

Supplementary Table 1 List of genes regulated by OxyR, SoxRS and genes involved in SOS response, of which transcription was significantly changed by H₂O₂ under anaerobic condition (p < 0.05, |Fold change| > 2)

b. No.	Gene	Gene product name	p value [#]	Fold change [§]
OxyR				
b0475	<i>hemH</i>	ferrochelatase	0.005	12.7
b0606	<i>ahpF</i>	alkyl hydroperoxide reductase, F52a subunit, FAD/NAD(P)-binding	0.004	36.7
b0683	<i>fur</i>	DNA-binding transcriptional dual regulator of siderophore biosynthesis and transport	0.041	2.0
b0849	<i>grxA</i>	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)	0.002	99.3
b1679	<i>sufE</i>	sulfur acceptor protein	0.000	112.7
b1680	<i>sufS</i>	selenocysteine lyase, PLP-dependent	0.000	117.3
b1681	<i>sufD</i>	component of SufBCD complex	0.000	249.5
b1682	<i>sufC</i>	component of SufBCD complex, ATP-binding component of ABC superfamily	0.001	256.9
b1683	<i>sufB</i>	component of SufBCD complex	0.001	394.3
b1684	<i>sufA</i>	Fe-S cluster assembly protein	0.002	665.0
b2392	<i>mntH</i>	manganese/divalent cation transporter	0.001	60.1
b2582	<i>trxC</i>	thioredoxin 2	0.002	66.8
b3500	<i>gor</i>	glutathione oxidoreductase	0.002	2.6
b3518	<i>yhjA</i>	predicted cytochrome C peroxidase	0.045	3.7
b3942	<i>katG</i>	catalase/hydroperoxidase HPI(I)	0.021	24.7
SoxRS				
b0462	<i>acrB</i>	multidrug efflux system protein	0.005	2.1
b0683	<i>fur</i>	DNA-binding transcriptional dual regulator of siderophore biosynthesis and transport	0.041	2.0
b0850	<i>ybjC</i>	predicted inner membrane protein	0.010	-2.6
b0851	<i>nfsA</i>	nitroreductase A, NADPH-dependent, FMN-dependent	0.010	-2.8
b0852	<i>rimK</i>	ribosomal protein S6 modification protein	0.016	-3.0
b0853	<i>ybjN</i>	predicted oxidoreductase	0.003	-2.2
b0950	<i>pqiA</i>	paraquat-inducible membrane protein A	0.026	-4.1
b1530	<i>marR</i>	DNA-binding transcriptional repressor of multiple antibiotic resistance	0.008	3.4
b1531	<i>marA</i>	DNA-binding transcriptional dual activator of multiple antibiotic resistance	0.038	3.8
b1532	<i>marB</i>	predicted protein	0.017	3.2
b1611	<i>fumC</i>	fumarate hydratase (fumarase C), aerobic Class II	0.000	81.1
b2159	<i>nfo</i>	endonuclease IV with intrinsic 3'-5' exonuclease activity	0.001	10.5
b2895	<i>fldB</i>	flavodoxin 2	0.019	2.4
b3908	<i>sodA</i>	superoxide dismutase, Mn	0.007	102.5

b3924	<i>fpr</i>	ferredoxin-NADP reductase	0.002	7.3
b4062	<i>soxS</i>	DNA-binding transcriptional dual regulator	0.002	18.2
b4063	<i>soxR</i>	DNA-binding transcriptional dual regulator, Fe-S center for redox-sensing	0.008	10.1
SOS response				
b0060	<i>polB</i>	DNA polymerase II	0.001	7.1
b0231	<i>dinB</i>	DNA polymerase IV	0.007	6.7
b0779	<i>uvrB</i>	excinuclease of nucleotide excision repair, DNA damage recognition component	0.005	8.4
b0799	<i>dinG</i>	ATP-dependent DNA helicase	0.006	2.5
b0958	<i>sulA</i>	SOS cell division inhibitor	0.007	6.1
b1183	<i>umuD</i>		0.033	2.3
b1184	<i>umuC</i>		0.031	2.1
b1728	<i>ydjM</i>	predicted inner membrane protein regulated by LexA	0.001	5.2
b1848	<i>yebG</i>	conserved protein regulated by LexA	0.031	7.1
b1860	<i>ruvB</i>	ATP-dependent DNA helicase, component of RuvABC resolvosome	0.016	2.8
b2009	<i>sbmC</i>	DNA gyrase inhibitor	0.005	2.9
b2616	<i>recN</i>	recombination and repair protein	0.003	12.5
b2699	<i>recA</i>	DNA strand exchange and recombination protein with protease and nuclease activity	0.004	6.8
b3631	<i>rfaG</i>	glucosyltransferase I	0.041	2.4
b3813	<i>uvrD</i>	DNA-dependent ATPase I and helicase II	0.005	2.3
b4058	<i>uvrA</i>	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC	0.009	7.2
b4347	<i>symE</i>	conserved protein	0.001	7.7

Supplementary Table 2 List of genes in “Cellular respiration (GO: 0045333)” with fold changes (FC) by H₂O₂ under aerobic or anaerobic condition

b. No.	Gene	Description	Aerobic FC	Anaerobic FC
b0114	<i>aceE</i>	pyruvate dehydrogenase	1.9	3.2
b0115	<i>aceF</i>	pyruvate dehydrogenase	1.5	3.9
b0116	<i>lpd</i>	lipoamide dehydrogenase	2.1	3.1
b0118	<i>acnB</i>	aconitate hydratase B	3.9	4.3
b0720	<i>glta</i>	citrate synthase	-1.2	6.3
b0824	<i>ybiY</i>	putative pyruvate formate-lyase 2 activating enzyme	-12.6	-2.4
b0851	<i>nfsA</i>	modulator of drug activity A	5.3	-2.9
b0894	<i>dmsA</i>	anaerobic dimethyl sulfoxide reductase subunit A	-4.6	-2.6
b0895	<i>dmsB</i>	anaerobic dimethyl sulfoxide reductase subunit B	-6.3	-2.0
b0972	<i>hyaA</i>	hydrogenase-1 small subunit	-3.9	-2.9
b0973	<i>hyaB</i>	hydrogenase-1 large subunit	-3.5	-2.2
b0974	<i>hyaC</i>	probable Ni/Fe-hydrogenase 1 b-type cytochrome subunit	-2.7	-3.6
b0975	<i>hyaD</i>	processing of HyaA and HyaB proteins	-4.5	-3.3
b0976	<i>hyaE</i>	processing of HyaA and HyaB proteins	-2.6	-3.2
b0977	<i>hyaF</i>	nickel incorporation into hydrogenase-1 proteins	-7.9	-9.7
b0995	<i>torR</i>	response transcriptional regulator for torA	-3.2	2.2
b0996	<i>torC</i>	trimethylamine N-oxide reductase, cytochrome c-type subunit	4.6	1.4
b1109	<i>ndh</i>	respiratory NADH dehydrogenase	3.8	4.6
b1136	<i>icd</i>	isocitrate dehydrogenase, specific for NADP ⁺	-1.4	3.0
b1224	<i>narG</i>	nitrate reductase 1, alpha subunit	-14.5	-4.3
b1225	<i>narH</i>	nitrate reductase 1, beta subunit	-17.9	-3.3
b1226	<i>narJ</i>	nitrate reductase 1, delta subunit, assembly function	-3.2	-1.5
b1227	<i>narI</i>	nitrate reductase 1, cytochrome b	-6.0	-1.4
b1276	<i>acnA</i>	aconitate hydratase 1	-1.8	23.6
		transcriptional regulation of aerobic, anaerobic respiration, osmotic		
b1334	<i>fnr</i>	balance	3.0	3.4
b1468	<i>narZ</i>	cryptic nitrate reductase 2, alpha subunit	-6.6	-2.5
b1474	<i>fdnG</i>	formate dehydrogenase-N, nitrate-inducible, alpha subunit	1.1	-1.0
b1475	<i>fdnH</i>	formate dehydrogenase-N, nitrate-inducible, iron-sulfur beta subunit	-2.8	1.5
b1476	<i>fdnI</i>	formate dehydrogenase-N, nitrate-inducible, cytochrome B556	-1.1	1.6
b1478	<i>adhP</i>	alcohol dehydrogenase	2.8	-1.7
b1590	<i>ynfH</i>	putative DMSO reductase anchor subunit	-2.8	1.1
b1611	<i>fumC</i>	fumarase C= fumarate hydratase Class II; isozyme	1.2	100.1
b1676	<i>pykF</i>	pyruvate kinase I	2.0	-3.2
b2202	<i>napC</i>	cytochrome c-type protein	-6.0	-1.9
b2203	<i>napB</i>	cytochrome c-type protein	-4.0	-2.6
b2204	<i>napH</i>	ferredoxin-type protein: electron transfer	-9.2	-3.0
b2206	<i>napA</i>	probable nitrate reductase 3	-5.1	-2.0
b2207	<i>napD</i>	orf, hypothetical protein	-3.2	-13.4

b2208	<i>napF</i>	ferredoxin-type protein: electron transfer	-20.4	-5.2
b2242	<i>glpB</i>	sn-glycerol-3-phosphate dehydrogenase	1.6	2.1
b2260	<i>menE</i>	o-succinylbenzoate-CoA ligase	-2.3	-1.7
b2264	<i>menD</i>	2-oxoglutarate decarboxylase; SHCHC synthase	-4.4	-3.6
b2265	<i>menF</i>	isochorismate hydroxymutase 2, menaquinone biosynthesis	-2.7	-5.4
b2281	<i>nuoI</i>	NADH dehydrogenase I chain I	-4.4	-1.4
b2285	<i>nuoE</i>	NADH dehydrogenase I chain E	-2.7	-2.5
b2287	<i>nuoB</i>	NADH dehydrogenase I chain B	-2.8	-4.9
b2469	<i>narQ</i>	sensor for nitrate reductase system, protein histidine kinase	-3.0	1.4
b2486	<i>hyfF</i>	hydrogenase 4 membrane subunit	-7.6	1.4
b2489	<i>hyfI</i>	hydrogenase 4 Fe-S subunit	-7.2	-1.2
b2712	<i>hypF</i>	transcriptional regulatory protein	-3.8	-2.0
b2713	<i>hydN</i>	involved in electron transport from formate to hydrogen, Fe-S centers	-3.3	-1.5
b2726	<i>hypA</i>	pleiotrophic effects on 3 hydrogenase isozymes	-5.6	1.5
b2728	<i>hypC</i>	pleiotrophic effects on 3 hydrogenase isozymes	-8.5	-6.1
b2729	<i>hypD</i>	pleiotrophic effects on 3 hydrogenase isozymes	-3.8	-4.0
		hydrogenase-2 operon protein: may effect maturation of large subunit of		
b2990	<i>hybG</i>	hydrogenase-2	-3.5	-1.5
b2993	<i>hybD</i>	probable processing element for hydrogenase-2	-2.0	-1.1
b2994	<i>hybC</i>	probable large subunit, hydrogenase-2	1.3	-1.4
b2995	<i>hybB</i>	probable cytochrome Ni/Fe component of hydrogenase-2	-4.0	-2.4
b2997	<i>hybO</i>	putative hydrogenase subunit	-17.5	-4.2
b3236	<i>mdh</i>	malate dehydrogenase	-2.3	2.1
b3365	<i>nirB</i>	nitrite reductase	-5.1	-4.3
b3366	<i>nirD</i>	nitrite reductase	-4.0	-4.4
b3453	<i>ugpB</i>	sn-glycerol 3-phosphate transport system; periplasmic binding protein	-1.6	3.5
b3479	<i>nikD</i>	ATP-binding protein of nickel transport system	-7.7	-2.5
b3605	<i>lldD</i>	L-lactate dehydrogenase	-1.4	3.7
b3892	<i>fdoI</i>	formate dehydrogenase, cytochrome B556	1.8	7.2
b3893	<i>fdoH</i>	formate dehydrogenase-O, iron-sulfur subunit	-1.3	9.3
b3894	<i>fdoG</i>	formate dehydrogenase-O, major subunit	2.2	8.9
b3930	<i>menA</i>	1,4-dihydroxy-2-naphthoate --> dimethylmenaquinone	-1.6	-1.5
b4070	<i>nrFA</i>	periplasmic cytochrome c	-24.6	-6.7
b4071	<i>nrFB</i>	formate-dependent nitrite reductase; a penta-haeme cytochrome c	-25.0	-5.6
b4072	<i>nrFC</i>	formate-dependent nitrite reductase; Fe-S centers	-8.7	-5.6
b4076	<i>nrFG</i>	part of formate-dependent nitrite reductase complex	-6.2	-5.1
b4125	<i>dcuS</i>	putative 2-component sensor protein	-2.2	2.5
b4151	<i>frdD</i>	fumarate reductase, anaerobic, membrane anchor polypeptide	-2.4	1.2
b4152	<i>frdC</i>	fumarate reductase, anaerobic, membrane anchor polypeptide	-1.7	1.1
b4153	<i>frdB</i>	fumarate reductase, anaerobic, iron-sulfur protein subunit	-4.2	-1.1
b4154	<i>frdA</i>	fumarate reductase, anaerobic, flavoprotein subunit	-3.6	-1.2
b4379	<i>yjjW</i>	putative activating enzyme	-11.9	-2.0