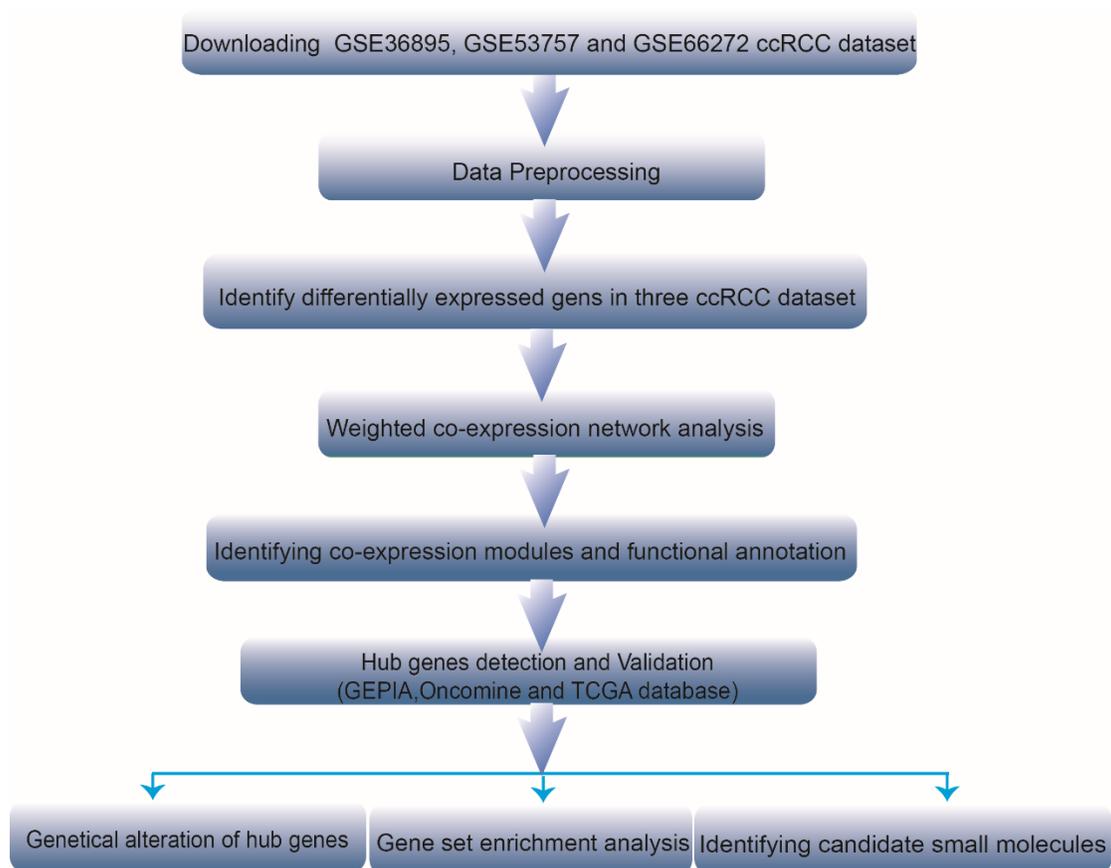
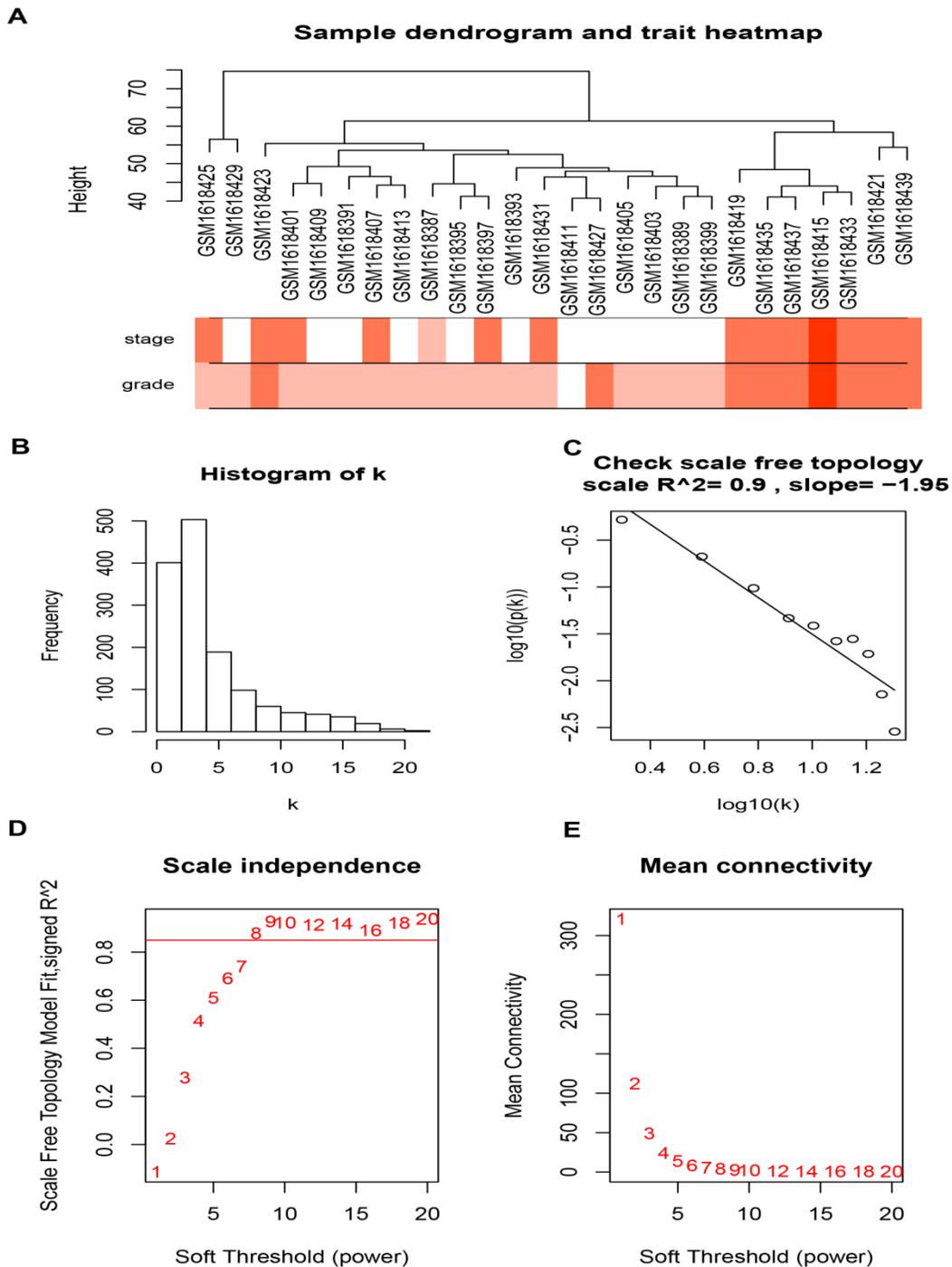


SUPPLEMENTARY FIGURES



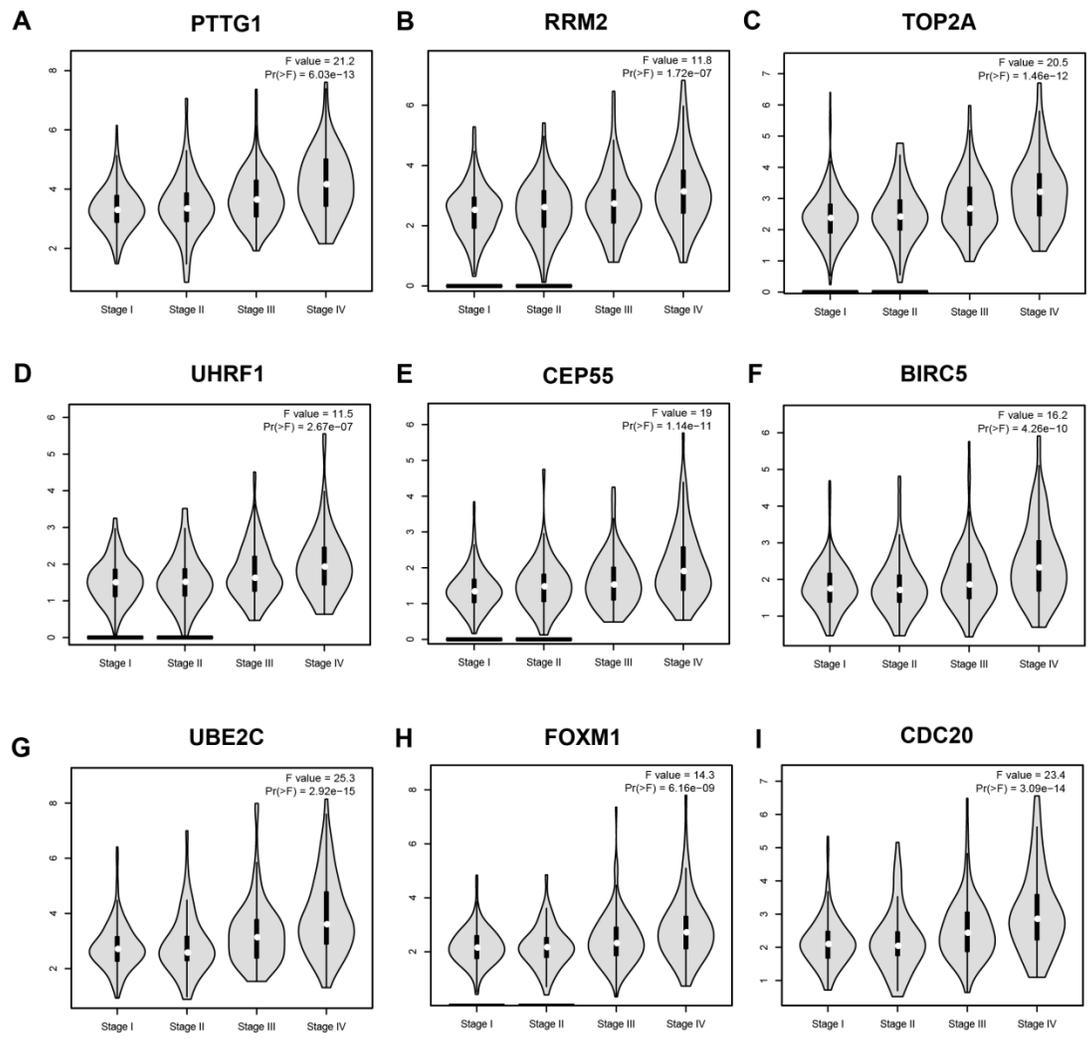
Supplementary Figure 1. Flow chart of data preparation, processing, analysis and validation in this study.



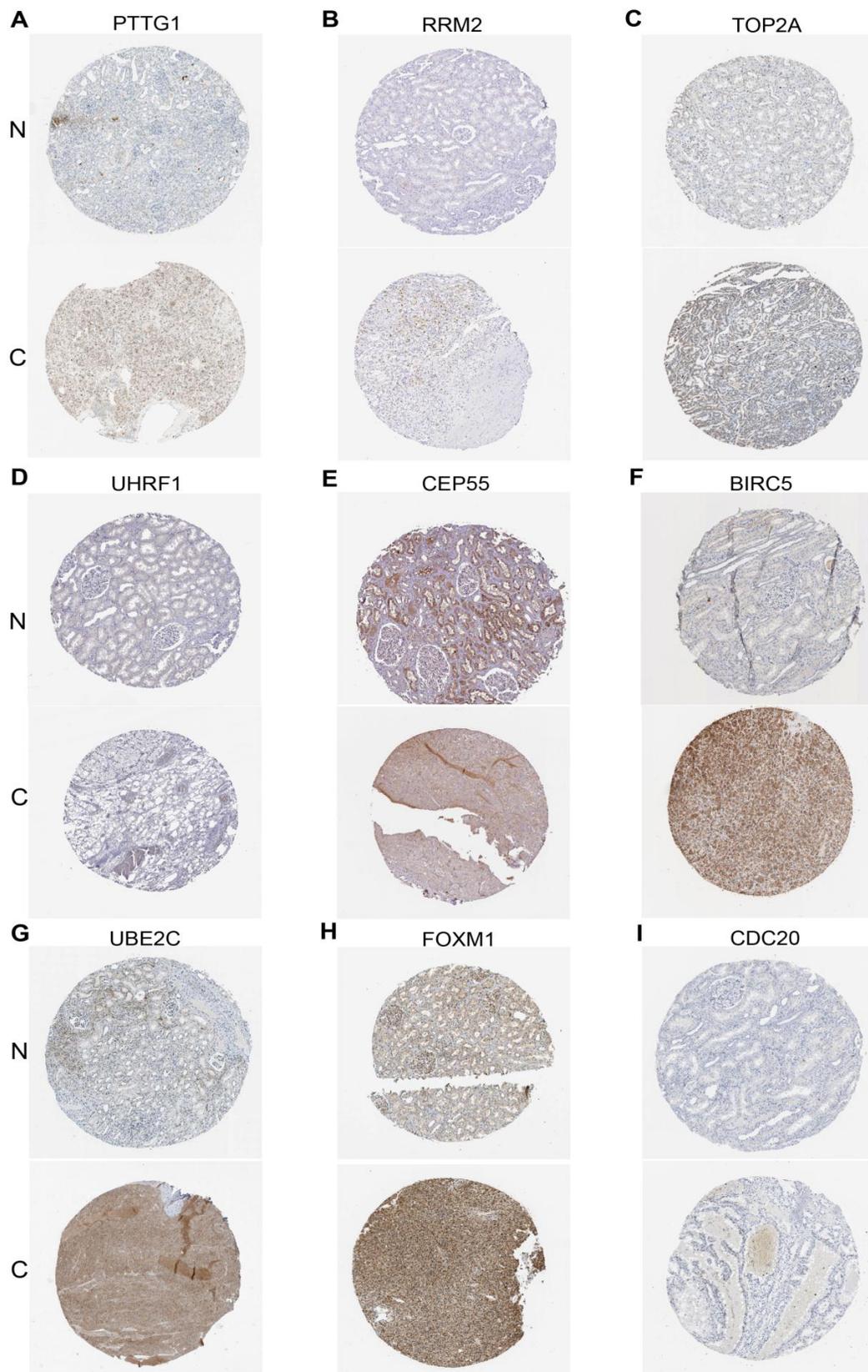
Supplementary Figure 2. Clustering dendrogram of ccRCC tumor samples and the clinical traits, and determination of soft-thresholding power. (A) The clustering was based on the common differentially expressed genes in ccRCC. The red color represented stage and grade. The color intensity was proportional to higher pathological stage and grade. (B) Analysis of the scale-free fit index for various soft-thresholding powers (β). (C) Analysis of the mean connectivity for various soft-thresholding powers. (D) Histogram of connectivity distribution when $\beta = 8$. (E) Checking the scale free topology when $\beta = 8$.

Analysis Type by Cancer	PTTG1	RRM2	TOP2A	UHRF1	CEP55	BIRC5	UBE2C	FOXM1	CDC20
	Cancer vs. Normal								
Bladder Cancer	5	6 1	9	1	4	3	6	4	6
Brain and CNS Cancer	7 1	12 1	15 1	10 1	7 1	12 1	14 1	14 1	8 2
Breast Cancer	30 1	19 1	31 1	21 1	24 1	16 1	31	17	21 1
Cervical Cancer	3	4	5	2	4	3	3	4	3
Colorectal Cancer	11	18	23	15	20	12	20	9	9
Esophageal Cancer	2 2	3	5	2	6	2	6	5	3
Gastric Cancer	6	5	11	5	7	5 1	9	7	5
Head and Neck Cancer	6	9	12	5	11	6	6	7	9
Kidney Cancer	3	4	5	1	5 1	2 5	3	2	1
Leukemia	1 3	2 11	3 10	8 4	2 2	4 8	6	1 3	1 9
Liver Cancer	4	5	4	1	2	3 1	4	4	3
Lung Cancer	15	15	21 1	5	11	12 2	19 1	15	12 1
Lymphoma	12 1	22 1	12 2	6	9	16	9	13	12 2
Melanoma	3	2	3 1	1	3	3	2	2	2
Myeloma	1	2	2		1	1			2
Other Cancer	5 10	9	11 5	6 1	7 7	7 2	13	10 1	6 2
Ovarian Cancer	4	5	7	3	5	3	8	6	4
Pancreatic Cancer	5	2	6 1	2	3	2 1	2	3	3
Prostate Cancer		2	3	2	1	4	1		
Sarcoma	11	11	14		9	13	11 1	12	12 1
Significant Unique Analyses	132 18	155 15	200 22	96 7	139 12	126 22	166 9	134 5	118 20
Total Unique Analyses	422	449	462	291	387	464	450	455	415

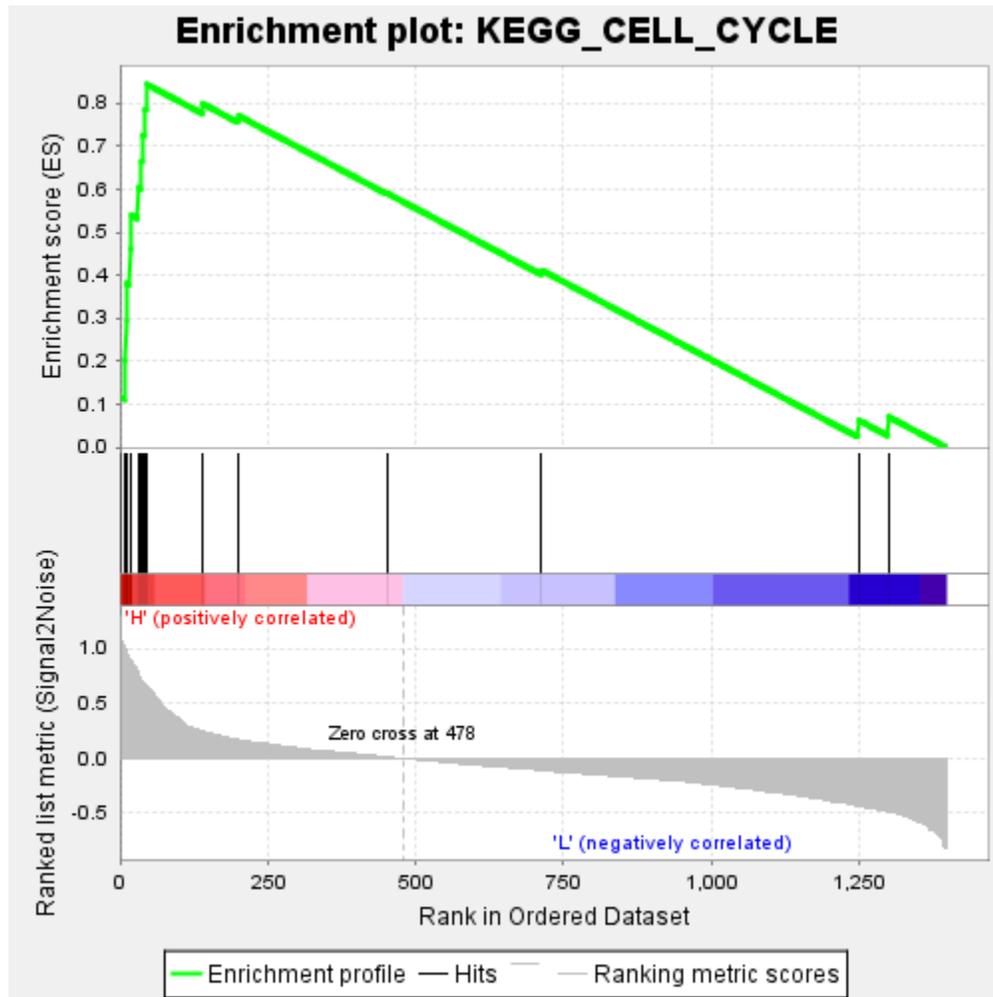
Supplementary Figure 3. Gene expression level of 9 key genes (based on OncoPrint database).



Supplementary Figure 4. Validation of the correlation between 9 key genes expression levels and the pathologic stages of ccRCC (based on ccRCC data in GEPIA database). (A) PTTG1, (B) RRM2, (C) TOP2A, (D) UHRF1, (E) CEP55, (F) BIRC5, (G) UBE2C, (H) FOXM1 and (I) CDC20.



Supplementary Figure 5. Immunohistochemistry of the 9 key genes based on the Human Protein Atlas. (A) PTTG1, (B) RRM2, (C) TOP2A, (D) UHRF1, (E) CEP55, (F) BIRC5, (G) UBE2C, (H) FOXM1, (I) CDC20.



Supplementary Figure 6. Gene set enrichment analysis (GSEA). Only listed the common functional gene sets enriched in ccTCC with 9 key genes highly expressed.