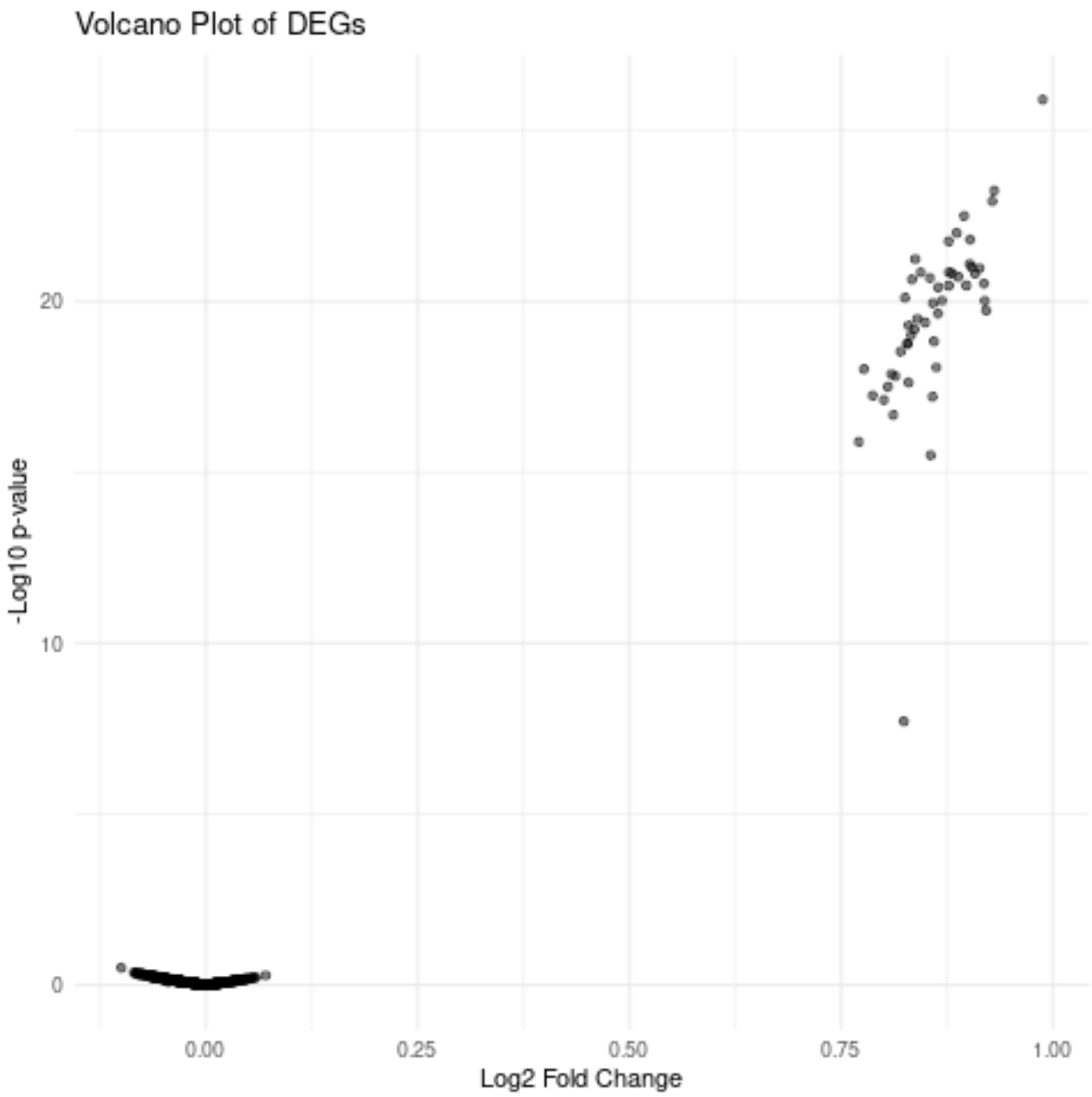
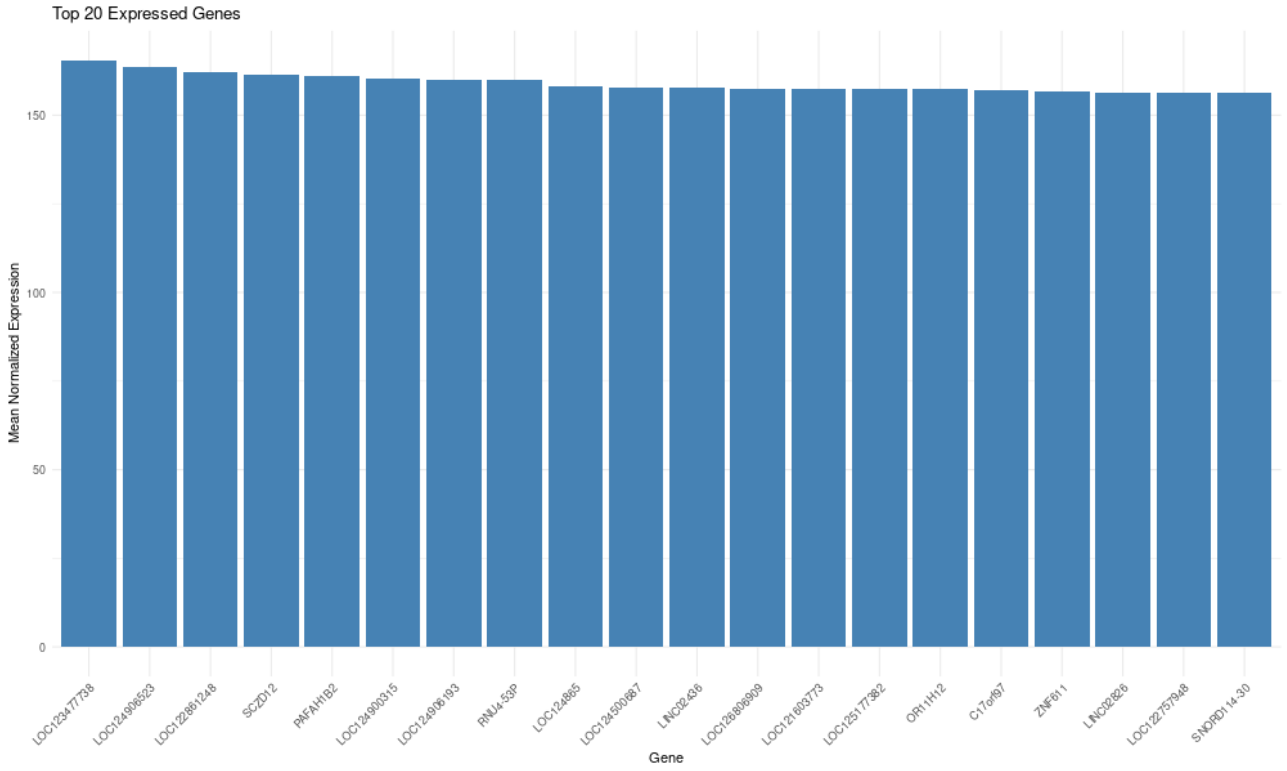
Melanoma Drug Resistance Analysis
Comprehensive Report

Volcano Plot of Differentially Expressed Genes



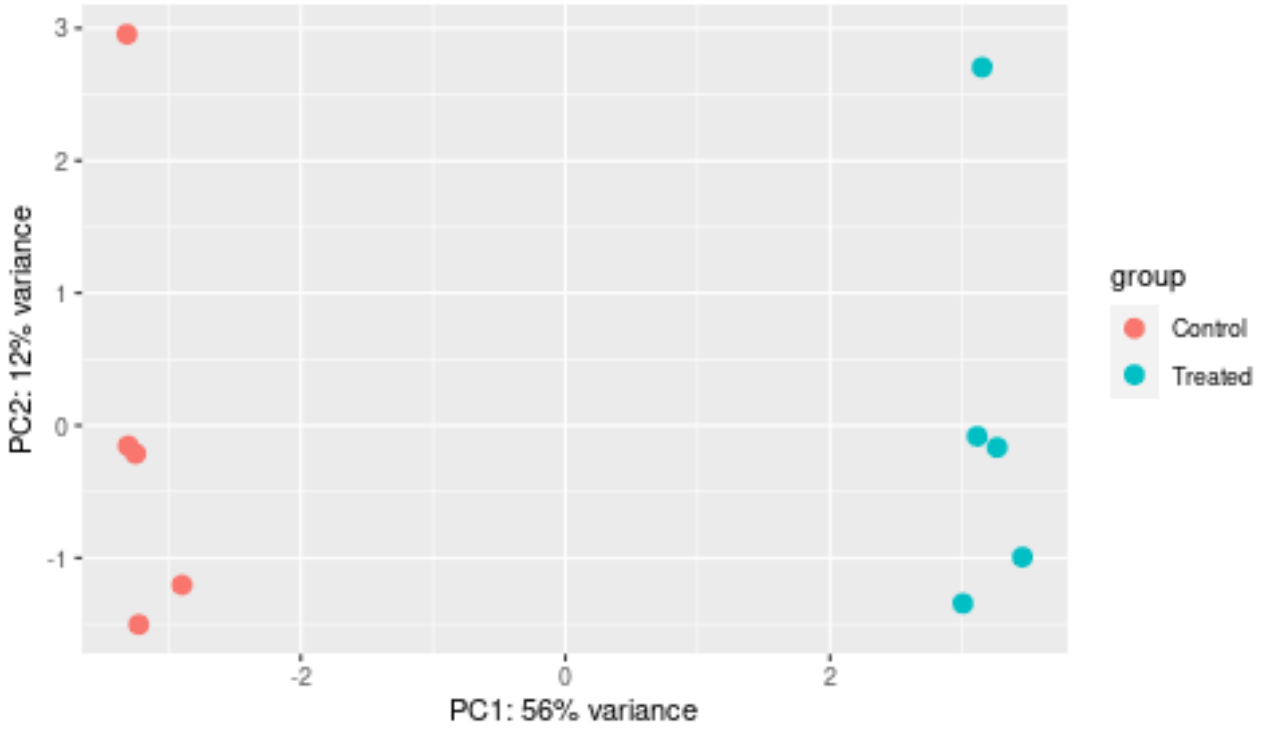
This volcano plot displays the relationship between log2 fold change and statistical significance (-log10 adjusted p-value) of all genes analyzed. Genes in the upper right corner are highly upregulated in treated melanoma cells, indicating possible drug-resistance markers.

Top 20 Expressed Genes



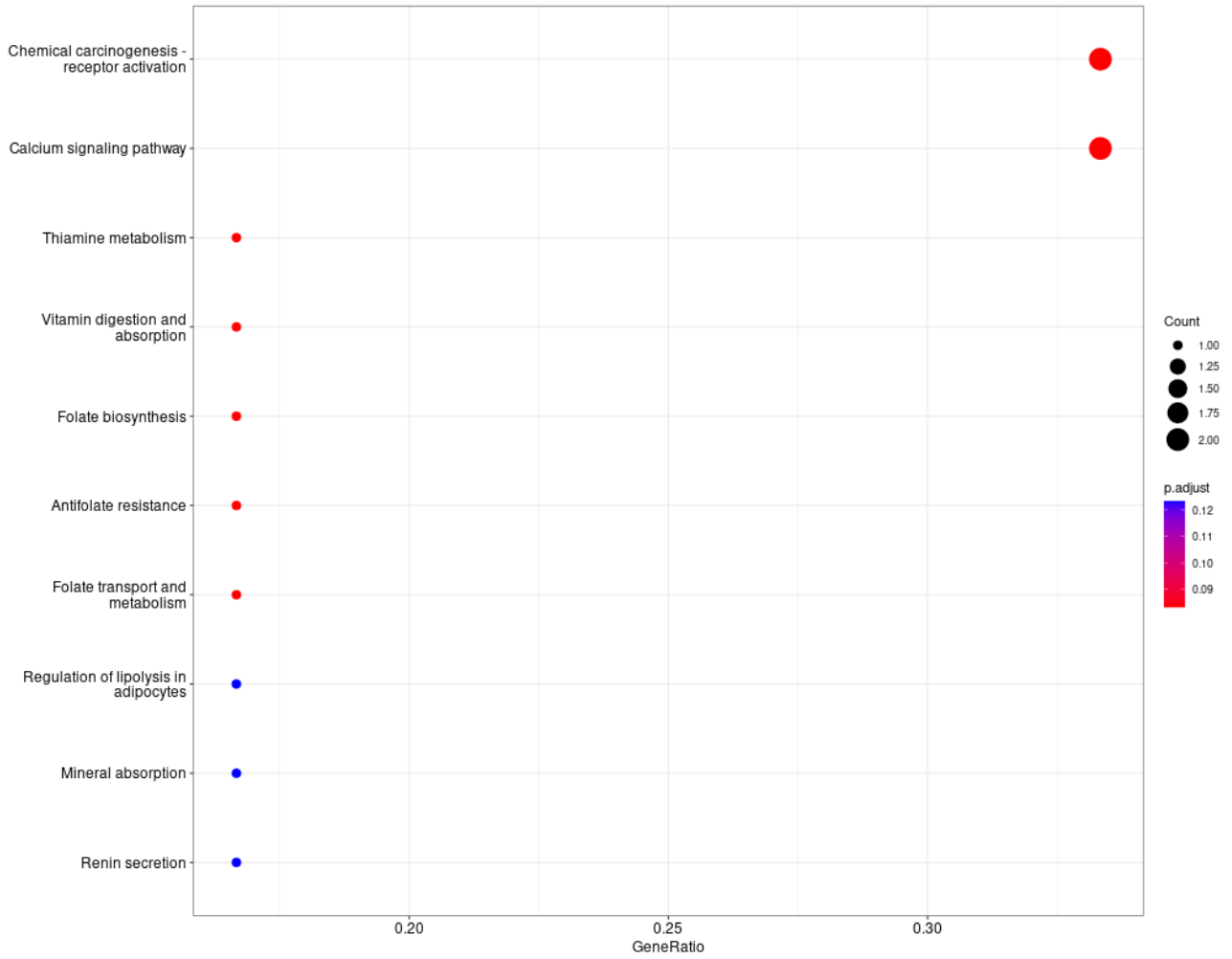
Bar plot showing the top 20 most expressed genes across all samples. These genes represent strong baseline expression and may include housekeeping genes or treatment-influenced transcripts.

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 melanoma 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.