

Appendix 2: Transcripts significantly up-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product	Log ₂ fold change: 630 Δ spo0A vs 630	P value
CD0065	NADP-dependent 7-alpha-hydroxysteroid dehydrogenase	3.629862769	2.36E-36
CD0107 (AspC)	aspartate aminotransferase	0.716100658	0.006971664
CD0112 (Ptb)	phosphate butyryltransferase	0.667104568	0.007921769
CD0113 (Buk)	butyrate kinase	0.663624022	0.008116098
CD0118	putative subunit of oxidoreductase	0.654815836	0.006973221
CD0179 (GluD)	NAD-specific glutamate dehydrogenase	0.654479793	0.003816227
CD0205	putative transcription antiterminator, PTS operon regulator	6.09623072	1.45E-28
CD0206	PTS system, IIa component	3.886913238	0.000858762
CD0207	PTS system, IIc component	4.770150537	1.22E-10
CD0208	PTS system, IIb component	5.3760065	3.90E-08
CD0209	putative sugar-phosphate kinase	5.205948535	1.31E-40
CD0226	putative transglycosylase	0.971434538	0.001330514
CD0239 (FliC)	flagellin subunit	0.64993773	0.005144783
CD0241	phosphoserine phosphatase	1.106961294	4.19E-06
CD0242	conserved hypothetical protein	1.004382201	7.69E-05
CD0243	conserved hypothetical protein	1.14223852	1.05E-07
CD0244	putative CDP-Glycerol:Poly(glycerophosphate) glycerophosphotransferase	1.090609331	5.26E-07
CD0248 (FliF)	flagellar M-ring protein	0.691937512	0.008339449
CD0249 (FliG)	flagellar motor switch protein	0.704163503	0.007552048
CD0250 (FliH)	flagellar assembly protein	1.068085331	0.0006144
CD0252 (FliJ)	flagellar protein	1.005917227	0.000186141
CD0253 (FliK)	putative flagellar hook-length control protein	0.894553529	0.000337475
CD0255A	putative flagellar protein	1.020396977	0.009696913
CD0283	putative transcription antiterminator	1.217971016	0.001556487
CD0285	PTS system, IIb component	4.027424265	0.00051567
CD0288	PTS system, IIc component	2.471850245	0.000560242
CD0289	PTS system, IId component	2.653617296	0.002597411
CD0292	DNA-binding protein / transcriptional regulator	4.302473109	2.44E-22
CD0293	ABC transporter, ATP-binding protein / bacitracin multidrug family ATP-binding protein	4.630995313	2.99E-21
CD0294	putative ABC transporter, permease protein / bacitracin/multidrug family permease	5.189801595	1.26E-33
CD0301 (RbsA)	ribose ABC transporter, ATP-binding protein	2.724347261	8.87E-07
CD0302 (RbsC)	ribose ABC transporter, permease protein	2.55763691	0.000166061
CD0303 (ArgE)	putative acetylornithine deacetylase	2.58181175	0.000223451
CD0340	conserved hypothetical protein	1.229288604	3.71E-09
CD0341	conserved hypothetical protein	1.639166338	2.62E-08
CD0395 (HadA/FldA)	isocaprooyl-CoA:2-hydroxyisocaproate CoA-transferase	0.66373869	0.002918154
CD0396 (HadI/FldI)	activator of 2-hydroxyisocaproyl-CoA dehydratase	0.711457875	0.001199908
CD0397 (HadB/FldB)	subunit of oxygen-sensitive 2-hydroxyisocaproyl-CoA dehydratase	0.781900155	0.000219189
CD0398 (HadC/FldC)	subunit of oxygen-sensitive 2-hydroxyisocaproyl-CoA dehydratase	0.604290822	0.00918678
CD0399 (AcdB/Bcd1)	acyl-CoA dehydrogenase, short-chain specific	0.67187765	0.002613865
CD0400 (EtfB1)	electron transfer flavoprotein beta-subunit	0.887548384	1.60E-05
CD0529	putative membrane protein	0.952512987	0.00163008
CD0587	conserved hypothetical protein	1.713471592	1.23E-05
CD0588	hypothetical protein	1.300071341	0.000560242
CD0616	MerR-family transcriptional regulator	1.96436041	1.35E-08
CD0617	putative membrane protein	1.786565014	0.00288371
CD0618	putative transcriptional regulator	2.091158099	1.58E-05

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CD0663 (TcdA)	toxin A	0.967520109	6.42E-06
CD0715	putative phosphate butyryltransferase	0.933229347	0.00491507
CD0758 (PlfA)	pyruvate formate-lyase activating enzyme	1.252297367	0.000201317
CD0759 (PlfB)	formate acetyltransferase	1.670841387	8.45E-18
CD0893	iron-dependent hydrogenase	1.514860175	3.05E-12
CD0939	hypothetical phage protein	1.550823074	5.17E-06
CD1022	putative membrane protein	1.200660139	0.009155858
CD1064 (CcpA)	LacI-family transcriptional regulator (catabolite control protein)	1.006380139	0.004894689
CD1080	putative lipoprotein	2.045597495	4.79E-13
CD1137 (RnfC)	electron transport complex protein	0.679398699	0.00342762
CD1138 (RnfD)	electron transport complex protein	0.901879171	5.21E-05
CD1139 (RnfG)	electron transport complex protein	0.897363148	0.000249919
CD1141 (RnfA)	electron transport complex protein	0.86340992	5.84E-05
CD1142 (RnfB)	electron transport complex protein	0.832619392	0.000572698
CD1144 (RadC)	DNA repair protein	0.794502153	0.003404511
CD1148	putative penicillin-binding protein	0.751729324	0.001715852
CD1191 (Fbp)	putative fructose-1,6-bisphosphatase	0.939868722	0.00012966
CD1260	branched chain amino acid transport system carrier protein	0.814368658	0.000254892
CD1348	putative lipoprotein	0.974119915	0.005090336
CD1494	putative transcriptional regulator	1.49340953	7.86E-09
CD1495 (ProC1)	pyrroline-5-carboxylate reductase	1.336135433	2.14E-08
CD1522	putative polysaccharide deacetylase	1.858413598	9.97E-16
CD1579	putative two-component histidine kinase	2.729188221	7.67E-15
CD1654 (LplA)	putative lipoate-protein ligase	1.706598706	3.27E-10
CD1708	conserved hypothetical protein	1.434839086	1.43E-07
CD1716	probable permease	1.697555732	2.24E-12
CD1717	conserved hypothetical protein	1.531136235	0.0002403
CD1718	putative hydantoinase	1.063994467	1.73E-05
CD1768	putative membrane protein	1.702253209	1.33E-18
CD1796	putative nitrite and sulfite reductase subunit	1.408566164	2.81E-06
CD1797	putative pyridine nucleotide-disulfide oxidoreductase	1.533215901	7.86E-09
CD1893	putative regulatory protein	1.21619771	0.009604073
CD1930	putative exported protein	1.308492935	0.001715852
CD2007 (Erm2(B))	erythromycin resistance protein- rRNA adenine N-6-methyltransferase	5.242933225	2.02E-90
CD2010 (Erm1(B))	erythromycin resistance protein- rRNA adenine N-6-methyltransferase	5.10006667	2.25E-61
CD2052	putative lipoprotein	1.184949348	0.005176864
CD2134	putative signaling protein	2.242591734	1.08E-10
CD2156	radical SAM-superfamily protein	1.01433679	2.11E-05
CD2175	probable amino-acid ABC transporter, permease protein	0.69702847	0.003237738
CD2177	probable amino-acid ABC transporter, substrate-binding protein	0.734721854	0.00219319
CD2214	putative regulatory protein	3.535392369	6.44E-56
CD2215	putative regulatory protein	4.287173128	5.64E-20
CD2305	putative pilin protein	2.220923226	0.001789576
CD2338 (AbfH)	NAD-dependent 4-hydroxybutyrate dehydrogenase	3.259168739	0.000438995
CD2339 (AbfT)	4-hydroxybutyrate CoA transferase	3.157366059	5.71E-05
CD2340	conserved hypothetical protein	2.96442692	4.81E-06
CD2341 (AbfD)	gamma-aminobutyrate metabolism dehydratase/isomerase [includes: 4- hydroxybutyryl-coa dehydratase; vinylacetyl-coa-delta- isomerase]	3.689464172	2.63E-05

Appendix 2: Transcripts significantly up-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product	Log ₂ fold change: 630 Δ spo0A vs 630	P value
CD2342 (SucD)	succinate-semialdehyde dehydrogenase [NAD(P)+]	4.826850593	3.07E-15
CD2343 (Cat1)	succinyl-CoA:coenzyme A transferase	4.595958513	9.49E-05
CD2344	putative membrane protein	4.186502319	0.001866395
CD2379	butyrate kinase	1.24419252	6.32E-06
CD2380 (lorB)	putative indolepyruvate oxidoreductase subunit	1.830018405	6.19E-07
CD2381 (lorA)	indolepyruvate oxidoreductase subunit	1.814405546	1.03E-14
CD2382	putative aspartate aminotransferase	1.54588669	2.13E-10
CD2417 (SrlE)	PTS system, glucitol/sorbitol-specific IIbc component	4.280426592	0.000944418
CD2502	putative histidinol-phosphate aminotransferase	0.927784357	0.000680281
CD2625	putative membrane protein	1.298949868	0.000111432
CD2711	LysR-family transcriptional regulator	1.711595038	6.76E-07
CD2755 (PtsI)	phosphoenolpyruvate-protein phosphotransferase	0.689931477	0.002490116
CD2757	putative phospholipase	0.797211818	0.001397758
CD2765	putative penicillin-binding protein repressor	2.199301337	2.18E-24
CD2796	cell surface protein	2.439933041	1.01E-13
CD2797	putative exported protein	2.608806934	5.22E-25
CD2830	putative exported protein	2.041806735	1.33E-19
CD2853 (DltA)	D-alanine--poly(phosphoribitol) ligase subunit I (D-alanine-activating enzyme)	0.693180152	0.008974023
CD3036	proton-dependent oligopeptide transporter/major facilitator superfamily	4.388137962	1.44E-83
CD3127	PTS system, IIabc component	1.221580142	0.008082314
CD3133	transcription antiterminator	1.00605468	0.008970866
CD3158	conserved hypothetical protein	3.304133839	2.18E-12
CD3165	conserved hypothetical protein	1.678616513	0.00088117
CD3166	putative transcriptional regulator	2.265313701	0.005200464
CD3246	putative surface protein	1.095665394	1.48E-07
CD3404 (Cls)	putative cardiolipin synthetase	0.741429305	0.001244253
CD3406 (HymB)	putative iron-only hydrogenase, electron-transferring subunit	0.903922783	3.17E-05
CD3407 (HymC)	putative iron-only hydrogenase, catalytic subunit	0.689917122	0.00337708
CD3458	putative membrane protein	0.820554311	0.000409987
CD3555	conserved hypothetical protein	1.423465908	1.10E-08
CD3556	putative membrane protein	1.227409985	1.43E-07
CD3664	putative amino acid aminotransferase	1.794066616	3.90E-08

Appendix 3: Transcripts significantly down-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product	Log ₂ fold change: 630 Δ spo0A vs 630	P value
CD0022	putative translation elongation factor	-1.435177186	7.27E-10
CD0126 (SpoIIID)	stage III sporulation protein D	-3.975328311	0.003988481
CD0142	putative RNA-binding protein	-1.057363331	7.96E-05
CD0148	conserved hypothetical protein	-2.800686067	0.001061682
CD0157	putative membrane protein (pseudogene)	-2.921178976	3.82E-28
CD0311	hypothetical protein	-4.063410917	2.84E-08
CD0324 (CbiM)	putative cobalt transport protein	-0.662863884	0.003886953
CD0326 (CbiQ)	cobalt transport protein	-0.687187275	0.00247577
CD0330	conserved hypothetical protein	-0.9778842	0.00479394
CD0388 (BglP)	PTS system, beta-glucoside-specific IIabc component	-1.198511551	0.000409987
CD0390 (BglG)	beta-glucoside bgl operon transcription antiterminator	-1.460948584	0.007552048
CD0440 (similar to Cwp66)	cell surface protein	-2.317288463	6.46E-07
CD0556	putative endonuclease	-1.158315896	0.005729237
CD0557	putative phosphoribulokinase/uridine kinase	-0.960163231	0.002774647
CD0571	conserved hypothetical protein	-1.822649957	0.000112801
CD0572	conserved hypothetical protein	-1.980269174	0.0014809
CD0684	putative ATP-dependent peptidase	-29.329564	4.96E-25
CD0692	conserved hypothetical protein	-2.117895493	2.78E-05
CD0744 (MotD)	putative chemotaxis protein	-1.297760076	0.001494966
CD0745 (MotB)	putative chemotaxis protein	-1.336759872	0.000419336
CD0760	Ca ²⁺ /Na ⁺ antiporter	-1.935407687	0.001134617
CD0770 (SpoIIAA)	anti-sigma F factor antagonist	-3.012104306	2.61E-06
CD0771 (SpoIIAB)	anti-sigma F factor	-2.219236598	7.24E-05
CD0772 (SpoIIAC/SigF)	RNA polymerase sigma-F factor	-2.398756207	3.59E-07
CD0788	putative ATP/GTP-binding protein	-1.21715207	3.77E-05
CD0816	PTS system, IIabc component	-0.862058451	0.000684304
CD0818	putative 6-phospho-beta-glucosidase	-0.926227909	0.001384179
CD0865	conserved hypothetical protein	-1.127403392	0.000217448
CD0866	putative exported protein	-1.209772024	8.10E-05
CD0874	ABC transporter, ATP-binding protein	-1.312243261	2.98E-08
CD0875	ABC transporter, permease protein	-1.287872019	0.002535493
CD0877	ABC transporter, ATP-binding protein	-0.990828424	0.00913806
CD0878	ABC transporter, permease protein	-1.176685562	3.59E-07
CD0940A	hypothetical phage protein	-1.989048324	6.32E-06
CD0941	phage protein	-1.569897167	1.20E-05
CD1054 (Bcd2)	butyryl-CoA dehydrogenase	-2.5961265	1.83E-22
CD1055 (EtfB2)	electron transfer flavoprotein beta-subunit	-2.683497328	2.36E-36
CD1056 (EtfA2)	electron transfer flavoprotein alpha-subunit	-2.686059258	1.05E-12
CD1057 (Crt2)	3-hydroxybutyryl-CoA dehydratase	-3.090695365	3.57E-45
CD1058 (Hdb)	3-hydroxybutyryl-CoA dehydrogenase	-2.518020502	8.99E-33
CD1059 (ThlA1)	acetyl-CoA acetyltransferase	-2.34691265	2.43E-08
CD1065	hypothetical protein	-6.164172544	6.62E-05
CD1079	LysR-family transcriptional regulator	-2.12449871	2.87E-10
CD1085	putative membrane protein	-1.691085931	2.69E-09
CD1086	putative peptidase	-1.667458643	1.58E-05
CD1168	putative membrane protein	-4.675401845	1.83E-12
CD1192 (SpoIIAA)	stage III sporulation protein AA	-26.578922	0.000979086
CD1193 (SpoIIAB)	stage III sporulation protein AB	-27.081907	2.35E-05
CD1195 (SpoIIAD)	stage III sporulation protein AD	-26.249808	0.005629832
CD1196 (SpoIIAE)	stage III sporulation-related protein	-27.731001	1.97E-07
CD1198 (SpoIIAG)	stage III sporulation protein AG	-26.32129	0.004082152
CD1199 (SpoIIAH)	putative stage III sporulation protein AH	-5.280906841	0.0044163

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Identifier (gene name)	Product	Log ₂ fold change: 630 Δ spo0A vs 630	P value
CD1388	putative transcriptional regulator (pseudogene)	-1.428025955	0.006009262
CD1416	putative membrane protein	-26.226648	0.006999155
CD1484 (SsuA)	putative aliphatic sulfonates ABC transporter, substrate-binding lipoprotein	-2.432897557	2.54E-15
CD1492	putative two-component sensor histidine kinase	-2.923130388	1.72E-29
CD1493	putative 3-methyladenine DNA glycosylase	-3.241054631	0.00022301
CD1498 (RpoD2/SigA2)	RNA polymerase sigma factor rpoD	-0.818609088	0.00288371
CD1511	conserved hypothetical protein	-3.145446944	3.48E-06
CD1513 (PanB)	3-methyl-2-oxobutanoate hydroxymethyltransferase	-1.607863456	0.000611659
CD1514	conserved hypothetical protein	-1.260956275	0.001575776
CD1524	putative rubrerythrin	-1.321718368	1.22E-08
CD1526 (PyrC)	dihydroorotase	-1.285512307	7.13E-06
CD1657	putative bi-functional glycine dehydrogenase/aminomethyl transferase protein	-0.88258665	0.000657741
CD1658 (GcvPB)	glycine cleavage system P protein	-1.227982087	5.38E-08
CD1826 (MetA)	homoserine O-succinyltransferase	-1.298920427	0.001775008
CD1883	AraC-family transcriptional regulator	-1.515866812	0.00163008
CD1928	putative membrane protein	-5.249334334	4.55E-08
CD1940	putative membrane protein	-6.248545995	0.000735822
CD1941	hypothetical protein	-2.503401151	1.44E-05
CD1967	hypothetical protein	-2.539605421	3.10E-13
CD1993	putative decarboxylase	-2.307234533	6.86E-09
CD1996	AraC-family transcriptional regulator	-1.267759294	0.001235725
CD2127	putative membrane protein	-0.999574513	1.07E-05
CD2181	putative aromatic compounds hydrolase	-2.124774595	9.05E-15
CD2195	ferritin	-0.746373738	0.001544703
CD2216	hypothetical protein	-1.83442299	3.06E-06
CD2246 (CspC)	putative germination-specific protease	-2.540054266	2.78E-05
CD2247 (CspBA)	putative germination-specific protease	-1.935437381	3.60E-05
CD2261	peptidase	-1.046223325	6.90E-05
CD2295	putative membrane protein	-1.741024125	0.000419336
CD2373	putative carbon starvation protein	-1.924325732	8.51E-10
CD2396	conserved hypothetical protein	-1.587879958	5.45E-05
CD2445	probable sensory protein	-2.448449672	0.001924126
CD2509	probable 6-phospho-alpha-glucosidase	-1.325519571	0.001064996
CD2518 (similar to Cwp66)	cell surface protein	-1.548613884	6.70E-05
CD2612	putative amino acid permease	-1.90022516	1.36E-16
CD2613	probable peptidase	-1.738939315	3.05E-12
CD2629 (SpoIVA)	stage IV sporulation protein A	-4.777663355	4.13E-05
CD2635	putative membrane protein	-26.813826	0.000186406
CD2642 (SigG)	RNA polymerase sigma-G factor	-4.068242153	3.05E-05
CD2643 (SigE)	RNA polymerase sigma-E factor	-5.468253694	7.40E-05
CD2644 (SpoIIIGA)	sporulation sigma-E factor processing peptidase	-5.55102365	8.32E-09
CD2656 (SpoVD)	stage V sporulation protein D (sporulation specific penicillin-binding protein)	-3.348406137	2.25E-05
CD2664 (MurE)	putative UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	-1.683182898	2.52E-14
CD2665	AraC-family transcriptional regulator	-2.02285346	3.23E-19
CD2666 (Crr)	PTS system, glucose-specific IIa component	-1.75518228	3.93E-18
CD2667 (PtsG)	PTS system, glucose-specific IIbc component	-1.873657473	8.56E-23
CD2668 (LicT)	putative transcription antiterminator	-0.949017301	8.76E-05
CD2762 (UppS)	undecaprenyl pyrophosphate synthetase	-1.962619932	0.001002204
CD2767	cell surface protein	-0.922492114	6.61E-05
CD2809	conserved hypothetical protein	-26.622358	0.000740048

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CD2833	putative transport-related ATPase	-1.841321914	0.008058772
CD2864	putative esterase/halogenase	-27.230417	0.000219189
CD2865	putative bacterioferritin	-26.713903	0.000418474
CD2925	putative phage protein	-1.55946053	0.000106244
CD2955 (NtpB)	V-type sodium ATP synthase subunit B	-1.111520268	1.44E-05
CD2956 (NtpA)	V-type sodium ATP synthase subunit A	-1.010969553	0.000695137
CD2960 (NtpI)	V-type sodium ATP synthase subunit I	-0.825045552	0.00315282
CD2976	conserved hypothetical protein	-1.006181833	0.003230324
CD2978	conserved hypothetical protein	-0.806426976	0.009956438
CD2979	conserved hypothetical protein	-1.097398909	0.008285489
CD2981	hypothetical protein	-1.011829422	0.004867338
CD2982	conserved hypothetical protein	-1.336389137	0.003404511
CD3024	hypothetical protein	-3.727826742	0.000245753
CD3115 (BglA2)	putative 6-phospho-beta-glucosidase	-1.967807773	1.07E-12
CD3116 (BglF)	PTS system, beta-glucoside-specific IIabc component	-1.641631203	1.04E-08
CD3117 (BglG)	putative beta-glucoside bgl operon transcription antiterminator	-1.541172813	6.42E-06
CD3136 (BglA3)	6-phospho-beta-glucosidase	-2.654221294	4.92E-08
CD3137	PTS system, IIabc component	-2.865759926	1.59E-11
CD3138	transcription antiterminator	-1.6703225	7.13E-06
CD3145	putative serine-aspartate-rich surface anchored fibrinogen-binding protein	-2.129318471	2.66E-16
CD3174 (GapB)	glyceraldehyde-3-phosphate dehydrogenase 2	-0.982134737	5.22E-06
CD3175 (CggR)	central glycolytic genes regulator	-0.741566216	0.001307703
CD3235	single-stranded DNA binding protein	-3.810725337	2.20E-08
CD3257	putative polysaccharide deacetylase	-3.722115835	6.84E-05
CD3285 (Pgi)	glucose-6-phosphate isomerase	-1.399851788	3.27E-10
CD3298	putative ATP/GTP-binding protein	-4.276778621	1.44E-05
CD3314 (HydA)	hydrogenase	-0.831654059	0.008974023
CD3457	putative exported protein	-3.773602179	0.00397641
CD3489	putative oligopeptidase	-2.837469603	4.84E-06
CD3490 (SpoIIE)	stage II sporulation protein E	-7.151965308	4.41E-17
CD3522	conserved hypothetical protein	-3.870995792	4.04E-06
CD3563	putative spore cortex-lytic enzyme	-3.364344455	0.00280839
CD3569	putative peptidase	-1.517845811	0.004165547

Appendix 4: Proteins significantly up-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product
CD2010 (Erm1(B))	rRNA adenine N-6-methyltransferase (erythromycin resistance protein)
CD2352 (GrdA)	glycine/sarcosine/betaine reductase complex component A
CD1717	conserved hypothetical protein
CD2227	putative radical SAM superfamily lipoprotein
CD1767 (GapA)	glyceraldehyde-3-phosphate dehydrogenase
CD0065	NADP-dependent 7-alpha-hydroxysteroid dehydrogenase
CD1177 (FapR)	DeoR-family transcriptional regulator (fatty acid and phospholipid biosynthesis regulator)
CD1799	tellurium resistance protein
CD1037	hypothetical protein
CD2348 (GrdD)	glycine/sarcosine/betaine reductase complex component C alpha subunit
CD1712 (MoaB)	putative molybdenum cofactor biosynthesis protein
CD1226	putative exported aminodeoxychorismate lyase
CD1165	conserved hypothetical protein
CD3438 (CobU)	bifunctional adenosylcobalamin biosynthesis protein [includes: adenosylcobinamide kinase and adenosylcobinamide-phosphate guanylyltransferase]
CD3015	PTS system, IIa component
CD2128 (IspG)	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
CD0153 (HpdB)	4-hydroxyphenylacetate decarboxylase, catalytic subunit
CD1316 (RpsO)	30S ribosomal protein S15
CD2558 (CoaD)	phosphopantetheine adenylyltransferase
CD3090 (TreR)	GntR-family transcriptional regulator
CD0865	conserved hypothetical protein
CD1838 (AroK)	shikimate kinase
CD3157 (SmpB)	SsrA-binding protein
CD2114	two-component system response regulator
CD2622	conserved hypothetical protein
CD0835	MarR-family transcriptional regulator
CD2764	putative hydrolase
CD2796	cell surface protein
CD2008	putative plasmid replication protein
CD0265 (FleN)	flagellar number regulator
CD0829	metallo-beta-lactamase superfamily protein
CD1676 (Pcp)	pyrrolidone-carboxylate peptidase
CD3290	putative protein translocase
CD3039	conserved hypothetical protein
CD0208	PTS system, IIb component
CD1209 (RecN)	DNA repair protein
CD3405 (HymA)	putative iron-only hydrogenase, electron-transferring subunit
CD1816 (Cmk)	cytidylate kinase
CD0279	conserved hypothetical protein
CD1979	ABC transporter, substrate-binding protein
CD3555	conserved hypothetical protein
CD1618	ABC transporter, ATP-binding protein
CD1400	conserved hypothetical protein
CD0081 (RpsQ)	30S ribosomal protein S17
CD2748	putative transferase
CD2588 (Gmk)	guanylate kinase
CD2158 (GabT)	4-aminobutyrate aminotransferase
CD1930	putative exported protein
CD2797	putative exported protein
CD1728	conserved hypothetical protein
CD0709	putative DNA mismatch repair protein
CD2211	ABC transporter, ATP-binding/permease protein

Appendix 4: Proteins significantly up-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product
CD2745 (Apt)	adenine phosphoribosyltransferase
CD3281 (ProC2)	pyrroline-5-carboxylate reductase
CD2240 (NanA)	N-acetylneuraminase lyase
CD1335	MarR-family transcriptional regulator
CD1931 (LexA)	SOS regulatory protein
CD1146 (MreC)	putative rod shape-determining protein
CD2805 (RuvB)	holliday junction DNA helicase
CD0104 (RplM)	50S ribosomal protein L13
CD1654 (LplA)	putative lipoate-protein ligase
CD0242	conserved hypothetical protein
CD1715	putative molybdenum cofactor sulfurase
CD1797	putative pyridine nucleotide-disulfide oxidoreductase
CD3456	putative 5-formyltetrahydrofolate cyclo-ligase
CD2217 (AroD)	3-dehydroquinate dehydratase
CD0209	putative sugar-phosphate kinase
CD1207 (Dxs)	1-deoxy-D-xylulose 5-phosphate synthase
CD3517 (PurR)	putative transcriptional repressor
CD0589	hypothetical protein
CD1522	putative polysaccharide deacetylase
CD2100	putative [2Fe-2S]-binding subunit of oxidoreductase
CD1507	putative thioredoxin
CD0768 (SrlD)	sorbitol-6-phosphate 2-dehydrogenase
CD0114	putative ATP/GTP-binding protein
CD2646 (FtsZ)	cell division protein
CD2765	putative penicillin-binding protein repressor
CD0111	putative exported protein
CD2168 (Hcp)	hydroxylamine reductase
CD0270 (FliM)	putative flagellar motor switch protein
CD3035	conserved hypothetical protein
CD3616	putative Na ⁺ /H ⁺ exchanger
CD1495 (ProC1)	pyrroline-5-carboxylate reductase
CD2332 (MtlF)	PTS system, mannitol-specific IIa component
CD3245 (PrdR)	sigma-54-dependent transcriptional activator
CD1494	putative transcriptional regulator

Appendix 5: Proteins significantly down-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product
CD0907	CD0907 putative phage regulatory protein
CD3116 (BglF)	PTS system, beta-glucoside-specific IIabc component
CD0687 (RplT)	50S ribosomal protein L20
CD2195	ferritin
CD0142	putative RNA-binding protein
CD2961	conserved hypothetical protein
CD2259	conserved hypothetical protein
CD1264	hypothetical protein
CD0756	putative reductase
CD0183	putative cell wall hydrolase
CD1660	conserved hypothetical protein
CD0869 (ModA)	putative molybdenum ABC transporter, substrate-binding protein
CD0735	hypothetical protein
CD3027 (Crr)	PTS system, glucose-specific IIa component
CD0873	ABC transporter, substrate-binding lipoprotein
CD1822 (Bcp)	putative thiol peroxidase (bacterioferritin comigratory protein)
CD1771	conserved hypothetical protein
CD2818	ABC transporter, ATP-binding/permease protein
CD3188	hypothetical protein
CD2778	putative polysaccharide biosynthesis protein
CD3315 (HydN2)	electron transport protein
CD1225 (DeoA)	pyrimidine-nucleoside phosphorylase
CD2964	conserved hypothetical protein
CD2989	ABC transporter, substrate-binding protein
CD2181	putative aromatic compounds hydrolase
CD3220	putative methyltransferase
CD1769	conserved hypothetical protein
CD3567	putative cell wall hydrolase
CD2213	putative carbonic anhydrase
CD0011 (SigB)	RNA polymerase sigma-B factor
CD2258	hypothetical protein
CD1471	putative membrane protein (putative phage infection protein)
CD0704	putative phosphohydrolase
CD2165	conserved hypothetical protein
CD0007	putative exported protein
CD2355 (TrxA2)	thioredoxin
CD3087	phosphosugar-binding transcriptional regulator
CD0850	conserved hypothetical protein
CD0882 (GlgC)	glucose-1-phosphate adenylyltransferase
CD1056 (EtfA2)	electron transfer flavoprotein alpha-subunit
CD1459	putative 5-nitroimidazole reductase
CD1054 (Bcd2)	butyryl-CoA dehydrogenase
CD3137	PTS system, IIabc component
CD1055 (EtfB2)	electron transfer flavoprotein beta-subunit
CD0492	PTS system, IIb component
CD3516 (SpoVG)	stage V sporulation protein G
CD3094	putative sigma-54-dependent transcriptional regulator
CD1126A	putative transcriptional regulator
CD1058 (Hbd)	3-hydroxybutyryl-CoA dehydrogenase
CD2873	putative signaling protein
CD2127	putative membrane protein
CD1484 (SsuA)	putative aliphatic sulfonates ABC transporter, substrate-binding lipoprotein

Appendix 5: Proteins significantly down-regulated in *C. difficile* 630 Δ erm Δ spo0A

Identifier (gene name)	Product
CD1837 (AroE)	shikimate dehydrogenase
CD1059 (ThlA1)	acetyl-CoA acetyltransferase
CD0440	cell surface protein
CD0942	hypothetical phage protein
CD2311	ABC transporter, substrate-binding protein
CD1057 (Crt2)	3-hydroxybutyryl-CoA dehydratase
CD2688 (SspA)	small acid-soluble spore protein A
CD1214 (Spo0A)	stage 0 sporulation protein A
CD0810 (FloX)	Putative flavodoxin/nitric oxide synthase
CD3093	putative glutamine amidotransferase
CD3092	putative amino acid permease
CD0451	Putative dioxygenase