**Table S2. Differently expressed genes involved in regulation of adaptation of *P. aeruginosa* PAO1 to urinary tract conditions.** Pairwise comparisons between late logarithmic biofilms grown anaerobically on AUM and 10-fold diluted LB supplemented with 50 mM nitrate was performed. A fold change cut-off of two and a ppde above 0.99999 was applied.

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| --- | --- | --- | --- |
| **Locus tag** | **Gene name** | **Function** | **Fold change** |
|  |  | **FUR regulon** |  |
| PA4764 | *fur* | ferric uptake regulation protein |  1.6 |
| PA2426 | *pvdS* | sigma factor PvdS |  6.6 |
| PA4227 | *pchR* | transcriptional regulator PchR |  4.5 |
| PA2258 | *ptxR* | transcriptional regulator PtxR |  1.1 |
| PA2686 | *pfeR* | two-component response regulator PfeR |  3.1 |
| PA0471 | *fiuR* | probable transmembrane sensor |  4.2 |
| PA0472 | *fiuI* | probable sigma-70 factor. ECF subfamily |  4.3 |
| PA1300 |  | probable sigma-70 factor. ECF subfamily |  11.7 |
| PA1301 |  | probable transmembrane sensor |  10.1 |
| PA1911 | *femR* | probable transmembrane sensor |  6.8 |
| PA1912 | *femI* | probable sigma-70 factor. ECF subfamily |  9.9 |
| PA2093 |  | probable sigma-70 factor. ECF subfamily |  6.3 |
| PA2094 |  | probable transmembrane sensor |  5.7 |
| PA2387 | *fpvI* | probable sigma-70 factor. ECF subfamily |  1.4  |
| PA2388 | *fpvR* | probable transmembrane sensor |  1.3 |
| PA2467 | *foxR* | Anti-sigma factor FoxR |  3.3 |
| PA2468 | *foxI* | ECF sigma factor FoxI |  4.3  |
| PA3409 |  | probable transmembrane sensor |  3.7 |
| PA3410 |  | probable sigma-70 factor. ECF subfamily |  8.4 |
| PA3899 | *fecI* | probable sigma-70 factor. ECF subfamily |  7.1 |
| PA3900 | *fecR* | probable transmembrane sensor |  3.2 |
| PA4895 |  | probable transmembrane sensor |  4.8 |
| PA4896 |  | probable sigma-70 factor. ECF subfamily |  10.3 |
| PA2385 | *pvdQ* | PvdQ |  6.7 |
| PA2386 | *pvdA*  | L-ornithine N5-oxygenase | 53.5 |
| PA2389 |  | conserved hypothetical protein |  6.1 |
| PA2390 |  | probable ATP-binding ABC transporter |  3.4 |
| PA2391 | *opmQ* | probable outer membrane protein precursor |  2.7 |
| PA2392 | *pvdP* | PvdP |  12.2 |
| PA2393 |  | probable dipeptidase precursor |  21.5 |
| PA2394 | *pvdN* | PvdN |  17.5 |
| PA2395 | *pvdO* | PvdO |  8.8 |
| PA2396 | *pvdF*  | pyoverdine synthetase F |  12.4 |
| PA2397 | *pvdE* | pyoverdine biosynthesis protein PvdE |  14.8 |
| PA2398 | *fpvA* | ferripyoverdine receptor |  27.6 |
| PA2399 | *pvdD* | pyoverdine synthetase D |  7.2 |
| PA2400 | *pvdJ* | PvdJ |  8.1 |
| PA2401 | *pvdI* | PvdI |  6.6 |
| PA2402 |  | probable non-ribosomal peptide synthetase |  11.3 |
| PA2403 |  | hypothetical protein |  15.6 |
| PA2404 |  | hypothetical protein |  12.2 |
| PA2405 |  | hypothetical protein |  22.8 |
| PA2406 |  | hypothetical protein |  9.5 |
| PA2407 |  | probable adhesion protein |  6.4 |
| PA2408 |  | ATP-binding component of ABC transporter |  4.6 |
| PA2409 |  | probable permease of ABC transporter |  2.9 |
| PA2410 |  | hypothetical protein |  4.8 |
| PA2411 |  | probable thioesterase | 42.8 |
| PA2412 |  | conserved hypothetical protein | 70.2 |
| PA2413 | *pvdH* | diaminobutyrate-2-ketoglutarate 4-aminotransferase  | 33.3 |
| PA2424 | *pvdL* | PvdL |  13.3 |
| PA2425 | *pvdG* | PvdG | 9.0 |
| PA2254 | *pvcA* | pyoverdine biosynthesis protein PvcA | 1.0 |
| PA2255 | *pvcB* | pyoverdine biosynthesis protein PvcB | 0.9 |
| PA2256 | *pvcC* | pyoverdine biosynthesis protein PvcC | 1.0 |
| PA2257 | *pvcD* | pyoverdine biosynthesis protein PvcD | 1.0 |
| PA0707 | *toxR* | transcriptional regulator ToxR |  7.4 |
| PA1134 |  | hypothetical protein |  2.7  |
| PA2531 |  | probable aminotransferase |  3.4 |
| PA2451 |  | hypothetical protein |  3.1 |
| PA4221 | *fptA* | Fe(III)-pyochelin outer membrane receptor precursor |  3.2  |
| PA4220 | *fptB* | hypothetical protein | 4.0 |
| PA4222 | *pchI* | ATP-binding component of ABC transporter |  7.2 |
| PA4223 | *pchH* | ATP-binding component of ABC transporter |  6.3 |
| PA4224 | *pchG* | pyochelin biosynthetic protein PchG |  7.1 |
| PA4225 | *pchF* | pyochelin synthetase |  8.9  |
| PA4226 | *pchE* | dihydroaeruginoic acid synthetase |  8.1 |
| PA4227 | *pchR* | transcriptional regulator PchR |  4.5 |
| PA4228 | *pchD* | pyochelin biosynthesis protein PchD |  3.6 |
| PA4229 | *pchC* | pyochelin biosynthetic protein PchC |  3.7 |
| PA4230 | *pchB* | salicylate biosynthesis protein PchB |  5.2 |
| PA4231 | *pchA* | salicylate biosynthesis isochorismate synthase |  3.9 |
| PA4467 |  | hypothetical protein |  12.3 |
| PA4468 | *sodM* | sodA ; superoxide dismutase |  19.8 |
| PA4469 |  | hypothetical protein |  22.1 |
| PA4470 | *fumC1* | fumarate hydratase |  18.9 |
| PA4471 | *fagA* | hypothetical protein |  18.9 |
| PA2688 | *pfeA* | Ferric enterobactin receptor. outer membrane protein |  2.5 |
| PA4705 | *phuW* | hypothetical protein |  1.5 |
| PA4706 | *phuV* | ATP-binding component of ABC transporter |  2.6 |
| PA4707 | *phuU* | probable permease of ABC transporter |  1.9 |
| PA4708 | *phuT* | Heme-transport protein. PhuT |  5.5 |
| PA4709 | *phuS* | probable hemin degrading factor |  5.6 |
| PA4710 | *phuR* | Haem/Haemoglobin uptake outer membrane receptor  |  5.1  |
| PA4514  | *piuA* | probable outer membrane receptor for iron transport | 0.5 |
| PA4168 | *fpvB* | ferric pyoverdine receptor FpvB | 5.0 |
| PA2466 | *foxA* | Ferrioxamine receptor FoxA | 2.0 |
| PA3405 | *hasE*  | metalloprotease secretion protein |  2.4 |
| PA3406  | *hasD*  | transport protein HasD |  3.2 |
| PA3407  | *hasAp* | heme acquisition protein HasAp | 64.0 |
| PA3408 | *hasR* | Haem uptake outer membrane receptor HasR precursor | 10.00 |
| PA3901  | *fecA*  | Fe(III) dicitrate transport protein FecA |  17.1 |
| PA0929  | *pirR*  | two-component response regulator |  3.6 |
| PA0930 | *pirS*  | two-component sensor |  1.9 |
| PA0931 | *pirA* | ferric enterobactin receptor PirA |  2.4 |
|  |  | **Quorum sensing regulon** |  |
| PA3476  | *rhlI* | autoinducer synthesis protein RhlI |  1.9 |
| PA3477  | *rhlR*  | transcriptional regulator RhlR |  1.1 |
| PA3478 | *rhlB*  | rhamnosyltransferase chain B |  1.7 |
| PA3479  | *rhlA*  | rhamnosyltransferase chain A |  2.8 |
| PA2570 | *lecA*  | galactophilic lectin LecA |  1.8 |
| PA3361  | *lecB* | fucose-binding lectin LecB |  2.3 |
| PA4209 | *phzM*  | phenazine-specific methyltransferase |  1.4 |
| PA4210 | *phzA1* | phenazine biosynthesis protein | 0.9 |
| PA4211 | *phzB1* | phenazine biosynthesis protein |  1.1 |
| PA4217 | *phzS* | flavin-containing monooxygenase | 0.8 |
| PA1901 | *phzC2* | phenazine biosynthesis protein PhzC |  1.4 |
| PA1902 | *phzD2* | phenazine biosynthesis protein PhzD |  1.1 |
| PA1903 | *phzE2* | phenazine biosynthesis protein PhzE | 0.9 |
| PA1904 | *phzF2* | probable phenazine biosynthesis protein |  1.1 |
| PA1905 | *phzG2* | probable pyridoxamine 5'-phosphate oxidase | 1.0 |
| PA1430 | *lasR* | transcriptional regulator LasR |  1.2 |
| PA1432 | *lasI* | autoinducer synthesis protein LasI |  1.5 |
| PA1871  | *lasA* | LasA protease precursor |  1.8 |
| PA2193  | *hcnA*  | hydrogen cyanide synthase HcnA | 0.5 |
| PA2194  | *hcnB* | hydrogen cyanide synthase HcnB | 0.4 |
| PA2195 | *hcnC* | hydrogen cyanide synthase HcnC  | 0.5 |
| PA3724 | *lasB* | elastase LasB |  4.8 |
| PA2862  | *lipA* | lactonizing lipase precursor |  8.8 |
| PA2863  | *lipH* | lipase modulator protein |  2.1 |
| PA1245  | *aprX* | hypothetical protein |  9.1 |
| PA1246  | *aprD* | alkaline protease secretion protein AprD |  3.4 |
| PA1247  | *aprE* | alkaline protease secretion protein AprE |  3.4 |
| PA1248  | *aprF* | Alkaline protease secretion protein AprF |  2.7 |
| PA1249  | *aprA* | alkaline metalloproteinase precursor AprA |  24.7 |
| PA1003  | *pqsR* | Transcriptional regulator MvfR |  6.1 |
| PA0996  | *pqsA*  | probable coenzyme A ligase |  2.3 |
| PA0997  | *pqsB* | beta-keto-acyl-acyl-carrier protein synthase |  2.1 |
| PA0998  | *pqsC* | beta-keto-acyl-acyl-carrier protein synthase |  2.1 |
| PA0999  | *pqsD* | 3-oxoacyl-[acyl-carrier-protein] synthase III | 2.0 |
| PA1000 | *pqsE*  | Quinolone signal response protein |  1.5 |
| PA1001  | *phnA*  | anthranilate synthase component I |  1.7 |
| PA1002 | *phnB* | anthranilate synthase component II |  1.8 |
|  |  | **ANR regulon** |  |
| PA1544  | *anr* | transcriptional regulator Anr | 0.8 |
| PA0527 | *dnr*  | transcriptional regulator Dnr | 0.6 |
| PA3878 | *narX* | two-component sensor NarX |  2.7 |
| PA3879 | *narL* | two-component response regulator NarL |  2.5 |
| PA3872 | *narI* | respiratory nitrate reductase gamma chain | 0.2 |
| PA3873 | *narJ* | respiratory nitrate reductase delta chain | 0.2 |
| PA3874 | *narH* | respiratory nitrate reductase beta chain | 0.1 |
| PA3875 | *narG* | respiratory nitrate reductase alpha chain | 0.2 |
| PA3876 | *narK2* | nitrite extrusion protein 2 | 0.5 |
| PA3877 | *narK1* | nitrite extrusion protein 1 | 0.2 |
| PA3870 | *moaA1* | molybdopterin biosynthetic protein A1 | 0.6 |
| PA4666 | *hemA* | delta-aminolevulinic synthase  | 0.8 |
| PA3871 | *nifM* | peptidyl-prolyl cis-trans isomerase. PpiC-type | 0.3 |
| PA5170 | *arcD*  | arginine/ornithine antiporter |  1.2 |
| PA5171 | *arcA*  | arginine deiminase |  1.2 |
| PA5172 | *arcB*  | ornithine carbamoyltransferase. catabolic |  1.6 |
| PA5173 | *arcC*  | carbamate kinase | 1.0 |
| PA0835 | *pta* | phosphate acetyltransferase | 1.0 |
| PA0836 | *ackA* | acetate kinase |  1.2 |
| PA3929  | *cioB*  | cyanide insensitive terminal oxidase | 0.8 |
| PA3930 | *cioA* | cyanide insensitive terminal oxidase | 0.8 |
| PA1553 | *cooO/fixO* | probable cytochrome oxidase subunit (cbb3-type) | 0.5 |
| PA1554  | *cooN/fixN* | probable cytochrome oxidase subunit (cbb3-type) | 0.6 |
| PA1555  | *ccoP/fixP* | probable cytochrome c | 0.4 |
| PA1556 | *cooO/fixO* | probable cytochrome c oxidase subunit | 0.4 |
| PA1557  | *cooQ/fixQ* | probable cytochrome oxidase subunit (cbb3-type) | 0.5 |
| PA0509  | *nirN* | probable c-type cytochrome | 0.3 |
| PA0510  | *nirE* | probable uroporphyrin-III c-methyltransferase | 0.2 |
| PA0511  | *nirJ* | heme d1 biosynthesis protein NirJ | 0.3 |
|  PA0512  | *nirH* | conserved hypothetical protein | 0.3 |
| PA0513 | *nirG* | probable transcriptional regulator | 0.2 |
| PA0514  | *nirL* | heme d1 biosynthesis protein NirL | 0.3 |
| PA0515  | *nirD* | probable transcriptional regulator | 0.2 |
| PA0516  | *nirF* | heme d1 biosynthesis protein NirF | 0.2 |
| PA0517  | *nirC* | probable c-type cytochrome precursor | 0.1 |
|  PA0518 | *nirM* | cytochrome c-551 precursor | 0.1 |
| PA0519 | *nirS* | nitrite reductase precursor | 0.2 |
| PA0520 | *nirQ* | regulatory protein NirQ | 0.4 |
| PA0521  | *nirO* | probable cytochrome c oxidase subunit | 0.3 |
| PA0522  | *nirP* | hypothetical protein | 0.7 |
| PA0523 | *norC* | nitric-oxide reductase subunit C | 0.1 |
| PA0524  | *norB* | nitric-oxide reductase subunit B | 0.1 |
| PA0525  | *norD* | probable dinitrification protein NorD | 0.2 |
| PA0526 |  | hypothetical protein | 0.4 |
| PA3391  | *nosR* | regulatory protein NosR | 0.2 |
| PA3392 | *nosZ* | nitrous-oxide reductase precursor | 0.1 |
| PA3393  | *nosD* | NosD protein | 0.2 |
| PA3394  | *nosF* | NosF protein | 0.2 |
| PA3395 | *nosY* | NosY protein | 0.3 |
| PA3396 | *nosL* | NosL protein | 0.4 |
|  |  | **PhoBR regulon** |  |
| PA5360 | *phoB* | two-component response regulator PhoB | 0.03 |
| PA5361 | *phoR* | two-component sensor PhoR | 0.1 |
| PA5362  |  | conserved hypothetical protein | 0.4 |
| PA5363  |  | hypothetical protein |  1.4 |
| PA5364  |  | probable two-component response regulator | 0.7 |
| PA5365  | *phoU* | phosphate uptake regulatory protein PhoU | 0.1 |
| PA5366 | *pstB* | ATP-binding component of phosphate transporter | 0.04 |
| PA5367  | *pstA* | membrane protein of phosphate transporter | 0.04 |
| PA5368  | *pstC* | membrane protein of phosphate transporter | 0.04 |
| PA5369  | *pstS* | periplasmic phosphate-binding protein PstS | 0.03 |
| PA3375  | *phnL* | probable ATP-binding component of transporter | 0.3 |
| PA3376  | *phnK* | probable ATP-binding component of transporter | 0.3 |
| PA3377  | *phnJ* | conserved hypothetical protein | 0.1 |
| PA3378  | *phnI* | conserved hypothetical protein | 0.1 |
| PA3379  | *phnH* | conserved hypothetical protein | 0.2 |
| PA3380  | *phnG* | conserved hypothetical protein | 0.1 |
| PA3381 | *phnF* | probable transcriptional regulator | 0.1 |
| PA3382  | *phnE* | phosphonate transport protein PhnE | 0.2 |
|  PA3383  | *phnD* | binding protein of phosphonate transporter | 0.05 |
| PA3384 | *phnC* | ATP-binding component of phosphonate transporter | 0.2 |
| PA3296  | *phoA* | alkaline phosphatase | 0.05 |
| PA3319 | *plcN* | non-hemolytic phospholipase C precursor | 0.2 |
|  |  | **FleQ regulon** |  |
| PA1097 | *fleQ* | transcriptional regulator FleQ |  1.2 |
| PA1077 | *flgB*  | flagellar basal-body rod protein FlgB | 0.2 |
| PA1078 | *flgC* | flagellar basal-body rod protein FlgC | 0.2 |
| PA1079  | *flgD* | flagellar basal-body rod modification protein FlgD | 0.1 |
|  PA1080  | *flgE* | flagellar hook protein FlgE | 0.2 |
|  PA1081 | *flgF* | flagellar basal-body rod protein FlgF | 0.2 |
| PA1082 | *flgG* | flagellar basal-body rod protein FlgG | 0.3 |
| PA1083  | *flgH* | flagellar L-ring protein precursor FlgH | 0.3 |
|  PA1084 | *flgI* | flagellar P-ring protein precursor FlgI | 0.3 |
|  PA1085  | *flgJ* | flagellar protein FlgJ | 0.3 |
|  PA1086  | *flgK* | flagellar hook-associated protein 1 FlgK | 0.2 |
|  PA1087 | *flgL* | flagellar hook-associated protein type 3 FlgL | 0.2 |
| PA1088 |  | hypothetical protein | 0.3 |
|  PA1089 |  | conserved hypothetical protein | 0.3 |
|  PA1090  |  | hypothetical protein | 0.3 |
|  PA1091 | *fgtA* | flagellar glycosyl transferase. FgtA | 0.3 |
| PA1092 | *fliC* | flagellin type B | 0.5 |
|  PA1093 | *flaG*  | hypothetical protein | 0.4 |
| PA1094  | *fliD* | flagellar capping protein FliD | 0.5 |
| PA1095  | *fliS* | hypothetical protein | 0.3 |
| PA1096  |  | hypothetical protein | 0.2 |
|  PA1097 | *fleQ* | transcriptional regulator FleQ |  1.2 |
| PA1098  | *fleS* | two-component sensor | 0.4 |
|  PA1099  | *fleR* | two-component response regulator | 0.4 |
| PA1100  | *fliE* | flagellar hook-basal body complex protein FliE | 0.4 |
| PA1101 | *fliF* | Flagella M-ring outer membrane protein precursor | 0.4 |
| PA1102 | *fliG* | flagellar motor switch protein FliG | 0.7 |
| PA1103  | *fliH* | probable flagellar assembly protein | 0.6 |
| PA1104 | *fliI* | flagellum-specific ATP synthase FliI | 0.6 |
| PA1105  | *fliJ* | flagellar protein FliJ | 0.5 |
|  |  | **Vfr regulon** |  |
| PA0652 | *vfr* | transcriptional regulator Vfr, cyclic AMP receptor | 1.3 |
| PA1148 | *toxA* | exotoxin A precursor | 1.0 |
| PA0707 | *regA/toxR* | transcriptional regulator ToxR | 7.4 |
| PA3477  | *rhlR* | transcriptional regulator RhlR | 1.1 |
| PA1430 | *lasR* | transcriptional regulator LasR | 1.2 |
| PA5261 | *algR* | alginate biosynthesis regulatory protein AlgR | 1.7 |
| PA5262 | *algZ* | alginate biosynthesis protein AlgZ | 1.4 |
| PA1097 | *fleQ* | transcriptional regulator FleQ | 1.1 |