



Fig. S2 Summary statistics of RNA-seq samples. **(a)** Percentage of mapped and uniquely mapped reads over the initial number of reads. On average 92% of reads were mapped and 85% of the initial number of reads were uniquely mapped to the fly dm6 genome. **(b)** Percentage of split and continuous mapping through genomic regions. As expected from our experimental design, on average 92% of the reads mapped to exonic regions of the genome. **(c)** Spearman coefficient of correlation of gene expression. Pair of replicates show high coefficient of correlation. Samples first cluster by early and late developmental stages and next early samples split among neural and non-neural tissues.