	<i>Pph</i> 1448A T3SS-2	Pstab T3SS-2	Psory T3SS-2	Rhizobium NGR 234 T3SS-2	Rhizobium NGR234 T3SS-1	B. japonicum T3SS	R. etti CNF42 T3SS
Hrp <i>II</i> Q	PSPPH_2517		62%	32%	24%	25%	
	PSPPH_2518	100%	85%	36%			
	PSPPH_2519		86%	48%			
Hrc IN	PSPPH_2520		77%	46%	40%		
Hrc IIC2	PSPPH_2521			51%	40%	38%	
	PSPPH_2522		82%	37%			
TPR protein	PSPPH_2523			38%			
Hrc IIC1	PSPPH_2524		87%	40%	32%	32%	
	PSPPH_2525	94%	86%				
	PSPPH_2526	100%	87%	39%			
Hrc //J	PSPPH_2527		94%	58%	54%	54%	32%
NolU homolog	PSPPH_2528		70%	32%	28%	30%	16%
Hrp //E	PSPPH_2529		84%	36%	28%	31%	27%
Hrc//N	PSPPH_2530		91%	62%	52%	53%	51%
Hrp IIO	PSPPH_2532		63%				
Hrc//Q	PSPPH_2534		65%	26%	31%	32%	30%
Hrc//R	PSPPH_2535		98%	71%	56%	50%	43%
Hrc IIS	PSPPH_2536			76%	39%		
Hrc//T	PSPPH_2537	100%		50%	33%	33%	30%
Hrc//U	PSPPH_2538		91%	46%	36%	38%	30%
transription regulator	PSPPH_2539		80%				
Hrp IIK	PSPPH_2540	98%	85%				28%

Additional file 6. Table S1:

Sequence comparisons of T3SS-2 proteins with proteins from from subgroups I-III of *Rhc* T3SS gene clusters. Percentage identities of various T3SS proteins in comparison to the *Pph* T3SS-2 proteins. *Pph* T3SS-2 cluster shares a higher degree of common genes with T3SS-2 of *Rhizobium* sp. NGR234 than with *Rhc* T3SS gene clusters of subgroup I or III. Shading in grayscale is according to percentage identity.