

**Additional file 3.** Dendrogram of average  $\omega$  estimates of genes falling under slow, clock-like and accelerated rate categories. Branch lengths represent the proportion of genes with  $\omega$  values greater than background  $\omega$  values. P-values for the different tests were corrected using a Bonferroni correction prior to the comparisons. mel: *D. melanogaster*, sim: *D. simulans*, sec: *D. sechellia*, simsecmel: branch leading to the *D. melanogaster* clade, yak: *D. yakuba*, ere: *D. erecta*, yakere, branch leading to the *D. yakuba* clade, ana: *D. ananassae*.

