Supplementary Table 2: Full list of *P. aeruginosa* genes with expression up- or down-regulated in the *metR* mutant compared to the PA14 wild-type.

			Liquid swarming condition		**Semi-viscous swarming condition**	
Gene	**Name**	**Function**	**Fold change**	**P-value**	**Fold change**	**P-value**
PA0044	*exoT*	exoenzyme T			-2.08	0.010
PA0045		hypothetical protein			-3.43	0.022
PA0047		hypothetical protein			-2.23	0.025
PA0051	*phzH*	potential phenazine-modifying enzyme			3.62	0.002
PA0096		hypothetical protein			-5.82	0.008
PA0103		probable sulfate transporter			3.69	0.000
PA0137		probable permease of ABC transporter			2.01	0.040
PA0208	*mdcA*	malonate decarboxylase alpha subunit			-2.40	0.004
PA0248		probable transcriptional regulator			-2.72	0.029
PA0252		hypothetical protein			-4.28	0.001
PA0293	*aguB*	N-carbamoylputrescine amidohydrolase			2.30	0.004
PA0298	*spuB*	probable glutamine synthetase			-4.22	0.012
PA0326		probable ATP-binding component of ABC transporter			2.17	0.002
PA0430	*metF*	5,10-methylenetetrahydrofolate reductase			-2.08	0.013
PA0434		hypothetical protein			2.33	0.043
PA0523	*norC*	nitric-oxide reductase subunit C			2.37	0.010
PA0588		putative protein kinase	-2.06	0.000		
PA0606		probable permease of ABC transporter			-2.39	0.040
PA0610	*prtN*	transcriptional regulator PrtN			2.84	0.000
PA0612		hypothetical protein			11.27	0.000
PA0613		hypothetical protein			5.45	0.000
PA0614		hypothetical protein			4.98	0.002
PA0615		hypothetical protein			4.65	0.000
PA0616		hypothetical protein			5.44	0.000
PA0617		probable bacteriophage protein			6.37	0.000
PA0618		probable bacteriophage protein			5.29	0.001
PA0619		probable bacteriophage protein			8.07	0.000
PA0620		probable bacteriophage protein			6.66	0.000
PA0621		hypothetical protein			3.13	0.010
PA0622		probable bacteriophage protein			6.17	0.000
PA0623		probable bacteriophage protein			6.86	0.000
PA0624		hypothetical protein			5.44	0.000

PA0625		hypothetical protein			5.45	0.000
PA0626		hypothetical protein			5.35	0.000
PA0627		hypothetical protein			7.09	0.000
PA0628		hypothetical protein			5.85	0.000
PA0629		hypothetical protein			7.03	0.000
PA0630		hypothetical protein			5.93	0.001
PA0631		hypothetical protein			8.65	0.000
PA0633		hypothetical protein			9.28	0.000
PA0634		hypothetical protein			6.22	0.000
PA0635		hypothetical protein			6.42	0.000
PA0636		hypothetical protein			5.93	0.000
PA0637		hypothetical protein			5.24	0.000
PA0638		probable bacteriophage protein			6.60	0.000
PA0639		hypothetical protein			8.23	0.000
PA0647		hypothetical protein			2.66	0.026
PA0671		hypothetical protein			2.13	0.002
PA0703		probable major facilitator superfamily (MFS) transporter			-2.07	0.011
PA0707	*toxR*	transcriptional regulator ToxR			-5.38	0.000
PA0713		hypothetical protein			-2.63	0.032
PA0717		hypothetical protein of bacteriophage Pf1	10.08	0.000	342.12	0.000
PA0718		hypothetical protein of bacteriophage Pf1	5.74	0.000	271.30	0.000
PA0719		hypothetical protein of bacteriophage Pf1			109.98	0.000
PA0720		helix destabilizing protein of bacteriophage Pf1	24.11	0.000	325.95	0.000
PA0721		hypothetical protein of bacteriophage Pf1			375.78	0.000
PA0723	*coaB*	coat protein B of bacteriophage Pf1	91.94	0.000		
PA0725		hypothetical protein of bacteriophage Pf1	3.69	0.000	7.01	0.000
PA0726		hypothetical protein of bacteriophage Pf1			47.72	0.000
PA0727		hypothetical protein from bacteriophage Pf1			11.96	0.000
PA0730		probable transferase			2.44	0.002
PA0775		conserved hypothetical protein	2.56	0.003		
PA0807		hypothetical protein			3.10	0.000
PA0848		probable alkyl hydroperoxide reductase			2.12	0.008
PA0865	*hpd*	4-hydroxyphenylpyruvate dioxygenase	5.38	0.023		
PA0866	*aroP2*	aromatic amino acid transport protein AroP2	2.51	0.002		
PA0906		probable transcriptional regulator			2.92	0.025
PA0908		hypothetical protein			3.08	0.029
PA0909		hypothetical protein			2.94	0.010
PA0910		hypothetical protein	-3.99	0.000		
PA0913	*mgtE*	probable Mg transporter MgtE			2.72	0.005

PA0929		two-component response regulator			-3.33	0.019
PA0979		hypothetical protein			-3.37	0.019
PA0994	*cupC3*	usher CupC3	-2.50	0.003		
PA1035		hypothetical protein			-2.54	0.035
PA1178	*oprH*	PhoP/Q and low Mg2+ inducible outer membrane protein H1 precursor			3.37	0.000
PA1267		hypothetical protein			-4.50	0.011
PA1286		putative MFS transporter	-2.10	0.000		
PA1317	*cyoA*	cytochrome o ubiquinol oxidase subunit II			-3.17	0.002
PA1318	*cyoB*	cytochrome o ubiquinol oxidase subunit I			-2.15	0.006
PA1319	*cyoC*	cytochrome o ubiquinol oxidase subunit III			-2.41	0.000
PA1320	*cyoD*	cytochrome o ubiquinol oxidase subunit IV			-3.26	0.001
PA1321	*cyoE*	cytochrome o ubiquinol oxidase protein CyoE			-2.25	0.002
PA1326	*ilvA2*	threonine dehydratase, biosynthetic			3.19	0.002
PA1327		probable protease			2.01	0.012
PA1343		hypothetical protein			2.58	0.026
PA1421	*gbuA*	guanidinobutyrase	2.11	0.008		
PA1466		hypothetical protein			2.44	0.011
PA1498	*pykF*	pyruvate kinase I	7.07	0.000		
PA1539		hypothetical protein			-3.95	0.014
PA1541		probable drug efflux transporter			-2.48	0.037
PA1542		hypothetical protein			2.43	0.039
PA1549		probable cation-transporting P-type ATPase			-2.31	0.044
PA1566		hypothetical protein			2.08	0.010
PA1600		probable cytochrome c			-3.86	0.015
PA1601		probable aldehyde dehydrogenase			-3.21	0.021
PA1626		probable major facilitator superfamily (MFS) transporter			2.53	0.035
PA1637	*kdpE*	two-component response regulator KdpE			-2.37	0.041
PA1691	*pscT*	translocation protein in type III secretion	2.71	0.002		
PA1693	*pscR*	translocation protein in type III secretion	2.52	0.003		
PA1695	*pscP*	translocation protein in type III secretion			-3.85	0.015
PA1696	*pscO*	translocation protein in type III secretion			21.12	0.002
PA1699		conserved hypothetical protein in type III secretion			-3.57	0.017
PA1705	*pcrG*	regulator in type III secretion			-2.19	0.007
PA1708	*popB*	translocator protein PopB	2.16	0.005		
PA1710	*exsC*	exoenzyme S synthesis protein C precursor	2.26	0.000		
PA1716	*pscC*	Type III secretion outer membrane protein PscC precursor	2.42	0.001	-2.11	0.001
PA1717	*pscD*	type III export protein PscD			-2.80	0.012

PA1718	*pscE*	type III export protein PscE			-7.61	0.005
PA1719	*pscF*	type III export protein PscF			-2.19	0.002
PA1721	*pscH*	type III export protein PscH			-3.50	0.002
PA1723	*pscJ*	type III export protein PscJ	2.00	0.001		
PA1724	*pscK*	type III export protein PscK			-2.32	0.002
PA1740		hypothetical protein			-2.83	0.027
PA1778	*cobA*	uroporphyrin-III C-methyltransferase			2.10	0.001
PA1781	*nirB*	assimilatory nitrite reductase large subunit			4.34	0.001
PA1785		hypothetical protein			4.14	0.000
PA1799		putative two-component response regulator	3.06	0.001		
PA1823	*nudC*	NADH pyrophosphatase			9.50	0.004
PA1842		hypothetical protein			-3.26	0.000
PA1843	*metH*	methionine synthase			-2.90	0.001
PA1863	*modA*	molybdate-binding periplasmic protein precursor ModA			2.61	0.032
PA1879		hypothetical protein			-2.02	0.016
PA1882		probable transporter			3.31	0.001
PA1888		hypothetical protein			-2.31	0.044
PA1925		hypothetical protein			-2.41	0.039
PA1971	*braZ*	branched chain amino acid transporter BraZ			-4.83	0.010
PA1977		hypothetical protein			-2.73	0.029
PA2014	*gnyB*	beta subunit of geranoyl-CoA carboxylase, GnyB			-2.00	0.005
PA2030		hypothetical protein			2.55	0.000
PA2041		probable amino acid permease			-4.16	0.013
PA2056		probable transcriptional regulator			2.16	0.019
PA2082		probable transcriptional regulator			-3.72	0.016
PA2083		probable ring-hydroxylating dioxygenase subunit			2.30	0.045
PA2086		probable epoxide hydrolase			-5.41	0.009
PA2088		hypothetical protein			-7.93	0.005
PA2140		probable metallothionein			6.14	0.007
PA2156		putative metal-dependent hydrolase	2.88	0.002		
PA2202		probable amino acid permease			-6.35	0.000
PA2203		probable amino acid permease			-5.98	0.007
PA2204		probable binding protein component of ABC transporter			-3.30	0.001
PA2205		hypothetical protein			2.66	0.031
PA2211		putative hydrolase	3.84	0.001		
PA2228		hypothetical protein			15.10	0.003
PA2259	*ptxS*	transcriptional regulator PtxS			2.44	0.026
PA2260		hypothetical protein			2.50	0.004
PA2288		hypothetical protein			3.78	0.000

PA2291		carbohydrate-selective porin	2.42	0.000	2.25	0.001
PA2324		hypothetical protein			-3.18	0.021
PA2328		hypothetical protein			-2.28	0.001
PA2329		probable ATP-binding component of ABC transporter			-4.01	0.014
PA2337	*mtlR*	transcriptional regulator MtlR			2.13	0.002
PA2377		hypothetical protein			-4.63	0.011
PA2383		probable transcriptional regulator			-2.16	0.017
PA2384		hypothetical protein			-4.97	0.000
PA2385	*pvdQ*	PvdQ			-18.74	0.001
PA2386	*pvdA*	L-ornithine N5-oxygenase			-9.60	0.000
PA2389		hypothetical protein			-5.19	0.001
PA2390		probable ATP-binding/permease fusion ABC transporter			-2.45	0.001
PA2391	*opmQ*	probable outer membrane protein precursor			-7.75	0.002
PA2392	*pvdP*	PvdP			-31.94	0.000
PA2393		probable dipeptidase precursor			-5.00	0.002
PA2394	*pvdN*	PvdN			-15.56	0.000
PA2395	*pvdO*	PvdO			-7.55	0.001
PA2396	*pvdF*	pyoverdine synthetase F			-5.07	0.001
PA2397	*pvdE*	pyoverdine biosynthesis protein PvdE			-7.66	0.001
PA2399	*pvdD*	pyoverdine synthetase D			-5.28	0.022
PA2400	*pvdJ*	PvdJ			-10.38	0.000
PA2402		probable non-ribosomal peptide synthetase			-13.28	0.000
PA2407		probable adhesion protein			-2.31	0.007
PA2411		probable thioesterase			-8.27	0.000
PA2412		hypothetical protein			-8.60	0.000
PA2413	*pvdH*	diaminobutyrate--2-oxoglutarate aminotransferase			-7.53	0.000
PA2418		hypothetical protein			-2.39	0.040
PA2424	*pvdL*	PvdL			-15.24	0.000
PA2425	*pvdG*	PvdG			-8.19	0.000
PA2427		hypothetical protein			-7.40	0.000
PA2428		hypothetical protein	2.22	0.006		
PA2451		hypothetical protein			-5.38	0.000
PA2452		hypothetical protein			-3.95	0.014
PA2469		probable transcriptional regulator	-4.06	0.000		
PA2505		probable porin			2.28	0.046
PA2508	*catC*	muconolactone delta-isomerase			2.21	0.050
PA2509	*catB*	muconate cycloisomerase I			2.53	0.035
PA2513	*antB*	anthranilate dioxygenase small subunit			2.11	0.037
PA2542		hypothetical protein			-2.48	0.037

PA2577		probable transcriptional regulator			2.57	0.001
PA2665		anaerobic nitric oxide reductase transcription regulator			3.73	0.016
PA2677		probable type II secretion protein			-2.31	0.044
PA2694		probable thioredoxin			-2.84	0.027
PA2780		hypothetical protein			2.78	0.009
PA2782		hypothetical protein			2.37	0.005
PA2783		hypothetical protein			2.34	0.043
PA2784		hypothetical protein			2.81	0.003
PA2787	*cpg2*	glutamate carboxypepticase			2.79	0.028
PA2835		putative multidrug efflux MFS transporter	-4.52	0.000		
PA2844		hypothetical protein			-2.13	0.032
PA2846		probable transcriptional regulator			-2.60	0.033
PA2868		hypothetical protein			2.75	0.029
PA2891		probable biotin carboxylase/biotin carboxyl carrier protein			-2.23	0.049
PA2910		hypothetical protein			-2.88	0.026
PA2917		probable transcriptional regulator			-2.68	0.031
PA2927		hypothetical protein			3.12	0.047
PA2939		probable aminopeptidase			3.82	0.015
PA3007	*lexA*	LexA repressor			3.72	0.000
PA3008		hypothetical protein			3.50	0.000
PA3039		probable transporter			2.48	0.007
PA3079		hypothetical protein			-2.48	0.002
PA3126	*ibpA*	putative small heat shock protein	-3.56	0.005		
PA3205		hypothetical protein			14.38	0.000
PA3206		probable two-component sensor			2.92	0.002
PA3235		hypothetical protein			-2.18	0.001
PA3251		hypothetical protein			2.32	0.002
PA3253		probable permease of ABC transporter			3.12	0.022
PA3273		conserved hypothetical protein	2.38	0.000		
PA3284		hypothetical protein			3.12	0.002
PA3315		probable permease of ABC transporter			2.95	0.010
PA3320		hypothetical protein			-2.45	0.038
PA3407	*hasAp*	heme acquisition protein HasAp			-8.04	0.000
PA3413		hypothetical protein			2.07	0.003
PA3414		hypothetical protein			6.48	0.007
PA3415		probable dihydrolipoamide acetyltransferase			2.52	0.006
PA3416		probable pyruvate dehydrogenase E1 component, beta chain			2.43	0.012

PA3431		hypothetical protein			2.49	0.035
PA3441		probable molybdopterin-binding protein			-5.62	0.001
PA3443		probable permease of ABC transporter			-3.59	0.017
PA3499		endonuclease III	7.22	0.002		
PA3508		probable transcriptional regulator			-2.51	0.036
PA3532		hypothetical protein			-2.12	0.043
PA3540	*algD*	GDP-mannose 6-dehydrogenase AlgD			3.09	0.000
PA3550	*algF*	alginate o-acetyltransferase AlgF			2.72	0.017
PA3560	*fruA*	phosphotransferase system, fructose-specific IIBC component			-3.59	0.017
PA3575		hypothetical protein			5.32	0.000
PA3583	*glpR*	glycerol-3-phosphate regulon repressor			-2.27	0.004
PA3586		probable hydrolase	2.06	0.000	17.30	0.000
PA3590		putative 3-hydroxyacyl-CoA dehydrogenase	2.05	0.009		
PA3601		hypothetical protein			2.40	0.004
PA3617	*recA*	RecA protein			2.34	0.002
PA3633	*ispD*	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase			-3.08	0.022
PA3688		hypothetical protein			2.11	0.009
PA3712		hypothetical protein			2.37	0.001
PA3830		probable transcriptional regulator			-3.00	0.003
PA3842		probable chaperone	2.51	0.000		
PA3843		hypothetical protein			-5.50	0.008
PA3845		putative transcriptional regulator, LysR family	4.32	0.000		
PA3870	*moaA1*	molybdenum cofactor biosynthesis protein A	2.62	0.002		
PA3911		hypothetical protein			-2.21	0.028
PA3914	*moeA1*	MoeA1, molybdopterin biosynthesis enzyme	2.35	0.009		
PA3915	*moaB1*	molybdopterin biosynthetic protein B1	2.31	0.038		
PA3935	*tauD*	taurine dioxygenase			-3.05	0.009
PA3957		possible short-chain dehydrogenase	4.00	0.000		
PA3959		hypothetical protein			-2.47	0.037
PA4024	*eutB*	ethanolamine ammonia-lyase large subunit			2.11	0.006
PA4110	*ampC*	beta-lactamase precursor			2.83	0.027
PA4143		probable toxin transporter			-2.46	0.000
PA4144		probable outer membrane protein precursor			-3.16	0.003
PA4181		hypothetical protein			-2.53	0.035
PA4218		probable transporter			-3.50	0.001
PA4219		hypothetical protein			-2.79	0.001
PA4220		conserved hypothetical protein			-2.82	0.008
PA4221	*fptA*	Fe(III)-pyochelin outer membrane receptor precursor			-6.97	0.006

PA4222		probable ATP-binding component of ABC transporter	-3.54	0.004	-4.06	0.000
PA4223		probable ATP-binding component of ABC transporter	-2.77	0.001	-3.85	0.012
PA4224	*pchG*	pyochelin biosynthetic protein PchG			-4.67	0.000
PA4225	*pchF*	pyochelin synthetase			-5.06	0.000
PA4226	*pchE*	dihydroaeruginoic acid synthetase			-3.15	0.000
PA4229	*pchC*	pyochelin biosynthetic protein PchC			-2.27	0.001
PA4230	*pchB*	salicylate biosynthesis protein PchB	-2.93	0.000	-2.83	0.001
PA4231	*pchA*	salicylate biosynthesis isochorismate synthase			-3.45	0.000
PA4278		conserved hypothetical protein				
PA4281	*sbcD*	exonuclease SbcD			-3.04	0.023
PA4302		probable type II secretion system protein			-2.69	0.030
PA4320		hypothetical protein			-2.37	0.013
PA4321		hypothetical protein			-2.19	0.019
PA4357		hypothetical protein			-3.79	0.001
PA4364		hypothetical protein			3.95	0.015
PA4467		hypothetical protein			-3.71	0.000
PA4468	*sodM*	superoxide dismutase			-9.19	0.000
PA4469		hypothetical protein			-4.59	0.000
PA4515		putative iron-regulated protein	2.42	0.004		
PA4525	*pilA*	type 4 fimbrial precursor PilA			3.90	0.014
PA4582		hypothetical protein			3.45	0.002
PA4587	*ccpR*	cytochrome c551 peroxidase precursor			3.30	0.019
PA4632		putative lipoprotein	-2.03	0.009		
PA4649		hypothetical protein			2.70	0.011
PA4652		putative type 1 pili usher protein CsuD	2.87	0.000		
PA4683		hypothetical protein			-3.95	0.000
PA4707		probable permease of ABC transporter			-2.59	0.003
PA4710	*phuR*	putative haem/haemoglobin uptake outer membrane receptor PhuR precursor	4.98	0.000		
PA4714		hypothetical protein			2.26	0.000
PA4763	*recN*	DNA repair protein RecN			2.98	0.000
PA4836		hypothetical protein			4.28	0.012
PA4837		probable outer membrane protein precursor			2.41	0.009
PA4858		hypothetical protein			2.33	0.029
PA4893	*ureG*	urease accessory protein UreG			2.13	0.041
PA4908		ornithine cyclodeaminase			2.51	0.021
PA4919	*pncB1*	nicotinate phosphoribosyltransferase	2.09	0.008		
PA4980		probable enoyl-CoA hydratase/isomerase			3.93	0.014
PA5011	*waaC*	heptosyltransferase I			-2.29	0.002

PA5096		probable binding protein component of ABC transporter			2.25	0.026
PA5125	*ntrC*	two-component response regulator NtrC			2.22	0.001
PA5169		probable C4-dicarboxylate transporter	-3.60	0.000		
PA5229		hypothetical protein			2.45	0.038
PA5294		multidrug efflux protein NorA			2.73	0.029
PA5354	*glcE*	glycolate oxidase subunit GlcE	3.16	0.001		
PA5380		probable transcriptional regulator			2.40	0.019
PA5420	*purU2*	formyltetrahydrofolate deformylase			2.24	0.048
PA5433		hypothetical protein			-2.72	0.030
PA5439		probable glucose-6-phosphate dehydrogenase			2.16	0.009
PA5490	*cc4*	cytochrome c4 precursor			-4.62	0.011
PA5509		hypothetical protein			-2.62	0.044
PA5535		hypothetical protein			2.36	0.012