## Supplementary information to "Efficiency of RNA interference is improved by knockdown of dsRNA nucleases in tephritid fruit flies" in Open Biology

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**Figure S1.** Neighbour-joining phylogenetic trees of a) *dsRNase1* and b) *dsRNase2* with evolutionary distance computed using the maximum composite likelihood method shown on the x-axis. Bootstrap values of 500 replicates are shown at nodes. Alignments were done using CLUSTAL O (1.2.4) and phylogenetic trees constructed and tested using MEGA X.