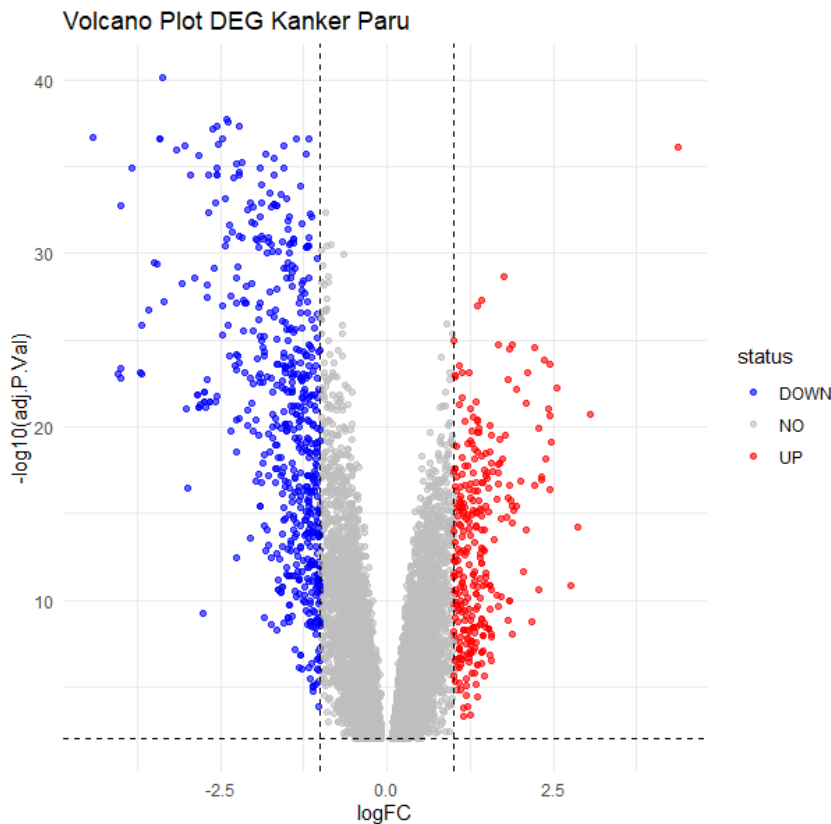GSE10072 Analysis

1. Introduction

   This analysis was done to identify DEGs between adenocarcinoma of the lung and normal lung tissue from a group of samples totalling in the number of 180. DEG identification was then followed by a number of other analyses to determine the degree of expressions and genetic profiles. These resulted in a number of data that can be interpreted for further biological and medical implications.
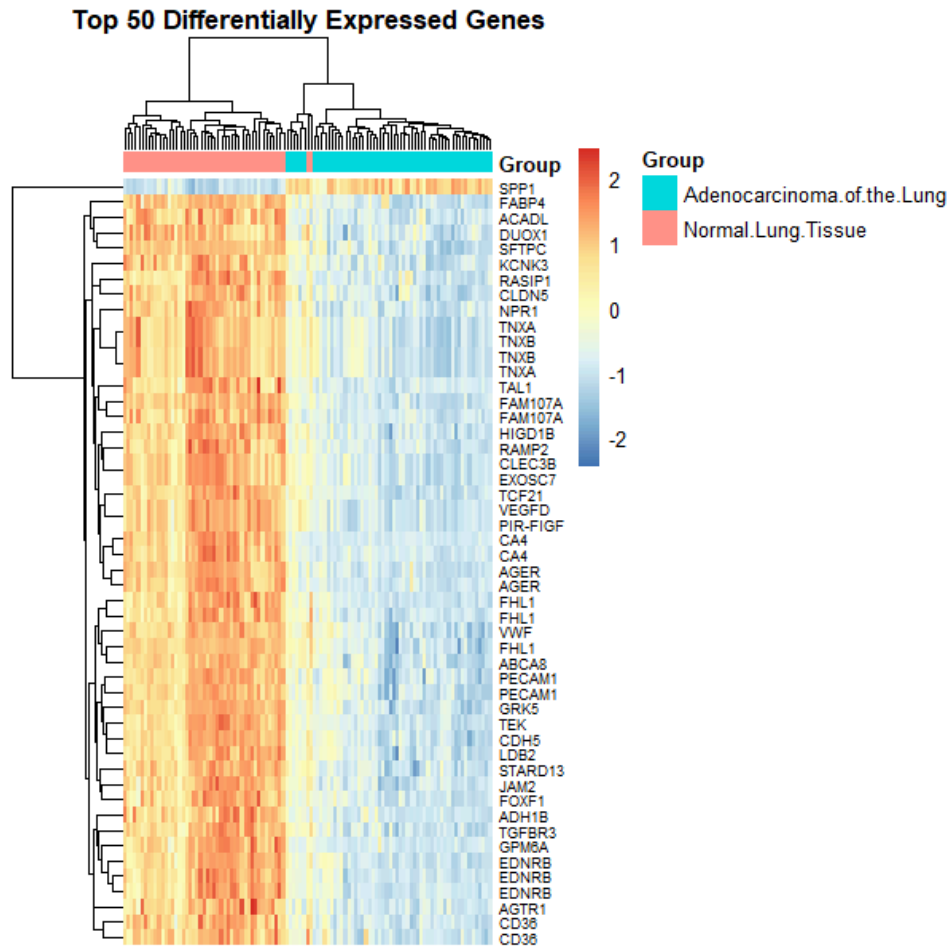
2. Method

   The dataset GSE10072 was processed and analysed using R, which script had been provided prior as guide. Using R, two groups were made to be compared. They were "Adenocarcinoma of The Lung" and "Normal Lung Tissue". DEGs were described as having p-value of less than 0.01, log2FC value of less than -1 for downregulated genes, and greater than 1 for upregulated genes. Volcano plot of the DEGs and heatmap of top 50 DEGs were also made using R guided by the script that had been provided. Additionally, GO term and KEGG pathway analyses of the top 50 DEGs were also performed using ShinyGO.
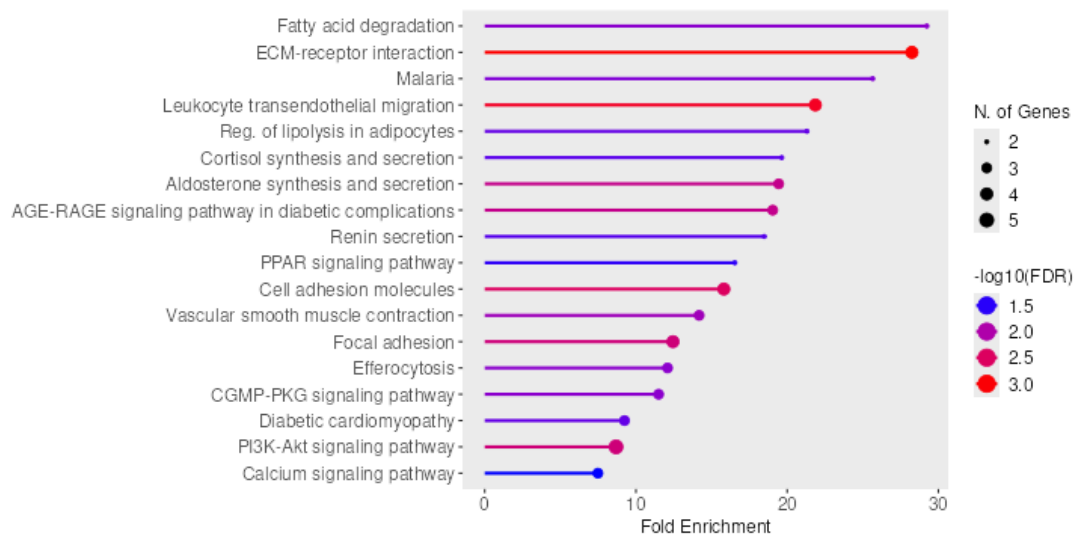
3. Results

   Volcano plot of the identified DEGs is as follows.

   There were 920 differentially expressed genes, which consist of 336 upregulated and 584 downregulated genes. Of the 920 DEGs, the top 50 of those genes were selected and represented in the form of a heatmap provided below.
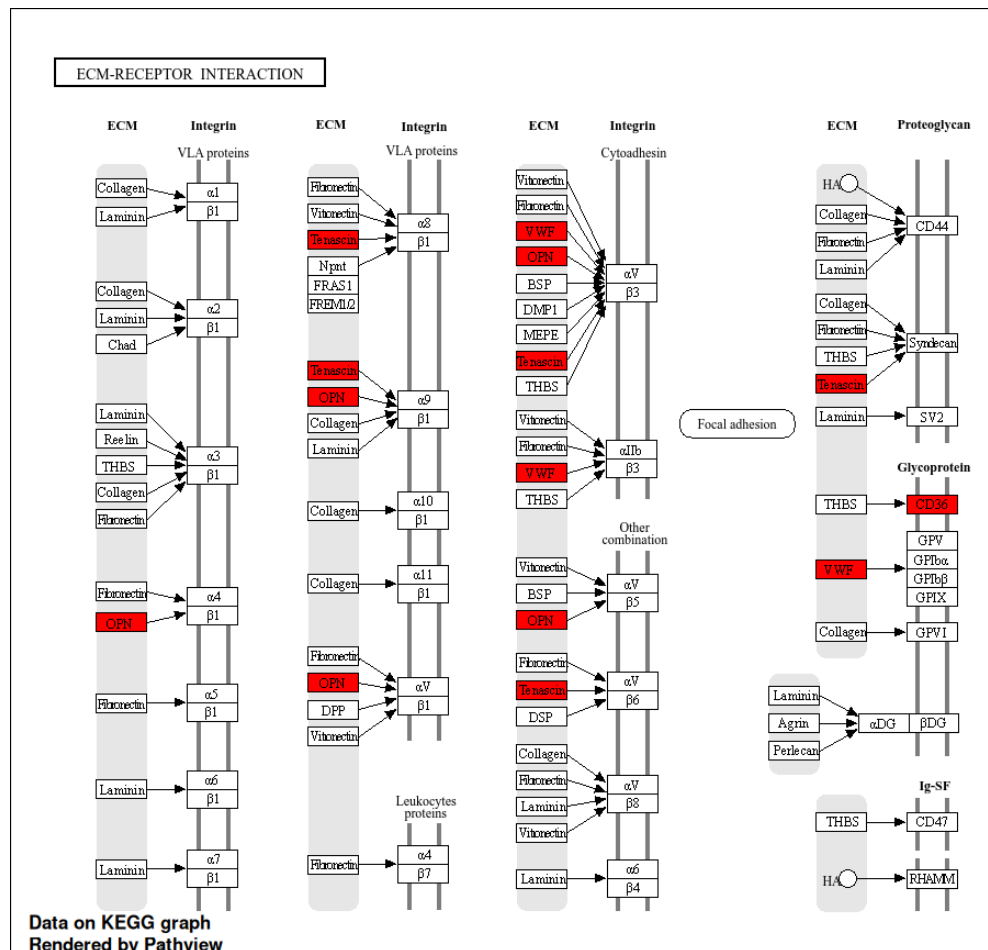
Top 50 Differentially Expressed Genes

Those genes were then processed through ShinyGO to obtain their GO terms and KEGG pathway results. Fatty acid degradation and ECM receptor interaction were among the top identified. There were two and four genes involved respectively.

I want to highlight the KEGG pathway of ECM receptor interaction, which involves four different genes and is one of the most significant pathways. This is because there's a paper

published that also discusses the promotion of a transcription factor which is caused by the stiffening of ECM.[1] That resulted in the proliferation of the cancer cells. This finding and the results of this enrichment analysis may or may not have something in common with one another but it is worth to dive deeper into.

4. Conclusion

DEGs between adenocarcinoma of the lung and normal lung tissue have been identified and so have their GO terms and KEGG pathway results. The analyses sorted top 50 DEGs and presented them in heatmap, GO terms, and one of the most significant KEGG pathways identified. It showed that there are genes involved in ECM receptor interaction. It may or may not have a link to a study conducted in 2025 that found cancer cell proliferation is driven by the stiffening of the ECM of the cancerous cells.

[1] Ishihara, S., Enomoto, A., Sakai, A., Iida, T., Tange, S., Kioka, N., Nukuda, A., Nagasato, A. I., Yasuda, M., Tokino, T., & Haga, H. (2025). Stiff extracellular matrix activates the transcription factor ATF5 to promote the proliferation of cancer cells. iScience, 28(3), 112057. https://doi.org/10.1016/j.isci.2025.112057