

Additional file 2 – Complete set of genes differentially expressed in the *S. lividans adpA* mutant^a.

gene ^b	annotated function ^b	Fc ^c	P-value ^d	class ^e	classification details ^e
SCO0148	putative transcriptional regulatory protein	0.421	0.00E+00	r.	6.5.0 Others (237)
SCO0169	conserved hypothetical protein SCJ1.18	0.621	2.70E-08	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0171	conserved hypothetical protein SCJ1.20	0.615	1.30E-08	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0188	putative methylesterase	0.531	4.90E-13	s. m	3.8.0 Secondary metabolism (165)
SCO0197	conserved hypothetical protein	1.820	1.29E-11	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0199	putative alcohol dehydrogenase	1.927	0.00E+00	s. m	3.5.2 Anaerobic respiration (22)
SCO0200	conserved hypothetical protein SCJ12.12c	1.656	2.53E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0205	putative pyruvate formate-lyase activating enzyme (pseudogene)	1.684	5.42E-10	s. m	3.5.2 Anaerobic respiration (22)
SCO0216	nitrate reductase alpha chain NarG2	1.745	1.86E-11	s. m	3.5.2 Anaerobic respiration (22)
SCO0218	putative nitrate reductase delta chain NarJ2	1.650	8.44E-07	s. m	3.5.2 Anaerobic respiration (22)
SCO0224	conserved hypothetical protein	1.782	2.14E-12	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0229	putative oxidoreductase (putative secreted protein)	1.988	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO0231	small hydrophobic hypothetical protein	0.122	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO0268	hypothetical protein	0.100	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO0280	conserved hypothetical protein SCF85.08c	0.332	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0338	putative dehydrogenase	1.865	0.00E+00	s. m	3.5.6 Oxidative branch, pentose pwy (9)
SCO0370	possible DNA-binding protein (putative secreted protein)	0.575	2.38E-08	r.	6.5.0 Others (237)
SCO0379	catalase (EC 1.11.1.6)	0.483	0.00E+00	c. p.	1.4.2 Detoxification (90)
SCO0382	UDP-glucose/GDP-mannose family dehydrogenase	0.491	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0383	hypothetical protein SCF62.09	0.527	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0384	putative membrane protein	0.611	7.01E-09	s. m	3.8.0 Secondary metabolism (165)
SCO0391	putative transferase	0.613	3.94E-03	s. m	3.8.0 Secondary metabolism (165)
SCO0392	putative methyltransferase	0.606	1.24E-05	s. m	3.8.0 Secondary metabolism (165)
SCO0394	hypothetical protein SCF62.20	0.518	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0396	hypothetical protein SCF62.22	0.454	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0397	putative integral membrane protein	0.312	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0399	putative membrane protein	0.532	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0402	putative integral membrane protein	0.578	4.02E-11	c. e.	4.1.6 Gram positive membrane (836)
SCO0423	putative membrane transport protein	0.621	3.44E-07	c. p.	1.5.0 Transport/binding proteins (520)
SCO0438	pyrrolidone-carboxylate peptidase (EC 3.4.19.3)	1.605	6.06E-04	m. m.	2.1.4 Degradation of proteins, peptides, glycoproteins (126)
SCO0439	putative membrane protein	1.840	1.10E-13	c. e.	4.1.6 Gram positive membrane (836)
SCO0453	probable secreted solute-binding lipoprotein.	1.876	5.78E-11	c. p.	1.5.0 Transport/binding proteins (520)
SCO0464	putative integral membrane protein	1.723	6.14E-11	c. e.	4.1.6 Gram positive membrane (836)
SCO0494	putative iron-siderophore binding lipoprotein	0.615	1.26E-08	s. m	3.8.0 Secondary metabolism (165)
SCO0496	putative iron-siderophore permease transmembrane protein	0.505	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0497	putative iron-siderophore permease transmembrane protein	0.492	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0498	putative peptide monooxygenase	0.336	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0499	putative formyltransferase	0.374	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO0560	catalase/peroxidase	0.565	4.51E-12	c. p.	1.4.2 Detoxification (90)

Additional file 2 – Complete set of genes differentially expressed in the *S. lividans adpA* mutant^a.

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SCO0561	Fe regulatory protein	0.613	9.49E-09	r.	6.5.0 Others (237)
SCO0592	hypothetical protein SCF55.16c	0.624	4.10E-08	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO0611	putative membrane protein	1.682	6.22E-10	c. e.	4.1.6 Gram positive membrane (836)
SCO0643	putative secreted cellulose-binding protein.	2.002	0.00E+00	c. p.	1.5.3 Carbohydrates, organic acids and alcohols (9)
SCO0682	hypothetical protein SCF15.03c	0.375	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO0705	conserved hypothetical protein	0.579	4.55E-11	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0762	protease inhibitor precursor	0.124	0.00E+00	m. m.	2.1.4 Degradation of proteins, peptides, glycoproteins (126)
SCO0771	conserved hypothetical protein	0.612	1.66E-06	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0772	putative regulatory protein	0.618	1.81E-08	r.	6.3.8 TetR (122)
SCO0773	putative ferredoxin	0.098	0.00E+00	s. m	3.5.3 Electron transport (71)
SCO0774	putative cytochrome P450	0.075	0.00E+00	s. m	3.5.3 Electron transport (71)
SCO0775	conserved hypothetical protein	0.424	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0827	hypothetical protein SCF43A.17c	0.516	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO0860	probable cation-transporting ATPase	0.526	0.00E+00	c. p.	1.5.2 Cations (40)
SCO0862	putative integral membrane protein.	0.243	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO0863	putative integral membrane protein	0.225	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO0864	probable ECF-family sigma factor.	0.574	1.97E-11	r.	6.2.1 sigma factor (66)
SCO0865	putative integral-membrane protein.	0.621	2.97E-08	c. e.	4.1.6 Gram positive membrane (836)
SCO0919	hypothetical protein SCM10.07c	0.621	2.94E-08	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO0920	putative acyltransferase	0.503	0.00E+00	m. m.	2.2.7 Phospholipids (14)
SCO0923	putative reductase flavoprotein subunit	1.752	1.23E-11	s. m	3.5.8 TCA cycle (26)
SCO0928	conserved hypothetical protein SCM10.16c	0.584	1.14E-10	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO0929	conserved hypothetical protein SCM10.17c	0.419	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1032	putative ABC transport system ATP-binding protein	2.138	0.00E+00	c. p.	1.5.0 Transport/binding proteins (520)
SCO1048	putative secreted protein	0.311	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO1088	putative oxidoreductase	1.701	2.09E-10	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO1132	putative oxidoreductase	0.559	2.83E-09	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO1134	putative oxidoreductase, iron-sulphur binding subunit	0.584	1.06E-10	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO1155	conserved hypothetical protein	0.608	4.34E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1179	conserved hypothetical protein SCG11A.10c	1.649	3.71E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1183	conserved hypothetical protein SCG11A.14	1.682	6.10E-10	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1184	conserved hypothetical protein SCG11A.15	1.611	2.75E-08	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1186	putative lacI-family transcriptional regulator	1.657	2.42E-09	r.	6.3.5 LacI (34)
SCO1196	putative secreted protein	0.493	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO1222	conserved hypothetical protein	0.509	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1223	ornithine aminotransferase	0.617	1.77E-08	s. m	3.1.2 Arginine (10)
SCO1269	putative pyruvate dehydrogenase beta subunit	1.752	1.22E-11	s. m	3.8.1 PKS (102)
SCO1282	putative oxidoreductase	1.620	1.77E-08	s. m	3.8.0 Secondary metabolism (165)
SCO1361	conserved hypothetical protein	0.407	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1379	hypothetical protein	1.800	7.80E-13	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)

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SCO1407	hypothetical protein	0.617	2.13E-07	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO1430	putative TetR-family transcriptional regulator.	1.685	5.26E-10	r.	6.3.8 TetR (122)
SCO1435	putative integral membrane protein	1.743	2.01E-11	c. e.	4.1.6 Gram positive membrane (836)
SCO1444	putative chitinase precursor	1.984	0.00E+00	m. m.	2.1.3 Degradation of polysaccharides (92)
SCO1499	putative integral membrane protein	1.659	2.21E-09	c. e.	4.1.6 Gram positive membrane (836)
SCO1565	putative glycerophosphoryl diester phosphodiesterase	0.531	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO1593	putative transcriptional regulator	1.860	0.00E+00	r.	6.3.2 AraC (33)
SCO1626	putative cytochrome P450	0.518	0.00E+00	s. m	3.5.3 Electron transport (71)
SCO1627	putative ATP-GTP binding protein	0.423	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO1628	conserved hypothetical protein	0.414	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1629	conserved hypothetical protein SCI41_12c	0.375	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1630	putative integral membrane protein	0.505	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO1674	putative secreted protein	0.564	3.74E-12	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO1675	putative small membrane protein	0.237	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO1684	hypothetical protein	1.626	1.68E-07	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO1688	putative membrane protein	1.609	3.10E-08	c. e.	4.1.6 Gram positive membrane (836)
SCO1700	putative membrane protein	0.524	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO1715	putative homogentisate 1,2-dioxygenase	0.601	1.65E-09	s. m	3.4.2 Amino acids (28)
SCO1769	conserved hypothetical protein	1.619	1.85E-08	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO1776	putative CTP synthetase	1.744	1.93E-11	s. m	3.3.11 Nucleotide interconversions (25)
SCO1800	putative small secreted protein	0.256	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO1821	molybdenum cofactor biosynthesis protein A	1.679	7.20E-10	s. m	3.2.9 Molybdopterin (8)
SCO1860	putative secreted protein	0.344	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO1864	putative acetyltransferase	2.903	0.00E+00	c. p.	1.6.2 Osmotic adaptation (7)
SCO1865	putative aminotransferase	3.154	0.00E+00	c. p.	1.6.2 Osmotic adaptation (7)
SCO1866	putative condensing enzyme	2.552	0.00E+00	c. p.	1.6.2 Osmotic adaptation (7)
SCO1867	putative hydroxylase	3.029	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO1887	putative integral membrane transport protein	1.656	2.56E-09	c. p.	1.5.0 Transport/binding proteins (520)
SCO1968	putative secreted hydrolase	0.537	0.00E+00	m. m.	2.2.7 Phospholipids (14)
SCO1969	putative DNA-methyltransferase	0.564	3.48E-12	m. m.	2.2.3 DNA - replication, repair, restr./modific'n (85)
SCO2068	putative secreted alkaline phosphatase	0.621	2.77E-08	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO2174	putative transferase	1.819	3.00E-13	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO2180	putative dihydrolipoamide dehydrogenase	1.784	1.88E-12	s. m	3.5.7 Pyruvate dehydrogenase (10)
SCO2181	putative dihydrolipoamide succinyltransferase	1.713	1.09E-10	s. m	3.5.5 Glycolysis (25)
SCO2183	putative pyruvate dehydrogenase E1 component	1.647	4.20E-09	s. m	3.5.7 Pyruvate dehydrogenase (10)
SCO2212	hypothetical protein SC10B7.07	0.516	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO2286	putative alkaline phosphatase	0.623	3.62E-08	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO2289	putative membrane protein.	0.621	2.71E-08	c. e.	4.1.6 Gram positive membrane (836)
SCO2362	hypothetical protein	1.797	9.60E-13	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO2396	conserved hypothetical protein	1.734	3.42E-11	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)

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SCO2424	putative secreted protein	1.617	2.01E-08	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO2435	conserved hypothetical protein	0.526	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2468	DNA primase	1.643	5.18E-09	m. m.	2.2.3 DNA - replication, repair, restr./modific'n (85)
SCO2480	putative secreted protein	1.918	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO2520	putative membrane protein	0.526	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO2525	hypothetical protein SCC121.28c	0.405	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO2550	putative lipoprotein	0.474	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO2640	aspartate semialdehyde dehydrogenase	1.824	2.10E-13	s. m	3.1.13 Lysine (13)
SCO2691	hypothetical protein	2.234	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO2751	conserved hypothetical protein SCC57A.22c	2.009	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2780	putative secreted protein	1.757	9.44E-12	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO2790	conserved hypothetical protein SCC105.21c	1.710	1.29E-10	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2791	hypothetical protein SCC105.22c	2.430	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO2792	araC-family transcriptional regulator	0.383	0.00E+00	r.	6.3.2 AraC (33)
SCO2793	oligoribonuclease	1.966	0.00E+00	m. m.	2.1.2 Degradation of RNA (8)
SCO2797	putative cellobiose transport permease	1.722	6.51E-11	c. p.	1.5.0 Transport/binding proteins (520)
SCO2818	conserved hypothetical protein	1.613	2.55E-08	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2822	putative decarboxylase	0.424	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO2823	putative decarboxylase	0.489	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO2879	putative membrane protein	0.359	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO2880	conserved hypothetical protein SCE6.17	0.426	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2881	conserved hypothetical protein SCE6.18	0.499	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2883	putative cytochrome P450	0.617	1.66E-08	s. m	3.5.3 Electron transport (71)
SCO2884	putative cytochrome P450	0.624	4.40E-08	s. m	3.5.3 Electron transport (71)
SCO2911	conserved hypothetical protein	0.609	5.34E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO2912	hypothetical protein	0.551	3.00E-13	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO2919	hypothetical protein	0.408	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO2921	putative membrane protein	0.196	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO2927	putative 4-hydroxyphenylpyruvate dioxygenase	0.236	0.00E+00	s. m	3.4.2 Amino acids (28)
SCO2962	putative bi-functional transferase/deacetylase	1.746	1.73E-11	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO2987	putative regulatory protein	1.647	4.21E-09	r.	6.3.7 MarR (40)
SCO2994	putative tetR-family transcriptional regulator (fragment)	1.879	0.00E+00	r.	6.3.8 TetR (122)
SCO2995	putative ABC transporter integral membrane protein	2.315	0.00E+00	c. p.	1.5.0 Transport/binding proteins (520)
SCO2997	putative transferase	1.837	1.10E-13	m. m.	2.2.4 Glycoprotein (11)
SCO3061	putative integral membrane protein	1.632	9.45E-09	c. e.	4.1.6 Gram positive membrane (836)
SCO3089	putative ABC transporter ATP-binding protein	1.600	4.87E-08	c. p.	1.5.0 Transport/binding proteins (520)
SCO3123	ribose-phosphate pyrophosphokinase	1.891	0.00E+00	s. m	3.7.1 Purine ribonucleotide biosynthesis (21)
SCO3167	putative tetR-family transcriptional regulator	2.650	0.00E+00	r.	6.3.8 TetR (122)
SCO3177	putative membrane protein	1.618	1.90E-08	c. e.	4.1.6 Gram positive membrane (836)
SCO3197	putative 1-phosphofructokinase	1.958	0.00E+00	s. m	3.5.5 Glycolysis (25)

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SCO3202	RNA polymerase principal sigma factor	2.499	0.00E+00	r.	6.2.1 sigma factor (66)
SCO3319	putative glutamyl-tRNA reductase	1.878	0.00E+00	s. m	3.2.6 Heme, porphyrin (16)
SCO3323	putative RNA polymerase sigma factor	0.389	0.00E+00	r.	6.2.1 sigma factor (66)
SCO3357	hypothetical protein	1.656	2.56E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO3421	conserved hypothetical protein	0.594	6.01E-10	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO3495	putative aldolase	0.623	3.49E-08	s. m	3.4.3 Carbon compounds (91)
SCO3579	putative regulatory protein	0.310	0.00E+00	r.	6.5.0 Others (237)
SCO3752	putative ABC transporter ATP-binding protein	0.562	2.32E-12	c. p.	1.5.0 Transport/binding proteins (520)
SCO3767	conserved hypothetical protein	0.534	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO3768	putative translocase protein	0.601	1.57E-09	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO3776	putative membrane protein	1.722	1.75E-09	c. e.	4.1.6 Gram positive membrane (836)
SCO3810	putative gntR-family transcriptional regulator	1.762	6.98E-12	r.	6.3.3 GntR (51)
SCO3811	putative D-alanyl-D-alanine carboxypeptidase	1.628	1.12E-08	c. e.	4.1.9 Gram positive peptidoglycan, teichoic acid (40)
SCO3830	putative branched-chain alpha keto acid dehydrogenase E1 beta subunit	1.837	1.10E-13	s. m	3.5.7 Pyruvate dehydrogenase (10)
SCO3831	E1-alpha branched-chain alpha keto acid dehydrogenase	2.230	0.00E+00	s. m	3.5.7 Pyruvate dehydrogenase (10)
SCO3835	putative dehydrogenase	2.207	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO3877	putative 6-phosphogluconate dehydrogenase	2.020	0.00E+00	s. m	3.5.6 Oxidative branch, pentose pwy (9)
SCO3917	conserved hypothetical protein	0.504	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO3945	putative cytochrome oxidase subunit I	3.386	0.00E+00	s. m	3.5.3 Electron transport (71)
SCO3946	putative cytochrome oxidase subunit II	3.594	0.00E+00	s. m	3.5.3 Electron transport (71)
SCO3947	putative ABC transporter	2.653	0.00E+00	c. p.	1.5.0 Transport/binding proteins (520)
SCO3965	conserved hypothetical protein	0.603	2.24E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO3966	putative secreted protein	0.549	2.10E-13	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO3967	conserved hypothetical membrane protein	0.406	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO3968	putative integral membrane protein	0.443	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO3971	conserved hypothetical protein	1.631	9.87E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4000	hypothetical protein 2SC10A7.04c	1.877	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO4032	putative marR regulatory protein	1.807	4.90E-13	r.	6.3.7 MarR (40)
SCO4034	putative RNA polymerase sigma factor	0.582	7.93E-11	r.	6.2.1 sigma factor (66)
SCO4049	putative antibiotic binding protein	1.708	1.40E-10	c. p.	1.4.2 Detoxification (90)
SCO4065	putative transposase	0.612	8.67E-09	e.	5.1.4 Transposon/insertion element-related functions (85)
SCO4113	conserved hypothetical protein	0.568	7.03E-12	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4114	sporulation associated protein	0.487	0.00E+00	c. p.	1.8.1 Differentiation/sporulation (11)
SCO4140	phosphate ABC transport system permease protein	0.584	1.14E-10	c. p.	1.5.0 Transport/binding proteins (520)
SCO4164	putative thiosulfate sulfurtransferase	0.483	0.00E+00	s. m	3.3.19 Sulfur metabolism (13)
SCO4165	conserved hypothetical protein	0.486	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4187	putative membrane protein	0.245	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO4215	putative GntR-family regulatory protein	1.964	0.00E+00	r.	6.3.3 GntR (51)
SCO4271	putative NADP-dependent alcohol dehydrogenase	1.795	1.05E-12	n. c.	7.0.0 Not classified (included putative assignments) (565)

Additional file 2 – Complete set of genes differentially expressed in the *S. lividans adpA* mutant^a.

gene ^b	annotated function ^b	Fc ^c	P-value ^d	class ^e	classification details ^e
SCO4275	putative histidine autokinase	1.730	4.26E-11	r.	6.1.1 Sensor kinase (85)
SCO4293	putative threonine synthase	0.362	0.00E+00	s. m	3.1.18 Threonine (4)
SCO4294	conserved hypothetical protein	0.431	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4295	cold shock protein	0.217	0.00E+00	c. p.	1.6.1 Adaptations, atypical conditions (25)
SCO4296	chaperonin 2	0.566	5.11E-12	c. p.	1.3.1 Chaperones (15)
SCO4327	conserved hypothetical protein SCD12A.10c	1.662	1.88E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4338	hypothetical protein SCD12A.21	0.544	1.10E-13	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4383	4-coumarate:CoA ligase	1.810	4.00E-13	m. m.	2.2.8 Polysaccharides - (cytoplasmic) (25)
SCO4393	conserved hypothetical protein	1.724	5.77E-11	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4427	conserved hypothetical protein	0.534	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO4428	putative secreted protein	0.550	3.00E-13	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO4498	putative proton transport protein	0.592	4.45E-10	c. p.	1.5.2 Cations (40)
SCO4513	hypothetical protein SCD35.20c	0.621	2.97E-08	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO4514	putative integral membrane protein	0.548	2.10E-13	c. e.	4.1.6 Gram positive membrane (836)
SCO4516	hypothetical protein SCD35.23c	0.374	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO4521	putative secreted protein	0.610	1.78E-05	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO4671	putative lysR-family regulatory protein	1.734	9.99E-10	r.	6.3.6 LysR (38)
SCO4761	10 kD chaperonin cpn10	0.401	0.00E+00	c. p.	1.3.1 Chaperones (15)
SCO4762	60 kD chaperonin cpn60	0.440	0.00E+00	c. p.	1.3.1 Chaperones (15)
SCO4768	putative two-component regulator	0.586	1.44E-10	r.	6.3.11 LuxR (GerR) (23)
SCO4875	putative sugar transferase	0.600	1.42E-09	m. m.	2.2.8 Polysaccharides - (cytoplasmic) (25)
SCO4876	putative sugar translocase	0.586	1.44E-10	c. p.	1.5.5 Other (11)
SCO4880	putative transferase	0.597	9.05E-10	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO4881	putative polysaccharide biosynthesis related protein	0.558	1.24E-12	m. m.	2.2.8 Polysaccharides - (cytoplasmic) (25)
SCO4920	putative deoR-family transcriptional regulator	0.523	0.00E+00	r.	6.3.10 DeoR (13)
SCO4950	nitrate reductase gamma chain NarI3	0.211	0.00E+00	s. m	3.5.2 Anaerobic respiration (22)
SCO4951	putative aldoketoreductase	0.440	0.00E+00	s. m	3.8.1 PKS (102)
SCO4952	putative tetR-family transcriptional regulator	0.301	0.00E+00	r.	6.3.8 TetR (122)
SCO4974	putative deaminase	1.826	2.10E-13	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO5011	putative integral membrane protein	0.454	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO5012	putative integral membrane protein	0.466	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO5029	putative secreted protein	0.566	5.35E-12	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO5032	alkyl hydroperoxide reductase	0.576	2.95E-11	c. p.	1.4.2 Detoxification (90)
SCO5050	putative nucleotide-sugar dehydrogenase	1.852	0.00E+00	s. m	3.3.18 Sugar-nucleotide biosynthesis, conversions (11)
SCO5077	hypothetical protein	0.600	1.46E-09	s. m	3.8.1 PKS (102)
SCO5101	conserved hypothetical protein	0.584	1.11E-10	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO5123	putative small membrane protein	0.343	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO5240	hypothetical protein	2.246	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO5249	putative nucleotide-binding protein	0.551	3.00E-13	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO5390	putative alkanal monooxygenase (luciferase)	0.608	6.79E-08	n. c.	7.0.0 Not classified (included putative assignments) (565)

Additional file 2 – Complete set of genes differentially expressed in the *S. lividans* *adpA* mutant^a.

gene ^b	annotated function ^b	Fc ^c	P-value ^d	class ^e	classification details ^e
SCO5512	acetolactate synthase	1.672	1.06E-09	s. m	3.4.3 Carbon compounds (91)
SCO5521	hypothetical protein SC1C2.02	0.502	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO5555	hypothetical protein SC1C2.36	2.828	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO5556	histone-like DNA binding protein	2.388	0.00E+00	m. m.	2.2.2 Basic proteins - synthesis, modification (1)
SCO5650	putative membrane protein	0.578	4.33E-11	c. e.	4.1.6 Gram positive membrane (836)
SCO5741	putative membrane protein	2.502	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO5742	putative membrane protein	2.094	0.00E+00	c. e.	4.1.6 Gram positive membrane (836)
SCO5751	putative membrane protein	0.613	9.87E-09	c. e.	4.1.6 Gram positive membrane (836)
SCO5789	hypothetical protein SC4H2.10c	2.001	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO5790	hypothetical protein SC4H2.11c	1.704	1.81E-10	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO5793	diaminopimelate epimerase	1.784	1.97E-12	s. m	3.1.13 Lysine (13)
SCO5818	putative ABC transporter	1.666	1.52E-09	c. p.	1.5.0 Transport/binding proteins (520)
SCO5862	two-component regulator CutR	1.927	0.00E+00	r.	6.1.2 Response regulator (79)
SCO5863	two-component sensor (kinase)	1.714	1.04E-10	r.	6.1.1 Sensor kinase (85)
SCO6000	hypothetical protein	0.560	1.70E-12	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6004	putative secreted ATP/GTP binding protein	0.603	2.16E-09	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO6009	solute-binding protein	1.736	3.03E-11	c. p.	1.5.0 Transport/binding proteins (520)
SCO6010	probable ABC-transport system ATP binding protein	1.620	1.76E-08	c. p.	1.5.0 Transport/binding proteins (520)
SCO6019	conserved hypothetical protein SC1C3.07	1.727	3.78E-08	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6073	putative cyclase	0.466	0.00E+00	s. m	3.8.0 Secondary metabolism (165)
SCO6075	conserved hypothetical protein	1.892	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6096	putative lipoprotein	0.557	9.60E-13	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO6097	sulfate adenylyltransferase subunit 1	0.579	4.60E-11	s. m	3.3.19 Sulfur metabolism (13)
SCO6098	sulfate adenylyltransferase subunit 2	0.519	0.00E+00	s. m	3.3.19 Sulfur metabolism (13)
SCO6099	adenylylsulfate kinase	0.544	1.10E-13	s. m	3.3.19 Sulfur metabolism (13)
SCO6100	phosphoadenosine phosphosulfate reductase	0.623	3.88E-08	s. m	3.3.19 Sulfur metabolism (13)
SCO6101	hypothetical protein SCBAC1A6.25c	0.476	0.00E+00	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO6102	putative nitrite/sulphite reductase	0.532	0.00E+00	s. m	3.5.2 Anaerobic respiration (22)
SCO6130	hypothetical protein SC9B2.17	0.410	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6174	hypothetical protein SC6C5.10	0.538	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6176	conserved hypothetical protein	0.459	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6197	putative secreted protein	0.147	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO6198	putative secreted protein	0.618	1.94E-08	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO6227	hypothetical protein SC2H4.09	1.713	2.68E-09	u. f.	0.0.0 Unknown function. no known homologs (1049)
SCO6230	putative sugar transport system permease protein	1.626	1.24E-08	c. p.	1.5.0 Transport/binding proteins (520)
SCO6306	putative oxidoreductase	1.604	4.50E-07	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO6373	putative integral membrane protein	0.585	4.21E-05	c. e.	4.1.6 Gram positive membrane (836)
SCO6376	putative integral membrane protein	0.603	3.94E-08	c. e.	4.1.6 Gram positive membrane (836)
SCO6384	putative integral membrane lysyl-tRNA synthetase	0.590	1.39E-07	m. m.	2.2.1 Amino acyl tRNA syn; tRNA modif'n (34)
SCO6458	conserved hypothetical protein SC9B5.25	1.636	7.37E-09	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)

Additional file 2 – Complete set of genes differentially expressed in the *S. lividans adpA* mutant^a.

gene ^b	annotated function ^b	Fc ^c	P-value ^d	class ^e	classification details ^e
SCO6482	conserved hypothetical protein	0.538	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6507	putative gas vesicle synthesis protein	0.410	0.00E+00	c. p.	1.6.1 Adaptations, atypical conditions (25)
SCO6509	hydrophobic protein	0.398	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO6510	conserved hypothetical protein SC1E6.19c	0.406	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6645	putative transport system permease protein	1.864	0.00E+00	c. p.	1.5.0 Transport/binding proteins (520)
SCO6659	glucose-6-phosphate isomerase	2.018	0.00E+00	s. m	3.5.5 Glycolysis (25)
SCO6660	hypothetical protein SC5A7.10c	2.207	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6661	glucose-6-phosphate 1-dehydrogenase	2.614	0.00E+00	s. m	3.5.6 Oxidative branch, pentose pwy (9)
SCO6662	transaldolase	2.180	0.00E+00	s. m	3.3.9 Non-oxidative branch, pentose pwy (8)
SCO6685	putative two-component system response regulator	0.624	3.94E-08	r.	6.1.2 Response regulator (79)
SCO6691	putative phospholipase C	0.414	0.00E+00	s. m	3.4.4 Fatty acids (59)
SCO6799	threonine 3-dehydrogenase	1.638	6.68E-09	s. m	3.4.2 Amino acids (28)
SCO6808	putative ArsR-family transcriptional regulator	0.268	0.00E+00	r.	6.3.13 ArsR (15)
SCO6818	putative phosphoglycerate mutase	0.389	0.00E+00	s. m	3.5.5 Glycolysis (25)
SCO6820	putative oxidoreductase	0.338	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO6824	putative phosphonopyruvate decarboxylase (fragment)	0.564	3.48E-12	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO6830	putative ArsR-family transcriptional regulator	0.284	0.00E+00	r.	6.3.13 ArsR (15)
SCO6831	hypothetical protein SC4A9.08	0.602	3.14E-08	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO6903	hypothetical protein SC1B2.09	0.617	2.03E-07	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6926	hypothetical protein SC1B2.32	0.600	4.20E-07	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6937	putative DNA-binding protein	0.545	1.10E-13	r.	6.5.0 Others (237)
SCO6939	conserved hypothetical protein SC1G8.11c	0.485	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO6979	probable solute-binding lipoprotein	0.611	7.37E-09	c. p.	1.5.0 Transport/binding proteins (520)
SCO7011	putative membrane transport protein	1.764	6.21E-12	c. p.	1.5.0 Transport/binding proteins (520)
SCO7070	hypothetical protein SC4G1.36	1.649	8.68E-07	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO7221	putative polyketide synthase	1.692	3.42E-10	s. m	3.8.1 PKS (102)
SCO7233	putative secreted protein	0.309	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO7251	conserved hypothetical protein	0.574	2.21E-11	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO7344	putative secreted protein	0.467	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO7398	putative membrane transport protein	1.678	1.52E-08	c. p.	1.5.0 Transport/binding proteins (520)
SCO7399	possible binding-protein-dependent transport lipoprotein	1.807	4.90E-13	c. p.	1.5.0 Transport/binding proteins (520)
SCO7400	putative ABC-transport protein, ATP-binding component	1.772	3.90E-12	c. p.	1.5.0 Transport/binding proteins (520)
SCO7409	putative binding-protein dependent transport protein	2.072	0.00E+00	c. p.	1.5.0 Transport/binding proteins (520)
SCO7410	putative binding-protein dependent transport protein	1.707	1.47E-10	c. p.	1.5.0 Transport/binding proteins (520)
SCO7449	putative membrane protein	1.634	8.47E-09	c. e.	4.1.6 Gram positive membrane (836)
SCO7472	putative phenylacetic acid degradation protein PaaB	1.811	4.00E-13	s. m	3.4.3 Carbon compounds (91)
SCO7473	putative phenylacetic acid degradation protein PaaC	1.716	9.44E-11	s. m	3.4.3 Carbon compounds (91)
SCO7474	putative phenylacetic acid degradation protein PaaD	2.033	0.00E+00	s. m	3.4.3 Carbon compounds (91)
SCO7475	putative phenylacetic acid degradation NADH oxidoreductase PaaE	1.737	2.93E-11	s. m	3.4.3 Carbon compounds (91)

Additional file 2 – Complete set of genes differentially expressed in the *S. lividans adpA* mutant^a.

gene ^b	annotated function ^b	Fc ^c	P-value ^d	class ^e	classification details ^e
SCO7477	putative membrane protein	1.657	2.44E-09	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO7549	hypothetical protein	0.447	0.00E+00	u. f.	0.0.2 Conserved in organism other than Escherichia coli (1322)
SCO7550	putative secreted hydrolase	0.334	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO7603	putative LysR-family transcriptional regulator	1.600	4.70E-08	r.	6.3.6 LysR (38)
SCO7631	putative secreted protein	0.355	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO7648	putative two-component system response regulator	0.616	1.48E-08	r.	6.1.2 Response regulator (79)
SCO7657	putative secreted protein	0.033	0.00E+00	c. e.	4.1.7 Gram positive exported/lipoprotein (439)
SCO7658	hypothetical protein SC10F4.31	0.103	0.00E+00	u. f.	0.0.0 Unknown function, no known homologs (1049)
SCO7659	putative oxidoreductase	0.511	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO7685	conserved hypothetical protein	1.632	9.11E-09	s. m	3.8.0 Secondary metabolism (165)
SCO7697	putative secreted hydrolase	0.557	9.60E-13	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO7700	putative cyclase	1.636	1.49E-06	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO7714	putative acetyltransferase	0.516	0.00E+00	n. c.	7.0.0 Not classified (included putative assignments) (565)
SCO7774	putative secreted protein	0.589	2.62E-10	c. e.	4.1.7 Gram positive exported/lipoprotein (439)

a. Genes expression in the *S. lividans adpA* mutant was compared to that in the wild-type, using *S. coelicolor* microarrays. The complete data set is presented in this file. A selected subset of the genes extracted from Additional file 2 is shown in Table 1.

b. Gene names and annotated function are from the StrepDB database [7].

c. Fold change (Fc) in gene expression in the *S. lividans adpA* mutant with respect to the wild-type strain 1326.

d. From a Student's *t*-test applying the Benjamini and Hochberg multiple testing correction (*P*-value <0.05).

e. From the protein classification scheme for the *S. coelicolor* genome available on the Wellcome Trust Sanger Institute database [37]: unknown function (u. f.), cell process (c. p.), macromolecule metabolism (m. m.), small molecule metabolism (s. m.), cell envelope (c. e.), extrachromosomal (e.), regulation (r.) and not classified (n. c.).