A   GO Analysis

glycosaminoglycan binding
heparin binding
sulfur compound binding
response to lipid
response to hormone
response to steroid hormone
response to organic cyclic compound

PROS1
KRT19
RXRG
CCND1
CITED1
SLC34A2
MDK
FN1
GABRB2
LTPH
TENM1
CFH

B   Pathway Analysis

KEGG_CELL ADHESION MOLECULES CAMS
KEGG_LEUKOCYTE TRANSENDOTHELIAL MIGRATION
REACTOME_TIGHT JUNCTION INTERACTIONS
REACTOME_CELL JUNCTION ORGANIZATION
REACTOME_CELL CELL ADHESION SYSTEMS
KEGG_TIGHT JUNCTION
KEGG_PATHWAYS IN CANCER
KEGG_SMALL CELL LUNG CANCER
KEGG_NON SMALL CELL LUNG CANCER
KEGG_THYROID CANCER
KEGG_COMPLEMENT AND COAGULATION CASCADES
REACTOME_CELL SURFACE INTERACTIONS AT THE VASCULAR WALL
REACTOME_FORMATION OF PLATELET PLUG
REACTOME_PLATELET ACTIVATION
REACTOME_PLATELET DEGRANULATION

RXRG
CCND1
PROS1
CFH
FN1
PPP2R2B
CLDN1
CLDN16

Corresponding gene-term association positively reported

Corresponding gene-term association not reported yet

The proportion of genes associated with the term:

0%
20%
40%
60%
80%
100%

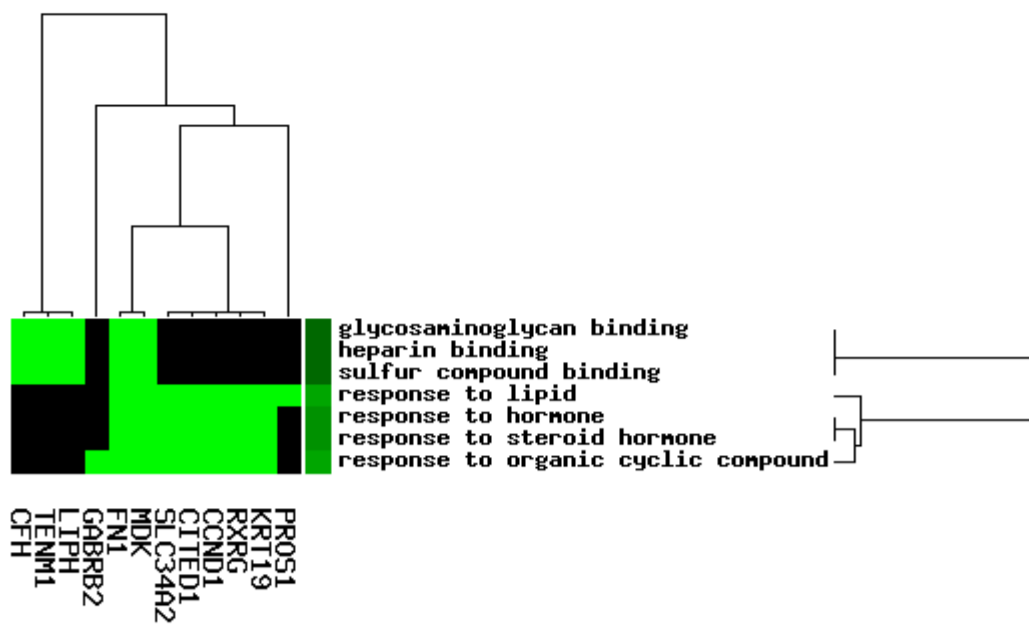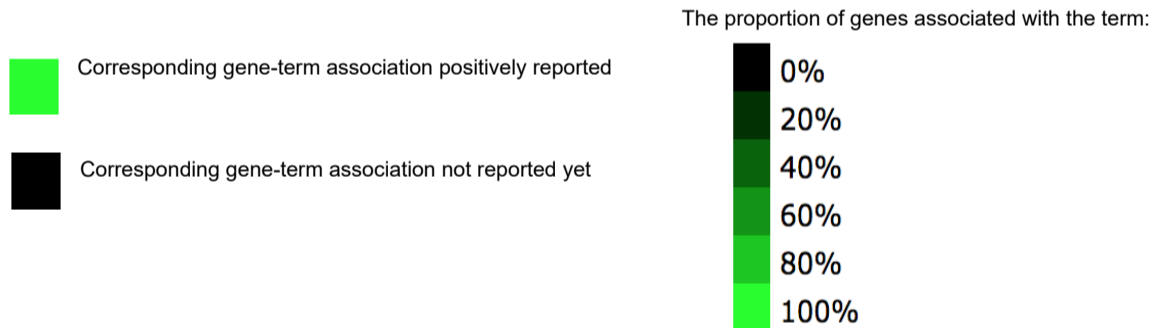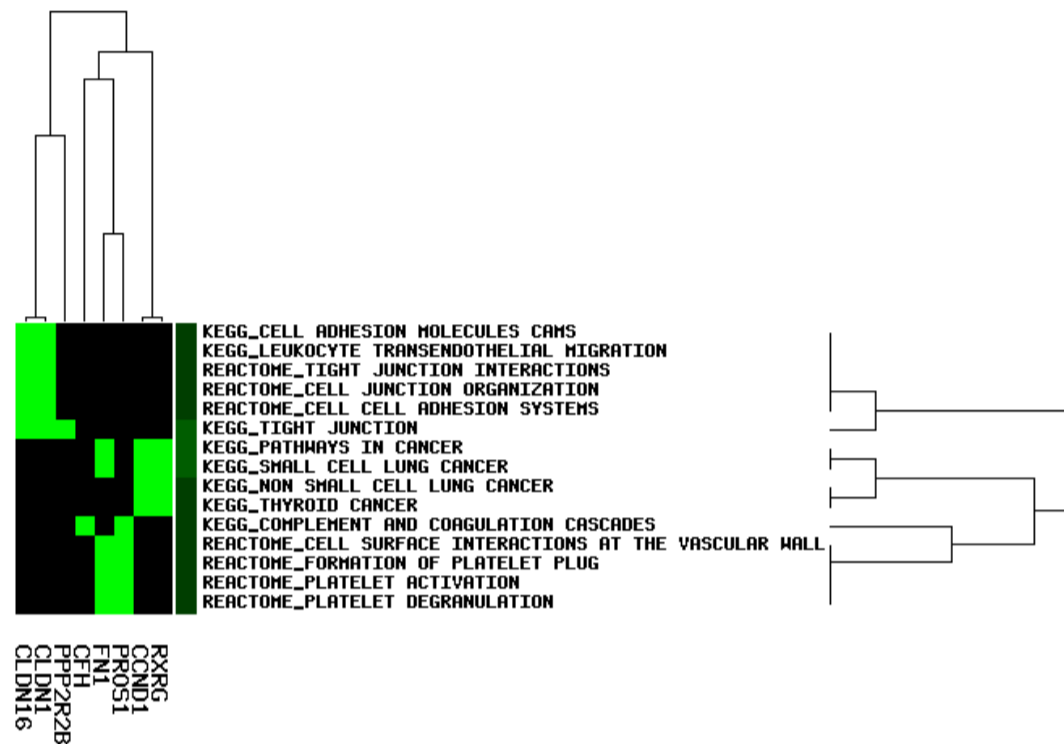**Supporting Figure 6.** GO and pathway analysis of Genes Significant (GS). Clustering analysis of the biological functions of 22 genes in previous studies for GO (A) and Pathway (B) generated by the GenClip software. In the heatmap, the black color represents that the biological function of the corresponding gene-term association has not been reported yet. While light green color means that the corresponding gene-term association positively has been reported. The color scale bar for proportion of genes associated were labelled.