

Dataset S3. Transcription unit analysis for RNA-Seq data

region	log2 fold change wt after 30min Fe(II) shock	log2 fold change Δ bqsR after 30min Fe(II) shock	1 st -2 nd column (WT vs Δ bqsR)	FDR	Predicted function
regionPA14_04180	11.62	-0.91	12.53	1.36E-08	Bacterial OB-Fold protein (pfam)
regionPA14_04270	8.54	-0.29	8.83	8.23E-12	transcription factor (PseudoCAP Function Class)
regionPA14_29710-PA14_29740	8.27	-0.03	8.30	4.74E-13	bqs operon; Two-component system (PseudoCAP Function Class)
regionPA14_04190 PA14_04210	7.44	-0.41	7.85	1.43E-12	deacetylase (cog); amino acid transporter, potE homologue (polyamine transporter) (cog)
regionPA14_04290	6.75	-0.19	6.94	4.53E-12	arginine-specific autotransporter (doi: 10.1371/journal.ppat.1002854)
regionPA14_07070	7.10	0.65	6.46	8.57E-12	Predicted ferric reductase (cog)
regionPA14_29750	5.96	0.19	5.77	1.11E-09	hypothetical
regionPA14_52340	5.32	-0.41	5.73	2.77E-06	hypothetical
regionPA14_01240	2.98	-1.04	4.02	1.07E-08	Zn-binding carbonic anhydrase (doi: 10.1099/mic.0.066357-0)
regionPA14_63110-PA14_63160	2.99	-0.15	3.14	2.57E-09	S-adenosylmethionine decarboxylase (cog, pfam, tigrfam); Spermidine synthase (cog, pfam, tigrfam); hypothetical; pmrA; pmrB
regionPA14_01250	2.45	-0.42	2.87	2.75E-08	sulfate transporter (cog, pfam)

regionPA14_57850-PA14_57880	2.82	0.33	2.49	7.17E-09	57830/57840 in operon (DOOR operon predictor) ABC-type transport system involved in resistance to organic solvents, periplasmic component (cog); ABC-type transport system involved in resistance to organic solvents, permease component (cog); ABC-type transport system involved in resistance to organic solvents, ATPase component (cog)
regionPA14_57830 PA14_57840	2.35	0.34	2.01	2.22E-05	ABC-type transport system involved in resistance to organic solvents, auxiliary component (cog); Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor) (cog)
regionPA14_52330	1.83	0.02	1.81	1.12E-04	hypothetical
regionPA14_03710	3.48	1.85	1.63	5.11E-04	hypothetical
regionPA14_28070	3.21	1.61	1.60	6.11E-03	FOG: GAF domain (cog)
regionPA14_07000	1.43	-0.13	1.56	4.23E-07	Disulfide bond formation protein DsbB (cog)
regionPA14_29760	2.28	0.73	1.55	1.98E-07	Methyl-accepting chemotaxis protein (cog, pfam, SMART)
regionPA14_49170 PA14_49180	1.17	-0.38	1.55	2.41E-06	PhoP/PhoQ (predicted to be part of the oprH operon)
regionPA14_46900	1.45	-0.10	1.55	5.24E-04	hypothetical
regionPA14_19970	-2.98	-4.45	1.48	2.10E-06	hypothetical
regionPA14_49200	1.17	-0.26	1.44	1.15E-05	oprH- outer membrane porin stabilizes outer membrane by LPS binding and increases antibiotic resistance (doi: 10.1074/jbc.M111.280933)
regionPA14_70860	1.44	0.05	1.39	1.65E-06	ABC-type phosphate transport system, periplasmic component (cog)
regionPA14_37830	3.60	2.30	1.30	3.67E-04	cysteine desulfurase (cog, tigrfam, prk)
regionPA14_50740	1.12	0.03	1.09	1.58E-06	Outer membrane lipoprotein (cog)
regionPA14_17930	2.40	1.39	1.01	6.80E-06	glycerol-3-phosphate dehydrogenase (cog, tigrfam)
regionPA14_63470	0.91	-0.09	1.00	2.14E-04	S-adenosylmethionine-dependent methyltransferases (CD), Methyltransferase domain (pfam)

regionPA14_39590	0.31	1.73	-1.42	4.15E-04	metE, cobalamine independent methione synthetase (PMID: 1339288)
regionPA14_39570 PA14_39580	-0.63	1.02	-1.66	8.30E-03	rimJ Acetyltransferase, including N-acetylases of ribosomal proteins (cog), This enzyme acetylates the N-terminal alanine of ribosomal protein S5. Plays also a role in the temperature regulation of pap pilin transcription (uniprot) ; hypothetical