**List of Supplemental Files:**

Figure S1: Fly hormone axis illustration

Figure S2: Principle component analysis of biological replicates.

Figure S3: Correlation plots.

Figure S4: Relative quantification plots using qRT-PCR for each comparison.

Figure S5: Gene list overlap.

Figure S6: Strain and treatment differences in sleep.

Figure S7: Genome wide associations on rank transformed data.

Table S1: Publication Summary. Summarized previous genomics studies that examined gene expression changes in females post-mating.

Table S2: Full Results. Shows FPKM values for all replicates, the average for each condition, as well as, raw *P*-values, FDR corrected *P*-values, fold change, and filters for each comparison.

Table S3: Primer sequences for qRT-PCR

Table S4: Gene Ontology Results. Biological process, cellular component, molecular function, protein domain, and pathway enrichment are all included for each list.

Table S5: ANOVA and Tukey-HSD *post-hoc* test results. Statistical analysis for Figure 4A, B and D and Figure S5A and B.

Table S6: Gene lists. All genes that are differentially expressed with a FDR cut-off of <0.05 for each comparison.

Table S7: Rank Transformation of re-mating results. For each strain shows the average percent re-mating and the ranking after transformation.

Table S8: DGRP2 Top 100. For each associated SNP shows the location of the SNP, the major and minor alleles and counts, the minor allele frequency, p-value, and nearest gene within a 10kb window.