

Differential Expression

RaNA-seq

2026-10-08 02:53:51.862265586853

Volcano plot

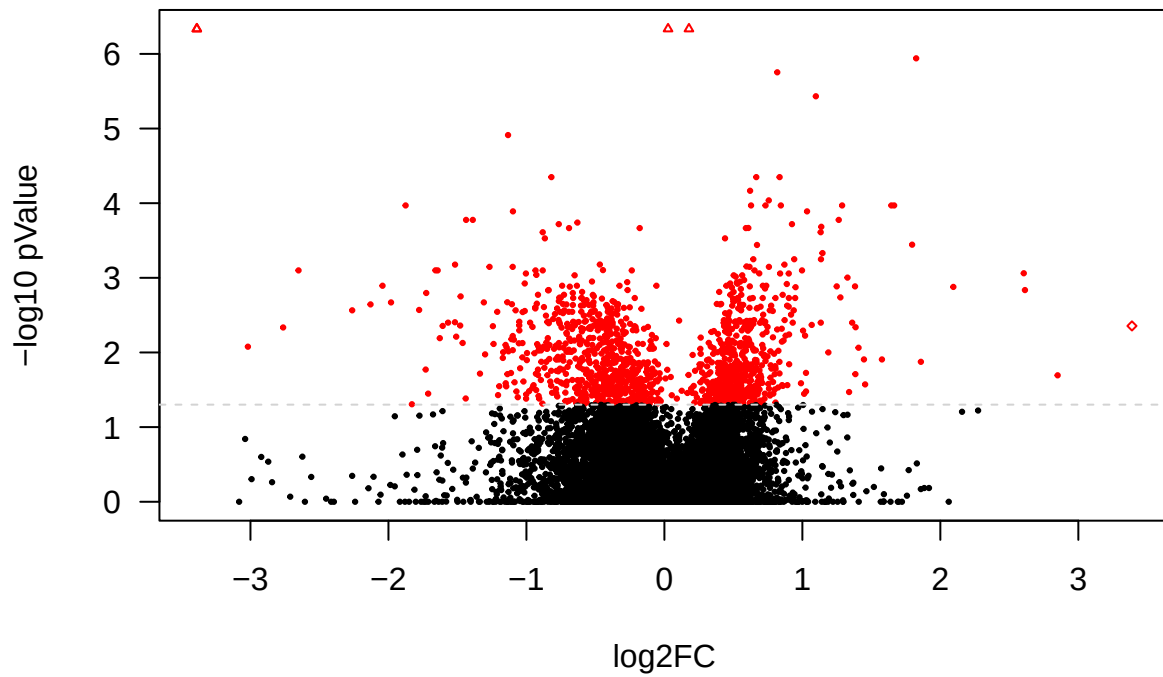


Figure 1 Volcano plot of differential expression results. It shows the log2 scaled fold change (x axis) and the minus log10 p-value (y axis) of each gene in the differential expression analysis. Genes with a significant expression change are highlighted as red dots.

MA plot

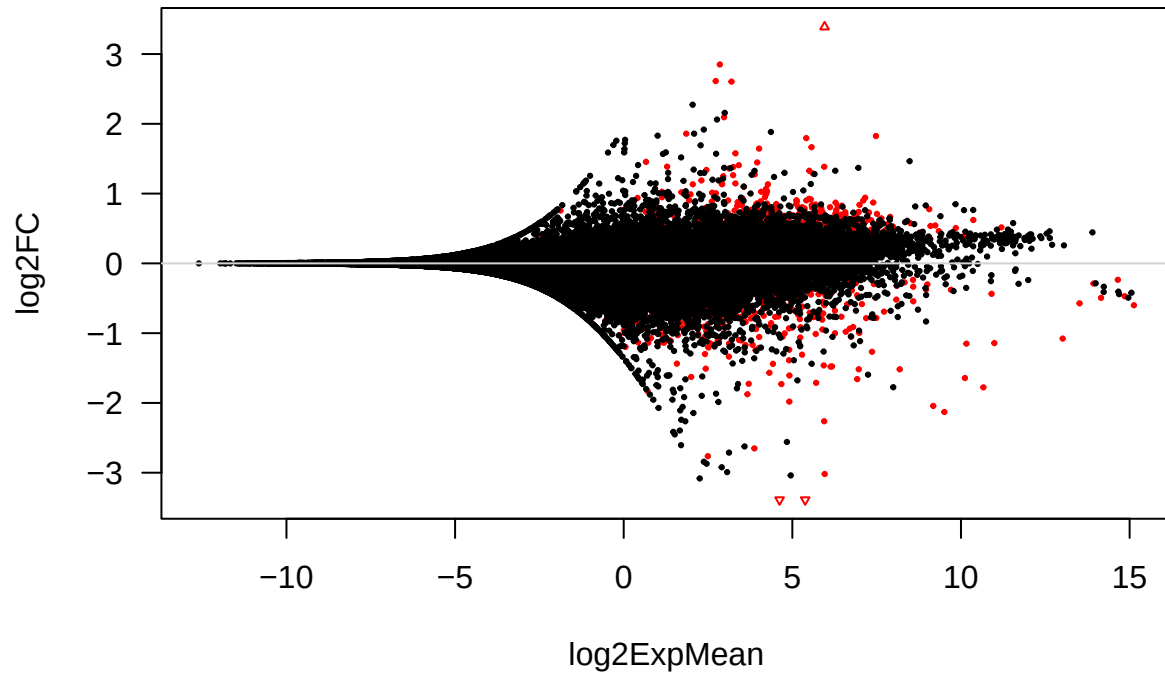


Figure 2 MA plot of differential expression results. It shows the log2 scaled mean of expression (x axis) and the log2 scaled fold change (y axis) of each gene in the differential expression analysis. Genes with a significant expression change are highlighted as red dots.

Methods

Samples were quantified with Salmon algorithm (Patro et al. 2017) setting following parameters: paired-end, default parameters.

Differential Expression analysis was performed with DESeq2 (Love, Anders, and Huber 2014). It was executed with following parameters: test: Wald; fitType: parametric. It found 1308 significant genes for a cutoff of 0.05.

Protocol executed by RaNA-seq(Prieto and Barrios 2019).

References

- Love, M. I., Simon Anders, and Wolfgang Huber. 2014. *Differential analysis of count data - the DESeq2 package*. Vol. 15. 12. <https://doi.org/110.1186/s13059-014-0550-8>.
- Patro, Rob, Geet Duggal, Michael I. Love, Rafael A. Irizarry, and Carl Kingsford. 2017. "Salmon provides fast and bias-aware quantification of transcript expression." *Nature Methods* 14 (4): 417–19. <https://doi.org/10.1038/nmeth.4197>.
- Prieto, Carlos, and David Barrios. 2019. "RaNA-Seq: interactive RNA-Seq analysis from FASTQ files to functional analysis." *Bioinformatics* 36 (6): 1955–56. <https://doi.org/10.1093/bioinformatics/btz854>.