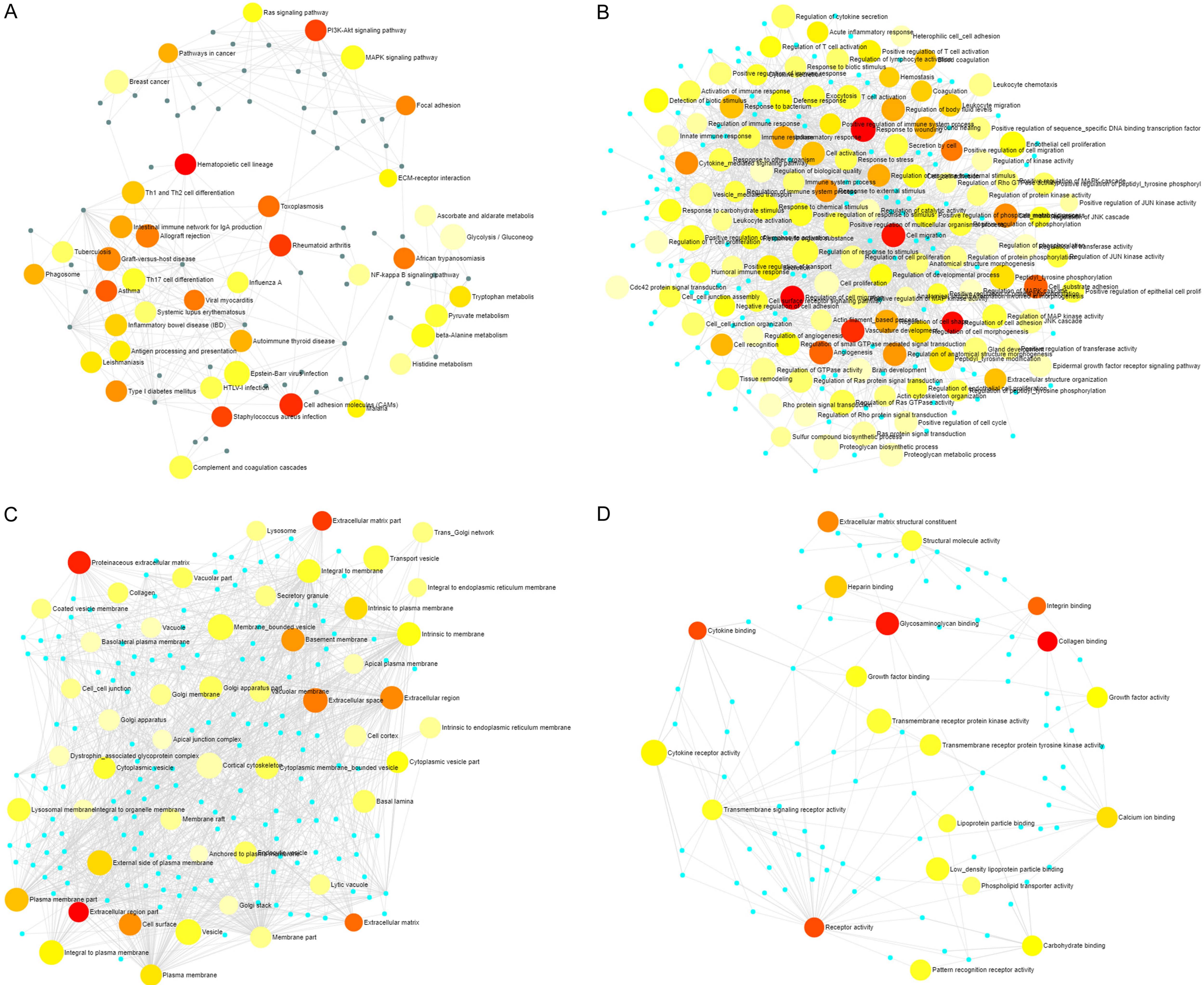


Figure S1. The expression of marker genes in each cell lineage. A. The t-SNE map of all cells generated from ASAP. B-I. The t-SNE plots showing specific marker genes' expression level by color gradient.



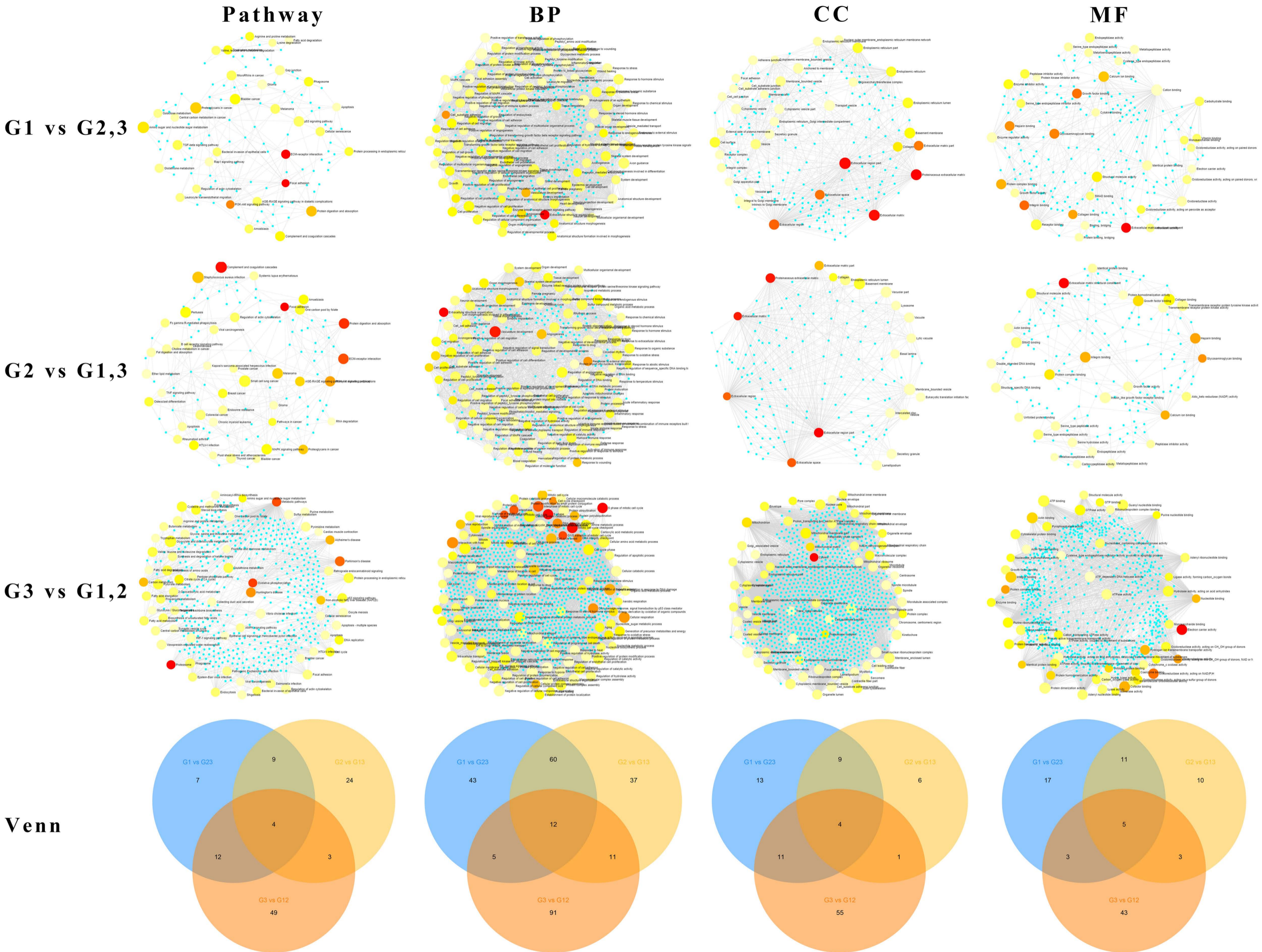


Figure S3. The networks of DEGs-pathways and DEGs-GOs in CAFs. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets were shown successively. The last row shows the Venn diagrams of each network type. The bigger colorful circles represent function items and the blue points represent DEGs.

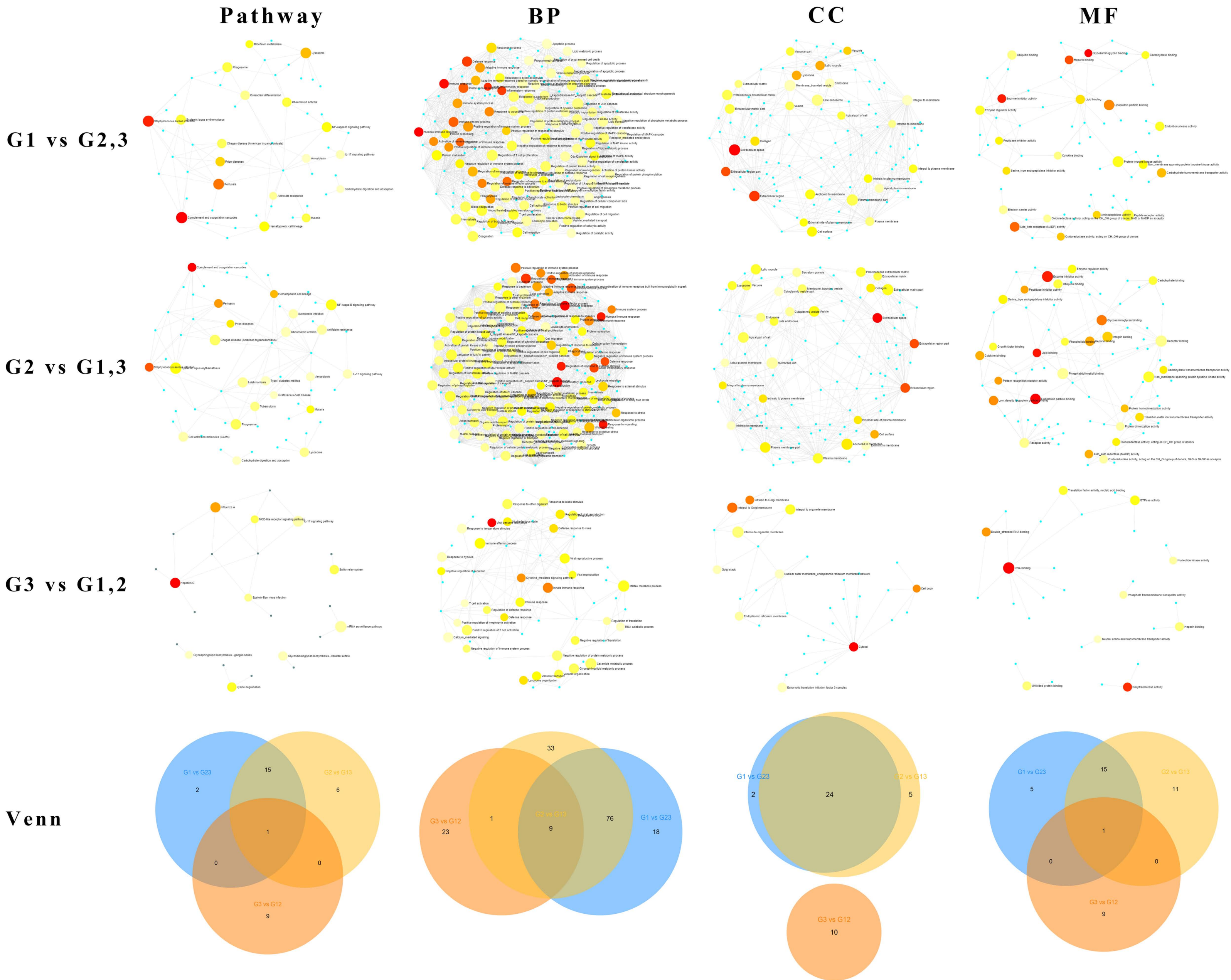


Figure S4. The networks of DEGs-pathways and DEGs-GOs in macrophages. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets were shown successively. The last row shows the Venn diagrams of each network type. The bigger colorful circles represent function items and the blue points represent DEGs.

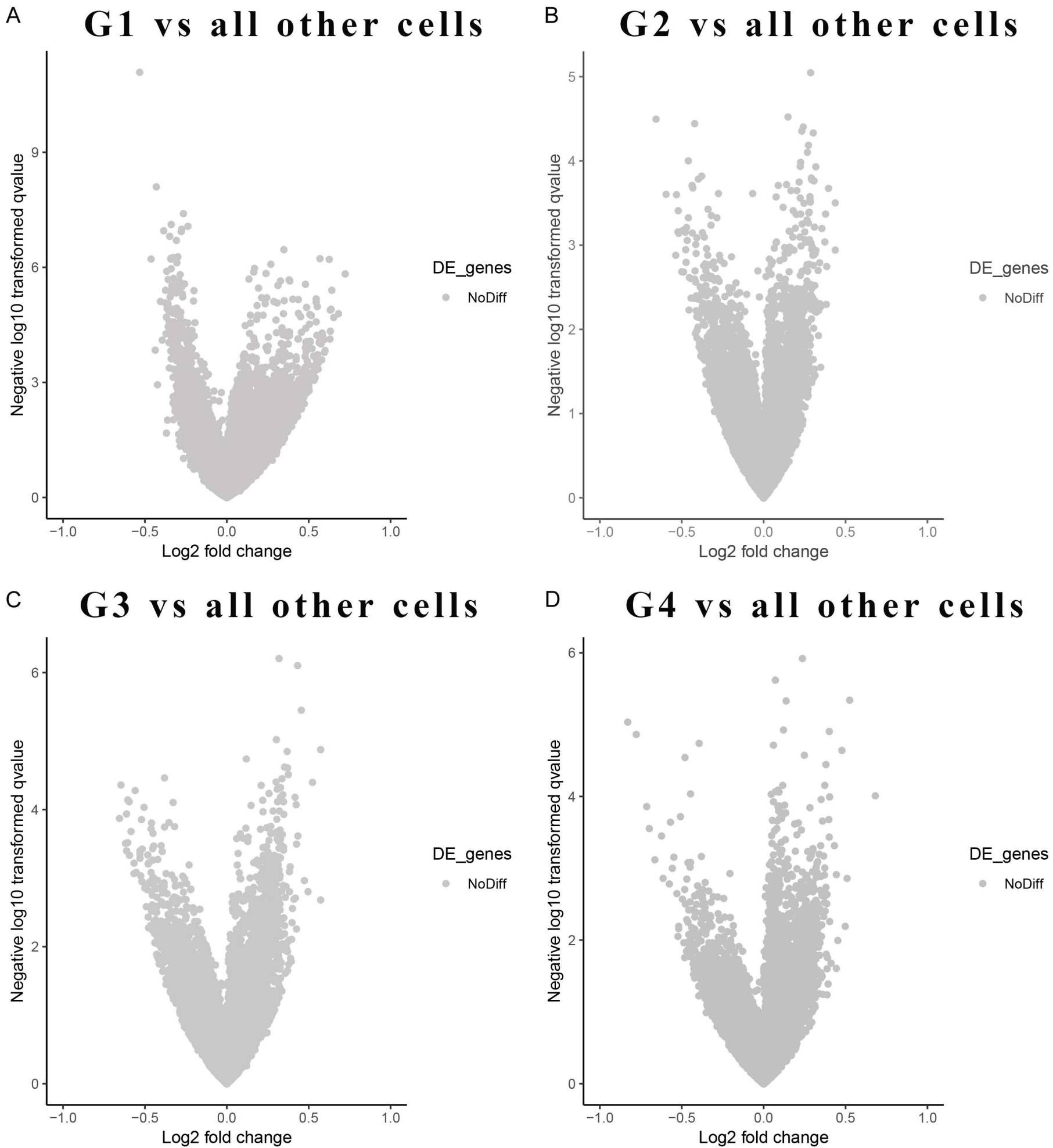


Figure S5. There was no significant DEGs in 4 B cell groups (G1-4) when compared with others. The gray dots represent genes without significant difference.

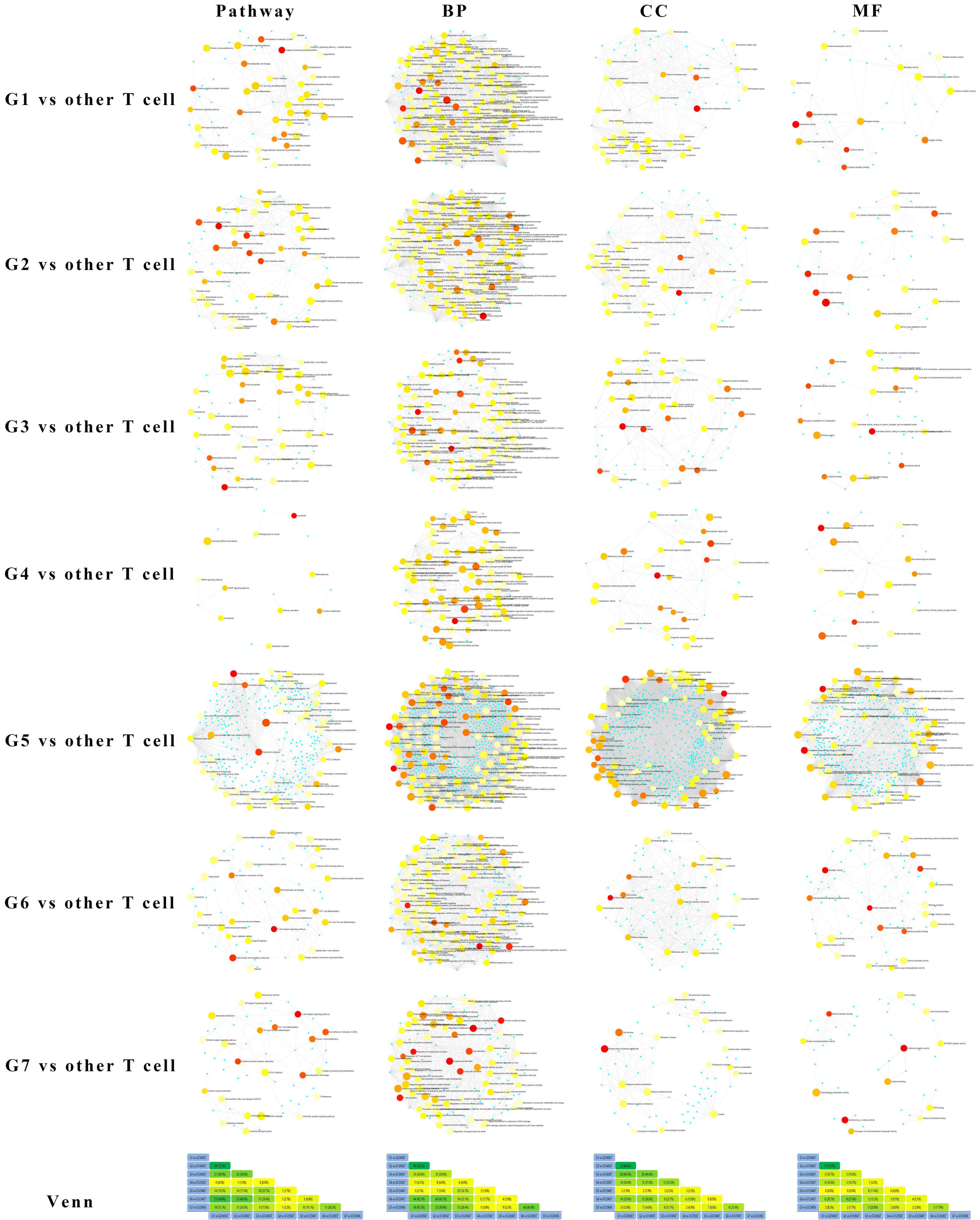


Figure S7. The networks of DEGs-pathways and DEGs-GOs in T cell. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets were shown successively. The last row shows the Venn diagrams of each network type. The bigger colorful circles represent function items and the blue points represent DEGs.

Heatmap

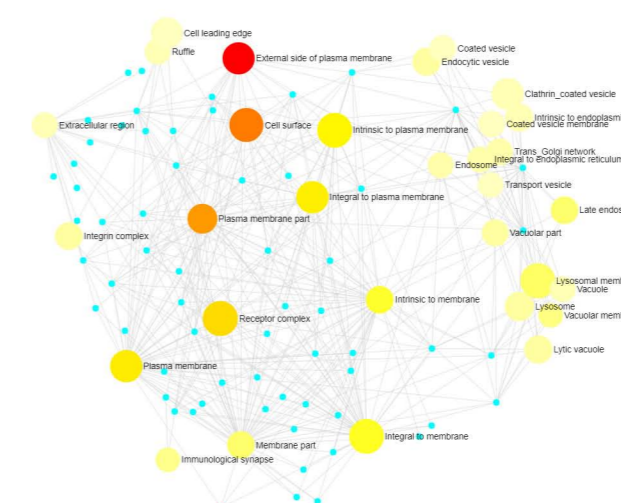
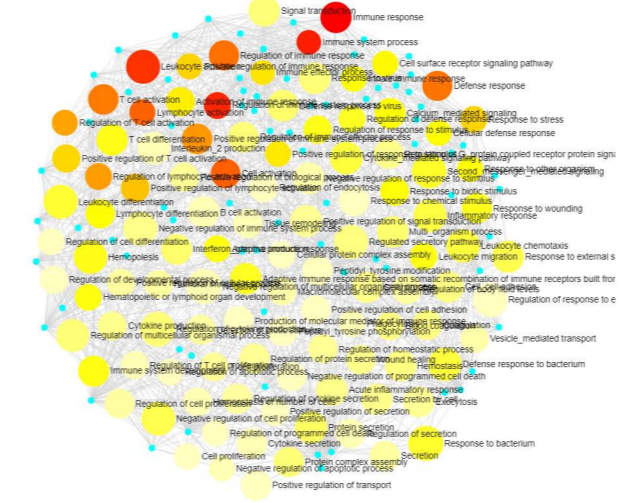
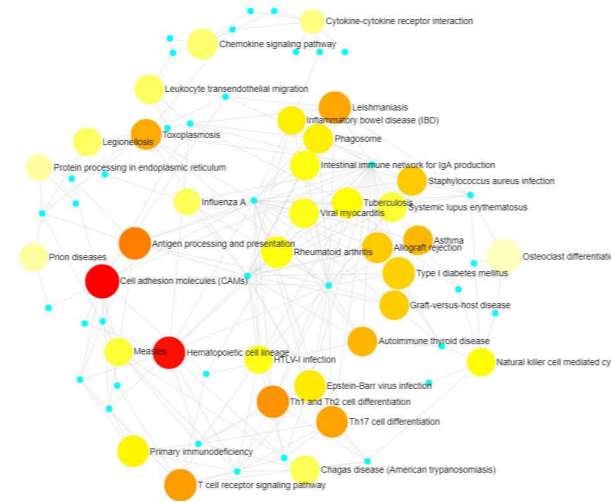
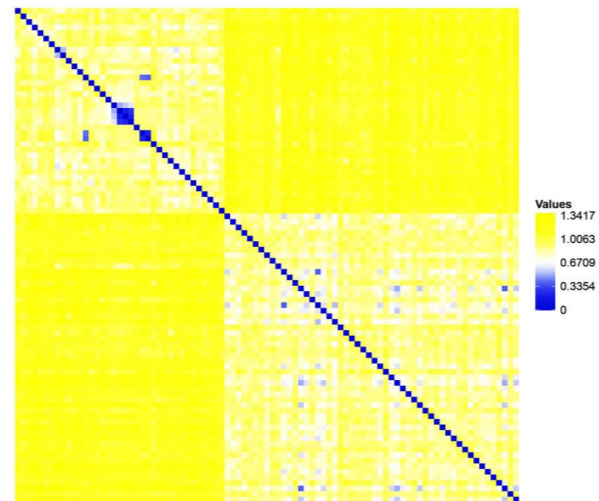
Pathway

BP

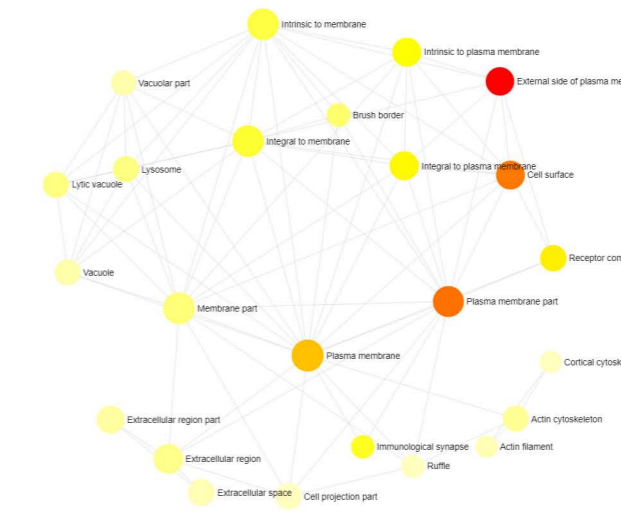
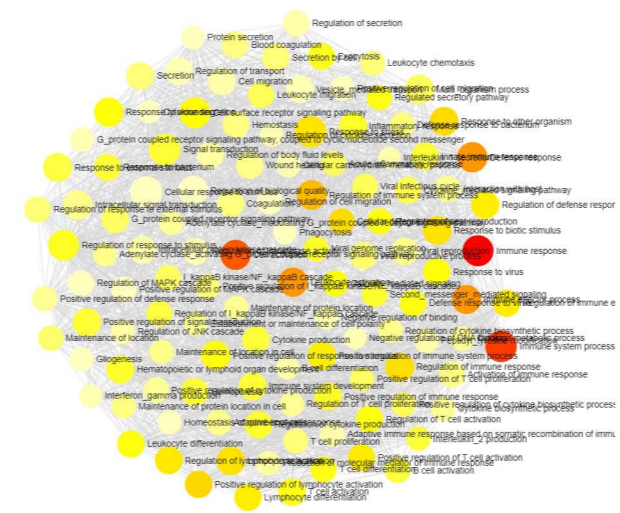
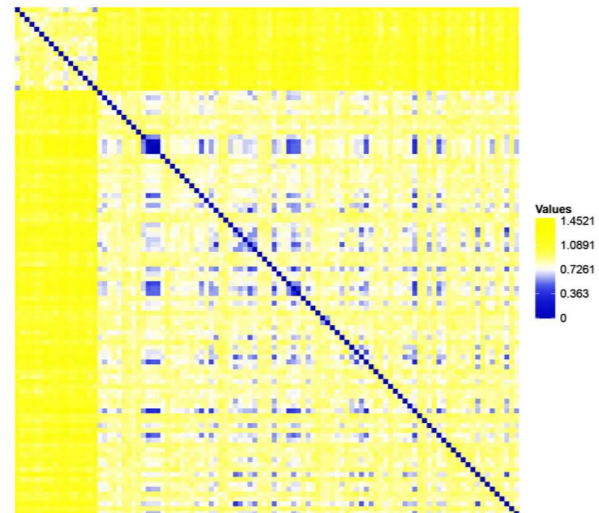
CC

MF

G NK cell vs G T cell
(G 6 vs G1, 5)



G NK cell vs G T memory cell
(G 6 vs G 2, 3, 4, 7)



G T cell vs G T memory cell
(G 1, 5 vs G2, 3, 4, 7)

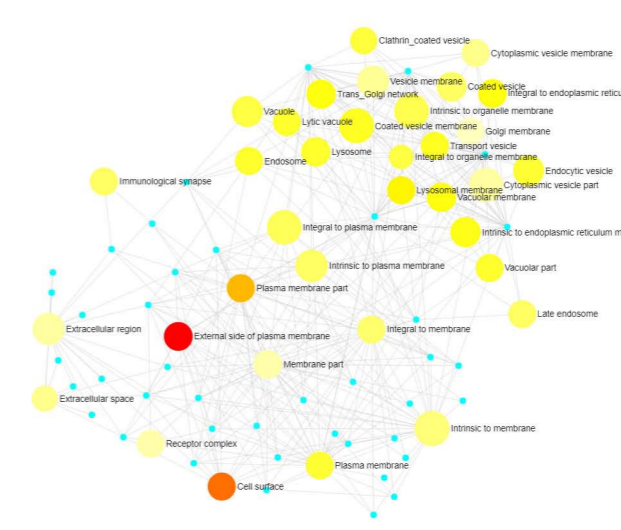
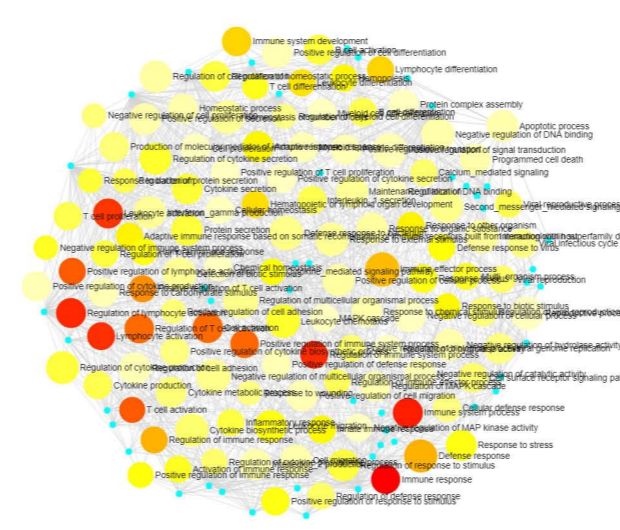
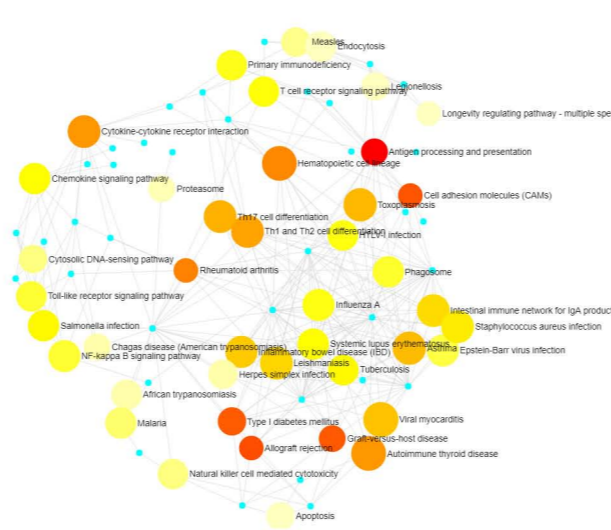
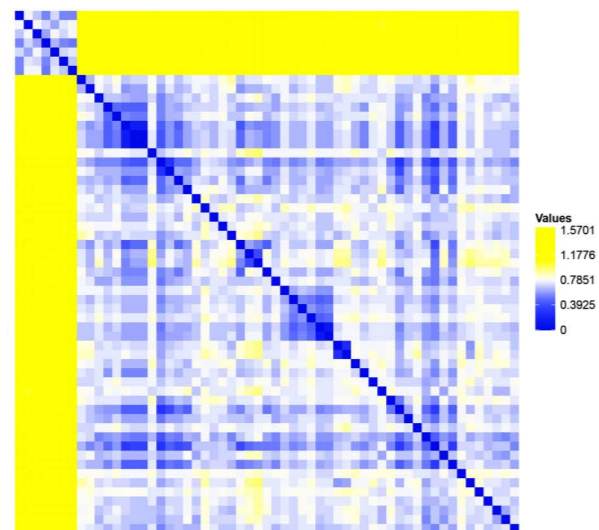


Figure S8. The networks of DEGs-pathways and DEGs-GOs in T cell (3 clusters include T cells, memory T cells and NK cells). The heatmap and networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets (G NK cell vs. G T cell, G NK cell vs. G memory T cell and G T cell vs. G memory T cell) were shown successively.

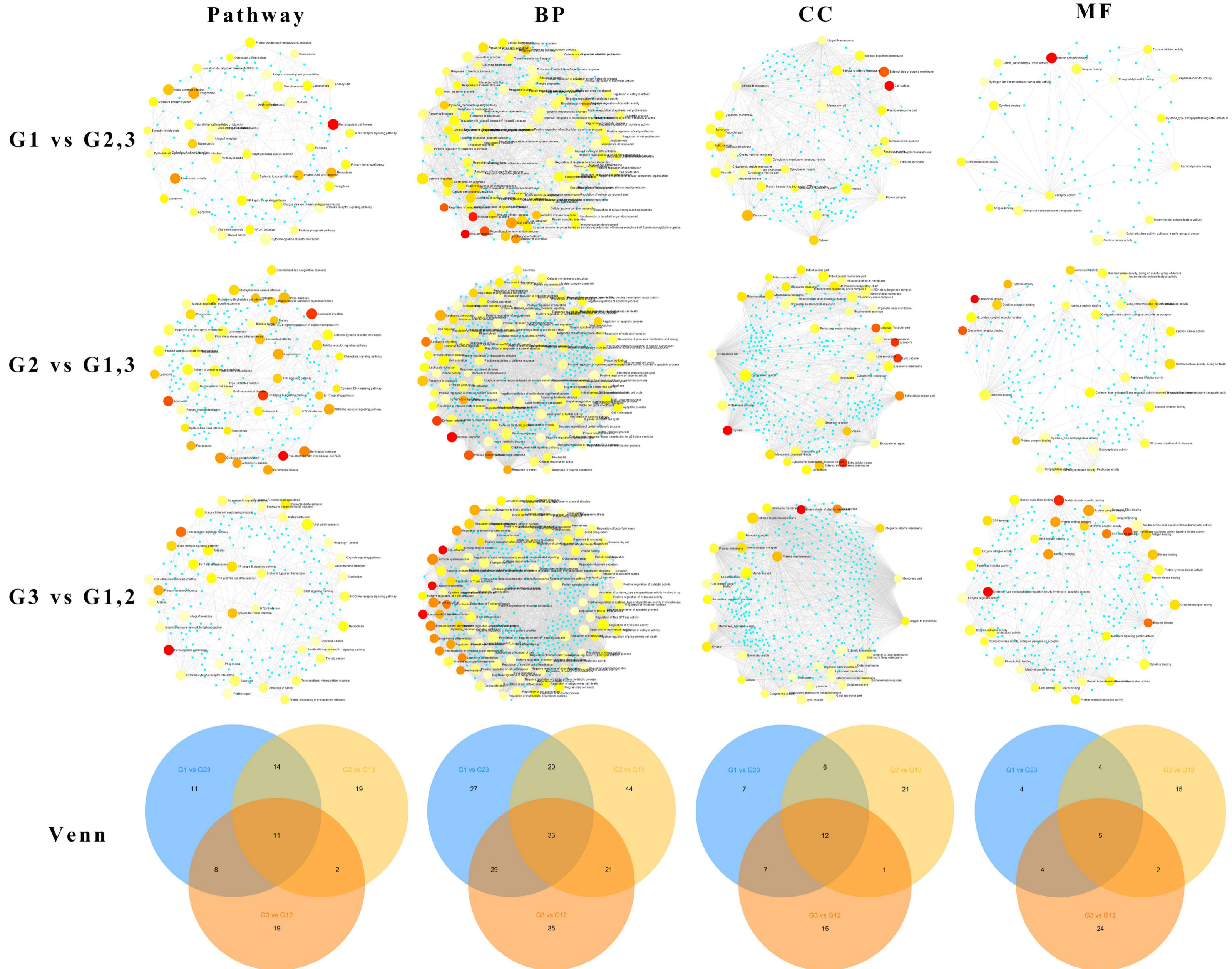


Figure S9. The networks of DEGs-pathways and DEGs-GOs in memory T cell. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets were shown successively. The last row shows the Venn diagrams of each network type. The bigger colorful circles represent function items and the blue points represent DEGs.

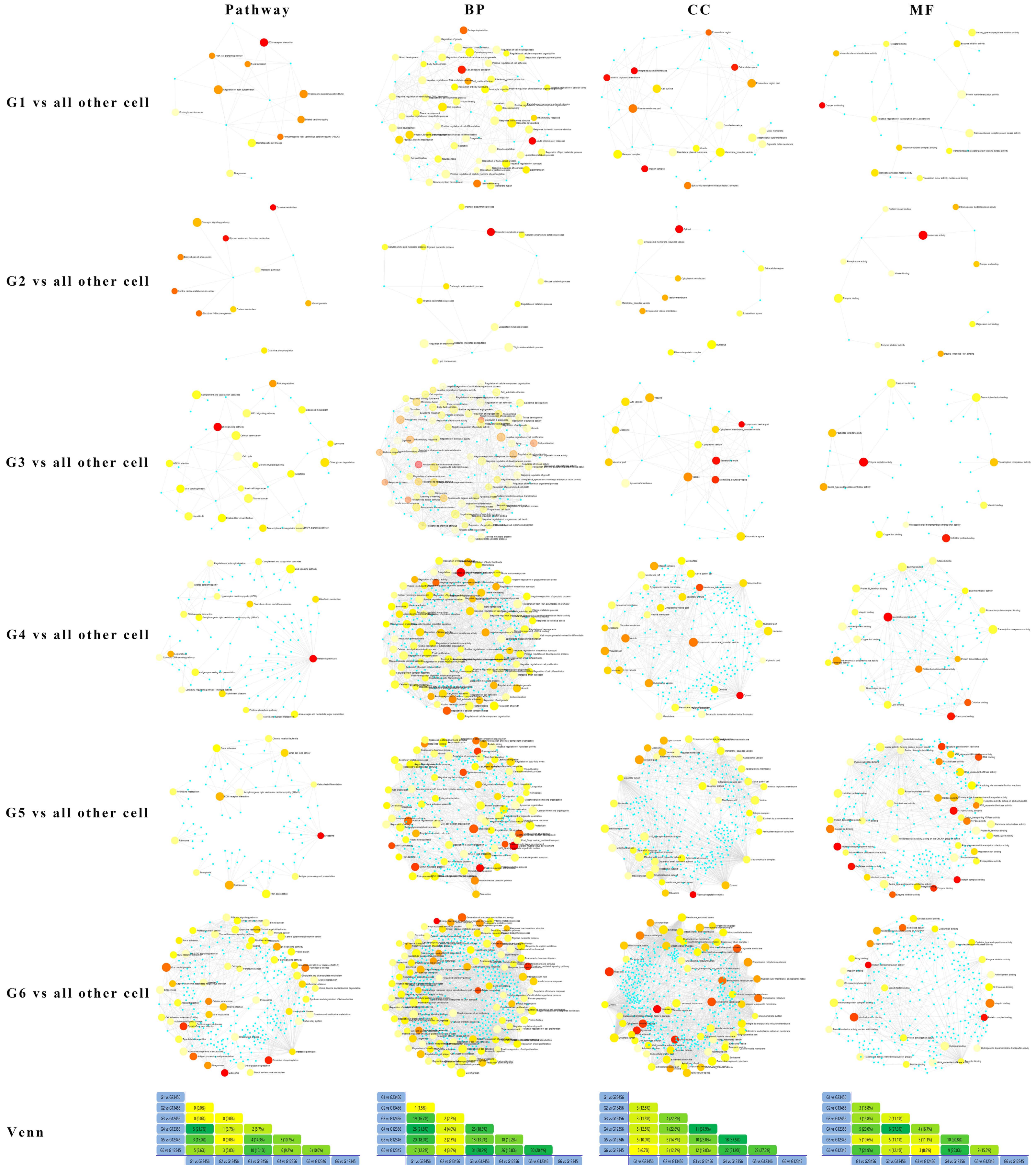


Figure S10. The networks of DEGs-pathways and DEGs-GOs in melanocytes. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets were shown successively. The last row shows the Venn diagrams of each network type. The bigger colorful circles represent function items and the blue points represent DEGs.

tSNE of melanocyte

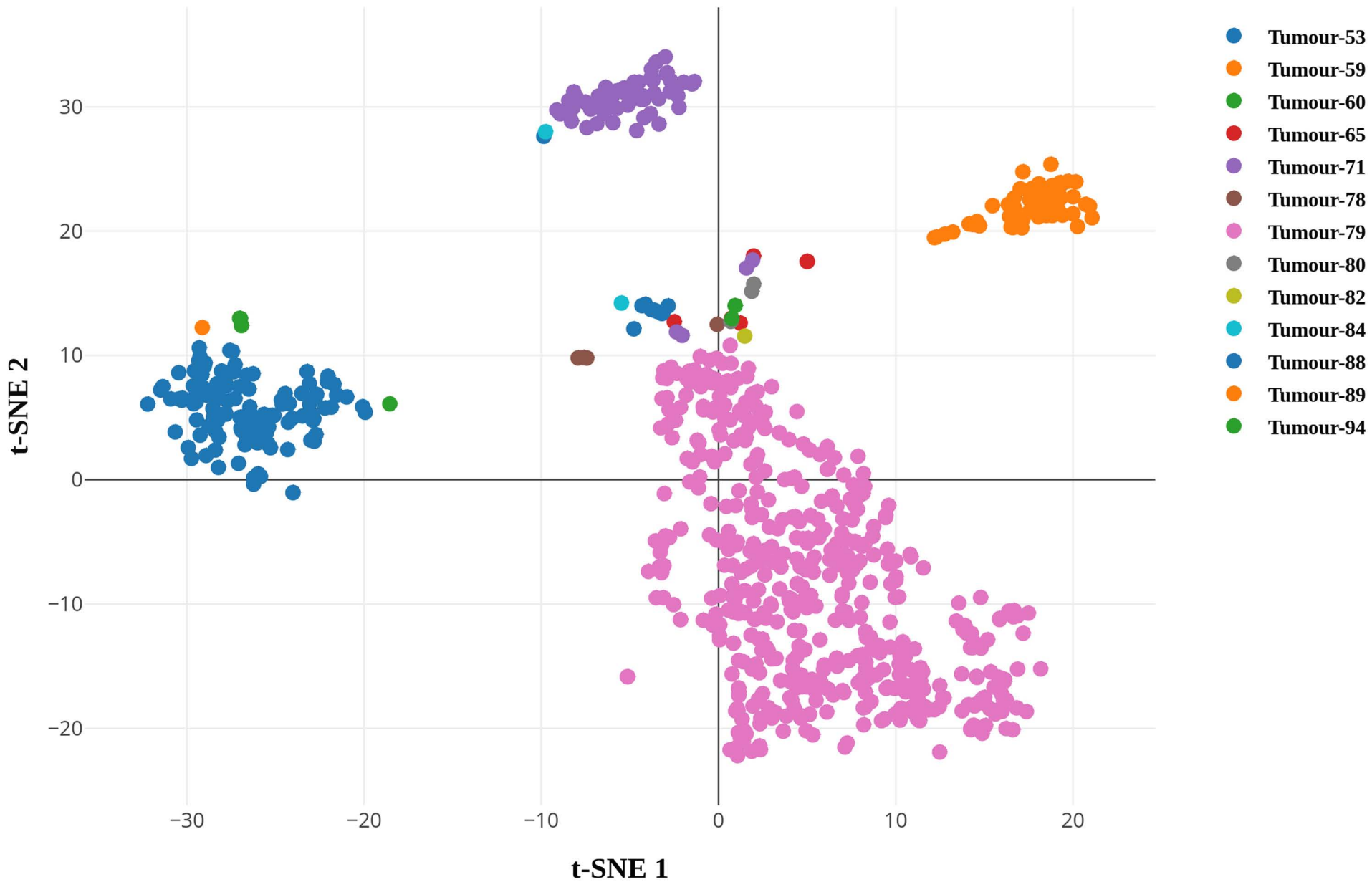


Figure S11. The t-SNE of melanocyte colored by sample ID.

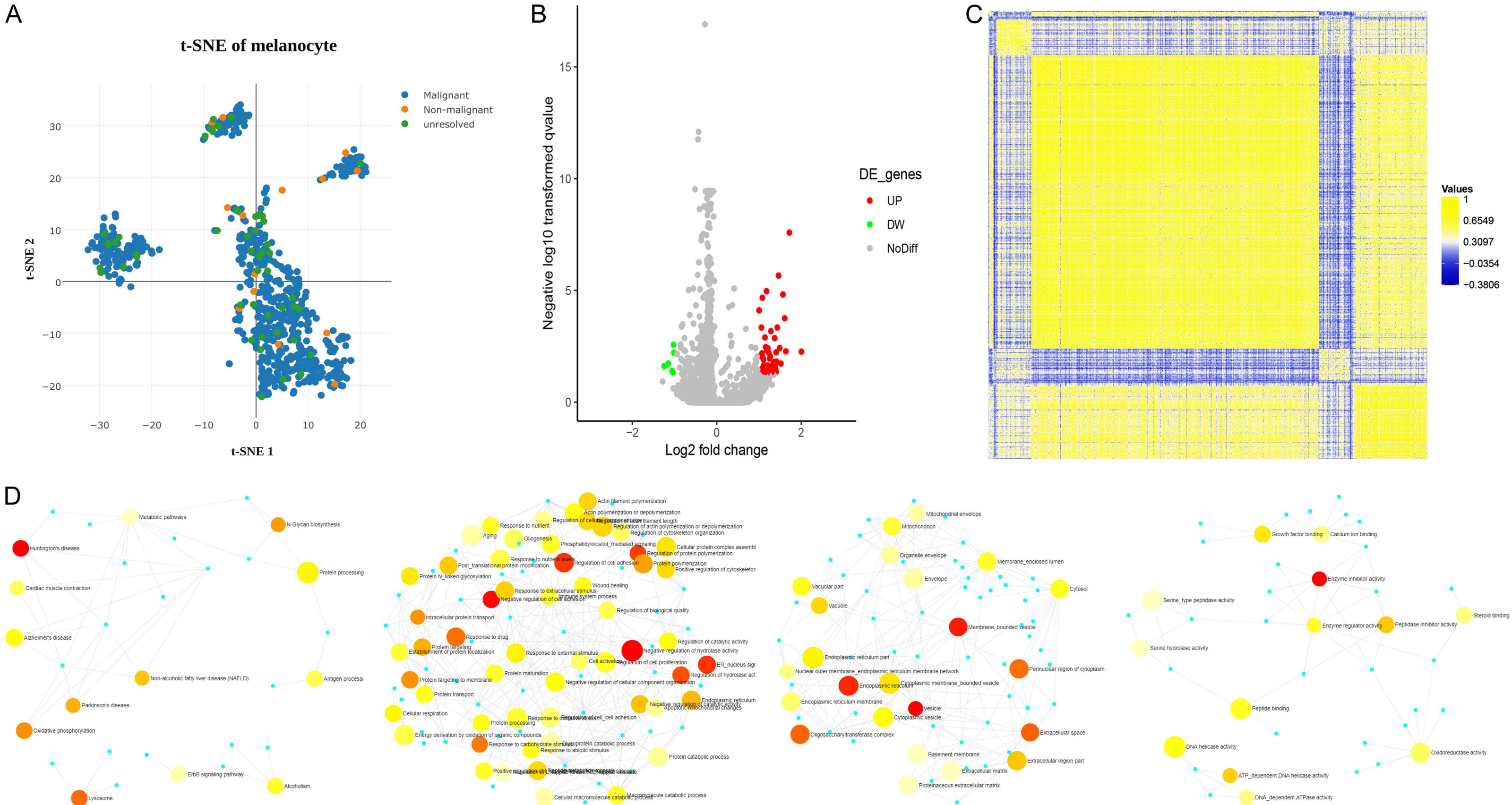


Figure S12. The networks of DEGs-pathways and DEGs-GOs in melanocytes (malignant vs. non-malignant). A. The t-SNE plot of melanocytes which colored by malignance. B. The volcano plots of DEGs in malignant cells when compared with non-malignant ones, each dot represents a gene. The gray ones represent genes without significant difference while the green and red ones represent decreased and increased genes in malignant group. C. The heatmap of DEGs, legend for relative expression from lowest expression (blue) to highest expression (yellow) (top right). D. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of DEGs in malignant cells.

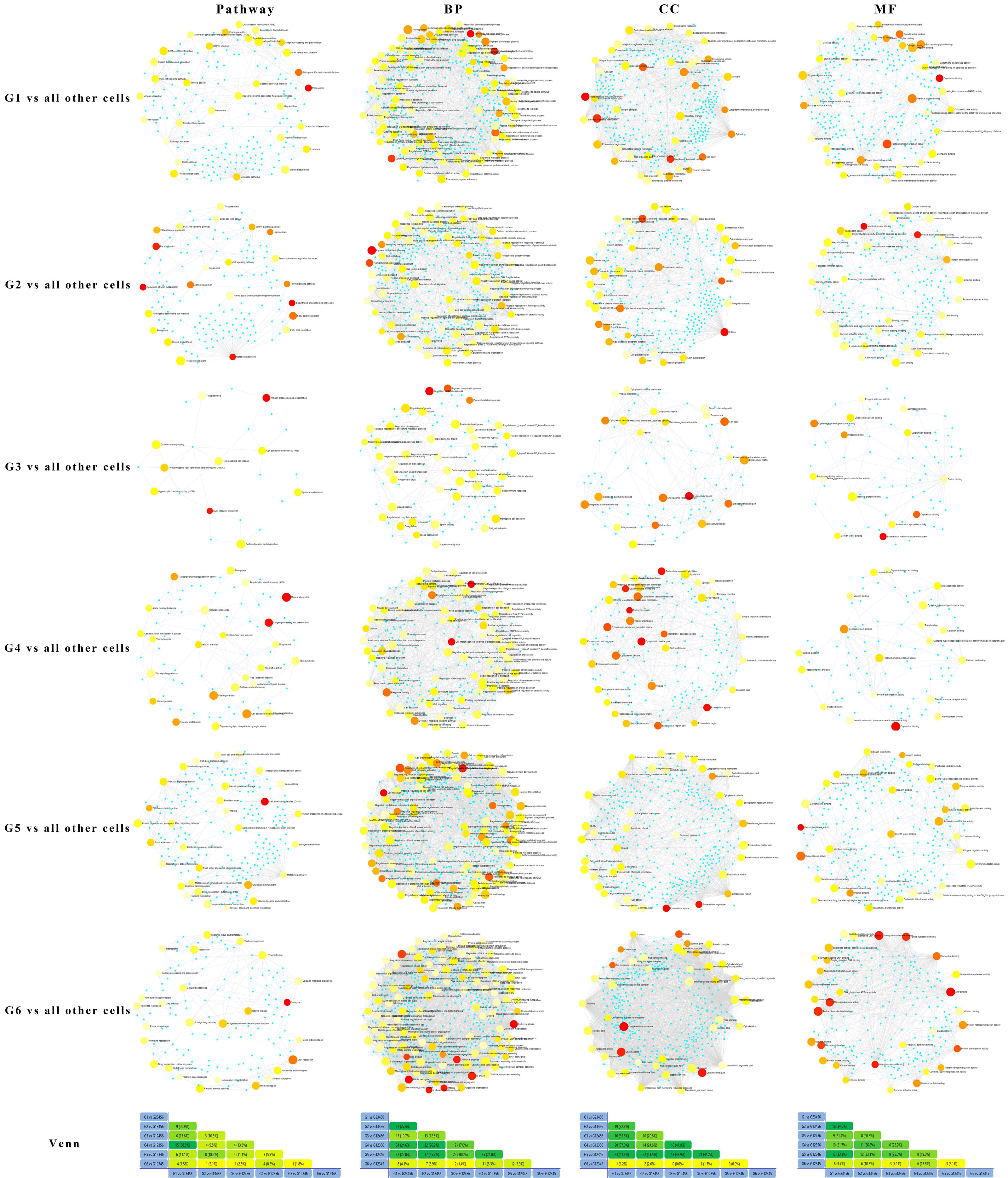


Figure S13. The networks of DEGs-pathways and DEGs-GOs in podocyte cell. The networks of DEGs-pathways, DEGs-BPs, DEGs-CCs and DEGs-MFs of each DEG-sets were shown successively. The last row shows the Venn diagrams of each network type. The bigger colorful circles represent function items and the blue points represent DEGs.

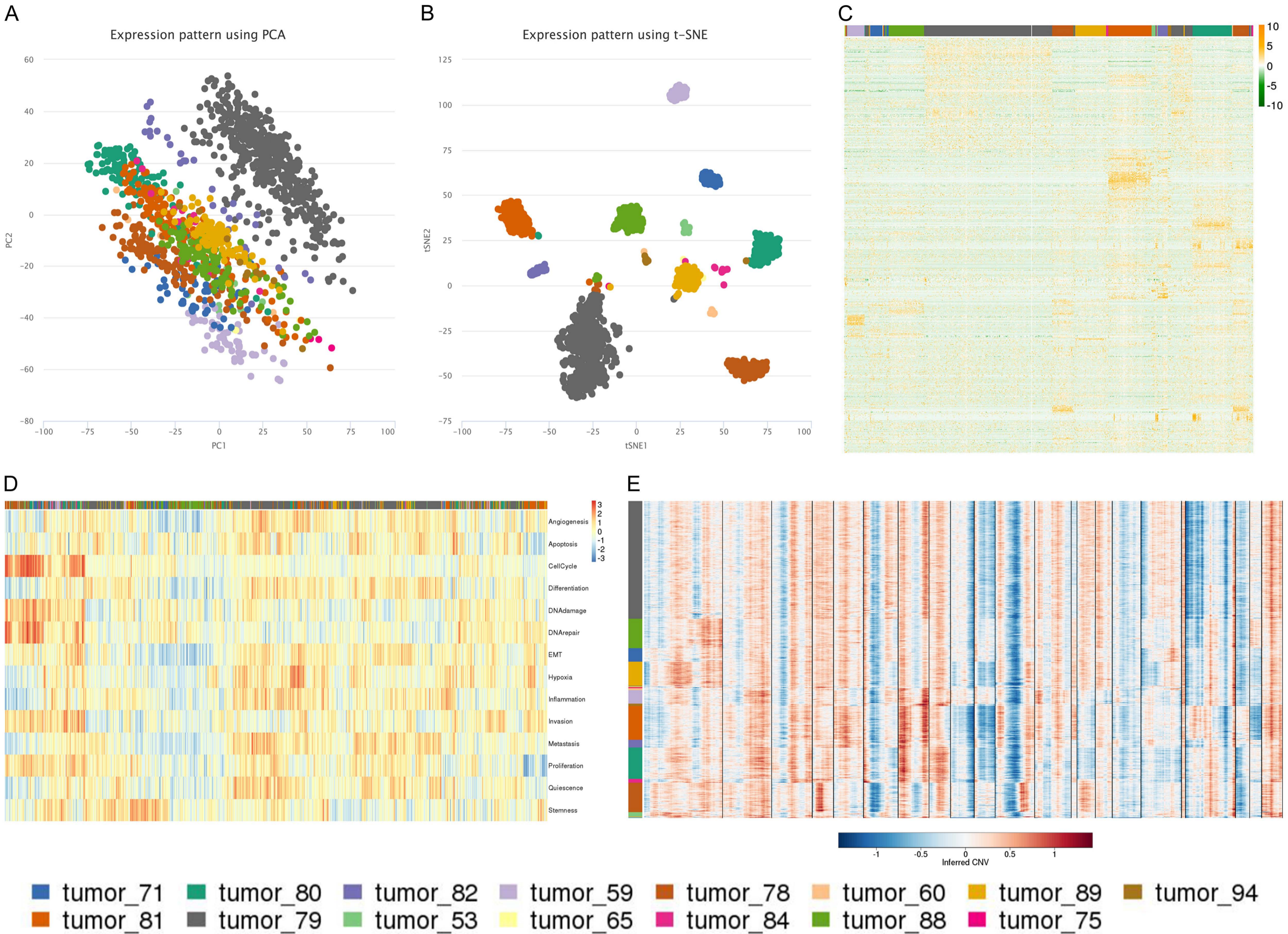


Figure S14. Analysis of 1257 malignant cells in CancerSEA. A and B. PCA and t-SNE plots of 1257 malignant cells colored by sample ID. C. The heatmap shows the expression profile of highly variable genes. Row represents hierarchically clustered highly variable genes, and columns represent single cells. D. The heatmap displays the activity of function states of cells in 1257 malignant cells. Rows represent function states, columns represent hierarchically clustered cells. E. The heatmap shows the inferred CNV profile of cells. Rows represent hierarchically clustered cells, columns represent genes which ordered by genomic location (1-22 and X), and separation represents the gap of chromosomes. Colorful labels indicates the cell groups.

Expression distribution with t-SNE plot

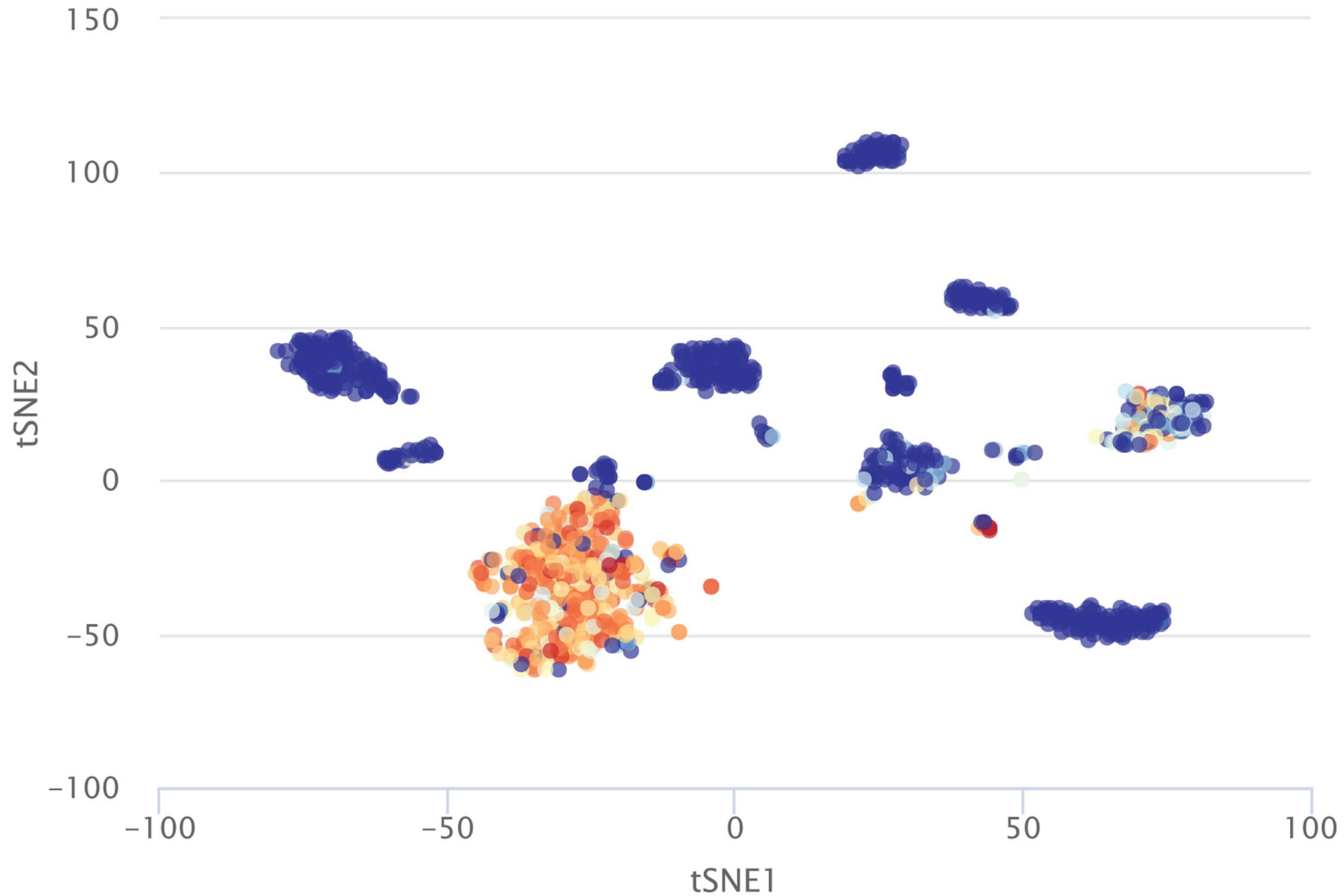


Figure S15. The expression of APOC2 in 15 tumor samples. T-SNE describes the distribution of cells depend on APOC2 level, every point represents a single cell, and the color of the point represents the expression level of the gene in the cell.

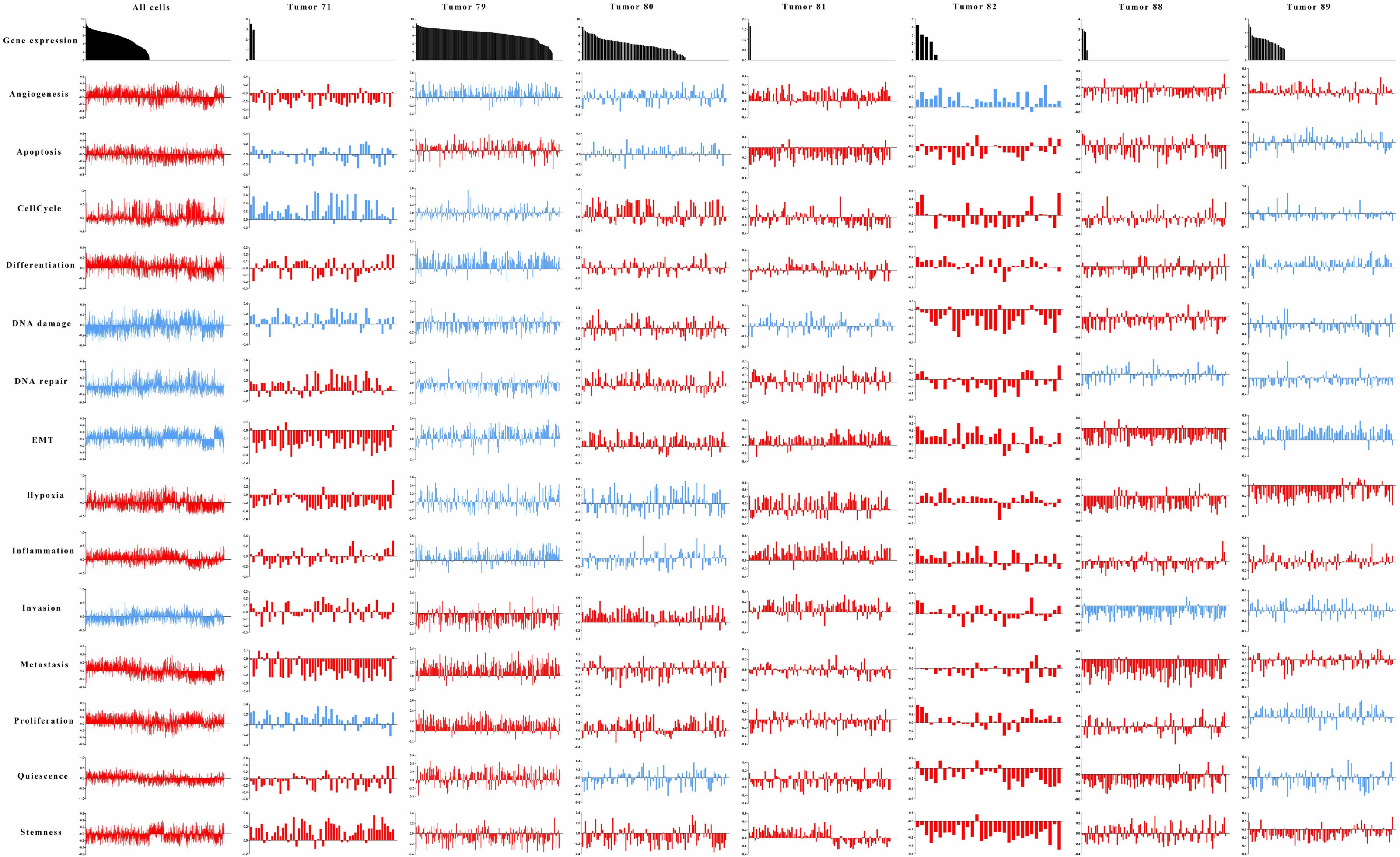


Figure S16. The association of APOC2 and 14 function states in 1257 malignant cells and each single tumor. The histograms in first line showed the relative expression of APOC2 in each cell. Other histograms represent the correlation of each cancer function and APOC2 level. Red means positive correlation while blue represents negative correlation.