RNAseq analysis Workflow

Raw reads

Quality evaluation

(**FastQC**, MultiQC or fastp)

Remove low quality reads

(**trimmomatic** or fastqp)

Transcriptome Assembly

Genome guided

(Cufflinks pipeline)

Interactive results using several R packages

De novo

(**Trinity** or any other)

Transcriptome assembly quality assessment

(**TransRate** and BUSCO)

Estimate transcript abundances

(**kallisto**, salmon, bowtie or any other)

Functional annotation

Trinotate pipeline

Differential gene expression analyses

(**edgeR**)

GO and KEGG Enrichment analyses

(**Goseq** or TopGo)

Interactive results using several R packages