

Table S1 Amino acid sequence homology analysis of selected VirB2 family proteins.

Protein ^a name	<i>A. t.</i> C58 pTiC58 VirB2	<i>A. r.</i> pRi1724 Riorf154	<i>A. t.</i> pTiA6 VirB2	<i>A. v.</i> S4 pTiS4 VirB2	<i>R. e.</i> CFN42 p42a VirB2a	<i>S. m.</i> WSM419 pSMED02 VirB2	<i>M. c. bv.</i> <i>biserrulae</i> TrbC	<i>A. r.</i> K84 AvhB2	<i>A. t.</i> C58 pAtC58 AvhB2	<i>R. e.</i> CFN42 p42d VirB2	<i>S. m.</i> 1021 pSymA VirB2
VirB2p ^b	100 (100)	75 (81)	90 (95)	74 (82)	93 (98)	69 (76)	71 (77)	40 (56)	36 (56)	35 (56)	35 (50)
VirB2m ^c	100 (100)	96 (96)	99 (100)	96 (96)	95 (100)	93 (94)	91 (92)	44 (61)	35 (55)	38 (57)	35 (59)

^a: Organism full name and protein UniProt accession number: *Agrobacterium tumefaciens* pTiC58, P17792; *Agrobacterium rhizogenes* pRi1724, Q9F5A1; *Agrobacterium tumefaciens* pTiA6, P05351; *Agrobacterium vitis* pTiS4, B9K417; *Rhizobium etli* p42a, Q2K2L1; *Sinorhizobium medicae* pSMED02; A6UMA7, *Mesorhizobium ciceri* chromosome, E8TGI0; *Agrobacterium radiobacter* K84 chromosome, B9JE70; *Agrobacterium tumefaciens* pAtC58, Q7D3S1; *Rhizobium etli* p42d, Q8KIM6; *Sinorhizobium meliloti* pSymA, Q92YZ4.

^b identity % (similarity %) of full-length pTiC58 VirB2 against other VirB2 homologs.

^c identity % (similarity %) of processed pTiC58 VirB2 against other VirB2 homologs.