

Liver Cancer RNA-seq Analysis

This report summarizes the analysis of a liver cancer RNA-seq dataset (TCGA). The analysis includes PCA, differential gene expression, heatmap, volcano plot, and 3D PCA visualization.

Dataset Overview:

- Genes: 20,531
- Samples: Cancer and Normal
- sample_type_id: 0 = Normal, 1 = Cancer

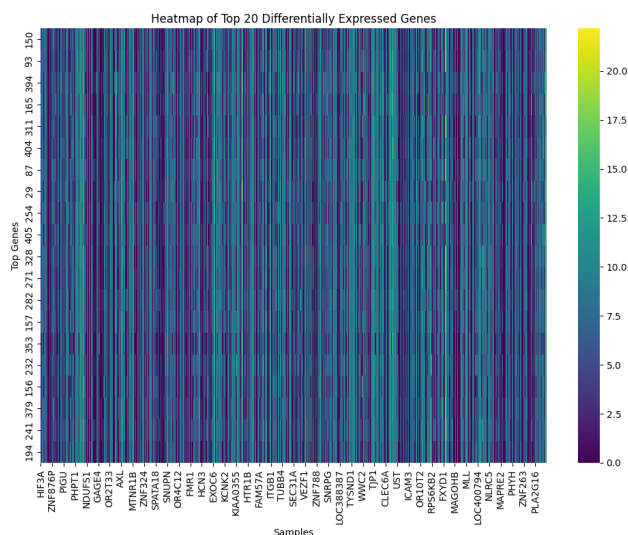
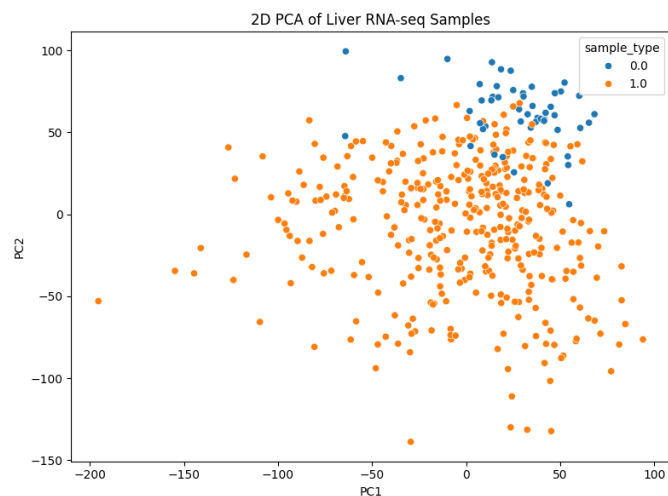
Analysis Steps:

1. PCA (2D and 3D) for sample distribution.
2. Differential gene expression analysis (Top 20 genes) using log2 fold change and t-test.
3. Heatmap of Top 20 genes.
4. Volcano plot of all genes.
5. Clustering (optional) for sample grouping.

Key Results:

- Top 20 genes identified and saved in 'Top_20_Genes.csv'.
- PCA shows clear separation of cancer and normal samples.
- Heatmap visualizes expression patterns of Top 20 genes.
- Volcano plot highlights significantly differentially expressed genes.
- 3D PCA interactive plot saved as '3D_PCA.html'.

Visualizations:



Note: For full interactive visualization, open '3D_PCA.html'. This report summarizes the main findings for CV or Devpost use.