

Supplementary Table S1. Spot intensities of 11 proteins or protein constituents that were induced in the outer-membrane fraction of *S. oneidensis* COAG, compared to the MR-1 wild-type, in three replicate 2D-PAGE gels

The spot volume as a percentage of the total volume of all spots is given for both MR-1 and COAG, and for each gel. In total, 16 COAG upregulated (Student's *t* test value ≥ 0.95) spots were detected, of which 11 could be identified by mass fingerprinting. The upregulated proteins that were confirmed by a microarray study are indicated by grey shading.

Identified protein	Monomer no.	Spot volume (percentage of total volume of all spots)					
		MR-1			COAG		
		Gel no. 1	Gel no. 2	Gel no. 3	Gel no. 1	Gel no. 2	Gel no. 3
Agglutination protein (trimeric)	1st	0.105	0.120	0.130	0.165	0.185	0.210
	2nd	0.240	0.250	0.255	0.360	0.415	0.465
	3rd	0.280	0.290	0.300	0.500	0.610	0.720
Outer-membrane protein precursor MtrB	–	0.080	0.085	0.095	0.154	0.165	0.185
Bacterial surface antigen (trimeric)	1st	0.050	0.051	0.060	0.130	0.145	0.160
	2nd	0.150	0.150	0.150	0.230	0.250	0.275
Outer-membrane protein TolC	–	0.160	0.170	0.180	0.255	0.260	0.265
TonB-dependent receptor, putative	–	0.170	0.240	0.305	0.395	0.475	0.550
TonB-dependent receptor, putative	–	0.015	0.040	0.060	0.095	0.120	0.150
Conserved hypothetical protein	–	0.070	0.070	0.070	0.235	0.300	0.370
Conserved hypothetical protein	–	0.110	0.190	0.230	0.415	0.500	0.605

Supplementary Table S2. Average fold-change and *P* value for each of the 249 genes that showed significant upregulation in COAG, following spot intensity quantification and data normalization, in at least one sampling event

Significance levels were determined as follows: average fold-change ≥ 2.0 and *P* value ≤ 0.05 . The COAG overexpressed genes related to the expression of outer-membrane-associated proteins, that were confirmed to be upregulated by 2D-PAGE, are indicated by grey shading.

Name	Locus	0 h (fold)	<i>P</i> value	2 h (fold)	<i>P</i> value	4 h (fold)	<i>P</i> value	8 h (fold)	<i>P</i> value	Product
so0027	so0027	8,43E+00	4,77E-05	3,13E+00	7,66E-03	3,14E+00	2,77E-05	3,27E+00	2,65E-03	protoporphyrinogen oxidase, putative
so0045	so0045	2,56E+00	2,36E-03	2,31E+00	3,80E-02	1,86E+00	1,63E-02	2,20E+00	1,56E-03	Rrf2 family protein
so0047	so0047	2,31E+00	1,77E-03	2,20E+00	2,41E-02	1,81E+00	1,04E-02	1,60E+00	8,85E-02	carboxyl-terminal protease, putative
so0119	so0119	2,27E+00	6,56E-03	1,84E+00	7,55E-02	1,67E+00	1,53E-01	3,06E+00	2,29E-03	conserved hypothetical protein
so0154	so0154	7,72E+00	1,69E-06	2,49E+00	4,93E-02	2,02E+00	3,25E-03	2,27E+00	2,66E-03	conserved hypothetical protein
so0203	so0203	2,16E+00	3,46E-03	1,70E+00	1,66E-02	1,97E+00	1,98E-03	2,23E+00	6,14E-05	hypothetical protein
so0204	so0204	2,71E+00	4,48E-04	1,66E+00	4,58E-02	1,41E+00	2,80E-01	2,30E+00	9,22E-04	hypothetical protein
tufa	so0229	1,84E+00	6,42E-03	2,36E+00	5,57E-03	1,97E+00	5,09E-03	2,37E+00	6,74E-04	translation elongation factor Tu
spef	so0314	2,10E+00	2,20E-02	2,13E+00	5,37E-02	2,55E+00	4,02E-04	2,21E+00	6,96E-03	ornithine decarboxylase, inducible
so0325	so0325	8,13E+00	7,58E-04	2,53E+00	9,57E-03	2,56E+00	2,18E-04	2,51E+00	7,04E-04	dsrE-related protein
fdrc	so0396	2,65E+00	7,11E-04	1,89E+00	4,05E-03	1,83E+00	3,77E-03	2,30E+00	8,72E-05	fumarate reductase cytochrome B subunit
frda	so0398	2,26E+00	7,52E-03	1,78E+00	6,22E-02	2,19E+00	2,60E-03	1,33E+00	1,84E-01	fumarate reductase flavoprotein subunit
so0400	so0400	2,07E+00	1,10E-02	1,74E+00	1,40E-02	2,01E+00	8,84E-04	1,95E+00	1,23E-02	conserved hypothetical protein
so0439	so0439	1,64E+00	5,95E-02	1,85E+00	1,03E-02	2,06E+00	1,87E-04	2,43E+00	1,47E-04	hypothetical protein
so0444	so0444	2,51E+00	1,74E-03	1,68E+00	2,77E-02	1,48E+00	9,59E-02	2,50E+00	2,89E-04	hypothetical protein
ccmf-2	so0478	2,18E+00	3,72E-02	1,57E+00	1,48E-01	2,14E+00	9,24E-04	1,67E+00	4,29E-02	cytochrome c-type biogenesis protein CcmF
so0479	so0479	2,52E+00	1,91E-03	2,15E+00	1,30E-02	2,07E+00	2,02E-03	1,81E+00	1,35E-02	cytochrome c, putative
nosd	so0486	2,01E+00	4,13E-02	1,69E+00	1,59E-01	1,48E+00	2,75E-01	6,20E+00	3,29E-03	copper ABC transporter, periplasmic copper-binding protein
nosf	so0487	9,24E+00	1,01E-05	2,19E+00	5,53E-03	1,98E+00	4,06E-04	1,58E+00	4,37E-02	copper ABC transporter, ATP-binding protein
so0490	so0490	2,43E+00	1,29E-03	1,56E+00	1,01E-01	1,77E+00	1,69E-02	2,08E+00	5,11E-04	transcriptional regulator
so0541	so0541	2,46E+00	4,00E-02	1,82E+00	2,36E-01	2,78E+00	7,13E-03	1,59E+00	1,88E-01	metallo-beta-lactamase family protein
fhs	so0560	9,85E-01	9,59E-01	8,44E-01	7,08E-01	2,58E+00	1,67E-04	4,93E+00	2,14E-04	formate--tetrahydrofolate ligase
so0576	so0576	6,93E+00	2,47E-07	4,31E+00	6,14E-03	4,48E+00	8,97E-10	4,39E+00	2,06E-04	PhoH family protein
so0581	so0581	1,88E+00	5,43E-03	1,97E+00	5,87E-02	2,47E+00	1,04E-03	3,14E+00	9,45E-03	hypothetical protein
so0584	so0584	1,83E+00	1,35E-02	2,86E+00	1,84E-01	5,13E+00	2,92E-02	3,46E+00	2,34E-02	methyl-accepting chemotaxis protein
so0594	so0594	2,90E+00	6,45E-04	5,06E+00	6,98E-02	7,52E+00	5,51E-02	6,18E+00	7,92E-04	hypothetical protein
so0595	so0595	4,25E+00	1,08E-04	3,27E+00	2,65E-03	2,73E+00	4,75E-04	2,77E+00	4,12E-05	hypothetical protein
so0599	so0599	3,20E+00	2,01E-05	2,71E+00	2,03E-04	2,88E+00	1,11E-06	3,00E+00	7,62E-04	conserved hypothetical protein TIGR00150
so0699	so0699	9,63E+00	2,55E-05	2,91E+00	1,95E-02	3,41E+00	2,22E-03	3,67E+00	4,72E-03	hypothetical protein
so0740	so0740	1,97E+00	5,52E-03	2,16E+00	6,65E-03	3,89E+00	1,07E-08	3,28E+00	2,05E-06	melanin biosynthesis protein TyrA, putative
so0750	so0750	4,60E+00	3,88E-05	2,03E+00	1,09E-02	2,23E+00	8,25E-03	2,56E+00	8,45E-05	glutamate synthase, putative
so0762	so0762	4,76E+00	2,59E-06	2,67E+00	5,87E-02	4,27E+00	4,10E-04	5,65E+00	4,13E-03	isochorismatase family protein
so0767	so0767	3,56E+00	1,64E-03	1,79E+00	6,20E-02	2,60E+00	9,52E-04	2,20E+00	3,33E-03	transcriptional regulator, LysR family

so0843	so0843	1,56E+01	1,53E-04	3,30E+00	7,59E-02	3,63E+00	5,80E-03	2,70E+00	7,17E-02	transcriptional regulator, LysR family
napg	so0847	3,19E+00	1,28E-02	5,88E-01	9,85E-01	2,76E+00	8,67E-02	5,82E+00	1,83E-02	iron-sulfur cluster-binding protein NapG
napd	so0849	8,31E+00	4,12E-05	3,68E+00	3,03E-03	4,16E+00	3,89E-04	5,69E+00	3,70E-04	napD protein
so0864	so0864	8,32E+00	1,27E-06	4,05E+00	7,28E-04	3,65E+00	1,73E-05	3,91E+00	9,47E-06	transcriptional regulator, LuxR family
nqra-1	so0902	2,60E+00	1,53E-03	1,40E+00	2,41E-01	2,22E+00	6,77E-03	2,12E+00	1,93E-02	NADH:ubiquinone oxidoreductase, Na translocating, alpha subunit
nqrd-1	so0905	4,28E+00	2,14E-05	2,42E+00	5,05E-04	2,53E+00	2,09E-04	3,87E+00	7,05E-07	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrD
nqre-1	so0906	1,83E+00	4,53E-03	1,46E+00	6,14E-02	2,04E+00	3,79E-04	2,22E+00	4,05E-03	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrE
so0919	so0919	8,68E-01	6,22E-01	1,50E+00	1,54E-01	2,63E+00	6,82E-03	2,72E+00	2,29E-04	serine transporter, putative
nhad	so0935	1,47E+00	8,87E-02	1,58E+00	1,51E-01	2,60E+00	5,72E-03	2,51E+00	1,59E-04	Na ⁺ /H ⁺ antiporter
so0939	so0939	3,82E+00	1,27E-05	1,56E+00	1,73E-01	2,01E+00	2,55E-02	1,69E+00	1,03E-01	cytochrome c, putative
so0940	so0940	7,22E-01	5,15E-01	2,33E+00	4,92E-02	2,97E+00	6,12E-02	2,04E+00	3,42E-01	transcriptional regulator-related protein
so0970	so0970	2,14E+00	3,10E-02	2,04E+00	3,58E-01	2,24E+00	4,70E-02	3,49E+00	7,46E-02	fumarate reductase flavoprotein subunit precursor
so0975	so0975	2,03E+00	8,82E-03	2,93E+00	1,68E-03	2,40E+00	1,89E-04	3,99E+00	2,18E-05	hypothetical protein
so1146	so1146	3,25E+00	4,04E-04	1,46E+00	1,93E-01	2,08E+00	1,38E-02	1,97E+00	1,69E-02	hypothetical protein
so1175	so1175	1,06E+01	3,40E-05	2,07E+00	1,08E-01	2,18E+00	1,08E-01	1,50E+00	3,88E-01	conserved hypothetical protein
nusa	so1203	8,79E+00	1,46E-04	1,68E+00	3,02E-01	2,81E+00	2,30E-02	2,74E+00	3,73E-03	N utilization substance protein A
infb	so1204	3,49E+00	2,97E-03	1,56E+00	3,76E-01	3,54E+00	3,95E-02	2,76E+00	3,73E-03	translation initiation factor IF-2
rbfa	so1205	5,44E+00	5,55E-04	1,83E+00	1,75E-01	1,78E+00	2,04E-01	2,20E+00	3,34E-02	ribosome-binding factor A
rpsa	so1207	5,03E+00	1,82E-05	1,99E+00	9,82E-02	1,50E+00	1,09E-02	2,39E+00	5,59E-03	ribosomal protein S15
deoc	so1217	8,03E+00	5,37E-05	2,31E+00	3,70E-02	1,51E+00	4,59E-01	1,70E+00	1,31E-01	deoxyribose-phosphate aldolase
deoa	so1218	1,66E+00	7,87E-02	4,43E+00	2,42E-01	5,20E+00	5,82E-02	2,65E+01	1,28E-02	thymidine phosphorylase
deob	so1219	4,27E+00	9,36E-06	2,25E+00	4,70E-03	2,36E+00	4,65E-05	2,66E+00	7,46E-04	phosphopentomutase
deod-2	so1221	4,10E+00	5,28E-03	3,42E+00	3,09E-04	3,30E+00	2,36E-04	5,21E+00	1,75E-07	purine nucleoside phosphorylase
tord	so1231	1,50E+01	2,55E-04	4,06E+00	2,21E-03	4,39E+00	1,22E-05	5,16E+00	1,27E-04	TorA specific chaperone
so1265	so1265	1,82E+00	2,84E-02	5,14E+00	7,66E-02	2,32E+00	2,50E-02	3,32E+00	4,17E-03	transcriptional regulator, putative
so1268	so1268	4,24E+00	4,55E-05	2,64E+00	8,12E-03	3,44E+00	1,27E-06	3,74E+00	1,54E-04	glutamine synthetase
so1274	so1274	1,25E+00	2,63E-01	2,12E+00	2,57E-02	2,13E+00	1,46E-03	1,91E+00	3,39E-03	conserved hypothetical protein
gabd	so1275	1,29E+00	1,99E-01	2,01E+00	8,77E-02	2,05E+00	4,30E-03	2,42E+00	3,16E-03	succinate-semialdehyde dehydrogenase
so1278	so1278	2,30E+00	3,97E-03	2,97E+00	2,13E-03	2,49E+00	1,65E-04	3,22E+00	2,49E-06	methyl-accepting chemotaxis protein
so1317	so1317	1,74E+00	1,41E-02	3,42E+00	8,31E-03	2,87E+00	1,30E-04	2,75E+00	2,78E-05	hypothetical protein
so1326	so1326	2,51E+00	4,73E-03	2,16E+00	3,55E-04	2,58E+00	9,58E-06	3,16E+00	2,65E-05	conserved hypothetical protein
so1337	so1337	4,73E+00	4,75E-06	3,46E+00	4,12E-03	4,24E+00	1,30E-05	5,12E+00	5,37E-09	hypothetical protein
hcp	so1363	3,24E+00	1,41E-03	2,21E+00	1,98E-02	2,65E+00	1,49E-07	3,18E+00	1,48E-05	prismane protein
so1378	so1378	1,27E+00	2,60E-01	1,91E+00	1,43E-01	2,08E+00	2,97E-03	2,63E+00	1,81E-02	ThiJ/PfpI family protein
so1410	so1410	2,05E+00	6,16E-03	1,63E+00	3,74E-02	1,38E+00	9,58E-02	2,30E+00	1,57E-03	hypothetical protein

so1427	so1427	2,83E+00	1,18E-03	2,86E+00	1,27E-02	3,48E+00	2,04E-04	5,98E+00	9,10E-07	decaheme cytochrome c
so1428	so1428	1,72E+00	1,74E-02	1,82E+00	2,27E-02	2,26E+00	6,70E-05	3,01E+00	3,20E-05	outer membrane protein
dmaa-1	so1429	2,21E+00	7,36E-03	3,59E+00	2,79E-03	3,72E+00	1,91E-06	3,95E+00	2,86E-05	anaerobic dimethyl sulfoxide reductase, A subunit
dmsb-1	so1430	2,20E+00	1,24E-02	3,13E+00	2,89E-03	3,17E+00	2,65E-07	2,78E+00	1,46E-05	anaerobic dimethyl sulfoxide reductase, B subunit
so1431	so1431	4,79E+00	1,22E-06	2,38E+00	1,32E-03	2,01E+00	2,48E-03	2,21E+00	9,90E-04	conserved hypothetical protein
so1489	so1489	2,59E+00	2,68E-02	2,10E+00	9,69E-03	2,24E+00	1,32E-04	1,44E+00	3,80E-02	hypothetical protein
adhb	so1490	4,37E+00	6,62E-06	3,09E+00	6,70E-04	2,46E+00	8,21E-05	2,57E+00	9,42E-04	alcohol dehydrogenase II
so1521	so1521	1,98E+00	1,27E-02	1,62E+00	3,02E-02	3,07E+00	5,59E-05	6,46E+00	1,03E-03	iron-sulfur cluster-binding protein
so1522	so1522	4,90E+00	5,78E-03	2,37E+00	6,87E-03	3,13E+00	1,66E-04	1,93E+00	1,74E-02	L-lactate permease, putative
so1532	so1532	2,71E+00	1,43E-03	3,21E+00	2,80E-02	2,05E+00	1,44E-02	2,54E+00	1,12E-02	hypothetical protein
so1659	so1659	4,84E+00	1,36E-05	2,58E+00	4,58E-02	2,16E+00	1,75E-04	2,58E+00	1,12E-03	decaheme cytochrome c
so1673	so1673	6,76E+00	4,55E-07	1,98E+00	1,03E-01	2,66E+00	1,83E-02	3,14E+00	1,21E-03	outer membrane protein OmpW, putative
so1703	so1703	5,27E+00	2,73E-05	3,34E+00	3,18E-02	3,14E+00	2,14E-03	6,54E+00	4,74E-03	transcriptional regulator, TetR family
so1706	so1706	3,88E+00	2,54E-04	2,72E+00	2,44E-02	2,95E+00	4,59E-03	3,60E+00	4,85E-05	ABC transporter, ATP-binding protein, putative
mtrb	so1776	4,31E+00	9,77E-06	1,66E+00	7,18E-02	1,80E+00	4,04E-02	1,72E+00	1,36E-01	outer membrane protein precursor MtrB
so1821	so1821	3,20E+00	8,38E-05	2,54E+00	6,90E-03	3,30E+00	2,37E-05	3,83E+00	2,89E-05	outer membrane porin, putative
rmf	so1855	2,22E+00	1,21E-03	1,42E+00	2,78E-01	1,52E+00	6,42E-02	2,72E+00	5,76E-05	ribosome modulation factor
so1907	so1907	8,63E+00	4,82E-05	2,94E+00	2,02E-03	3,25E+00	1,30E-05	2,56E+00	4,28E-04	transcriptional regulator, LysR family
so1909	so1909	3,90E+00	9,52E-07	2,99E+00	4,47E-02	3,58E+00	1,15E-03	3,74E+00	1,59E-03	conserved hypothetical protein
so1911	so1911	2,41E+00	5,32E-03	1,55E+00	2,68E-02	1,65E+00	8,29E-03	2,55E+00	8,27E-04	oxidoreductase, short chain dehydrogenase/reductase family
so1968	so1968	4,22E+00	4,14E-05	1,73E+00	4,54E-03	1,75E+00	1,92E-03	2,18E+00	2,68E-04	hypothetical protein
so2059	so2059	5,77E+00	5,59E-03	6,27E+00	2,51E-02	8,11E+00	2,54E-04	1,35E+01	5,11E-03	hypothetical protein
hisd	so2073	2,58E+00	6,64E-04	1,92E+00	2,95E-03	2,55E+00	1,14E-03	2,78E+00	6,36E-06	histidinol dehydrogenase
hisg	so2074	6,75E+00	2,86E-05	2,38E+00	1,85E-01	3,84E+00	7,80E-03	3,12E+00	1,58E-02	ATP phosphoribosyltransferase
hypa	so2089	1,65E+00	2,54E-02	1,40E+00	1,31E-01	2,23E+00	1,13E-03	2,76E+00	5,09E-05	hydrogenase expression/formation protein HypA
hype	so2090	2,58E+00	5,68E-03	1,46E+00	3,54E-01	2,54E+00	1,12E-02	2,26E+00	1,41E-02	hydrogenase expression/formation protein HypE
hypd	so2091	1,62E+00	1,39E-01	3,17E+00	4,25E-04	3,03E+00	2,07E-04	2,14E+00	1,67E-02	hydrogenase expression/formation protein HypD
hypc	so2092	5,35E+00	2,94E-06	1,94E+00	1,90E-02	3,48E+00	1,24E-02	5,70E+00	2,49E-04	hydrogenase assembly chaperone hypC/hupF
hydc	so2097	1,07E+00	8,23E-01	2,17E+00	2,19E-01	5,96E+00	2,54E-03	6,76E+00	3,18E-03	quinone-reactive Ni/Fe hydrogenase, cytochrome b subunit
hyab	so2098	1,23E+00	3,39E-01	2,05E+00	9,68E-03	3,22E+00	1,83E-06	4,42E+00	3,88E-06	quinone-reactive Ni/Fe hydrogenase, large subunit
hoxk	so2099	1,66E+01	9,90E-09	1,50E+00	4,13E-01	1,50E+00	2,87E-01	2,40E+00	4,18E-02	quinone-reactive Ni/Fe hydrogenase, small subunit precursor
so2109	so2109	2,31E+00	8,06E-03	1,71E+00	7,26E-03	1,76E+00	1,04E-03	2,05E+00	7,56E-04	conserved hypothetical protein
adhe	so2136	2,65E+00	2,59E-03	1,72E+00	1,80E-02	2,81E+00	1,10E-04	1,95E+00	7,58E-02	aldehyde-alcohol dehydrogenase
ccpa	so2178	2,19E+00	2,14E-02	1,80E+00	1,45E-02	2,45E+00	6,62E-04	1,63E+00	6,32E-01	cytochrome c551 peroxidase
ppx	so2185	2,62E+00	6,09E-04	1,93E+00	1,22E-02	2,71E+00	2,02E-06	2,74E+00	2,75E-05	exopolyphosphatase

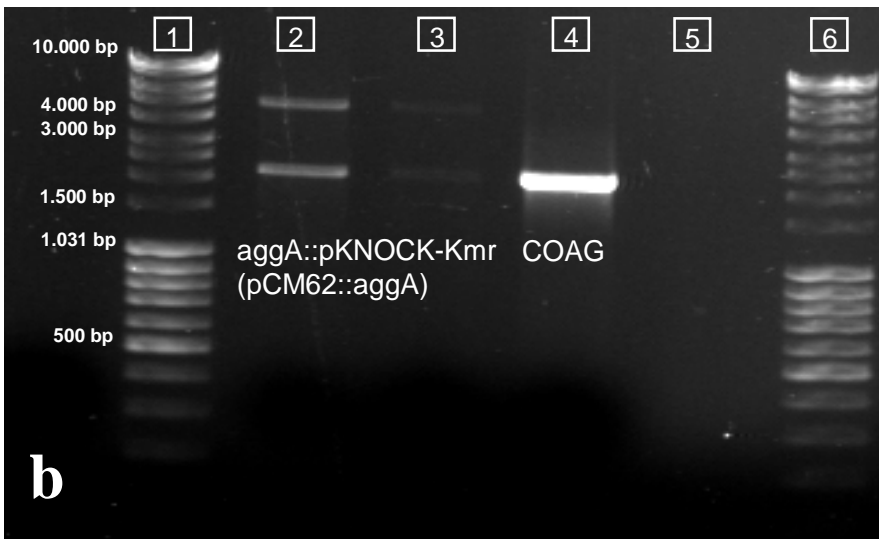
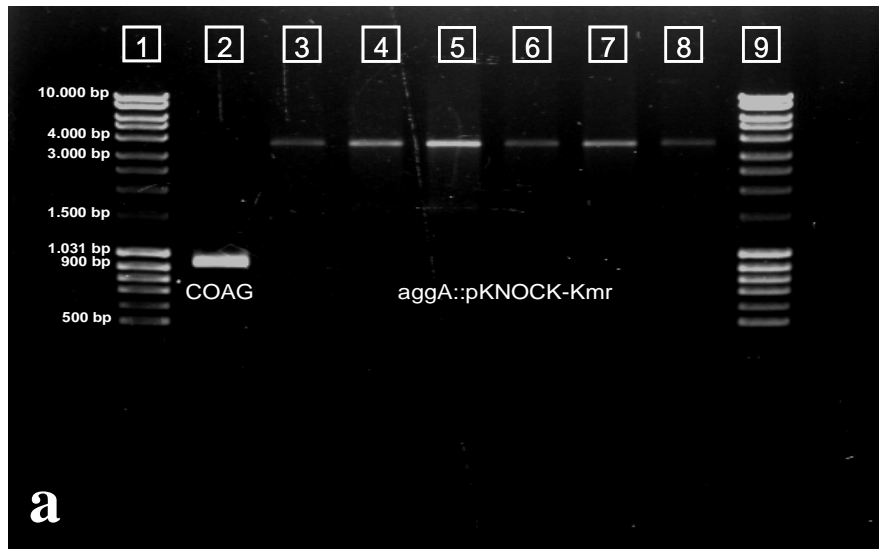
crea	so2190	3,27E+00	6,70E-03	1,74E+00	1,40E-01	2,32E+00	1,38E-03	2,48E+00	1,88E-01	creA protein
so2219	so2219	2,66E+00	6,13E-02	2,03E+00	1,30E-01	2,02E+00	7,20E-03	2,03E+00	5,61E-02	hypothetical protein
so2228	so2228	2,62E+00	1,72E-02	1,52E+00	4,31E-01	2,36E+00	3,30E-02	1,67E+00	1,55E-01	CBS domain protein
sdaa	so2248	5,09E+00	7,68E-03	1,72E+00	5,04E-01	2,21E+00	5,87E-02	3,14E+00	2,86E-01	L-serine dehydratase 1
so2251	so2251	4,82E+00	5,60E-05	3,73E+00	1,62E-02	5,67E+00	3,68E-05	5,31E+00	1,36E-07	conserved hypothetical protein
so2273	so2273	1,03E+01	3,89E-04	4,68E+00	1,85E-02	9,86E+00	6,39E-05	5,07E+00	1,18E-03	hypothetical protein
ibpA	so2277	4,60E+00	1,92E-04	4,41E+00	1,15E-02	6,59E+00	6,05E-06	4,82E+00	1,05E-04	16 kDa heat shock protein A
so2281	so2281	3,21E+00	1,36E-04	1,93E+00	1,13E-02	2,48E+00	1,09E-04	2,49E+00	5,16E-04	alkaline phosphatase
so2346	so2346	2,44E+00	1,10E-03	2,12E+00	2,08E-03	2,77E+00	6,04E-07	2,95E+00	2,07E-05	conserved hypothetical protein
so2355	so2355	9,98E+00	1,09E-05	2,33E+00	6,46E-02	2,32E+00	2,60E-04	1,72E+00	5,58E-02	universal stress protein family
emrd	so2389	9,84E+00	4,24E-08	3,96E+00	1,07E-02	3,45E+00	4,45E-05	2,62E+00	1,14E-02	multidrug resistance protein D
dacb	so2394	3,78E+00	3,65E-04	2,39E+00	4,73E-04	2,90E+00	4,69E-05	3,78E+00	3,74E-05	penicillin-binding protein 4
serc	so2410	2,62E+00	3,60E-04	1,42E+00	1,58E-01	2,12E+00	7,35E-03	1,85E+00	5,34E-04	phosphoserine aminotransferase
so2439	so2439	2,02E+00	7,09E-03	1,46E+00	6,26E-02	1,35E+00	2,97E-01	2,00E+00	3,45E-03	srpA-related protein
so2458	so2458	4,13E+00	4,64E-06	2,02E+00	2,07E-02	1,65E+00	9,85E-03	2,13E+00	2,50E-03	transporter, putative
so2499	so2499	4,11E+00	3,56E-04	2,67E+00	3,59E-03	3,57E+00	4,63E-06	2,37E+00	4,57E-03	conserved hypothetical protein
so2542	so2542	6,36E+00	1,86E-03	2,49E+00	1,92E-01	2,17E+00	1,23E-02	2,38E+00	1,23E-02	conserved hypothetical protein
so2553	so2553	7,41E-01	3,82E-01	2,12E+00	5,16E-03	3,60E+00	7,51E-06	9,25E+00	2,39E-04	conserved hypothetical protein
so2555	so2555	2,63E+00	9,61E-04	1,59E+00	1,05E-01	2,18E+00	1,93E-03	1,93E+00	1,34E-02	hypothetical protein
so2556	so2556	3,37E+00	2,06E-04	1,55E+00	6,25E-02	2,00E+00	3,73E-04	1,55E+00	6,43E-02	hypothetical protein
so2640	so2640	2,06E+00	3,44E-03	2,09E+00	1,91E-02	2,26E+00	1,05E-04	2,29E+00	1,10E-04	transcriptional regulator, MarR family
so2672	so2672	4,12E+00	7,30E-06	2,15E+00	7,80E-03	1,86E+00	3,12E-02	1,92E+00	3,91E-03	conserved hypothetical protein
so2701	so2701	3,24E+00	7,30E-04	1,65E+00	7,29E-02	1,88E+00	6,77E-03	2,08E+00	8,91E-04	conserved hypothetical protein
deod-3	so2719	2,74E+00	3,44E-04	2,19E+00	1,96E-02	2,03E+00	5,79E-04	1,87E+00	1,67E-02	purine nucleoside phosphorylase
upp	so2759	2,99E+00	2,37E-04	1,78E+00	3,26E-01	2,61E+00	2,05E-02	2,07E+00	1,90E-01	uracil phosphoribosyltransferase
purm	so2760	2,50E+00	3,89E-03	1,83E+00	2,06E-02	2,45E+00	9,29E-05	2,48E+00	2,41E-03	phosphoribosylformylglycinamide cyclo-ligase
so2768	so2768	5,61E+00	3,40E-05	2,10E+00	2,02E-02	2,68E+00	5,03E-03	2,62E+00	1,77E-04	acyl-CoA dehydrogenase family protein
so2795	so2795	2,88E+00	1,52E-04	2,08E+00	3,72E-02	2,44E+00	1,37E-03	2,17E+00	2,35E-02	glyoxalase family protein
so2819	so2819	2,95E+00	2,48E-03	2,38E+00	2,23E-02	2,57E+00	4,08E-02	6,59E+00	3,17E-02	ISSod11, transposase
nrdg	so2833	2,89E+00	3,17E-02	2,06E+00	4,75E-03	2,20E+00	2,66E-03	2,06E+00	1,21E-02	anaerobic ribonucleoside-triphosphate reductase activating protein
nrd	so2834	3,07E+00	2,47E-03	3,24E+00	6,19E-03	1,95E+00	9,64E-03	3,10E+00	1,15E-02	anaerobic ribonucleoside-triphosphate reductase
so2841	so2841	2,10E+00	3,59E-03	1,34E+00	1,25E-01	1,84E+00	7,55E-04	2,09E+00	7,17E-04	hypothetical protein
so2882	so2882	1,72E+00	4,29E-02	2,91E+00	1,15E-01	4,47E+00	2,23E-03	7,21E+00	6,42E-03	conserved hypothetical protein
so2883	so2883	3,13E+00	4,32E-03	2,25E+00	5,76E-03	4,62E+00	1,18E-02	4,91E+00	2,00E-03	conserved hypothetical protein
so2884	so2884	1,64E+00	1,16E-01	2,31E+00	5,78E-03	2,28E+00	9,38E-05	1,90E+00	1,10E-02	conserved hypothetical protein

liga	so2896	3,58E+00	1,96E-04	2,39E+00	4,26E-03	2,19E+00	5,70E-04	2,19E+00	4,93E-04	DNA ligase, NAD-dependent
so2911	so2911	3,54E+00	4,47E-02	4,77E-01	8,93E-01	2,37E+00	3,49E-01	3,89E+00	9,18E-02	formate transporter, putative
pflb	so2912	2,25E+00	6,18E-03	1,97E+00	3,61E-01	3,60E+00	8,83E-03	4,41E+00	5,95E-04	formate acetyltransferase
pfla	so2913	2,70E+00	3,34E-02	2,01E+00	6,77E-02	1,88E+00	1,16E-02	1,66E+00	3,10E-01	pyruvate formate-lyase 1 activating enzyme
acka	so2915	2,96E+00	1,18E-03	2,23E+00	9,03E-02	1,77E+00	1,96E-01	2,59E+00	2,48E-01	acetate kinase
pta	so2916	4,97E+00	6,63E-03	2,53E+00	2,92E-03	2,06E+00	3,38E-04	2,67E+00	3,51E-04	phosphate acetyltransferase
so2941	so2941	1,02E+01	3,11E-04	3,85E+00	1,92E-02	4,22E+00	2,56E-03	3,45E+00	7,36E-04	prophage LambdaSo, tail assembly protein I
so2944	so2944	4,37E+00	2,84E-04	2,07E+00	3,95E-02	1,99E+00	2,00E-03	1,59E+00	4,32E-02	hypothetical protein
so2945	so2945	4,21E+00	1,36E-03	3,07E+00	1,58E-01	5,74E+00	4,24E-03	4,89E+00	9,41E-03	hypothetical protein
so3052	so3052	3,51E+00	7,62E-05	4,09E+00	8,49E-02	5,52E+00	1,74E-03	3,59E+00	3,03E-02	methyl-accepting chemotaxis protein
so3053	so3053	3,78E+00	1,48E-04	3,30E+00	1,03E-01	4,56E+00	4,92E-03	5,22E+00	1,36E-02	hypothetical protein
so3054	so3054	3,12E+00	2,76E-04	2,48E+00	3,61E-04	2,34E+00	1,29E-05	2,21E+00	7,68E-04	metallo-beta-lactamase family protein
so3059	so3059	1,77E+01	3,64E-07	3,05E+00	1,70E-02	2,06E+00	1,72E-04	1,80E+00	3,67E-02	formate hydrogenlyase transcriptional activator, putative
so3119	so3119	7,70E+00	6,32E-05	3,06E+00	6,74E-03	3,36E+00	2,64E-08	5,93E+00	1,41E-07	hypothetical protein
so3324	so3324	7,30E+00	3,11E-04	2,45E+00	9,21E-03	1,48E+00	9,48E-01	2,43E+00	2,05E-02	acetyltransferase, GNAT family
so3325	so3325	7,33E+00	2,22E-05	3,71E+00	4,43E-03	2,54E+00	4,12E-05	3,26E+00	2,66E-03	nrfJ-related protein
so3342	so3342	3,57E+00	1,03E-04	1,88E+00	1,10E-01	1,72E+00	3,60E-03	2,00E+00	1,41E-02	conserved hypothetical protein
so3386	so3386	3,16E+00	4,61E-05	2,49E+00	1,04E-02	2,05E+00	8,20E-03	9,48E-01	9,09E-01	conserved hypothetical protein
so3395	so3395	1,78E+00	2,40E-02	2,07E+00	2,05E-02	2,08E+00	2,79E-03	8,47E-01	9,20E-01	hypothetical protein
so3409	so3409	2,40E+00	1,80E-03	1,79E+00	2,91E-02	2,05E+00	4,11E-03	1,25E+00	4,94E-01	OsmC/Ohr family protein
thra	so3415	2,55E+00	6,31E-04	1,73E+00	1,26E-02	2,24E+00	6,66E-04	2,66E+00	3,54E-04	aspartokinase I/homoserine dehydrogenase, threonine-sensitive
yfia-2	so3422	6,52E+00	5,12E-05	2,64E+00	3,91E-02	3,09E+00	2,93E-03	3,31E+00	1,33E-01	ribosomal subunit interface protein
mexe	so3493	3,73E+00	5,52E-03	2,01E+00	4,87E-03	2,40E+00	4,52E-04	1,90E+00	1,06E-03	RND multidrug efflux membrane fusion protein MexE
so3525	so3525	5,97E+00	8,40E-04	3,01E+00	1,43E-02	4,57E+00	3,45E-03	4,42E+00	3,17E-03	type IV pilin biogenesis protein, putative
so3528	so3528	6,51E+00	5,32E-04	4,42E+00	2,93E-04	7,00E+00	1,86E-09	6,39E+00	1,71E-05	hypothetical protein
hlyu	so3538	6,07E+00	1,30E-04	3,41E+00	3,71E-03	2,13E+00	3,57E-04	2,17E+00	2,90E-02	transcriptional regulator HlyU
tal	so3546	4,82E+00	2,15E-04	2,88E+00	3,75E-05	2,45E+00	9,42E-04	3,31E+00	4,68E-06	Transaldolase
so3549	so3549	3,10E+00	1,98E-03	2,54E+00	1,74E-02	3,12E+00	7,37E-02	2,40E+00	2,14E-02	conserved hypothetical protein
so3553	so3553	2,03E+00	1,11E-02	2,06E+00	3,79E-03	3,20E+00	8,89E-06	2,83E+00	6,82E-04	sulfate permease family protein
so3616	so3616	2,37E+00	2,85E-03	1,35E+00	3,30E-01	1,70E+00	2,71E-02	2,55E+00	3,74E-03	hypothetical protein
so3620	so3620	2,35E+00	2,98E-03	1,75E+00	3,94E-02	1,98E+00	6,48E-05	2,07E+00	2,48E-03	hypothetical protein
so3625	so3625	5,60E+00	1,17E-03	1,96E+00	2,19E-02	1,72E+00	1,37E-02	2,55E+00	3,06E-05	ISSod3, transposase
so3626	so3626	8,41E+00	2,49E-04	2,88E+00	3,08E-03	4,56E+00	5,76E-05	5,82E+00	4,64E-03	hypothetical protein
so3678	so3678	1,13E+00	5,89E-01	2,63E+00	1,42E-01	1,86E+00	1,99E-02	3,18E+00	3,14E-02	conserved hypothetical protein
so3679	so3679	2,68E+00	7,34E-03	1,71E+00	8,34E-02	2,13E+00	9,57E-04	1,83E+00	2,67E-02	conserved hypothetical protein

so3680	so3680	1,68E+00	2,50E-02	1,54E+00	4,40E-02	2,36E+00	7,13E-04	2,17E+00	5,47E-04	universal stress protein family
so3681	so3681	7,96E+00	3,35E-05	2,68E+00	1,31E-03	2,75E+00	5,11E-05	4,54E+00	3,19E-05	universal stress protein family
so3682	so3682	3,17E+00	1,84E-04	2,30E+00	3,64E-03	2,46E+00	2,80E-05	2,27E+00	1,12E-03	hypothetical protein
so3699	so3699	5,98E+00	6,90E-05	2,69E+00	7,17E-03	4,27E+00	1,45E-03	4,67E+00	1,17E-04	hypothetical protein
so3714	so3714	5,18E+00	1,38E-05	2,36E+00	5,13E-03	2,57E+00	2,14E-05	1,71E+00	1,78E-02	sugar-binding protein, putative
so3715	so3715	1,86E+00	1,07E-02	1,33E+00	2,22E-01	2,83E+00	3,05E-02	2,84E+00	4,60E-06	oxygen-insensitive NAD(P)H nitroreductase
so3718	so3718	4,42E+00	3,44E-02	3,19E+00	4,10E-02	1,09E+00	8,35E-01	1,59E+00	9,74E-01	thiol:disulfide interchange protein, DsbA family
so3719	so3719	2,10E+00	1,18E-02	8,51E-01	8,93E-01	1,37E+00	1,59E-01	2,65E+00	2,42E-03	hypothetical protein
so3720	so3720	2,00E+01	8,32E-04	2,41E+00	1,70E-03	1,79E+00	1,48E-02	1,42E+00	1,85E-01	conserved hypothetical protein
so3846	so3846	2,78E+00	4,38E-03	1,77E+00	1,58E-01	2,10E+00	4,85E-03	1,66E+00	1,16E-02	conserved hypothetical protein
modb	so3864	2,21E+00	2,86E-03	1,70E+00	2,01E-02	2,04E+00	3,03E-04	1,39E+00	1,22E-01	molybdenum ABC transporter, permease protein
modc	so3865	3,21E+00	3,82E-04	2,79E+00	9,96E-03	3,20E+00	1,00E-05	2,54E+00	1,65E-04	molybdenum ABC transporter, ATP-binding protein
so3872	so3872	9,33E+00	5,35E-05	4,21E+00	7,24E-02	7,06E+00	1,23E-03	6,09E+00	8,44E-03	arylsulfate sulfotransferase
so3888	so3888	7,57E+00	4,83E-06	3,18E+00	8,63E-02	7,02E+00	1,59E-03	4,96E+00	1,33E-03	conserved hypothetical protein
so3912	so3912	6,42E+00	4,29E-05	2,48E+00	4,17E-03	2,32E+00	5,37E-04	2,17E+00	3,02E-03	TIM-barrel protein, yjbN family
so3915	so3915	4,23E+00	1,04E-04	2,84E+00	6,56E-04	4,97E+00	3,06E-07	6,97E+00	9,67E-06	conserved hypothetical protein
so3925	so3925	2,16E+00	5,82E-03	1,39E+00	7,91E-02	2,01E+00	2,67E-04	1,51E+00	7,67E-02	biotin synthase family protein
so4053	so4053	4,47E+00	2,79E-05	1,64E+00	3,38E-02	1,65E+00	1,24E-03	2,26E+00	2,08E-04	methyl-accepting chemotaxis protein
psrc	so4060	8,31E+00	2,72E-06	2,20E+00	2,03E-02	2,58E+00	9,00E-04	2,30E+00	1,11E-02	polysulfide reductase, subunit C
psrb	so4061	8,76E+00	8,84E-07	4,43E+00	7,14E-02	3,66E+00	1,30E-04	4,55E+00	1,34E-03	polysulfide reductase, subunit B
psra	so4062	2,23E+00	1,39E-03	1,93E+00	2,61E-02	2,55E+00	8,44E-05	1,38E+00	1,75E-01	polysulfide reductase, subunit A
so4126	so4126	2,74E+00	9,53E-03	1,87E+00	2,35E-01	2,82E+00	1,74E-02	3,95E+00	4,02E-04	hypothetical protein
udp	so4133	2,49E+00	9,15E-04	1,30E+00	6,26E-01	1,37E+00	3,95E-01	2,11E+00	6,63E-03	uridine phosphorylase
so4138	so4138	1,30E+01	6,47E-03	2,66E+00	2,15E-02	2,29E+00	4,03E-03	3,26E+00	6,51E-03	conserved hypothetical protein
so4151	so4151	9,32E+00	1,70E-03	7,15E+00	2,12E-03	1,25E+01	3,77E-04	1,62E+01	6,40E-04	polysaccharide deacetylase family protein
so4152	so4152	2,78E+00	4,11E-04	2,32E+00	6,11E-03	2,40E+00	4,18E-04	2,47E+00	3,32E-04	hypothetical protein
so4153	so4153	4,44E+00	4,65E-05	2,31E+00	3,84E-03	2,45E+00	3,24E-06	4,66E+00	3,65E-06	N-ethylmaleimide reductase, putative
so4155	so4155	3,85E+00	1,28E-04	2,42E+00	8,64E-05	1,92E+00	1,06E-03	1,56E+00	4,04E-02	sensor histidine kinase
so4157	so4157	1,88E+01	8,13E-09	3,17E+00	7,16E-04	3,48E+00	2,83E-03	8,94E+00	6,05E-02	DNA-binding response regulator
meng-2	so4197	9,43E-01	8,10E-01	1,96E+00	3,09E-02	3,96E+00	2,81E-04	5,10E+00	1,28E-04	S-adenosylmethionine:2-demethylmenaquinone methyltransferase
so4229	so4229	4,34E-01	1,81E-01	2,54E+00	1,56E-02	5,25E+00	4,59E-03	9,93E+00	8,68E-04	hypothetical protein
leua	so4236	7,16E-01	3,59E-01	3,04E+00	6,77E-03	6,71E+00	2,68E-03	7,60E+00	2,01E-03	2-isopropylmalate synthase
so4274	so4274	1,84E+01	1,76E-03	6,70E+00	3,12E-03	5,21E+00	6,61E-06	2,46E+00	7,60E-03	undecaprenol kinase, putative
so4304	so4304	1,81E+00	1,16E-02	1,97E+00	3,19E-03	2,15E+00	1,21E-03	3,05E+00	3,54E-06	conserved hypothetical protein
so4317	so4317	4,35E+00	6,19E-05	2,10E+00	1,00E-02	2,12E+00	8,03E-03	2,17E+00	9,14E-04	RTX toxin, putative

rtxB	so4318	1,75E+00	1,84E-02	2,57E+00	1,55E-03	1,41E+00	4,07E-02	1,25E+00	3,84E-01	toxin secretion ATP-binding protein
so4319	so4319	2,01E+00	6,74E-03	1,67E+00	2,84E-02	1,31E+00	1,20E-01	1,61E+00	6,38E-02	HlyD family secretion protein
agga	so4320	1,18E+00	4,26E-01	1,31E+00	2,37E-01	1,41E+00	1,87E-02	2,97E+00	1,62E-04	agglutination protein
so4321	so4321	2,17E+00	6,81E-03	1,71E+00	4,06E-02	2,47E+00	1,71E-03	3,40E+00	2,86E-03	OmpA family protein
so4326	so4326	1,96E+00	1,58E-01	2,06E+00	1,07E-01	6,90E+00	1,05E-02	5,75E+00	3,16E-02	transcriptional regulator, TetR family
ilvd	so4345	1,12E+00	6,83E-01	1,26E+00	2,82E-01	3,44E+00	3,98E-06	3,28E+00	1,60E-05	dihydroxy-acid dehydratase
katg-2	so4405	1,20E+01	3,91E-05	3,95E+00	8,22E-03	5,50E+00	5,96E-03	8,61E+00	1,18E-04	catalase/peroxidase HPI
so4407	so4407	7,51E+00	2,28E-05	2,53E+00	1,96E-02	2,45E+00	2,01E-03	1,56E+00	2,85E-01	GGDEF family protein
dcub	so4417	2,34E+00	4,96E-04	1,97E+00	6,76E-02	1,84E+00	3,44E-04	2,06E+00	1,33E-03	anaerobic C4-dicarboxylate membrane transporter
so4446	so4446	1,90E+00	1,13E-02	1,71E+00	8,40E-03	2,31E+00	3,86E-04	2,44E+00	1,41E-03	molybdenum ABC transporter, ATP-binding protein
so4447	so4447	1,38E+00	1,36E-01	2,03E+00	2,67E-02	1,86E+00	1,19E-03	2,48E+00	1,85E-04	molybdenum ABC transporter, permease protein
so4448	so4448	2,56E+00	6,50E-03	2,03E+00	6,71E-03	1,04E+00	7,98E-01	9,95E-01	9,88E-01	molybdenum ABC transporter, periplasmic molybdenum-binding protein
moae	so4449	2,37E+00	1,52E-03	1,60E+00	2,08E-02	2,05E+00	3,57E-05	2,00E+00	2,54E-03	molybdenum cofactor biosynthesis protein E
moad	so4450	2,86E+00	1,59E-04	2,60E+00	1,78E-04	2,86E+00	3,31E-05	4,72E+00	1,63E-06	molybdenum cofactor biosynthesis protein D
moac	so4451	2,07E+00	5,92E-03	2,23E+00	5,10E-02	2,06E+00	3,51E-04	3,89E+00	1,74E-05	molybdenum cofactor biosynthesis protein C
moaa	so4452	1,17E+00	4,86E-01	2,41E+00	1,61E-01	1,87E+00	2,78E-02	2,45E+00	1,15E-02	molybdenum cofactor biosynthesis protein A
so4508	so4508	2,40E+00	1,18E-03	1,99E+00	3,33E-03	2,00E+00	1,51E-04	2,39E+00	1,75E-03	hypothetical protein
fdhb-1	so4510	6,04E+00	5,57E-04	3,28E+00	2,22E-04	3,32E+00	1,97E-04	6,14E+00	5,68E-06	formate dehydrogenase, iron-sulfur subunit
so4512	so4512	3,29E+00	1,29E-04	2,75E+00	2,31E-03	6,62E+00	4,42E-07	5,49E+00	6,09E-05	conserved hypothetical protein
so4513	so4513	9,64E+00	1,18E-03	4,30E+00	1,91E-02	4,31E+00	4,39E-04	6,57E+00	3,44E-03	formate dehydrogenase, alpha subunit
so4515	so4515	2,20E+00	1,30E-02	1,88E+00	8,38E-02	2,14E+00	1,22E-03	2,28E+00	2,95E-03	formate dehydrogenase, C subunit, putative
so4520	so4520	2,80E+00	5,98E-04	2,13E+00	5,03E-03	2,66E+00	3,56E-03	3,37E+00	4,35E-04	oxygen-independent coproporphyrinogen III oxidase, putative
so4558	so4558	3,07E+00	2,62E-04	2,74E+00	1,24E-03	4,13E+00	6,68E-05	5,16E+00	1,09E-05	hypothetical protein
cyma	so4591	2,71E+00	1,18E-04	2,25E+00	1,40E-02	3,40E+00	2,83E-04	5,34E+00	1,14E-05	tetraheme cytochrome c
so4594	so4594	2,89E+00	3,12E-04	3,28E+00	1,01E-02	3,34E+00	1,38E-03	6,02E+00	1,86E-06	hypothetical protein
so4606	so4606	2,36E+00	4,66E-02	2,42E+00	2,11E-02	3,58E+00	5,63E-05	4,37E+00	6,20E-08	cytochrome c oxidase, subunit II
so4623	so4623	1,88E+00	1,22E-02	2,31E+00	2,71E-03	3,08E+00	1,46E-04	4,24E+00	3,97E-06	DNA-binding response regulator
so4627	so4627	3,77E+00	1,01E-02	1,78E+00	2,53E-01	4,58E+00	1,70E-02	6,47E+00	2,00E-02	hypothetical protein
so4716	so4716	1,69E+00	1,03E-01	2,02E+00	8,43E-02	2,41E+00	1,06E-02	2,78E+00	9,71E-01	acetyltransferase, GNAT family
hemn	so4730	5,66E+00	3,16E-05	2,87E+00	1,44E-05	2,53E+00	4,96E-06	2,09E+00	2,28E-04	oxygen-independent coproporphyrinogen III oxidase
nqrb-1	so903	1,08E+01	1,67E-05	3,23E+00	3,75E-02	2,70E+00	5,48E-03	2,60E+00	1,77E-02	NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein NqrB
nqrc-1	so904	4,13E+00	8,11E-04	2,03E+00	6,14E-02	1,81E+00	8,08E-04	1,24E+00	1,68E-01	NADH:ubiquinone oxidoreductase, Na translocating, gamma subunit
soa0058	soa0058	5,41E+00	8,66E-05	1,80E+00	1,12E-01	2,07E+00	4,33E-02	1,32E+00	4,53E-01	hypothetical protein
soa0060	soa0060	4,73E+00	4,09E-02	3,13E+00	2,70E-03	3,36E+00	5,25E-06	2,52E+00	1,69E-03	acetyltransferase, GNAT family
soa0070	soa0070	4,93E+00	5,19E-05	2,26E+00	1,78E-04	2,53E+00	1,56E-05	3,06E+00	2,27E-03	hypothetical protein

soa0127	soa0127	2,63E+00	1,09E-03	1,95E+00	1,58E-01	2,29E+00	2,48E-05	2,04E+00	9,22E-03	hypothetical protein
soa0137	soa0137	1,91E+00	1,54E-02	2,81E+00	1,10E-03	3,35E+00	1,65E-05	2,91E+00	5,11E-05	conserved domain protein
soa0155	soa0155	5,37E+00	3,18E-04	2,90E+00	2,74E-05	2,95E+00	4,07E-07	3,55E+00	6,74E-06	conserved domain protein
soa0158	soa0158	4,65E+00	7,23E-04	3,13E+00	5,04E-02	5,08E+00	2,72E-03	4,06E+00	1,46E-02	hypothetical protein
soa0159	soa0159	2,93E+00	1,49E-02	3,47E+00	9,71E-03	3,24E+00	1,05E-04	3,12E+00	1,41E-04	multidrug efflux transporter
soa0172	soa0172	4,56E+00	1,39E-06	2,46E+00	6,84E-03	2,33E+00	5,17E-04	3,01E+00	2,37E-05	site-specific recombinase, resolvase family



Supplementary Fig. S1. (a) PCR products of *aggA* amplification with primers AGG183F and AGG1122R for COAG (lane 2), and of *aggA::pKNOCK-Km^r* amplification for six different transconjugants (lanes 3–8). (b) PCR products for *aggA* amplification with primers AGGf and AGGr for COAG (lane 4) and for complemented *aggA::pKNOCK-Km^r*(pCM62::aggA) (lanes 2–3).