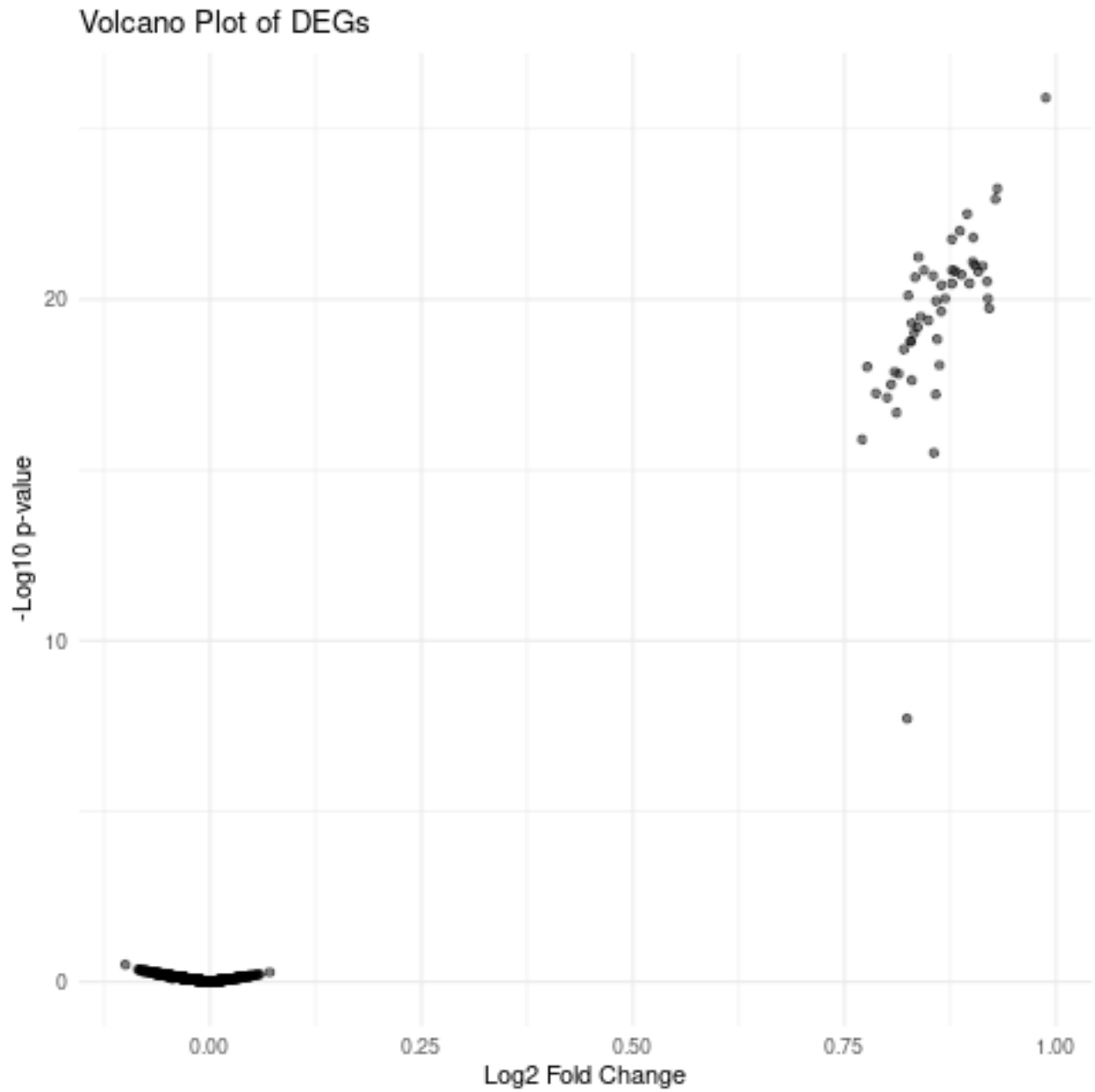


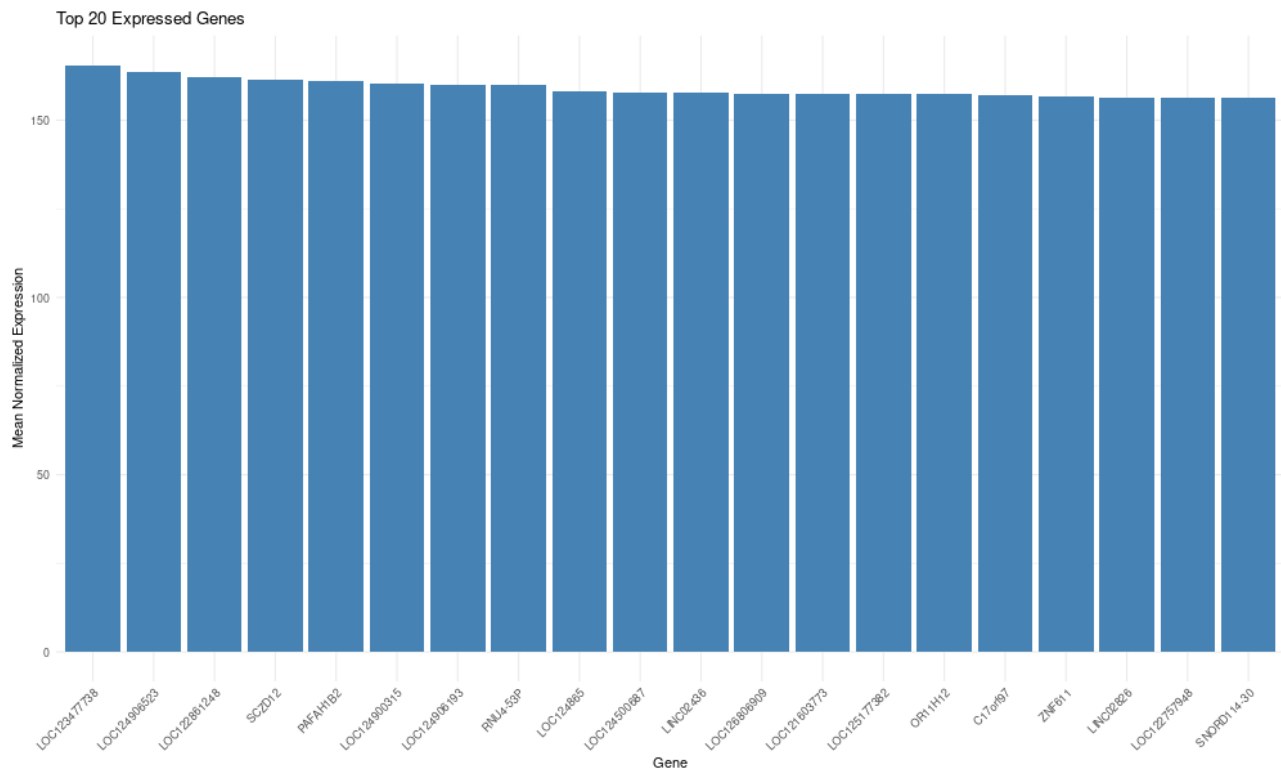
**Drug Resistance Analysis**  
**Comprehensive Report**

## Volcano Plot of Differentially Expressed Genes



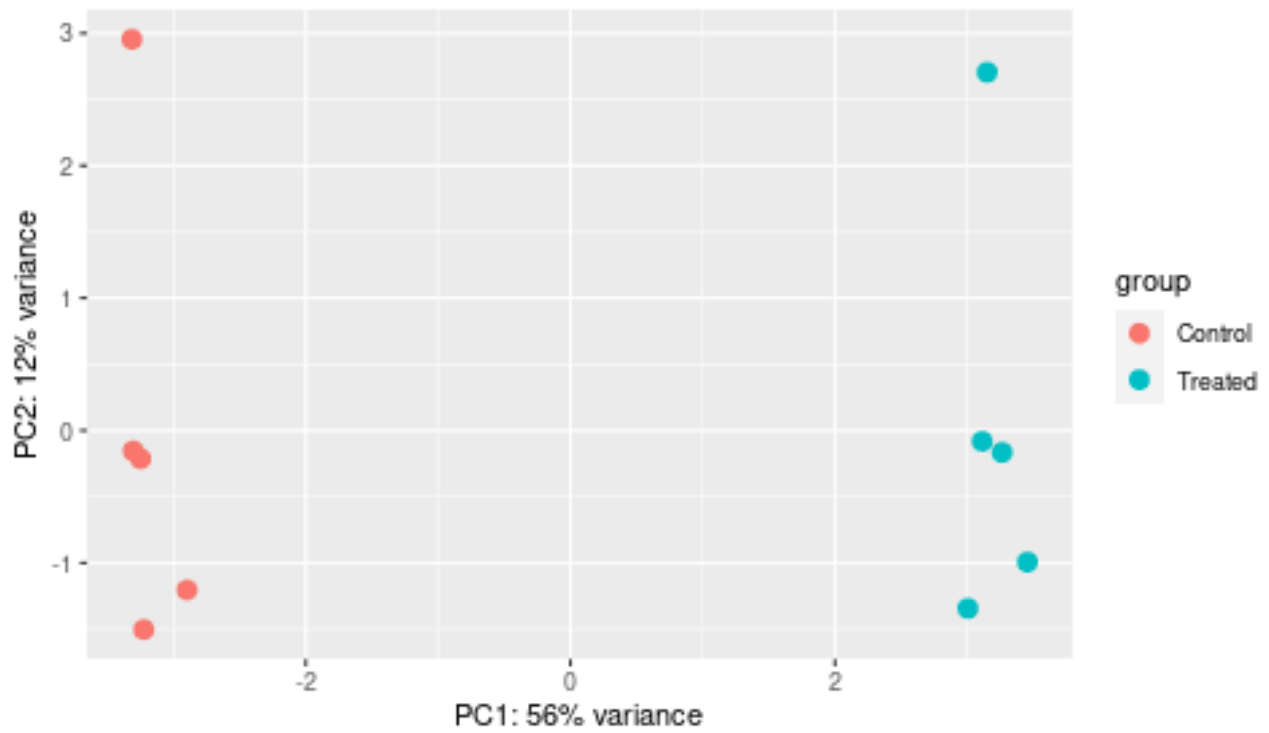
This volcano plot displays the relationship between log2 fold change and statistical significance ( $-\log_{10}$  adjusted p-value) of all genes analyzed. Genes in the upper right corner are highly upregulated in treated cells, indicating possible drug-resistance markers.

## Top 20 Expressed Genes



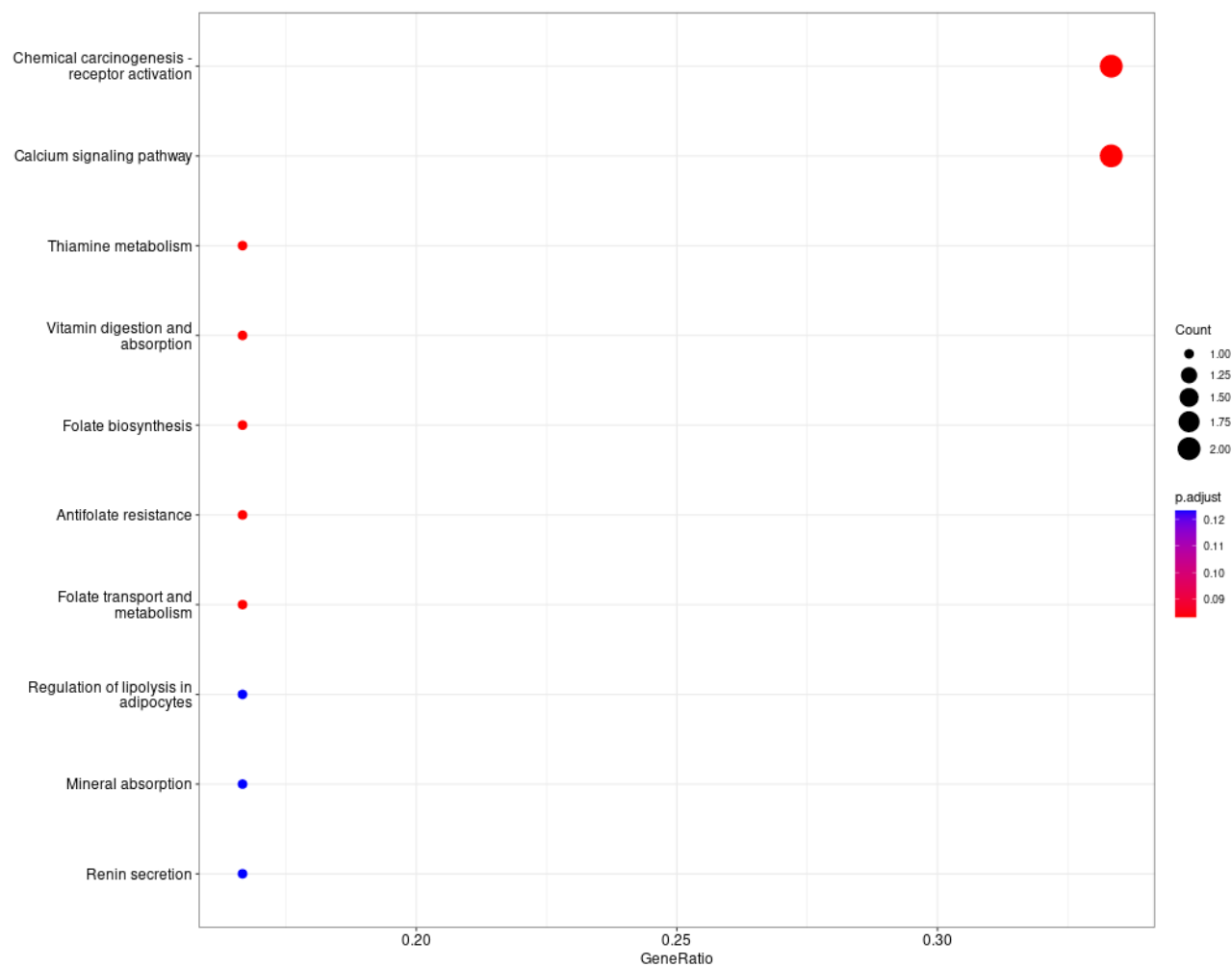
Bar plot showing the top 20 most expressed genes across all samples. These genes represent strong baseline expression and may include housekeeping genes or treatment-influenced transcripts.

## Principal Component Analysis (PCA)



The PCA plot illustrates variance across samples. Control and treated samples are distinctly clustered, indicating that treatment induced major changes in gene expression.

# KEGG Pathway Enrichment Analysis



Top 10 enriched KEGG pathways among the significantly upregulated genes. Pathways such as chemical carcinogenesis and antifolate resistance suggest molecular mechanisms associated with drug resistance.

## Summary of Analysis

This analysis explores gene expression changes in cells treated with a drug. The pipeline includes RNA-seq count processing, differential expression using DESeq2, pathway enrichment via KEGG, and PCA for exploratory data analysis.

Key findings:

- Volcano plot highlights genes significantly upregulated post-treatment.
- Top 20 expressed genes may serve as key biomarkers or controls.
- PCA confirms distinct clustering between control and treated groups.
- Enriched KEGG pathways such as antifolate resistance and chemical carcinogenesis indicate potential molecular mechanisms involved in resistance.

These insights form a strong foundation for further biological validation and therapeutic targeting.