**Gene Expression and KEGG Pathway Enrichment Analysis in Glioblastoma Using R**

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**Introduction**

This report considers the analysis of gene expression data from the Glioblastoma.csv dataset. We use heat maps to illustrate gene expression patterns, perform functional enrichment analysis, interpret the outcomes' biological significance, and use Shiny GO to uncover important pathways associated with genes.

**Data Overview**

The dataset comprises 582 genes (observations) and 11 samples (variables) with no missing values. It includes 5 primary tumors and 5 solid tumor cell samples. The normalization process utilized was log transformation, ensuring the data is on the same scale. Using the DESeq2 package, differential gene expression analysis was conducted. The results show:

* Out of 454 genes with nonzero total read count:
* Upregulated Genes: 25 genes (5.5%) with an adjusted p-value < 0.05 and log2 fold change (LFC) > 0.
* Downregulated Genes: 78 genes (17%) with an adjusted p-value < 0.05 and LFC < 0.
* Outliers: 229 genes (50%).
* Low Counts: 41 genes (9%) with mean count < 5.

Filtered results identified 25 upregulated genes and 78 downregulated genes.

**A graph showing a volcano plot

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Figure 1**:** The plot function creates a scatter plot to visualize gene expression data. Red points indicate significant differences; a blue line marks the significance threshold.

**Visualization: Heatmaps**

The gplots library was used to visualize gene expression patterns and the data was normalized by log2-transformed. Five types of heatmaps were created:

**A yellow and black striped pattern

Description automatically generated with medium confidence**

Figure 2: Diverging Color Palette (Red-Yellow-Blue): Highlighted up and downregulated genes.

A blue and black graph

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Figure 3**:** Sequential Color Palette (White to Blue): displays gradual changes in gene expression.

**A blue and black graph

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Figure 4: Heatmap of glioblastoma in both clusters.

**A graph showing a heatmap

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Figure 5 Heatmap of glioblastoma in column clustering

**A blue and black graph

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Figure 6: Heatmap of Glioblastoma in both clusters.

**Functional Enrichment Analysis Results**

This bar graph displays the top enriched pathways, with "Viral protein interaction with cytokine and cytokine receptor" showing the highest fold enrichment highlighting key immune pathways, including IL-17 signaling.

Description: A graph with different colored bars

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Figure 7:The key enriched pathways identified through functional enrichment analysis.

Viral protein interactions with cytokines, such as the IL-17 signaling and hematopoietic cell lineage pathway, are crucial for immune regulation and cancer progression. Viruses can manipulate the immune system to promote tumor growth by disrupting cytokine signaling, which leads to immune suppression and facilitates tumor expansion. Understanding these viral-host interactions is vital for targeted cancer therapies (Smith *et al*., 2023).

Cytokines are small proteins that can regulate immune cell growth and differentiation (Garg *et al.*, 2020). Dysregulation of cytokines, such as through the CCL21-CCR7 pathway, can enhance cancer cell proliferation (Geraldo *et al*., 2023). Targeting these pathways, for instance, with temozolomide, may offer effective therapies (Vakilian *et al*., 2016).

IL-17 signaling pathway, driven by T-helper 17 cells, activates inflammatory pathways like MAPK and NF-κB. While IL-17 is crucial for immune defense, it also fosters a pro-tumor microenvironment in glioblastoma, contributing to tumor growth through inflammation, angiogenesis, and immune evasion (Li *et al.*, 2020; Ngiow *et al*., 2015).

The hematopoietic cell lineage pathway governs blood cell differentiation from hematopoietic stem cells. In glioblastoma, disruptions lead to abnormal immune cell infiltration and an immunosuppressive environment, promoting tumor growth and metastasis (Xu *et al*., 2021; Pérez *et al*., 2020).

**Conclusion**

Scientists can explore new therapeutic strategies by focusing on specific pathways, inhibiting tumor growth. This interconnected signaling pathway is vital for immune homeostasis and effective response.

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