

Figure S1. Heat map of differentially expressed genes belonging to the “Proteolysis” functional group in flies infected with wMelPlus and wMelCS112 Wolbachia strains compared to uninfected flies. Uninfected_1, Uninfected_2, Uninfected_3 – gene expression of the uninfected *Drosophila melanogaster* line; wMelCS112_1, wMelCS112_2, wMelCS112_3 – the *Drosophila melanogaster* line infected with wMelCS112; wMelPlus_1, wMelPlus_2, wMelPlus_3 – the *Drosophila melanogaster* line infected with wMelPlus. Genes were clustered using the linkage method. The heat maps were generated using the Python3 package seaborn.

