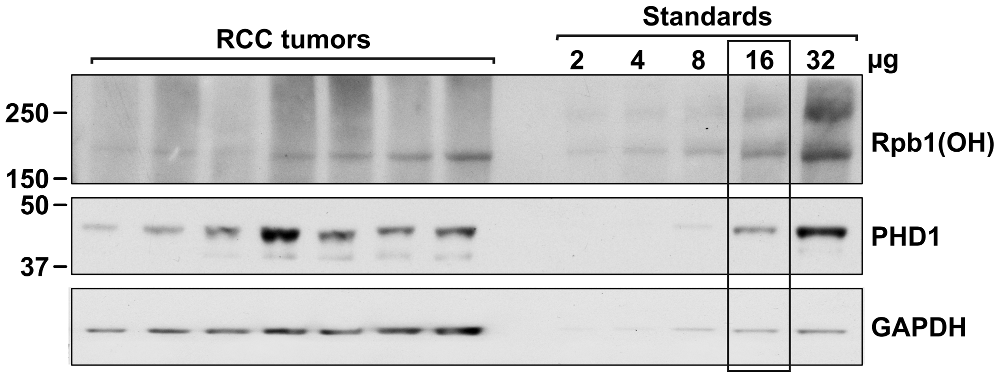

Figure S1. Representative western blot showing molecular standards used for normalization of individual proteins among all the gels run for all the tumors or kidneys. A sample running in the linear range of standards (rectangle) was used for normalization. In addition, all samples were normalized to the levels of GAPDH.

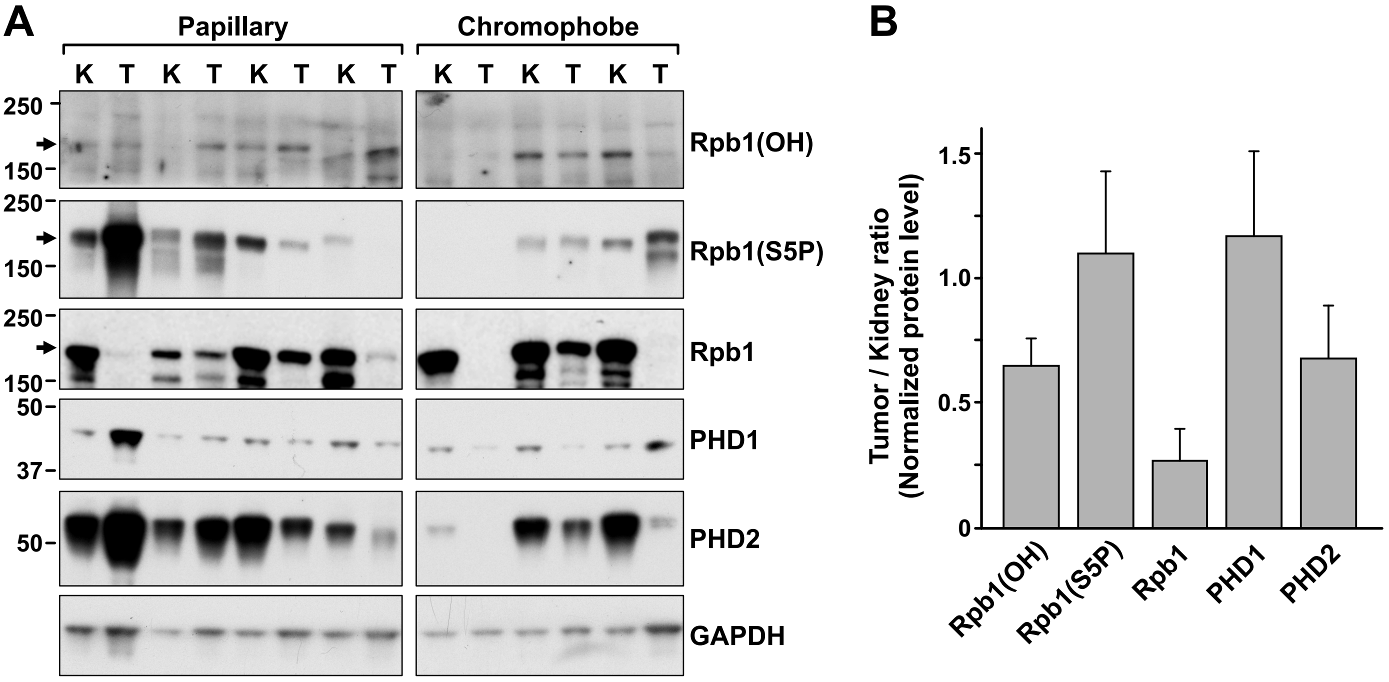

Figure S2. Western blots of extracts from four papillary and three chromophobe renal tumors and matched normal kidneys probed with the indicated antibodies (**A**). (**B**) Quantification of the tumor/kidney ratio was performed by first normalizing the optical density of relevant bands to the optical density of GAPDH bands and then calculating the T/K ratio. The analysis to date, although on a very small sample, does not indicate increases in Rpb(OH), PHD1 or PHD2 in these tumors as compared to matched kidneys.

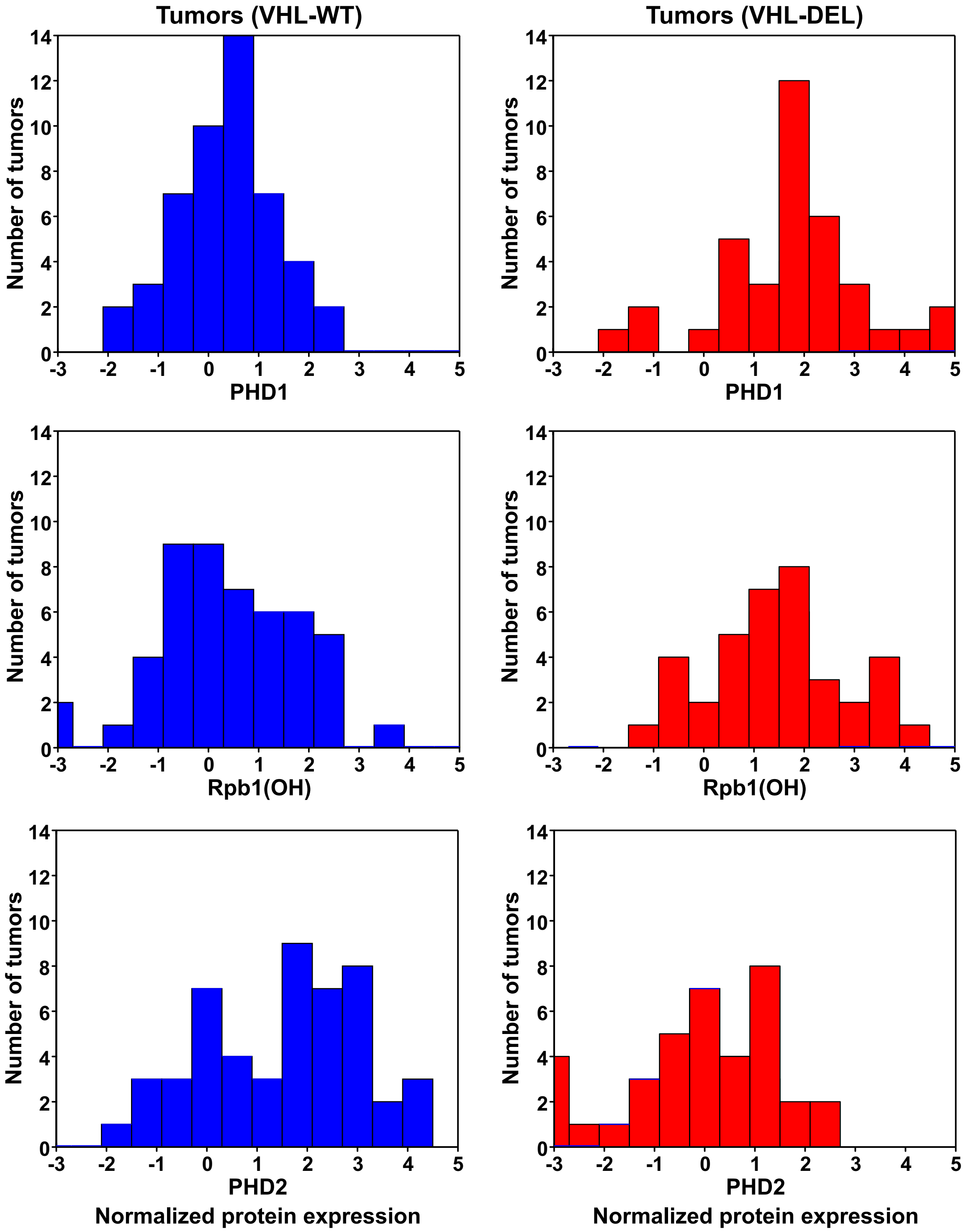

Figure S3. **Histograms of the distributions of PHD1, Rpb1(OH), and PHD2 levels in VHL-WT (red bars) and -DEL (blue bars) tumors.** The normalized expression levels for each protein are shown on the x-axis, and the number of tumors at a given expression level are shown on the y-axis. For example, there are 10 VHL-DEL and 1 VHL-WT tumors with PHD1 expression levels in the interval around 0 (bar #4 in the top panels). The bars at either end of the histogram account for all cases with values below -3 or above 5. The separation between distributions for VHL-WT and -DEL cases is most pronounced for PHD1, which is also reflected in multivariate decision tree-based analysis Fig. 3A).

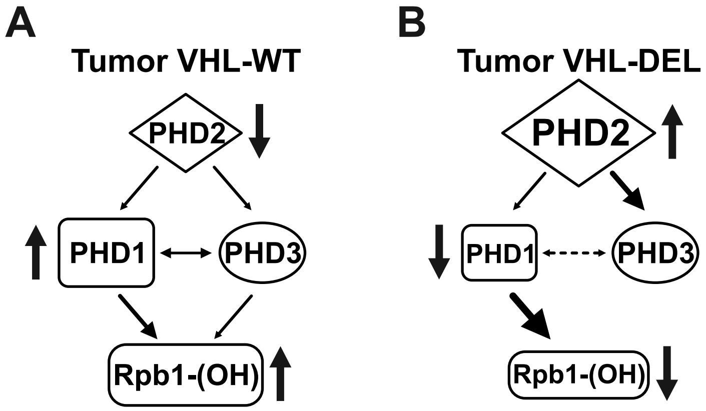

Figure S4. **Proposed model for the regulation of Rpb1(OH) in RCC VHL-WT (A) and VHL-DEL (B) tumors.** In VHL-WT tumors, Rpb1 is hydroxylated by PHD1 and PHD3, and relatively lower levels of PHD2 do not inhibit this hydroxylation, or inhibit it to a lesser degree. In VHL-DEL tumors, higher levels of PHD2 titrate PHD3 away from Rpb1, leaving PHD1 as the only hydroxylase and resulting in an overall lower, but primarily PHD1-mediated, Rpb1 hydroxylation.

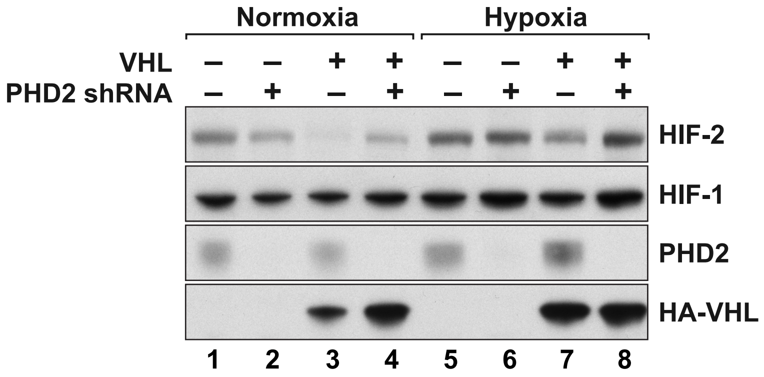

Figure S5. Knockdown of PHD2 in 786-O VHL cells induces accumulation of HIF-2 to levels similar to those measured in VHL(-) cells under both normoxic and hypoxic conditions. Western blot analysis of the indicated proteins. The control samples were treated with scramble shRNA.

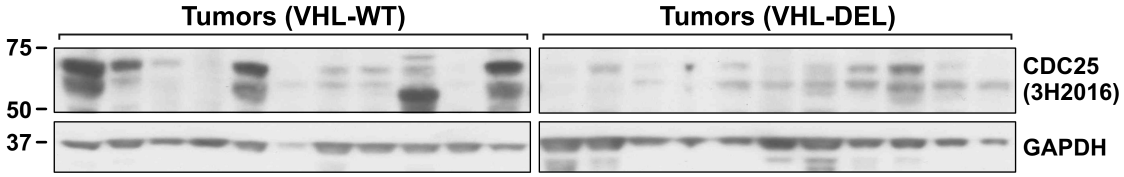

Figure S6. **Western blot of CDC25A in a representative set of VHL-WT and VHL-DEL RCC tumors.** Santa Cruz monoclonal antibody 3H2016 was used for immunoblotting. In human RCC tumors, the antibody detects two bands between 50 and 75 kD markers. These bands most likely correspond to different phosphorylation forms or splice variants of CDC25A.

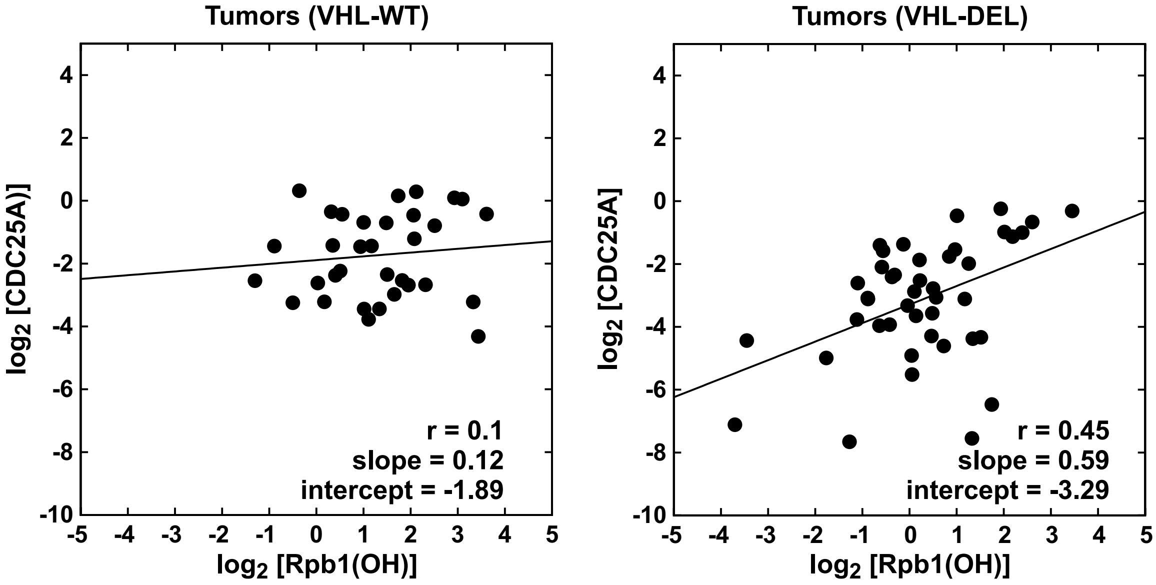

Figure S7. Regression analysis of CDC25A levels as function of Rpb1(OH) levels in tumor samples stratified by *VHL* gene status. Each dot represents a sample and the solid line represents the linear regression fit, with the Pearson correlation coefficients (r) as well as the slope and intercept of the fitted line shown in the lower right corner of each box. ** $p<0.01$

Table S1. Sequence of forward and reverse primers used for RT-PCR of the indicated human mRNAs.

hVEGF-A	F	5’	TTTCTGCTGTCTTGGGTGCATTGG	3’	**hVEGFb**	5'	CTGCGAAGGTGACACATGGCTTTT
hVEGF-A	F	5’	TTTCTGCTGTCTTGGGTGCATTGG	3’	**hVEGFb**	3'	GCAAGTCACCCTGCTGAGTCT
GLUT-1	F	5’	CCGGCGGAATTCAATGCTGATGAT	3’	**hVEGFc**	5'	CCAGAAATCAACCCCTAAATCCTGGAAAA
hGLUT-1	F	5’	CCGGCGGAATTCAATGCTGATGAT	3’	**hVEGFc**	3'	CCATAATAGAAAATCGATGAACTGGAAAA
GLUT-1	B	5’	TCAGCATCTCAAAGGACTTGCCCA	3’			

Table S2. Summary of general information on all human RCC tumors used for analysis

total # of kidneys	114
total # of tumors	128
# of tumors with known grade	114
G1	10
G2	64
G3	32
G4	8
unknown	14
tumor stage:	
0	1
1	6
1a	25
1b	20
2	11
3	3
3a	11
3b	11
3c	1
unknown	39
VHL gene status:	
wild type	46
missense point mutations	17
hypermethylation	13
frameshift, nonsense mutations	52

Table S3. Status of the *VHL* gene sequence and promoter hypermethylation in all investigated RCC tumors. (WT - wild-type; PM/MS - missense point mutations; HypMe - hypermethylated; DEL - frameshift (FS), nonsense (Non), in-frame-deletion (IFD) mutations; nd - not determined

Tumor ID	VHL Gene	Grade and pTNM	HypMe	Mutation				
				Genomic change	mRNA change	Exon	Codon and predicted amino acid change	Mutation type
1	WT	G2 T1a	No	–	–	–	–	–
2	WT	G2 T1a	No	–	–	–	–	–
3	WT	G2 T1a	No	–	–	–	–	–
4	WT	G2 T1a	No	–	–	–	–	–
5	WT	G2 T1a	No	–	–	–	–	–
6	WT	G2 T1a	No	–	–	–	–	–
7	WT	G2 T1a	No	–	–	–	–	–
8	WT	G2 T1a	No	–	–	–	–	–
9	WT	G2 T1a	No	–	–	–	–	–
10	WT	G2 T1a	No	–	–	–	–	–
11	WT	G2 T1b	No	–	–	–	–	–
12	WT	G2 T1b	No	–	–	–	–	–
13	WT	G2 T1b	No	–	–	–	–	–
14	WT	G2 T1b	No	–	–	–	–	–
15	WT	G2 T1b	No	–	–	–	–	–
16	WT	G2 T1b	No	–	–	–	–	–
17	WT	G2 T1b	No	–	–	–	–	–
18	WT	G2 T2	No	–	–	–	–	–
19	WT	G2 T3a	No	–	–	–	–	–
20	WT	G2 T3b	No	–	–	–	–	–
21	WT	G2 T3b	No	–	–	–	–	–
22	WT	G2 T3b	No	–	–	–	–	–
23	WT	G2 T3b	No	–	–	–	–	–
24	WT	G2 T3b	No	–	–	–	–	–
25	WT	G2	No	–	–	–	–	–
26	WT	G2	No	–	–	–	–	–
27	WT	G2	No	–	–	–	–	–
28	WT	G2	No	–	–	–	–	–
29	WT	G3 T1a	No	–	–	–	–	–
30	WT	G3 T1b	No	–	–	–	–	–
31	WT	G3 T1b	No	–	–	–	–	–
32	WT	G3 T2	No	–	–	–	–	–
33	WT	G3 T3a	No	–	–	–	–	–
34	WT	G3 T3b	No	–	–	–	–	–
35	WT	G3	No	–	–	–	–	–
36	WT	G3	No	–	–	–	–	–
37	WT	G3	No	–	–	–	–	–
38	WT	G3	No	–	–	–	–	–
39	WT	G4 T3a	No	–	–	–	–	–
40	WT	G4 T3a	No	–	–	–	–	–
41	WT	G4 T3b	No	–	–	–	–	–
42	WT	G4	No	–	–	–	–	–
43	WT	nd	No	–	–	–	–	–
44	WT	nd	No	–	–	–	–	–
45	WT	nd	No	–	–	–	–	–
46	WT	nd	No	–	–	–	–	–
47	PM	G1 T1b	No	445 A>C	445 A>C	1	N78H	MS
48	PM	G1 T1b	No	434 T>A	434 T>A	1	V74D	MS
49	PM	G1 T3	No	470 C>T	470 C>T	1	P86L	MS
50	PM	G2 T1a	No	446 A>T	446 A>T	1	N78I	MS
51	PM	G2 T1a	No	458 G>C	458 G>C	1	R82P	MS
52	PM	G2 T1a	No	4928 T>A	602 T>A	2	V130D	MS
53	PM	G2 T1a	No	4922 T>A	596 T>A	2	L128H	MS
54	PM	G2 T1b	No	8188 C>G	712 C>G	3	R167G	MS
55	PM	G2	No	4900 G>T	574 G>T	2	D121Y	MS
56	PM	G3 T1a	No	407 C>T	407 C>T	1	S65L	MS
57	PM	G3 T1b	No	8180 A>T	704 A>T	3	Q164L	MS
58	PM	G3 T3b	No	4991T>A	665 T>A	2	I151N	MS
59	PM	G3 T3c	No	4889 G>C	563 G>C	2	W117S	MS
60	PM	G3	No	4997 T>G	671 T>G	2	L153R	MS
61	PM	G3	No	4889 G>C	563 G>C	2	W117S	MS
62	PM	G3	No	4882 C>A	556 C>A	2	H115N	MS
63	PM	nd	No	445 A>G	445 A>G	1	N78D	MS
64	HypMe	G1 T1b	Yes	-	-	-	-	-
65	HypMe	G2 T1	Yes	-	-	-	-	
66	HypMe	G2 T2	Yes	-	-	-	-	-
67	HypMe	G2	Yes	-	-	-	-	-
68	HypMe	G2	Yes	-	-	-	-	-
69	HypMe	G3 T2	Yes	-	-	-	-	-
70	HypMe	G3 T3a	Yes	-	-	-	-	-
71	HypMe	G3	Yes	-	-	-	-	-
72	HypMe	nd	Yes	-	-	-	-	-
73	HypMe	nd	Yes	-	-	-	-	-
74	HypMe	nd	Yes	-	-	-	-	-
75	HypMe	nd	Yes	-	-	-	-	-
76	HypMe	nd	Yes	-	-	-	-	-
77	DEL	G1 T1	No	440 del T	440 del T	1	F76fsX158	FS
78	DEL	G1 T1	No	8161-8162 insT	685-686 insT	3	L158fsX173	FS
79	DEL	G1 T1a	No	512 del C	512 del C	1	T100fsX158	FS
80	DEL	G1 T1a	No	5004 T>C	IVS2+2 T>C	IVS2+2	Splicing effect	Spl
81	DEL	G1 T1b	No	421 G>T	421 G>T	1	E70X	Non
82	DEL	G1	No	374-375 insG	374-375 insG	1	m54fsX131	FS
83	DEL	G2 T1	No	4937 ins2	611 ins2	2	T133fsX159	FS
84	DEL	G2 T1	No	8155 ins2	678 ins2	3	Y156fsX159	FS
85	DEL	G2 T1a	No	499-509 del11 ins3	499-509 del11 ins3	1	Q96fsX128	FS
86	DEL	G2 T1a	No	287 C>T, 8219-8221 del2	287 C>T, 743-744 del2	1, 3	P25L, R177fsX94	MS, FS
87	DEL	G2 T1a	No	8168 del A ins6	692 del A ins6	3	E160fsX171	FS
88	DEL	G2 T1a	No	8214 C>A	738 C>A	3	Y175X	Non
89	DEL	G2 T1a	No	8191-8195 del5	715-719 del5	3	S168fsX171	FS
90	DEL	G2 T1b	No	4943 delT	617 delT	2	L135fsX158	FS
91	DEL	G2 T1b	No	5005 A>C	IVS2+3 A>C	IVS2+3	Splicing effect	Spl
92	DEL	G2 T1b	No	8279-8285 del7	803-809 del7	3	D197fsX199	FS
93	DEL	G2 T2	No	520- Deleted	520- Deleted	1	P103truncated	truncated
94	DEL	G2 T2	No	553-556 del4	553+3 del4	1	Splicing effect	Spl/FS
95	DEL	G2 T2	No	482-488 del 7	482-488 del 7	1	N90fsX156	FS
96	DEL	G2 T2	No	4939-4942 del4	613-616 del4	2	Y134fsX157	FS
97	DEL	G2 T3	No	4885-4890 del 6	559 del 6	2	L116IFD	IFD
98	DEL	G2 T3a	No	447 del T	447 del T	1	N78fxX158	FS
99	DEL	G2 T3a	No	500-520 del21	500-521 del21	1	Q96IFD	IFD
100	DEL	G2 T3b	No	4983 del T	657 del T	2	F148fsX157	FS
101	DEL	G2 T3b	No	8160 del T	684 del T	3	T157fxX158	FS
102	DEL	G2	No	544 del A	544 del A	1	S111fsX158	FS
103	DEL	G2	No	4989-4991 del3 ins2	663-665 del3 ins2	2	N150fsX158	FS
104	DEL	G2	No	4884 ins C	558 ins C	2	H115fs131	FS
105	DEL	G2	No	8187 del C	711 del C	3	V166fsX169	FS
106	DEL	G2	No	8179 C>T	703 C>T	3	Q164X	Non
107	DEL	G2	No	8275 A>T	799 A>T	3	K196X	Non
108	DEL	G2	No	8176-8194 del 19 insG	700-718 del 19 insG	3	L163IFD	IFD
109	DEL	G3 T1	Yes	446 ins C	446 ins C	1	N78fsX131	FS
110	DEL	G3 T1a	No	523 del G ins 3	523 del G ins 3	1	G104fsX159	FS
111	DEL	G3 T1a	No	384-409 del26	384-409 del26	1	G57fsX122	FS
112	DEL	G3 T1b	No	416-422 del7 insT	416-422 del7 insT	1	S68IFD	IFD
113	DEL	G3 T1b	No	485 delT	485 delT	1	F91fsX158	FS
114	DEL	G3 T2	No	544-557 del14, 8227 A>G	544-553+4 del14, 751 A>G	1, 3	S111fsX115, I180V	FS/Spl, MS
115	DEL	G3 T2	No	4965 delT	638 delT	2	V142fsX158	FS
116	DEL	G3 T3a	No	424-427 del4	424-427 del4	1	P71fsX157	FS
117	DEL	G3 T3a	No	4889 G>A	563 G>A	2	W117X	Non
118	DEL	G3 T3a	No	8146-8160 del15	S2-(7-1) del7, 677-684 de	IVS2, 3	Splicing effect	Spl/FS
119	DEL	G3 T3b	No	384-409 del26	384-409 del26	1	G57fsX122	FS
120	DEL	G3	No	375 ins2	375 ins2	1	M54fsX67	FS
121	DEL	G4 T0	No	8163-8165 del3 insC	687-689 del 3 insC	3	I158fsX165	FS
122	DEL	G4 T2	No	4944-4946 del3	618-620 del3	2	L135IFD	IFD
123	DEL	G4 T3	No	555 T>A	553+2 T>A	IVS1+1	Splicing effect	Spl
124	DEL	G4 T3a	No	8229 del C	753 del C	3	I180fsX201	FS
125	DEL	nd	No	482 del A	482 del A	1	N90fsX158	FS
126	DEL	nd	No	512-514 del3 insA	512-514 del3 insA	1	T100fsX130	FS
127	DEL	nd	No	4966 del G	640 del G	2	D143fsX158	FS
128	DEL	nd	No	8202 del G	726 del G	3	K171fsX201	FS

Table S4. Normalized values of indicated protein levels in all samples of kidneys (left) and RCC tumors (right) where meaningful values were obtained for all proteins of interest. The same ID number is used to indicate samples where kidneys and tumors are from the same patient, and correspond to the ID numbers in Table S3. Each value is an average of at least two independent runs and quantification procedures. While tumor stage is known for some tumors, it is not shown in the table because we did not detect any meaningful correlation between the levels of the investigated proteins and tumor stage. Note that for some statistical analyses in Figures 1, 2, and 3 a log2 transformation of these normalized values was used (data not shown).

Kidney ID	Rpb1(OH)	Rpb1(S5P)	Rpb1	PHD1	PHD2	PHD3	VHL
1	0.779134	0.330303874	0.675807	0.351504	0.602262	0.734235	0.149277
2	0.852668	1.403032937	0.600851	1.176604	0.540309	0.99428	1.032996
4	1.399742	1.542422989	0.918707	0.459954	1.172805	0.95796	0.643101
5	2.086502	2.9323137	0.178467	0.117408	0.185177	0.319598	0.404281
7	1.73543	0.660043959	1.701935	0.703419	1.002106	1.813295	1.034266
8	1.529465	2.392883249	1.142019	0.718516	0.978171	1.620433	1.233934
10	1.238125	2.140309109	1.283523	1.362834	1.650705	1.138483	0.167285
11	0.439318	0.617201666	1.01269	1.192838	1.261866	1.210608	0.462562
12	1.525342	0.368016167	0.846772	0.829452	0.679163	0.889435	1.471188
13	0.711689	1.265966774	0.29769	0.974965	0.047785	0.719737	0.564606
14	0.634307	0.254380638	0.64452	0.237525	0.070996	0.70618	0.353888
15	1.032809	0.521782931	0.746261	0.424122	1.932919	0.877271	2.518942
16	0.848916	0.684038133	0.279306	0.654626	0.471584	0.857188	1.514478
17	0.977678	0.377061674	0.754522	1.41923	1.767182	1.828016	0.619576
18	1.830559	0.16488071	0.722557	0.91794	1.15639	3.403458	0.983551
19	1.014508	0.050713271	0.329183	0.174989	0.116834	1.399744	0.30872
20	1.104317	0.6800587	0.426616	0.625111	0.884925	0.902793	0.639178
21	1.224991	0.243276298	0.702925	0.974546	0.337203	0.870618	0.153836
23	1.234885	0.767624921	0.891906	1.07107	1.076205	1.204561	2.479155
24	0.484898	3.025389807	0.883321	0.947498	1.385623	1.2104	0.207341
25	0.855548	1.209648434	0.824362	0.753569	0.332653	1.299855	2.649292
26	1.021742	0.822667153	0.786866	1.343752	1.40269	1.156253	0.131166
27	0.363271	0.649626853	0.435652	0.386448	0.053826	1.209378	3.158267
29	2.048585	0.422187099	0.638977	0.710106	0.935307	1.522553	2.451929
31	2.234053	1.023556791	0.129195	0.490583	3.879793	1.194947	0.113855
32	0.505768	0.474709321	0.995073	0.95836	1.560713	1.153602	0.884373
33	1.304056	2.718241413	0.966777	1.090319	1.497746	0.892243	0.493036
34	0.171719	0.997167073	0.198455	0.096584	0.074189	1.80349	0.116223
35	0.495588	0.574924406	0.50145	0.898915	0.125229	3.188219	1.73294
41	0.482683	0.096620516	0.506842	1.149068	0.043023	0.996746	0.743588
47	1.511765	0.257129455	1.131149	0.837439	0.548138	0.772244	0.221933
48	1.360669	0.293700695	0.571919	0.390878	0.133033	1.279247	1.171562
49	2.862962	0.247613326	0.760236	1.052349	0.860655	1.277219	1.145268
50	1.601027	0.489600067	0.329988	1.625675	0.706196	8.591856	1.773688
51	2.040814	0.81862637	1.218039	2.295907	1.119129	9.206772	1.278299
52	2.810401	1.022906864	0.715666	1.569299	0.892665	9.001847	1.63274
53	3.710821	0.461967208	0.843589	1.797918	0.690993	1.620706	0.066228
55	2.559682	2.430764061	0.988361	2.353551	1.135427	5.345315	1.523431
59	1.765817	0.481772374	0.631826	1.595579	0.19648	1.492636	0.327719
60	1.191854	0.401445276	0.407765	0.476334	1.031579	3.930477	1.099106
61	1.478438	0.408591186	0.754191	0.732454	0.296469	0.944954	0.502396
62	1.536529	0.229698056	0.769479	0.465753	0.591049	1.567046	1.164647
63	1.535551	2.012883433	0.568629	0.845062	0.485807	0.715738	0.241184
64	0.912197	0.488389451	0.685033	0.518994	0.099616	0.576273	1.421832
65	0.93767	2.24105825	0.671299	1.257413	1.056329	0.702945	2.146823
66	0.80784	0.440106076	0.187093	0.834032	0.201834	0.576493	1.856333
67	0.431643	0.152568349	0.118973	0.133646	0.337996	0.241392	4.396002
68	1.0543	0.385725553	0.120433	0.865638	0.198605	0.731791	4.240861
69	0.895915	1.070821074	0.195994	0.392517	0.196027	0.114244	0.66725
70	1.915905	0.228843467	0.181357	0.595851	0.075702	0.931205	1.764072
74	2.041246	3.503818277	0.814435	0.880212	0.310937	0.978289	0.49049
76	2.17015	4.443728238	1.534715	1.917723	0.716948	1.201576	2.913961
77	1.266122	4.404313408	0.369737	0.128792	0.365433	2.118486	0.061251
78	0.504606	0.322566838	0.460629	0.402672	0.460208	1.668013	2.650926
80	1.160283	0.892027295	0.535365	0.714516	0.670535	1.960343	0.668234
81	0.983911	0.149940119	0.098063	0.407764	0.428582	2.105715	1.446902
82	1.223418	0.130632071	0.500156	1.720964	1.071939	0.886998	1.688551
85	1.112827	1.882790783	0.678788	1.825175	1.423132	0.710859	0.095459
86	0.325931	0.07670219	0.664801	0.892664	1.415415	0.622333	2.644109
87	0.552779	0.154609691	0.250962	0.045084	0.608498	0.74336	0.239469
88	0.69272	0.130108225	0.159014	0.839741	0.582802	1.368429	0.359779
89	0.785025	0.708017815	0.153022	0.054239	0.216993	0.375296	1.042601
90	0.920864	0.318711582	0.546047	0.55992	0.875294	1.07582	1.118818
91	0.791605	2.487599389	0.150301	0.23367	0.516533	1.237536	0.129756
92	0.730808	1.009960175	0.229852	0.380718	0.849046	0.71968	0.209537
93	0.479583	0.075861927	0.140772	0.166071	0.157749	1.305202	1.148087
94	0.555194	0.97610874	0.189323	0.262924	0.046054	2.219977	1.480894
95	0.117793	0.217816082	0.381427	0.201844	0.718753	0.683009	0.064093
96	0.534986	0.236821136	0.443411	0.063383	0.163622	0.661192	1.091792
97	0.493944	0.179334206	0.293079	0.306832	0.555243	0.668346	1.022983
98	0.308335	2.528040354	0.097072	0.432547	0.052135	0.596227	0.212845
99	0.719215	0.955363657	0.706924	0.617725	1.000056	1.254876	1.555337
100	1.090603	1.030930147	0.885545	0.571725	0.926412	2.292522	2.134515
101	0.660999	1.464702248	0.566917	0.207128	0.967793	0.607775	0.436621
102	0.388452	1.199284118	0.704458	0.390897	0.649801	0.824551	1.308767
103	0.688715	1.84316221	1.298607	0.669841	1.13763	0.743965	1.592677
104	0.614685	0.771028154	0.786159	0.398113	0.993879	0.39233	0.122065
105	0.484335	0.913844072	0.804162	0.462881	0.724614	0.630243	1.687428
107	0.832011	2.353406858	0.971168	1.485424	2.980207	0.556605	0.03692
108	0.763594	0.777111124	0.850274	0.378068	0.448012	0.296036	0.856128
109	0.802975	0.855442158	1.124393	0.742572	0.39761	0.609028	1.660823
112	0.873256	0.161201344	0.171173	0.246413	0.079312	0.87181	0.657967
113	0.849006	0.895651368	0.372349	0.5814	0.720885	1.224465	0.754454
114	0.539957	1.015248736	0.032049	0.195297	0.10165	0.72363	0.153658
115	1.312454	0.601587389	0.375738	0.997299	0.593963	0.694079	0.340924
116	0.460186	2.884265107	0.458894	0.936203	0.582209	1.047004	0.128621
117	0.517799	1.387580854	0.191947	0.525759	0.694635	0.139838	0.207386
118	0.723718	0.418806262	0.048664	0.370568	0.445127	0.716893	0.385461
120	1.077945	0.056276677	0.353246	0.775431	0.807636	1.216286	0.615088
121	0.78961	0.063628582	0.419934	0.29992	0.372052	0.61458	0.180799
122	0.723545	0.672405556	0.320635	0.78674	0.915699	1.224465	1.274335
123	0.4286	1.896259925	1.495605	0.892856	2.159733	1.019804	0.221136
124	0.741011	1.791905955	0.448085	0.391341	0.830929	0.75038	0.72417
127	0.744852	2.337983089	0.455631	0.774862	1.068174	1.280256	0.195771
128	0.381876	3.668867351	0.294194	0.233235	0.546196	1.469392	1.078616

Tumor ID	VHL Gene	Tumor Grade	Rpb1(OH)	Rpb1(S5P)	Rpb1	PHD1	PHD2	PHD3
1	WT	G2	7.610721	2.609797488	2.166894	7.549522	3.209464	2.30729
2	WT	G2	4.221295	2.928816489	0.934721	2.853641	2.044011	1.090349
4	WT	G2	2.83374	0.912482714	2.851552	5.752435	0.066321	2.53494
5	WT	G2	10.04669	0.433463901	1.961252	4.26345	1.94647	4.800583
6	WT	G2	4.17295	1.671309893	1.394931	5.853612	2.256066	1.822048
7	WT	G2	12.2131	0.858607543	1.716053	6.195441	0.170077	1.621158
8	WT	G2	3.144421	0.840287077	1.32382	2.855549	1.234943	1.331657
10	WT	G2	3.532139	0.412943931	1.261965	3.623387	1.141059	1.519409
11	WT	G2	1.460306	1.626966231	1.256497	3.978753	0.757928	2.723771
12	WT	G2	3.87533	2.061466465	1.826423	2.693131	2.347028	0.306002
13	WT	G2	4.342426	3.087447961	2.732057	14.88925	5.96958	2.418347
14	WT	G2	8.545708	1.41363241	1.23494	9.104568	3.781291	0.673659
15	WT	G2	2.527555	0.615177313	0.212113	1.868718	1.725931	0.245523
16	WT	G2	0.706526	0.974716435	0.639101	3.679075	0.083415	1.788212
17	WT	G2	3.126437	0.999783556	1.713818	3.771628	2.157587	0.362602
18	WT	G2	5.698271	1.910628554	0.742363	1.955665	1.797571	0.27312
19	WT	G2	2.249171	1.807538702	0.730466	4.593919	0.96836	0.657196
20	WT	G2	2.01575	0.619447536	0.177615	6.155768	1.334911	0.287366
21	WT	G2	15.90326	2.356500303	1.559703	26.54102	4.652444	6.758368
23	WT	G2	0.639568	0.63622467	0.527932	1.801526	0.820324	0.075701
24	WT	G2	10.82134	2.066354159	0.301164	3.480229	0.928283	1.146996
26	WT	G2	0.405188	0.751005193	0.300873	3.601277	1.794225	0.122568
28	WT	G2	3.331607	0.779156723	1.386426	6.177442	2.459399	1.208647
29	WT	G3	4.977022	4.99826329	1.144375	28.0426	0.854764	2.453674
31	WT	G3	2.154387	0.253352712	0.644823	3.273449	0.0895	1.12008
32	WT	G3	2.0051	1.129993914	1.858506	8.307124	2.769522	1.475267
33	WT	G3	1.418504	0.824179367	0.397504	0.51321	0.728931	0.491974
34	WT	G3	0.53923	0.653988007	1.732395	0.289925	0.392766	1.219036
35	WT	G3	1.91411	1.169328133	1.453236	1.460506	1.040441	0.087264
36	WT	G3	1.124474	0.864471544	0.433973	0.490456	0.34083	0.495563
37	WT	G3	1.273205	0.630082856	1.609168	1.344365	0.761081	1.168957
38	WT	G3	1.322905	0.134880849	1.733695	1.678658	0.072821	2.093644
41	WT	G4	1.020683	0.158251636	2.040644	1.04664	0.423803	0.482065
42	WT	G4	1.245149	10.56668652	1.893975	1.334592	0.449199	2.113997
43	WT	n/a	2.79529	0.443972722	1.371594	4.091988	0.802756	0.84924
44	WT	n/a	14.62169	1.097825758	2.328005	17.94265	2.603325	1.991075
46	WT	n/a	0.777681	0.809551446	2.919566	3.66551	0.643682	1.074374
47	PM	G1	0.413175	0.709353049	0.585986	0.129344	1.142549	0.700506
48	PM	G1	4.064763	0.79218263	1.274302	0.135973	0.974876	0.077954
49	PM	G1	0.653213	1.96730497	0.364796	1.487869	2.466269	0.798019
50	PM	G2	0.729352	0.819891976	0.211021	0.397197	1.468764	0.545863
51	PM	G2	0.883799	0.823782647	0.591822	1.753487	1.285709	1.203407
52	PM	G2	0.74397	1.35523819	0.194719	0.311698	1.540084	0.097874
53	PM	G2	1.724725	0.395567366	2.320984	1.045391	0.22306	1.504693
54	PM	G2	1.720062	1.787136817	0.174928	0.557648	0.426695	0.554927
55	PM	G2	8.014753	0.444387833	1.744045	2.957151	2.850078	0.628903
57	PM	G3	2.071958	0.689497641	2.002178	0.82125	0.737635	0.553994
58	PM	G3	0.271502	0.644634107	0.17898	0.679413	1.171833	0.791511
59	PM	G3	0.365757	0.82959042	0.92952	0.626758	0.308191	0.512916
60	PM	G3	1.698567	0.547605748	1.488895	1.012565	1.710302	0.373082
61	PM	G3	0.478659	1.572846238	1.13507	0.757503	1.229741	0.307612
62	PM	G3	0.660622	1.80883773	0.834177	0.860632	0.82084	1.163759
64	HyMe	G1	2.172738	2.932247086	2.174975	1.380005	1.175618	1.278285
65	HyMe	G2	0.911852	0.703876368	2.150089	13.54938	2.675955	5.850135
66	HyMe	G2	2.878463	0.815843689	2.374903	4.254424	1.662132	3.220068
67	HyMe	G2	0.79097	0.656084987	1.32907	0.9783	1.954192	0.760038
69	HyMe	G3	1.002207	2.282286701	0.414736	0.566107	1.059738	0.482342
70	HyMe	G3	0.801813	0.664866943	0.165744	0.309386	1.20129	0.534226
72	HyMe	n/a	3.83223	0.847883797	0.993861	2.740708	1.894164	0.592035
73	HyMe	n/a	1.171514	1.634192168	0.851392	1.602859	1.881267	0.699691
74	HyMe	n/a	1.234273	0.841439318	1.264025	0.310827	0.788237	0.236136
76	HyMe	n/a	0.302381	0.601206474	2.569974	0.126637	0.947291	4.713769
77	DEL	G1	10.93368	2.79717593	2.102091	5.149172	3.643285	1.871108
78	DEL	G1	1.95169	1.593871085	1.728668	2.006133	2.671203	1.752016
79	DEL	G1	1.037842	0.47908202	0.819575	0.770581	0.372664	0.697402
80	DEL	G1	3.828927	1.633617857	2.411425	1.666323	0.81826	1.353178
81	DEL	G1	1.030997	2.815230496	1.086823	0.432985	3.759378	0.41133
82	DEL	G1	0.642688	1.801435932	0.87234	0.567813	1.531569	0.492339
84	DEL	G2	1.07899	1.438652203	0.892419	0.781482	2.932282	0.311157
85	DEL	G2	1.672288	2.424590425	0.437922	1.470619	6.42915	0.621277
86	DEL	G2	0.294238	0.915863031	0.615892	1.148848	1.37454	0.619328
87	DEL	G2	0.091348	0.701286907	0.617502	0.448662	1.298645	0.84751
88	DEL	G2	0.542466	1.618705646	0.842947	1.064071	3.083829	2.006862
89	DEL	G2	0.747215	2.113641965	0.866508	0.884467	2.375451	0.339822
90	DEL	G2	1.479075	2.557185786	0.912503	1.593964	7.067708	0.6679
91	DEL	G2	0.772278	4.481698438	1.112043	0.733157	2.089405	0.329518
92	DEL	G2	0.678033	4.271260524	1.630265	0.54492	4.756769	0.378315
93	DEL	G2	1.166704	3.181305734	3.68067	1.354806	3.498827	1.400942
94	DEL	G2	1.074372	1.929951879	1.843037	1.546114	1.146542	0.562802
95	DEL	G2	2.253194	0.515627171	2.497294	1.409559	4.890749	2.956121
96	DEL	G2	4.96909	0.588209176	1.586007	3.538579	10.34674	1.215133
97	DEL	G2	0.478047	0.252682118	0.737646	0.326845	0.272129	0.871952
98	DEL	G2	2.856576	1.001292303	1.045898	1.644986	0.666681	1.866715
99	DEL	G2	1.791492	1.818168141	0.889099	1.839371	9.743216	0.830614
100	DEL	G2	1.100157	0.440722794	1.386186	1.605608	4.245797	1.405288
101	DEL	G2	2.534317	0.797318596	0.712848	1.670218	3.81863	0.466343
102	DEL	G2	0.914195	0.901634994	0.716565	1.185194	4.379809	1.603964
103	DEL	G2	1.157519	1.235460521	1.843277	0.92735	5.596091	1.249693
104	DEL	G2	0.6469	1.381746398	1.966667	0.917486	4.329536	0.802466
105	DEL	G2	3.418783	1.303166902	2.077023	2.144153	8.111778	0.291925
106	DEL	G2	3.136425	1.469298011	2.702146	3.996055	15.03456	1.626949
107	DEL	G2	1.414038	1.471250279	1.032927	1.046952	8.729734	0.253805
108	DEL	G2	4.66128	1.212528618	1.786955	2.614972	16.15785	2.227012
109	DEL	G3	1.396624	0.61438726	0.749201	1.099558	4.024603	0.596855
110	DEL	G3	0.540394	0.896759393	0.604795	1.28297	5.462258	0.307029
112	DEL	G3	2.504886	1.968016394	0.762007	1.825035	7.423363	0.998059
113	DEL	G3	6.078416	1.32925455	0.961282	2.904793	12.44928	1.227376
114	DEL	G3	4.555193	2.345164805	2.79806	4.678641	16.90912	1.950924
115	DEL	G3	0.803258	1.211746122	0.861694	1.289684	3.142019	0.177281
116	DEL	G3	0.666361	0.837269179	1.183237	0.528925	1.004104	0.791445
117	DEL	G3	5.247643	0.742261232	0.576544	2.23215	0.751285	0.420897
118	DEL	G3	2.010347	0.342314208	1.343775	2.474461	0.388587	4.227386
119	DEL	G3	0.076737	0.549168521	0.186389	0.710884	0.631053	0.697317
120	DEL	G3	4.042164	0.479557064	1.886306	2.937851	9.12943	0.652834
121	DEL	G4	1.380741	3.100850921	1.837431	1.783075	1.356776	1.469719
122	DEL	G4	3.353545	7.700686522	0.802593	2.012554	1.024386	0.494977
123	DEL	G4	2.390136	2.71038919	1.506958	2.071223	7.812385	0.160052
124	DEL	G4	1.654069	0.604418684	0.594829	0.860821	9.657967	0.258953
125	DEL	n/a	0.413885	0.568665118	2.246495	0.903623	1.002361	3.433822
126	DEL	n/a	0.971672	5.296318971	1.483754	1.417686	0.481837	0.291428
127	DEL	n/a	0.461794	6.09365325	0.809109	0.253539	1.078245	2.255607
128	DEL	n/a	0.466668	0.738645436	0.741915	0.576747	0.917696	1.386492