Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

eTable 1: Genes on MSK-IMPACT and syndromes associated with germline mutations

ABL1	
ACVR1	
AKT1	
AKT2	
AKT3	
ALK	Familial neuroblastoma
ALOX12B	
AMER1	
ANKRD11	
APC	Familial adenomatous polyposis
AR	
ARAF	
ARID1A	
ARID1B	
ARID2	
ARID5B	
ASXL1	
ASXL2	
ATM	Ataxia-telangiectasia; ATM-related cancer risk
ATR	
ATRX	
AURKA	
AURKB	
AXIN1	
AXIN2	
AXL	
B2M	
BABAM1	
BAP1	Mesothelioma, uveal melanoma, RCC
BARD1	Hereditary breast and ovarian cancer syndrome
BBC3	
BCL10	
BCL2	
BCL2L11	
BCL2L1	
BCL6	
BCOR	
BIRC3	
BLM	Bloom syndrome
BMPR1A	Juvenile polyposis syndrome
BRAF	
BRCA1	Hereditary breast and ovarian cancer syndrome
BRCA2	Hereditary breast and ovarian cancer syndrome; Fanconi anemia
BRD4	
BRIP1	BRIP1-related cancer; Fanconi anemia
BTK	
KNSTRN	
CALR	
CARD11	
CARM1	
CASP8	
CBFB	
CBL	
CCND1	
CCND2	
CCND3	
CCNE1	
CD274	
CD276	
CD79A	
CD79B	
CDC42	
CDC73	
CDH1	Hereditary diffuse gastric cancer
CDK12	
CDK4	Familial cutaneous melanoma
CDK6	
CDK8	
CDKN1A	
CDKN1B	
CDKN2A	Familial cutaneous melanoma
CDKN2B	
CDKN2C	
CEBPA	
CENPA	
CHEK1	
CHEK2	CHEK2-related cancer
CIC	
CREBBP	
CRKL	
CRLF2	
CSDE1	
CSF1R	
CSF3R	
CTCF	
CTLA4	
CTNNB1	
CUL3	
CXCR4	
CYLD	
CYSLTR2	
DAXX	
DCUN1D1	
DDR2	
DICER1	DICER1-related disorders

DIS3	
DNAJB1	
DNMT1	
DNMT3A	
DNMT3B	
DOT1L	
DROSHA	
DUSP4	
E2F3	
EED	
EGFL7	
EGFR	Familial lung cancer
EIF1AX	
AGO2	
EIF4A2	
EIF4E	
ELF3	
EP300	
EPAS1	
EPCAM	Lynch syndrome
EPHA3	
EPHA5	
EPHA7	
EPHB1	
ERBB2	
ERBB3	
ERBB4	
ERCC2	
ERCC3	
ERCC4	
ERCC5	
ERF	
ERG	
ERRFI1	
ESR1	
ETV1	
ETV6	
EZH1	
EZH2	
FAM175A	Hereditary breast cancer syndrome
FAM46C	
FAM58A	
FANCA	
FANCC	
FAT1	
FBXW7	
FGF19	
FGF3	
FGF4	
FGFR1	
FGFR2	
FGFR3	
FGFR4	

FH	Hereditary Leiomyomatosis and Renal Cell Cancer
FLCN	Birt-Hogg-Dubé syndrome
FLT1	
FLT3	
FLT4	
FOXA1	
FOXL2	
FOXO1	
FOXP1	
FUBP1	
FYN	
GATA1	
GATA2	Familial MDS-AML
GATA3	
GLI1	
GNA11	
GNAQ	
GNAS	
GPS2	
GREM1	Hereditary mixed polyposis syndrome (HMPS)
GRIN2A	
GSK3B	
H3F3A	
H3F3B	
H3F3C	
HGF	
HIST1H1C	
HIST1H2BD	
HIST1H3A	
HIST1H3B	
HIST1H3C	
HIST1H3D	
HIST1H3E	
HIST1H3F	
HIST1H3G	
HIST1H3H	
HIST1H3I	
HIST1H3J	
HIST2H3C	
HIST2H3D	
HIST3H3	
HLA-A	
HLA-B	
HNF1A	
HOXB13	
HRAS	Costello syndrome
ICOSLG	
ID3	
IDH1	
IDH2	
IFNGR1	
IGF1	

IGF1R	
IGF2	
IKBKE	
IKZF1	
IL10	
IL7R	
INHA	
INHBA	
INPP4A	
INPP4B	
INPPL1	
INSR	
IRF4	
IRS1	
IRS2	
JAK1	
JAK2	Familial thrombocytosis
JAK3	
JUN	
KDM5A	
KDM5C	
KDM6A	
KDR	
KEAP1	
KIT	Hereditary Gastrointestinal stromal tumors (GISTs)
KLF4	
KRAS	Noonan Syndrome
LATS1	
LATS2	
LMO1	
LYN	
MALT1	
MAP2K1	
MAP2K2	
MAP2K4	
MAP3K13	
MAP3K14	
MAP3K1	
MAPK1	
MAPK3	
MAPKAP1	
MAX	Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes
MCL1	
MDC1	
MDM2	
MDM4	
MED12	
MEF2B	
MEN1	Multiple endocrine neoplasia, type 1
MET	Hereditary papillary renal carcinoma
MGA	
MITF	Familial melanoma and renal cell carcinoma
MLH1	Lynch syndrome
MLL2	
MLL3	
MLL4	
MLL	
MPL	
MRE11A	Ataxia-telangiectasia-like disorder (recessive); breast cancer
MSH2	Lynch syndrome
MSH3	
MSH6	Lynch syndrome
MSI1	
MSI2	
MST1	
MST1R	
MTOR	
MUTYH	MUTYH-associated polyposis (MAP)
MYC	
MYCL1	
MYCN	
MYD88	
MYOD1	
NBN	Nijmegen breakage syndrome; NBN-related cancer risk
NCOA3	
NCOR1	
NEGR1	
NF1	Neurofibromatosis, type 1
NF2	Neurofibromatosis, type 2
NFE2L2	
NFKBIA	
NKX2-1	
NKX3-1	
NOTCH1	
NOTCH2	
NOTCH3	
NOTCH4	
NPM1	
NRAS	Autoimmune lymphoproliferative syndrome (ALPS)
NSD1	
NTHL1	
NTRK1	
NTRK2	
NTRK3	
NUF2	
NUP93	
PAK1	

PAK7	
PALB2	PALB2-related cancer; Fanconi anemia
PARK2	
PARP1	
PAX5	B cell precursor acute lymphoblastic leukemia (B-ALL)
PBRM1	
PDCD1	
PDCD1LG2	
PDGFRA	Hereditary Gastrointestinal stromal tumors (GISTs)
PDGFRB	
PDPK1	
PGR	
PHOX2B	Familial neuroblastoma; Congenital central hypoventilation syndrome (CCHS)
PIK3C2G	
PIK3C3	
PIK3CA	
PIK3CB	
PIK3CD	
PIK3CG	
PIK3R1	
PIK3R2	
PIK3R3	
PIM1	
PLCG2	
PLK2	
PMAIP1	
PMS1	
PMS2	Lynch syndrome
PNRC1	
POLD1	
POLE	Colorectal cancer and endometrial cancer
PPARG	
PPM1D	
PPP2R1A	
PPP4R2	
PPP6C	
PRDM14	
PRDM1	
PREX2	
PRKAR1A	
PRKCI	
PRKD1	
PTCH1	Nevoid basal cell carcinoma syndrome (NBCCS)
PTEN	PTEN hamartoma tumor syndrome
PTP4A1	
PTPN11	
PTPRD	
PTPRS	
PTPRT	
RAB35	
RAC1	
RAC2	
RAD21	
RAD50	Nijmegen breakage syndrome-like disorder
RAD51	Hereditary breast cancer
RAD51B	Hereditary breast cancer
RAD51C	RAD51C-related cancer; Fanconi anemia
RAD51D	Hereditary ovarian cancer
RAD52	
RAD54L	
RAF1	
RARA	
RASA1	
RB1	Retinoblastoma
RBM10	
RECQL4	Rothmund-Thomson syndrome (RTS)
RECQL	
REL	
RET	Multiple endocrine neoplasia, type 2
RFWD2	
RHEB	
RHOA	
RICTOR	
RIT1	
RNF43	
ROS1	
RPS6KA4	
RPS6KB2	
RPTOR	
RRAGC	
RRAS2	
RRAS	
RTEL1	
RUNX1	Familial platelet disorder with predisposition to acute myelogenous leukaemia
RXRA	
RYBP	
SDHA	Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes
SDHAF2	Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes
SDHB	Hereditary paraganglioma-

	pheochromocytoma (PGL/PCC) syndromes
SDHC	Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes
SDHD	Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes
SESN1	
SESN2	
SESN3	
SETD2	
SETD8	
SF3B1	
SH2B3	
SH2D1A	
SHOC2	
SHQ1	
SLX4	
SMAD2	
SMAD3	Thoracic aortic aneurysms and aortic dissections (TAAD)
SMAD4	Juvenile polyposis syndrome
SMARCA4	Rhabdoid tumor predisposition syndrome type 2
SMARCB1	Rhabdoid tumor predisposition syndrome type 1
SMARCD1	
SMO	
SMYD3	
SOCS1	
SOS1	
SOX17	
SOX2	
SOX9	
SPEN	
SPOP	
SPRED1	
SRC	
SRSF2	
STAG2	
STAT3	
STAT5A	
STAT5B	
STK11	Peutz-Jeghers syndrome
STK19	
STK40	
SUFU	Medulloblastoma
SUZ12	
SYK	
TAP1	
TAP2	
TBX3	
TCEB1	
TCF3	
TCF7L2	
TEK	
TERT	Familial pulmonary fibrosis (FPF); Dyskeratosis congenita (DC)
TET1	
TET2	
TGFBR1	Thoracic aortic aneurysms and aortic dissections (TAAD)
TGFBR2	Thoracic aortic aneurysms and aortic dissections (TAAD)
TMEM127	Familial pheochromocytoma syndrome
TMPRSS2	
TNFAIP3	
TNFRSF14	
TOP1	
TP53	Li-Fraumeni syndrome
TP53BP1	
TP63	
TRAF2	
TRAF7	
TSC1	Tuberous sclerosis complex (TSC)
TSC2	Tuberous sclerosis complex (TSC)
TSHR	
U2AF1	
UPF1	
VEGFA	
VHL	Von Hippel-Lindau syndrome; Familial erythrocytosis, type 2
VTCN1	
WHSC1	
WHSC1L1	
WT1	WAGR (Wilms tumor-aniridia-genital anomalies-retardation) syndrome, Denys-Drash syndrome (DDS), Frasier syndrome, and isolated Wilms tumor
WWTR1	
XIAP	
XPO1	
XRCC2	
YAP1	
YES1	
ZFHX3	
ZRSR2	

Genes in bold were included for germline analysis

eTable 2. Current Indications for Genetic Counseling Referral for Patients with Renal Cell Carcinoma

1. Clear cell RCC with any of the following criteria: age of diagnosis <50, bilateral or multifocal tumors, ≥1 close relative with clear cell RCC
2. RCC with papillary type 1 histology
3. RCC with papillary type 2 histology
4. RCC with collecting duct histology
5. RCC with tubulopapillary histology
6. RCC with Birt-Hogg-Dubé related histology (chromophobe, oncocytoma, oncocytic hybrid)
7. RCC with 2 additional features of Cowden syndrome
8. Angiomyolipomas of the kidney and one additional feature of tuberous sclerosis complex

Abbreviations: RCC, renal cell carcinoma

eTable 3: Reasons for Declining Germline Genetic Testing

Reasons for declining germline genetic testing	Number of patients
Potential cause of worry or anxiety	5
Lack of interest	3
Not wanting to know the information	2
Unsure	2
Concerned about insurance coverage	1

eTable 4. Demographic Characteristics

	No.	%
Total	254	
Age at diagnosis		
Median	56	
Range	13 to 79 years	
Age 46 or younger	49	19
Age 47 or older	205	81
Sex		
Female	75	30
Male	179	70
Race or ethnic background		
Non-Hispanic white	211	83
Hispanic	6	2
Non-Hispanic African American	19	8
Asian or Pacific Islander	12	5
Other or unknown	6	2
Ashkenazi Jewish ethnicity		
Yes	31	12
No	199	78
Unknown	24	10
Family History of RCC		
First-degree relative	19	8
First, second or third-degree relative	24	10
More than 1 relative	7	3
Tumor histologic subtype[a]		
Clear Cell	177	69
Unclassified	29	11
Unclassified, HLRCC features	7	3
Unclassified, SDHB-deficient	1	<1
Papillary	14	5
Chromophobe	11	4
Translocation-associated	10	4
Other	12	5
Patient history of prior malignancy[b]		
Yes	33	13
No	221	87
Bilateral or multifocal RCC at diagnosis		
Yes	14	6
No	240	94
Nephrectomy		
Yes	240	94

No	14	6
Stage at diagnosis		
Stage I	25	10
Stage II	22	9
Stage III	103	41
Stage IV	102	40
Stage at time of analysis		
Stage I	0	0
Stage II	0	0
Stage III	28	11
Stage IV	226	89

Abbreviations: RCC, renal cell carcinoma; HLRCC, hereditary leiomyomatosis and renal cell carcinoma.
aThree patients had both a clear cell and a non-clear cell tumor.
bExcludes nonmelanoma skin cancers

eTable 5. Detail on Pathogenic Mutations

Study ID	GENE 1	VARIANT 1	PROTEIN 1	TRANSCRIPT NM_#S	PENETRANCE	Zygosity	Pathogenicity
RCC4	CHEK2	deletion exons 9-10		NM_007194	MODERATE	WT	P
RCC15	APC	c.3920T>A	p.Ile1307Lys	NM_000038	LOW	LOH	P
RCC20	FH	deletion exon 1		NM_000143	HIGH	PATH LOS	P
RCC26	VHL	c.154G>T	p.Glu52*	NM_000551	HIGH	LOH	P
RCC29	CHEK2	c.216T>G	p.Tyr72*	NM_007194	MODERATE	WT	P
RCC31	CHEK2	c.1100delC	p.Thr367Metfs*15	NM_007194	MODERATE	LOH	P
RCC34	CHEK2	c.1283C>T	p.Ser428Phe	NM_007194	MODERATE	LOH	P
RCC35	APC	c.3920T>A	p.Ile1307Lys	NM_000038	LOW	WT	P
RCC36	CHEK2	c.1283C>T	p.Ser428Phe	NM_007194	MODERATE	LOH	P
RCC46	MUTYH	c.1187G>A	p.Gly396Asp	NM_001128425	LOW	WT	P
RCC47	SDHA	c.91C>T	p.Arg31*	NM_004168	HIGH	CN-LOH	LP
RCC65	CHEK2	c.1100delC	p.Thr367Metfs*15	NM_007194	MODERATE	LOH	P
RCC94	MUTYH	c.207delC	p.Arg70Glyfs*21	NM_001128425	LOW	LOH	P
RCC98	PALB2	c.3234T>A	p.Cys1078*	NM_024675	HIGH	WT	P
RCC102	MUTYH	c.1187G>A	p.Gly396Asp	NM_001128425	LOW	WT	P
RCC120	BARD1	c.1111A>T	p. Lys371*	NM_000465	UNCERTAIN	WT	P
RCC131	CHEK2	c.470T>C	p.Ile157Thr	NM_007194	UNCERTAIN	WT	P
RCC139	FH	deletion exon 1		NM_000143	HIGH	LOH	LP
RCC142	BAP1	deletion exons 15-17		NM_004656	HIGH	LOH	P
RCC151	CHEK2	deletion exons 9-10		NM_007194	MODERATE	WT	P
RCC155	BAP1	c.1983+1_1983+3delinsAT		NM_004656	HIGH	LOH	LP
RCC159	FH	c.584T>C	p.Met195Thr	NM_000143	HIGH	2nd somatic mutation	LP
RCC161	MSH6	c.2731C>T	p.Arg911*	NM_000179	HIGH	WT	P

RCC165	RECQL4	c.1391-2A>G		NM_004260	RECESSIVE	WT	LP
RCC169	EPCAM	c.556-14A>G	p.Tyr186Phefs*6	NM_002354	RECESSIVE	WT	P
RCC173	MUTYH	c.1187G>A	p.Gly396Asp	NM_001128425	LOW	LOH	P
RCC176	APC	c.3920T>A	p.Ile1307Lys	NM_000038	LOW	WT	P
RCC185	CHEK2	c.470T>C	p.Ile157Thr	NM_007194	UNCERTAIN	WT	P
RCC186	MET	c.3239T>C	p.Phe1080Ser	NM_000245	HIGH	WT	LP
RCC187	BAP1	c.437G>A	p.Arg146Lys	NM_004656	HIGH	LOS	LP
RCC199	RECQL4	c.2662C>T	p.Gln888*	NM_004260	RECESSIVE	WT	P
RCC203	APC	c.3920T>A	p.Ile1307Lys	NM_000038	LOW	WT	P
RCC206	FH	c. 556-2A>T		NM_000143	HIGH	PATH LOS	LP
RCC207	BRCA2	c. 5946delT	p.Ser1982Argfs*22	NM_000059	HIGH	WT	P
RCC211	FH	c.1083_1086delTGAA	p.Glu362Glnfs*10	NM_000143	HIGH	PATH LOS	P
RCC212	SDHB	c.587G>A	p.Cys196Tyr	NM_003000	HIGH	LOH	LP
RCC222	APC	c.3920T>A	p.Ile1307Lys	NM_000038	LOW	WT	P
RCC228	ATM	c.-30-2A>G		NM_000051	MODERATE	WT	LP
RCC230	FH	c.824_835delGAGGCACTGCTG	p.Gly275_Ala278del	NM_000143	HIGH	PATH LOS	LP
RCC240	FH	deletion of exons 7-10		NM_000143	HIGH	PATH LOS	P
RCC244	RAD51C	c.1026+5_1026+7delGTA		NM_058216	MODERATE	WT	LP

Abbreviations: LOH, loss of heterozygosity; CN-LOH, copy neutral- loss of heterozygosity; WT, wild-type; ND, could not be determined; PATH LOS, loss of staining on pathology; P, pathogenic; LP, likely pathogenic

eTable 6. *CHEK2* Variants and Association with Renal Cell Carcinoma

Variant (Protein change)	Allele Carriers in Cohort	Non-Allele Carriers in Cohort	Allele Carriers in ExAC	Non-Allele Carriers in ExAC	Odds Ratio (CI)	P Value
c.1283C>T (p.Ser428Phe)	2	506	29	106208		
c.470T>C (p.Ile157Thr)	2	506	411	106206		
c.1100delC (p.Thr367Metfs*15)	2	506	189	106160		
c216T>G exon 2 (p.Tyr72*)	1	506	Absent	na		
Intragenic deletion of the exons 9-10	2	506	Absent	na		
CHEK2 burden test	9	499	629	106208	3.0 (1.3-5.8)	0.003**
CHEK2 burden test without (p.Ile157Thr)	7	497	600	106183	2.4 (0.99-5.2)	0.025**
Burden test without the founder[a] mutations	5	503	411	106208	2.5 (0.8-6)	0.04

[a]Founder mutations:
c.1100delC (p.Thr367Metfs*15)
c.1283C>T (p.Ser428Phe)

eTable 7. Associations between Clinicopathologic Characteristics and Presence of RCC-Associated Germline Mutation

	Germline Mutation in RCC-Associated Gene	No RCC-Associated Germline Mutation	P-Value*
Age at Diagnosis			
≤46years	5 (36%)	44 (18%)	0.15
>46 years	9 (64%)	196 (82%)	
Subtype			
Clear Cell	3 (22%)	174 (72.5%)	<0.001
Non-Clear Cell	9 (64%)	65 (27%)	
Both	2 (14%)	1 (0.5%)	
Family History RCC FDR			
Yes	1 (7%)	18 (8%)	1
No	13 (93%)	222 (92%)	
Metastatic Disease			
Yes	13 (93%)	212 (88%)	1
No	1 (7%)	28 (12%)	
Multiple Malignancy (other than RCC)			
Yes	2 (14%)	39 (16%)	1
No	12 (86%)	201 (84%)	
Bilateral or Multifocal RCC			
Yes	4 (29%)	10 (4%)	0.004
No	10 (71%)	230 (96%)	

[a]RCC-associated germline mutations include mutations in *BAP1*, *FH*, *MET*, *SDHA*, *SDHB*, and *VHL*

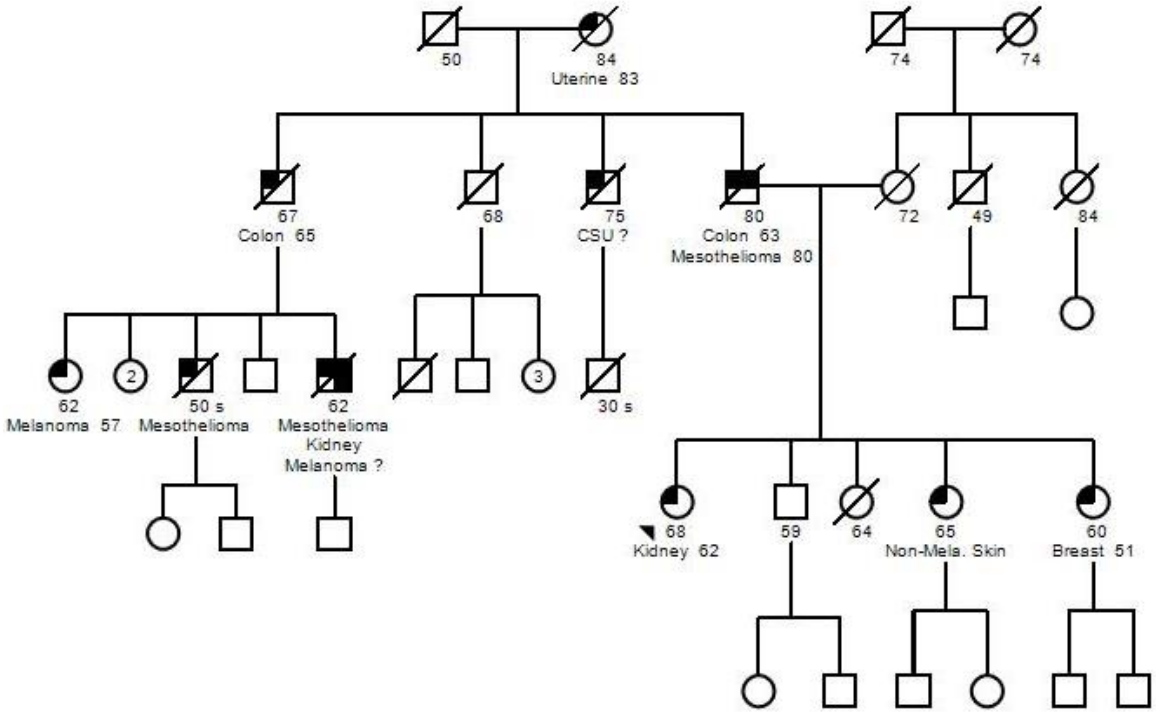
eTable 8. OncoKB Levels of Evidence and Somatic Biomarkers in Cohort

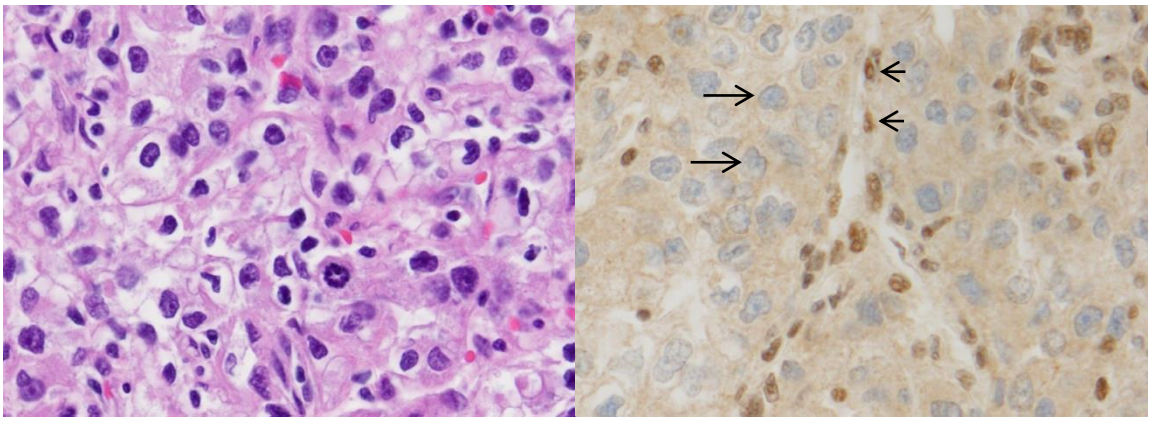
Study ID	Somatic Gene Altered	OncoKB Level of Evidence[a]
RCC221	TSC2	Level 2B
RCC186	BRCA1	Level 2B
RCC11	TSC1	Level 2B
RCC126	ALK (fusion)	Level 2B
RCC219	TSC2	Level 2B
RCC176	BRCA2	Level 2B
RCC63	TSC2	Level 2B
RCC69	TSC2	Level 2B
RCC239	TSC1	Level 2B
RCC142	TSC2	Level 2B
RCC223	TSC1	Level 2B
RCC41	TSC1	Level 2B
RCC95	TSC1	Level 2B
RCC10	TSC2	Level 2B
RCC211	TSC1	Level 2B
RCC228	MET	Level 3
RCC98	ERBB2	Level 3
RCC229	PIK3CA	Level 3
RCC102	ERBB2	Level 3
RCC48	PIK3CA	Level 3
RCC161	PIK3CA	Level 3
RCC147	PIK3CA	Level 3
RCC5	AKT1	Level 3
RCC20	PIK3CA	Level 3
RCC120	PIK3CA	Level 3
RCC124	AKT1	Level 3
RCC214	PIK3CA	Level 3
RCC173	ERBB2	Level 3
RCC106	MAP2K1	Level 3
RCC12	PIK3CA	Level 3
RCC151	PIK3CA	Level 3
RCC104	PIK3CA	Level 3
RCC133	PIK3CA	Level 3
RCC33	PIK3CA	Level 3
RCC254	PIK3CA	Level 3
RCC171	ERBB2	Level 3

[a]**Level 2B**: Standard of care biomarker predictive of response to and FDA-approved drug in another indication, but not a standard of care for this indication
Level 3: Compelling clinical evidence supports the biomarker as being predictive of response to a drug in this or another indication, but neither biomarker not drug are standard of care

eFigure 1 A-C. Families of *BAP1* Germline Mutant Patients and Tumor Immunohistochemistry

eFigure 1A: 62F with clear cell RCC



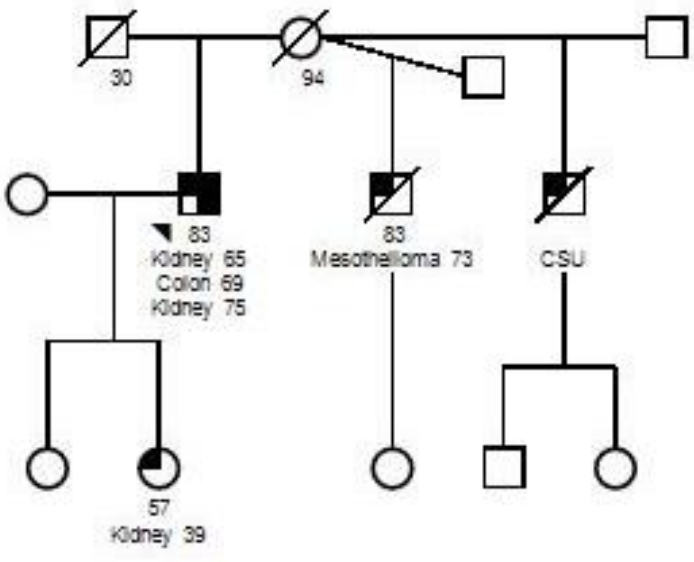


Top panel: Pedigree showing proband with an arrow. Ages, gender and family composition of unaffected relatives may have been altered to preserve anonymity.

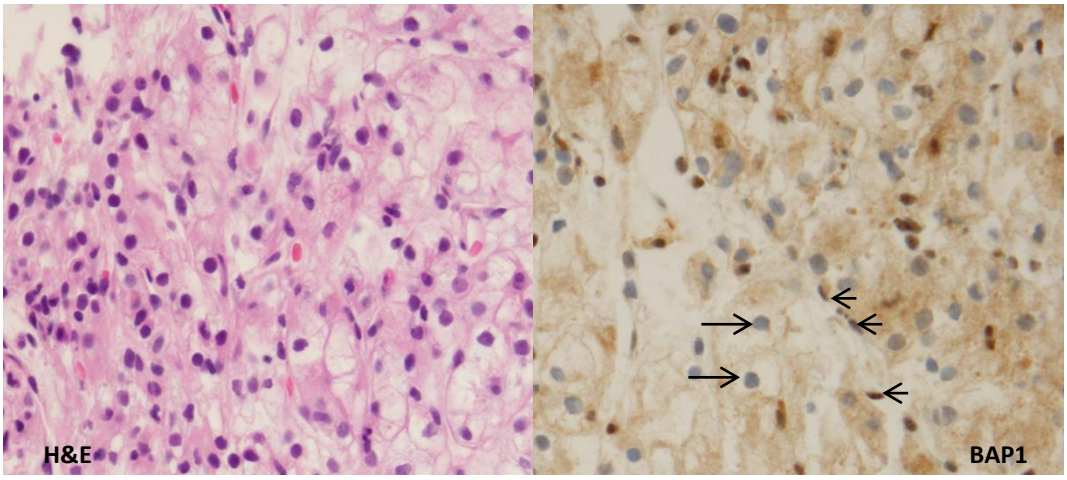
Left bottom panel: H&E staining showing clear cell RCC arranged in alveolar architecture and intervening fine fibrovasculature. Right bottom panel: corresponding BAP1 staining demonstrating absent BAP1 nuclear staining in the neoplastic cells (long arrows). Endothelial cell within the “alveolar” fibrovasculatures show retained BAP1 nuclear expression (short arrows). Stromal and lymphocytic cells also show retain nuclear BAP1 expression.

eFigure 1B

eFigure 1B: 83M with clear cell RCC and papillary RCC



Clear cell RCC

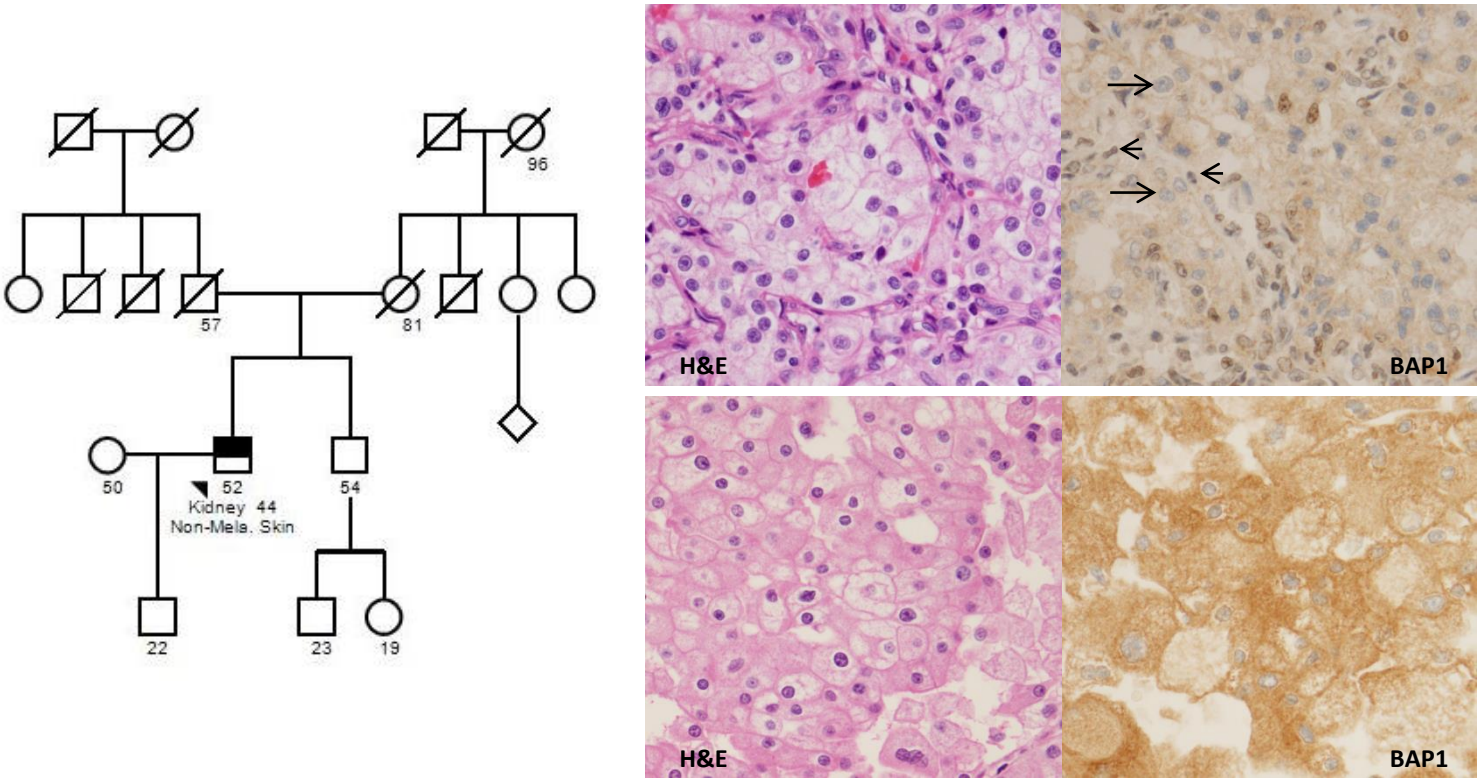


Top panel: Pedigree showing proband with an arrow. Ages, gender and family composition of unaffected relatives may have been altered to preserve anonymity. Abbreviations: CSU, cancer-site unspecified

Left bottom panel: H&E staining showing clear cell RCC histologic features. Right bottom panel: corresponding BAP1 staining demonstrating absent BAP1 nuclear staining in the neoplastic cells (long arrows). Endothelial cell within the "alveolar" fibrovasculatures show retained BAP1 nuclear expression (short arrows). Stromal and lymphocytic cells also show retain nuclear BAP1 expression.

eFigure 1C

eFigure 1C: 52M with clear cell RCC and chromophobe RCC



Left panel: Pedigree showing proband with an arrow. Ages, gender and family composition of unaffected relatives may have been altered to preserve anonymity.

Right panels. Single nephrectomy specimen harboring spatially separated clear cell (right upper panels) and chromophobe (right lower panels) RCCs. Left panels: H&E staining showing respective histologic features with fine “alveolar” fibrovasculatures in the clear cell RCC and perinuclear halos and focal “raisinoid” nuclei in the chromophobe RCC. Right panels: corresponding BAP1 staining demonstrating absent BAP1 nuclear staining in the neoplastic cells (long arrows). Endothelial cell within the “alveolar” fibrovasculatures in the clear cell RCC show retained BAP1 nuclear expression (short arrows). Stromal and lymphocytic cells also show retain nuclear BAP1 expression.