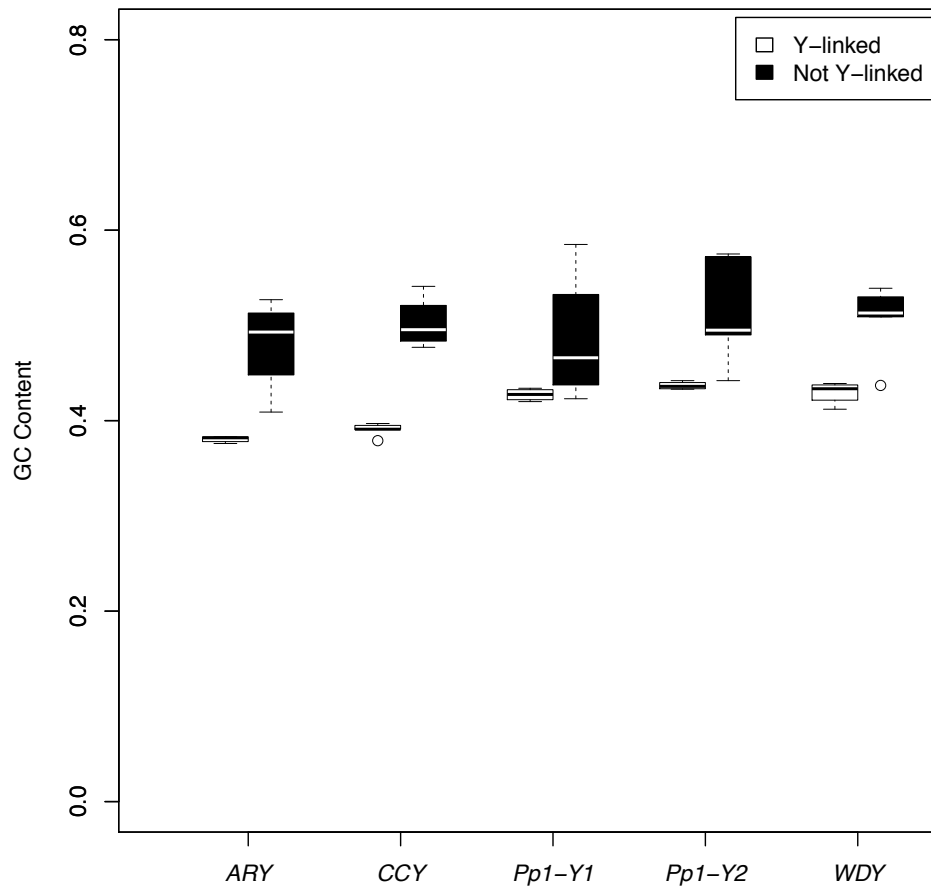
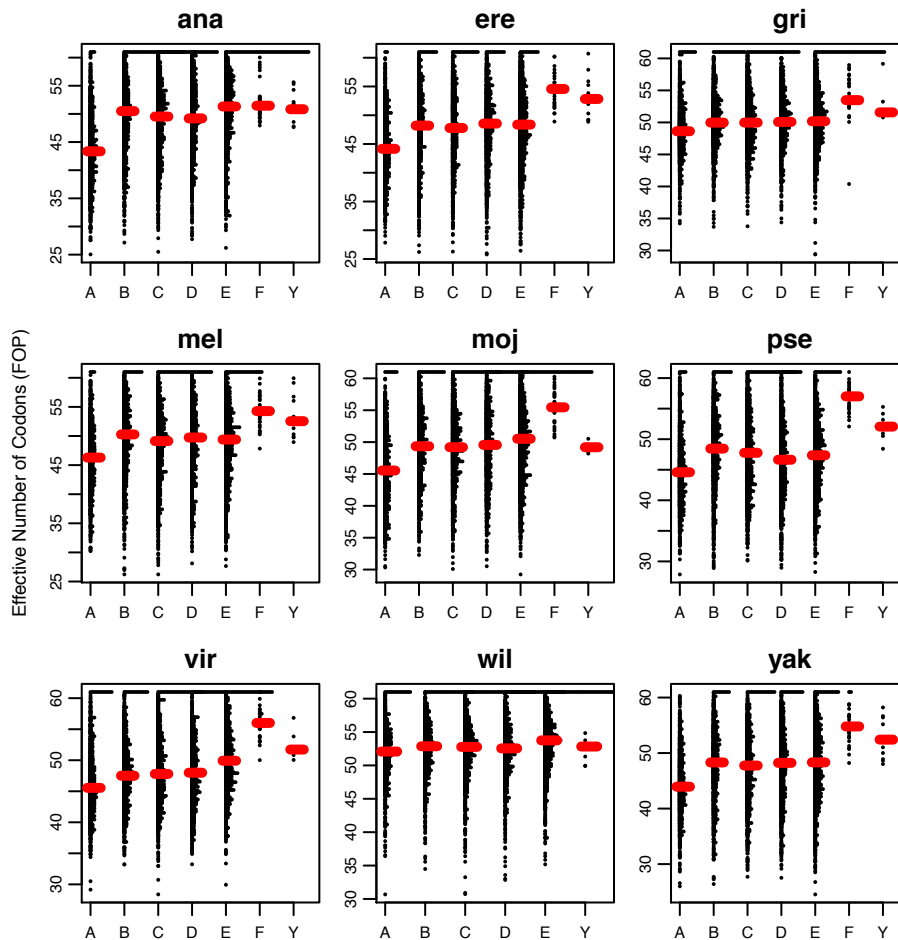


Supplemental Figure 1



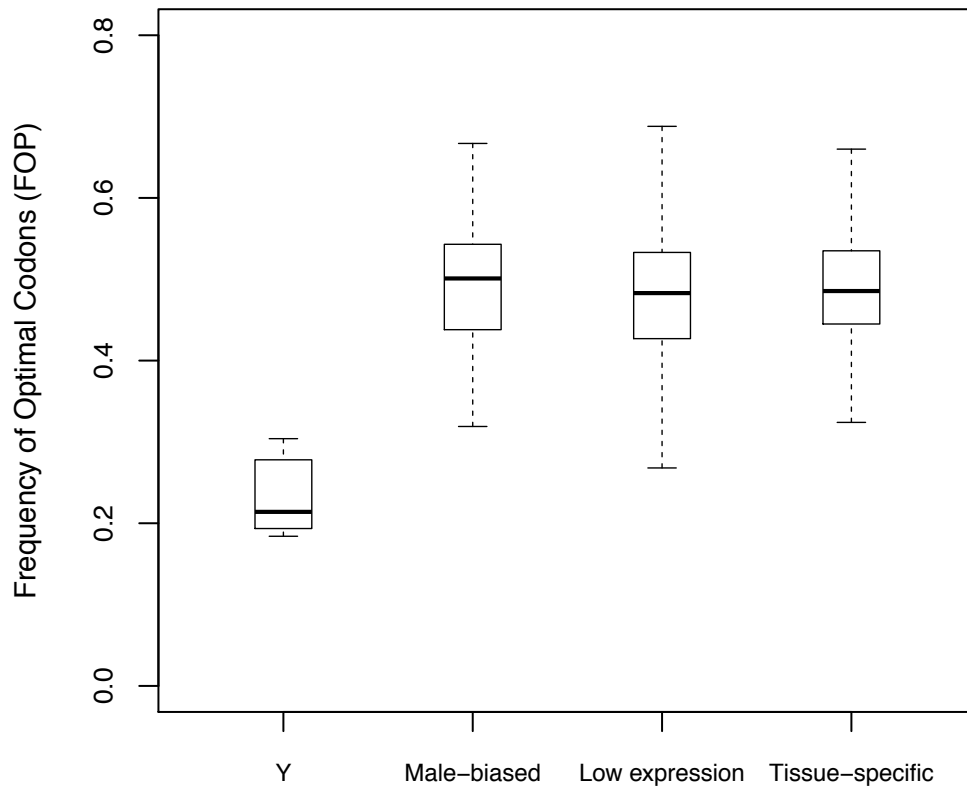
Supplemental Figure 1: GC content of Y-linked (white) and not Y-linked (black) orthologs of *ARY*, *CCY*, *Pp1-Y1*, *Pp1-Y2*, and *WDY*. The top and bottom edges of each box represent the 3rd and 1st quartile, respectively. Median values are shown in black for Y-linked orthologs and white for not Y-linked genes.

Supplemental Figure 2



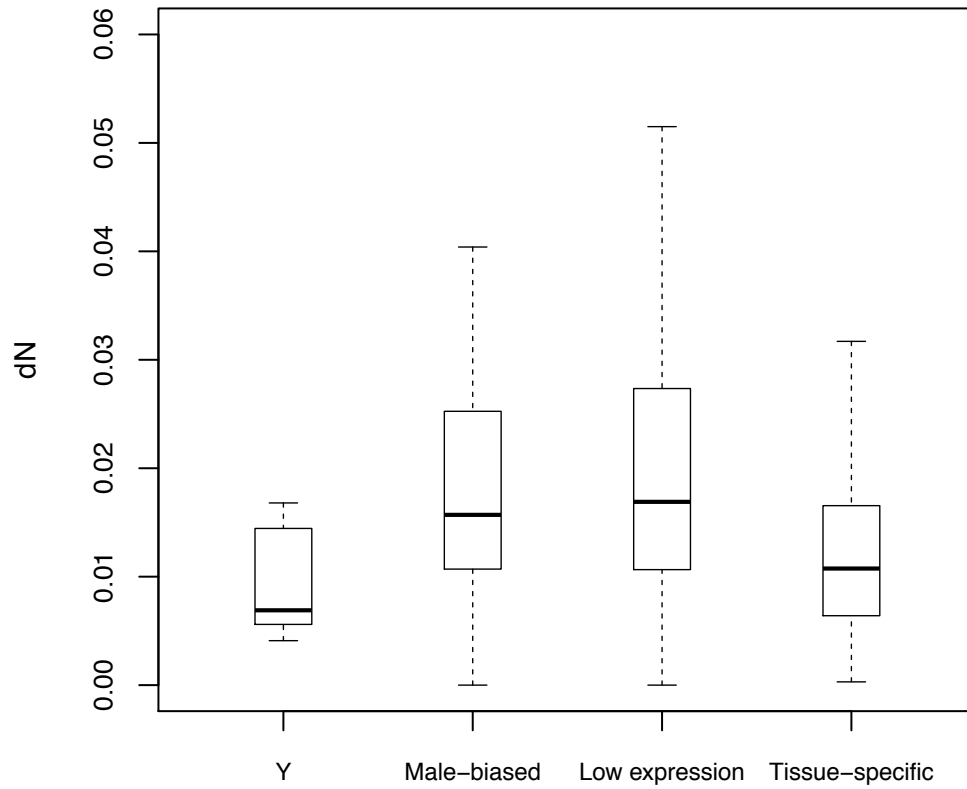
Supplemental Figure 2: Distributions of codon bias as measured by the effective number of codons (ENC) of all 1:1 orthologs and Y-linked genes separated by chromosome arm for *D. ananassae* (“ana”), *D. erecta* (“ere”), *D. grimshawi* (“gri”), *D. melanogaster* (“mel”), *D. mojavensis* (“moj”), *D. pseudoobscura* (“pse”), *D. virilis* (“vir”), *D. willistoni* (“wil”) and *D. yakuba* (“yak”). Median values are overlaid in red. Higher values of ENC correspond to less biased patterns of codon usage. Note that for *D. pseudoobscura* ‘Y’-linked genes are those genes that have some history of Y-linkage in this species but are not currently Y-linked (*ARY*, *kl-2*, *kl-3*, *ORY*, *Ppr-Y*, and *PRY*). Levels of codon bias as measured by ENC are significantly lower on the Y chromosome than on the X and pooled autosomes in all species ($P < 0.05$, 1-tailed MWU test) except *D. ananassae*, *D. mojavensis*, and *D. willistoni*.

Supplemental Figure 3



Supplemental Figure 3: Boxplot of codon bias as measured by the frequency of optimal codons for genes in *D. melanogaster* that are Y-linked, have male-biased patterns of gene expression (based on Sturgill et al. 2007), low levels of gene expression (defined as the bottom 10% of genes in Larracunte et al. 2008) or tissue-specific patterns of gene expression (as curated in Larracunte et al. 2008).

Supplemental Figure 4



Supplemental Figure 4: Rates of evolution at nonsynonymous sites (dN) on the *D. melanogaster* branch for genes that are Y-linked, have male-biased patterns of gene expression (based on Sturgill et al. 2007), low levels of gene expression (defined as the bottom 10% of genes in Larracunte et al. 2008) or tissue-specific patterns of gene expression (as curated in Larracunte et al. 2008).