Received: 5 June 2020 | Revised: 12 August 2020 | Accepted: 19 August 2020

DOI: 10.1002/gcc.22893

RESEARCH ARTICLE

WILEY

Pathogenic germline variants in patients with features of hereditary renal cell carcinoma: Evidence for further locus heterogeneity

Philip S. Smith[1] | Hannah West[1] | James Whitworth[1] | Bruce Castle[2] | Francis H. Sansbury[2,3] | Anne Y. Warren[4] | Emma R. Woodward[5] | Marc Tischkowitz[1] | Eamonn R. Maher[1]

[1]Department of Medical Genetics, University of Cambridge and NIHR Cambridge Biomedical Research Centre, and Cancer Research UK Cambridge Centre, Cambridge Biomedical Campus, Cambridge, UK

[2]Peninsula Clinical Genetics Service, Royal Devon and Exeter NHS Foundation Trust, Royal Devon and Exeter Hospital (Heavitree), Exeter, UK University of Exeter Medical School, University of Exeter, Exeter, UK

[3]All Wales Medical Genomics Service, Cardiff and Vale University Health Board, Institute of Medical Genetics, University Hospital of Wales, Cardiff, UK

[4]Department of Histopathology, Cambridge University NHS Foundation Trust and Cancer Research UK Cambridge Centre, Cambridge, UK

[5]Manchester Centre for Genomic Medicine and NW Laboratory Genetics Hub, Manchester University Hospitals NHS Foundation Trust, and Division of Evolution and Genomic Sciences, School of Biological Sciences, Faculty of Biology, Medicine and Health, University of Manchester, Health Innovation Manchester, Manchester, UK

Correspondence
Professor Eamonn R. Maher, Department of Medical Genetics, University of Cambridge and NIHR Cambridge Biomedical 6 Research Centre, and Cancer Research UK Cambridge Centre, Box 238, Cambridge Biomedical Campus, Cambridge CB2 0QQ, United Kingdom.
Email: erm1000@medschl.cam.ac.uk

Funding information
Cancer Research UK; H2020 European Research Council, Grant/Award Number: OncoTreat; National Institute for Health Research

Abstract

Inherited renal cell carcinoma (RCC) is associated with multiple familial cancer syndromes but most individuals with features of non-syndromic inherited RCC do not harbor variants in the most commonly tested renal cancer predisposition genes (CPGs). We investigated whether undiagnosed cases might harbor mutations in CPGs that are not routinely tested for by testing 118 individuals with features suggestive of inherited RCC (family history of RCC, two or more primary RCC aged <60 years, or early onset RCC ≤46 years) for the presence of pathogenic variants in a large panel of CPGs. All individuals had been prescreened for pathogenic variants in the major RCC genes. We detected pathogenic or likely pathogenic (P/LP) variants of potential clinical relevance in 16.1% (19/118) of individuals, including P/LP variants in *BRIP1* (n = 4), *CHEK2* (n = 3), *MITF* (n = 1), and *BRCA1* (n = 1). Though the power to detect rare variants was limited by sample size the frequency of truncating variants in *BRIP1*, 4/118, was significantly higher than in controls (P = 5.92E-03). These findings suggest that the application of genetic testing for larger inherited cancer gene panels in patients with indicators of a potential inherited RCC can increase the diagnostic yield for P/LP variants. However, the clinical utility of such a diagnostic strategy requires validation and further evaluation and in particular, confirmation of rarer RCC genotype-phenotype associations is required.

KEYWORDS

inherited, predisposition, renal cell carcinoma

1 | INTRODUCTION

Renal cell carcinoma (RCC) is a group of human cancers derived from renal epithelium that comprise a variety of histological and genetic backgrounds. Worldwide, RCCs account for around 2.4% of all malignancies, with a prevalence of about 4.4 per 100 000 individuals and a cumulative lifetime risk (to age 75 years) of approximately 0.5%.[1] Molecular genetic studies have identified multiple genetic causes for RCC predisposition. The best recognized cause of familial RCC is the dominantly inherited familial cancer syndrome von Hippel-Lindau (VHL) disease caused by germline mutations in the *VHL* tumor suppressor gene.[2,3] Inactivating mutations in a number of tumor suppressor genes including *VHL*, *FH*, *FLCN*, *SDHB*, and *BAP1*, activating mutations in the *MET* proto-oncogene and constitutional chromosome 3 translocations are well established causes of inherited predisposition to renal cancers.[4] Though it has been suggested that 24% to 33% of individuals with RCC may meet referral criteria for genetic testing,[5] the majority of patients who undergo routine genetic testing for germline variants in the "major inherited RCC genes" (ie, . *VHL*, *FH*, *FLCN*, *SDHB*, *BAP1*, *MET*) do not have detectable pathogenic variants (unpublished observations).

Recently, studies in a number of different human cancer types have identified pathogenic variants in a wider range of cancer predisposition genes (CPGs) than have been traditionally associated with the cancer of interest.[6,7] In addition, germline genetic testing of a cohort of individuals with advanced RCC revealed 16% of individuals presented with a pathogenic cancer-associated germline variant, of which only about a third occurred in the widely recognized RCC-associated genes.[8] We hypothesized that applying a wider CPG testing strategy to a cohort of affected individuals with features of inherited RCC might increase the diagnostic yield of pathogenic/likely pathogenic (P/LP) variants and we proceeded to investigate a large panel of CPGs in 118 unrelated probands pre-screened for germline mutations in *VHL*, *MET*, *FLCN*, *SDHB*, *FH*, and *BAP1*.

2 | MATERIALS AND METHODS

2.1 | Subjects

Individuals diagnosed with RCC referred to Regional Genetics Centres for consideration of genetic testing were assessed for eligibility based on the presence of clinical features associated with inherited RCC. Individuals were recruited if they matched one or more of the following criteria: (a) At least one first or second degree relative with RCC, (b) no family history of RCC but two or more separate primary RCC before age 60 years, or (c) diagnosed with RCC at age 45 years or less. Assignment of groupings based on clinical criteria was carried out hierarchically in the order given, where, for example, a patient with bilateral RCC aged under 45 years with a family history of RCC would be categorized as familial and a patient with bilateral RCC aged under 45 years without a family history of RCC would be categorized as multiple RCC. For four individuals in whom the precise age at diagnosis of RCC was not available the age at genetic testing was used. Individuals with confirmed or likely pathogenic variants in *BAP1*, *FH*, *FLCN*, *MET*, *SDHB* and *VHL* were excluded from the study. All study participants gave written informed consent, and the study was approved by the South Birmingham Research Ethics Committee.

2.2 | Molecular genetics studies

DNA was extracted from peripheral blood lymphocytes in a regional genetics laboratory using standard techniques. A total of 100 samples were analyzed using Illumina TruSight Cancer Sequencing Panel (Illumina, San Diego, CA) on the Illumina MiSeq platform. Seventy five probands (18 of whom were also analyzed by the Illumina TruSight Cancer Sequencing Panel) had exome sequencing data generated by Illumina TruSeq Exome library preparation on the Illumina HiSeq 4000 or Illumina NextSeq platform. In total 118 probands were analyzed by panel and/or exome sequencing.

2.3 | Bioinformatics

Further details of bioinformatic protocols and methodology can be found in the Appendix S1. FASTQ files for both case and ICR1000UK exomes[9] were aligned to genome reference GRCh38 using BWA-MEM (version 0.7.15-r1140) with ALT-contig post-processing. PCR duplicates were flagged by SAMtools rmdup (version 1.4.1) and variant calling carried out using GATK unified genotyper (version 3.7-0-gcfedb67). Variants from targeted sequencing panel and exome datasets were called independently and a "virtual" panel applied to the exome variants via vcftools, restricting the reported variants to the Illumina TruSight Cancer sequencing panel target bed intervals (with an additional 3 bp paddingAppendix S1). Full alignment and variant calling pipeline provided in Appendix S1. VCF files were filtered to remove low quality calls and sequencing artefacts using vcftools and in-house bioinformatics pipelines (supplementary Table S1). Lastly, genomic regions were restricted to a total of 67 cancer-related genes sub-selected from the original cancer gene panel as utilized previously[7] which were targeted on the Illumina TruSight Cancer sequencing panel. In addition, a single variant in *MITF* (rs149617956) was also assessed in conjunction with the previously described genes due to previous associations with RCC risk[10] (Supplementary Table S2, S3).

Variants passing quality filtering were annotated with ANNOVAR to provide genomic region annotation, variant consequence, functional in silico prediction, reference minor allele frequencies for datasets of 1000 genomes project (1KG) and Exome Aggregation Consortium (ExAC),[11] and reported ClinVar data, where available. Variants were selected by variant consequence, filtered to be rarer than 1% (minor AF < 0.01) in both 1KG and ExAC, in order to exclude common SNPs. In silico predictive metrics provided by ANNOVAR were used to inform potential pathogenicity but were not used as filtering cutoffs for candidate selection. ACMG guidelines[12,13] were applied to all candidate variants to determine clinical significance utilizing

InterVar (version 20 180 827). Somatic variant calling was performed jointly using both Strelka2 (version 2.9.10) and Mutect2 (version 3.7-0-gcfedb67) with annotation performed as described for germline variant calls. The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

Structural variant calling was performed using SvABA (version 1.1.3)[14] to identify any large indels or structural variants within the same genomic regions described for SNV calling. Full details of structural variant calling process are described in the Appendix S1.

2.4 | Statistical analysis

Proportion confidence intervals were calculated using R base function binom.test at CI 95%, Odds ratios were calculated using the oddsratio.fisher function in epitools package (version 0.5-10), and two-tailed Fisher's exact tests were calculated using the fisher. test function in base, using R (version 3.5.1).

3 | RESULTS

3.1 | Clinical features

The 118 unrelated individuals with RCC eligible for inclusion were subdivided into three clinical subsets: 44 cases with a positive family history and 74 sporadic cases comprising 30 cases with multifocal or bilateral disease and 44 cases with early onset RCC only). Median age of onset across all cases was 42 years (range 10-74) and 52 years (range 29-74) in the familial cases, 48 years (range 31-72) in multifocal/bilateral cases and 33 years (range 10-46) in early onset cases). Histological subtype was available for 70 of 118 cases (59.3%) and comprised of 68.6% clear cell RCC, 27.1% papillary RCC, and 4.29% chromophobe RCC. Summary of the distribution of clinical features are given in Table 1 (full details in Supplementary Table S6).

TABLE 1 Summary of clinical features of individuals with suspected inherited RCC where available

Clinical feature	Value
Sex, num. (%)	
Male	71 (60.2)
Female	47 (39.8)
Age, median (range)	
All	43 (10-74)
Familial	52 (29-74)
Early onset	33 (10-46)
Bi/multi	48 (31-74)
Case type, num. (%)	
Familial	44 (37.2)
Early onset	44 (37.2)
Bi/multi	30 (25.4)
Histology, num. (%)	
Clear cell RCC	48 (68.6)
Papillary RCC	19 (27.1)
Chromophobe RCC	3 (4.29)
Nonspecified RCC	48
Family history, num. (%)	
First degree	27 (61.4)
Second degree	8 (18.2)
Unspecified	9 (20.5)

Abbreviation: RCC, renal cell carcinoma.

3.2 | Variant filtering

A total of 1955 and 237 variants passed quality control filtering requirements (Appendix S1) in the targeted sequencing and virtual panel sets, respectively. After variant filtering (Appendix S1), a total of 159 variants were retained from the targeted sequencing and 25 variants were retained from the virtual panel sets, respectively. Variants present in both sets were merged resulting in a total of 174 variants across the targeted regions.

Analysis of the pathogenic or likely pathogenic (P/LP) variants identified in this set were divided into three categories subpanels based on the clinical associations and inheritance patterns of the affected genes: (a) Category I genes (n = 14) had a known association with syndromic or non-syndromic RCC predisposition, (b) Category II genes (n = 18) were those in which heterozygous pathogenic variants are known to be associated with predisposition to multiple tumor types, and (c) Category III genes (n = 35) which are associated with cancer predisposition when there are biallelic pathogenic variants or those which have been associated with a single non-RCC tumor phenotype. List of targeted genomic regions are listed in supplemental information Table S2.

Of the 174 variants assessed, 16 were classified as pathogenic or likely pathogenic (P-LP) variants (three pathogenic, 13 likely pathogenic), corresponding to four nonsense variants, three frameshift deletions, one frameshift insertions, and eight nonsynonymous substitutions. The 16 variants were observed in 19 cases (16.1%; 95% CI: 9.98-23.0). P/LP variants were equally distributed by count across the inherited subtypes (nine variants in familial, six variants in early onset, and four variants in bilateral/multifocal). All 16 P/LP variants are described in Table 2 and all 19 patients harboring the aforementioned variants in Table 3. Structural variant calling, performed using SvABA, did not identify any structural variants which passed quality control in the targeted genomic regions.

3.3 | Detection of variants in category I: RCC predisposition genes

As expected, no P/LP variants were detected in genes that had previously been analyzed before inclusion in this study (*VHL*, *MET*, *FLCN*,

TABLE 2 Sixteen variants identified as pathogenic or likely pathogenic by ACMG guideline classifications assigned by InterVar

Gene	Pos (GRCh38)	rsID	Consequence	(Canonical)	DNA	Exon	AA	Genomad AF	InterVar classification
BRCA1	chr17:43074505	N/a	Frameshift deletion	NM_007300.3	c.4563delA	Exon 15	p.Lys1521Asnfs*5	NS	Likely pathogenic
BRIP1	chr17:61780325	rs587781321	Nonsense	NM_032043.2	c.1871C>A	Exon 13	p.Ser624*	1.86E-05	Pathogenic
BRIP1	chr17:61799278	N/a	Frameshift insertion	NM_032043.2	c.1161dupA	Exon 9	p.Gln388Thrfs*7	NS	Likely pathogenic
BRIP1	chr17:61716051	rs137852986	Nonsense	NM_032043.2	c.2392C>T	Exon 17	p.Arg798*	1.40E-04	Pathogenic
CHEK2	chr22:28694066	rs142763740	Nonsynonymous	NM_007194.4	c.1427C>T	Exon 13	p.Thr476Met	3.00E-04	Likely pathogenic
CHEK2	chr22:28695238	rs587780174	Frameshift deletion	NM_007194.4	c.1263delT	Exon 12	p.Ser422Valfs*15	4.49E-05	Pathogenic
ERCC2	chr19:45352315	rs746618110	Nonsynonymous	NM_000400.3	c.2084G>A	Exon 22	p.Arg695His	1.19E-05	Likely pathogenic
ERCC2	chr19:45353112	rs140522180	Nonsynonymous	NM_000400.3	c.1802G>A	Exon 19	p.Arg601Gln	1.81E-04	Likely pathogenic
ERCC2	chr19:45364278	rs767916267	Nonsynonymous	NM_000400.3	c.772C>T	Exon 9	p.Arg258Trp	4.00E-06	Likely pathogenic
MITF	chr3:69964940	rs149617956	Nonsynonymous	NM_000248.3	c.952G>A	Exon 9	p.Glu318Lys	1.37E-03	Likely pathogenic
MUTYH	chr1:45331556	rs36053993	Nonsynonymous	NM_012222.2	c.1178G>A	Exon 13	p.Gly393Asp	3.06E-03	Likely pathogenic
MUTYH	chr1:45332803	rs34612342	Nonsynonymous	NM_012222.2	c.527A>G	Exon 7	p.Tyr176Cys	1.54E-03	Likely pathogenic
PMS2	chr7:5982932	rs1254554953	Nonsynonymous	NM_000535.4	c.2066C>T	Exon 12	p.Thr689Ile	4.63E-06	Likely pathogenic
PMS2	chr7:6002670	rs200029834	Nonsense	NM_001322015.2	c.11C>G	Exon 5	p.Ser4*	2.48E-04	Likely pathogenic
XPA	chr9:97687186	N/a	Nonsense	NM_000380.3	c.464delT	Exon 4	p.Leu155*	NS	Likely pathogenic
XPC	chr3:14172946	N/a	Frameshift deletion	NM_004628.4	c.219delG	Exon 2	p.Val75Trpfs*4	NS	Likely pathogenic

TABLE 3 Nineteen RCC samples carrying variants identified as pathogenic or likely pathogenic by ACMG guideline classifications assigned by InterVar

Full Id	Sex	Subtype	Histology	Age	Gene	Variants
RCC-022	F	Familial	ccRCC	46	*XPA*	*XPA:c.464delT:p.Leu155**
RCC-030	M	Early onset	pRCC	40	*BRCA1*	*BRCA1:c.4563delA:p.Lys1521Asnfs*5*
RCC-023	F	Bi/multi	nsRCC	56	*CHEK2*	*CHEK2:c.1263delT:p.Ser422Valfs*15*
RCC-070	M	Familial	pRCC	44	*XPC*	*XPC:c.219delG:p.Val75Trpfs*4*
RCC-074	F	Familial	nsRCC	64	*BRIP1*	*BRIP1:c.1161dupA:p.Gln388Thrfs*7*
RCC-011	M	Familial	nsRCC	58	*CHEK2*	*CHEK2:c.1427C>T:p.Thr476Met*
RCC-089	F	Bi/multi	nsRCC	40	*ERCC2*	*ERCC2:c.2084G>A:p.Arg695His*
RCC-025	F	Familial	ccRCC	N/a	*ERCC2*	*ERCC2:c.1802G>A:p.Arg601Gln*
RCC-052	F	Bi/multi	nsRCC	61	*ERCC2*	*ERCC2:c.772C>T:p.Arg258Trp*
RCC-068	M	Familial	ccRCC	74	*MITF*	*MITF:c.952G>A:p.Glu318Lys*
RCC-059	M	Bi/multi	nsRCC	56	*CHEK2*	*CHEK2:c.1263delT:p.Ser422Valfs*15*
					MUTYH	*MUTYH:c.1178G>A:p.Gly393Asp*
RCC-088	F	Early onset	nsRCC	45	*MUTYH*	*MUTYH:c.527A>G:p.Tyr176Cys*
RCC-099	M	Early onset	nsRCC	27	*PMS2*	*PMS2:c.2066C>T:p.Thr689Ile*
RCC-031	M	Bi/multi	nsRCC	46	*BRIP1*	*BRIP1:c.1871C>A:p.Ser624**
RCC-001	M	Familial	nsRCC	38	*PMS2*	*PMS2:c.11C>G:p.Ser4**
RCC-043	M	Bi/multi	pRCC	54	*BRIP1*	*BRIP1:c.1871C>A:p.Ser624**
RCC-029	F	Familial	ccRCC	47	*PMS2*	*PMS2:c.11C>G:p.Ser4**
RCC-096	F	Early onset	nsRCC	34	*PMS2*	*PMS2:c.11C>G:p.Ser4**
RCC-102	M	Familial	ccRCC	39	*BRIP1*	*BRIP1:c.2392C>T:p.Arg798**

Abbreviation: RCC, renal cell carcinoma.

SDHB, or *BAP1*) and only a single P/LP variant was identified in a gene previously linked to RCC: a *MITF* nonsynonymous variant in (NM_000248.3: c.952G>A: p.E318K) was identified in an individual who presented with clear cell RCC at age 74 years and whose son was reported to have presented with clear cell RCC at age 53 years. Sequencing in the individual's unaffected brother did not reveal the variant. Though this variant had been previously associated with predisposition to RCC and melanoma [10] there was no reported family history of melanoma.

3.4 | Detection of variants in category II: Multisite CPGs

Six distinct P/LP variants in three genes in which heterozygous pathogenic variants are known to be associated with predisposition to multiple non-RCC tumor types were identified in 8/118 cases. Two category II genes, *BRIP1* and *CHEK2*, harbored germline P/LP variants in more than one proband. Four probands harbored a heterozygous truncating variants in *BRIP1* (two cases with NM_032043.3: c.1871C>A: p.Ser624*, and one each with NM_032043.3: c.1161dupA: p.Gln388Thrfs*7, and NM_032043.3: c.2392C>T: p.Arg798*) (Supplementary Table S4). The four probands consisted of two familial cases and two multifocal/bilateral cases. Age at diagnosis of RCC was 54, 64, 46, and 39 years and these patients presented with papillary, two nonspecified, and clear cell RCC, respectively (Table 3; Individuals RCC-043, RCC-074, RCC-031, RCC-102). DNA from an affected family member (second-degree relative) was available for one of the familial cases (RCC-102) and the affected relative (who developed clear cell RCC at age 57 years) harbored the *BRIP1* nonsense variant (NM_032043.3: c.2698G>A: p.Arg798*) identified in the proband (see Supplementary Figure S1).

To compare the frequency of *BRIP1* truncating variants (3.39%; 4/118) in the patient cohort to controls, the ICR1000UK control set was analyzed for number of truncating variants. The ICR1000UK control cohort harbored *BRIP1* truncating variants in 0.4% (4/999) of individuals (Supplementary Table S7), corresponding to an enrichment of truncating variants in our cases (P = 5.92E-03, OR = 8.70, 95% CI: 1.60-47.4). In addition, evaluation of rare truncating variants in *BRIP1* detected in both the ExAC non-TCGA dataset and gnomAD exome dataset[15] revealed an estimated at 0.24% (123/51300) and 0.20% (252/124984), respectively, which results in a significant enrichment in the case set (P = 2.19E-04, OR = 14.6, 95% CI: 3.85-39.3 and P = 1.09E-04, OR = 17.4, 95% CI: 4.61-46.3). This association is still present in ExAC non-TCGA and gnomAD exome datasets after false discovery rate correction (Table 4). Finally, statistical comparison to data published by Easton et al[16] also demonstrated a statistical enrichment in this series (P = 1.21E-04, OR = 18.2, 95% CI: 4.55-53.1) when compared to truncating variants in *BRIP1* in breast

TABLE 4 Statistical association of truncating variant carrier status between the case set 1958 birth control, gnomAD exomes, and ExAC non-TCGA (Fisher's exact test with FDR correction)

Gene	Cases		gnomAD		gnomAD (*P* value)	gnomAD (q value) (n = 65)	ExAC non-TCGA		ExAC (*P* value)	ExAC (q value) (n = 58)	ICR 1958 BC		1958-BC (*P* value)	1958-BC (q value) (n = 19)
	Carrier	Noncarrier	Carrier	Noncarrier			Carrier	Noncarrier			Carrier	Noncarrier		
AIP	0	118	150	124 530	1.00E+00	1.00E+00	60	53 032	1.00E+00	1.00E+00	0	999	N/a	N/a
ALK	0	118	415	123 175	1.00E+00	1.00E+00	24	53 080	1.00E+00	1.00E+00	2	994	1.00E+00	1.00E+00
APC	0	118	51	120 997	1.00E+00	1.00E+00	186	48 761	1.00E+00	1.00E+00	0	999	N/a	N/a
ATM	0	118	401	124 424	1.00E+00	1.00E+00	398	52 703	1.00E+00	1.00E+00	4	994	1.00E+00	1.00E+00
BAP1	0	118	45	125 458	1.00E+00	1.00E+00	20	53 084	1.00E+00	1.00E+00	0	999	N/a	N/a
BMPR1A	0	118	7	125 516	1.00E+00	1.00E+00	13	53 092	1.00E+00	1.00E+00	0	999	N/a	N/a
BRCA1	1	117	328	124 617	2.67E-01	1.00E+00	154	52 085	2.95E-01	1.00E+00	1	998	2.00E-01	5.43E-01
BRCA2	0	118	2146	121 389	2.77E-01	1.00E+00	929	52 165	2.77E-01	1.00E+00	24	974	1.00E-01	4.03E-01
BRIP1	4	114	252	124 984	1 .09E-04	7.06E-03	174	52 927	6.90E-04	4.00E-02	4	994	5.94E-03	1.13E-01
CDC73	0	118	7	124 886	1.00E+00	1.00E+00	3	53 100	1.00E+00	1.00E+00	1	998	1.00E+00	1.00E+00
CDH1	0	118	21	121 649	1.00E+00	1.00E+00	9	48 329	1.00E+00	1.00E+00	0	999	N/a	N/a
CDK4	0	118	14	125 686	1.00E+00	1.00E+00	3	53 102	1.00E+00	1.00E+00	1	998	1.00E+00	1.00E+00
CDKN2A	0	118	18	117 900	1.00E+00	1.00E+00	6	53 021	1.00E+00	1.00E+00	0	999	N/a	N/a
CEBPA	0	118	0	118 332	N/a	N/a	0	52 127	N/a	N/a	0	999	N/a	N/a
CHEK2	2	116	728	119 600	1.61E-01	1.00E+00	266	51 488	1.25E-01	1.00E+00	5	992	1.64E-01	5.19E-01
CYLD	0	118	10	124 515	1.00E+00	1.00E+00	3	52 828	1.00E+00	1.00E+00	0	999	N/a	N/a
DDB2	0	118	40	125 271	1.00E+00	1.00E+00	13	53 092	1.00E+00	1.00E+00	0	999	N/a	N/a
DICER1	0	118	17	125 424	1.00E+00	1.00E+00	9	53 096	1.00E+00	1.00E+00	1	998	1.00E+00	1.00E+00
EGFR	0	118	79	118 688	1.00E+00	1.00E+00	26	52 854	1.00E+00	1.00E+00	0	999	N/a	N/a
EPCAM	0	118	43	122 455	1.00E+00	1.00E+00	30	52 947	1.00E+00	1.00E+00	0	999	N/a	N/a
ERCC2	0	118	189	119 333	1.00E+00	1.00E+00	70	52 787	1.00E+00	1.00E+00	0	999	N/a	N/a
ERCC3	0	118	295	124 460	1.00E+00	1.00E+00	113	52 991	1.00E+00	1.00E+00	0	999	N/a	N/a
ERCC4	0	118	101	124 884	1.00E+00	1.00E+00	46	53 053	1.00E+00	1.00E+00	0	999	N/a	N/a
ERCC5	0	118	146	125 186	1.00E+00	1.00E+00	41	53 055	1.00E+00	1.00E+00	0	999	N/a	N/a
EXT1	0	118	7	125 399	1.00E+00	1.00E+00	2	53 103	1.00E+00	1.00E+00	0	999	N/a	N/a
EXT2	0	118	74	123 212	1.00E+00	1.00E+00	22	52 900	1.00E+00	1.00E+00	0	999	N/a	N/a
FH	0	118	16	116 752	1.00E+00	1.00E+00	5	47 640	1.00E+00	1.00E+00	1	998	1.00E+00	1.00E+00
FLCN	0	118	189	125 301	1.00E+00	1.00E+00	128	52 976	1.00E+00	1.00E+00	0	999	N/a	N/a
GATA2	0	118	2	114 936	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
HNF1A	0	118	15	122 880	1.00E+00	1.00E+00	6	53 097	1.00E+00	1.00E+00	0	999	N/a	N/a
KIT	0	118	21	125 545	1.00E+00	1.00E+00	4	53 101	1.00E+00	1.00E+00	0	999	N/a	N/a
MAX	0	118	21	125 062	1.00E+00	1.00E+00	6	53 043	1.00E+00	1.00E+00	0	999	N/a	N/a

TABLE 4 (Continued)

Gene	Cases		gnomAD		gnomAD (*P* value)	gnomAD (q value) (n = 65)	ExAC non-TCGA		ExAC (*P* value)	ExAC (q value) (n = 58)	ICR 1958 BC		1958-BC (*P* value)	1958-BC (q value) (n = 19)
	Carrier	Noncarrier	Carrier	Noncarrier			Carrier	Noncarrier			Carrier	Noncarrier		
MEN1	0	118	2	122 596	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
MET	0	118	26	122 952	1.00E+00	1.00E+00	9	52 843	1.00E+00	1.00E+00	0	999	N/a	N/a
MLH1	0	118	80	122 372	1.00E+00	1.00E+00	10	53 095	1.00E+00	1.00E+00	0	999	N/a	N/a
MSH2	0	118	61	122 691	1.00E+00	1.00E+00	25	53 053	1.00E+00	1.00E+00	0	999	N/a	N/a
MSH6	0	118	1149	123 628	6.32E-01	1.00E+00	949	52 149	2.80E-01	1.00E+00	7	992	1.00E+00	1.00E+00
MUTYH	0	118	533	123 827	1.00E+00	1.00E+00	348	52 754	1.00E+00	1.00E+00	2	996	1.00E+00	1.00E+00
NF1	0	118	97	122 299	1.00E+00	1.00E+00	52	53 020	1.00E+00	1.00E+00	1	998	1.00E+00	1.00E+00
NF2	0	118	8	120 896	1.00E+00	1.00E+00	1	53 104	1.00E+00	1.00E+00	0	999	N/a	N/a
PALB2	0	118	222	125 060	1.00E+00	1.00E+00	83	53 020	1.00E+00	1.00E+00	1	998	1.00E+00	1.00E+00
PHOX2B	0	118	0	118 332	N/a	N/a	0	52 127	N/a	N/a	0	999	N/a	N/a
PMS2	3	115	259	119 201	2.30E-03	7.49E-02	454	52 338	8.29E-02	1.00E+00	4	994	2.94E-02	2.79E-01
PRKAR1A	0	118	2	125 224	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
PTCH1	0	118	40	123 146	1.00E+00	1.00E+00	14	52 903	1.00E+00	1.00E+00	0	999	N/a	N/a
PTEN	0	118	25	122 703	1.00E+00	1.00E+00	1	53 104	1.00E+00	1.00E+00	0	999	N/a	N/a
RAD51C	0	118	121	125 258	1.00E+00	1.00E+00	50	53 054	1.00E+00	1.00E+00	2	996	1.00E+00	1.00E+00
RAD51D	0	118	85	121 475	1.00E+00	1.00E+00	31	52 911	1.00E+00	1.00E+00	1	997	1.00E+00	1.00E+00
RB1	0	118	5	120 731	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
RET	0	118	6	125 729	1.00E+00	1.00E+00	3	53 102	1.00E+00	1.00E+00	0	999	N/a	N/a
RHBDF2	0	118	36	119 924	1.00E+00	1.00E+00	20	53 035	1.00E+00	1.00E+00	0	999	N/a	N/a
RUNX1	0	118	13	103 237	1.00E+00	1.00E+00	7	52 745	1.00E+00	1.00E+00	0	999	N/a	N/a
SDHAF2	0	118	27	125 597	1.00E+00	1.00E+00	15	53 090	1.00E+00	1.00E+00	0	999	N/a	N/a
SDHB	0	118	27	125 031	1.00E+00	1.00E+00	12	53 093	1.00E+00	1.00E+00	0	999	N/a	N/a
SDHC	0	118	27	123 500	1.00E+00	1.00E+00	7	53 075	1.00E+00	1.00E+00	0	999	N/a	N/a
SDHD	0	118	30	88 498	1.00E+00	1.00E+00	6	21 717	1.00E+00	1.00E+00	0	999	N/a	N/a
SMAD4	0	118	14	114 572	1.00E+00	1.00E+00	1	53 104	1.00E+00	1.00E+00	0	999	N/a	N/a
SMARCB1	0	118	4	125 639	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
STK11	0	118	4	80 810	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
SUFU	0	118	2	124 946	1.00E+00	1.00E+00	0	52 127	N/a	N/a	0	999	N/a	N/a
TMEM127	0	118	15	122 589	1.00E+00	1.00E+00	3	53 102	1.00E+00	1.00E+00	0	999	N/a	N/a
TP53	0	118	32	119 966	1.00E+00	1.00E+00	6	52 658	1.00E+00	1.00E+00	0	999	N/a	N/a
TSC1	0	118	8	125 513	1.00E+00	1.00E+00	3	53 100	1.00E+00	1.00E+00	0	999	N/a	N/a
TSC2	0	118	36	122 583	1.00E+00	1.00E+00	6	53 093	1.00E+00	1.00E+00	0	999	N/a	N/a

(Continues)

TABLE 4 (Continued)

Gene	Cases		gnomAD		gnomAD (*P* value)	gnomAD (q value) (n = 65)	ExAC non-TCGA		ExAC (*P* value)	ExAC (q value) (n = 58)	ICR 1958 BC		1958-BC (*P* value)	1958-BC (q value) (n = 19)
	Carrier	Noncarrier	Carrier	Noncarrier			Carrier	Noncarrier			Carrier	Noncarrier		
VHL	0	118	13	106 153	1.00E+00	1.00E+00	14	52 727	1.00E+00	1.00E+00	0	999	N/a	N/a
XPA	1	117	155	124 232	1.38E-01	1.00E+00	60	53 038	1.27E-01	1.00E+00	0	995	1.06E-01	4.03E-01
XPC	1	117	132	122 045	1.21E-01	1.00E+00	71	52 812	1.48E-01	1.00E+00	0	995	1.06E-01	4.03E-01

Abbreviation: ExAC, Exome Aggregation Consortium.

cancer, found at a rate of 0.19% (28/14526) (Supplementary Table S5).

A frameshift deletion in *CHEK2* (NM_007194.4: c.1263delT: p.Ser422Valfs*15) was identified in two individuals, both of whom presented with multifocal RCC in their fifth decade. The frameshift deletion is considered to be pathogenic and has previously been detected in both germline sequencing of breast[17] and prostate cancer.[18,19] An additional *CHEK2* nonsynonymous variant (NM_007194.4: c.1427C>T: p.Thr476Met) was also identified in one individual with nonspecified RCC at 58 years and had a reported family history. The variant falls within the protein kinase domain of *CHEK2* and in vitro studies had reported loss of kinase activity and loss of DNA repair function.[20,21] A single individual with early onset papillary RCC at age 40 years was found to carry a *BRCA1* frameshift deletion in exon 15 (NM_007300.3: c.4563delA: p.Lys1521Asnfs*5), which was absent in the noncancer gnomAD data set.

A *PMS2* nonsense variant was identified in three individuals, purported to occur within the fourth amino acid (NM_001322015: c.11C>G: p.Ser4*) but on review was found only to affect noncanonical isoform 14, resulting in an intronic substitution within the canonical isoforms of *PMS2*. Furthermore, one individual was identified with a *PMS2* nonsynonymous variant, occurring within the canonical transcript (NM_000535: c.2066C>T: p.Thr689Ile). The *PMS2* nonsynonymous substitution occurs within exon 12 resulting a threonine to isoleucine substitution in a c-terminal dimerization domain. The variant occurs as a singleton in the gnomAD data set[15] and is considered to be highly deleterious by multiple in silico predictive tools.

3.5 | Analysis of tumors from cases with germline BRIP1 truncating variants

Pathology blocks from RCC from two related patients with a truncating *BRIP1* variant (*BRIP1* NM_032043: c.2698G>A: p.Arg798*) were available for analysis. The proband (RCC-102) presented with a 63 mm RCC at age 39 years. Histopathological review revealed that the tumor contained some sheets of cells with clear cytoplasm, in keeping with classification as a clear cell RCC. However, in many areas the tumor showed very variable morphology, with a tubulo-papillary architecture and areas where the cells had very abundant eosinophilic cytoplasm (see Figure S2). The tumor cell nuclei were predominantly WHO/ISUP grade 2, but some were interpreted as grade 3. There was no sarcomatoid or rhabdoid morphology. There was no tumor necrosis but there was a marked infiltrate of chronic inflammatory cells within the tumor, including lymphocytes and macrophages. Immunohistochemistry studies were performed and the tumor showed positive staining for CA-IX, CD10, RCC, EMA, CD15, CAM5.2, AMACR, MNF116, AE1/3, and Vimentin and there was very weak and patchy staining for E-Cadherin. SDHB and FH expression was retained. The tumor was negative for CD117, CK7, CK20, Mel-A, and HMB45. This immunoprofile was in keeping with the diagnosis. In summary the tumor was categorized as a clear cell RCC WHO/ISUP

grade 3; pT1b pNX (UICC TNM eighth Edition); Leibovich score: 3. The affected relative (RCC102.1) had a >120 mm diameter tumor with involvement of a renal vein tributary, stage pT3a with a Leibovitch score = 5. Histopathological review showed typical morphological features of a clear cell RCC (see Figure S2), with WHO/ISUP grade 2 tumor cells and no tumor necrosis. Immunohistochemistry was positive for Vimentin, RCC, CA-IX, AE1/3, and EMA (focal). SDHB and FH expression were retained. Targeted somatic gene panel sequencing was performed as described previously[22] to assess 68 cancer-related genes including several associated with RCC. Only a single *VHL* variant in the tumor from the affected relative (RCC102.1) was identified. The variant was consistent with clonal heterozygous inactivation of *VHL* resulting from a large deletion within Exon 3. Both Strelka2 and Mutect2 called the somatic variant but were not identically. Strelka2 called a single 30 bp nonframeshift deletion (NM_000551; c.492_521del; p.Gln164_Asn174delinsHis) at a variant allelic fraction of 0.31. Mutect2 called two separate but contiguous frameshift deletions (NM_000551; c.492_501del; p.Val165AlafsTer2 and NM_000551: c.503_522del: p.Ser168IlefsTer81) at variant allelic fractions of 0.31 and 0.46, respectively. No additional protein-altering somatic mutations were detected at variant allele fraction greater than 10% in either tumor.

4 | DISCUSSION

We analyzed a cohort of 118 individuals with clinical characteristics suggestive of inherited RCC (but no known genetic cause) for germline variants in 68 cancer-related genes. This gene panel strategy was previously used to analyse a large cohort of patients with multiple primary tumors and in that study we found that there was a significant diagnostic yield of P/LP variants in CPGs for which the tumor phenotype in the relevant patient was atypical.[7]

The only pathogenic variant identified in a category I gene was a previously described nonsynonymous variant in *MITF* (c.952G>A: p.E318K). The E318K variant was linked to non-syndromic RCC predisposition in a cohort of individuals presenting with both RCC and melanoma in which variant carriers demonstrated a 5-fold increased risk for melanoma, RCC, or both and functional studies demonstrated MITF upregulation and differential expression of MITF target transcripts.[10,23] Subsequently the E318K variant was confirmed to be associated with a melanoma predisposition[24,25]; however, the association of *MITF* E318K with RCC predisposition has been less well studied and provides limited support for the association between RCC predisposition and *MITF* E318K.[26,27] In this instance, the identification of *MITF* E318K in this cohort is difficult to interpret given the limited sample sizes and the identification of only a single carrier. The category I genes also included rarer RCC cancer predisposition genes such as *CDC73*, *PTEN*, *TSC1*, and *TSC2* that have been linked to syndromic forms of inherited RCC and we did not identify pathogenic variants in these genes (the cohort had been ascertained via clinical geneticists and so we would have expected syndromic cases to have been identified prior to recruitment).

Several VUS variants were identified in *TSC2* and *MET*. Three variants in *MET* (NM_000245: c.T2543C: p.V848A, NM_000245: c.G1406C: p.R469P, and NM_000245: c.A1336G: p.I446V) were present at allelic frequencies lower than 8.5E-05, with in silico predictions being variable, but none of the variants fall within the tyrosine kinase domain associated with constitutional activation of c-MET,[28,29] and none had been reported as somatic events in sporadic RCC based on data from the catalogue of somatic mutations in cancer (COSMIC).[30]

Six missense variants were identified in *TSC2*, associated with tuberous sclerosis complex (MIM: 613254) which predisposes individuals to renal angiomyolipomas and cysts, as well as hybrid or oncocytic RCC in between 2% and 4% of cases.[31,32] Histological information was not available for these individuals to assess if they presented with histologies consistent with loss of *TSC2*. The predicted pathogenicity of these missense variants, as well as the allele rarity, is variable but two variants (NM_000548 c.G4657T: p.G1553C & NM_000548: c.G5117A: p.R1706H) occur within the Rap GTPase activating protein domain implicated in RHEB inhibition[33] and one variant (NM_000548: c.C2476A: p.L826M) arises in a Tuberin-type domain, though its direct function is not known. None of the 6 variants identified in *TSC2* had been reported as somatic events in sporadic RCC in COSMIC. All VUS variants are detailed in the Appendix S1.

Previously, segregation analysis of non-syndromic familial RCC was found to be consistent with an autosomal dominant inheritance pattern with incomplete penetrance.[34] Together with recent findings that the cancer phenotype of well-established cancer predisposition genes may be wider than initially recognized[6,7,35,36] this raised the possibility that we might find pathogenic variants in category II genes in individuals with features of inherited RCC. We identified pathogenic variants in three category II genes (*BRIP1*, *BRCA1*, *CHEK2*) in 6.8% (8/118 probands), of our cohort (6.8% of familial cases, 9.1% of multi/bilateral cases and 2.3% of early onset cases). Four probands harbored truncating mutations in *BRIP1*. Pathogenic *BRIP1* variants were initially reported to predispose individuals to both breast and ovarian cancers,[37,38] though more recent evidence from epidemiological studies of pathogenic *BRIP1* variants in breast cancer have found no association with breast cancer susceptibility.[16,39] We note that the potential link between RCC predisposition and pathogenic BRIP1 variants would be strengthened if any of the rare non-truncating BRIP1 variants identified in probands were to be proved to be pathogenic. Only a single additional variant in *BRIP1* (NM_032043: c.C1207T: p.R403W) was identified as at least a VUS. This variant was enriched in comparison to the gnomAD noncancer population (P = 7.0E-04), but singleton variants in lower sample sizes are more difficult to accurately assess. A recent study assessed the functional impact of several novel or rare nonsynonymous variants[40] and, though none of these variants were present in our cohort, it highlights the potential for non-truncating variants to contribute to cancer predisposition and need for thorough functional evaluation of variants of uncertain significance.

Pathogenic variants were also detected in two other DNA repair genes, *BRCA1* (n = 1) and *CHEK2* (n = 3). While in this study we did

not demonstrate statistical enrichment of *CHEK2* P-LP variants in our cohort of individuals with features of inherited RCC, joint assessment of the frequency of P-LP variants in *CHEK2* in this case series and our cohort of individuals with multiple primary tumor-associated RCC that we analyzed with a similar cancer predisposition gene panel strategy,[7] demonstrated that P-LP *CHEK2* variants are overrepresented after multiple testing correction (7/192; P = 2.14E-04, FDR corrected = 1.77E-02). This is also strengthened the association described by Carlo et al. which reported an enrichment of germline *CHEK2* variants in patients with advanced RCC.[8]

The significance of the *BRCA1* mutation in a single individual with early onset papillary RCC is difficult to interpret. Germline *BRCA1* and *BRCA2* variants have been reported previously and in a recent study of 190 unrelated Chinese patients with RCC aged <45 years, analysis of 23 CPGs revealed four RCC patients with pathogenic *BRCA1* (n = 1) or *BRCA2* (n = 3) germline variants.[41] However, in BRCA1 and BRCA2 mutation carriers ascertained through a personal and/or family history of breast/ovarian cancer the risk of RCC had not been reported to be increased.[42]

While some inherited RCC cases are caused by genes (eg, *VHL*, *MET*, *BAP1*) which show high somatic alteration rates in sporadic RCC, others inherited RCC genes (eg, *FLCN* and *SDHB*) do not display frequent somatic alteration in sporadic RCC. *BRCA1*, *CHEK2*, or *BRIP1* are frequently somatically altered in sporadic RCC in the TCGA dataset (1.2%, 1%, and 1.1%, respectively) at a rate that would be indicative of common somatic driver genes.[43] However, *BAP1*, *BRCA1*, *BRCA2*, *BRIP1*, and *CHEK2* gene products have related functions in DNA repair pathways that may make a common role in RCC predisposition more plausible. BAP1 (BRCA1 associated protein) was originally identified due to direct interactions with the RING finger domain of BRCA1 and functions as a de-ubiquitinating enzyme. BAP1 has been determined to form multiple protein complexes and known functions include removal ubiquitin groups from histone H2A lysine 119 residues to regulate gene expression,[44] modulation of DNA damage repair by de-ubiquitinating BARD1 (which binds to BRCA1), indirectly modulating the efficacy of BRCA1-driven DNA repair pathways,[45] and mediates the recruitment of homologous recombination proteins to DNA damage foci.[46] Given the interconnected functions and pathways associated with *CHEK2*, *BRIP1*, and *BRCA1*, it can be hypothesized that germline pathogenic variants in these gene might predispose to a broader range of cancers in a manner similar to that described with *BAP1* predisposition syndrome, including RCC. Two P-LP variants were also identified in *PMS2* across four individuals though the truncating variant present in three of these individuals occurs in a noncanonical isoform, annotated as an intronic substitution. The *PMS2* variants in this study were not independently confirmed and known issues regarding *PMS2* pseudogenes[47] make interpretation more complex.

The observation that eight of the nine genes identified in this study with P or LP variants are associated with DNA repair pathways in some capacity could suggest a potential enrichment across all DNA repair pathways but interpretation should be cautious given that cancer panels are biased towards DNA repair pathway components due to frequent alterations in somatic sequencing, and several of these genes only result in cancer presentation under autosomal recessive inheritance, which was not demonstrated here.

Epidemiological studies have reported multiple risk factors including smoking, obesity and hypertension[48,49] but these features were not reported in this study. An interesting further examination of the results described herein is the relationship between what appear to be generalized cancer predisposition genes, or at least rare causes of cancers outside of the canonical cancer spectrum, and impact of environmental factors in the resulting genotype-phenotype correlations.

In summary we found that in a cohort of patients with features associated with inherited predisposition to RCC and no detectable mutation in routinely tested RCC CPGs, extension of testing to a larger CPG panel revealed pathogenic variants in CPGs associated with multiple cancer types in a subset of patients. This finding is consistent with previous studies of patients with early onset or advanced RCC that have been analyzed by larger gene panels and with the results of patients with multiple primary tumors[7,8,43] If patients with germline mutations in DNA repair genes, such as *BRCA1*, *BRCA2*, *BRIP1*, and *CHEK2* were shown to benefit from specific targeted therapies there would be a clear case for incorporating a wider genetic testing protocol into clinical care. However, we suggest that before the implementation into routine clinical practice of wider CPG testing for patients with potential non-syndromic inherited RCC proceeds, further studies are required to establish a causal link between RCC predisposition and pathogenic variants in *BRIP1*, *BRCA1*, *BRCA2*, and *CHEK2* and to determine more accurately renal cancer risks in patients with pathogenic variants in these genes so that appropriate renal screening protocols for asymptomatic gene carriers can be defined.

ACKNOWLEDGEMENTS

This research was funded by the European Research Council (Advanced Researcher Award), NIHR (Senior Investigator Award and Cambridge NIHR Biomedical Research Centre), Cancer Research UK Cambridge Cancer Centre and National Institute for Health Research (NIHR, grant number RG65966). We thank NIHR BioResource volunteers for their participation, and gratefully acknowledge NIHR BioResource centres, NHS Trusts and staff for their contribution. We thank the National Institute for Health Research and NHS Blood and Transplant. The views expressed are those of the authors and not necessarily those of the NHS, NIHR or Department of Health. The University of Cambridge has received salary support in respect of EM from the NHS in the East of England through the Clinical Academic Reserve. ERW is supported by the Manchester NIHR Biomedical Research Centre (IS-BRC-1215-20007). We acknowledge support from the NIHR UK Rare Genetic Disease Research Consortium. This work made use of data and samples generated by the 1958 Birth Cohort (NCDS), which is managed by the Centre for Longitudinal Studies at the UCL Institute of Education, funded by the Economic and Social Research Council (grant number ES/M001660/1). Access to these resources was enabled via the Wellcome Trust & MRC: 58FORWARDS grant [108439/Z/15/Z] (The 1958 Birth Cohort: Fostering new Opportunities for Research via Wider Access to Reliable

Data and Samples). Before 2015 biomedical resources were maintained under the Wellcome Trust and Medical Research Council 58READIE Project (grant numbers WT095219MA and G1001799).

CONFLICT OF INTEREST

E. R. M. has received funding from Illumina to attend a clinical genetics advisory group.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

ORCID

Philip S. Smith https://orcid.org/0000-0002-9306-1747
James Whitworth https://orcid.org/0000-0002-3682-2298
Francis H. Sansbury https://orcid.org/0000-0002-5048-3309
Emma R. Woodward https://orcid.org/0000-0002-6297-2855
Marc Tischkowitz https://orcid.org/0000-0002-7880-0628
Eamonn R. Maher https://orcid.org/0000-0002-6226-6918

REFERENCES

1. Ferlay J, Soerjomataram II, Dikshit R, et al. Cancer incidence and mortality worldwide: sources, methods and major patterns in GLOBOCAN 2012. *Int J Cancer*. 2014;136(5):E359-E386. https://doi.org/10.1002/ijc.29210.
2. Latif F, Tory K, Gnarra J, et al. Identification of the von Hippel-Lindau disease tumor suppressor gene. *Science*. 1993;260(5112):1317-1320. https://doi.org/10.1126/science.8493574.
3. Gossage L, Eisen T, Maher ER. VHL, the story of a tumour suppressor gene. *Nat Rev Cancer*. 2015;15(1):55-64. https://doi.org/10.1038/nrc3844.
4. Maher ER. Genomics and epigenomics of renal cell carcinoma. *Semin Cancer Biol*. 2013;23(1):10-17. https://doi.org/10.1016/j.semcancer.2012.06.003.
5. Truong H, Hegarty SE, Gomella LG, et al. Prevalence and characteristics of patients with suspected inherited renal cell cancer: application of the ACMG/NSGC genetic referral guidelines to patient cohorts. *J Genet Couns*. 2017;26(3):548-555. https://doi.org/10.1007/s10897-016-0020-4.
6. Pearlman R, Frankel WL, Swanson B, et al. Prevalence and spectrum of germline cancer susceptibility gene mutations among patients with early-onset colorectal cancer. *JAMA Oncol*. 2017;3(4):464-471. https://doi.org/10.1001/JAMAONCOL.2016.5194.
7. Whitworth J, Smith PS, Martin J-E, et al. Comprehensive cancer-predisposition gene testing in an adult multiple primary tumor series shows a broad range of deleterious variants and atypical tumor phenotypes. *Am J Hum Genet*. 2018;103(1):3-18. https://doi.org/10.1016/j.ajhg.2018.04.013.
8. Carlo MI, Mukherjee S, Mandelker D, et al. Prevalence of germline mutations in cancer susceptibility genes in patients with advanced renal cell carcinoma. *JAMA Oncol*. 2018;4(9):1228-1235. https://doi.org/10.1001/jamaoncol.2018.1986.
9. Ruark E, Münz M, Renwick A, et al. The ICR1000 UKexome series: a resource of gene variation in an outbred population. *F1000Res*. 2015;4:883. https://doi.org/10.12688/f1000research.7049.1.
10. Bertolotto C, Lesueur F, Giuliano S, et al. A SUMOylation-defective MITF germline mutation predisposes to melanoma and renal carcinoma. *Nature*. 2011;480(7375):94-98. https://doi.org/10.1038/nature10539.
11. Karczewski KJ, Weisburd B, The Exome Aggregation Consortium, et al. The ExAC browser: displaying reference data information from over 60 000 exomes. *Nucleic Acids Res*. 2017;45(D1):D840-D845. https://doi.org/10.1093/nar/gkw971.
12. Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med*. 2015;17(5):405-423. https://doi.org/10.1038/gim.2015.30.
13. Nykamp K, Anderson M, Powers M, et al. Sherloc: a comprehensive refinement of the ACMG–AMP variant classification criteria. *Genet Med*. 2017;19(10):1105-1117. https://doi.org/10.1038/gim.2017.37.
14. Wala JA, Bandopadhayay P, Greenwald NF, et al. SvABA: genome-wide detection of structural variants and indels by local assembly. *Genome Res*. 2018;28(4):581-591. https://doi.org/10.1101/gr.221028.117.
15. Karczewski KJ, Francioli LC, Tiao G, et al. Variation across 141,456 human exomes and genomes reveals the spectrum of loss-of-function intolerance across human protein-coding genes. *bioRxiv*. 2019:531210. https://doi.org/10.1101/531210.
16. Easton DF, Lesueur F, Decker B, et al. No evidence that protein truncating variants in *BRIP1* are associated with breast cancer risk: implications for gene panel testing. *J Med Genet*. 2016;53(5):298-309. https://doi.org/10.1136/jmedgenet-2015-103529.
17. Byers H, Wallis Y, van Veen EM, et al. Sensitivity of BRCA1/2 testing in high-risk breast/ovarian/male breast cancer families: little contribution of comprehensive RNA/NGS panel testing. *Eur J Hum Genet*. 2016;24(11):1591-1597. https://doi.org/10.1038/ejhg.2016.57.
18. Leongamornlert D, Saunders E, Dadaev T, et al. Frequent germline deleterious mutations in DNA repair genes in familial prostate cancer cases are associated with advanced disease. *Br J Cancer*. 2014;110(6):1663-1672. https://doi.org/10.1038/bjc.2014.30.
19. Wu Y, Yu H, Zheng SL, et al. A comprehensive evaluation of *CHEK2* germline mutations in men with prostate cancer. *Prostate*. 2018;78(8):607-615. https://doi.org/10.1002/pros.23505.
20. Desrichard A, Bidet Y, Uhrhammer N, Bignon Y-J. CHEK2 contribution to hereditary breast cancer in non-BRCA families. *Breast Cancer Res*. 2011;13(6):R119. https://doi.org/10.1186/bcr3062.
21. Roeb W, Higgins J, King M-C. Response to DNA damage of CHEK2 missense mutations in familial breast cancer. *Hum Mol Genet*. 2012;21(12):2738-2744. https://doi.org/10.1093/hmg/dds101.
22. Casey RT, Warren AY, Rodrigues JE, et al. Clinical and molecular features of renal and phaeochromocytoma/paraganglioma tumour association syndrome (RAPTAS): case series and literature review. *J Clin Endocrinol Metab*. 2017;102:4013-4022. https://doi.org/10.1210/jc.2017-00562.
23. Yokoyama S, Woods SL, Boyle GM, et al. A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. *Nature*. 2011;480(7375):99-103. https://doi.org/10.1038/nature10630.
24. Potrony M, Puig-Butille JA, Aguilera P, et al. Prevalence of MITF p.E318K in patients with melanoma independent of the presence of CDKN2A causative mutations. *JAMA Dermatol*. 2016;152(4):405-412. https://doi.org/10.1001/jamadermatol.2015.4356.
25. Potjer TP, Bollen S, Grimbergen AJEM, et al. Multigene panel sequencing of established and candidate melanoma susceptibility genes in a large cohort of Dutch non-CDKN2A/CDK4 melanoma families. *Int J Cancer*. 2019;144(10):2453-2464. https://doi.org/10.1002/ijc.31984.
26. Gromowski T, Masojć B, Scott RJ, et al. Prevalence of the E318K and V320I MITF germline mutations in polish cancer patients and multiorgan cancer risk-a population-based study. *Cancer Genet*. 2014;207(4):128-132. https://doi.org/10.1016/j.cancergen.2014.03.003.
27. Stoehr CG, Walter B, Denzinger S, et al. The microphthalmia-associated transcription factor p.E318K mutation does not play

a major role in sporadic renal cell tumors from Caucasian patients. *Pathobiology*. 2016;83(4):165-169. https://doi.org/10.1159/000443311.
28. Schmidt L, Duh F-M, Chen F, et al. Germline and somatic mutations in the tyrosine kinase domain of the MET proto-oncogene in papillary renal carcinomas. *Nat Genet*. 1997;16(1):68-73. https://doi.org/10.1038/ng0597-68.
29. Miller M, Ginalski K, Lesyng B, Nakaigawa N, Schmidt L, Zbar B. Structural basis of oncogenic activation caused by point mutations in the kinase domain of the MET proto-oncogene: modeling studies. *Proteins*. 2001;44(1):32-43. http://www.ncbi.nlm.nih.gov/pubmed/11354004. Accessed March 3, 2019.
30. Forbes SA, Beare D, Gunasekaran P, et al. COSMIC: exploring the world's knowledge of somatic mutations in human cancer. *Nucleic Acids Res*. 2015;43(D1):D805-D811. https://doi.org/10.1093/nar/gku1075.
31. Yang P, Cornejo KM, Sadow PM, et al. Renal cell carcinoma in tuberous sclerosis complex. *Am J Surg Pathol*. 2014;38(7):895-909. https://doi.org/10.1097/PAS.0000000000000237.
32. Guo J, Tretiakova MS, Troxell ML, et al. Tuberous sclerosis-associated renal cell carcinoma: a clinicopathologic study of 57 separate carcinomas in 18 patients. *Am J Surg Pathol*. 2014;38(11):1457-1467. https://doi.org/10.1097/PAS.0000000000000248.
33. Zhang Y, Gao X, Saucedo LJ, Ru B, Edgar BA, Pan D. Rheb is a direct target of the tuberous sclerosis tumour suppressor proteins. *Nat Cell Biol*. 2003;5(6):578-581. https://doi.org/10.1038/ncb999.
34. Woodward ER, Clifford SC, Astuti D, Affara NA, Maher ER. Familial clear cell renal cell carcinoma (FCRC): clinical features and mutation analysis of the VHL, MET, and CUL2 candidate genes. *J Med Genet*. 2000;37(5):348-353. https://doi.org/10.1136/JMG.37.5.348.
35. Schrader KA, Cheng DT, Joseph V, et al. Germline variants in targeted tumor sequencing using matched normal DNA. *JAMA Oncol*. 2016;2. American Medical Association:104-111. https://doi.org/10.1001/jamaoncol.2015.5208.
36. Parsons DW, Roy A, Yang Y, et al. Diagnostic yield of clinical tumor and germline whole-exome sequencing for children with solid tumors. *JAMA Oncol*. 2016;2(5):616-624. https://doi.org/10.1001/jamaoncol.2015.5699.
37. Seal S, Thompson D, Renwick A, et al. Truncating mutations in the Fanconi anemia J gene BRIP1 are low-penetrance breast cancer susceptibility alleles. *Nat Genet*. 2006;38(11):1239-1241. https://doi.org/10.1038/ng1902.
38. Rafnar T, Gudbjartsson DF, Sulem P, et al. Mutations in BRIP1 confer high risk of ovarian cancer. *Nat Genet*. 2011;43(11):1104-1107. https://doi.org/10.1038/ng.955.
39. Weber-Lassalle N, Hauke J, Ramser J, et al. BRIP1 loss-of-function mutations confer high risk for familial ovarian cancer, but not familial breast cancer. *Breast Cancer Res*. 2018;20(1):7. https://doi.org/10.1186/s13058-018-0935-9.
40. Moyer CL, Ivanovich J, Gillespie JL, et al. Rare BRIP1 missense alleles confer risk for ovarian and breast cancer. *Cancer Res*. 2020;80(4):857-867. https://doi.org/10.1158/0008-5472.CAN-19-1991.
41. Wu J, Wang H, Ricketts CJ, et al. Germline mutations of renal cancer predisposition genes and clinical relevance in Chinese patients with sporadic, early-onset disease. *Cancer*. 2018;125(7):1060-1069. https://doi.org/10.1002/cncr.31908.
42. Mersch J, Jackson MA, Park M, et al. Cancers associated with BRCA1 and BRCA2 mutations other than breast and ovarian. *Cancer*. 2015;121(2):269-275. https://doi.org/10.1002/cncr.29041.
43. Cancer Genome Atlas Research Network, Weinstein JN, Collison EA, et al. The cancer genome atlas Pan-cancer analysis project. *Nat Genet*. 2013;45(10):1113-1120. https://doi.org/10.1038/ng.2764.
44. Scheuermann JC, de Ayala Alonso AG, Oktaba K, et al. Histone H2A deubiquitinase activity of the Polycomb repressive complex PR-DUB. *Nature*. 2010;465(7295):243-247. https://doi.org/10.1038/nature08966.
45. Nishikawa H, Wu W, Koike A, et al. BRCA1-associated protein 1 interferes with BRCA1/BARD1 RING heterodimer activity. *Cancer Res*. 2009;69(1):111-119. https://doi.org/10.1158/0008-5472.CAN-08-3355.
46. Yu H, Pak H, Hammond-Martel I, et al. Tumor suppressor and deubiquitinase BAP1 promotes DNA double-strand break repair. *Proc Natl Acad Sci U S A*. 2014;111(1):285-290. https://doi.org/10.1073/pnas.1309085110.
47. Vaughn CP, Robles J, Swensen JJ, et al. Clinical analysis of PMS2: mutation detection and avoidance of pseudogenes. *Hum Mutat*. 2010;31(5):588-593. https://doi.org/10.1002/humu.21230.
48. Patel NH, Attwood KM, Hanzly M, et al. Comparative analysis of smoking as a risk factor among renal cell carcinoma histological subtypes. *J Urol*. 2015;194(3):640-646. https://doi.org/10.1016/j.juro.2015.03.125.
49. MacLeod LC, Hotaling JM, Wright JL, et al. Risk factors for renal cell carcinoma in the VITAL study. *J Urol*. 2013;190(5):1657-1661. https://doi.org/10.1016/j.juro.2013.04.130.

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

How to cite this article: Smith PS, West H, Whitworth J, et al. Pathogenic germline variants in patients with features of hereditary renal cell carcinoma: Evidence for further locus heterogeneity. *Genes Chromosomes Cancer*. 2021;60:5–16. https://doi.org/10.1002/gcc.22893