

**Supplementary Table****Table S1. Clinical characteristics of RCC patients**

<b>Variables</b>	<b>RCC patients (n=160)</b>
<b>Gender (%)</b>	
Male	108 (67.5)
Female	52 (32.5)
<b>Age (%)</b>	
≤60	94 (58.8)
>60	66 (41.2)
<b>Tumor size (%)</b>	
≤4cm	85 (53.1)
>4cm	75(46.9)
<b>Fuhrman grade (%)</b>	
I / II	123 (76.9)
III/VI	37 (23.1)
<b>TNM stage (%)</b>	
I / II	126 (78.8)
III/VI	44 (21.2)
<b>Tumor thrombus (%)</b>	
No	148 (92.5)
Yes	12 (7.5)
<b>Distant metastasis (%)</b>	
No	144 (90.0)
Yes	16(10.0)

**Table S2. Sequences of primers used for qRT-PCR in this study**

CD44 Forward	GGATCACCGACAGCACAGAC
CD44 Reverse	TTCTTGCCTCTTGGTTGCTG
CD86 Forward	TAGGTCACAGCAGAAGCAGC
CD86 Reverse	AATCAAAACTTGTGCGGCC
EGFR Forward	TGGTCAAGTGCTGGATGATAGA
EGFR Reverse	ACGGTAGAAGTTGGAGTCTGTA
EGF Forward	ACGCAGTTCCCACCCATTT
EGF Reverse	AACTCTGACTCTGAATGC
VEGFA Forward	AGGCCAGCACATAGGAGAGA
VEGFA Reverse	CTGGTTCCCGAAACCCTGAG
FN1 Forward	GACACATTCCACAAGCGTCA
FN1 Reverse	CTCCAATTTGATAAAACGTCCC
TLR2 Forward	CTCCCAGTGTTTGGTGTTC
TLR2 Reverse	GGCTTGAACCAGGAAGACGA
ITGAM Forward	TCAGCCCCTCCCATAGCCA
ITGAM Reverse	GCTCCTACAGTCAGGTCTACCA
ITGB2 Forward	CCAGGGCAGACTGGTAGCAA
ITGB2 Reverse	AGAGGACTGAGGGACGAGGC

## Supplementary Figure

Figure S1. Gene ontology (a-c) and KEGG pathway (d) analysis of the down-regulated differentially expressed genes associated with renal cancer. The threshold was a fold change  $\geq 2.0$  and a p-value  $< 0.05$ . BP: biological process; MF: molecular function; CC: cellular component.

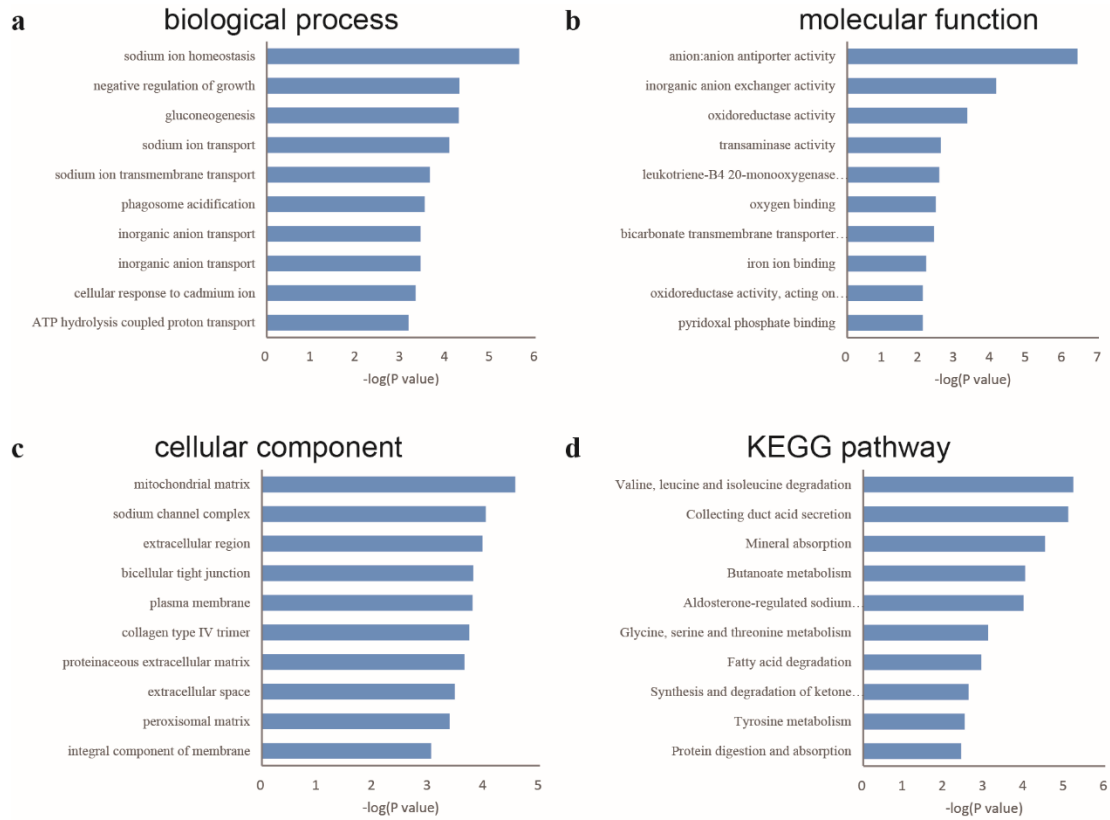
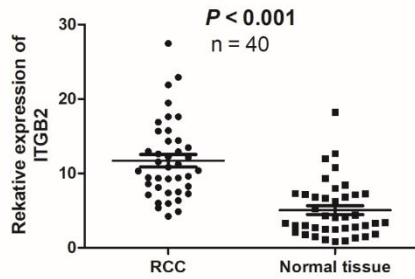


Figure S2. (a) The ITGB2 mRNA expression between RCC samples and paired normal tissues was compared using qRT-PCR analysis (n = 40). (b) The survival analyses of hub genes, including EGF, VEGFA, TLR2, PTPRC, ITGAM and ITGB2.  $p < 0.05$  was considered statistically significant.

**a**



**b**

