACAGCCACT	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	CCGGAATTCCGGGTGGAAGCACTTGTAAATGAA	654bp
<i>abal</i> (Xhol)-R	CCGCTCGAGCGGCTCATTTGCTCGTCATA	
<i>abaR</i> (EcoRI)-F	CCGGAATTCCGGCTACAAAGCCCTAGCATT	808bp
<i>abaR</i> (Xhol)-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	TTGGCGTAACCTCACTT
AUO97_RS08710-F	ATGCCGAGTTGCTTA

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AU097_RS08710-R	AACACGCTGTGAATCTTT
AU097_RS13835-F	CGGTGCTTGATGTGCT
AU097_RS13835-R	AAATGCGATAACGTGGA
AU097_RS17125-F	GTCTACGCCGCTCTGT
AU097_RS17125-R	AGGTTATTGAAGGTGGG
AU097_RS17130-F	CCACATACGCCTTGCT
AU097_RS17130-R	CCTCGGGAGATTCAATT
AU097_RS17135-F	TTTTGGGCATACTGACTTT
AU097_RS17135-R	CTTCTGGACTCGGTAATGT
AU097_RS17140-F	CCTTTGGTGCCGTAGA
AU097_RS17140-R	ACCCGAACCTCACAGAC
AU097_RS17145-F	GCGTTCCCAAGCCTCA
AU097_RS17145-R	CTCGGTGATTACGATGGATG
AU097_RS17160-F	CACCCAACCCACTGAA
AU097_RS17160-R	AGCGTATGTGAGCCAAG
16S_qF	CAGCTCGTGTGAGATGT
16S_qR	CGTAAGGGCCATGATGACTT

---

791 Table 4 MICs of antibiotics used in this study

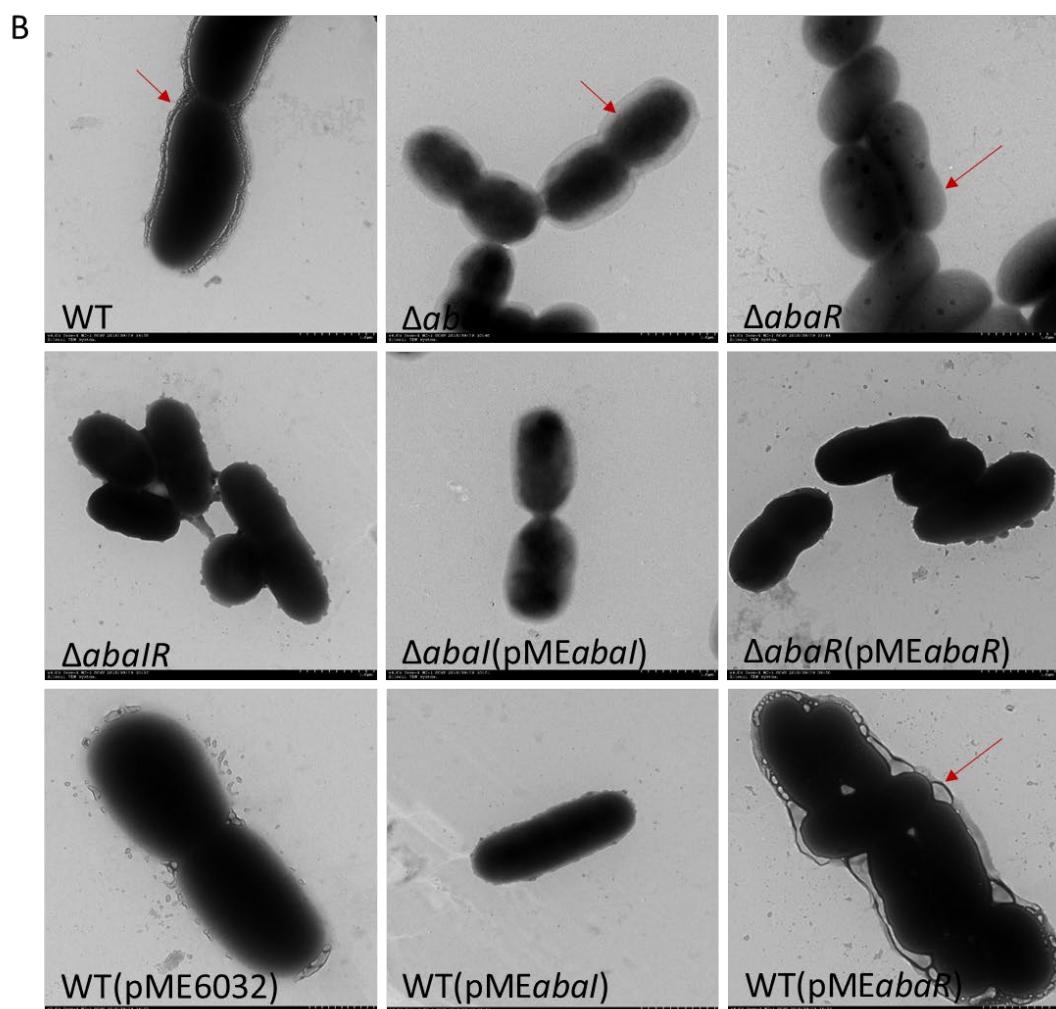
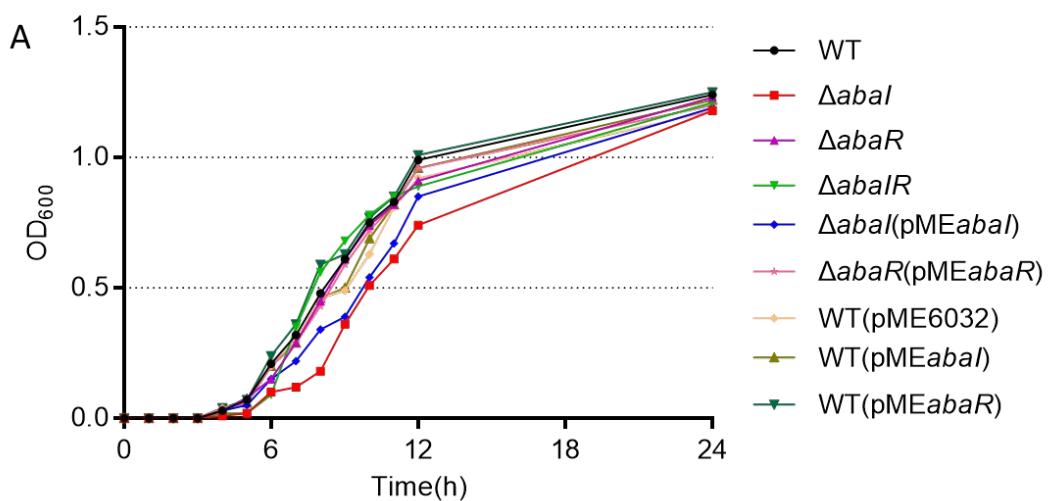
Antibiotic	MIC(µg/ml)									
	$\Delta a$		$\Delta a$		$\Delta a$		$\Delta a$		$\Delta a$	
	$\Delta a$	$ba$	$bal$	$\Delta abal(p)$	$\Delta abar(p)$	WT(pM)	WT(	WT(	WT(	WT(
	WT	<i>bal</i>	R	R	ME <i>abal</i> )	ME <i>abar</i> )	E6032)	pME	pME	

								<i>ab</i> al	<i>ab</i> a
								)	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

Spectinomycin

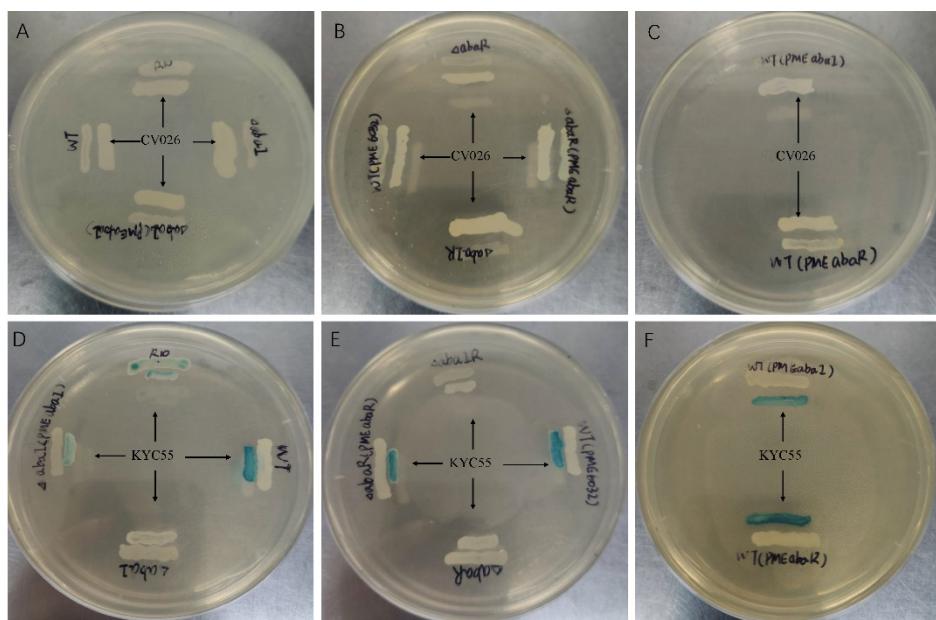
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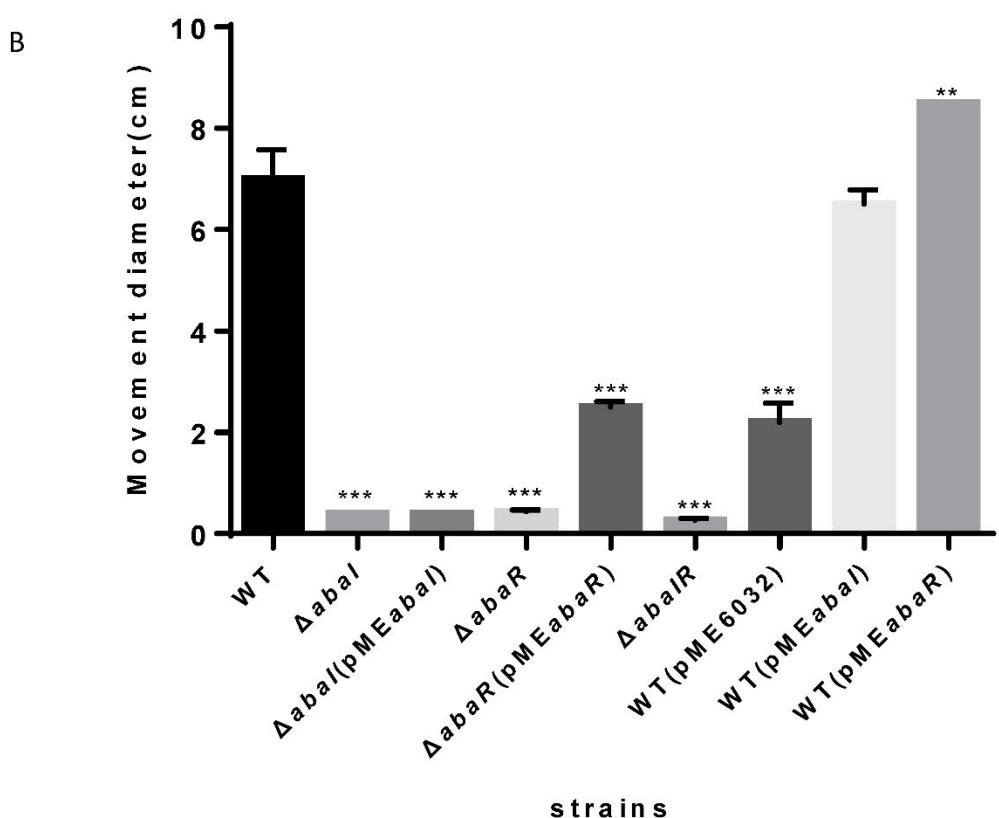
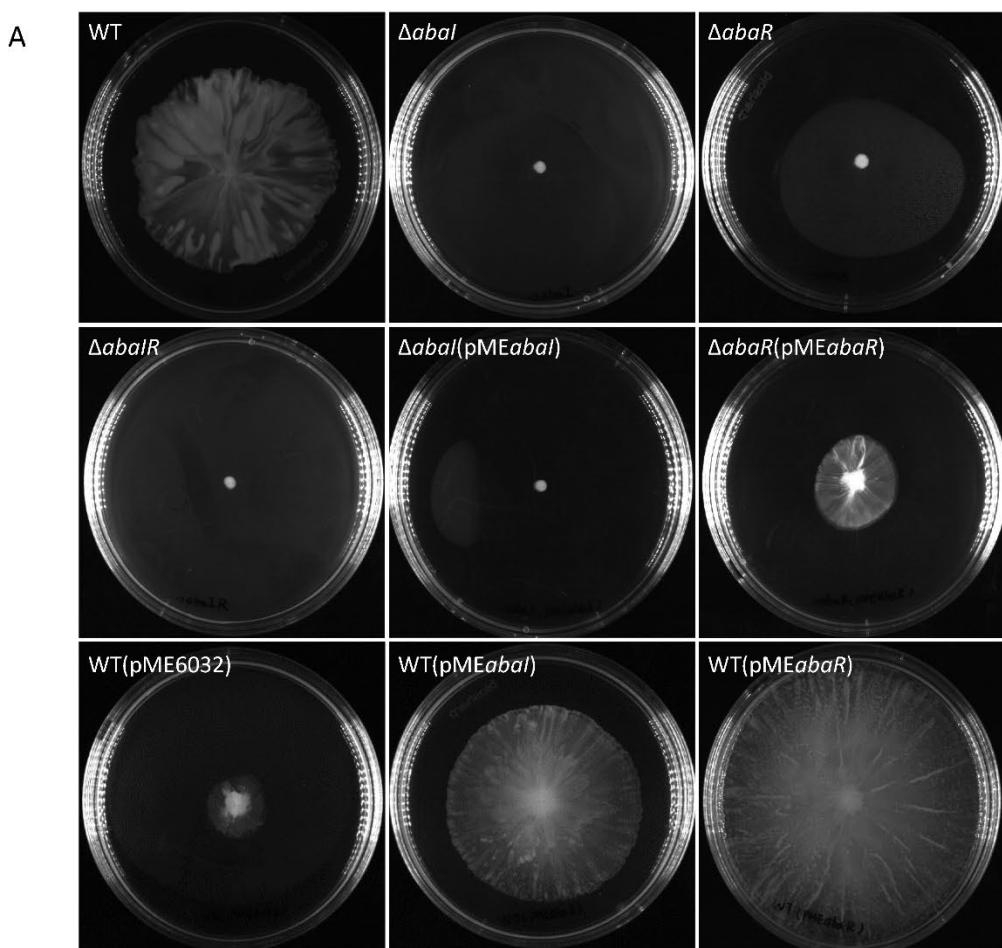
793

794 **Figure 1.** A) Growth curve analysis of *A.baumannii* and mutants in broth. B)  
795 Transmission electron microscope images of the targeted bacteria. Cells were  
796 observed with a HITACHI H-7650 TEM transmission electron microscope operated at  
797 120 kv. Scale bar = 500 nm.

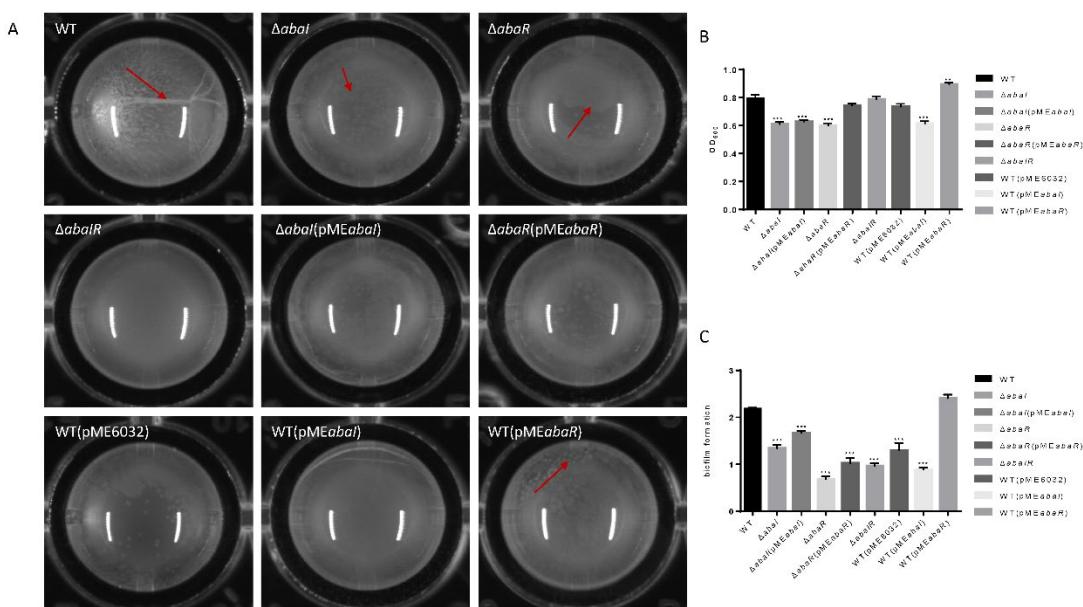


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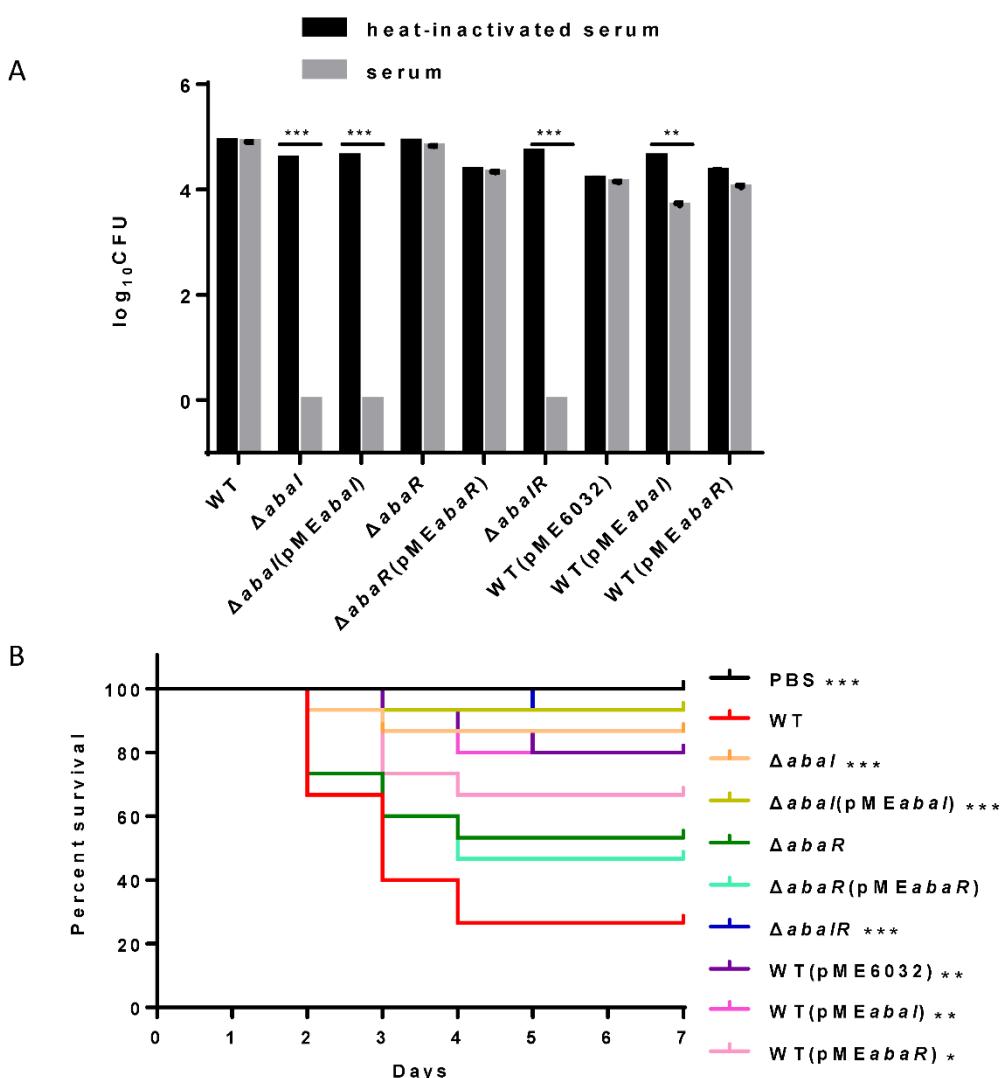
799 **Figure 2.** Screening of WT and mutants for AHLs production using agar-plate well  
800 diffusion assay with *C. violaceum* CV026 and *A. tumefaciens* KYC55 reporter strain.



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



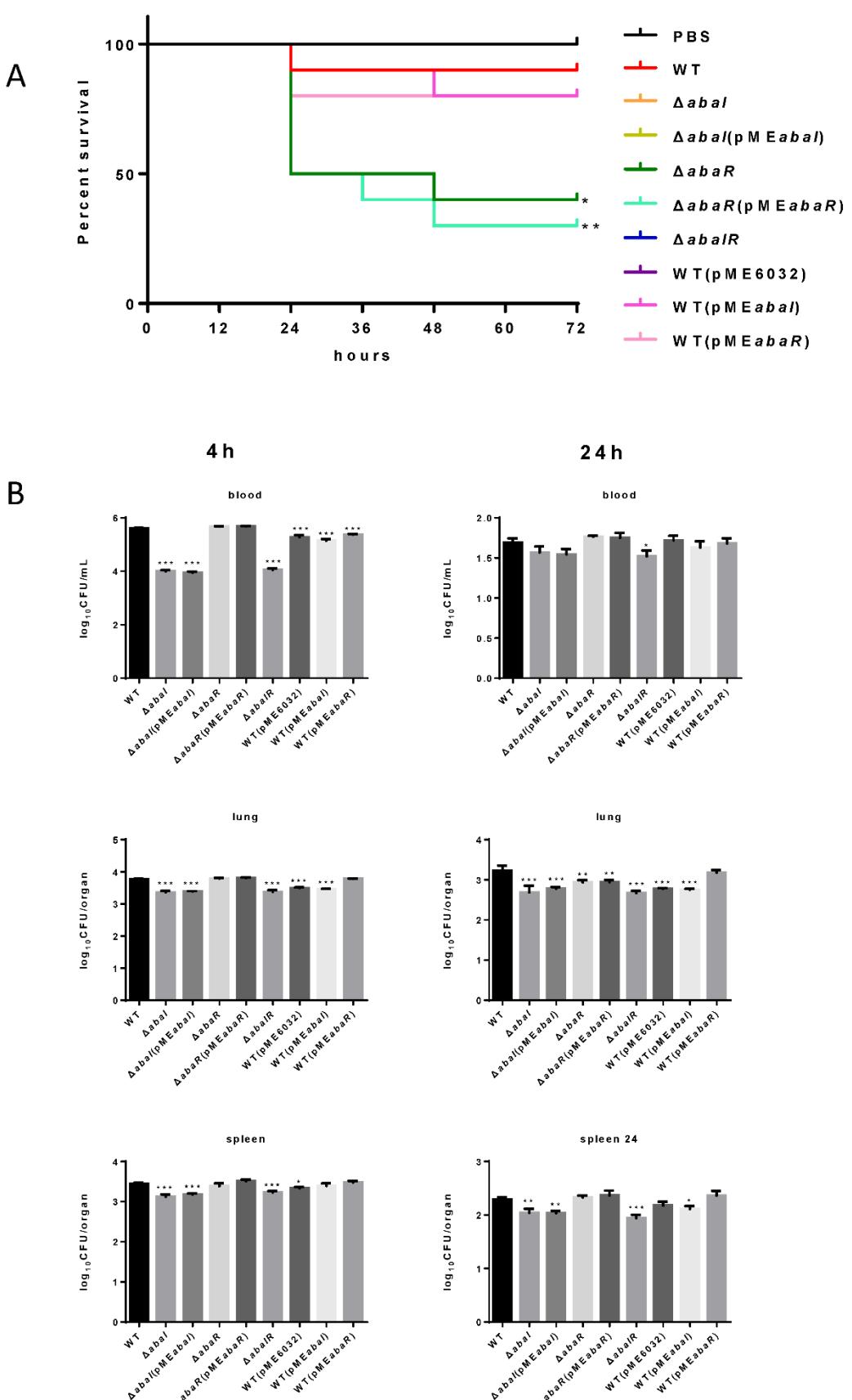
807 **Figure 4. A)** Visual changes in biofilm formation in 96-well plates for 24 h at 37°C,  
808 images were taken after 24 of growth. B) The absorbance of bacterial solution was  
809 detected by OD595. C) Biofilm formation on plastic at 37°C as determined by crystal  
810 violet staining. Markers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



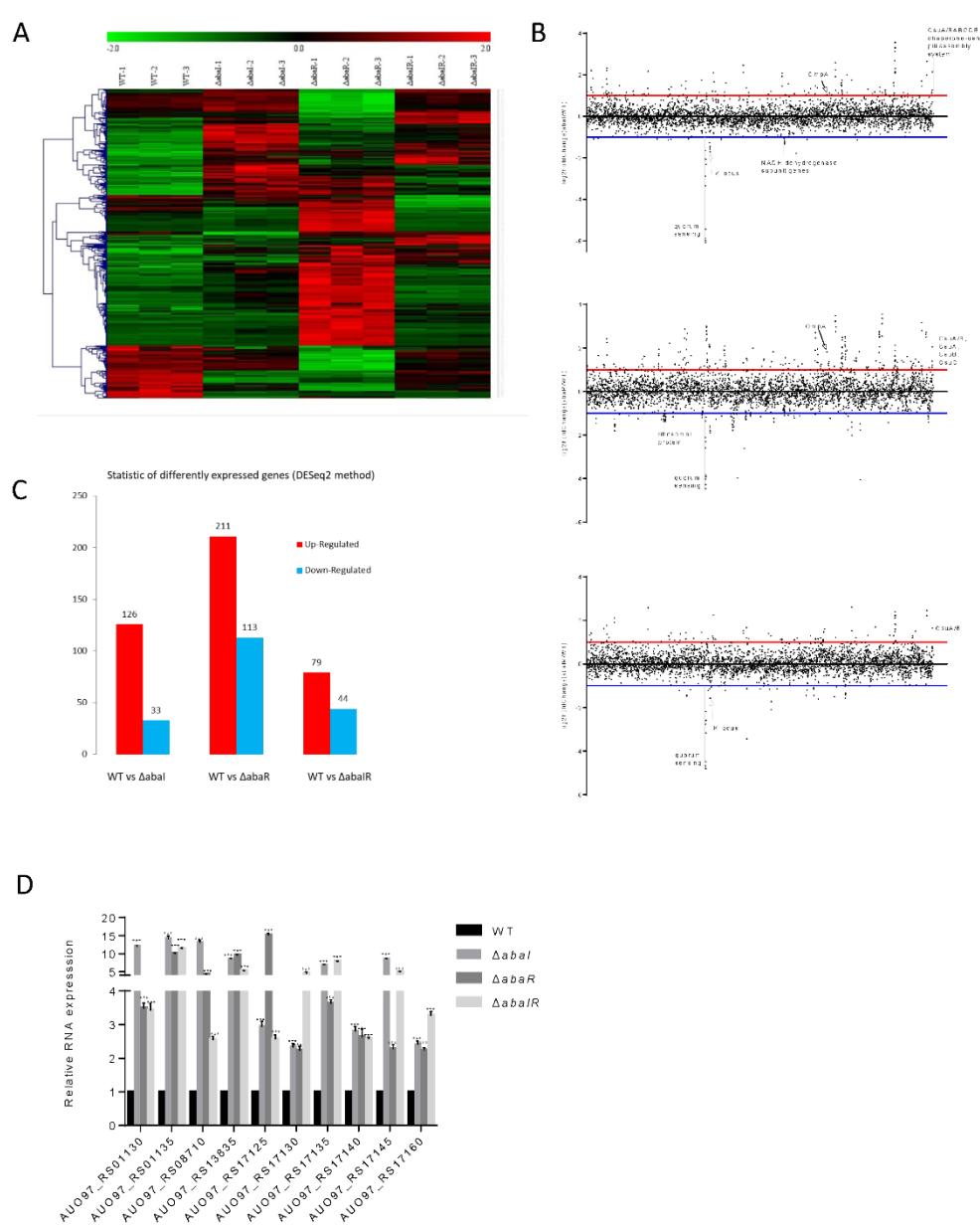
813

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

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

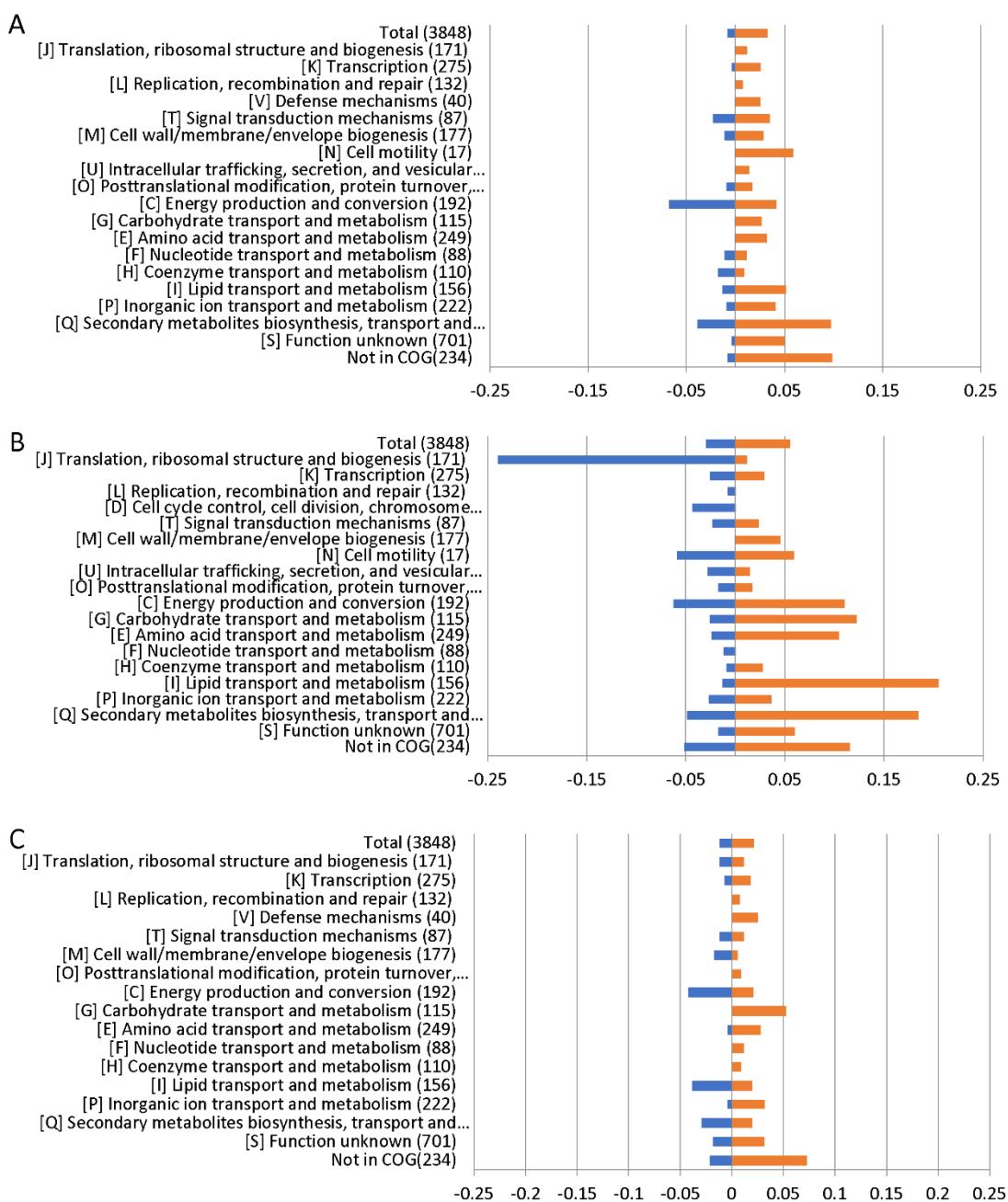


824 **Figure 6.** A) Kaplan-Meier survival curve of mouse inoculated with strains at a dose  
825 of  $1.2 \times 10^8$  CFUs (n=10). Survival curves were compared using the log-rank (Mantel-  
826 Cox) test, \*p < 0.05. B) *A. baumannii* bacterial burdens in the lungs, spleen, and  
827 blood. Bacterial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



830  
831 **Figure 7.** A) Heat map representation and hierarchical clustering of gene expression

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



848

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

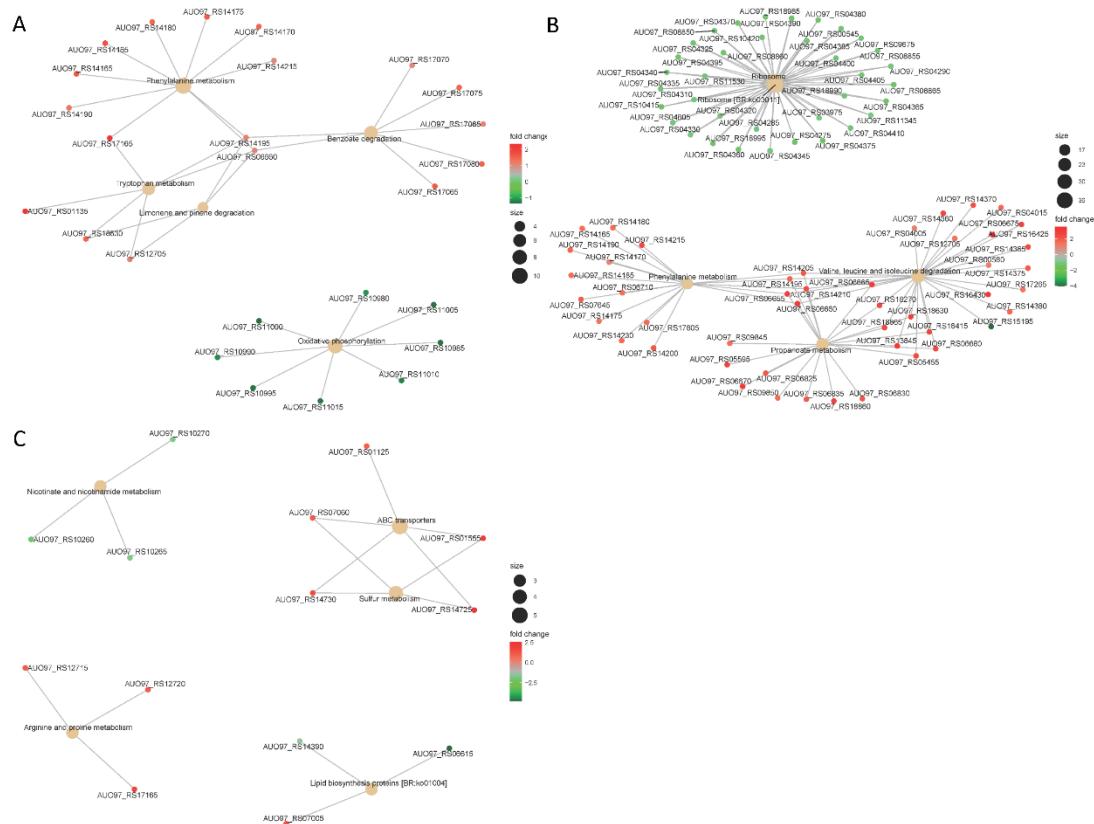


854

855

856 **Figure 9.** A) Top 30 of GO enrichment of DEGs in  $\Delta abai$ . The shape of the point  
857 indicates the different ontology. The enrichment q value of each GO term was  
858 normalized as negative  $\log_{10}(q$  value) and is shown as a color gradient. The number  
859 of genes enriched in each GO term is represented by the size of the points. B) The  
860 significantly enriched KEGG pathway of DEGs in  $\Delta abai$ . The enrichment P adjustvalue  
861 of each pathway was shown as a color gradient. GeneRatio, number of differentially  
862 expressed genes/total number of genes in this KEGG pathway. The number of genes

863 enriched in each pathway is represented by the size of the points. C) Top 30 of GO  
864 enrichment of DEGs in  $\Delta abaR$ . The shape of the point indicates the different  
865 ontology. The enrichment q value of each GO term was normalized as negative  
866  $\log_{10}(q \text{ value})$  and is shown as a color gradient. The number of genes enriched in  
867 each GO term is represented by the size of the points. D) The significantly enriched  
868 KEGG pathway of DEGs in  $\Delta abaR$ . The enrichment P adjustvalue of each pathway was  
869 shown as a color gradient. GeneRatio, number of differentially expressed genes/total  
870 number of genes in this KEGG pathway. The number of genes enriched in each  
871 pathway is represented by the size of the points. E) Top 30 of GO enrichment of DEGs  
872 in  $\Delta abalR$ . The shape of the point indicates the different ontology. The enrichment q  
873 value of each GO term was normalized as negative  $\log_{10}(q \text{ value})$  and is shown as a  
874 color gradient. The number of genes enriched in each GO term is represented by the  
875 size of the points. F) The significantly enriched KEGG pathway of DEGs in  $\Delta abalR$ . The  
876 enrichment P adjustvalue of each pathway was shown as a color gradient. GeneRatio,  
877 number of differentially expressed genes/total number of genes in this KEGG  
878 pathway. The number of genes enriched in each pathway is represented by the size  
879 of the points.



880

881 **Figure 10.** A) The top 5 of significantly enriched KEGG pathway of DEGs in *ΔabaI*.

882 The size of the nodes shows the number of genes enriched in each pathway. The  
 883 color gradient shows log2-fold change of gene expression. B) The top 5 of  
 884 significantly enriched KEGG pathway of DEGs in *ΔabaR*. The size of the nodes shows  
 885 the number of genes enriched in each pathway. The color gradient shows log2-fold  
 886 change of gene expression. C) The top 5 of significantly enriched KEGG pathway of  
 887 DEGs in *ΔabaIR*. The size of the nodes shows the number of genes enriched in each  
 888 pathway. The color gradient shows log2-fold change of gene expression.

889 **Supplemental Material**

890 Table 5 Differential expressed genes in *ΔabaI* strain

GeneID	log2FoldChange( $\Delta$ )	Up-Down-	Pvalu	Product
	<i>abai</i> /WT)	Regulation( $\Delta ab$	e	
		<i>ai</i> /WT)		
AU097_RS	-6.0744	Down	0	acyl-CoA
06625				dehydrogenase
AU097_RS	-5.9747	Down	0	non-ribosomal
06615				peptide synthetase
AU097_RS	-5.88657	Down	0	outer membrane
06610				lipoprotein-sorting
				protein
AU097_RS	-5.44259	Down	0	acyl-CoA synthetase
06630				
AU097_RS	-3.3445	Down	1.1E-	hypothetical protein
06605			107	
AU097_RS	-2.88721	Down	4.97E-	alpha/beta
06600			78	hydrolase
AU097_RS	-2.30926	Down	1.64E-	GNAT family N-
06645			07	acetyltransferase
AU097_RS	-2.06687	Down	3.24E-	acyl carrier protein
06620			06	
AU097_RS	-1.78566	Down	1.77E-	hemerythrin
11650			32	

---

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

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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	

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AUO97_RS	-1.09799	Down	1.5E-	GGDEF domain-containing protein
03915			12	
AUO97_RS	-1.09371	Down	8.57E-	U32 family peptidase
00400			25	
AUO97_RS	-1.08569	Down	0.000	MBL fold metallo-hydrolase
05665			189	
AUO97_RS	-1.06889	Down	2.64E-	NADH-quinone oxidoreductase subunit NuoG
10980			57	
AUO97_RS	-1.06411	Down	1.08E-	efflux RND transporter
07485			09	periplasmic adaptor subunit
AUO97_RS	-1.02016	Down	7.07E-	DUF2147 domain-containing protein
05775			23	
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

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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-

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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	

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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

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				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

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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

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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

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				permease subunit
				PstC
AUO97_RS	1.246926	Up	2.2E-	phenylacetate-CoA
14190			06	oxygenase/reductase
				e subunit PaaK
AUO97_RS	1.253491	Up	1.81E-	allophanate
13840			20	hydrolase
AUO97_RS	1.264522	Up	4.69E-	PAAR domain-containing protein
16595			19	
AUO97_RS	1.274509	Up	0.000	SCPU domain-containing protein
19205			646	
AUO97_RS	1.27559	Up	4.91E-	molecular chaperone
19200			09	
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 protein
15625			06	
AUO97_RS	1.328101	Up	2.33E-	amino acid transporter
12450			19	
AUO97_RS	1.333536	Up	1.76E-	NADPH:quinone

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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

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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-	deoxyguanosinetriphosphohydrolase
01840			65	hosphate
				triphasphohydrolase
AUO97_RS	1.487037	Up	1.93E-	1,2-phenylacetyl-CoA epoxidase
14170			27	subunit A
AUO97_RS	1.493798	Up	1.05E-	hypothetical protein
05275			18	
AUO97_RS	1.496273	Up	1.16E-	3-oxoadipate CoA-transferase subunit A
17080			05	
AUO97_RS	1.534021	Up	1.12E-	1,2-phenylacetyl-CoA epoxidase
14175			19	subunit B
AUO97_RS	1.557012	Up	2.02E-	NAD-dependent

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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

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AUO97_RS	1.743263	Up	4E-17	taurine ABC transporter
14725				substrate-binding protein
AUO97_RS	1.744985	Up	1.2E-	MFS transporter
06395			73	
AUO97_RS	1.794527	Up	4.22E-	phosphonate ABC transporter
01125			35	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 protein
13830			13	
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-containing protein
10860			191	

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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

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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

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dioxygenase subunit

alpha

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

GenelID	log2FoldChange( $\Delta abaR/WT$ )	Up-Down-Regulation( $\Delta abaR/WT$ )	Pvalu	Product
AUO97_RS	-1.46697	Down	7.01E-97	elongation factor Ts
00540				
AUO97_RS	-1.23446	Down	6.5E-101	30S ribosomal protein S2
00545				
AUO97_RS	-1.25779	Down	7.5E-12	sulfate ABC transporter substrate-binding protein
01555				
AUO97_RS	-1.60798	Down	9.23E-07	alpha/beta hydrolase
01560				
AUO97_RS	-1.80619	Down	3.15E-14	sulfate ABC transporter permease
01565				subunit CysT
AUO97_RS	-1.51136	Down	1.53E-08	sulfate ABC transporter permease
01570				subunit CysW
AUO97_RS	-1.55706	Down	1.89E-01	sulfate ABC

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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-
03220			-08	containing protein
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

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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

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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

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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]	

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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 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

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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

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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

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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/antitermination 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	

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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

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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		

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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

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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	

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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]

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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

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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-	methylmalonate-
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

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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

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AUO97_RS	1.903493	Up	1.1E-	4-
07645			213	hydroxyphenylpyruvate 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-	fumarylacetoacetate
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	imidazolonepropionase
07715			-54	e
AUO97_RS	1.392517	Up	2.47E	formimidoylglutamase
07720			-69	
AUO97_RS	1.165672	Up	1.52E	DUF885 domain-containing protein
07725			-07	
AUO97_RS	1.186045	Up	2.89E	hypothetical protein
07745			-16	
AUO97_RS	1.313813	Up	3.7E-	TetR/AcrR family

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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

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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

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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	

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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 <sup>+</sup>
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

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13830			131	protein
AUO97_RS	3.473384	Up	8.5E-	DUF1445 domain-containing protein
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-containing protein
13845			213	containing protein
AUO97_RS	1.08262	Up	2.65E	DUF333 domain-containing protein
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

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					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	

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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	$\gamma$ lcrotonyl-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	

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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

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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

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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

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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

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				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	carboxymuconolactone	
				decarboxylase	
				[Acinetobacter]	
AUO97_RS	1.117003	Up	0.000	aromatic acid/H <sup>+</sup>	
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	

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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	

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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 CsxA
19210			104	
AUO97_RS	2.042194	Up	3.42E	SCPU domain-
19215			-59	containing protein

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892

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

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GenelID	log2FoldChange( $\Delta a$ <i>balR</i> /WT)	Up-Down- Regulation( $\Delta ab$ )	Pvalue	Product

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<i>alR</i> /WT)				
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

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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-

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				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	

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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-

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				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
				aminotransferas
				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				

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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-containing protein
01160				
AUO97_RS	1.022615214	Up	0.010216	hypothetical protein
14910				
AUO97_RS	1.027289495	Up	1.33E-12	DUF3108 domain-containing protein
04145				
AUO97_RS	1.027636888	Up	0.000313	DUF2184 domain-containing protein
13145				
AUO97_RS	1.050221533	Up	0.001537	transcriptional regulator
02595				
AUO97_RS	1.059975124	Up	0.000226	MFS transporter

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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	

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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
04620				family transporter
AUO97_RS	1.127777848	Up	0.001455	sulfonate ABC transporter
07060				substrate-binding protein
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
12860				family

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AUO97_RS	1.145856951	Up	1.85E-31	NADPH:quinone oxidoreductase
05515				
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 aminotransferase family protein
12715				
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

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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

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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

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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

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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

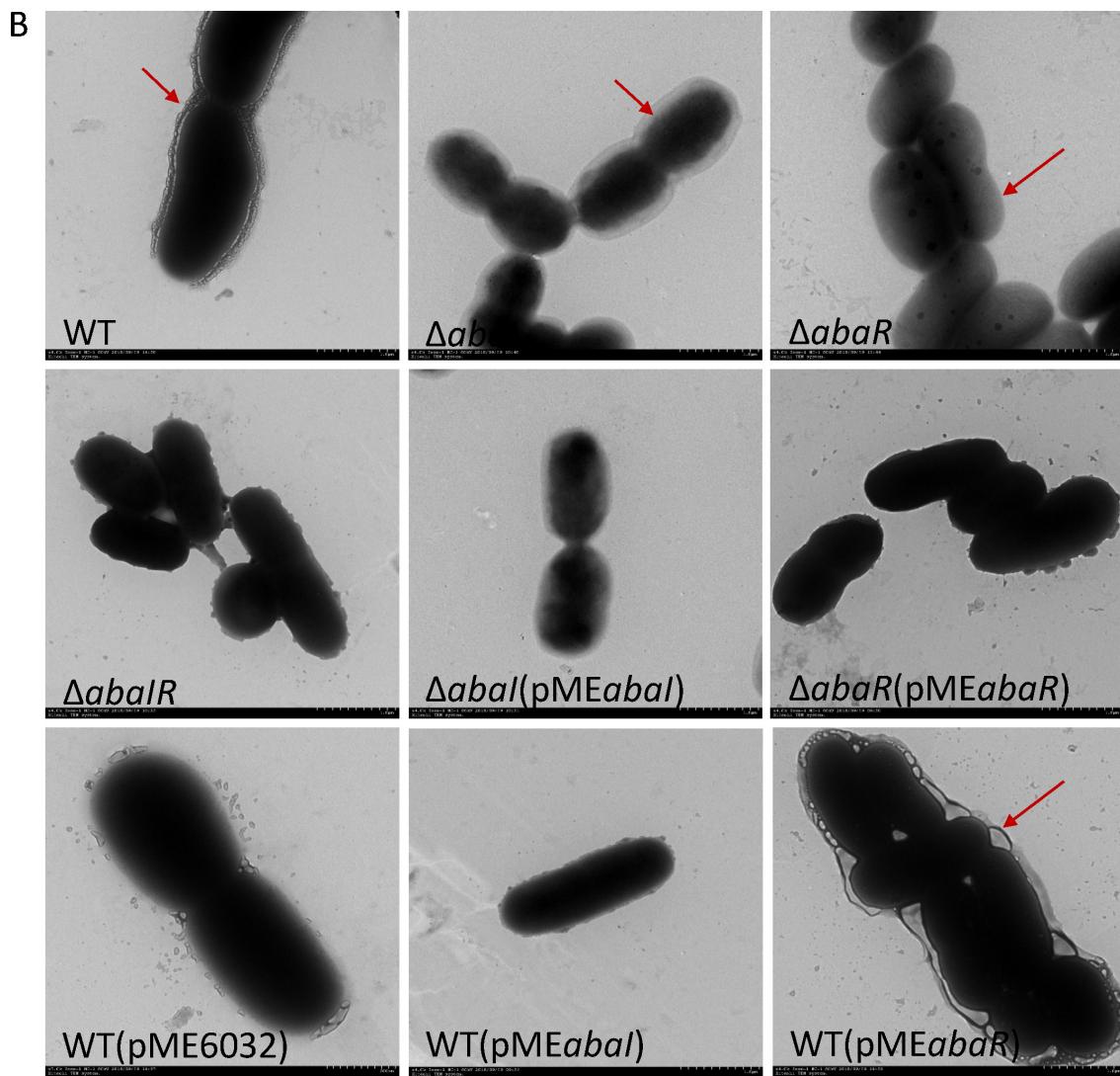
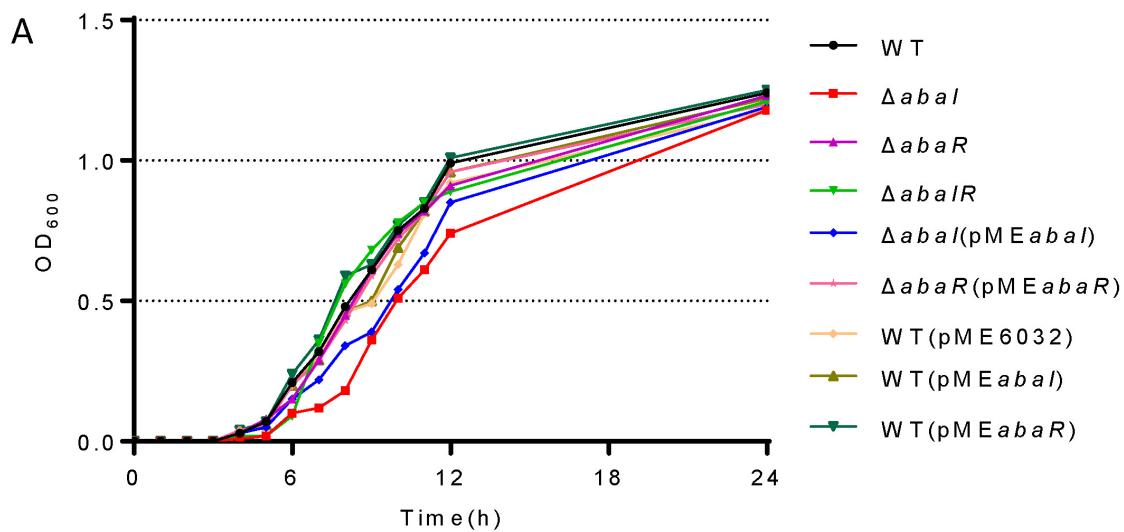
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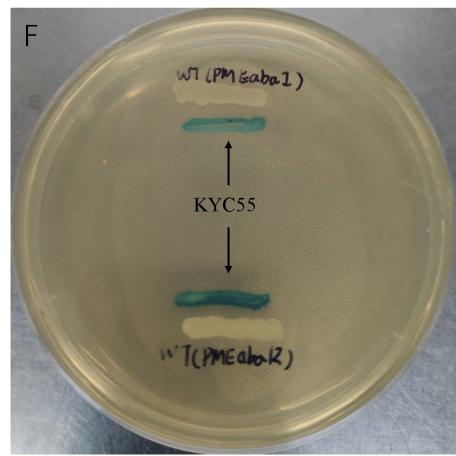
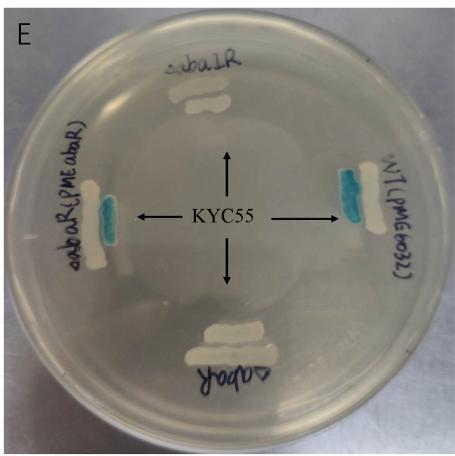
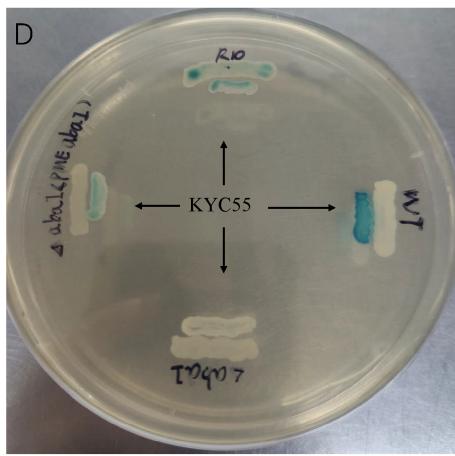
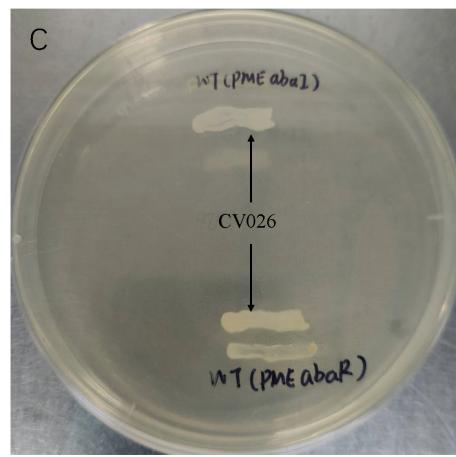
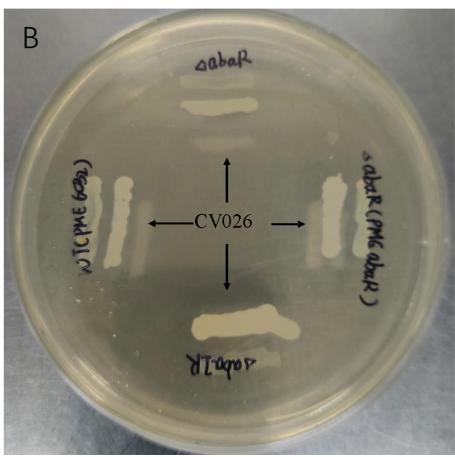
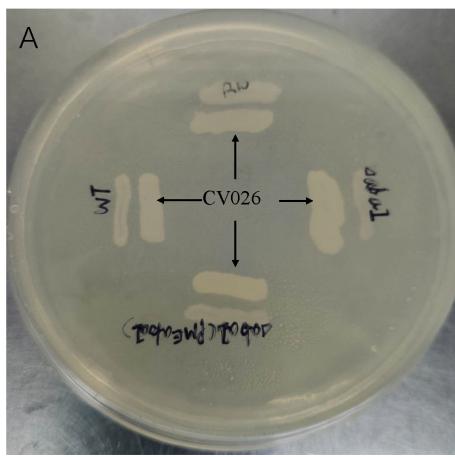
17165					
AUO97_RS	1.839119762	Up	2.78E-05	aromatic-ring-	
17140				hydroxylating	
				dioxygenase	
				subunit beta	
AUO97_RS	1.905157138	Up	5.15E-26	alpha/beta	
01560				hydrolase	
AUO97_RS	2.110174475	Up	2.41E-10	KR domain-	
17135				containing	
				protein	
AUO97_RS	2.113312655	Up	9.47E-77	sulfate 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	

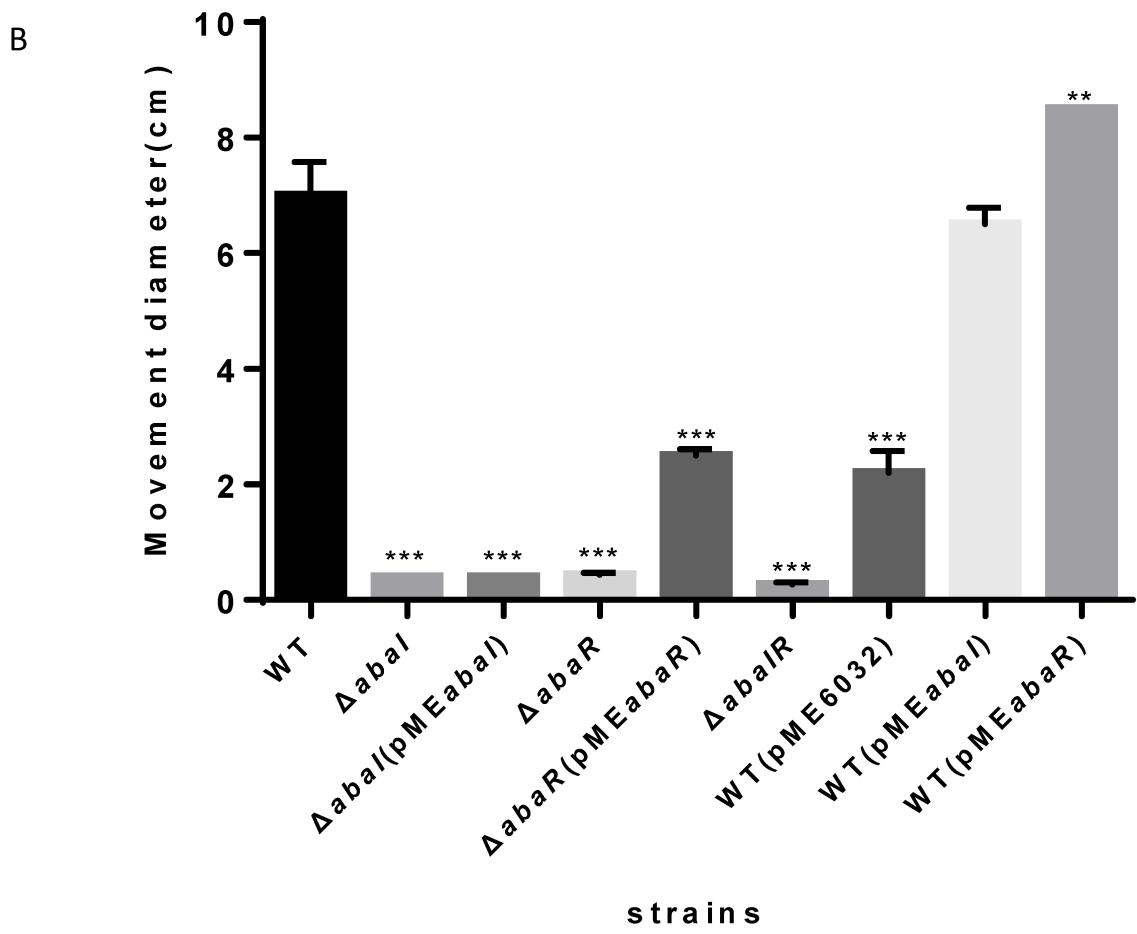
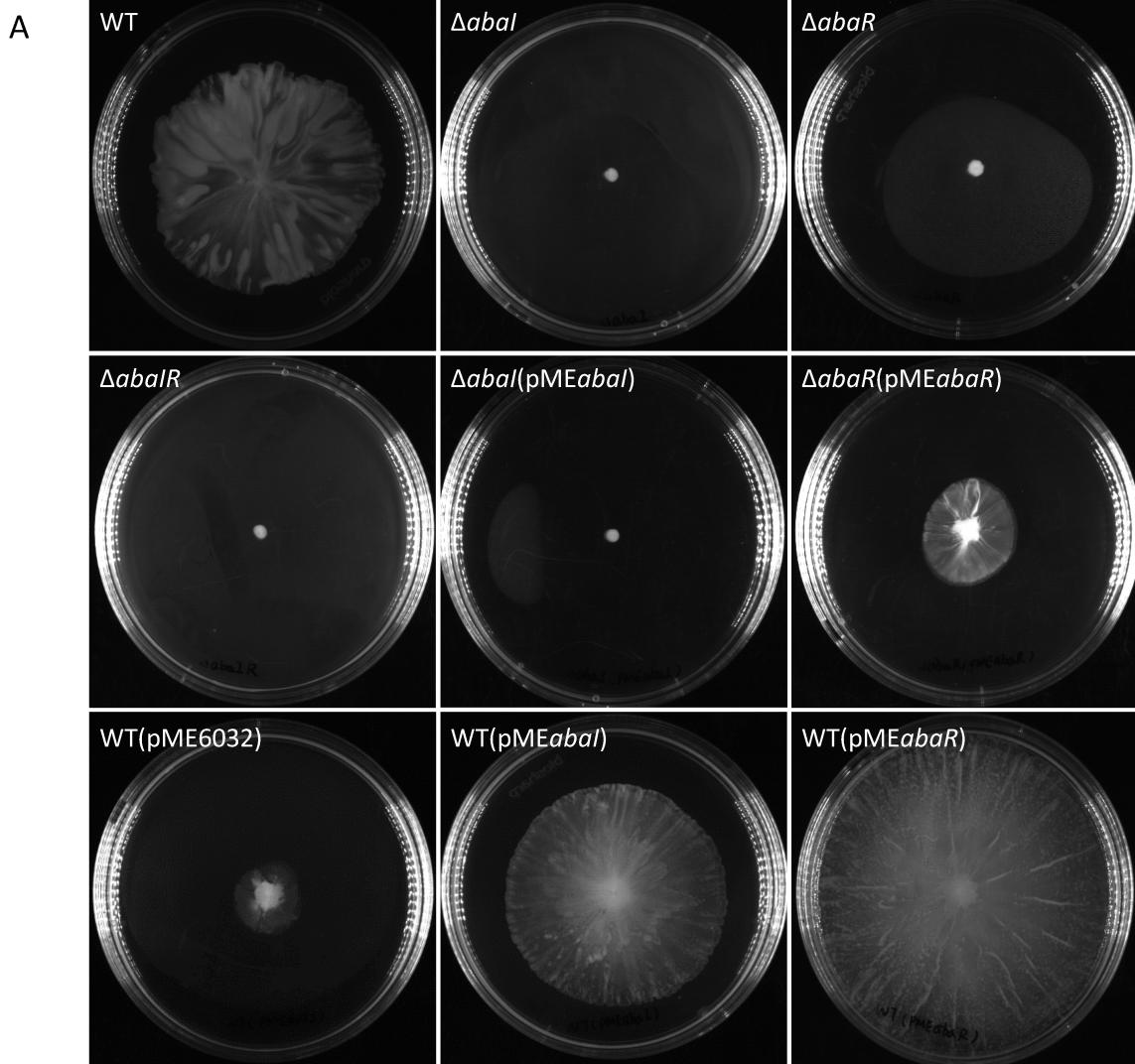
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AUO97_RS	2.394634424	Up	3.66E-18	aromatic ring-
17145				hydroxylating
				dioxygenase
				subunit alpha
AUO97_RS	2.455858156	Up	5.07E-14	hypothetical
18910				protein
AUO97_RS	2.581083497	Up	1.35E-17	hypothetical
03425				protein
AUO97_RS	2.601467607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

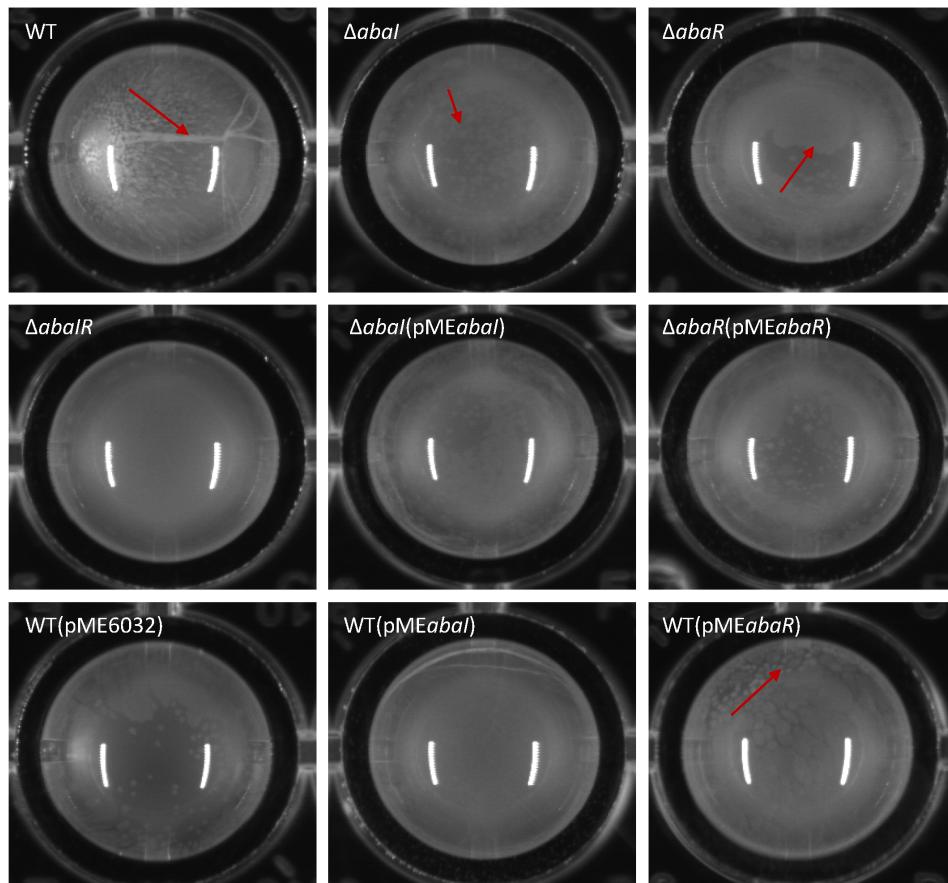
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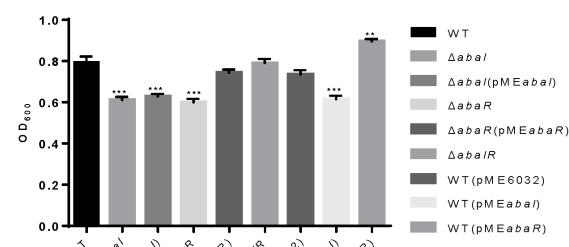




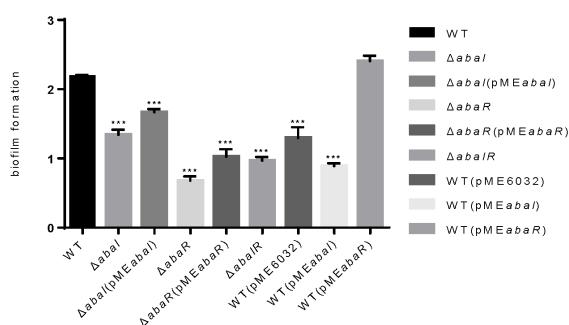
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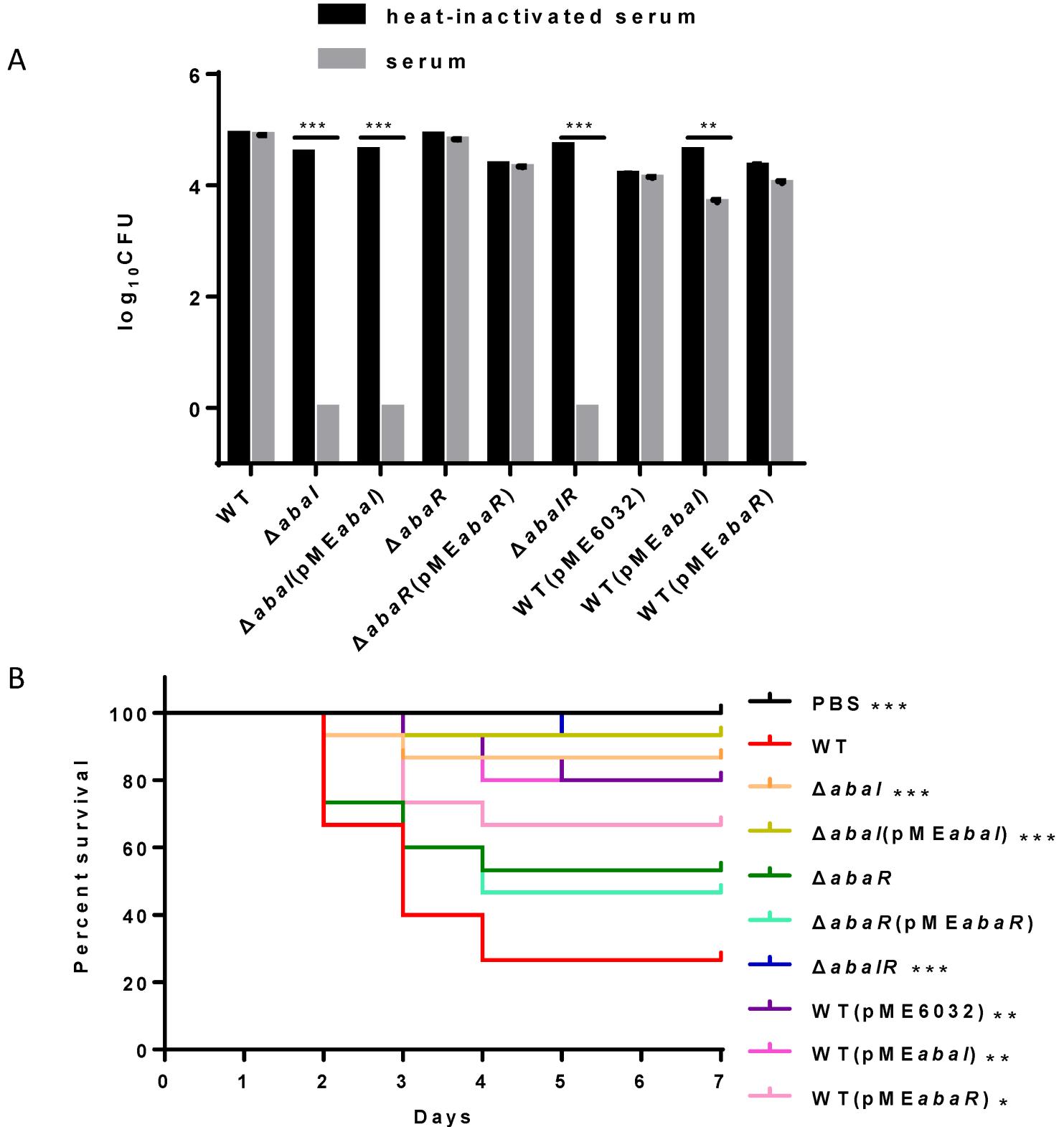


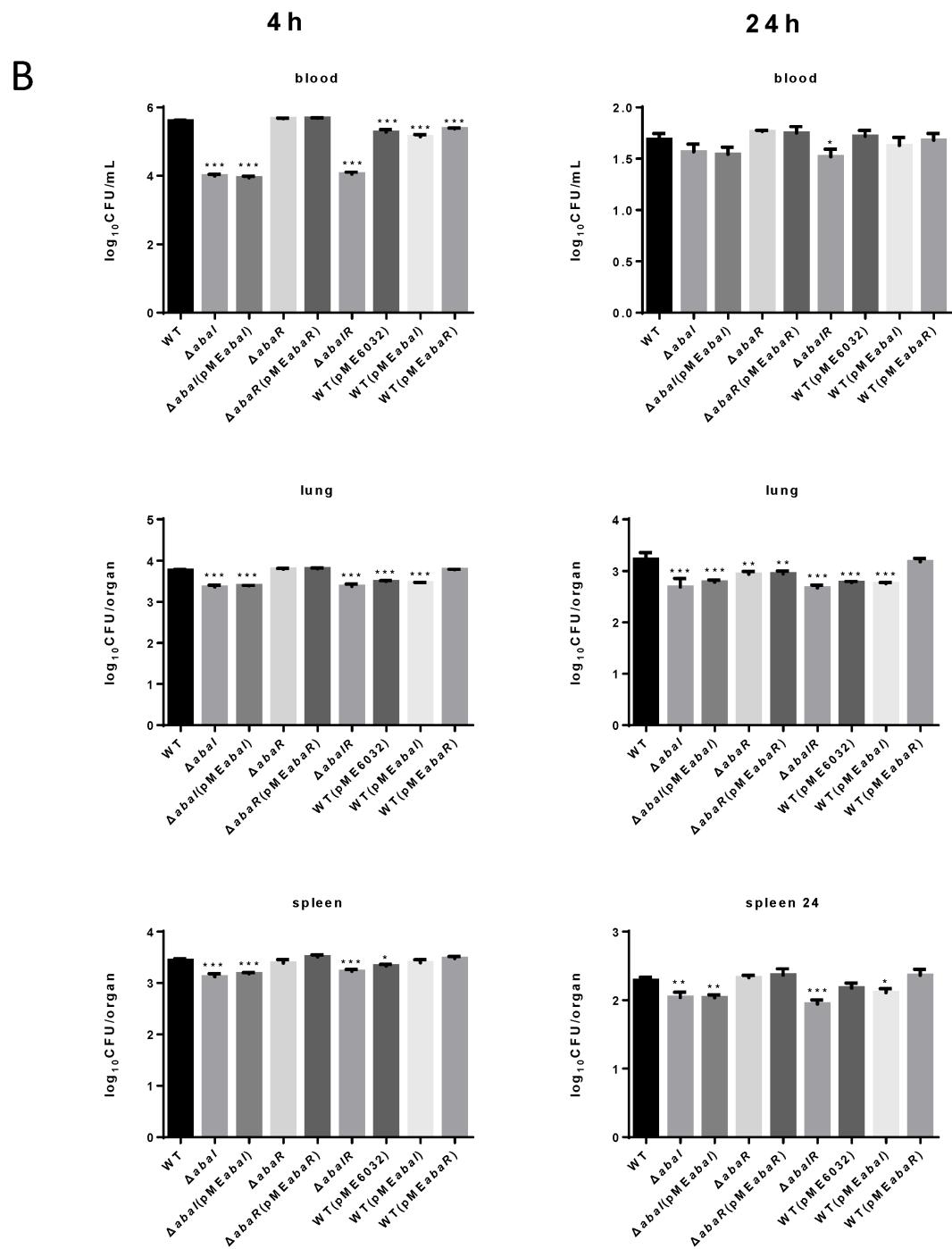
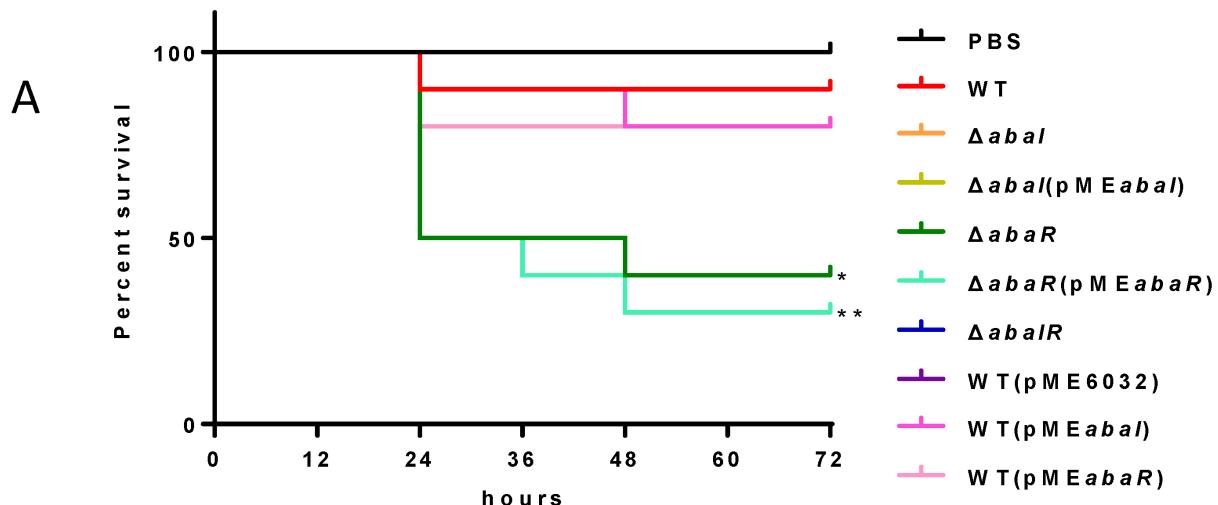
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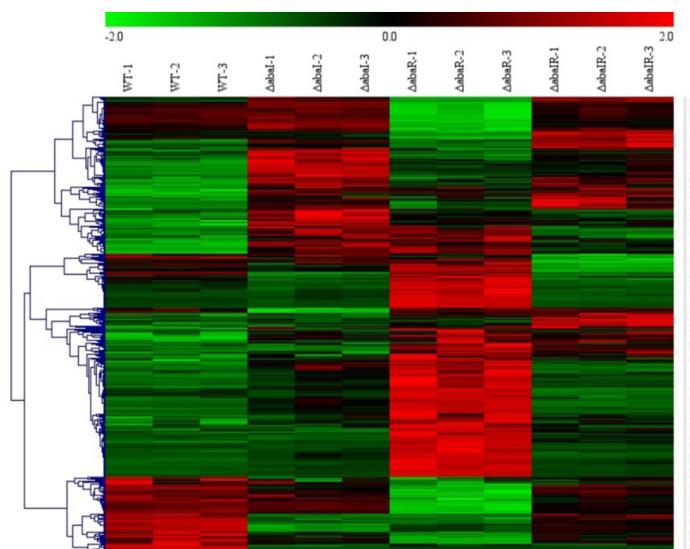
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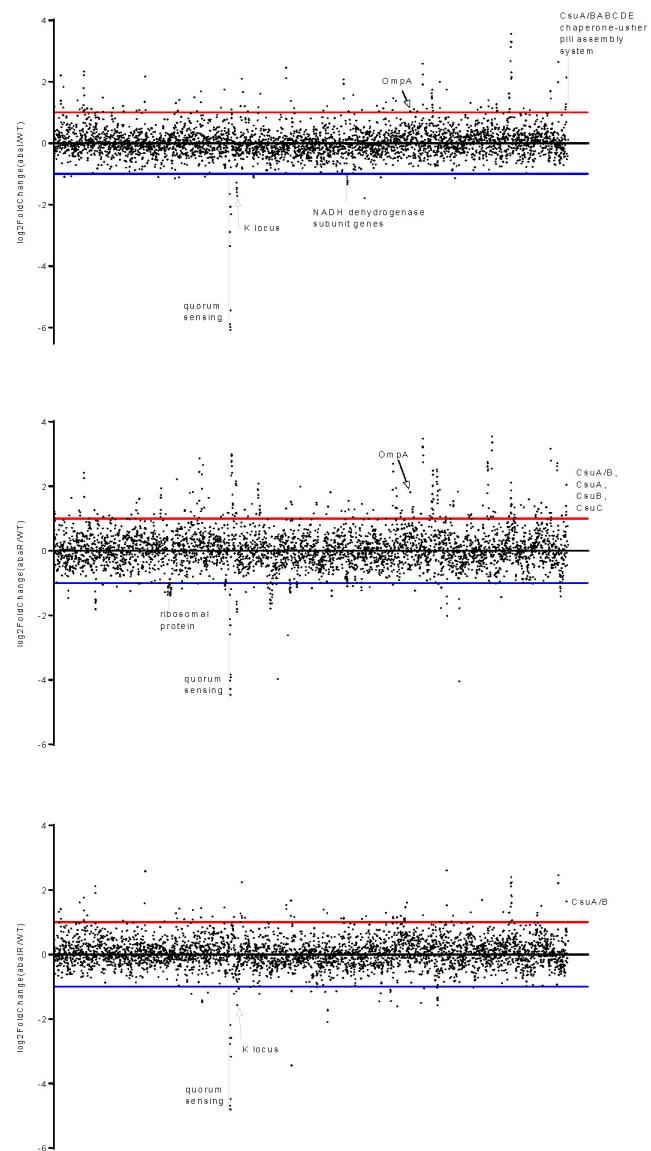




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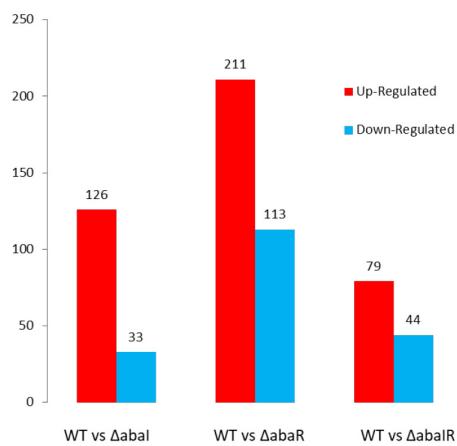


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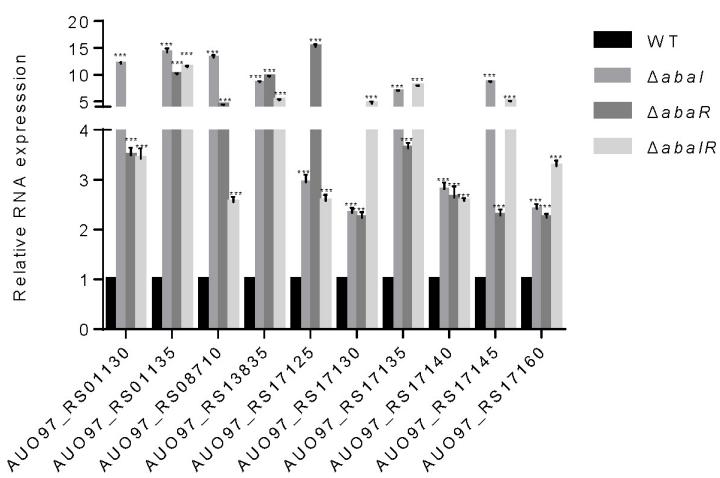


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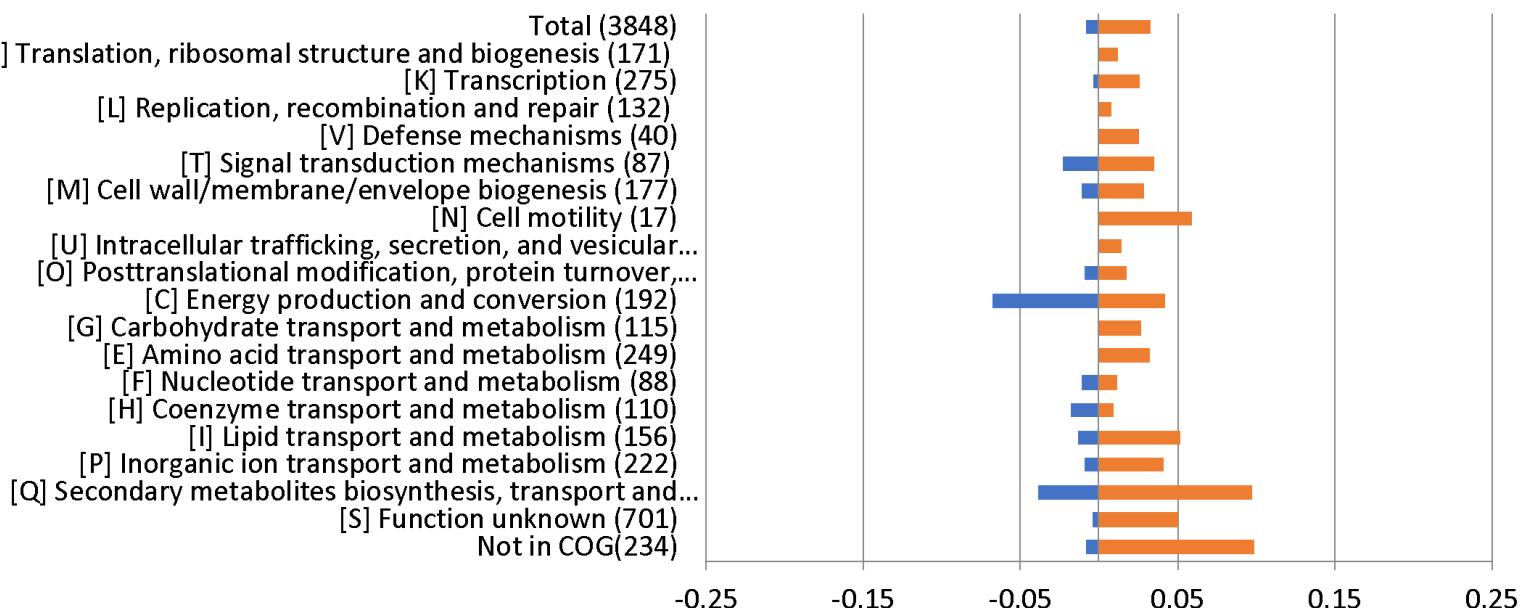
Statistic of differently expressed genes (DESeq2 method)



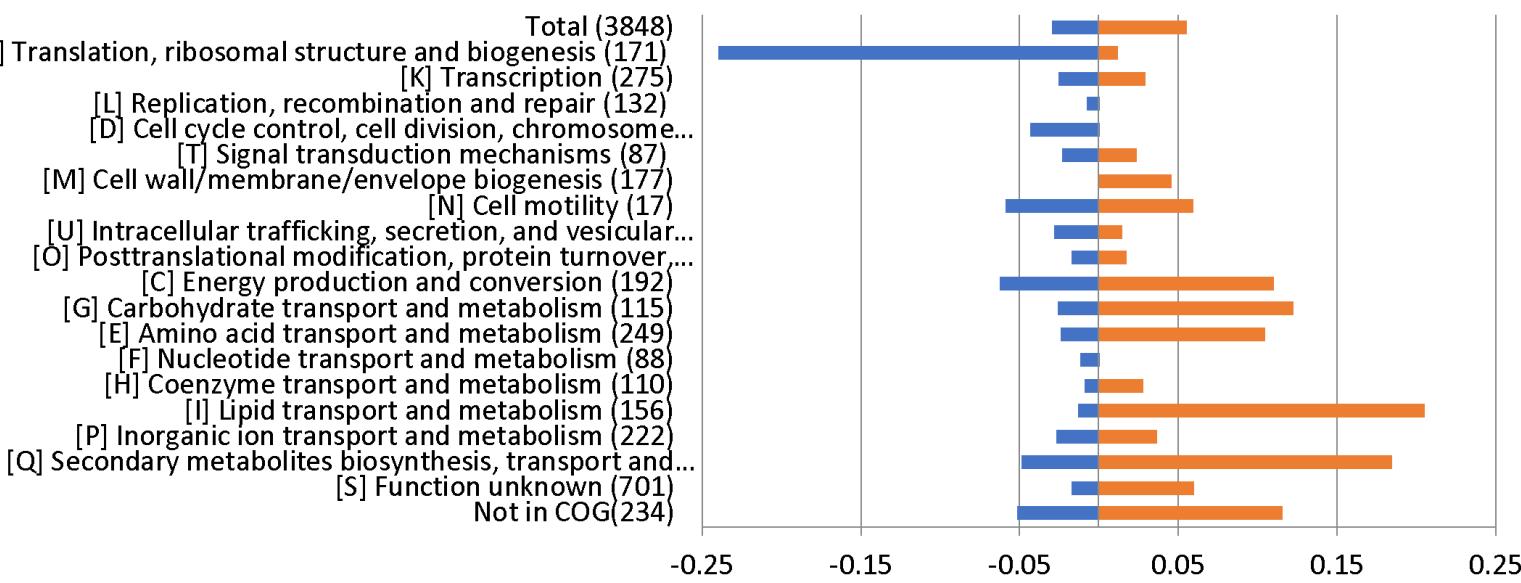
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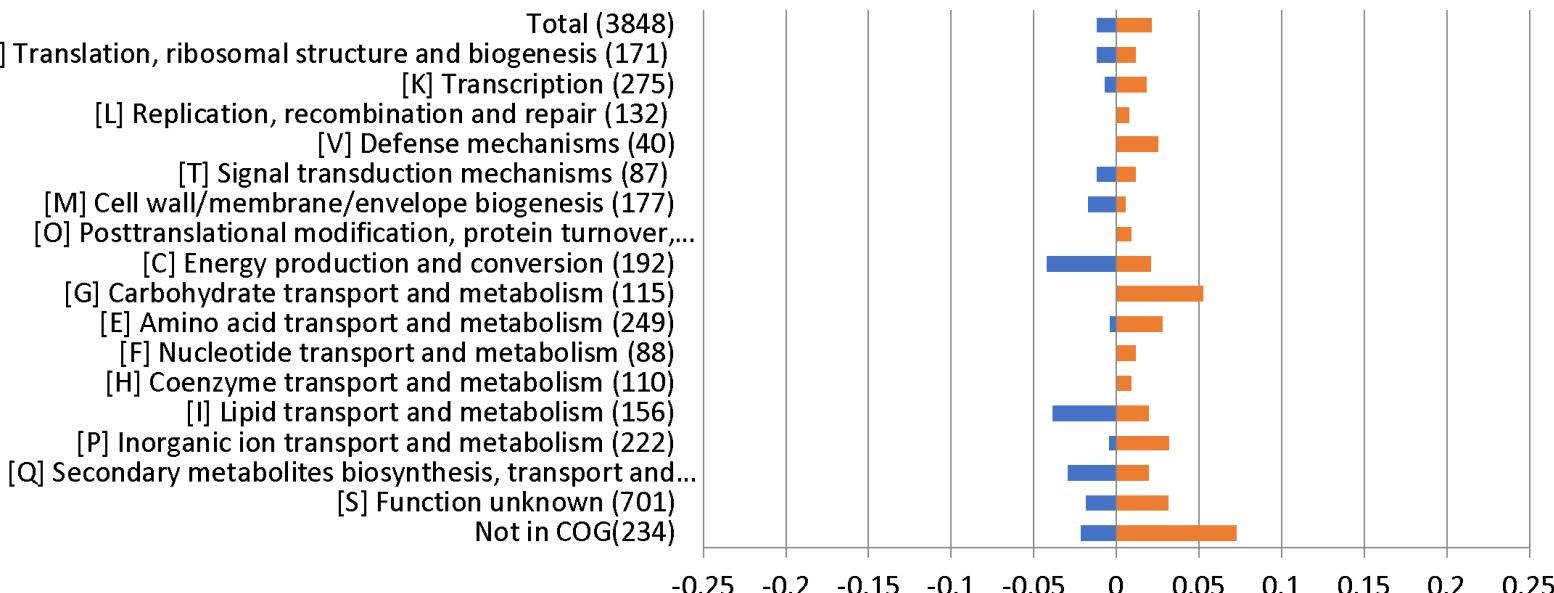
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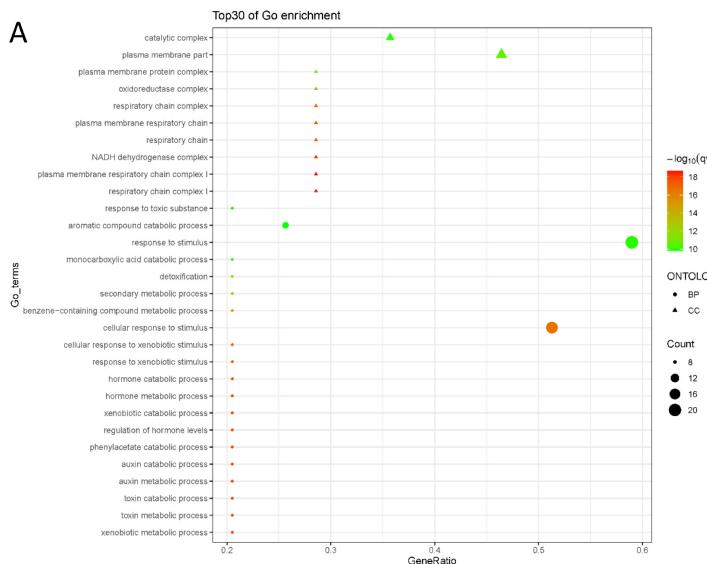
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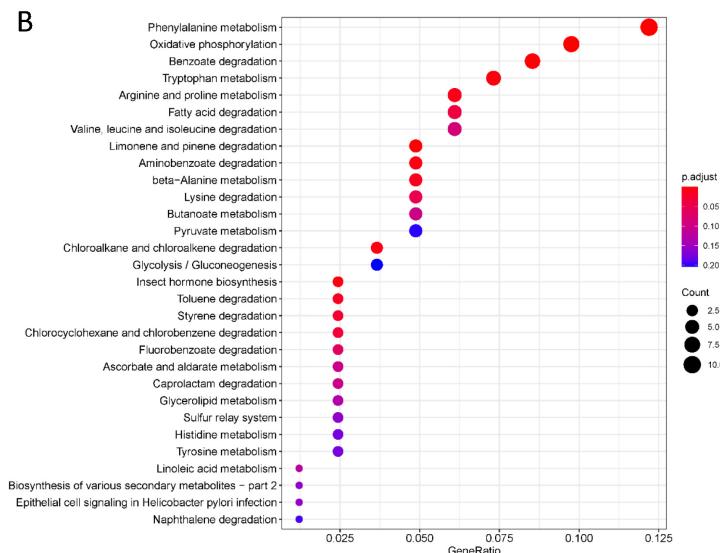
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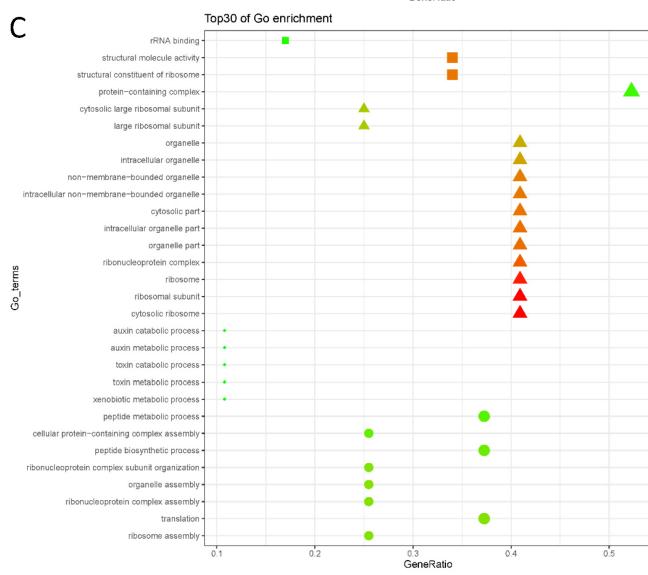
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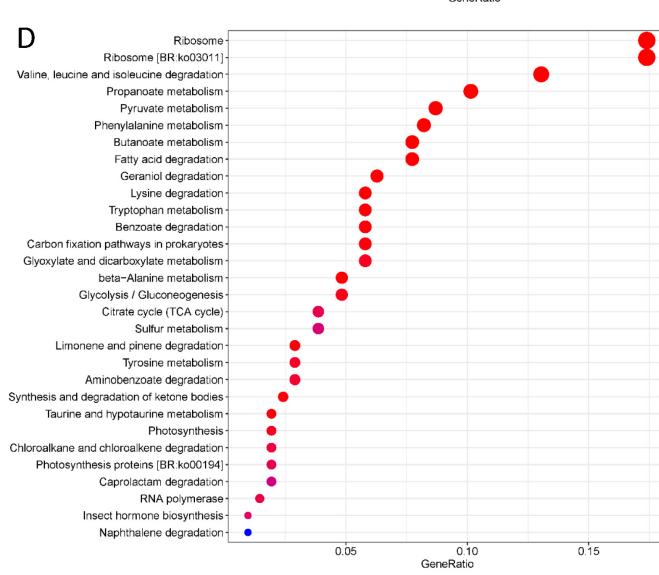
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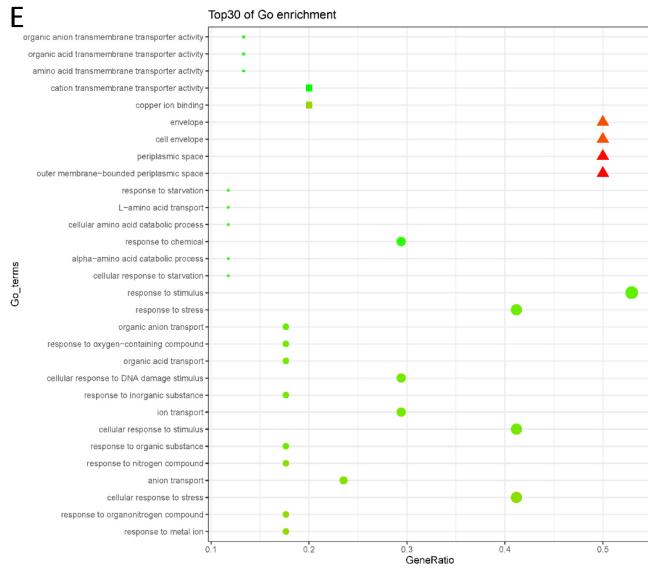
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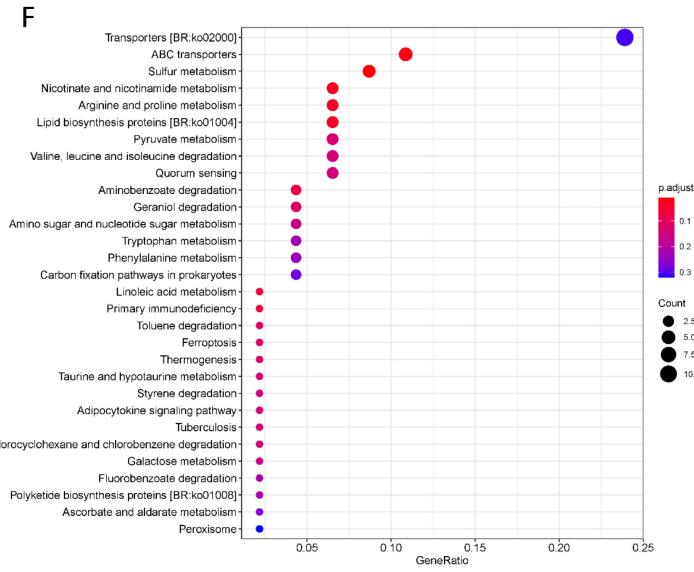
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E



F



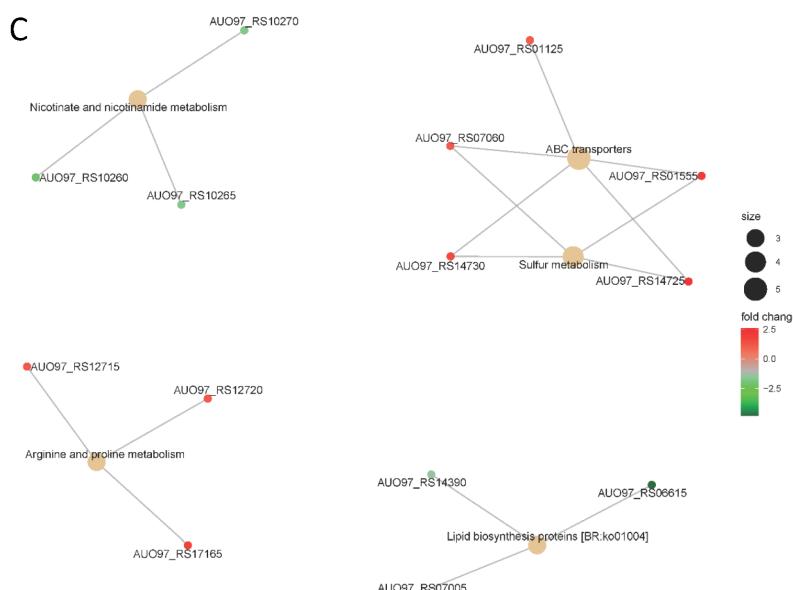


Table 4 Differential expressed genes in  $\Delta$ abal strain

GenelD	log2FoldChange( $\Delta$ ab al/WT)	Up-Down-Regulation( $\Delta$ a bal/WT)	Pvalue	Product
AU097_RS0 6625	-6.0744	Down	0	acyl-CoA dehydrogenase
AU097_RS0 6615	-5.9747	Down	0	non-ribosomal peptide synthetase
AU097_RS0 6610	-5.88657	Down	0	outer membrane lipoprotein-sorting protein
AU097_RS0 6630	-5.44259	Down	0	acyl-CoA synthetase
AU097_RS0 6605	-3.3445	Down	1.1E-1 07	hypothetical protein
AU097_RS0 6600	-2.88721	Down	4.97E- 78	alpha/beta hydrolase
AU097_RS0 6645	-2.30926	Down	1.64E- 07	GNAT family N-acetyltransferase
AU097_RS0 6620	-2.06687	Down	3.24E- 06	acyl carrier protein
AU097_RS1 1650	-1.78566	Down	1.77E- 32	hemerythrin
AU097_RS0 6875	-1.71559	Down	1.47E- 59	UDP-glucose 4-epimerase GalE
AU097_RS0 6595	-1.64711	Down	1.23E- 07	phosphopantetheine- protein transferase
AU097_RS0 6865	-1.58854	Down	5.17E- 94	L-lactate permease
AU097_RS0 6855	-1.50567	Down	7.58E- 53	alpha-hydroxy-acid oxidizing enzyme
AU097_RS0 6860	-1.45419	Down	3.24E- 26	transcriptional regulator LldR
AU097_RS1 1000	-1.33315	Down	9.15E- 17	NADH-quinone oxidoreductase subunit K
AU097_RS0 6850	-1.28401	Down	1.16E- 24	D-lactate dehydrogenase
AU097_RS1 1005	-1.27855	Down	4.17E- 96	NADH-quinone oxidoreductase subunit L
AU097_RS1 0995	-1.27133	Down	2.73E- 39	NADH-quinone oxidoreductase subunit J
AU097_RS1	-1.25693	Down	1.91E-	NADH-quinone

1015			85	oxidoreductase subunit N
AU097_RS1	-1.25538	Down	4.49E-80	NADH-quinone oxidoreductase subunit H
0985				
AU097_RS1	-1.21787	Down	3.2E-73	NADH-quinone oxidoreductase subunit M
1010				
AU097_RS1	-1.14605	Down	7.24E-42	NADH-quinone oxidoreductase subunit I
0990				
AU097_RS0	-1.14342	Down	7.7E-49	oxygen-dependent coproporphyrinogen oxidase
4545				
AU097_RS1	-1.13713	Down	4.45E-15	cytosine permease
5040				
AU097_RS0	-1.11951	Down	1.42E-20	AcrB/AcrD/AcrF family protein
7490				
AU097_RS1	-1.11535	Down	3.08E-46	isocitrate lyase
2255				
AU097_RS0	-1.11028	Down	3.71E-16	hypothetical protein
4690				
AU097_RS0	-1.09799	Down	1.5E-12	GGDEF domain-containing protein
3915				
AU097_RS0	-1.09371	Down	8.57E-25	U32 family peptidase
0400				
AU097_RS0	-1.08569	Down	0.0001	MBL fold
5665			89	metallo-hydrolase
AU097_RS1	-1.06889	Down	2.64E-57	NADH-quinone oxidoreductase subunit NuoG
0980				
AU097_RS0	-1.06411	Down	1.08E-09	efflux RND transporter
7485				periplasmic adaptor subunit
AU097_RS0	-1.02016	Down	7.07E-23	DUF2147 domain-containing protein
5775				
AU097_RS0	1.001374	Up	1.2E-16	putative DNA
4585				modification/repair
				radical SAM protein
AU097_RS1	1.011794	Up	0.0054	TetR/AcrR family
1080			96	transcriptional

					regulator
AU097_RS0 1645	1.013889	Up	1.31E- 06	heteromeric transposase endonuclease subunit TnsA	
AU097_RS1 7070	1.014466	Up	0.0115 44	muconolactone delta-isomerase	
AU097_RS0 1845	1.025133	Up	1.34E- 12	Holliday junction branch migration protein RuvA	
AU097_RS0 2620	1.033632	Up	8.86E- 13	outer membrane lipoprotein carrier protein LolA	
AU097_RS1 3365	1.03403	Up	4.16E- 23	OmpA family protein	
AU097_RS1 3625	1.034741	Up	7.53E- 10	hypothetical protein	
AU097_RS1 1050	1.034749	Up	0.0109 09	hypothetical protein	
AU097_RS0 7280	1.037826	Up	0.0033 11	GlsB/YeaQ/YmgE family stress response membrane protein	
AU097_RS1 2195	1.042847	Up	2.75E- 05	SRPBCC domain-containing protein	
AU097_RS0 5370	1.043606	Up	0.0091 18	GNAT family N-acetyltransferase	
AU097_RS1 6615	1.047928	Up	5.3E-5 0	ImmA/IrrE family metallo-endopeptidase	
AU097_RS0 1115	1.052979	Up	2.83E- 17	phosphate ABC transporter, permease protein PstA	
AU097_RS1 4215	1.060287	Up	2.86E- 13	phenylacetate--CoA ligase	
AU097_RS0 4650	1.061309	Up	4.72E- 18	SPOR domain-containing protein	
AU097_RS1 0110	1.063226	Up	1.44E- 20	MacA family efflux pump subunit	
AU097_RS0 3105	1.065265	Up	2.54E- 05	toxin	
AU097_RS1 6620	1.066128	Up	4.92E- 29	hypothetical protein	

AU097_RS0	1.07437	Up	1.36E-05	VOC family protein
3210				
AU097_RS1	1.076757	Up	2.31E-13	sulfurtransferase TusD
7840				
AU097_RS1	1.080796	Up	8.18E-05	hypothetical protein
2700				
AU097_RS0	1.084479	Up	0.001824	DUF4184 domain-containing protein
3445				
AU097_RS1	1.084642	Up	1.05E-10	gamma-aminobutyral dehyde dehydrogenase
2705				
AU097_RS1	1.084666	Up	1.11E-05	metal-dependent hydrolase
1550				
AU097_RS0	1.086385	Up	6.24E-17	DUF541 domain-containing protein
1160				
AU097_RS1	1.089957	Up	5.57E-27	transcriptional regulator
5885				
AU097_RS0	1.094631	Up	4.41E-06	enoyl-CoA hydratase
6660				
AU097_RS1	1.100387	Up	3.94E-07	proline/glycine betaine transporter ProP
9180				
AU097_RS0	1.100706	Up	0.002029	PaaX family transcriptional regulator
0970				
AU097_RS1	1.108039	Up	2.06E-05	hypothetical protein
3500				
AU097_RS0	1.109955	Up	5.76E-15	membrane protein
1405				
AU097_RS1	1.111993	Up	0.00072	3-oxoadipate CoA-transferase
7085				
AU097_RS1	1.125222	Up	2.47E-07	type VI secretion system baseplate subunit TssE
3980				
AU097_RS0	1.130874	Up	1.28E-29	LysR family transcriptional regulator
1255				
AU097_RS1	1.132006	Up	3.99E-55	META domain-containing protein
2355				
AU097_RS1	1.135218	Up	1.36E-07	universal stress protein
7615				

AU097_RS1	1.135699	Up	9.01E-06	CoA subunit A	transferase
6430					
AU097_RS0	1.136286	Up	1.71E-38	FUSC family protein	
9015					
AU097_RS1	1.14236	Up	7.91E-09	DNA polymerase V	
4475					
AU097_RS0	1.148054	Up	5.78E-38	ABC transporter	
2225				substrate-binding	
				protein	
AU097_RS0	1.151745	Up	1.11E-10	hypothetical protein	
1060					
AU097_RS1	1.153076	Up	4.64E-10	hypothetical protein	
6600					
AU097_RS1	1.154194	Up	1.2E-05	enoyl-CoA hydratase	
4195					
AU097_RS0	1.155982	Up	1.36E-07	DNA-binding response	
0360				regulator	
AU097_RS0	1.156561	Up	4.43E-10	DUF2726	
6270				domain-containing	
				protein	
AU097_RS0	1.165001	Up	4.24E-11	aromatic amino acid	
7670				transporter AroP	
AU097_RS0	1.166185	Up	1.94E-63	fumarylacetoacetate	
7665					
AU097_RS1	1.168526	Up	1.13E-32	haloacid	
6010				dehalogenase	
AU097_RS1	1.176465	Up	1E-07	SCPU	
9190				domain-containing	
				protein	
AU097_RS1	1.188775	Up	4.99E-16	fimbrial biogenesis	
9195				outer membrane	
				usher protein	
AU097_RS0	1.189934	Up	0.005552	hypothetical protein	
0020					
AU097_RS1	1.202481	Up	1.73E-45	TIGR01244 family	
6300				phosphatase	
AU097_RS0	1.204777	Up	0.005296	hypothetical protein	
7165					
AU097_RS1	1.204815	Up	0.003704	RidA family protein	
0250					
AU097_RS0	1.210701	Up	0.000229	transcriptional	
2595				regulator	
AU097_RS0	1.211821	Up	1.5E-37	acyl-CoA desaturase	
7005					

AU097_RS1 6305	1.212542	Up	1.27E- 08	sulfite TauE/SafE protein	exporter family
AU097_RS1 2115	1.214564	Up	2.84E- 32	Fe-S protein	biogenesis NfuA
AU097_RS0 1120	1.243207	Up	3.6E-1 8	phosphate transporter	ABC permease subunit PstC
AU097_RS1 4190	1.246926	Up	2.2E-0 6	phenylacetate-CoA oxygenase/reductase	subunit PaaK
AU097_RS1 3840	1.253491	Up	1.81E- 20	allophanate hydrolase	
AU097_RS1 6595	1.264522	Up	4.69E- 19	PAAR domain-containing	protein
AU097_RS1 9205	1.274509	Up	0.0006 46	SCPU domain-containing	protein
AU097_RS1 9200	1.275559	Up	4.91E- 09	molecular chaperone	
AU097_RS0 0270	1.276369	Up	8.02E- 05	hypothetical protein	
AU097_RS0 4580	1.307287	Up	1.03E- 07	hypothetical protein	
AU097_RS1 5625	1.309804	Up	9.99E- 06	phage major capsid protein	
AU097_RS1 2450	1.328101	Up	2.33E- 19	amino acid transporter	
AU097_RS0 5515	1.333536	Up	1.76E- 40	NADPH:quinone oxidoreductase	
AU097_RS0 3405	1.346309	Up	0.0002 18	hypothetical protein	
AU097_RS1 2825	1.375679	Up	2.99E- 06	crotonase	
AU097_RS0 8885	1.376611	Up	0.0003 94	DNA transfer protein p32	
AU097_RS0 0265	1.381641	Up	0.0007 4	hypothetical protein	
AU097_RS1 6295	1.396496	Up	6.32E- 27	MBL metallo-hydrolase	fold
AU097_RS0 0890	1.398657	Up	7.72E- 28	hypothetical protein	
AU097_RS0	1.410219	Up	9.19E-	hypothetical protein	

4705				16	
AU097_RS1	1.454416	Up		1.2E-2	flavin reductase
0870				6	
AU097_RS1	1.4574	Up		3.51E-	phenylacetate-CoA
4180				11	oxygenase subunit
					Paal
AU097_RS1	1.457907	Up		3.68E-	aldehyde
8630				75	dehydrogenase
AU097_RS1	1.458908	Up		1.83E-	aspartate
2715				09	aminotransferase
					family protein
AU097_RS1	1.468197	Up		3.65E-	catechol
7075				14	1,2-dioxygenase
AU097_RS1	1.470222	Up		6.53E-	arginine
2720				08	N-succinyltransferase
AU097_RS0	1.484748	Up		1.28E-	deoxyguanosinetripho
1840				65	sphate
					triphosphohydrolase
AU097_RS1	1.487037	Up		1.93E-	1,2-phenylacetyl-CoA
4170				27	epoxidase subunit A
AU097_RS0	1.493798	Up		1.05E-	hypothetical protein
5275				18	
AU097_RS1	1.496273	Up		1.16E-	3-oxoadipate
7080				05	CoA-transferase
					subunit A
AU097_RS1	1.534021	Up		1.12E-	1,2-phenylacetyl-CoA
4175				19	epoxidase subunit B
AU097_RS0	1.557012	Up		2.02E-	NAD-dependent
1145				49	aldehyde
					dehydrogenase
AU097_RS1	1.567974	Up		2.97E-	trehalose-phosphatas
1225				14	e
AU097_RS0	1.607067	Up		3.22E-	DNA transfer protein
7745				31	p32
AU097_RS1	1.619212	Up		1.95E-	muconate
7065				10	cycloisomerase
AU097_RS1	1.628035	Up		6.97E-	phenylacetic acid
4165				17	degradation
					bifunctional protein
					PaaZ
AU097_RS0	1.660574	Up		6.92E-	C4-dicarboxylate ABC
7095				08	transporter
AU097_RS0	1.685455	Up		2.39E-	TetR/AcrR family
5520				30	transcriptional

					regulator
AU097_RS1	1.695967	Up	4.07E-46	alcohol dehydrogenase	
8615					
AU097_RS1	1.739369	Up	1.42E-35	phenylacetate-CoA oxygenase subunit	
4185					
AU097_RS1	1.743263	Up	4E-17	taurine transporter	ABC
4725					
				substrate-binding protein	
AU097_RS0	1.744985	Up	1.2E-7	MFS transporter	
6395			3		
AU097_RS0	1.794527	Up	4.22E-35	phosphonate transporter	ABC
1125					
				substrate-binding protein	
AU097_RS0	1.83163	Up	7.99E-22	DNA-binding protein	
0365					
AU097_RS1	1.910832	Up	7.76E-13	LamB/YcsF family	
3830					
AU097_RS1	1.926934	Up	5.8E-205	methionine synthase	
0865					
AU097_RS1	1.984749	Up	6.85E-17	hypothetical protein	
8900					
AU097_RS1	1.998418	Up	5.49E-06	hypothetical protein	
4470					
AU097_RS1	2.07496	Up	2.1E-191	DUF1852	
0860					
				domain-containing protein	
AU097_RS0	2.095124	Up	6.19E-12	hypothetical protein	
7050					
AU097_RS1	2.097862	Up	5.78E-08	nuclear transport factor 2 family protein	
7150					
AU097_RS0	2.116025	Up	7.01E-29	EamA family	
8715					
AU097_RS1	2.141387	Up	5.07E-60	SCPU	
9215					
				domain-containing protein	
AU097_RS1	2.147861	Up	7.66E-23	amidase	
7165					
AU097_RS0	2.174702	Up	4.1E-13	hypothetical protein	
3425					
AU097_RS0	2.205577	Up	1.57E-67	RtcB family protein	
0260					

AU097_RS0 1130	2.216359	Up	6.67E- 33	aromatic amino acid transporter AroP
AU097_RS1 3835	2.236657	Up	1.63E- 29	DUF1445 domain-containing protein
AU097_RS1 7155	2.307109	Up	1.38E- 08	hypothetical protein
AU097_RS0 1135	2.335458	Up	2.75E- 62	pyruvate decarboxylase
AU097_RS0 8710	2.459453	Up	2.56E- 34	TetR/AcrR family transcriptional regulator
AU097_RS1 3825	2.587926	Up	3.04E- 24	divalent metal cation transporter
AU097_RS1 8910	2.644973	Up	3.5E-4 8	hypothetical protein
AU097_RS1 7125	2.673537	Up	8.63E- 24	flavin reductase
AU097_RS1 7130	3.134825	Up	5.49E- 24	oxidoreductase
AU097_RS1 7135	3.137551	Up	8.58E- 27	KR domain-containing protein
AU097_RS1 7160	3.296468	Up	8.85E- 48	acyl-CoA dehydrogenase
AU097_RS1 7140	3.302273	Up	5.99E- 17	aromatic-ring-hydroxy lating dioxygenase subunit beta
AU097_RS1 7145	3.557326	Up	8.79E- 58	aromatic ring-hydroxylating dioxygenase subunit alpha

Table 5 Differential expressed genes in  $\Delta$ abaR strain

GeneID	log2FoldChange( $\Delta$ abaR/WT)	Up-Down-Regulation( $\Delta$ abaR/WT)	Pvalue	Product
AU097_RS 00540	-1.46697	Down	7.01E- -97	elongation factor Ts
AU097_RS 00545	-1.23446	Down	6.5E- 101	30S ribosomal protein S2
AU097_RS 01555	-1.25779	Down	7.5E- 12	sulfate ABC transporter substrate-binding protein
AU097_RS 01560	-1.60798	Down	9.23E- -07	alpha/beta hydrolase
AU097_RS 01565	-1.80619	Down	3.15E- -14	sulfate ABC transporter permease subunit CysT

AU097_RS	-1.51136	Down	1.53E	sulfate	ABC	transporter
01570			-08	permease subunit CysW		
AU097_RS	-1.55706	Down	1.89E	sulfate	ABC	transporter
01575			-17	ATP-binding protein		
AU097_RS	-1.04633	Down	1.47E	phosphoribosylformylglycina		
01835			-50	midine synthase		
AU097_RS	-1.24855	Down	7.89E	septum formation inhibitor		
02870			-07	Maf		
AU097_RS	-1.006	Down	1.04E	translational GTPase TypA		
03165			-52			
AU097_RS	-1.02069	Down	2.64E	DUF934 domain-containing		
03220			-08	protein		
AU097_RS	-1.00367	Down	7.42E	50S ribosomal protein L13		
03975			-47			
AU097_RS	-1.27941	Down	8.69E	EamA/RhaT family		
04165			-08	transporter		
AU097_RS	-1.36319	Down	2.43E	50S ribosomal protein L17		
04275			-55			
AU097_RS	-1.26373	Down	9.25E	DNA-directed RNA		
04280			-80	polymerase subunit alpha		
AU097_RS	-1.14133	Down	7.65E	30S ribosomal protein S4		
04285			-54			
AU097_RS	-1.09269	Down	1.17E	30S ribosomal protein S11		
04290			-38			
AU097_RS	-1.29326	Down	1.32E	preprotein translocase		
04305			-74	subunit SecY		
AU097_RS	-1.09864	Down	1.39E	50S ribosomal protein L15		
04310			-44			
AU097_RS	-1.15251	Down	1.55E	30S ribosomal protein S5		
04320			-40			
AU097_RS	-1.14007	Down	2.33E	50S ribosomal protein L18		
04325			-45			
AU097_RS	-1.03587	Down	5.13E	50S ribosomal protein L6		
04330			-39			
AU097_RS	-1.12717	Down	1.21E	30S ribosomal protein S8		
04335			-37			
AU097_RS	-1.00921	Down	2.04E	30S ribosomal protein S14		
04340			-22			
AU097_RS	-1.04986	Down	2.5E-	50S ribosomal protein L5		
04345			52			
AU097_RS	-1.33542	Down	2.89E	30S ribosomal protein S17		
04360			-22			
AU097_RS	-1.38332	Down	9.06E	50S ribosomal protein L29		
04365			-15			

AU097_RS	-1.30303	Down	6.38E	50S ribosomal protein L16
04370			-42	
AU097_RS	-1.38848	Down	3.29E	30S ribosomal protein S3
04375			-60	
AU097_RS	-1.32586	Down	3.99E	50S ribosomal protein L22
04380			-40	
AU097_RS	-1.2558	Down	3.56E	30S ribosomal protein S19
04385			-34	
AU097_RS	-1.25482	Down	9.97E	50S ribosomal protein L2
04390			-55	
AU097_RS	-1.33758	Down	3.92E	50S ribosomal protein L23
04395			-37	
AU097_RS	-1.14341	Down	4.11E	50S ribosomal protein L4
04400			-43	
AU097_RS	-1.19034	Down	3.39E	50S ribosomal protein L3
04405			-50	
AU097_RS	-1.18708	Down	2.7E-	30S ribosomal protein S10
04410			30	
AU097_RS	-1.0042	Down	1.6E-	flavohemoprotein
04430			53	
AU097_RS	-1.16847	Down	2.27E	50S ribosomal protein L19
04805			-41	
AU097_RS	-1.0155	Down	1.78E	MFS transporter
05405			-11	
AU097_RS	-1.08048	Down	2.86E	ATP synthase epsilon chain
06420			-48	
AU097_RS	-1.0439	Down	3.37E	ATP synthase subunit beta
06425			-50	
AU097_RS	-1.19299	Down	3.17E	ATP synthase subunit
06430			-60	gamma
AU097_RS	-1.00172	Down	5.3E-	ATP synthase subunit alpha
06435			52	
AU097_RS	-1.3648	Down	3.66E	phosphopantetheine-protein
06595			-06	transferase
AU097_RS	-2.11825	Down	8.13E	alpha/beta hydrolase
06600			-56	
AU097_RS	-2.58786	Down	4.19E	hypothetical protein
06605			-97	
AU097_RS	-4.02394	Down	0	outer membrane
06610				lipoprotein-sorting protein
AU097_RS	-4.2825	Down	0	non-ribosomal peptide
06615				synthetase
AU097_RS	-2.30484	Down	1.32E	acyl carrier protein
06620			-05	[Acinetobacter]

AU097_RS	-4.46229	Down	0	acyl-CoA dehydrogenase
06625				
AU097_RS	-3.82819	Down	0	acyl-CoA synthetase
06630				
AU097_RS	-3.91695	Down	1.44E -13	LuxR family transcriptional regulator
06635				
AU097_RS	-1.18831	Down	0.010	GNAT family
06645			518	N-acetyltransferase
AU097_RS	-1.57625	Down	9.75E -39	D-lactate dehydrogenase
06850				
AU097_RS	-1.66135	Down	2.76E -57	alpha-hydroxy-acid oxidizing enzyme
06855				
AU097_RS	-1.89372	Down	8E-42	transcriptional regulator
06860			LldR	
AU097_RS	-1.80838	Down	1.65E -24	L-lactate permease
06865				[Acinetobacter]
AU097_RS	-1.27639	Down	4.66E -18	dual-action HEIGH
07200				metallo-peptidase
AU097_RS	-1.0278	Down	0.000	hypothetical protein
08005			671	
AU097_RS	-1.18969	Down	1.46E -36	ATP-binding protein
08095				
AU097_RS	-1.00682	Down	4.07E -06	hypothetical protein
08100				
AU097_RS	-1.50123	Down	4.68E -08	type VI secretion protein
08105				
AU097_RS	-1.6293	Down	3.47E -44	hypothetical protein
08110				
AU097_RS	-1.32724	Down	3.42E -11	type VI secretion protein
08115				
AU097_RS	-1.78941	Down	6.98E -25	hypothetical protein
08120				
AU097_RS	-1.63462	Down	1.71E -25	conjugal transfer protein
08125				Trbl
AU097_RS	-1.53505	Down	1E-14	hypothetical protein
08130				
AU097_RS	-1.78221	Down	2.31E -11	conjugal transfer protein
08135				
AU097_RS	-1.63347	Down	2.54E -07	hypothetical protein
08175				
AU097_RS	-1.43919	Down	5.89E -15	hypothetical protein
08180				
AU097_RS	-1.2236	Down	5.97E -15	type IV pili twitching motility
08185				protein PilT

AU097_RS	-1.35697	Down	2.13E	hypothetical protein
08195			-17	
AU097_RS	-1.00648	Down	0.000	hypothetical protein
08200			214	
AU097_RS	-1.03879	Down	1.12E	hypothetical protein
08205			-06	
AU097_RS	-1.0272	Down	1.39E	hypothetical protein
08345			-09	
AU097_RS	-3.96826	Down	3.8E-	IS5 family transposase
08400			191	
AU097_RS	-2.61617	Down	1.95E	DNA-binding protein
08775			-12	[Acinetobacter]
AU097_RS	-1.19333	Down	1.89E	elongation factor Tu
08830			-65	
AU097_RS	-1.12568	Down	8.29E	50S ribosomal protein L11
08850			-60	
AU097_RS	-1.15414	Down	4.74E	50S ribosomal protein L1
08855			-68	
AU097_RS	-1.25299	Down	6.63E	50S ribosomal protein L10
08860			-61	
AU097_RS	-1.29006	Down	8.87E	50S ribosomal protein L7/L12 [Acinetobacter]
08865			-84	
AU097_RS	-1.03148	Down	2.36E	DNA-directed RNA
08870			-50	polymerase subunit beta
AU097_RS	-1.14418	Down	2.9E-	DNA-directed RNA
08875			73	polymerase subunit beta'
AU097_RS	-1.04917	Down	4.83E	transcription
09110			-48	termination/antitermination
				protein NusA
AU097_RS	-1.11845	Down	2.33E	translation initiation factor
09115			-57	IF-2
AU097_RS	-1.02517	Down	3E-23	ribosome-binding factor A
09120				
AU097_RS	-1.15939	Down	0.000	50S ribosomal protein L28
09675			133	[Moraxellaceae]
AU097_RS	-1.39769	Down	3.91E	50S ribosomal protein L35
10415			-09	
AU097_RS	-1.23068	Down	1.37E	50S ribosomal protein L20
10420			-68	[Acinetobacter]
AU097_RS	-1.10035	Down	4.37E	NADH-quinone
11000			-14	oxidoreductase subunit K
				[Acinetobacter]
AU097_RS	-1.00922	Down	9.05E	NADH-quinone
11015			-51	oxidoreductase subunit N

AU097_RS	-1.09784	Down	1.27E	MFS transporter
11215			-35	
AU097_RS	-1.00307	Down	1.11E	50S ribosomal protein L25
11345			-16	
AU097_RS	-1.12853	Down	2.42E	30S ribosomal protein S7
11530			-59	
AU097_RS	-1.22746	Down	1.66E	elongation factor G
11535			-65	
AU097_RS	-1.1171	Down	1.64E	malate:quinone
11840			-58	oxidoreductase
AU097_RS	-1.05094	Down	0.008	Lrp/AsnC family
12710			596	transcriptional regulator
AU097_RS	-1.23454	Down	0.000	transposase
13535			918	
AU097_RS	-1.77276	Down	0.000	amino acid ABC transporter
14515			107	permease [Acinetobacter]
AU097_RS	-1.13951	Down	1.92E	ArtI protein [Acinetobacter]
14525			-06	
AU097_RS	-1.41173	Down	1.07E	taurine ABC transporter
14730			-09	ATP-binding protein
AU097_RS	-1.63502	Down	9.12E	taurine ABC transporter
14735			-15	permease
AU097_RS	-2.01495	Down	7.36E	taurine dioxygenase
14740			-21	
AU097_RS	-1.4971	Down	0.000	hypothetical protein
15190			116	
AU097_RS	-4.0442	Down	0	trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase
15195				
AU097_RS	-1.779	Down	1.1E-	sodium/proline symporter
15205			174	PutP
AU097_RS	-1.43715	Down	4.91E	NAD(P)-dependent alcohol dehydrogenase
16765			-05	
AU097_RS	-1.02093	Down	0.001	3-dehydroquinate dehydratase
17945			295	
AU097_RS	-1.10603	Down	6.31E	protoheme IX
18980			-29	farnesyltransferase
AU097_RS	-1.2489	Down	4.3E-	30S ribosomal protein S6
18985			72	
AU097_RS	-1.16315	Down	5.79E	30S ribosomal protein S18
18990			-09	
AU097_RS	-1.41125	Down	8.4E-	50S ribosomal protein L9

18995				118	
AU097_RS	1.222331	Up	0.016	hypothetical protein	
00020			824		
AU097_RS	1.135363	Up	0.000	glycosyl transferase	
00035			104		
AU097_RS	1.1511	Up	5.99E-08	PIG-L family deacetylase	
00045					
AU097_RS	1.098532	Up	7.5E-35	acyl-CoA dehydrogenase	
00580					
AU097_RS	1.639534	Up	6.49E-71	alpha/beta hydrolase	
00665					
AU097_RS	1.245914	Up	5.65E-06	hydrolase	
00945					
AU097_RS	1.091104	Up	0.000	DUF466 domain-containing	
00985			167	protein	
AU097_RS	1.196287	Up	1.09E-52	carbon starvation protein A	
00990					
AU097_RS	2.419967	Up	6.12E-42	MFS transporter	
01130					
AU097_RS	2.254064	Up	1.16E-83	ATP-dependent protease	
01135					
AU097_RS	1.668297	Up	1.74E-90	NAD-dependent aldehyde	
01145				dehydrogenase	
AU097_RS	1.013324	Up	2.48E-20	hypothetical protein	
01330					
AU097_RS	1.258765	Up	1.74E-42	PDZ domain-containing	
01525				protein	
AU097_RS	1.134019	Up	0.017	NIF3 1	
01635			089		
AU097_RS	1.056825	Up	5.66E-05	amidohydrolase	
01855					
AU097_RS	1.096169	Up	2.03E-37	amino acid permease	
02080					
AU097_RS	1.126299	Up	1.17E-16	glutamine amidotransferase	
02905					
AU097_RS	1.255559	Up	7.25E-17	DUF1508 domain-containing	
03090				protein	
AU097_RS	1.492233	Up	1.04E-09	toxin	
03105					
AU097_RS	1.158869	Up	6.14E-24	large conductance	
03160				mechanosensitive channel	
				protein MscL	
AU097_RS	1.611018	Up	6.12E-14	VOC family protein	
03210					

AU097_RS 04000	1.156133	Up	1.9E- 16	acetyl/propionyl/methylcrotonyl-CoA carboxylase subunit alpha
AU097_RS 04005	1.052399	Up	4.02E- 05	enoyl-CoA hydratase
AU097_RS 04010	1.271182	Up	8.42E- 15	acyl-CoA dehydrogenase
AU097_RS 04015	1.648108	Up	9.91E- 27	acetyl-CoA carboxylase carboxyltransferase subunit
AU097_RS 04020	1.729121	Up	2.87E- 19	KR domain-containing protein
AU097_RS 04025	1.935767	Up	1.05E- 53	DUF1446 domain-containing protein
AU097_RS 04195	1.138211	Up	4.47E- 65	hypothetical protein
AU097_RS 04615	2.218472	Up	1.38E- 19	hypothetical protein
AU097_RS 04620	5.633865	Up	4.3E- 106	EamA/RhaT family transporter
AU097_RS 04905	1.264872	Up	2.7E- 05	hypothetical protein
AU097_RS 04915	1.231286	Up	4.4E- 31	LemA family protein
AU097_RS 05105	1.791924	Up	5.78E- 67	hypothetical protein
AU097_RS 05140	1.207876	Up	7.53E- 08	sulfate permease
AU097_RS 05215	1.821676	Up	9.5E- 28	EamA/RhaT family transporter
AU097_RS 05275	1.081392	Up	7.43E- 10	hypothetical protein
AU097_RS 05370	1.46563	Up	0.000 574	GNAT family N-acetyltransferase
AU097_RS 05440	1.02368	Up	2.04E- 12	hydrolase
AU097_RS 05450	1.550398	Up	9.3E- 115	NAD-dependent succinate-semialdehyde dehydrogenase
AU097_RS 05455	2.444237	Up	9.5E- 158	4-aminobutyrate--2-oxoglutarate transaminase
AU097_RS 05465	2.866641	Up	1.4E- 170	amino acid permease
AU097_RS 05515	1.227311	Up	1.59E- 21	NADPH:quinone oxidoreductase

AU097_RS	1.298715	Up	6.71E	hypothetical protein
05545			-05	
AU097_RS	2.370634	Up	1.4E-	cation acetate symporter
05550			202	
AU097_RS	1.922574	Up	6.03E	DUF485 domain-containing
05555			-29	protein [Acinetobacter]
AU097_RS	2.656199	Up	3.7E-	acetate--CoA ligase
05595			278	
AU097_RS	1.336995	Up	2.19E	carbapenem susceptibility
05635			-84	porin CarO
AU097_RS	1.641335	Up	2.51E	hypothetical protein
05805			-71	
AU097_RS	1.057684	Up	5.68E	DUF2726 domain-containing
06270			-08	protein
AU097_RS	1.175945	Up	0.014	DUF3861 domain-containing
06525			654	protein
AU097_RS	1.175091	Up	4.65E	DoxX family protein
06550			-05	
AU097_RS	2.333258	Up	6.99E	MFS transporter
06650			-28	
AU097_RS	2.75065	Up	7.52E	enoyl-CoA
06655			-90	hydratase/isomerase family
				protein
AU097_RS	2.947701	Up	1.15E	enoyl-CoA hydratase
06660			-61	
AU097_RS	2.788771	Up	2.4E-	acyl-CoA dehydrogenase
06665			101	
AU097_RS	2.99023	Up	6.78E	AMP-binding protein
06670			-31	
AU097_RS	2.626672	Up	1.8E-	3-hydroxyisobutyrate
06675			101	dehydrogenase
AU097_RS	2.412876	Up	5.5E-	methylmalonate-semialdehy
06680			215	de dehydrogenase
				(acylating)
AU097_RS	1.738202	Up	2.05E	amino acid permease
06695			-58	
AU097_RS	1.327951	Up	3.98E	RidA family protein
06700			-13	[Acinetobacter]
AU097_RS	1.11741	Up	1.41E	alanine racemase
06705			-34	
AU097_RS	1.417227	Up	3.65E	D-amino-acid
06710			-61	dehydrogenase
AU097_RS	1.465739	Up	0.000	AsnC family transcriptional
06715			52	regulator [Acinetobacter]

AU097_RS	1.075741	Up	0.002	sel1 repeat family protein
06785			995	
AU097_RS	1.16987	Up	8.02E-09	DUF4126 domain-containing protein
06810				
AU097_RS	2.083996	Up	5.4E-190	Fe/S-dependent 2-methylisocitrate dehydratase AcnD
06825				
AU097_RS	2.154844	Up	7.5E-125	2-methylcitrate synthase
06830				
AU097_RS	2.034936	Up	2.1E-108	methylisocitrate lyase
06835				
AU097_RS	1.166137	Up	1.01E-23	GntR family transcriptional regulator
06840				
AU097_RS	1.277517	Up	0.012	hypothetical protein
07165			728	
AU097_RS	1.067484	Up	0.004	GlsB/YeaQ/YmgE family
07280			097	stress response membrane protein [Acinetobacter]
AU097_RS	1.453655	Up	7.14E-70	sodium-dependent transporter
07430				
AU097_RS	1.141851	Up	1.13E-09	PQQ-dependent sugar dehydrogenase
07590				
AU097_RS	1.903493	Up	1.1E-213	4-hydroxyphenylpyruvate dioxygenase
07645				
AU097_RS	1.885403	Up	5.1E-107	VOC family protein
07655				
AU097_RS	1.644119	Up	1.7E-102	maleylacetoacetate isomerase
07660				
AU097_RS	1.732833	Up	6.8E-139	fumarylacetoacetate
07665				
AU097_RS	2.082498	Up	2.6E-191	aromatic amino acid transporter AroP
07670				
AU097_RS	1.109972	Up	2.23E-40	amino acid permease
07710				
AU097_RS	1.277428	Up	7.06E-54	imidazolonepropionase
07715				
AU097_RS	1.392517	Up	2.47E-69	formimidoylglutamase
07720				
AU097_RS	1.165672	Up	1.52E-07	DUF885 domain-containing protein
07725				
AU097_RS	1.186045	Up	2.89E-16	hypothetical protein
07745				
AU097_RS	1.313813	Up	3.7E-08	TetR/AcrR family transcriptional regulator
08710				

AU097_RS	1.522507	Up	0.000	DNA transfer protein p32
08885			292	
AU097_RS	1.441162	Up	1.05E	hypothetical protein
08925			-45	
AU097_RS	1.990121	Up	9.89E	MerR family transcriptional
09240			-17	regulator
AU097_RS	1.159549	Up	2.63E	hypothetical protein
09745			-05	
AU097_RS	1.430921	Up	1.56E	phosphate acetyltransferase
09845			-62	
AU097_RS	1.495476	Up	5.58E	acetate kinase
09850			-67	
AU097_RS	1.130523	Up	6.26E	aconitate hydratase AcnA
10220			-63	
AU097_RS	1.368536	Up	9.08E	hydroxypyruvate isomerase
10285			-22	
AU097_RS	1.815771	Up	7.89E	acyl-CoA synthetase
10375			-80	
AU097_RS	1.238882	Up	5.12E	acyl-CoA dehydrogenase
10780			-22	
AU097_RS	1.219079	Up	1.81E	Ig-like domain
10915			-60	
AU097_RS	1.547215	Up	0.000	hypothetical protein
11050			298	
AU097_RS	1.277695	Up	2.06E	hypothetical protein
11055			-85	
AU097_RS	1.046402	Up	3.48E	trehalose-6-phosphate
11220			-27	synthase
AU097_RS	1.287005	Up	3.58E	threonylcarbamoyl-AMP
11270			-12	synthase
AU097_RS	1.451916	Up	2.38E	metal-dependent hydrolase
11550			-10	
AU097_RS	1.160465	Up	3.76E	gamma-glutamyltransferase
11750			-21	family protein
AU097_RS	1.267775	Up	0.006	cupin domain-containing
11975			622	protein [Acinetobacter]
AU097_RS	1.001019	Up	9.88E	amino acid transporter
12450			-12	
AU097_RS	1.891923	Up	1E-13	hypothetical protein
12700				
AU097_RS	1.395535	Up	2.52E	gamma-aminobutyraldehyd
12705			-22	e dehydrogenase
AU097_RS	2.700051	Up	1E-42	aspartate aminotransferase
12715				family protein

AU097_RS	2.456076	Up	4.22E	arginine
12720			-24	N-succinyltransferase
AU097_RS	1.332388	Up	1.17E	feruloyl-CoA synthase
12815			-05	
AU097_RS	1.944957	Up	1E-12	crotonase
12825				
AU097_RS	1.696962	Up	4.2E-	aromatic ring-hydroxylating
12850			09	dioxygenase subunit alpha
AU097_RS	1.327513	Up	0.008	MFS transporter
12855			247	
AU097_RS	1.063488	Up	0.004	hypothetical protein
13000			539	
AU097_RS	1.167699	Up	0.003	hypothetical protein
13005			181	
AU097_RS	1.254068	Up	0.011	hypothetical protein
13050			311	
AU097_RS	1.816626	Up	1.1E-	OmpA family protein
13365			103	
AU097_RS	1.28526	Up	2.37E	aromatic acid/H <sup>+</sup> symport
13440			-07	family MFS transporter
AU097_RS	1.198891	Up	0.000	KR domain-containing
13450			264	protein
AU097_RS	1.354883	Up	1.45E	benzoate 1,2-dioxygenase
13465			-13	large subunit
AU097_RS	1.043153	Up	3.76E	Cu(I)-responsive
13485			-05	transcriptional regulator
				[Acinetobacter]
AU097_RS	1.143059	Up	9.1E-	MFS transporter
13760			05	
AU097_RS	3.234393	Up	6.8E-	divalent metal cation
13825			158	transporter
AU097_RS	3.201213	Up	2.6E-	LamB/YcsF family protein
13830			131	
AU097_RS	3.473384	Up	8.5E-	DUF1445 domain-containing
13835			107	protein
AU097_RS	2.743149	Up	1.4E-	allophanate hydrolase
13840			134	
AU097_RS	2.961316	Up	3.2E-	ATP-grasp
13845			213	domain-containing protein
AU097_RS	1.08262	Up	2.65E	DUF333 domain-containing
14095			-11	protein
AU097_RS	1.53906	Up	3.3E-	phenylacetic acid
14165			101	degradation bifunctional
				protein PaaZ

AU097_RS	1.032446	Up	2.82E	1,2-phenylacetyl-CoA
14170			-49	epoxidase subunit A
AU097_RS	1.3148	Up	1.55E	1,2-phenylacetyl-CoA
14175			-15	epoxidase subunit B [Acinetobacter]
AU097_RS	1.499868	Up	1.65E	phenylacetate-CoA
14180			-67	oxygenase subunit Paal
AU097_RS	1.536227	Up	1.89E	phenylacetate-CoA
14185			-33	oxygenase subunit PaaJ [Acinetobacter]
AU097_RS	1.751782	Up	4.95E	phenylacetate-CoA
14190			-74	oxygenase/reductase subunit PaaK
AU097_RS	1.762544	Up	1.76E	enoyl-CoA hydratase
14195			-44	
AU097_RS	2.024242	Up	1.93E	2-(1,2-epoxy-1,2-dihydrophe
14200			-52	nyl)acetyl-CoA isomerase
AU097_RS	1.999641	Up	3.01E	3-hydroxyacyl-CoA
14205			-78	dehydrogenase
AU097_RS	2.356772	Up	1.47E	3-oxoadipyl-CoA thiolase
14210			-86	
AU097_RS	2.48519	Up	1E-99	phenylacetate--CoA ligase
14215				[Acinetobacter]
AU097_RS	1.148118	Up	3.32E	phenylacetic acid
14220			-18	degradation operon negative regulatory protein PaaX
AU097_RS	1.268769	Up	1.59E	carbonic anhydrase
14225			-07	
AU097_RS	1.60666	Up	0.005	Paal family thioesterase
14230			131	
AU097_RS	2.142704	Up	3.8E-	hypothetical protein
14350			210	
AU097_RS	2.522866	Up	4.7E-	hydroxymethylglutaryl-CoA
14360			198	lyase
AU097_RS	2.454808	Up	4.6E-	acetyl/propionyl/methylcro
14365			216	onyl-CoA carboxylase subunit alpha
AU097_RS	2.29445	Up	1E-13	enoyl-CoA hydratase
14370			0	
AU097_RS	2.072343	Up	2.5E-	methylcrotonoyl-CoA
14375			231	carboxylase subunit beta
AU097_RS	1.70927	Up	3.3E-	isovaleryl-CoA
14380			142	dehydrogenase

					[Acinetobacter]
AU097_RS	1.473479	Up	6.7E-88	TetR/AcrR family	transcriptional regulator
14385					
AU097_RS	1.584436	Up	2.3E-99	AMP-binding protein	
14390					
AU097_RS	1.860351	Up	2.77E-29	class I SAM-dependent methyltransferase	
14395					
AU097_RS	1.850229	Up	2.47E-24	porin	
14400					
AU097_RS	1.887777	Up	0.000657	hypothetical protein	
14470					
AU097_RS	1.066247	Up	1.68E-06	LysE family translocator	
14480					
AU097_RS	1.049086	Up	3.4E-28	cytochrome ubiquinol oxidase subunit I	
14690					
AU097_RS	1.419848	Up	5.24E-21	peptide-methionine (R)-S-oxide reductase	
14855					
AU097_RS	1.54179	Up	9.37E-77	amino acid ABC transporter substrate-binding protein	
14970					
AU097_RS	1.38723	Up	7.4E-36	amino acid ABC transporter permease	
14975					
AU097_RS	1.428635	Up	7.26E-24	amino acid ABC transporter permease	
14980					
AU097_RS	1.5406	Up	2.68E-41	amino acid ABC transporter ATP-binding protein	
14985					
AU097_RS	1.837935	Up	2.31E-06	hypothetical protein	
15145					
AU097_RS	1.100482	Up	0.000393	phage major capsid protein	
15625					
AU097_RS	1.402496	Up	3E-06	membrane protein	
16085					
AU097_RS	1.070249	Up	9.77E-14	helix-turn-helix domain-containing protein	
16245					
AU097_RS	1.783306	Up	1.04E-38	lipoyl synthase	
16250					
AU097_RS	2.613427	Up	5.1E-147	thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha	
16255					
					[Acinetobacter]
AU097_RS	2.751704	Up	4.6E-128	alpha-ketoacid dehydrogenase subunit beta	
16260					
					[Acinetobacter]
AU097_RS	2.709018	Up	3.3E-	pyruvate dehydrogenase	

16265			146	complex	dihydrolipoamide acetyltransferase
AU097_RS	2.482195	Up	1.3E-	dihydrolipoyl	
16270			103	dehydrogenase	
AU097_RS	2.532405	Up	7.87E	3-oxoacyl-ACP reductase	
16275			-35		
AU097_RS	2.044181	Up	8.99E	2,3-butanediol	
16280			-68	dehydrogenase	
				[Acinetobacter]	
AU097_RS	1.320639	Up	5.63E	sulfite exporter	TauE/SafE
16305			-11	family protein	
AU097_RS	1.063217	Up	1.95E	MFS transporter	
16380			-06		
AU097_RS	2.547582	Up	1.8E-	acetyl-CoA C-acyltransferase	
16415			236		
AU097_RS	3.111344	Up	1.4E-	hypothetical protein	
16420			138		
AU097_RS	3.545127	Up	5E-27	CoA transferase subunit B	
16425			6		
AU097_RS	3.355226	Up	2.2E-	CoA transferase subunit A	
16430			212		
AU097_RS	1.065725	Up	1.2E-	GntP family permease	
16465			37		
AU097_RS	1.220277	Up	2.06E	3-hydroxybutyrate	
16470			-27	dehydrogenase	
AU097_RS	1.198637	Up	7.03E	AdeA/Adel family multidrug	
16540			-05	efflux RND transporter	
				periplasmic adaptor subunit	
AU097_RS	1.072523	Up	0.000	muconate cycloisomerase	
17065			169		
AU097_RS	1.183404	Up	0.000	flavin reductase	
17125			615		
AU097_RS	1.630775	Up	5.91E	oxidoreductase	
17130			-05		
AU097_RS	1.379569	Up	0.000	KR domain-containing	
17135			479	protein	
AU097_RS	2.112924	Up	7.35E	aromatic-ring-hydroxylating	
17140			-05	dioxygenase subunit beta	
AU097_RS	1.870779	Up	2.13E	aromatic ring-hydroxylating	
17145			-11	dioxygenase subunit alpha	
AU097_RS	1.445298	Up	0.005	hypothetical protein	
17155			927		
AU097_RS	1.417474	Up	1.19E	acyl-CoA dehydrogenase	
17160			-07		

AU097_RS	1.037498	Up	0.006	protocatechuate
17255			082	3,4-dioxygenase subunit alpha
AU097_RS	1.339034	Up	0.016	4-carboxymuconolactone
17265			976	decarboxylase [Acinetobacter]
AU097_RS	1.117003	Up	0.000	aromatic acid/H <sup>+</sup> symport
17270			133	family MFS transporter
AU097_RS	1.031416	Up	0.001	3-oxoadipate
17295			354	CoA-transferase subunit A
AU097_RS	1.418298	Up	7.41E-19	hypothetical protein
17510				
AU097_RS	1.348617	Up	1.88E-12	univeal stress protein
17615				
AU097_RS	1.595015	Up	5.1E-125	D-amino acid dehydrogenase
17805				
AU097_RS	1.379384	Up	0.016	hypothetical protein
18020			194	
AU097_RS	1.120939	Up	0.010	hypothetical protein
18065			31	
AU097_RS	1.293585	Up	0.013	hypothetical protein
18165			585	
AU097_RS	1.483132	Up	0.007	hypothetical protein
18270			185	
AU097_RS	1.352626	Up	3.22E-05	RDD family protein
18455				
AU097_RS	3.165241	Up	2.2E-227	alcohol dehydrogenase
18615				
AU097_RS	2.790133	Up	6.7E-289	aldehyde dehydrogenase
18630				
AU097_RS	1.045856	Up	1.34E-06	ethanolamine permease
18635				
AU097_RS	1.168491	Up	0.000	ethanolamine
18640			154	ammonia-lyase subunit EutB
AU097_RS	2.626809	Up	4.9E-108	AMP-binding protein
18860				
AU097_RS	2.497141	Up	1.3E-129	butyryl-CoA dehydrogenase
18865				
AU097_RS	2.711438	Up	1.4E-155	3-hydroxyacyl-CoA
18870				dehydrogenase
AU097_RS	1.091354	Up	0.000	hypothetical protein
19040			146	[Acinetobacter]
AU097_RS	1.109533	Up	5.26E-07	molecular chaperone
19200				

AU097_RS 19205	1.38997	Up	0.000	SCP4	domain-containing protein
AU097_RS 19210	1.208871	Up	0.000	protein CsA	104
AU097_RS 19215	2.042194	Up	3.42E-59	SCP4	domain-containing protein

Table 6 Differential expressed genes in  $\Delta$ abaIR strain

GenelD	log2FoldChange( $\Delta$ a balR/WT)	Up-Down-Regulation( $\Delta$ abaIR/WT)	Pvalue	Product
AU097_RS 06625	-4.810564081	Down	0	acyl-CoA dehydrogenase
AU097_RS 06615	-4.798341091	Down	0	non-ribosomal peptide synthetase
AU097_RS 06610	-4.684191859	Down	0	outer membrane lipoprotein-sorting protein
AU097_RS 06630	-4.479849984	Down	0	acyl-CoA synthetase
AU097_RS 08905	-3.443053657	Down	0	membrane protein
AU097_RS 06635	-3.169896529	Down	1.77E-13	LuxR family transcriptional regulator
AU097_RS 06605	-2.775977102	Down	1.2E-108	hypothetical protein
AU097_RS 06600	-2.592760202	Down	1.05E-77	alpha/beta hydrolase
AU097_RS 06645	-2.580535991	Down	5.26E-09	GNAT family N-acetyltransferase
AU097_RS 06620	-2.187695047	Down	8.04E-07	acyl carrier protein
AU097_RS 10260	-2.092687691	Down	1.5E-128	NAD(P)(+)-transhydrogenase (Re/Si-specific) subunit alpha
AU097_RS 10270	-1.736715963	Down	1.03E-89	NAD(P)-transhydrogenase subunit beta
AU097_RS 10265	-1.715456717	Down	5.71E-10	NAD(P)-transhydrogenase subunit alpha
AU097_RS 12875	-1.610454816	Down	5.57E-10	SDR family NAD(P)-dependent

					oxidoreductase
AU097_RS 06875	-1.571786385	Down	1.63E-66	UDP-glucose 4-epimerase GalE	
AU097_RS 14380	-1.571062479	Down	1.04E-66	isovaleryl-CoA dehydrogenase	
AU097_RS 13765	-1.504167019	Down	1.89E-08	DUF2147 domain-containing protein	
AU097_RS 05565	-1.467640693	Down	7.99E-23	hypothetical protein	
AU097_RS 12200	-1.450434646	Down	1.71E-06	esterase	
AU097_RS 12630	-1.447421801	Down	2.09E-77	hypothetical protein	
AU097_RS 05555	-1.418971886	Down	2.68E-07	DUF485 domain-containing protein	
AU097_RS 14390	-1.416019051	Down	6.55E-44	AMP-binding protein	
AU097_RS 14375	-1.363301003	Down	1.35E-64	methylcrotonoyl-Co A carboxylase subunit beta	
AU097_RS 14395	-1.333055716	Down	3.01E-07	class I SAM-dependent methyltransferase	
gene2510	-1.254200121	Down	0.000113	#N/A	
AU097_RS 07705	-1.221452269	Down	5.3E-91	histidine ammonia-lyase	
AU097_RS 06750	-1.218989942	Down	6.02E-21	short-chain dehydrogenase	
AU097_RS 05160	-1.216497945	Down	4E-69	acetyl-CoA hydrolase	
AU097_RS 12255	-1.2055697	Down	7E-106	isocitrate lyase	
AU097_RS 05775	-1.18255173	Down	1.22E-39	DUF2147 domain-containing protein	
AU097_RS 12620	-1.159218991	Down	1.38E-62	D-amino acid dehydrogenase	
AU097_RS 10175	-1.15568351	Down	2.52E-33	hypothetical protein	
AU097_RS 09645	-1.148829981	Down	0.008712	RNA-binding protein	
AU097_RS	-1.146164239	Down	6.59E-12	GntR family	

06840					transcriptional regulator
AU097_RS	-1.136579054	Down	3.51E-05	DUF1311	
08910				domain-containing protein	
AU097_RS	-1.136034285	Down	3.57E-11	ribosome-associated translation inhibitor	
10590				RaiA	
AU097_RS	-1.09534896	Down	1.37E-11	RidA family protein	
12615					
AU097_RS	-1.062020065	Down	2.24E-40	DegT/DnrJ/EryC1/Str S family	
06935				aminotransferase	
AU097_RS	-1.053989883	Down	0.001534	SRPBCC family	
13875				protein	
AU097_RS	-1.027361924	Down	1.64E-13	enoyl-CoA hydratase	
14370					
AU097_RS	-1.01932917	Down	6.13E-84	malate synthase G	
15725					
AU097_RS	-1.012081007	Down	3.26E-22	acetate kinase	
09850					
AU097_RS	-1.007776244	Down	2.76E-26	RND transporter	
07365					
AU097_RS	-1.00310968	Down	1.46E-42	Ig-like domain	
10915					
AU097_RS	1.000516557	Up	3.19E-06	LysE family	
14480				translocator	
AU097_RS	1.0133961	Up	8.83E-37	ferredoxin reductase	
07010					
AU097_RS	1.016484113	Up	3.04E-12	DUF541	
01160				domain-containing protein	
AU097_RS	1.022615214	Up	0.010216	hypothetical protein	
14910					
AU097_RS	1.027289495	Up	1.33E-12	DUF3108	
04145				domain-containing protein	
AU097_RS	1.027636888	Up	0.000313	DUF2184	
13145				domain-containing protein	
AU097_RS	1.050221533	Up	0.001537	transcriptional regulator	
02595					
AU097_RS	1.059975124	Up	0.000226	MFS transporter	
17175					

AU097_RS 01125	1.065129674	Up	4.77E-12	phosphonate transporter	ABC
AU097_RS 05210	1.083855153	Up	7.7E-06	XRE transcriptional regulator	family
AU097_RS 04890	1.089851492	Up	5.25E-28	bacterioferritin	
AU097_RS 11550	1.102335386	Up	2.83E-06	metal-dependent hydrolase	
AU097_RS 00265	1.10618527	Up	0.00818	hypothetical protein	
AU097_RS 10860	1.109814353	Up	1.46E-41	DUF1852 domain-containing protein	
AU097_RS 13165	1.111887863	Up	0.008051	hypothetical protein	
AU097_RS 10765	1.117361686	Up	2.1E-12	adenosine deaminase	
AU097_RS 13135	1.12070687	Up	0.001552	DUF2213 domain-containing protein	
AU097_RS 12720	1.121710543	Up	5.81E-05	arginine N-succinyltransferase	
AU097_RS 04620	1.122555825	Up	0.002472	EamA/RhaT family transporter	
AU097_RS 07060	1.127777848	Up	0.001455	sulfonate transporter	ABC
				substrate-binding protein	
AU097_RS 07165	1.134673245	Up	0.009058	hypothetical protein	
AU097_RS 10870	1.135437723	Up	5.34E-19	flavin reductase	
AU097_RS 12860	1.145646353	Up	0.002439	outer membrane porin, OprD family	
AU097_RS 05515	1.145856951	Up	1.85E-31	NADPH:quinone oxidoreductase	
AU097_RS 09015	1.161085465	Up	1.95E-46	FUSC family protein	
AU097_RS 06745	1.162966485	Up	0.001507	DUF1003 domain-containing	

AU097_RS 12715	1.16516071	Up	1.69E-06	protein aspartate aminotransferase family protein
AU097_RS 05945	1.175348599	Up	6.55E-17	replication protein C [Proteobacteria]
AU097_RS 11705	1.187305046	Up	8.43E-06	hypothetical protein
AU097_RS 13005	1.19521274	Up	0.000815	hypothetical protein
AU097_RS 07045	1.197457681	Up	5.63E-15	hypothetical protein
AU097_RS 08880	1.200746597	Up	0.003007	DNA transfer protein p32
AU097_RS 14960	1.202220672	Up	0.000235	SfnB family sulfur acquisition oxidoreductase
AU097_RS 18115	1.206540056	Up	0.00495	stress-responsive nuclear envelope protein
AU097_RS 01255	1.211481854	Up	1.01E-39	LysR family transcriptional regulator
AU097_RS 13835	1.218264558	Up	9.15E-09	DUF1445 domain-containing protein
AU097_RS 07005	1.273658088	Up	3.63E-49	acyl-CoA desaturase
AU097_RS 04575	1.274976219	Up	2.47E-25	HPP family protein
AU097_RS 10250	1.279002189	Up	0.001758	RidA family protein
AU097_RS 18125	1.290037253	Up	0.000228	hypothetical protein
AU097_RS 12450	1.291462344	Up	6.13E-21	amino acid transporter
AU097_RS 17065	1.294967434	Up	1.56E-06	muconate cycloisomerase
AU097_RS 15625	1.311448775	Up	3.38E-06	phage major capsid protein
AU097_RS 16845	1.31494929	Up	0.000124	SMP-30/gluconolact onase/LRE family protein
AU097_RS	1.319981098	Up	2.03E-07	hypothetical protein

00195					
AU097_RS	1.364315635	Up	2.3E-28	pyruvate	
01135				decarboxylase	
AU097_RS	1.376815835	Up	4.79E-15	EamA/RhaT	family
05215				transporter	
AU097_RS	1.390886913	Up	1.88E-28	MacA	family efflux
10110				pump subunit	
AU097_RS	1.406842394	Up	6.74E-23	RtcB	family protein
00260					
AU097_RS	1.408770151	Up	1.15E-13	EamA	family
08715				transporter	
AU097_RS	1.424467059	Up	5.57E-05	hypothetical	protein
04705					
AU097_RS	1.434908162	Up	6.18E-21	TetR/AcrR	family
05520				transcriptional	
				regulator	
AU097_RS	1.455698678	Up	1.21E-48	MFS	transporter
06395					
AU097_RS	1.463500264	Up	0.000157	hypothetical	protein
13175					
AU097_RS	1.482712098	Up	2.03E-06	flavin	reductase
17125					
AU097_RS	1.506892192	Up	0.0006	hypothetical	protein
18270					
AU097_RS	1.525928785	Up	8.33E-26	taurine	ABC
14730				transporter	
				ATP-binding	protein
AU097_RS	1.53094861	Up	9.1E-12	TetR/AcrR	family
08710				transcriptional	
				regulator	
AU097_RS	1.583794725	Up	5.9E-06	hypothetical	protein
03405					
AU097_RS	1.597978381	Up	8.73E-05	nuclear	transport
17150				factor	2 family
				protein	
AU097_RS	1.608502109	Up	0.000235	hypothetical	protein
13235					
AU097_RS	1.610222783	Up	5E-07	PaaX	family
00970				transcriptional	
				regulator	
AU097_RS	1.646501685	Up	1.18E-36	SCPU	
19215				domain-containing	
				protein	
AU097_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	