Figure S8. Sequence alignment of ψ proteins from different members of the Pseudomonadaceae. Protein sequences were aligned based on a ClustalW2 result [1] and amino acid residues were colored according to their chemical properties (GeneDoc, http://www.nrbsc.org/). Conserved positively charged residues in the N-terminal region of ψ, possibly implicated in DNA-binding, are marked with red arrows. 1: *P. aeruginosa* PAO1, 2: *P. putida* KT2440, 3: *P. syringae* pv. *tomato* T1, 4: *P. fluorescens* Pf0-1, 5: *A. vinelandii* DJ / ATCC BAA-1303, 6: *P. entomophila* L48, 7: *P. mendocina* ymp, 8: *P. savastanoi* pv. *savastanoi* NCPPB 3335, 9: *P. fluorescens* Pf-5 / ATCC BAA-477.