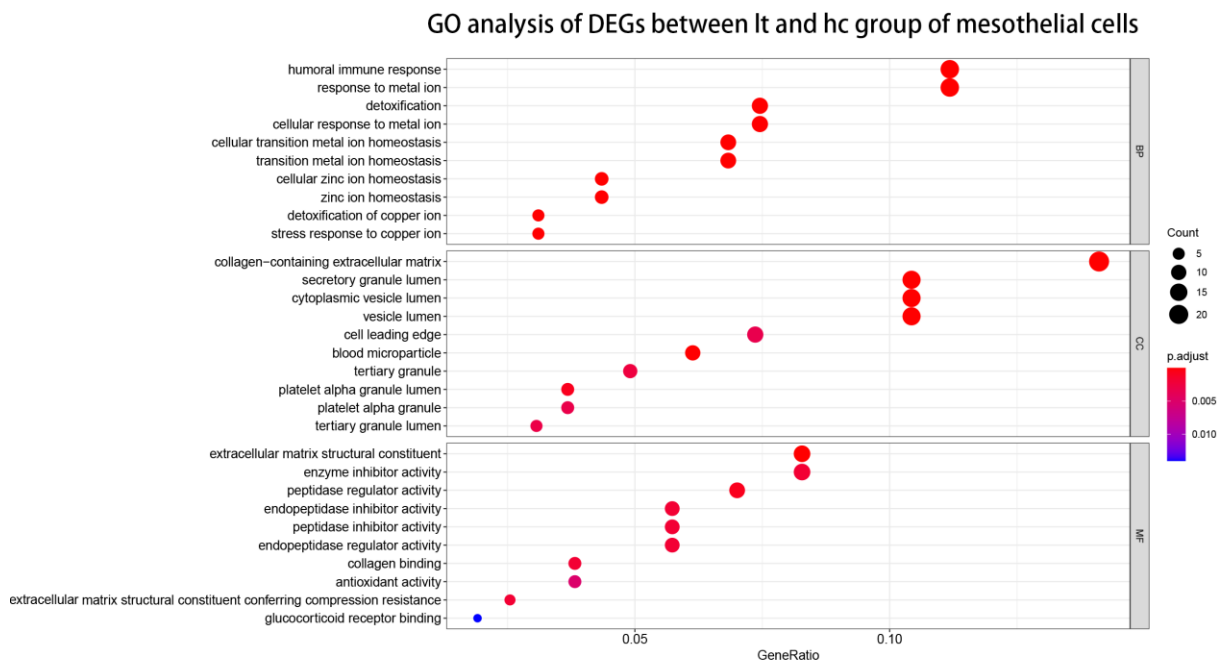
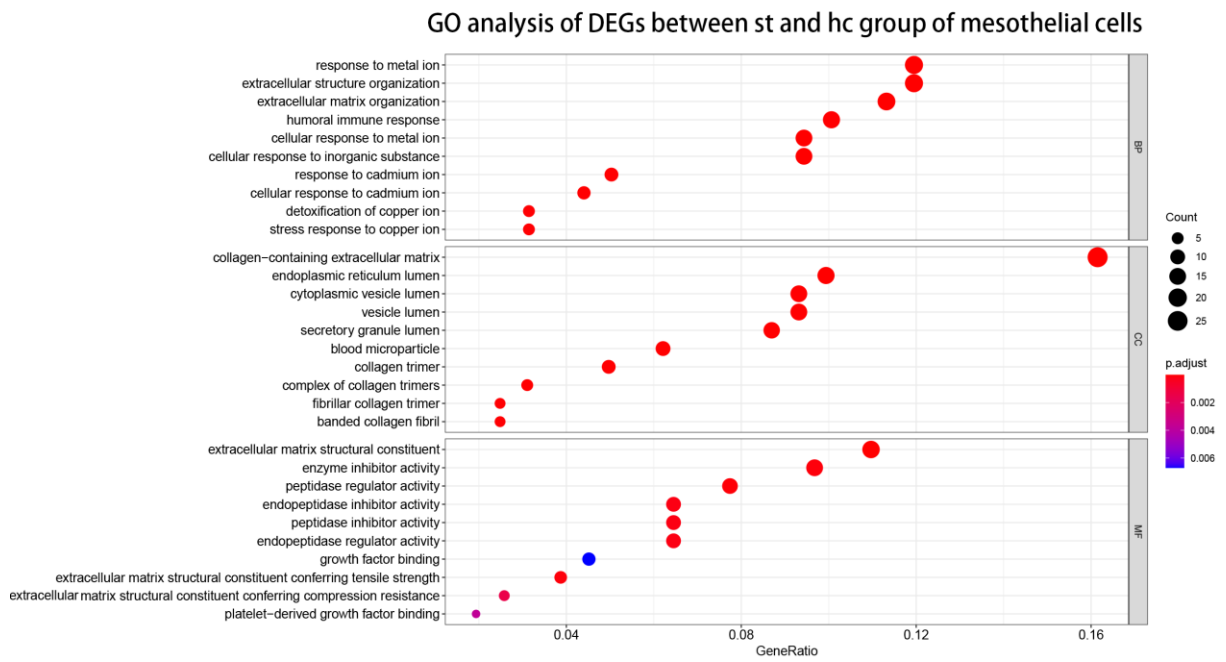
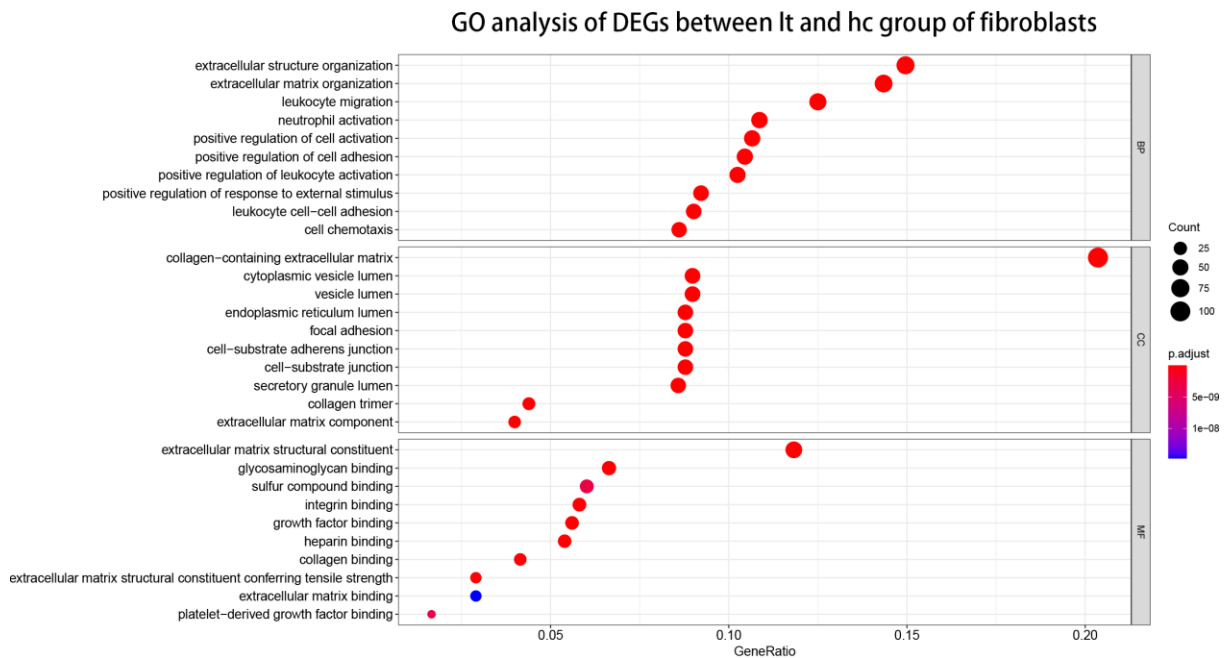
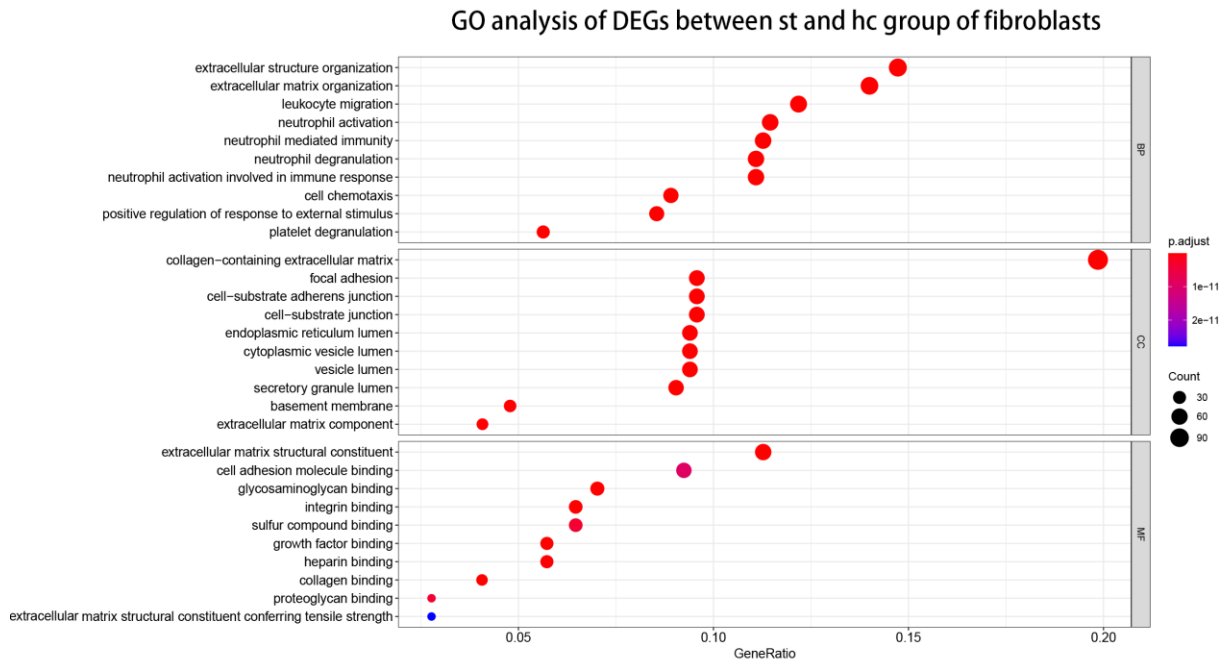


Supplemental Figure 1



Supplemental Figure 1. Gene Ontology enrichment analysis (GO analysis) of DEGs (st vs. hc and lt vs. hc) in mesothelial cells.

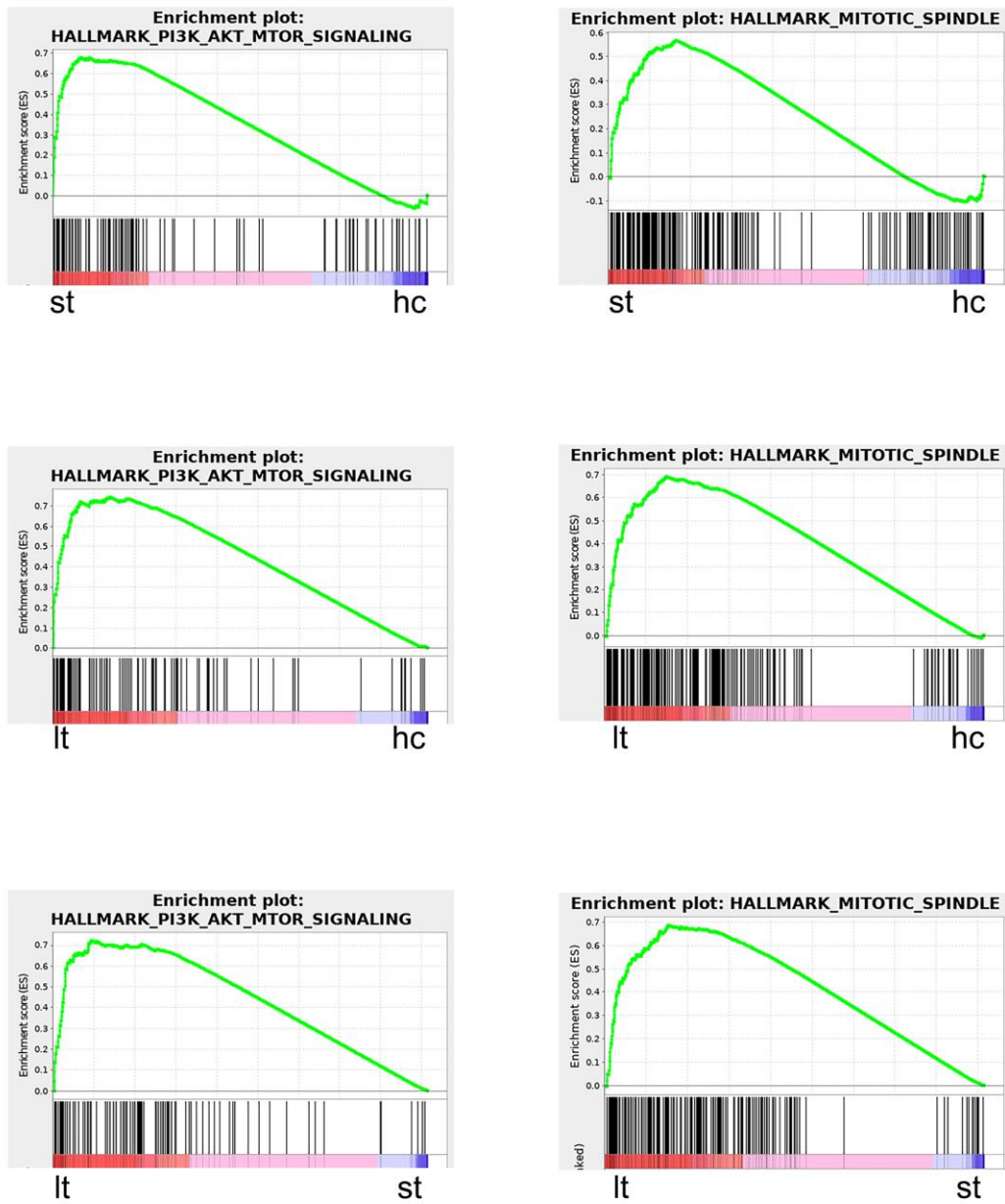
Supplemental Figure 2



Supplemental Figure 2. Gene Ontology enrichment analysis (GO analysis) of DEGs (st vs. hc and lt vs. hc) in fibroblasts.

Supplemental Figure 3

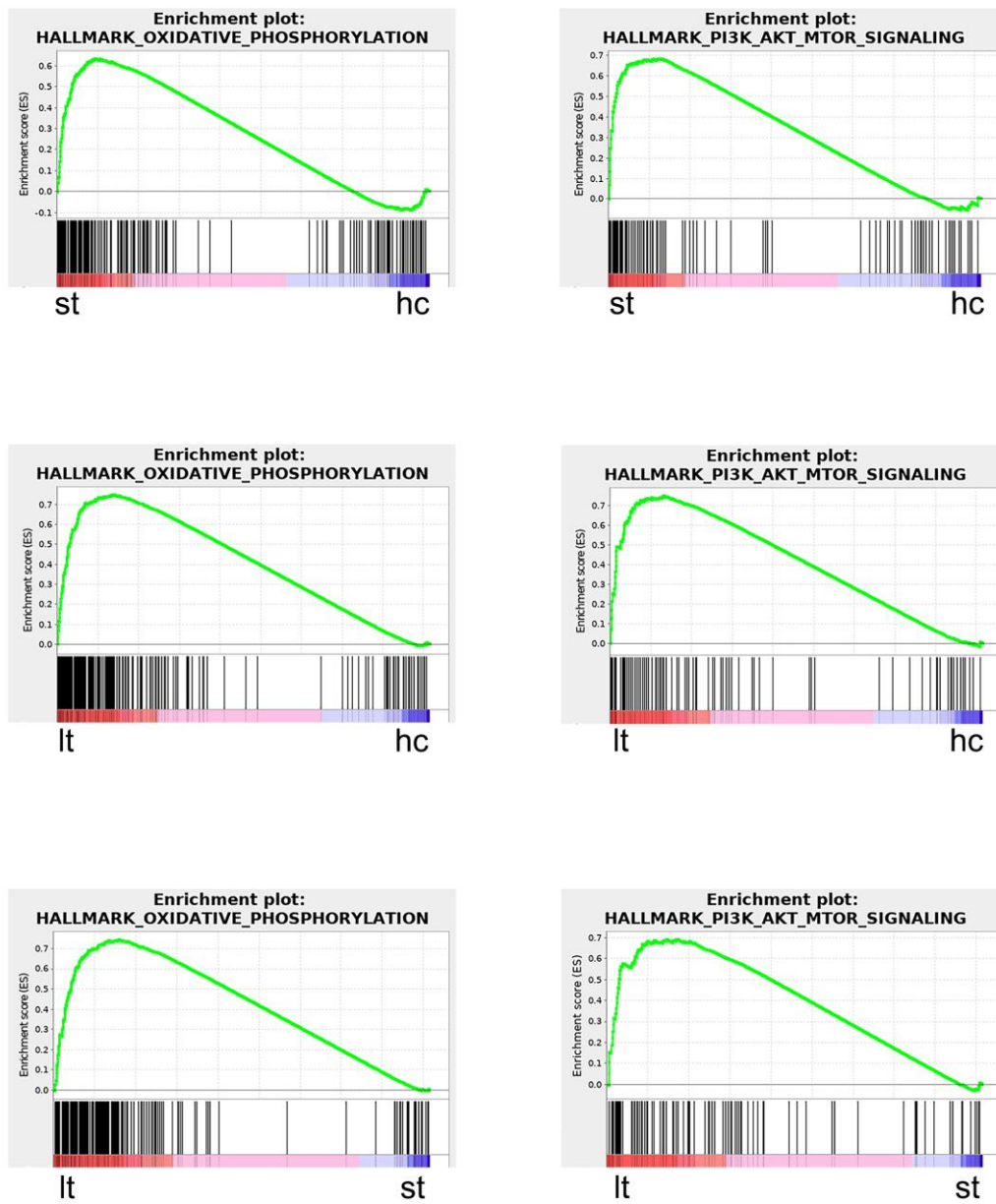
Enriched Gene Sets of Mesothelial cells



Supplemental Figure 3. Intersection gene sets of significantly enriched hallmark sets from GSEA result of each comparison in mesothelial cells corresponding to Figure 3G.

Supplementary Figure S4

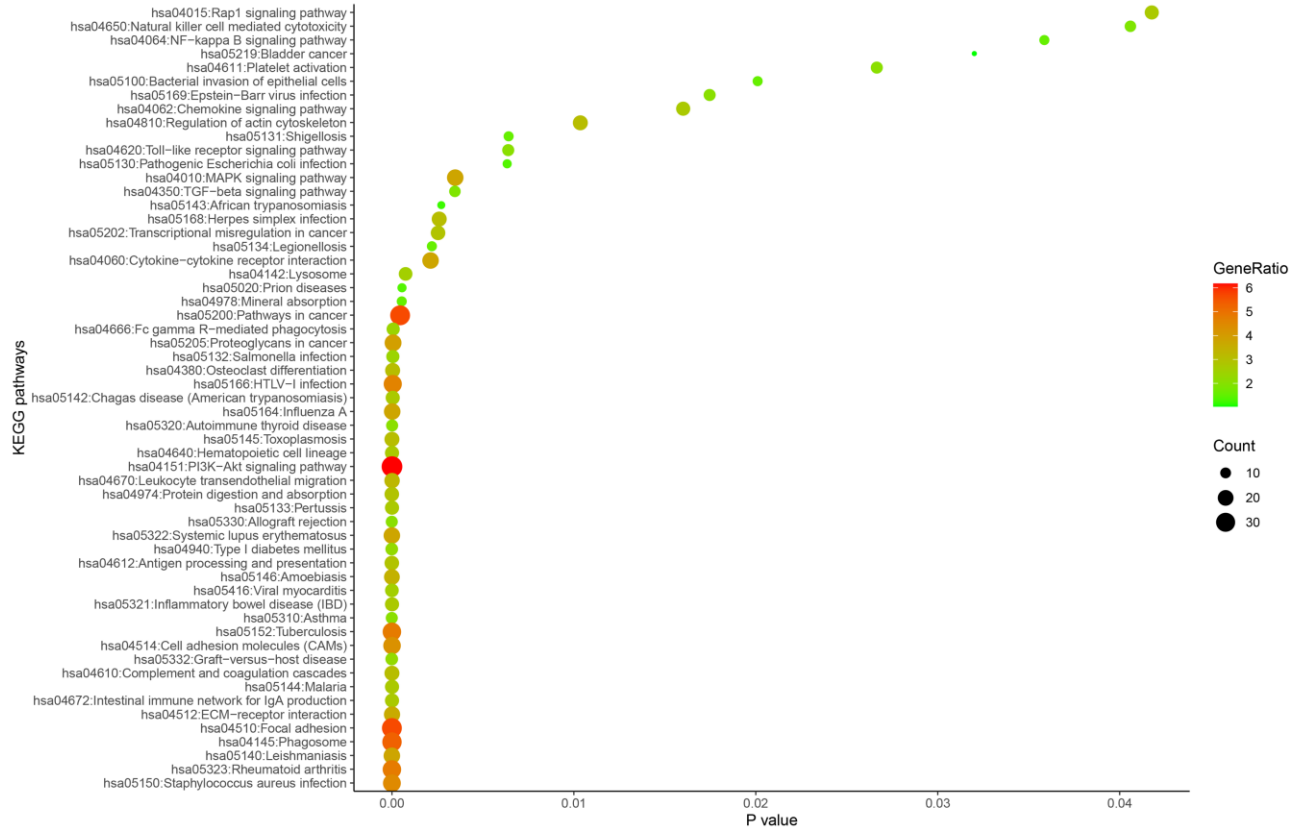
Enriched Gene Sets of Fibroblasts



Supplemental Figure 4. Intersection gene sets of significantly enriched hallmark sets from GSEA result of each comparison in fibroblasts corresponding to Figure 3H.

Supplemental Figure 5

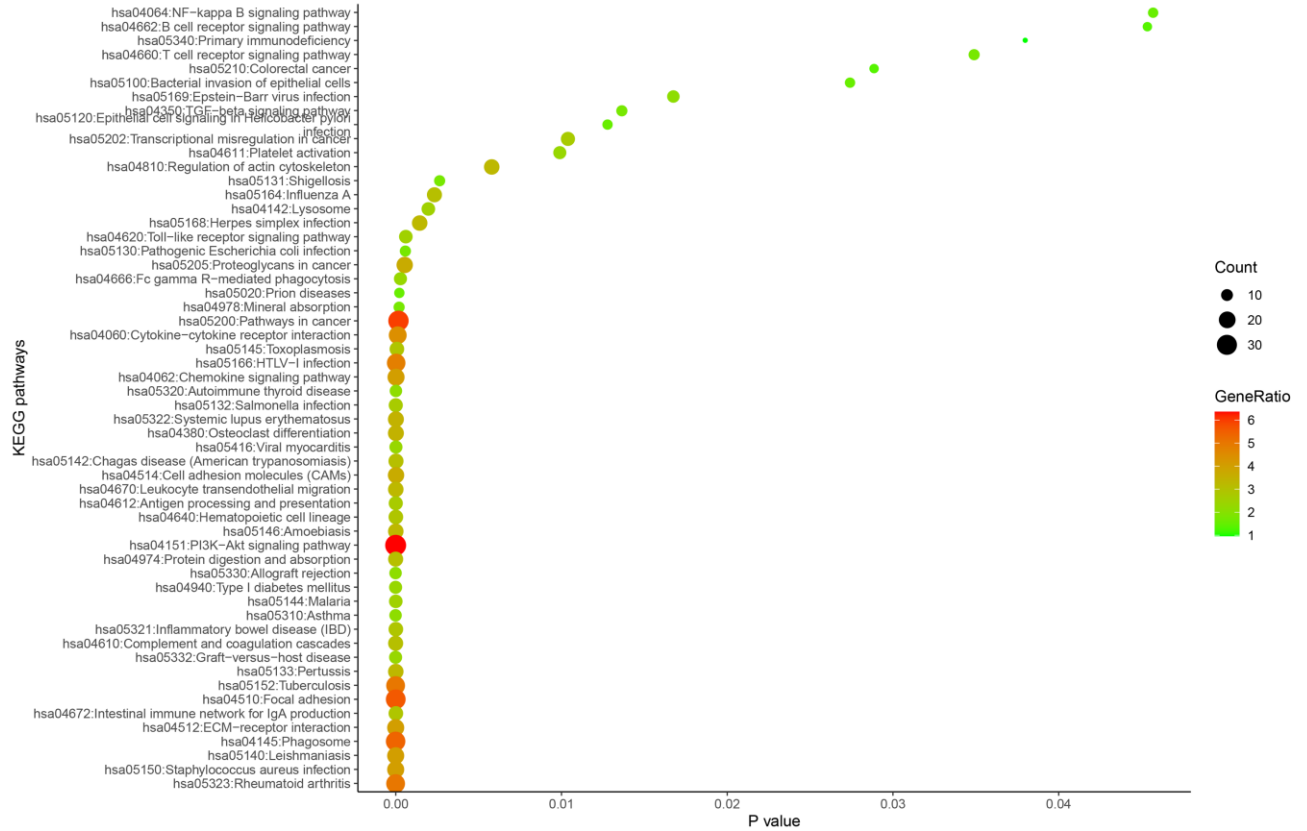
KEGG for DEGs between st and hc group of fibroblasts



Supplemental Figure 5. Enriched pathways in KEGG analysis of DEGs from comparison between st and hc group in fibroblasts.

Supplemental Figure 6

KEGG for DEGs between lt and hc group of fibroblasts



Supplemental Figure 6. Enriched pathways in KEGG analysis of DEGs from comparison between lt and hc group in fibroblasts.