Table S2. Genes whose expression is most affected by the overexpression of CpxR.

ORF	Gene	Description	A[a]	SD
HD1109		putative oxalate/formate antiporter	3.90	0.25
HD0281	*fimA*	possible fimbrial major pilin protein	3.62	0.41
HD0282	*fimB*	possible fimbrial structural subunit	3.16	0.41
HD1640		hypothetical protein	3.06	0.34
HD0283	*fimC*	probable fimbrial outer membrane usher protein	2.80	0.41
HD0262	*argR*	arginine repressor	2.46	0.32
HD0261		conserved hypothetical protein	2.45	0.35
HD0284	*fimD*	probable periplasmic fimbrial chaperone	2.27	0.31
HD1815		putative sulfite reductase	2.27	0.25
HD0025	*dcuB1*	anaerobic C4-dicarboxylate transporter	2.24	0.30
HD0811	*artP*	arginine ABC transporter, ATP-binding protein	2.16	0.67
HD1325		conserved hypothetical protein	2.13	0.23
HD1512		acriflavine resistance protein	2.12	0.41
HD0564	*aspA*	aspartate ammonia-lyase	2.11	0.33
HD2016	*dacA*	penicillin-binding protein 5	2.02	0.28
HD0614	*kefB*	glutathione-regulated potassium-efflux system protein	2.00	0.19
HD1814		probable transport protein	1.89	0.17
HD0285		possible minor fimbrial subunit	1.86	0.17
HD0097		conserved hypothetical protein	1.72	0.18
HD2017		possible rare lipoprotein A	1.72	0.23
HD1282	*fhs*	putative formate--tetrahydrofolate ligase	1.71	0.14
HD0351	*prfC*	peptide chain release factor 3	1.65	0.23
HD0189	*dnaK*	chaperone protein DnaK	1.61	0.20
HD2012	*lipA*	lipoic acid synthetase	1.60	0.38
HD0286		hypothetical protein	1.60	0.33
HD0812	*artI*	arginine ABC transporter, periplasmic-binding protein	1.60	0.31
HD1084		HesB family protein	1.59	0.29
HD1161	*ribD*	riboflavin-specific deaminase	1.58	0.31
HD0338		hypothetical protein	1.57	0.21
HD2015		conserved hypothetical protein	1.57	0.23
HD1163	*ribAB*	riboflavin biosynthesis protein RibA	1.56	0.30
HD0266	*lpp*	15kd outer membrane lipoprotein	1.55	0.24
HD0565	*clpB*	ATP-dependant Clp protease chain B	1.51	0.18
HD0287		hypothetical protein	1.51	0.19
HD0337	*rluB*	probable pseudouridylate synthase	1.49	0.22
HD0876		conserved probable ribonuclease	1.46	0.20
HD0096		hypothetical protein	1.46	0.27
HD1142	*sdaA*	L-serine dehydratase	1.44	0.28
HD1513		putative RND efflux membrane fusion protein	1.44	0.34
HD2013	*lipB*	lipoate-protein ligase B	1.43	0.27

HD0098		hypothetical protein	1.42	0.23
HD0767	*manY*	mannose-specific phosphotransferase system IIC component	1.41	0.26
HD0766	*manZ*	mannose-specific phosphotransferase system IID component	1.40	0.25
HD0988	*prlC*	oligopeptidase A	1.39	0.19
HD0765	*manA*	mannose-6-phosphate isomerase	1.39	0.33
HD1343		hypothetical protein	1.38	0.30
HD2014		hypothetical protein	1.32	0.24
HD1076	*recB*	exodeoxyribonuclease V, beta subunit	1.31	0.17
HD0738	*crp*	cyclic AMP receptor protein	1.31	0.18
HD1165	*ribH*	6,7-dimethyl-8-ribityllumazine synthase	1.28	0.25
HD1400		putative soluble lytic murein transglycosylase	1.27	0.19
HD1354		conserved hypothetical protein	1.27	0.26
HD1654		conserved hypothetical protein	1.26	0.23
HD0090	*ner*	possible DNA-binding protein	1.24	0.26
HD1786	*mutT*	mutator MutT protein	1.22	0.16
HD0400	*rnfD*	putative Na-translocating NADH-quinone reductase	1.21	0.25
HD1994	*selA*	L-seryl-tRNA (Sec) selenium transferase	1.21	0.23
HD0313	*dppC*	dipeptide transport system permease protein	1.20	0.23
HD1073	*grpE*	heat shock protein GrpE	1.20	0.25
HD0108		hypothetical protein	1.20	0.14
HD0889	*deoD*	purine nucleoside phosphorylase	1.19	0.24
HD1202	*WaaQ*	ADP-heptose--lipooligosaccharide heptosyltransferase III	1.18	0.25
HD0264	*mdh*	malate dehydrogenase	1.17	0.21
HD1817	*yfeB*	iron (chelated) transporter, ATP-binding protein	1.15	0.31
HD1655		conserved hypothetical protein	1.14	0.35
HD1075	*norM*	multidrug resistance protein NorM	1.14	0.22
HD0472	*lgtB*	lipooligosaccharide galactosyltransferase II	1.13	0.24
HD0188	*dnaJ*	chaperone protein DnaJ	1.13	0.25
HD1143	*sdaC*	serine transporter	1.12	0.27
HD1088	*fdx2*	ferredoxin	1.11	0.28
HD1146	*glpF*	glycerol uptake facilitator protein	1.11	0.33
HD1089		conserved hypothetical protein	1.09	0.27
HD0783	*oadA*	oxaloacetate decarboxylase alpha chain	1.09	0.20
HD1784	*groEL*	60 kDa chaperonin	1.09	0.21
HD0404	*lpxM*	lipid A acyltransferase	1.09	0.22
HD0177	*trpS*	tryptophanyl-tRNA synthetase	1.08	0.13
HD1507	*manB*	probable phosphomannomutase	1.08	0.23
HD0403	*rnfE*	probable Na-translocating NADH-quinone reductase	1.07	0.21
HD2006	*hslV*	ATP-dependent protease HslV	1.06	0.23
HD1074	*potD2*	spermidine/putrescine-binding periplasmic protein	1.06	0.19
HD0181	*fabA*	3-hydroxydecanoyl-(acyl-carrier protein) dehydratase	1.05	0.25
HD0768	*manX*	mannose-specific phosphotransferase IIAB component	1.05	0.22
HD1011		hypothetical protein	1.05	0.25

HD1254		putative Na/dicarboxylate symporter	1.04	0.15
HD0095		Mu phage DNA transposition protein B	1.04	0.25
HD0816	*lpxC*	UDP-3-O-acyl-GlcNAc deacetylase	1.03	0.25
HD1205		conserved hypothetical protein	1.03	0.21
HD2007	*hslU*	ATP-dependent hsl protease ATP-binding subunit HslU	1.01	0.24
HD0176	*gph*	phosphoglycolate phosphatase	1.01	0.23
HD1853	*menD*	menaquinone biosynthesis protein	1.01	0.23
HD1355		conserved hypothetical protein	1.00	0.25
HD1766	*moeB*	molybdopterin biosynthesis protein MoeB	0.99	0.24
HD1087	*hscA*	chaperone protein HscA	0.99	0.25
HD0687	*rmlB*	dTDP-D-glucose 4,6-dehydratase	0.97	0.17
HD0470		conserved putative lipoprotein	0.97	0.23
HD1511	*glmU*	bifunctional GlmU protein	0.96	0.23
HD0697		thioredoxin-like protein	0.95	0.27
HD1085	*hscB*	chaperone protein HscB	0.94	0.24
HD0419		conserved putative sodium-dependent transporter	0.94	0.16
HD0475	*recQ*	ATP-dependent DNA helicase	0.94	0.20
HD1086		conserved hypothetical protein	0.94	0.26
HD0725		conserved hypothetical protein	0.93	0.26
HD1353	*ihfB*	integration host factor, beta subunit	0.93	0.21
HD1083	*iscU*	NifU protein homolog	0.92	0.21
HD1180	*surA*	survival protein SurA homolog	0.92	0.23
HD1160	*glpC*	anaerobic glycerol-3-phosphate dehydrogenase, subunit C	0.89	0.23
HD0989	*pflA*	pyruvate formate-lyase activating enzyme	0.89	0.22
HD1007	*bioB*	biotin synthetase	0.89	0.24
HD1471		conserved hypothetical protein	0.87	0.24
HD1706		conserved hypothetical protein	0.87	0.23
HD0001	*gidA*	glucose inhibited division protein A	0.86	0.23
HD1747		hypothetical protein	0.86	0.25
HD0835		putative transport protein	0.85	0.23
HD0892	*argD*	acetylornithine aminotransferase	0.85	0.19
HD1810	*trxA*	thioredoxin	0.84	0.25
HD0408	*pabB*	p-aminobenzoate synthase component I	0.82	0.21
HD0174	*lgt*	prolipoprotein diacylglyceryl transferase	0.81	0.21
HD1854		conserved hypothetical protein	0.81	0.20
HD1824	*modB*	molybdenum ABC transporter, permease protein	0.81	0.20
HD1256	*rec2*	recombination protein 2	0.80	0.17
HD1540		hypothetical protein	0.80	0.21
HD1286	*uvrA*	excinuclease ABC subunit A	0.79	0.23
HD1173	*rseA*	possible sigma-E factor negative regulatory protein	0.79	0.24
HD0723	*trmA*	tRNA (uracil-5-)-methyltransferase	0.79	0.32
HD0300	*grxA*	glutaredoxin	0.79	0.24
HD0890	*argC*	N-acetyl-gamma-glutamyl-phosphate reductase	0.78	0.17

HD1705		putative coproporphyrinogen III oxidase	0.77	0.22
HD0647		conserved hypothetical protein	0.77	0.22
HD0706		conserved hypothetical protein	0.73	0.19
HD1820		putative ABC transporter, ATP-binding protein	0.71	0.17
HD0545	*lexA*	probable LexA repressor	0.70	0.20
HD1825		hypothetical protein	0.70	0.20
HD0040	*yidC*	60 kD inner-membrane protein	0.69	0.22
HD1992	*sun*	SUN protein	0.69	0.17
HD0372	*ansB*	L-asparaginase II	0.68	0.22
HD1753	*secF*	protein-export membrane protein SecF	0.68	0.22
HD1296		conserved hypothetical protein	0.67	0.18
HD0615	*nfrE*	cytochrome c-type biogenesis protein	0.64	0.22
HD0544	*mutH*	DNA mismatch repair protein	0.63	0.24
HD0054	*tufA*	elongation factor tu, EF-Tu	0.60	0.23
HD0034	*frdD*	fumarate reductase, 13 kD hydrophobic protein	0.58	0.17
HD0891	*argB*	acetylglutamate kinase	0.58	0.20
HD1247	*maeA*	malate oxidoreductase (NAD)	0.57	0.20
HD0838	*zwf*	glucose-6-phosphate 1-dehydrogenase	0.51	0.18
HD1767	*moeA*	molybdopterin biosynthesis protein MoeA	0.51	0.16
HD1826	*modC*	molybdenum ABC transporter, ATP-binding protein	0.48	0.17
HD1991	*trkA*	TRK system potassium uptake protein	0.46	0.17
HD1186	*dxr*	1-deoxy-D-xylulose 5-phosphate reductoisomerase	0.45	0.15
HD1417		hypothetical protein	0.43	0.19
HD0688	*rmlA*	glucose-1-phosphate thymidyltransferase	0.42	0.13
HD0815	*recN*	DNA repair protein	0.40	0.18

HD0436	*thiL*	thiamin-monophosphate kinase	-0.48	0.18
HD1911	*asnC*	transcription regulatory protein, AsnC	-0.60	0.18
HD1014		hypothetical protein	-0.61	0.16
HD0435	*nusB*	transcription termination factor	-0.61	0.18
HD1780		hypothetical protein	-0.63	0.19
HD0365		conserved hypothetical protein	-0.66	0.15
HD0575	*prfB*	peptide chain release factor 2	-0.68	0.16
HD0455		putative protease	-0.74	0.18
HD1625	*aceE*	2-oxoglutarate dehydrogenase	-0.79	0.18
HD0010	*atpD*	ATP synthase beta chain	-0.80	0.21
HD1809	*hflK*	HflK protein	-0.80	0.18
HD0081	*murB*	UDP-N-acetylenolpyruvoylglucosamine reductase	-0.84	0.19
HD0257		conserved hypothetical protein	-0.84	0.20
HD1892		conserved hypothetical protein	-0.85	0.24
HD0426	*mrcA*	penicillin-binding protein 1A	-0.86	0.20
HD1271	*menE*	O-succinylbenzoic acid--CoA ligase	-0.87	0.19
HD0008	*atpA*	ATP synthase alpha chain	-0.87	0.20

HD1779		hypothetical protein	-0.91	0.19
HD0874	*ndh*	NADH dehydrogenase	-0.92	0.18
HD0258		probable permease	-0.93	0.26
HD1219		conserved hypothetical protein	-0.94	0.22
HD1893		hypothetical protein	-0.95	0.15
HD0580	*hlp*	lipoprotein Hlp	-0.96	0.18
HD1016		hypothetical protein	-0.96	0.18
HD1902		conserved hypothetical protein	-0.97	0.15
HD0750	*glnA*	glutamine synthetase	-0.97	0.22
HD1015		hypothetical protein	-0.98	0.19
HD1642		possible integral membrane protein of DedA family	-0.99	0.25
HD1060		hypothetical protein	-1.01	0.14
HD0449	*fis*	DNA-binding protein	-1.02	0.19
HD1759	*pryE*	orotate phosphoribosyltransferase	-1.03	0.13
HD1104	*truA*	tRNA pseudouridine synthase A	-1.04	0.19
HD1662	*pntB*	NAD(P) transhydrogenase, beta subunit	-1.04	0.21
HD1999	*ffh*	signal recognition particle protein	-1.04	0.18
HD0066		hypothetical protein	-1.05	0.21
HD1372	*dnaB2*	replicative DNA helicase	-1.06	0.19
HD1896		conserved hypothetical protein	-1.06	0.22
HD1485	*frxA*	NAD(P)H nitroreductase	-1.06	0.20
HD0004	*atpB*	ATP synthase A chain	-1.06	0.24
HD0009	*atpG*	ATP synthase gamma chain	-1.07	0.23
HD1371		conserved hypothetical protein	-1.07	0.24
HD1118	*folA*	dihydrofolate reductase	-1.08	0.22
HD0201	*mrsA*	phosphoglucosamine mutase	-1.09	0.23
HD0821	*ddlB*	D-alanine-D-alanine ligase B	-1.10	0.14
HD1103	*folE*	GTP cyclohydrolase I	-1.10	0.19
HD1291	*gapA*	glyceraldehyde 3-phosphate dehydrogenase	-1.10	0.26
HD0007	*atpH*	ATP synthase delta chain	-1.10	0.21
HD1379		conserved hypothetical protein	-1.10	0.19
HD1017		hypothetical protein	-1.13	0.27
HD0005	*atpE*	ATP synthase C chain	-1.13	0.19
HD0440	*suhB*	inositol-1-monophosphatase	-1.15	0.15
HD1727	*fadR*	fatty acid metabolism regulator protein	-1.15	0.19
HD0006	*atpF*	ATP synthase B chain	-1.15	0.21
HD0448		putative dehydrogenase	-1.15	0.25
HD1468	*mazG*	MazG protein	-1.16	0.23
HD1728	*nhaB*	Na+/H+ antiporter protein	-1.16	0.23
HD1737	*ppiD*	peptidyl-prolyl cis-trans isomerase D	-1.16	0.20
HD1020		glyoxalase II family protein	-1.18	0.18
HD0668		hypothetical protein	-1.18	0.23
HD0194	*rne*	ribonuclease E	-1.19	0.21

HD1327	*hhdA*	hemolysin	-1.20	0.11
HD0441	*dxs*	1-deoxyxylulose-5-phosphate synthase	-1.20	0.15
HD1411	*asnS*	asparaginyl-tRNA synthetase	-1.20	0.23
HD1663	*pntA*	NAD(P) transhydrogenase, alpha subunit	-1.20	0.19
HD1857	*sgaH*	probable hexulose-6-phosphate synthase	-1.21	0.21
HD1369		conserved hypothetical protein	-1.22	0.18
HD0865	*pgk*	phosphoglycerate kinase	-1.24	0.18
HD0042		conserved hypothetical protein	-1.26	0.16
HD0669	*valS*	valyl-tRNA synthetase	-1.26	0.19
HD1782	*cydA*	cytochrome D ubiquinol oxidase, subunit I	-1.27	0.21
HD2025	*hgbA*	hemoglobin-binding protein HgbA	-1.27	0.28
HD0581	*HlpB*	lipoprotein HlpB	-1.30	0.18
HD1220	*ykgF*	putative iron-sulfur electron transport protein	-1.30	0.19
HD1913	*asnA*	asparagine synthetase A	-1.30	0.27
HD1859		PTS system Enzyme II-A permease component	-1.32	0.18
HD0997		hypothetical protein	-1.34	0.33
HD1115	*nth*	endonuclease III, DNA (apurinic or apyrimidinic site) lyase	-1.35	0.21
HD1456	*ackA*	acetate kinase	-1.37	0.21
HD0824	*murG*	UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	-1.38	0.21
HD0076	*napG*	ferredoxin-type protein NapG	-1.39	0.18
HD0003		conserved hypothetical protein	-1.39	0.27
HD1428	*uspA*	universal stress protein A	-1.41	0.19
HD0848	*sodC*	superoxide dismutase [Cu-Zn]	-1.42	0.25
HD1735		putative oligopeptide transporter, periplasmic-binding protein	-1.42	0.20
HD0770		conserved hypothetical protein	-1.42	0.21
HD0646		conserved hypothetical protein	-1.46	0.18
HD1489		hypothetical protein	-1.47	0.22
HD1641	*purR*	purine nucleotide synthesis repressor	-1.49	0.20
HD1221	*ykgE*	conserved putative dehydrogenase subunit	-1.51	0.16
HD0074	*napA*	periplasmic nitrate reductase	-1.52	0.18
HD0667	*holC*	DNA polymerase III chi subunit	-1.52	0.27
HD0613	*cyaA*	adenylate cyclase	-1.56	0.19
HD1290	*msrB*	peptide methionine sulfoxide reductase MsrB	-1.57	0.31
HD1409		conserved hypothetical protein	-1.59	0.21
HD1494	*rplM*	50S ribosomal protein L13	-1.60	0.20
HD0349	*nrfC*	nitrate reductase, Fe-S protein	-1.60	0.36
HD1299	*tadF*	tight adherence protein F	-1.62	0.16
HD1493	*rpsI*	30S ribosomal protein S9	-1.66	0.25
HD1480	*bioD1*	probable dethiobiotin synthetase	-1.66	0.30
HD1986	*fumC*	fumarate hydratase class II	-1.68	0.22
HD1666		probable phosphatase	-1.68	0.24
HD1253	*dgkA*	diacylglycerol kinase	-1.68	0.32

HD1298	*tadG*	tight adherence protein G	-1.69	0.16
HD1860	*sgaT*	putative PTS system Enzyme II sga subunit	-1.70	0.27
HD1301	*tadD*	tight adherence protein D	-1.75	0.12
HD1300	*tadE*	tight adherence protein E	-1.78	0.22
HD1304	*tadA*	tight adherence protein A	-1.80	0.19
HD1755	*ftnB*	ferritin-like protein 2	-1.80	0.26
HD1303	*tadB*	tight adherence protein B	-1.80	0.21
HD1387		conserved hypothetical protein	-1.83	0.16
HD1667	*bcp*	bacterioferritin comigratory protein	-1.83	0.25
HD1754	*ftnA*	ferritin-like protein 1	-1.84	0.25
HD1030	*cysB*	*cys* regulon transcriptional activator	-1.87	0.22
HD1305		*flp* operon protein D	-1.88	0.17
HD1504	*guaA*	GMP synthase [glutamine-hydrolyzing]	-1.92	0.25
HD0347	*nrfB*	nitrate reductase, cytochrome-C type protein	-1.94	0.32
HD1280		possible serine protease homolog	-1.94	0.29
HD0073	*napD*	possible NapD protein	-1.98	0.15
HD0577	*selD*	selenide, water dikinase	-1.99	0.16
HD0072	*napF*	ferredoxin-type protein NapF	-2.01	0.19
HD1389	*moaE*	molybdopterin converting factor subunit 2	-2.03	0.15
HD1407	*efp*	elongation factor P	-2.03	0.15
HD1018	*macA*	probable macrolide-specific efflux protein	-2.05	0.20
HD0344	*nrfA*	nitrate reductase, cytochrome c552	-2.11	0.33
HD1306	*rcpB*	rough colony protein B	-2.16	0.20
HD1150	*glpT*	glycerol 3-phosphate transporter	-2.18	0.20
HD1394	*torZ*	trimethylamine-N-oxide reductase 2	-2.20	0.16
HD1302	*tadC*	tight adherence protein C	-2.20	0.14
HD1029		putative haloacid dehalogenase-like hydrolase	-2.25	0.20
HD1307	*rcpA*	rough colony protein A	-2.26	0.16
HD0998	*uraA*	uracil permease	-2.27	0.42
HD0202	*slyD*	FkbP-type peptidyl-prolyl cis-trans isomerase	-2.31	0.14
HD1985		possible DNA transformation protein	-2.31	0.44
HD1308		*flp* operon protein C	-2.37	0.17
HD1390	*moaD*	molybdopterin converting factor subunit 1	-2.41	0.17
HD1503	*guaB*	inosine-5-monophosphate dehydrogenase	-2.43	0.17
HD1028	*gcvA*	glycine cleavage system transcriptional activator	-2.47	0.27
HD1312	*flp1*	*flp* operon protein Flp1	-2.51	0.28
HD1078	*ompP1*	outer membrane protein P1	-2.56	0.18
HD1856		hypothetical protein	-2.58	0.29
HD1151		hypothetical protein	-2.60	0.26
HD1900	*fkpA*	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA	-2.61	0.15
HD1393	*torY*	cytochrome c-type protein TorY	-2.68	0.18
HD0233	*carB*	carbamoyl-phosphate synthase, large subunit	-2.72	0.50
HD0589		conserved hypothetical protein	-2.90	0.26

HD1432		conserved hypothetical protein	-2.91	0.28
HD1278		possible serine protease	-2.92	0.26
HD1156	*lspA2*	large supernatant protein 2	-2.95	0.20
HD1309		*flp* operon protein B	-2.95	0.22
HD0084	*lldD*	L-lactate dehydrogenase	-2.98	0.31
HD0590		conserved hypothetical protein	-2.99	0.21
HD0805		conserved hypothetical protein	-3.04	0.31
HD0235	*carA*	carbamoyl-phosphate synthase, small subunit	-3.21	0.52
HD0047		hypothetical protein not likely	-3.31	0.43
HD0048		hypothetical protein	-3.34	0.36
HD0591		conserved hypothetical protein	-3.37	0.16
HD1310	*flp3*	*flp* operon protein Flp3	-3.37	0.39
HD1433	*ompP2A*	outer membrane protein P2 homolog	-3.49	0.43
HD1920		hypothetical protein	-3.51	0.25
HD1311	*flp2*	*flp* operon protein Flp2	-3.66	0.35
HD0896	*cysK*	cysteine synthase	-3.92	0.23
HD0769	*dsrA*	serum resistance protein DrsA	-4.38	0.32
HD0046	*ompA2*	major outer membrane protein homolog, OmpA2	-5.72	0.21

[a] Median $\log_2$ ratio of expression comparing 35000HPΔ*cpxR*(pML125) to 35000HPΔ*cpxR*(pLS88) from three independent experiments ($p < 0.05$).