**Fig. 1** Transcriptional profiling of *Drosophila* imaginal dics. (**a**) Overview of sequenced tissues and respective developmental stages. (**b**) Control genes for each tissue and for each developmental stage described in literature. (**c**) Principal component analysis based on the expression of 1000 most variable genes in 3 tissues and 3 developmental stages. PC1 indicates time, mainly separating the early stages and the late stage. PC2 separates neural and non neural tissues. PC3 separates eye late stage to the other samples. Selected genes show expression levels of at least 5 TPMs in at least 2 samples. Gene expression is computed as log10-normalized TPM with pseudocount of 0.01.