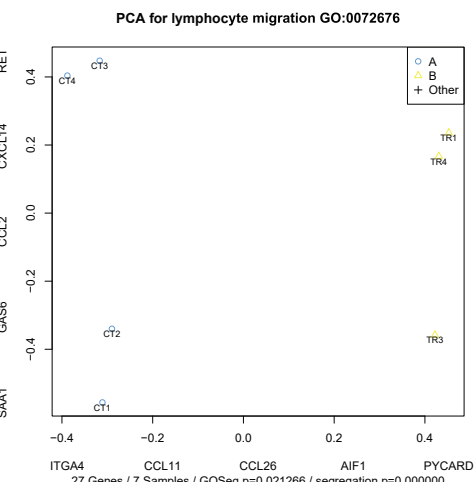
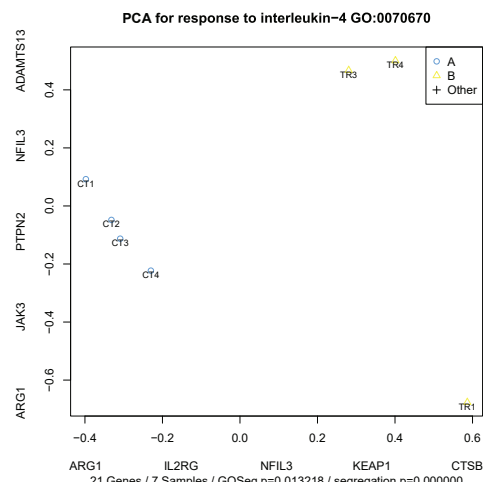
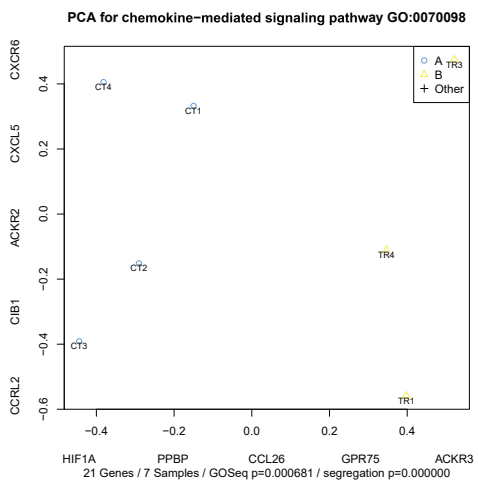
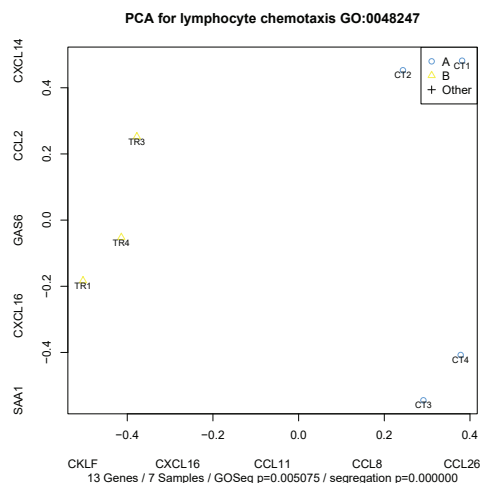
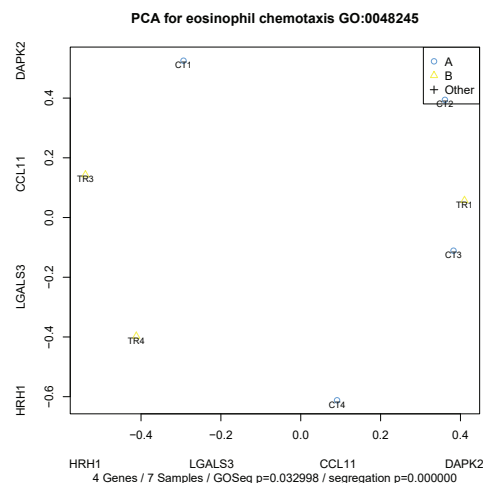
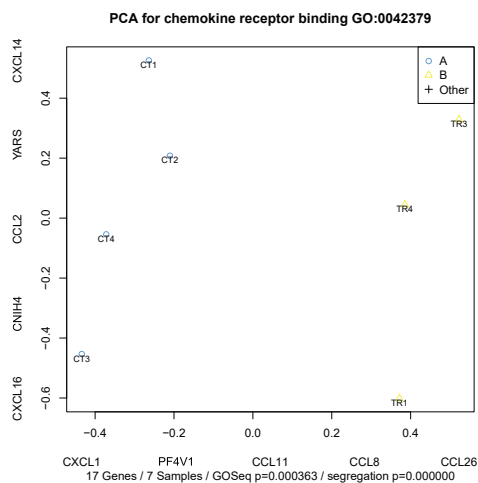
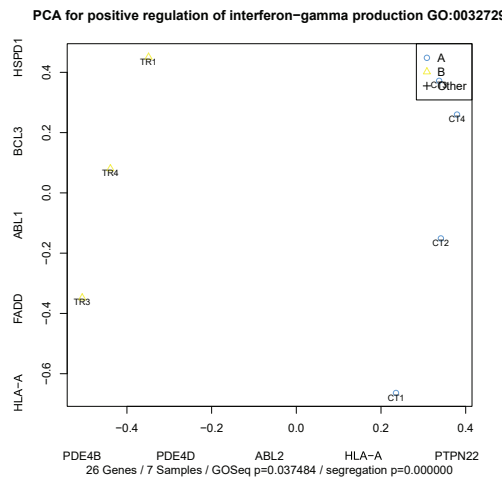
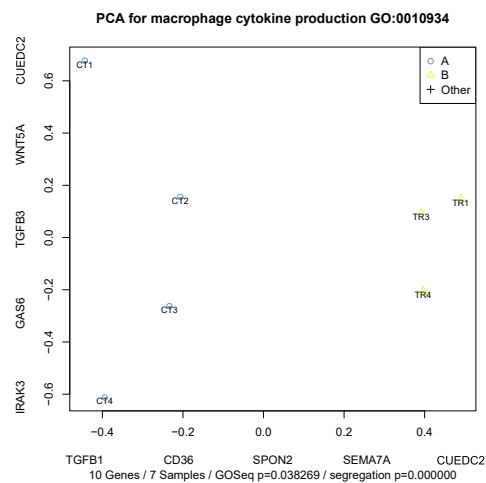
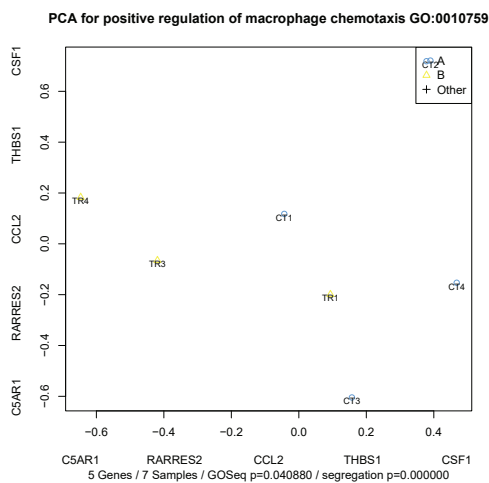
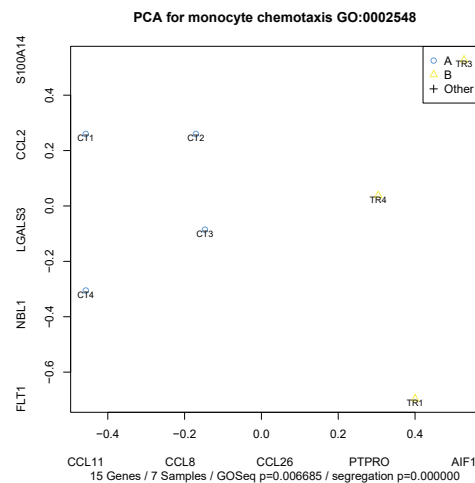
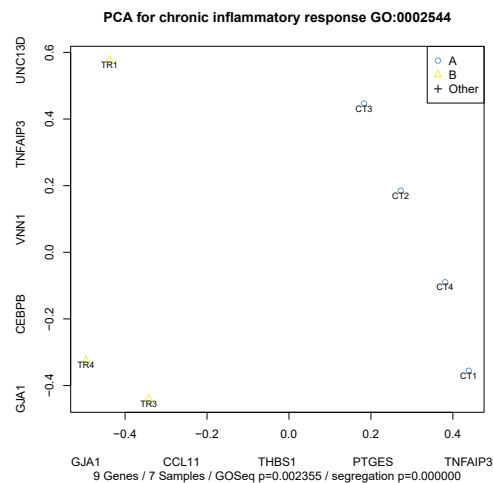
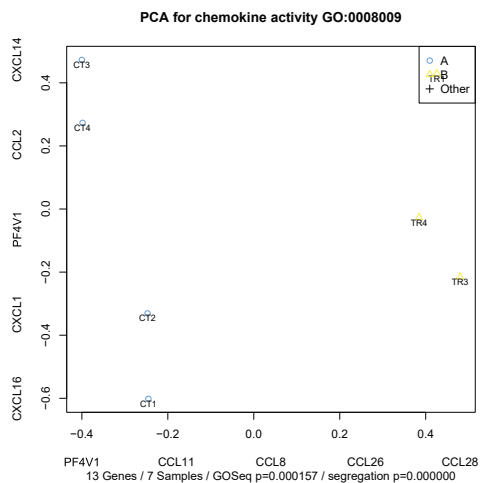


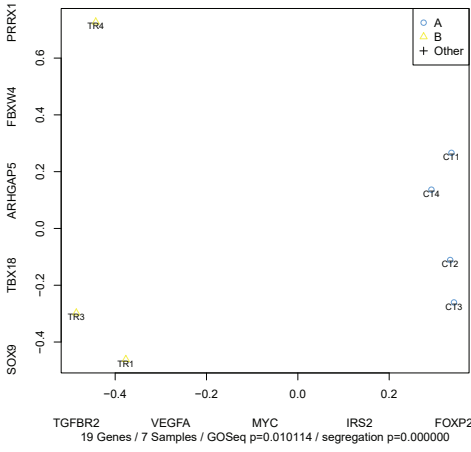
# A. Immune-related GO terms

# Fig S3.

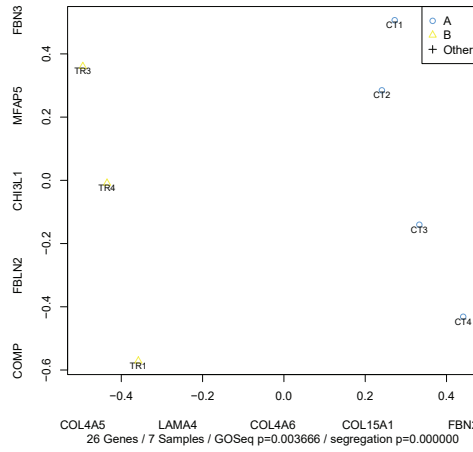


# B. Atherosclerosis related GO terms

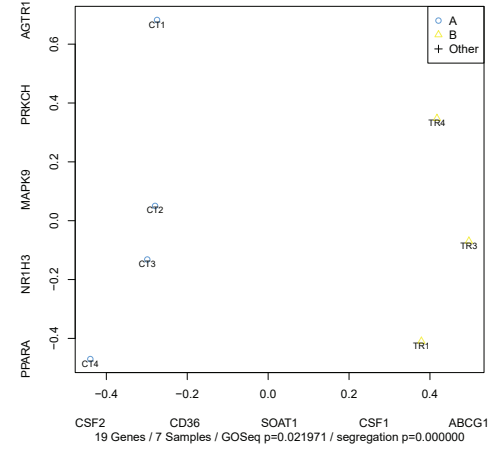
PCA for positive regulation of mesenchymal cell proliferation GO:000205



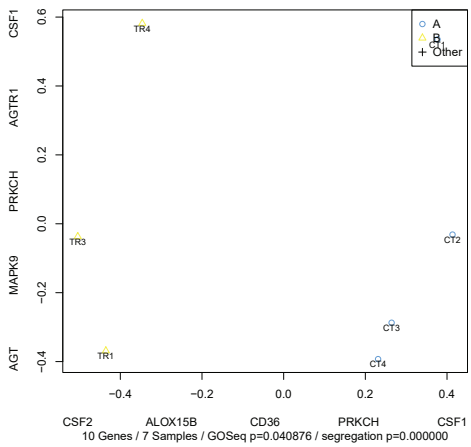
PCA for extracellular matrix structural constituent GO:0005201



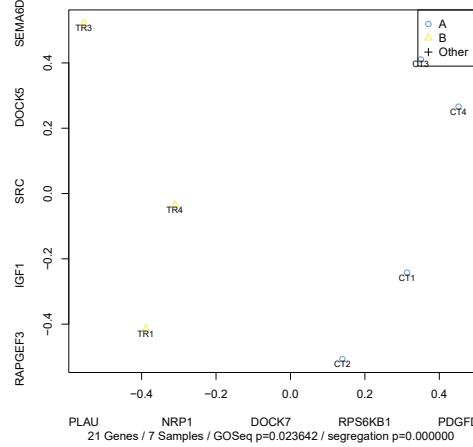
PCA for macrophage derived foam cell differentiation GO:0010742



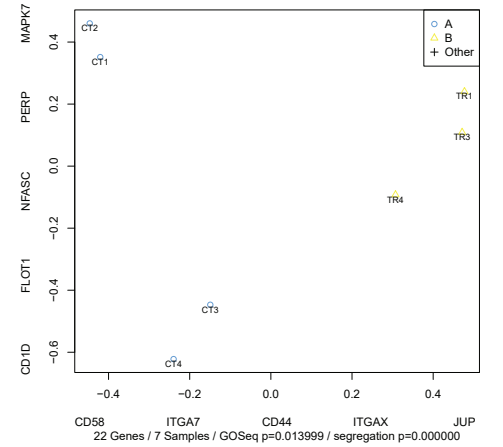
PCA for positive regulation of macrophage derived foam cell differentiation GO:



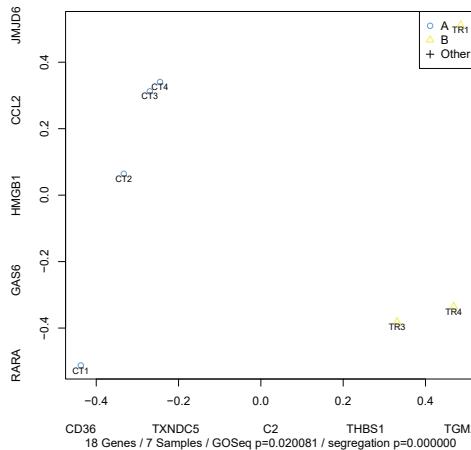
PCA for positive regulation of smooth muscle cell migration GO:0014911



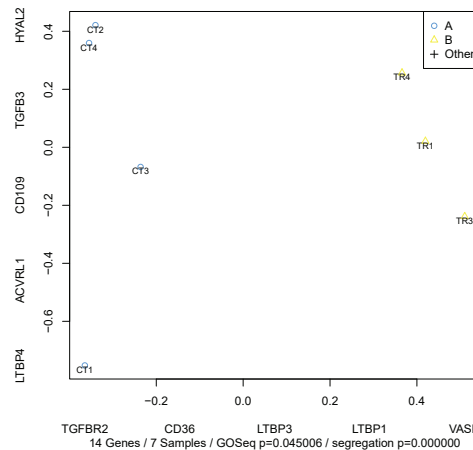
PCA for heterotypic cell-cell adhesion GO:0034113



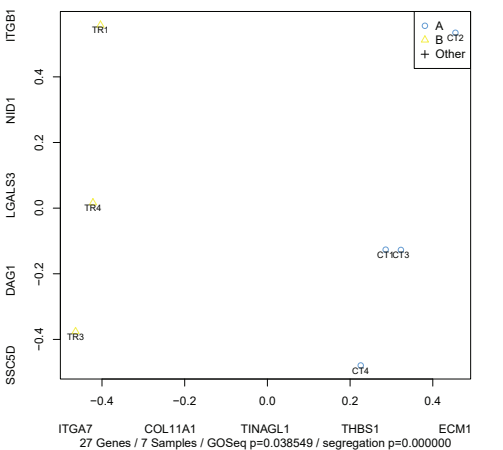
PCA for apoptotic cell clearance GO:0043277



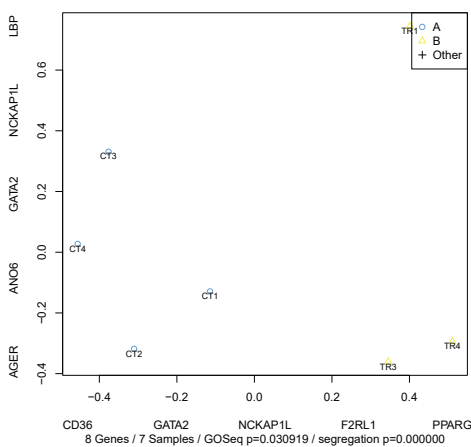
PCA for transforming growth factor beta binding GO:0050431



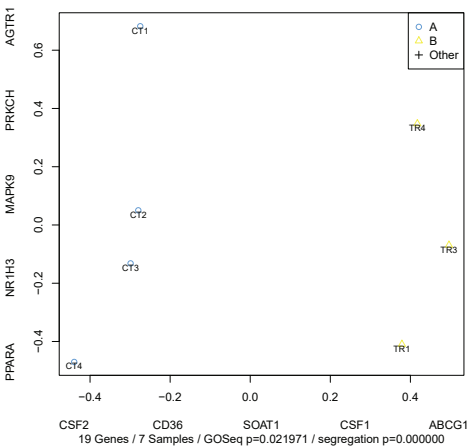
PCA for extracellular matrix binding GO:0050840



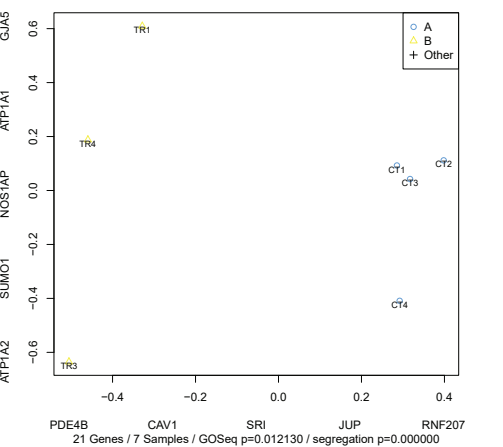
PCA for positive regulation of phagocytosis, engulfment GO:0060100



PCA for foam cell differentiation GO:0090077



PCA for regulation of actin filament-based movement GO:1903115



**Figure S3.**

**GO terms identified with *TCF21* overexpression in HCASMC.**

Differential expression of exons, genes, and transcripts were assayed using the DESeq2 R package from Bioconductor, which uses negative binomial distribution to estimate dispersion and model differential expression such as to permit biological variability to be different among tested genes (transcripts). GO terms enrichment and PCA analysis was performed using goseq and Gene Set Enrichment and Projection Displays – GSEPD Bioconductor package. Gene Ontology (GO) terms were grouped into following categories: A. Immune- related GO terms. B. Atherosclerosis- related terms.