Table S1. PCR Primer of Exons of *PBRM1* and *VHL*, Related to Table1

Gene Name	Exon ID	PCR Primer-F	PCR Primer-R
PBRM1	1	ACCCAAAACCAAGAAAACAA	CAGGAGGTAGAGGTTGCAGT
	2	ATGCAAAGAAACTCCAAACC	GAGCCTCTAACTGTGCCATT
	3	GGTAGGCCTCTGAGTGAAGA	ACAAAGATTCAAGGGCAGAG
	4	AGTATGCCTCTTGTCCCTTG	AAGGGTGCTTTATTCATTGG
	5	CCTACCAATTACCAGGGTTG	GCTTTCTGAATGTGTGTTGC
	6	ATTTGCAGGGGAAAATACAA	ACCTTGTGATCCACCTGTCT
	7	TGGCACTGACAAAATCTGTT	ATCCCAACTTTGGACACAAT
	8	AAGTGTTTCTGCCTCATTCC	AAGAGATCTGCCCACTTCAG
	9	TGCCCTAATTACCACCTGAT	AACAGCCAGTGAAACTCCTC
	10	GAAGAAAACAAAAGAGCCCA	CCAAGCTGGTCTCAAACTCT
	11	GCACTTGGCCTGATTTACTT	ATAAGTCCATTCCGTAGCCA
	12	CAAGTGGTCTTTCACAACGA	TGAGCTGGACACAGTGACTT
	13	CTGTGACACTTGCCCAATAG	CTATTGCTGATTCCTGCCTT
	14	ATCTTTCCCAGGTCTGATGA	CGTGTGCCATATATCTCCAA
	15	CTTCTCTCCCCCACAGAATA	TCCAGGATACCAGAGGTGAT
	16	AGGGCTTGACAAGAACAAAG	CCTAGGCTCTCCCACAGATA
	17	GAAGAAATTGAGGCTCAGGA	ACTGCTCCTGCCAGAATTAC
	18	ATAAACTGGCACCCCAATAA	TGCTGTGTATGATTCTGCCT
	19	ACATGTTTTGCCAAGCTACA	TCATGCAGGCTTTTGTTAAA
	20	CAAGCTGGTCTTGAACTCCT	GCTTTTGCCTCCTTACTTTG
	21	CTGAGGCAAGAGAATCACCT	AATTAGCTGGGTGTGATGGT
	22	GTACTTCCCAAACCAGCAAA	GTTTCCTCGGCTAAGATTGA
	23	ATCTCAAGTGATTCACCCGT	TACCAGGTCCTCTGGTCACT
	24	CCTCCCAAGTAGCTGTGACT	ATTGAATGGAAGTCTGCTCC
	25	CGCCCAGCTAATTTTTGTAT	TGAGAATAATGCAGCTCTGG
	26	TGTCCTAAGATGCAATCCAA	CTCACAAAGCTGCTTCACTG
	27	GTAGAGATGGGGTTTCTCCA	TTGCAGTGAGCTGAAATTGT
	28	CTCTGGCTGAATGTCCTTTT	TCATTTGTCTTCTGCCTCAA
	29	TGTAACAGAGCAAGACCCTG	TGAGTGTGCATCTTGCTTTT
	30	CTTGCCTTAGTCTCCCATGT	AAGACAAAATCACCAGGAGC
	31	GGCTATATCCCAACCATGAG	ATTTGGAGCCAGAAGTTGAG
VHL	1	CAGTAACGAGTTGGCCTAGC	AAAAAGAATGCTCTGACGCT
	2	GAGTAGCTGGGACTACAGGC	TCTTAAGAGCCCAAAGTGCT
	3	GCCACATACATGCACTCACT	TACTTCTCTAATGGGCAGGC

Table S2. Raw Sequencing Data Count, Related to Figure 2 and Table 1

Sample Name	Mean Fold Coverage	Fraction of targets covered by at least 1 ×	Fraction of targets covered by at least 5 ×
RC-1	34.63	95.84%	90.83%
RC-2	33.82	90.92%	78.81%
RC-3	36.42	86.81%	73.37%
RC-4	24.99	89.36%	74.93%
RC-5	32.63	92.84%	82.20%
RC-6	32.56	95.86%	90.54%
RC-7	41.03	95.37%	89.30%
RC-8	27.29	92.51%	80.96%
RC-9	32.13	82.71%	66.93%
RC-10	35.2	94.52%	86.72%
RC-11	24.72	81.77%	64.49%
RC-12	27.59	81.74%	65.03%
RC-13	36.06	91.73%	80.43%
RC-14	30.4	81.65%	67.29%
RC-15	34.42	93.95%	75.86%
RC-16	41.32	92.52%	84.70%
RC-17	38.1	92.85%	75.38%
RC-18	23.91	89.36%	74.88%
RC-19	51.74	87.74%	76.51%
RC-20	30.76	92.87%	73.22%
RN-1	25.85	94.74%	87.37%
RN-2	27.45	95.52%	89.25%
RN-3	37.41	90.84%	84.74%
RN-4	32.65	89.95%	75.87%
RN-5	31.56	96.05%	90.96%

Sample Name	Mean Fold Coverage	Fraction of targets covered by at least 1 ×	Fraction of targets covered by at least 20 ×
ccRCC mix carcinoma (RC-T)	117.77	96.32%	95.01%
normal tissue mix DNA (RN-T)	32.97	95.73%	65.70%