

Table S2. Primer information

Primer	Plasmid	Sequence (5'-3') ^a	Source / reference
PpkA F-XhoI	pPpkA	5'-CCGCTCGAGAGGTAGCCGGA CGTTTTTC-3'	This study
PpkA R-XbaI		5'-GCTCTAGACGTGTTCCAGAA GAGTGTGC-3'	This study
PppA F-BamHI	pPppA	5'-CGGGATCCTTATGATGAAGG CAAGCACG-3'	This study
PppA R-XbaI		5'-GCTCTAGAGGATAGGCAGGC TCATCAAG-3'	This study
TssL F-XhoI	1. pTssL-His (TssL F-XhoI/TssL-His R-XbaI) 2. pTssL-Strep (TssL F-XhoI/TssL-Strep R-XbaI) 3. pTssL ^{T14A} -His (pJQ200KS- <i>tssL</i> ^{T14A} as template) (TssL F-XhoI/TssL-His R-XbaI) 4. pTssL ^{T14A} -Strep (pJQ200KS- <i>tssL</i> ^{T14A} as template) (TssL F-XhoI/TssL-Strep R-XbaI)	5'-CCGCTCGAGTGCCATTGCCCT GCATCTGG-3'	[1]
TssL-His R-XbaI		5'-GCTCTAGATCAGTGGTGGTG GTGGTGGTGTGGCTGGGCCTCT CCCGGCT-3'	This study
TssL-Strep R-XbaI		5'-GCTCTAGATCACTTTTCGAAC TGCGGGTGGCTCCATGGCTGGG CCTCTCCCGGCTG-3'	This study
TssL F-XhoI		5'-CCGCTCGAGTGCCATTGCCCT GCATCTGG-3'	[1]
TssL R-XbaI	pTssL ^{T14A} (pJQ200KS- <i>tssL</i> ^{T14A} as template)	5'-GCTCTAGATCTCGACATAGG AACGGATCG-3'	[1]
Fha F-NdeI	1. pET-Fha7-267 ^{WT} -His 2. pET-Fha7-267 ^{R30AS46A} - His (pJQ200KS- <i>fha</i> ^{R30AS46A} as template)	5'-GAACATATGAACACACGGAA CATCGGGAC-3'	This study
Fha ²⁶⁷ R-XhoI		5'-CCGCTCGAGGCAATCGGCAC TTCCCTTTC-3'	This study
Fha F-NdeI	pET-Fha7-309 ^{WT} -His	5'-GAACATATGAACACACGGAA CATCGGGAC-3'	This study
Fha ³⁰⁹ R-XhoI		5'-CCGCTCGAGATGCATGAGGG TTTCGAGC-3'	This study
PpkA 2F-BamHI	pJQ200KS- $\Delta t6$	5'-CGGGATCCCTGTAGCGCCGG CGTCAGTTG-3'	[2]
PpkA 2R-XmaI		5'-TCCCCCGGGCCCGTCAGGA GCGTGTACTTG-3'	[2]
Atu4352 2F-BamHI		5'-CGGGATCCGAGTGACGACGA TATCCAGC-3'	[2]
Atu4352 2R-XbaI		5'- GCTCTAGACTCGATCTTGAAAT CACCAG-3'	[2]
Fha 1F-XbaI	pJQ200KS- <i>fha</i> ^{ΔFHA}	5'-GCTCTAGATGCCGAAGACAC ACTTCTGC-3'	This study
Fha 2R-XmaI		5'-TCCCCCGGGGGAGGAATGA AATCCGGATCG-3'	This study
Fha ^{ΔFHA} -1		5'-GACGCGCGCTTTCGCCCTCA AGGCCTCGCTCGAAGCTCCACT G-3'	This study
Fha ^{ΔFHA} -2		5'-CAGTGGAGCTTCGAGCGAGG CCTTGAGGGCGAAAGCGCGCGT C-3'	This study

Fha 1F-XbaI	pJQ200KS- <i>fha</i> ^{R30A}	5'- <u>GCTCTAGAT</u> GCCGAAGACAC ACTTCTGC-3'	This study
Fha 2R-XmaI		5'-TCCCCCGGGGAGGAATGA AATCCGGATCG-3'	This study
Fha ^{R30A} -1		5'-CAGTCGCAATCACGAGAC CGC GCCAATTGCGCGGCGGCCTC-3'	This study
Fha ^{R30A} -2		5'-CCGCCGCGCAATTGGC GCGT CTCGTGATTGCGACTGGCAG-3'	This study
Fha 1F-XbaI	1. pJQ200KS- <i>fha</i> ^{S46A} 2. pJQ200KS- <i>fha</i> ^{R30AS46A} (pJQ200KS- <i>fha</i> ^{R30A} as template)	5'- <u>GCTCTAGAT</u> GCCGAAGACAC ACTTCTGC-3'	This study
Fha 2R-XmaI		5'-TCCCCCGGGGAGGAATGA AATCCGGATCG-3'	This study
Fha ^{S46A} -1		5'-GCGTGCAATGCAGCTT GGCA ACGCGCCGCTCATTGTCATC-3'	This study
Fha ^{S46A} -2		5'-ACAATGAGCGGCGGTT GCC AAGCTGCATTGCACGCTGAG-3'	This study
TssL 1F-XbaI	pJQ200KS- <i>tssL</i> ^{T14A}	5'-GCTCTAGACGAAGACTGCAT CCAGCTTGC-3'	[1]
TssL 2R-XmaI		5'-TCCCCCGGGAGTGTCGATA AGGATCGCCTC-3'	[1]
TssL ^{T14A} -1		5'-CCTCGGTGATCTCGACCACC GCCGGCAAATCCTGCCAGG -3'	This study
TssL ^{T14A} -2		5'-CCTGGCAGGATTTGCC GCG GTGGTCGAGATCACCGAGG-3'	This study
TssL 1F-XbaI	pJQ200KS- <i>tssL</i> ^{T14D}	5'-GCTCTAGACGAAGACTGCAT CCAGCTTGC-3'	[1]
TssL 2R-XmaI		5'-TCCCCCGGGAGTGTCGATA AGGATCGCCTC-3'	[1]
TssL ^{T14D} -1		5'-CCTCGGTGATCTCGACCACA TCCGGCAAATCCTGCCAGG -3'	This study
TssL ^{T14D} -2		5'-CCTGGCAGGATTTGCC GGAT GTGGTCGAGATCACCGAGG-3'	This study
TssL 1F-XbaI	pJQ200KS- <i>tssL</i> ^{T14E}	5'-GCTCTAGACGAAGACTGCAT CCAGCTTGC-3'	[1]
TssL 2R-XmaI		5'-TCCCCCGGGAGTGTCGATA AGGATCGCCTC-3'	[1]
TssL ^{T14E} -1		5'-CCTCGGTGATCTCGACCACC TCCGGCAAATCCTGCCAGG -3'	This study
TssL ^{T14E} -2		5'-CCTGGCAGGATTTGCC GGAG GTGGTCGAGATCACCGAGG-3'	This study
PpkA 1F-XbaI	pJQ200KS- <i>ppkA</i> ^{D161AN166A}	5'-GCTCTAGAGGAGATGATGGC ACAGCAGATC-3'	This study
PpkA 2R-XmaI		5'-TCCCCCGGGCCCGTCAGGA GCGTGTACTTG-3'	This study
PpkA ^{D161AN166A} - 1		5'-CATCCGCCAGCAGAAT AGCG GCTGGCGTGAC GGCG CAATGC ACATATCC-3'	This study
PpkA ^{D161AN166A} - 2		5'-GGATATGTGCATTGCGCCGT CACGCCAGCC GCT ATTCTGCTG GCGGATG-3'	This study

a: Restriction enzyme sites are underlined, and mutated sequences are indicated by bold type.

References

1. Ma LS, Lin JS, Lai EM (2009) An IcmF family protein, Imp_{L_M}, is an integral inner membrane protein interacting with ImpK_L, and its walker a motif is required for type VI secretion system-mediated Hcp secretion in *Agrobacterium tumefaciens*. J Bacteriol 191: 4316-4329.
2. Lin JS, Ma LS, Lai EM (2013) Systematic Dissection of the *Agrobacterium* Type VI Secretion System Reveals Machinery and Secreted Components for Subcomplex Formation. PLoS One 8: e67647.