SUPLEMENTAL DATA

Table S1. Cytochrome *c* maturation (Ccm) components and their role

Ccm protein	Structural Features	Proposed Funtion
CcmA	Peripheral membrane protein with ATP-binding domain (Walker A and B motifs)	Part of the CcmABCD complex, a predicted ABC-type transporter; required for the ATP-dependent release of holoCcmE from the CcmABCDE complex.
CcmB	Six TM helices and a conserved FXXDXXDGSL motif	Part of the CcmABCD complex, a predicted ABC-type transporter; required for the release of holoCcmE from the CcmABCDE complex
CcmC	Six TM helices with a tryptophan-rich (WGX[F,Y,W]WXWDXRLT) motif, and two conserved His residues	Part of the CcmABCD complex, a predicted ABC-type transporter; transfers heme to apoCcmE, providing axial ligands to the heme iron; acts as a CcmE-specific heme lyase.
CcmD	Small single TM helix protein with no conserved domains	Part of the CcmABCD complex, a predicted ABC-type transporter; required for the release of holoCcmE from the CcmABCDE complex
CcmE	Single TM helix with a periplasmic domain containing a conserved HXXXY motif	Heme chaperone binding covalently vinyl-2 of heme via the conserved His residue; delivers heme to the apocytochrome *c* substrates
CcmF	Eleven TM helices with a tryptophan-rich (WGGXWFWDPVEN) motif, and four conserved His residues (two of them are ligands of a *b*-type heme)	Part of the CcmFHI heme ligation complex; interacts with apocytochromes *c* and CcmE, and suggested to reduce heme in holoCcmE for its transfer to the apocytochrome
CcmG	Single TM helix with a periplasmic domain containing a thioredoxin motif (CXXC)	Binds poorly apocytochromes *c*, and suggested to reduce the disulfide at the heme binding site of apocytochrome *c* either directly or via CcmH
CcmH	Single TM helix with a periplasmic domain containing a thioredoxin-like motif (LRCXXC)	Part of the CcmFHI heme ligation complex; interacts with apocytochrome *c* and suggested to reduce its disulfide bond for the stereo-specific heme ligation
CcmI	Two TM helices, linked by a cytoplasmic loop with a leucine-zipper-like motif, and a large periplasmic domain containing three TPR repeats	Part of the CcmFHI heme ligation complex; is an apocytochrome *c* chaperone binding to the C-terminal portion of the apocytochrome *c* via its periplasmic domain
CcdA	Six TM helices with two conserved redox active Cys residues	Thiol-reduction of CcmG

Table S2. Nucleotide sequences of the oligonucleotide primers used in this study.

Designation	Constructs	Nucleotide sequence (5' to 3')
CcmE-NdeI-Fwd	pAV4	CGG CAT ATG AGA AAC CTG AAG AAA ACG CGG
CcmE-BamHI-Rv		ATT GGA TCC TTA TGC CGC TCA GCC CTC GGG CT
CcmEH123A-Fwd	pAV4H123A	CGA AAT CCT GGC CAA GGC TGA CGA AAA CTA CAT G
CcmEH123A-Rv		CAT GTA GTT TTC GTC AGC CTT GGC CAG GAT TTC G
FLAG-Fw	pFLAG-CcmI	TAC CAT GGG CGA CTA CAA GGA CGA CGA CGA CAA GAG CAG CGG CCA TAT CG
FLAG-Rv		GGC CGC TGC TCT TGT CGT CGT CGT CCT TGT AGT CGC CCA TGG TAT ATC TCC

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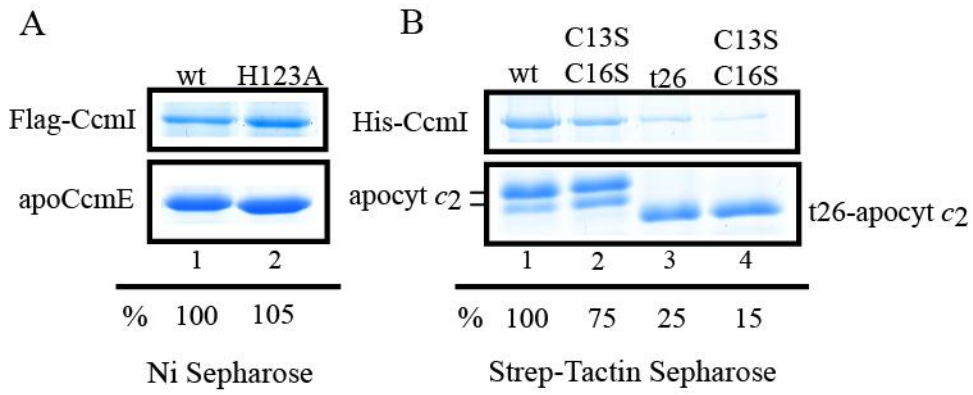

Figure S1. A) Co-purification of Flag-CcmI with His-apoCcmE (lane 1) and its His-apoCcmE-H123A mutant (lane 2) using Ni Sepharose resin. **B**) Co-purification of FlagCcmI with Strep-apocytochrome c_2 (lane 1), its C13SC16S mutant (lane 2), the t26-truncated Strep-apocytochrome c_2 (lane 3) and its cysteine-less derivative (lane 4) using the Strep-Tactin Sepharose resin. The data show that apoCcmE interacts specifically with CcmI and that the Flag-fused CcmI shows the same behavior towards apocytochrome c_2 that its His-derivative, indicating that the different tags do not interfere with the observed protein-protein interactions.