



**Fig. 1** Transcriptional profiling of *Drosophila* imaginal discs. **(a)** Overview of sequenced tissues and wing compartments and respective developmental stages. **(b)** t-distributed stochastic neighbor embedding (t-SNE) based on the expression of 10045 genes in 5 tissues, 4 wing compartments and 3 developmental stages. The samples show a predominant clustering by the late stage followed by the clusters of neural tissues and genitalia in the early stages. Selected genes show expression levels of at least 5 TPMs in at least 2 samples. Gene expression is computed as log<sub>10</sub>-normalized TPM with pseudocount of 0.01. Pearson's correlation was computed for each pair of samples. **(c)** control genes described in literature (see Supplemental Fig. SX for more details).