## Supplementary material

## Protein interactions within and between two F-type type IV secretion systems

Birgit Koch<sup>1</sup>, Melanie M. Callaghan<sup>2</sup>, Jonathan Tellechea Luzardo<sup>1</sup>, Ami Y. Seeger<sup>2</sup>, Joseph P. Dillard<sup>2</sup>, and Natalio Krasnogor<sup>1</sup>

<sup>1</sup> Interdisciplinary Computing and Complex BioSystems (ICOS), School of Computing Science, Urban Sciences Building, Newcastle University, 1 Science Square Science Central, Newcastle upon Tyne NE4 5TG, U.K

<sup>2</sup>Department of Medical Microbiology and Immunology, University of Wisconsin-Madison,

Madison, Wisconsin, 53706-1521 USA

Corresponding author: Natalio Krasnogor; E-mail: natalio.krasnogor@ncl.ac.uk; Tel: + 44 191 208 5035, Faxe: +44 191 208 8232

Content

Table S1. Strain and plasmid list, including link to Cellrepo.	Page 2 – 6
Table S2 Primer list	Page 7 - 8
Fig. S1. Two-hybrid interactions. Neisseria proteins and corresponding	
mixed interactions	Page 9
Fig. S2. Two-hybrid interactions. F-plasmid proteins and corresponding	
mixed interactions	Page 10
Fig. S3 Mixed two-hybrid interactions corresponding to shared interactions	Page 11
Fig. S4 Pull-down experiments	Page 12 –13
References	Page 14

Table S1. Strains and plasmids used in this study				
	Relevant description	Reference or source		
Neisseria gonorrheae	· · ·			
MS11	WT N. gonorrhoeae	(Swanson, 1972)		
AY529	MS11 transformed with pAY28	This study		
AY534	MS11 transformed with pAY27	This study		
PK127	$MS11\Delta atlA$	(Kohler et al. 2007)		
MR535	$MS11\Delta traK$	(Ramsey et al. 2014)		
PK186	$MS11\Delta traG$	(Kohler et al. 2013)		
AY534∆atlA	PK127 transformed with pAY27	This study		
AY534∆traK	MR535 transformed with pAY27	This study		
AY534∆traG	PK186 transformed with pAY27	This study		
Escherichia coli				
JM101	F' traD36 pro $A^+B^+$ lac $I^q \Delta(lacZ)M15/\Delta(lac-proAB)$	New England Biolabs		
	glnV thi	C		
BTH101	(F-, cya-99, araD139, galE15, galK16, rpsL1 (Str r),	Euromedex		
	hsdR2, mcrA1, mcrB1)			
10-beta	$\Delta$ (ara-leu) 7697 araD139 fhuA $\Delta$ lacX74 galK16 galE15	New England Biolabs		
	$e14- \phi 80 dlac Z \Delta M15 \ recA1 \ relA1 \ endA1 \ nupG \ rpsL$	č		
	$(Str^{R})$ rph spoT1 $\Delta(mrr-hsdRMS-mcrBC)$			
BL21(DE3)	F-, $lon-11$ , $\Delta(ompT-nfrA)885$ , $\Delta(galM-ybhJ)884$ , $\lambda DE3$	Novagen		
. ,	[lacI, lacUV5-T7 gene 1, ind1, sam7, nin5], 446,	5		
	$[mal^+]_{K-12}(\lambda^{S}), hsdS10$			
Origami2(DE3)	$\Delta$ (ara-leu)7697 $\Delta$ lacX74 $\Delta$ phoA PvuII phoR araD139	Novagen		
	ahpC galE galK rpsL F'[lac <sup>+</sup> lacI <sup>q</sup> pro] (DE3)	6		
	gor 522::Tn10 trxB (Str <sup>R</sup> , Tet <sup>R</sup> )			
Plasmids	0			
pMR100	plasmid for constructing C-terminal linker-FLAG3	(Ramsey et al. 2014)		
Pittico	fusions	(Italiisely et al. 2011)		
pAY25	pMR100 with TraH-FLAG3	This study		
pMR68	<i>iga-trpB</i> complementation construct contains the	(Ramsey et al. 2012)		
Prozenos	tetracyline-inducible promoter	(11111100) 00 411 2012)		
pAY27	pMR68 with TraH-FLAG3 under control of the	This study		
<b>F</b>	tetracycline inducible promoter	1110 50000		
pAY28	pAY25 with sequence downstream of <i>traH</i> added after	This study		
P	FLAG3 tag, used to place the FLAG3 tag at the <i>traH</i>	This study		
	native site			
pUT18C	Bacterial two-hybrid vector designed to express a given	(Karimova et al.,		
perioe	polypeptide fused in frame at its N-terminal end with T18	(Ramio va et al., 2001)		
	fragment; ColE1 ori, Amp <sup>R</sup>	_001)		
pUT18	Bacterial two-hybrid vector designed to express a given	(Karimova et al.,		
pe 110	polypeptide fused in frame at its C-terminal end with T18	2001)		
	fragment; ColE1 ori, Amp <sup>R</sup>	2001)		
pUTM18C	As pUT18C but designed to insert the TM domain 1 of <i>E</i> .	(Quellette et el 2014)		
PO IMIOC	<i>coli</i> oppB between the cloned polypeptide and the T18	(Ouellette et al., 2014)		
	fragment; ColE1 ori, Amp <sup>R</sup>			
pKT25	Bacterial two-hybrid vector designed to express a given			
pK125				
	polypeptide fused in frame at its N-terminal end with T25 fragment; p15 ori, Km <sup>R</sup>			
n25N	0	(Classer at al 2000)		
p25N	Bacterial two-hybrid vector designed to express a given	(Claessen et al., 2008)		
	polypeptide fused in frame at its C-terminal end with T25			
	fragment; p15 ori, Km <sup>R</sup>	(O		
pSTM25	Bacterial two-hybrid vector designed to express a given	(Ouellette et al., 2014)		
	polypeptide fused in frame at its N-terminal end with TM			
	domain 1 of <i>E. coli</i> oppB and T25 fragment, p15 ori, Sm <sup>R</sup>			
pKTM25	Bacterial two-hybrid vector designed to express a given	This study		
	polypeptide fused in frame at its N-terminal end with TM			
	domain 1 of <i>E. coli</i> oppB and T25 fragment, p15 ori,			
	Km <sup>R</sup> The TM region was PCR amplified from pSTM25			

	with primer pair 1/2 cut with Sall/EcoRI and cloned into	
pUTM18CltgX <sub>N</sub>	Sall/EcoRI digested pKT25 LtgX <sub>N</sub> was PCR amplified using primer pair 3/4 and	This study
permittengan	cloned into pUTM18C	This study
pKTM25ltgX <sub>N</sub>	LtgX <sub>N</sub> was PCR amplified using primer pair 3/4 and cloned into pKTM25	This study
pUTM18CYag <sub>N</sub>	Yag <sub>N</sub> was PCR amplified using primer pair $5/7$ and	This study
	cloned into pUTM18C	-
pKTM25Yag <sub>N</sub>	Yag <sub>N</sub> was PCR amplified using primer pair 5/7 and cloned into pKTM25	This study
pUT18TraL <sub>N</sub>	TraL <sub>N</sub> was PCR amplified using primer pair $7/8$ and	This study
<b>25</b> N/T 1	cloned into pUT18	This storday
p25NTraL <sub>N</sub>	$TraL_N$ was PCR amplified using primer pair 7/8 and cloned into p25N	This study
pUT18CTraE <sub>N</sub>	$TraE_N$ was PCR amplified using primer pair 9/10 and	This study
	cloned in pUT18C	<b>TT1 1</b>
pKT25TraE <sub>N</sub>	$TraE_N$ was PCR amplified using primer pair 9/10 and cloned in pKT25	This study
pUT18CTraK <sub>N</sub>	TraK <sub>N</sub> was PCR amplified using primer pair $11/12$ and	This study
-	cloned in pUT18C	
pUTM18CTraK <sub>N</sub>	TraK <sub>N</sub> was PCR amplified using primer pair 11/12 and	This study
pKT25TraK <sub>N</sub>	cloned in pUTM18C TraK <sub>N</sub> was PCR amplified using primer pair 11/12 and	This study
<b>P</b>	cloned in pKT25	11115 500005
pKTM25TraK <sub>N</sub>	$TraK_N$ was PCR amplified using primer pair 11/12 and	This study
nITT18CTmoD.	cloned in pKTM25	This study
pUT18CTraB <sub>N</sub>	$TraB_N$ was PCR amplified using primer pair 13/14 and cloned into pUT18C	This study
pKT25TraB <sub>N</sub>	$TraB_N$ was PCR amplified using primer pair 13/14 and	This study
	cloned into pKT25	
pUTM18CDsbC <sub>N</sub>	DsbC <sub>N</sub> was PCR amplified using primer pair 15/16 and cloned into pUTM18C	This study
pKTM25DsbC <sub>N</sub>	$DsbC_N$ was PCR amplified using primer pair 15/16 and	This study
1	cloned into pKTM25	
pUT18CTraV <sub>N</sub>	$TraV_N$ was PCR amplified using primer pair 17/18 and	This study
pUTM18CTraV <sub>N</sub>	cloned into pUT18C TraV <sub>N</sub> was PCR amplified using primer pair 17/18 and	This study
	cloned into pUTM18C	This study
pKT25TraV <sub>N</sub>	$TraV_N$ was PCR amplified using primer pair 17/18 and	This study
IZTM <b>35</b> T 57	cloned into pKT25	This storday
pKTM25TraV <sub>N</sub>	TraV <sub>N</sub> was PCR amplified using primer pair $17/18$ and cloned into pKTM25	This study
pUT18CTraC <sub>N</sub>	$TraC_N$ was PCR amplified using primer pair 19/20 and	This study
	cloned into pUT18C	
pUT18TraC <sub>N</sub>	$TraC_N$ was PCR amplified using primer pair 19/21 and cloned into pUT18C	This study
pKT25TraC <sub>N</sub>	TraC <sub>N</sub> was PCR amplified using primer pair 19/20 and	This study
•	cloned into pKT25	-
p25NTraC <sub>N</sub>	$TraC_N$ was PCR amplified using primer pair 19/21 and	This study
pUTM18CTraW <sub>N</sub>	cloned into pUT18C TraW <sub>N</sub> was PCR amplified using primer pair 22/23 and	This study
	cloned into pUTM18C	This study
pKTM25TraW <sub>N</sub>	$TraW_N$ was PCR amplified using primer pair 22/23 and	This study
	cloned into pKTM25	This storday
pUT18CTraU <sub>N</sub>	TraU <sub>N</sub> was PCR amplified using primer pair 24/26 and cloned into pUT18C	This study
pUTM18CTraU <sub>N</sub>	TraU <sub>N</sub> was PCR amplified using primer pair $24/26$ and	This study
	cloned into pUTM18C	-
pKT25TraU <sub>N</sub>	TraU <sub>N</sub> was PCR amplified using primer pair 24/26 and cloned into pKT25	This study
	cioned into pre125	

pKTM25TraU <sub>N</sub>	$TraU_N$ was PCR amplified using primer pair 24/26 and cloned into pKTM25	This study
pUTM18CTrbC <sub>N</sub>	TrbC <sub>N</sub> was PCR amplified using primer pair $26/28$ and cloned into pUTM18C	This study
pKTM25TrbC <sub>N</sub>	TrbC <sub>N</sub> was PCR amplified using primer pair 26/28 and	This study
pUT18CTraN <sub>N</sub>	cloned into pKTM125 TraN <sub>N</sub> was PCR amplified using primer pair 28/30 and cloned into pUT18C	This study
pUTM18CTraN <sub>N</sub>	TraN <sub>N</sub> was cut out from pKT25TraN <sub>N</sub> with XbaI/BamHI and cloned into XbaI/BamHI digested pUTM18C	This study
pKT25TraN <sub>N</sub>	$TraN_N$ was PCR amplified using primer pair 29/30 and	This study
pKTM25TraN <sub>N</sub>	cloned into pKT25 TraN <sub>N</sub> was cut out from pUTM18CTraN <sub>N</sub> with XbaI/BamHI and cloned into XbaI/BamHI digested	This study
pUTM18CTraF <sub>N</sub>	pKTM25 TraF <sub>N</sub> was PCR amplified using primer pair 32/34 and cloned into pUTM18C	This study
pKTM25TraF <sub>N</sub>	TraF <sub>N</sub> was PCR amplified using primer pair $32/34$ and cloned into pKTM25	This study
pUT18CTraH <sub>N</sub>	TraH <sub>N</sub> was PCR amplified using primer pair $34/35$ and cloned into pUT18C	This study
pUTM18CTraH <sub>N</sub>	TraH <sub>N</sub> was PCR amplified using primer pair $34/35$ and cloned into pUTM18C	This study
pKT25TraH <sub>N</sub>	TraH <sub>N</sub> was PCR amplified using primer pair 34/35 and cloned into pKT25	This study
pKTM25TraH <sub>N</sub>	TraH <sub>N</sub> was PCR amplified using primer pair $34/35$ and cloned into pKTM25	This study
pUT18TraG <sub>N</sub>	Tra $G_N$ was PCR amplified using primer pair 36/37 and cloned into pUT18	This study
p25NTraG <sub>N</sub>	Tra $G_N$ was PCR amplified using primer pair 36/37 and cloned into p25N	This study
pUT18CAtlA <sub>N</sub>	AtlA <sub>N</sub> was PCR amplified using primer pair $38/39$ and cloned into pUT18C	This study
pUT18AtlA <sub>N</sub>	AtlA <sub>N</sub> was PCR amplified using primer pair $40/41$ and cloned into pUT18	This study
pUTM18CAtlA <sub>N</sub>	AtlA <sub>N</sub> was PCR amplified using primer pair $40/42$ and cloned into pUTM18C	This study
pKT25AtlA <sub>N</sub>	AtlA <sub>N</sub> was PCR amplified using primer pair $40/42$ and cloned into pKT25	This study
p25NAtlA <sub>N</sub>	AtlA <sub>N</sub> was PCR amplified using primer pair $38/43$ and cloned into pKT25	This study
pKTM25AtlA <sub>N</sub>	AtlA <sub>N</sub> was PCR amplified using primer pair 40/42 and cloned into pKTM25	This study
pUT18CTraB <sub>F</sub>	TraB <sub>F</sub> was PCR amplified using primer pair 44/45 and cloned into pUT18C	This study
pKT25TraB <sub>F</sub>	TraB <sub>F</sub> was PCR amplified using primer pair $44/45$ and cloned into pKT25	This study
pUT18CTraC <sub>F</sub>	TraC <sub>F</sub> was PCR amplified using primer pair $46/48$ and cloned into pUT18C	This study
pUT18TraC <sub>F</sub>	TraC <sub>F</sub> was PCR amplified using primer pair $46/48$ and cloned into pUT18	This study
pKT25TraC <sub>F</sub>	TraC <sub>F</sub> was PCR amplified using primer pair $46/48$ and cloned into pKT25	This study
p25NTraC <sub>F</sub>	TraC <sub>F</sub> was PCR amplified using primer pair 46/47 and	This study
pUT18CTraE <sub>F</sub>	cloned into p25N TraE <sub>F</sub> was PCR amplified using primer pair 49/50 and cloned into pUT18C	This study
pKT25TraE <sub>F</sub>	cloned into pUT18C TraE <sub>F</sub> was PCR amplified using primer pair 49/50 and cloned into pKT25	This study

pUTM18CTraF <sub>F</sub>	$TraF_F$ was PCR amplified using primer pair 51/52 and cloned into pUTM18C	This study
pKTM25TraF <sub>F</sub>	$TraF_F$ was PCR amplified using primer pair 51/52 and	This study
pUTM18CTraH <sub>F</sub>	cloned into pKTM25 TraH <sub>F</sub> was PCR amplified using primer pair 53/54and	This study
	cloned into pUTM18C	
pKTM25TraH <sub>F</sub>	TraH <sub>F</sub> was PCR amplified using primer pair 53/54 and cloned into pKTM25	This study
pUT18CTraK <sub>F</sub>	TraK <sub>F</sub> was PCR amplified using primer pair 55/56 and cloned into pUT18C	This study
pUTM18CTraK <sub>F</sub>	TraK <sub>F</sub> was PCR amplified using primer pair 55/56 and cloned into pUTM18C	This study
pKT25TraK <sub>F</sub>	TraK <sub>F</sub> was PCR amplified using primer pair $55/56$ and	This study
-	cloned into pKT25	
pKTM25TraK <sub>F</sub>	$TraK_F$ was PCR amplified using primer pair 55/56 and	This study
pUTM18CTraU <sub>F</sub>	cloned into pKTM25 TraU <sub>F</sub> was PCR amplified using primer pair 57/58 and	This study
permitter	cloned into pUTM18C	This study
pKTM25TraU <sub>F</sub>	$TraU_F$ was PCR amplified using primer pair 57/58 and	This study
UT100T V	cloned into pKTM25	TT1.'
pUT18CTraV <sub>F</sub>	TraV <sub>F</sub> was PCR amplified using primer pair 59/60 and cloned into pUT18C	This study
pUTM18CTraV <sub>F</sub>	TraV <sub>F</sub> was PCR amplified using primer pair 59/60 and	This study
-	cloned into pUTM18C	
pKT25TraV <sub>F</sub>	$TraV_F$ was PCR amplified using primer pair 59/60 and	This study
pKTM25TraV <sub>F</sub>	cloned into pKT25 TraV <sub>F</sub> was PCR amplified using primer pair 59/60 and	This study
	cloned into pKTM25	This study
pUTM18CTraW <sub>F</sub>	$TraW_F$ was PCR amplified using primer pair 61/62 and	This study
• KTM <b>125</b> Tro W-	cloned into pUTM18C TraW <sub>F</sub> was PCR amplified using primer pair 61/62 and	This study
pKTM25TraW <sub>F</sub>	cloned into pKTM25	This study
pUTM18CTrbC <sub>F</sub>	$TrbC_F$ was PCR amplified using primer pair 63/64 and	This study
	cloned into pUTM18C	
pKTM25TrbC <sub>F</sub>	$TrbC_F$ was PCR amplified using primer pair 63/64 and cloned into pKTM25	This study
pCOLADuet-1	Protein expression vector. Kan <sup>R</sup>	Novagen
pET22b	Protein expression vector. $Amp^R$	Novagen
pET22bTraV <sub>N</sub>	TraV <sub>N</sub> and pET22b were PCR amplified using primer	This study
	pair 67/68 and primer pair 65/66 respectively. The PCR	
	products were combined using the NEBuilder HiFi DNA Assembly Cloning Kit (New England Biolabs.).	
pET22bTraV <sub>F</sub>	TraV <sub>F</sub> and pET22b were PCR amplified using primer pair	This study
P	75/76 and primer pair 73/74 respectively. The PCR	11110 00000
	products were combined using the NEBuilder HiFi DNA	
	Assembly Cloning Kit (New England Biolabs.).	TT1 · / 1
pCOLATraW <sub>N</sub>	TraW <sub>N</sub> and pCOLADuet were PCR amplified using primer pair $71/72$ and primer pair $69/70$ respectively. The	This study
	PCR products were combined using the NEBuilder HiFi	
	DNA Assembly Cloning Kit (New England Biolabs.).	
pCOLATrbC <sub>F</sub> -SP	TrbC <sub>F</sub> -SP and pCOLADuet were PCR amplified using	
	primer pair 77/78 and primer pair 69/70 respectively. The	This study
	PCR products were combined using the NEBuilder HiFi DNA Assembly Cloning Kit (New England Biolabs.).	
	Errer resentory croning fat (new England Diolaos.).	

## **Version Controlled Strains:**

Version-controlled cell repositories (Tellechea-Luzardo et al., 2020) to facilitate reproduction and derivative work from this paper can be found here:

TraV<sub>N</sub>: <u>https://cellrepo.herokuapp.com/repositories/53?branch\_id=68&locale=en</u>

 $TraV_{F:} \ \underline{https://cellrepo.herokuapp.com/repositories/56?branch_id=75\&locale=en}$ 



TraV<sub>N</sub>

TraV<sub>F</sub>

This repository focuses on TraV proteins and describes the plasmids containing them.

Table S2. Primers used in this study. Restriction sites used for cloning are underlined

- 1. CCGACAACGACGTCAACAG
- 2. CCAGGGTTTTTCCCAGTCA
- 3. GGAA<u>GGATCC</u>CTGTTATAAGGAAGCCGGCAGCAA
- 4. GCTAC<u>GAATTC</u>CTACGAAGAGCGTGTTTTTAATCGTT
- 5. GGAA<u>GGATCC</u>CATGATTCTGACAGCCTGTGCC
- 6. GCTAC<u>GAATTC</u>TTACCAAGTGATTACAACGGTTCTC
- 7. CAAGA<u>TCTAGAG</u>ATGAGAGATTATCATGTGCC
- 8. GCTAC<u>GAATTC</u>GAATTTAGAAACTCCCGTTTAT
- 9. GGAA<u>GGATCC</u>CATGTTGAGTGAATTGGCGATA A
- 10. GCTAC GAATTCTCAATTACCTCGATTACCGCC
- 11. GGAAGGATCCCGCGCAACGAGTGCCGGCAACA
- 12. GCTAC<u>GAATTC</u>TCAACCTCCCGGACGGCTGAT
- 13. GGAA<u>GGATCC</u>CATGAGGGTGAAAGTAAACAAATT
- 14. GCTACGAATTCCTATTTGGTTTCGCCGGTAT
- 15. GGAA<u>GGATCC</u>CGATGTCAAAACTGTTGGAAGCACT
- 16. GCTAC<u>GAATTC</u>TCATTCTGCTCCCGCTCCATTTAA
- 17. CAA GA<u>TCTAGAG</u>TCAACCTTAACCATGTCCGGT
- 18. AAGG<u>GGATCC</u>CTATCGAACGGTACCGGGAAT
- 19. GCTAC<u>TCTAGA</u>GATGGGCGTCCTGTCAAAATTT
- 20. AAGG<u>GGATCC</u>TTAGCGGGTTGCGGCACGGTCCCTT
- 21. AATTC<u>GGATCC</u>TCGCGGGTTGCGGCACGGTCCCTT
- 22. GGAA<u>GGATCC</u>CTCGACACCCCCTGTCGAGA
- 23. GCTAC<u>GAATTC</u>TCACGGTTTCATGACCTCTACAC
- 24. GCTAC<u>TCTAGA</u>GGCTGAAGCTGTTCCTACT
- 25. AAGG<u>GGATCC</u>TCAATTAGTCTTAAATTTATATGCACCA
- 26. GGAAGGATCCCGCGGATGTAGAGGCGGC
- 27. GCTAC<u>GAATTC</u>TCATTTTCTGCCTTCCAGAACGG
- 28. GCTAC<u>GGATCC</u>CGCCGCACTCAGGGAA
- 29. AAGG<u>CCCGGGG</u>TTATTGATATTCATAATAGTTCTTCACTTCCAA
- 30. GCTACTCTAGAGGCCGCACTCAGGGAAA
- 31. AAGG<u>GGATCC</u>TTATTGATATTCATAATAGTTCTTCACTTCCAAATTTTTCC
- 32. GGAA<u>GGATCC</u>CGCGGATGATGGCATGGGAT
- 33. GCTAC<u>GAATTC</u>TTAATACAATGTCCCGACAGGGCG
- 34. GGAAGGATCCCGGCATAGAGAAGAACATGGCT
- 35. GCTAC<u>GAATTC</u>TTAGAAACGGTTCATCGAATCAAA
- 36. GCTAC<u>TCTAGA</u>GATGGCTGTCGAATACTTTACTTTC
- 37. CTAC<u>GGTACC</u>CGTTCCTTTGGGCGGAATACAGC
- 38. CAAGA<u>TCTAGA</u>GATGTGGCGTGGAATATCAAGTGGA
- 39. TTCGC<u>GGTACC</u>TTAAAATCCTCTCTGCCTAAAGAA

40. GGAAGGATCCCATGTGGCGTGGAATATCAAGT 41. GCTACGAATTCAGAAATCCTCTCTGCCTAAAGAAATT 42. GCTACGAATTCTTAAAATCCTCTCTGCCTAAAGAAATT 43. CTACGGTACCCGAAATCCTCTCTGCCTAAAGAAATT 44. GGAAGGATCCCATGGCCAGTATCAATACCATTGTG 45. GCTACGAATTCTTATTTGCCATCGTTGCCCC 46. GGAAGGATCCCGTGAATAACCCACTTGAGGCC 47. GCTACGAATTCGATGCCACACTCCTGTATTTCT 48. GCTACGAATTCTCATGCCACACTCCTGTATTTCT 49. GGAAGGATCCCATGGAACACGGTGCCCG 50. GCTACGAATTCTTATTTTTTTCTCATCGTCTG 51. GGAAGGATCCCAAAGATGCAGGCTGGCAGT 52. GCTACGAATTCTTAAAAATTGGGTTTAAAATCTTCAGAAACGTTCAG 53. GGAAGGATCCCGATGTGAACAGCGACATGAATCAG 54. GCTACGAATTCTCACAGCGTGCTCCCTC 55. GGAAGGATCCCGCAAACGGTACGCTGGC 56. GCTACGAATTCTCAGTTGCCCTCCCCG 57. GGAAGGATCCCGATTCTGCCTGTGAGGGGC 58. GCTACGAATTCTCACAGGAAGACACAGTTACGTTTACG 59. GGAAGGATCCCAGTACGGAATTTGAGTGTAACGC 60. GCTACGAATTCTTAATTAATACGTGGTTTTCCCCACG 61. GGAAGGATCCCGCCGATCTTGGTACCTGGG 62. GCTACGAATTCTCATTTTCTGCCCTCCTCTG 63. GGAAGGATCCCTCAGAAAACGTGAACACTCCTG 64. GCTACGAATTCTCATTTCCCGGAATCTCCTTTC 65. TACCGTTCGACTCGAGCACCACCACCAC 66. TACCGGACATATCCATGGCCATCGCCGG 67. GGCCATGGATATGTCCGGTATCGGCGGTAG 68. GGTGCTCGAGTCGAACGGTACCGGGAATAC 69. CTCGAGTCTGGTAAAGAAAC 70. TGTATATCTCCTTCTTATACTTAAC 71. GTATAAGAAGGAGATATACAATGTCCCACAAGAAAAAAATAG 72. GTTTCTTTACCAGACTCGAGCGGTTTCATGACCTCTAC 73. ACGTATTAATCTCGAGCACCACCACCAC 74. ATTCCGTACTATCCATGGCCATCGCCGG 75. GGCCATGGATAGTACGGAATTTGAGTGTAAC 76. GGTGCTCGAGATTAATACGTGGTTTTCCC 77. GTATAAGAAGGAGATATACAATGTCAGAAAACGTGAAC 78. GTTTCTTTACCAGACTCGAGTTTCCCGGAATCTCCTTTC

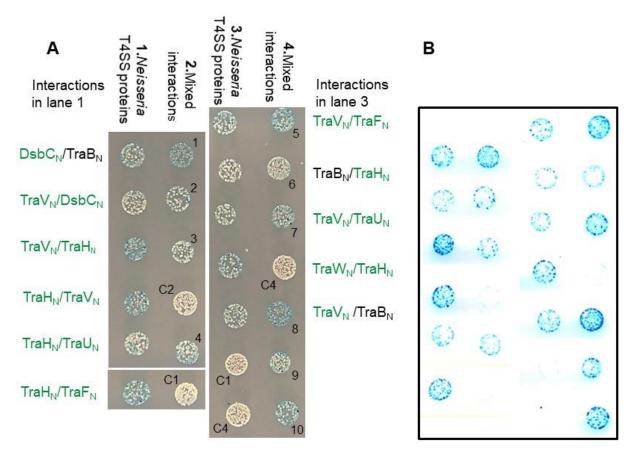
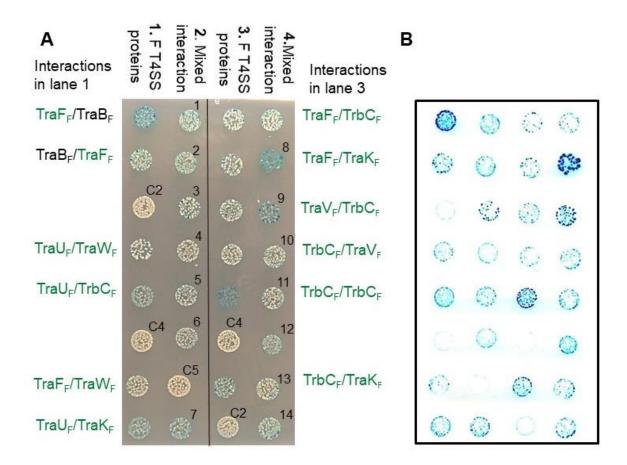
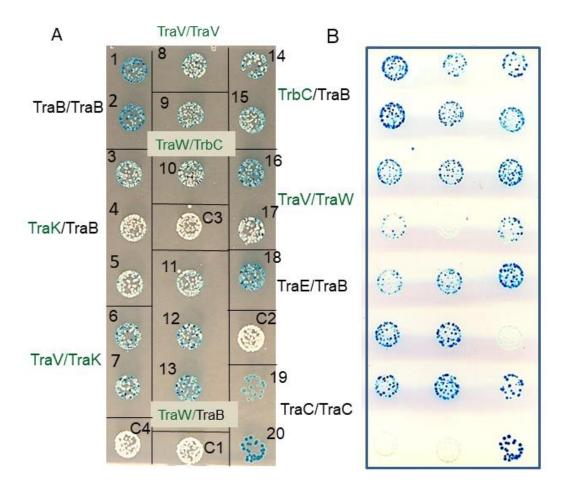


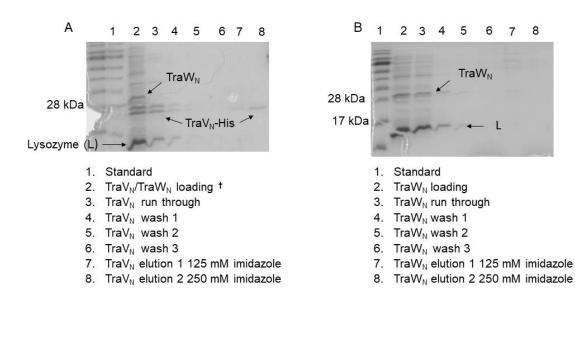
Fig.S1. Bacterial two-hybrid interactions between Neisseria proteins (lane 1 and 3) and corresponding mixed interactions defined as an interaction between a protein from the N. gonorrhoeae T4SS and a protein from the T4SS encoded by the F-plasmid. The figure shows colonies of E. coli BTH101 transformants carrying plasmids encoding the proteins indicated in the order T18/T25. Protein names in green indicate that the gene encoding the protein was cloned in a BACTH-TM system vector, black names indicate that the gene was cloned in the BACTH system vector. C1, C2, C3, C4 and C5 are vector controls; respectively pUTM18C/pKTM25, pUT18/pKT25, pUT18C/pKT25, pUT18C/pKTM25 and pUTM18C/pKT25. The mixed interactions are: 1. DsbC<sub>N</sub>/TraB<sub>F</sub>, 2. TM-TraV<sub>F</sub>/DsbC<sub>N</sub>, 3 TM-TraV<sub>F</sub>/TraH<sub>N</sub>, 4. TraU<sub>F</sub>/TraH<sub>N</sub>, 5. TM-TraV<sub>N</sub>/TraF<sub>F</sub>, 6. TraB<sub>F</sub>/TraH<sub>N</sub>, 7. TraH<sub>N</sub>/TraB<sub>F</sub>. 8. TM-TraV<sub>N</sub>/TraB<sub>F</sub>, 9. TraB<sub>F</sub>/TM-TraV<sub>N</sub>, 10. TM-TraV<sub>F</sub>/TraB<sub>N</sub>. B. Image obtained by scanning the agar plate.

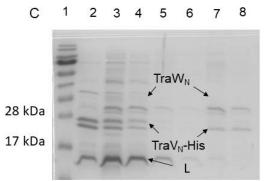


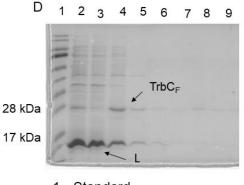
**Fig.S2.** Bacterial two-hybrid interactions between F-plasmid proteins (lane 1 and 3) and corresponding mixed interactions defined as an interaction between a protein from the *N*. *gonorrhoeae* T4SS and a protein from the T4SS encoded by the F-plasmid. The figure shows colonies of *E. coli* BTH101 transformants carrying plasmids encoding the proteins indicated in the order T18/T25. Protein names in green indicate that the gene encoding the protein was cloned in a BACTH-TM system vector, black names indicate that the gene was cloned in the BACTH system vector.C2, C3, C4 and C5 are vector controls; respectively pUT18C/pKT25, pUT18C/pKT25, pUT18C/pKTM25 and pUTM18C/pKT25. The mixed interactions are: 1 TraF<sub>F</sub>/TraB<sub>N</sub>, 2. TraF<sub>N</sub>/TraB<sub>F</sub>, 3. TraB<sub>F</sub>/TraF<sub>N</sub>, 4. TraU<sub>F</sub>/TraW<sub>N</sub> 5. TrbC<sub>F</sub>/TraU<sub>N</sub>, 6. TaU<sub>N</sub>/TrbC<sub>F</sub>, 7. TraU<sub>N</sub>/TM-TraK<sub>F</sub>, 8. TraF<sub>N</sub>/TM-TraK<sub>F</sub> 9. TM-TraV<sub>N</sub>/TrbC<sub>F</sub> 10. TrbC<sub>F</sub>/TM-TraV<sub>N</sub> 11. TrbC<sub>F</sub>/TrbC<sub>N</sub>, 12. TrbC<sub>N</sub>/TrbC<sub>F</sub>, 13. TrbC<sub>N</sub>/TM-TraK<sub>F</sub>, 14.TM-TraK<sub>N</sub>/TrbC<sub>F</sub>. B. Image obtained by scanning the agar plate.



**Fig. S3.** Mixed interactions (defined as interactions between a protein from the *N. gonorrhoeae* T4SS and a protein from the F-plasmid T4SS) corresponding to interactions observed with both *N. gonorrhoeae* and F-plasmid proteins. **A.** Photograph of colonies of *E. coli* BTH101 transformants carrying plasmids encoding the proteins indicated in the order T18/T25. Protein names in green indicate that the gene encoding the protein was cloned in a BACTH-TM system vector, black names indicate that the gene was cloned into the BACTH system vector. C1, C2 and C4 are vector controls; respectively pUT18C/pKT25, pUTM18C/pKTM25 and pUT18C/pKTM25. The following interactions are shown: 1. TraB<sub>N</sub>/TraB<sub>F</sub>. 2. TraB<sub>F</sub>/TraB<sub>N</sub>, 3. TraB<sub>N</sub>/TM-TraK<sub>F</sub>, 4. TM-TraK<sub>F</sub>/TraB<sub>N</sub>, 5.TM-TraK<sub>N</sub>/TraB<sub>F</sub>, 6. TM-TraV<sub>F</sub>/TM-TraK<sub>N</sub>, 7. TM-TraV<sub>N</sub>/TM-TraK<sub>F</sub>, 8. TM-TraV<sub>F</sub>/TM-TraV<sub>N</sub>, 9. TM-TrbC<sub>F</sub>/TM-TraW<sub>N</sub>, 10. TM-TraW<sub>N</sub>/TM-TrbC<sub>F</sub>/TraB<sub>N</sub>, 12. TraB<sub>F</sub>/TraW<sub>N</sub>, 13. TM-TraW<sub>N</sub>/TraB<sub>F</sub>, 14. TM-TrbC<sub>F</sub>/TraB<sub>N</sub>, 15. TM-TrbC<sub>N</sub>/TraB<sub>F</sub>, 16. TM-TraV<sub>N</sub>/TM-TraW<sub>F</sub>, 17. TM-TraV<sub>F</sub>/TM-TraW<sub>N</sub>, 18. TraE<sub>N</sub>,/TraB<sub>F</sub> 19. pUT18TraC<sub>N</sub>/pKT25TraC<sub>F</sub>, 20. pUT18CTraC<sub>N</sub>/pKT25TraC<sub>F</sub>. B. Image obtained by scanning the agar plate



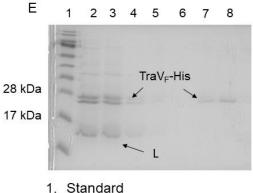




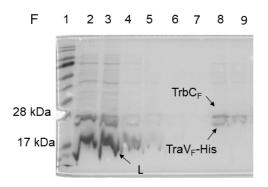
- 1. Standard
- 2. TrbC<sub>F</sub> loading
- 3. TrbC<sub>F</sub> run through
- 4. TrbC<sub>F</sub> wash 1
- 5. TrbC<sub>F</sub> wash 2
- 6. TrbC<sub>F</sub> wash 3
- 7. TrbC<sub>F</sub> wash 4
- 8. TrbC<sub>F</sub> elution 1 125 mM imidazole
- 9. TrbC<sub>c</sub> elution 2 250 mM imidazole



- TraV<sub>N</sub> loading <sup>†</sup>
- 3. TraV<sub>N</sub> /TraW<sub>N</sub> run through
- 4. TraV<sub>N</sub> /TraW<sub>N</sub> wash 1
- 5. TraV<sub>N</sub> /TraW<sub>N</sub> wash 2
- 6. TraV<sub>N</sub>/TraW<sub>N</sub> wash3
- 7. TraV<sub>N</sub> / TraW<sub>N</sub> elution 125 mM imidazole
- 8. TraV<sub>n</sub>/TraW<sub>N</sub> elution 250 mM imidazole



- 2. TraV<sub>F</sub> loading
- 3. TraV<sub>F</sub> run through
- 4. Tra $V_F$  wash 1
- 5. TraV<sub>F</sub> wash 2
- 6. TraV<sub>F</sub> wash 3
- 7. TraV<sub>F</sub> elution 1 125 mM imidazole
- 8. TraV<sub>F</sub> elution 2 250 mM imidazole



- 1 .Standard
- 2.  $TraV_F/TrbC_F$  loading
- 3. TraV<sub>F</sub> /TrbC<sub>F</sub> run through
- 4.  $TraV_F/TrbC_F$  wash 1
- 5. TraV<sub>F</sub> /TrbC<sub>F</sub> wash 2
- 6.  $TraV_F/TrbC_F$  wash 3
- 7.  $TraV_F/TrbC_F$  wash 4
- 8. TraV<sub>F</sub> /TrbC<sub>F</sub> elution 1 125 mM imidazole
- 9. TraV<sub>F</sub>/TrbC<sub>F</sub> elution 2 250 mM imidazole

**Fig. S4. Pull-down experiments. A.** Pull-down results for lysate from *E. coli* BL21(DE3)(pET22bTraV<sub>N</sub>) mixed with lysate from *E. coli* BL21(DE3)(pCOLADuet). † By a mistake TraV<sub>N</sub>/TraW<sub>N</sub> loading is shown on Gel A while the TraV<sub>N</sub> loading is shown on Gel C. **B.** Pull-down results for lysate from *E. coli* BL21(DE3)(pCOLADuetTraW<sub>N</sub>) mixed with lysate from *E. coli* BL21(DE3)(pET22b). **C.** Pull-down results for lysate from *E. coli* BL21(DE3)(pCOLADuetTraW<sub>N</sub>). **D.** Pull-down results for lysate from *E. coli* Origami-2(DE3)(pCOLADuetTrbC<sub>F</sub>) mixed with lysate from *E. coli* BL21(DE3)(pET22b). **E.** Pull-down results for lysate from *E. coli* BL21(DE3)(pCOLADuetTrbC<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuet). **F.** Pull-down results for lysate from *E. coli* BL21(pET22bTraV<sub>F</sub>) mixed with lysate from *E. coli* Origami-2(DE3)(pCOLADuetTrbC<sub>F</sub>). Only a partial resin binding of His-TraV<sub>N</sub> and His-TraV<sub>F</sub> was observed probably due to some His-TraV<sub>N</sub> and His-TraV<sub>F</sub> being trapped in inclusion bodies (**A**, **C** and **E**).

## References

Claessen, D., Emmins, R., Hamoen, L.W., Daniel, R.A., Errington, J., and Edwards, D.H. (2008) Control of the cell elongation–division cycle by shuttling of PBP1 protein in *Bacillus subtilis. Mol Microbiol* **68**: 1029–1046.

Karimova, G., Ullmann, A., and Ladant, D. (2001) Protein-protein interaction between *Bacillus* stearothermophilus tyrosyl-tRNA synthetase subdomains revealed by a bacterial two-hybrid system. *J Mol Microbiol Biotechnol* **3**: 73–82.

Kohler, P.L., Chan, Y.A., Hackett, K.T., Turner, N., Hamilton, H.L., Cloud-Hansen, K.A., and Dillard, J.P. (2013) Mating pair formation homologue TraG is a variable membrane protein essential for contact-independent type IV secretion of chromosomal DNA by *Neisseria* gonorrhoeae. J Bacteriol **195**: 1666–1679.

Kohler, P.L., Hamilton, H.L., Cloud-Hansen, K., and Dillard, J.P. (2007) AtlA functions as a peptidoglycan lytic transglycosylase in the *Neisseria gonorrhoeae* type IV secretion system. *J Bacteriol* **189**: 5421–5428.

Tellechea-Luzardo, J., Winterhalter, C., Widera, P., Kozyra, J., de Lorenzo, V. and Krasnogor, N. (2020) Linking Engineered Cells to Their Digital Twins: A Version Control System for Strain Engineering. *ACS Synthetic Biology* **9**: 536-545

Ouellette, S.P., Gauliard, E., Antosová, Z., and Ladant, D. (2014) A Gateway <sup>®</sup> -compatible bacterial adenylate cyclase-based two-hybrid system: A Gateway-compatible bacterial two-hybrid system. *Environ Microbiol Rep* **6**: 259–267.

Ramsey, M.E., Hackett, K.T., Kotha, C., and Dillard, J.P. (2012) New complementation constructs for inducible and constitutive gene expression in *Neisseria gonorrhoeae* and *Neisseria meningitidis*. *Appl Environ Microbiol* **78**: 3068–3078.

Ramsey, M.E., Hackett, K.T., Bender, T., Kotha, C., van der Does, C., and Dillard, J.P. (2014) TraK and TraB are conserved outer membrane proteins of the *Neisseria gonorrhoeae* Type IV secretion system and are expressed at low levels in wild-type cells. *J Bacteriol* **196**: 2954–2968.

Swanson, J. (1972) Studies on gonococcus infection. II. Freeze-fracture, freeze-etch studies on gonocci. *J Exp Med* **136**: 1258–1271.