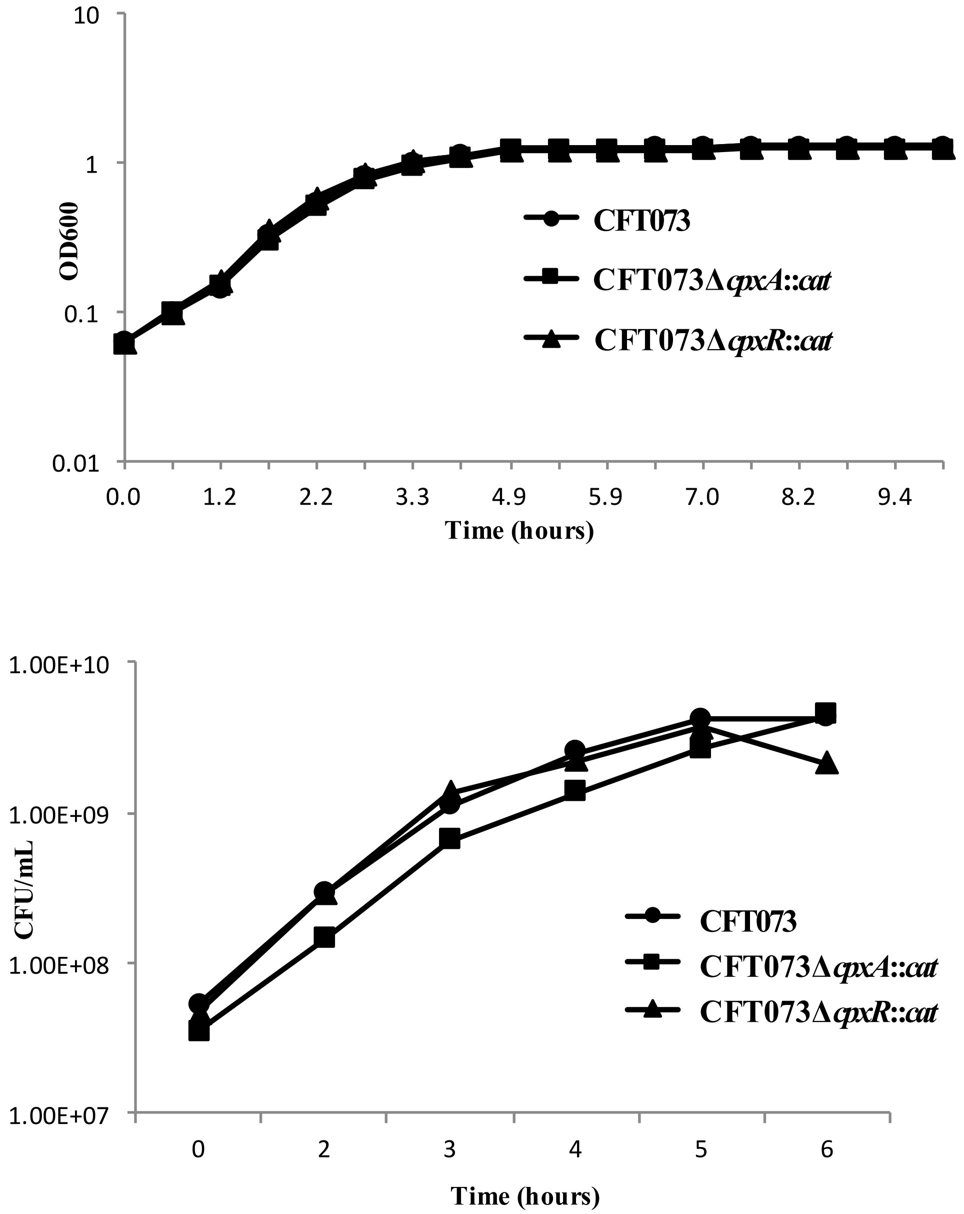

FIG S1 Growth kinetics of CFT073, CFT073Δ*cpxA*::*cat*, and CFT073Δ*cpxR*::*cat* in TB broth with 0.4% glucose determined by measuring the optical density at 600 nm (OD_{600}) (top panel) and CFU/mL (bottom panel) at different time points following inoculation from overnight cultures.

Table S1 Functional classification of genes differentially regulated between the parent, the *cpxA* mutant, and the *cpxR* mutant

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
CELLULAR PROCESSES AND SIGNALING					
Cell cycle control, cell division, and chromosome partitioning					
c0715	*ccrB*	Camphor resistance protein	-2.00		
c0171	*ecpD*	Chaperone protein EcpD	2.48	2.80	
c0172	*yadN*	Fimbrial-like protein YadN	4.53	5.11	
c3163		Tail component of prophage	2.07		
Adhesins, chaperones, secretion, and trafficking					
c1239	*focA*	F1C major fimbrial subunit	-5.32	-4.68	
c1238	*sfaB*	F1C and S fimbrial switch regulatory protein	-4.64	-4.23	
c1240	*sfaD*	F1C minor fimbrial subunit	-4.91	-4.20	
c1241	*focC*	F1C periplasmic chaperone	-4.62	-3.89	
c1242	*focD*	F1C fimbrial usher	-3.61	-2.88	
c1243	*focF*	F1C minor fimbrial subunit F	-3.82	-3.25	
c1244	*focG*	F1C minor fimbrial subunit protein G	-4.63	-3.92	
c1245	*focH*	F1C fimbrial adhesin	-4.19	-3.69	
c3592	*papA*	PapA protein	-3.71	-3.34	
c3593	*papI*	PapI protein	-3.34	-2.53	
c4214		Major fimbrial subunit	-2.07	-2.19	
c5188	*papA_2*	PapA protein	-3.50	-3.06	
c5393	*fimA*	Type-1 fimbrial protein A chain	-4.49	-3.75	
c5394	*fimI*	Fimbrin-like protein FimI	-3.90	-3.13	
c5395	*fimC*	Chaperone protein FimC	-3.40	-2.68	
c5396	*fimD*	Outer membrane usher protein FimD	-2.99	-2.12	
c5397	*fimF*	FimF protein	-2.18		
c5399	*fimG*	FimG protein	-2.31		
c5400	*fimH*	FimH protein	-2.39	-2.02	
c2143	*spy*	Spheroplast protein Y precursor	4.42	4.38	
c3740	*exbD*	Biopolymer transport protein ExbD	3.78	3.42	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c3741	*exbB*	Biopolymer transport protein ExbB	3.72	3.56	
c4865	*cpxP*	Periplasmic repressor CpxP	5.22	4.45	
Cell wall/membrane/envelope biogenesis					
c0388	*phoE*	Outer membrane phosphoporin protein E	-4.42	-2.67	
c0426	*upaB*	Putative autotransporter	-2.40	-2.21	
c0652	*ompT*	Outer membrane protease	-4.18	-3.63	
c0658	*cusC*	Copper/silver efflux system outer membrane protein	-7.35	-5.88	
c0660	*cusB*	Copper/silver efflux system membrane fusion protein	-4.41	-3.79	
c0924	*dacC*	D-alanyl-D-alanine carboxypeptidase fraction C	-3.67	-3.92	
c1071	*ompF*	Outer membrane protein F	-2.53	-2.34	
c1800		Putative oxidoreductase		-2.01	
c1804	*ynaI*	Putative mechanosensitive channel	-3.03	-2.58	
c1937		Putative NAD-dependent dehydratase	-2.68	-2.31	
c2049	*ydhO*	Putative murein DD-endopeptidase	-3.11	-2.54	
c2055	*cfa*	Cyclopropane fatty acyl phospholipid synthase	-2.03	-2.01	
c2554	*wzzB*	Chain length determinant protein	-2.16		
c2555	*ugd*	UDP-glucose 6-dehydrogenase	-3.14	-2.56	
c2567	*galF*	UTP-glucose-1-phosphate uridylyltransferase	-2.36	-2.35	
c2795	*yfbE*	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase	-3.59	-3.56	
c2796		Putative glycosyl transferase	-3.38	-3.50	
c2799	*arnT*	4-amino-4-deoxy-L-arabinose transferase	-2.57	-2.49	
c3655		Antigen 43		-2.64	-2.89
c4324	*yhiU*	Putative multidrug efflux system protein MdtE	-5.22	-4.90	
c5388		N-acetylneuraminic acid mutarotase	-3.67		
c1391	*lolC*	Outer membrane-specific lipoprotein transporter subunit	2.54	2.09	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c1717	*tonB*	Transport protein TonB	3.18	2.95	
c2915	*ddg*	Palmetoleoyl acyl transferase	3.61	2.37	
c4370	*yiaD*	Outer membrane lipoprotein	2.24	2.17	
c5245	*yjeP*	Putative mechanosensitive channel	2.35	2.20	
c5479	*slt*	Lytic murein transglycosylase	3.53	2.63	
c4316	*chuY*	Hypothetical protein	5.45	5.19	
Defense mechanisms					
c1392	*lolD*	Lipoprotein transporter ATP-binding subunit	2.61	2.39	
c4325	*yhiV*	Putative multidrug efflux transporter	-3.95	-3.91	
Posttranslational modification, protein turnover, and chaperones					
c0019	*dnaK*	Molecular chaperone DnaK	-2.27	-2.18	
c0539	*cyoE*	Protoheme IX farnesyltransferase	-2.38	-2.34	
c0982	*grxA*	Glutaredoxin 1	-2.53		
c1879		Putative glutathione S transferase	-2.11		
c3114	*clpB*	Protein disaggregation chaperone	-2.25	-2.28	
c4606	*ibpB*	Heat shock chaperone IbpB	-3.31		
c4607	*ibpA*	Heat shock protein IbpA	-2.50		
c0197	*htrA*	Serine endoprotease	2.60		
c1572		Capsid assembly protein of prophage	2.66	2.46	
c2238	*htpX*	Heat shock protein HtpX	5.09	4.09	
c3226	*nrdH*	Glutaredoxin-like protein	2.74	2.84	
c3287	*hypB*	Hydrogenase nickel incorporation protein HypB	2.40		
c3288	*hypC*	Hydrogenase assembly chaperone	2.24	2.78	
c4138	*ppiA*	Peptidyl-prolyl cis-trans isomerase	3.71		
c5462	*yjjW*	Putative glycine radical enzyme activase	3.06	2.46	
Signal transduction mechanisms					
c0435		Putative phosphodiesterase, c-di-GMP-specific		-2.43	
c0509	*phoR*	Phosphate regulon sensor protein	-2.62		

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c0435		Putative phosphodiesterase, c-di-GMP-specific	-2.69		
c0508	*phoB*	Transcriptional regulator PhoB	-2.89	-2.24	
c0940	*ybiI*	Putative catecholate siderophore receptor	-2.08	-3.32	
c1159	*phoH*	Putative phosphate-starvation inducible protein	-5.75	-6.04	
c1821	*ynaF*	Putative universal stress protein UspF	-2.82	-2.41	
c1918		Putative sensor kinase	-2.85	-3.04	
c3564		Putative response regulator	-2.07		
c3565		Putative response regulator	-2.48		
c4323	*yhiE*	Putative transcriptional regulator GadE	-6.49	-5.76	
c4331	*yhjB*	Transcriptional regulator YhjB	-2.80	-2.58	
c4875	*yiiT*	Universal stress protein UspD	-3.27	-3.29	
c5052	*yjcC*	Putative c-di-GMP-specific phosphodiesterase	-3.41	-3.20	
c4818	*glnL*	Nitrogen regulation protein	2.42		
INFORMATION STORAGE AND PROCESSING					
Replication, recombination, and repair					
c1011	*ybjD*	Hypothetical protein	-2.11		
c2405		Hypothetical protein	-2.12		
c2473		Transposase	-2.08		
c2474		Transposase	-2.45		
c4511		Putative TatD hydrolase	-2.04	-2.01	
c5196		Transposase	-2.84	-2.57	
c0880	*rhlE*	ATP-dependent RNA helicase RhlE	2.04		
c2254		Exodeoxyribonuclease X	2.34	2.18	
c4167	*nudE*	ADP-ribose diphosphatase	2.11		
c4818	*glnL*	Nitrogen regulation protein		2.29	
c5254	*mutL*	DNA mismatch repair protein	2.81	2.46	
Transcription					

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c0405	*matA*	Putative transcription factor	-2.70	-3.12	
c1169	*alpA*	Prophage CP4-57 regulatory protein AlpA	-2.34		
c1237	*sfaC*	F1C and S fimbrial switch regulatory protein	-4.19	-3.33	
c1247	*focX*	Regulatory protein	-2.93	-2.31	
c1938	*oprR*	Transcriptional regulator YcjZ	-2.21		
c2330	*sdiA*	DNA-binding transcriptional activator SdiA	-2.14		
c2447	*cbl*	Transcriptional regulator Cbl	-3.50	-3.75	
c3212	*ygaE*	DNA-binding transcriptional regulator CsiR	-2.04	-2.30	
c3600		Putative TetR protein	-2.70	-2.29	
c4306	*yhiF*	Transcriptional regulator YhiF	-5.01	-4.71	
c4550		Hypothetical protein	-2.05		
c5142	*cadC*	DNA-binding transcriptional activator CadC	-3.00	-2.79	
c5189	*papI_2*	P fimbrial regulatory protein	-3.24	-3.05	
c5436	*yjjM*	Putative transcriptional regulator	-2.36		
c2830	*lrhA*	Transcriptional regulator LrhA	2.12	2.09	
c3237	*emrR*	Transcriptional repressor	2.59	2.28	
c3626	*iucB*	Putative aerobactin siderophore biosynthesis protein		2.00	
c3770		Putative transcriptional regulator	2.38	2.59	
c3863	*yhaJ*	Transcriptional regulator	2.37	2.07	
c3976	*yhcH*	N-acetylmannosamine kinase	2.31		
Translation, ribosomal structure, and biogenesis					
c0516	*tgt*	Queuine tRNA-ribosyltransferase	3.10	2.54	
c3119	*yfiA*	Translation inhibitor protein RaiA	2.88		
c4076	*rpsQ*	30S ribosomal protein S17	2.34	2.39	
c4079	*rplP*	50S ribosomal protein L16	2.43	2.58	
c4080		30S ribosomal protein S3	2.73	2.87	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c4083	*rpsS*	30S ribosomal protein S19	2.79	3.09	
c4085	*rplB*	50S ribosomal protein L2	2.81	2.98	
c4087	*rplW*	50S ribosomal protein L23	2.81	3.16	
c4092	*rpsJ*	30S ribosomal protein S10	2.75	3.07	
c4941	*rplJ*	50S ribosomal protein L10	2.09	2.26	
c4943	*rplL*	50S ribosomal protein		2.07	
c5018	*yjbN*	Trna-dihydrouridine synthase A	2.16		
METABOLISM					
Amino acid transport and metabolism					
c0431	*betA*	Choline dehydrogenase	-2.07	-2.10	
c0606	*ybaT*	Transport protein YbaT	-2.97	-2.99	
c0988	*potG*	Putrescine transporter ATP-binding subunit		-2.02	
c1707	*oppA*	Periplasmic oligopeptide-binding protein	-2.06	-2.23	
c1708	*oppB*	Oligopeptide transporter permease		-2.04	
c1803	*mppA*	Periplasmic murein peptide-binding	-2.43	-2.31	
c1921	*xasA*	Amino acid antiporter	-7.63	-7.28	
c1922	*gadB*	Glutamate decarboxylase beta	-7.17	-6.89	
c2335	*fliY*	Cystine transporter subunit	-2.84	-2.87	
c2679	*yeiT*	Oxidoreductase	-3.15	-2.73	
c3211	*gabP*	Gamma-aminobutyrate transporter	-2.69	-2.94	
c3319	*cysD*	Sulfate adenylyltransferase subunit 2	-2.65	-3.33	
c3407		Beta-cystathionase	-2.16		
c4328	*gadA*	Glutamate decarboxylase alpha	-8.09	-7.78	
c4501		Putative arginine decarboxylase	-2.44	-2.50	
c4502		Antiporter	-2.33		
c5081		Putative ABC transporter substrate binding protein	-2.31	-2.31	
c0040	*carA*	Carbamoyl phosphate synthase small subunit	3.26	3.14	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c0041	*carB*	Carbamoyl phosphate synthase large subunit	2.95	3.23	
c0568	*glnK*	Nitrogen regulatory protein P-II 2	3.92	3.45	
c0737	*gltK*	Glutamate/aspartate transport system permease GltK		2.01	
c0738	*gltJ*	Glutamate/aspartate transport system permease GltJ		2.37	
c0739	*ybeJ*	Glutamate and aspartate transporter subunit transporter	2.39	2.08	
c2256	*ptrB*	Protease II	2.36	2.21	
c2831		Aminotransferase	2.37	2.13	
c3122	*aroF*	Phospho-2-dehydro-3-deoxyheptonate aldolase	4.39	3.94	
c3235	*ygaZ*	Putative L-valine exporter	2.77	2.02	
c3639		N-acetylneuraminate lyase	2.59	2.74	
c3974	*gltD*	Glutamate synthase subunit beta	3.05	2.84	
c3979	*nanA*	N-acetylneuraminate lyase	3.29	2.62	
c4269	*nikA*	Nickel-binding periplasmic protein		2.14	
c4270	*nikB*	Nickel transporter permease NikB	2.35	2.13	
c4271	*nikC*	Nickel transporter permease NikC	2.45	2.22	
c4272	*nikD*	Nickel transporter ATP-binding protein NikD	2.38		
c4273	*nikE*	Nickel transporter ATP-binding protein NikE	2.41		
c4690	*ilvG*	Acetolactate synthase 2 catalytic subunit	2.45	2.08	
c4692	*ilvE*	Branched-chain amino acid aminotransferase	2.15		
c4694	*ilvA*	Threonine dehydratase	2.72	2.19	
c5473	*serB*	Phosphoserine phosphatase	2.18		
Carbohydrate transport and metabolism					
c0153	*gcd*	Glucose dehydrogenase	-2.40	-2.28	
c1843		Glyceraldehyde 3-phosphate dehydrogenase A	-2.48	-2.59	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c2136	*celB*	PTS system N,N-diacetylchitobiose-specific transporter subunit IIC	-2.26		
c3070	*yphF*	ABC transporter periplasmic-binding protein	-2.19		
c4241	*ugpA*	Glycerol-3-phosphate transporter permease	-2.21		
c4242	*ugpB*	Glycerol-3-phosphate transporter periplasmic binding protein	-2.87		
c4283		Phosphocarrier protein	-2.61	-2.50	
c4330	*treF*	Trehalase		-2.24	
c0922	*yliI*	Putative aldose sugar dehydrogenase	4.37	2.27	-2.10
c1254	*iroB*	Glucosyltransferase	3.43	3.22	
c3977	*yhcJ*	N-acetylmannosamine-6-phosphate 2-epimerase	2.22	2.26	
c4749	*yigM*	Membrane protein YigM	2.61	2.25	
Coenzyme transport and metabolism					
c2471		Putative 4'-phosphopantetheinyl transferase	-2.61		
c3715		Putative 8-amino-7-oxononanoate synthase	-2.41	-2.54	
c0680	*entC*	Isochorismate synthase	4.96	4.15	
c0853	*bioA*	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	2.41	3.12	
c0855	*bioB*	Biotin synthase	2.45	2.37	
c0856	*bioF*	8-amino-7-oxononanoate synthase	3.20	2.98	
c0858	*bioD*	Dithiobiotin synthetase	2.12		
c3541	*yggW*	Coproporphyrinogen III oxidase	2.19		
c4314	*chuW*	Coproporphyrinogen III oxidase	5.82	5.91	
Energy production and conversion					
c0409		Oxidoreductase	-2.40	-2.05	
c0420	*ykgC*	Pyridine nucleotide-disulfide oxidoreductase	-3.87	-3.62	
c0540	*cyoD*	Cytochrome o ubiquinol oxidase subunit IV		-2.32	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c0541	*cyoC*	Cytochrome o ubiquinol oxidase subunit III	-2.98	-2.63	
c0543	*cyoA*	Cytochrome o ubiquinol oxidase subunit II	-2.11	-2.19	
c1078	*ycbN*	Alkanesulfonate monooxygenase	-2.34	-2.62	
c1119	*appC*	Cytochrome bd-II oxidase subunit I	-2.45	-2.61	
c1120	*appB*	Cytochrome bd-II oxidase subunit II	-2.12	-2.07	
c1897	*narV*	Respiratory nitrate reductase 2 subunit gamma	-2.15	-2.27	
c1898	*narW*	Respiratory nitrate reductase 2 subunit delta	-2.87	-3.12	
c1899	*narY*	Respiratory nitrate reductase 2 subunit beta	-2.89	-3.00	
c1900	*narZ*	Respiratory nitrate reductase 2 subunit alpha	-3.80	-3.85	
c2003	*fumC*	Fumarate hydratase		-2.11	
c2820	*nuoK*	NADH dehydrogenase subunit K	-2.31	-2.32	
c2821	*nuoJ*	NADH dehydrogenase subunit J	-2.11		
c2822	*nuoI*	NADH dehydrogenase subunit I	-2.16		
c3566		Putative thiosulfate reductase cytochrome B	-3.06	-2.76	
c3704	*yghK*	Glycolate transporter	-2.92	-2.71	
c3709	*glcD*	Glycolate oxidase subunit GlcD	-3.86	-3.90	
c3991	*mdh*	Malate dehydrogenase	-2.29	-2.61	
c4971	*aceB*	Malate synthase	-2.37	-2.28	
c4972	*aceA*	Isocitrate lyase	-2.80	-2.69	
c0142	*aceE*	Pyruvate dehydrogenase subunit E1	3.24	3.12	
c1323		Cytochrome b561 2	2.96	2.32	
c2782	*glpA*	Sn-glycerol-3-phosphate dehydrogenase subunit A	3.00	2.86	
c4141	*nirB*	Nitrite reductase [NAD(P)H] large subunit	2.41	2.08	
c5241	*frdB*	Fumarate reductase iron-sulfur subunit	2.13		
c5242	*frdA*	Fumarate reductase flavoprotein subunit	2.11		

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
Inorganic ion transport and metabolism					
c0472	*tauA*	Taurine transporter substrate binding subunit		-3.78	-2.07
c0473	*tauB*	Taurine transporter ATP-binding subunit		-2.06	
c0475	*tauC*	Taurine transporter subunit		-2.78	
c0490	*phoA*	Alkaline phosphatase	-3.13	-3.13	
c0659	*cusX*	Periplasmic copper-binding protein	-5.80		
c0490	*phoA*	Alkaline phosphatase	-3.84		
c1079	*ycbO*	Alkanesulfonate transporter substrate-binding subunit		-2.07	
c1155		Cytochrome	-2.52		
c1156	*ycdO*	Putative periplasmic lipoprotein	-3.72	-2.26	
c1157	*ycdB*	Putative iron-dependent peroxidase	-2.39		
c1715	*kch*	Voltage-gated potassium channel	-2.83	-2.55	
c1901	*narU*	Nitrite extrusion protein 2	-5.59	-5.25	
c2321	*ftn*	Ferritin	-4.37	-3.89	
c2352	*emrE*	Multidrug efflux protein	-2.23		
c2998	*yffB*	Putative arsenate reductase	-2.17	-2.13	
c3317	*cysC*	Adenylylsulfate kinase	-2.83	-3.12	
c3318	*cysN*	Sulfate adenylyltransferase subunit 1	-2.46	-3.01	
c4107	*bfr*	Bacterioferritin	-2.89	-2.71	
c4262	*zntA*	Zinc/cadmium/mercury/lead-transporting ATPase	-3.11	-3.22	
c4319	*yhiD*	Mg transport ATPase	-6.75		
c4329	*yhjA*	Cytochrome C peroxidase	-2.04		
c4583	*nlpA*	Cytoplasmic membrane lipoprotein-28	-4.39	-4.50	
c4648	*phoU*	Transcriptional regulator PhoU	-3.74	-3.25	
c4649	*pstB*	Phosphate transporter ATP-binding protein	-3.02	-2.54	
c4651	*pstA*	Phosphate transporter permease subunit PstA	-2.84	-2.23	
c4652	*pstC*	Phosphate transporter permease subunit PstC	-3.35	-2.48	

Locus tag	**Gene**	**Description**	***cpxA* mutant vs *cpxR* mutant**[a]	***cpxA* mutant vs parent**[b]	***cpxR* mutant vs parent**[c]
c4653	*pstS*	Phosphate ABC transporter periplasmic substrate-binding protein PstS	-4.52	-3.64	
c4869	*sbp*	Sulfate transporter subunit	-3.07	-3.57	
c5110	*phnD*	Phosphonates-binding periplasmic protein	-2.53		
c5341	*mgtA*	Magnesium-transporting ATPase MgtA	-2.32	-2.15	
c0185	*fhuA*	Ferrichrome outer membrane transporter	3.74	4.15	
c0186	*fhuC*	Iron-hydroxamate transporter ATP-binding subunit	3.64	4.24	
c0187	*fhuD*	Iron-hydroxamate transporter substrate-binding subunit	4.09	4.06	
c0188	*fhuB*	Iron-hydroxamate transporter permease subunit	3.41	3.43	
c0669	*fepA*	Outer membrane receptor FepA	3.27	2.98	
c0671	*fes*	Enterobactin esterase	4.68	4.76	
c0675	*fepC*	Iron-enterobactin transporter ATP-binding protein	4.05	3.98	
c0676	*fepG*	Iron-enterobactin transporter permease	4.90	4.28	
c0677	*fepD*	Iron-enterobactin transporter membrane protein	3.26	4.63	
c0679	*fepB*	Iron-enterobactin transporter periplasmic binding protein	3.60	3.74	
c1597	*sitD*	SitD protein	2.34	2.51	
c1598	*sitC*	SitC protein	3.60	3.85	
c1599	*sitB*	SitB protein	3.91	4.14	
c1600	*sitA*	SitA protein	4.35	4.78	
c1676	*chaA*	Calcium/sodium:proton antiporter	4.45	3.44	
c1684	*narK*	Nitrite extrusion protein 1	2.34	2.50	
c1991	*ydgE*	Multidrug efflux system protein MdtI	2.80	2.24	
c1992	*ydgF*	Multidrug efflux system protein MdtJ	2.55		
c2101	*ydiE*	Hypothetical protein	2.84	3.46	
c2315	*yecI*	Ferritin	3.44	2.57	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c3217	*ygaP*	Hypothetical protein, membrane protein	2.00		
c3771		Iron ABC transporter substrate-binding protein	2.67	2.87	
c3772		Iron ABC transporter permease	2.29	2.98	
c3773		Iron ABC transporter permease	2.51	3.23	
c3774		Ferric enterobactin transport ATP-binding protein	3.31	3.48	
c3823	*yqjH*	Putative ferric reductase	3.68	3.25	
c4108	*yheA*	Bacterioferritin-associated ferredoxin	2.10	2.27	
c4142	*nirD*	Nitrite reductase small subunit	2.75		
c4143	*nirC*	Nitrite transporter NirC	2.81		
c4186	*feoB*	Ferrous iron transport protein B	2.67	2.38	
c4308	*chuA*	Outer membrane heme/hemoglobin receptor	3.16	3.01	
c4313	*chuT*	Periplasmic binding protein	5.75	6.33	
c4317	*chuU*	Iron ABC transporter permease	4.62	4.91	
c4318	*hmuV*	Hemin importer ATP-binding subunit	3.03	3.08	
Lipid transport and metabolism					
c0926	*ybjG*	Undecaprenyl pyrophosphate phosphatase	-3.40	-3.04	
c1200		Acyl carrier protein	-2.18	-2.25	
c2011	*hdhA*	7-alpha-hydroxysteroid dehydrogenase	-2.94	-2.67	
c2467		3-hydroxyacyl-coa dehydrogenase	-2.28		
c3467		Isopentenyl-diphosphate delta-isomerase	-2.81	-2.63	
c3714		Putative acyl carrier protein	-3.46	-3.28	
c5275	*aidB*	Isovaleryl CoA dehydrogenase	-3.12	-3.13	
c0683	*entA*	2,3-dihydroxybenzoate-2,3-dehydrogenase	4.38	4.51	
c4011	*accB*	Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	2.35		
c4012	*accC*	Acetyl-CoA carboxylase biotin carboxylase subunit	2.38	2.03	

Locus tag	Gene	Description	***cpxA* mutant vs *cpxR* mutant**[a]	***cpxA* mutant vs parent**[b]	***cpxR* mutant vs parent**[c]
c5247	*psd*	Phosphatidylserine decarboxylase	2.92	2.43	
Nucleotide transport and metabolism					
c3460	*ygfO*	Purine permease YgfO	-2.07		
c0636	*purK*	Phosphoribosylaminoimidazole carboxylase ATPase subunit	2.42	2.54	
c0637	*purE*	Phosphoribosylaminoimidazole carboxylase catalytic subunit		2.15	
c3017	*purM*	Phosphoribosylaminoimidazole synthetase	2.76	2.79	
c3227	*nrdI*	Ribonucleotide reductase stimulatory protein	3.12	2.96	
c3228	*nrdE*	Ribonucleotide-diphosphate reductase subunit	2.76	2.96	
c3229	*nrdF*	Ribonucleotide-diphosphate reductase subunit beta	2.02	2.18	
c3540	*yggV*	Deoxyribonucleotide triphosphate pyrophosphatase	2.22	2.01	
c4479	*yicE*	Putatuve purine permease YicE		2.21	
c4963	*purD*	Phosphoribosylamine-glycine ligase	3.06	3.66	
Secondary metabolites biosynthesis, transport, and catabolism					
c1034	*ycaC*	Putative amidases	-2.53	-2.31	
c2451		Thioesterase	-2.24	-2.05	
c0616	*ybbA*	ABC transporter ATP-binding protein YbbA	4.02	3.42	
c0617	*ybbP*	Putative transport protein	3.96	3.28	
c0681	*entE*	Enterobactin synthase subunit E	4.10	4.61	
c0684	*ybdB*	Putative proofreading thioesterase in enterobactin biosynthesis	3.75	3.56	
c2752	*yojI*	Multidrug transporter membrane - ATP-binding component		2.04	

[a] Genes differentially expressed in CFT073Δ*cpxA*::*cat* vs CFT073Δ*cpxR*::*cat*.

[b] Genes differentially expressed in CFT073Δ*cpxA*::*cat* vs CFT073.

[c] Genes differentially expressed in CFT073Δ*cpxR*::*cat* vs CFT073.

Values indicate fold change in expression of gene transcription; (-) minus sign indicates downregulation.

Table S2 Genes with no defined functional category differentially regulated between the parent, the *cpxA* mutant, and the *cpxR* mutant

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
POORLY CHARACTERIZED					
Function unknown					
c0659	*cusX*	Periplasmic copper-binding protein		-4.76	
c2200	*yeaQ*	Hypothetical protein, membrane protein	-2.85	-2.46	
c2450		Hypothetical protein	-3.13	-2.77	
c3065	*yphA*	Hypothetical protein, membrane protein		-2.21	
c4319	*yhiD*	Mg transport ATPase		-6.36	
c4322	*hdeD*	Acid-resistance membrane protein	-7.19	-6.84	
c5016	*yjbJ*	Stress-response protein	-2.13		
c5388		N-acetylneuraminic acid mutarotase		-3.26	
c0587	*ybaN*	Hypothetical protein	2.81	2.53	
c1387	*ycfS*	Putative L,D-transpeptidase	4.61	4.33	
c1877	*yncE*	Hypothetical protein	3.05	3.66	
c2141	*ydjR*	Hypothetical protein		3.40	
c3539	*yggU*	Hypothetical protein	2.03		
c3783	*ygiB*	Hypothetical protein, membrane protein	3.03		
c3853	*yqjA*	Hypothetical protein	3.52	3.28	
c4691	*ilvM*	Acetolactate synthase 2 regulatory subunit	2.12		
c5409	*yjiG*	Hypothetical protein	2.08		
General function prediction only					
c0284		Putative phospholipase		-3.14	-2.51
c0410		Putative alpha/beta hydrolase	-3.18	-2.96	
c0417		2,5-diketo-D-gluconate reductase A	-2.90	-2.70	
c0457	*lacA*	Galactoside O-acetyltransferase	-2.41	-2.02	
c0611	*ybbL*	ABC transporter ATP-binding protein YbbL	-2.19	-2.23	
c0629	*ylbA*	Putative S-ureidoglycine aminohydrolase	-2.15	-2.18	
c1269		Hypothetical protein	-2.04		
c2350	*ybcL*	Kinase inhibitor	-2.76	-2.09	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c2385	*yedU*	Chaperone protein HchA	-2.30	-2.16	
c2389	*yedY*	Sulfite oxidase subunit YedY		-2.16	
c2411		DNA-binding protein H-NS	-2.81	-2.39	
c2495		Phosphotriesterase-related protein	-2.50		
c3455	*ygfJ*	Hypothetical protein	-3.50	-2.71	
c3567		Putative oxidoreductase	-2.68	-2.51	
c3706	*glcG*	Hypothetical protein	-2.01		
c4512		Hypothetical protein	-2.15	-2.05	
c5223	*fxsA*	FxsA, inhibits F exclusion of bacteriophage T7	-2.48		
c5457	*osmY*	Osmotically inducible protein Y precursor	-3.79	-3.81	
c1110	*yccA*	Putative Bax inhibitor	5.25		-3.95
c1569	*nohA*	DNA packaging protein of prophage	2.08		
c1571		Putative capsid protein of prophage	2.05		
c1925	*yddA*	ABC transporter ATP-binding protein		2.05	
c1993	*ydgG*	Putative quorum signal AI-2 exporter	3.09		-2.15
c2253	*yobB*	Hypothetical protein	4.43	4.24	
c4803	*yihE*	Serine/threonine protein kinase	3.53	3.07	
c5446	*fhuF*	Ferric iron reductase	4.11	3.70	
UNCLASSIFIED					
c0043	*caiF*	DNA-binding transcriptional activator	-2.57	-2.47	
c0200	*yaeH*	Hypothetical protein	-2.38	-2.28	
c0279		Hypothetical protein	-2.43	-2.88	
c0280		Hypothetical protein	-2.56	-3.52	
c0281		Hypothetical protein	-2.71	-3.79	
c0282		Hypothetical protein	-2.08	-4.61	-2.53
c0283		Hypothetical protein	-2.33	-4.54	-2.21
c0286		Hypothetical protein		-3.80	-3.36
c0370	*yfkE*	C-lysozyme inhibitor	-6.03	-5.68	
c0166	*yadC*	Fimbrial-like adhesin protein	-2.15		

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c0402	*yagX*	Putative usher protein		-2.20	
c0399	*yagU*	Hypothetical protein	-6.27	-3.54	2.73
c0403	*yagY*	Putative fimbrial chaperone	-2.21	-2.84	
c0404	*matB*	Putative common pilus-major subunit	-2.40	-2.86	
c0449	*yahO*	Hypothetical protein	-4.71	-4.55	
c0489	*yaiB*	Putative anti-adaptor protein	-3.90	-3.45	
c0491	*psiF*	Phosphate starvation-inducible protein	-2.20		
c0501	*ykiA*	Hypothetical protein	-2.51	-2.42	
c0605	*ybaS*	Glutaminase	-3.19	-2.90	
c0651		Hypothetical protein	-2.30		
c0697		Hypothetical protein	-2.03		
c0713	*pagP*	Palmitoyl transferase	-3.53	-3.46	
c0807		Hypothetical protein	-2.45		
c0829	*ybgS*	Hypothetical protein	-2.20	-2.05	
c0935	*coxT*	Regulator for prophage	-2.95	-3.55	
c0936		Putative phage regulatory protein	-2.95	-3.69	
c0937		Hypothetical protein	-2.93	-3.65	
c0938		Hypothetical protein	-3.29	-3.99	
c0939		Hypothetical protein	-2.78	-3.27	
c0943		Putative DNA damage inducible protein-like family protein	-3.22	-3.72	
c0944		Hypothetical protein	-2.27	-2.30	
c0945		Hypothetical protein	-2.20	-2.38	
c0946		Hypothetical protein		-2.05	
c0979	*ogrK*	Prophage P2 Ogr protein	-2.28	-2.98	
c1009	*aqpZ*	Aquaporin Z	-3.51	-3.33	
c1082	*ycbW*	Hypothetical protein	-3.16	-2.87	
c1124	*sfa*	Cold shock gene	-2.66	-2.28	
c1160	*pgaD*	PGA biosynthesis protein	-2.25		
c1125		GnsB protein		-2.11	
c1202		Hypothetical protein	-2.25	-2.47	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c1203		O-methyltransferase	-2.31	-2.48	
c1204		Hypothetical protein	-2.80	-2.76	
c1246		Putative diguanylate phosphodiesterase	-4.07	-3.57	
c1270		Hypothetical protein	-2.08		
c1308	*ymdA*	Hypothetical protein	-2.51	-2.12	
c1327	*bssS*	Biofilm formation regulatory protein BssS	-3.78	-3.47	
c1386	*ycfR*	Hypothetical protein	-2.01		
c1418		Hypothetical protein	-2.91	-2.23	
c1429	*ycgW*	Enhancing lycopene biosynthesis protein 1	-2.86	-2.41	
c1474		Putative SAM-dependent methyltransferase	-2.21		
c1564	*ybcU*	Lambdoid prophage DLP12 Bor-like protein	-2.65	-2.04	
c1609	*ymgB*	Putative regulator of acid resistance and biofilm formation	-2.39	-2.11	
c1625	*ycgJ*	Hypothetical protein	-3.03	-2.79	
c1663	*ychH*	Putative stress induced protein	-2.31	-2.11	
c1856	*ydcL*	Lipoprotein YdcL	-3.48	-3.08	
c1885		Hypothetical protein	-2.21		
c1886		Hypothetical protein	-3.24	-2.69	
c1913	*rpsV*	30S ribosomal subunit S22	-2.17		
c1914		Biofilm-dependent modulation protein	-2.06	-2.12	
c1919		Hypothetical protein	-3.39	-3.18	
c1939	*oprR*	Putative transcriptional regulator	-2.37		
c2017	*ydgT*	OriC-binding nucleoid-associated protein	-4.03	-3.10	
c2018	*ydgK*	Hypothetical protein	-2.34		
c2091	*ydiP*	Transcriptional regulator	-2.80	-2.52	
c2092		Hypothetical protein	-3.04	-2.62	
c2099	*ydiA*	Putaive phosphoenolpyruvate synthase regulatory protein	-2.57	-2.46	
c2103	*ydiV*	Putative anti-flhdc factor	-2.44	-2.24	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c2201		Hypothetical protein	-2.64		
c2214	*yoaC*	Hypothetical protein	-3.76	-3.33	
c2215		Hypothetical protein	-2.48	-2.05	
c2233	*yebO*	Hypothetical protein	-2.40	-2.06	
c2234	*yobG*	Putative Pho family transcriptional regulator	-2.67	-2.32	
c2235		Hypothetical protein	-2.54	-2.50	
c2320		Hypothetical protein	-2.60	-2.24	
c2329	*yecF*	Hypothetical protein	-2.01		
c2336	*fliZ*	Flagella biosynthesis protein FliZ	-2.11		
c2349	*ybcM*	Transcriptional regulator YbcM	-2.55	-2.01	
c2351	*ybcL*	Putative phospholipid-binding protein	-2.17		
c2388		Transthyretin-like protein	-2.89	-2.64	
c2406		Hypothetical protein	-2.08		
c2466		Putative D-alanine--poly(phosphoribitol) ligase	-2.29		
c2470		Peptide/polyketide synthase	-2.51		
c2490		Hypothetical protein	-2.11		
c2606	*yegP*	Hypothetical protein	-2.49	-2.49	
c2640	*yehE*	Hypothetical protein	-2.40	-2.13	
c2748		Hypothetical protein	-2.02		
c2794	*ais*	Ais protein	-4.03	-3.74	
c2797	*yfbG*	Bifunctional UDP-glucuronic acid decarboxylase, UDP-4-amino-4-deoxy-L-arabinose formyltransferase	-3.20	-3.16	
c2798	*yfbH*	Putative deformylase	-2.91	-2.71	
c2800		Putative 4-amino-4-deoxy-L-arabinose phosphoundercaprenol flippase	-2.65	-2.27	
c2801	*yfbJ*	Putative undecaprenyl-phosphate-α-L-Ara4N flippase	-2.03		
c2893		Hypothetical protein	-2.92	-2.35	
c3207	*ygaT*	Hypothetical protein	-2.02	-2.63	
c3221	*ygaW*	Putative L-alanine exporter	-2.15		

Locus tag	**Gene**	**Description**	***cpxA* mutant vs *cpxR* mutant**[a]	***cpxA* mutant vs parent**[b]	***cpxR* mutant vs parent**[c]
c3316	*ygbE*	Hypothetical protein, membrane protein	-2.04		
c3394		Hypothetical protein	-2.28		
c3557		ShiA-like protein	-2.82	-2.51	
c3568		Hypothetical protein	-3.77	-3.17	
c3599		Hypothetical protein	-2.39		
c3601		Hypothetical protein, membrane protein	-3.15	-2.67	
c3682		Hypothetical protein	-2.00		
c3797	*glgS*	Glycogen synthesis protein GlgS	-2.91	-2.59	
c3798	*yqiJ*	Hypothetical protein, membrane protein	-2.24		
c4051	*mscL*	Large-conductance mechanosensitive channel	-3.13	-2.82	
c4177		Hypothetical protein	-2.16		
c4178		Putative toxin RelE	-2.09		
c4250		Hypothetical protein	-3.19	-2.70	
c4289	*yhiM*	Putative inner membrane protein with a role in acid resistance	-7.72	-7.19	
c4304	*slp*	Outer membrane protein Slp	-5.41	-4.93	
c4305		Hypothetical protein	-5.04	-4.57	
c4320	*hdeB*	Acid-resistance protein	-7.36	-6.66	
c4321	*hdeA*	Acid-resistance protein	-7.36	-6.74	
c4326	*yhiW*	Transcriptional regulator GadW	-3.83	-3.58	
c4327	*yhiX*	DNA-binding transcriptional regulator GadX	-2.85	-2.63	
c4366	*yhjY*	Hypothetical protein	-2.20		
c4380		Hypothetical protein, membrane protein	-2.04		
c4517		Hypothetical protein	-2.39	-2.13	
c4519		Hypothetical protein	-2.16		
c4585		Hypothetical protein	-2.76	-2.52	
c4650		Hypothetical protein	-2.24		
c4686	*yifE*	Hypothetical protein	-2.49	-2.05	
c4754		Hypothetical protein	-2.56	-2.34	
c4755		Putative HNH endonuclease	-2.32		

Locus tag	**Gene**	**Description**	***cpxA* mutant vs *cpxR* mutant**[a]	***cpxA* mutant vs parent**[b]	***cpxR* mutant vs parent**[c]
c4874	*yiiS*	Hypothetical protein	-3.23	-3.37	
c5000		Hypothetical protein	-2.09		
c5121	*adiY*	Regulatory protein	-2.93		
c5136		Toxin of the GhoTS toxin-antitoxin system	-2.62	-2.02	
c5197		Transposase	-2.70	-2.62	
c5205		Hypothetical protein	-2.02		
c5212		Hypothetical protein	-2.09		
c5387		Putative 9-O-acetyl-N-acetylneuraminate esterase	-2.56	-2.29	
c5405		Putative DNA replication/recombination/repair protein	-3.40	-3.33	
c5458		Hypothetical protein	-3.16	-3.15	
c5459		Hypothetical protein	-4.58	-4.26	
c0173		Hypothetical protein	6.10	6.17	
c0290		Hypothetical protein	2.02		
c0672		Hypothetical protein	6.88	5.06	
c0673	*entF*	Enterobactin synthase subunit F	4.43	4.61	
c0678	*ybdA*	Enterobactin exporter EntS	2.71	3.21	
c0682	*entB*	Isochorismatase	4.64	4.71	
c1233		Putative CAAX amino protease		2.13	
c1322	*yceI*	Hypothetical protein	2.79	2.30	
c1452		Hypothetical protein		2.01	
c1498		Hypothetical protein	3.01	2.61	
c1499		Capsid protein of prophage	2.71	2.50	
c1563	*ybcS*	Endopeptidase from lambdoid prophage DLP12	2.51		
c1570		DNA packaging protein of prophage		2.36	
c1574		Capsid protein of prophage	3.06	2.51	
c1575		Capsid protein of prophage	2.69	2.29	
c1576		Hypothetical protein	2.41		
c1577		Head-tail joining protein of prophage	2.14		

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c1578		Tail fiber component Z of prophage	2.11		
c1579		Tail component of prophage	2.76	2.46	
c1583		Tail component of prophage	2.46		
c1584		Tail component of prophage	2.20		
c1596		Hypothetical protein		2.07	
c1675		Putative small toxic polypeptide	4.06	3.93	
c1849	*ydcg*	Glucan biosynthesis protein D	2.41		
c1860	*yncJ*	Hypothetical protein	5.93	6.30	
c1963	*ydeH*	Putative diguanylate cyclase	3.31	3.32	
c2142		Hypothetical protein	2.99	3.08	
c2257		Hypothetical protein	2.67	3.07	
c2258	*yebE*	Hypothetical protein	6.44	5.65	
c2423		AraC type regulator	2.97	3.07	
c3004	*purC*	Phosphoribosylaminoimidazole-succinocarboxamide synthase		2.37	
c3030		SinI-like protein	2.82	2.83	
c3031		SinH-like protein	2.42	2.70	
c3080	*purL*	Phosphoribosylformylglycinamidine synthase	2.81	3.17	
c3104		Hypothetical protein		2.18	
c3121	*tyrA*	Bifunctional chorismate mutase/prephenate dehydrogenase	3.68	3.48	
c3127	*rplS*	50S ribosomal protein L19		2.13	
c3177	*cspI*	Cold shock-like protein CspI	4.53	3.37	
c3178		Hypothetical protein	4.83	3.39	
c3236	*ygaH*	Putative L-valine efflux transporter	3.27	2.77	
c3285	*hycA*	Formate hydrogenlyase regulatory protein HycA		2.61	
c3627	*iucA*	Putative aerobactin synthase		2.00	
c3782	*ygiA*	Hypothetical protein	2.38		
c3784	*ygiC*	Hypothetical protein	3.34		

Locus tag	Gene	Description	***cpxA* mutant vs *cpxR* mutant**[a]	***cpxA* mutant vs parent**[b]	***cpxR* mutant vs parent**[c]
c3854	*yqjB*	Putative component of osmoregulatory two-component signal transduction system	3.40	3.20	
c3911	*yhbU*	Putative protease YhbU	2.15		
c3912	*yhbV*	Hypothetical protein	2.21		
c3973	*gltB*	Glutamate synthase subunit alpha	2.83	2.48	
c3978	*nanT*	Putative sialic acid transporter	3.07	2.66	
c4077	*rpmC*	50S ribosomal protein L29	2.39	2.59	
c4078		Hypothetical protein		2.65	
c4081	*rpsC*	Hypothetical protein	2.59	2.74	
c4082	*rplV*	50S ribosomal protein L22	2.75	3.02	
c4086		Hypothetical protein	2.58	3.34	
c4088		Hypothetical protein		2.24	
c4089	*rplD*	50S ribosomal protein L4	2.83	3.09	
c4091	*rplC*	50S ribosomal protein L3	2.77	3.05	
c4185	*feoA*	Ferrous iron transport protein A	2.17	2.14	
c4187	*yhgG*	Putative DNA-binding transcriptional regulator		2.24	
c4310		Hypothetical protein	3.42	3.71	
c4312		Hypothetical protein	4.16	3.36	
c4315	*chuX*	Putative heme utilization carrier protein	5.57	5.56	
c4365	*yhjX*	Putative transporter	5.52	5.68	
c4376		Hypothetical protein	2.20	2.04	
c4693	*ilvD*	Dihydroxy-acid dehydratase	2.73	2.09	
c4804	*dsbA*	Periplasmic protein disulfide isomerase I	2.45	2.27	
c4819	*glnA*	Glutamine synthetase	3.27	2.95	
c4942		Hypothetical protein	2.19	2.39	
c4964	*purH*	Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase-IMP cyclohydrolase	2.48	3.25	
c5055		Hypothetical protein		3.05	
c5276	*yjfN*	Hypothetical protein	6.26	5.93	

Locus tag	Gene	Description	*cpxA* mutant vs *cpxR* mutant[a]	*cpxA* mutant vs parent[b]	*cpxR* mutant vs parent[c]
c5292	*rpsR*	30S ribosomal protein S18	2.07		
c5447		Hypothetical protein	2.42	2.29	
c5448		Hypothetical protein		2.12	
c5463	*yjjI*	Hypothetical protein	2.47	2.29	

[a] Genes differentially expressed in CFT073Δ*cpxA*::*cat* vs CFT073Δ*cpxR*::*cat*.

[b] Genes differentially expressed in CFT073Δ*cpxA*::*cat* vs CFT073.

[c] Genes differentially expressed in CFT073Δ*cpxR*::*cat* vs CFT073.

Values indicate fold change in expression of gene transcription; (-) minus sign indicates downregulation.

Table S3 Promoters of differentially regulated genes containing a consensus CpxR binding logo

Locus tag	Gene	Motif[a]	Strand[b]	Score[c]	Position[d]
c0040	*carA*	GTAAATCAATGCAAA	-	8.36735	-45, -31
c0197	*htrA*	GTAAATTACCGTCAG	+	15.6122	-269, -255
c0290		GCAAAAAACCGTAAA	-	17.7347	-108, -94
c0605	*ybaS*	GTAAAAGTCCGTAAA	+	17.7347	-171, -157
c0611	*ybbL*	GTAAAAATCAGAAAA	+	12.4592	-23, -9
c0652	*ompT*	GTAAAACCTTGCAAG	+	7.34694	-347, -333
c0924	*dacC*	GCAAAAAAATGACAC	+	11.4592	-144, -130
c0926	*ybjG*	GTTAAACTGGGTAAA	-	8.35714	-79, -65
c1009	*aqpZ*	GCAAATGTCTGAAAA	+	9.70408	-327, -313
c1011	*ybjD*	GCAAATGTCTGAAAA	-	9.70408	-106, -92
c1034	*ycaC*	GCAAAAGCATGACAG	+	10.8571	-247, -233
c1110	*yccA*	GTAAAGATGGGTAAA	+	16.9082	-84, -70
c1155		GCAAAGAAAAGTAAA	-	15.4694	-116, -102
c1204		TCAAAAAAATGTCAA	+	7.21429	-401, -387
c1418		GTAACGCTATGTAAG	+	8.20408	-61, -47
c1625	*ycgJ*	GCAAAAAATGGAAAG	-	12.8469	-201, -187
c1663	*ychH*	GTAAAGTATAGACAA	-	11.9184	-70, -56
c1676	*chaA*	ATAAAAAATCGTAAA	-	9.57143	-413, -399
c1676	*chaA*	GTAAAAATTCGTAAA	+	17.7449	-14, 0
c1676	*chaA*	GTAAAAAATCGACAG	+	14.5918	-33, -19
c1717	*tonB*	ATAAAGTAAGGTCAA	+	7.7449	-78, -64
c1849	*ydcg*	GTAAAATCAGGCAAA	-	7.65306	-198, -184
c1919		GCAAAGCATCGTTAA	-	7.92857	-435, -421
c1963	*ydeH*	GCAAAATTACGTCAA	-	15.7449	-59, -45
c1992	*ydgF*	GTAAAGAAGTGAAAA	+	15.898	-330, -316
c1993	*ydgG*	GTAAAGAAGTGAAAA	-	15.898	-95, -81
c2011	*hdhA*	GCAAAGCGGGGAAAG	+	11.9898	-339, -325
c2143	*spy*	GTAAAACAATGAAAG	-	16.7245	-119, -105
c2201		GCAAAGCAACGTATA	+	8.60204	-191, -177
c2238	*htpX*	GCAAGATGCCGTAAA	+	6.94898	-147, -133
c2253	*yobB*	GTAAGAAAGTGTAAC	-	8.14286	-90, -76
c2315	*yecI*	GTAAAAATATATAAA	+	8.71429	-194, -180
c2351	*ybcL*	ATAAAGTAGGGTAAG	-	8.42857	-173, -159
c2352	*emrE*	GCAAAGCGAAGACAA	-	10.0306	-190, -176
c2411		ATAAAACAACGTACA	+	7.83673	-284, -270
c2470		GCAAAAACATGTAAG	-	15.5816	-198, -184
c2471		GCAAAAACATGTAAG	+	15.5816	-429, -415
c2794	*ais*	GAAAAAAAATGTCAG	-	9.43878	-286, -272
c2915	*ddg*	GTAAAGACTAGTCAG	-	12.6327	-123, -109
c3217	*ygaP*	GTAAATGAGAGTAAA	-	15.0612	-394, -380
c3221	*ygaW*	GAAAATAAAGGTAAA	+	7.58163	-252, -238
c3460	*ygfO*	GGAAATCGGTGTAAA	+	7.13265	-231, -217
c3682		GTAAACGAAGGTAAG	+	16.449	-268, -254
c3863	*yhaJ*	GTAAAGAGAGGTCAA	-	16.2041	-98, -84
c4011	*accB*	GTGAAAAGCTGTAAA	-	8.55102	-447, -433
c4081	*rpsC*	GAAAAACTGCGTAAG	-	9.40816	-266, -252
c4138	*ppiA*	GTAAAATTAGGTAAA	+	17.7551	-91, -77
c4141	*nirB*	GCAAAAAACAGACAA	-	11.0408	-175, -161
c4323	*yhiE*	GCAAAAAAATGAACC	-	9.56122	-419,
c4607	*ibpA*	GCAAAAAAAAGTCCG	+	11.7347	-154
c4803	*yihE*	GTAAAAGCTTGTAAG	+	16.1633	-80, -66

Locus tag	**Gene**	**Motif**[a]	**Strand**[b]	**Score**[c]	**Position**[d]
c4864	*cpxR*	GTAAAACAACGTAAA	+	20.6122	-69, -55
c4864	*cpxR*	GCAAACATGCGTCAG	+	13.0204	-89, -75
c4865	*cpxP*	GTAAAACAACGTAAA	-	20.6122	-94, -80
c4865	*cpxP*	GCAAACATGCGTCAG	-	13.0204	-74, -60
c4964	*purH*	GTAAAAAGGTATAAA	-	8.86735	-240, -226
c5081		GTAATACCGCGTAAA	+	8.64286	-377, -363
c5247	*psd*	GTAAAAACGCGTAAA	+	17.9082	-134, -120
c5276	*yjfN*	GCAAAGCAATGTAAA	-	17.7449	-97, -83
c5393	*fimA*	GAAAAAATACGTAAC	-	7.27551	-346, -332
c5458		GCAAAAGCCAGTCCG	+	8.43878	-289, -275
c5463	*yjjI*	GCAAAACTCTGAAAG	-	12.551	-440, -426
c5479	*slt*	GTAAAAAAGTGTCCG	+	15.4694	-106, -92
c5479	*slt*	GTAACGTGGCGTAAA	+	8.65306	-92, -78

[a] Corresponds to the motif with the highest match score.

[b] +Template strand; -Complementary strand.

[c] Match score is the sum of individual position scores from each letter in the sequence.

[d] Position of the motif is relative to the position of the transcriptional start site for the gene/operon.

Table S4 qRT-PCR validation of RNA-Seq data

Expression Level	**Gene**	**RNA-Seq**[a]	**qRT-PCR**[b]
Low	*cusB*	-4.4	-22.7
	fimH	-2.4	-5.0
	nikC	2.4	13.6
	fepC	4.0	11.8
Medium	*sfaD*	-4.9	-84.1
	phoU	-3.7	-20.0
	dsbA	2.4	8.5
	ppiA	3.7	14.9
	chuW	5.8	408.9
High	*gadA*	-8.1	-620.5
	oppA	-2.1	-4.3
	glnA	3.3	14.1
	cpxP	5.2	46.5

[a] Fold change in the expression of select genes in the *cpxA* mutant relative to the *cpxR* mutant from RNA-Seq.

[b] Fold change in the expression of select genes in the *cpxA* mutant relative to the *cpxR* mutant from qRT-PCR. The expression levels of target genes were normalized to that of *gapA*. The data represent the mean of four independent experiments.

(-) minus sign indicates downregulation of gene expression in the *cpxA* mutant relative to the *cpxR* mutant.

Table S5 Primers used in this study

Primer (gene)	Purpose	5' to 3' sequence
P1	*cpxR* deletion	GACGTAATTTCTGCCTCGGAGGTATTTAAACAATGGTGTAGGCTGGAGCTGCTTC
P2	*cpxR* deletion	GATGGCGAAGATGCGCGCGGTTAAGCTGCCTATCAATGGGAATTAGCCATGGTCC
P3	*cpxA* deletion	CGTGGTCGCGGCTATCTGATGGTTTCTGCTTCATGATAGTGTAGGCTGGAGCTGCTT
P4	*cpxA* deletion	TAAACGCCTTATCCTGCCTACAAATGCGGAGTTTAATGGGAATTAGCCATGGTCC
P5	SDM[a]	GTCGCCAGGAAGCCAGCTTCGACGGGCAAAC
P6	SDM	GTTTGCCCGTCGAAGCTGGCTTCCTGGCGAC
P7	SDM	GTAATGCTCTGCGTTATTCCCATACGAAGATTG
P8	SDM	CAATCTTCGTATGGGAATAACGCAGAGCATTAC
P9 (*cusB* F)	qRT-PCR[b]	GCTTACCGTGGGCGATAAA
P10 (*cusB* R)	qRT-PCR	TAAATACTCACTCTGCGCTTCC
P11 (*fimH* F)	qRT-PCR	CTTATGGCGGCGTGTTATCT
P12 (*fimH* R)	qRT-PCR	CGGCTTATCCGTTCTCGAATTA
P13 (*nikC* F)	qRT-PCR	CGCGTCGCTGATATGTTTATG
P14 (*nikC* R)	qRT-PCR	GACAGGGCGATGGCTATAAT
P15 (*fepC* F)	qRT-PCR	AACCGCGAGAAAGGCTATAC
P16 (*fepC* R)	qRT-PCR	CTTCCCGCAATGCAATCAAA
P17 (*sfaD* F)	qRT-PCR	AGAACTGGGTGCATCTTACC
P18 (*sfaD* R)	qRT-PCR	CATACCTGTCCATTTGCCTTTC
P19 (*phoU* F)	qRT-PCR	GTCATCGAAGGCGACAAGAA
P20 (*phoU* R)	qRT-PCR	GCTGACGTTTGGCGATAATG
P21 (*dsbA* F)	qRT-PCR	AGTCACAGTTCCGCTGTTT
P22 (*dsbA* R)	qRT-PCR	GCGTCGTACTCTTCACCTTT
P23 (*ppiA* F)	qRT-PCR	CCACCAGCCAGTTCTTTATCA
P24 (*ppiA* R)	qRT-PCR	GCCTTTCACCACTTTACCAAATAC
P25 (*chuW* F)	qRT-PCR	ACGCGAACGCAATCTCTATAA
P26 (*chuW* R)	qRT-PCR	GTTCGTTCATCCAGGAGTACC
P27 (*gadA* F)	qRT-PCR	CAGGCAAACCAACGGATAAAC
P28 (*gadA* R)	qRT-PCR	CATAGGGATCTCACGCAACTC
P29 (*oppA* F)	qRT-PCR	TCTCGGCGTGAAAGCTATTG
P30 (*oppA* R)	qRT-PCR	CGGTGAAGTTGATGGGTGAA
P31 (*glnA* F)	qRT-PCR	TGTTCGGTGATAACGGTTCC
P32 (*glnA* R)	qRT-PCR	GTTCAGACAGACCTGCGTATT
P33 (*cpxP* F)	qRT-PCR	CGCTGGCAGTCAGTTCATTA
P34 (*cpxP* R)	qRT-PCR	AACATATGGCTCTGCGTACTG
P35 (*cpxR* F)	qRT-PCR	ACCGACACTGGAAGTTGATG
P36 (*cpxR* R)	qRT-PCR	CCAGCAAATAGAGCAGGGTAA
P37 (*cpxA* F)	qRT-PCR	CCGATCATCCGCAGAAGAAA
P38 (*cpxA* R)	qRT-PCR	GGCCGGACGAATCAGATAAA
P39 (*gapA* F)	qRT-PCR	CGGTACCGTTGAAGTGAAAGA
P40 (*gapA* R)	qRT-PCR	CTAACCTGAAATGGGACGAAGT
P41 (*fimA* promoter F)	Reporter construct	GGA**AGATCT**TTGCCGGATTATGGGAAAGA
P42 (*fimA* promoter R)	Reporter construct	GGA**AGATCT**TTTGTTTTGTCAACGAGTTTG
P43 (*hlyA* promoter F)	Reporter construct	GGA**AGATCT**ATATTTTAGAGTATACTTGCGCACC
P44 (*hlyA* promoter R)	Reporter construct	GGA**AGATCT**TGCGGTGGCAGGTAAAAAAAAG
P45 (*gfp* R)	Reporter construct	CCTTCACCCTCTCCACTGACAG

[a] SDM, site directed mutagenesis; [b] qRT-PCR, quantitative real time polymerase chain reaction; underline indicates mutagenic nucleotide; boldfaced text indicates regions corresponding to restriction enzyme sites as mentioned in the text.