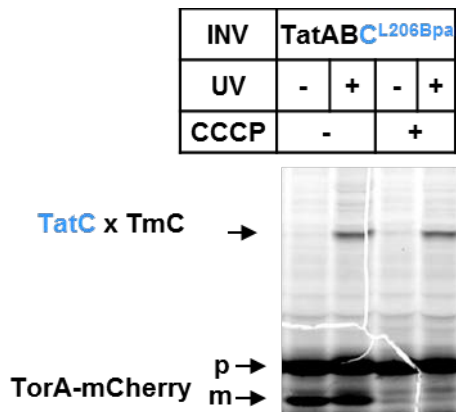
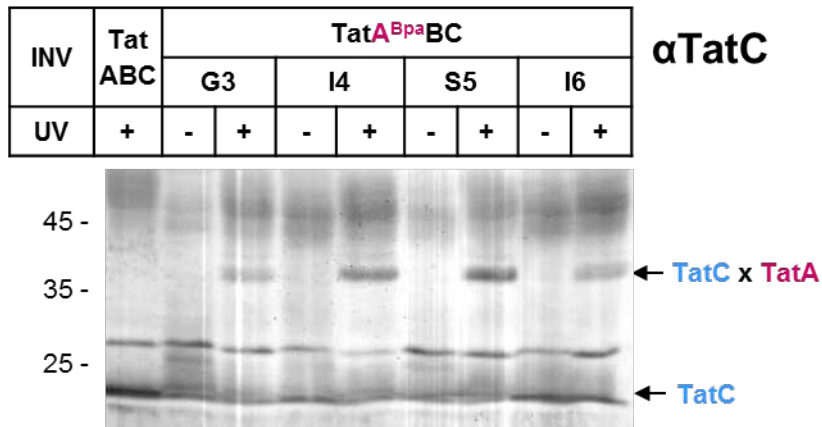
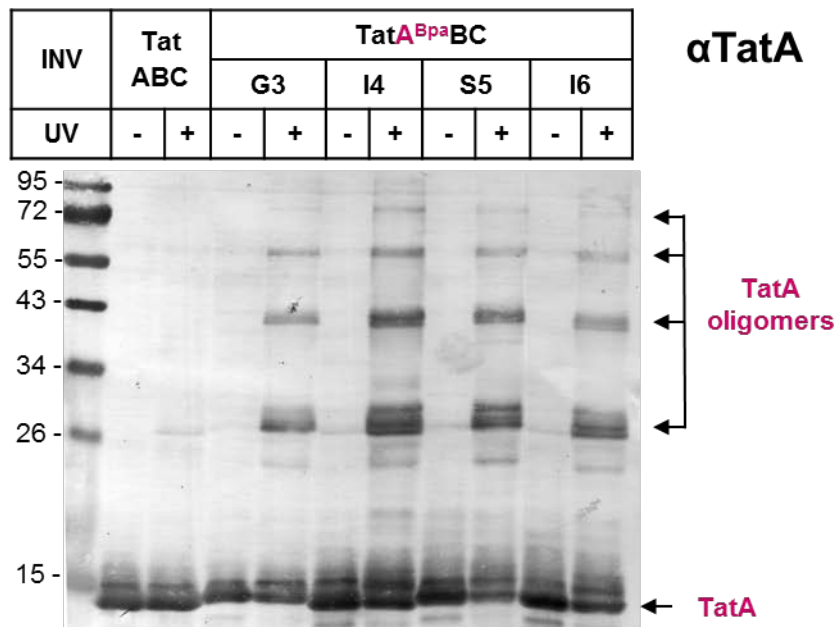


SUPPLEMENTARY INFORMATION

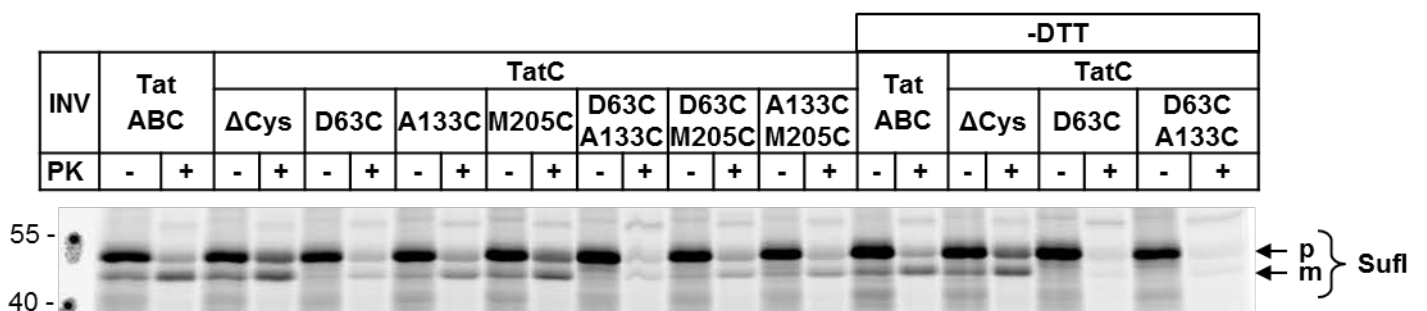
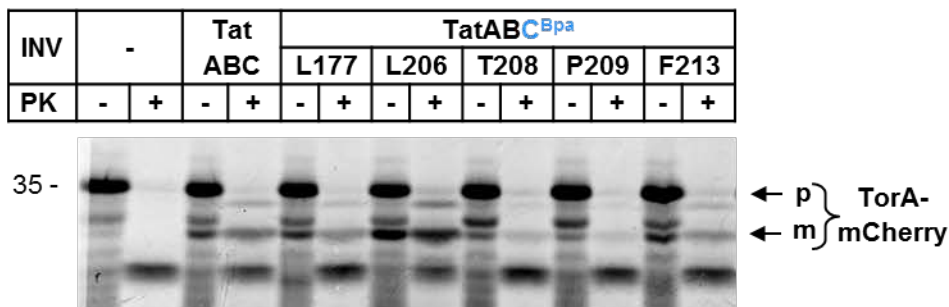
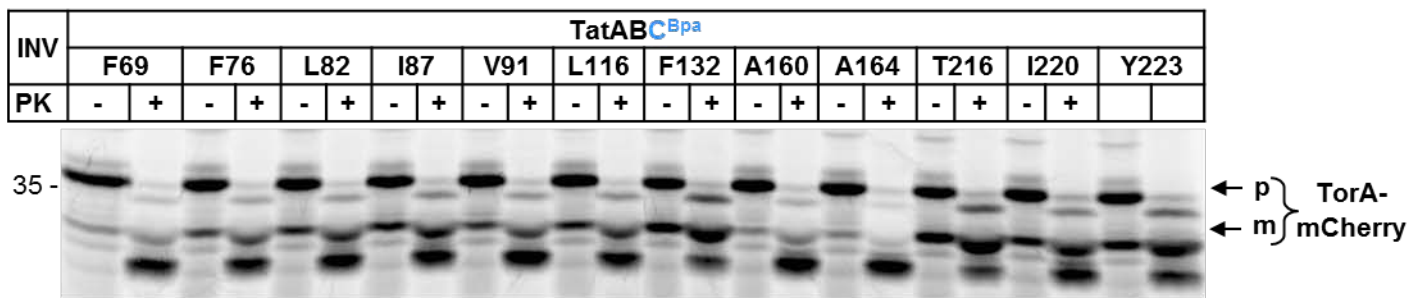
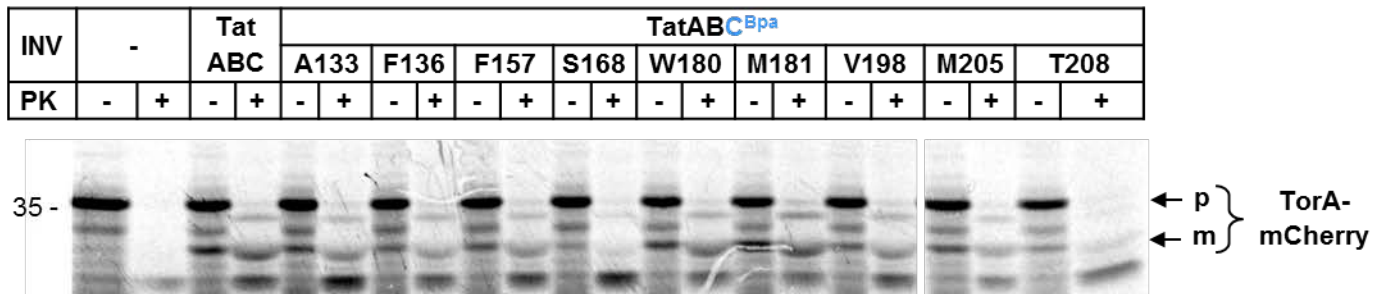
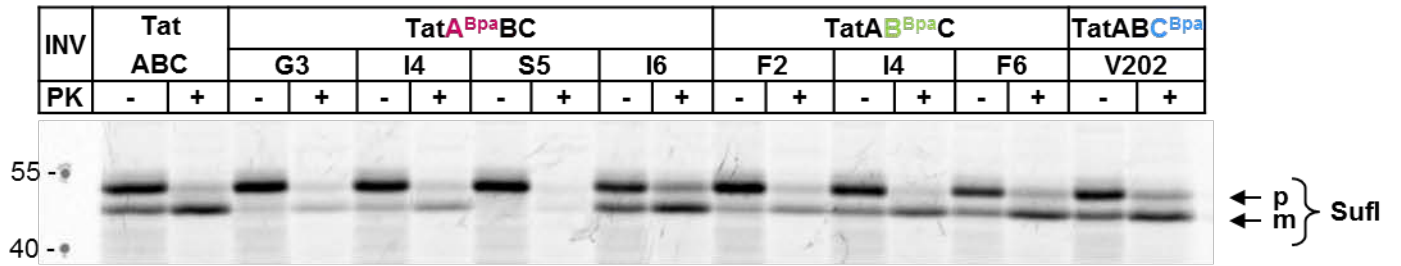
Supplementary Figures



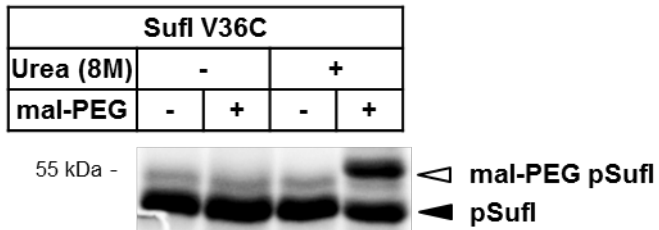
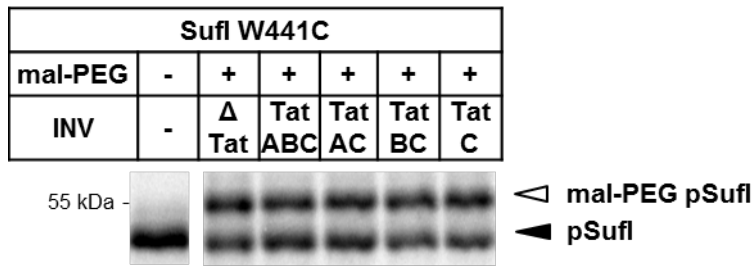
Supplementary Figure 1. Contacts between TatC and a membrane-inserted RR-precursor do not require the H⁺-motive force. The model RR-precursor TorA-mCherry was synthesized and radioactively labeled by *in vitro* transcription/translation in the presence of *E. coli* inner membrane vesicles containing TatA, TatB, and the L206Bpa variant of TatC. In samples labeled (+), cross-linking was initiated by irradiation with UV light. Radiolabeled translation products were separated by SDS-PAGE and visualized by phosphorimaging. Cross-linking between TatC and TorA-mCherry (TatC x TmC) was not influenced by the uncoupler CCCP, which, however, blocks transport into the vesicles, as indicated by a lack of conversion of the precursor (p) to the mature form (m) of TorA-mCherry.

a**b**

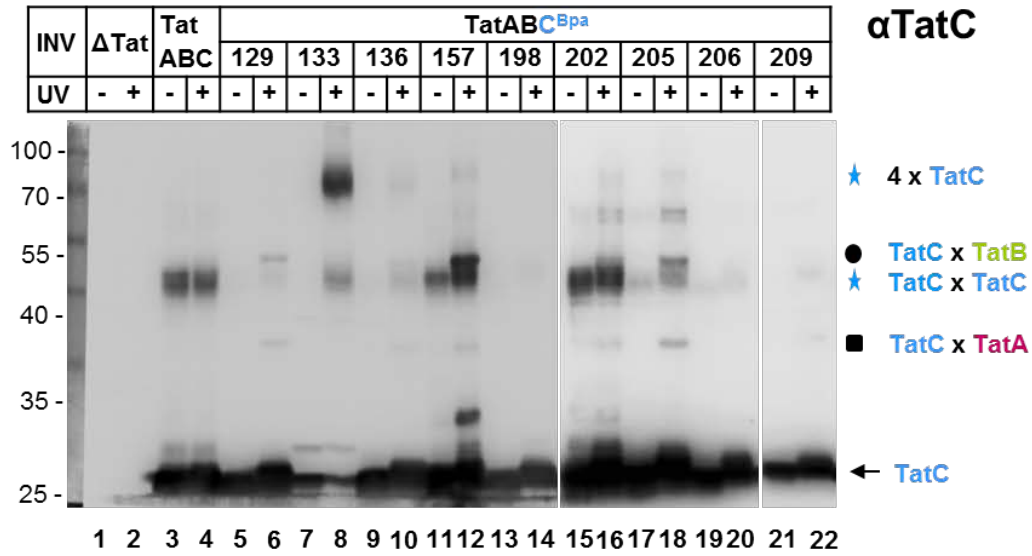
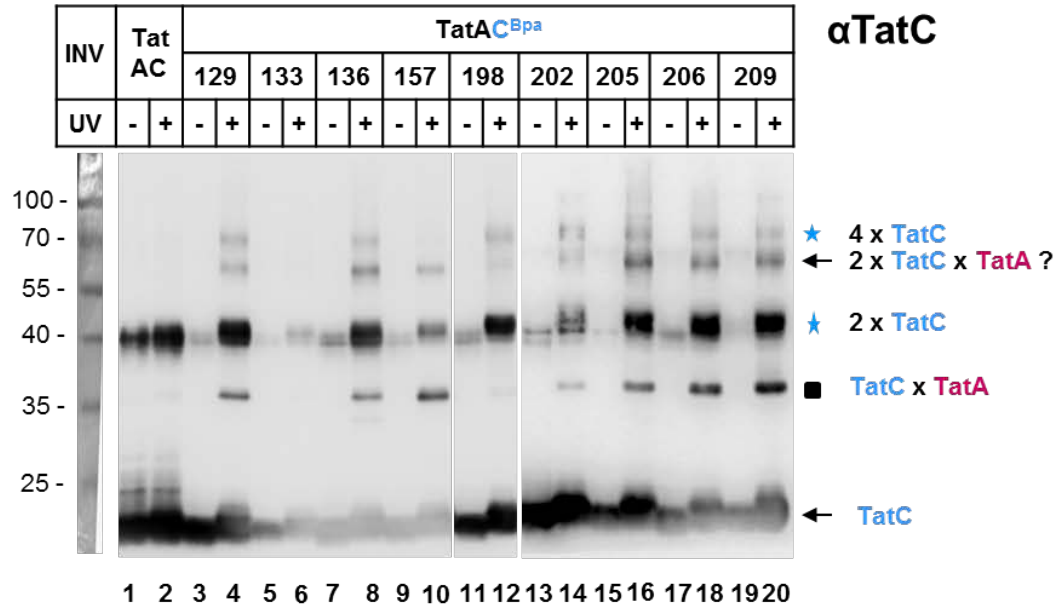
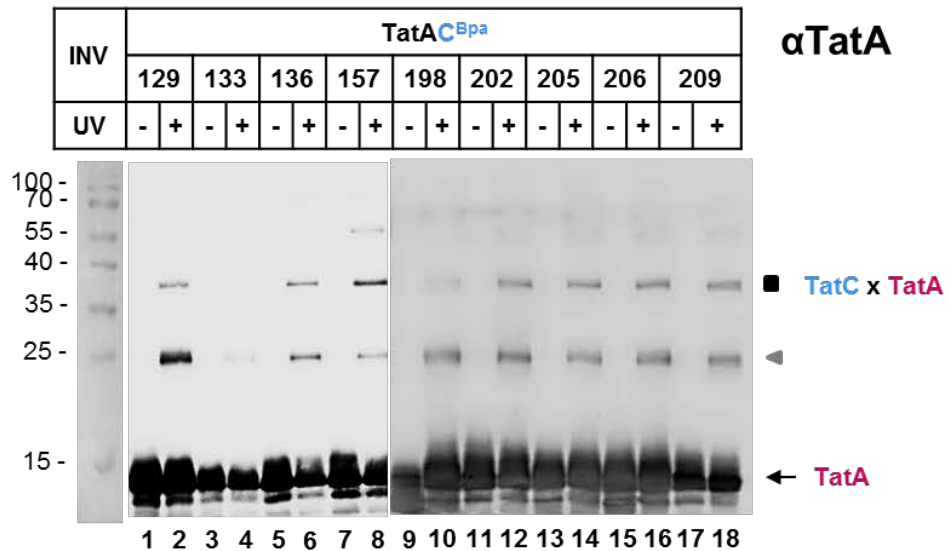
Supplementary Figure 2. The N-terminus of TatA cross-links to TatC and mediates oligomerization of TatA. (a, b) Inner membrane vesicles (INV) carrying the indicated Bpa variants in the N-terminus of TatA were probed for TatA adducts on Western blots using antibodies against TatC (α TatC) and TatA (α TatA). Cross-linking was induced by irradiation with UV light (+). Indicated are complexes between TatA and TatC as well as N-terminally colligated oligomers of TatA. TatABC, Bpa-free vesicles.



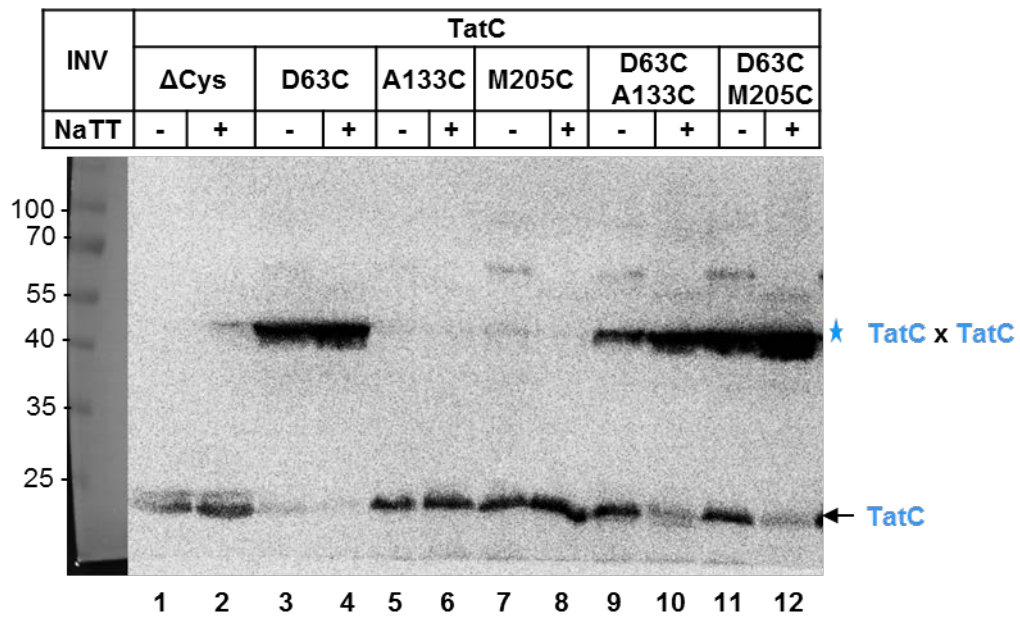
Supplementary Figure 3. Translocation activity of membrane vesicles carrying Bpa-containing Tat variants used in this study. The RR-precursors TorA-mCherry and pSufI were synthesized *in vitro* in the presence of membrane vesicles (INV) containing the wild-type TatABC proteins or any of the indicated Bpa variants of TatA (A^{Bpa}), TatB (B^{Bpa}), or TatC (C^{Bpa}). Shown are the radioactively labeled translation products obtained without (-) or after (+) digestion with proteinase K (PK). The positions of the precursors (p) and mature forms (m) of TorA-mCherry and SufI are indicated. (Bottom panel), vesicles were prepared from *E. coli* strain BL21(DE3) Δ Tat expressing extra-chromosomally a Cys-less mutant of TatC (TatC Δ Cys) carrying single or double cysteine mutations where indicated. Assays performed in the total absence of DTT (- DTT) revealed that TatC dimers, which formed through disulfide bridges at position D63, are inactive.



Supplementary Figure 4. Control experiments to Figure 5. The surface exposed residue W441 of SufI is accessible to mal-PEG, whereas residue V36 in the early mature region can be labeled only after denaturation of SufI with 8M urea. Experimental details are as described in the legend to Fig. 5 and in the Materials section.

a**b****c**

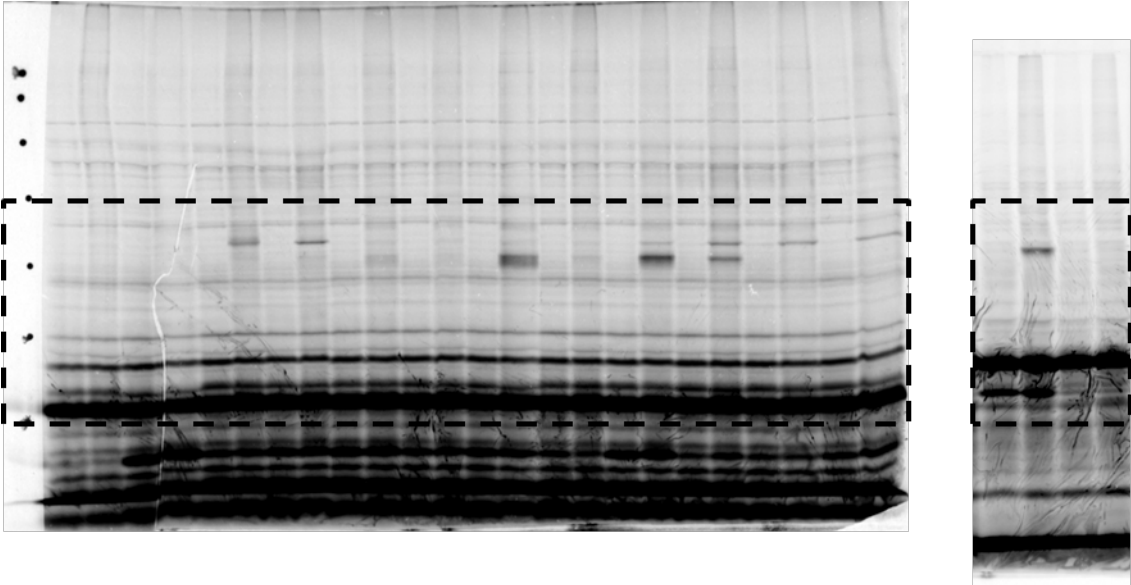
Supplementary Figure 5. TatB is required for tetramerization of TatC through residue 133, whereas it impairs interaction between TatC and TatA. (a) Membrane vesicles (INV) containing the indicated Bpa variants of TatC were probed for inter-TatC cross-links (blue stars). TatB-TatC adducts (black dots) had been identified as such in Fig. 2a and TatA-TatC adducts (squares) are addressed in **b, c**. Δ Tat, vesicles lacking the Tat proteins; TatABC, Bpa-free vesicles. (b, c) As in a, except that membrane vesicles used were devoid of TatB. UV-dependent adducts to the indicated Bpa variants of TatC were probed by antibodies against TatC (α TatC) and TatA (α TatA) revealing the 37 kDa TatA-TatC complexes (squares). TatA dimers formed independently of Bpa, are indicated by a grey arrow head.



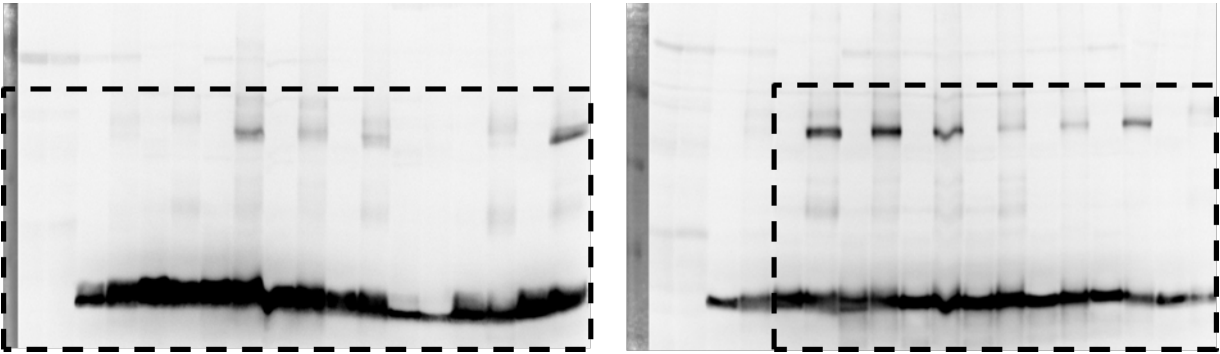
Supplementary Figure 6. No direct cross-linking between the D63 and A133 residues of two adjacent TatC monomers. In contrast to the about 13 Å long, bifunctional cysteine cross-linker Bismaleimido-hexane (Fig. 7b), sodium tetrathionate (NaTT) did not yield adducts larger than 70 kDa that would have been indicative of tetramerization and hexamerization of TatC through residues D63 and A133.

Supplementary Figure 7. Uncropped images of Figs. 1-7 and Supplementary Figs. 1-6.

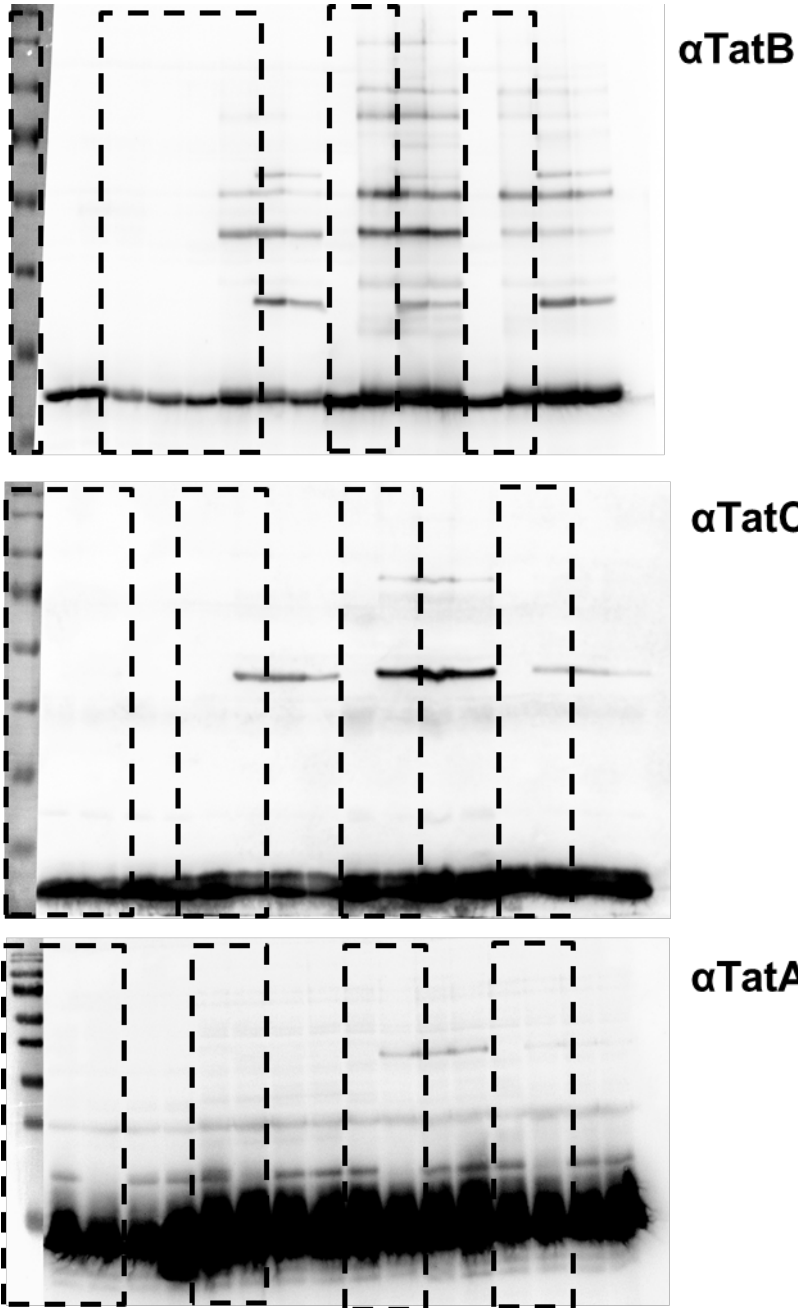
Uncropped Figure 1b



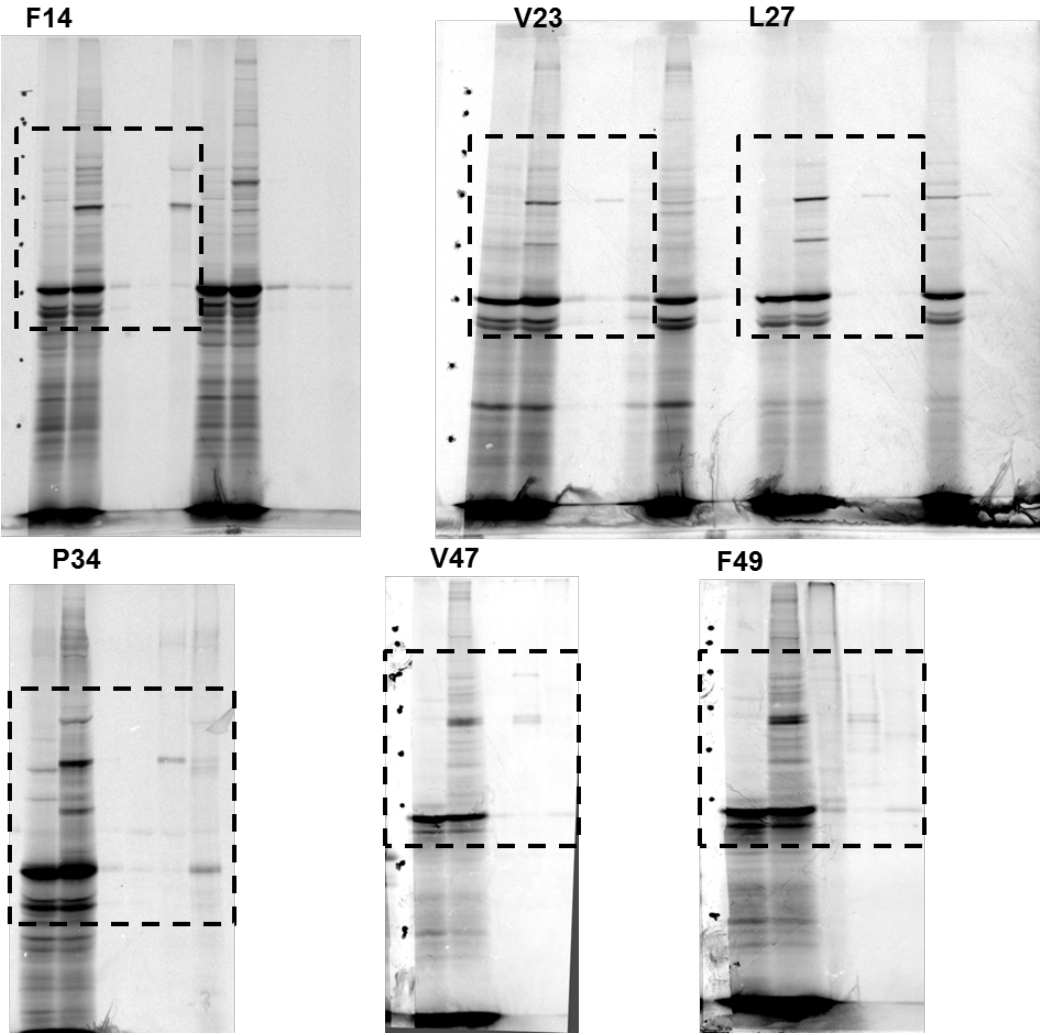
Uncropped Figure 2a



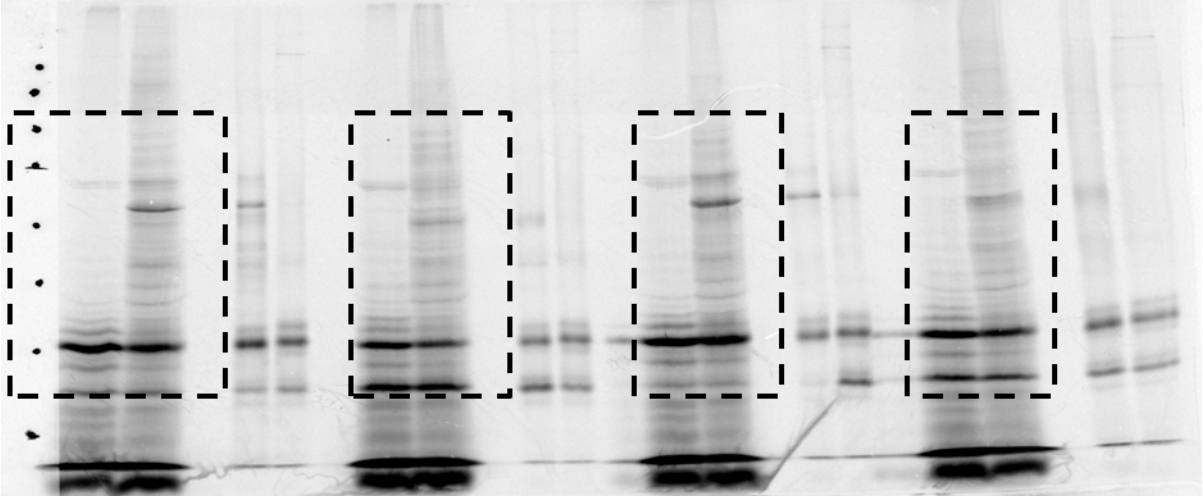
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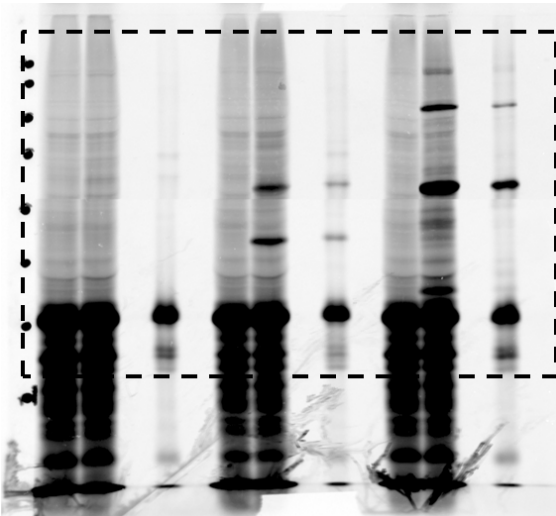
Uncropped Figure 3b



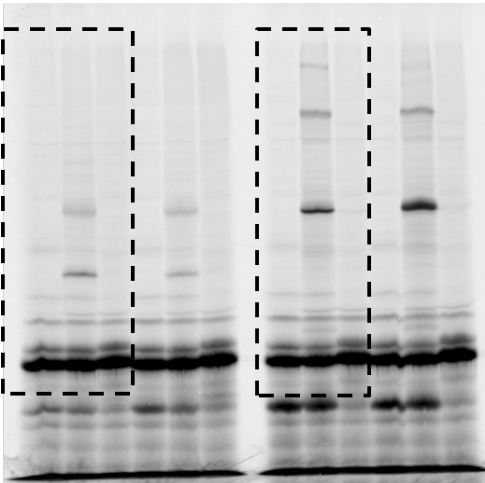
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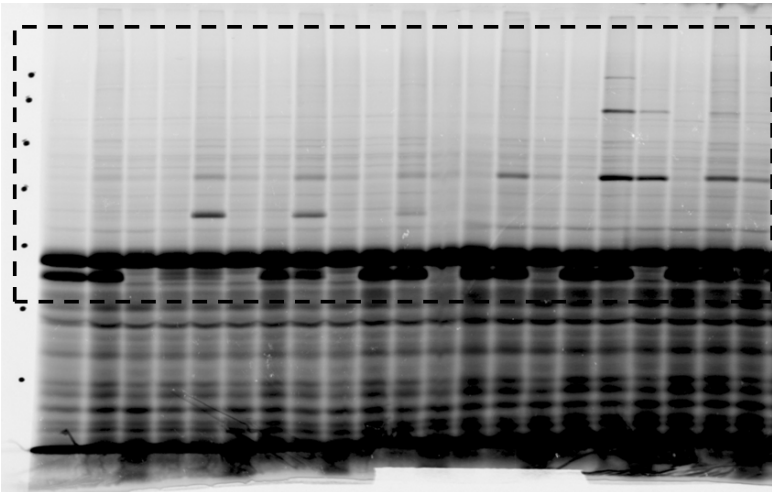
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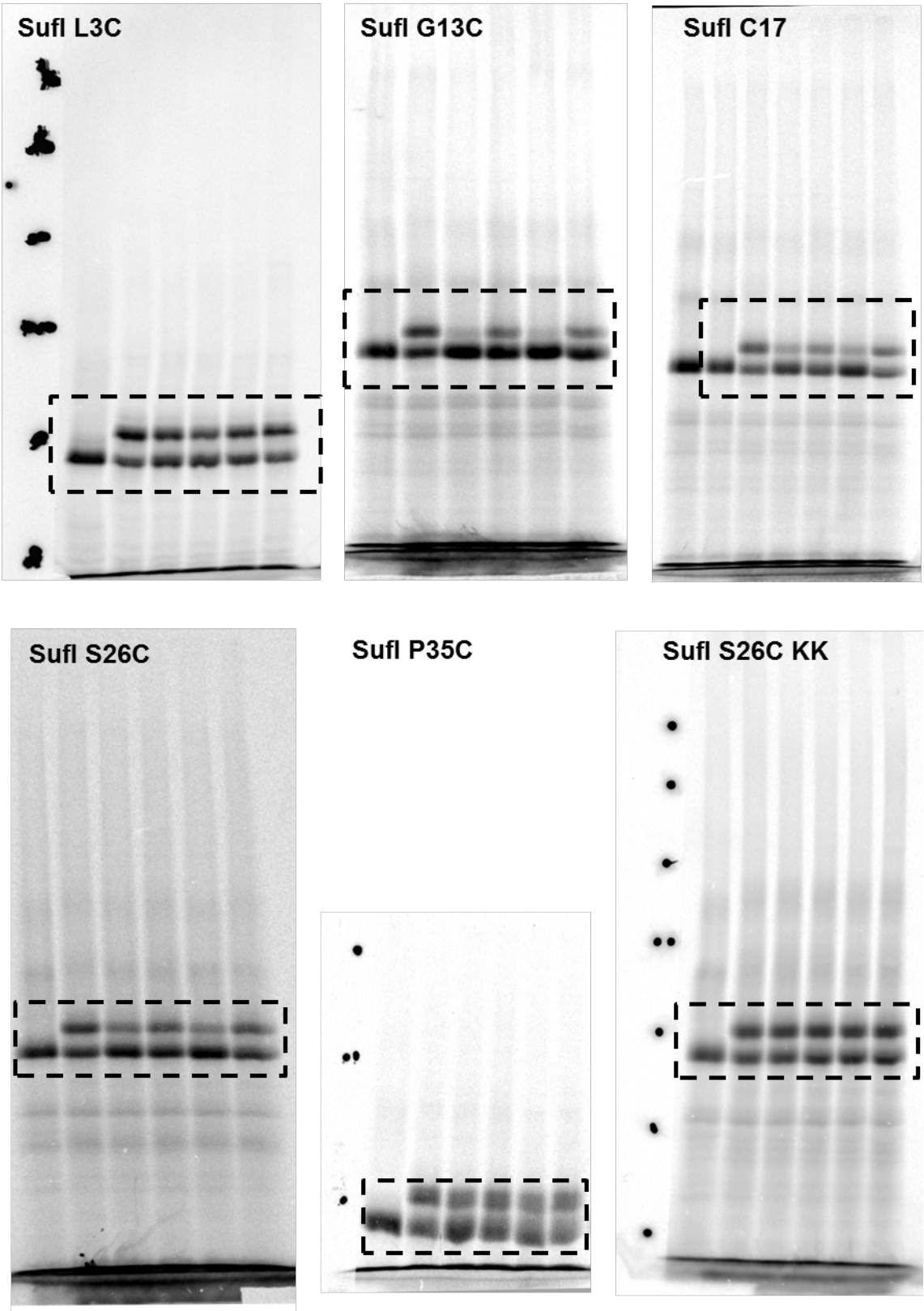
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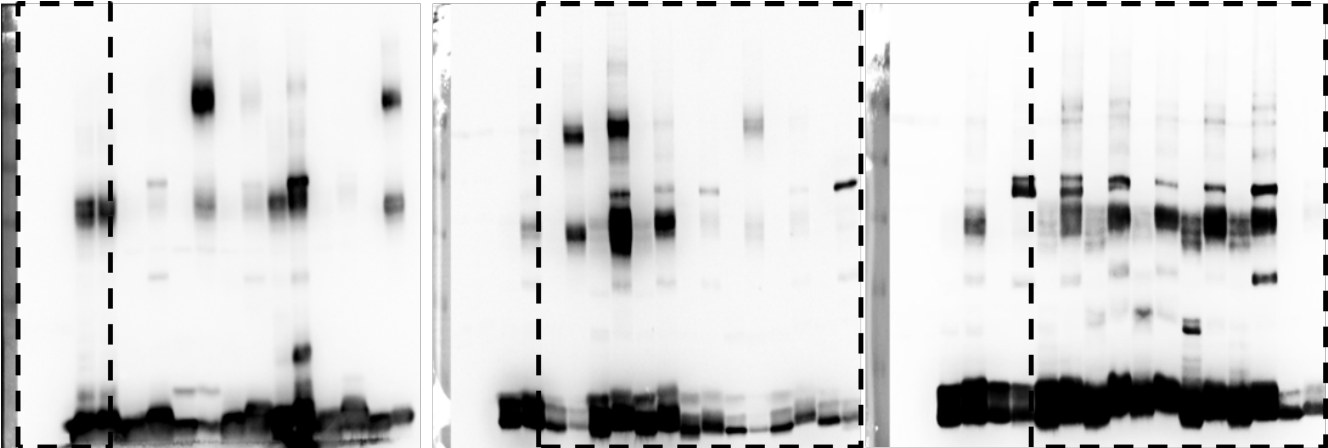
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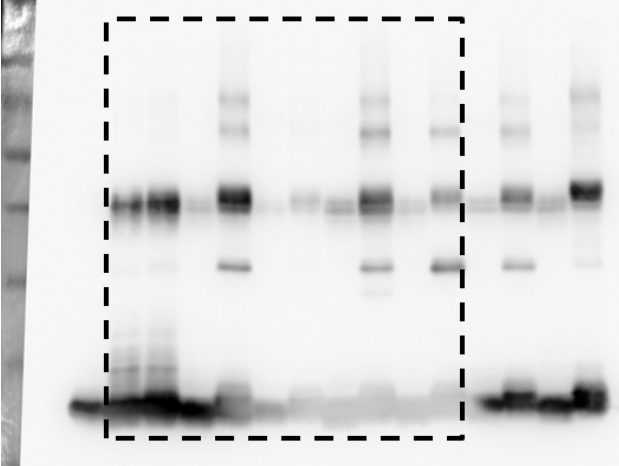
Uncropped Figure 5c



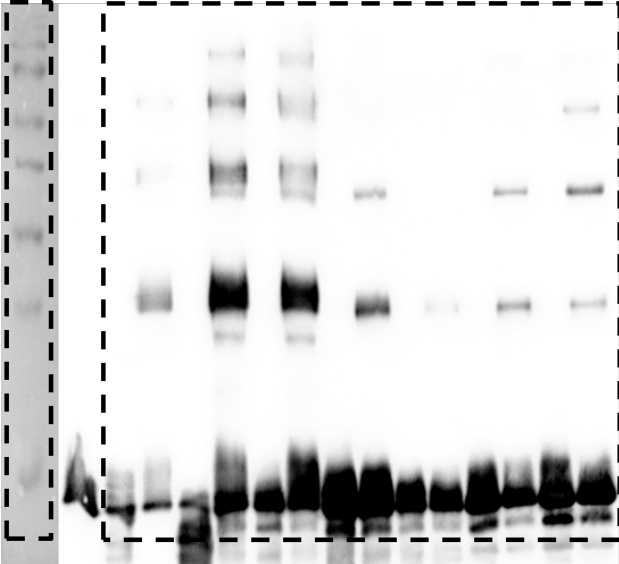
Uncropped Figure 6a



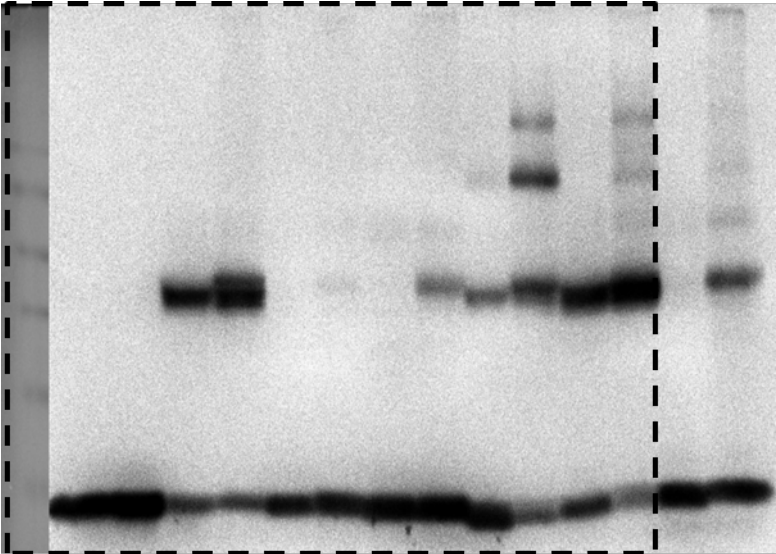
Uncropped Figure 6b



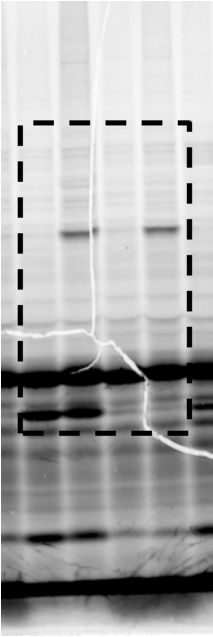
Uncropped Figure 6c



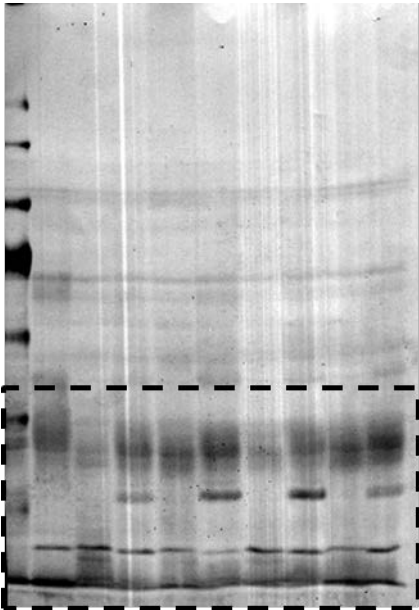
Uncropped Figure 7b



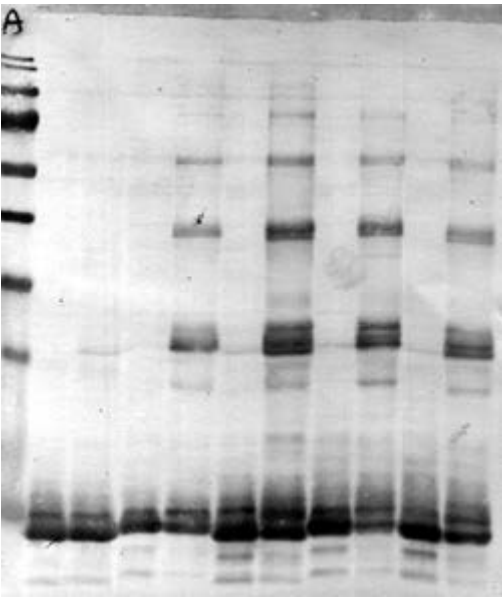
Uncropped Supplementary Figure 1



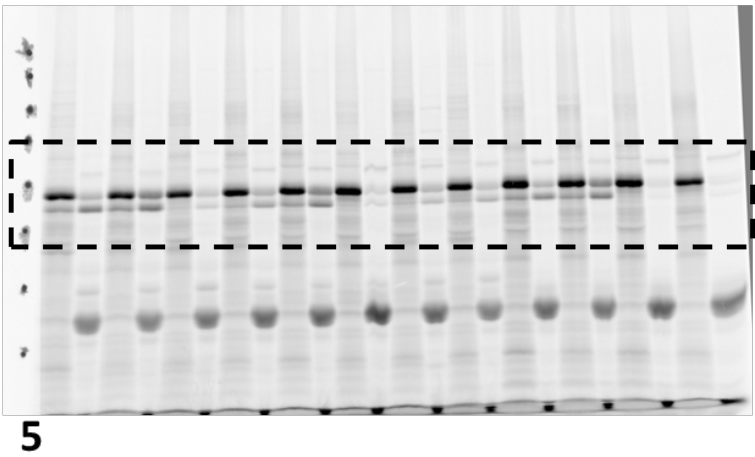
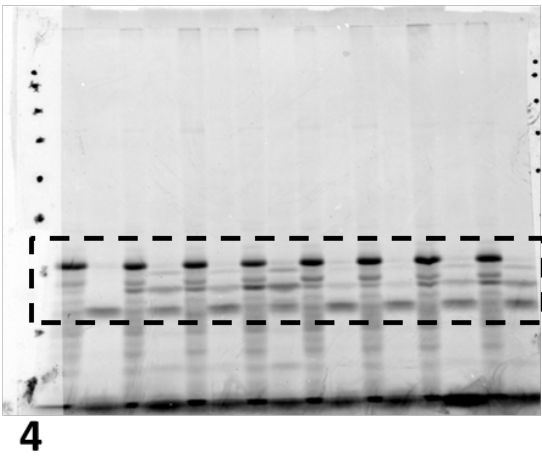
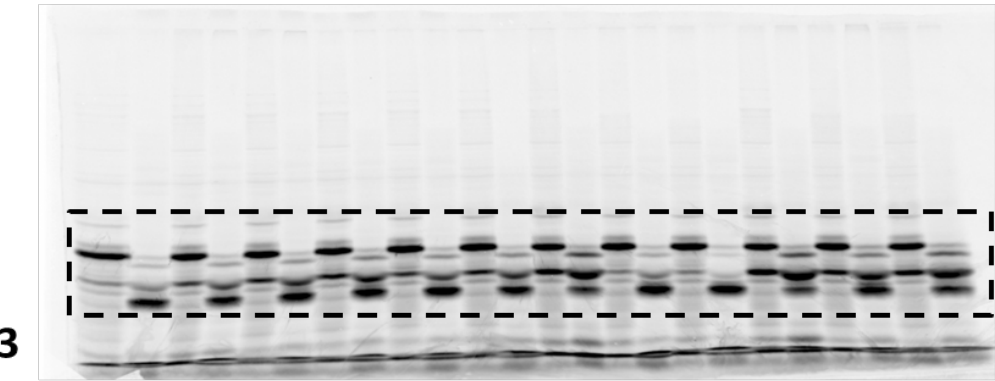
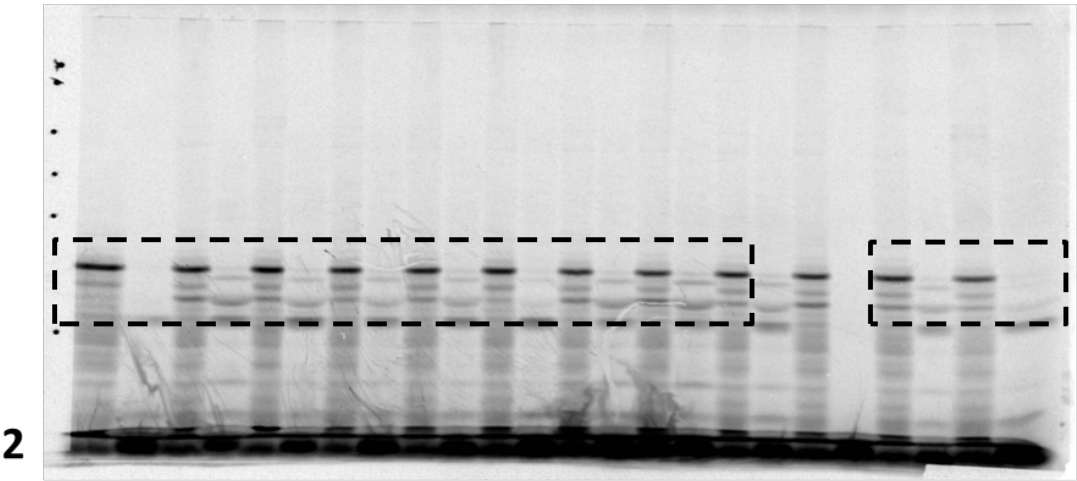
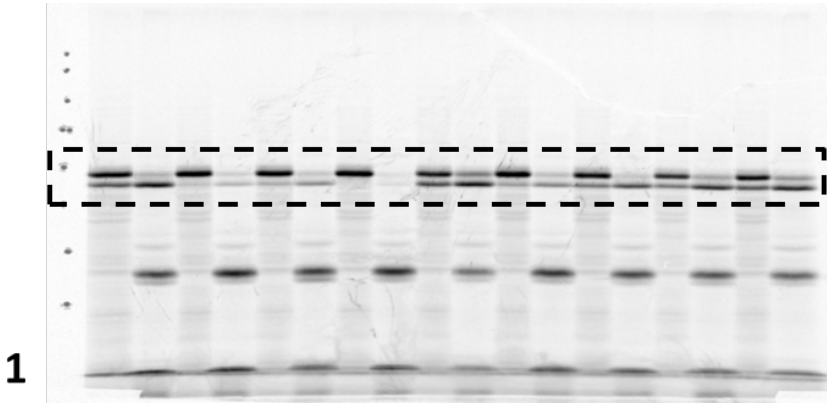
Uncropped Supplementary Figure 2a



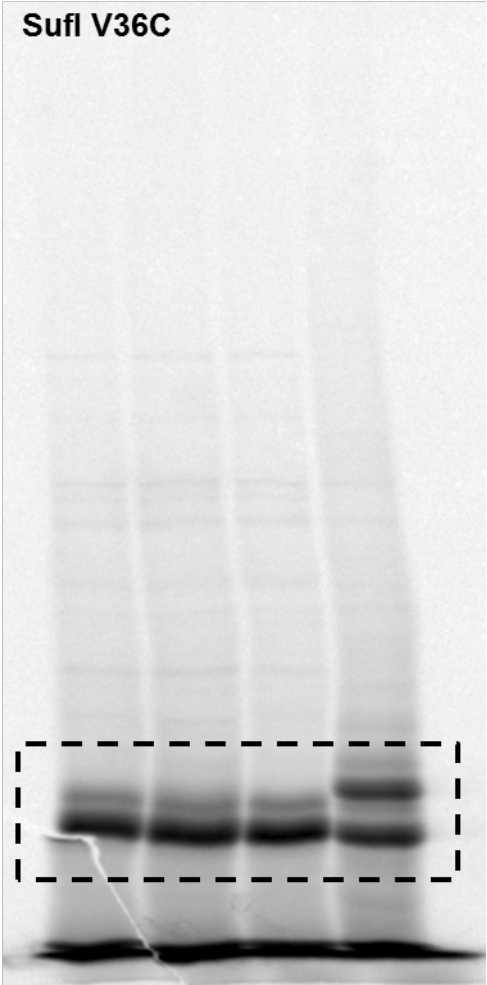
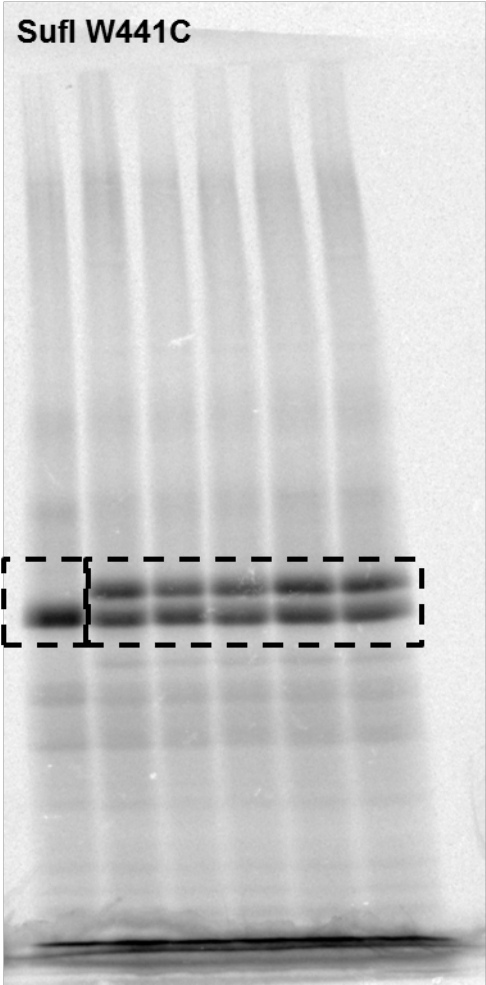
Uncropped Supplementary Figure 2b



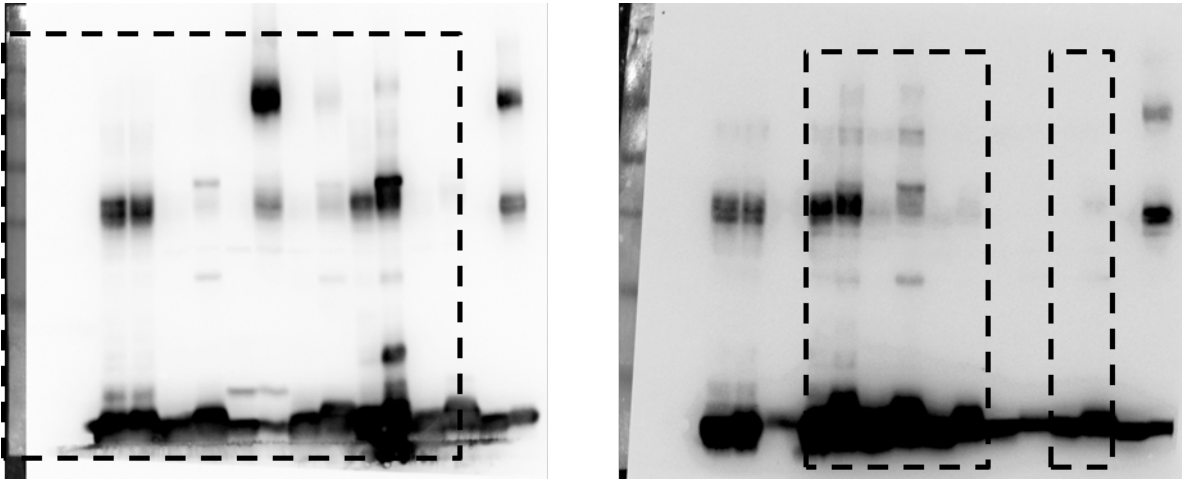
Uncropped Supplementary Figure 3



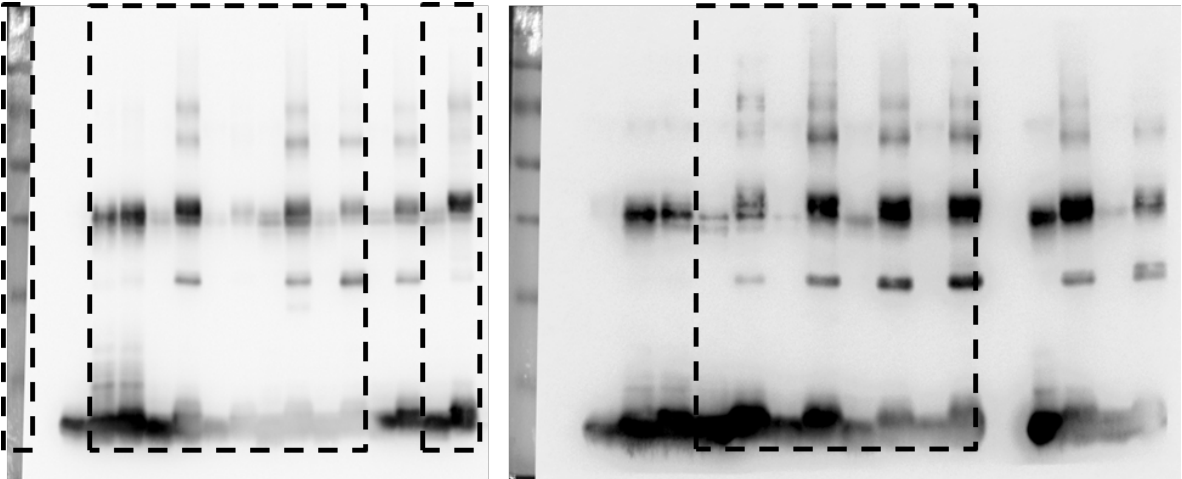
Uncropped Supplementary Figure 4



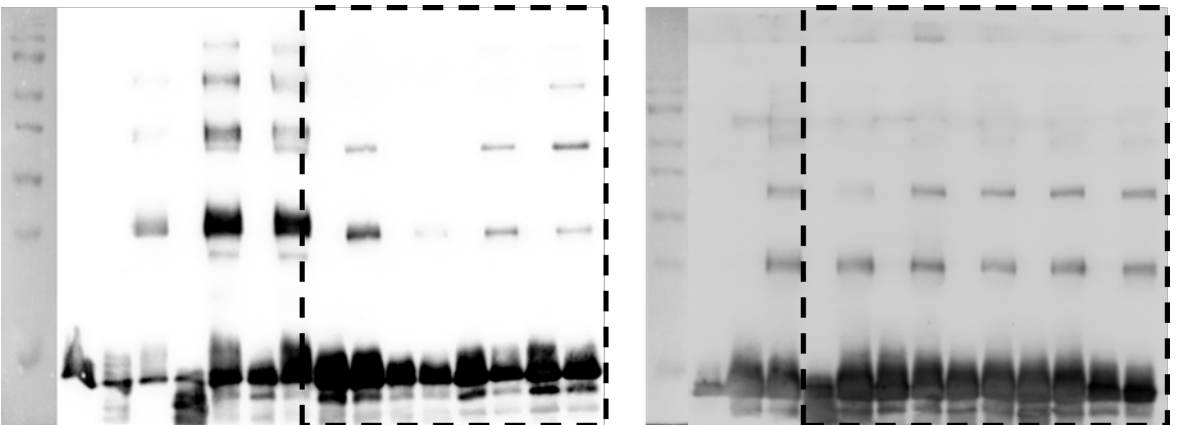
Uncropped Supplementary Figure 5a



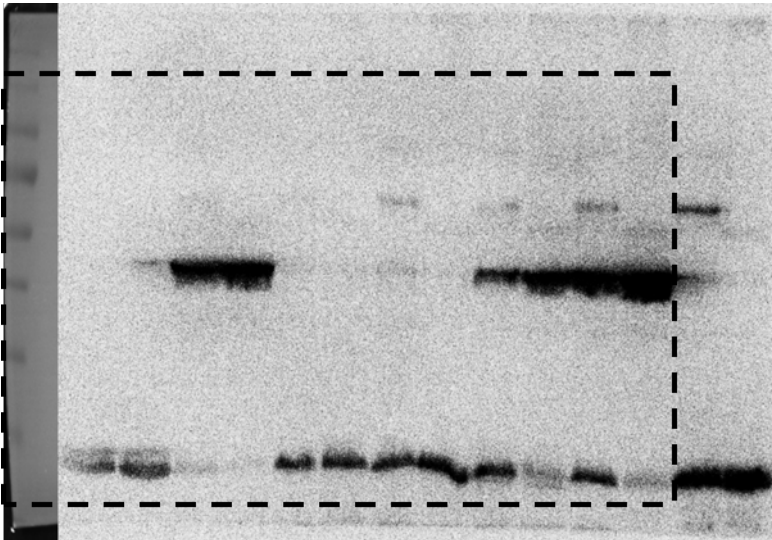
Uncropped Supplementary Figure 5b



Uncropped Supplementary Figure 5c



Uncropped Supplementary Figure 6



Supplementary Tables

Supplementary Table 1. Quantitative data depicted in Fig. 5b

	Exp.I	Exp.II	Exp.III	mean	S.D.
ΔTat-INV					
L3C		0.610	0.673	0.642	
A11C	0.536	0.607		0.572	
G13C	0.468	0.530		0.499	
II4C	0.551	0.629		0.590	
A15C	0.501	0.656		0.579	
L16C	0.417	0.698	0.766	0.627	0.185
C17	0.497	0.655	0.648	0.600	0.089
A18C	0.617	0.716		0.666	
G19C	0.503	0.575		0.539	
A20C	0.370	0.532		0.451	
V21C	0.556	0.589	0.657	0.600	0.051
P22C	0.234	0.258		0.246	
L23C	0.538	0.590		0.564	
A25C	0.483	0.541		0.512	
S26C	0.442	0.481		0.461	
A28C	0.502	0.350		0.426	
G29C	0.491	0.347		0.419	
Q30C	0.293	0.640		0.466	
Q31C	0.314	0.155		0.234	
Q32C	0.147	0.258		0.202	
P33C	0.116	0.094		0.105	
L34C	0.148	0.081		0.114	
P35C	0.500	0.454	0.720	0.558	0.142
V36C	0.062	0.046		0.054	
W441C	0.492	0.532		0.512	
S26CKK	0.530	0.349		0.439	

Supplementary Table 2. Quantitative data depicted in Fig. 5d

	Exp.I	Exp.II	Exp.III	mean	S.D.
ΔTat-INV					
L3C		0.610	0.673	0.642	
G13C	0.468	0.530		0.499	
C17	0.497	0.655	0.648	0.600	0.089
S26C	0.442	0.481		0.461	
P35C	0.500	0.454	0.720	0.558	
W441C	0.492	0.532		0.512	
S26CKK	0.530	0.349		0.439	0.128
TatABC-INV					
L3C		0.476	0.515	0.495	
G13C	0.152	0.137		0.145	
C17	0.244	0.378	0.298	0.307	0.068
S26C	0.218	0.263		0.240	
P35C	0.394	0.331	0.500	0.408	
W441C	0.418	0.419		0.418	
S26CKK	0.525	0.394		0.459	0.093
TatAC-INV					
L3C		0.413	0.476	0.444	
G13C	0.274	0.266		0.270	
C17	0.337	0.373	0.270	0.326	0.052
S26C	0.339	0.342		0.340	
P35C	0.446	0.333	0.328	0.369	
W441C	0.459	0.400		0.429	
S26CKK	0.504	0.408		0.456	0.067
TatBC-INV					
L3C		0.497	0.553	0.525	
G13C	0.127	0.109		0.118	
C17	0.216	0.269	0.278	0.254	0.033
S26C	0.132	0.203		0.167	
P35C	0.388	0.221	0.414	0.341	
W441C	0.545	0.593		0.569	
S26CKK	0.492	0.445		0.469	0.033
TatC-INV					
L3C		0.573	0.618	0.596	
G13C	0.302	0.311		0.307	
C17	0.446	0.446	0.516	0.469	0.041
S26C	0.423	0.394		0.409	
P35C	0.500	0.389	0.535	0.474	
W441C	0.545	0.514		0.529	
S26CKK	0.494	0.383		0.438	0.079

Supplementary Table 3. Plasmids used in this study

Name	Vector	Insert	Reference
pSup-BpaRS-6TRN(D286R)			1
pEVOL-pBpF			2
p8737	pET22b+	TatABCD	3
p8737-tatAC	pET22b+	TatAC	4
pFAT588	pQE	TatCHis	5
pFAT75CH Δ A	pQE	TatBCHis	
pPJ3	pET22b+	TorA-mCherry	6
pPJ5	pET22b+	TorA(KK)-mCherry	
pPJ11	pET22b+	TorA-MalE	7
pKSM SufI-RR	pKSM	SufI	8
pEJ	pET22b+	SufI	this study
pETRick	pET22b+	SufI(KK)	
pLJ1	pET22b+	SufI Δ Cys	
pLJ2	pET22b+	SufI(KK) Δ Cys	
pUNITATCC4	pQE60	TatABC Δ Cys	9

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2. Young, T.S., Ahmad, I., Yin, J.A. & Schultz, P.G. An enhanced system for unnatural amino acid mutagenesis in *E. coli*. *J Mol Biol* **395**, 361-374 (2010).
3. Alami, M., Trescher, D., Wu, L.F. & Müller, M. Separate analysis of twin-arginine translocation (Tat)-specific membrane binding and translocation in *Escherichia coli*. *J Biol Chem* **277**, 20499-20503 (2002).
4. Fröbel, J. et al. Transmembrane insertion of twin-arginine signal peptides is driven by TatC and regulated by TatB. *Nat Commun* **3**, 1311 (2012).
5. Orriss, G.L. et al. TatBC, TatB, and TatC form structurally autonomous units within the twin arginine protein transport system of *Escherichia coli*. *FEBS Lett* **581**, 4091-4097 (2007).
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7. Zoufaly, S. et al. Mapping Precursor-binding Site on TatC Subunit of Twin Arginine-specific Protein Translocase by Site-specific Photo Cross-linking. *J Biol Chem* **287**, 13430-13441 (2012).
8. Alami, M. et al. Differential interactions between a twin-arginine signal peptide and its translocase in *Escherichia coli*. *Mol Cell* **12**, 937-946 (2003).
9. Lee, P.A. et al. Cysteine-scanning mutagenesis and disulfide mapping studies of the conserved domain of the twin-arginine translocase TatB component. *J Biol Chem* **281**, 34072-85 (2006).

Supplementary Table 4. List of primers (mutations are given in bold)

Sufl NdeI	for	GCCATATGTCACTCAGTCGGCG
Sufl XhoI	rev	GCCTCGAGTACCGGATTGACC
Sufl KK F	for	CATATGTCACTCAGTAAGAAGCAGTTCATTCAGGCATCGG
Sufl KK R	rev	CCGATGCCTGAATGAACTGCTTCTTACTGAGTGACATATG
TatA G3	for	GGAACATGTATGGGT TAG ATCAGTATTTGGCAG
	rev	CTGCCAAATACTGAT CTA ACCCATACATGTTCC
TatA I4	for	CATGTATGGGTGGT TAG AGTATTTGGCAGTTATTG
	rev	CAATAACTGCCAAATACT CTA ACCACCCATACATG
TatA S5	for	GTATGGGTGGTAT CTAG ATTTGGCAGTTATTG
	rev	CAATAACTGCCAAAT CTAG ATACCACCCATAC
TatA I6	for	GGTGGTATCAGT TAG TGGCAGTTATTGATTATTG
	rev	CAATAATCAATAACTGCC CTA ACTGATACCACC
TatB F2	for	GCAGGTGTAATCCGTG TAG GATATCGGTTTTAGCG
	rev	CGCTAAAACCGATATC CTAC ACGGATTACACCTGC
TatB I4	for	GGTGTAAATCCGTGTTT GATTAG GGTTTTAGCGAACTGC
	rev	GCAGTTCGCTAAAACC CTA ATCAAACACGGATTACACC
TatB F6	for	CCGTGTTT GATATCGGTTAG AGCGAACTGCTATTGG
	rev	CCAATAGCAGTTCGCT CTA ACCGATATCAAACACGG
TatC F69	for	GGCCTCGCCGTT CTAG ACGCCGATCAAGC
	rev	GCTTGATCGGCGT CTAG AACGGCGAGGCC
TatC F76	for	GCCGATCAAGCTGAC CTAG ATGGTGTGCGCTGATTC
	rev	GAATCAGCGACACCAT CTAG GT CTAG CTT GATCGGC
TatC L82	for	GGTGTGCGCTGATTT TAG TCAGCGCCGGTG
	rev	CACCGGCGCTG ACTA ATCAGCGACACC
TatC I87	for	CTGTCAGCGCCGGT TAG CTCTATCAGGTGTGG
	rev	CCACACCTGATAGAG CTAC ACCGGCGCTGACAG
TatC V91	for	CCGGTGATTCTCTATCAG TAG TGGGCATTTATCGCCCC
	rev	GGGGCGATAAATGCC CTA CTGATAGAGAATCACCGG
TatC L116	for	GCTGCTGGTTTCCAGCT CTTAG CTGTTTTATATCGGCATGG
	rev	CCATGCCGATATAAAACAG CTA AGAGCTGGAAACCAGCAGC
TatC V129	for	GCATTGCGCTACTTTGT TAG TTTCCGCTGGCATTGG
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	rev	GGCAAGGAAGCCAAATGC CTAC GGAAAGACCACAAAGTAG
TatC A133	for	CTTTGTGGTCTTTCCGCT TAG TTTGGCTTCCTTGCC
	rev	GGCAAGGAAGCCAA CTAC AGCGGAAAGACCACAAAG
TatC F136	for	CTTTCCGCTGGCATTGG CTAG CTTGCCAATACCGCG
	rev	CGCGGTATTGGCAAG CTAG CCAAATGCCAGCGGAAAG
TatC F157	for	CGCCAGCTATTTAAG CTAG GTATGGCGCTGTTTATGG
	rev	CCATAAACAGCGCCATA CTAG CTTAAATAGCTGGCG
TatC A160	for	CTATTTAAGCTTCGTTAT TAG CTGTTTATGGCGTTTGG
	rev	CCAAACGCCATAAACAG CTAC ATAACGAAGCTTAAATAG
TatC A164	for	CTTCGTTATGGCGCTGTTTAT TAG TTTGGTGTCTCCTTTGA AGTGC
	rev	GCACTTCAAAGGAGACACCAA CTAC ATAAACAGCGCCATA

		ACGAAG
TatC F165	for	GGCGCTGTTTATGGCGT AGGGT GTCTCCTTTGAAGTGC
	rev	GCACTTCAAAGGAGACACC CTAC GCCATAAACAGCGCC
TatC S168	for	GTTTATGGCGTTTGGTGTCT AG TTTGAAGTGCCGGTAG
	rev	CTACCGGCACTTCAA ACTAG ACACCAAACGCCATAAAC
TatC L177	for	GAAGTGCCGGTAGCAATTGTGT AGCT GTGCTGGATGGG
	rev	CCCATCCAGCACAG CTAC ACAATTGCTACCGGCACTTC
TatC W180	for	GCAATTGTGCTGCTGTG CTAG ATGGGGATTACCTCGCC
	rev	GGCGAGGTAATCCCCAT CTAG CACAGCAGCACAATTGC
TatC M181	for	GCAATTGTGCTGCTGTG CTGGTAG GGGATTACCTCGCC
	rev	GGCGAGGTAATCCC CTACC AGCACAGCAGCACAATTGC
TatC V198	for	CAAAAACGCCCGTATGTGCTGT AGGGT GCATTCTGTTG
	rev	CAACGAATGCACC CTAC AGCACATACGGGCGTTTTTTG
TatC V202	for	GTGCTGGTTGGTGCATT CTAGG TCGGGATGTTGCTGAC
	rev	GTCAGCAACATCCCGAC CTAGA ATGCACCAACCAGCAC
TatC M205	for	GTTGGTGCATTCTGTTGT CGGGTAG TTGCTGACGCCGCC
	rev	GGCGGCGTCAGCA ACTACC CGACAACGAATGCACCAAC
TatC L206	for	GCATTCTGTTGTCGGGATGT AGCT GACGCCGCCGGATG
	rev	CATCCGGCGGCGTCAG CTAC ATCCCGACAACGAATGC
TatC T208	for	GTTGTCGGGATGTTGCTGT AGCC GCCGGATGTCTTCTC
	rev	GAGAAGACATCCGGCG GCTAC AGCAACATCCCGACAAC
TatC P209	for	GTTGTCGGGATGTTGCTGACGT AGCC GGATGTCTTCTC
	rev	GAGAAGACATCCGG CTAC GTCAGCAACATCCCGACAAC
TatC F213	for	GCTGACGCCGCCGGATGT CTAGT CGCAAACGCTGTTGG
	rev	CCAACAGCGTTT GCGACTAG ACATCCGGCGGCGTCAGC
TatC T216	for	GGATGTCTTCTCGCA ATAGCT GTTGGCGATCCCG
	rev	CGGGATCGCCAACAG CTATT GCGAGAAGACATCC
TatC I220	for	CGCAAACGCTGTTGGCGT AGCC GATGTACTGTCTGTTTG
	rev	CAAACAGACAGTACATCG GCTAC GCCAACAGCGTTTGCG
TatC Y223	for	GCTGTTGGCGATCCCGATGT AGT GTCTGTTTGAATCGGTG
	rev	CACCGATTTCAAACAGAC ACTAC ATCGGGATCGCCAACAGC
TatC A133C	for	CTACTTTGTGGTCTTTCCGCTGT GTTTT GGCTTCCTTGC
	rev	GCAAGGAAGCCAAA ACAC AGCGGAAAGACCACAAAGTAG
TatC D63C	for	GTTCAACGATGATCGCCAC CTGT GTGGCCTCGCCGTTTC
	rev	GAACGGCGAGGCCAC ACAGG TGGCGATCATCGTTGAAC
TatC M205C	for	GGTGCATTCTGTTGTCGGGT GTTT GCTGACGCCGCCCG
	rev	CGGCGGCGTCAGCAA ACACCC GACAACGAATGCACC
TorA SS F14_f	for	CATCACGT CGGCGTTAGCT GGCACAAC CTCGGCGGC
TorA SS F14_r	rev	GCCGCCGAGTTGTGCCAG CTAAC GCCGACGTGATG
TorA SS V23_f	for	CAACTCGGCGGCTTAAC CTAGG CCGGGATGCTGG
TorA SS V23_r	rev	CCAGCATCCCGG CTAGG TTTAGCCGCCGAGTTG
TorA SS L27_f	for	CCGTCGCCGGGATGT AGGGG CCGTCATTGTTAACGC

TorA SS L27_r	rev	GCGTTAACAATGACGGCCCC CTACAT CCCGGGCGACGG
TorA SS P34_f	for	CCGTCATTGTTAACGT AGCGACGTGCGACTGCG
TorA SS P34_r	rev	CGCAGTCGCACGT CGCTACGTTAACAATGACGG
TorA-MalE V47	for	GCGGCGACTGACGCT TAGGAATT CGATATCATCGAAG
	rev	CTTCGATGATATCGAATT CCTAAGCGTCAGTCGCCGC
TorA-MalE F49	for	CGACTGACGCTGT CGAATAGGATAT CATCGAAGAAGG
	rev	CCTTCTTCGATGATAT CCTATT CGACAGCGTCAGTCG
TorA- mCherry V47	for	GCGGCGACTGACGCT TAGGAATT CATGGTGAGCAAGGG
	rev	CCCTTGCTCACCATGAATT CCTAAGCGTCAGTCGCCGC
TorA- mCherry F49	for	GCGACTGACGCTGT CGAATAGATGGT GAGCAAGGGC
	rev	GCCCTTGCTCACCAT CTATT CGACAGCGTCAGTCGC
SufI C17A	for	GGG ATT GCA CTT GCG GCA GGC GCT G
	rev	C AGC GCC TGC CGC AAG TGC AAT CCC
SufI C295A	for	GTG TCG ATC ACC GCG GGC GAA GCG G
	rev	C CGC TTC GCC CGC GGT GAT CGA CAC
SufI L3C	for	GGAGATATACATATGTCAT GCAGTCGGCGTCAGTTCATTC
	rev	GAATGAACTGACGCCGACT GCATGACATATGTATATCTCC
SufI A11C	for	CGTCAGTTCATTCAGT GCTCGGGGATTGCACTTGCG
	rev	CGCAAGTGCAATCCCC GAGCACTGAATGAACTGACG
SufI G13C	for	GTCAGTTCATTCAGGCATCGT GCATTGCACTTGCGGCAGG
	rev	CCTGCCGCAAGTGCAAT GCACGATGCCTGAATGAACTGAC
SufI I14C	for	CAGGCATCGGGGT GTGCACTTGCGGCAGGC
	rev	GCCTGCCGCAAGTGC ACACCCCGATGCCTG
SufI A15C	for	GGCATCGGGGATT GCCTTGCGGCAGGCG
	rev	CGCCTGCCGCAAG GCAATCCCCGATGCC
SufI L16C	for	CGGGGATTGCAT GTGCGGCAGGCGC
	rev	GCGCCTGCCG CACATGCAATCCCCG
SufI A18C	for	GGGATTGCACTTGCGT GC GGCGCTGTTCCCC
	rev	GGGGAACAGCGCC GCACGCAAGT GCAATCCC
SufI G19C	for	GGATTGCACTTGCGGCAT GC GCTGTTCCCCTGAAGG
	rev	CCTTCAGGGGAACAG GCATGCCGCAAGT GCAATCC
SufI A20C	for	GGGATTGCACTTGCGGCAGGCT GTGTTCCCCTGAAGGCC
	rev	GGCCTTCAGGGGAAC ACAGCCTGCCGCAAGT GCAATCCC
SufI V21C	for	GCACTTGCGGCAGGCGCT TGTCCCCTGAAGGCCAGC
	rev	GCTGGCCTTCAGGG GACAAGCGCCTGCCGCAAGTGC
SufI P22C	for	GCGGCAGGCGCTGTT GCCTGAAGGCCAGCGC
	rev	GCGCTGGCCTTCAG GCAACAGCGCCTGCCGC
SufI L23C	for	GCAGGCGCTGTTCC CTGCAAGGCCAGCGCAGC
	rev	GCTGCGCTGGCCT GCAGGGAACAGCGCCTGC
SufI A25C	for	GCTGTTCCCCTGAAG TCAGCGCAGCCGGG
	rev	CCCGGCTGCGCT GCACTTCAGGGGAACAGC
SufI S26C	for	CCTGAAGGCCT GTGCAAGCCGGGCAAC
	rev	GTTGCCCGGCTGC ACAGGCCTTCAGG
SufI A28C	for	CCTGAAGGCCAGCGCAT GC GGGCAACAGCAACC

	rev	GGTTGCTGTTGCCCG GC ATGCGCTGGCCTTCAGG
SufI G29C	for	GGCCAGCGCAGCCT GC CAACAGCAACCGC
	rev	GCGGTTGCTGTTGG GC AGGCTGCGCTGGCC
SufI Q30C	for	GCGCAGCCGGGT GC CAGCAACCGCTACC
	rev	GGTAGCGGTTGCTGG GC ACCCGGCTGCGC
SufI Q31C	for	CGCAGCCGGGCAAT GC CAACCGCTACCCG
	rev	CGGGTAGCGGTTGG GC ATTGCCCGGCTGCG
SufI Q32C	for	GCCGGGCAACAGT GC CCCGCTACCCGTTCCG
	rev	CGGAACGGGTAGCGGG GC ACTGTTGCCCGGC
SufI P33C	for	GGGCAACAGCAAT GC CCTACCCGTTCCGCCG
	rev	CGGCGGAACGGGTAG GC ATTGCTGTTGCC
SufI L34C	for	GGCAACAGCAACCGT GC CCCGTTCCGCCG
	rev	GCGGCGGAACGGGG GC ACGGTTGCTGTTGCC
SufI P35C	for	GCAACAGCAACCGCTAT GC GTTCCGCCGCTACTTGAATCTC
	rev	GAGATTCAAGTAGCGGGCGGAAC GC ATAGCGGTTGCTGTTG CC
SufI V36C	for	CAACCGCTACCCT GT CCGCCGCTACCTG
	rev	CAAGTAGCGGGCGG GC AGGGTAGCGGTTG
SufI W441C	for	GGTCAGCCTTCCT GC GCGCACTTCCCG
	rev	CGGGAAGTGCGC GC AGGAAGGCTGACC