

**Table S2** Bioinformatics parameters used in the mRNA-seq data analysis

**General hardware settings:** 40 CPU and RAM 150 GB.

**Parameters settings:**

- Tophat: -p 20, --bowtie1, -i30, -I200000, --min-segment-intron 30, --max-segment-intron 200000, --min-coverage-intron 30, --max-coverage-intron 200000, other default parameters
- cufflinks: -p20, --min-intron-length 30, other default parameters
- cuffcompare: -p20, -R, other default parameters
- Cuffmerge: -p20, other default parameters
- Cuffdiff: -p20, -u, -v, other default parameters