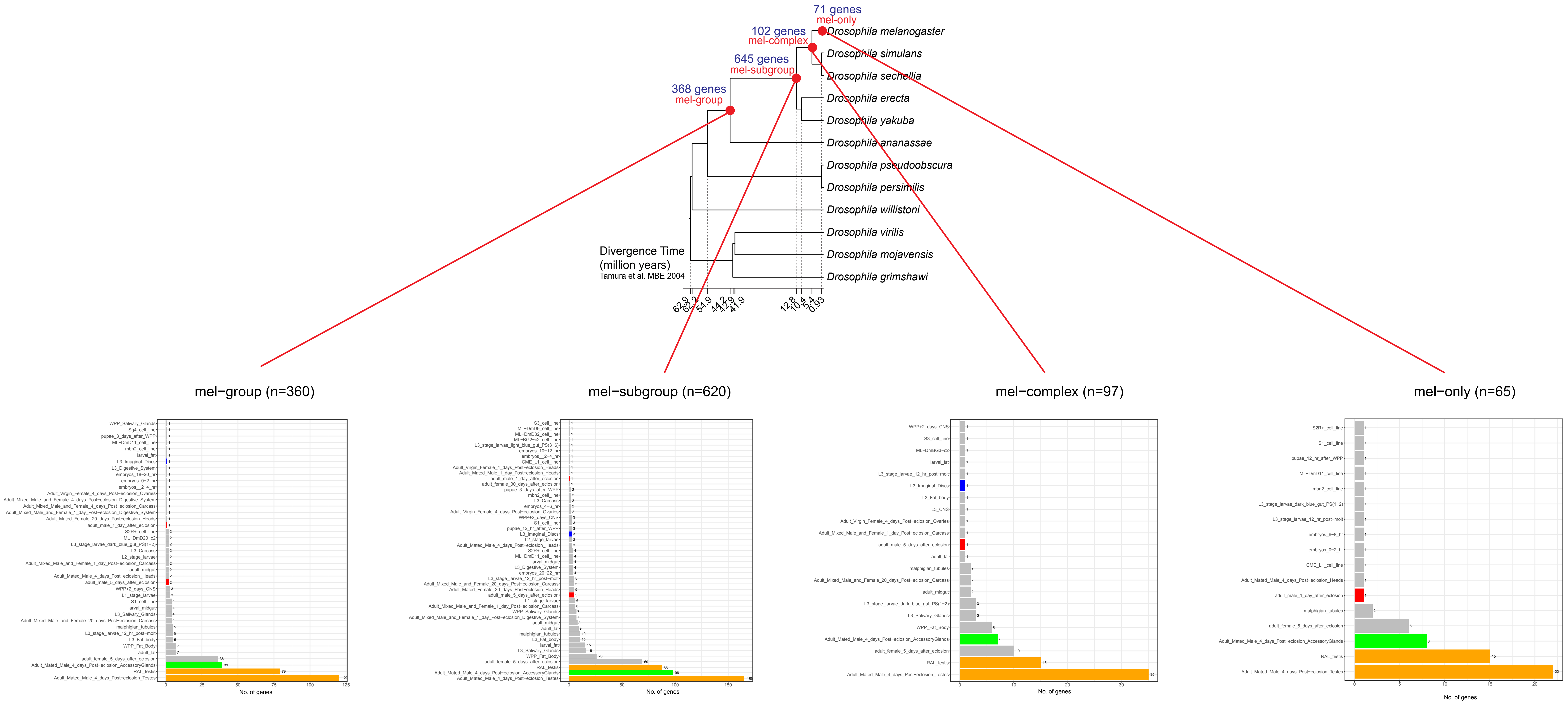

Supplementary Figure 6. Summary of expression biases of young Drosophila genes to the male reproductive system.

These barplots summarize the library type of maximal expression (”xmax”) from ~80 developmental stages/tissues/cell lines RNA-seq datasets, for sets of evolutionarily young Drosophila genes across various age groups. These data represent summaries of individual gene expression plots provided in Supplementary Figures 7-10 for mel-group genes (present in Dmel/sim/sech/ere/yak/ana), mel-subgroup genes (present in Dmel/sim/sech/ere/yak), mel-complex genes (present in Dmel/sim/sech) and genes that are present only in Dmel. Only those genes with expression are plotted; thus, there are fewer loci analyzed by expression than are analyzed by genomic alignment/homology. Note the preponderance of genes whose “xmax” is in testis or accessory glands.

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Supplementary Figure 6