Fig. S1. Mean expression trajectories per Drosophila Genetic Reference Panel (DGRP) line, each of which either had high performance as adults (HA) or as larvae (HL). The Y-axis is the $\log_2$ fold change at each sampling time point compared to the first (0) time point. **(A)** The trajectories for the only gene significantly (FDR < 0.05) differentially expressed between phenotypes from time 0 to time 30 minutes, a time period with active differential expression for larvae (see results in main text). **(B)** The trajectories for one representative gene out of 329 genes significantly differentially expressed between phenotypes from time 0 to time 90 (30 minutes into recovery), a time period with active differential expression for adults (see main text). In both cases, one outlier line is primarily driving differential expression – there are not consistent differences between HA and HL lines in either case. Visual inspection of trajectories for many more genes confirmed that these likely spurious cases of phenotypic effects were common.
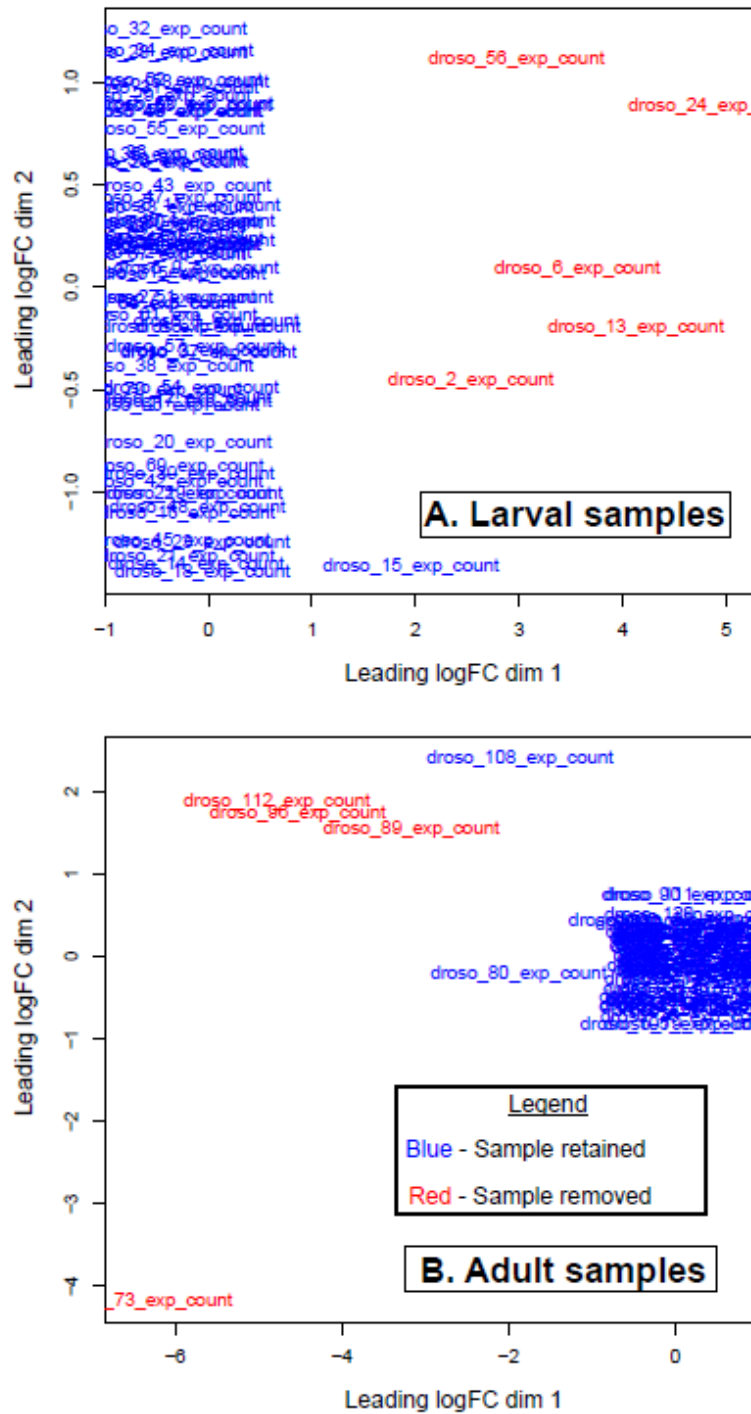
Fig. S2. Results of Multidimensional Scaling (MDS) analysis of the 500 most differentially expressed transcripts in cold-shocked **(A)** larvae and **(B)** adults. Each RNA library (sample) is plotted as its ID. We removed all samples appearing in red that were clear outliers and had a low (<200,000) number of reads mapping.
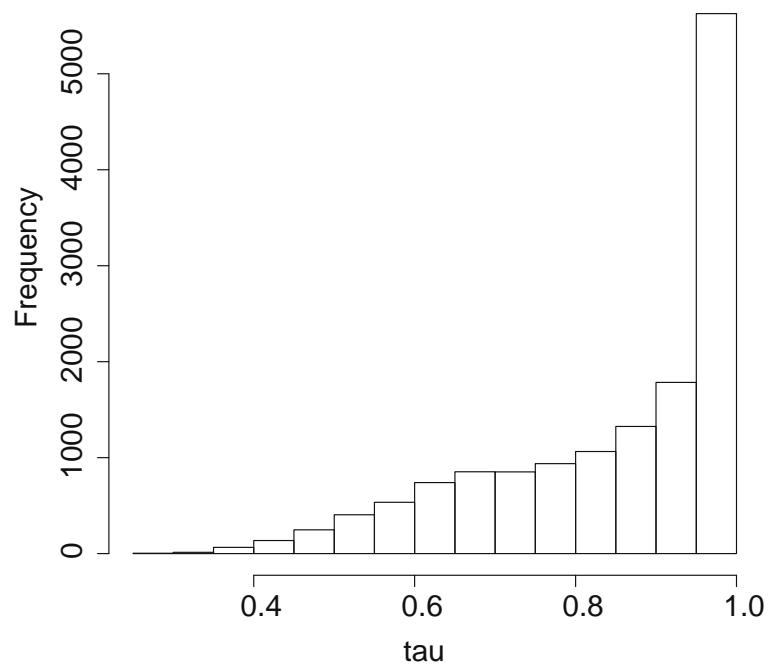
Fig. S3. Frequency distribution of the index of tissue specificity, τ (tau) for all genes in the *Drosophila melanogaster* genome as calculated following the methods described in the main text.

Table S1. Sample IDs for each RNA library in the RNASeq experiment (Experiment 1), library sizes (number of mapped reads), and a column to indicate which samples were excluded from further analysis because of outlier status and small library size (see methods).

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Table S2. Number of replicate libraries for each line-stage-time combination in Experiment 1 after removal of libraries as summarized in Table S2.

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TableS3. Full results of functional enrichment analysis of genes with a significant stage × time interaction (FDR < 0.05) and significantly differentially expressed across at least one time point in larvae or adults in Experiment 1. Enrichment analysis conducted with the David functional annotation tool v6.8, https://david.ncifcrf.gov/summary.jsp This tool produces functional enrichment results for categories that 'cluster' together based on member gene overlap (the 'clustered' results) and categories that do not cluster with other categoreis ('unclustered' results).

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