Table S1. Genes whose expression is most affected by the constitutive phosphorylation of CpxR.

ORF	Gene	Description	A[a]	SD
HD0281	*fimA*	possible fimbrial major pilin protein	3.47	1.05
HD0282	*fimB*	possible fimbrial structural subunit	3.01	0.32
HD0283	*fimC*	probable fimbrial outer membrane usher protein	2.55	0.54
HD1109		putative oxalate/formate antiporter	2.41	0.06
HD1435	*ompP2B*	outer membrane protein P2 homolog	2.30	0.15
HD0284	*fimD*	probable periplasmic fimbrial chaperone	2.29	0.08
HD1512		acriflavine resistance protein	2.20	0.14
HD1163	*ribAB*	riboflavin biosynthesis protein ribA	2.19	0.52
HD1590	*deaD*	cold-shock DEAD box protein-A	2.13	0.15
HD1591		conserved hypothetical protein	2.09	0.26
HD1343		hypothetical protein	1.90	0.15
HD1434		hypothetical protein	1.90	0.10
HD0386	*apbE*	thiamine biosynthesis lipoprotein	1.88	0.05
HD1165	*ribH*	6,7-dimethyl-8-ribityllumazine synthase	1.82	0.14
HD1162	*ribE*	riboflavin synthase, alpha chain	1.78	0.13
HD0312	*dppB*	dipeptide transport system permease protein	1.74	0.17
HD1161	*ribD*	riboflavin-specific deaminase	1.73	0.20
HD1621		conserved hypothetical protein	1.71	0.19
HD1513		putative RND efflux membrane fusion protein	1.69	0.15
HD1629	*lolB*	outer membrane lipoprotein LolB	1.67	0.15
HD0313	*dppC*	dipeptide transport system permease protein	1.66	0.16
HD1084		hesB family protein	1.66	0.12
HD1622		conserved hypothetical protein	1.66	0.25
HD1142	*sdaA*	L-serine dehydratase	1.65	0.54
HD0765	*manA*	mannose-6-phosphate isomerase	1.62	0.05
HD0286		hypothetical protein	1.62	0.16
HD0812	*artI*	arginine ABC transporter, periplasmic-binding protein	1.61	0.21
HD0792	*ccmF*	cytochrome c-type biogenesis protein	1.57	0.17
HD0287		hypothetical protein	1.57	0.15
HD1179	*ksgA*	dimethyladenosine transferase	1.56	0.57
HD1640		hypothetical protein	1.54	0.57
HD1511	*glmU*	bifunctional GlmU protein	1.50	0.08
HD0352		hypothetical protein	1.50	0.13
HD0634	*accB*	probable biotin carboxyl carrier protein of acetyl-CoA carboxylase	1.48	0.17
HD0635	*accC*	biotin carboxylase	1.46	0.11
HD0382	*nqrD*	Na+-translocating NADH-ubiquinone oxidoreductase, subunit D	1.42	0.05
HD0383	*nqrE*	Na+-translocating NADH-ubiquinone oxidoreductase, subunit E	1.42	0.05
HD0351	*prfC*	peptide chain release factor 3	1.42	0.16
HD0381	*nqrC*	Na+-translocating NADH-ubiquinone oxidoreductase, subunit C	1.41	0.07

HD0994	*potD1*	spermidine/putrescine-binding periplasmic protein	1.41	0.45
HD0384	*nqrF*	Na+-translocating NADH-ubiquinone oxidoreductase, subunit F	1.40	0.10
HD0195		hypothetical protein	1.39	0.09
HD1007	*bioB*	biotin synthetase	1.39	0.12
HD1628	*ispE*	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	1.38	0.08
HD0564	*aspA*	aspartate ammonia-lyase	1.37	0.05
HD2012	*lipA*	lipoic acid synthetase	1.36	0.20
HD1354		conserved hypothetical protein	1.36	0.10
HD0766	*manZ*	mannose-specific phosphotransferase system IID component	1.32	0.08
HD1010	*prc*	tail-specific protease	1.31	0.21
HD1146	*glpF*	glycerol uptake facilitator protein	1.30	0.06
HD1974	*rpsQ*	30S ribosomal protein S17	1.29	0.18
HD2017		possible rare lipoprotein A	1.29	0.06
HD0380	*nqrB*	NADH dehydrogenase	1.29	0.08
HD0315	*dppD*	dipeptide transport ATP-binding protein	1.28	0.09
HD2016	*dacA*	penicillin-binding protein 5	1.27	0.08
HD1355		conserved hypothetical protein	1.26	0.05
HD1342	*recJ*	single-stranded-DNA-specific exonuclease RecJ	1.25	0.04
HD0648	*tnaB*	tryptophan-specific transport protein	1.24	0.09
HD0767	*manY*	mannose-specific phosphotransferase system IIC component	1.23	0.08
HD1806	*thiI*	thiamine biosynthesis protein ThiI	1.23	0.15
HD1357		conserved possible translation initiation factor	1.22	0.05
HD1876	*rpoC*	RNA polymerase beta subunit	1.22	0.11
HD1086		conserved hypothetical protein	1.20	0.07
HD0404	*lpxM*	lipid A acyltransferase	1.20	0.13
HD1712	*ispZ*	probable intracellular septation protein	1.20	0.05
HD1975	*rpmC*	50S ribosomal protein L29	1.18	0.11
HD0246	*ftsW*	cell division protein FtsW	1.18	0.12
HD0471	*gcp*	putative sialylglycoprotease	1.18	0.18
HD1624	*aceF*	dihydrolipoamide acetyltransferase	1.18	0.07
HD1085	*hscB*	chaperone protein HscB	1.17	0.10
HD1978	*rplV*	50S ribosomal protein L22	1.16	0.09
HD1353	*ihfB*	integration host factor, beta subunit	1.14	0.16
HD0445		possible ADP-heptose--lipooligosaccharide heptosyltransferase I	1.13	0.15
HD0449	*fis*	DNA-binding protein	1.12	0.16
HD1630	*msbA*	ABC transporter ATP-binding protein MsbA	1.12	0.11
HD1648	*glpR*	glycerol-3-phosphate regulon repressor	1.12	0.15
HD0300	*grxA*	glutaredoxin	1.11	0.14
HD0614	*kefB*	glutathione-regulated potassium-efflux system protein	1.11	0.06
HD1771	*djlA*	DnaJ-like protein DjlA	1.10	0.10
HD1325		conserved hypothetical protein	1.10	0.07
HD1087	*hscA*	chaperone protein HscA	1.09	0.07
HD1089		conserved hypothetical protein	1.09	0.08

HD0316	*dppF*	dipeptide transport ATP-binding protein	1.09	0.09
HD1462	*nusA*	transcription termination-antitermination factor nusA, N utilization substance protein A	1.09	0.07
HD0400	*rnfD*	putative Na-translocating NADH-quinone reductase	1.09	0.07
HD0647		conserved hypothetical protein	1.08	0.13
HD1982	*rplD*	50S ribosomal protein L4	1.08	0.12
HD1471		conserved hypothetical protein	1.08	0.07
HD1160	*glpC*	anaerobic glycerol-3-phosphate dehydrogenase, subunit C	1.08	0.02
HD0250		conserved hypothetical protein	1.08	0.10
HD0353	*htpX*	putative protease	1.08	0.08
HD1158	*glpB*	anaerobic glycerol-3-phosphate dehydrogenase, subunit B	1.06	0.05
HD1088	*fdx2*	ferredoxin	1.04	0.06
HD1199	*pgpB*	phosphatidylglycerophosphatase B	1.02	0.20
HD1786	*mutT*	mutator MutT protein	1.02	0.05
HD0318		possible fimbrial biogenesis and twitching motility protein PilF	1.02	0.17
HD1356	*pyrF*	orotidine 5`-phosphate decarboxylase	1.00	0.06
HD1957	*secY*	preprotein translocase SecY subunit	1.00	0.08
HD1189	*lpxD*	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase	1.00	0.06
HD1805		putative MAF protein	0.98	0.15
HD1011		hypothetical protein	0.96	0.08
HD1219		conserved hypothetical protein	0.96	0.14
HD1220	*ykgF*	putative iron-sulfur electron transport protein	0.96	0.08
HD1731	*nrdA*	ribonucleoside-diphosphate reductase, alpha chain	0.96	0.11
HD1191	*D15*	outer membrane protein D-15	0.95	0.09
HD0889	*deoD*	purine nucleoside phosphorylase	0.94	0.07
HD0451		conserved hypothetical protein	0.92	0.07
HD1143	*sdaC*	serine transporter	0.92	0.07
HD0835		putative transport protein	0.91	0.08
HD1461	*infB*	translation initiation factor IF-2	0.91	0.08
HD1983	*rplC*	50S ribosomal protein L3	0.91	0.10
HD0223	*dnaQ*	DNA polymerase III epsilon chain	0.90	0.12
HD1400		putative soluble lytic murein transglycosylase	0.90	0.07
HD1824	*modB*	molybdenum ABC transporter, permease protein	0.89	0.08
HD0876		conserved probable ribonuclease	0.88	0.09
HD0989	*pflA*	pyruvate formate-lyase activating enzyme	0.87	0.10
HD1747		hypothetical protein	0.87	0.15
HD1282	*fhs*	putative formate--tetrahydrofolate ligase	0.85	0.08
HD0990	*pflB*	formate acetyltransferase	0.84	0.07
HD1623	*lpdA*	dihydrolipoamide dehydrogenase	0.84	0.07
HD0371		conserved hypothetical protein	0.83	0.09
HD1607	*lepB*	signal peptidase I	0.83	0.11
HD0425		hypothetical protein	0.83	0.12
HD1033	*argH*	argininosuccinate lyase	0.82	0.11

HD1473	*tdk*	thymidine kinase	0.82	0.09
HD1961	*rpsE*	30S ribosomal protein S5	0.82	0.12
HD1895		putative adhesin processing HmwC-like protein	0.82	0.13
HD1180	*surA*	survival protein SurA homolog	0.81	0.11
HD0357		probable carbon starvation protein A	0.81	0.08
HD1589	*nlpI*	lipoprotein NlpI homolog	0.81	0.07
HD0830	*ligA*	DNA ligase	0.81	0.14
HD0419		conserved putative sodium-dependent transporter	0.80	0.07
HD0615	*nfrE*	cytochrome c-type biogenesis protein	0.80	0.09
HD0394		hypothetical protein	0.80	0.16
HD0827	*ampG*	permease and possible signal transducer	0.79	0.09
HD1756		putative xanthine/uracil permease	0.77	0.14
HD0244	*mraY*	phospho-N-acetylmuramoyl-pentapeptide-transferase E	0.77	0.07
HD1816	*yfeA*	iron (chelated) ABC transporter, periplasmic-binding protein	0.77	0.09
HD1923	*rpoZ*	RNA polymerase omega subunit	0.75	0.12
HD1654		conserved hypothetical protein	0.75	0.14
HD1460	*rbfA*	ribosome binding factor A	0.75	0.09
HD1745	*uup*	ABC-type transport protein Uup	0.74	0.11
HD1962	*rplR*	50S ribosomal protein L18	0.74	0.10
HD2013	*lipB*	lipoate-protein ligase B	0.74	0.07
HD1459	*truB*	tRNA pseudouridine synthase B	0.73	0.10
HD1785	*groES*	10 kDa chaperonin	0.73	0.13
HD1803	*thrS*	threonyl-tRNA synthetase	0.73	0.09
HD1784	*groEL*	60 kDa chaperonin	0.73	0.13
HD0411	*recX*	possible regulatory protein RecX homolog	0.72	0.10
HD1939		conserved hypothetical protein	0.72	0.17
HD1463		conserved hypothetical protein	0.70	0.10
HD1469	*cpxR*	transcriptional regulatory protein CpxR	0.70	0.12
HD0396	*rnfA*	probable Na+-translocating NADH-quinone oxidoreductase	0.68	0.14
HD0226		conserved hypothetical protein	0.66	0.14
HD1604	*recO*	DNA repair protein RecO	0.66	0.10
HD0605	*folK*	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	0.64	0.11
HD1606	*rnc*	ribonuclease III	0.64	0.12
HD0567		hypothetical protein	0.63	0.07
HD1605	*era*	GTP-binding protein era homolog	0.63	0.10
HD1331	*pckA*	phosphoenolpyruvate carboxykinase	0.62	0.09
HD0379	*nqrA*	Na+-translocating NADH-ubiquinone oxidoreductase, subunit A	0.61	0.08
HD0260	*degP*	periplasmic serine protease	0.60	0.09
HD0189	*dnaK*	chaperone protein DnaK	0.60	0.07
HD1410		conserved hypothetical protein	0.56	0.10
HD1472		conserved hypothetical protein	0.55	0.14
HD0771		conserved hypothetical protein	0.54	0.10

HD1024	*yfeD*	iron (chelated) transport system membrane protein	0.52	0.13
HD1249	*rplY*	50S ribosomal protein L25	0.48	0.11
HD1443		putative single stranded DNA-binding protien	0.48	0.13
HD1237	*lolA*	outer membrane lipoprotein carrier protein	0.30	0.11
HD1020		glyoxalase II family protein	-0.33	0.10
HD1016		hypothetical protein	-0.42	0.09
HD0361	*infA*	translation initiation factor IF-1	-0.42	0.12
HD0222		conserved hypothetical protein	-0.44	0.11
HD1105		conserved hypothetical protein	-0.45	0.11
HD0903	*cdtB*	cytolethal distending toxin protein B	-0.48	0.09
HD1111	*fdnI*	formate dehydrogenase, gamma subunit	-0.49	0.08
HD1935	*holB*	DNA polymerase III delta subunit	-0.56	0.09
HD1798		hypothetical protein	-0.57	0.07
HD0786	*ccmA*	cytochrome c-type biogenesis ATP-binding protein	-0.57	0.11
HD0014	*mesJ*	probable cell-cycle protein MesJ	-0.58	0.09
HD0846	*lpxB*	lipid-A-disaccharide synthase	-0.59	0.14
HD1212	*smpA*	small protein A	-0.60	0.13
HD0700		putative peroxiredoxin/glutaredoxin family protein	-0.60	0.12
HD1665		possible GTP cyclohydrolase I	-0.60	0.15
HD0004	*atpB*	ATP synthase A chain	-0.63	0.09
HD1632		conserved hypothetical protein	-0.64	0.07
HD1170	*ompP4*	outer membrane protein P4	-0.65	0.06
HD0076	*napG*	ferredoxin-type protein NapG	-0.67	0.11
HD1493	*rpsI*	30S ribosomal protein S9	-0.69	0.13
HD0169	*ppa*	inorganic pyrophosphatase	-0.69	0.15
HD0902	*cdtA*	cytolethal distending toxin protein A	-0.69	0.12
HD0161		hypothetical protein	-0.69	0.14
HD1218		hypothetical protein	-0.69	0.17
HD0901		hypothetical protein	-0.70	0.05
HD1141		conserved hypothetical protein	-0.70	0.09
HD1332	*LapB*	putative membrane protein	-0.71	0.12
HD1494	*rplM*	50S ribosomal protein L13	-0.72	0.09
HD1892		conserved hypothetical protein	-0.73	0.10
HD0595		conserved hypothetical protein	-0.76	0.09
HD1053	*ndk*	nucleoside diphosphate kinase	-0.78	0.09
HD1018	*macA*	probable macrolide-specific efflux protein	-0.81	0.07
HD0624	*alr*	alanine racemase	-0.83	0.08
HD1917		probable RNA polymerase sigma factor	-0.84	0.09
HD1666		probable phosphatase	-0.84	0.12
HD1029		putative haloacid dehalogenase-like hydrolase	-0.84	0.05
HD1667	*bcp*	bacterioferritin comigratory protein	-0.85	0.09
HD0668		hypothetical protein	-0.86	0.09

HD1211		hypothetical protein	-0.87	0.17
HD1377		conserved hypothetical protein	-0.87	0.20
HD1545		hypothetical protein	-0.89	0.15
HD0229	*ptsH*	PTS system phosphocarrier protein HPr	-0.89	0.12
HD0479		possible DNA-binding protein	-0.90	0.09
HD0741	*hfq*	putative host factor-I protein	-0.90	0.10
HD1302	*tadC*	tight adherence protein C	-0.91	0.10
HD1515		conserved hypothetical protein	-0.91	0.13
HD1783		hypothetical protein	-0.92	0.19
HD1495		conserved hypothetical protein	-0.93	0.22
HD1393	*torY*	cytochrome c-type protein TorY	-0.93	0.06
HD0848	*sodC*	superoxide dismutase [Cu-Zn]	-0.94	0.10
HD0923		hypothetical protein	-0.95	0.18
HD1600	*rpsB*	30S ribosomal protein S2	-0.96	0.08
HD0591		conserved hypothetical protein	-1.01	0.29
HD1859		PTS system Enzyme II-A permease component	-1.01	0.07
HD0667	*holC*	DNA polymerase III chi subunit	-1.02	0.07
HD1030	*cysB*	cys regulon transcriptional activator	-1.03	0.09
HD0770		conserved hypothetical protein	-1.04	0.13
HD1754	*ftnA*	ferritin-like protein 1	-1.06	0.10
HD1945		conserved hypothetical protein	-1.06	0.08
HD1115	*nth*	endonuclease III, DNA (apurinic or apyrimidinic site) lyase	-1.07	0.09
HD0073	*napD*	possible NapD protein	-1.08	0.05
HD1755	*ftnB*	ferritin-like protein 2	-1.09	0.08
HD0646		conserved hypothetical protein	-1.09	0.16
HD1078	*ompP1*	outer membrane protein P1	-1.10	0.05
HD0072	*napF*	ferredoxin-type protein NapF	-1.14	0.09
HD1028	*gcvA*	glycine cleavage system transcriptional activator	-1.16	0.06
HD1387		conserved hypothetical protein	-1.18	0.08
HD0084	*lldD*	L-lactate dehydrogenase	-1.18	0.09
HD0068	*ftpA*	fine tangled pili major subunit	-1.19	0.08
HD1156	*lspA2*	large supernatant protein 2	-1.19	0.12
HD1304	*tadA*	tight adherence protein A	-1.20	0.12
HD1327	*hhdA*	hemolysin	-1.25	0.06
HD1077	*ogt*	methylated-DNA--protein-cysteine S-methyltransferase	-1.25	0.07
HD1480	*bioD1*	probable dethiobiotin synthetase	-1.28	0.07
HD1530		hypothetical protein	-1.29	0.14
HD1857	*sgaH*	probable hexulose-6-phosphate synthase	-1.29	0.05
HD1503	*guaB*	inosine-5-monophosphate dehydrogenase	-1.31	0.05
HD1326	*hhdB*	hemolysin activation/secretion protein	-1.37	0.44
HD1525	*gam*	putative mu-phage host-nuclease inhibitor protein	-1.38	0.10
HD1305		*flp* operon protein D	-1.39	0.09
HD1291	*gapA*	glyceraldehyde 3-phosphate dehydrogenase	-1.41	0.13

HD0740	*hflX*	GTP-binding protein HflX	-1.46	0.12
HD1986	*fumC*	fumarate hydratase class II	-1.46	0.05
HD0925		hypothetical protein	-1.49	0.11
HD1290	*msrB*	peptide methionine sulfoxide reductase MsrB	-1.50	0.11
HD1389	*moaE*	molybdopterin converting factor subunit 2	-1.50	0.56
HD1306	*rcpB*	rough colony protein B	-1.53	0.13
HD1920		hypothetical protein	-1.54	0.12
HD1391	*moaC*	molybdenum cofactor biosynthesis protein C	-1.57	0.55
HD0600		conserved hypothetical protein	-1.58	0.09
HD1280		possible serine protease homolog	-1.63	0.11
HD1096		hypothetical protein	-1.64	0.26
HD1390	*moaD*	molybdopterin converting factor subunit 1	-1.66	0.62
HD0066		hypothetical protein	-1.78	0.58
HD1392	*moaA*	molybdenum cofactor biosynthesis protein A	-1.80	0.52
HD1307	*rcpA*	rough colony protein A	-1.83	0.20
HD1518		hypothetical protein	-1.85	0.67
HD0347	*nrfB*	nitrate reductase, cytochrome-C type protein	-1.92	0.25
HD1432		conserved hypothetical protein	-1.98	0.07
HD1308		*flp* operon protein C	-2.06	0.09
HD0344	*nrfA*	nitrate reductase, cytochrome c552	-2.12	0.19
HD1309		*flp* operon protein B	-2.43	0.45
HD1278		possible serine protease	-2.51	0.87
HD1856		hypothetical protein	-2.54	0.50
HD0896	*cysK*	cysteine synthase	-2.56	0.12
HD0047		hypothetical protein not likely	-2.69	0.16
HD1312	*flp1*	*flp* operon protein Flp1	-2.85	0.94
HD0998	*uraA*	uracil permease	-2.92	0.26
HD0048		hypothetical protein	-3.05	0.26
HD0232	*arcB1*	ornithine carbamoyltransferase	-3.10	0.13
HD1310	*flp3*	*flp* operon protein Flp3	-3.10	0.66
HD1311	*flp2*	*flp* operon protein Flp2	-3.11	0.71
HD1985		possible DNA transformation protein	-3.16	0.61
HD0233	*carB*	carbamoyl-phosphate synthase, large subunit	-3.34	0.21
HD0235	*carA*	carbamoyl-phosphate synthase, small subunit	-3.63	0.26
HD0769	*dsrA*	serum resistance protein DrsA	-3.68	0.15
HD0805		conserved hypothetical protein	-3.70	1.52
HD0046	*ompA2*	major outer membrane protein homolog, OmpA2	-4.61	0.10
HD1433	*ompP2A*	outer membrane protein P2 homolog	-4.68	0.35

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