**Material & Methods:**

All samples were subjected to ***FastQC 0.3*** (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) check and segment with poor quality bases trimmed in each sample by ***FASTQ Trimmer 1.0.0*** (Blankenberg, Gordon et al. 2010). Read mapping was carried out using TopHat 1.4.1 ([Trapnell, Pachter et al. 2009](#_ENREF_2)) with supplied annotations (mm9.gtf) against the mouse genome build mm9. Afterwards, alignment was reduce to contain only uniquely mapping reads and HTSeq-count script was used at default parameters (<http://www-huber.embl.de/users/anders/HTSeq/doc/count.html>) to obtained the count of reads mapped to genes. Differential expression analysis between two groups was performed (using raw count uniquely mapped data) by using R package *edgeR* ([Robinson, McCarthy et al. 2010](#_ENREF_1)) and only genes ≥ 1count per million in at least 3 samples were used during the analysis.

**References:**

Blankenberg, D., A. Gordon, et al. (2010). "Manipulation of FASTQ data with Galaxy." Bioinformatics **26**(14): 1783-1785.

Robinson, M. D., D. J. McCarthy, et al. (2010). "edgeR: a Bioconductor package for differential expression analysis of digital gene expression data." Bioinformatics **26**(1): 139-140.

Trapnell, C., L. Pachter, et al. (2009). "TopHat: discovering splice junctions with RNA-Seq." Bioinformatics **25**(9): 1105-1111.