

**Revised annotations, sex-biased expression, and lineage-specific genes in the *Drosophila melanogaster* group**

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DOI: [10.1534/g3.114.013532](https://doi.org/10.1534/g3.114.013532)

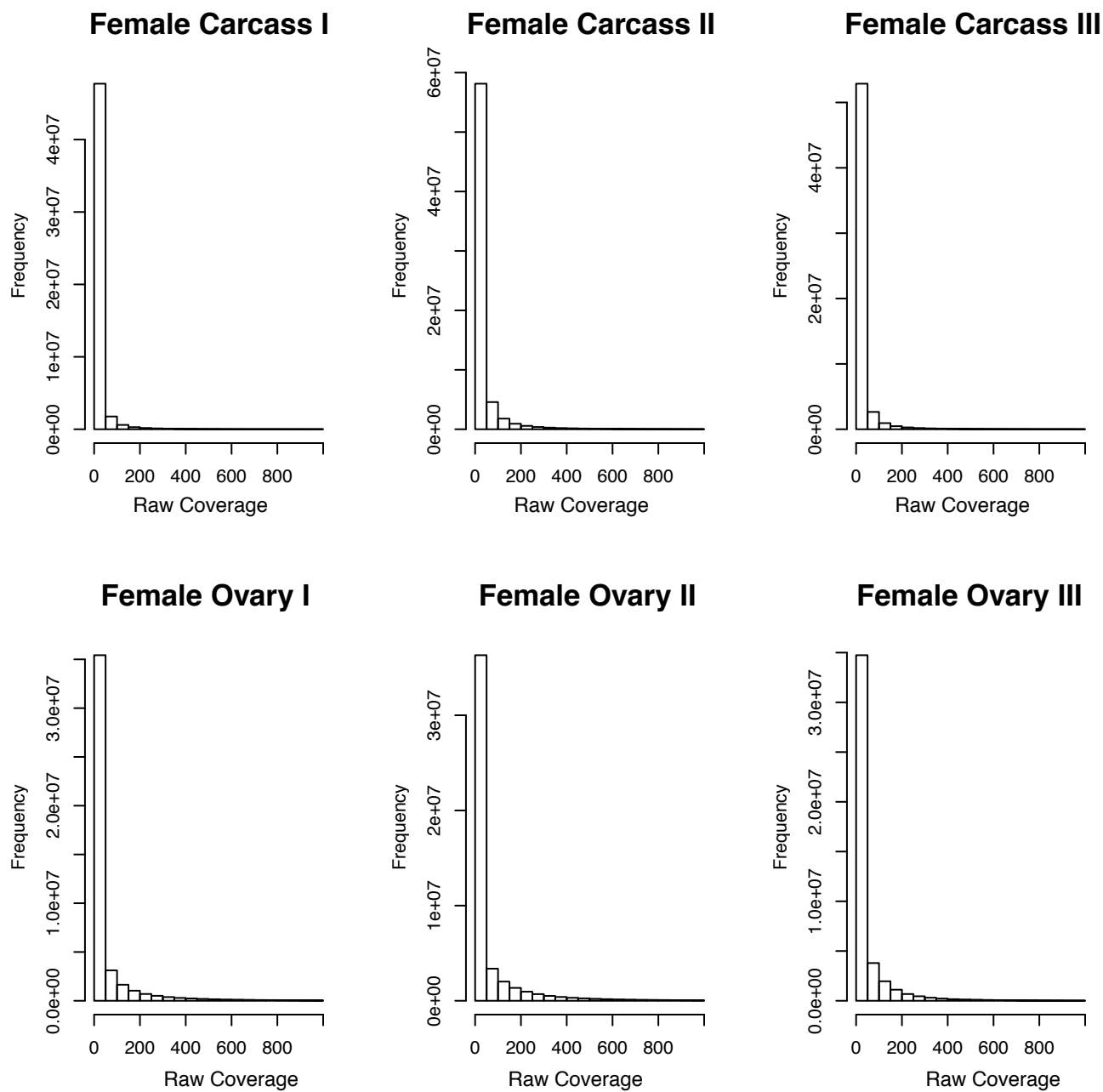


Figure S1: Raw coverage for sites with coverage sequencing depth between 1 and 1000 reads in RNA-seq data for replicates of female tissues in *D. simulans*.

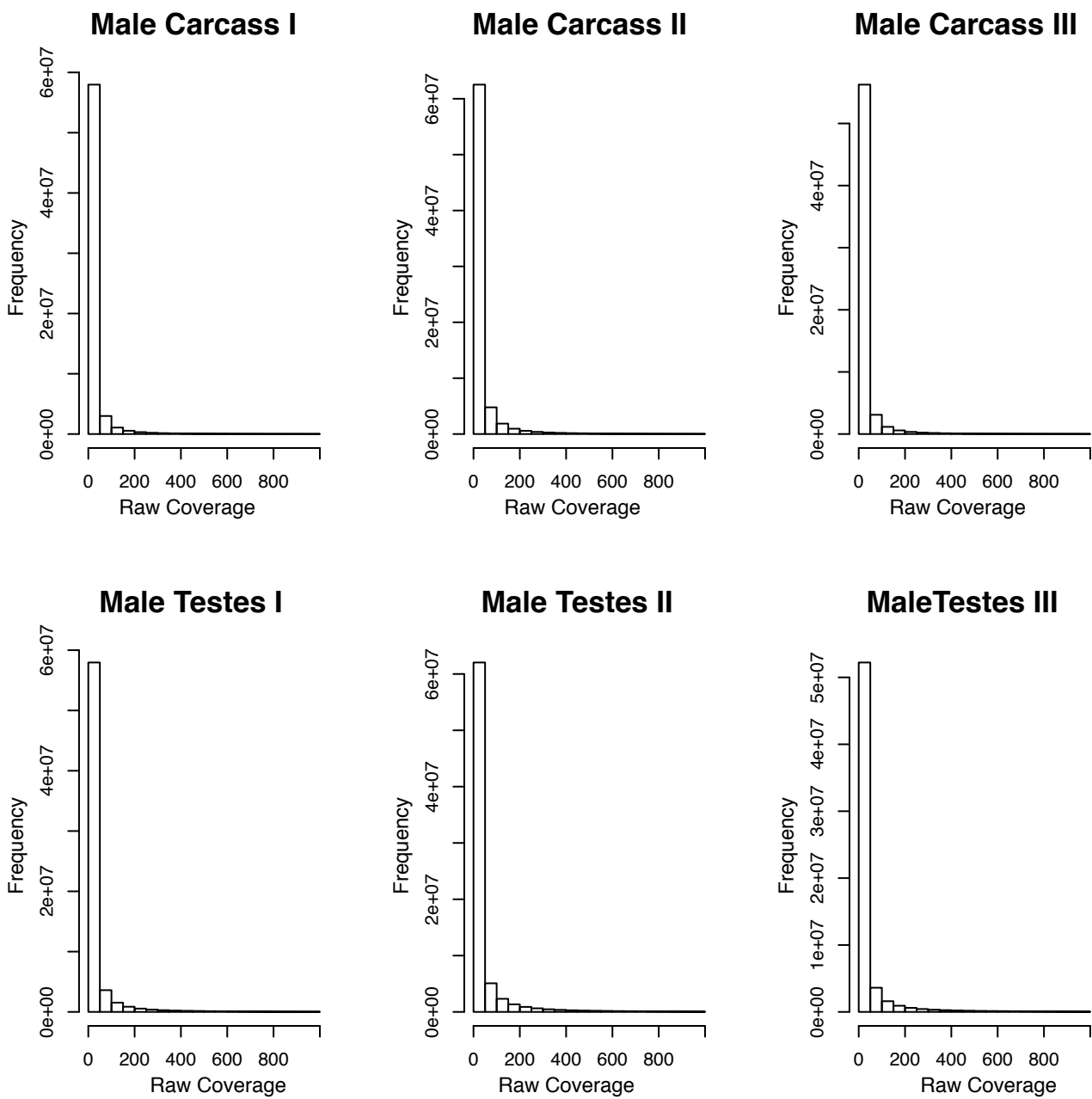


Figure S2: Raw coverage for sites with coverage sequencing depth between 1 and 1000 reads in RNA-seq data for replicates of male tissues in *D. simulans*.

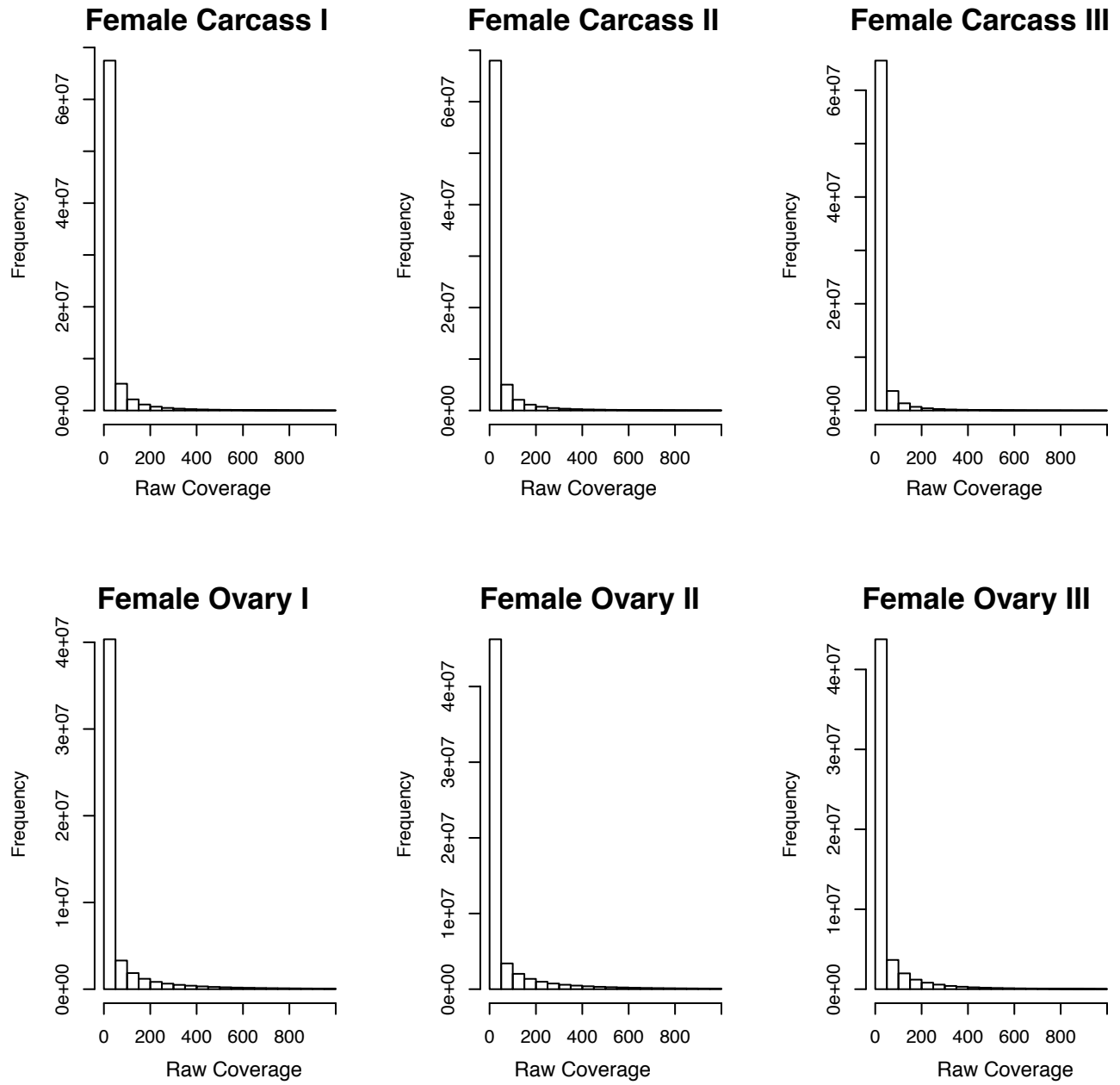


Figure S3: Raw coverage for sites with coverage sequencing depth between 1 and 1000 reads in RNA-seq data for replicates of female tissues in *D. yakuba*.

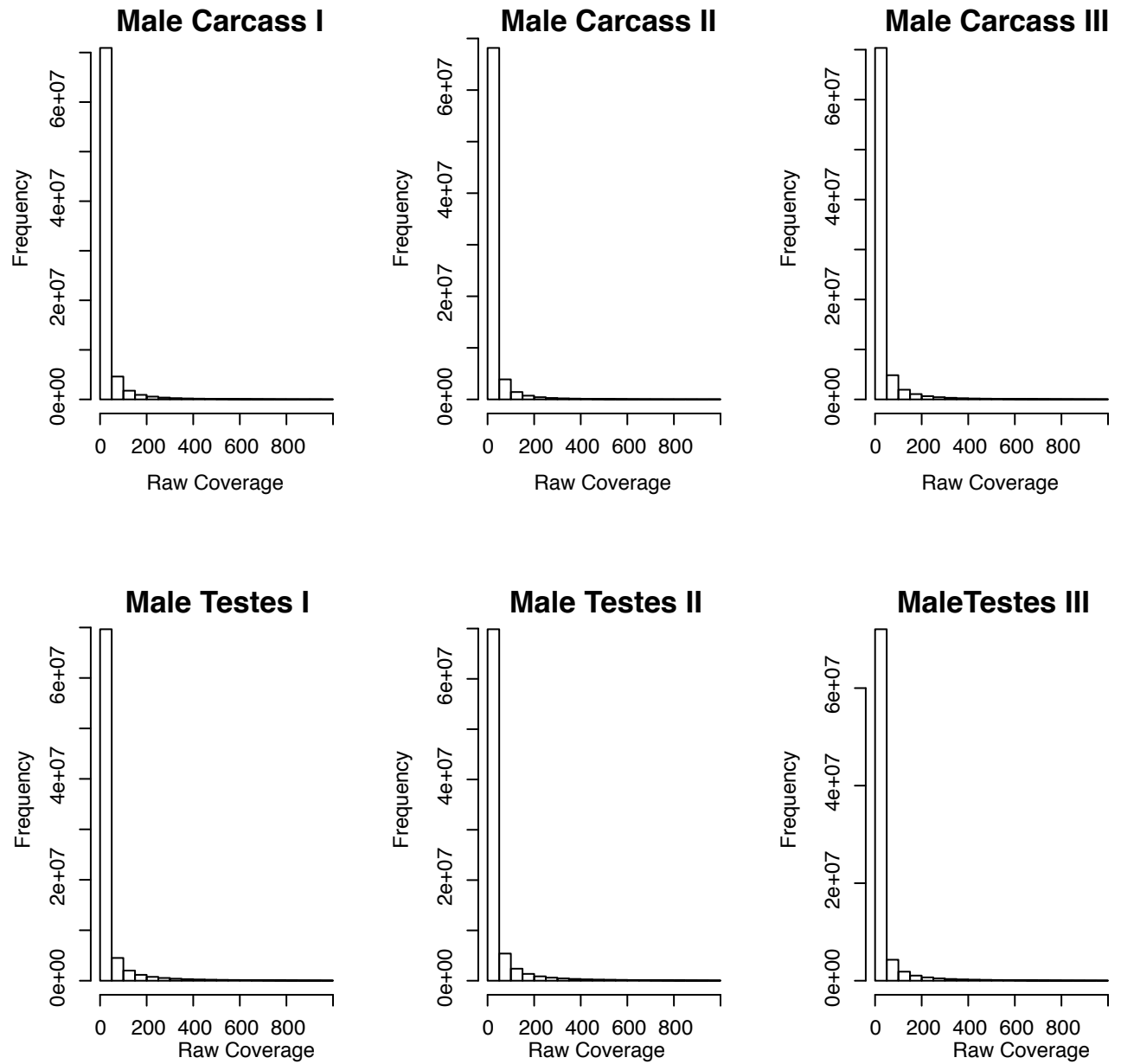


Figure S4: Raw coverage for sites with coverage sequencing depth between 1 and 1000 reads in RNA-seq data for replicates of male tissues in *D. simulans*.

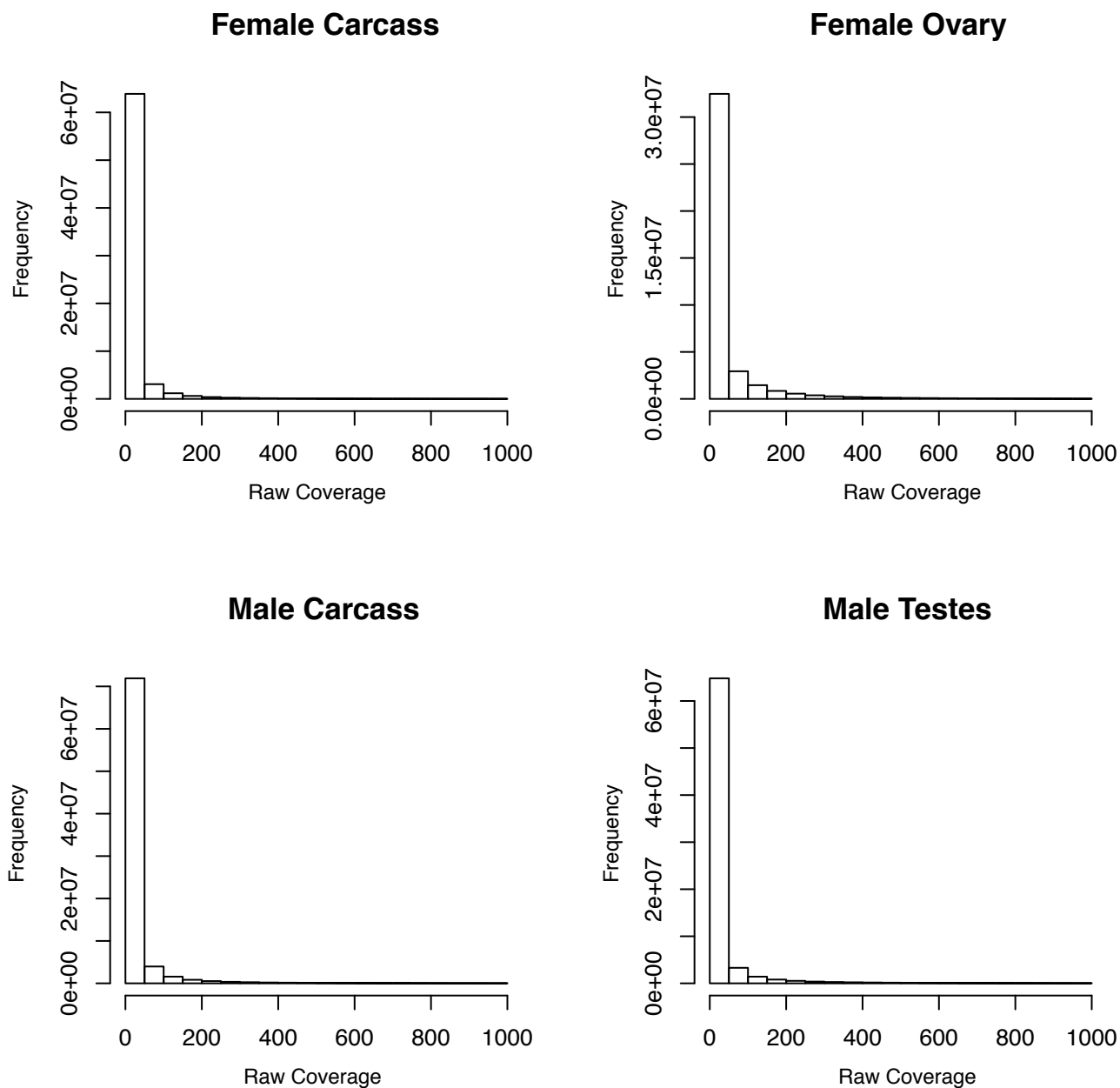


Figure S5: Raw coverage for sites with coverage sequencing depth between 1 and 1000 reads in RNA-seq data for tissues in *D. ananassae*.

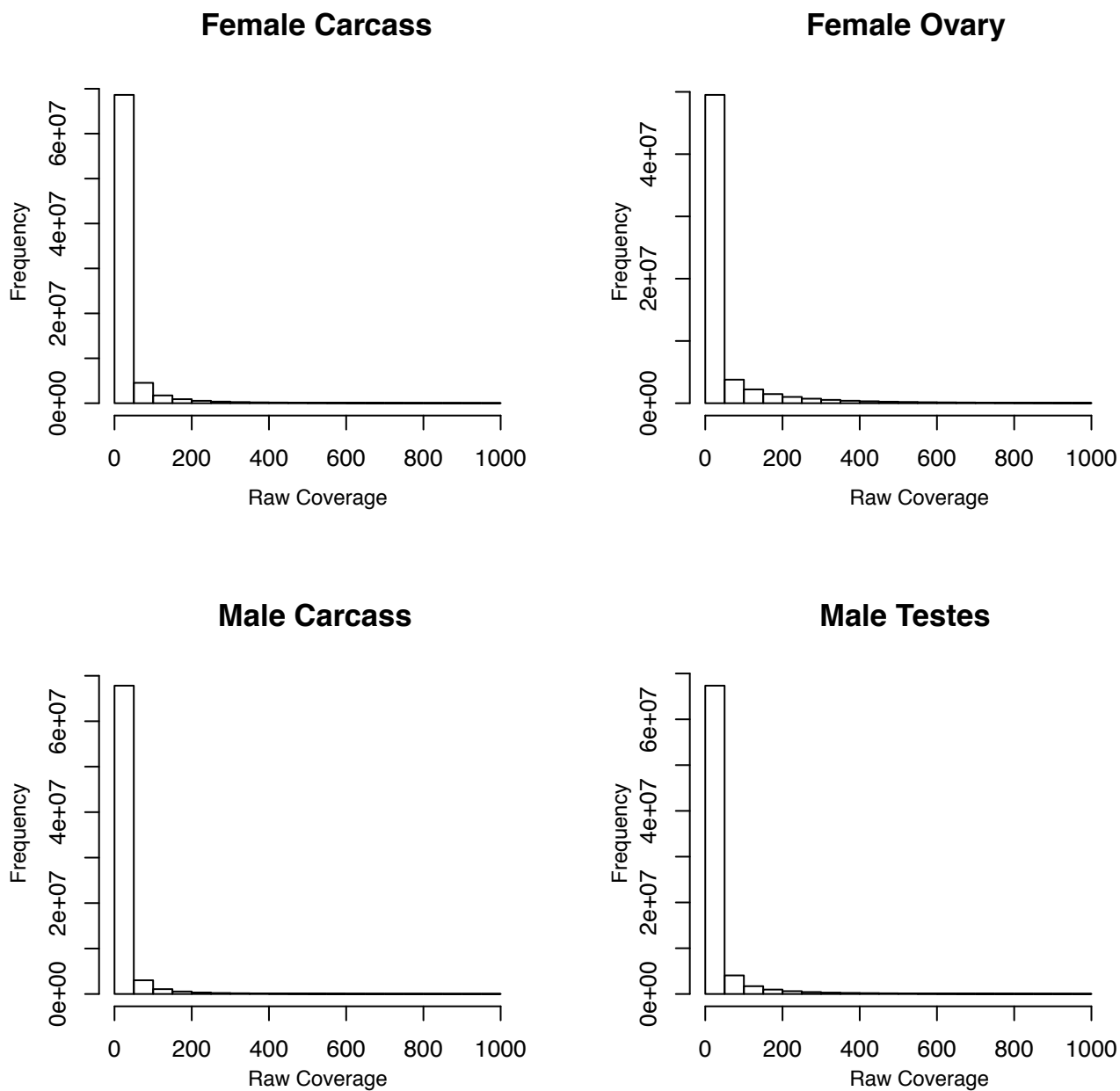


Figure S6: Raw coverage for sites with coverage sequencing depth between 1 and 1000 reads in RNA-seq data for tissues in *D. melanogaster*.

**File S1**

**Data Archive**

Available for download as a .zip file at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.013532/-/DC1>