

# RUVseq Data: GSVA analysis on cell lines gene expression (RNAseq)

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## Background

- The input for this set GSVA analysis is the RUVseq normalized counts from RNASeq data. A total of nine databases are used for the following GSVA analysis.

## Hallmark gene sets

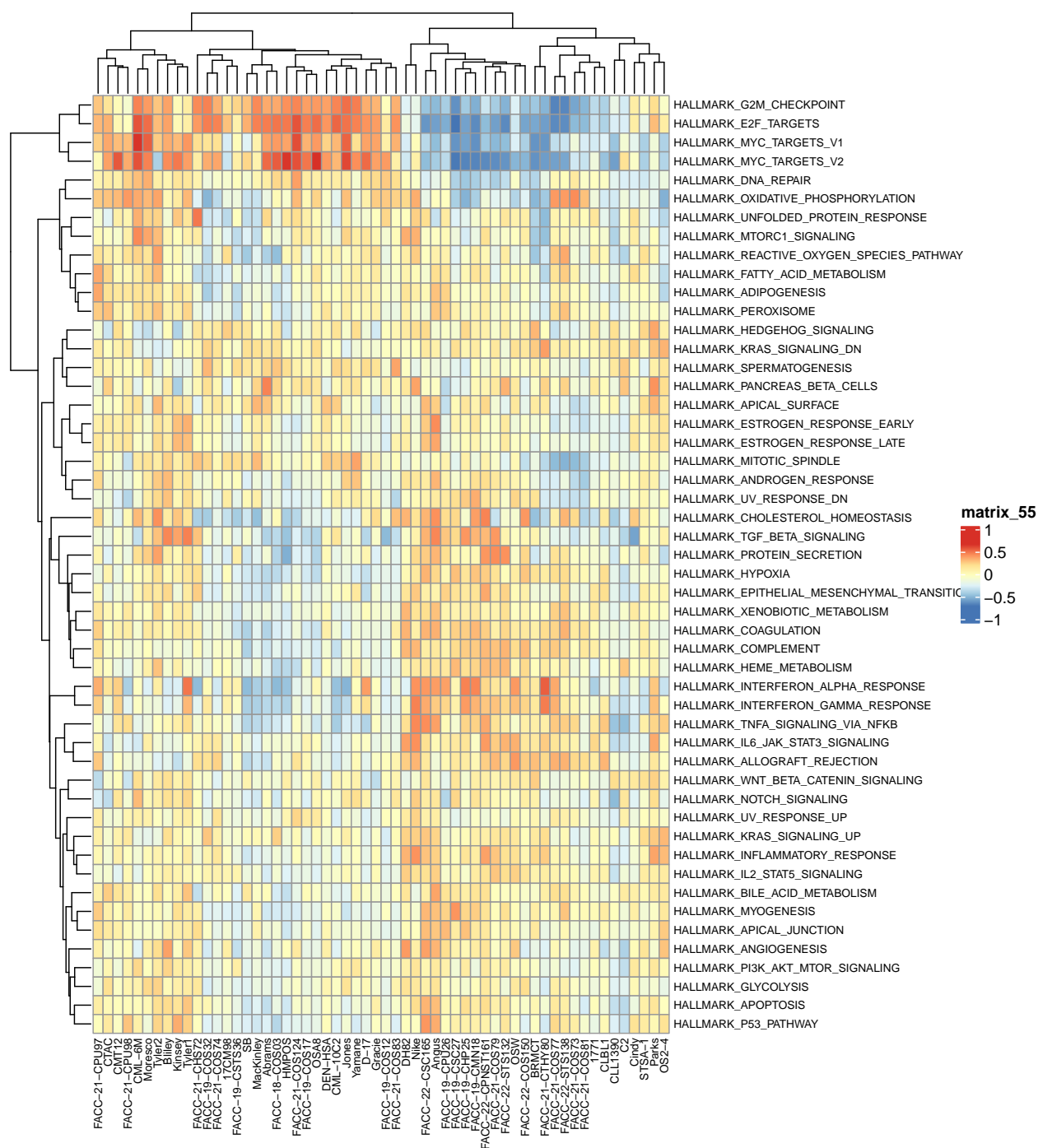
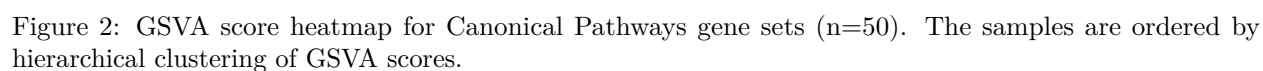


Figure 1: GSVA score heatmap for Hallmark gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

## Canonical Pathways



Input: RUVseq normalized counts

Chemical and Genetic Perturbations

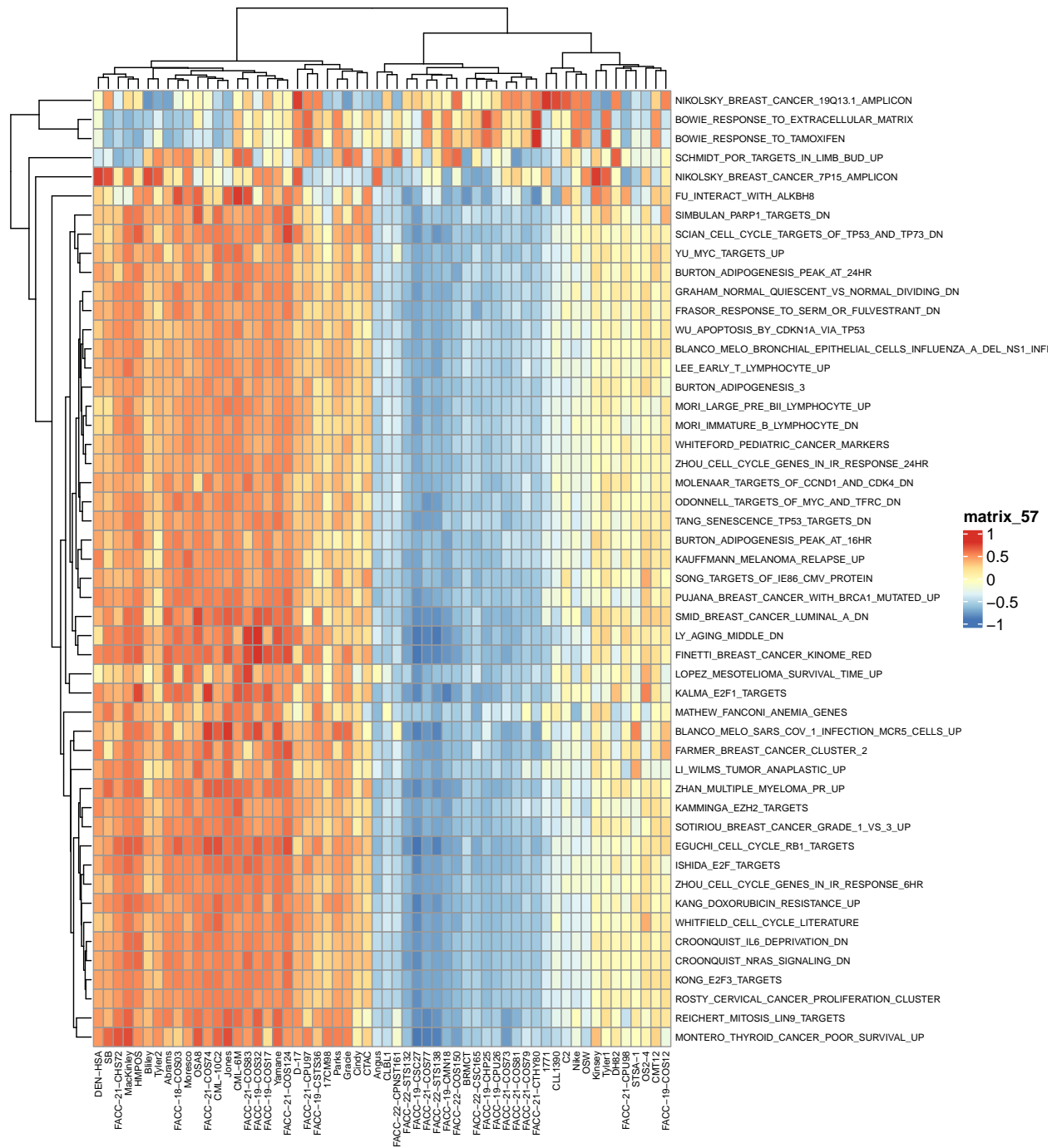


Figure 3: GSVA score heatmap for Chemical and Genetic Perturbations gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Input: RUVseq normalized counts

Cancer Gene Neighborhood gene sets

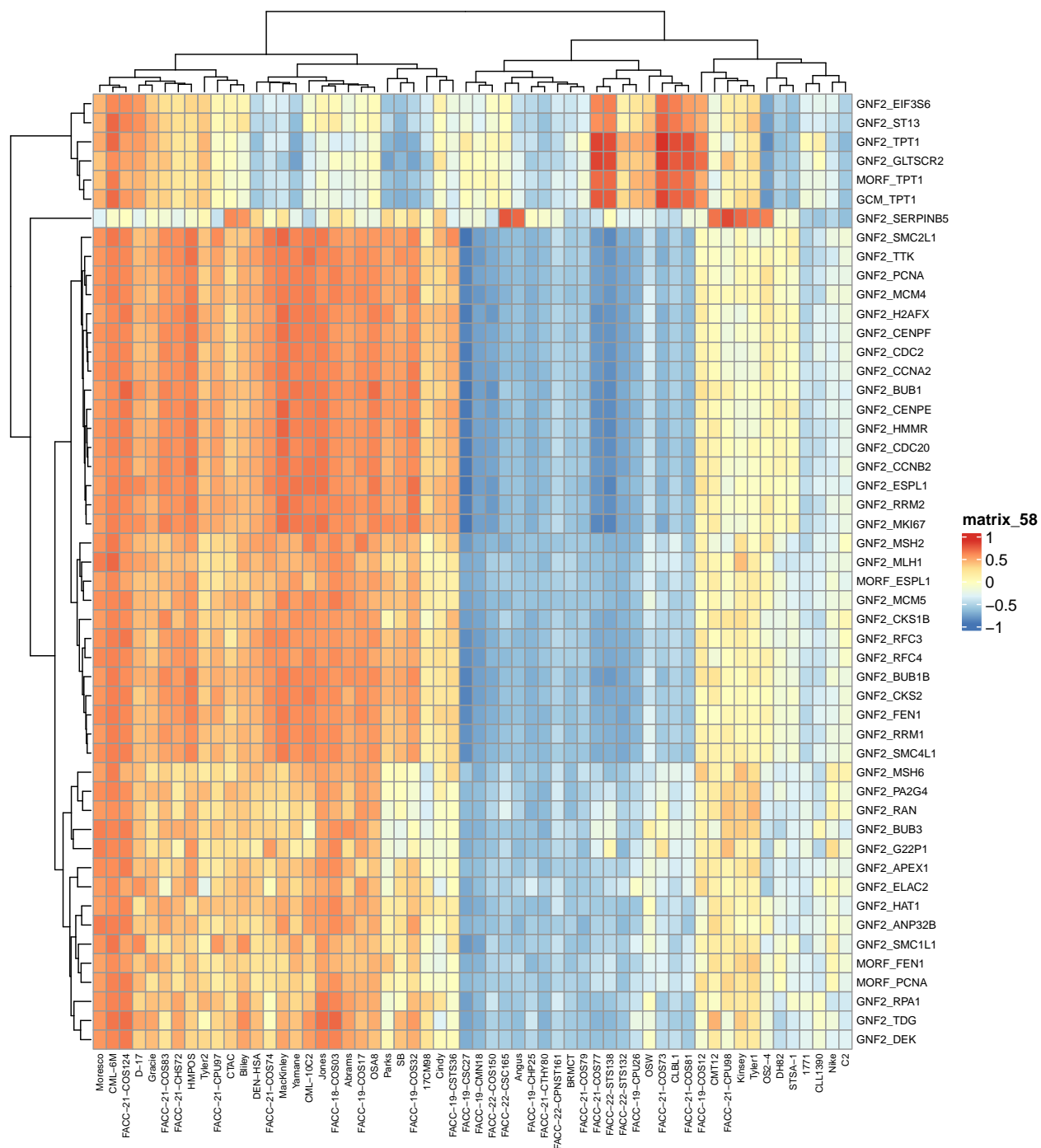


Figure 4: GSVAscore heatmap for Cancer Gene Neighborhoods gene sets (n=50). The samples are ordered by hierarchical clustering of GSVAscore.

Input: RUVseq normalized counts

Biological Processes gene sets

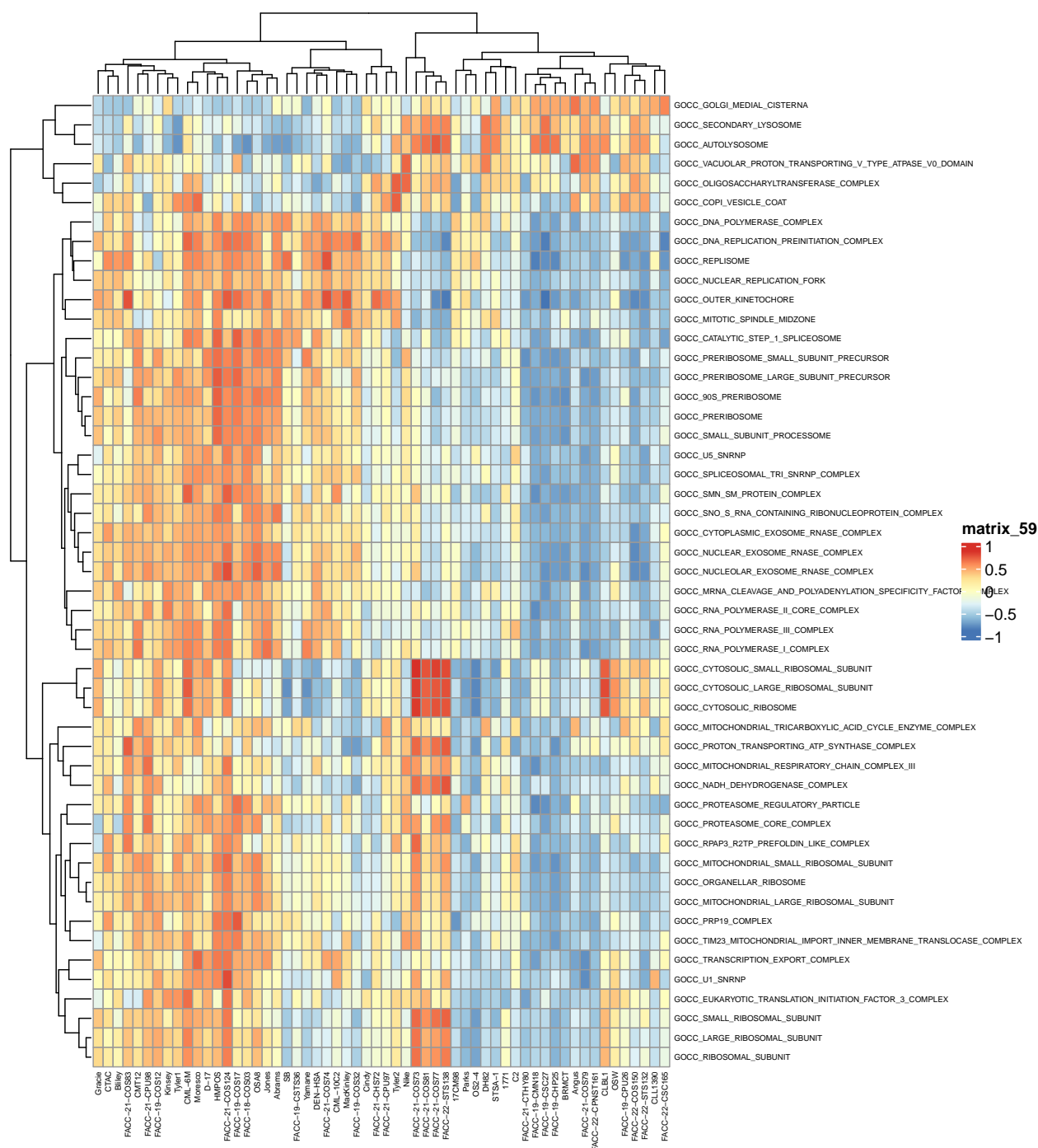
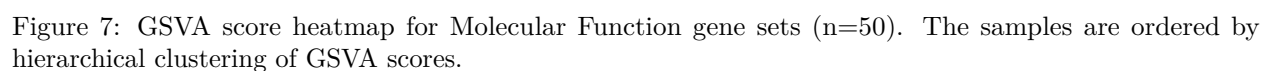


Figure 5: GSVA score heatmap for Biological Processes gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

### Component Ontology gene sets



## Molecular Function gene sets





## Oncogenic Signature gene sets



Input: RUVseq normalized counts

Cell Type Signature gene sets

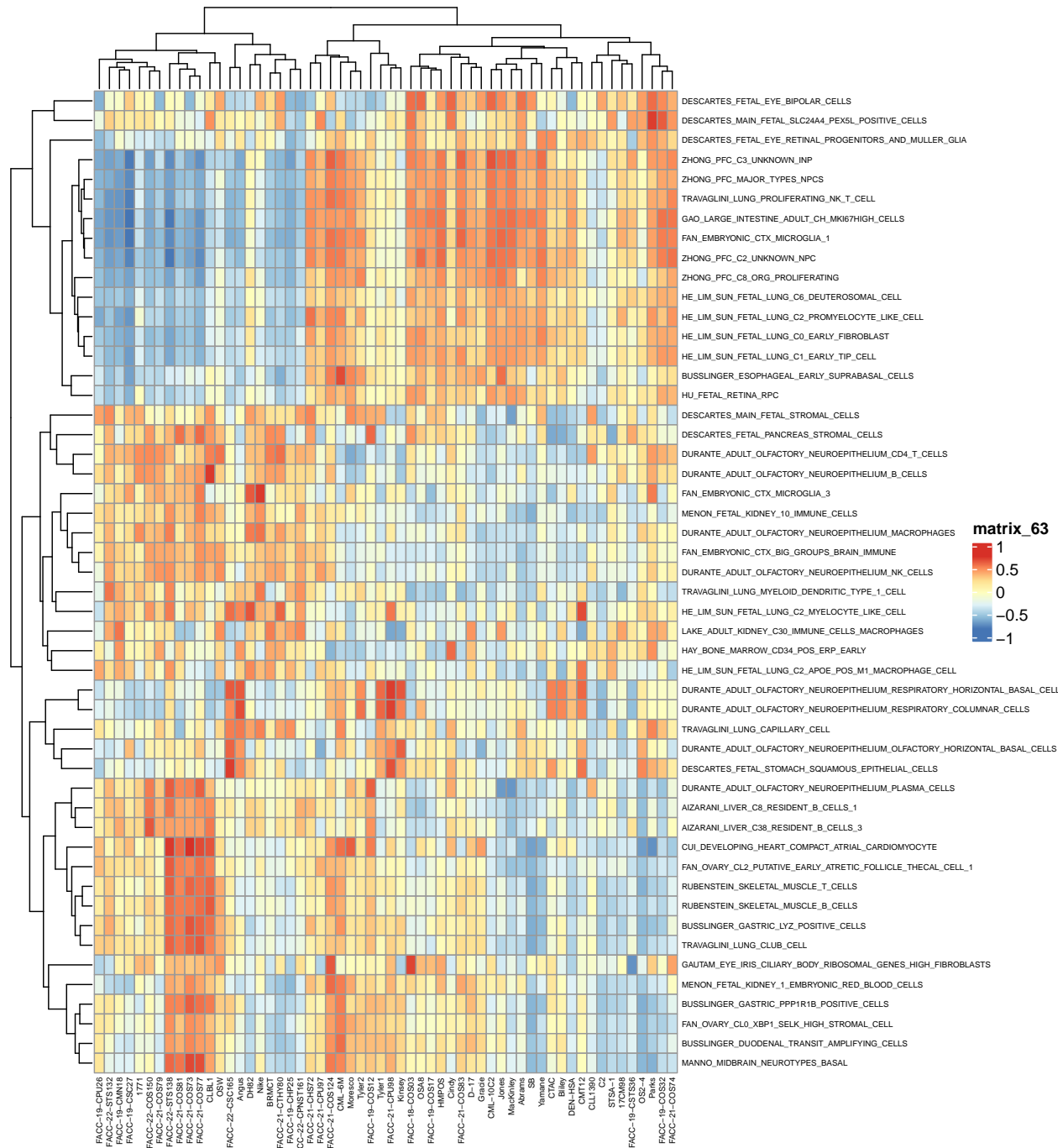


Figure 9: GSVA score heatmap for Cell Type Signature gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.