

SI Table 1. Frequency of LOH on VHL and SETD2 amongst TCGA ccRCC samples.

Complete sequencing and CGH data were available for 262 cases (dbGaP accession number: phs000178.v5.;

Copy Number

Mutations	Total	VHL LOH	SETD2 LOH	Both LOH	None LOH	NA	
	Total	262	241	239	238	20	31
	VHL	122	115	112	112	7	14
	SETD2	30	28	28	28	2	4
	Both	15	13	13	13	2	3
	None	125	111	112	111	13	16
	NA	188	155	157	153	29	0

SI Table 2. MutSig analysis to identify significantly recurrent mutations in ccRCC

gene	expr	reptime	hic	N_nonsilent	N_silent	N_noncoding	n_nonsilent	n_silent	n_noncoding	nnei	x	X	p	q
BAP1	1078407	229	62	2134715	617419	3086688	33	1	2	49	79	122827716	0	0
CLOCK	235221	384	22	2550669	649572	3800973	4	0	3	7	25	28356911	0	0
EBPL	425192	296	62	596662	178673	796092	8	0	0	29	57	77303545	0	0
KANK3	752886	204	7	2270653	789173	842490	5	0	1	50	117	146031193	0	0
PBRM1	1217701	231	47	4894582	1236059	7560432	127	1	7	20	60	67076856	0	0
SETD2	593886	365	46	7464787	2030930	4683756	47	2	4	4	11	15229533	0	0
VHL	825905	170	39	608872	184778	614163	167	6	2	1	8	1088318	1.110223e-16	2.991575e-13
KDM5C	877207	NaN	80	4592588	1364671	3296700	22	0	1	5	6	13384195	5.884182e-15	1.387343e-11
PTEN	259678	300	34	1232396	286528	2108667	18	2	3	3	9	5492872	6.459899e-11	1.353851e-07
TP53	2069567	213	34	1257223	347171	2181927	13	1	1	4	4	9060227	1.145001e-06	2.159700e-03
STAG3L2	745065	173	55	416768	107041	1590963	6	0	6	3	6	4242161	1.386555e-06	2.377563e-03
CR1	442029	361	18	7377689	1967845	6235647	13	0	2	4	4	17610076	3.076631e-06	4.835951e-03
MTOR	577167	416	32	7527058	2091980	16137957	28	3	6	7	26	41772852	1.110749e-05	1.611611e-02
PIK3CA	401889	613	11	3212858	800569	4134306	15	1	3	12	39	45527834	1.668844e-05	2.248410e-02

SI Table 3.

Differential enrichment of adult kidney H3K36me3 marks within defined chromosomal segment and breakpoint region lengths.

lSeg	lBrk	WT/LOH (n=210)				Mutant (n=28+1)		
		nBrk	AvgBrk	k36<expect)	k27<expect)	nBrk	AvgBrk	k36>expect)
1Mb	10kb	3505	16.7	0.0628	0.0114	352	12.1	0.217
1Mb	20kb	3636	17.3	0.352	0.135	370	12.8	0.0446
1Mb	50kb	3829	18.2	0.0472	0.951	406	14.0	0.313
1Mb	100kb	4054	19.3	0.0012	0.831	441	15.2	0.697
2Mb	10kb	1658	7.9	0.331	0.229	202	7.0	0.085
2Mb	20kb	1741	8.3	0.231	0.815	211	7.3	0.0064
2Mb	50kb	1880	9.0	0.0368	0.966	236	8.1	0.0796
2Mb	100kb	2025	9.6	0.0052	0.589	259	8.9	0.382
5Mb	10kb	685	3.3	0.0386	0.182	94	3.2	0.238
5Mb	20kb	710	3.4	0.0216	0.452	99	3.4	0.247
5Mb	50kb	766	3.6	<.0002	0.496	107	3.7	0.0746
5Mb	100kb	825	3.9	0.007	0.0892	114	3.9	0.156
10Mb	10kb	321	1.5	0.0144	0.597	35	1.2	0.412
10Mb	20kb	327	1.6	0.0046	0.288	37	1.3	0.0584
10Mb	50kb	349	1.7	0.002	0.404	39	1.3	0.005
10Mb	100kb	368	1.8	0.0046	0.389	41	1.4	0.354

Footnote:

lSeg Minimum segment length

lBrk Maximum breakpoint region length

AvgBrk Average number of breakpoint regions per sample

<expect p-value for the observed mark frequency to be inferior to expectations, as given by 5,000 randomizations

>expect p-value for the observed mark frequency to be superior to expectations