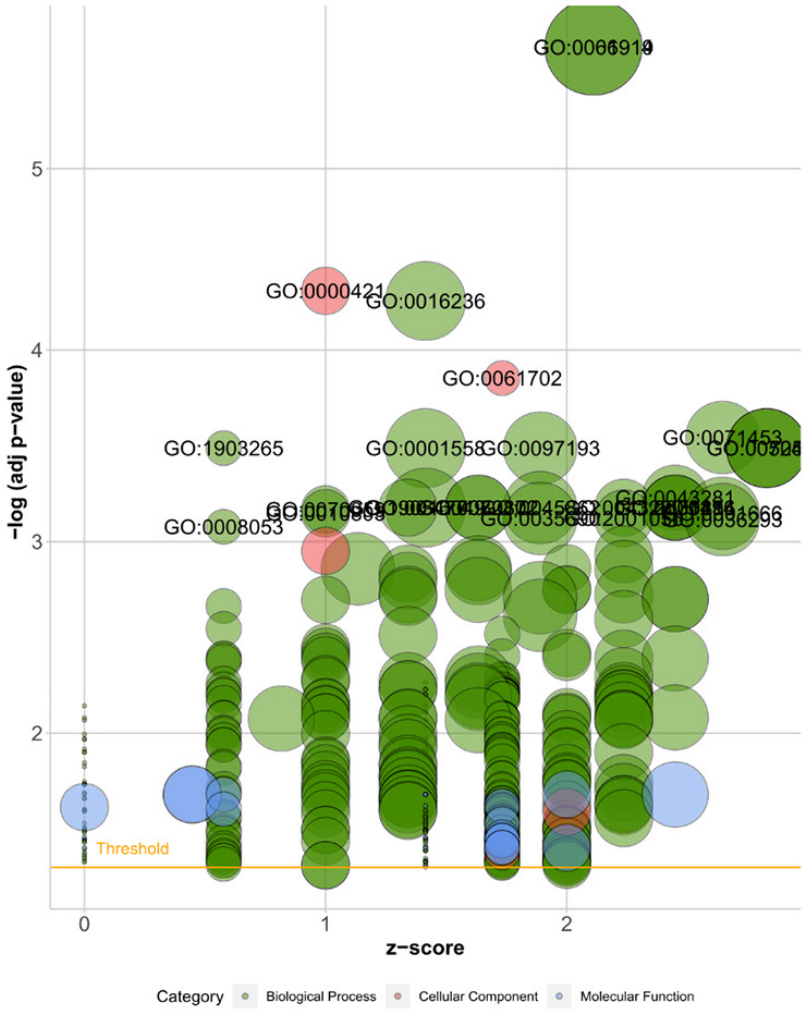
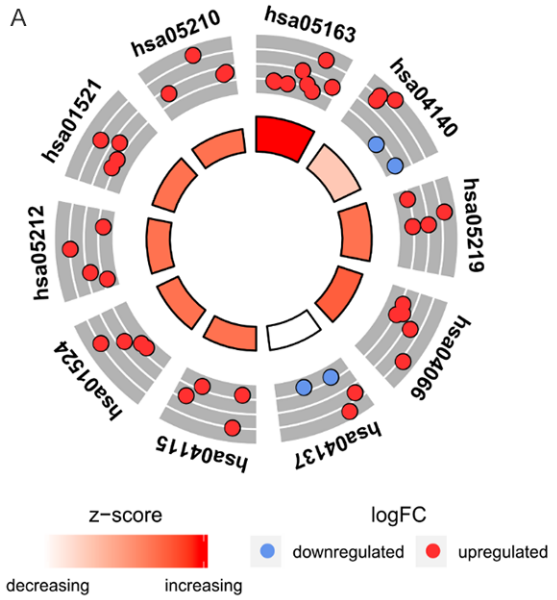
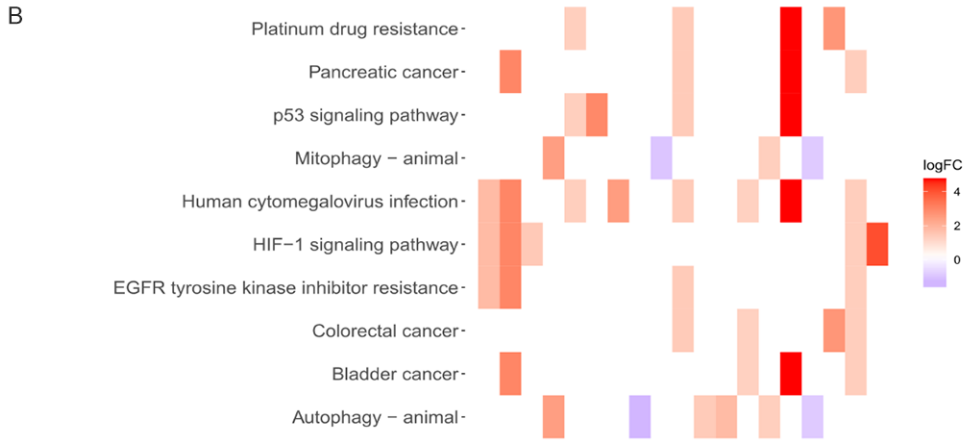


ID	Description
GO:0006914	autophagy
GO:0061919	process utilizing autophagic mechanism
GO:0016236	macroautophagy
GO:0071453	cellular response to oxygen levels
GO:1903265	positive regulation of tumor necrosis factor−mediated signaling pathway
GO:0070482	response to oxygen levels
GO:0001558	regulation of cell growth
GO:0052547	regulation of peptidase activity
GO:0097193	intrinsic apoptotic signaling pathway
GO:0043281	regulation of cysteine−type endopeptidase activity involved in apoptotic process
GO:0043280	positive regulation of cysteine−type endopeptidase activity involved in apoptotic process
GO:0016049	cell growth
GO:0071456	cellular response to hypoxia
GO:1905477	positive regulation of protein localization to membrane
GO:0045862	positive regulation of proteolysis
GO:0032872	regulation of stress−activated MAPK cascade
GO:0036294	cellular response to decreased oxygen levels
GO:0070302	regulation of stress−activated protein kinase signaling cascade
GO:2000116	regulation of cysteine−type endopeptidase activity
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
GO:0010803	regulation of tumor necrosis factor−mediated signaling pathway
GO:0001666	response to hypoxia
GO:2001056	positive regulation of cysteine−type endopeptidase activity
GO:0035690	cellular response to drug
GO:0036293	response to decreased oxygen levels
GO:0008053	mitochondrial fusion
GO:0000421	autophagosome membrane
GO:0061702	inflammasome complex

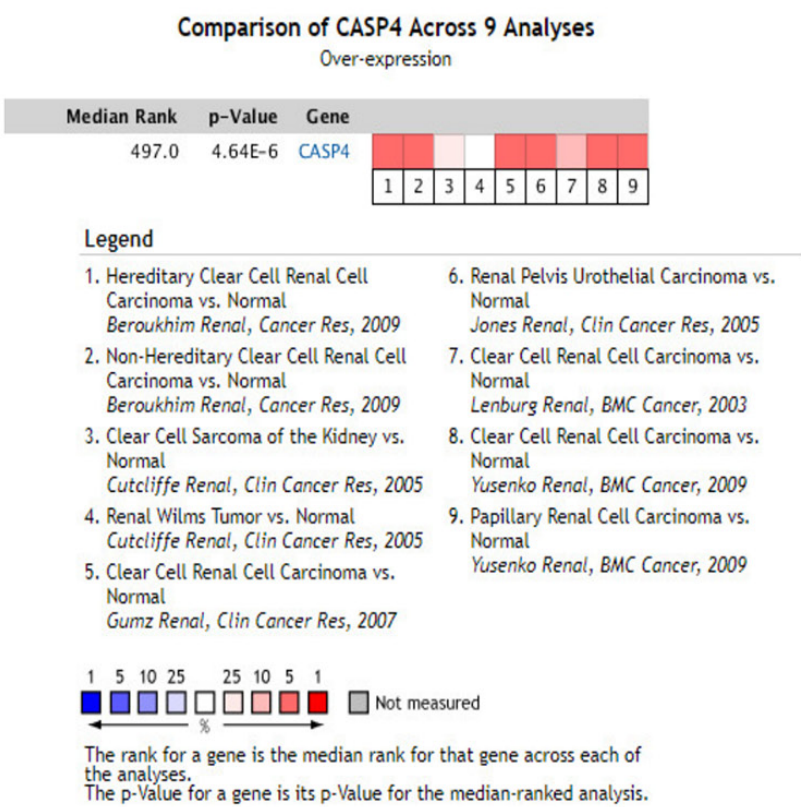
Supplementary Figure 1. Bubble plot of Gene Ontology (GO) enrichment analysis for differentially expressed autophagy-related genes in renal cancer. The green circles show biological process terms, red circles indicate the cellular component terms, and the blue circles represent molecular function terms.

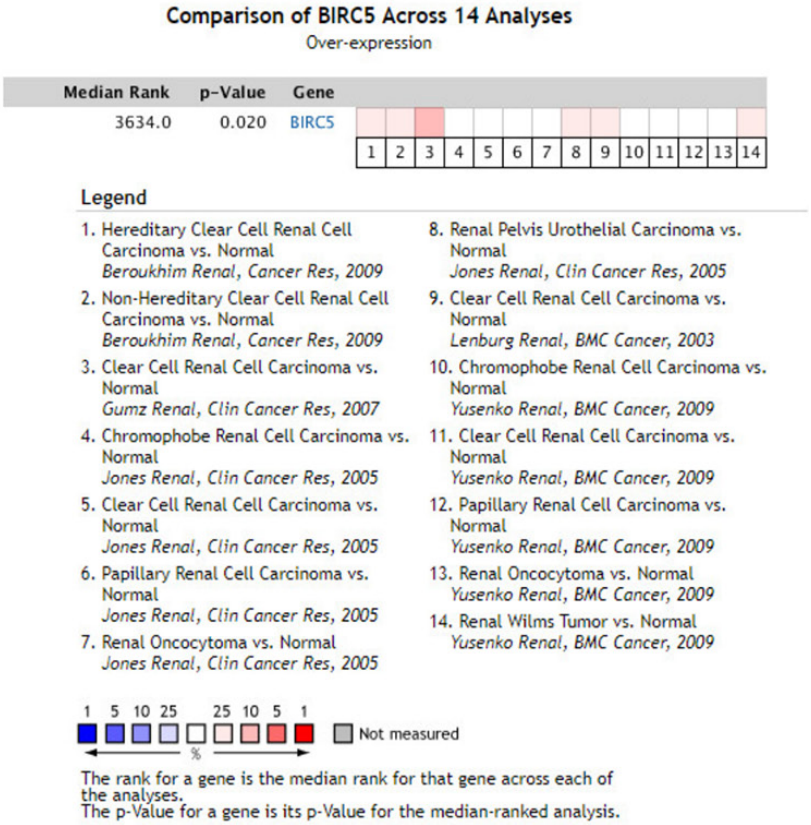


ID	Description
hsa05163	Human cytomegalovirus infection
hsa04140	Autophagy − animal
hsa05219	Bladder cancer
hsa04066	HIF−1 signaling pathway
hsa04137	Mitophagy − animal
hsa04115	p53 signaling pathway
hsa01524	Platinum drug resistance
hsa05212	Pancreatic cancer
hsa01521	EGFR tyrosine kinase inhibitor resistance
hsa05210	Colorectal cancer



Supplementary Figure 2. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of differentially expressed autophagy-related genes. A. A scatter plot for each term of the log fold change (FC) of the assigned genes was shown with the outer circle. The red circles indicate upregulation and the blue circles indicate downregulation. B. Heatmap of the KEGG pathway enrichment results. The color of each module depends on its corresponding logFC values.





Supplementary Figure 3. Search of the Oncomine database demonstrating that the expression levels of *CASP4* and *BIRC5* mRNA in RC tissues were significantly higher than those in normal tissues.