Supplementary information, Table S2 Summary of RNA-seq.

		Total reads	Uniquely mapped reads	Uniquely mapped rate
Patient 1	**Normal**	76,073,808	53,039,193	69.72%
	ccRCC	78,465,446	51,331,691	65.42%
Patient 2	**Normal**	80,348,492	57,402,303	71.44%
	ccRCC	104,481,634	66,394,548	63.55%

Uniquely mapped reads with mapping quality larger than or equal to 20 were used in the downstream analysis. Read counts per exon were obtained, followed by summarizing the read counts for all exons within a gene for all genes in UCSC HG19 RefGene table.