

Figure S1. PPI network and functional enrichment analysis of the overlapping DEGs. (A) PPI network of proteins encoded by the DEGs and their neighbor genes, including 34 nodes and 251 edges. The node size represents the degree and association of the DEGs. The blue nodes represent 14 DEGs, while the red nodes represent 20 neighbor genes. S100 calcium-binding protein P did not exhibit binding ability with other genes, thus it was not included in the network diagram. (B) Biological process, (C) cellular component and (D) molecular function analyses of the overlapping DEGs. (E) KEGG pathway analysis of the overlapping DEGs. PPI, protein-protein interaction; DEGs, differentially expressed genes; KEGG, Kyoto Encyclopedia of Genes and Genomes.

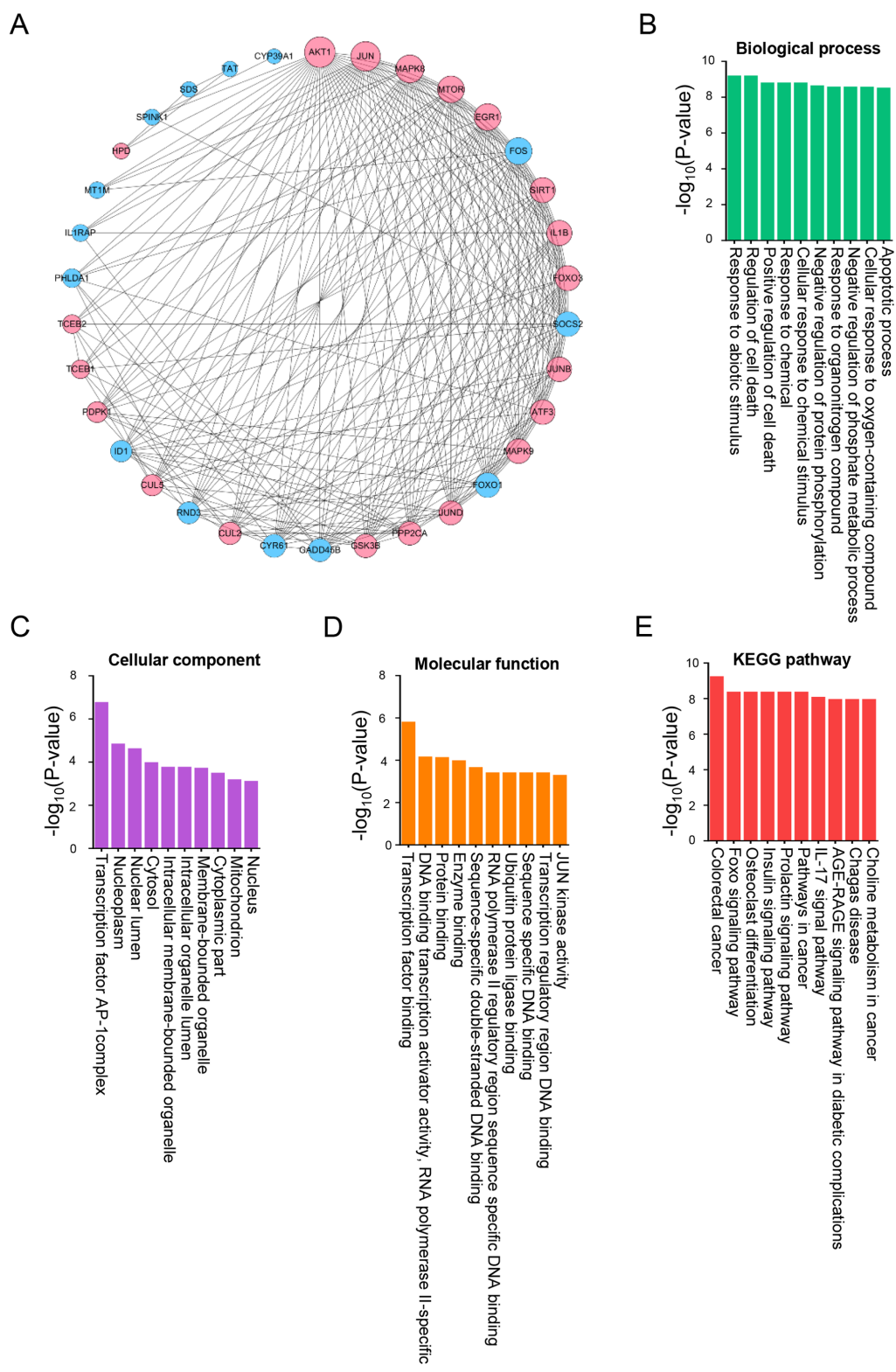


Figure S2. Overall survival analysis of the other 11 differentially expressed genes in patients with hepatocellular carcinoma.

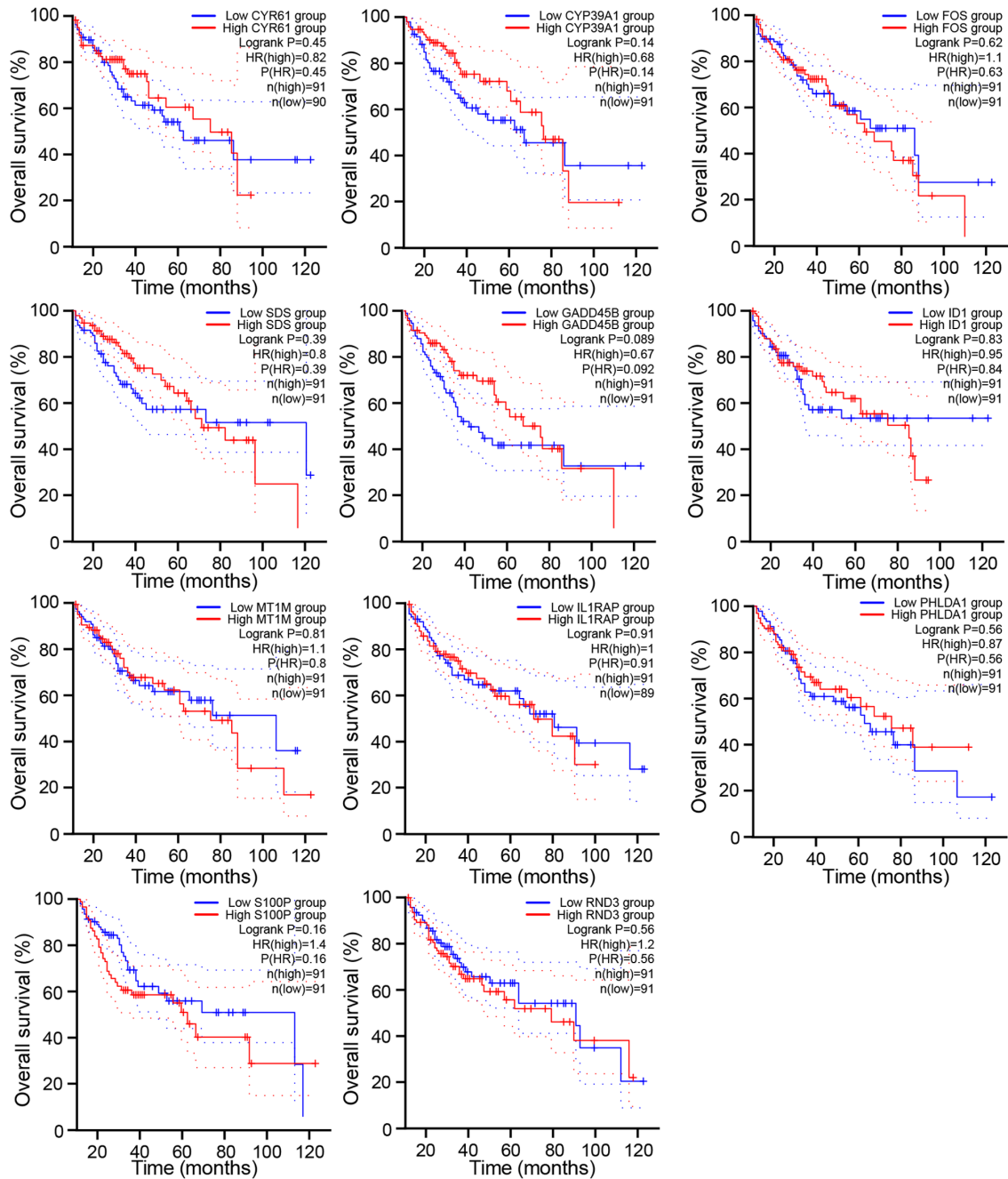


Table SI. Top 10 enriched biological processes.

Term ID	Term description	-logFDR
GO:0009628	Response to abiotic stimulus	9.157391
GO:0010941	Regulation of cell death	9.157391
GO:0010942	Positive regulation of cell death	8.769551
GO:0042221	Response to chemical	8.769551
GO:0070887	Cellular response to chemical stimulus	8.769551
GO:0001933	Negative regulation of protein phosphorylation	8.609065
GO:0010243	Response to organonitrogen compound	8.543634
GO:0045936	Negative regulation of phosphate metabolic process	8.543634
GO:1901701	Cellular response to oxygen-containing compound	8.537602
GO:0006915	Apoptotic process	8.485452

GO, Gene Ontology.

Table SII. Top 10 enriched molecular functions.

Term ID	Term description	-logFDR
GO:0008134	Transcription factor binding	5.782516
GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	4.133713
GO:0005515	Protein binding	4.108463
GO:0019899	Enzyme binding	3.958607
GO:1990837	Sequence-specific double-stranded DNA binding	3.638272
GO:0000977	RNA polymerase II regulatory region sequence-specific DNA binding	3.387216
GO:0031625	Ubiquitin protein ligase binding	3.387216
GO:0043565	Sequence-specific DNA binding	3.387216
GO:0044212	Transcription regulatory region DNA binding	3.387216
GO:0004705	JUN kinase activity	3.267606

GO, Gene Ontology.

Table SIII. Top 10 enriched cellular components.

Term ID	Term description	-logFDR
GO:0035976	Transcription factor AP-1 complex	6.742321
GO:0005654	Nucleoplasm	4.818156
GO:0031981	Nuclear lumen	4.603801
GO:0005829	Cytosol	3.958607
GO:0043231	Intracellular membrane-bounded organelle	3.744727
GO:0070013	Intracellular organelle lumen	3.744727
GO:0043227	Membrane-bounded organelle	3.69897
GO:0044444	Cytoplasmic part	3.468521
GO:0005739	Mitochondrion	3.161151
GO:0005634	Nucleus	3.091515

GO, Gene Ontology.

Table SIV. Top 10 enriched KEGG pathways.

Term ID	Term description	-logFDR
hsa05210	Colorectal cancer	9.207608
hsa04068	FoxO signaling pathway	8.333482
hsa04380	Osteoclast differentiation	8.333482
hsa04910	Insulin signaling pathway	8.333482
hsa04917	Prolactin signaling pathway	8.333482
hsa05200	Pathways in cancer	8.333482
hsa04657	IL-17 signaling pathway	8.047208
hsa04933	AGE-RAGE signaling pathway in diabetic complications	7.924453
hsa05142	Chagas disease (American trypanosomiasis)	7.924453
hsa05231	Choline metabolism in cancer	7.924453

KEGG, Kyoto Encyclopedia of Genes and Genomes; IL, interleukin.