



Figure S6 Phylogenetic analysis of the *STE24* paralogs in *Drosophila*, including the potential non-processed pseudogene *CG30461*. Maximum Likelihood phylogeny for *CG9000* and paralogs including *CG30461*. CG numbers denote the clades of *Drosophila* species for the respective locus. The figures above the nodes are the results from bootstrap analysis with 500 replicates (only bootstrap values ≥ 95 are shown). The scale is given as substitutions per site.

Tamura, K., D. Peterson, N. Peterson, G. Stecher, M. Nei, et al., 2011 MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Mol. Biol and Evol.* **10.1093/molbev/msr121**.