



**Additional file 1. Figure S1 :**

**Unrooted neighbor-joining phylogenetic tree of SctQ proteins of flagellar and non-flagellar T3S proteins. The tree was calculated by CLUSTALW (1.82) using**

bootstrapping (500 replicates) as a method for deriving confidence values for the groupings and was drawn by MEGA 4.0. Bootstrap values are indicated in each branching point. Scale bar represents numbers of substitution per site. The arrow indicates a possible position of root so that the tree will be compatible with the monophyly of the flagellar T3SS. Consistently with phylograms based on other conserved proteins of the *Pph* T3SS-2, the *Hrc<sub>II</sub>Q* polypeptide does not fall into any of the two *Hrc1/Hrc2* T3SS families but it is grouped with the *Rhc* family.