

Supplementary Material: To B or not to B: *Arsenophonus* as a source of B-vitamins in whiteflies.

1 SUPPLEMENTARY FIGURES

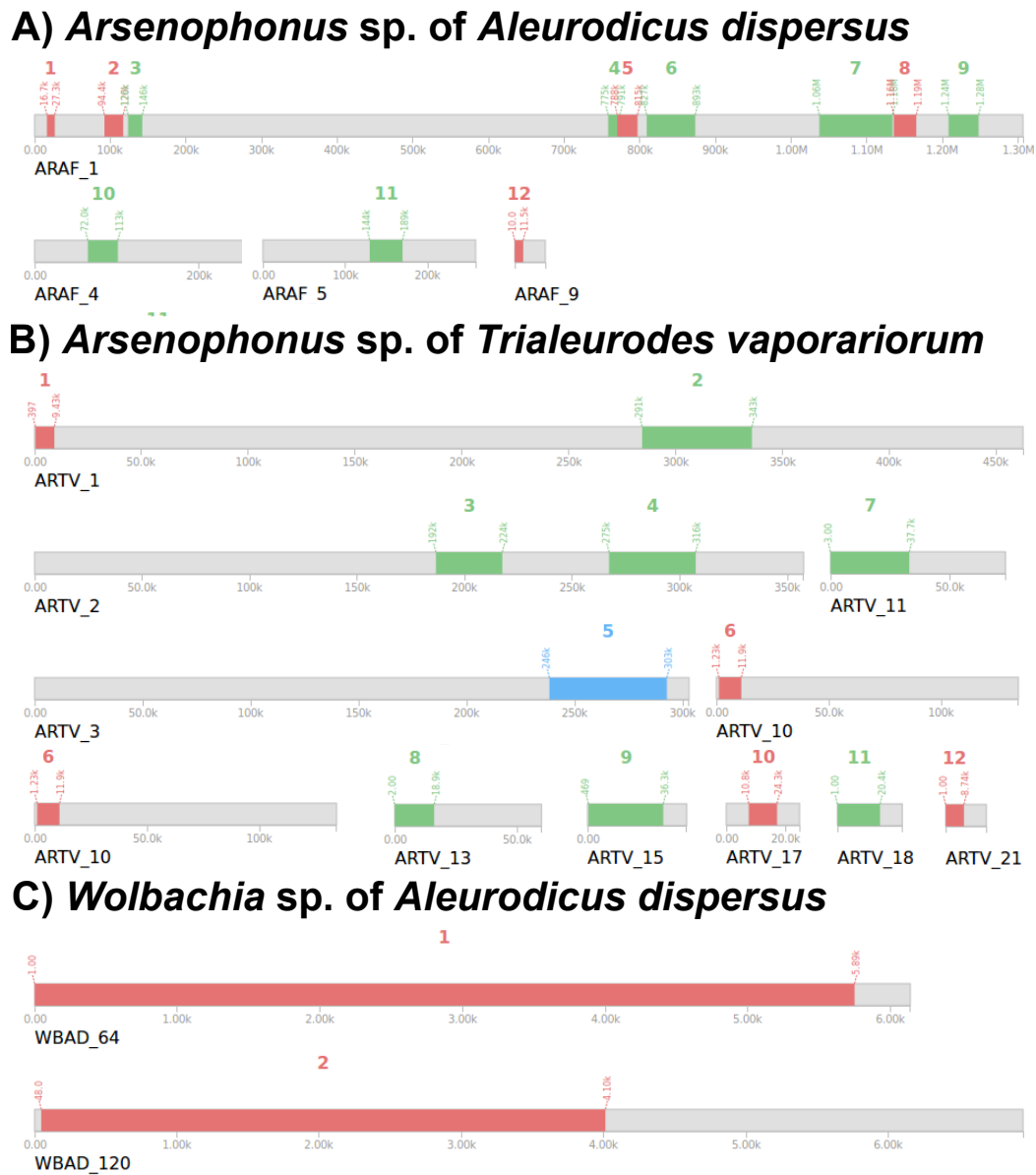


Figure S1. Prophages regions detected in *Arsenophonus* (A) ARAF, (B) ARTV and (C) *Wolbachia* WBAD. Red bars represents incomplete prophages, green bars complete prophages and blue bars questionable complete prophages.

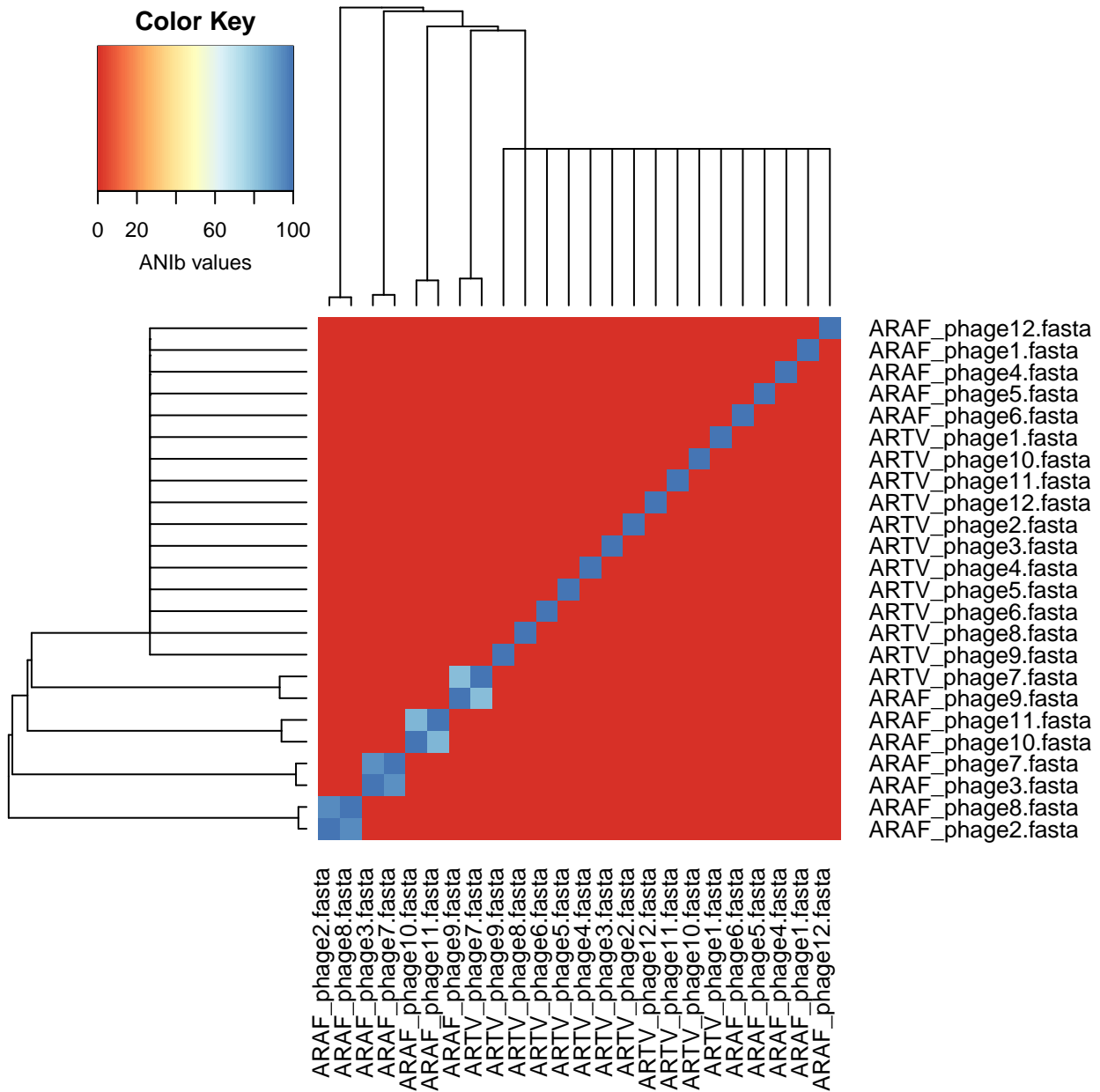


Figure S2. Hierarchical clustering of pairwise Average Nucleotide Identity (ANI) between the *Arsenophonus* ARAF and ARTV detected phages.

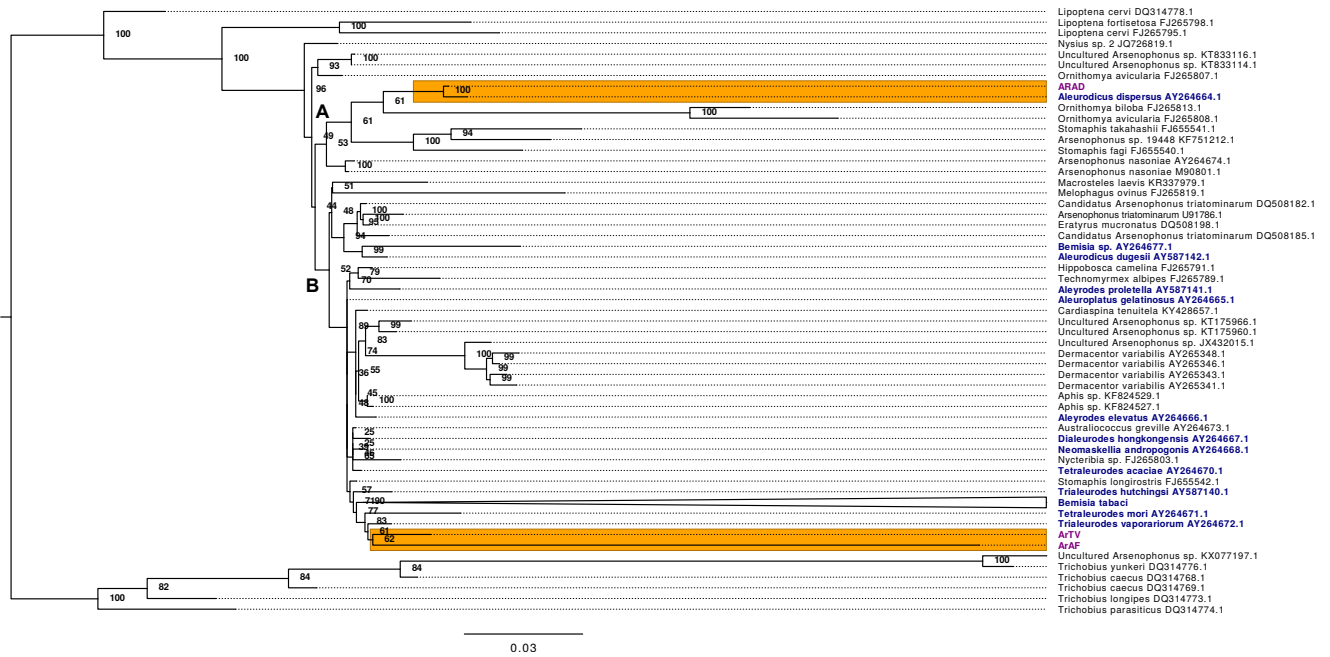


Figure S3. Midpoint rooted maximum likelihood tree obtained for several *16S rRNA* genes from *Arsenophonus* infecting different hosts. The tree was inferred using a TVM+F+R3 substitution model and 1000 ultrafast bootstraps (node labels). *Arsenophonus* from *Aleurodicus dispersus* (ARAD), *A. floccissimus* (ARAF) and *Trialeurodes vaporariorum* (ARTV) are highlighted in purple. *Arsenophonus* from different whiteflies are highlighted in blue. Two potential clades are denoted with letters A and B

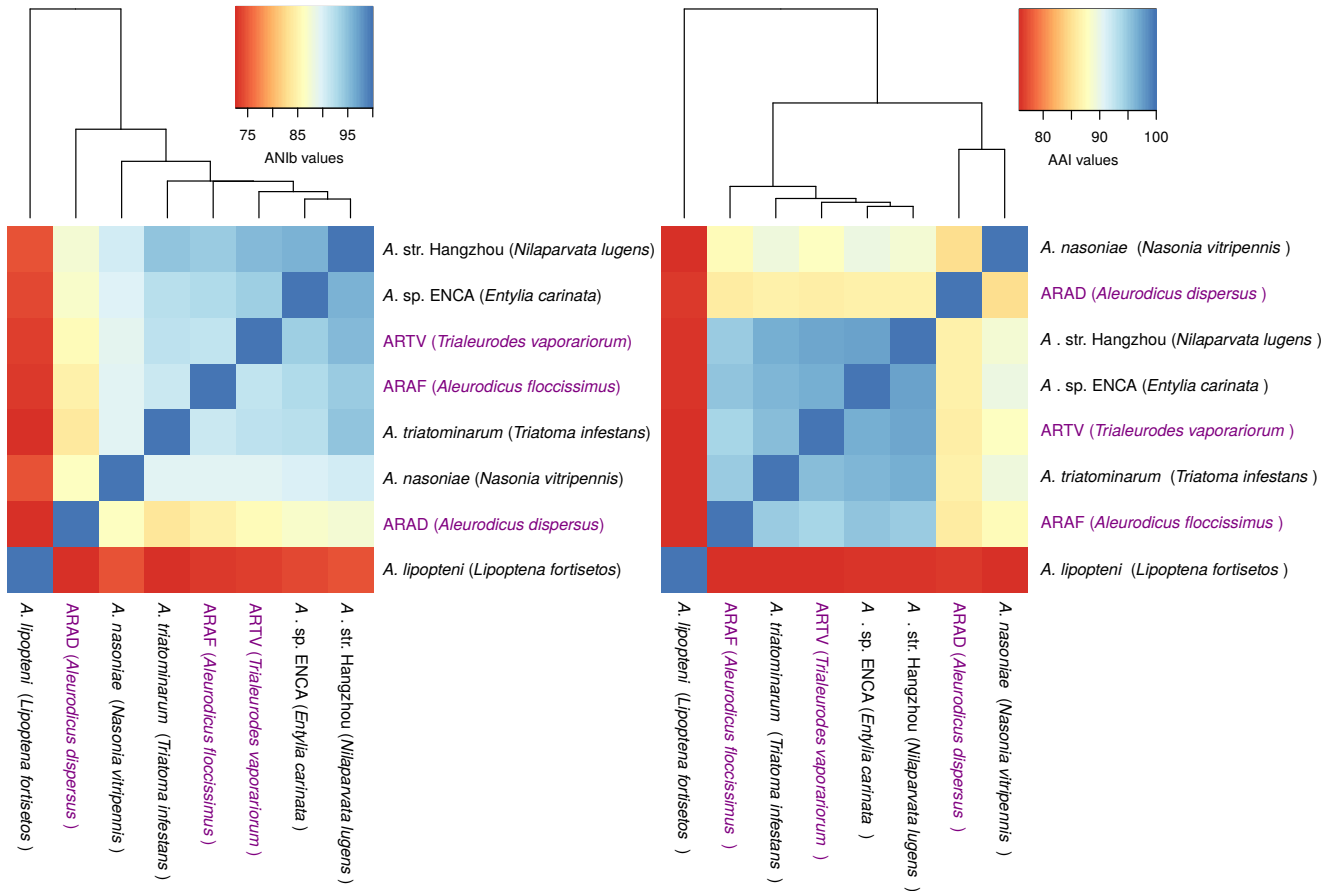


Figure S4. Hierarchical clustering of pairwise Average Nucleotide Identity (ANI, left) and Average Amino Acid Identity (AAI, right) of several *Arsenophonus* genomes. *Arsenophonus* from *Aleurodicus dispersus* (ARAD), *A. floccissimus* (ARAF) and *Trialeurodes vaporariorum* (ARTV) are highlighted in purple. Names for the eukaryotic hosts are shown after the strain names inside parentheses.

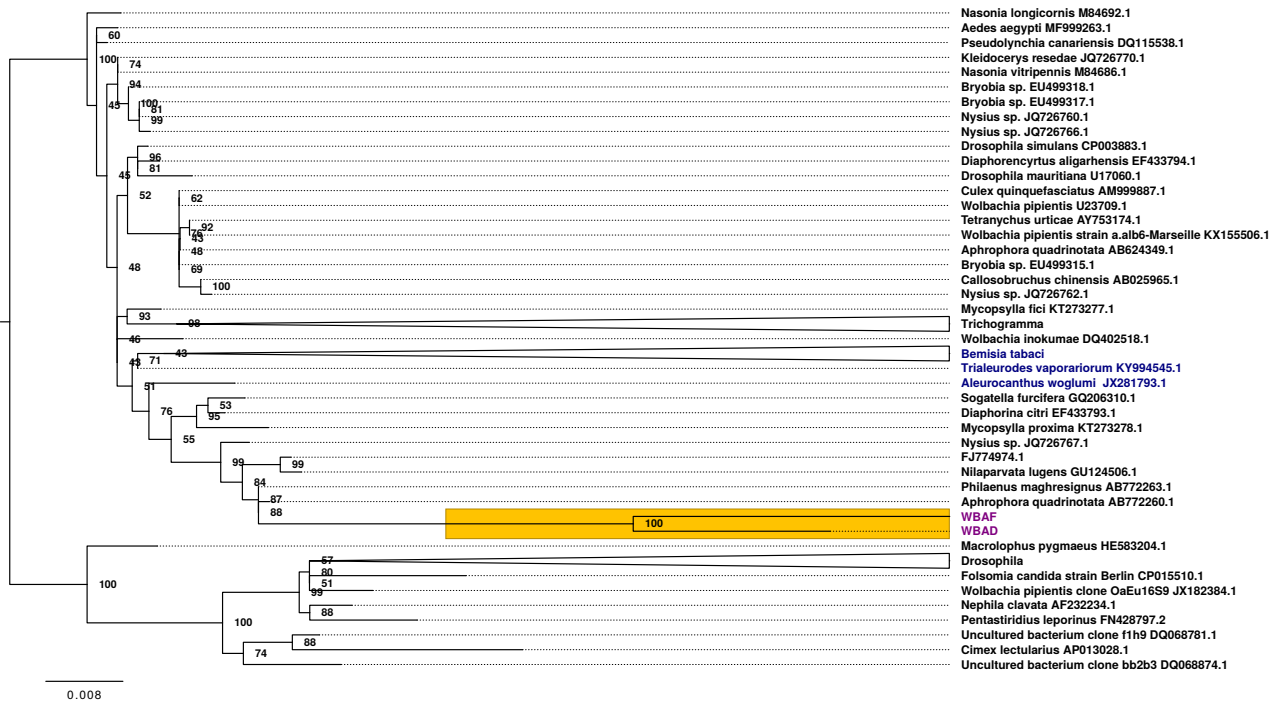


Figure S5. Midpoint rooted maximum likelihood tree obtained for several *16S rRNA* genes from *Wolbachia* infecting different hosts. The tree was inferred using a TN+F+R2 substitution model and 1000 ultrafast bootstraps (node labels). *Wolbachia* from *Aleurodicus dispersus* (WBAD) and *A. floccissicums* (WBAF) are highlighted in purple. *Wolbachia* from different whiteflies are highlighted in blue.