

## Figure S2: Differentially expressed genes identified in Gutzwiller et al., 2015 are a high fold-change subset of all differentially expressed genes across the *D. melanogaster* life cycle.

Maximum log2 fold change across stages in the *D. melanogaster* life cycle for each of the 473 *w*Mel genes identified as differentially expressed in the current study, partitioned by whether they were identified as differentially expressed in the Gutzwiller et al., 2015 study (red) or only in the current study (grey). Omission of the design matrix in the Gutzwiller et al., 2015 life-cycle edgeR analysis caused an over-estimation of common and tagwise dispersion, leading to detection of only a subset of genes with high maximum fold-change across life-cycle stages in Gutzwiller et al., 2015. All 60 genes detected as differentially expressed in Gutzwiller et al., 2015 that pass the edgeR minimum expression filters and are in the current RefSeq annotation for *w*Mel are also differentially expressed in the current study.