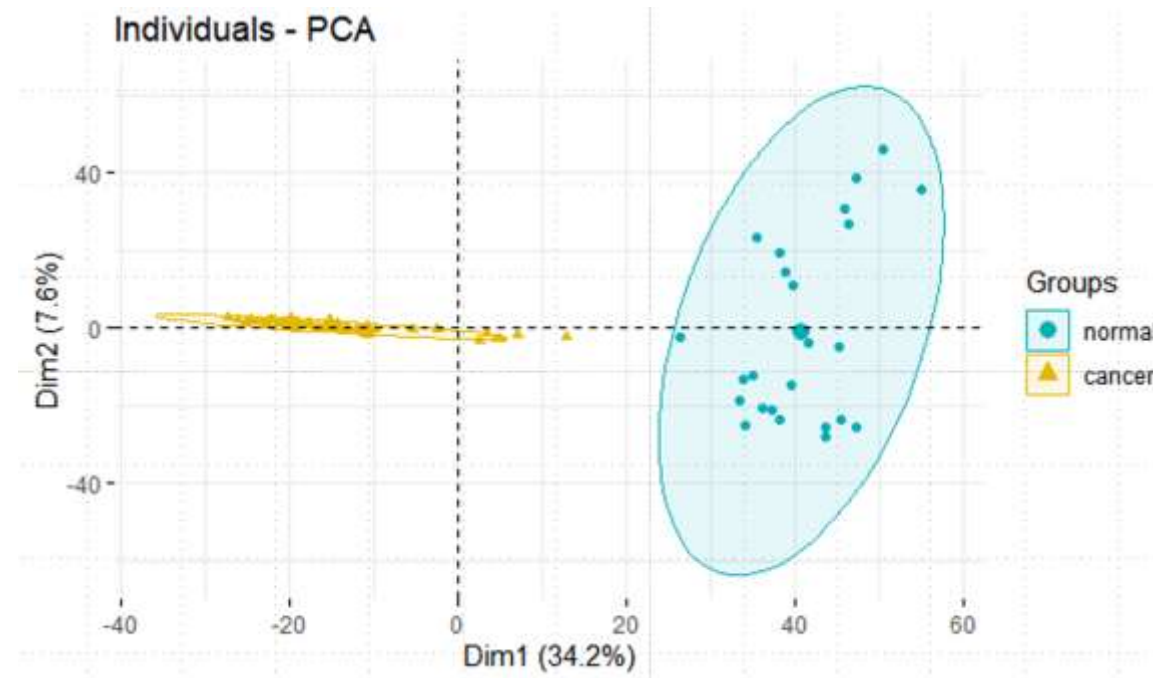
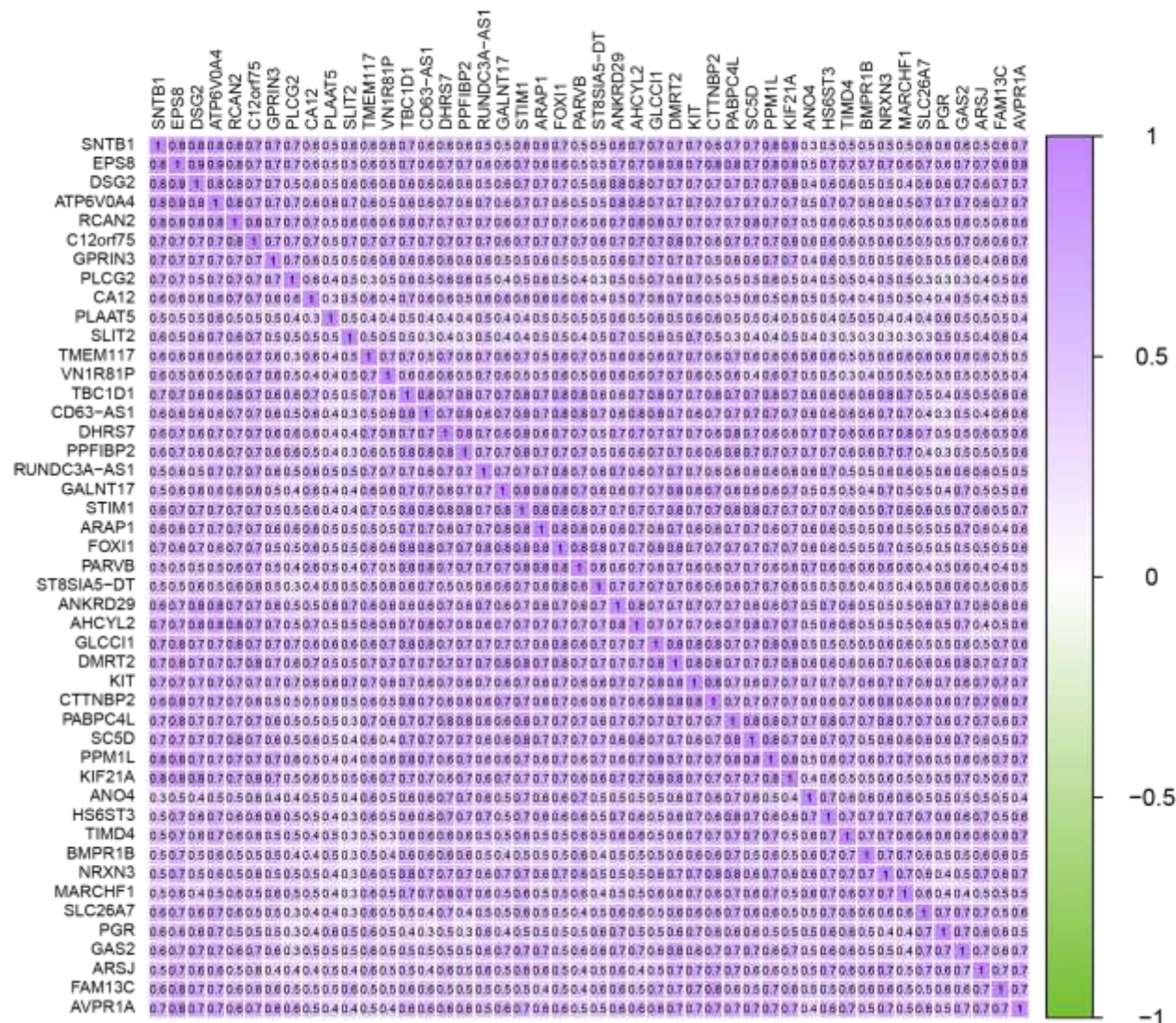


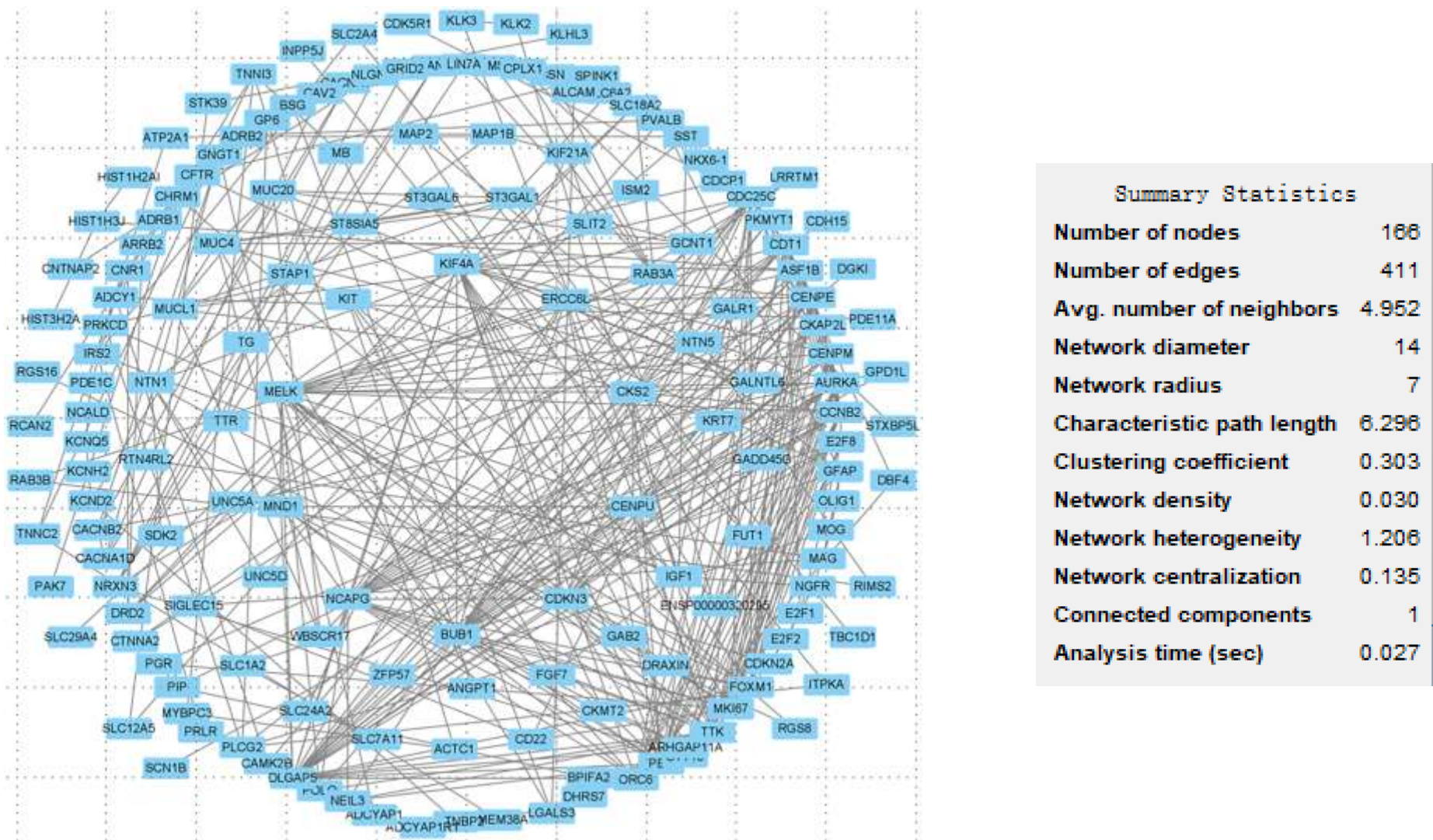
Supplementary figure 1 PCA analysis of ChRCC cancer samples and normal samples in the TCGA cohort



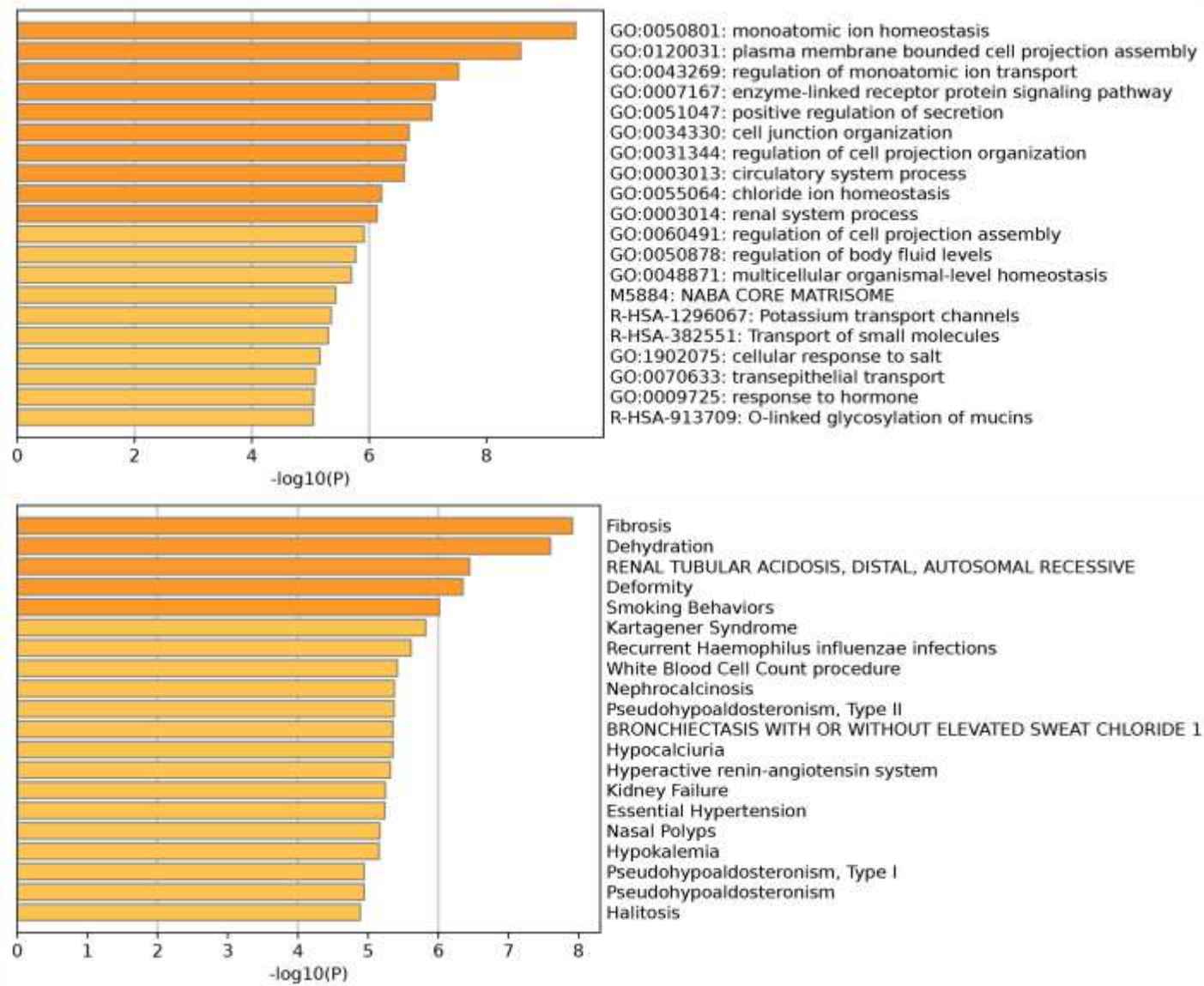
Supplementary figure 2 KIT-correlated genes in ChRCC. Correlation index ≥ 0.4 , $P < 0.05$



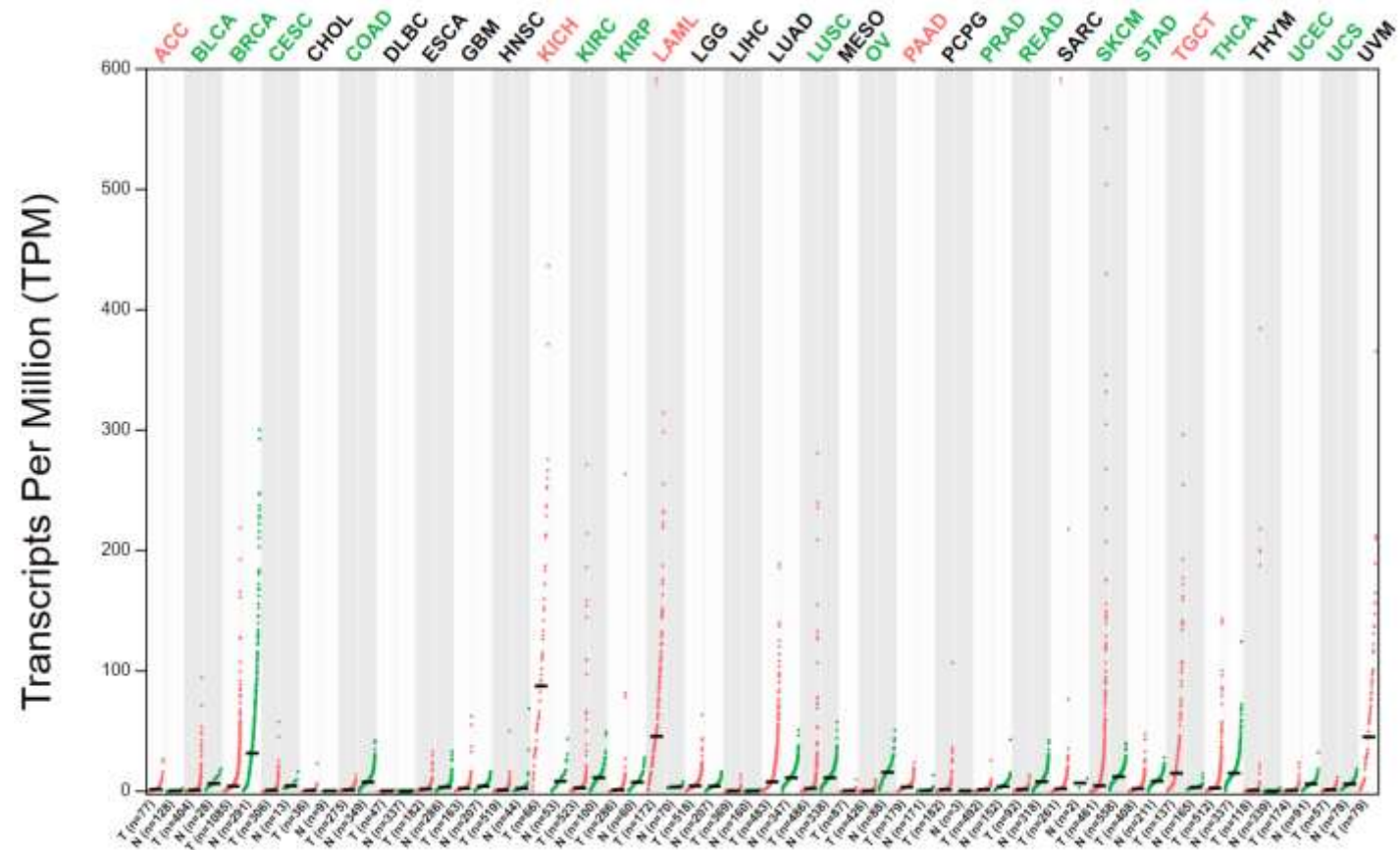
Supplementary figure 3 PPI networks of KIT and its correlated DEGs.



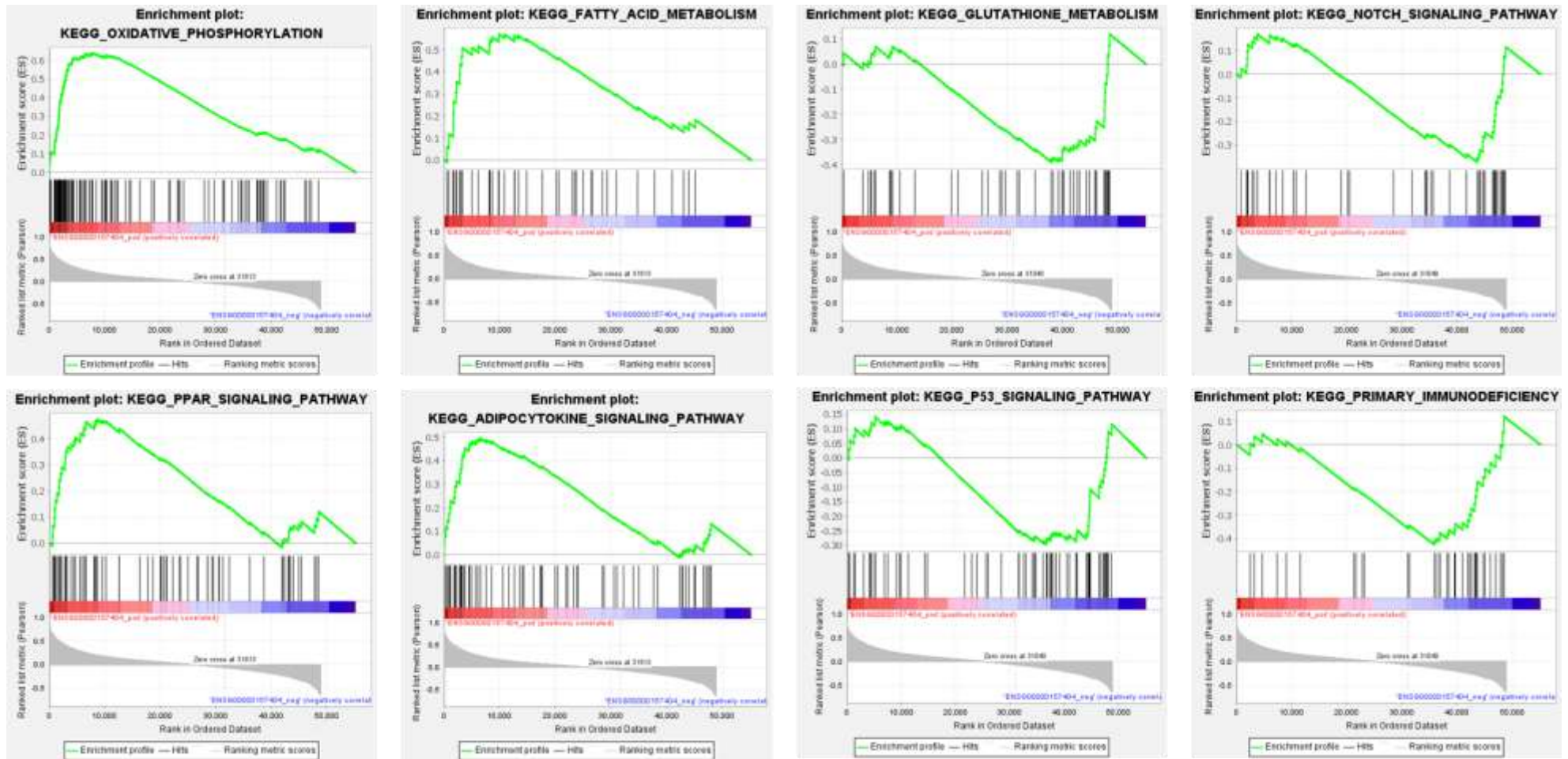
Supplementary figure 4 GO and KEGG enrichment pathway analysis based on the DEGs and summary of enrichment analysis in DisGeNET.



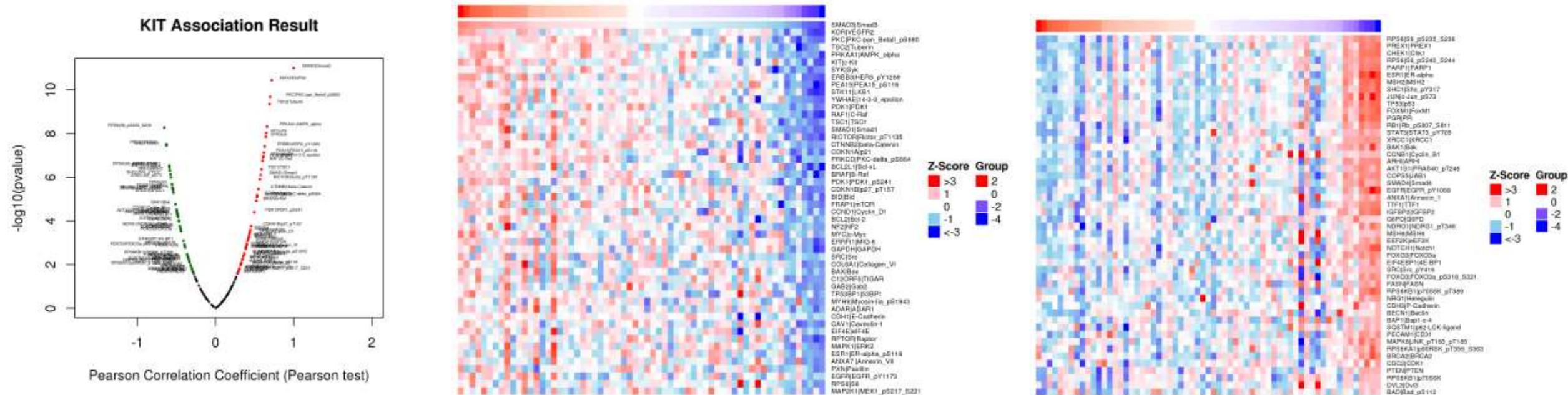
Supplementary figure 5 Differential expression of KIT in cancer tissues and adjacent tissues in GEPIA database.



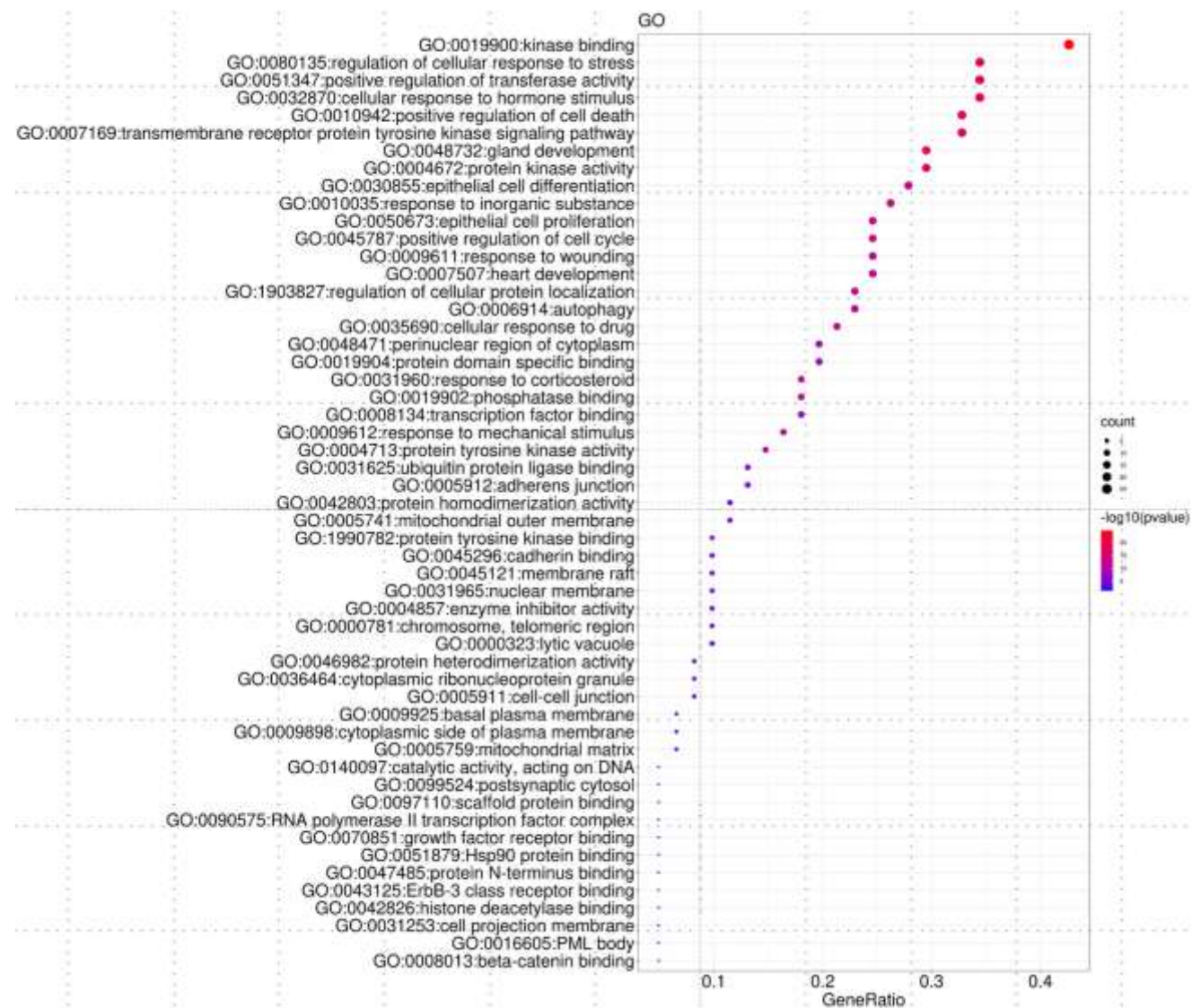
Supplementary Figure 6 KEGG pathway of KIT in ChRCC. GSEA analysis in the TCGA cohort. The result of GSEA showed that high KIT expression samples were enriched into Notch and P53 signaling pathway, etc. GSEA: Gene Set Enrichment Analysis.



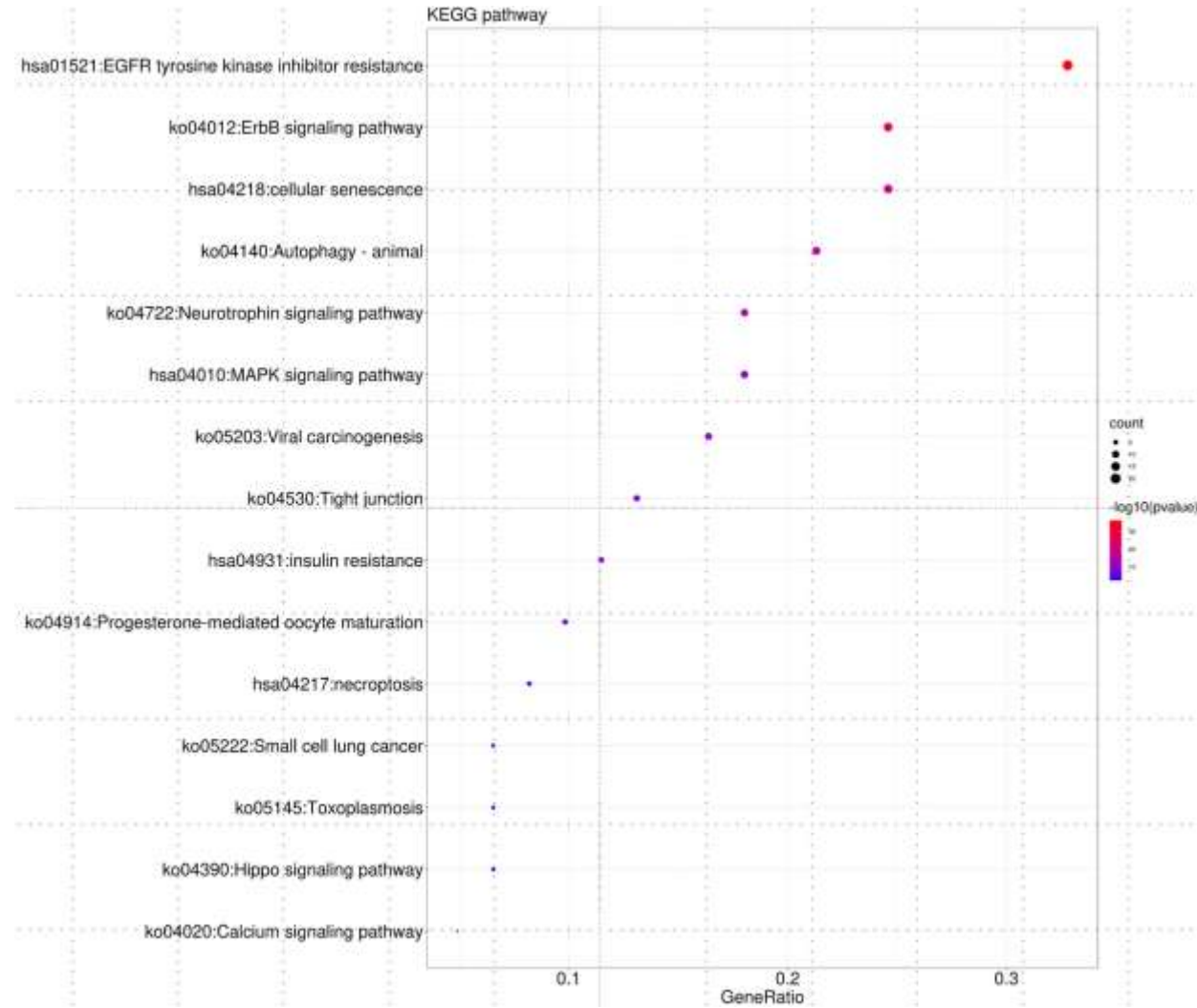
Supplementary Figure 7 Functional enrichment analysis of KIT and its co-expressed Genes. All KIT-related genes, the first 50 genes positively related to KIT and the first 50 genes negatively related to KIT.



Supplementary figure 8 The GO function of KIT co-expression gene enriched.



Supplementary figure 9 The KEGG pathway of KIT co-expression gene.



Supplementary figure 10 The enrichment network diagram of related genes

