

Dataset S2. Gene and sRNA analysis for RNA-Seq data

locusID	Gene name	log2 fold change WT after 30 min Fe(II) shock	log2 fold change $\Delta bqsR$ after 30 min Fe(II) shock	FDR	1st - 2nd column (WT vs $\Delta bqsR$)	Predicted function
PA14_04180		11.61	-0.90	5.68E-08	12.51	Bacterial OB-Fold protein (pfam)
PA14_29710	<i>bqsP</i>	9.03	-0.14	6.68E-12	9.17	Predicted membrane protein (COG)
PA14_04270		8.55	-0.28	1.04E-11	8.84	transcription factor (PseudoCAP Function Class)
PA14_04190		8.43	-0.27	1.78E-12	8.70	acytyl polyamine deacetylase (COG)
PA14_29720	<i>bqsQ</i>	8.61	0.06	1.78E-12	8.54	Predicted membrane protein (COG)
PA14_29730	<i>bqsR</i>	7.79	-0.29	6.83E-12	8.08	Fe(II) responsive response regulator
PA14_29740	<i>bqsS</i>	6.99	0.05	1.78E-12	6.94	Fe(II) responsive sensor histidine kinase
PA14_04290		6.74	-0.19	3.58E-12	6.92	arginine-specific autotransporter (doi: 10.1371/journal.ppat.1002854)
PA14_07070		7.09	0.65	1.05E-11	6.44	Predicted ferric reductase (cog)
PA14_04210		5.38	-0.50	2.75E-11	5.88	amino acid transporter, potE homologue (polyamine transporter) (cog)
PA14_29750	<i>bqsT</i>	5.95	0.20	7.42E-10	5.75	hypothetical
PA14_52340		5.31	-0.41	1.61E-06	5.71	hypothetical
PA14_63110		4.78	-0.18	2.07E-08	4.96	S-adenosylmethionine decarboxylase (cog, pfam, tigrfam)
PA14_63120		3.86	-0.16	1.88E-09	4.02	Spermidine synthase (cog, pfam, tigrfam)
PA14_01240		2.97	-1.04	9.80E-09	4.01	Zn-binding carbonic anhydrase (doi: 10.1099/mic.0.066357-0)
PA14_01250		2.44	-0.41	2.66E-08	2.85	sulfate transporter (cog, pfam)
PA14_57880		3.08	0.31	1.62E-09	2.77	ABC-type transport system involved in resistance to organic solvents, ATPase component (cog)
PA14_57870		2.59	0.28	1.67E-08	2.32	ABC-type transport system involved in resistance to organic solvents, permease component (cog)
PA14_63150	<i>pmrA</i>	2.19	-0.08	7.34E-08	2.26	pmrA two-compenent regulator
PA14_63130		1.97	-0.13	8.73E-07	2.10	hypothetical
PA14_57840		2.41	0.32	1.09E-04	2.09	Anti-anti-sigma regulatory factor

						(antagonist of anti-sigma factor) (cog)
PA14_49100		1.40	-0.59	3.11E-06	1.99	Glutathione S-transferase (COG)
PA14_57850		2.33	0.47	2.33E-06	1.86	ABC-type transport system involved in resistance to organic solvents, periplasmic component (cog)
PA14_52330		1.82	0.02	1.16E-04	1.80	hypothetical
PA14_57830		2.18	0.43	1.17E-05	1.75	ABC-type transport system involved in resistance to organic solvents, auxiliary component (cog)
PA14_49180	<i>phoP</i>	1.37	-0.37	1.59E-06	1.74	two component system
PA14sr_013		1.94	0.22	4.62E-06	1.72	regulatory RNA
PA14_63160	<i>pmrB</i>	1.48	-0.17	1.34E-07	1.65	pmrB two-component sensor
PA14_03710		3.47	1.86	4.52E-04	1.61	hypothetical
PA14_28070		3.20	1.62	5.23E-03	1.59	hypothetical
PA14_07000	<i>dsbB</i>	1.42	-0.12	4.56E-07	1.54	Disulfide bond formation protein DsbB (cog)
PA14_29760		2.27	0.73	1.95E-07	1.54	Methyl-accepting chemotaxis protein (cog, pfam, SMART)
PA14_46900		1.44	-0.09	6.09E-04	1.53	hypothetical
PA14_19970		-2.99	-4.45	1.88E-06	1.46	hypothetical
PA14_49200	<i>oprH</i>	1.16	-0.26	1.53E-05	1.42	outer membrane porin stabilizes outer membrane by LPS binding and increases antibiotic resistance (doi: 10.1074/jbc.M111.280933)
PA14_70860		1.43	0.06	1.73E-06	1.37	ABC-type phosphate transport system, periplasmic component (cog)
PA14_37830		3.60	2.31	3.17E-04	1.30	cysteine desulfurase (cog, tigrfam, prk)
PA14_13010		3.20	1.95	6.41E-05	1.25	ABC-type metal ion transport system, periplasmic component/surface antigen (COG)
PA14_03700		3.19	2.00	6.15E-04	1.19	ABC-type sulfate transport system, periplasmic component (COG)
PA14_04220		1.09	-0.04	3.35E-04	1.13	Spermidine/putrescine-binding periplasmic protein (COG)
PA14sr_109		1.18	0.08	2.45E-05	1.10	regulatory RNA
PA14_50740		1.10	0.04	2.59E-06	1.07	hypothetical
PA14_34740		2.80	1.76	2.34E-03	1.05	hypothetical
P35		1.52	0.48	1.64E-05	1.05	Non-coding RNA gene
PA14_57720		2.91	1.90	3.13E-04	1.01	sulfate adenylyltransferase subunit 2 (PRK)