



**S1 Fig. Analysis framework for the *D. melanogaster* mRNA-seq data.**

Required inputs (sequencing data in FASTQ format, and the corresponding reference genome and transcriptome in FASTA/GFF) and the six main steps of the analysis are shown in a workflow diagram, following Conesa et al. 2016 (Genome Biology, 17:13). The steps, for which additional details are included, are: Quality check (QC), alignment, normalization of gene abundances, identification of DE, functional enrichment and finally low-throughput validation