Supplementary

Table S1 The number of the ccRCC tissues and normal kidney tissues in GEO datasets enrolled in this study

Dataset	ccRCC tissues (n)	Normal tissues (n)	Total tissues (n)	Platform
GSE53757	72	72	144	GPL570
GSE53000	53	6	59	GPL6244
GSE36895	29	23	52	GPL570
GSE15641	32	23	55	GPL96
GSE66272	27	27	54	GPL570
GSE68417	29	14	43	GPL6244
GSE40435	101	101	202	GPL10558
GSE12606	3	3	6	GPL570
GSE46699	67	63	130	GPL570
GSE11151	26	5	31	GPL570
Total	439	337	776	–

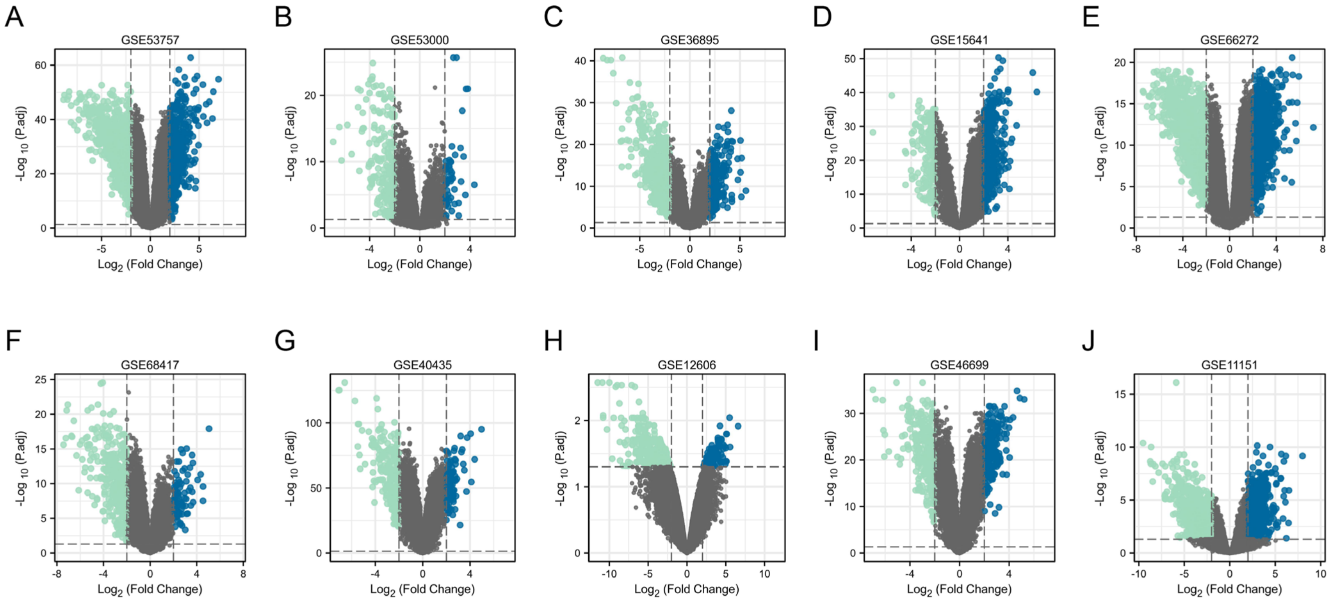
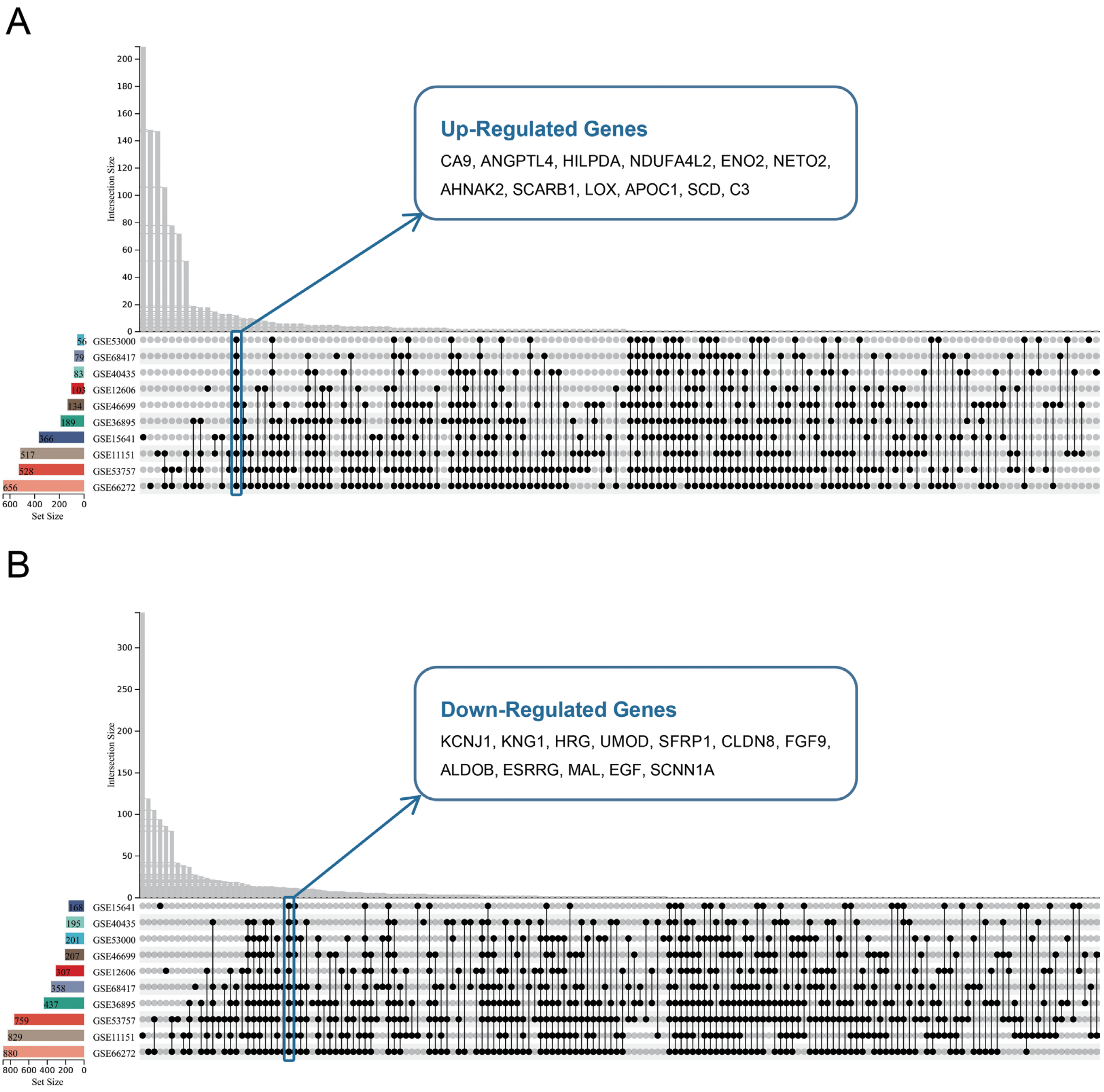


Figure S1 Volcano plots of DEGs between ccRCC tissues and normal kidney tissues in each GEO dataset. (A) GSE53757; (B) GSE53000; (C) GSE36895; (D) GSE15641; (E) GSE66272; (F) GSE68417; (G) GSE40435; (H) GSE12606; (I) GSE46699; (J) GSE11151.



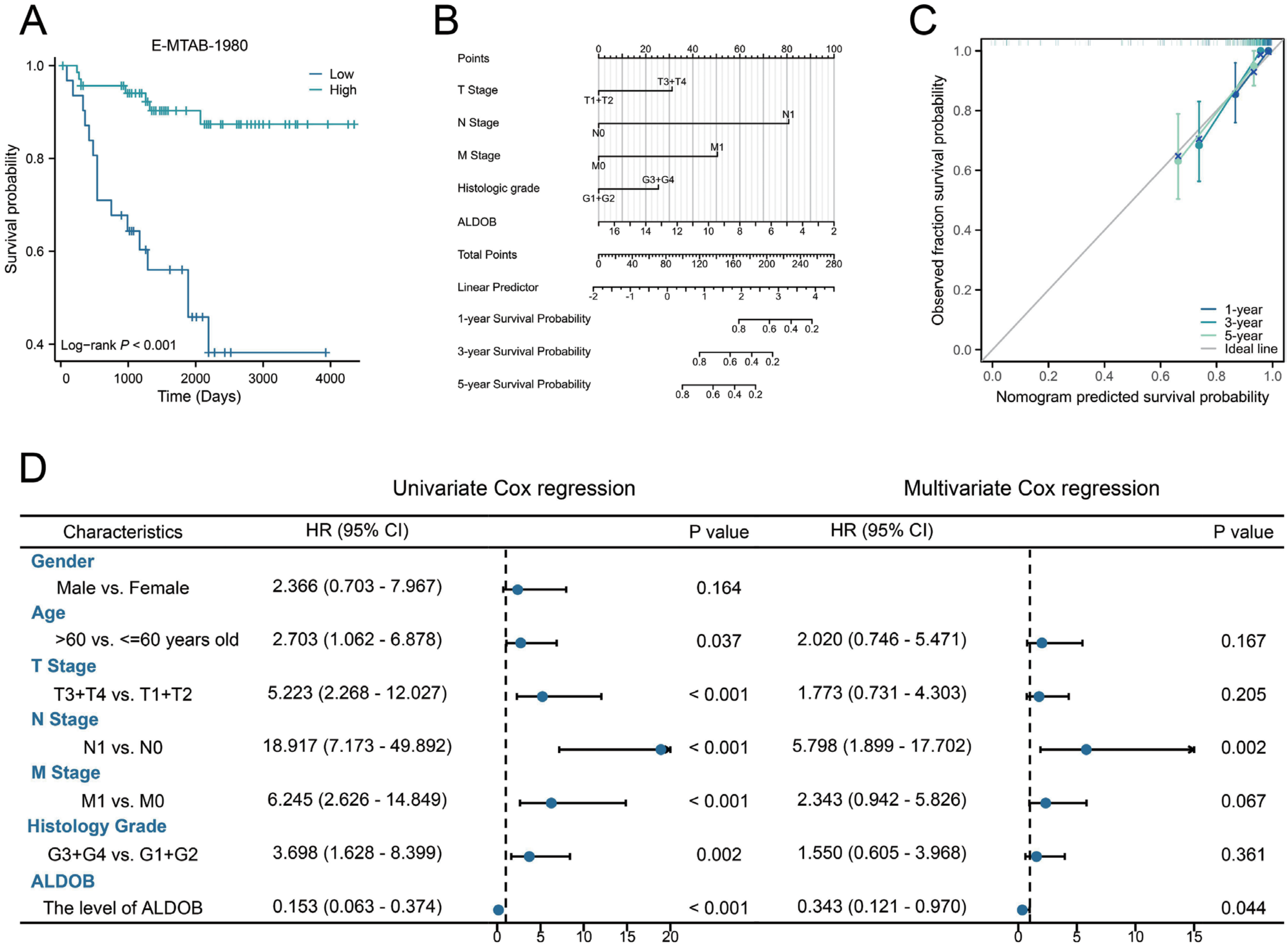
Up-Regulated Genes

CA9, ANGPTL4, HILPDA, NDUFA4L2, ENO2, NETO2, AHNAK2, SCARB1, LOX, APOC1, SCD, C3

Down-Regulated Genes

KCNJ1, KNG1, HRG, UMOD, SFRP1, CLDN8, FGF9, ALDOB, ESRRG, MAL, EGF, SCNN1A

Figure S2 Upset plots of common DEGs between ccRCC tissues and normal kidney tissues of ten GEO datasets. (A) Common up-regulated DEGs between ccRCC tissues and normal kidney tissues; (B) common down-regulated DEGs between ccRCC tissues and normal kidney tissues.



Characteristics	Univariate Cox regression HR (95% CI)	Univariate P value	Multivariate Cox regression HR (95% CI)	Multivariate P value
Gender				
Male vs. Female	2.366 (0.703 - 7.967)	0.164		
Age				
>60 vs. <=60 years old	2.703 (1.062 - 6.878)	0.037	2.020 (0.746 - 5.471)	0.167
T Stage				
T3+T4 vs. T1+T2	5.223 (2.268 - 12.027)	< 0.001	1.773 (0.731 - 4.303)	0.205
N Stage				
N1 vs. N0	18.917 (7.173 - 49.892)	< 0.001	5.798 (1.899 - 17.702)	0.002
M Stage				
M1 vs. M0	6.245 (2.626 - 14.849)	< 0.001	2.343 (0.942 - 5.826)	0.067
Histology Grade				
G3+G4 vs. G1+G2	3.698 (1.628 - 8.399)	0.002	1.550 (0.605 - 3.968)	0.361
ALDOB				
The level of ALDOB	0.153 (0.063 - 0.374)	< 0.001	0.343 (0.121 - 0.970)	0.044

Figure S3 External validation of the prognostic value of ALDOB in the E-MTAB-1980 dataset from the ArrayExpress database (OS). (A) The Kaplan-Meier survival curve comparing the high and low expression of ALDOB in OS of ccRCC patients; (B) Nomogram for the prediction of the OS in ccRCC patients; (C) calibration plot for the prediction of the OS in ccRCC patients; (D) forest plots of univariate and multivariate Cox regression analysis of factors affecting the OS of ccRCC patients. TNM, tumor node metastasis.

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Table S2 The association between the mRNA expression of ALDOB and the clinicopathological features of ccRCC patients from TCGA-KIRC dataset

Clinicopathological features	Low expression of ALDOB (n=265)	High expression of ALDOB (n=265)	P
Age (years), mean ± SD	60.55±11.92	60.57±12.38	0.986
Gender, n (%)			0.036
Female	81 (15.3)	105 (19.8)	
Male	184 (34.7)	160 (30.2)	
T stage, n (%)			0.002
T1	116 (21.9)	155 (29.2)	
T2	42 (7.9)	27 (5.1)	
T3	98 (18.5)	81 (15.3)	
T4	9 (1.7)	2 (0.4)	
N stage, n (%)			0.141
N0	126 (49.4)	113 (44.3)	
N1	12 (4.7)	4 (1.6)	
M stage, n (%)			0.109
M0	204 (40.8)	218 (43.6)	
M1	46 (9.2)	32 (6.4)	
AJCC stage, n (%)			0.005
Stage I	113 (21.3)	152 (28.7)	
Stage II	35 (6.6)	22 (4.2)	
Stage III	67 (12.6)	58 (10.9)	
Stage IV	50 (9.4)	33 (6.2)	
Histologic grade, n (%)			<0.001
G1	4 (0.8)	10 (1.9)	
G2	101 (19.3)	126 (24.1)	
G3	102 (19.5)	104 (19.9)	
G4	53 (10.2)	22 (4.2)	

TCGA, The Cancer Genome Atlas; KIRC, kidney renal clear cell carcinoma; T, tumor; N, node; M, metastasis; AJCC, American Joint Committee on Cancer.

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