**Supplemental Figure 1**

A) Changes in mRNA expression in the SP117 and TY1916 strains compared to N2 are shown. In each graph, the x-axis shows the entire chromosomes from which the duplications originated from. The y-axis is the genome-median centered log2 ratio (mutant/N2) as determined by DESeq2. Genes that are lowly expressed (FPKM<1 in any wild type mRNA-seq replicate) have been removed. The duplicated genes are highlighted in blue, deleted genes in orange, and unaffected genes in gray. B) Scatter plot analysis of FPKM expression level for the X chromosomal genes in the SP117 strain. The duplicated genes are shown in blue. Trendlines were fitted in R using ggplot’s linear model (lm()) function. D) Expression noise for each chromosome is analyzed through calculating the coefficient of variation from FPKM values of mRNA-seq replicates. N2 wild type data was used and genes that showed FPKM<1 in any of the replicates were removed.