

Figure S1. One-way analysis of variance (ANOVA) and Tukey post-hoc test results of selected gene expressions in normal and stage I RCC tissue samples. (A) *VIM* (B) *ATXN1* (C) *RFTN1* (D) *TNFAIP6* (E) *TM4SF19* (F) *GRAMD1B*. Significance values: ns: not significant; * $p < 0.05$; ** $p < 0.01$, * $p < 0.001$, **** $p < 0.0001$.**

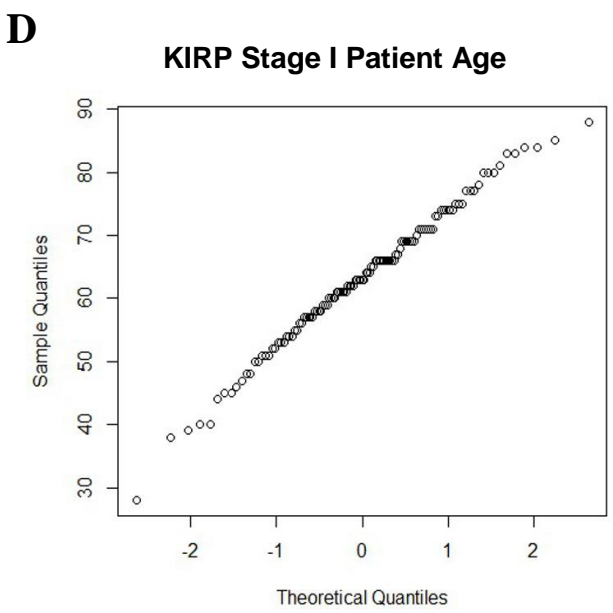
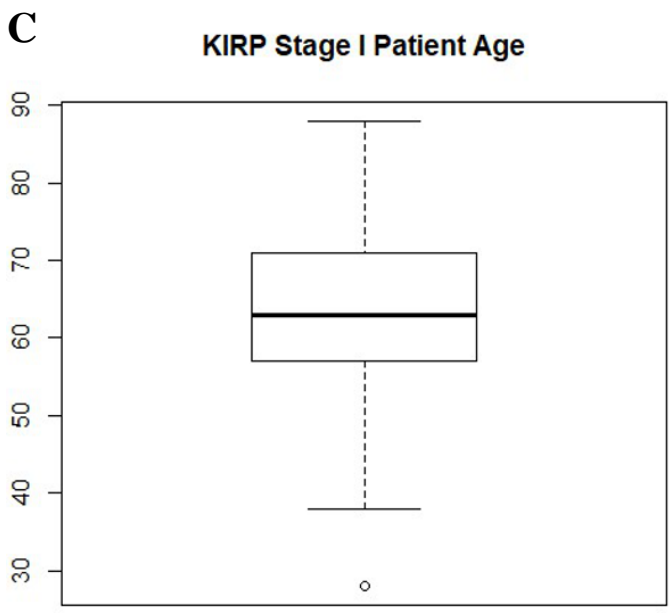
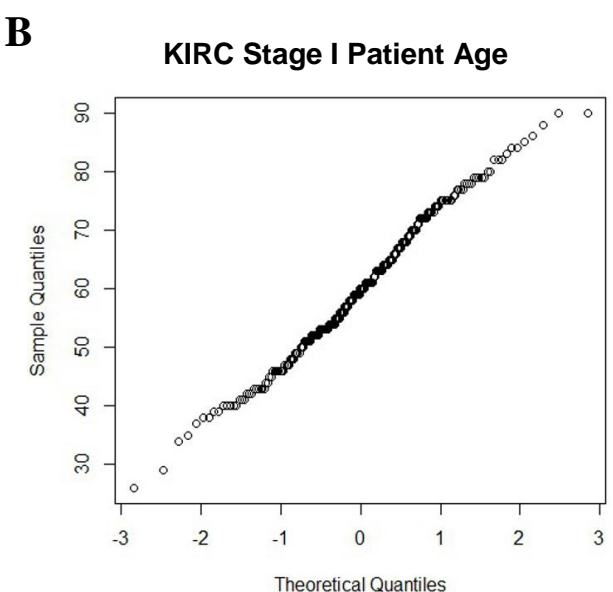
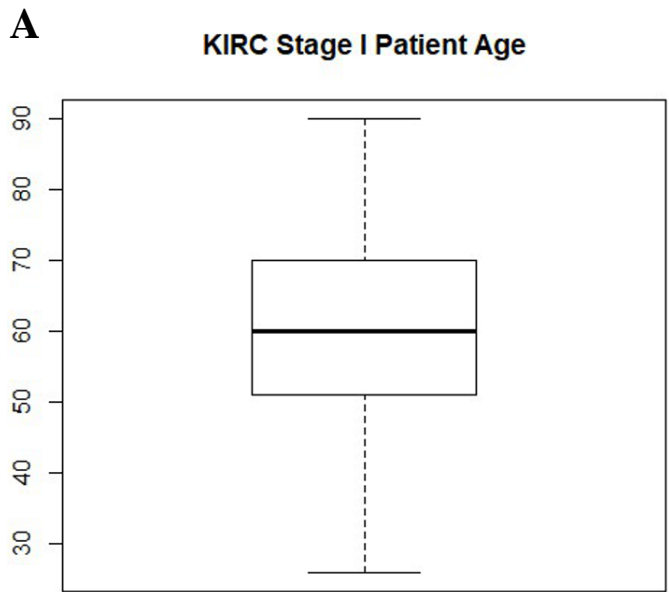


Figure S2. Boxplots and normal Q-Q plots of age distribution in stage I KIRC (A-B) and KIRP (C-D) patients. A linear Q-Q plot indicates normally distributed data.

Table S1. Functional enrichment analysis of genes of most significant nodules in KIRC.

Term Name	Pathway	-log(FDR)
hsa04612	Antigen Processing and Presentation	17.5157
GO.0001916	Positive Regulation of T-cell mediated cytotoxicity	7.5867
hsa05332	Graft-versus-host disease	7.53313
GO.0006082	Antigen Processing via MHC Class I pathway	6.80134
GO.1903039	Positive Regulation of Leukocyte Cell Adhesion	4
GO.0052548	Regulation of Endopeptidase Activity	1.93181
GO.0002664	Regulation of Translation	3.95861
hsa04136	Autophagy	3.65758
GO.0002486	Regulation of T-cell tolerance induction	3.50864
GO.0006457	Protein Folding	2.4437
GO.2001238	Positive Regulation of Extrinsic Apoptosis	2.4437
hsa04640	Hematopoietic cell lineage	2.39794
GO.0006417	Organic Acid Metabolic Process	1.95861
hsa05164	Influenza A	1.93554

Table S2. Functional enrichment analysis of genes of most significant nodules in KIRP.

Term Name	Pathway	-log(FDR)
GO.0043312	Neutrophil Degranulation	46.31247104
GO.0019730	Antimicrobial Humoral Response	6.910094889
GO.0030574	Collagen Catabolic Process	4.863279433
GO.0006954	Inflammatory Response	4.744727495
hsa04922	Glucagon Signaling	3.568636236
GO.0000041	Transition Metal Ion Transport	3.008773924
GO.0030388	Fructose-1,6-biphosphate metabolic process	2.744727495
GO.0044793	Negative Regulation of Viral Process	2.585026652
GO.0002682	Regulation of immune system	2.397940009
GO.0009056	Catabolic Process	2.180456064
GO.0019370	Leukotriene biosynthesis	2.148741651
GO.0002478	Antigen processing and presentation	1.866461092

GO.0019835	Cytolysis	1.801342913
GO.0044283	Small molecule biosynthetic process	1.690369833
GO.0006953	Acute-phase Response	1.619788758
GO.0031343	Positive Regulation of Cell Killing	1.602059991
GO.0032757	Positive Regulation of IL-8 Production	1.595166283
GO.1903556	Negative Regulation of TNF superfamily	1.580044252
GO.0019221	Cytokine-mediated Signaling Pathway	1.536107011
GO.0031347	Regulation of Defense Response	1.49757288
GO.0010951	Negative Regulation of Endopeptidase Activity	1.338187314
GO.0051289	Protein Homotetramerization	1.327902142

Table S3. Cut-off points for selected genes in KIRC for overall survival analysis.

Gene Symbol	Cut-off point (Normalized counts)
<i>ATXN1</i>	1,321.56
<i>VIM</i>	133,004.59
<i>RFTN1</i>	1,564.90
<i>HLA-B</i>	94,525.33
<i>RIN1</i>	400,93

Table S4. Cutoff points of selected genes in KIRP for overall survival analysis.

Gene Symbol	Cut-off point (Normalized counts)
<i>TNFAIP6</i>	851.11
<i>TM4SF19</i>	76.92
<i>GRAMD1B</i>	14.48
<i>CHI3L2</i>	11.13
<i>EGR3</i>	262.85
<i>THY1</i>	2,167.99
<i>CPNE7</i>	262.14
<i>TRPM8</i>	79.04