

## **Final task - RNA analysis**

Analyze RNA-seq samples prepared with QuantSeq 3' mRNA-Seq Library Prep Kit from human cell-line. There are 3 replicates of wildtype samples and 3 replicates of VeR treated samples. Raw reads in fastq format are provided for all 6 sequenced samples. Ligated UMIs were removed from the reads and written to the reads headers.

The goal is to identify genes with statistically significant expression changes.

The expected deliverables are:

1. Table with a list of differential expressed genes (can be a resulting DEseq table)
2. MultiQC report in html format summarizing pre- and post-alignment QC
3. A workflow that can reproduce these results with a single command