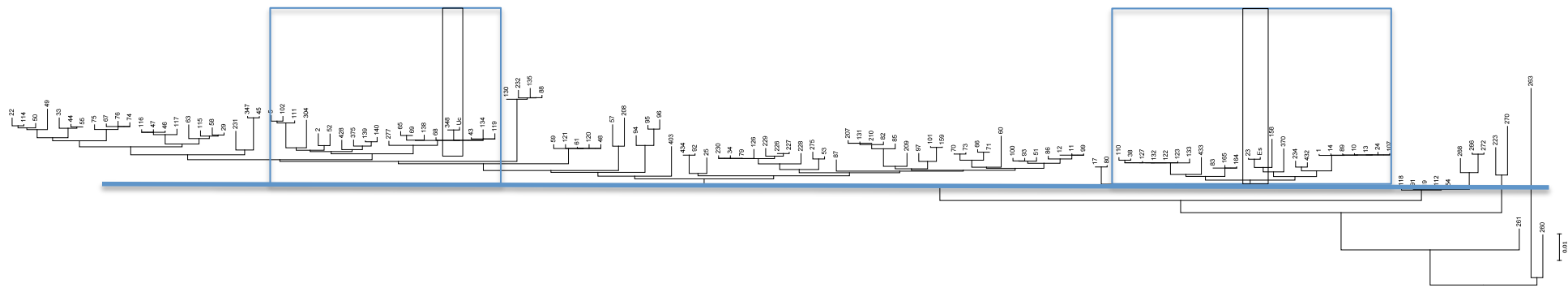


# Appendix S4

Johannesen, J.: Tracing the history and ecological context of *Wolbachia* double infection in a specialist host (*Urophora cardui*) – parasitoid (*Eurytoma serratulae*) system



Neighbor-Joining tree (K2P model) of 131 *Wolbachia* supergroup A strains based on full MLST. Boxes in blue show the position of subtrees with Ucar\_A1 (Uc) and Eser\_A (Es) presented in Fig. 3. Black boxes show the positions of Ucar\_A1 and Eser\_A within subtrees. The tree was calculated from 2071 positions in the final data set (gaps deleted). Total branch length of optimal tree = 0.67672.