



Figure S1. Phylogenetic relationship of the transferred *Wolbachia* genes to the *Wolbachia* genes of wMel from a fruit fly, wPip from a mosquito, and wBm from a filarial nematode. A total of 6,653 unambiguously aligned amino acid sites, representing partial sequences of 56 genes (see Table S1), were subjected to the analysis. A neighbor-joining (NJ) tree is shown, while maximum likelihood (ML) and Bayesian analysis (BA) trees exhibited the same topologies. On each of the nodes, support values (NJ/ML/BA) are indicated.