

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_0003	<i>trmE</i>	-1.06	tRNA modification GTPase TrmE	General function prediction only
SO_0017	-	1.22	amidohydrolase	Intracellular trafficking, secretion, and vesicular transport, Secondary metabolites biosynthesis, transport and catabolism
SO_0020	<i>fadA</i>	1.45	3-ketoacyl-CoA thiolase	Lipid transport and metabolism
SO_0027	-	2.04	protoporphyrinogen oxidase, putative	Energy production and conversion, Coenzyme transport and metabolism
SO_0055	-	1.18	hypothetical protein	General function prediction only
SO_0075	-	-1.36	AMP-binding family protein	Lipid transport and metabolism
SO_0084	-	-1.16	HAD-superfamily hydrolase, subfamily IA, variant 1 family protein	Energy production and conversion
SO_0086	-	-1.47	hypothetical protein	Function unknown
SO_0088	-	1.00	hypothetical protein	Function unknown
SO_0090	-	3.47	hypothetical protein	Function unknown
SO_0094	-	-1.07	hypothetical protein	Function unknown
SO_0095	<i>hutI</i>	-1.64	imidazolonepropionase	Secondary metabolites biosynthesis, transport and catabolism
SO_0120	-	-2.95	hypothetical protein	Function unknown
SO_0138	<i>moeA</i>	1.07	molybdopterin biosynthesis MoeA protein	Coenzyme transport and metabolism
SO_0151	-	-1.20	SAM-dependent methyltransferase	Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_0160	-	-1.04	transporter, putative	Coenzyme transport and metabolism
SO_0166	<i>gspD</i>	1.56	general secretion pathway protein D	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_0169	<i>gspG</i>	1.30	general secretion pathway protein G	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_0171	<i>gspI</i>	1.07	general secretion pathway protein I	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_0172	<i>gspJ</i>	1.70	general secretion pathway protein J	Intracellular trafficking, secretion, and vesicular transport
SO_0174	<i>gspL</i>	1.20	general secretion pathway protein L	Intracellular trafficking, secretion, and vesicular transport
SO_0182	-	1.10	hypothetical protein	Function unknown
SO_0184	-	1.44	microcystin dependent protein	Function unknown
SO_0185	-	1.17	microcystin dependent protein	Function unknown
SO_0186	-	1.17	microcystin dependent protein	Function unknown
SO_0187	-	1.31	serine protease	Posttranslational modification, protein turnover, chaperones
SO_0188	-	1.16	hypothetical protein	Function unknown
SO_0189	-	1.27	fibronectin type III domain-containing protein	Secondary metabolites biosynthesis, transport and catabolism
SO_0206	<i>trmA</i>	-1.02	tRNA (uracil-5-)-methyltransferase	Translation, ribosomal structure and biogenesis
SO_0216	-	-1.28	hypothetical protein	Function unknown

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SO_0260	<i>ccmD</i>	1.01	heme exporter protein CcmD	Intracellular trafficking, secretion, and vesicular transport
SO_0261	<i>ccmC</i>	1.02	heme exporter protein CcmC	Posttranslational modification, protein turnover, chaperones
SO_0262	<i>ccmB</i>	1.25	heme exporter protein CcmB	Posttranslational modification, protein turnover, chaperones
SO_0263	<i>ccmA</i>	1.79	cytochrome c biogenesis protein CcmA	Posttranslational modification, protein turnover, chaperones
SO_0264	<i>scyA</i>	-1.10	cytochrome c	Energy production and conversion
SO_0265	-	1.57	hypothetical protein	Posttranslational modification, protein turnover, chaperones
SO_0266	<i>ccmF-1</i>	1.09	cytochrome c-type biogenesis protein CcmF	Posttranslational modification, protein turnover, chaperones
SO_0312	-	-3.62	outer membrane porin, putative	Cell wall/membrane/envelope biogenesis
SO_0313	<i>potE</i>	-4.21	putrescine transporter	Amino acid transport and metabolism
SO_0314	<i>speF</i>	-4.35	ornithine decarboxylase	Amino acid transport and metabolism
SO_0322	-	1.08	hypothetical protein	Function unknown
SO_0324	-	2.16	hypothetical protein	Function unknown
SO_0325	-	1.18	dsrE-related protein	Inorganic ion transport and metabolism
SO_0326	-	1.83	hypothetical protein	Function unknown
SO_0334	-	2.36	hypothetical protein	Function unknown
SO_0335	-	-2.85	hypothetical protein	Function unknown
SO_0347	-	-1.10	acyltransferase family protein	Lipid transport and metabolism
SO_0354	-	-1.21	sodium/calcium exchanger	Inorganic ion transport and metabolism
SO_0365	-	-1.12	major facilitator superfamily permease	Carbohydrate transport and metabolism, Amino acid transport and metabolism, Inorganic ion transport and metabolism, General function prediction only
SO_0396	<i>frdC</i>	2.53	fumarate reductase cytochrome b-556 subunit	Energy production and conversion
SO_0397	<i>frdC</i>	1.10	fumarate reductase cytochrome B subunit	Function unknown
SO_0403	-	-3.63	hypothetical protein	Energy production and conversion
SO_0404	-	-6.22	hypothetical protein	Function unknown
SO_0468	<i>ubiA</i>	-1.09	4-hydroxybenzoate octaprenyltransferase	Coenzyme transport and metabolism
SO_0490	-	1.15	transcriptional regulator	Transcription
SO_0504	<i>fre</i>	-1.46	FMN reductase	Coenzyme transport and metabolism, Energy production and conversion
SO_0524	-	-1.77	HlyD family secretion protein	Defense mechanisms
SO_0552	-	2.00	hypothetical protein	Function unknown
SO_0553	-	1.58	hypothetical protein	Function unknown
SO_0556	-	-1.61	hypothetical protein	Function unknown
SO_0559	-	-1.13	MaoC domain-containing protein	Lipid transport and metabolism

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SO_0562	-	-1.18	hypothetical protein	Function unknown
SO_0563	-	-2.80	hypothetical protein	Function unknown
SO_0569	-	1.22	sensory box/GGDEF family protein	Signal transduction mechanisms
SO_0570	-	1.78	response regulator	Signal transduction mechanisms
SO_0575	<i>hepA</i>	-1.19	ATP-dependent helicase HepA	Transcription, Replication, recombination and repair
SO_0577	-	-1.85	sensory box histidine kinase/response regulator	Signal transduction mechanisms
SO_0581	-	3.09	hypothetical protein	Function unknown
SO_0582	<i>tpm</i>	1.40	thiopurine S-methyltransferase	Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_0583	<i>bfd</i>	-1.61	bacterioferritin-associated ferredoxin	Inorganic ion transport and metabolism
SO_0588	-	-1.12	transporter, putative	Cell wall/membrane/envelope biogenesis
SO_0595	-	1.53	hypothetical protein	General function prediction only
SO_0613	<i>pabA</i>	-1.09	para-aminobenzoate synthase glutamine amidotransferase, component II	Amino acid transport and metabolism, Coenzyme transport and metabolism
SO_0616	-	1.25	esterase, putative	Lipid transport and metabolism
SO_0620	-	1.11	hypothetical protein	Function unknown
SO_0639	-	1.75	collagenase family protein	Function unknown
SO_0671	-	1.32	hypothetical protein	Function unknown
SO_0672	-	1.22	hypothetical protein	Function unknown
SO_0696	<i>dipZ</i>	1.20	thiol:disulfide interchange protein precursor	Posttranslational modification, protein turnover, chaperones, Energy production and conversion
SO_0697	<i>cutA</i>	1.57	periplasmic divalent cation tolerance protein CutA	Inorganic ion transport and metabolism
SO_0702	-	-1.36	MATE efflux family protein	Defense mechanisms
SO_0703	<i>groES</i>	1.07	co-chaperonin GroES	Posttranslational modification, protein turnover, chaperones
SO_0704	<i>groEL</i>	1.01	chaperonin GroEL	Posttranslational modification, protein turnover, chaperones
SO_0717	-	1.11	monoheme cytochrome c	Energy production and conversion
SO_0721	-	-2.20	hypothetical protein	Function unknown
SO_0752	-	-3.31	hypothetical protein	Function unknown
SO_0755	-	-1.47	hypothetical protein	Function unknown
SO_0761	<i>glnB-1</i>	-1.35	nitrogen regulatory protein P-II 1	Amino acid transport and metabolism
SO_0775	-	-1.63	hypothetical protein	Function unknown
SO_0785	-	-1.43	hypothetical protein	Function unknown
SO_0788	-	-1.51	hypothetical protein	Function unknown
SO_0797	-	1.10	hypothetical protein	Posttranslational modification, protein turnover, chaperones, Energy production and conversion

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SO_0798	-	1.83	hypothetical protein	Inorganic ion transport and metabolism, Coenzyme transport and metabolism
SO_0806	-	1.86	alkaline phosphatase, putative	Inorganic ion transport and metabolism
SO_0839	-	-1.03	LysR family transcriptional regulator	Transcription
SO_0843	-	2.38	LysR family transcriptional regulator	Transcription
SO_0844	-	-1.90	hypothetical protein	Function unknown
SO_0848	<i>napA</i>	1.79	nitrate reductase	Energy production and conversion
SO_0849	<i>napD</i>	2.33	napD protein	Inorganic ion transport and metabolism
SO_0850	-	-1.59	hypothetical protein	Function unknown
SO_0852	-	-1.07	hypothetical protein	Function unknown
SO_0853	-	-1.30	pilin, putative	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_0858	-	-1.65	sodium:alanine symporter family protein	Amino acid transport and metabolism
SO_0863	-	-1.18	hypothetical protein	Function unknown
SO_0864	-	2.15	LuxR family transcriptional regulator	Signal transduction mechanisms, Transcription
SO_0865	-	5.02	hypothetical protein	Function unknown
SO_0866	-	6.39	minor curlin subunit CsgB, putative	Function unknown
SO_0867	-	3.47	serine protease	Posttranslational modification, protein turnover, chaperones, General function prediction only
SO_0883	-	1.01	hypothetical protein	Function unknown
SO_0894	-	-1.37	hypothetical protein	Function unknown
SO_0900	-	1.14	aldo/keto reductase family oxidoreductase	Energy production and conversion
SO_0902	<i>nqrA-1</i>	2.97	Na(+)-translocating NADH-quinone reductase subunit A	Energy production and conversion
SO_0903	<i>nqrB-1</i>	1.21	Na(+)-translocating NADH-quinone reductase subunit B	Energy production and conversion
SO_0904	<i>nqrC-1</i>	1.93	Na(+)-translocating NADH-quinone reductase subunit C	Energy production and conversion
SO_0906	<i>nqrE-1</i>	1.36	Na(+)-translocating NADH-quinone reductase subunit E	Energy production and conversion
SO_0916	-	1.28	MarR family transcriptional regulator	Transcription, General function prediction only
SO_0918	<i>aac</i>	1.54	aculeacin A acylase	General function prediction only
SO_0919	-	-1.28	serine transporter, putative	Amino acid transport and metabolism
SO_0923	-	-1.28	hypothetical protein	Posttranslational modification, protein turnover, chaperones
SO_0940	-	2.37	transcriptional regulator-related protein	Transcription
SO_0941	-	3.18	hypothetical protein	Function unknown
SO_0944	-	1.70	hypothetical protein	General function prediction only
SO_0945	-	3.80	AcrB/AcrD/AcrF family protein	Defense mechanisms

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SO_0946	-	4.44	hypothetical protein	Cell wall/membrane/envelope biogenesis
SO_0956	<i>ahpF</i>	-1.09	alkyl hydroperoxide reductase, F subunit	Posttranslational modification, protein turnover, chaperones
SO_0961	-	-1.35	hypothetical protein	Cell wall/membrane/envelope biogenesis
SO_0970	-	1.15	fumarate reductase flavoprotein subunit precursor	Energy production and conversion
SO_0974	-	-1.51	hypothetical protein	Function unknown
SO_0994	-	2.14	hypothetical protein	Function unknown
SO_0999	<i>pbpG</i>	-1.07	D-alanyl-D-alanine endopeptidase	Cell wall/membrane/envelope biogenesis
SO_1064	-	1.21	hypothetical protein	General function prediction only
SO_1066	-	1.35	extracellular nuclease	General function prediction only
SO_1071	-	-1.91	hypothetical protein	Function unknown
SO_1074	-	-1.14	tyrosine-specific transport protein, putative	Amino acid transport and metabolism
SO_1075	-	1.19	hypothetical protein	Function unknown
SO_1087	-	-1.73	Na ⁺ /H ⁺ antiporter family protein	Energy production and conversion
SO_1091	-	-1.32	hypothetical protein	Carbohydrate transport and metabolism, Amino acid transport and metabolism, General function prediction only
SO_1092	-	-1.02	AraC/XylS family transcriptional regulator	Transcription
SO_1094	-	-1.80	putative transcription elongation factor	Transcription
SO_1102	-	1.16	TonB-dependent receptor domain-containing protein	Inorganic ion transport and metabolism
SO_1112	<i>bfr1</i>	-1.27	bacterioferritin subunit 1	Inorganic ion transport and metabolism
SO_1120	-	-1.03	xanthine/uracil permease family protein	General function prediction only
SO_1126	<i>dnaK</i>	1.35	chaperone protein DnaK	Posttranslational modification, protein turnover, chaperones
SO_1128	-	-1.05	hypothetical protein	Function unknown
SO_1144	-	-1.25	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms
SO_1155	-	-2.72	hypothetical protein	Function unknown
SO_1159	-	-1.24	hypothetical protein	Cell cycle control, cell division, chromosome partitioning
SO_1167	<i>rodA</i>	-1.04	rod shape-determining protein RodA	Cell cycle control, cell division, chromosome partitioning
SO_1190	-	1.11	hypothetical protein	Inorganic ion transport and metabolism
SO_1195	-	-2.16	hypothetical protein	Translation, ribosomal structure and biogenesis
SO_1207	<i>rpsO</i>	-1.38	30S ribosomal protein S15	Translation, ribosomal structure and biogenesis
SO_1218	<i>deoA</i>	1.20	thymidine phosphorylase	Nucleotide transport and metabolism
SO_1268	-	1.09	glutamine synthetase	Amino acid transport and metabolism
SO_1278	-	1.58	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms

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SO_1279	-	1.01	hypothetical protein	Function unknown
SO_1281	-	-1.18	hypothetical protein	Function unknown
SO_1297	<i>gspA</i>	1.15	general secretion pathway protein a	Intracellular trafficking, secretion, and vesicular transport, Cell wall/membrane/envelope biogenesis
SO_1317	-	1.01	hypothetical protein	Function unknown
SO_1325	<i>gltB</i>	1.30	glutamate synthase subunit alpha	Amino acid transport and metabolism
SO_1326	-	1.71	hypothetical protein	General function prediction only
SO_1329	-	-1.28	adenylate cyclase-related protein	Signal transduction mechanisms
SO_1343	<i>rseA</i>	1.39	sigma-E factor negative regulatory protein	Signal transduction mechanisms
SO_1369	-	-1.00	hypothetical protein	General function prediction only
SO_1370	-	-1.11	hypothetical protein	General function prediction only
SO_1383	-	-1.51	DEAD-box ATP dependent DNA helicase	Replication, recombination and repair, Transcription, Translation, ribosomal structure and biogenesis
SO_1390	-	-1.20	peptidyl-prolyl cis-trans isomerase, FKBP-type	Posttranslational modification, protein turnover, chaperones
SO_1407	-	1.18	mercuric transport periplasmic protein MerP, putative	Inorganic ion transport and metabolism
SO_1415	-	2.36	TetR family transcriptional regulator	Transcription
SO_1416	-	1.44	DNA-binding response regulator	Signal transduction mechanisms
SO_1417	-	1.01	sensor histidine kinase	Signal transduction mechanisms
SO_1443	-	-1.32	hypothetical protein	Function unknown
SO_1469	-	-1.12	Cro/CI family transcriptional regulator	Transcription
SO_1478	-	3.14	methylase, putative	Coenzyme transport and metabolism
SO_1479	-	2.84	hypothetical protein	Function unknown
SO_1480	-	1.31	GGDEF family protein	Signal transduction mechanisms
SO_1483	<i>aceB</i>	1.83	malate synthase	Energy production and conversion
SO_1484	<i>aceA</i>	1.84	isocitrate lyase	Energy production and conversion
SO_1506	-	-1.19	MATE efflux family protein	Defense mechanisms
SO_1507	-	-1.30	hypothetical protein	Function unknown
SO_1508	-	-1.08	hypothetical protein	Amino acid transport and metabolism
SO_1512	-	-1.37	hypothetical protein	Energy production and conversion
SO_1513	-	-1.73	hypothetical protein	Nucleotide transport and metabolism
SO_1543	-	-1.18	hypothetical protein	Function unknown
SO_1568	-	-2.90	hypothetical protein	Function unknown
SO_1572	-	-1.94	hypothetical protein	Function unknown

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SO_1581	<i>phnA</i>	-1.36	phnA protein	Inorganic ion transport and metabolism
SO_1589	-	1.23	hypothetical protein	Function unknown
SO_1591	-	1.74	hypothetical protein	Function unknown
SO_1635	<i>dxr</i>	1.15	1-deoxy-D-xylulose 5-phosphate reductoisomerase	Lipid transport and metabolism
SO_1643	<i>rnhB</i>	1.09	ribonuclease HII	Replication, recombination and repair
SO_1649	-	1.87	hypothetical protein	Function unknown
SO_1650	-	1.47	hypothetical protein	Function unknown
SO_1666	<i>phhA</i>	2.84	phenylalanine 4-monooxygenase	Amino acid transport and metabolism
SO_1667	<i>phhB</i>	2.55	pterin-4-alpha-carbinolamine dehydratase	Coenzyme transport and metabolism
SO_1673	-	2.10	outer membrane protein W	Cell wall/membrane/envelope biogenesis
SO_1678	<i>mmsA</i>	1.08	methylmalonate-semialdehyde dehydrogenase	Energy production and conversion
SO_1698	-	2.43	hypothetical protein	Function unknown
SO_1700	-	3.05	hypothetical protein	Function unknown
SO_1701	-	3.26	hypothetical protein	Function unknown
SO_1708	<i>cat2</i>	1.02	4-hydroxybutyrate coenzyme A transferase	Energy production and conversion
SO_1710	-	1.15	hypothetical protein	Function unknown
SO_1751	-	1.06	hypothetical protein	Amino acid transport and metabolism
SO_1759	-	-1.07	hypothetical protein	Function unknown
SO_1769	-	-1.43	glutamate decarboxylase, putative	Amino acid transport and metabolism
SO_1770	-	1.66	glycerate kinase, putative	Carbohydrate transport and metabolism
SO_1775	-	-1.25	phage SPO1 DNA polymerase domain-containing protein	Replication, recombination and repair
SO_1796	<i>lon</i>	1.43	ATP-dependent protease La	Posttranslational modification, protein turnover, chaperones
SO_1806	<i>pspF</i>	1.93	psp operon transcriptional activator	Transcription, Signal transduction mechanisms
SO_1812	<i>mdeA</i>	2.65	methionine gamma-lyase	Amino acid transport and metabolism
SO_1813	-	1.68	DNA-binding protein, putative	Replication, recombination and repair
SO_1821	-	-2.19	outer membrane porin, putative	Cell wall/membrane/envelope biogenesis
SO_1822	-	3.79	TonB-dependent receptor, putative	Inorganic ion transport and metabolism
SO_1835	-	-1.31	hypothetical protein	Function unknown
SO_1836	-	-1.40	hypothetical protein	Function unknown
SO_1844	-	1.31	extracellular nuclease, putative	General function prediction only
SO_1858	-	-4.16	hypothetical protein	Function unknown

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SO_1863	-	-1.71	HU family DNA-binding protein	Replication, recombination and repair
SO_1881	-	1.16	HlyD family-like protein	Cell wall/membrane/envelope biogenesis
SO_1888	-	1.01	hypothetical protein	Function unknown
SO_1895	-	1.12	enoyl-CoA hydratase/isomerase family protein	Lipid transport and metabolism
SO_1901	<i>sugE</i>	-1.16	sugE protein	Inorganic ion transport and metabolism
SO_1909	-	1.01	hypothetical protein	Function unknown
SO_1911	-	2.97	short chain dehydrogenase/reductase family oxidoreductase	Lipid transport and metabolism, Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_1915	-	2.51	serine protease	Posttranslational modification, protein turnover, chaperones, General function prediction only
SO_1921	-	-2.12	hypothetical protein	Function unknown
SO_1961	<i>maa</i>	-1.08	maltose O-acetyltransferase	General function prediction only
SO_1962	-	1.39	4-hydroxyphenylpyruvate dioxygenase	Amino acid transport and metabolism, General function prediction only
SO_1963	-	1.87	hypothetical protein	Secondary metabolites biosynthesis, transport and catabolism
SO_1964	-	1.16	hypothetical protein	Function unknown
SO_1985	-	-1.80	transcriptional activator, putative	Signal transduction mechanisms
SO_1986	-	-1.91	RNA polymerase sigma-70 factor	Transcription
SO_1987	-	-1.35	ATP-dependent protease La	General function prediction only
SO_2004	-	-1.92	TonB-dependent receptor domain-containing protein	Inorganic ion transport and metabolism
SO_2010	-	-1.67	hypothetical protein	Function unknown
SO_2011	-	-1.22	hypothetical protein	Function unknown
SO_2016	<i>htpG</i>	1.88	heat shock protein 90	Posttranslational modification, protein turnover, chaperones
SO_2017	-	2.90	thioredoxin-like protein	Posttranslational modification, protein turnover, chaperones
SO_2042	-	1.11	putative sulfite oxidase subunit YedY	General function prediction only
SO_2044	<i>gloA</i>	-1.39	lactoylglutathione lyase	Amino acid transport and metabolism
SO_2047	-	1.13	prolyl oligopeptidase family protein	Amino acid transport and metabolism
SO_2049	-	1.12	GGDEF family protein	Signal transduction mechanisms
SO_2065	<i>tyrP</i>	-1.20	tyrosine-specific transport protein	Amino acid transport and metabolism
SO_2083	-	1.61	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms
SO_2090	<i>hypE</i>	1.33	hydrogenase expression/formation protein HypE	Posttranslational modification, protein turnover, chaperones
SO_2091	<i>hypD</i>	3.30	hydrogenase expression/formation protein HypD	Posttranslational modification, protein turnover, chaperones
SO_2092	<i>hypC</i>	2.38	hydrogenase assembly chaperone hypC/hupF	Posttranslational modification, protein turnover, chaperones
SO_2093	<i>hypB</i>	2.37	hydrogenase accessory protein HypB	Posttranslational modification, protein turnover, chaperones, Transcription

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SO_2096	-	1.63	hydrogenase expression/formation protein	Energy production and conversion
SO_2097	<i>hydC</i>	1.50	quinone-reactive Ni/Fe hydrogenase, cytochrome b subunit	Energy production and conversion
SO_2098	<i>hyaB</i>	3.88	quinone-reactive Ni/Fe hydrogenase, large subunit	Energy production and conversion
SO_2099	<i>hoxK</i>	3.81	quinone-reactive Ni/Fe hydrogenase, small subunit precursor	Energy production and conversion
SO_2109	-	1.90	hypothetical protein	Function unknown
SO_2110	-	1.47	hypothetical protein	Function unknown
SO_2111	-	-1.44	hypothetical protein	Function unknown
SO_2113	-	-1.23	hypothetical protein	Function unknown
SO_2114	-	-1.03	hypothetical protein	Cell wall/membrane/envelope biogenesis
SO_2123	-	1.30	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms
SO_2167	-	1.14	hypothetical protein	Energy production and conversion
SO_2191	<i>metC</i>	-1.04	cystathionine beta-lyase	Amino acid transport and metabolism
SO_2192	-	-1.12	sensor histidine kinase	Signal transduction mechanisms
SO_2203	<i>dgkA</i>	-1.18	diacylglycerol kinase	Cell wall/membrane/envelope biogenesis
SO_2215	-	-1.17	sun protein, putative	Translation, ribosomal structure and biogenesis
SO_2216	-	1.34	sensory box protein	Signal transduction mechanisms
SO_2241	-	1.14	hypothetical protein	Function unknown
SO_2251	-	1.10	hypothetical protein	General function prediction only
SO_2253	-	-1.55	acylphosphatase	Energy production and conversion
SO_2260	<i>suhB</i>	-1.79	extragenic suppressor protein SuhB	Carbohydrate transport and metabolism
SO_2279	<i>ilvI</i>	1.11	acetolactate synthase 3 catalytic subunit	Amino acid transport and metabolism, Coenzyme transport and metabolism
SO_2354	-	-1.33	hypothetical protein	Cell cycle control, cell division, chromosome partitioning
SO_2373	-	-1.16	inner membrane transport protein YdhC	Carbohydrate transport and metabolism, Amino acid transport and metabolism, Inorganic ion transport and metabolism, General function prediction only
SO_2389	<i>emrD</i>	-3.55	multidrug resistance protein D	Carbohydrate transport and metabolism, Amino acid transport and metabolism, Inorganic ion transport and metabolism, General function prediction only
SO_2394	<i>dacB</i>	1.23	penicillin-binding protein 4	Cell wall/membrane/envelope biogenesis
SO_2395	-	1.85	acyl-CoA dehydrogenase family protein	Lipid transport and metabolism
SO_2399	-	-1.04	hypothetical protein	Carbohydrate transport and metabolism
SO_2426	-	1.48	DNA-binding response regulator	Signal transduction mechanisms, Transcription
SO_2427	-	-4.79	TonB-dependent receptor, putative	Inorganic ion transport and metabolism
SO_2446	-	2.69	hypothetical protein	Function unknown

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SO_2483	-	-2.38	aminotransferase AlaT	Amino acid transport and metabolism
SO_2490	-	1.04	DNA-binding transcriptional regulator HexR	Transcription
SO_2493	-	1.34	TetR family transcriptional regulator	Transcription
SO_2515	-	-1.02	hypothetical protein	Function unknown
SO_2516	-	-1.97	hypothetical protein	Function unknown
SO_2525	-	-1.11	ABC transporter, ATP-binding protein	General function prediction only
SO_2530	<i>def</i>	-1.38	peptide deformylase	Translation, ribosomal structure and biogenesis
SO_2566	<i>asmA</i>	1.51	asmA protein	Cell wall/membrane/envelope biogenesis
SO_2569	-	-2.21	hypothetical protein	Function unknown
SO_2570	-	1.71	putative lipoprotein	Function unknown
SO_2587	<i>hemB-1</i>	2.02	delta-aminolevulinic acid dehydratase	Coenzyme transport and metabolism
SO_2594	-	1.91	hypothetical protein	General function prediction only
SO_2595	-	3.88	BNR repeat-containing protein	General function prediction only
SO_2596	-	3.50	hypothetical protein	Function unknown
SO_2597	-	4.16	hypothetical protein	Function unknown
SO_2625	<i>infA</i>	-1.63	translation initiation factor IF-1	Translation, ribosomal structure and biogenesis
SO_2628	<i>cspD</i>	2.81	stress response protein CspD	Transcription
SO_2647	-	-1.61	cytosolic long-chain acyl-CoA thioester hydrolase family protein	Lipid transport and metabolism
SO_2653	-	-2.33	Ner family transcriptional regulator	Transcription
SO_2654	-	-2.42	transposase, putative	Replication, recombination and repair
SO_2657	-	-1.79	hypothetical protein	Function unknown
SO_2658	-	-1.62	hypothetical protein	Function unknown
SO_2660	-	-1.75	hypothetical protein	Function unknown
SO_2661	-	-1.43	hypothetical protein	Function unknown
SO_2663	-	-1.69	hypothetical protein	Function unknown
SO_2665	-	-1.72	hypothetical protein	Function unknown
SO_2682	-	-1.10	hypothetical protein	Function unknown
SO_2683	-	-1.27	hypothetical protein	Function unknown
SO_2711	-	1.59	hypothetical protein	Function unknown
SO_2727	-	-1.17	cytochrome c3	Replication, recombination and repair, Posttranslational modification, protein turnover, chaperones
SO_2745	<i>grxA</i>	-1.88	glutaredoxin 1	Posttranslational modification, protein turnover, chaperones

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_2751	-	1.00	MotA/TolQ/ExbB proton channel family protein	Intracellular trafficking, secretion, and vesicular transport
SO_2755	<i>mt</i>	-1.38	ribonuclease T	Replication, recombination and repair
SO_2797	-	-2.64	hypothetical protein	Posttranslational modification, protein turnover, chaperones
SO_2801	<i>lpxK</i>	-1.10	tetraacyldisaccharide 4'-kinase	Cell wall/membrane/envelope biogenesis
SO_2849	-	-1.37	acetyltransferase	Transcription, General function prediction only
SO_2850	-	-1.02	acetyltransferase	Translation, ribosomal structure and biogenesis
SO_2856	-	1.41	CBS domain-containing protein	Signal transduction mechanisms
SO_2857	-	1.86	sodium/solute symporter family protein	General function prediction only
SO_2858	-	1.45	hypothetical protein	Function unknown
SO_2861	-	-1.03	hypothetical protein	Cell wall/membrane/envelope biogenesis, Carbohydrate transport and metabolism
SO_2863	-	-1.07	hypothetical protein	Function unknown
SO_2865	-	-1.56	L-lysine exporter, putative	General function prediction only
SO_2868	-	-1.36	hypothetical protein	Posttranslational modification, protein turnover, chaperones
SO_2888	-	1.50	hypothetical protein	Function unknown
SO_2889	-	1.12	sensory box histidine kinase	Signal transduction mechanisms, Cell motility
SO_2905	-	1.09	O-methyltransferase, putative	Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_2913	<i>pflA</i>	1.84	pyruvate formate lyase-activating enzyme 1	Posttranslational modification, protein turnover, chaperones
SO_2918	-	-1.98	hypothetical protein	Function unknown
SO_2923	<i>gltS</i>	-1.20	sodium/glutamate symporter	Amino acid transport and metabolism
SO_2924	-	1.43	signal peptidase I family protein	Intracellular trafficking, secretion, and vesicular transport
SO_2926	-	1.69	ABC transporter, permease, putative	Secondary metabolites biosynthesis, transport and catabolism
SO_2927	-	2.92	ABC transporter, ATP-binding protein	Secondary metabolites biosynthesis, transport and catabolism
SO_2934	-	3.71	hypothetical protein	General function prediction only
SO_2945	-	2.15	hypothetical protein	Function unknown
SO_2954	-	1.87	hypothetical protein	Function unknown
SO_2955	-	1.64	hypothetical protein	Function unknown
SO_2960	-	1.16	hypothetical protein	Function unknown
SO_2962	-	1.20	hypothetical protein	Function unknown
SO_2963	-	1.19	prophage LambdaSo, HK97 family major capsid protein	Function unknown
SO_2964	-	1.28	ClpP protease family protein	Posttranslational modification, protein turnover, chaperones, Intracellular trafficking, secretion, and vesicular transport
SO_2968	-	1.05	phage terminase small subunit	Replication, recombination and repair

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_2974	-	1.84	hypothetical protein	Function unknown
SO_2977	-	-1.67	hypothetical protein	Function unknown
SO_2988	-	-1.30	hypothetical protein	Function unknown
SO_2999	-	-1.06	hypothetical protein	Function unknown
SO_3029	-	-1.11	hypothetical protein	Function unknown
SO_3030	<i>alcA</i>	3.38	siderophore biosynthesis protein	Secondary metabolites biosynthesis, transport and catabolism
SO_3031	-	1.34	siderophore biosynthesis protein, putative	Translation, ribosomal structure and biogenesis
SO_3032	-	1.18	siderophore biosynthesis protein, putative	Secondary metabolites biosynthesis, transport and catabolism
SO_3033	-	1.40	ferric alcaligin siderophore receptor	Inorganic ion transport and metabolism
SO_3047	-	1.18	hypothetical protein	Function unknown
SO_3048	-	1.24	isoquinoline 1-oxidoreductase, beta subunit, putative	Energy production and conversion
SO_3051	-	1.01	xanthine dehydrogenase accessory factor	Posttranslational modification, protein turnover, chaperones
SO_3053	-	1.37	hypothetical protein	Function unknown
SO_3054	-	1.35	metallo-beta-lactamase family protein	General function prediction only
SO_3059	-	1.91	formate hydrogenlyase transcriptional activator, putative	Transcription, Signal transduction mechanisms
SO_3060	-	-1.19	outer membrane porin, putative	Cell wall/membrane/envelope biogenesis
SO_3063	-	1.29	sodium:alanine symporter family protein	Amino acid transport and metabolism
SO_3090	-	1.69	MoxR domain-containing protein	General function prediction only
SO_3091	-	1.85	hypothetical protein	General function prediction only
SO_3092	-	1.45	hypothetical protein	Function unknown
SO_3093	-	1.36	von Willebrand factor type A domain-containing protein	General function prediction only
SO_3094	-	1.60	TPR domain-containing protein	General function prediction only
SO_3095	-	1.07	hypothetical protein	Function unknown
SO_3099	-	-6.40	long-chain fatty acid transport protein, putative	Lipid transport and metabolism
SO_3101	-	1.13	hypothetical protein	Function unknown
SO_3102	-	1.07	AcrA/AcrE family protein	Cell wall/membrane/envelope biogenesis
SO_3106	<i>aprE</i>	4.16	cold-active serine alkaline protease	Posttranslational modification, protein turnover, chaperones
SO_3122	-	-1.47	serine/threonine transporter SstT	Amino acid transport and metabolism
SO_3132	-	-2.77	hypothetical protein	Function unknown
SO_3135	-	-1.33	C4-dicarboxylate transporter, putative	Carbohydrate transport and metabolism
SO_3136	<i>dctM</i>	-1.24	C4-dicarboxylate transport protein	Carbohydrate transport and metabolism

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_3145	<i>etfB</i>	1.33	electron transfer flavoprotein, beta subunit	Energy production and conversion
SO_3161	-	-1.15	glucose-1-phosphate thymidyltransferase-related protein	Cell wall/membrane/envelope biogenesis
SO_3275	-	-1.92	hypothetical protein	Function unknown
SO_3279	-	1.80	AcrB/AcrD/AcrF family protein	Defense mechanisms
SO_3301	-	-1.23	flavocytochrome c flavin subunit	Energy production and conversion
SO_3305	-	-1.86	LuxR family DNA-binding response regulator	Signal transduction mechanisms, Transcription
SO_3342	-	-1.71	hypothetical protein	Function unknown
SO_3350	<i>pilU</i>	1.79	twitching motility protein PilU	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_3351	<i>pilT</i>	1.79	twitching motility protein PilT	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_3377	-	-1.22	hypothetical protein	Function unknown
SO_3378	-	-1.22	hypothetical protein	Function unknown
SO_3380	-	-1.24	hypothetical protein	Function unknown
SO_3381	-	-1.34	hypothetical protein	General function prediction only
SO_3382	-	-1.69	short chain dehydrogenase/reductase family oxidoreductase	Lipid transport and metabolism, Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_3383	-	-1.74	transcriptional regulator-related protein	Function unknown
SO_3386	-	-1.05	hypothetical protein	Function unknown
SO_3395	-	2.61	hypothetical protein	Function unknown
SO_3403	<i>yfiA-1</i>	1.41	ribosomal subunit interface protein	Translation, ribosomal structure and biogenesis
SO_3404	-	1.23	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms
SO_3408	-	1.11	hypothetical protein	Function unknown
SO_3418	-	-1.07	hypothetical protein	Function unknown
SO_3422	<i>yfiA-2</i>	2.20	ribosomal subunit interface protein	Translation, ribosomal structure and biogenesis
SO_3432	<i>rpoS</i>	2.02	RNA polymerase sigma-38 factor	Transcription
SO_3433	<i>nlpD</i>	2.26	lipoprotein NlpD	Cell wall/membrane/envelope biogenesis
SO_3469	<i>ribD</i>	1.05	riboflavin biosynthesis protein RibD	Coenzyme transport and metabolism
SO_3480	-	1.20	phosphatase	Signal transduction mechanisms
SO_3489	-	3.06	GGDEF domain-containing protein	Signal transduction mechanisms
SO_3507	-	1.08	hypothetical protein	Carbohydrate transport and metabolism
SO_3514	-	1.08	TonB-dependent receptor	Inorganic ion transport and metabolism
SO_3527	-	1.05	hypothetical protein	Cell motility, Intracellular trafficking, secretion, and vesicular transport
SO_3537	<i>rpsT</i>	-1.75	30S ribosomal protein S20	Translation, ribosomal structure and biogenesis

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_3538	<i>hlyU</i>	1.25	transcriptional regulator HlyU	Transcription
SO_3540	-	-1.16	hypothetical protein	Function unknown
SO_3542	-	1.44	putative phosphoketolase	Carbohydrate transport and metabolism
SO_3558	-	1.32	hypothetical protein	Function unknown
SO_3559	<i>gshA</i>	1.33	glutamate--cysteine ligase	Coenzyme transport and metabolism
SO_3560	-	2.53	M16 family peptidase	General function prediction only
SO_3562	-	-1.56	proton/glutamate symporter, putative	Energy production and conversion
SO_3573	-	-1.52	hypothetical protein	Function unknown
SO_3577	<i>clpB</i>	1.08	clpB protein	Posttranslational modification, protein turnover, chaperones
SO_3582	-	-1.33	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms
SO_3611	-	1.24	AAA family ATPase	Posttranslational modification, protein turnover, chaperones
SO_3627	-	1.65	TetR family transcriptional regulator	Transcription
SO_3638	<i>pdxA</i>	1.02	pyridoxal phosphate biosynthetic protein PdxA	Coenzyme transport and metabolism
SO_3656	-	-1.43	hypothetical protein	Function unknown
SO_3657	-	-1.25	amino acid transporter LysE	Amino acid transport and metabolism
SO_3668	-	1.27	hypothetical protein	Inorganic ion transport and metabolism
SO_3679	-	1.05	hypothetical protein	Function unknown
SO_3685	-	2.13	curli production assembly/transport component CsgG, putative	Cell wall/membrane/envelope biogenesis
SO_3686	-	1.57	curli production assembly/transport component CsgF, putative	Function unknown
SO_3687	-	3.42	curli production assembly/transport component CsgE, putative	Function unknown
SO_3688	-	1.26	nitrogen regulation protein NtrY, putative	Signal transduction mechanisms
SO_3689	-	1.30	sigma-54 dependent nitrogen response regulator	Signal transduction mechanisms
SO_3705	-	-2.68	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase, putative	Nucleotide transport and metabolism
SO_3706	-	-3.53	NupC family protein	Nucleotide transport and metabolism
SO_3715	-	-1.00	dihydropteridine reductase	Energy production and conversion
SO_3720	-	1.55	hypothetical protein	Energy production and conversion, Coenzyme transport and metabolism
SO_3774	-	1.17	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	Amino acid transport and metabolism, Energy production and conversion
SO_3800	-	2.66	serine protease	Posttranslational modification, protein turnover, chaperones
SO_3808	-	1.57	hypothetical protein	Function unknown
SO_3813	-	-1.22	hypothetical protein	Function unknown

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_3840	-	-1.31	ECF subfamily RNA polymerase sigma factor	Transcription
SO_3847	-	-1.41	hypothetical protein	Function unknown
SO_3848	-	-1.20	hypothetical protein	Function unknown
SO_3857	-	-1.41	PAP2 family protein	Lipid transport and metabolism
SO_3864	<i>modB</i>	1.20	molybdate ABC transporter permease protein	Inorganic ion transport and metabolism
SO_3867	-	-1.53	Cro/CI family transcriptional regulator	Transcription
SO_3877	-	-1.09	hypothetical protein	Function unknown
SO_3884	-	-1.45	phage integrase family site specific recombinase	Replication, recombination and repair
SO_3895	-	-1.08	HesA/MoeB/ThiF family protein	Coenzyme transport and metabolism
SO_3913	-	2.57	putative hydroxylase	Function unknown
SO_3914	-	2.58	TonB-dependent receptor, putative	Inorganic ion transport and metabolism
SO_3915	-	1.39	hypothetical protein	Cell motility
SO_3942	-	1.68	serine protease	Posttranslational modification, protein turnover, chaperones
SO_3967	-	-1.08	hypothetical protein	Inorganic ion transport and metabolism
SO_3969	-	-3.20	OmpA family protein	Cell wall/membrane/envelope biogenesis
SO_3980	<i>nrfA</i>	1.43	cytochrome c nitrite reductase	Inorganic ion transport and metabolism
SO_3983	-	-1.23	hypothetical protein	Function unknown
SO_3987	-	-1.00	hypothetical protein	Function unknown
SO_4012	-	-1.83	hypothetical protein	Function unknown
SO_4013	-	-2.49	hypothetical protein	Function unknown
SO_4014	-	-3.18	AcrB/AcrD/AcrF family protein	Defense mechanisms
SO_4015	-	-4.20	hypothetical protein	Cell wall/membrane/envelope biogenesis
SO_4051	-	-1.24	HlyD family secretion protein	Defense mechanisms
SO_4052	-	-1.31	MarR family transcriptional regulator	Transcription
SO_4054	<i>metF</i>	-1.02	5,10-methylenetetrahydrofolate reductase	Amino acid transport and metabolism
SO_4057	<i>metJ</i>	-1.26	transcriptional repressor protein MetJ	Transcription, Amino acid transport and metabolism
SO_4058	-	-1.27	hypothetical protein	General function prediction only
SO_4069	-	-1.20	hypothetical protein	Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_4139	-	-1.27	hypothetical protein	General function prediction only
SO_4145	-	3.19	hypothetical protein	Signal transduction mechanisms
SO_4147	-	1.59	ABC transporter, ATP-binding/permease protein	Defense mechanisms

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_4148	-	1.78	HlyD family secretion protein	Cell wall/membrane/envelope biogenesis
SO_4149	-	3.18	RTX toxin, putative	Secondary metabolites biosynthesis, transport and catabolism
SO_4157	-	2.07	DNA-binding response regulator	Signal transduction mechanisms
SO_4159	-	-1.35	hypothetical protein	Function unknown
SO_4164	-	1.43	hypothetical protein	Function unknown
SO_4170	-	-1.06	C factor cell-cell signaling protein	Lipid transport and metabolism, Secondary metabolites biosynthesis, transport and catabolism, General function prediction only
SO_4178	-	-1.58	hypothetical protein	Cell wall/membrane/envelope biogenesis, Defense mechanisms
SO_4179	-	-1.49	glycosyl transferase, group 2 family protein	Cell wall/membrane/envelope biogenesis
SO_4180	-	-1.44	hypothetical protein	Signal transduction mechanisms
SO_4186	-	-1.00	hypothetical protein	Function unknown
SO_4209	-	-1.88	hypothetical protein	Replication, recombination and repair
SO_4210	-	-2.36	hypothetical protein	Replication, recombination and repair
SO_4232	-	-1.21	long-chain fatty acid transport protein	Lipid transport and metabolism
SO_4238	-	-1.17	TPR domain-containing protein	General function prediction only
SO_4245	<i>argA</i>	-1.08	N-acetylglutamate synthase	Amino acid transport and metabolism
SO_4252	-	1.96	prolyl oligopeptidase family protein	Amino acid transport and metabolism
SO_4254	<i>folE</i>	-1.24	GTP cyclohydrolase I	Coenzyme transport and metabolism
SO_4255	<i>pyrE</i>	-1.16	orotate phosphoribosyltransferase	Nucleotide transport and metabolism
SO_4264	<i>hsdS-2</i>	1.82	type I restriction-modification system, S subunit	Defense mechanisms
SO_4265	<i>hsdM-2</i>	1.51	type I restriction-modification system, M subunit	Defense mechanisms
SO_4266	-	1.32	hypothetical protein	Function unknown
SO_4285	-	-1.27	hypothetical protein	Function unknown
SO_4314	<i>hemD</i>	1.21	uroporphyrinogen-III synthase	Coenzyme transport and metabolism
SO_4320	<i>aggA</i>	1.13	agglutination protein	Cell wall/membrane/envelope biogenesis, Intracellular trafficking, secretion, and vesicular transport
SO_4321	-	1.12	OmpA family protein	Cell wall/membrane/envelope biogenesis
SO_4335	-	-1.42	phosphatidylglycerophosphatase B, putative	Lipid transport and metabolism
SO_4340	-	-1.41	hypothetical protein	Function unknown
SO_4342	-	-1.07	hypothetical protein	Function unknown
SO_4343	-	-1.02	aminotransferase, class V	Amino acid transport and metabolism
SO_4356	-	-1.91	hypothetical protein	Function unknown
SO_4361	-	-1.12	hypothetical protein	Function unknown

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_4412	-	-1.72	hypothetical protein	Function unknown
SO_4413	-	3.12	kynureninase	Amino acid transport and metabolism
SO_4414	-	2.67	hypothetical protein	Function unknown
SO_4418	-	-1.31	trypanothione synthetase domain-containing protein	Function unknown
SO_4419	-	-1.44	hypothetical protein	Amino acid transport and metabolism
SO_4420	-	-1.39	M24/M37 family peptidase	Cell wall/membrane/envelope biogenesis
SO_4425	-	-1.50	GGDEF family protein	Signal transduction mechanisms
SO_4457	-	1.48	GGDEF domain-containing protein	Signal transduction mechanisms
SO_4463	-	1.90	prolyl 4-hydroxylase alpha subunit	Function unknown
SO_4469	-	-1.38	alcohol dehydrogenase, iron-containing	Energy production and conversion
SO_4474	-	-1.69	hypothetical protein	Function unknown
SO_4481	-	-1.10	hypothetical protein	Function unknown
SO_4498	-	-1.52	hypothetical protein	Amino acid transport and metabolism
SO_4505	-	1.19	hypothetical protein	Function unknown
SO_4515	-	-1.43	formate dehydrogenase, C subunit, putative	Energy production and conversion
SO_4520	-	1.34	coproporphyrinogen III oxidase	Coenzyme transport and metabolism
SO_4527	-	-1.03	integral membrane domain-containing protein	Carbohydrate transport and metabolism, Amino acid transport and metabolism, General function prediction only
SO_4544	-	-1.11	hypothetical protein	Function unknown
SO_4555	-	-1.02	drug resistance transporter, Bcr/CflA family protein	Carbohydrate transport and metabolism, Amino acid transport and metabolism, Inorganic ion transport and metabolism, General function prediction only
SO_4557	-	-3.72	methyl-accepting chemotaxis protein	Cell motility, Signal transduction mechanisms
SO_4561	-	-1.21	hypothetical protein	Function unknown
SO_4570	-	-1.25	hypothetical protein	Function unknown
SO_4577	-	-1.22	hypothetical protein	Signal transduction mechanisms
SO_4592	-	1.57	hypothetical protein	Function unknown
SO_4593	-	1.68	hypothetical protein	Function unknown
SO_4604	-	-1.10	hypothetical protein	Function unknown
SO_4623	-	1.94	DNA-binding response regulator	Signal transduction mechanisms, Transcription
SO_4628	-	1.74	sulfatase	Cell wall/membrane/envelope biogenesis
SO_4681	-	-1.65	glycosyl transferase, group 1 family protein	Cell wall/membrane/envelope biogenesis
SO_4700	-	3.55	hypothetical protein	Function unknown
SO_4705	-	1.51	transcriptional regulator, putative	Transcription

Table S3: significantly regulated genes in $\Delta arcS$ mutants under aerobic growth conditions

ORF	Gene	Regulation ¹	Product	COG description
SO_4708	-	-1.34	hypothetical protein	Function unknown
SO_4718	-	1.78	sigma-54 dependent response regulator	Signal transduction mechanisms
SO_4727	-	-1.54	hypothetical protein	Coenzyme transport and metabolism
SO_4728	-	-1.64	hypothetical protein	Function unknown
SO_4729	-	-1.12	hypothetical protein	Function unknown
SO_4730	<i>hemN</i>	1.53	coproporphyrinogen III oxidase	Coenzyme transport and metabolism
SO_4743	-	1.39	TonB-dependent receptor, putative	Inorganic ion transport and metabolism
SO_A0006	-	1.70	ParA family protein	Cell cycle control, cell division, chromosome partitioning
SO_A0012	<i>rulB</i>	-1.20	SOS mutagenesis protein RulB	Replication, recombination and repair
SO_A0013	<i>rulA</i>	-1.28	SOS mutagenesis protein RulA	Transcription, Signal transduction mechanisms
SO_A0023	<i>higA</i>	-1.47	plasmid maintenance system antidote protein HigA	General function prediction only
SO_A0036	-	-1.22	HicB-related protein	Function unknown
SO_A0043	-	-1.17	hypothetical protein	Function unknown
SO_A0047	-	1.60	hypothetical protein	Function unknown
SO_A0049	-	1.74	toxin secretion ABC transporter, ATP-binding subunit/permease protein, putative	Defense mechanisms
SO_A0050	-	1.34	toxin secretion, membrane fusion protein	Cell wall/membrane/envelope biogenesis
SO_A0056	-	-1.19	hypothetical protein	Function unknown
SO_A0057	-	-1.91	hypothetical protein	Function unknown
SO_A0058	-	-1.82	hypothetical protein	Function unknown
SO_A0059	-	-1.28	hypothetical protein	Function unknown
SO_A0068	-	-1.95	hypothetical protein	Transcription
SO_A0070	-	-1.63	hypothetical protein	Amino acid transport and metabolism
SO_A0087	-	-1.36	hypothetical protein	Cell cycle control, cell division, chromosome partitioning
SO_A0185	-	-1.02	transcriptional regulator	Transcription
SO_A0159	-	-1.29	multidrug efflux transporter	Inorganic ion transport and metabolism

¹regulation is given in log fold change