Figure S1. The CspB prodomain can be supplied *in trans* to largely reconstitute CspB function.

(A) Schematic of wild-type CspBA and a construct encoding the prodomain *in trans* ($Q66_{TAG}$). "Pro" denotes the prodomain. Q66-TAG encodes a variant in which the CspB prodomain is produced *in trans* from the remainder of CspBA through the introduction of a stop codon after codon 66 and a ribosome binding site and start codon before codon 67. (B) Western blot analyses of CspB(A) and CspC in sporulating cells and purified spores from wild type 630Δ*erm*-p, Δ*cspBA*, and Δ*cspBA* complemented with either wild-type *cspBA* or the *cspBA* trans-complementation variant. A-P refers to CspB(A) that has undergone autoprocessing to release the CspB prodomain. Δ*spo0A* (Δ*0A*) was used as a negative control for sporulating cells. SpoIVA was used as a loading control for sporulating cells, while CotA was used as a loading control for purified spores. An anti-CspB antibody was used to detect full-length CspBA in sporulating cells. A non-specific band in the anti-CspB blot is indicated with an asterisk. The germination efficiency of spores from the indicated strains plated on BHIS media containing 0.1% taurocholate is also shown relative to wild type. The mean and standard deviations shown are based on multiple replicates performed on two independent spore purifications. Statistical significance relative to wild type was determined using a one-way ANOVA and Tukey's test. (C) Germinant sensitivity of $Q66_{TAG}$ spores plated on BHIS containing increasing concentrations of taurocholate. The number of colony forming units (CFUs) produced by germinating spores is shown. The mean and standard deviations shown are based on multiple replicates performed on two independent spore purifications. Statistical significance relative to wild type was determined using a one-way ANOVA and Tukey's test. **** $p < 0.0001$, *** $p < 0.001$, **$p < 0.01$.

Figure S2. Restoring CspC's catalytic triad appears to impair protein folding in *E. coli*. (A) CspC space fill model with jelly roll domain in cyan, prodomain in pink and subtilase domain in grey. Residues identified as being required for *C. difficile* spore germination by Francis et al. [1] in a genetic screen are shown in black. The S443N substitution was identified in combination with V272G. The pseudoactive site residues Thr170 and Gly485 are shown in blue. (B) Purification of CspC-His_6 variants from the soluble fraction. G171R was included because this substitution had been predicted to destabilize CspC by steric occlusion [2, 3]. Cultures expressing the *cspC* variants were induced with IPTG overnight at 18˚C, and aliquots were removed for analysis of the "induced" fraction. Cultures were harvested, and cells were lysed using sonication. Following a high-speed centrifugation, the cleared lysate containing soluble proteins was incubated with Ni^{2+}-NTA agarose beads. CspC-His_6 variants were eluted from the beads using imidazole (elution fraction). Equivalent volumes of samples were resolved by SDS-PAGE and analyzed by western blotting (top) and Coomassie staining (bottom).

Figure S3. Purification of CspC variants using the CPD self-cleaving tag and SEC. (A) Coomassie stains of the CspC-CPD-His_6 purifications. The variants purified are listed above the gels. "+" shows IPTG-induced cell lysates; CL refers to the soluble proteins present in cleared lysates of IPTG-induced cell lysates; E1 and E2 refer to the elutions obtained from the supernatant fraction following inositol hexakisphosphase ($InsP_6$)-induced cleavage of CspC-CPD-His_6 variants. $CspC_{EL}$ refers to the glutamate and leucine residues that are added to the C-terminus of the CspC variants following $InsP_6$-mediated cleavage. We note that WT CspC-CPD was present in higher levels in the cleared lysate fraction than the other CspC variants. (B) SEC profiles of $CspC_{2xcat}$ and $CspC_{G171R}$ variants. These traces are identical to those shown in **Figure**

3, except the y-axis has been scaled for these variants, which are purified with much lower yields. The black rectangle and blue and pink arrows identify the fraction that contained these variants. (C) Coomassie stain of fractions taken from the SEC shown in (B). The black rectangle highlights the fraction that was concentrated for the thermal shift assays and Coomassie gels shown in **Figure 3**. Lane 1 in the bottom gel includes SEC-purified $CspC_{T170H}$, which highlights how $CspC_{G171R}$ runs at a slightly smaller apparent MW relative to $CspC_{T170H}$ (and WT CspC, **Figure 3**). This slight difference in mobility is likely due to CPD-mediated trimming of the partially unfolded $CspC_{2xcat}$ and $CspC_{G171R}$ variants (compare the mobility of these variants in Figure 3 vs. S3). The CPD cleaves after leucine residues [4], and CspC carries a leucine at its C-terminus (residue 557) prior to the LEHHHHHH tag created by the pET22b cloning construct as well as a leucine at position 544.

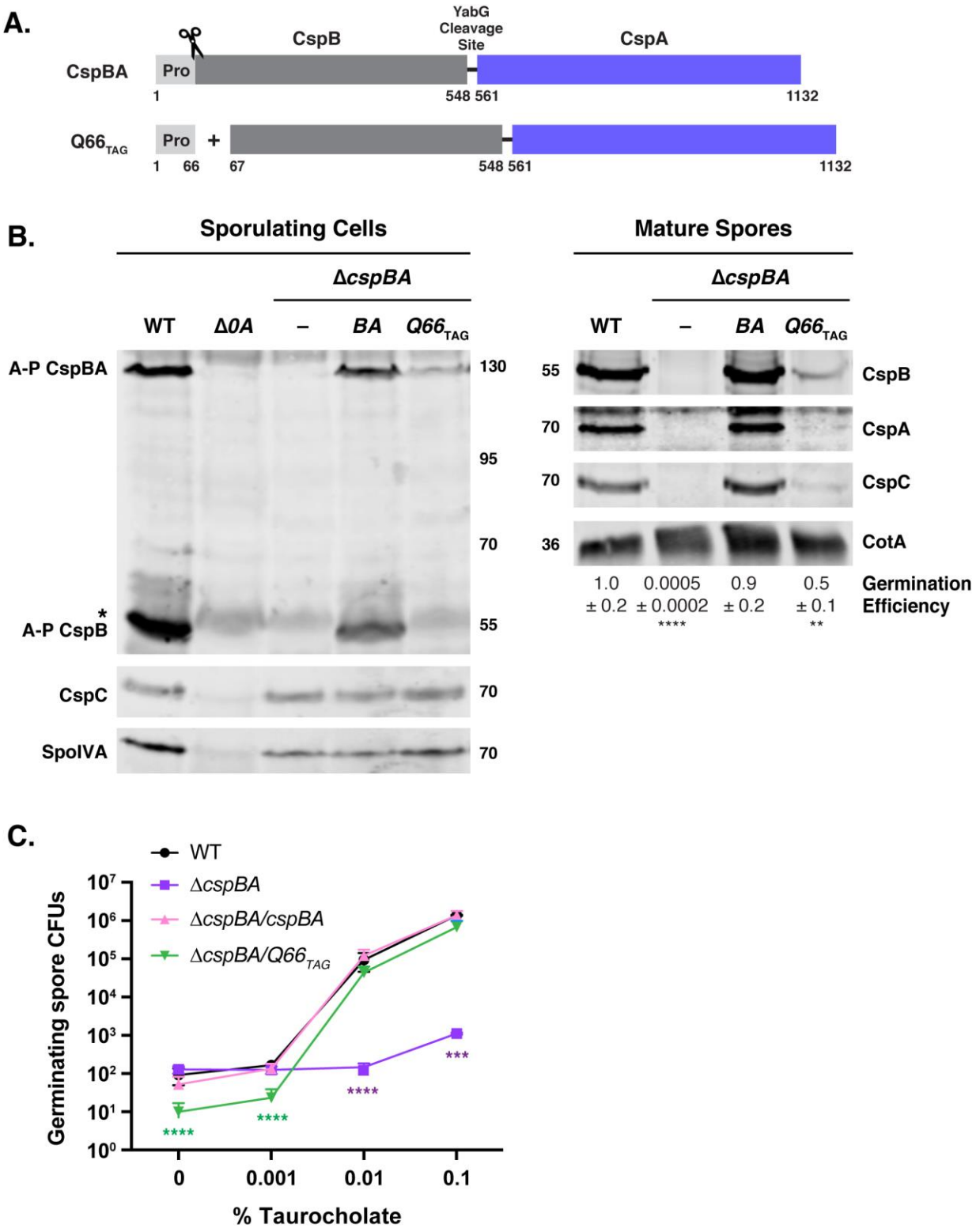

Figure S1. The CspB prodomain can be supplied *in trans* to largely re-constitute CspB function

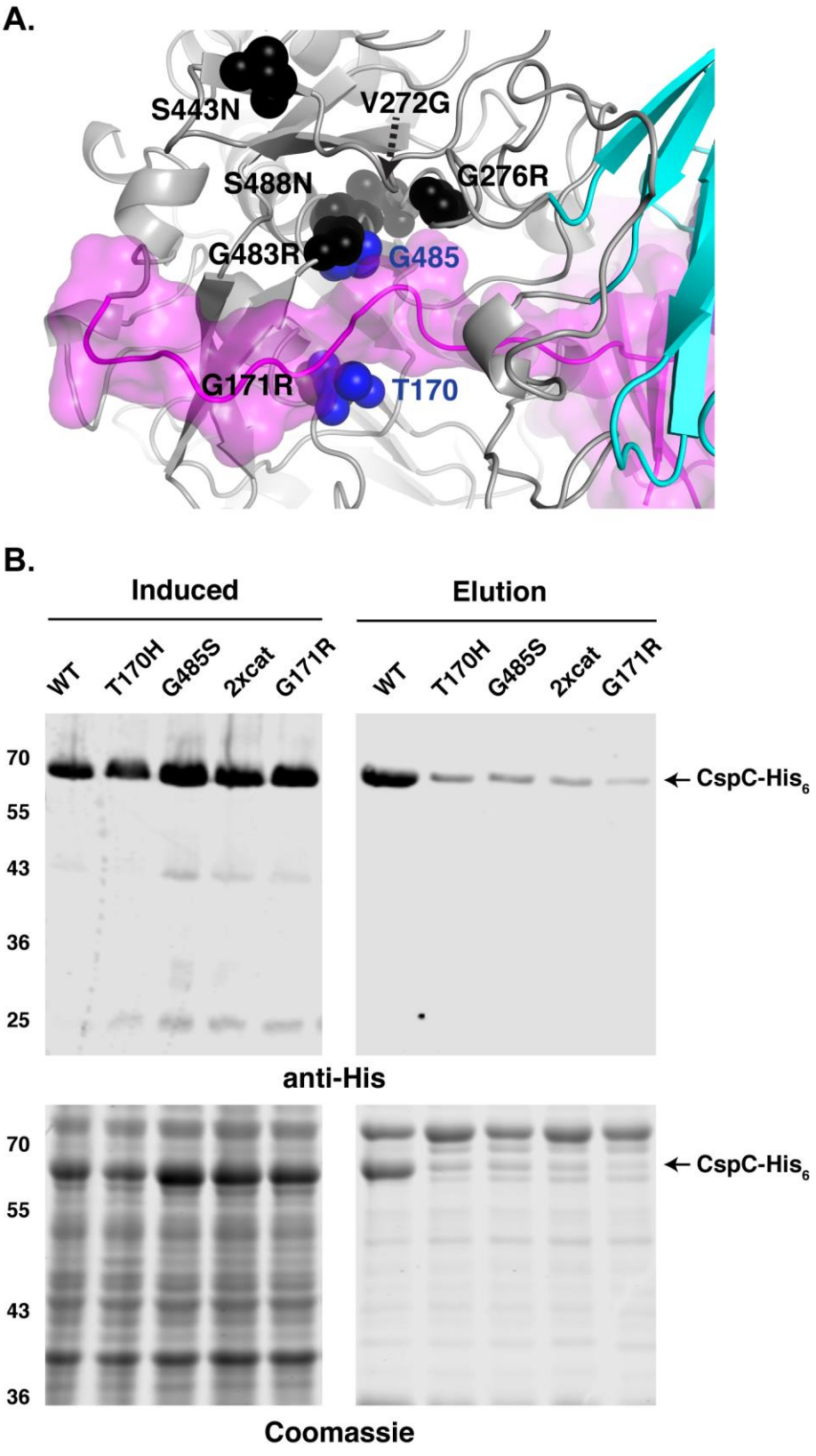

Figure S2. Restoring CspC's catalytic triad appears to impair folding in *E. coli*.

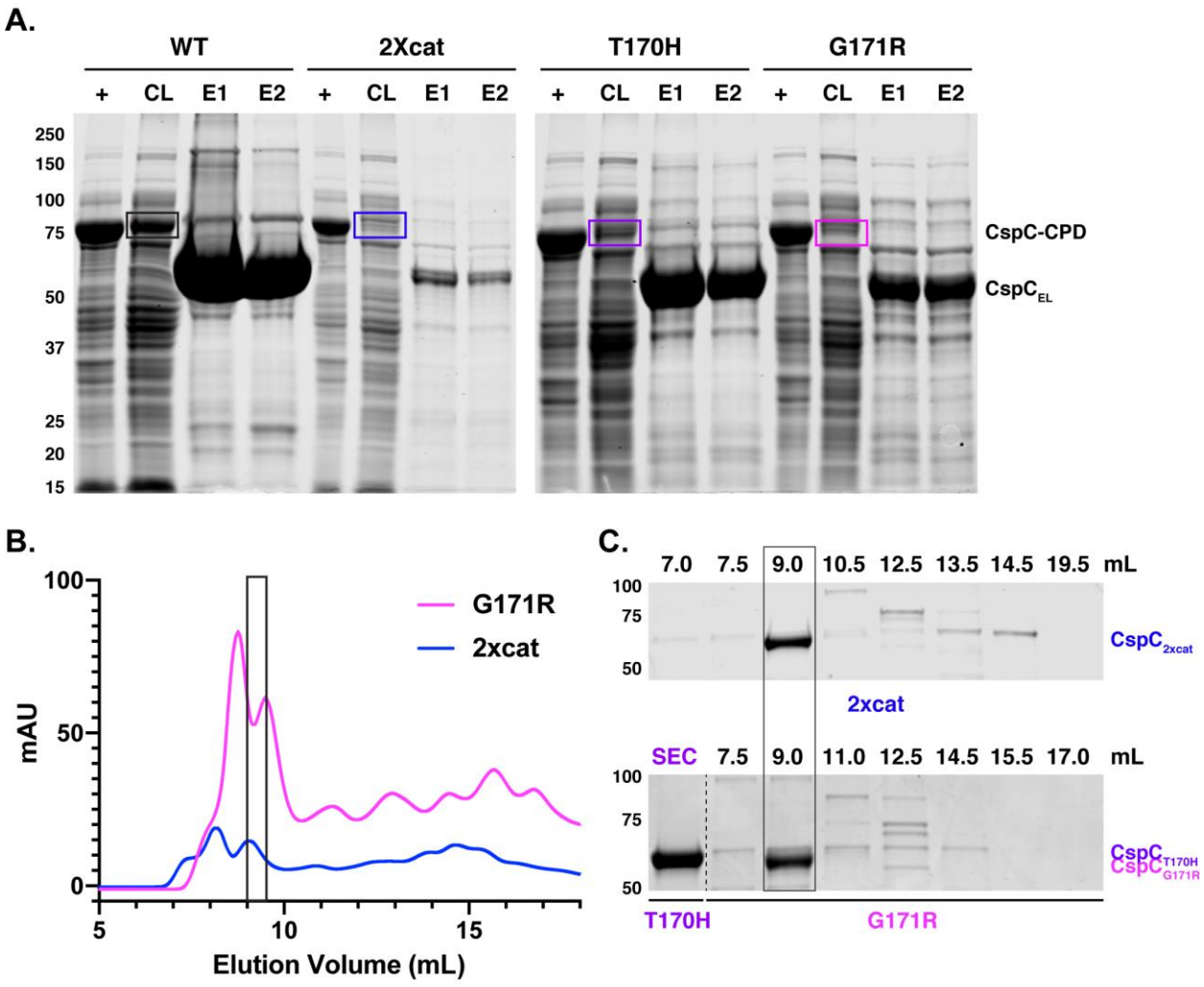

Figure S3. Purification of CspC variants using the CPD self-cleaving tag and SEC.

Supplementary Table S1 – *C. difficile* and *E. coli* strains used in this study.

Strain#	Strain name	Relevant genotype or features	Source/reference
***C. difficile* strains**			
789	630Δ*erm*Δ*pyrE*Δ*cspBA*	630Δ*erm*Δ*pyrE* with *cspBA* deleted	[5]
799	630Δ*erm*Δ*pyrE*Δ*cspC*	630Δ*erm*Δ*pyrE* with *cspC* deleted	[6]
831	630Δ*erm*Δ*cspC*/*cspC*	630Δ*erm*Δ*cspC* with *cspC* in the *pyrE* locus	[6]
846	630Δ*erm*-p	*erm*-sensitive derivate of 630 with *pyrE* restored	[5]
849	630Δ*erm*Δ*spo0A*-p	630Δ*erm*Δ*spo0A* with *pyrE* restored	[5]
859	630Δ*erm*Δ*cspBA*-p	630Δ*erm*Δ*cspBA* with *pyrE* restored	[6]
862	630Δ*erm*Δ*cspBA*/*cspBA*	630Δ*erm*Δ*cspBA* with *cspBA* in the *pyrE* locus	[6]
1238	630Δ*erm*Δ*cspC*-p	630Δ*erm*Δ*cspC* with *pyrE* restored	[6]
1438	630Δ*erm*-Δ*cspC*/*cspC*$_{T170H}$	630Δ*erm*Δ*cspC* with *cspC*$_{T170H}$ in the *pyrE* locus	This study
1441	630Δ*erm*-Δ*cspC*/*cspC*$_{G485S}$	630Δ*erm*Δ*cspC* with *cspC*$_{G485S}$ in the *pyrE* locus	This study
1751	630Δ*erm*Δ*cspC*/*cspC*$_{L64\text{-}TAG}$	630Δ*erm*Δ*cspC* with *cspC*$_{L64\text{-}TAG}$ in the *pyrE* locus	This study
1768	630Δ*erm*Δ*cspC*/*cspC*$_{T170H/G485S}$	630Δ*erm*Δ*cspC* with *cspC*$_{T170H/G485S}$ in the *pyrE* locus	This study
1864	630Δ*erm*Δ*cspBA*/*cspBA*$_{Q66\text{-}TAG}$	630Δ*erm*Δ*cspBA* with *cspBA*$_{Q55\text{-}TAG}$ in the *pyrE* locus	This study
2517	630*Δerm-p* Δ*cspBA*/*cspBA*$_{Q757H}$	630Δ*erm*Δ*cspBA* with *cspBA*Δ*C*$_{Q757H}$ in the *pyrE* locus	This study
2520	630*Δerm-p* Δ*cspBA*/*cspBA*$_{A1064S}$	630Δ*erm*Δ*cspBA* with *cspBA*Δ*C*$_{A1064S}$ in the *pyrE* locus	This study
2559	630*Δerm-p* Δ*cspBA*/*cspBA*$_{Q757H/A1064S}$	630Δ*erm*Δ*cspBA* with *cspBA*Δ*C*$_{Q757H/A1064S}$ in the *pyrE* locus	This study

***E. coli* strains**

Strain#	Strain Background	Plasmid carried	
41	DH5α	F– Φ80*lacZ*ΔM15 Δ(*lacZYA-argF*) U169 *recA1 endA1 hsdR17* (rK$^-$, mK$^+$) *phoA supE44* λ– *thi-1 gyrA96 relA1*	D. Cameron
455	BL21	pET28a-*cspB*(548aa)	[7]
471	BL21	pET28a-*cspB*(548aa)-S461A	[7]
531	HB101/pRK24	F- *mcrB mrr hsdS20*(rB$^-$mB$^-$) *recA13 leuB6 ara-13 proA2 lavYI galK2 xyl-6 mtl-1 rpsL20* carrying pRK24	C. Ellermeier
981	BL21(DE3)	pET22b *cspC*-His$_6$ codon-optimized	This study
982	BL21	pET22b *cspC*-CPD codon-optimized	This study
1185	BL21	pET22b *cspC*$_{T170H}$-CPD codon-optimized	This study
1169	BL21	pET22b *cspC*$_{G171R}$-CPD codon-optimized	This study
1281	BL21(DE3)	pET28a *cspBA* codon-optimized	This study
1889	HB101	pMTL-YN1C Δ*cspBA*-*cspC*$_{T170H}$	This study
1890	HB101	pMTL-YN1C Δ*cspBA*-*cspC*$_{G485S}$	This study
2018	HB101	pMTL-YN1C Δ*cspBA*-*cspC*$_{T170H/G485Sr}$	This study
2062	HB101	pMTL-YN1C Δ*cspBA*-*cspC*$_{L64\text{-}TAG}$	This study
2076	HB101	pMTL-YN1C *cspBA*$_{Q66\text{-}TAG}$-Δ*cspC*	This study
2098	BL21(DE3)	pET22b *cspC*$_{T170H/G485S}$-His$_6$ codon-optimized	This study
2099	BL21(DE3)	pET22b *cspC*$_{G485S}$-His$_6$ codon-optimized	This study
2126	BL21(DE3)	pET22b *cspC*$_{T170H}$-His$_6$ codon-optimized	This study
2127	BL21(DE3)	pET22b *cspC*$_{G171R}$-His$_6$ codon-optimized	This study
2368	HB101	pMTL-YN1C *cspBA*Δ*C*$_{A1064S}$	This study
2370	HB101	pMTL-YN1C *cspBA*Δ*C*$_{Q757H}$	This study
2382	HB101	pMTL-YN1C *cspBA*Δ*C*$_{Q757H/A1064S}$	This study

2372	BL21(DE3)	pET28a *cspBA*$_{Q757H}$ codon-optimized	This study
2384	BL21(DE3)	pET28a *cspBA*$_{A1064S}$ codon-optimized	This study
2385	BL21(DE3)	pET28a *cspBA*$_{Q757H/A1064S}$ codon-optimized	This study
2646	BL21	pET22b *cspC*$_{T170H/G485S}$-CPD codon-optimized	This study

Plasmids

Plasmids	**Relevant features**	**Source/reference**
pMTL-YN1C	Unstable plasmid for restoring *pyrE* locus in 630Δ*ermpyrE*	[8]
pET22b	Expression vector for IPTG-inducible production of C-terminally His_6-tagged proteins	Novagen
pET28a	Expression vector for IPTG-inducible production of His_6-tagged proteins	Novagen
pET22b-CPD$_{SacI}$	Expression vector for IPTG-inducible production of C-terminally CPD-His_6-tagged proteins	[9]

Supplementary Table S2 – Primers used in this study.

Primer	Name	Sequence
950	5' *cspBA* Q66+TAG RBS_ATG	GACTCAGTAGGAGGGATTTATGGATGTGCAAAGTTTTTCAAGTACAGG
951	3' *cspB* Q66+TAG RBS rev	AAATCCCTCCTACTGAGTCTGTAATATAAAAGGCTTTTCTATAAATTCAATTTC
1128	5' NdeI *cspC* CO	AAAAAACATATGGAGAAAAGCTACTGCATTATTTATC
1129	3' XhoI *cspC* no stop CO	AAAAAACTCGAGAAGGGTGTTGGCAATCTG
1166	3' SacI *cspC* codon opt no TAA	AAATGAGCTCAAGGGTGTTGGCAATCTGCTG
1340	5' T170H *cspC* CO SOE	CTCAGCCAGGATAACATTGGGCATGGCACGTTGGTATCTGGTA
1341	3' T170H *cspC* CO rev oes	TACCAGATACCAACGTGCCATGCCCAATGTTATCCTGGCTGAG
1342	5' G171R *cspC* CO SOE	AGCCAGGATAACATTGGGACACGCACGTTGGTATCTGGTATTCTG
1343	3' G171R *cspC* CO rev oes	CAGAATACCAGATACCAACGTGCGTGTCCCAATGTTATCCTGGCT
1372	5' *cspC* CO BamHI 307-331	ACCGGGCGTGGGATCCTGCTTGCGG
1505	5' NcoI *cspB* codon opt	ATACCATGGCTATTATCATTAATTACGAACTGATTGTGAAGTAC
1507	5' linker *cspA* SOE	GACGAGGAAAATAGCTACAAGTTTATCGATGGATACAACATTCAGATTCATAACGATC
1508	3' XhoI *cspA* codon opt no stop	AATCTCGAGGCGCAGTACATCAAACATGCCACG
1529	3' HindIII *cspBA* CO 2439	TTTGAAGCTTTTATTAATGCTGCGATAGCC
1530	5' HindIII *cspBA* linker 2482	TAAAAGCTTCAAAGACGAGGAAAATAGCTACAAGTTTATCGATGGA
2189	5' NotI *cspBA* promoter gibson	AATTAGGGATGTAATAAGCGGCCGCTTCAATTAATTATTGGTATCAAACT
2242	3' XhoI *cspC* Gibson	CAAGCTTGCATGTCTGCAGGCCTCGAGCTATAGAGTATTTGCTATCTGTTGAATCG
2311	5' NdeI pET22b *cspC* CO Gibson	GTTTAACTTTAAGAAGGAGATATACATATGGAGAAAAGCTACTGCATTATTTATCAG
2312	3' XhoI pET22b *cspC* CO gibson	GTGGTGGTGGTGGTGGTGCTCGAGAAGGGTGTTGGCAATCTGCTGAATG
2354	5' *cspC* T170H SOE	GGGAGTTTGAGTCAAGATAATATAGGTCATGGAACTTTAGTTTCTGGTATATTAGTTGG
2355	3' *cspC* T170H rev eos	CCAACTAATATACCAGAAACTAAAGTTCCATGACCTATATTATCTTGACTCAAACTCCC
2356	5' *cspC* G485S SOE	GGAACATATAATACAGGAACAGGAACATCAGTGAGCAGTTCTATAGTCACAGGTG
2357	3' *cspC* G485 rev eos	CACCTGTGACTATAGAACTGCTCACTGATGTTCCTGTTCCTGTATTATATGTTCC
2552	5' L64-TAG *cspC* SOE	GAACCAATGAGCAGTCTATAGGAGGGATTTATGATTGAAATAACTAATAATGTAAATAAT
2553	3' L64-TAG *cspC* rev eos	ATTATTTACATTATTAGTTATTTCAATCATAAATCCCTCCTATAGACTGCTCATTGGTTC
2600	5' G485S cspC CO SOE	AACGGTACCTATAATACTGGCACCGGAACTAGCGTGTCCAGTTCCATTGTGACG
2601	3' G485S cspC rev eos	CGTCACAATGGAACTGGACACGCTAGTTCCGGTGCCAGTATTATAGGTACCGTT
2602	3' SacI *cspC* CO-CPD Gibson	GATTATGGAGTATTTTTCCATCCGCGAGCTCAAGGGTGTTGGCAATCTGCTGAATGG

3034	5' NcoI *cspBA* CO pET28a Gibson	CTTTAAGAAGGAGATATACCATGGCTATTATCATTAATTACGAACTGATTGTGAA GTAC
3035	3' XhoI *cspBA* CO pET28a Gibson	CAGTGGTGGTGGTGGTGGTGCTCGAGGCGCAGTACATCAAACATGCCACG
3036	5' Q757H SOE *cspBA* codon opt	CTCTCTCAGGATGAGGTCGGTCACGGCACCATGCTGTCCGGCATCTGCTC
3037	3' Q757H rev eos *cspBA* codon opt	GAGCAGATGCCGGACAGCATGGTGCCGTGACCGACCTCATCCTGAGAGAG
3038	5' A1064S SOE *cspBA* codon opt	CAATACATATGCAACCATTACTGGGACCTCAGCGGCGAGCGCGCATGCGGCTG
3039	3' A1064S rev eos *cspBA* codon opt	CAGCCGCATGCGCGCTCGCCGCTGAGGTCCCAGTAATGGTTGCATATGTATTG
3040	5' Q757H SOE *cspBA* 630	CTAGTCTATCTCAGGATGAAGTTGGTCATGGAACTATGTTGAGTGGGATATGTGC
3041	3' Q757H rev eos *cspBA* 630	GCACATATCCCACTCAACATAGTTCCATGACCAACTTCATCCTGAGATAGACTAG

[a]Restriction sites are underlined

Supplementary Table S3– Peptostreptococcaceae CspBA homologs

Organism genus and species	**Accession**	**CspB**			**CspA**		
Clostridioides difficile 630	CAJ69133.1	DSG	HGTH	GTSMATP	DTG	HGTM	GTSAAAA
Clostridioides difficile R20291	CDR20291_2147	DSG	HGTH	GTSMATP	DSG	RGTM	GTAAASA
Clostridioides difficile Y165	EQI24072.1	DSG	HGTH	GTSMATP	GSG	YGTI	GTAASAS
Romboutsia maritimum	WP_095405957.1	DSG	HGTH	GTSMATP	DTG	SGTM	GTAVAAA
Romboutsia weinsteinii	WP_094368045.1	DSG	HGTH	GTSMATP	DSG	NGTM	GTAPAAA
Romboutsia sp. Marseille-P6047	WP_122638576.1	DSG	HGTH	GTSMATP	DSG	NGTM	GTAPAAA
Romboutsia lituseburensis	WP_092722645.1	DSG	HGTH	GTSMATP	DSG	NGTM	GTAPAAA
Paeniclostridium sordellii	CEN89310.1	DSG	HGTH	GTSMATP	DSG	TGTM	GTAASAA
Paeniclostridium sordellii	WP_081015910.1	DSG	HGTH	GTSMATP	DSG	SGTM	GTAPAAA
Paeniclostridium sordellii	CEQ11710.1	DSG	HGTH	GTSMATP	DSG	HGTM	GTSAAGA
Romboutsia hominis	CEI72315.1	DSG	HGTH	GTSMATP	DSG	SGTM	GTAPAAA
Romboutsia timonensis	WP_071121078.1	DSG	HGTH	GTSMATP	DSG	HGTM	GTSAAGA
Paraclostridium bifermentans	WP_142730225.1	DSG	HGTH	GTSMATP	DSG	TGTL	GTSAAAA
Romboutsia ilealis	CED93323.1	DSG	HGTH	GTSMATP	DTG	HGTM	GSSAAGA
Paraclostridium bifermentans	WP_025162001.1	DSG	HGTH	GTSMATP	DTG	HGTM	GSSAAGA
Peptostreptococcaceae bacterium	WP_148487629.1	DSG	HGTH	GTSMATP	DTG	HGTM	GSSAAGA

Paraclostridium bifermentans	WP_148550927.1	DSG	HGTH	GTSMATP	DSG	SGTL	GTAASSA
Paraclostridium benzoelyticum	OXX84749.1	DSG	HGTH	GTSMATP	DSG	SGTL	GTAASSA
Paraclostridium benzoelyticum	WP_046823062.1	DSG	HGTH	GTSISAA	DSG	SGTM	GTAVAAA
Terrisporobacter glycolicus	WP_148557837.1	DSG	HGTH	GTSISAA	DSG	SGTM	GTAVAAA
Terrisporobacter glycolicus	WP_083399335.1	DSG	HGTH	GTSMATP	DSG	TGTL	GTAAAAA
Romboutsia lituseburensis	WP_092722648.1	DSG	HGTH	GTSMATP	DSG	TGTL	GTAAAAA
Romboutsia lituseburensis	SDL34486.1	DSG	HGTH	GTSMATP	DSG	SGTL	GTAASAA
Terrisporobacter othiniensis	KHS58529.1	DSG	HGTH	GTSMATP	DTG	SGTL	GTSAAAA
Terrisporobacter othiniensis	WP_082007783.1	DSG	HGTH	GTSMATP	DTG	SGTL	GTSAAAA
Terrisporobacter glycolicus	WP_018589409.1	DSG	HGTH	GTSMATP	DTG	SGTL	GTSAAAA
Intestinibacter bartlettii	WP_055088383.1	DSE	NNED	-------	DSG	HGTM	GTAPAAA
Intestinibacter bartlettii	WP_078687908.1	DSG	HGTH	GTSMSAP	DSG	HGTL	GTSAAGA
Intestinibacter bartlettii	WP_147616711.1	DSG	HGTH	GTSMAAP	DSG	HGTR	GTSASGA
Asaccharospora irregularis	WP_073125354.1	DSG	HGTH	GTSMAAP	DSG	HGTK	GTSASAA
Tepidibacter mesophilus	WP_099188795.1	DSG	HGTH	GTSMAAP	DSG	HGTM	GTSVAAA
Tepidibacter formicigenes	WP_072888171.1	DSG	HGTH	GTSMAAP	DSG	HGTM	GTSVAAA
Tepidibacter thalassicus	WP_084601981.1	DSG	HGTH	GTSMAAP	DSG	HGTM	GTSVAAA
Clostridium paradoxum	WP_083528235.1	DSG	HGTH	GTSMATP	DTG	QGTM	GTAAASA
Clostridium paradoxum	KXZ39276.1	DSG	HGTH	GTSMATP	DTG	QGTM	GTAAASA
Clostridium thermoalcaliphilum	WP_079411776.1	DSG	HGTH	GTSMATP	DTG	QGTM	GTAAASA

Supplementary Table S4. Peptostreptococcaceae CspC homologs.

Organism genus and species	Accession	CspC		
Clostridium difficile 630	CAJ69132.1	DSG	TGTM	GTGVSAS
Clostridioides difficile R20291	6MW4_A	DSG	TGTI	GTGISSS
Clostridioides difficile Y165	EQF98486.1	DSG	TGTI	GTGISSS
Romboutsia weinsteinii	WP_094368046.1	DSG	TGTI	GTGVSSS
Romboutsia maritimum	WP_115975881.1	DSG	TGTI	GTGVSSS
Romboutsia maritimum	WP_115975890.1	DSG	TGTI	GTGVSSS
Paeniclostridium sordellii	WP_055341573.1	DSG	TGTM	GTGVSSS
Paeniclostridium sordellii	WP_057564142.1	DSG	TGTT	GTGVSSS
Paeniclostridium sordellii	CEK30389.1	DSG	TGTT	GTGVSSS
Clostridium dakarense	WP_042275205.1	DSG	TGTM	GTGVSSS
Clostridiales	WP_053830978.1	DSG	TGTT	GTGVSSS
Paraclostridium bifermentans	WP_148550882.1	DSG	TGTT	GTGVSSS
Romboutsia sp. MT17	WP_092926789.1	DSG	TGTM	GTGVSSS
Paraclostridium bifermentans	WP_142730224.1	DSG	TGTT	GTGVSSS
Paraclostridium bifermentans	WP_025162002.1	DSG	TGTI	GTGVSSS
Romboutsia hominis	CEI72316.1	DSG	TGTT	GTGVSSS
Paraclostridium benzoelyticum	WP_046821862.1	DSG	TGTI	GTGVSTS
Romboutsia weinsteinii	WP_094369213.1	DSG	TGTM	GTGISSS
Paraclostridium benzoelyticum	OXX84577.1	DSG	TGTI	GTGVSSS
Romboutsia lituseburensis	WP_092722643.1	DSG	TGTM	GTGISSS
Clostridioides mangenotii	WP_024620345.1	DSG	TGTM	GTGVSSS
Romboutsia sp. Marseille-P6047	WP_122638577.1	DSG	TGTM	GTGISSS
Clostridioides mangenotii	WP_027702696.1	DSG	TGTI	GTGISSS
Peptostreptococcaceae bacterium VA2	WP_026901720.1	DSG	TGTM	GTGISSS
Clostridioides mangenotii	WP_024620469.1	DSG	TGTI	GTGVSSS
Romboutsia timonensis	WP_071121077.1	DSG	TGTI	GTGISAS
Asaccharospora irregularis	WP_073125363.1	DSG	TGTI	GTGVSSS
Romboutsia ilealis	CED93324.1	DSG	TGTI	GTGVSSS
Terrisporobacter glycolicus	WP_148557830.1	DSG	TGTL	GTGVSSS
Terrisporobacter glycolicus	WP_018589415.1	DSG	TGTL	GTGVSSS

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