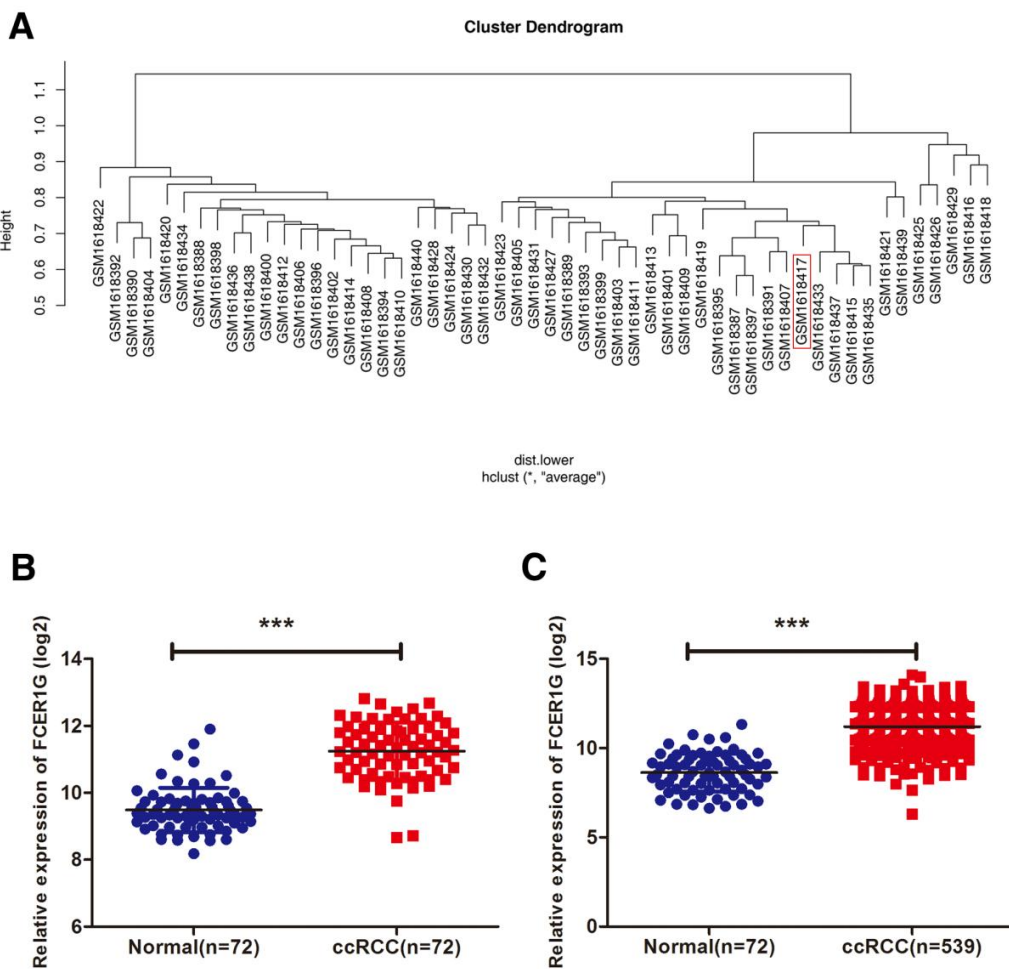**Co-expression network analysis identified FCER1G in association with progression and prognosis in human clear cell renal cell carcinoma**

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Supplementary Information 1

Supplementary Figure 1. Samples clustering and FCER1G expression in the two testing datasets. (A) Total samples clustering of GSE66272 to detect outliers. One sarcoma sample GSM1618417 with red marker was removed from the subsequent analysis. **(B-C)** FCER1G mRNA expression was significantly higher in ccRCC tissues compared with normal kidney tissues based on the microarray dataset GSE53757 (B) and TCGA RNA sequencing dataset (C). Two-tailed Student's t-test was used for significance of differences between subgroups, ***p<0.001.

Supplementary Information 2

Supplementary Table 1. Clinical information of ccRCC patients in training dataset and testing dataset.

Characteristics	Training dataset GSE66272	Testing dataset GSE53757[*]	Testing dataset TCGA[*#]
Age			
≥ 65	13	-	-
< 65	13	-	-
Sex			-
Female	8	-	-
Male	18	-	-
Pathological stage			
Stage I	12	24	261
Stage II	1	19	56
Stage III	12	14	123
Stage IV	1	15	82
Tumor grade			
Grade 1	1	-	-
Grade 2	16	-	-
Grade 3	8	-	-
Grade 4	1	-	-
Metastasis	1	-	-
Yes	12	-	-
No	14	-	-

*In both GSE53757 and TCGA datasets, only pathological stage was used in our analysis.

#The testing dataset TCGA contained 539 ccRCC tissue samples, of which 522 samples have definite pathological stage.

Supplementary Table 2. Correlation between FCER1G and clinical parameters in ccRCC.

Characteristics	Number of cases	FCER1G expression		P value
		Low (n=13)	High (n=13)	
Age				
≥ 65	13	7	6	0.694
< 65	13	6	7	
Gender				
Male	18	9	9	1
Female	8	4	4	
Tumor stage				
Stage I-II	12	5	7	0.239
Stage III-IV	14	8	6	
Tumor grade				
Grade 1, 2	17	6	11	0.039*
Grade 3, 4	9	7	2	
Metastasis				
Yes	12	10	2	0.0016**
No	14	3	11	

*$p<0.05$, **$p<0.01$