

RNA-seq analysis of NELFE KO vs EV

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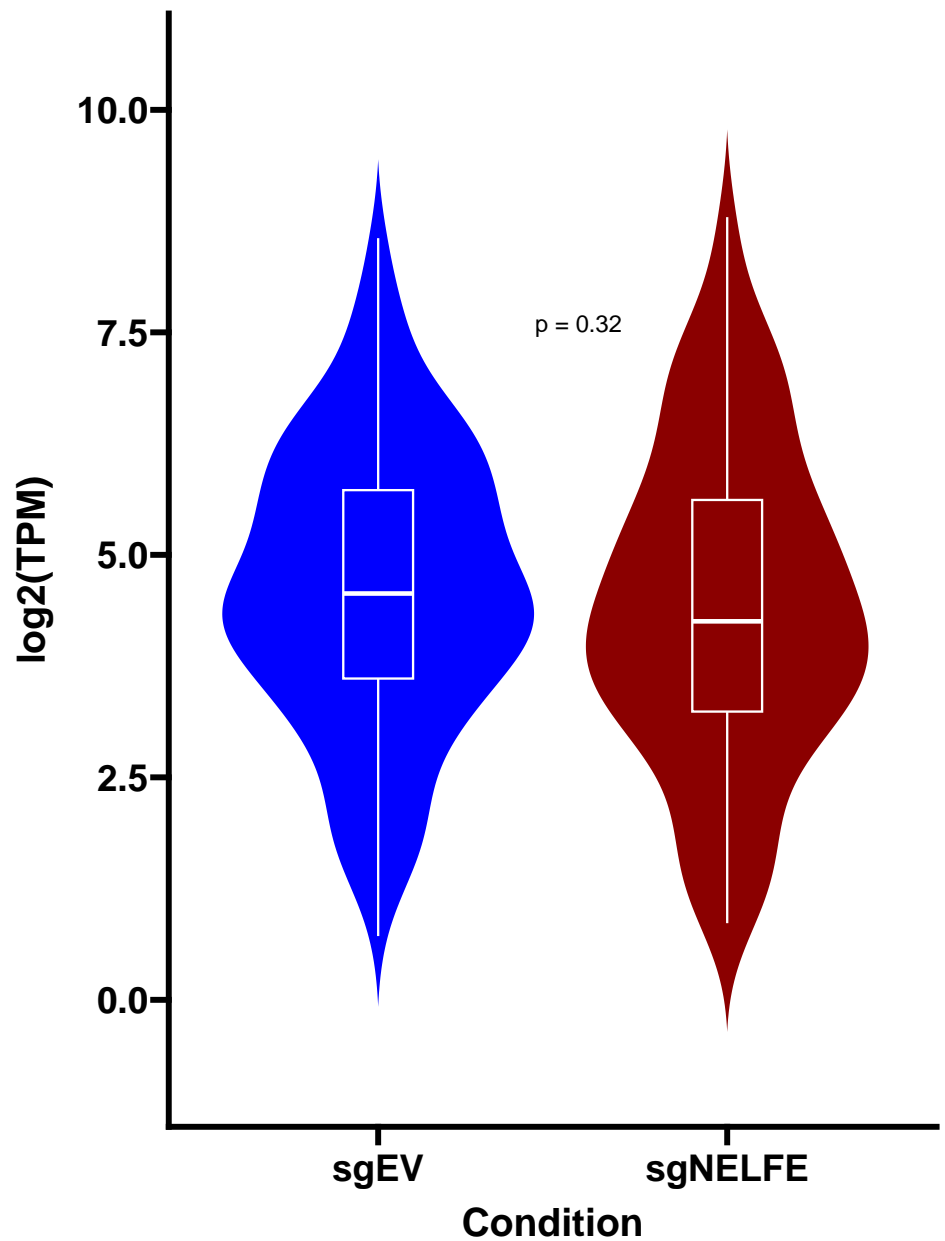
Description

This document is the analysis of RNA-seq experiment on HEP3B sgNELFE Knock-out (KO) and sgEV (EV) between group I and group II genes identified by common regions based on ATAC-seq, H3K-seq, and GRO-seq analyses.

The assumption for this analysis is that the common regions that are affected by NELFE KO will have less RNA accessibility, thereby make the RNA expression lower too.

[1] TRUE

RNAseq Group I up-regulated Genes, n=168



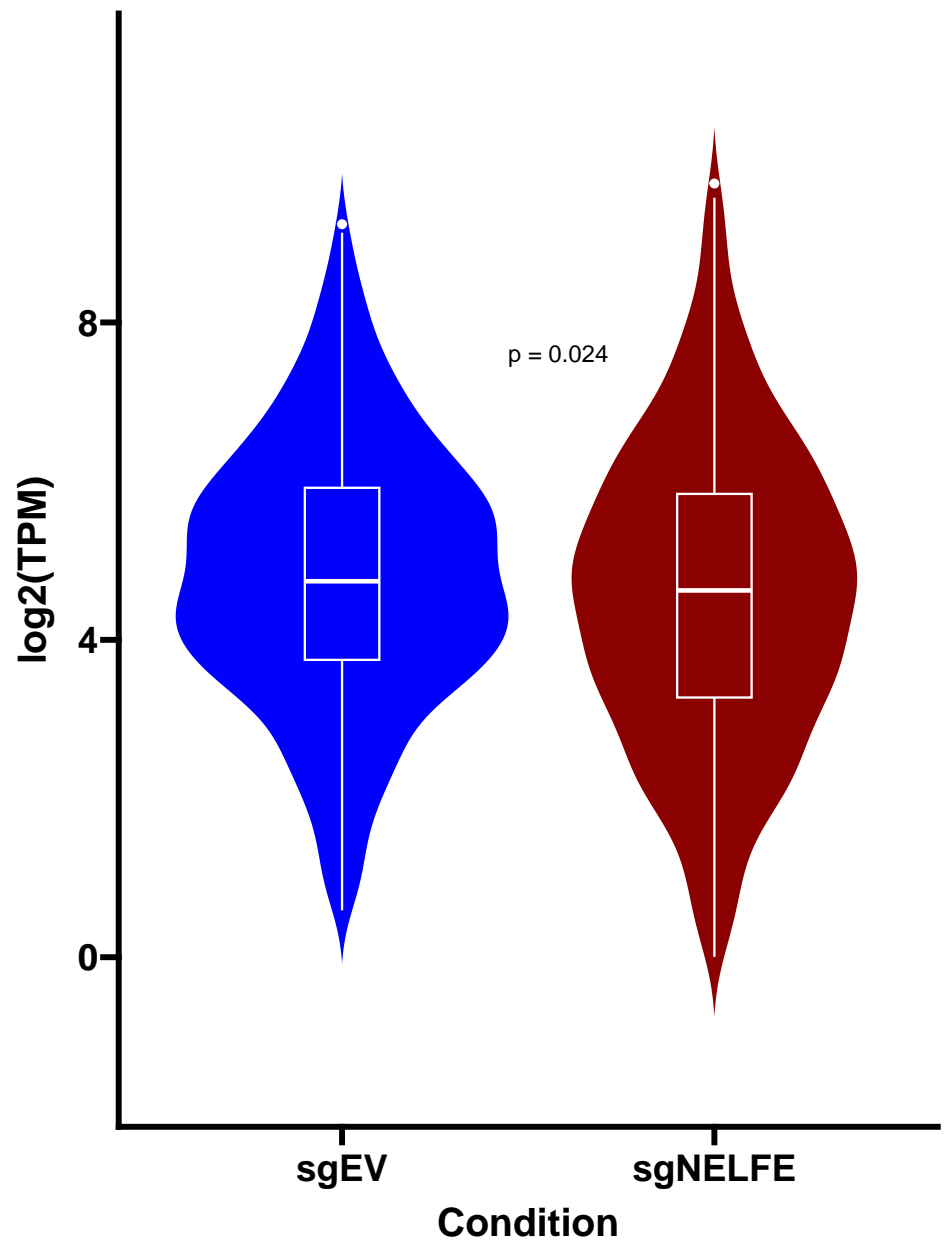
Group I genes Up-regulated-1.pdf

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## ('stat_ydensity()').

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## ('stat_boxplot()').

## Warning: Removed 19 rows containing non-finite outside the scale range
## ('stat_compare_means()').
```

RNAseq Group II up-regulated Genes, n=472



Group II genes Up-regulated-1.pdf