

Table S3. Running times of different R packages for analyzing the development transcriptome of *Drosophila*

deGPS		DESeq*	DESeq2	edgeR	SAMseq
Number of cores	Runtime	14 min	14 sec	10 sec	15 sec
1	37.6 min				
4	10.3 min				
8	5.4 min				
16	3.1 min				

*Note: DESeq, DESeq2 and edgeR do not use parallel computation and thus one core was used in their analyses.