Table S1 The most changed genes in *Pseudomonas fluorescens* induced by calcium

|  |  |  |  |
| --- | --- | --- | --- |
| Gene ID | Gene Description | Fold change | P-value |
| Up Regulation |  |  |  |
| gene 5078 | PepSY domain-containing protein | 19.39 | 0.00 |
| gene 4174 | PepSY domain-containing protein | 24.39 | 0.00 |
| *lgrC* | Linear gramicidin synthase subunit C | 3.54 | 0.00 |
| gene 4451 | hypothetical protein | 17.22 | 0.00 |
| *lgrD* | Linear gramicidin synthase subunit D | 3.33 | 0.00 |
| *tcpJ* | Dipeptidase tcpJ | 3.61 | 0.00 |
| *grsT* | Gramicidin S biosynthesis protein GrsT | 6.88 | 0.00 |
| *Sumf1* | Formylglycine-generating enzyme | 6.35 | 0.00 |
| gene 3851 | N(5)-hydroxyornithine transformylase PvdF | 3.11 | 0.00 |
| gene 3855 | PvdJ/PvdD/PvdP-like protein | 3.05 | 0.00 |
| *fumC2* | Fumarate hydratase class II 2 | 2.73 | 0.00 |
| *fecI* | Probable RNA polymerase sigma factor FecI | 2.09 | 0.00 |
| *syrD* | ATP-binding protein SyrD | 3.81 | 0.00 |
| *hasA* | Hemophore HasA | 3.28 | 0.00 |
| *pvdA* | L-ornithine N(5)-monooxygenase | 2.82 | 0.00 |
| *pvdQ* | Acyl-homoserine lactone acylase PvdQ | 2.87 | 0.00 |
| *mntA* | Manganese-binding lipoprotein MntA | 3.42 | 0.00 |
| *mntC* | Manganese transport system membrane protein MntC | 2.54 | 0.00 |
| *ELI5* | Phenylacetaldehyde synthase | 3.42 | 0.00 |
| gene 35 | 2OG-Fe(II) oxygenase | 2.67 | 0.00 |
| *carS* | Sensor protein kinase CarS | 3.22 | 0.00 |
| *macA* | Macrolide export protein MacA | 2.43 | 0.00 |
| *tap* | Tripeptidyl aminopeptidase | 3.59 | 0.00 |
| *all1319* | 2-dehydropantoate 2-reductase | 2.47 | 0.00 |
| *cefD* | Isopenicillin N epimerase | 2.40 | 0.00 |
| *oprM* | Outer membrane protein OprM | 2.25 | 0.00 |
| gene 4878 | zinc ABC transporter substrate-binding protein | 2.45 | 0.00 |
| gene 2637 | acyl-CoA/acyl-ACP dehydrogenase | 2.95 | 0.00 |
| *moaF* | Protein MoaF | 2.77 | 0.00 |
| *ribD* | Riboflavin biosynthesis protein RibD | 2.51 | 0.00 |
| *citE* | Citrate lyase subunit beta-like protein | 2.96 | 0.00 |
| *frk* | Fructokinase | 2.52 | 0.00 |
| *nimR* | HTH-type transcriptional regulator NimR | 3.98 | 0.00 |
| *plsC* | 1-acyl-sn-glycerol-3-phosphate acyltransferase | 2.70 | 0.00 |
| gene 2190 | FtsX-like permease family protein | 2.29 | 0.00 |
| gene 4266 | DUF1853 family protein | 3.06 | 0.00 |
| *pbuA* | Ferric-pyoverdine M114 receptor PbuA | 2.07 | 0.00 |
| *aotP* | ATP-binding cassette domain-containing protein | 2.21 | 0.00 |
| gene 4681 | TIM barrel protein | 2.28 | 0.00 |
| gene 5157 | Succinylglutamate desuccinylase/aspartoacylase family protein | 2.17 | 0.00 |
| *F17a-A* | F17 fimbrial protein | 3.05 | 0.00 |
| *ghrB* | Glyoxylate/hydroxypyruvate reductase B | 2.22 | 0.00 |
| *rlmA* | 23S rRNA (guanine(745)-N(1))-methyltransferase | 2.32 | 0.00 |
| *hutH* | Histidine ammonia-lyase | 2.03 | 0.00 |
| *AF\_0788* | DMT family transporter | 2.36 | 0.00 |
| gene 4839 | TIGR03915 family putative DNA repair protein | 2.45 | 0.00 |
| *MJ0087* | ABC transporter permease protein MJ0087 | 2.07 | 0.00 |
| Down Regulation |  |  |  |
| *PH0782* | Alanine/serine racemase | 8.33 | 0.00 |
| *MJ1311* | Sugar phosphate isomerase/epimerase | 3.23 | 0.00 |
| *cadA* | Cadmium-transporting ATPase | 3.85 | 0.00 |
| *dmlR* | HTH-type transcriptional regulator DmlR | 3.33 | 0.00 |
| *arnC* | Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase | 3.13 | 0.00 |
| gene 4536 | Pentapeptide repeat-containing protein | 3.23 | 0.00 |
| *czcR* | Transcriptional activator protein CzcR | 3.61 | 0.00 |
| *lgt* | Phosphatidylglycerol--prolipoprotein diacylglyceryl transferase | 3.03 | 0.00 |
| *nemA* | N-ethylmaleimide reductase | 2.75 | 0.00 |
| *nemR* | HTH-type transcriptional repressor NemR | 2.57 | 0.00 |
| *yerO* | HTH-type transcriptional regulator YerO | 3.00 | 0.00 |
| *slr1025* | Uncharacterized protein slr1025 | 2.91 | 0.00 |
| *hxlR* | HTH-type transcriptional activator HxlR | 4.61 | 0.00 |
| *irlS* | Sensor protein IrlS | 2.87 | 0.00 |
| *bigR* | Biofilm growth-associated repressor | 3.19 | 0.00 |
| *umuC* | Translesion error-prone DNA polymerase V subunit UmuC | 2.61 | 0.00 |
| gene 2082 | DUF3077 domain-containing protein | 5.10 | 0.00 |
| *yeiE* | HTH-type transcriptional regulator YeiE | 2.35 | 0.00 |
| *HD\_0322* | RutC family protein HD\_0322 | 2.44 | 0.00 |
| *udg* | UDP-glucose 6-dehydrogenase | 2.48 | 0.00 |
| gene 4737 | DUF1289 domain-containing protein | 2.54 | 0.00 |
| *ywbI* | HTH-type transcriptional regulator YwbI | 2.44 | 0.00 |
| *tatB* | Sec-independent protein translocase protein TatB | 2.38 | 0.00 |
| gene 3331 | DNA-binding protein | 2.23 | 0.00 |
| *srlR* | Glucitol operon repressor | 2.55 | 0.00 |
| gene 2710 | XRE family transcriptional regulator | 2.35 | 0.00 |
| gene 4038 | pilus assembly protein | 2.26 | 0.00 |
| SSP1627 | SDR family oxidoreductase | 2.25 | 0.00 |
| gene 665 | hypothetical protein | 2.24 | 0.00 |
| gene 1149 | DUF4160 domain-containing protein | 2.12 | 0.00 |
| gene 2575 | hypothetical protein | 2.48 | 0.00 |
| gene 1204 | hypothetical protein | 2.19 | 0.00 |