Transcriptomic

Raw files

Quality assessment (FastQC)

After trimming

Mapping*
(TopHat 2)

Quantification
(Cufflinks 2 and HTSeq-count)

Normalisation and Tissue averaging

Analyses and Comparison

Filtering
(Expression thresholds, …)

Automatized through iRAP

*Annotation and reference: ENSEMBL 76