



**A.** The phylogram of 253 SctN sequences subdivided in seven main families, depicted with different colors and named according to [8], while the flagellum proteins are depicted in black. The evolutionary history was inferred as in case of Fig. 2

**B.** The *Rhc* T3SS clade as derived from the phylogram in A, groups clearly the *P. syringae* Hrc<sub>II</sub>V sequences close to the Rhc<sub>II</sub>V protein of the *Rhizobium* sp. NGR234 T3SS-2. The values at the nodes are the bootstrap percentages out of 1000 replicates. The locus numbers or the protein accession number of each sequence is indicated.