Lung Adenocarcinoma Analysis

This study conducted to analyze differential gene expression between lung adenocarcinoma tissues and normal lung tissues in order to identify potential biomarker candidates. The dataset used in this study was GSE10072, obtained from the Affymetrix Human Genome U133A microarray platform (GPL96).

In this study, the analysis was performed using R software. The initial procedure in R involved installing all required packages until the libraries could be successfully loaded without errors. Subsequently, data were retrieved and processed from the GEO database. The next step involved data visualization, resulting in boxplots, density plots, UMAP, volcano plots, and heatmaps.

R-based analysis identified differentially expressed genes, including upregulated and downregulated genes, as shown in **Figure 1**. Among them, SPP1, NME1, KDELR2, MIF, and LDHA genes were upregulated, whereas FAM107A, CD36, GRK5, CA4, and EDNRB genes were downregulated.
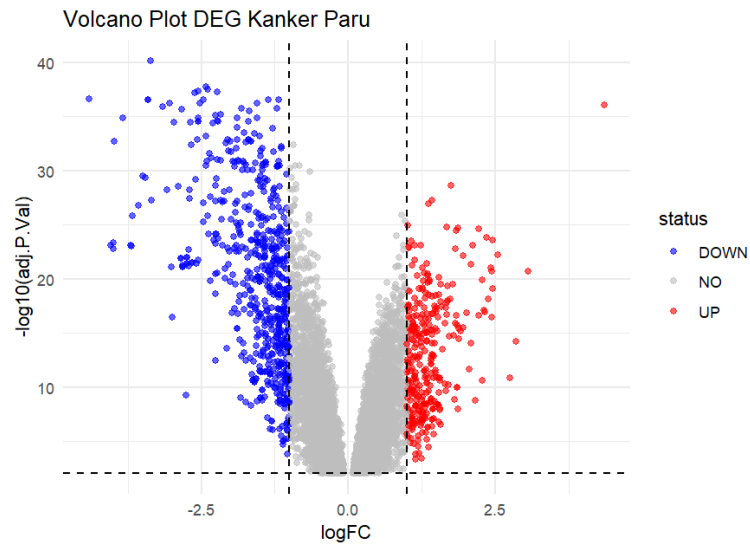

Figure 1. Volcano plot of differentially expressed genes in lung adenocarcinoma

Heatmap visualization was performed to explore gene expression patterns across samples based on the most significant genes or differentially expressed genes (DEGs). The heatmap is presented in **Figure 2**.
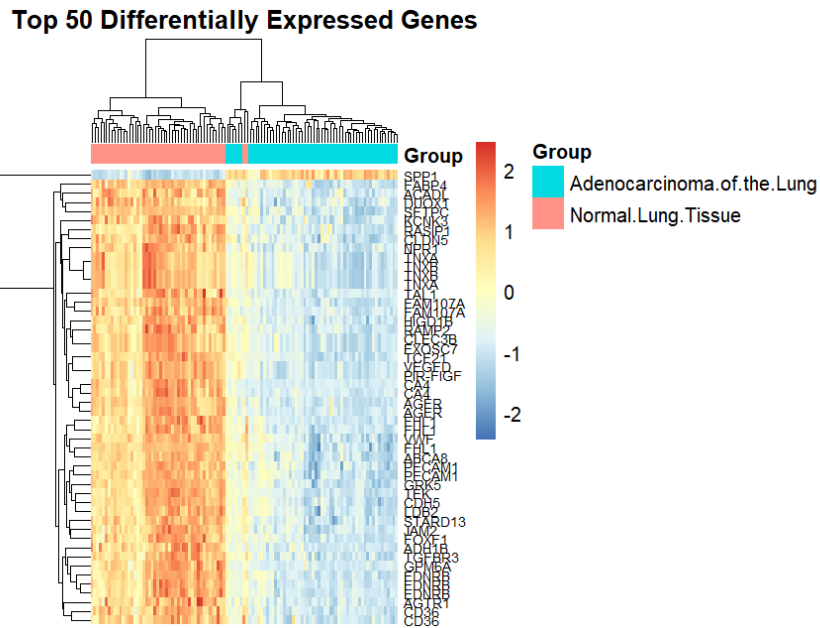
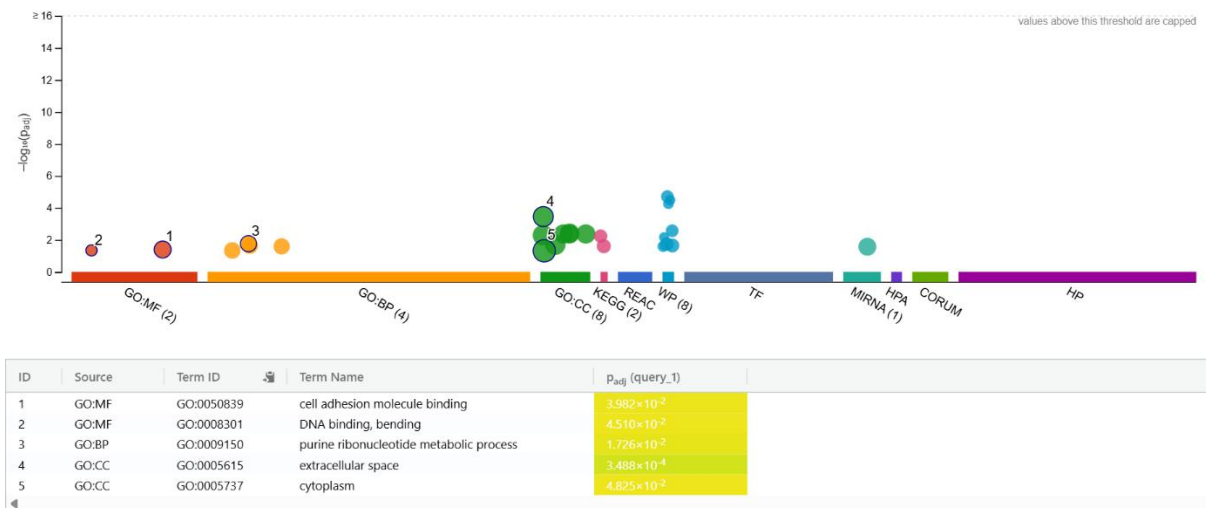**Figure 2.** Top 50 differentially expressed genes by heatmap visualization

Gene Ontology (GO) enrichment analysis was conducted on the upregulated and downregulated genes. The results indicated that lung adenocarcinoma was associated with molecular functions, biological processes, and cell cycle-related processes. GO visualization is shown in **Figure 3** and **Figure 4**.

Figure 3. Upregulated gene ontology

ID	Source	Term ID	Term Name	p_{adj} (query_1)
1	GO:MF	GO:0033218	amide binding	4.186×10^{-2}
2	GO:BP	GO:0048518	positive regulation of biological process	3.672×10^{-4}
3	GO:BP	GO:0003018	vascular process in circulatory system	5.815×10^{-4}
4	GO:BP	GO:0032835	glomerulus development	1.573×10^{-3}
5	GO:BP	GO:0019934	cGMP-mediated signaling	1.143×10^{-2}
6	GO:BP	GO:0001568	blood vessel development	1.417×10^{-2}
7	GO:BP	GO:0035633	maintenance of blood-brain barrier	1.591×10^{-2}
8	GO:BP	GO:0035295	tube development	2.085×10^{-2}
9	GO:BP	GO:0003158	endothelium development	2.231×10^{-2}
10	GO:BP	GO:1900271	regulation of long-term synaptic potentiation	2.630×10^{-2}
11	GO:BP	GO:0061028	establishment of endothelial barrier	3.185×10^{-2}
12	GO:BP	GO:0001525	angiogenesis	3.262×10^{-2}
13	GO:BP	GO:0006954	inflammatory response	4.089×10^{-2}
14	GO:CC	GO:0031091	platelet alpha granule	4.318×10^{-4}
15	GO:CC	GO:0071944	cell periphery	1.666×10^{-3}
16	GO:CC	GO:0009986	cell surface	5.078×10^{-3}
17	GO:CC	GO:0045121	membrane raft	4.156×10^{-2}

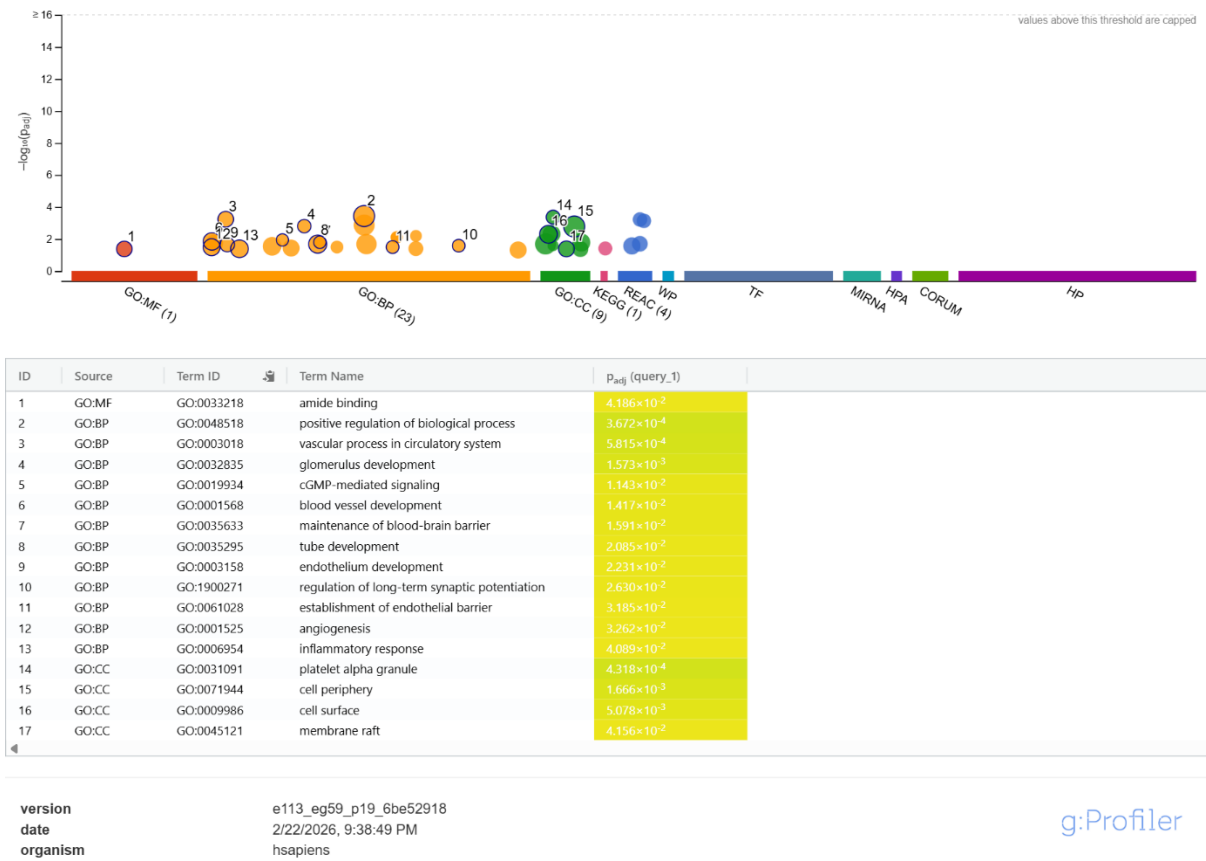|	
version	e113_eg59_p19_6be52918
date	2/22/2026, 9:38:49 PM
organism	hsapiens

g:Profiler

Figure 4. Downregulated gene ontology

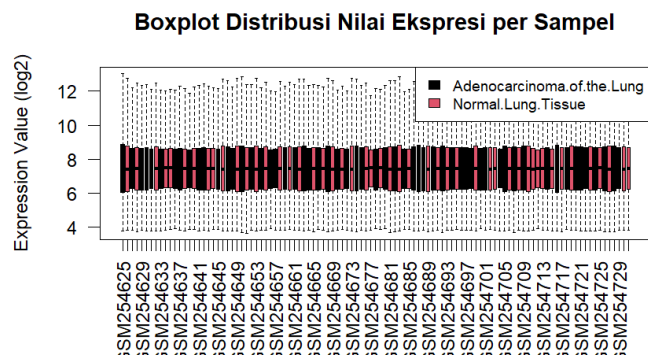Furthermore, boxplot, density plot, and UMAP visualizations were generated, as shown in **Figures 5**, **Figure 6**, and **Figure 7**.

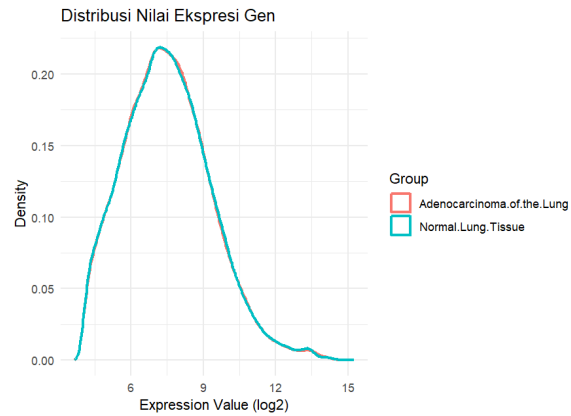**Figure 5**. Boxplot visualization

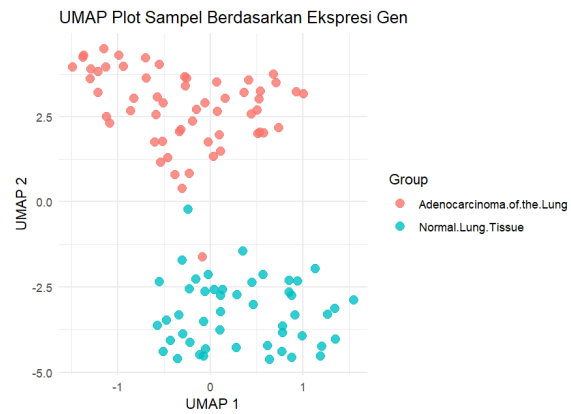**Figure 6**. Density plot visualization

Figure 7. UMAP Plot visualization

Analysis of the GSE10072 dataset revealed that the identified DEGs were significantly associated with molecular functions, biological processes, and cell cycle–related pathways.