Supplementary data file for the manuscript:

Polar N-terminal residues conserved in type 2 secretion pseudopilins determine subunit targeting and membrane extraction steps during fibre assembly

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Supplementary Table S1

Oligo Name	Sequence
PulG T2A 5	CAGCGCGGATTCGCCTTACTGGAAATC
PulG T2A Rev	GATTTCCAGTAAGGCGAATCCGCGCTG
PulG T2A Kpn	CGGGTACCATTCGCCTTACTGGAAATC
PulG P22A 5	CCAGCCTCGTGGTGGCCAACCTGATGGGCAAC
PulG P22A 3	GTTGCCCATCAGGTTGGCCACCACGAGGCTGG
PuilL Eco 3	CACGAATTCCTGTTGCCATAAGGCGAG
PulM 3	GACTGCAAGCTTGCAGGCCGATAGTGAGTCTA
PulM 5-1	TGAGGCGAATTCGAGGTTTCGCGTGCAGAC
PulL Eco	CAAGAATTCAGCGGCGCTACGGAATC
PulL Hind	CACAAGCTTCTGTTGCCATAAGGCGAG

Supplementary Figures

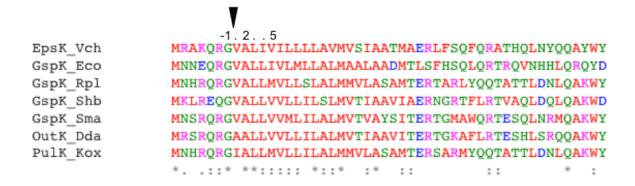


Fig. S1. Sequence alignment of the N-terminal region of pseudopilins of the T2SS GspK family, showing conservation of residue A2 and the lack of residue E at the 5th position. The arrowhead indicates the prepilin peptidase cleavage site, and residue positions 2 and 5 of the mature sequence are indicated. The alignment was generated using the T-Coffee server http://www.ebi.ac.uk/Tools/services/web/. This figure is related to the Fig. 5 or the main text.

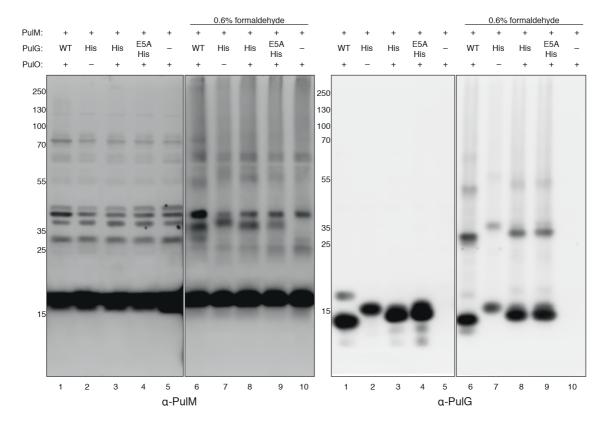


Fig. S2. PulM and PulG interact in the context of the functional Pul T2SS.

Uncropped α -PulM and α -PulG blots showing samples corresponding to the *in vivo* cross-linking described in Fig. 6 before and after the FA treatment. Mw markers (in kDa) and lane numbers are indicated. The strains and technical procedures are described in Fig. 6 and in the Materials and Methods.