

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

Maritza Morales

2023-09-19

Contents

Background	1
Input: DESeq normalized counts	2
Hallmark gene sets	2
Input: DESeq normalized counts	3
Canonical Pathways	3
Input: DESeq normalized counts	4
Chemical and Genetic Perturbations	4
Input: DESeq normalized counts	5
Cancer Gene Neighborhood gene sets	5
Input: DESeq normalized counts	6
Biological Processes gene sets	6
Input: DESeq normalized counts	7
Component Ontology gene sets	7
Input: DESeq normalized counts	8
Molecular Function gene sets	8
Input: DESeq normalized counts	9
Oncogenic Signature gene sets	9
Input: DESeq normalized counts	10
Cell Type Signature gene sets	10

Background

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

Input: DESeq normalized counts

Hallmark gene sets

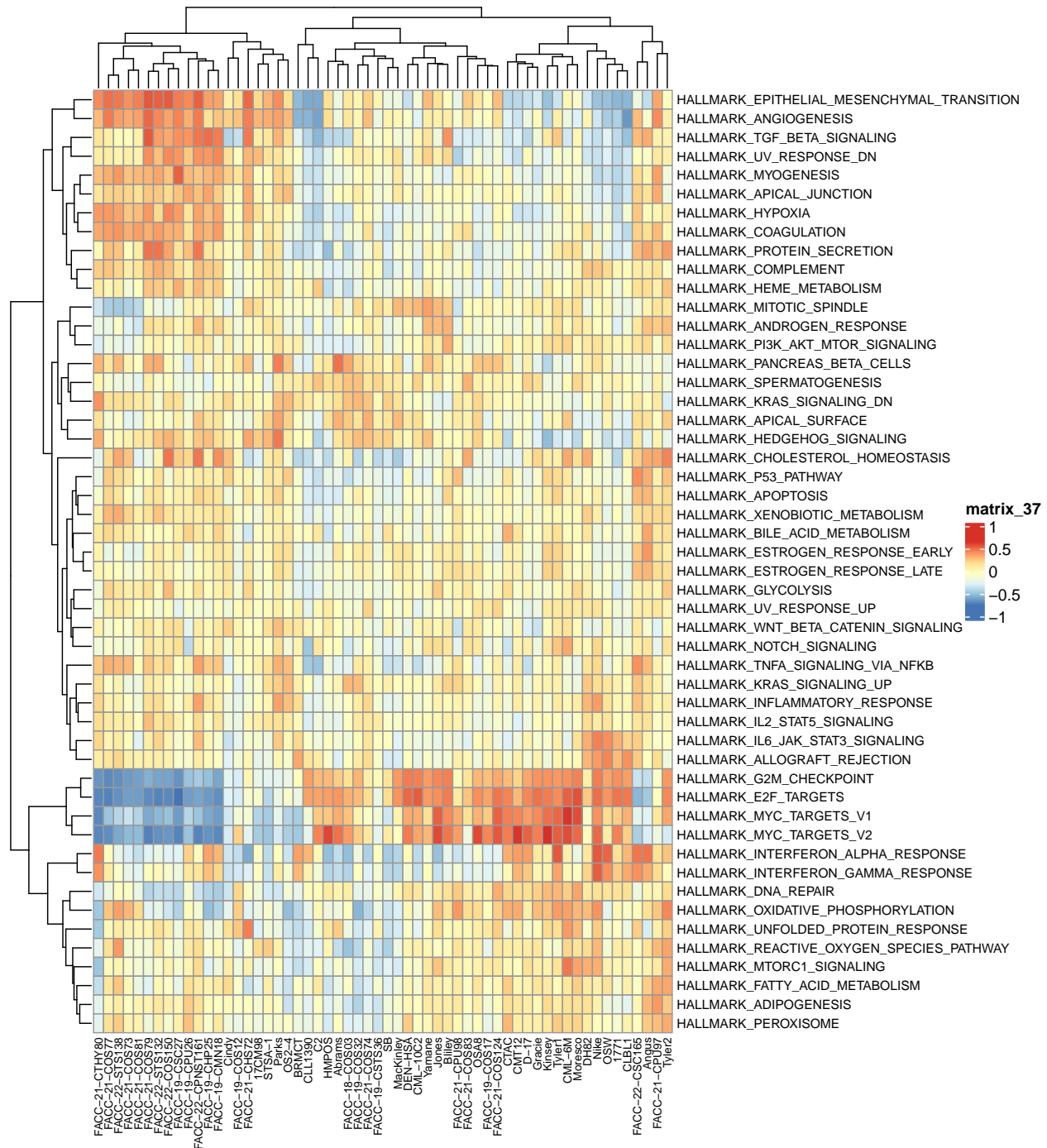


Figure 1: GSVA score heatmap for Hallmark gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Canonical Pathways

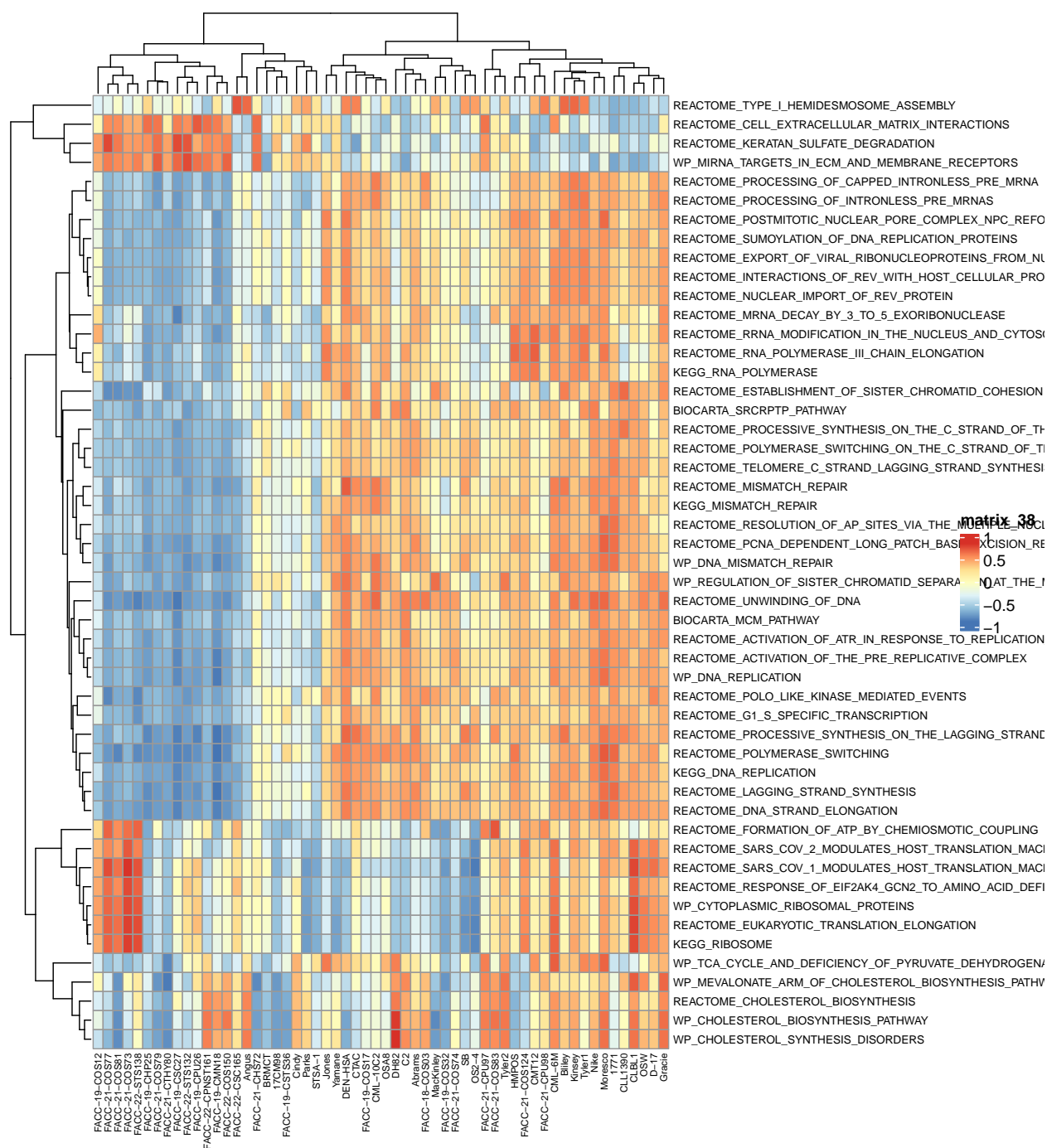


Figure 2: GSVA score heatmap for Canonical Pathways gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Chemical and Genetic Perturbations



Input: DESeq normalized counts

Cancer Gene Neighborhood gene sets

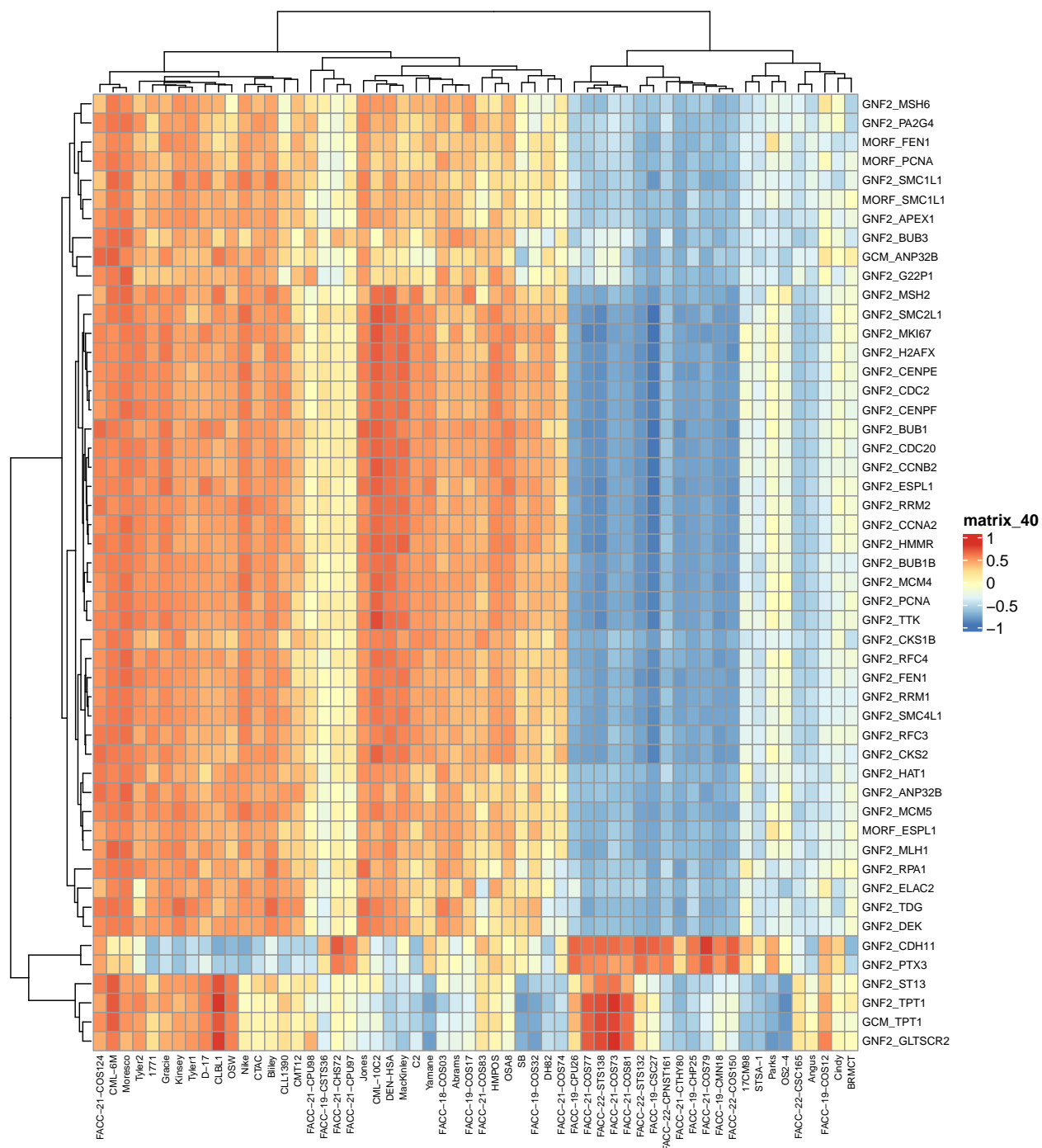


Figure 4: GSVAscore heatmap for Cancer Gene Neighborhoods gene sets (n=50). The samples are ordered by hierarchical clustering of GSVAscore.

Input: DESeq normalized counts

Biological Processes gene sets

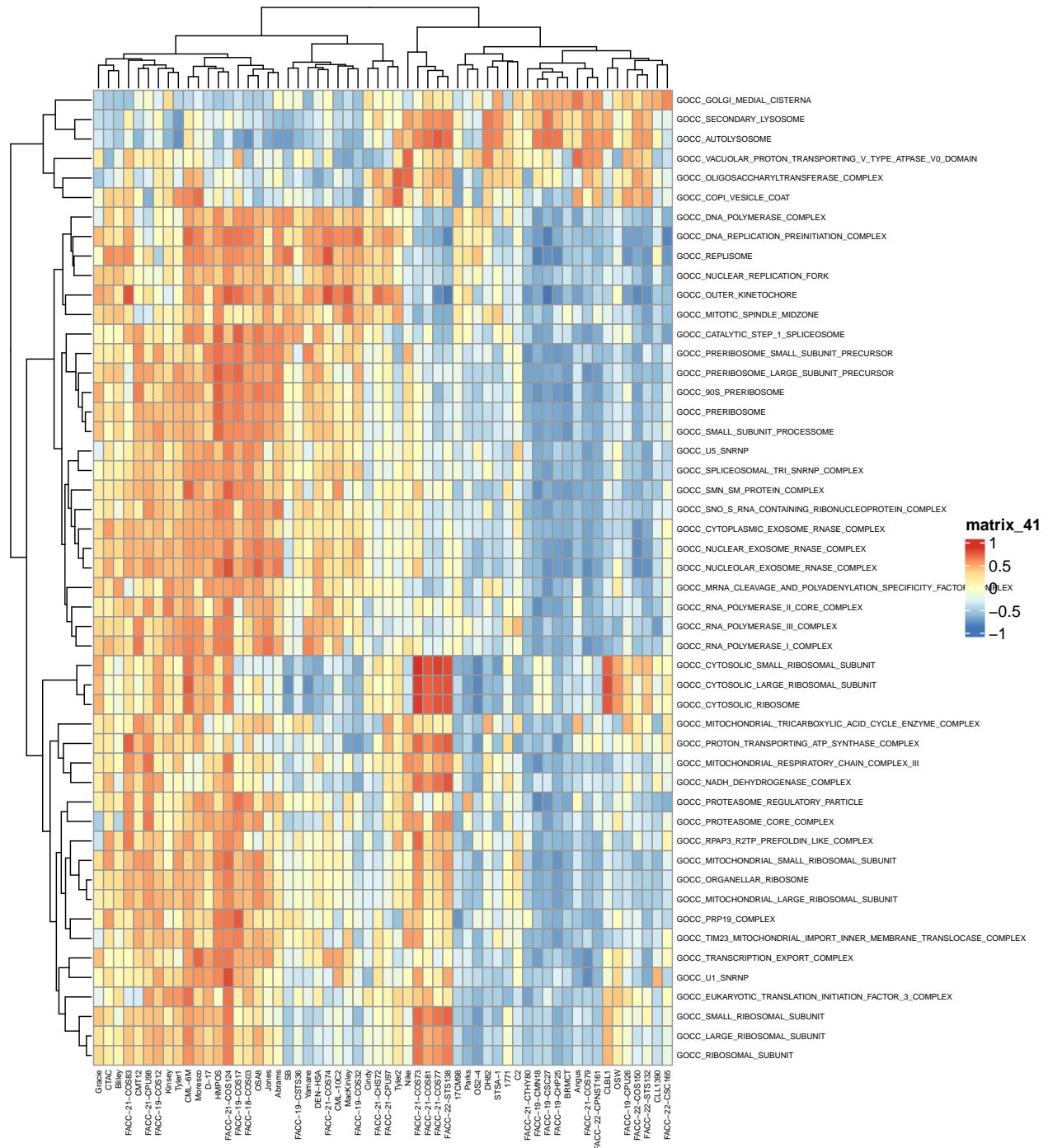


Figure 5: GSVA score heatmap for Biological Processes gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Component Ontology gene sets

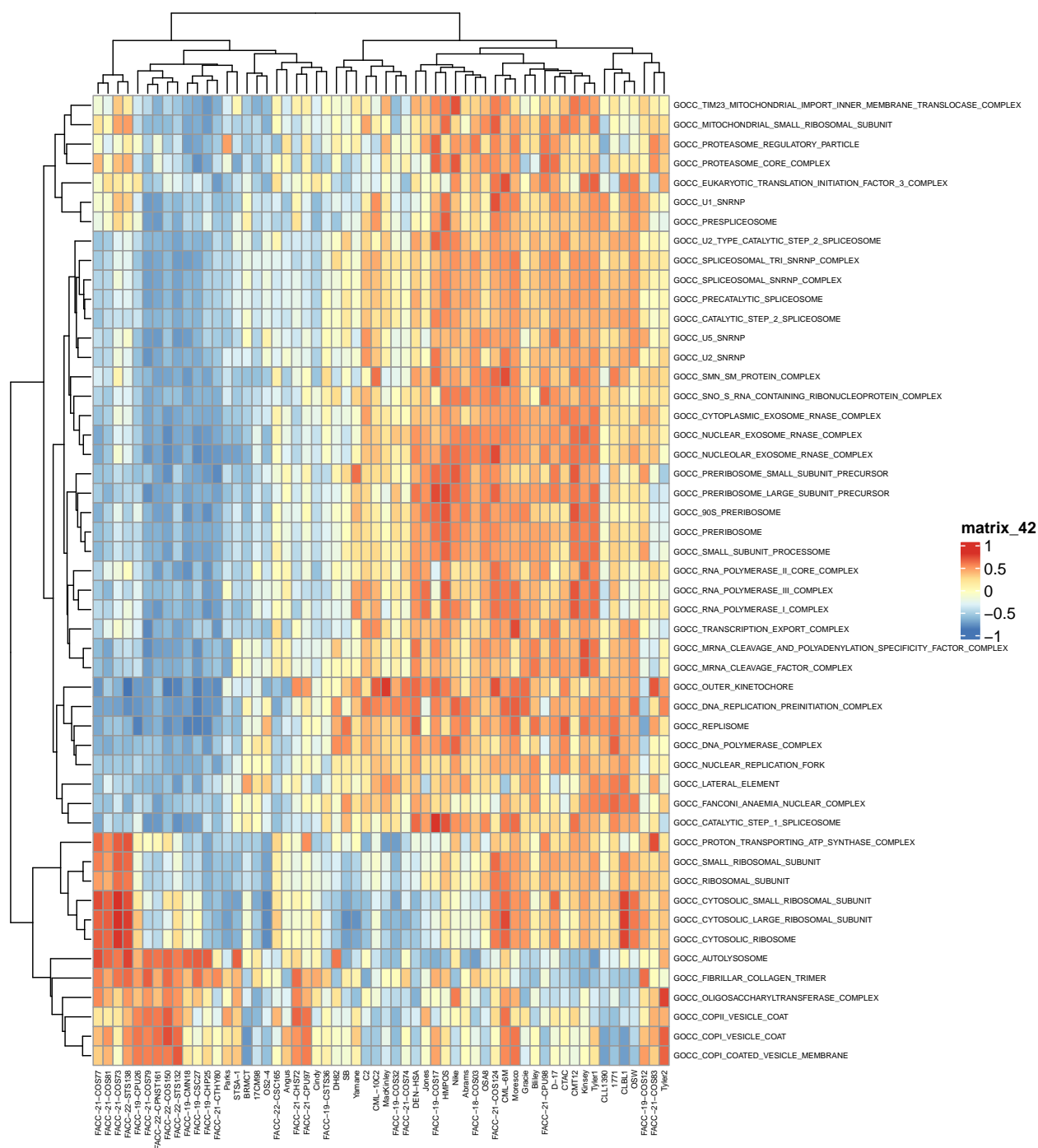


Figure 6: GSVA score heatmap for Component Ontology gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Input: DESeq normalized counts

Molecular Function gene sets

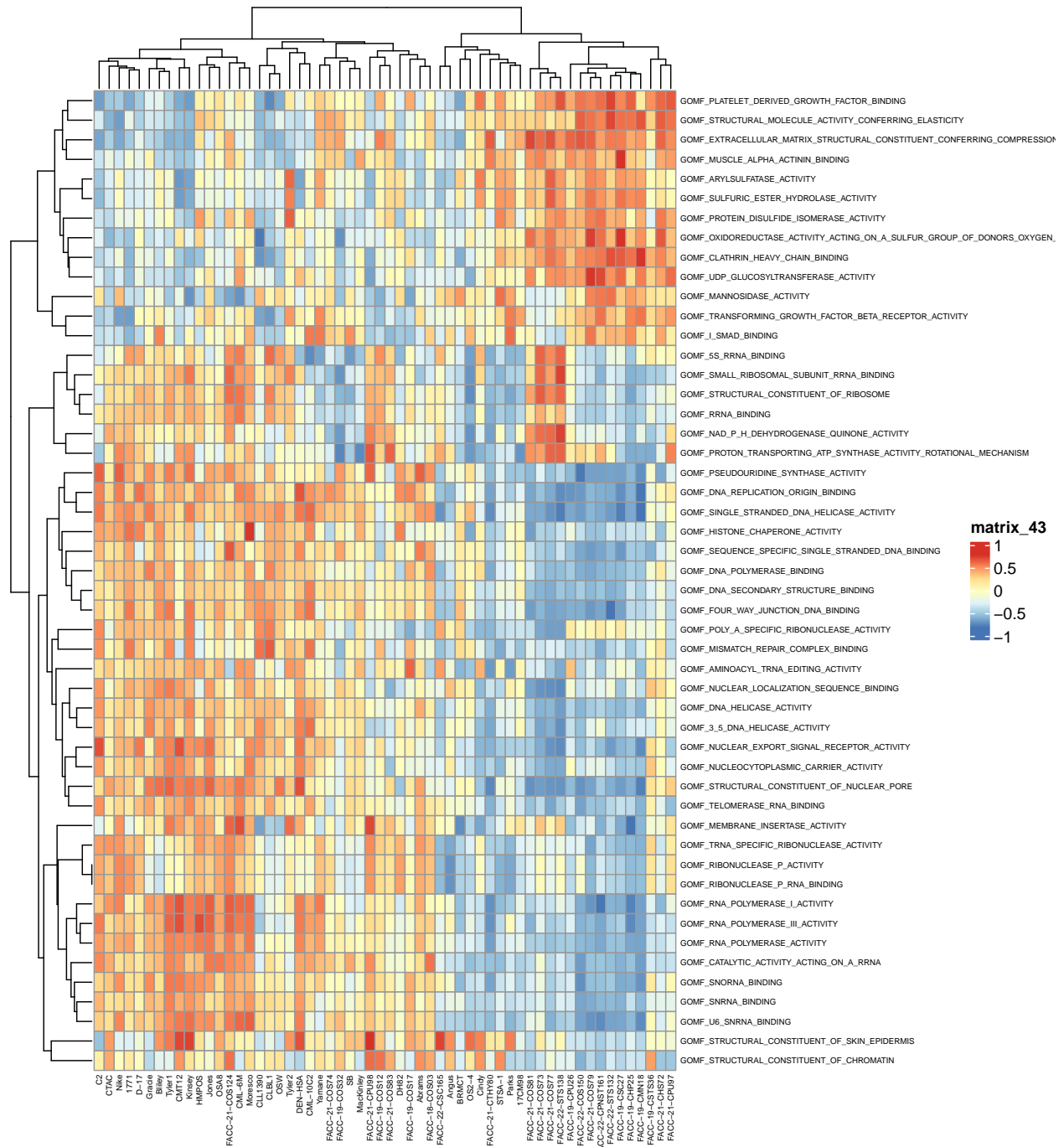


Figure 7: GSVA score heatmap for Molecular Function gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Input: DESeq normalized counts

Oncogenic Signature gene sets

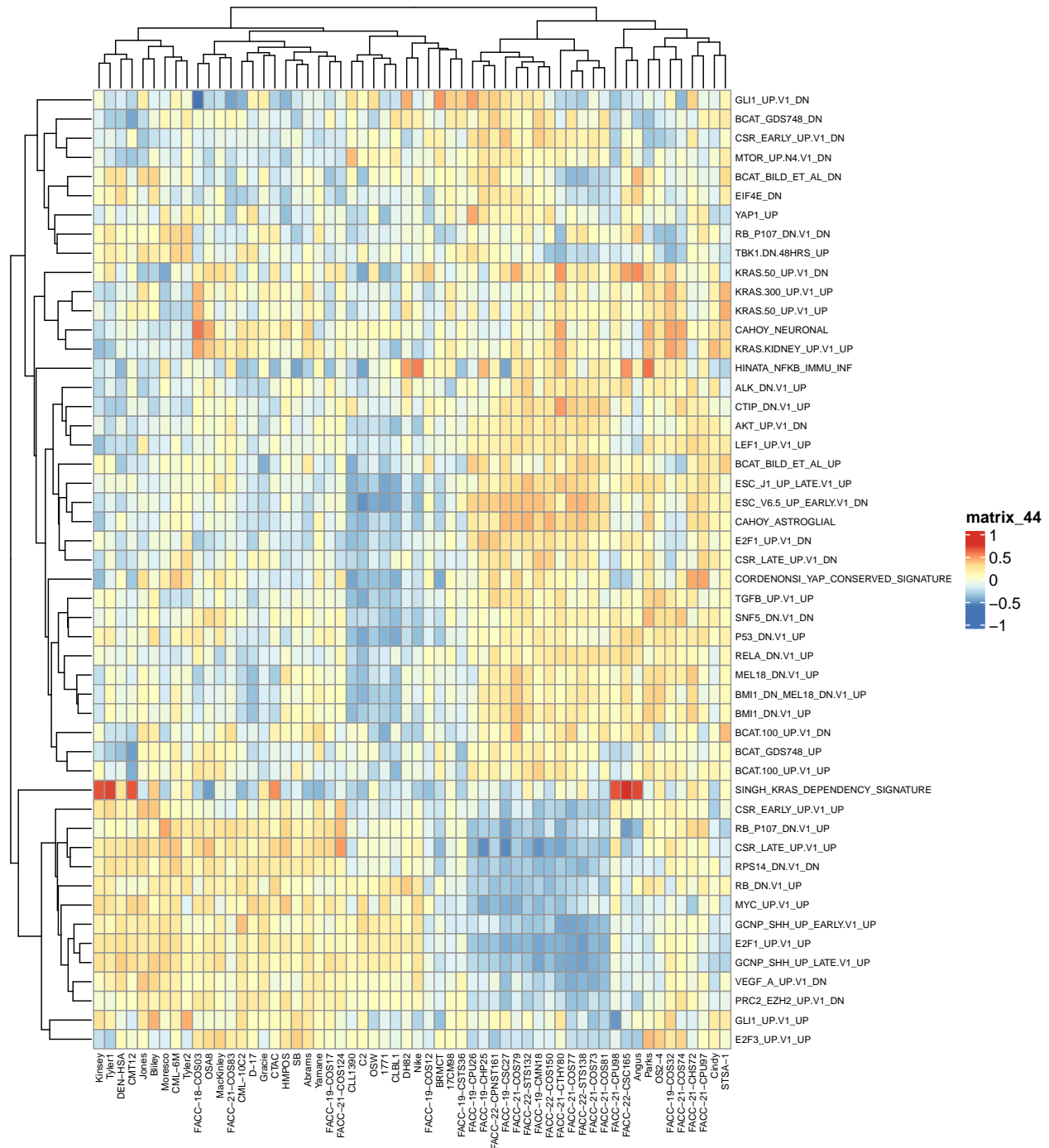


Figure 8: GSVA score heatmap for Oncogenic Signature gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.

Cell Type Signature gene sets

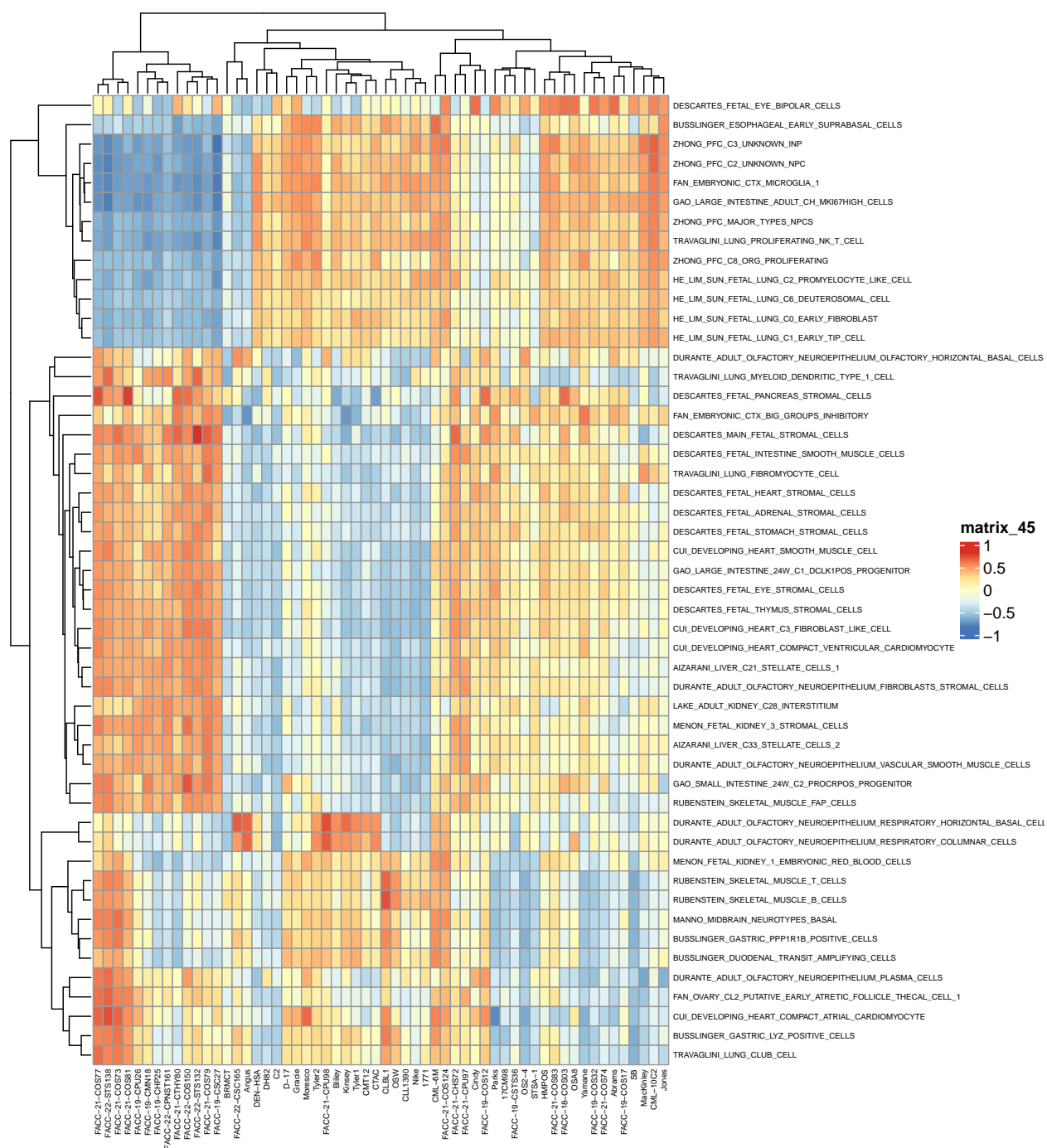


Figure 9: GSVA score heatmap for Cell Type Signature gene sets (n=50). The samples are ordered by hierarchical clustering of GSVA scores.