

Differential Expression Analysis

Differential expression analysis is determined via a two-sample t-test to compare the fibroid and normal samples for all genes. The p-values were adjusted, and genes with a p-value < 0.05 and absolute log2 fold change > 1 suggest that their differential expression was significant.

Heatmap Visualization

The heatmap provides a visualization of the expression patterns for the most significant genes using the z-score normalized expression values between fibroid and normal samples. The hierarchical clustering emphasizes the results of the differential expression analysis and fibroid development.

Volcano Plot

The volcano plot summarizes the results of the differential expression analysis by displaying the genes with high statistical significance and strong fold changes. There is an obvious separation in the upregulated and downregulated genes in the fibroid tissue, which helps to identify candidates for further reference.

Principal Component Analysis (PCA)

PCA assists in visualizing the sample variation in the gene expression data. The initial two principal components displayed a strong proportion of variance, where the plot displays a separation between the fibroid and normal samples. Thus suggesting that there may be transcriptional differences between the fibroid and normal tissues to determine disease and non-disease.

Quality Control and Distribution Analysis

QC was performed to confirm the reliability of the data analyzed. The distribution plots reveal the overall distribution of expression values and the gene-wise means and standard deviations. These plots allow for confirmation to reveal that the data was well-normalized and suitable to undergo statistical analysis.