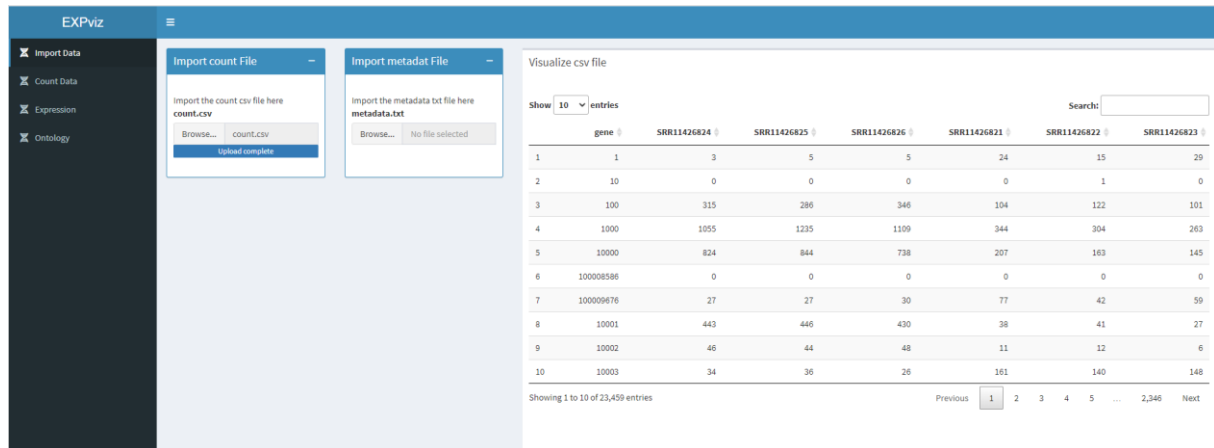
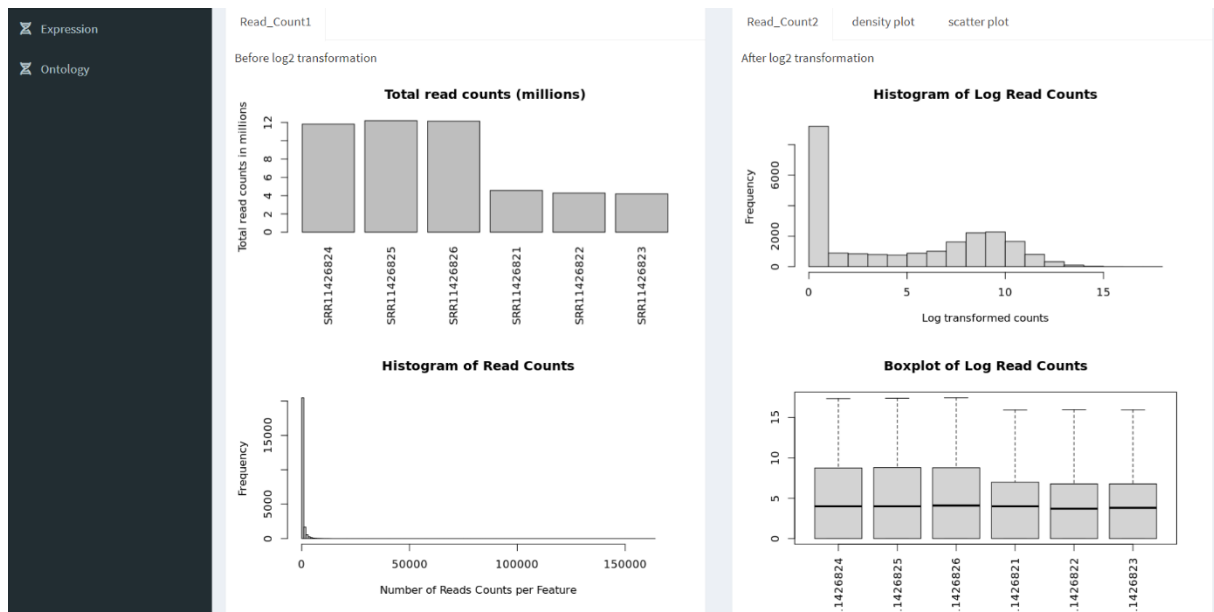


# EXPviz App

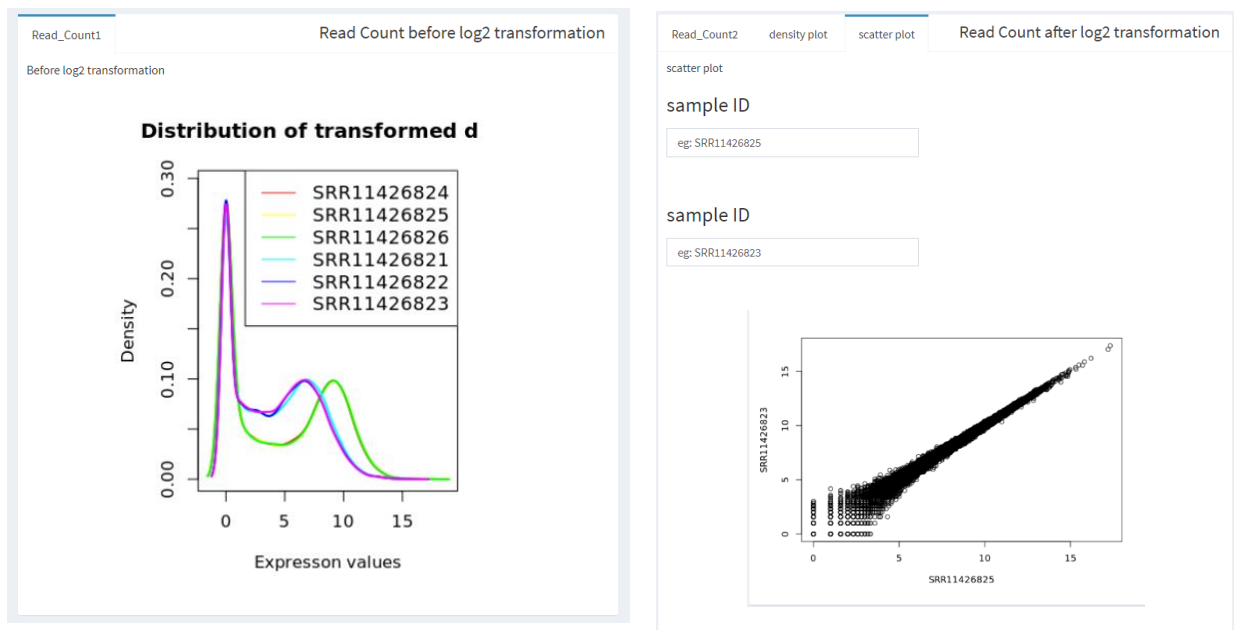
## For genetic expression data visualization



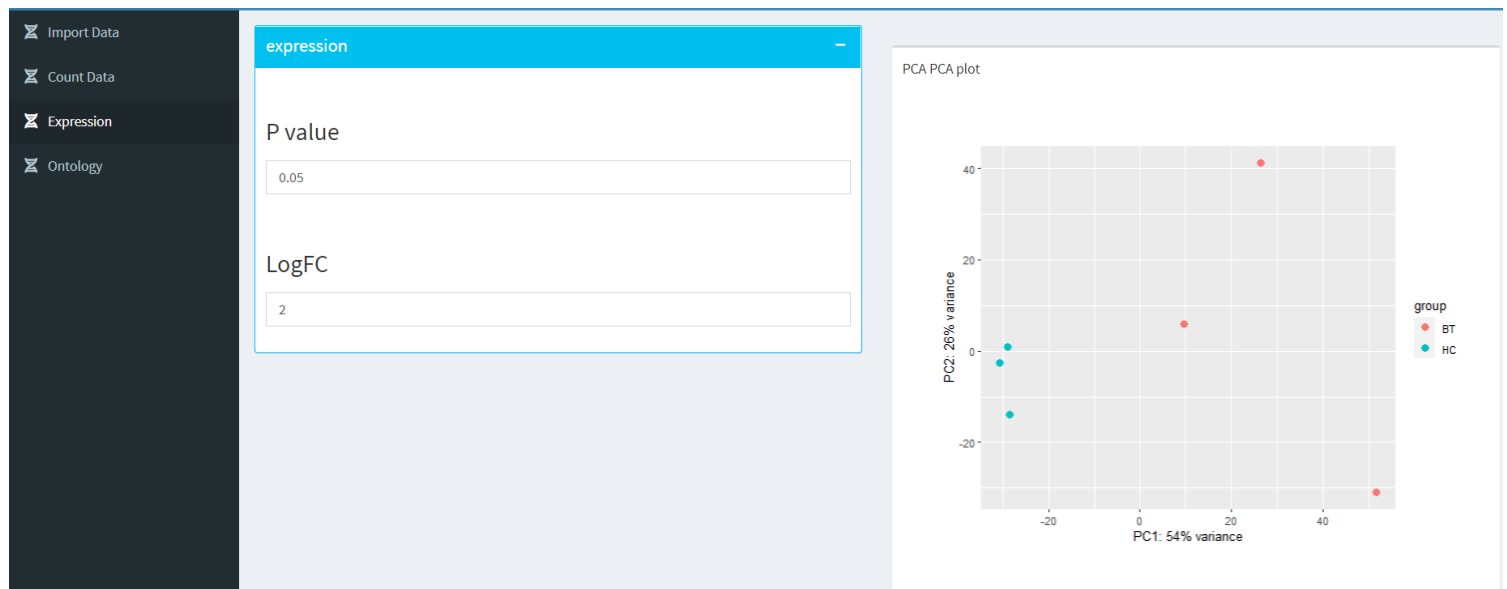
**Figure 1:** EXPviz app interface. The user is required to import a csv file for gene counts, and optionally a text file containing the metadata



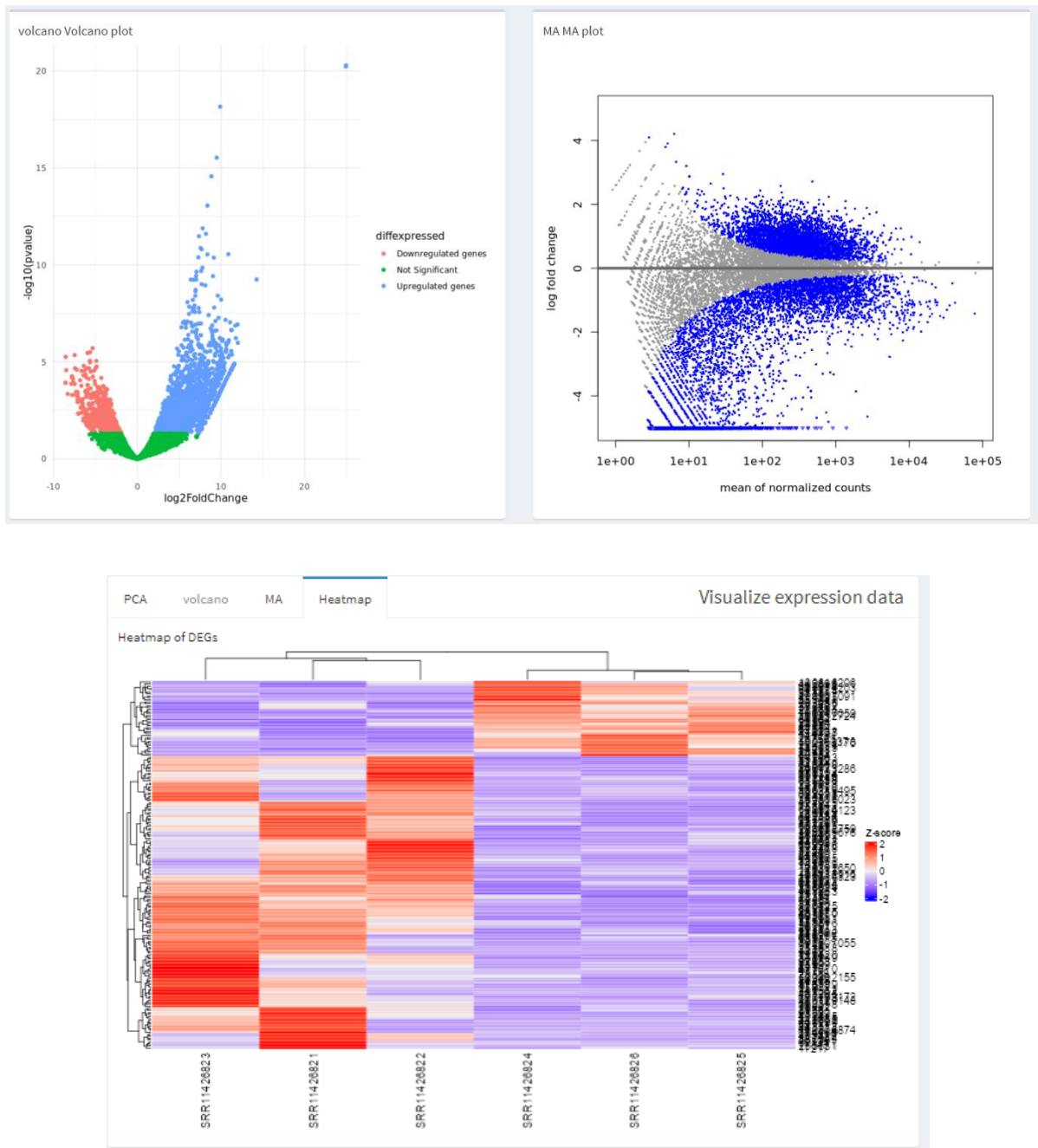
**Figure 2:** Plots showing the gene count per sample before and after log2 transformation (for quality control purposes)



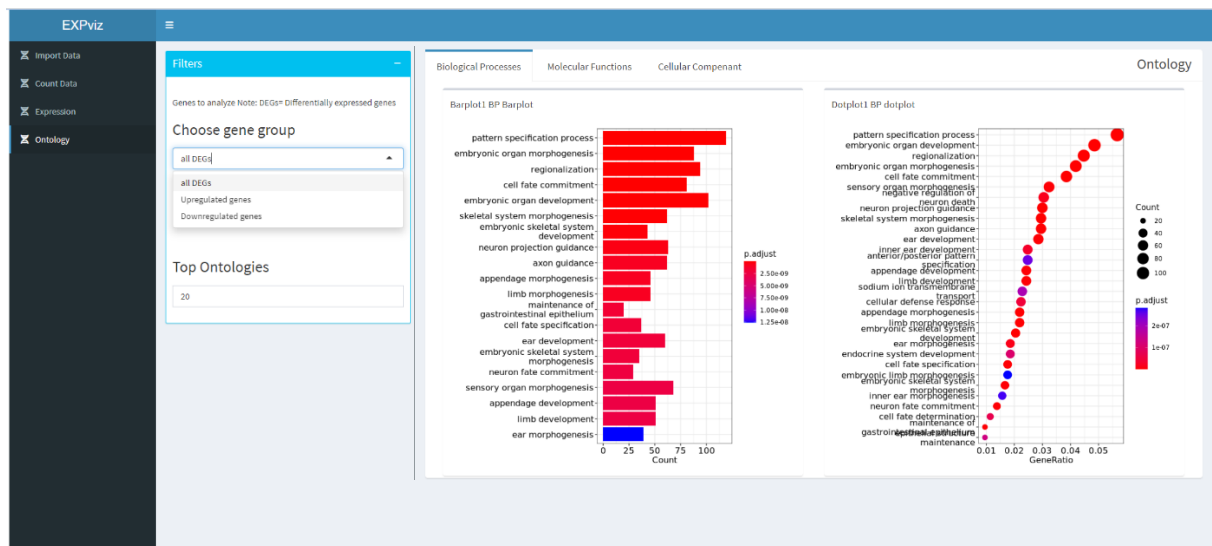
**Figure 3:** Density plot and scatter plot of gene expression before and after log2 transformation. The user defines the p-value and the LogFC value to be used to identify the DEGs.



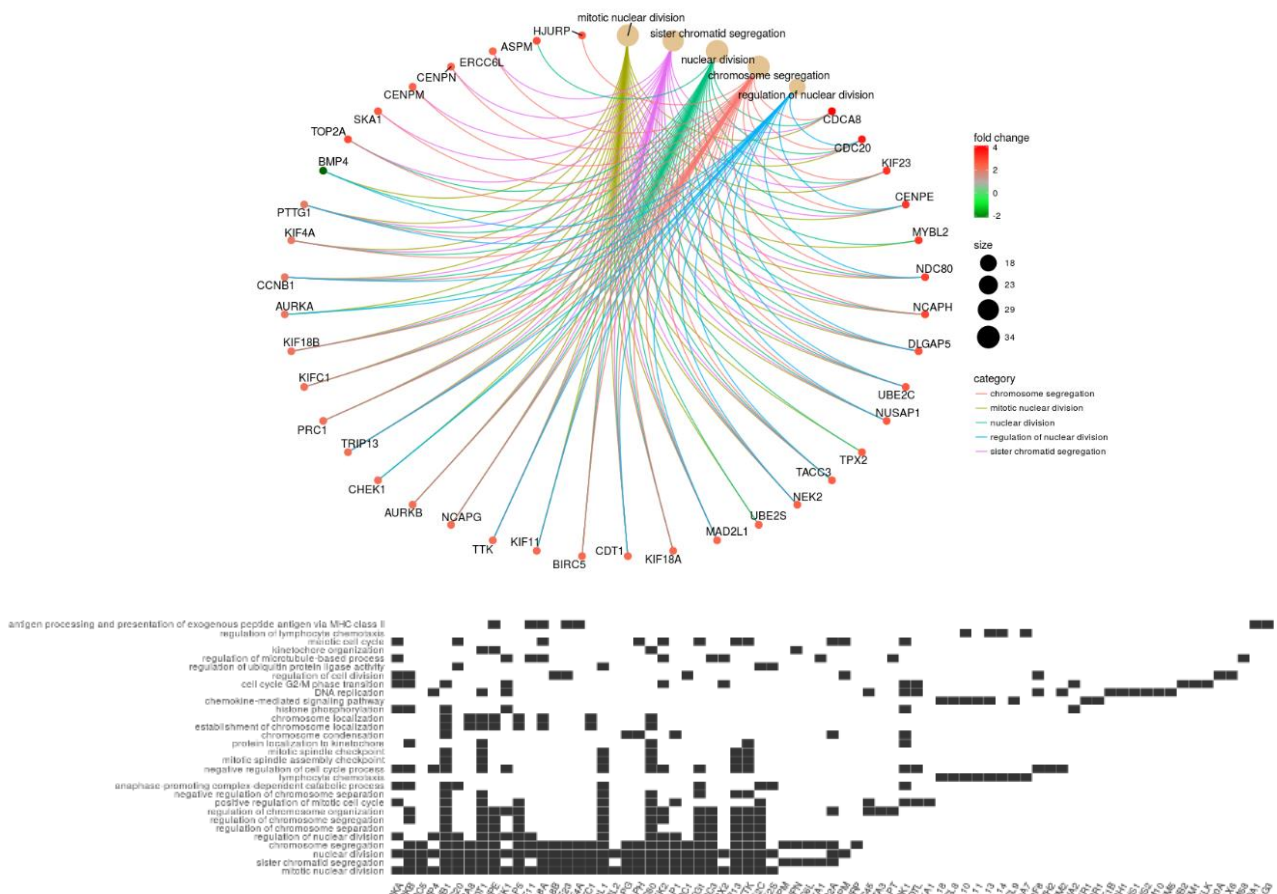
**Figure 4:** Principal Component Analysis displaying 2 groups. The p-value and the LogFC are set to default and can be changed by the user



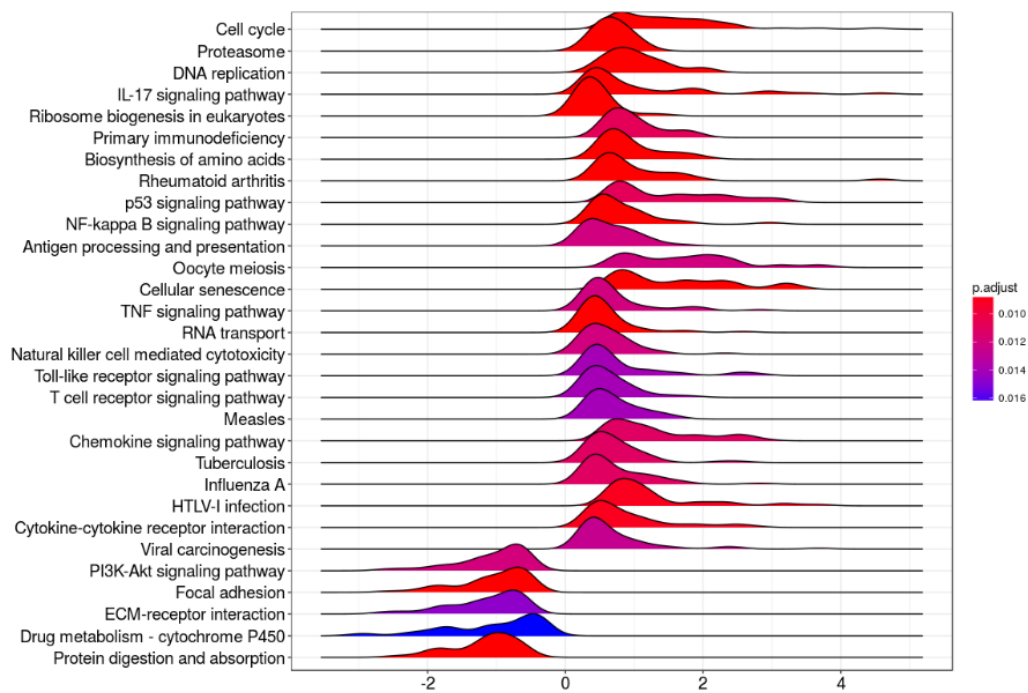
**Figure 5:** Volcano plot, MA plot and Heatmap of differentially expressed genes. The non-significant genes, the upregulated, and the downregulated gene are marked in different colors in the volcano plot.



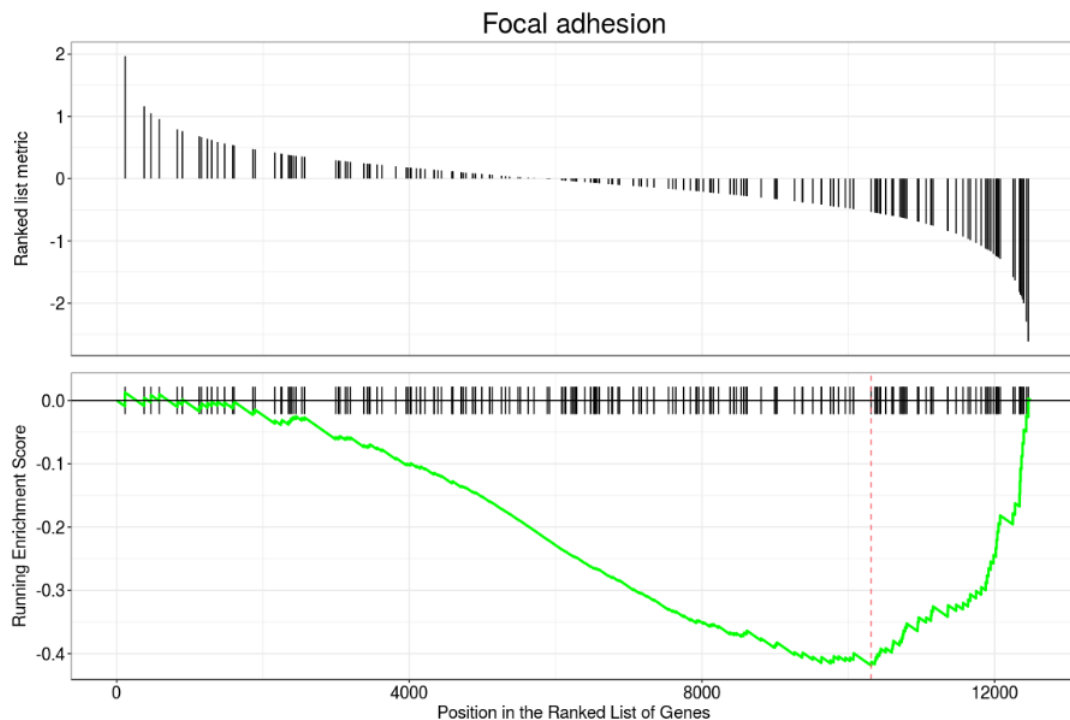
**Figure 6:** Gene Ontology represented by bar- and dotplots. The user has the option to choose the gene group as well as how many enriched terms to display. The adjusted p-value  $< 0.05$  is set as default to identify significant ontologies and could be customized



**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