UOM-BC: expression - RNAseq, RNA-Seq

Analysis Description:

Data process by aligment of Fastq files to **GRCh38**.p12   using STAR v2.5.1b and quantified at the gene-level with Gencode.v22. Mismatching and multi-mapping reads and were excluded during alignment using the parameters "outFilterMisMatchNmax = 0" and "outFilterMultimapNmax = 1". Raw counts were normalised using the median ratio method implemented in the DESeq2 package (PDF). **References and Links**

- https://www.ncbi.nlm.nih.gov/assembly/GCF_000001405.38
- https://academic.oup.com/bioinformatics/article/29/1/15/272537
- https://intranet.birmingham.ac.uk/it/teams/infrastructure/research/bear/bluebear/applications/star-aligner-v2-4-2a.aspx
- https://www.encodeproject.org/files/gencode.v22.annotation/
- http://bioconductor.org/packages/devel/bioc/vignettes/DESeq2/inst/doc/DESeq2.html
- https://www.bioconductor.org/packages/devel/bioc/manuals/DESeq2/man/DESeq2.pdf
- https://bioc.ism.ac.jp/packages/2.14/bioc/vignettes/DESeq2/inst/doc/beginner.pdf