

Supplementary Table S1. List of genes in the RNA-Seq result that were found to be significantly up-regulated in *P. aeruginosa* upon 500 μ M iberin treatment. Up-regulation was defined as greater than 2-fold increase in the RNA-Seq result. Only genes showing a significant difference in expression from the control (i.e. p-value < 0.05) were selected.

PA No.	Gene Name	QS ^a	Description	Fold Change	P value
PA0119			Probable dicarboxylate transporter	2.2	0.03
PA0132			Beta-alanine--pyruvate transaminase	2.9	0.05
PA0133			Probable transcriptional regulator	4.2	0.01
PA0161			Hypothetical protein	4.7	0.01
PA0181			Probable transcriptional regulator	2.2	0.03
PA0182			Probable short-chain dehydrogenase	7.6	0.04
PA0185			Probable permease of ABC transporter	8.9	0.04
PA0201			Hypothetical protein	25.9	0.01
PA0202			Probable amidase	20.7	0.03
PA0234			Hypothetical protein	2.5	0.03
PA0283	<i>sbp</i>		Sulfate-binding protein precursor	26.0	0.01
PA0284			Hypothetical protein	32.9	0.04
PA0450			Probable phosphate transporter	2.1	0.05
PA0485			Conserved hypothetical protein	2.1	0.04
PA0539			Hypothetical protein	2.1	0.04
PA0709			Hypothetical protein	2.3	0.01
PA0865	<i>hpd</i>		4-hydroxyphenylpyruvate dioxygenase	42.2	0.04
PA0878			Hypothetical protein	7.9	0.04
PA0879			Probable acyl-CoA dehydrogenase	4.1	0.05
PA0905	<i>rsmA</i>		RsmA, regulator of secondary metabolites	3.6	0.01
PA1223			Probable transcriptional regulator	2.7	0.04
PA1226			Probable transcriptional regulator	2.9	0.01
PA1253			Probable semialdehyde dehydrogenase	2.3	0.02
PA1284			Probable acyl-CoA dehydrogenase	2.2	0.01
PA1285			Probable transcriptional regulator	5.2	0.05
PA1310	<i>phnW</i>		2-aminoethylphosphonate:pyruvate aminotransferase	19.3	0.05
PA1332			Hypothetical protein	17.7	0.05
PA1334			Probable oxidoreductase	74.7	0.04
PA1493	<i>cysP</i>		Sulfate-binding protein of ABC transporter	8.2	<0.01
PA1569			Probable major facilitator superfamily (MFS) transporter	4.7	0.03
PA1570			Probable transcriptional regulator	2.7	0.05
PA1602			Probable oxidoreductase	2.4	<0.01
PA1621			Probable hydrolase	2.8	0.04
PA1738			Probable transcriptional regulator	2.6	0.01
PA1742			Probable amidotransferase	3.1	<0.01
PA1756	<i>cysH</i>		3-phosphoadenosine-5-phosphosulfate reductase	3.4	0.04

PA1936			Hypothetical protein	2.1	0.02
PA1999	<i>dhcA</i>		Probable CoA transferase, subunit A	9.1	0.01
PA2000	<i>dhcB</i>		Probable CoA transferase, subunit B	9.5	<0.01
PA2001	<i>atoB</i>		Acetyl-CoA acetyltransferase	5.0	0.02
PA2008	<i>fahA</i>		Fumarylacetoacetase	54.8	0.03
PA2009	<i>hmgA</i>		Homogentisate 1,2-dioxygenase	62.0	0.02
PA2047			Probable transcriptional regulator	2.1	0.04
PA2086			Probable epoxide hydrolase	3.7	0.05
PA2087			Hypothetical protein	2.4	0.05
PA2090			Hypothetical protein	2.2	0.02
PA2095			Hypothetical protein	4.4	0.03
PA2220			Probable transcriptional regulator	2.9	0.03
PA2247	<i>bkdA1</i>		2-oxoisovalerate dehydrogenase (alpha subunit)	2.2	0.04
PA2250	<i>lpdV</i>		Lipoamide dehydrogenase-Val	2.5	0.04
PA2275			Probable alcohol dehydrogenase (Zn-dependent)	3.4	0.04
PA2277	<i>arsR</i>		ArsR protein	15.3	0.05
PA2278	<i>arsB</i>		ArsB protein	9.6	0.02
PA2310			Hypothetical protein	20.5	0.03
PA2311			Hypothetical protein	51.8	0.05
PA2312			Probable transcriptional regulator	29.6	<0.01
PA2326			Hypothetical protein	3.0	0.01
PA2327		x	Probable permease of ABC transporter	6.6	0.05
PA2359			Probable transcriptional regulator	34.5	0.03
PA2444	<i>glyA2</i>		Serine hydroxymethyltransferase	37.4	0.05
PA2481			Hypothetical protein	2.0	0.01
PA2483			Conserved hypothetical protein	3.7	0.03
PA2484			Conserved hypothetical protein	2.1	<0.01
PA2490			Conserved hypothetical protein	16.4	0.05
PA2491			Probable oxidoreductase	34.1	0.03
PA2494	<i>mexF</i>		Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter MexF	129.4	0.04
PA2495	<i>oprN</i>		Multidrug efflux outer membrane protein OprN precursor	102.3	0.03
PA2535			Probable oxidoreductase	4.8	0.05
PA2575			Hypothetical protein	28.5	0.02
PA2576			Hypothetical protein	2.3	0.01
PA2578			Probable acetyltransferase	2.7	0.02
PA2579	<i>kynA</i>		L-Tryptophan:oxygen 2,3-oxidoreductase (deacylizing) KynA	5.3	0.05
PA2580			Conserved hypothetical protein	26.1	0.01
PA2593	<i>qteE</i>	x	Hypothetical protein	2.1	<0.01
PA2594		x	Conserved hypothetical protein	9.0	0.02
PA2599			Conserved hypothetical protein	12.1	0.05
PA2600			Hypothetical protein	21.0	<0.01
PA2610			Conserved hypothetical protein	5.2	0.03

PA2636		Hypothetical protein	2.8	0.02
PA2641	<i>nuoF</i>	NADH dehydrogenase I chain F	2.4	0.02
PA2642	<i>nuoG</i>	NADH dehydrogenase I chain G	2.4	<0.01
PA2643	<i>nuoH</i>	NADH dehydrogenase I chain H	2.3	0.02
PA2645	<i>nuoJ</i>	NADH dehydrogenase I chain J	2.4	0.01
PA2647	<i>nuoL</i>	NADH dehydrogenase I chain L	2.1	0.01
PA2648	<i>nuoM</i>	NADH dehydrogenase I chain M	2.2	0.03
PA2649	<i>nuoN</i>	NADH dehydrogenase I chain N	2.1	0.05
PA2665		Probable transcriptional regulator	2.9	0.04
PA2711		Probable periplasmic spermidine/putrescine-binding protein	2.3	0.01
PA2714		Probable molybdopterin oxidoreductase	3.2	<0.01
PA2715		Probable ferredoxin	2.4	0.01
PA2758		Probable transcriptional regulator	63.7	0.02
PA2759		Hypothetical protein	179.3	0.01
PA2766		Probable transcriptional regulator	2.7	0.04
PA2767		Probable enoyl-CoA hydratase/isomerase	5.8	0.03
PA2768		Hypothetical protein	2.5	0.04
PA2786		Hypothetical protein	8.6	0.05
PA2812		Probable ATP-binding component of ABC transporter	20.4	0.03
PA2813		Probable glutathione S-transferase	32.7	0.04
PA2844		Conserved hypothetical protein	8.3	0.04
PA2845		Hypothetical protein	91.2	0.04
PA2846		Probable transcriptional regulator	2.9	0.03
PA2881		Probable two-component response regulator	4.3	0.03
PA2930		Probable transcriptional regulator	2.7	0.05
PA2931	<i>cifR</i>	CifR	10.4	0.03
PA2932	<i>morB</i>	Morphinone reductase	45.7	0.03
PA3035		Probable glutathione S-transferase	8.0	<0.01
PA3176	<i>gltS</i>	Glutamate/sodium ion symporter, GltS	2.2	0.02
PA3222		Hypothetical protein	5.4	0.04
PA3229		Hypothetical protein	311.5	0.04
PA3230		Conserved hypothetical protein	69.5	0.01
PA3424		Hypothetical protein	2.2	0.05
PA3446		Conserved hypothetical protein	63.5	0.05
PA3450		Probable antioxidant protein	39.4	0.01
PA3630		Probable transcriptional regulator	3.7	0.03
PA3663		Hypothetical protein	2.1	0.02
PA3893		Conserved hypothetical protein	2.5	0.05
PA3927		Probable transcriptional regulator	3.1	0.02
PA3931		Conserved hypothetical protein	44.7	0.05
PA3938		Probable periplasmic taurine-binding protein precursor	24.5	0.05
PA3971		Hypothetical protein	2.2	<0.01
PA4166		Probable acetyltransferase	77.6	0.02

PA4167		Probable oxidoreductase	112.0	<0.01
PA4173		Conserved hypothetical protein	12.4	0.01
PA4288		Probable transcriptional regulator	3.9	0.02
PA4355		Probable major facilitator superfamily (MFS) transporter	37.3	<0.01
PA4385	<i>groEL</i>	GroEL protein	6.4	0.04
PA4386	<i>groES</i>	GroES protein	6.4	0.03
PA4387		Conserved hypothetical protein	8.0	0.05
PA4442	<i>cysN</i>	ATP sulfurylase GTP-binding subunit/APS kinase	4.5	0.04
PA4443	<i>cysD</i>	ATP sulfurylase small subunit	3.8	<0.01
PA4475		Conserved hypothetical protein	2.4	0.05
PA4623		Hypothetical protein	727.4	0.01
PA4630		Hypothetical protein	3.2	0.03
PA4918		Hypothetical protein	3.0	0.01
PA4919	<i>pncB1</i>	Nicotinate phosphoribosyltransferase	2.8	0.02
PA4920	<i>nadE</i>	NH ₃ -dependent NAD synthetase	2.1	0.02
PA4921		Hypothetical protein	2.4	0.02
PA4980		Probable enoyl-CoA hydratase/isomerase	3.9	0.02
PA4985		Hypothetical protein	2.1	0.03
PA5103		Hypothetical protein	2.4	0.04
PA5105	<i>hutC</i>	Histidine utilization repressor HutC	2.1	0.02
PA5106		Conserved hypothetical protein	2.2	0.02
PA5246		Conserved hypothetical protein	2.2	0.02
PA5429	<i>aspA</i>	Aspartate ammonia-lyase	4.6	<0.01
PA5446		Hypothetical protein	2.8	0.02

^aAn 'X' in the box indicates that the gene/protein is regulated by quorum sensing (1), in reference to the QS-regulated genes/proteins as determined previously.

Supplementary Table S2. List of genes in the RNA-Seq result that were found to be significantly down-regulated in *P. aeruginosa* upon 500 μ M iberin treatment. Down-regulation was defined as greater than 2-fold increase in the RNA-Seq result. Only genes showing a significant difference in expression from the control (i.e. p-value < 0.05) were selected.

PA No.	Gene Name	QS ^a	Description	Fold Change	P value
PA0027		x	Hypothetical protein	-3.3	0.04
PA0028			Hypothetical protein	-3.3	0.04
PA0029			Probable sulfate transporter	-2.0	0.03
PA0039			Hypothetical protein	-2.5	0.05
PA0044	<i>exoT</i>		Exoenzyme T	-2.0	0.02
PA0122	<i>rahU</i>	x	RahU	-32.8	0.05
PA0123			Probable transcriptional regulator	-4.6	0.05
PA0143	<i>nuh</i>	x	Purine nucleosidase Nuh	-3.8	0.05
PA0179			Probable two-component response regulator	-3.1	0.03
PA0200			Hypothetical protein	-4.6	0.04
PA0208	<i>mdcA</i>		Malonate decarboxylase alpha subunit	-3.1	0.01
PA0211	<i>mdcD</i>		Malonate decarboxylase beta subunit	-3.6	0.02
PA0212	<i>mdcE</i>		Malonate decarboxylase gamma subunit	-3.2	0.03
PA0346			Hypothetical protein	-3.6	0.03
PA0460			Hypothetical protein	-2.3	0.05
PA0471			Probable transmembrane sensor	-3.1	0.02
PA0472			Probable sigma-70 factor	-3.6	0.03
PA0519	<i>nirS</i>		Nitrite reductase precursor	-2.2	0.04
PA0523	<i>norC</i>		Nitric-oxide reductase subunit C	-10.9	0.04
PA0524	<i>norB</i>		Nitric-oxide reductase subunit B	-3.9	<0.01
PA0526			Hypothetical protein	-4.7	0.05
PA0572		x	Hypothetical protein	-3.7	<0.01
PA0619			Probable bacteriophage protein	-2.5	0.03
PA0623			Probable bacteriophage protein	-2.6	0.04
PA0625			Hypothetical protein	-2.6	0.05
PA0626			Hypothetical protein	-2.5	0.01
PA0629			Conserved hypothetical protein	-2.4	0.04
PA0633			Hypothetical protein	-2.4	<0.01
PA0634			Hypothetical protein	-2.5	0.05
PA0638			Probable bacteriophage protein	-2.4	0.01
PA0639			Conserved hypothetical protein	-2.2	0.04
PA0640			Probable bacteriophage protein	-2.2	0.05
PA0707	<i>toxR</i>		Transcriptional regulator ToxR	-5.4	0.02
PA0718			Hypothetical protein of bacteriophage Pf1	-3.1	0.05
PA0722			Hypothetical protein of bacteriophage Pf1	-2.3	0.04
PA0795	<i>prpC</i>		Citrate synthase 2	-2.4	0.05

PA0796	<i>prpB</i>		Carboxyphosphoenolpyruvate phosphonmutase	-3.9	0.05
PA0807	<i>ampDh3</i>		AmpDh3	-2.4	0.02
PA0852	<i>cbpD</i>	x	Chitin-binding protein CbpD precursor	-22.0	0.04
PA0958	<i>oprD</i>		Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	-2.0	0.01
PA0996	<i>pqsA</i>	x	Probable coenzyme A ligase	-3.1	0.05
PA0997	<i>pqsB</i>	x	PqsB	-4.0	0.05
PA1000	<i>pqsE</i>	x	Quinolone signal response protein	-4.4	0.05
PA1001	<i>phnA</i>	x	Anthranilate synthase component I	-7.2	0.01
PA1002	<i>phnB</i>	x	Anthranilate synthase component II	-4.8	0.02
PA1003	<i>mvfR</i>	x	Transcriptional regulator MvfR	-2.5	0.03
PA1092	<i>fliC</i>		Flagellin type B	-2.1	<0.01
PA1127			Probable oxidoreductase	-3.6	0.05
PA1129			Probable fosfomycin resistance protein	-3.9	0.02
PA1130	<i>rhIC</i>	x	Rhamnosyltransferase 2	-11.7	0.04
PA1131		x	Probable major facilitator superfamily (MFS) transporter	-8.9	0.05
PA1134			Hypothetical protein	-6.0	0.01
PA1196		x	Probable transcriptional regulator	-2.4	0.02
PA1212			Probable major facilitator superfamily (MFS) transporter	-3.3	<0.01
PA1214			Hypothetical protein	-8.2	0.03
PA1215			Hypothetical protein	-7.7	0.02
PA1216			Hypothetical protein	-9.0	0.04
PA1217			Probable 2-isopropylmalate synthase	-4.4	0.03
PA1219			Hypothetical protein	-2.9	0.05
PA1220			Hypothetical protein	-5.4	0.03
PA1221			Hypothetical protein	-6.8	0.04
PA1245			Hypothetical protein	-2.2	0.05
PA1289			Hypothetical protein	-4.0	0.01
PA1300			Probable sigma-70 factor, ECF subfamily	-5.5	0.03
PA1301			Probable transmembrane sensor	-3.7	0.04
PA1323		x	Hypothetical protein	-6.9	0.03
PA1324		x	Hypothetical protein	-7.7	0.05
PA1516			Hypothetical protein	-2.0	0.04
PA1518			Conserved hypothetical protein	-2.1	0.03
PA1519			Probable transporter	-2.2	0.01
PA1559			Hypothetical protein	-7.3	0.03
PA1560			Hypothetical protein	-8.9	0.02
PA1579			Hypothetical protein	-2.2	0.02
PA1673			Hypothetical protein	-3.1	0.01
PA1697			ATP synthase in type III secretion system	-2.3	0.02
PA1705	<i>pcrG</i>		Regulator in type III secretion	-7.3	0.03
PA1706	<i>pcrV</i>		Type III secretion protein PcrV	-6.1	0.03
PA1708			Translocator protein PopB	-6.7	0.03

PA1710	<i>exsC</i>		ExsC	-6.6	0.01
PA1711	<i>exsE</i>		ExsE	-4.4	0.01
PA1712	<i>exsB</i>		Exoenzyme S synthesis protein B	-4.5	0.04
PA1714	<i>exsD</i>		ExsD	-3.2	<0.01
PA1716	<i>pscC</i>		Type III secretion outer membrane protein PscC precursor	-2.1	0.01
PA1720	<i>pscG</i>		Type III export protein PscG	-2.6	0.03
PA1774	<i>cfrX</i>		CfrX protein	-3.8	0.03
PA1775	<i>cmpX</i>		Conserved cytoplasmic membrane protein, CmpX protein	-3.6	0.03
PA1871	<i>lasA</i>	x	LasA protease precursor	-25.5	0.02
PA1875		x	Probable outer membrane protein precursor	-5.1	0.04
PA1878			Hypothetical protein	-4.2	0.02
PA1891		x	Hypothetical protein	-2.5	0.04
PA1894			Hypothetical protein	-3.0	0.03
PA1898	<i>qscR</i>		Quorum-sensing control repressor	-3.0	0.02
PA1906			Hypothetical protein	-20.4	0.01
PA1911	<i>femR</i>		Probable transmembrane sensor	-3.2	0.03
PA1912	<i>femI</i>		Probable sigma-70 factor, ECF subfamily	-5.1	0.01
PA1914		x	Conserved hypothetical protein	-14.0	0.02
PA1934			Hypothetical protein	-2.1	0.02
PA2015	<i>liuA</i>		Putative isovaleryl-CoA dehydrogenase	-2.4	0.04
PA2016	<i>liuR</i>		Regulator of liu genes	-2.3	0.04
PA2018			Resistance-Nodulation-Cell Division (RND) multidrug efflux transporter	-2.2	<0.01
PA2020			Probable transcriptional regulator	-2.1	0.03
PA2064	<i>pcoB</i>		Copper resistance Protein B precursor	-2.2	0.02
PA2067			Probable hydrolase	-16.4	0.04
PA2068		x	Probable major facilitator superfamily (MFS) transporter	-37.5	0.02
PA2069		x	Probable carbamoyl transferase	-107.8	0.02
PA2070		x	Hypothetical protein	-2.6	<0.01
PA2076		x	Probable transcriptional regulator	-2.1	0.05
PA2081	<i>kynB</i>		Kynurenine formamidase, KynB	-2.1	0.01
PA2119			Alcohol dehydrogenase (Zn-dependent)	-2.1	0.05
PA2140			Probable metallothionein	-3.3	0.03
PA2149			Hypothetical protein	-4.5	0.02
PA2150			Conserved hypothetical protein	-3.3	0.04
PA2151			Conserved hypothetical protein	-2.3	0.04
PA2154			Conserved hypothetical protein	-3.2	0.02
PA2157			Hypothetical protein	-2.5	<0.01
PA2159			Conserved hypothetical protein	-5.4	0.04
PA2160			Probable glycosyl hydrolase	-3.6	0.02
PA2162			Probable glycosyl hydrolase	-3.7	0.02
PA2163			Hypothetical protein	-4.3	0.02
PA2164			Probable glycosyl hydrolase	-2.9	0.02

PA2165			Probable glycogen synthase	-3.4	<0.01
PA2167			Hypothetical protein	-5.3	0.02
PA2168			Hypothetical protein	-4.6	0.05
PA2169			Hypothetical protein	-6.7	0.03
PA2170			Hypothetical protein	-9.1	0.04
PA2175			Hypothetical protein	-2.4	0.01
PA2179			Hypothetical protein	-2.4	0.03
PA2193	<i>hcnA</i>	x	Hydrogen cyanide synthase HcnA	-27.7	0.05
PA2194	<i>hcnB</i>	x	Hydrogen cyanide synthase HcnB	-15.9	0.01
PA2195	<i>hcnC</i>	x	Hydrogen cyanide synthase HcnC	-12.6	<0.01
PA2300	<i>chiC</i>	x	Chitinase	-29.9	0.03
PA2320	<i>gntR</i>		Transcriptional regulator GntR	-3.2	0.01
PA2322			Gluconate permease	-11.4	0.02
PA2323			Probable glyceraldehyde-3-phosphate dehydrogenase	-3.7	0.01
PA2377			Hypothetical protein	-8.5	0.05
PA2383			Probable transcriptional regulator	-3.4	<0.01
PA2384			Hypothetical protein	-7.4	<0.01
PA2386	<i>pvdA</i>		L-ornithine N5-oxygenase	-3.2	0.01
PA2392	<i>pvdP</i>		PvdP	-3.6	0.03
PA2393			Probable dipeptidase precursor	-4.3	0.01
PA2403			Hypothetical protein	-2.9	0.01
PA2414		x	L-sorbose dehydrogenase	-10.5	0.02
PA2415		x	Hypothetical protein	-8.6	0.02
PA2425	<i>pvdG</i>		PvdG	-3.9	0.04
PA2426	<i>pvdS</i>		Sigma factor PvdS	-3.6	0.03
PA2427			Hypothetical protein	-6.9	0.01
PA2448			Hypothetical protein	-3.1	<0.01
PA2467	<i>foxR</i>		Anti-sigma factor FoxR	-2.1	0.03
PA2468	<i>foxI</i>		ECF sigma factor FoxI	-2.7	0.03
PA2564		x	Hypothetical protein	-4.0	0.04
PA2565			Hypothetical protein	-4.4	0.01
PA2566		x	Conserved hypothetical protein	-5.9	0.04
PA2570	<i>lecA</i>	x	LecA	-38.9	0.03
PA2587	<i>pqsH</i>	x	Probable FAD-dependent monooxygenase	-3.8	0.02
PA2588		x	Probable transcriptional regulator	-8.9	0.02
PA2589			Hypothetical protein	-4.4	0.03
PA2591		x	Probable transcriptional regulator	-3.9	0.01
PA2686	<i>pfeR</i>		Two-component response regulator PfeR	-2.2	0.03
PA2753		x	Hypothetical protein	-2.3	0.04
PA2788			Probable chemotaxis transducer	-5.8	0.03
PA2862	<i>lipA</i>		Lactonizing lipase precursor	-2.7	0.01
PA3023			Conserved hypothetical protein	-2.3	<0.01
PA3094			Probable transcriptional regulator	-2.9	0.03

PA3103	<i>xcpR</i>		General secretion pathway protein E Probable binding protein component of ABC sugar transporter	-2.2	0.02
PA3190				-2.3	0.01
PA3195	<i>gapA</i>		Glyceraldehyde 3-phosphate dehydrogenase	-2.3	0.05
PA3274		x	Hypothetical protein	-3.7	0.01
PA3283			Conserved hypothetical protein	-3.6	0.04
PA3284			Hypothetical protein	-3.0	<0.01
PA3305.1	<i>phrS</i>		PhrS	-6.5	0.05
PA3326		x	Probable Clp-family ATP-dependent protease	-12.7	0.04
PA3327		x	Probable non-ribosomal peptide synthetase	-8.1	0.02
PA3328		x	Probable FAD-dependent monooxygenase	-27.0	0.01
PA3329		x	Hypothetical protein	-11.4	0.04
PA3330		x	Probable short chain dehydrogenase	-31.5	0.03
PA3331		x	Cytochrome P450	-15.9	0.03
PA3332		x	Conserved hypothetical protein	-19.5	0.03
PA3333	<i>fabH2</i>	x	3-oxoacyl-[acyl-carrier-protein] synthase III	-19.0	0.03
PA3334		x	Probable acyl carrier protein	-14.0	0.02
PA3337	<i>rfaD</i>		ADP-L-glycero-D-mannoheptose 6-epimerase	-3.3	0.04
PA3361	<i>lecB</i>	x	Fucose-binding lectin PA-III	-35.3	0.02
PA3362			Hypothetical protein	-4.7	0.01
PA3407	<i>hasAp</i>		Heme acquisition protein HasAp	-2.7	0.01
PA3408	<i>hasR</i>		Haem uptake outer membrane receptor HasR precursor	-2.2	0.03
PA3431			Conserved hypothetical protein	-6.1	0.05
PA3452	<i>mqaA</i>		Malate:quinone oxidoreductase	-2.4	0.03
PA3459			Probable glutamine amidotransferase	-3.1	0.01
PA3460			Probable acetyltransferase	-3.7	0.05
PA3461			Conserved hypothetical protein	-4.0	0.04
PA3477	<i>rhlR</i>	x	Transcriptional regulator RhlR	-5.7	<0.01
PA3478	<i>rhlB</i>	x	Rhamnosyltransferase chain B	-27.6	<0.01
PA3479	<i>rhlA</i>	x	Rhamnosyltransferase chain A	-110.4	<0.01
PA3510			Hypothetical protein	-2.1	0.05
PA3530			Conserved hypothetical protein	-4.8	0.02
PA3535			Probable serine protease	-2.9	0.02
PA3554	<i>arnA</i>		ArnA	-3.2	0.03
PA3555	<i>arnD</i>		ArnD	-3.0	0.05
PA3557	<i>arnE</i>		ArnE	-2.9	<0.01
PA3558	<i>arnF</i>		ArnF	-3.5	0.03
PA3559			Probable nucleotide sugar dehydrogenase	-3.2	0.03
PA3621.1	<i>rsmZ</i>		Regulatory RNA RsmZ	-4.0	0.04
PA3622	<i>rpoS</i>		Sigma factor RpoS	-2.0	<0.01
PA3724	<i>lasB</i>	x	Elastase lasB	-124.4	0.02
PA3734			Hypothetical protein	-5.6	0.05
PA3808			Conserved hypothetical protein	-2.1	0.03

PA3809	<i>fdx2</i>		Ferredoxin [2Fe-2S]	-2.6	0.05
PA3841	<i>exoS</i>		Exoenzyme S	-3.0	0.05
PA3842			Probable chaperone	-3.9	0.02
PA3843			Hypothetical protein	-2.0	0.04
PA3899			Probable sigma-70 factor, ECF subfamily	-3.7	0.01
PA3906		x	Hypothetical protein	-3.5	0.01
PA3908		x	Hypothetical protein	-3.3	0.02
PA4078			Probable nonribosomal peptide synthetase	-3.4	0.02
PA4116	<i>bphO</i>		Heme oxygenase, BphO	-2.2	0.02
PA4117	<i>bphP</i>		Bacterial phytochrome, BphP	-3.0	0.03
PA4138	<i>tyrS</i>		Tyrosyl-tRNA synthetase	-2.3	0.04
PA4141		x	Hypothetical protein	-144.7	0.02
PA4142		x	Probable secretion protein	-43.3	0.01
PA4143			Probable toxin transporter	-20.8	0.02
PA4144			Probable outer membrane protein precursor	-16.2	<0.01
PA4156			Probable TonB-dependent receptor	-11.5	<0.01
PA4158	<i>fepC</i>		Ferric enterobactin transport protein FepC Ferrienterobactin-binding periplasmic protein precursor	-4.0	0.03
PA4159	<i>fepB</i>		FepB	-9.7	0.02
PA4160	<i>fepD</i>		Ferric enterobactin transport protein FepD	-5.0	0.03
PA4175	<i>piv</i>	x	Protease IV	-24.3	<0.01
PA4209	<i>phzM</i>	x	Probable phenazine-specific methyltransferase	-25.1	0.02
PA4213	<i>phzD1</i>		Phenazine biosynthesis protein PhzD	-71.8	0.05
PA4217	<i>phzS</i>		Flavin-containing monooxygenase	-3.4	0.04
PA4227	<i>pchR</i>		Transcriptional regulator PchR	-2.2	0.02
PA4294			Hypothetical protein	-2.9	<0.01
PA4338			Hypothetical protein	-2.1	0.03
PA4377			Hypothetical protein	-3.5	0.03
PA4394			Conserved hypothetical protein	-3.2	0.01
PA4470	<i>fumC1</i>		Fumarate hydratase	-3.9	0.01
PA4471			Hypothetical protein	-16.0	0.04
PA4570			Hypothetical protein	-5.7	0.01
PA4585	<i>rtcA</i>		RNA 3-terminal phosphate cyclase	-2.1	0.01
PA4586			Hypothetical protein	-2.7	<0.01
PA4587	<i>ccpR</i>		Cytochrome c551 peroxidase precursor	-2.9	0.05
PA4588	<i>gdhA</i>		Glutamate dehydrogenase	-4.9	0.01
PA4590	<i>pra</i>	x	Protein activator	-4.6	0.02
PA4675			Probable TonB-dependent receptor	-3.5	0.02
PA4774			Hypothetical protein	-2.3	0.05
PA4775			Hypothetical protein	-2.1	0.01
PA4813	<i>lipC</i>		Lipase LipC	-2.1	0.05
PA4847	<i>accB</i>		Biotin carboxyl carrier protein (BCCP)	-2.3	0.05
PA4925			Conserved hypothetical protein	-2.5	0.04

PA5111	<i>gloA3</i>	Lactoylglutathione lyase	-2.1	0.02
PA5150		Probable short-chain dehydrogenase	-3.2	0.02
PA5163	<i>rmlA</i>	Glucose-1-phosphate thymidyltransferase	-2.6	0.02
PA5164	<i>rmlC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	-2.4	0.02
PA5172	<i>arcB</i>	Ornithine carbamoyltransferase, catabolic	-2.8	0.01
PA5220		x Hypothetical protein	-8.5	0.01
PA5232		x Conserved hypothetical protein	-2.5	0.04
PA5424		Conserved hypothetical protein	-3.0	0.05
PA5475		Hypothetical protein	-3.6	0.02
PA5526		Hypothetical protein	-2.0	0.02
PA5531	<i>tonB1</i>	TonB protein	-2.1	0.01

^aAn 'X' in the box indicates that the gene/protein is regulated by quorum sensing (1), in reference to the QS-regulated genes/proteins as determined previously.

Reference

1. **Hentzer M, Wu H, Andersen JB, Riedel K, Rasmussen TB, Bagge N, Kumar N, Schembri MA, Song Z, Kristoffersen P, Manefield M, Costerton JW, Molin S, Eberl L, Steinberg P, Kjelleberg S, Høiby N, Givskov M.** 2003. Attenuation of *Pseudomonas aeruginosa* virulence by quorum sensing inhibitors. *EMBO J* **22**:3803-3815.