Supplemental Figures: Proprioceptive Genes as a Source of Genetic Variation Underlying Robustness for Flight Performance in *Drosophila*

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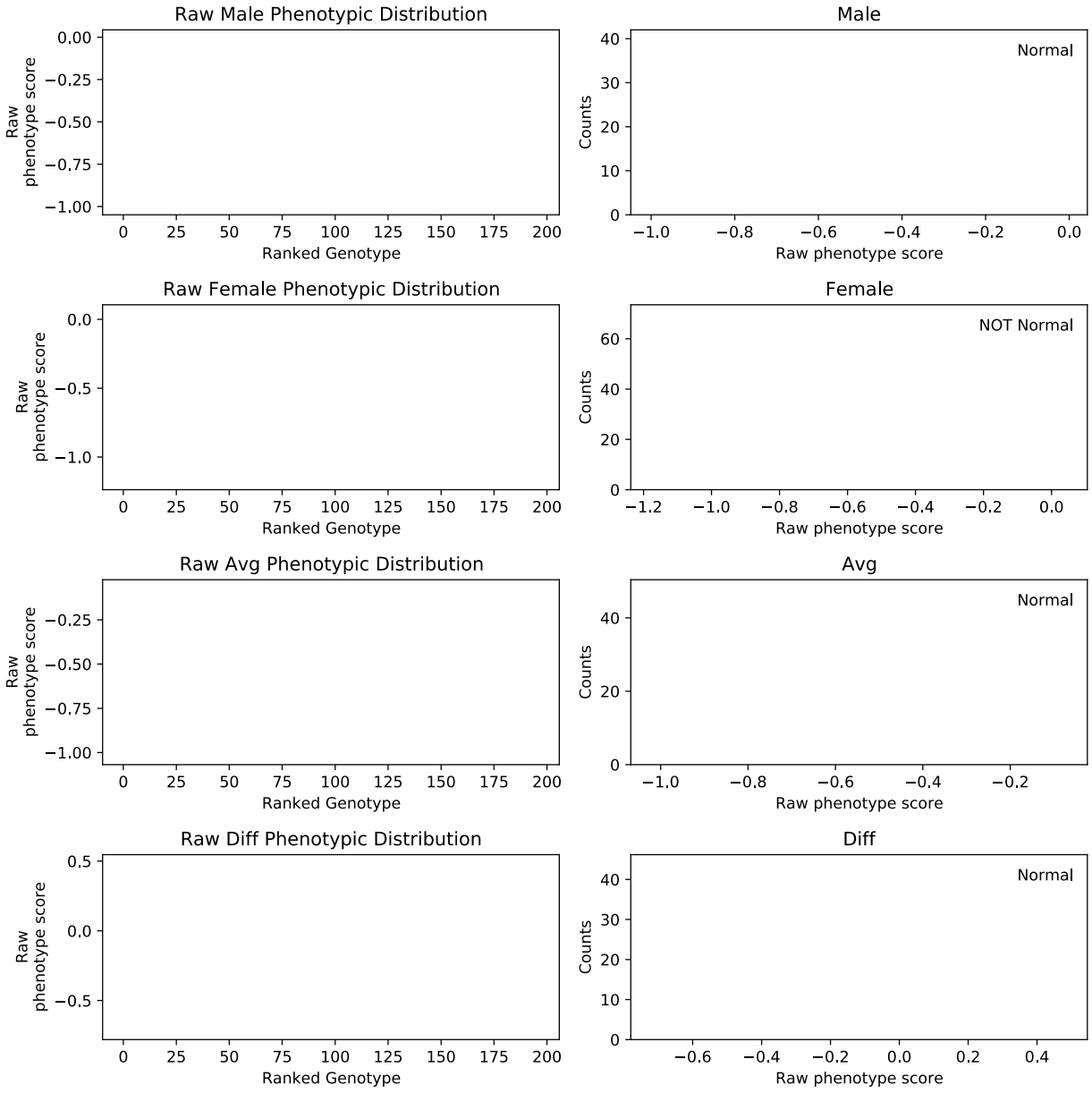

Figure S1. Natural log of the coefficient of variation is near-normally distributed for all sexes. Phenotypic distributions (left) and histograms of the raw phenotype score (right) help visualize the spread in the data. Male (P = 0.22), sex-average (P = 0.13), and sex-difference (P = 0.52) phenotypes are normally distributed under a Shapiro-Wilks test for normality, while the female phenotype is not (P = 0.013; no histogram border). Smaller, or more negative, phenotype scores correspond with tighter distributions in landing heights, and therefore more robust genotypes.

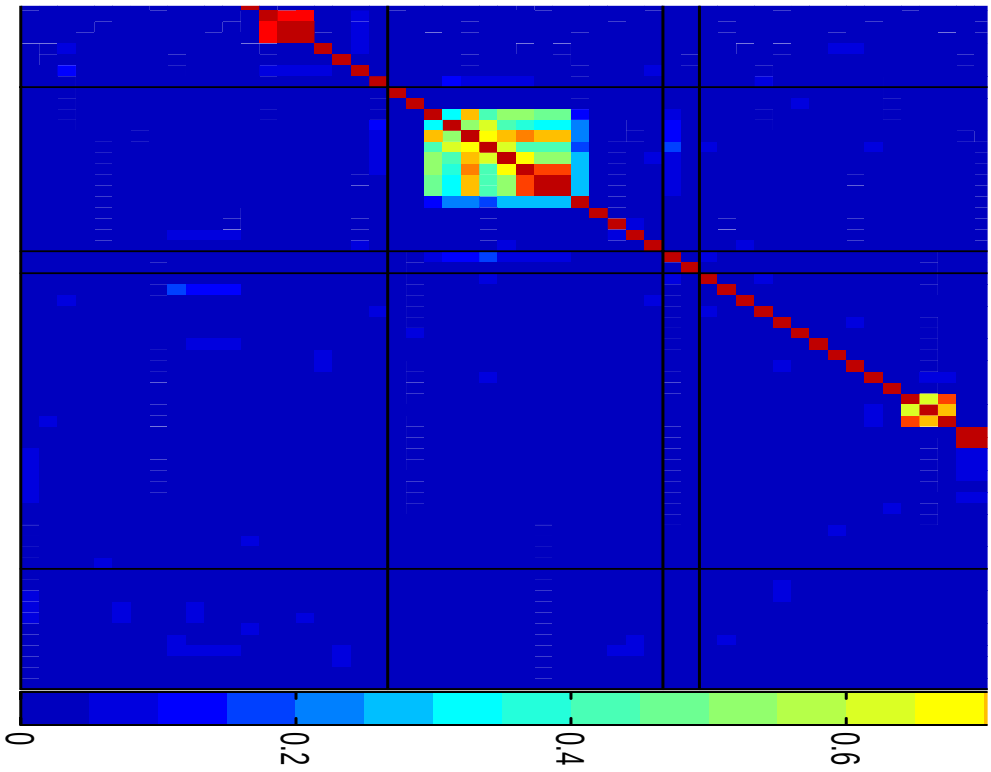

Figure S2. Significant additive variants are broadly distributed across the genome. Heat map illustrating the chromosomal location of each of the DGRP2 webserver's putative top hits colored from decreasing (0) to increasing (1) linkage score. Most variants were distributed throughout all but chromosome 4, with some variants in linkage blocks (multicolored squares).

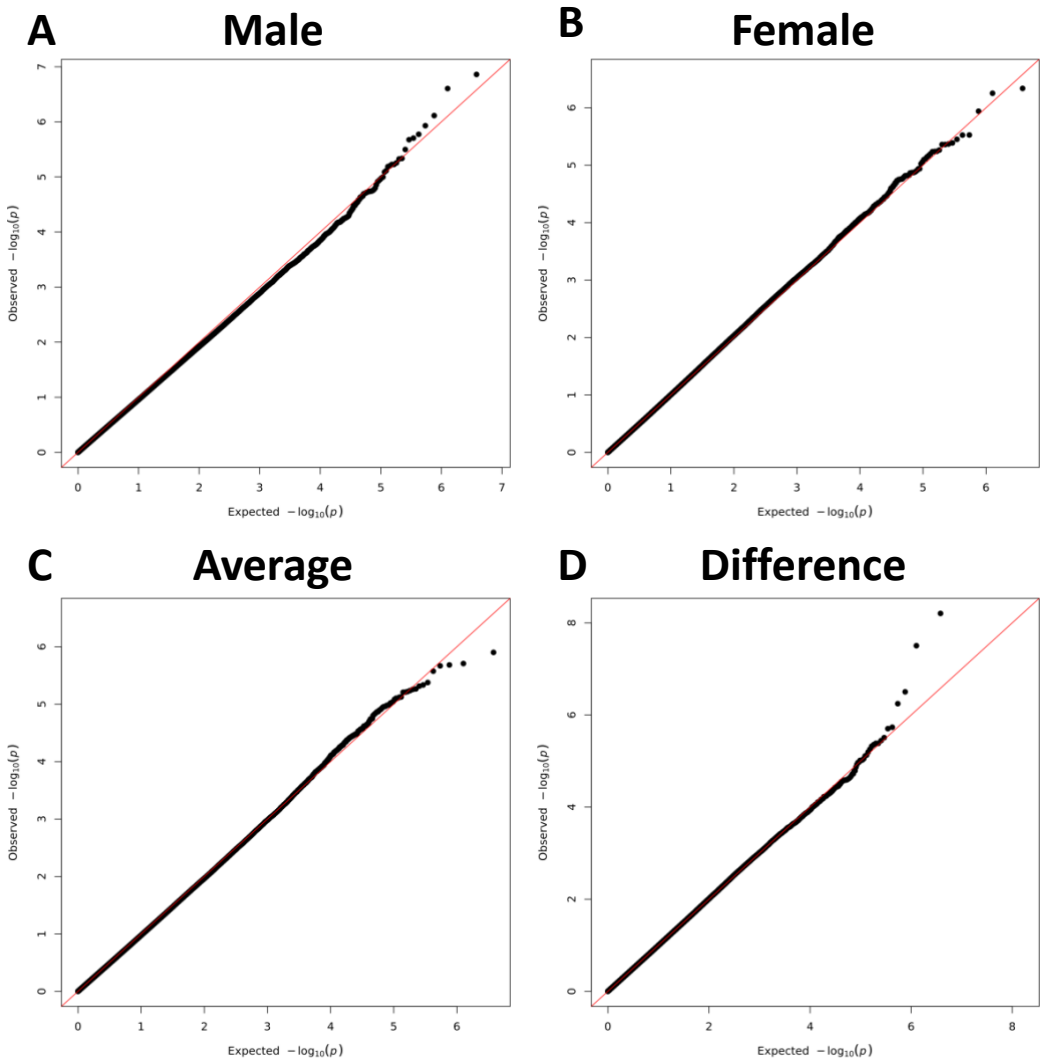

Figure S3. Quantile-quantile plots suggest GWAS contains significant variants with low population structure. Plots comparing the expected vs. observed distribution of *P*-values for each of the four sex-based phenotypes suggest significant variants exist in the analysis. Furthermore, since only a few points deviate from the 1:1 line (red), we can conclude that these points are the significant variants and are not significant due to anomalies in the population structure.

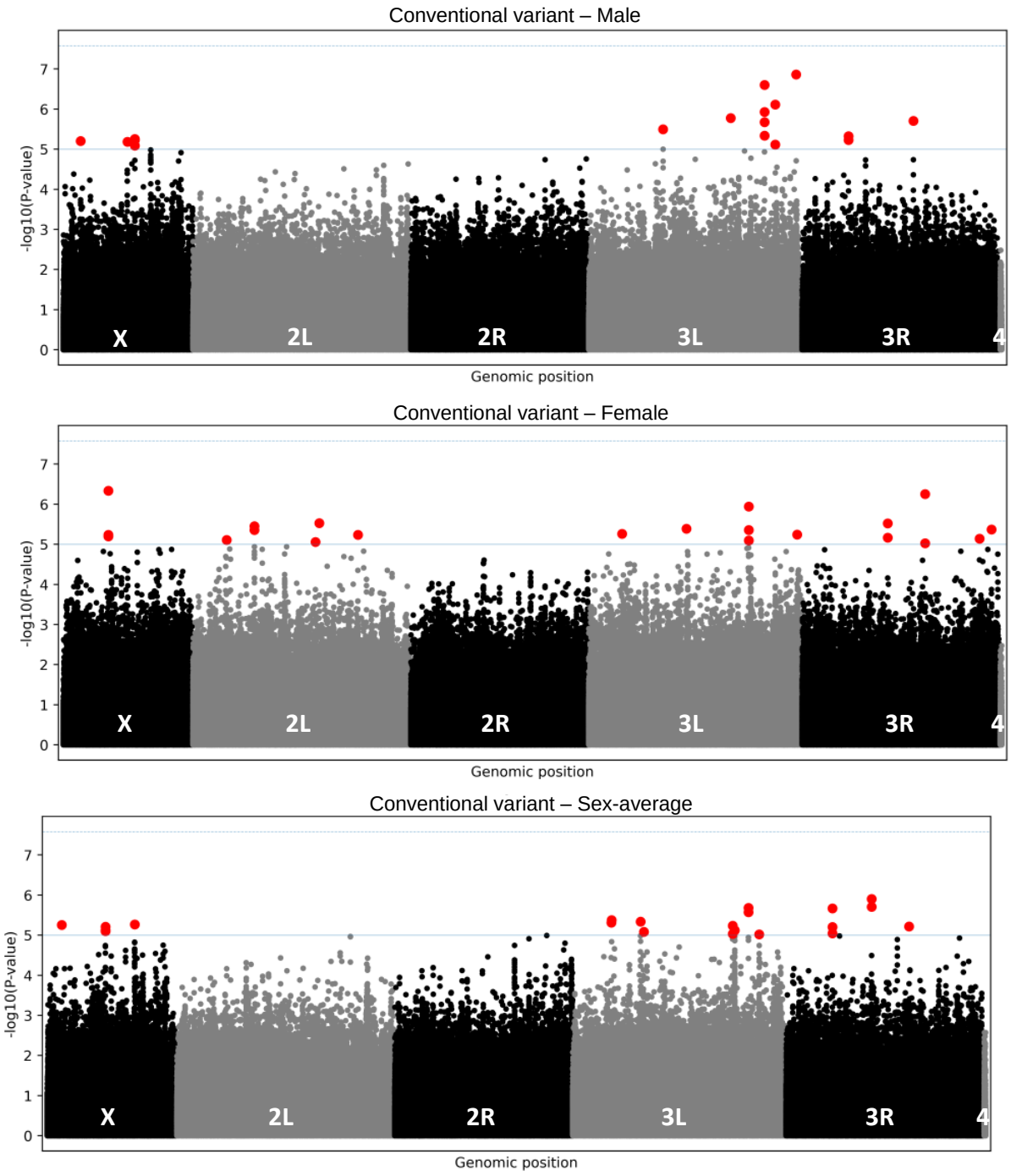

Figure S4. Manhattan plots of individual variant association analysis. Manhattan plots for the (A) male, (B) female, and (c) sex-average phenotypes visualize the distribution of variant *P*-values across the genome. Variants that fail to pass the standard significance threshold (*P* = 1E-5, solid blue line) are colored in gray or black, while variants that pass the threshold are colored in red. No variants passed the Bonferroni threshold (dashed blue line; *P* = 2.63E-8)

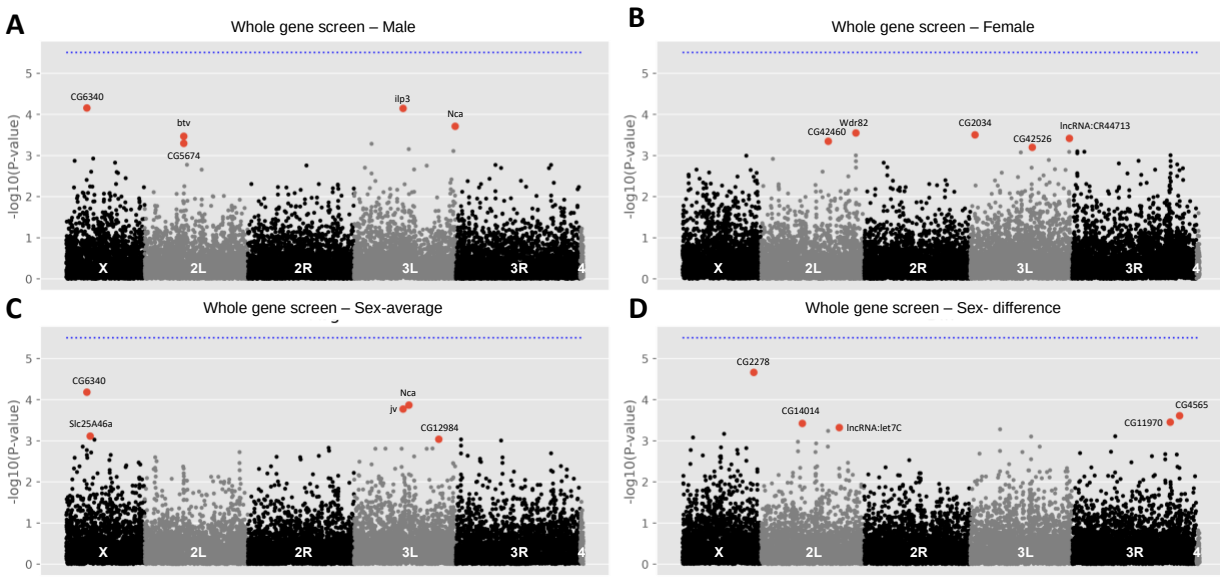

Figure S5. Top five genes from each sex-based phenotype in the whole gene search using `PEGASUS_flies`. Although no genes passed the strict Bonferroni significance threshold (*P* = 3.43E-6; blue dotted line), we explored the top five most significant genes (red points) in each of the sexes: (A) males, (B) females, (C) sex-average, and (D) sex-difference. All other genes (black and gray) were deemed not significant.