Deep Sequencing of Whole Transcriptomes Across the Drosophila Genetic Reference Panel

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ABSTRACT
Genetic variation influences phenotype in part by altering the transcriptional regulatory architecture that controls mRNA expression levels. However, there remain fundamental questions about the relationship between genetic, transcriptomic, and organismal phenotypic variation, in part because there are few data sets encompassing transcript and phenotype measurements from the same genotypes. The *Drosophila Genetic Reference Panel* (DGRP) is a collection of 205 inbred *Drosophila melanogaster* lines harboring natural genetic variation derived from wild-caught flies. Genetic variation was previously mapped across these lines, and multiple research groups have used this collection to map the genetic architecture of various quantitative traits, including alcohol sensitivity, aggression, feeding behavior, and growth control. We have now performed total RNA-seq on adult whole flies across this collection to map genetic variation in the entire transcriptome, including previously unknown lncRNA and anti-sense transcripts. We have developed novel analysis pipelines to unify RNA-seq data derived from distinct genomes, and have identified heritable expression patterns in the majority of known genes, as well as transposons and novel transcripts. Ultimately this data set will allow the mapping of trait-associated transcripts, eQTLs, and expression correlation networks in *Drosophila melanogaster* with unprecedented power and resolution.