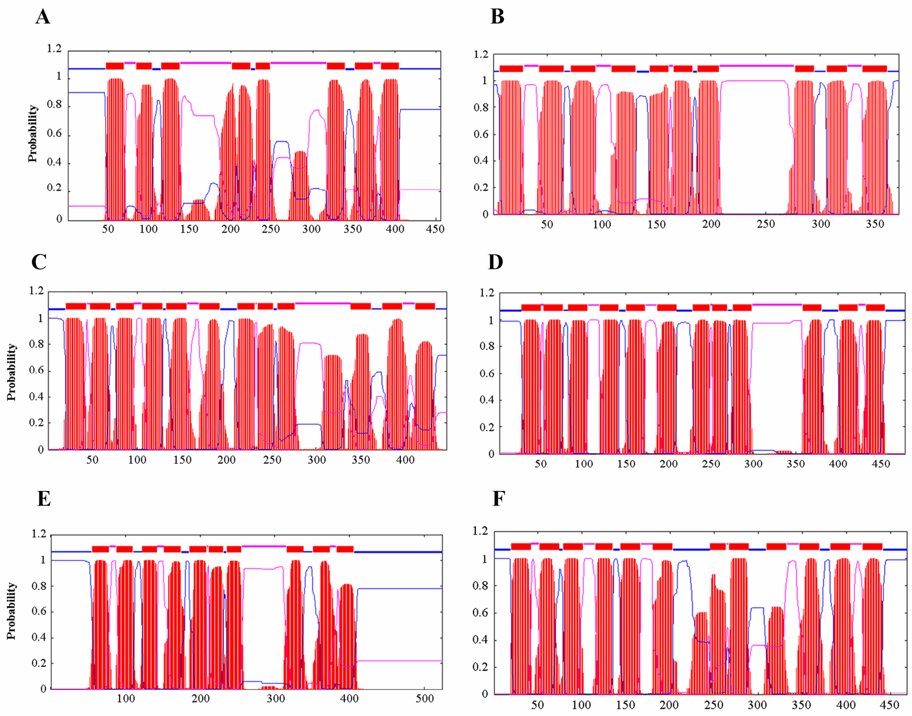
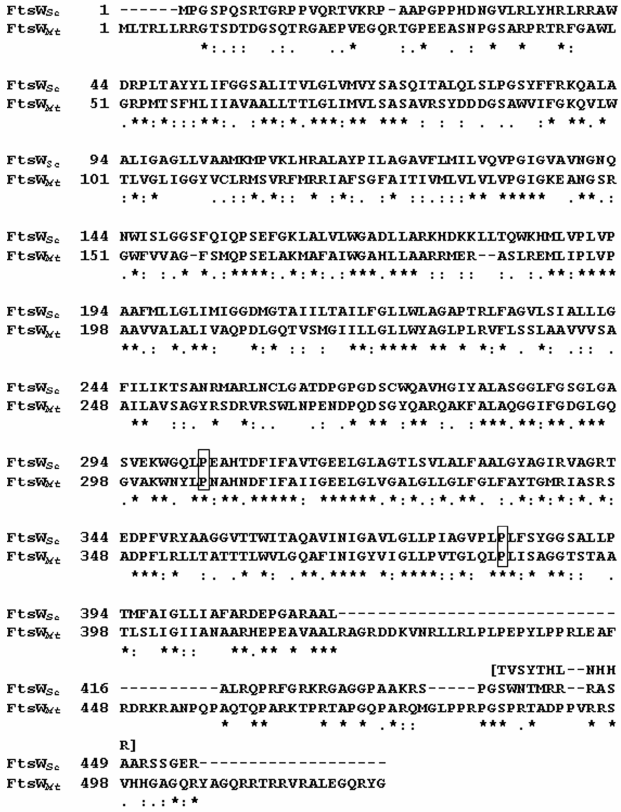
Supplementary Fig 1



Hydropathy plots of actinomycete SEDS proteins.

Protein sequences were analysed using TMHMM version 2.0 (http://www.cbs.dtu..dk/services/TMHMM-2.0/). (A) FtsW_{Sc}; (B) SCO2607 (Sfr); (C) SCO5302; (D) RodA_{Sc}; (E) FtsW_{Mt}; (F) RodA_{Mt}. The horizontal bars for each plot represent the topological predictions for a given protein: thick red bars are transmembrane helices, blue lines are cytoplasmic loops and pink lines are extracytoplasmic loops.

Supplementary Fig 2



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FtsWSc   1 ------MPGSPQSRTGRPPVQRTVKRP-AAPGPPHDNGVLRLYHRLRRAW
FtsWMt   1 MLTRLLRRGTSDTDGSQTRGAEPVEGQRTGPEEASNPGSARPRTRFGAWL
                   *:.::  .:.   ..*    :.*  . : *  *   *:

FtsWSc  44 DRPLTAYYLIFGGSALITVLGLVMVYSASQITALQLSLPGSYFFRKQALA
FtsWMt  51 GRPMTSFHLIIAVAALLTTLGLIMVLSASAVRSYDDDGSAWVIFGKQVLW
           .**:*:::**:. :**:*.***:** *** : : : . ..  :* **.*

FtsWSc  94 ALIGAGLLVAAMKMPVKLHRALAYPILAGAVFLMILVQVPGIGVAVNGNQ
FtsWMt 101 TLVGLIGGYVCLRMSVRFMRRIAFSGFAITIVMLVLVLVPGIGKEANGSR
           :*:*     ..::*.*:: * :*:. :* ::.:::** *****  .**.:

FtsWSc 144 NWISLGGSFQIQPSEFGKLALVLWGADLLARKHDKKLLTQWKHMLVPLVP
FtsWMt 151 GWFVVAG-FSMQPSELAKMAFAIWGAHLLAARRMER--ASLREMLIPLVP
           .*: :.* *.:****:.*:*:.:***.*** :: ::  :. :.**:****

FtsWSc 194 AAFMLLGLIMIGGDMGTAIILTAILFGLLWLAGAPTRLFAGVLSIALLLG
FtsWMt 198 AAVVALALIVAQPDLGQTVSMGIILLGLLWYAGLPLRVFLSSLAAVVVSA
           **.: *.**:   *:* :: :  **:**** ** * *:* . *: .:: .

FtsWSc 244 FILIKTSANRMARLNCLGATDPGPGDSCWQAVHGIYALASGGLFGSGLGA
FtsWMt 248 AILAVSAGYRSDRVRSWLNPENDPQDSGYQARQAKFALAQGGIFGDGLGQ
            **  ::. *  *:..   .: .* ** :** :. :***.**:**.***

FtsWSc 294 SVEKWGQLPEAHTDFIFAVTGEELGLAGTLSVLALFAALGYAGIRVAGRT
FtsWMt 298 GVAKWNYLPNAHNDFIFAIIGEELGLVGALGLLGLFGLFAYTGMRIASRS
           .* **. **:**.*****: ******.*:*.:*.**. :.*:*:*:*.*:

FtsWSc 344 EDPFVRYAAGGVTTWITAQAVINIGAVLGLLPIAGVPLPLFSYGGSALLP
FtsWMt 348 ADPFLRLLTATTTLWVLGQAFINIGYVIGLLPVTGLQLPLISAGGTSTAA
            ***:*  :. .* *: .**.**** *:****::*: ***:* **::  .

FtsWSc 394 TMFAIGLLIAFARDEPGARAAL----------------------------
FtsWMt 398 TLSLIGIIANAARHEPEAVAALRAGRDDKVNRLLRLPLPEPYLPPRLEAF
           *:  **::   **.** * ***

                                                [TVSYTHL--NHH
FtsWSc 416 ----------ALRQPRFGRKRGAGGPAAKRS-----PGSWNTMRR--RAS
FtsWMt 448 RDRKRANPQPAQTQPARKTPRTAPGQPARQMGLPPRPGSPRTADPPVRRS
                     *  **     * * * .*::      *** .*     * *

           R]
FtsWSc 449 AARSSGER-------------------
FtsWMt 498 VHHGAGQRYAGQRRTRRVRALEGQRYG
           . :.:*:*
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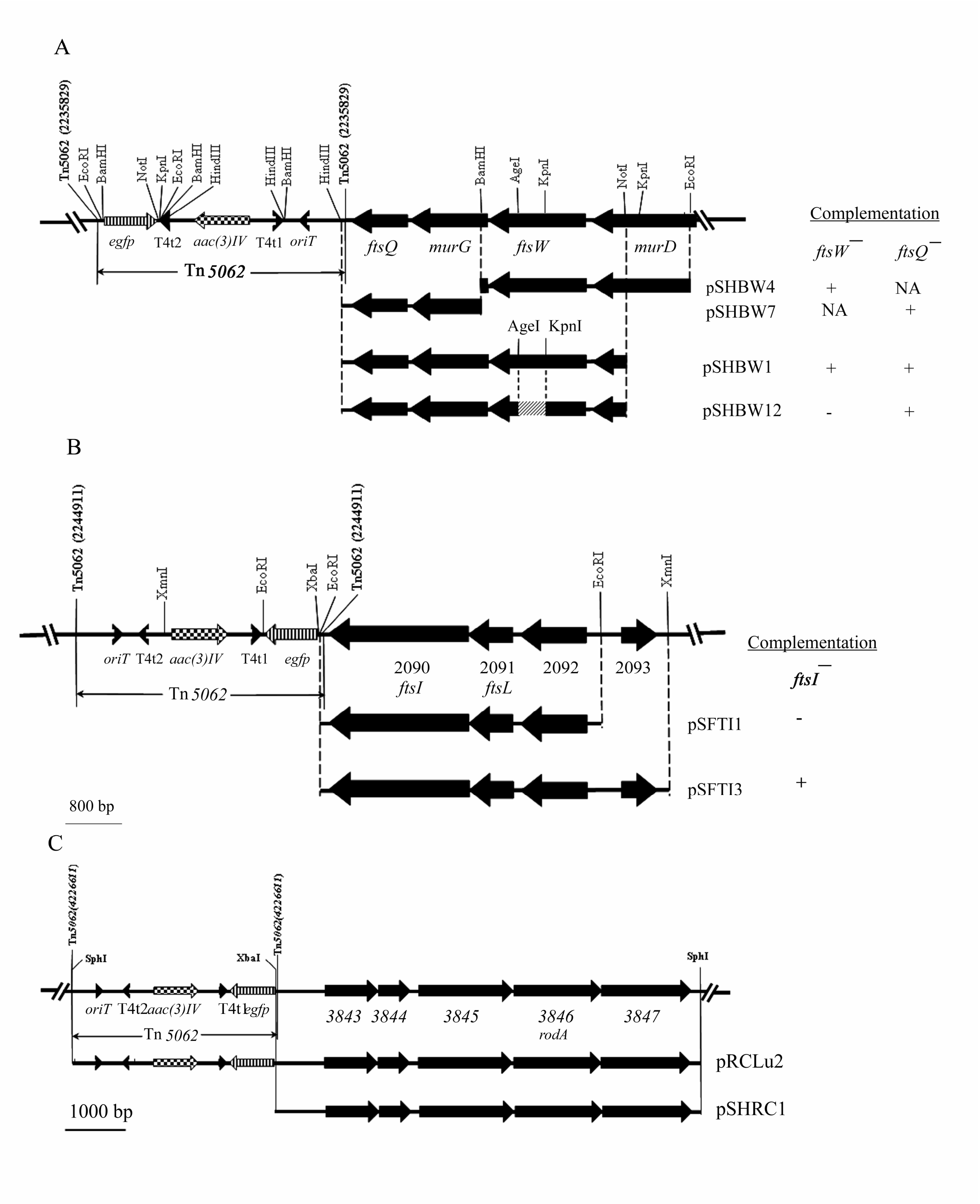
Amino acid alignment between FtsW$_{Sc}$ and FtsW$_{Mt}$.

An asterisk below the alignment indicates an identical amino acid at that position, a colon indicates a position of a conserved substitution, and a dot indicates a semi-conserved substitution. The positions of the two conserved proline residues implicated as being important for interactions between FtsW$_{Mt}$ and FtsI$_{Mt}$ are boxed. The C-terminal amino acid sequence of the truncated FtsW of DSCO2085-5 is indicated in square brackets above the polypeptide sequence replaced in this mutant.

Supplementary Fig 3



Maps of the relevant regions of cosmids derived from SC4A10 used to derive DNA fragments used for genetic complementation.

(A) SC4A10 containing a Tn*5062* insertion at position 15834 (equivalent to position 2235829 in the genome) and the restriction fragments derived from this used to test complementation of *ftsW* and *ftsQ* mutants.

(B) SC4A10 containing a Tn*5062* insertion at position 24916 (equivalent to position 2244911 in the genome) and the restriction fragments derived from this used to test complementation of the *ftsI* mutant.

(C) SCH69 containing a Tn*5062* insertion as position 16172 (equivalent to position 4226611 in the genome) and the restriction fragments derived from this used to construct the integrative plasmid pSHRC1.