

Quality Control

RaNA-seq

2026-10-08 02:53:41.3991272449493

Samples

##	id	name
##	1	SRR14409206
##	2	SRR14409207
##	3	SRR14409208
##	4	SRR14409209
##	5	SRR14409210
##	6	SRR14409211
##	7	SRR14409212
##	8	SRR14409213
##	9	SRR14409214
##	10	SRR14409215
##	11	SRR14409216
##	12	SRR14409217
##	13	SRR14409218
##	14	SRR14409219
##	15	SRR14409220
##	16	SRR14409221
##	17	SRR14409222
##	18	SRR14409223
##	19	SRR14409224
##	20	SRR14409225
##	21	SRR14409226
##	22	SRR14409227
##	23	SRR14409228
##	24	SRR14409229
##	25	SRR14409230
##	26	SRR14409231
##	27	SRR14409232
##	28	SRR14409233
##	29	SRR14409234
##	30	SRR14409235
##	31	SRR14409236
##	32	SRR14409237
##	33	SRR14409238
##	34	SRR14409239
##	35	SRR14409241
##	36	SRR14409242

Table 1 Table of samples.

Expression Value

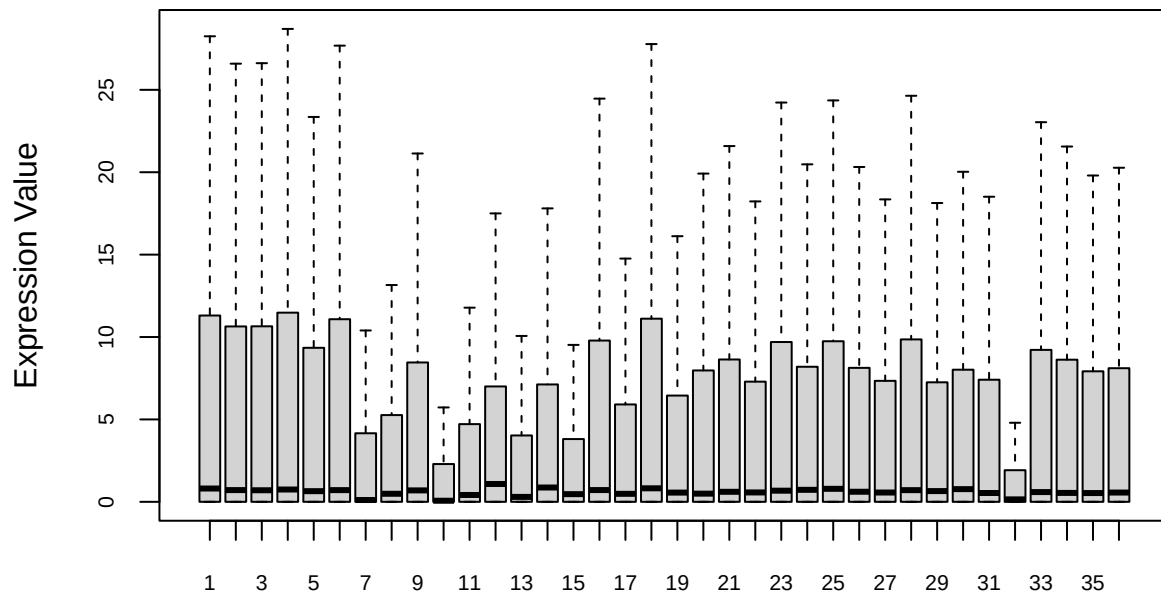


Figure 1 Box-and-whisker plots (boxplots) of the expression values (normalized as TPMs) for each sample.

ExpressedGenes

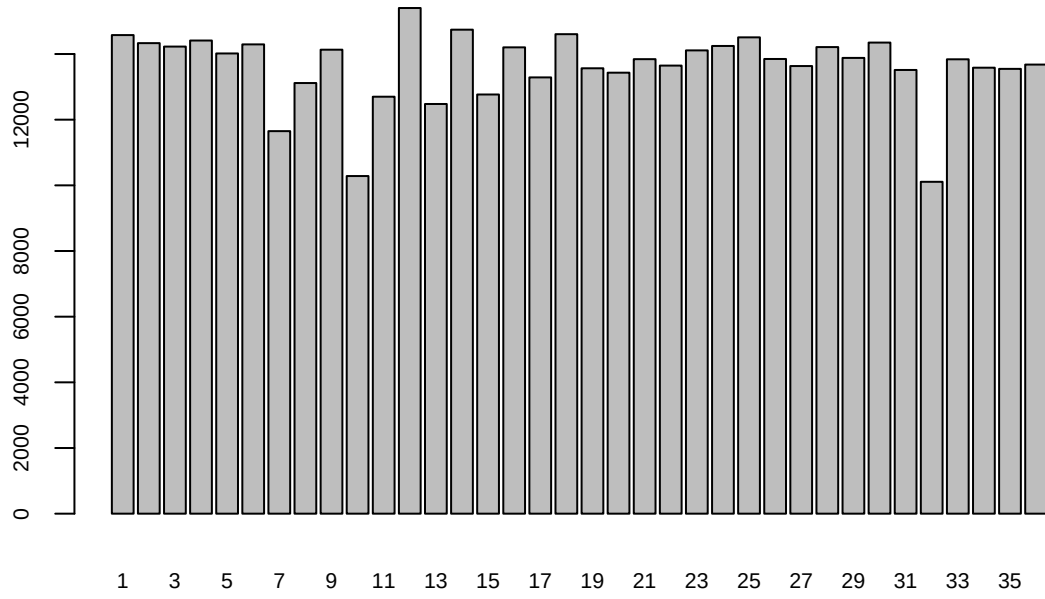


Figure 2 Barplot with the estimated expressed genes per sample.

Heatmap

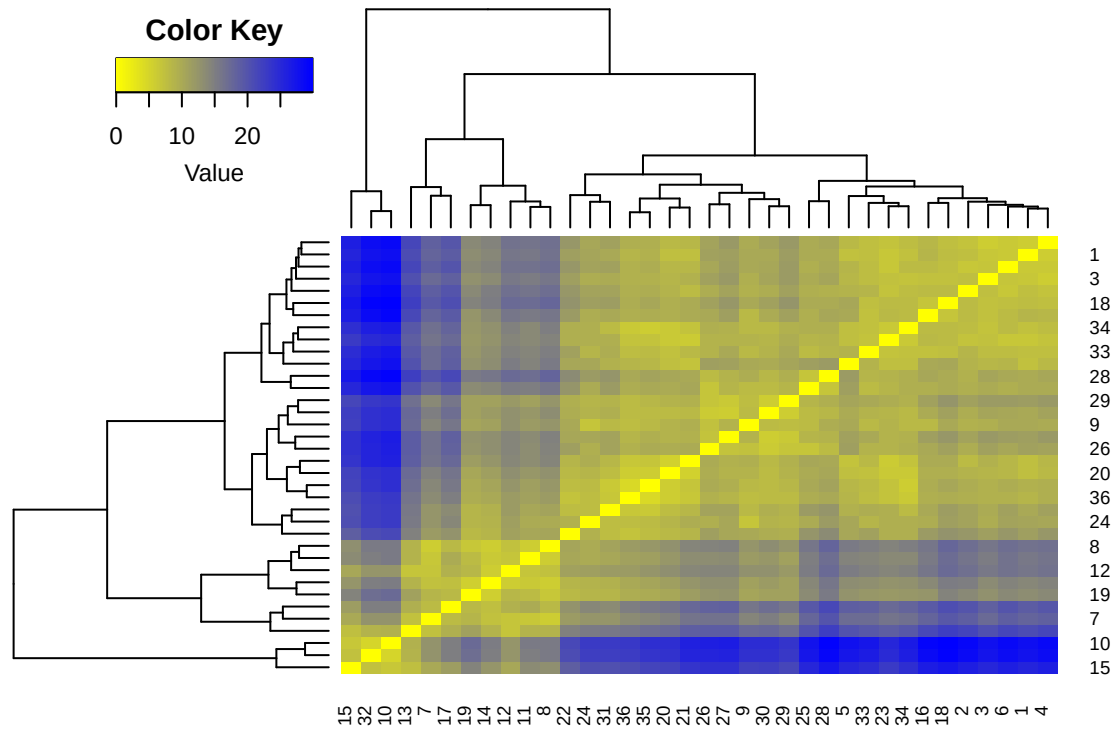


Figure 3 Heatmap of expression similarity between samples. It shows the distance between samples calculating the SERE coefficient (Schulze et al. 2012) between each pair of samples. Similar samples have lower values in the graph.

PCA plot

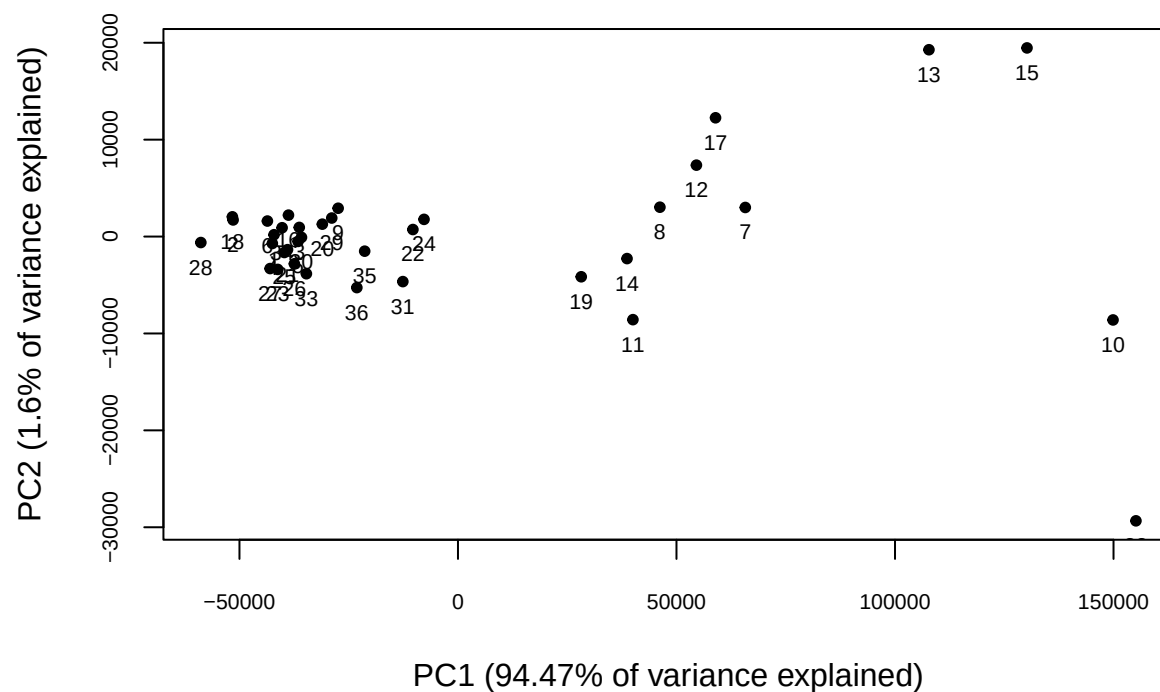


Figure 4 PCA plot of samples. It shows the two first PCs (principal components) values of each sample.

Methods

SERE coefficient was used as distance between samples on Figure 3 (Schulze et al. 2012). Graphs were generated using R (R Development Core Team 2011) and RJSplot (Barrios and Prieto 2018).

References

- Barrios, David, and Carlos Prieto. 2018. "RJSplot: Interactive Graphs with R." *Molecular Informatics* 37 (3). <https://doi.org/10.1002/minf.201700090>.
- R Development Core Team, R. 2011. *R: A Language and Environment for Statistical Computing*. Vol. 1. 2.11.1. <https://doi.org/10.1007/978-3-540-74686-7>.
- Schulze, Stefan K., Rahul Kanwar, Meike Gölzenleuchter, Terry M. Therneau, and Andreas S. Beutler. 2012. "SERE: Single-parameter quality control and sample comparison for RNA-Seq." *BMC Genomics* 13 (1). <https://doi.org/10.1186/1471-2164-13-524>.