Figure S1. Clinical trait-related modules were constructed and module genes were identified in the weighted gene co-expression network analysis package. (A) A hierarchical clustering analysis on the GSE40275 dataset samples was performed to exclude outliers. (B) The dynamic tree-cutting algorithm was used to segment modules to obtain the gene dendrogram and module colors. (C) Clustering of MEs. (D) The dynamic tree-cutting algorithm was used to segment modules and the dissimilarity threhold of MEs was set to 0.5 to merge similar modules to obtain the gene dendrogram and module colors. ME, module eigengene.

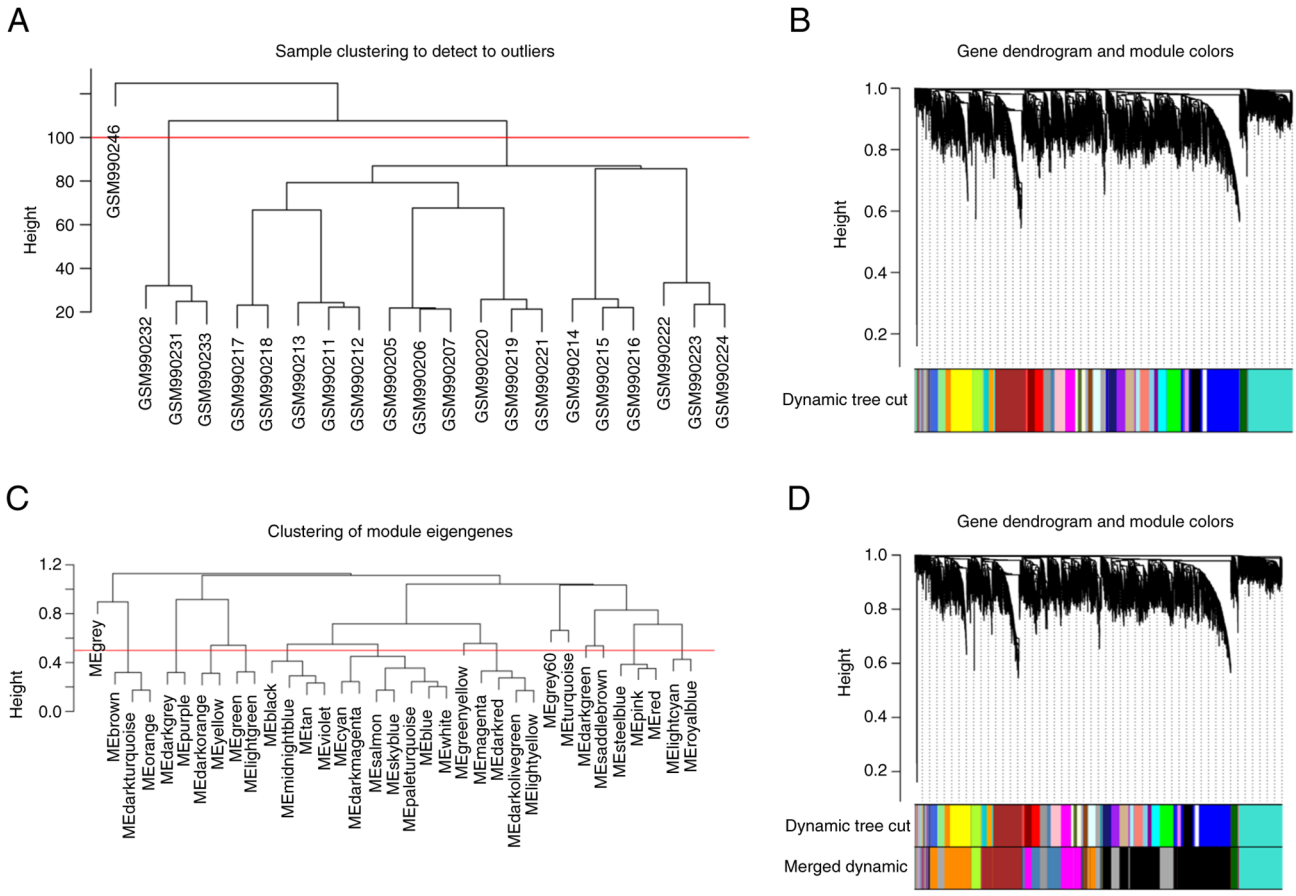

Figure S2. Correlation between DE-chr3 genes (n=33) and SCLC based on Metascape Gene Ontology analysis. DE-chr3 genes (n=33) in the (A) GSE40275 and (B) GSE60052 datasets. Results of GO-BP (C), GO-CC (D), GO-MF (E), and KEGG & Reactome (F) annotations of DE-chr3 genes. DE, differentially expressed; chr3, chromosome 3p; SCLC, small cell lung carcinoma; DN, downregulated; UP, upregulated.

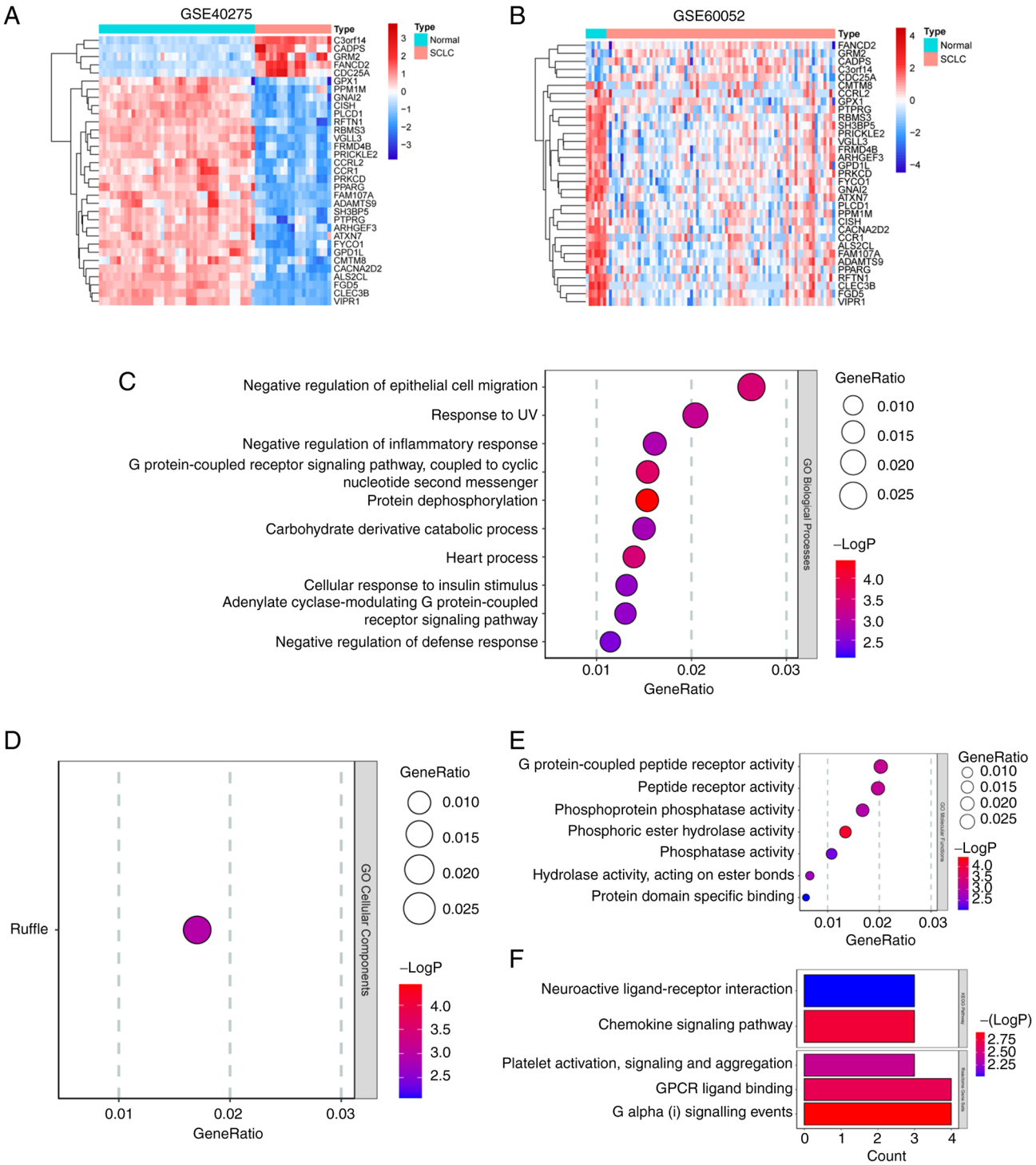

Figure S3. Association between the expression of diagnostic biomarkers and the clinical characteristics of small cell lung carcinoma in the GSE40275 dataset. (A) Cell division cycle 25 A was markedly overexpressed in pT4, stage IIIB and male patients. (B) Lipid raft linker 1 was significantly upregulated in pT4, stage III and male patients. (C) FYCO1 was overexpressed in pT2, stage I and female patients, and patients with pN0 had a higher expression of FYCO1. *P<0.05; **P<0.01; ***P<0.001; ns, no significance. CDC25A, cell division cycle 25 A; FYCO1, FYVE and coiled-coil domain autophagy adaptor 1; RFTN1, lipid raft linker 1.