

Minerva Access is the Institutional Repository of The University of Melbourne

Author/s:

Lim, BWX;Li, N;Mahale, S;McInerny, S;Zethoven, M;Rowley, SM;Huynh, J;Wang, T;Lee, JEA;Friedman, M;Devereux, L;Scott, RJ;Sloan, EK;James, PA;Campbell, IG

Title:

Somatic inactivation of breast cancer predisposition genes in tumors associated with pathogenic germline variants

Date:

2023-02-01

Citation:

Lim, B. W. X., Li, N., Mahale, S., McInerny, S., Zethoven, M., Rowley, S. M., Huynh, J., Wang, T., Lee, J. E. A., Friedman, M., Devereux, L., Scott, R. J., Sloan, E. K., James, P. A. & Campbell, I. G. (2023). Somatic inactivation of breast cancer predisposition genes in tumors associated with pathogenic germline variants. *Journal of the National Cancer Institute*, 115 (2), pp.181-189. <https://doi.org/10.1093/jnci/djac196>.

Persistent Link:

<https://hdl.handle.net/11343/327311>

License:

CC BY-NC

Somatic inactivation of breast cancer predisposition genes in tumors associated with pathogenic germline variants

Belle W. X. Lim , PhD,^{1,2,†} Na Li , PhD,^{1,3,4} Sakshi Mahale, MSc,¹ Simone McInerney, BSc,⁴ Magnus Zethoven , MSc,^{1,5} Simone M. Rowley, BSc,¹ Joanne Huynh, BSc,¹ Theresa Wang, BSc,^{1,4} Jue Er Amanda Lee, PhD,^{1,3,6} Mia Friedman, BSc,^{1,4} Lisa Devereux, MSc,^{3,7} Rodney J. Scott, PhD,^{8,9} Erica K. Sloan, PhD,^{2,10} Paul A. James, PhD,^{3,4,†} Ian G. Campbell , PhD^{1,3,7,*,†}

¹Cancer Genetics Laboratory, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

²Drug Discovery Biology, Monash Institute of Pharmaceutical Sciences, Monash University, Melbourne, Victoria, Australia

³Sir Peter MacCallum Department of Oncology, The University of Melbourne, Melbourne, Victoria, Australia

⁴Parkville Familial Cancer Centre, Peter MacCallum Cancer Centre and Royal Melbourne Hospital, Melbourne, Victoria, Australia

⁵Bioinformatics Core Facility, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

⁶Molecular Genomics Core, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

⁷Lifepool, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

⁸Discipline of Medical Genetics and The Centre for Cancer Detection and Therapy, The University of Newcastle and Hunter Medical Research Institute, Newcastle, New South Wales, Australia

⁹Division of Molecular Medicine, New South Wales Health Pathology North, Newcastle, New South Wales, Australia

¹⁰Division of Cancer Surgery, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

*Correspondence to: Ian Campbell, PhD, Cancer Genetics Laboratory, Research Division, Peter MacCallum Cancer Centre, 305 Grattan Street, Melbourne, VIC 3000, Australia (e-mail: ian.campbell@petermac.org).

†Authors contributed equally to this work.

Abstract

Background: Breast cancers (BCs) that arise in individuals heterozygous for a germline pathogenic variant in a susceptibility gene, such as BRCA1 and BRCA2, PALB2, and RAD51C, have been shown to exhibit biallelic loss in the respective genes and be associated with triple-negative breast cancer (TNBC) and distinctive somatic mutational signatures. Tumor sequencing thus presents an orthogonal approach to assess the role of candidate genes in BC development.

Methods: Exome sequencing was performed on paired normal-breast tumor DNA from 124 carriers of germline loss-of-function (LoF) or missense variant carriers in 15 known and candidate BC predisposition genes identified in the BEACCON case-control study. Biallelic inactivation and association with tumor genome features including mutational signatures and homologous recombination deficiency (HRD) score were investigated.

Results: BARD1-carrying TNBC (4 of 5) displayed biallelic loss and associated high HRD scores and mutational signature 3, as did a RAD51D-carrying TNBC and ovarian cancer. Biallelic loss was less frequent in BRIP1 BCs (4 of 13) and had low HRD scores. In contrast to other established BC genes, BCs from carriers of CHEK2 LoF (6 of 17) or missense (2 of 20) variant had low rates of biallelic loss. Exploratory analysis of BC from carriers of LoF variants in candidate genes such as BLM, FANCM, PARP2, and RAD50 found little evidence of biallelic inactivation.

Conclusions: BARD1 and RAD51D behave as classic BRCA-like predisposition genes with biallelic inactivation, but this was not observed for any of the candidate genes. However, as demonstrated for CHEK2, the absence of biallelic inactivation does not provide definitive evidence against the gene's involvement in BC predisposition.

Hereditary breast cancer (HBC) often clusters within families and can be attributed to germline variants in susceptibility genes directly or indirectly involved in DNA repair. The major contributors—BRCA1, BRCA2, and PALB2 (1,2)—collectively explain less than half of the familial aggregation of BC (3). Exploratory case-control studies in the past have found that potentially pathogenic variants in individual candidate genes are rare (3–5), precluding any confident conclusion about their role in HBC based solely on this approach.

An orthogonal approach to assess if a candidate gene is driving tumorigenesis is through genomic analysis of the cancers

from carriers of germline mutations. For example, approximately 90% of BRCA1 and 50%–60% of BRCA2 breast tumors from germline mutation carriers have a somatic “second-hit” (6–9), resulting in biallelic inactivation. Most commonly, this occurs through loss of heterozygosity (LOH) or, less frequently, through protein truncating somatic point mutations or promoter hypermethylation. Biallelic inactivation of genes such as BRCA1 and BRCA2 is almost invariably associated with specific somatic mutational signatures (10). The presence or absence of these tumor genomic features can provide strong evidence for or against a gene's cancer predisposition role, even if based on relatively few cancers as previously

Received: February 13, 2022. Revised: June 17, 2022. Accepted: October 18, 2022

© The Author(s) 2022. Published by Oxford University Press.

This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (<https://creativecommons.org/licenses/by-nc/4.0/>), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contact journals.permissions@oup.com

demonstrated for PALB2, RAD51C, and ATM (11–13). Recent large case-control studies involving more than 65 000 participants each confirmed the association of moderate risk genes RAD51C, RAD51D, and BARD1 but not BRIP1 with breast cancer (4,5).

In this study, we extend the tumor sequencing approach by performing exome sequencing on 124 BCs from individuals harboring germline variants in proposed and candidate HBC genes identified in the BEACCON case-control study (hereditary BrEAsT Case CONtrol study) (3) to look for evidence of biallelic inactivation as a means of validating the role of these genes in BC predisposition.

Methods

Case-control study and tumor sequencing

A total of 124 unique breast tumors were selected from cancers arising in individuals with a germline loss-of-function (LoF) or rare, likely pathogenic missense (MS) variant of interest in a known (BARD1, BRIP1, CHEK2, and RAD51D) or candidate (BLM, CDK9, CTH, ERCC5, FANCM, MUTYH, PARP2, RAD50, RAD51B, WRN, and XRCC2) BC predisposition gene detected in the BEACCON case-control study (3). LoF variants included stop-gained, frame-shift, or essential splice-site variants, and MS variants of interest were identified based on a combination of population frequency, in silico prediction, and location in key functional domains as detailed in [Supplementary Tables 1–4](#) (available online). Two ovarian cancers from carriers of BRIP1 and 1 of RAD51D LoF variants, respectively, were also included as these genes are known to be ovarian cancer predisposing genes. Since last reporting (5), this study has been expanded to include 6689 BRCA-negative female index familial BC patients and 14 381 cancer-free female participants ([Supplementary Table 5](#), available online). Candidate genes were selected for this analysis based on an excess of rare coding variants in the case group. Microdissection, DNA extraction, and exome sequencing are described in the [Supplementary Methods](#) (available online). Tumor characteristics and personal and family history of the individuals selected for the current study are summarized in [Supplementary Table 6](#) (available online).

Determination of variant allelic status and potential biallelic inactivation

For each tumor, the somatic sequencing data were assessed for the presence of somatic LoF or MS point mutations in the gene of interest as well as the allelic status of the germline variant as described previously (11,12). In summary, locus-specific LOH was determined by tumor variant allele frequency comparisons as adjusted according to estimated tumor purity. All cases had matched germline sequencing data for the gene of interest. Promoter hypermethylation, using targeted Twist Custom Panel methylation sequencing or Sanger sequencing on bisulfite converted DNA, was also assessed for cases where there was no somatic mutation or LOH across the gene of interest. Homologous recombination deficiency (HRD) scores were calculated for each tumor sample using copy number plots as a sum of the occurrence of telomeric allelic imbalances, large-scale state transitions, and homologous recombination deficiency—loss of heterozygosity from copy number plots as described previously (12), where a threshold of an HRD score of 42 or higher is defined as high-HRD (14,15). Mutational signatures were generated against COSMIC v2 catalogue (https://cancer.sanger.ac.uk/signatures/signatures_v2/) using the DeconstructSig package in R (16) on whole-exome sequenced samples.

Statistical analyses

Odds ratios and Fisher exact test (2-sided) were calculated in case-control analyses, with a 2-tailed *P* value of .05 or less defined as statistically significant. Confidence intervals (CIs) were calculated using a conditional maximum likelihood estimate. All calculations were carried out using R-in built function in R 3.3.2 (17).

Results

Tumor sequencing in individuals harboring a germline variant in known BC genes

Whole or targeted exome sequencing was performed on 41 tumors from individuals harboring germline LoF variants in genes commonly present in HBC panels: BARD1 (*n* = 7), BRIP1 (*n* = 13), RAD51D (*n* = 4), and CHEK2 (*n* = 17) ([Table 1](#)). BARD1, which in the BEACCON case-control data ([Figure 1](#)) and other published data (4) is associated specifically with triple-negative breast cancer (TNBC), showed loss of the wild-type (WT) allele via LOH in 4 of 5 assessable triple negative (TN) tumors. A sixth TN tumor also had LOH, but it was not possible to determine which allele had been lost, and the only BARD1 tumor to show loss of the mutant allele was estrogen receptor (ER) positive. The 6 BARD1 TN tumors including 1 in heterozygous status showed high HRD scores and 4 with strong HRD-related mutational signature 3. Carriers of RAD51D LoF mutations, which are also associated with TNBC, were rare in the BEACCON study. One of the 2 TNBC showed LOH of the WT allele, whereas 2 ER-positive tumors remained heterozygous. An additional high-grade serous ovarian cancer (HGSOC) that was available for analysis ([Supplementary Table 5](#), available online) showed biallelic inactivation through LOH. Nine carriers of rare RAD51D MS variants shortlisted based on likely pathogenicity assessment ([Supplementary Table 1](#), available online) were also analyzed, but only 2 cases showed loss of the WT allele with only 1 of these being a TNBC. This case was a compound heterozygote that showed loss of the p.Ala313Val and retention of the p.Ala52Val allele; it had a high HRD score and a strong mutational signature 3.

The role of BRIP1 in breast cancer predisposition is debated, and our analysis of BRIP1 LoF variants identified an equal number of tumors showing loss of the WT or mutant alleles (4 cases each) with the remaining 5 remaining heterozygous. By comparison, analysis of 2 HGSOCs showed both had loss of the WT ([Supplementary Table 5](#), available online), consistent with the established role of BRIP1 in ovarian cancer predisposition. Both HGSOCs also showed high HRD scores compared with only 2 of 4 BRIP1-null BCs. Mutational signature 3 was observed only in 1 BRIP1-null BC and not in the HGSOCs.

LoF mutations in CHEK2, predominantly the c.1100delC variant, are well established to confer a two- to threefold increase in BC risk (20), with the association being strongest for ER-positive BC. The current tumor data do not provide evidence that CHEK2 requires biallelic inactivation with the majority (9 of 17) of tumors remaining heterozygous, whereas only 6 showed loss of the WT allele, and 2 ER-positive tumors showed loss of the LoF allele. It appears that the 2 tumors with loss of pathogenic variants were not driven by CHEK2 LoF, and given that CHEK2 is only a moderate risk gene, several of the tumors without LOH could also not be driven by the CHEK2 pathogenic variants. In addition, 20 tumors from individuals with rare germline CHEK2 MS variants of interest ([Table 1](#); [Supplementary Table 2](#), available online) were analyzed. Most of these variants except for p.Ile157Thr and p.Arg117Gly are currently classified as variants

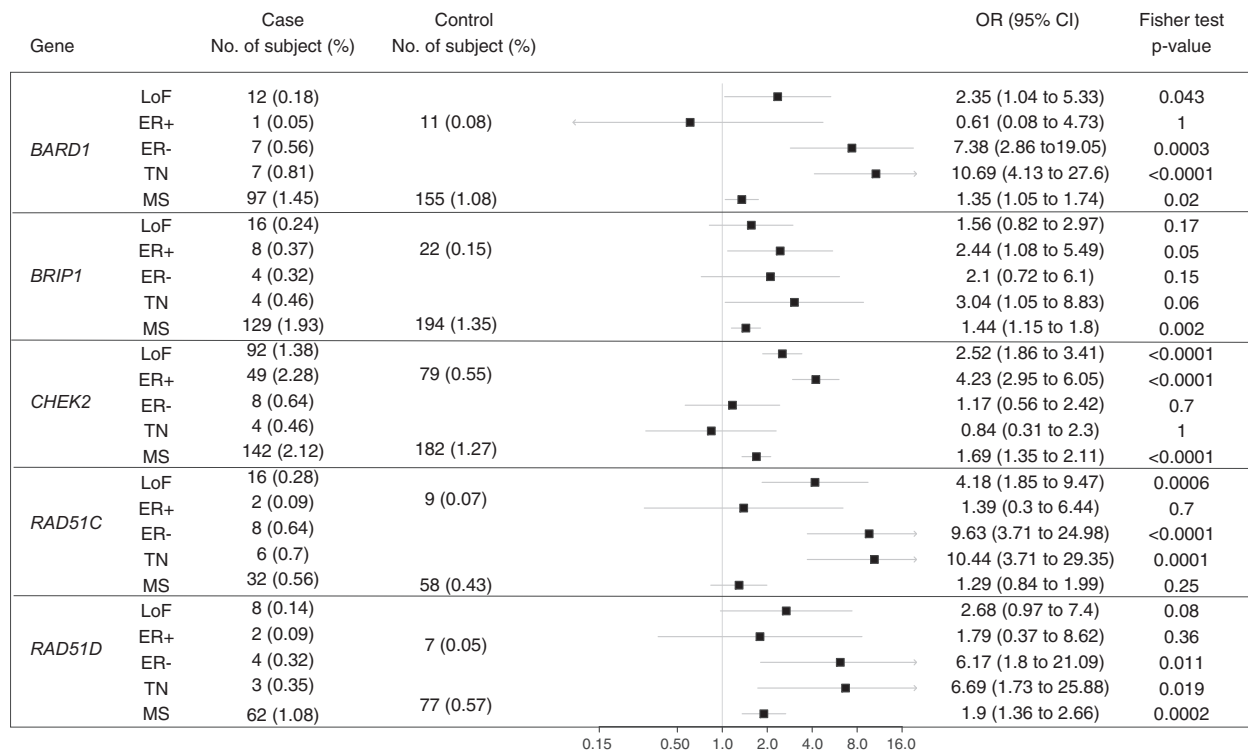


Figure 1. Case-control analysis of rare LoF variants (minor allele frequency [MAF] ≤ 0.005) and MS variants (MAF ≤ 0.001) in known or strongly proposed breast cancer genes, including subcategories of estrogen receptor-positive (ER+), ER-negative (ER-), and triple-negative (TN) breast tumor where diagnosis was available. ER+ and ER- groups were mutually exclusive, and the ER- groups include the TN samples. Participants without sufficient pathological information were only included in the overall LoF group and excluded from the subcategory analysis. CHEK2, BARD1, and BRIP1 were screened in 6689 cases and 14 381 controls; RAD51C and RAD51D were screened in 5726 cases and 13 428 controls. The sample sizes of ER+, ER-, and TN were 2146, 1246, and 862, respectively. CI = confidence interval; LoF = loss of function; MS = missense; OR = odds ratio (3,4,11,12,18,19).

of unknown significance, and tumor sequencing showed that most retained heterozygosity with only 2 showing loss of the WT allele and 2 showing loss of the variant allele. In particular, all 3 carriers of the known pathogenic, but reduced penetrance, variant CHEK2 p.Ile157Thr retained heterozygosity, and in the 2 tumors that were tested, neither were found to have promoter methylation.

Tumor sequencing in individuals with germline variants in candidate HBC genes

Tumor sequencing was performed on 57 BCs (Table 2) carrying LoF ($n=45$) or rare MS ($n=16$) variants in 11 genes that have been the subject of debate in the literature (FANCM, RAD50, RAD51B, and XRCC2) or were shortlisted from the BEACCON study (BLM, CDK9, CTH, ERCC5, MUTYH, PARP2, and WRN) (Supplementary Figure 1, available online). The 4 BCs from RAD50 LoF mutation carriers remained heterozygous, consistent with the accumulating literature that it does not predispose to BC (21). Literature support for a role of XRCC2 in BC predisposition is weak but with a potential association with ER-negative cancer (4,22,23). Of the 2 BCs from XRCC2 LoF variant carriers, only 1 (a TNBC) showed biallelic inactivation with both a high HRD score and mutational signature 3. For RAD51B, only tumors from carriers of rare MS variants were available with 2 remaining heterozygous and 2 showing loss of the variant allele.

LoF mutations in FANCM have previously been reported to be associated with a small increase in BC risk (24-26), but 4 of 6 tumors from individuals with FANCM LoF variants remained heterozygous with only 1 having lost the WT allele and did not show a high HRD score. Similarly, there was no consistent loss of the

WT allele in tumors associated with germline FANCM MS variants (Supplementary Table 3, available online). BLM has previously been implicated in BC predisposition (27-29) and in the BEACCON data (Supplementary Figure 1, available online), but 5 of the BCs with LoF variants remained heterozygous with no evidence of promoter hypermethylation, whereas 2 BCs lost the LoF allele.

For the candidate genes, loss of the WT allele was not observed for the majority. The BCs carrying LoF or MS variants in the candidate genes CDK9 and CTH (Supplementary Table 4, available online) remained heterozygous although promoter methylation assessment was not successful for these genes. Of the 4 PARP2 BCs with LoF mutations, 2 showed loss of the LoF allele with the other 2 remaining heterozygous. The 2 ERCC5 BCs showed loss of the LoF allele. In contrast, the WRN gene, which was found to have a statistically significant association with ER-positive BC in the BEACCON study (unadjusted $P=.003$), showed loss of the WT allele in 2 of 6 ER-positive cases. A WRN-heterozygous BC also carried an ATM germline variant that had experienced biallelic loss, suggesting that the ATM variant was instead responsible for the tumor. Overall, evidence of loss of the WT allele was rare among candidate genes despite evidence in case-control frequencies.

Discussion

The frequent observation of loss of the WT allele in BCs carrying germline pathogenic mutations in BRCA1 and BRCA2 supports the model of biallelic inactivation being required for BC predisposition, at least in some high penetrance genes. Recent studies

Table 1. Tumor sequencing data for 69 tumors from individuals heterozygous for a germline LoF (n = 41) or MS (n = 29) variant in a known breast cancer predisposition gene (BARD1, BRIP1, CHEK2, and RAD51D)

ID ^a	Gene	Germline variant	Variant type	Variant allelic status ^b	BC subtype	HRD	Somatic TP53	Somatic PIK3CA	Mutation signature 3 ^c	Dominant mutation signature	Promoter hypermethylation
3530	BARD1	c.1135A>T, p.Lys379Ter	LoF	Mutant loss	ER+/HER2-	na	na	na	na	na	Failed
3977	BARD1	c.1212C>G, p.Tyr404Ter	LoF	WT loss	TN	50	na	na	Strong	3, 11	DNT
1531	BARD1	c.1652C>G, p.Ser551Ter	LoF	WT loss	TN	83	LoF	—	Weak	19, 30	DNT
3828	BARD1	c.1652C>G, p.Ser551Ter	LoF	WT loss	TN	92	MS	—	Strong	1, 3	DNT
425	BARD1	c.1652C>G, p.Ser551Ter	LoF	LOH	TN	80	na	na	Strong	na	na
3496	BARD1	c.1905G>A, p.Trp635Ter	LoF	Het	TN	82	MS	—	Strong	3	Failed
1272	BARD1	c.2078_2079insTAATA, p.Lys693AsnfsTer23	LoF	WT loss	TN	76	LoF	—	No	19	DNT
2439	BRIP1	c.93 + 1G>T	LoF	WT loss	TN	59	LoF	—	Strong	3, 19	DNT
4160	BRIP1	c.103G>T, p.Gly35Ter	LoF	Mutant loss	ER-/HER2+	30	MS	—	Strong	1, 3	na
3259	BRIP1	c.1426del, p.Thr476LeufsTer50	LoF	WT loss	ER+/HER2-	41	—	MS	No	12, 20	DNT
3597	BRIP1	c.1888dup, p.Thr630AsnfsTer9	LoF	Het	ER+/HER2-	12	—	MS	No	30	Negative
3093	BRIP1	c.2298_2301delTGAG, p.Ser766ArgfsTer14	LoF	Het	ER+/HER2-	5	—	MS	na	na	na
227	BRIP1	c.2392C>T, p.Arg798Ter	LoF	WT loss	TN	58	MS	—	No	20, 21	DNT
1325	BRIP1	c.2392C>T, p.Arg798Ter	LoF	Mutant loss	TN	57	LoF	—	na	na	na
786	BRIP1	c.2392C>T, p.Arg798Ter	LoF	Het	ER+/HER2-	1	LoF	—	na	na	Failed
1928	BRIP1	c.2392C>T, p.Arg798Ter	LoF	Het	ER+/HER2-	11	MS	—	na	na	Negative
3829	BRIP1	c.2400C>G, p.Tyr800Ter	LoF	Mutant loss	TN	50	—	—	Weak	6	na
3635	BRIP1	c.2400C>G, p.Tyr800Ter	LoF	Het	ER+/HER2-	32	LoF	—	Weak	1	na
3354	BRIP1	c.2492_2492 + 5delGGTAAG	LoF	WT loss	ER+/HER2-	31	MS	MS	Weak	1	DNT
3468	BRIP1	c.3715del, p.Ser1239ProfsTer15	LoF	Mutant loss	ER+/HER2-	37	LoF	—	Weak	1, 13	na
4152	CHEK2	c.629_732delCAGT, p.Ser210PhefsTer6	LoF	Mutant loss	ER+/HER2-	47	MS	—	No	3	Negative
2320	CHEK2	c.630delA, p.Val211PhefsTer6	LoF	Het	na	7	—	—	Weak	5, 30	na
290	CHEK2	c.902delT, p.Leu301TrpfsTer3	LoF	Mutant loss	ER+/HER2-	27	—	—	Weak	1,6	na
3587	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	WT loss	ER+/HER2-	34	na	na	No	11	DNT
1825	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER+/HER2-	32	LoF	—	Strong	3	na
3174	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER+/HER2-	29	—	—	No	6, 30	na
2182	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER+/HER2-	45	—	—	No	11, 19	Failed
2410	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER+/HER2-	27	—	—	No	1, 30	Failed
2475	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	WT loss	ER+/HER2-	80	—	—	No	6, 19	DNT
1300	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	WT loss	ER+/HER2-	36	—	MS	No	10	Failed
2326	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	WT loss	ER+/HER2-	21	—	—	No	19, 30	Failed
2711	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	WT loss	ER+/HER2+	10	—	—	No	1, 11	Failed
3500	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER+/HER2unknown	37	—	—	Strong	3	na
2351	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER-/HER2+	4	na	na	Weak	19, 30	DNT
3076	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	Het	ER-/HER2+	1	—	—	No	1	na
1732	CHEK2	c.1100delC, p.Thr367MetfsTer15	LoF	WT Loss	TN	17	MS	MS	No	6	DNT
1853	CHEK2	c.1696delC, p.Thr533GlnfsTer33	LoF	Het	ER+/HER2-	28	MS	—	na	na	na
2625	CHEK2	c.14C>T, p.Ser5Leu	MS	Het	ER+/HER2-	85	—	—	Weak	19	Failed
1993	CHEK2	c.190G>A, p.Glu64Lys	MS	Het	ER+/HER2-	91	LoF	—	Weak	1, 6	na
811	CHEK2	c.349A>G, p.Arg117Gly	MS	Het	ER+/HER2+	0	—	MS	Weak	5	Negative
1103	CHEK2	c.349A>G, p.Arg117Gly	MS	Mutant loss	ER+/HER2-	16	—	MS	Weak	3	Negative
616	CHEK2	c.349A>G, p.Arg117Gly	MS	Het	ER-/HER2+	17	—	MS	Strong	1, 3	na
787	CHEK2	c.442A>G, p.Arg148Gly	MS	Het	ER+/HER2-	na	na	na	na	na	Failed
2531	CHEK2	c.470T>C, p.Ile157Thr	MS	Het	ER+/HER2-	34	—	—	Weak	19	Negative

(continued)

Table 1. (continued)

ID ^a	Gene	Germline variant	Variant type	Variant allelic status ^b	BC subtype	HRD	Somatic TP53	Somatic PIK3CA	Mutation signature 3 ^c	Dominant mutation signature	Promoter hypermethylation
1420	CHEK2	c.470T>C, p.Ile157Thr	MS	Het	ER+/HER2-	28	MS	MS	No	6	Negative
3240	CHEK2	c.470T>C, p.Ile157Thr	MS	Het	ER+/HER2-	16	—	—	Strong	3, 6	na
807	CHEK2	c.1036C>T, p.Arg346Cys; c.499G>A, p. Gly167Arg	MS	WT loss; mutant loss	ER+/HER2unknown	52	—	—	Weak	1	na
2091	CHEK2	c.1067C>T, p.Ser356Leu	MS	Het	ER+/HER2-	47	—	—	Weak	1, 19	Failed
2689	CHEK2	c.1211A>G, p.Tyr404Cys	MS	WT loss	ER+/HER2+	28	—	MS	Strong	3, 30	DNT
2221	CHEK2	c.1270T>C, p.Tyr424His	MS	WT loss	ER+/HER2-	13	—	MS	No	20	DNT
1830	CHEK2	c.1312G>T, p.Asp438Tyr	MS	Het	ER+/HER2-	17	—	—	na	na	na
2257	CHEK2	c.1312G>T, p.Asp438Tyr	MS	Het	ER+/HER2-	0	—	MS	Weak	6	Negative
200	CHEK2	c.1312G>T, p.Asp438Tyr	MS	Het	na	5	—	—	Strong	3	na
4164	CHEK2	c.1427C>T, p.Thr476Met	MS	Het	ER+/HER2-	13	—	—	No	11, 19	na
1410	CHEK2	c.1447C>T, p.His483Tyr	MS	Mutant loss	ER+/HER2-	30	MS	—	na	na	DNT
2345	CHEK2	c.1525C>T, p.Pro509Ser	MS	Mutant loss	ER+/HER2+	7	LoF	—	na	na	Negative
1198	CHEK2	c.1604G>A, p.Arg535His	MS	Het	TN	22	MS	—	No	6, 30	Failed
1897	RAD51D	c.616C>T, p.Arg206Ter	LoF	Het	ER+/HER2-	4	—	—	na	na	Negative
2734	RAD51D	c.754C>T, p.Arg252Ter	LoF	WT loss	TN	42	LoF	—	na	na	DNT
2866	RAD51D	c.808delC, p.His270ThrfsTer2	LoF	Het	TN	7	—	—	na	na	na
3500	RAD51D	c.863G>A, p.Trp288Ter	LoF	Het	ER+/HER2-	8	—	—	Weak	30	na
506	RAD51D	c.26G>C, p.Cys9Ser	MS	Het	ER+/HER2-	0	—	—	na	na	na
30	RAD51D	c.26G>C, p.Cys9Ser	MS	Het	ER+/HER2-	20	MS	—	na	na	na
2936	RAD51D	c.26G>C, p.Cys9Ser	MS	Het	ER+/HER2-	8	—	—	No	5	DNT
1980	RAD51D	c.26G>C, p.Cys9Ser	MS	Het	TN	3	LoF	—	No	1	Negative
2224	RAD51D	c.137C>G, p.Ser46Cys	MS	Het	ER+/HER2-	4	—	—	na	na	Negative
2219	RAD51D	c.155C>T, p.Ala52Val; c.938C>T, p. Ala313Val	MS compound homozygous	WT loss; mutant loss	TN	42	LoF	—	Strong	3	Negative
1686	RAD51D	c.308C>T, p.Ala103Val	MS	Het	TN	17	MS	—	na	na	Negative
3095	RAD51D	c.472A>C, p.Asn158His	MS	Mutant Loss	ER+/HER2+	20	—	—	na	na	na
2606	RAD51D	c.551T>C, p.Leu184Pro	MS	WT Loss	ER+/HER2-	11	MS	—	na	na	DNT

^a Subject 3093 carried 2 variants of interest in BRIP1; subject 2219 carried 2 variants in RAD51C; subject 3500 carried a variant of interest in both CHEK2 and RAD51D. “—” signifies feature not present. BC = breast cancer; DNT = did not test; na = not available; ER+ = estrogen receptor—positive breast cancer; HER2- = HER2 negative; HER2+ = HER2 positive; HRD = homologous recombination deficiency score; LoF = loss of function; MS = missense; TN = triple-negative; WT = wild type.

^b WT loss, somatic loss of the WT allele; mutant loss, somatic loss of the allele carrying the known germline variant; Het, heterozygous. Case 425 showed loss of heterozygosity across the gene regions but unable to determine which allele had been lost.

^c Proportion of mutational signature 3 (COSMIC v2, assessed on whole-exome sequenced tumors only) above 25% is classified as “strong”, under 25% as “weak”.

Table 2. Sequencing results of 57 tumors from individuals heterozygous for a germline LoF (n = 43) or MS (n = 16) variant in a candidate breast cancer predisposition gene (BLM, CDK9, CTH, ERCC5, FANCM, MUTYH, PARP2, RAD50, RAD51B, WRN, and PARP2)

ID ^a	Germline gene	Variant	Variant type	Variant status ^b	Subtype	HRD	Somatic TP53	Somatic PIK3CA	Mutation signature 3 ^c	Dominant signature	Hypermutated
2660	BLM	c.318_319insT, p.Leu107PhefsTer36	LoF	Het	ER+/HER2-	1	—	—	na	na	Negative
1471		c.768_769delCT, p.Leu258GluTer7	LoF	Mutant Loss	ER+/HER2unknown	5	—	MS	na	na	Negative
462		c.1624delG, p.Asp542ThrfsTer2	LoF	Mutant Loss	TN	44	LoF	—	na	na	Negative
3093		c.2695C>T, p.Arg899Ter	LoF	Het	ER+/HER2-	5	—	MS	na	na	na
2287		c.2875C>T, p.Arg959Ter	LoF	Het	ER+/HER2-	11	—	—	na	na	Negative
2083		c.3210 + 2delT	LoF	Het	ER+/HER2-	6	—	—	na	na	Failed
35		c.3558 + 1G>T	LoF	Het	ER+/HER2unknown	17	—	MS	na	na	Negative
1245	CDK9	c.130delA, p.Lys44ArgfsTer4	LoF	Het	ER+/HER2-	13	MS	—	na	na	Failed
2345		c.274delT, p.Tyr92IlefsTer23	LoF	Het	ER+/HER2+	4	LoF	—	na	na	Negative
3075		c.620_621insC, p.Ile210HisfsTer2	LoF	Het	TN	56	LoF	—	na	na	Failed
2723		c.689_690insG, p.Asn232GlnfsTer20	LoF	Het	ER+/HER2+	0	—	—	na	na	na
2045	CTH	c.465G>A, p.Trp155Ter	LoF	Het	ER+/HER2-	19	—	—	na	na	Failed
1322		c.465G>A, p.Trp155Ter	LoF	Het	ER+/HER2+	20	MS	—	na	na	Failed
3119		c.465G>A, p.Trp155Ter	LoF	Het	ER+/HER2+	0	—	—	na	na	na
1865		c.1064delC, p.Thr355IlefsTer19	LoF	Het	ER+/HER2-	36	MS	—	na	na	Failed
1092		c.230C>T, p.Ala77Val	MS	Het	ER+/HER2-	20	ESS	—	No	5, 12	Failed
307		c.323T>C, p.Ile108Thr	MS	Het	TN	24	LoF	—	na	na	Failed
2593		c.620T>C, p.Met207Thr	MS	Het	na	9	—	—	na	na	na
1065		c.718C>G, p.Gln240Glu	MS	Het	ER+/HER2-	0	—	—	na	na	na
4142		c.794G>A, p.Arg265Gln	MS	Het	ER+/HER2-	10	LoF	—	na	na	Failed
3197		c.1124G>A, p.Arg375Gln	MS	Het	ER+/HER2-	19	—	—	Weak	1, 12	na
2260	ERCC5	c.589delC, p.Pro198LeufsTer3	LoF	Mutant Loss	TN	41	—	—	Weak	15	Failed
901		c.1774_1775insAAGCA, p.Val592GluTer8	LoF	Mutant Loss	TN	83	—	MS	No	11	na
1367	FANCM	c.2267G>A, p.Arg756His	LoF	Het	ER+/HER2-	24	—	MS	No	6	Failed
1709		c.3589delG, p.Asp1197MetfsTer18	LoF	Mutant Loss	TN	26	MS	—	Weak	6	Failed
3147		c.5101C>T, p.Gln1701Ter	LoF	Het	ER+/HER2-	6	—	—	Weak	3, 6	Failed
691		c.5791C>T, p.Arg1931Ter	LoF	Het	ER+/HER2-	2	MS	MS	No	6	na
1172		c.5791C>T, p.Arg1931Ter	LoF	Het	ER+/HER2+	0	—	—	No	1	Failed
2771		c.5791C>T, p.Arg1931Ter	LoF	WT Loss	TN	18	LoF	—	No	1, 26	DNT
1127		c.163G>A, p.Asp55Asn	MS	Mutant Loss	TN	51	—	—	Weak	3	Failed
2094		c.2267G>A, p.Arg756His	MS	Het	TN	40	MS	—	Strong	1, 3	Failed
1879		c.2267G>A, p.Arg756His	MS cpd	Het	ER+/HER2-	72	LoF	—	Weak	1, 19	DNT
1222		c.3998A>C, p.Gln1333Pro	MS	WT Loss	TN	48	LoF	—	Weak	5	DNT
901		c.5108A>G, p.His1703Arg	MS	Het	TN	83	—	MS	No	5	na
2743	MUTYH	c.925-2A>G	LoF	Het	TN	10	MS	—	na	na	Failed
2727 [†]		c.925-2A>G	LoF	Het	TN	36	LoF	—	na	na	Failed
1253		c.384G>A, p.Trp128Ter	Biallelic LoF	Germline homozygous	TN	na	—	—	na	na	na
1474	PARP2	c.979_980insTT, p.Ser328CysfsTer8	LoF	Mutant Loss	ER+/HER2-	67	—	MS	na	na	DNT
2294		c.985_986insA, p.Ile331AsnfsTer11	LoF	Het	ER-/HER2+	81	—	—	na	na	Failed
333		c.1109_1110insT, p.Leu372ProfsTer2	LoF	Mutant Loss	ER+/HER2-	na	—	—	na	na	na
1185		c.1304delG, p.Val436TrpfsTer4	LoF	Het	ER-/HER2+	30	MS	MS	na	na	Failed
1327		c.965G>A, p.Arg322Gln	MS	WT Loss	ER+/HER2-	28	—	—	na	na	DNT
2883	RAD50	c.1291_1297delGAGATAA, p.Asp434LysfsTer7	LoF	Het	ER+/HER2-	47	—	—	No	16	Failed
2193		c.1958C>A, p.Ser653Ter	LoF	Het	ER+/HER2-	23	—	—	Strong	3	Failed
2251		c.2467C>T, p.Arg823Ter	LoF	Het	ER+/HER2-	24	—	MS	Strong	3, 5	na
1031		c.3207delA, p.Asn1070IlefsTer6	LoF	Het	ER+/HER2+	8	—	MS	No	25	Failed
2923	RAD51B	c.103C>T, p.Pro35Ser	MS	Het	TN	32	MS	—	na	na	na
1932		c.277G>A, p.Ala93Thr	MS	Het	TN	2	—	—	na	na	Failed

(continued)

Table 2. (continued)

ID ^a	Germline gene	Variant	Variant type	Variant status ^b	Subtype	HRD	Somatic TP53	Somatic PIK3CA	Mutation signature 3 ^c	Dominant signature	Hypermutated
1795		c.436G>A, p.Ala146Thr	MS	Mutant Loss	TN	30	LoF	—	na	na	na
3024		c.553T>G, p.Cys185Gly	MS	Mutant Loss	TN	76	—	—	na	na	DNT
3054	WRN	c.171C>A, p.Tyr57Ter	LoF	Het	ER+/HER2-	24	—	MS	Weak	5	Failed
2963		c.944_948delTAAAC, p.Leu315PhefsTer5	LoF	Het	ER+/HER2-	24	—	—	Weak	5	Failed
1115		c.3961C>T, p.Arg1321Ter	LoF	Het	ER+/HER2-	40	MS	MS	No	5, 6	Failed
1847		c.4216G>T, p.Arg1406Ter	LoF	WT Loss	ER+/HER2-	53	—	MS	Strong	3	DNT
2562		c.4216C>T, p.Arg1406Ter	LoF	Het	ER+/HER2-	29	—	—	Strong	3, 11	Failed
3093		c.4216G>T, p.Arg1406Ter	LoF	WT Loss	ER+/HER2-	5	—	MS	na	na	na
1349		c.4216C>T, p.Arg1406Ter	LoF	Het	TN	43	—	—	Strong	3	Failed
863	XRCC2	c.39 + 1G>A	LoF	Het	ER-/HER2+	12	LoF	—	Strong	3	Failed
3062		c.794T>A, p.Leu265Ter	LoF	WT Loss	TN	44	LoF	—	Strong	3	DNT

^a Subject 2727 also carried a germline ATM variant that had biallelic loss in tumor. Subject 3054 carried a germline RAD51C that had biallelic loss in tumor. Subject 3093 carried variants of interest in *BLM* and *WRN*. Subject 901 carried variants in both *ERCC5* and *FANCM*. "—" signifies feature not present. BC = breast cancer; DNT = did not test; na = not available; ER+ = estrogen receptor-positive breast cancer; HER2- = HER2 negative; HER2+ = HER2 positive; HRD = homologous recombination deficiency score; LoF = loss of function; MS = missense; TN = triple-negative; WT = wild type.

^b WT loss, somatic loss of the wild-type allele; Mutant loss, somatic loss of the allele carrying the known germline variant; Het, heterozygous. Case 425 showed loss of heterozygosity across the gene regions but unable to determine which allele had been lost.

^c Proportion of mutational signature 3 (COSMIC v2, assessed on whole-exome sequenced tumors only) above 25% is classified as "strong," below 25% as "weak."

indicate that biallelic inactivation is also common in BCs carrying pathogenic mutations in *PALB2* (12,30,31) and *ATM* (13) and has been used as a biomarker to support the role of *RAD51C* (11) as a TNBC predisposition gene. These examples suggest tumor sequencing can provide a useful orthogonal approach to validate new BC genes and rare MS variants in known genes.

In this study, tumor sequencing demonstrated that TN tumors from *BARD1* LoF mutation carriers frequently exhibit biallelic inactivation consistent with data from case-control studies (3-5) that indicate that *BARD1* pathogenic variants are associated with predisposition to TNBC. Recent case-control studies have also provided support for the role of *RAD51D* in TNBC predisposition (4). Although 1 of 2 LoF BCs studied here showed loss of the WT allele, the rarity of its variants precluded any confident conclusion to be drawn. *RAD51D* MS variants as a group showed an excess in the BEACON case-control analysis, but most of the tumors from rare MS variant carriers showed no evidence of a second hit, and the 2 cases with loss of the WT allele had low HRD scores suggesting they are benign variants.

The role of *BRIP1* in BC predisposition is debated with most, but not all, published case-control studies failing to identify a statistically significant excess of LoF mutations in cases (4,5). Tumor sequencing did not find evidence to support a role for *BRIP1* in BC predisposition with most BCs remaining heterozygous and, importantly, an equivalent number of cases losing the WT and LoF alleles. Previous tumor sequencing studies on *BRIP1* BCs are limited, but our findings are consistent with a previous report on 3 *BRIP1* BC where only 1 was found to have biallelic inactivation (10). Overall, our results for *BARD1*, *RAD51D*, and *BRIP1* are consistent with the findings of 2 recent large case-control studies cited previously (4,5) where *BARD1* and *RAD51D* are associated with BC, specifically TNBC, whereas no causative link was identified for *BRIP1*.

Based on the data for *BARD1* and the other previously studied BC predisposing genes *BRCA1*, *BRCA2*, *PALB2*, and *ATM*, it might be extrapolated that biallelic inactivation is a typical feature for all BC predisposition genes. However, the data for *CHEK2*, which has highly robust case-control evidence supporting its role as a moderate penetrance BC gene, suggest that this is not true in all cases. Of the 17 BCs with germline *CHEK2* LoF mutations, only 6 showed loss of the WT allele, and the majority (53%) showed no evidence of biallelic loss. The established low penetrance *CHEK2* variant p.Ile157Thr was also not detected with WT allele loss. This is consistent with previous studies that found that LOH across *CHEK2* in BCs from LoF mutation carriers was infrequent (32 of 93, 34%) (32-37) and occurs at a similar rate in sporadic BCs (40%, n = 560) (38). A recent sequencing-based study reported that 13 of 16 (81%) BC from *CHEK2* LoF carriers had biallelic inactivation (32), however, only 5 of the 8 (63%) *CHEK2*-null tumors were of ER-positive and HER2-negative ductal histological subtype that are known to be associated with *CHEK2* predisposition. Our data based on 17 LoF and 20 MS *CHEK2* variant-carrying tumors suggested that although *CHEK2* displayed a selective predisposition to ER-positive ductal BC, there was no consistent biallelic inactivation, and the BCs had low mutational burden and were not consistently associated with a characteristic mutational signature or somatic driver mutations. These data suggest that the effect of pathogenic variants in *CHEK2* is possibly mediated by haploinsufficiency (39), which has implications for the reliability of using biallelic inactivation as an indicator of disease association.

Candidate genes analyzed in this study were identified in the BEACON case-control and included *BLM*, *PARP2*, and *WRN*, which showed statistically significant association with BC with odds ratios of 2.5, 5.0, and 2.0, respectively, whereas other

candidate genes *CDK9*, *CTH*, and *XRCC2* also showed relatively high odds ratios despite the small number of cases. The BEACCON study included more than 11 500 subjects with enrichment for high-risk familial cases, however, LoF variants in candidate genes were still too rare to confidently assert a genuine association with BC predisposition. Inclusion of tumor sequencing from 57 cases did not provide definitive evidence for their roles in BC predisposition: 1 of 2 *XRCC2* and 2 of 7 *WRN* BCs were among the minority that showed loss of the WT allele. Despite multiple studies reporting an association with *BLM*, no instance of biallelic inactivation has been found in *BLM*-carrying tumors to date, including our study of 7 tumors and the previous evaluation of 22 cases across 3 studies (28,34,40). Despite early studies and inclusion of *RAD50* in many HBC gene panels (41,42), recent large studies have demonstrated that it is not a BC predisposition gene (4,5), consistent with the findings in the 4 *RAD50* tumors analyzed here, which all remained heterozygous.

Findings from this study have demonstrated that tumor sequencing is useful in validating BC predisposing genes that operate in carcinogenesis through a mechanism of biallelic inactivation, such as *BARD1*. However, based on the evidence from *CHEK2*-associated tumors, the absence of biallelic inactivation does not appear to preclude a role in BC predisposition. It is interesting to note that most of the established HBC genes that have been shown to undergo frequent biallelic inactivation in breast tumors, such as *BRCA1*, *BRCA2*, *PALB2*, and *RAD51C*, are highly penetrant and/or predispose selectively to TNBC, currently the sole exception being *ATM*, which is a moderate penetrance and ER-positive BC-associated gene. Interestingly, similar to *CHEK2*, the lower penetrance *BRCA2* variant p.Lys3326Ter does not appear to require biallelic activation. A recent study of 26 *BRCA2* p.Lys3326Ter-associated breast tumors found no instance of LOH (43).

Despite the ready availability of archival formalin-fixed, paraffin-embedded tumor blocks from BEACCON study participants, the main limitation to this study, was the small sample size for rare genes. In addition, the quality of formalin-fixed, paraffin-embedded tumor samples may cause potential errors in the determination of LOH. Tumor purity, especially in tumors that have high levels of infiltrating lymphocytes, may also introduce further complexity to the interpretation of allele frequency and copy number status, as addressed in the methods. Lastly, because of the greater requirements in terms of tumor DNA quality and quantity, methylation sequencing was not able to be carried out for all samples, therefore promoter hypermethylation cannot be ruled out for those samples, although in this study, no such instance was found.

In summary, this study demonstrates the utility of inclusion of tumor sequencing in HBC gene discovery and validation, but the absence of consistent biallelic inactivation in *CHEK2* suggests this approach might not be reliable for lower penetrance genes.

Funding

This work was supported by the National Breast Cancer Foundation (IF-15-004, IGC and PAJ), Cancer Australia/National Breast Cancer Foundation (PdCCRS_1107870, IGC and PAJ), Cancer Australia/National Breast Cancer Foundation (PdCCRS_1188547, IGC and PAJ), the Victorian Cancer Agency (Tumor Stream Grant, PAJ), the National Health and Medical Research Council of Australia (GNT1023698, PAJ; GNT1041975, IGC) and Cancer Australia (PdCCRS_1188547, IGC, PAJ, and EKS). EKS is supported by the National Health and Medical Research Council GNT114749, the

National Breast Cancer Foundation IIRS-20-025 and Cancer Council Victoria Grants-in-Aid. NL is supported by Cancer Council Victoria.

Notes

Role of the funder: The funding sources did not participate in the design and conduct of the study, the collection, analysis, and interpretation of the data, the preparation and writing of the manuscript, and the decision to submit the manuscript for publication.

Disclosures: The authors declare that there are no competing interests.

Author contributions: Conceptualization: IGC, PAJ. Data curation: BWXL, NL, SMR, MZ. Formal analysis: BWXL, IGC, PAJ. Funding acquisition: IGC, PAJ. Investigation: BWXL, NL, SM, SM, MZ, SMR, JH, TW, MF, AJEL, LD, RJS, EKS, PAJ, IGC. Methodology: BWXL, NL, MZ, PAJ, IGC. Resources: IGC, PAJ, RJS. Supervision: IGC, PAJ. Visualization: BWXL, NL, MZ. Writing—original draft: BWXL, IGC, PAJ, EKS. Writing—review & editing: BWXL, NL, SM, MZ, LD, EKS, RJS, PAJ, IGC.

Acknowledgements: The authors thank all the participants of the Variants in Practice and Lifepool studies for donating their DNA samples and clinical information. We also thank Norah Grewal, the Variants in Practice study site principal investigators Geoffrey Lindeman, Marion Harris, Lucinda Salmon, Ingrid Winship, and Yoland Antill and the staff at the Peter MacCallum Cancer Centre, Royal Melbourne Hospital, Monash Health, Cabrini Health and Barwon Health Familial Cancer Centres, and the Austin and Tasmanian Clinical Genetics Services, who enrolled participants and provided clinical data. We thank the following staff from Peter MacCallum Cancer Centre; Kaushalya Amarasinghe, Niko Thio, and Richard Lupat from Bioinformatics core facility for helping with the bioinformatic analysis and Steven Macaskill from Pathology Lab for Sanger sequencing services.

Prior presentations: Part of this study was presented at BRCA Symposium 2021, Montreal, Canada and Familial Aspects of Cancer Conference 2021, Melbourne, Australia.

Data availability

All sequencing data has been deposited to the European Genome-phenome Archive under accession numbers Study: EGAS00001006532 and Dataset: EGAD00001009299. Standard R codes were used. Code requests should be addressed to Prof. Ian Campbell.

References

1. Narod SA, Foulkes WD. *BRCA1* and *BRCA2*: 1994 and beyond. *Nat Rev Cancer*. 2004;4(9):665-676.
2. Antoniou AC, Casadei S, Heikkinen T, et al. Breast-cancer risk in families with mutations in *PALB2*. *N Engl J Med*. 2014;371(6):497-506.
3. Li N, Lim BWX, Thompson ER, et al. Investigation of monogenic causes of familial breast cancer: data from the BEACCON case-control study. *NPJ Breast Cancer*. 2021;7(1):76.
4. Breast Cancer Association Consortium. Breast cancer risk genes—association analysis in more than 113,000 women. *N Engl J Med*. 2021;384(5):428-439.

5. Hu C, Hart SN, Gnanaolivu R, et al. A population-based study of genes previously implicated in breast cancer. *N Engl J Med*. 2021; 384(5):440-451.
6. Maxwell KN, Wubbenhorst B, Wenz BM, et al. BRCA locus-specific loss of heterozygosity in germline BRCA1 and BRCA2 carriers. *Nat Commun*. 2017;8(1):319.
7. Sokol ES, Pavlick D, Khiabani H, et al. Pan-cancer analysis of BRCA1 and BRCA2 genomic alterations and their association with genomic instability as measured by genome-wide loss of heterozygosity. *J Clin Oncol Precis Oncol*. 2020;4:442-465.
8. Tung N, Miron A, Schnitt SJ, et al. Prevalence and predictors of loss of wild type BRCA1 in estrogen receptor positive and negative BRCA1-associated breast cancers. *Breast Cancer Res*. 2010;12(6):R95.
9. Osorio A, de la Hoya M, Rodriguez-Lopez R, et al. Loss of heterozygosity analysis at the BRCA loci in tumor samples from patients with familial breast cancer. *Int J Cancer*. 2002;99(2):305-309.
10. Polak P, Kim J, Braunstein LZ, et al. A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. *Nat Genet*. 2017;49(10):1476-1486.
11. Li N, McInerney S, Zethoven M, et al. Combined tumor sequencing and case/control analyses of RAD51C in breast cancer. *J Natl Cancer Inst*. 2019;111(12):1332-1338.
12. Lee JEA, Li N, Rowley SM, et al. Molecular analysis of PALB2-associated breast cancers. *J Pathol*. 2018;245(1):53-60.
13. Weigelt B, Bi R, Kumar R, et al.; for the kConFab Investigators. The landscape of somatic genetic alterations in breast cancers from ATM germline mutation carriers. *J Natl Cancer Inst*. 2018; 110(9):1030-1034.
14. Telli ML, Timms KM, Reid J, et al. Homologous recombination deficiency (HRD) score predicts response to platinum-containing neoadjuvant chemotherapy in patients with triple-negative breast cancer. *Clin Cancer Res*. 2016;22(15):3764-3773.
15. Lanchbury J, Timms K, Reid J, et al. 3-biomarker HRD score versus individual biomarker (LOH, TAI, LST) scores in platinum treated serous ovarian cancer (SOC). *Ann Oncol*. 2016;27(Suppl 6):vi34.
16. Rosenthal R, McGranahan N, Herrero J, Taylor BS, Swanton C. DeconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. *Genome Biol*. 2016;17:31.
17. R Core Team. R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing; 2016.
18. Thompson ER, Rowley SM, Li N, et al. Panel Testing for Familial Breast Cancer: Calibrating the Tension Between Research and Clinical Care. *J Clin Oncol*. 2016;34(13):1455-1459.
19. Rowley SM, Mascarenhas L, Devereux L, et al. Population-based genetic testing of asymptomatic women for breast and ovarian cancer susceptibility. *Genet Med*. 2019;21(4):913-922.
20. Weischer M, Bojesen SE, Ellervik C, Tybjaerg-Hansen A, Nordestgaard BG. CHEK21100delC genotyping for clinical assessment of breast cancer risk: meta-analyses of 26,000 patient cases and 27,000 controls. *J Clin Oncol*. 2008;26(4):542-548.
21. Couch FJ, Shimelis H, Hu C, et al. Associations between cancer predisposition testing panel genes and breast cancer. *JAMA Oncol*. 2017;3(9):1190-1196.
22. Hilbers FS, Wijnen JT, Hoogerbrugge N, et al. Rare variants in XRCC2 as breast cancer susceptibility alleles. *J Med Genet*. 2012; 49(10):618-620.
23. Park DJ, Lesueur F, Nguyen-Dumont T, et al.; for the Kathleen Cuninghame Foundation Consortium for Research into Familial Breast Cancer. Rare mutations in XRCC2 increase the risk of breast cancer. *Am J Hum Genet*. 2012;90(4):734-739.
24. Figlioli G, Bogliolo M, Catucci I, et al.; for kConFab. The FANCM:p.Arg658 truncating variant is associated with risk of triple-negative breast cancer. *NPJ Breast Cancer*. 2019; 5(1):38.
25. Kiiski JJ, Pelttari LM, Khan S, et al. Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. *Proc Natl Acad Sci USA*. 2014;111(42):15172-15177.
26. Neidhardt G, Hauke J, Ramser J, et al. Association between loss-of-function mutations within the FANCM gene and early-onset familial breast cancer. *JAMA Oncol*. 2017;3(9):1245-1248.
27. Prokofyeva D, Bogdanova N, Dubrowinskaja N, et al. Nonsense mutation p.Q548X in BLM, the gene mutated in Bloom's syndrome, is associated with breast cancer in Slavic populations. *Breast Cancer Res Treat*. 2013;137(2):533-539.
28. Sokolenko AP, Iyevleva AG, Preobrazhenskaya EV, et al. High prevalence and breast cancer predisposing role of the BLM c.1642 C>T (Q548X) mutation in Russia. *Int J Cancer*. 2012;130(12):2867-2873.
29. Thompson ER, Doyle MA, Ryland GL, et al.; for kConFab. Exome sequencing identifies rare deleterious mutations in DNA repair genes FANCC and BLM as potential breast cancer susceptibility alleles. *PLoS Genet*. 2012;8(9):e1002894.
30. Li A, Geyer FC, Bleuca P, et al.; for kConFab Investigators. Homologous recombination DNA repair defects in PALB2-associated breast cancers. *NPJ Breast Cancer*. 2019;5(1):23.
31. Ng PS, Pan JW, Ahmad Zabidi MM, et al. Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. *NPJ Breast Cancer*. 2021;7(1):46.
32. Mandelker D, Kumar R, Pei X, et al. The landscape of somatic genetic alterations in breast cancers from CHEK2 germline mutation carriers. *JNCI Cancer Spectr*. 2019;3(2):pkz027.
33. Massink MPG, Kooi IE, Martens JWM, Waisfisz Q, Meijers-Heijboer H. Genomic profiling of CHEK2*1100delC-mutated breast carcinomas. *BMC Cancer*. 2015;15:877.
34. Suspitsin EN, Yanus GA, Sokolenko AP, et al. Development of breast tumors in CHEK2, NBN/NBS1 and BLM mutation carriers does not commonly involve somatic inactivation of the wild-type allele. *Med Oncol*. 2014;31(2):828.
35. Muranen TA, Greco D, Fagerholm R, et al. Breast tumors from CHEK2 1100delC-mutation carriers: genomic landscape and clinical implications. *Breast Cancer Res*. 2011;13(5):R90.
36. Oldenburg RA, Kroeze-Jansema K, Kraan J, et al. The CHEK21100delC variant acts as a breast cancer risk modifier in non-BRCA1/BRCA2 multiple-case families. *Cancer Res*. 2003; 63(23):8153-8157.
37. Sodha N, Bullock S, Taylor R, et al. CHEK2 variants in susceptibility to breast cancer and evidence of retention of the wild type allele in tumours. *Br J Cancer*. 2002;87(12):1445-1448.
38. Nik-Zainal S, Davies H, Staaf J, et al. Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*. 2016;534(7605):47-54.
39. Teugels E, De Brakeleer S. An alternative model for (breast) cancer predisposition. *NPJ Breast Cancer*. 2017;3(1):13.
40. Kluźniak W, Wokołorczyk D, Rusak B, et al. Inherited variants in BLM and the risk and clinical characteristics of breast cancer. *Cancers (Basel)*. 2019;11(10):1548.
41. Heikkinen K, Rapakko K, Karppinen S-M, et al. RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. *Carcinogenesis*. 2006;27(8):1593-1599.
42. Tommiska J, Seal S, Renwick A, et al. Evaluation of RAD50 in familial breast cancer predisposition. *Int J Cancer*. 2006;118(11): 2911-2916.
43. Butz H, Papp J, Bozsik A, et al. Application of multilayer evidence for annotation of c-terminal BRCA2 variants. *Cancers (Basel)*. 2021;13(4):881.