Basic RNA-Seq Analysis (Eukaryotic)

Read mapping against the requested reference was performed with STAR[1]. Generated BAM files are provided in folders for each respective sample. Feature quantification was performed using RSEM[2]. Generated gene and isoform data from RSEM is provided with the individual sample folders.

Summary mapping statistics of all samples can be found in the ‘alignment.tsv’ file. Summaries of the raw, quantified counts are reported in the “*rsem_counts*.tsv” file.

Tool	Version	Parameters
STAR	2.7.10b	default parameters
RSEM	1.3.3	default parameters

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[1] Dobin A, Davis CA, Schlesinger F, et al. STAR: ultrafast universal RNA-seq aligner. Bioinformatics. 2013;29(1):15-21. doi:10.1093/bioinformatics/bts635

[2] Li, B., Dewey, C.N. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC Bioinformatics 12, 323 (2011). https://doi.org/10.1186/1471-2105-12-323

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