

Supplementary Table 1: Complete list of dysregulated genes in the microarray under sub-inhibitory concentrations of ciprofloxacin in the *lon* mutant compared to the wild type PAO1 under sub-inhibitory concentrations.

PA number	Gene Name	Fold change	p-eBayes	Gene Description
PA0040		-2.18	0.00	conserved hypothetical protein
PA0066		-2.28	0.00	conserved hypothetical protein
PA0069		-5.46	0.00	conserved hypothetical protein
PA0085		2.57	0.00	conserved hypothetical protein
PA0171		2.01	0.00	hypothetical protein
PA0253		-2.66	0.01	probable transcriptional regulator
PA0266	<i>gabT</i>	2.30	0.00	4-aminobutyrate aminotransferase
PA0277		4.05	0.00	conserved hypothetical protein
PA0386		-2.03	0.00	probable oxidase
PA0394		-2.01	0.00	conserved hypothetical protein
PA0426	<i>mexB</i>	3.30	0.01	RND multidrug efflux transporter MexB
PA0447	<i>gcdH</i>	2.42	0.02	glutaryl-CoA dehydrogenase
PA0577	<i>dnaG</i>	-2.10	0.00	DNA primase
PA0604		3.03	0.01	probable binding protein component of ABC transporter
PA0606		2.13	0.01	probable permease of ABC transporter
PA0610	<i>prtN</i>	-12.65	0.00	transcriptional regulator PrtN
PA0611	<i>prtR</i>	-3.00	0.00	transcriptional regulator PrtR
PA0612		-12.87	0.00	hypothetical protein
PA0613		-6.51	0.00	hypothetical protein
PA0614		-8.25	0.00	hypothetical protein
PA0615		-9.09	0.00	hypothetical protein
PA0616		-6.57	0.00	hypothetical protein
PA0617		-7.24	0.00	probable bacteriophage protein
PA0618		-2.21	0.00	probable bacteriophage protein
PA0619		-3.50	0.00	probable bacteriophage protein
PA0620		-9.93	0.00	probable bacteriophage protein
PA0621		-3.07	0.00	conserved hypothetical protein

PA0622		-5.10	0.00	probable bacteriophage protein
PA0623		-2.06	0.00	probable bacteriophage protein
PA0624		-7.63	0.00	hypothetical protein
PA0625		-5.61	0.00	hypothetical protein
PA0626		-7.32	0.00	hypothetical protein
PA0627		-6.30	0.00	conserved hypothetical protein
PA0628		-6.95	0.00	conserved hypothetical protein
PA0629		-7.79	0.00	conserved hypothetical protein
PA0630		-7.20	0.00	hypothetical protein
PA0631		-6.46	0.00	hypothetical protein
PA0632		-9.07	0.00	hypothetical protein
PA0633		-5.46	0.00	hypothetical protein
PA0634		-8.14	0.00	hypothetical protein
PA0635		-6.25	0.01	hypothetical protein
PA0636		-9.30	0.00	hypothetical protein
PA0637		-6.93	0.00	conserved hypothetical protein
PA0638		-7.61	0.00	probable bacteriophage protein
PA0640		-4.05	0.00	probable bacteriophage protein
PA0641		-8.94	0.00	probable bacteriophage protein
PA0642		-7.71	0.00	hypothetical protein
PA0643		-6.42	0.00	hypothetical protein
PA0644		-7.98	0.00	hypothetical protein
PA0645		-7.42	0.00	hypothetical protein
PA0646		-7.25	0.00	hypothetical protein
PA0648		-6.98	0.00	hypothetical protein
PA0649	<i>trpG</i>	-3.18	0.00	anthranilate synthase component II
PA0650	<i>trpD</i>	-3.46	0.00	anthranilate phosphoribosyltransferase
PA0651	<i>trpC</i>	-2.43	0.00	indole-3-glycerol-phosphate synthase
PA0654	<i>speD</i>	-2.11	0.00	S-adenosylmethionine decarboxylase proenzyme
PA0669		-3.08	0.00	probable DNA polymerase alpha chain
PA0670		-5.31	0.00	hypothetical protein
PA0671		-5.59	0.00	hypothetical protein

PA0782	<i>putA</i>	3.35	0.00	proline dehydrogenase PutA
PA0783	<i>putP</i>	4.74	0.00	sodium/proline symporter PutP
PA0789		2.21	0.00	probable amino acid permease
PA0807		-2.81	0.00	conserved hypothetical protein
PA0808		-3.75	0.00	hypothetical protein
PA0835	<i>pta</i>	3.80	0.01	phosphate acetyltransferase
PA0836		3.76	0.00	probable acetate kinase
PA0855		2.02	0.00	hypothetical protein
PA0865	<i>hpd</i>	2.80	0.00	4-hydroxyphenylpyruvate dioxygenase
PA0870	<i>phhC</i>	3.11	0.00	aromatic amino acid aminotransferase
PA0871	<i>phhB</i>	3.67	0.00	pterin-4-alpha-carbinolamine dehydratase
PA0872	<i>phhA</i>	2.84	0.00	phenylalanine-4-hydroxylase
PA0906		-2.26	0.00	probable transcriptional regulator
PA0907		-4.28	0.00	hypothetical protein
PA0908		-2.82	0.00	hypothetical protein
PA0910		-3.82	0.00	hypothetical protein
PA0911		-3.47	0.00	hypothetical protein
PA0922		-2.41	0.00	hypothetical protein
PA0958	<i>oprD</i>	4.42	0.00	outer membrane porin protein OprD precursor
PA0962		2.57	0.01	probable dna-binding stress protein
PA0985		-4.64	0.00	probable colicin-like toxin
PA1049	<i>pdxH</i>	2.16	0.00	pyridoxine 5-phosphate oxidase
PA1069		2.60	0.00	hypothetical protein
PA1071	<i>braF</i>	2.08	0.00	branched-chain amino acid transport protein BraF
PA1072	<i>braE</i>	2.12	0.00	branched-chain amino acid transport protein BraE
PA1074	<i>braC</i>	3.38	0.00	branched-chain amino acid transport protein BraC
PA1076		4.54	0.00	hypothetical protein
PA1151	<i>imm2</i>	-2.54	0.00	pyocin S2 immunity protein
PA1152		-2.09	0.01	hypothetical protein
PA1196		2.41	0.01	probable transcriptional regulator
PA1288		5.09	0.00	probable outer membrane protein
PA1337	<i>ansB</i>	2.68	0.00	glutaminase-asparaginase

PA1338	<i>ggt</i>	2.76	0.00	gamma-glutamyltranspeptidase precursor
PA1339		2.79	0.00	probable ATP-binding component of ABC transporter
PA1340		2.24	0.00	probable permease of ABC transporter
PA1341		2.21	0.00	probable permease of ABC transporter
PA1342		5.42	0.00	probable binding protein component of ABC transporter
PA1414		2.10	0.02	hypothetical protein
PA1418		2.09	0.00	probable sodium:solute symport protein
PA1419		2.35	0.00	probable transporter
PA1420		2.39	0.00	hypothetical protein
PA1421	<i>gbuA</i>	3.75	0.00	agmatinase
PA1498	<i>pykF</i>	2.52	0.01	pyruvate kinase I
PA1546	<i>hemN</i>	2.75	0.00	oxygen-independent coproporphyrinogen III oxidase
PA1557		3.36	0.01	probable cytochrome oxidase subunit (cbb3-type)
PA1647		2.03	0.00	probable sulfate transporter
PA1656		4.40	0.00	hypothetical protein
PA1657		11.03	0.00	conserved hypothetical protein
PA1658		3.45	0.00	conserved hypothetical protein
PA1659		2.60	0.00	hypothetical protein
PA1665		2.06	0.00	hypothetical protein
PA1673		3.29	0.00	hypothetical protein
PA1746		2.19	0.00	hypothetical protein
PA1865		-2.72	0.01	hypothetical protein
PA1866		-3.14	0.00	hypothetical protein
PA1892		2.33	0.00	hypothetical protein
PA1893		2.40	0.00	hypothetical protein
PA1894		3.10	0.00	hypothetical protein
PA1895		2.70	0.00	hypothetical protein
PA1896		2.83	0.00	hypothetical protein
PA1897		2.48	0.00	hypothetical protein
PA1948	<i>rbsC</i>	2.13	0.00	membrane protein component of ABC ribose transporter
PA2008	<i>fahA</i>	3.00	0.00	fumarylacetoacetase
PA2009	<i>hmgA</i>	8.12	0.00	homogentisate 1,2-dioxygenase

PA2026		3.43	0.00	conserved hypothetical protein
PA2040		2.44	0.00	probable glutamine synthetase
PA2041		2.09	0.00	probable amino acid permease
PA2064	<i>pcoB</i>	-2.00	0.03	copper resistance protein B precursor
PA2080	<i>kynU</i>	2.04	0.00	hypothetical protein
PA2119		2.81	0.00	alcohol dehydrogenase (Zn-dependent)
PA2126		2.18	0.01	conserved hypothetical protein
PA2127		3.84	0.00	conserved hypothetical protein
PA2193	<i>hcnA</i>	5.33	0.00	hydrogen cyanide synthase HcnA
PA2194	<i>hcnB</i>	3.21	0.00	hydrogen cyanide synthase HcnB
PA2195	<i>hcnC</i>	2.16	0.00	hydrogen cyanide synthase HcnC
PA2227		2.10	0.02	probable transcriptional regulator
PA2252		2.78	0.00	probable AGCS sodium/alanine/glycine symporter
PA2288		-2.14	0.00	hypothetical protein
PA2321		-2.04	0.00	gluconokinase
PA2501		3.02	0.00	hypothetical protein
PA2539		2.20	0.00	conserved hypothetical protein
PA2624	<i>idh</i>	2.24	0.01	isocitrate dehydrogenase
PA2753		2.59	0.01	hypothetical protein
PA2754		2.25	0.00	conserved hypothetical protein
PA2760		3.63	0.00	probable outer membrane protein
PA2840		-2.41	0.03	probable ATP-dependent RNA helicase
PA2886		2.03	0.03	hypothetical protein
PA2951	<i>etfA</i>	2.00	0.00	electron transfer flavoprotein alpha-subunit
PA2952	<i>etfB</i>	2.52	0.00	electron transfer flavoprotein beta-subunit
PA3007	<i>lexA</i>	-2.20	0.01	repressor protein LexA
PA3021		3.95	0.00	hypothetical protein
PA3054		2.04	0.00	hypothetical protein
PA3068	<i>gdhB</i>	2.10	0.00	conserved hypothetical protein
PA3126	<i>ibpA</i>	-3.97	0.00	heat-shock protein IbpA
PA3221	<i>csaA</i>	2.20	0.00	CsaA protein
PA3234		2.36	0.00	probable sodium:solute symporter

PA3278		3.24	0.02	hypothetical protein
PA3309		5.48	0.01	conserved hypothetical protein
PA3326		2.41	0.00	probable Clp-family ATP-dependent protease
PA3337	<i>rfaD</i>	3.13	0.01	ADP-L-glycero-D-mannoheptose 6-epimerase
PA3347		2.26	0.00	hypothetical protein
PA3356		3.26	0.00	conserved hypothetical protein
PA3413		-2.39	0.00	conserved hypothetical protein
PA3414		-2.69	0.00	hypothetical protein
PA3458		2.71	0.01	probable transcriptional regulator
PA3562		2.08	0.00	probable phosphotransferase system enzyme I
PA3613		6.09	0.00	hypothetical protein
PA3616		-2.18	0.00	conserved hypothetical protein
PA3661		2.19	0.00	hypothetical protein
PA3837		2.13	0.00	probable permease of ABC transporter
PA3839		3.07	0.03	probable sodium:sulfate symporter
PA3850		2.27	0.00	hypothetical protein
PA3859		2.25	0.00	probable carboxylesterase
PA3866		-8.25	0.00	pyocin protein
PA3876	<i>narK2</i>	3.01	0.03	nitrite extrusion protein 2
PA3877	<i>narK1</i>	4.29	0.00	nitrite extrusion protein 1
PA3880		2.51	0.01	conserved hypothetical protein
PA3905		2.37	0.00	hypothetical protein
PA3906		2.24	0.00	hypothetical protein
PA3915	<i>moaB1</i>	2.71	0.01	molybdopterin biosynthetic protein B1
PA3919		2.16	0.01	conserved hypothetical protein
PA4022		2.59	0.00	probable aldehyde dehydrogenase
PA4220		-3.04	0.00	hypothetical protein
PA4221	<i>fptA</i>	-2.14	0.01	Fe(III)-pyochelin receptor precursor
PA4224	<i>pchG</i>	-2.07	0.00	hypothetical protein
PA4225	<i>pchF</i>	-4.90	0.00	pyochelin synthetase
PA4226	<i>pchE</i>	-2.27	0.00	dihydroaeruginic acid synthetase
PA4230	<i>pchB</i>	-2.37	0.00	salicylate biosynthesis protein PchB

PA4328		2.73	0.02	hypothetical protein
PA4329	<i>pykA</i>	2.63	0.00	pyruvate kinase II
PA4348		2.13	0.00	conserved hypothetical protein
PA4463		2.08	0.01	conserved hypothetical protein
PA4571		3.79	0.01	probable cytochrome c
PA4579		2.32	0.01	hypothetical protein
PA4587	<i>ccpR</i>	3.42	0.01	cytochrome c551 peroxidase precursor
PA4605		2.63	0.00	conserved hypothetical protein
PA4606		2.51	0.00	conserved hypothetical protein
PA4610		2.04	0.01	hypothetical protein
PA4611		6.23	0.00	hypothetical protein
PA4625		2.55	0.00	hypothetical protein
PA4761	<i>dnaK</i>	-2.11	0.01	DnaK protein
PA4770	<i>lldP</i>	2.94	0.00	L-lactate permease
PA4771	<i>lldD</i>	2.19	0.00	L-lactate dehydrogenase
PA4772		2.08	0.00	probable ferredoxin
PA4846	<i>aroQ1</i>	-2.10	0.01	3-dehydroquinate dehydratase
PA5025	<i>metY</i>	2.52	0.00	homocysteine synthase
PA5027		3.67	0.01	hypothetical protein
PA5030		-2.58	0.00	probable MFS transporter
PA5053	<i>hslV</i>	-4.99	0.00	heat shock protein HslV
PA5054	<i>hslU</i>	-2.30	0.00	heat shock protein HslU
PA5112	<i>estA</i>	2.25	0.00	esterase EstA
PA5171	<i>arcA</i>	2.55	0.03	arginine deiminase
PA5180		-2.36	0.00	conserved hypothetical protein
PA5266		2.07	0.03	conserved hypothetical protein
PA5296	<i>rep</i>	-2.03	0.00	ATP-dependent DNA helicase Rep
PA5303		2.41	0.00	conserved hypothetical protein
PA5304	<i>dadA</i>	2.84	0.00	D-amino acid dehydrogenase, small subunit
PA5312		2.03	0.00	probable aldehyde dehydrogenase
PA5336	<i>gmk</i>	-2.13	0.00	guanylate kinase
PA5415	<i>glyA1</i>	2.05	0.03	serine hydroxymethyltransferase

PA5436		2.64	0.02	probable. biotin carboxylase subunit of a transcarboxylase
PA5463		-2.77	0.00	hypothetical protein
PA5464		-2.13	0.00	hypothetical protein
PA5470		-3.61	0.00	probable peptide chain release factor
PA5471		-2.66	0.00	hypothetical protein
PA5485		-2.06	0.00	conserved hypothetical protein
PA5486		-2.06	0.00	conserved hypothetical protein
PA5503		-2.04	0.00	probable ATP-binding component of ABC transporter
PA5504		-2.31	0.00	probable permease of ABC transporter
PA5510		2.03	0.01	probable transporter
PA5561	<i>atpI</i>	-2.76	0.00	ATP synthase protein I
PA5564	<i>gidB</i>	-2.11	0.00	glucose inhibited division protein B