Supplemental Material

TABLE S1 Genes showing altered expression in strain *G. oxydans* Δ*upp*Δ*cyoBACD* compared to the reference strain *G. oxydans* Δ*upp*. Cells were cultivated in baffled shake flasks with mannitol as carbon source and harvested at an OD_{600} of 1.5. RNA extraction, reverse transcription and cDNA labeling and DNA microarray analysis were performed as described previously (Hanke et al. 2012, J. Biotechnol. 157: 359-372). Genes showing an mRNA ratio (Δ*upp* Δ*cyoBACD* versus Δ*upp*) ≥2 and ≤0.5 and a p-value ≤0.05 are listed according to their locus tag number. The ratios represent mean values of three independent experiments.

Locus tag	**Annotation**	**Gene name**	**mRNA ratio**	***p* value**
	102 genes with an mRNA ratio ≥2			
GOX0057	Protein with GGDEF and EAL domain		2.11	1.36E-02
GOX0069	Hypothetical membrane-spanning protein		2.13	1.03E-02
GOX0135	Transcriptional regulator, Ros/MucR family		2.30	1.99E-04
GOX0278	Cytochrome *bd* ubiquinol oxidase subunit I	*cydA*	5.43	9.28E-03
GOX0279	Cytochrome *bd* ubiquinol oxidase subunit II	*cydB*	3.61	2.01E-02
GOX0290	Putative oxidoreductase		2.43	4.35E-02
GOX0291	Putative ferredoxin subunit of ring-hydroxylating dioxygenase	*hca*	3.69	9.29E-03
GOX0311	Transhydrogenase, subunit α2	*pntA2*	2.46	6.48E-03
GOX0312	Transhydrogenase, subunit b	*pntB*	2.19	1.36E-03
GOX0313	Alcohol:NAD^+ oxidoreductase		2.22	1.20E-02
GOX0433	Hypothetical protein		4.81	1.16E-02
GOX0442	Hypothetical protein		2.67	3.50E-02
GOX0475	Hypothetical protein		2.36	2.13E-02
GOX0498	Hypothetical protein		2.38	1.52E-02
GOX0502	Putative oxidoreductase		2.05	3.69E-02
GOX0503	Hypothetical protein		2.23	4.46E-02
GOX0519	Hypothetical outer membrane protein		2.35	2.05E-02
GOX0532	ExbB protein	*exbB*	3.40	2.46E-02
GOX0545	Putative outer membrane receptor for iron transport		2.72	9.08E-04
GOX0566	Ubiquinol-cytochrome *c* oxidoreductase, cytochrome *b*	*qrcB*	2.03	5.60E-03
GOX0570	Hypothetical protein		3.51	2.57E-02
GOX0576	Hypothetical protein		2.31	1.36E-02
GOX0635	Hypothetical protein		2.53	2.06E-02
GOX0646	Putative oxidoreductase		2.37	2.12E-02
GOX0647	Putative exporter protein, ArAE family	*fusB*	2.96	2.43E-02
GOX0673	Ferrous iron transport protein A	*feoA*	4.40	2.14E-04
GOX0674	Ferrous iron transport protein B	*feoB*	2.51	1.03E-02
GOX0679	Conserved protein of the SAM superfamily		3.71	1.90E-02
GOX0707	DNA starvation/stationary phase protection protein	*dps*	3.46	1.33E-02
GOX0726	Hypothetical protein		5.83	3.85E-02
GOX0756	Alcohol dehydrogenase, 15 kDa subunit		2.14	5.42E-02
GOX0814	PTS system IIA component	*ptsIIA*	2.13	2.38E-03

GOX0815	Hypothetical protein		2.39	1.75E-02
GOX0875	AtsE protein		2.19	9.83E-03
GOX0881	Arylesterase		2.31	3.51E-03
GOX0890	Hypothetical protein		2.39	2.47E-02
GOX0915	Hypothetical protein		2.28	1.34E-04
GOX1050	dTDP-4-dehydrorhamnose reductase		2.24	9.65E-04
GOX1051	dTDP-4-dehydrorhamnose 3.5-epimerase		2.62	4.93E-03
GOX1052	Glucose-1-phosphate thymidylyltransferase, C-terminus		2.64	2.93E-03
GOX1053	dTDP-glucose 4,6-dehydratase		2.32	4.02E-03
GOX1068	Alcohol dehydrogenase, large subunit		2.19	5.43E-03
GOX1107	O-antigen biosynthesis protein RfbC	*rfbC*	3.19	2.05E-03
GOX1132	Hypothetical protein		2.42	3.95E-04
GOX1246	TonB-dependent receptor protein		3.56	6.79E-03
GOX1276	Secreted protein of amidohydrolase family		2.01	2.53E-02
GOX1302	Paraquat-inducible protein A		2.43	1.10E-02
GOX1303	Paraquat-inducible protein B		2.18	2.57E-02
GOX1332	Alkyl hydroperoxide reductase subunit C		2.20	9.98E-03
GOX1357	Putative electron transport protein		2.63	1.81E-02
GOX1385	Hypothetical protein		2.01	1.11E-02
GOX1457	Hypothetical protein		2.11	3.65E-02
GOX1458	Putative oxidoreductase		2.47	1.90E-02
GOX1462	Putative oxidoreductase		3.88	3.47E-02
GOX1463	ATP-dependent Clp protease, ATP-binding subunit ClpV	*clpV*	2.41	4.16E-02
GOX1615	Putative oxidoreductase		4.34	2.11E-04
GOX1636	5-Aminolevulinate synthase		2.75	3.85E-02
GOX1697	Hypothetical protein		2.17	1.12E-02
GOX1698	Aminopeptidase		2.33	4.39E-03
GOX1712	Aldehyde dehydrogenase		2.90	4.34E-02
GOX1748	Bacterioferritin	*bfr*	4.90	2.82E-02
GOX1774	Putative ATP-sensitive potassium channel protein		3.17	6.71E-03
GOX1800	Superoxide dismutase	*sod*	2.00	1.92E-02
GOX1801	Putative oxidoreductase		2.38	3.63E-02
GOX1840	Hypothetical protein		5.16	4.51E-02
GOX1841	Hypothetical protein		14.16	7.46E-04
GOX1877	Glutathione peroxidase		2.06	1.57E-02
GOX1895	Hypothetical protein		2.00	1.04E-06
GOX1896	Coproporphyrinogen III oxidase		2.73	5.19E-02
GOX1899	Putative oxidoreductase		2.02	1.18E-02
GOX1900	Putative carboxymethylenebutenolidase		2.54	6.95E-03
GOX1951	Hypothetical protein		3.28	6.87E-03
GOX1953	5-Methylcytosine-specific restriction enzyme		4.05	2.70E-02
GOX1992	Osmotically inducible protein C, peroxyredoxin	*osmC*	4.90	1.37E-02
GOX2019	Putative esterase		2.11	1.17E-02
GOX2066	Glutaminase	*gls*	2.62	3.06E-02
GOX2069	Transcriptional regulator, DeoR family		2.52	7.54E-03
GOX2083	Hypothetical protein		2.40	1.72E-02
GOX2096	Major polyol dehydrogenase, large subunit	*sldA*	2.53	1.36E-02

GOX2097	Major polyol dehydrogenase small subunit	*sldB*	2.70	7.42E-05
GOX2108	NADH-dependent iron-containing alcohol dehydrogenase		2.15	6.69E-03
GOX2152	Hypothetical protein		3.12	1.77E-03
GOX2153	Hypothetical protein		2.97	9.32E-04
GOX2168	F_1F_o-ATP synthase subunit e	*atpC*	2.11	8.67E-03
GOX2170	F_1F_o-ATP synthase subunit r	*atpR**	2.36	2.71E-02
GOX2171	F_1F_o-ATP synthase subunit a	*atpB*	2.52	2.06E-02
GOX2172	F_1F_o-ATP synthase subunit c	*atpE*	2.25	5.27E-02
GOX2174	F_1F_o-ATP synthase subunit α	*atpA*	2.45	2.59E-02
GOX2199	Probable myosin-crossreactive antigen		4.46	6.39E-04
GOX2200	Probable myosin-crossreactive antigen		2.82	5.17E-02
GOX2246	Hypothetical protein		2.89	2.71E-02
GOX2253	Putative oxidoreductase		2.60	4.68E-03
GOX2308	Delta-aminolevulinic acid dehydratase		2.66	5.22E-03
GOX2407	Putative RNA polymerase sigma factor E (σ^{24})		2.32	5.02E-02
GOX2410	ABC transporter involved in cytochrome *bd* biogenesis	*cydC*	2.02	3.04E-02
GOX2413	Hypothetical protein		2.20	1.69E-02
GOX2470	Hypothetical protein		2.24	1.80E-03
GOX2494	Hypothetical protein		2.33	2.39E-02
GOX2683	Hypothetical protein		2.71	3.22E-02
GOX2684	NAD(P)H-dependent 2-cyclohexen-1-one reductase		2.10	6.24E-03
GOX2698	Hypothetical protein		2.30	1.23E-03
GOX2699	Hypothetical protein		2.89	1.78E-04
	208 genes with an mRNA ratio ≤0.5			
GOX0035	Hypothetical protein		0.39	4.60E-03
GOX0036	Enoyl-acyl-carrier-protein reductase	*fabL*	0.48	2.41E-02
GOX0053	Hypothetical protein		0.24	2.10E-02
GOX0066	Competence protein ComM		0.35	2.27E-02
GOX0074	Elongation factor Ts	*tsf*	0.40	3.11E-03
GOX0075	Ribosomal protein S2		0.34	4.92E-03
GOX0088	Trigger factor		0.44	3.84E-04
GOX0103	Carboxypeptidase-related protein		0.49	8.83E-03
GOX0116	Fatty acid/phospholipid synthesis protein		0.48	9.45E-03
GOX0126	Flagellar motor protein MotA	*motA*	0.41	3.37E-02
GOX0127	Chemotaxis MotB protein		0.13	3.39E-02
GOX0140	Ribosomal protein L27		0.38	1.16E-03
GOX0160	UDP-N-acetylenolpyruvoylglucosamine reductase		0.46	1.95E-02
GOX0193	Isopropylmalate isomerase, large subunit		0.30	4.74E-03
GOX0194	Ribosomal protein L19	*rplS*	0.38	6.37E-03
GOX0195	tRNA (Guanine-N(1)-)-methyltransferase		0.40	3.25E-03
GOX0196	Ribosomal protein S16	*rpsP*	0.35	6.27E-03
GOX0197	Signal recognition particle protein	*ffh*	0.38	7.30E-03
GOX0246	Hypothetical protein		0.15	1.79E-02
GOX0247	Hypothetical protein		0.47	3.35E-02
GOX0248	Hypothetical protein		0.44	8.34E-03
GOX0254	Putative Fe-S-cluster redox enzyme		0.38	6.64E-03

GOX0272	Hypothetical protein		0.36	2.50E-02
GOX0305	Ribosomal protein S18		0.42	1.28E-02
GOX0306	Ribosomal protein S6		0.36	5.90E-04
GOX0348	HlyD family secretion protein		0.48	4.34E-02
GOX0359	Adenylate kinase	*adk*	0.36	7.95E-03
GOX0360	Preprotein translocase subunit SecY	*secY*	0.37	2.13E-03
GOX0361	Ribosomal protein L15		0.33	3.13E-03
GOX0362	Ribosomal protein L30		0.29	7.76E-03
GOX0363	Ribosomal protein S5		0.29	3.66E-05
GOX0364	Ribosomal protein L18		0.23	8.89E-03
GOX0365	Ribosomal protein L6		0.31	1.63E-03
GOX0366	Ribosomal protein S8		0.31	6.46E-03
GOX0367	Ribosomal protein S14		0.37	9.81E-04
GOX0368	Ribosomal protein L5		0.24	1.00E-02
GOX0369	Ribosomal protein L24		0.22	3.05E-03
GOX0370	Ribosomal protein L14		0.22	6.73E-03
GOX0371	Ribosomal protein S17		0.31	9.17E-03
GOX0372	Ribosomal protein L29		0.32	3.24E-03
GOX0373	Ribosomal protein L16		0.26	6.00E-03
GOX0374	Ribosomal protein S3		0.39	5.13E-04
GOX0375	Ribosomal protein L22		0.37	4.80E-04
GOX0376	Ribosomal protein S19		0.34	2.97E-17
GOX0377	Ribosomal protein L2		0.40	3.77E-03
GOX0378	Ribosomal protein L23		0.40	6.36E-03
GOX0379	Ribosomal protein L4		0.42	2.00E-04
GOX0380	Ribosomal protein L3		0.40	9.82E-03
GOX0381	Ribosomal protein S10		0.34	2.79E-02
GOX0382	Elongation factor Tu	*tuf*	0.45	1.31E-02
GOX0383	Ribosomal protein S7		0.37	1.12E-03
GOX0384	Ribosomal protein S12		0.37	5.08E-03
GOX0385	RNA polymerase. subunit b’	*rpoC*	0.46	2.14E-02
GOX0387	Ribosomal protein L7/L12		0.31	7.17E-04
GOX0388	Ribosomal protein L10		0.33	5.98E-03
GOX0389	Ribosomal protein L1		0.29	1.46E-02
GOX0390	Ribosomal protein L11		0.37	3.38E-04
GOX0403	Hypothetical protein		0.49	5.66E-03
GOX0405	TonB-dependent outer membrane receptor		0.11	5.77E-03
GOX0415	Putative transport protein		0.49	2.44E-02
GOX0420	Flagellar biosynthesis protein A		0.18	2.25E-03
GOX0421	Flagellar motor switch protein		0.05	5.14E-03
GOX0422	Hypothetical protein		0.06	7.08E-05
GOX0423	Flagellar motor switch protein G		0.07	2.79E-03
GOX0424	Flagellar MS-ring protein		0.05	5.29E-03
GOX0425	Basal-body rod modification protein FlgD	*flgD*	0.14	2.36E-02
GOX0426	Hypothetical protein		0.10	2.44E-02
GOX0451	Ribosomal protein S9		0.34	3.38E-03
GOX0452	Ribosomal protein L13		0.38	2.59E-02

GOX0515	Hypothetical protein		0.42	6.22E-03
GOX0560	Diguanylate cyclase		0.39	3.61E-02
GOX0596	Ribosomal protein S1		0.34	1.32E-02
GOX0619	Hypothetical protein		0.34	2.95E-02
GOX0620	Chemotactic signal-response protein CheL	*cheL*	0.24	1.81E-02
GOX0621	Flagellar basal body P-ring protein		0.30	4.35E-02
GOX0693	Hypothetical protein		0.24	3.66E-02
GOX0694	Hypothetical protein		0.15	2.47E-02
GOX0695	Hypothetical protein		0.11	2.38E-02
GOX0696	Flagellar motor switch protein FliM		0.12	1.95E-02
GOX0697	Flagellar FliL protein	*fliL*	0.15	2.16E-02
GOX0699	L-Asparagine permease		0.37	2.72E-02
GOX0758	Porin		0.21	8.51E-03
GOX0766	Methyl-accepting chemotaxis protein		0.28	1.19E-02
GOX0772	Transcriptional regulator		0.47	1.70E-02
GOX0778	Two component sensor histidine kinase		0.42	1.49E-03
GOX0787	Flagellin B		0.06	3.66E-03
GOX0788	Flagellin assembly protein	*mviN*	0.13	1.79E-02
GOX0809	L-Asparaginase II		0.38	2.97E-03
GOX0825	Hypothetical protein		0.24	3.51E-02
GOX0835	Adenine phosphoribosyltransferase		0.49	1.79E-02
GOX0873	Levansucrase		0.48	1.27E-02
GOX0907	TonB-dependent outer membrane receptor		0.45	8.63E-03
GOX0909	Thiol:disulfide interchange protein DsbD	*dsbD*	0.48	8.45E-03
GOX0926	Sulfate adenylyltransferase subunit 1 / adenylylsulfate kinase		0.36	7.12E-03
GOX0927	Sulfate adenylyltransferase subunit 2		0.35	1.85E-03
GOX0928	Phosphoadenosine phosphosulfate reductase		0.28	4.45E-03
GOX0945	TonB-dependent outer membrane receptor		0.08	9.76E-03
GOX0952	Flagellar basal body P-ring biosynthesis protein FlgA	*flgA*	0.29	4.96E-02
GOX0953	Flagellar basal body rod protein FlgG	*flgG*	0.09	1.40E-02
GOX0954	Flagellar basal-body rod protein FlgF	*flgF*	0.11	2.11E-02
GOX0960	Protein with GGDEF and EAL domain		0.41	2.82E-02
GOX1003	Septum formation associated protein (Maf-like protein)		0.48	1.46E-03
GOX1017	TonB-dependent outer membrane receptor		0.17	4.55E-02
GOX1025	Flagellar hook-associated protein FlgL	*flgL*	0.10	1.50E-02
GOX1026	Flagellar hook-associated protein 1 FlgK	*flgK*	0.09	2.95E-02
GOX1027	Flagellar hook protein FlgE	*flgE*	0.07	1.23E-02
GOX1091	Spermidine synthase		0.50	4.35E-02
GOX1114	Vitamin B12-dependent ribonucleotide reductase		0.31	1.22E-03
GOX1141	Ribosomal protein L25		0.35	5.81E-03
GOX1142	Peptidyl-tRNA hydrolase		0.42	1.33E-02
GOX1197	Hypothetical protein		0.43	2.59E-02
GOX1198	Sulfite reductase (ferredoxin)		0.34	1.31E-02
GOX1199	Putative oxidoreductase		0.46	9.24E-03
GOX1208	Hypothetical protein		0.48	1.12E-02
GOX1209	Hypothetical protein		0.14	5.36E-03

GOX1210	Hypothetical protein		0.24	8.67E-03
GOX1211	Phage DNA packaging protein		0.22	1.10E-02
GOX1212	Phage portal protein		0.21	9.21E-03
GOX1213	Phage minor structual protein GP20		0.24	1.52E-02
GOX1214	Hypothetical protein		0.21	9.48E-03
GOX1215	Hypothetical protein		0.21	6.90E-03
GOX1216	Hypothetical protein		0.20	9.86E-03
GOX1217	Hypothetical protein		0.22	1.19E-02
GOX1218	Phage tail sheath protein		0.20	1.20E-02
GOX1219	Hypothetical protein		0.20	1.57E-02
GOX1220	Hypothetical protein		0.22	1.29E-02
GOX1221	Phage-recombinase-like protein		0.20	1.67E-02
GOX1222	Hypothetical protein		0.24	1.82E-02
GOX1223	Hypothetical protein		0.25	2.02E-02
GOX1224	Phage-related baseplate assembly protein		0.28	1.30E-02
GOX1225	Putative phage tail protein		0.20	1.35E-02
GOX1226	Hypothetical protein		0.24	6.60E-03
GOX1227	Hypothetical protein		0.25	1.50E-02
GOX1228	Hypothetical protein		0.24	1.90E-02
GOX1229	Hypothetical protein		0.26	2.30E-02
GOX1231	Gluconate 2-dehydrogenase subunit α	*gndB*	0.50	3.23E-03
GOX1237	Acetylornithine aminotransferase		0.47	5.34E-02
GOX1264	DNA processing chain A		0.48	7.95E-03
GOX1273	Hypothetical protein		0.49	3.11E-02
GOX1286	Hypothetical protein		0.23	1.14E-03
GOX1287	Biopolymer transport ExbB protein		0.32	7.75E-03
GOX1288	Biopolymer transport ExbD protein		0.36	1.75E-02
GOX1289	Biopolymer transport ExbD protein		0.42	1.11E-02
GOX1291	Flagellar basal body L-ring protein		0.19	2.77E-02
GOX1310	F_1F_o-ATP synthase subunit d	*atpH*	0.46	2.27E-03
GOX1317	Ile tRNA		0.31	8.31E-03
GOX1416	Porin B precursur		0.46	3.12E-02
GOX1436	Adenosine deaminase	*tadA*	0.49	1.43E-02
GOX1455	ATP-dependent RNA helicase		0.42	1.98E-02
GOX1523	Flagellar biosynthetic protein FlhB	*flhB*	0.29	4.47E-03
GOX1524	Flagellar biosynthetic protein FliR	*fliR*	0.39	1.89E-02
GOX1525	Flagellar biosynthetic protein FliQ	*fliQ*	0.06	1.98E-02
GOX1526	Flagellar hook-basal body protein FleE	*fleE*	0.06	2.66E-02
GOX1527	Flagellar basal body rod protein FlgC	*flgC*	0.06	1.68E-02
GOX1528	Flagellar basal-body rod protein FlgB	*flgB*	0.05	2.21E-02
GOX1530	Hypothetical protein		0.24	2.27E-02
GOX1531	Flagellar biosynthesis protein FliP	*fliP*	0.46	4.98E-03
GOX1543	Hypothetical protein		0.42	7.74E-03
GOX1549	Methyl-accepting chemotaxis protein		0.27	1.43E-02
GOX1550	Chemotaxis protein CheX	*cheX*	0.27	2.08E-02
GOX1551	Chemotaxis protein CheY	*cheY*	0.21	9.23E-03
GOX1552	Chemotaxis protein CheA	*cheA*	0.20	1.40E-02

GOX1553	Chemotaxis protein CheW	*cheW*	0.31	6.48E-03
GOX1554	Chemotaxis protein CheR	*cheR*	0.22	6.77E-03
GOX1579	Hypothetical protein associated with *nus* operon		0.46	1.87E-03
GOX1582	Translation initiation factor IF-2		0.48	3.45E-03
GOX1585	Ribosomal protein S15		0.49	3.06E-02
GOX1586	Polynucleotide phosphorylase/polyadenylase		0.46	4.24E-03
GOX1587	Putative 2-nitropropane dioxygenase		0.36	1.32E-02
GOX1613	Protein with GGDEF and EAL domain		0.13	2.65E-02
GOX1632	Hypothetical protein		0.15	6.36E-03
GOX1642	Carboxypeptidase-related protein		0.49	1.81E-02
GOX1661	Bacterioferritin comigratory protein		0.47	2.09E-02
GOX1674	Hypothetical protein		0.47	1.43E-02
GOX1693	Cell cycle transcriptional regulator CtrA	*ctrA*	0.11	9.35E-03
GOX1694	Flagellum-specific ATP synthase		0.26	1.63E-02
GOX1695	Hypothetical protein		0.42	8.87E-03
GOX1699	Hypothetical protein		0.24	7.45E-04
GOX1737	Rod shape-determining protein MreB		0.39	4.63E-03
GOX1780	Ribosomal protein S4	*rpsD*	0.34	7.62E-03
GOX1781	Bacterial Peptide Chain Release Factor 3 (RF-3)		0.39	1.36E-02
GOX1804	Hypothetical protein		0.36	1.38E-03
GOX1805	Hypothetical protein		0.36	5.66E-03
GOX1830	Hypothetical protein		0.30	1.73E-02
GOX1836	N-formylmethionylaminoacyl-tRNA deformylase		0.48	8.43E-03
GOX1857	Uncharacterized PQQ-containing dehydrogenase 1		0.06	2.35E-03
GOX1866	PmbA protein		0.47	2.57E-02
GOX1870	Hypothetical protein		0.34	3.69E-02
GOX1873	DNA mismatch repair protein		0.44	2.25E-02
GOX1903	TonB-dependent receptor protein		0.09	7.96E-03
GOX1911	Cytochrome bo_3 ubiquinol oxidase subunit II	*cyoB*	0.00	1.07E-03
GOX1912	Cytochrome bo_3 ubiquinol oxidase subunit I	*cyoA*	0.00	8.68E-04
GOX1913	Cytochrome bo_3 ubiquinol oxidase subunit III	*cyoC*	0.00	5.80E-04
GOX1914	Cytochrome bo_3 ubiquinol oxidase subunit IV	*cyoD*	0.01	3.21E-04
GOX1966	Hypothetical protein		0.39	2.35E-03
GOX2017	Hypothetical protein		0.33	1.81E-03
GOX2028	Hypothetical protein		0.24	5.41E-03
GOX2030	Chaperone protein DnaK	*dnaK*	0.48	2.44E-03
GOX2074	5-Methyltetrahydrofolate-S-homocysteine methyltransferase		0.49	3.09E-02
GOX2130	Hypothetical protein		0.38	2.79E-02
GOX2132	Hypothetical protein		0.28	1.16E-02
GOX2133	Hypothetical protein		0.24	2.84E-03
GOX2205	Hypothetical protein		0.18	1.32E-03
GOX2206	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase		0.17	3.44E-03
GOX2207	Methylenetetrahydrofolate reductase		0.29	6.54E-03
GOX2249	Aspartyl-tRNA synthetase		0.49	3.55E-02
GOX2373	Protein of Rieske non-heme iron oxygenase family, putative ring-hydroxylating dioxygenase		0.14	1.98E-02

GOX2386	Hypothetical protein	0.28	2.37E-02

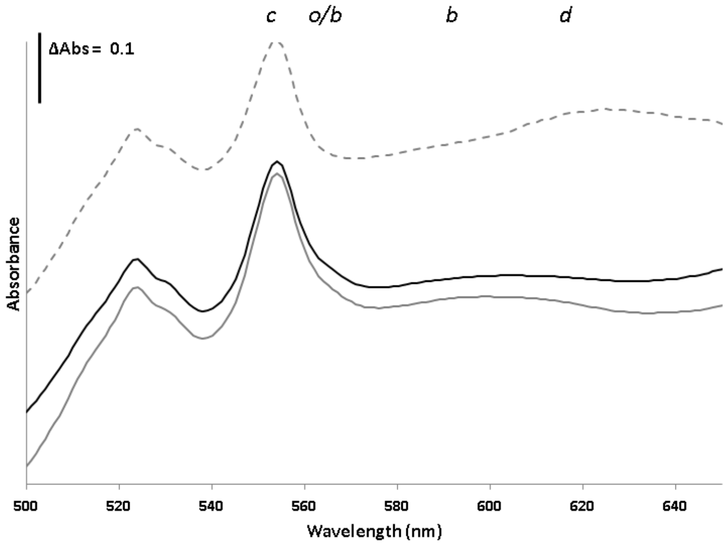

FIG S1 Dithionite-reduced minus ferricyanide-oxidized difference spectra of purified membranes. Spectra were recorded at room temperature using 10 mg ml^{-1} membrane protein each. Black line, *G. oxydans* Δ*upp*; grey line, *G. oxydans* Δ*upp* Δ*cydAB*; grey dashed line, *G. oxydans* Δ*upp* Δ*cyoBACD*. The experiments were conducted in triplicate; one exemplary curve for each strain is shown.

Difference spectroscopy with isolated membranes. For membrane isolation, cells were cultivated in 500 ml mannitol medium in a 2 l baffled shake flask at 30°C and 100 rpm in an Infors shaker (Basel, Switzerland). Cells were harvested after 16 h at an OD$_{600}$ of 2-2.5 (*G. oxydans* Δ*upp* Δ*cyoBACD*) or at an OD$_{600}$ of 3.5-4 (*G. oxydans* Δ*upp* and *G. oxydans* Δ*upp* Δ*cydAB*) by centrifugation for 20 min at 6000 rpm (Beckman Avanti TM J25) and 4°C, washed with 25 ml 100 mM Tris-HCl, 20 mM $MgSO_4$, pH 7.5 and centrifuged for 5 min at 10,414 x *g* and 4°C. The cells were resuspended in 10 ml of 100 mM Tris-HCl with 20 mM $MgSO_4$, pH 7.5, and disrupted by five passages at 207 MPa through a French pressure cell (SLM Aminco). Cell debris was removed by centrifugation at 16,100 x *g* for 30 min at 4°C. The supernatant was used for ultracentrifugation at 229.600 x *g* and 4°C for 60 min. The pellet containing the cytoplasmic membrane fraction was washed in 10 mM Tris-HCl, pH 7.5, and centrifuged again at 229.600 x *g* and 4°C for 60 min. The membranes were resuspended in a small volume of the same buffer. Protein concentration was determined according to Bradford (Bradford 1976 Anal. Biochem. 72: 248-254) using bovine serum albumin as standard. 10 mg ml^{-1} of membrane proteins were used for measurement of dithionite-reduced 'minus' ferricyanide-oxidized difference spectra. Recording was performed at room temperature with a Jasco V560 spectrophotometer using a special silicon photodiode detector as described (Niebisch and Bott 2001 Arch. Microbiol. 175: 282–294) and cuvettes with 5 mm lightpath. The instrument setting was 40 nm min^{-1} scanning velocity, 1 nm band width, and slow response. The reduced spectrum was recorded after addition of $Na_2S_2O_4$, the oxidized spectrum after addition of $K_4[Fe(CN)_6]$.