

EXPviz App

For genetic expression data visualization

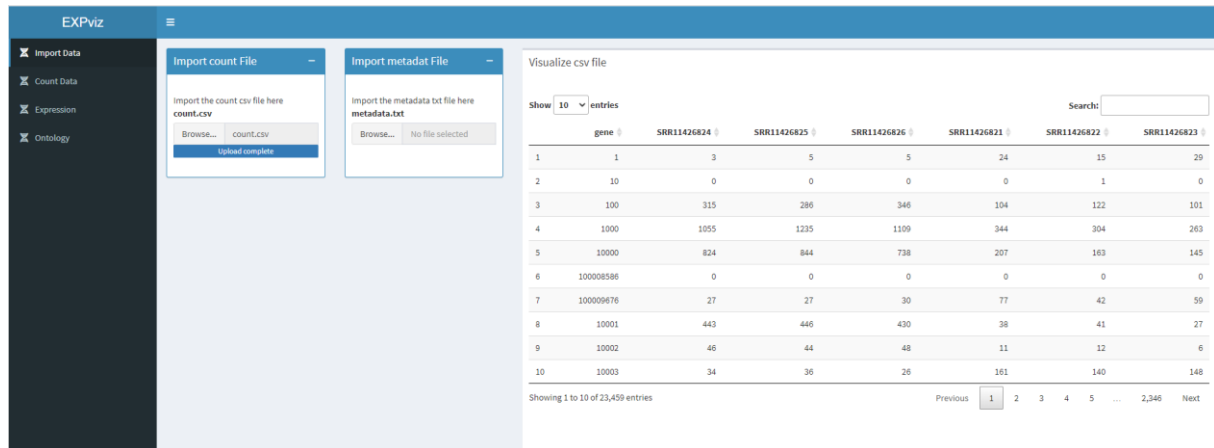


Figure 1: EXPviz app interface. The user is required to import a csv file for gene counts and a text file containing the metadata

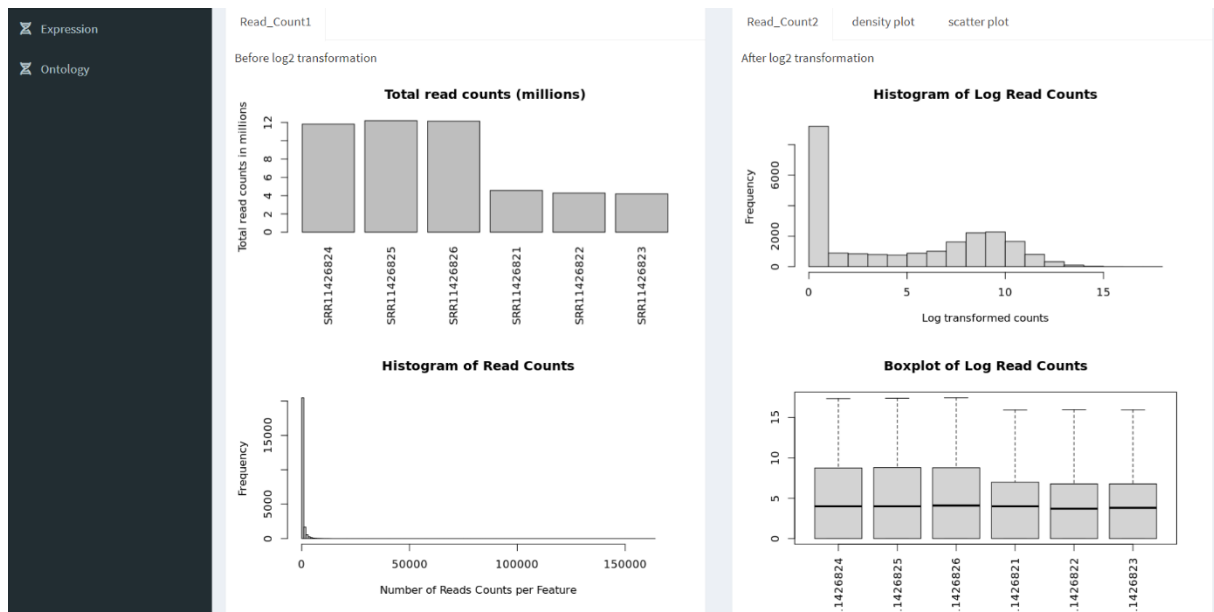


Figure 2: Plots showing the gene count per sample before and after log2 transformation (for quality control purposes)

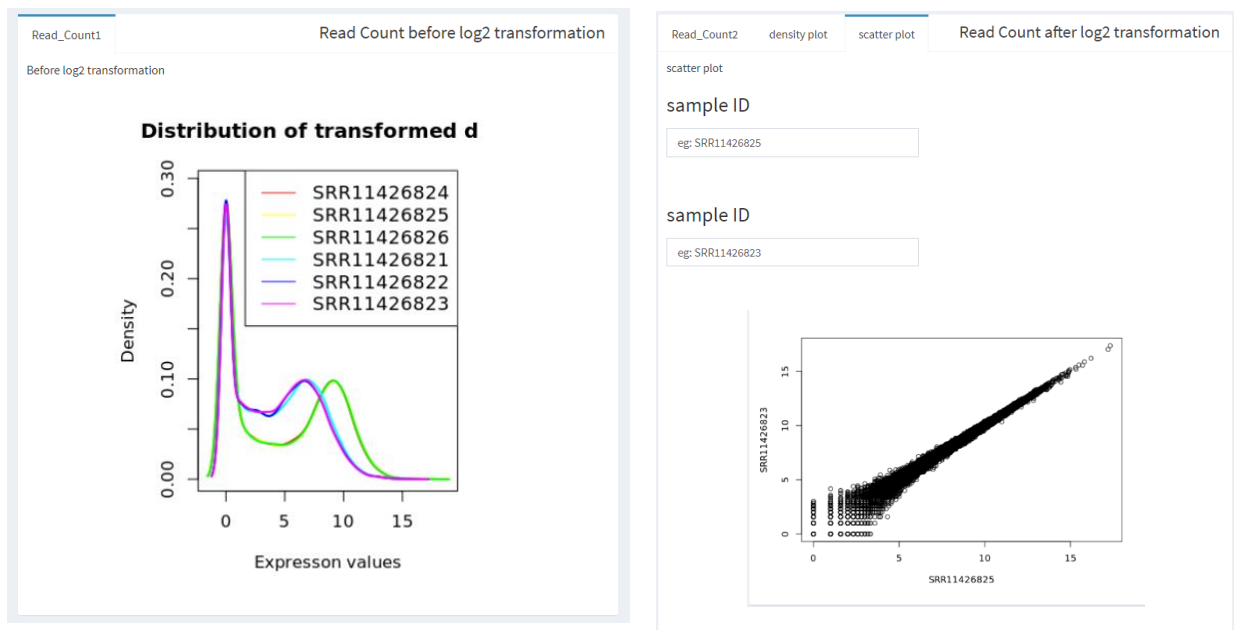


Figure 3: Density plot and scatter plot of gene expression before and after log2 transformation. The user defines the p-value and the LogFC value to be used to identify the DEGs.

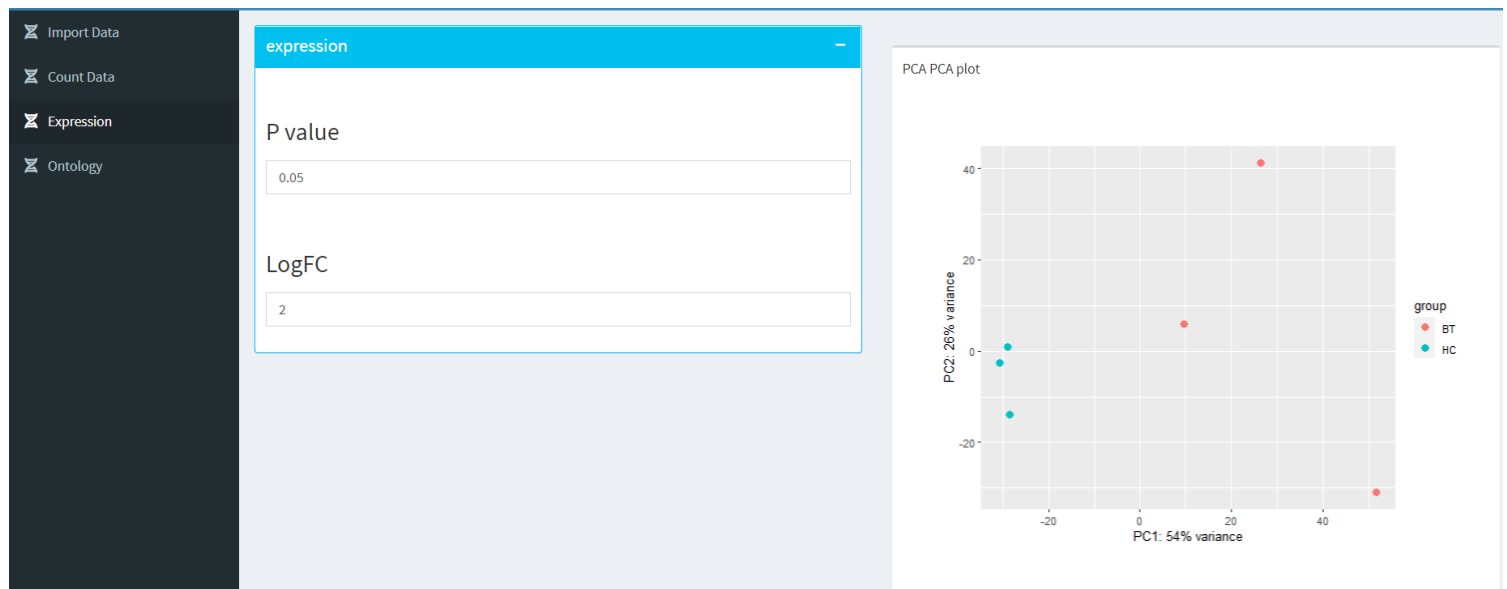


Figure 4: Principal Component Analysis displaying 2 groups. The p-value and the LogFC are set to default and can be changed by the user

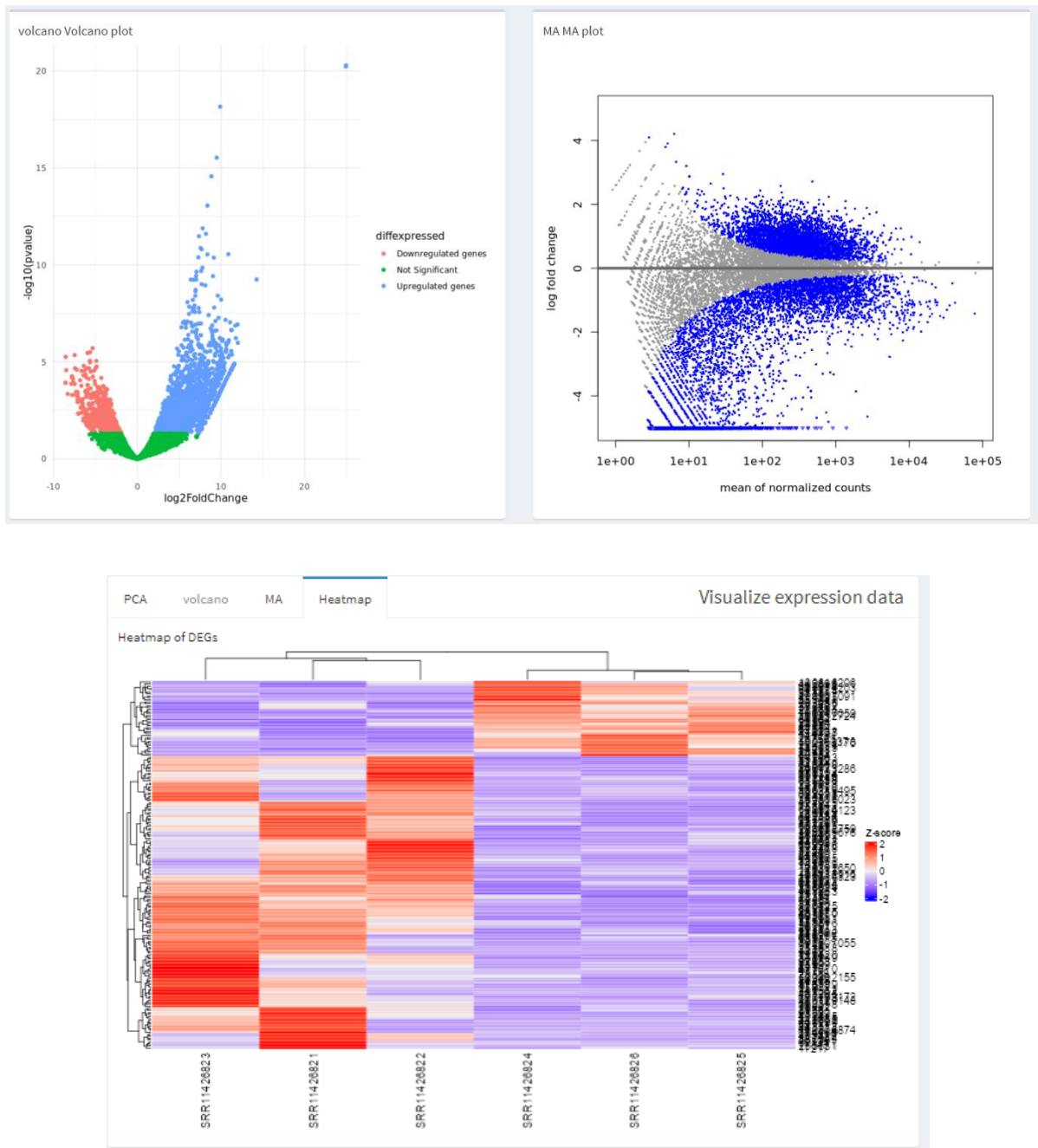


Figure 5: Volcano plot, MA plot and Heatmap of differentially expressed genes. The non-significant genes, the upregulated, and the downregulated gene are marked in different colors in the volcano plot.

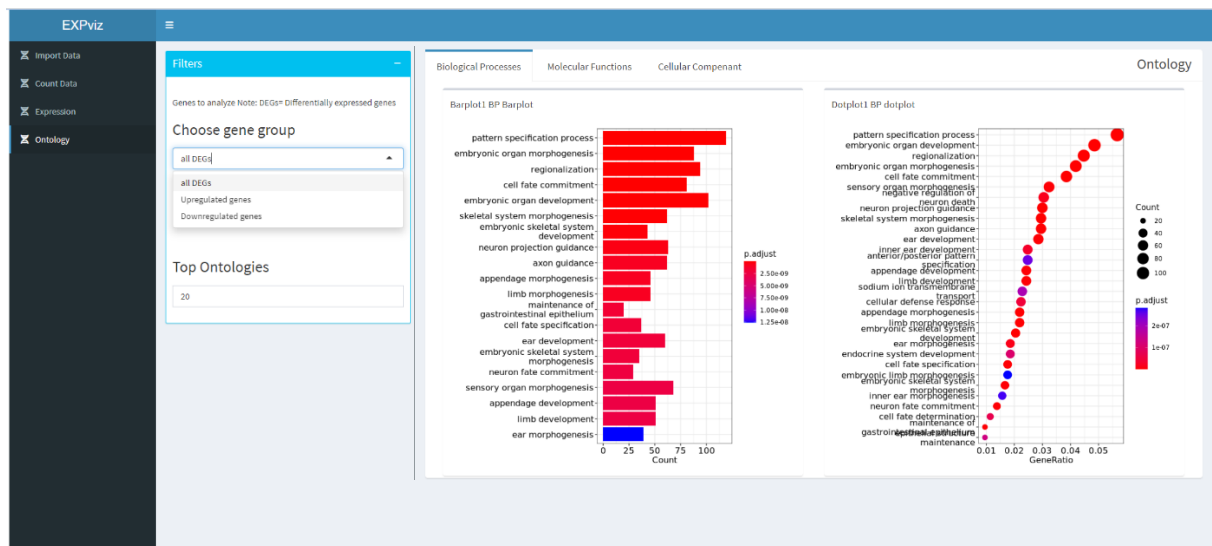


Figure 6: Gene Ontology represented by bar- and dotplots. The user has the option to choose the gene group as well as how many enriched terms to display. The adjusted p-value < 0.05 is set as default to identify significant ontologies and could be customized

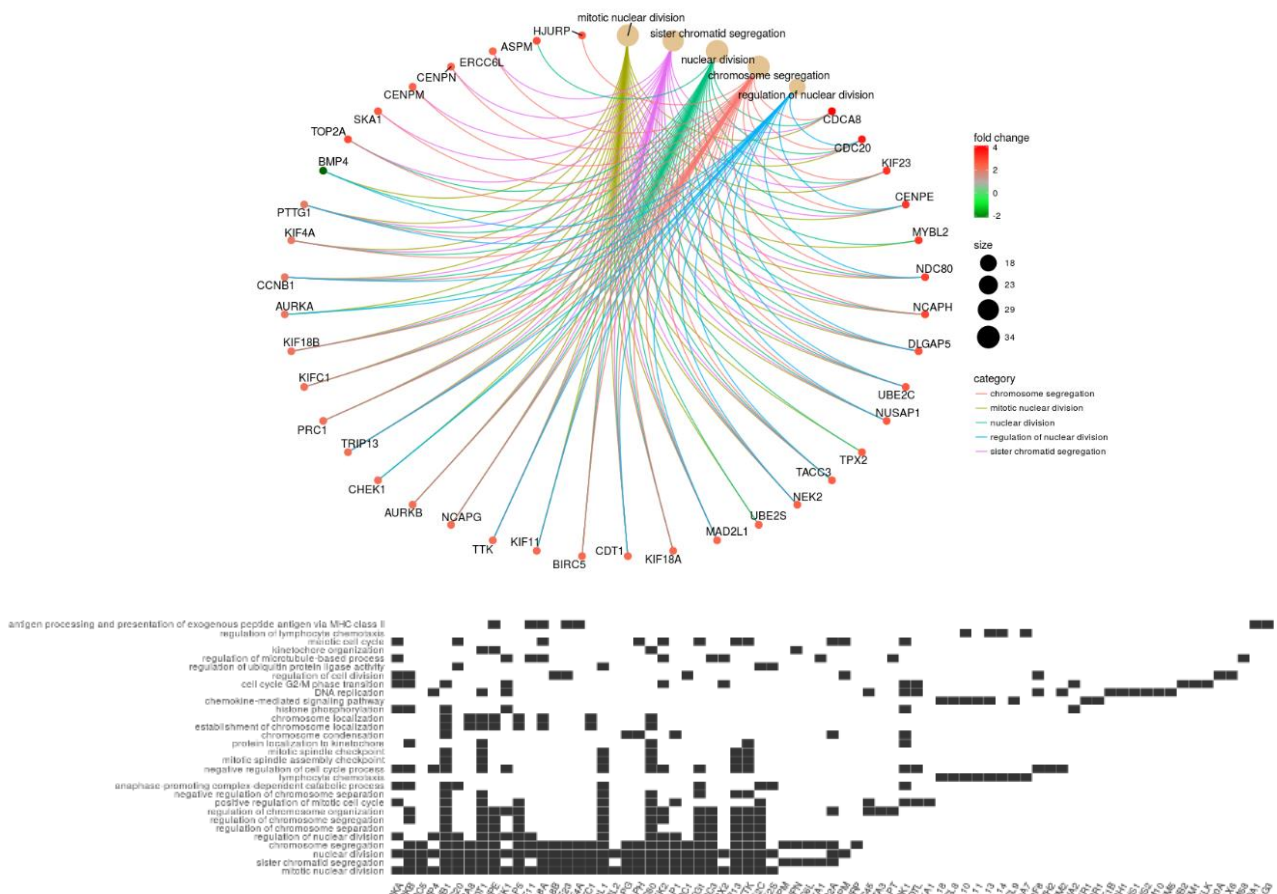


Figure 7: Gene Concept Network: Cnetplot and Heatplot displaying the relationship between genes and ontologies

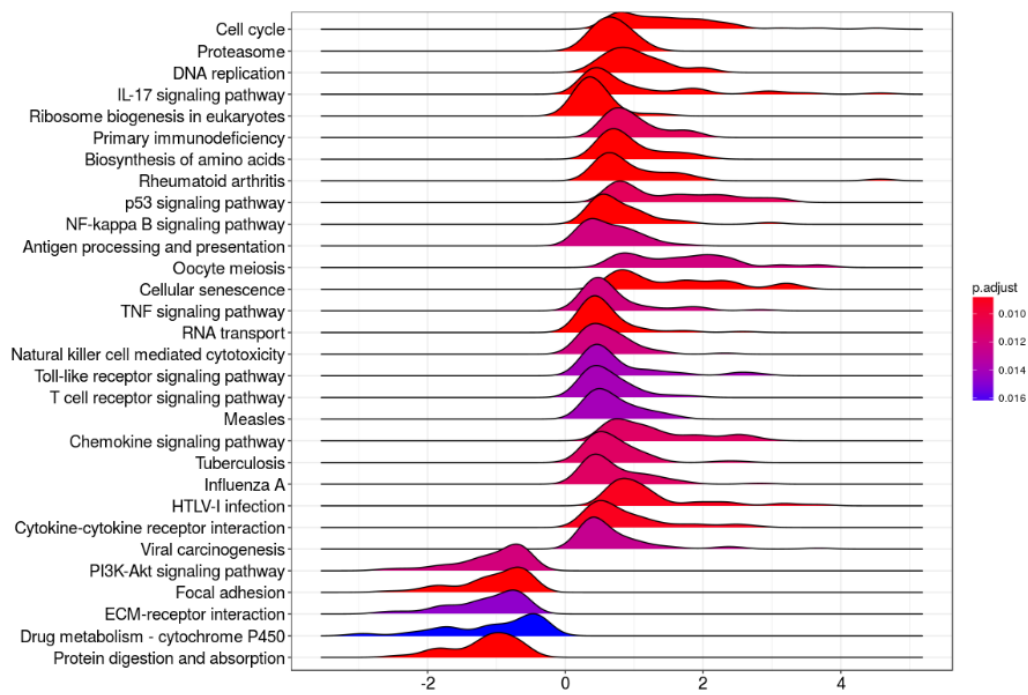


Figure 8: Ridgeline plot for expression distribution of GSEA result

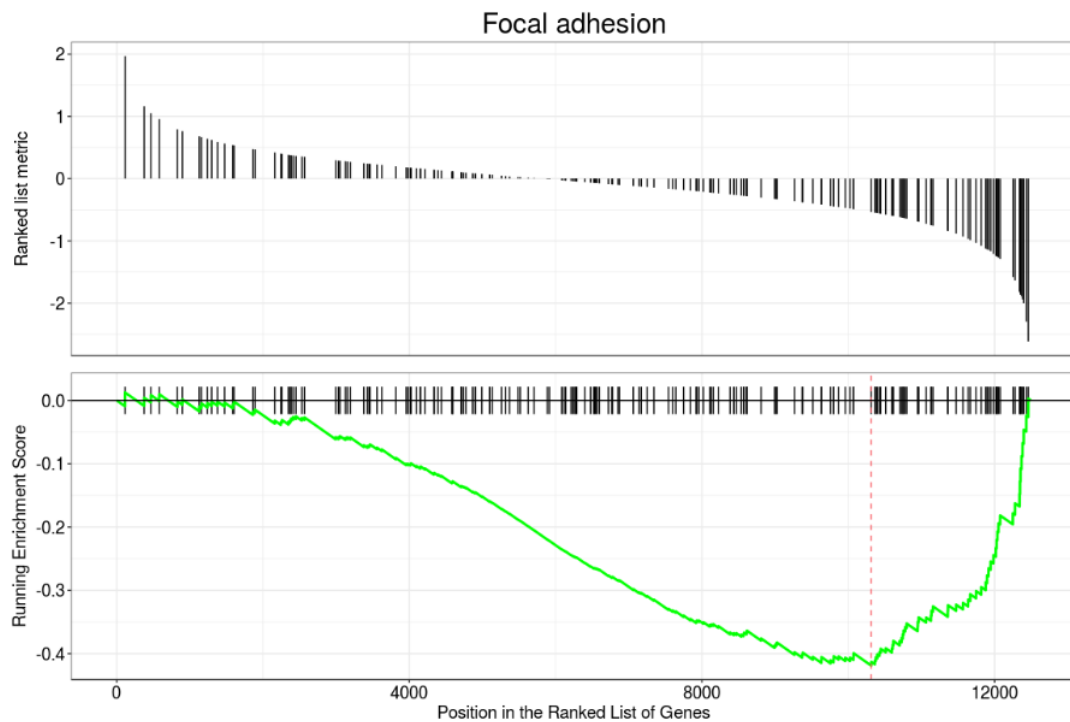


Figure 9: Running score and preranked list of GSEA result