Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk


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PLOS Genetics | www.plosgenetics.org 1 March 2013 | Volume 9 | Issue 3 | e1003173
Abstract

Common genetic variants contribute to the observed variation in breast cancer risk for BRCA2 mutation carriers; those known to date have all been found through population-based genome-wide association studies (GWAS). To complement these results, robustly identify breast cancer susceptibility alleles, we conducted a discovery phase of an ongoing GWAS discovery study. Using the ranked P-values of the breast cancer associations with the imputed genotype of 1.4 M SNPs, 19,029 SNPs were selected and designed for inclusion on a custom Illumina array that included a total of 211,155 SNPs as part of a multi-consortial project. DNA samples from 3,881 breast cancer affected and 4,330 unaffected BRCA2 mutation carriers from 47 studies belonging to the Consortium of Investigators of Modifiers of BRCA1/2 were genotyped and available for analysis. We replicated previously reported breast cancer susceptibility alleles in these BRCA2 mutation carriers and for several regions (including FGR2, MAP3K1, CDKN2A/B, and PTHLH) identified SNPs that have stronger evidence of association than those previously published. We also identified a novel susceptibility allele at 6p24 that was inversely associated with breast cancer risk either in the general population or in BRCA1 mutation carriers. The locus lies within a region containing TFAP2A, which encodes a transcriptional activation protein that interacts with several tumor suppressor genes. This report identifies the first breast cancer risk locus specific to a BRCA2 mutation background. This comprehensive update of novel and previously reported breast cancer susceptibility loci contributes to the establishment of a panel of SNPs that modify breast cancer risk in BRCA2 mutation carriers. This panel may have clinical utility for women with BRCA2 mutations weighing options for medical prevention of breast cancer.
Introduction

The lifetime risk of breast cancer associated with carrying a BRCA2 mutation varies from 40 to 84% [1]. To determine whether common genetic variants modify breast cancer risk for BRCA2 mutation carriers, we previously conducted a GWAS of BRCA2 mutation carriers from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA) [2]. Using the Affymetrix 6.0 platform, the discovery stage results were based on 899 young (<40 years) affected and 804 unaffected carriers of European ancestry. In a rapid replication stage wherein 85 discovery stage cases and controls were genotyped, 24 additional BRCA2 mutation carriers, only published loci associated with breast cancer risk in the general population, including FGF2 (10q26; rs2981575; \(P = 1.2 \times 10^{-6}\)), were associated with breast cancer risk at the genome-wide significance level among BRCA2 carriers.

Hospital grants, Cancer Fund of North Savo, the Finnish Cancer Organizations, the Academy of Finland, and by the strategic funding of the University of Eastern Finland. Kathleen Cuningham Consortium for Research into Familial Breast Cancer: KConFab is supported by grants from the National Breast Cancer Foundation and the National Health and Medical Research Council (NHMRC) and by the Queensland Cancer Fund; the Cancer Councils of New South Wales, Victoria, Tasmania, and South Australia; and the Cancer Foundation of Western Australia. G Chennevix-Trench and AB Spurdle are NHMRC Senior Research Fellows. Financial support for the ACOCS was provided by the United States Army Medical Research and Materiel Command (DAMD17-01-1-0729), the Cancer Council of Tasmania and Cancer Foundation of Western Australia, and the NHMRC (199660). G Chennevix-Trench is supported by the NHMRC. The Clinical Follow Up Study (funded 2007-2009) by NHMRC and currently by the National Breast Cancer Foundation (NBCCF). The Konstam Breast Cancer Study, Finland was supported by the Swedish Cancer Foundation and the Komen Foundation for the Cure. The Danish Breast Cancer Cooperative Study was supported by the Danish Cancer Society. The Early Stage Breast Cancer Short-term Follow-up Study was supported by the Danish Cancer Society. The Breast Cancer Family Registry (BCFR) New York. N. N. Petrov Institute of Oncology: The NPNIO study has been supported by the Russian Federation for Basic Research (grants 11-04-00227, 12-04-00298, and 12-04-01490) and the National Agency for Science and Innovation, Russian (contract 02.740.11.0780). Obou Breast Cancer Study: The ORBCS was supported by research grants from the Finnish Cancer Foundation, the Academy of Finland, the University of Oulu, and the Finnish Cancer Research Foundation. The Genotyping Center, Amsterdam: The VIB Leiden Multidisciplinary Breast Centre: LMBC is supported by the ‘Stichting tegen Kanker’ (232-2008 and 196-2010). D Lambrechts is supported by the FWO and the KULPV/10/016-SymBioSys. Mammary Carcinoma Risk Factor Investigation: The MARI study was supported by the Deutsche Krebsfille e.V. (70-2892-BRI), the Hamburg Cancer Society, the German Cancer Research Center, and the genotype work in part by the Federal Ministry of Education and Research (BMBF) Germany [0IKH0402]. Mayo Clinic: MAYO is supported by NIH grant AI28978, an NCI Specialized Program of Research Excellence (SPOR) in Breast Cancer (CA116201), a U.S. Department of Defence Ovarian Cancer Idea award (W81XWH-10-1-0341), and grants from the Breast Cancer Research Foundation and the Komen Foundation for the Cure. Milan Breast Cancer Study Group: MBCSG was funded by grants from Fondazione Italiana per la Ricerca sul Cancro Special Project ‘Hereditary tumors’; Italian Association for Cancer Research (AIRC, IG 8713); Italian Ministry of Health (‘Progetto Tumori Femminili’); and by Italian citizens who allocated the 5 million euro to the foundation. The Fondazione IRCCS Istituto Nazionale Tumori, according to Italian laws (INT-Institutional strategic projects ‘5 x 1000’). Melbourne Collaborative Cohort Study: MCCS cohort recruitment was funded by VicHealth and Cancer Council Victoria. The MCCS was further supported by Australian NHMRC grants 209057, 251353 and 504771 and by infrastructure provided by Cancer Council Victoria. McGill University: The McGill Study was supported by Jewish General Hospital Weekend to End Breast Cancer, Quebec Ministry of Economic Development, Innovation and Export Trade. Multi-Ethnic Cohort: The MEC was supported by NIH grants CA63464, CA54281, CA098758, and CA132839. Memorial Sloan-Kettering Cancer Center: The MSKCC was supported by Breast Cancer Research Foundation, Niehaus Clinical Cancer Genetics Initiative, Andrew Sabin Family Foundation, and Lymphoma Foundations. Montreal Gen Equ Mol Breast Cancer Study: The work of MTLGBCS was supported by the Quebec Breast Cancer Foundation, the Canadian Institutes of Health Research for the ‘CIHR Team in Familial Risks of Breast Cancer’ project grant CRN-87521 and the Ministry of Economic Development, Innovation and Export Trade grant PSRI-SHR-701. J Simard is Chairholder of the Canada Research Chair in Oncogenetics. National Cancer Institute: The research of MH Greene and PL Mai was supported by the Intramural Research Program of the US National Cancer Institute, NIH, and by support contracts NO2-CP-10193-01 and NO2-CP-65504 with Westat, Rockville, MD. National Israeli Cancer Control Center: NICCC is supported by Clalit Health Services in Israel. Some of its activities are supported by the Israel Cancer Association and the Breast Cancer Research Foundation (BCRF). New York. N. N. Petrov Institute of Oncology: The NPNIO study has been supported by the Russian Federation for Basic Research (grants 11-04-00227, 12-04-00298, and 12-04-01490) and the Federal Agency for Science and Innovations, Russia (contract 02.740.11.0780). Obou Breast Cancer Study: The ORBCS was supported by research grants from the Finnish Cancer Foundation, the Academy of Finland, the University of Oulu, and the Finnish Cancer Research Foundation. The Genotyping Center, Amsterdam: The VIB Leiden Multidisciplinary Breast Centre Cancer Study: The ORIGO study was supported by the Dutch Cancer Society (RUL 1997-1505) and the Biobanking and Biomolecular Resources Research Infrastructure (BBMRI-NL CP16). The Ohio State University Comprehensive Cancer Center: OSUCCG is supported by the Ohio State University Comprehensive Cancer Center. SEABASS is supported by the Ministry of Science, Technology and Innovation, Ministry of Higher Education (UM/ HR/ MOHE/06) and Cancer Research Initiatives Foundation. The U.S. National Cancer Institute Polish Breast Cancer Study: The PBCS was funded by Intramural Research Funds of the National Cancer Institute, Department of Health and Human Services, USA. Karolinska Mammography Project for Risk Prediction of Breast Cancer - prevalent cases: The pKARMA study was supported by Marit and Hans Rausings Initiative Against Breast Cancer. Rotterdam Breast Cancer Study: The RBCS was funded by the Dutch Cancer Society (DDHk 2004-3124, DDKH 2009-4318). Singapore and Sweden Breast Cancer Study: The SASBAC study was supported by funding from the Agency for Science, Technology and Research of Singapore (A*STAR), the U.S. National Institute of Health (NIH), and the Susan G. Komen Breast Cancer Foundation. Sheffield Breast Cancer Study: The SBCs was supported by Yorkshire Cancer Research S295, S299, and S305PA. South East Asian Breast Cancer Association Study: SEABASS is supported by the Ministry of Science, Technology and Innovation, Ministry of Higher Education (UM/CHIR/ MOHE/06) and Cancer Research Initiatives Foundation. The Malaysian Breast Cancer Genetic Study is funded by research grants from the Malaysian Ministry of Science, Technology and Innovation; Ministry of Higher Education (UM/CHIR/MOHE/06); and charitable funding from Cancer Research Initiatives Foundation. Study of Epidemiology and Risk Factors in Cancer Heredity: SEARCH is funded by programme grants from Cancer Research UK [C490/A10124][C8197/A10865]. Sheba Medical Centre: The SMC study was partially funded through a grant by the Israel Cancer Association and the funding for the Israeli Inherited Breast Cancer Consortium. Swedish Breast Cancer Consortium: SWE-BRCA collaborators are supported by the Swedish Cancer Society. IHCES-Siezeck Breast Cancer Study: The SZBSCs was supported by Grant PBZ_KBN_122/POS/2004. The University of Chicago Center for Clinical Genetics and Global Health: UChicago is supported by grants from the U.S. National Cancer Institute (NIH/NCI) and by the Ralph and Marion Falk Medical Research Trust, the Entertainment Industry Fund National Women’s Cancer Research Alliance, and the Breast Cancer Foundation. University of California Los Angeles: The UCLA study was supported by the Jonsson Comprehensive Cancer Center Foundation and the Breast Cancer Research Foundation. University of California San Francisco: The UCSF study was supported by the UCSF Cancer Risk Program and the Helen Diller Family Comprehensive Cancer Research United Kingdom Breakthrough Generations Study: The UKBGS is funded by Breaking Breast Cancer and the Institute of Cancer Research (ICR). ICR acknowledges NHS funding to the NIHR Biomedical Research Centre. United Kingdom Familial Ovarian Cancer Registries: UKFOCR was supported by a project grant from CRUK to PDP Pharoah. University of Pennsylvania: The UPENN study was supported by the National Institutes of Health (NIH) (R01-CA102776 and R01-CA102777). Singapore Breast Cancer Research Foundation, Rooney and the Sue-Ann Ong Foundation. Victorian Cancer Rates Study: The VFCG study was supported by the Victorian Cancer Agency, Cancer Australia, and the National Breast Cancer Foundation. Women’s Cancer Program: The WCP at the Samuel Oschin Comprehensive Cancer Institute is funded by the American Cancer Society Early Detection Professorship (SIOP-06-258-01-COUN). Genetic Modifiers of Cancer Risk in BRCA1/2 Mutation Carriers (GEMO) study: The study was supported in part by the Quebec Institute of Cancer, the Canadian Institutes of Health Research, the Canadian Cancer Society, the Canadian Institutes of Health Research-nidr funds for the “CIHR Team in Familial Risks of Breast Cancer” program. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

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Study subjects

Ethics statement

Each of the host institutions (Table S1) recruited under ethically-approved protocols. Written informed consent was obtained from all subjects.

Materials and Methods

Genotyping. The genotyping was performed on DNA samples from 10,048 BRCA2 mutation carriers at the McGill University and Génome Québec Innovation Centre (Montreal, Canada). As a quality control measure, each plate included DNA samples from six individuals who were members of two CEPH trios. Some plates also contained three duplicate pairs of quality control samples. Genotypes were called using GenCall [9]. Initial calling was based on a cluster file generated using 270 samples from Hapmap2. To generate the final calls, we first selected a subset of 3,018 individuals, including samples from each of the genotyping centers in the iCOGS project, each of the participating
consortia, and each major ethnicity. Only plates with a consistent high call rate in the initial calling were used. We also included 300 samples of European, African, and Asian ethnicity genotyped as part of the Hapmap and 1000 Genomes project, and 160 samples that were known positive controls for rare variants on the array. This subset was used to generate a cluster file that was then applied to call the genotypes for the remaining samples.

**Quality control of SNPs.** Of the 211,155 SNPs on the iCOGS array, we excluded SNPs for the following reasons (Table S2): on the Y-chromosome, call rate <95%; deviations from Hardy-Weinberg equilibrium (P<10^{-7}) using a stratified 1-d.f. test [10], and monomorphic. SNPs that gave discrepant genotypes among known duplicates were also excluded. After quality control filtering, 200,908 SNPs were available for analysis (Table S2); 18,086 of which were selected on the basis of the discovery BRCA2 GWAS [2]. Cluster plots of all reported SNPs were inspected manually for quality (Figure S1).

**Description of imputation.** Genotypes for SNPs identified through the 1000 Genomes Phase I data (released Jan 2012) [11] were imputed using SNPs on the iCOGS chip in a region of 500 kb around the novel modifier locus at 6p24. The boundaries were determined according to the linkage disequilibrium (LD) structure in the region based on HapMap data. The imputation was carried out using IMPUTE 2.2 [12]. SNPs with imputation information/accuracy r^2<0.30 were excluded in the analyses.

**Quality control of DNA samples.** Of 10,048 genotyped samples (Table S2), 742 were excluded because they did not meet the phenotypic eligibility criteria or had self-reported non-CEU ethnicity. Samples were then excluded for the following reasons: not female (XXY, XY), call rate <95%, low or high heterozygosity (P<10^{-7}), discordant genotypes from previous CIMBA genotyping efforts, or discordant duplicate samples. For duplicates with concordant phenotypic data, or in cases of cryptic monozygotic twins, only one of the samples was included. Cryptic duplicates for which phenotypic data indicated different individuals were all excluded. Samples of non-European ancestry were identified using multidimensional scaling, after combining the BRCA2 mutation carrier samples with the HapMap2 CEU, CHB, JPT and YRI samples using a set of 37,120 uncorrelated SNPs from the iCOGS array. Samples with >19% non-European ancestry were excluded (Figure S2). A total of 4,330 affected and 3,881 unaffected BRCA2 mutation carrier women of European ancestry from 42 studies remained in the analysis (Table S1), including 3,234 breast cancer cases and 3,490 unaffected carriers that were not in the discovery set.

**BRCA1 and BCAC samples.** Details of the sample collection, genotyping and quality control process for the BRCA1 and BCAC samples, are reported elsewhere [13,14].

**Statistical methods**

The associations between genotype and breast cancer risk were analyzed within a retrospective cohort framework with time to breast cancer diagnosis as the outcome [15]. Each BRCA2 carrier was followed until the first event: breast or ovarian cancer diagnosis, bilateral prophylactic mastectomy, or age at last observation. Only those with a breast cancer diagnosis were considered as cases in the analysis. The majority of mutation carriers were recruited through genetic counseling centers where genetic testing is targeted at women diagnosed with breast or ovarian cancer and in particular to those diagnosed with breast cancer at a young age. Therefore, these women are more likely to be sampled compared to unaffected mutation carriers or carriers diagnosed with the disease at older ages. As a consequence, sampling was not random with respect to disease phenotype and standard methods of survival analysis (such as Cox regression) may lead to biased estimates of the associations [16]. We therefore conducted the analysis by modelling the retrospective likelihood of the observed genotypes conditional on the disease phenotypes. This has been shown to provide unbiased estimates of the associations [15]. The implementation of the retrospective likelihoods has been described in detail elsewhere [15,17]. The associations between genotype and breast cancer risk were assessed using the 1degree of freedom score test statistic based on the retrospective likelihood [15]. In order to account for non-independence between relatives, an adjusted version of the score test was used in which the variance of the score was derived taking into account the correlation between the genotypes [18]. P-values were not adjusted using genomic control because there was little evidence of inflation. Inflation was assessed using the genomic inflation factor, λ. Since this estimate is dependent on sample size, we also calculated λ adjusted to 1000 affected and 1000 unaffacted samples. Per-allele and genotype-specific hazard-ratios (HR) and 95% confidence intervals (CI) were estimated by maximizing the retrospective likelihood.

Calendar-year and cohort-specific breast cancer incidences for BRCA2 were used [1]. All analyses were stratified by country of residence. The USA and Canada strata were further subdivided by self-reported Ashkenazi Jewish ancestry. The assumption of proportional hazards was assessed by fitting a model that included a genotype-by-age interaction term. Between-country heterogeneity was assessed by comparing the results of the main analysis to a model with country-specific log-HRs. A possible survival bias due to inclusion of prevalent cases was evaluated by re-fitting the model after excluding affected carriers that were diagnosed ≥5 years prior to study recruitment. The associations between genotypes and tumor subtypes were evaluated using an extension of the retrospective likelihood approach that models the association with two or more subtypes simultaneously [19]. To investigate whether any of the significant SNPs were associated with ovarian cancer risk for BRCA2 mutation carriers and whether the inclusion of ovarian cancer patients as unaffected subjects biased our results, we also analyzed the data within a competing risks framework and estimated HR simultaneously for breast and ovarian cancer using the methods described elsewhere [15]. Analyses were carried out in R using the GenABEL libraries [20] and custom-written software. The retrospective likelihood was modeled in the pedigree-analysis software MENDEL [21], as described in detail elsewhere [15].

**TCGA analysis.** Affymetrix SNP 6.0 genotype calls for normal (non-tumor) breast DNA were downloaded for all available individuals from The Cancer Genome Atlas in September 2011. Analyses were limited to the 401 individuals of European ancestry based on principal component analysis. Expression levels in breast tumor tissue were adjusted for the top two principal components, age, gender (there are some male breast cancer cases in TCGA), and average copy number across the gene in the tumor. Linear regression was then used to test for association between the SNP and the adjusted gene expression level for all genes within one megabase.

**Gene set enrichment analysis.** To investigate enrichment of genes associated with breast cancer risk, the gene-set enrichment approach was implemented using Versatile Gene-based Association Study [22] based on the ranked P-values from retrospective likelihood analysis. Association List Go Annotator was also used to prioritize gene pathways using functional annotation from gene ontology (GO) [23] to increase the power to detect association to a pathway, as opposed to individual genes in the pathway. Both analyses were corrected for LD between SNPs, variable gene size, and interdependence of GO categories.
where applicable, based on imputation. 100,000 Monte Carlo simulations were performed in VEGAS and 5000 replicate gene lists using random sampling of SNPs and 5000 replicate studies (sampling with replacement) were performed to estimate P-values.

**Predicted absolute breast cancer risks by combined SNP profile.** We estimated the absolute risks of developing breast cancer based on the joint distribution of SNPs associated with breast cancer for **BRCA2** mutation carriers. The methods have been described elsewhere [24]. To construct the SNP profiles, we considered the single SNP from each region with the strongest evidence of association in the present dataset. We included all loci that had previously been found to be associated with breast cancer risk through GWAS in the general population and demonstrated associations with breast cancer risk for **BRCA2** mutation carriers, and loci that had GWAS level of significance in the current study. We assumed that all loci in the profile were independent (i.e. they interact multiplicatively on **BRCA2** breast cancer risk). Genotype frequencies were obtained under the assumption of Hardy-Weinberg Equilibrium. For each SNP, the effect of each allele was assumed to be consistent with a multiplicative model (log-additive). We assumed that the average, age-specific breast cancer incidences, over all associated loci, agreed with published breast cancer risk estimates for **BRCA2** mutation carriers [1].

**Results**

The genomic inflation factor (λ) based on the 18,086 **BRCA2** GWAS SNPs in the 6,724 **BRCA2** mutation carriers who were not used in the SNP discovery set was 1.034 (λ adjusted to 1000 affected and 1000 unaffected: 1.010, Figure S3). Multiple variants were associated with breast cancer risk in the combined discovery and replication datasets (Figure S4). SNPs in three independent regions had P-values<5×10^{-8}; one was a region not previously associated with breast cancer.

The most significant associations were observed for known breast cancer susceptibility regions, rs2420946 (per allele P = 2×10^{-14}) in **FGFR2** and rs3803662 (P = 5.4×10^{-11}) near **TOX3** (Table 1). Breast cancer risk associations with other SNPs reported previously for **BRCA2** mutation carriers are summarized in Table 1. In this larger set of **BRCA2** mutation carriers, we also identified novel SNPs in the 12p11 (**PTHLH**, 5q11 (**MAP3K1**), and 9p21 (**CDK2A1/B**) regions with smaller P-values for association than those of previously reported SNPs. These novel SNPs were not correlated with the previously reported SNPs (r^2<0.14). For one of the novel SNPs identified in the discovery GWAS [2], **ZNFX3** rs16917302, there was weak evidence of association with breast cancer risk (P = 0.01); however, an uncorrelated SNP, rs17221319 (r^2<0.01), 54 kb upstream of rs16917302 had stronger evidence of association (P = 6×10^{-10}).

One SNP, rs9348512 at 6p24 not known to be associated with breast cancer, had a combined P-value of association of 3.9×10^{-8} amongst all **BRCA2** samples (Table 2), with strong evidence of replication in the set of **BRCA2** samples that were not used in the discovery stage (P = 5.2×10^{-8}). The minor allele of rs9348512 (MAF = 0.35) was associated with a 15% decreased risk of breast cancer among **BRCA2** mutation carriers (per allele HR = 0.85, 95% CI 0.80–0.90) with no evidence of between-country heterogeneity (P = 0.78, Figure S5). None of the genotyped (n = 68) or imputed (n = 3,507) SNPs in this region showed a stronger association with risk (Figure 1; Table S3), but there were 40 SNPs with P<10^{-4} (pairwise r^2>0.38 with rs9348512, with the exception of rs11526201 for which r^2 = 0.01, Table S3). The association with rs9348512 did not differ by 6174delT mutation status (P for difference = 0.33), age (P = 0.39), or estrogen receptor (ER) status of the breast tumor (P = 0.41). Exclusion of prevalent breast cancer cases (n = 1,752) produced results (HR = 0.83, 95% CI 0.77–0.89, P = 3.40×10^{-7}) consistent with those for all cases.

SNPs in two additional regions had P-values<10^{-5} for breast cancer risk associations for **BRCA2** mutation carriers (Table 2). The magnitude of associations for both SNPs was similar in the discovery and second stage samples. In the combined analysis of all samples, the minor allele of rs619373, located in **FGF13** (Xq26.3), was associated with higher breast cancer risk (HR = 1.30, 95% CI 1.17–1.43, P = 3.1×10^{-6}). The minor allele of rs184577, located in **C1P1B1-AS1** (2p22–p21), was associated with lower breast cancer risk (HR = 0.93, 95% CI 0.79–0.91, P = 3.6×10^{-4}). These findings were consistent across countries (P for heterogeneity between country strata = 0.39 and P = 0.30, respectively; Figure S6). There was no evidence that the HR estimates for rs619373 and rs184577 change with age of the **BRCA2** mutation carriers (P for the genotype-age interaction = 0.80 and P = 0.40, respectively) and no evidence of survival bias for either SNP (rs619373: HR = 1.35, 95% CI 1.20–1.53, P = 1.5×10^{-6} and rs184577: HR = 0.86, 95% CI 0.79–0.93, P = 2.0×10^{-4}, after excluding prevalent cases). The estimates for risk of ER-negative and ER-positive breast cancer were not significantly different (P for heterogeneity between tumor subtypes = 0.79 and 0.67, respectively). When associations were evaluated under a competing risks model, there was no evidence of association with ovarian cancer risk for SNPs rs9348512 at 6p24, rs619373 in **FGF13** or rs184577 at 2p22 and the breast cancer associations were virtually unchanged (Table S4).

Gene set enrichment analysis confirmed that strong associations exist for known breast cancer susceptibility loci and the novel loci identified here (gene-based P<1×10^{-5}). The pathways most strongly associated with breast cancer risk that contained statistically significant SNPs included those related to ATP binding, organ morphogenesis, and several nucleotide bindings (pathway-based P<0.05).

To begin to determine the functional effect of rs9348512, we examined associations of expression levels of any nearby gene in breast tumors with the minor A allele. Using data from The Cancer Genome Atlas, we found that the A allele of rs9348512 was strongly associated with mRNA levels of GCNT2 in breast tumors (p = 7.3×10^{-5}).

The hazard ratios for the percentiles of the combined genotype distribution of loci associated with breast cancer risk in **BRCA2** mutation carriers were translated into absolute breast cancer risks under the assumption that SNPs interact multiplicatively. Based on our results for SNPs in **FGFR2**, **TOX3**, 12p11, 5q11, **CDK2A1/B**, **LSP1**, 8q24, **ESR1**, **ZNF565**, 3p24, 12q24, 5p12, 11q13 and also the 6p24 locus, the 5% of the **BRCA2** mutation carriers at lowest risk were predicted to have breast cancer risks by age 80 in the range of 21–47% compared to 83–100% for the 5% of mutation carriers at highest risk on the basis of the combined SNP profile distribution (Figure 2). The breast cancer risk by age 50 was predicted to be 4–11% for the 5% of the carriers at lowest risk compared to 29–81% for the 5% at highest risk.

**Discussion**

In the largest assemblage of **BRCA2** mutation carriers, we identified a novel locus at 6q24 that is associated with breast cancer risk, and noted two potential SNPs of interest at Xq26 and 2p22. We also replicated associations with known breast cancer susceptibility SNPs previously reported in the general population and in **BRCA2** mutation carriers. For the 12p11 (**PTHLH**, 5q11 (**MAP3K1**), and 9p21 (**CDK2A1/B**), we found uncorrelated SNPs
Table 1. Per allele hazard ratios (HR) and 95% confidence intervals (CI) of previously published breast cancer loci among BRCA2 mutation carriers from previous reports and from the iCOGS array, ordered by statistical significance of the region.

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</table>

1. Reporting status of the SNP is either previously reported or novel to this report.
2. p-value was calculated based on the 1-degree of freedom score test statistic.
3. rs311499 could not be designed onto the iCOGS array. A surrogate (rs2 = 1.0), rs311498, was included, however, and reported here.
4. Stronger associations were originally reported for the SNP, assuming a dominant or recessive model of the ‘risk allele’.

doi:10.1371/journal.pgen.1003173.t001
<table>
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<th>SNP rs No. Chr. (Nearby Genes)</th>
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<td>Genotype</td>
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<td>368 (43.8)</td>
<td>299 (46.2)</td>
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<td>per allele</td>
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<td>per allele</td>
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1. P-value was calculated based on the 1-degree of freedom score test.

doi:10.1371/journal.pgen.1003173.t002
that had stronger associations than the originally identified SNP in the breast cancer susceptibility region that should be replicated in the general population. In BRCA2 mutation carriers, evidence for a breast cancer association with genetic variants in PTHLH has been restricted previously to ER-negative tumors [25]; however, the novel susceptibility variant we reported here was associated with risk of ER+ and ER- breast cancer.

The novel SNP rs9348512 (6p24) is located in a region with no known genes (Figure 1). C6orf218, a gene encoding a hypothetical protein LOC221718, and a possible tumor suppressor gene, TFAP2A, are within 100 kb of rs9348512. TFAP2A encodes the AP-2α transcription factor that is normally expressed in breast ductal epithelium nuclei, with progressive expression loss from normal, to ductal carcinoma in situ, to invasive cancer [26,27]. AP-2α also acts as a tumor suppressor via negative regulation of MYC [28] and augmented p53-dependent transcription [29]. However, the minor allele of rs9348512 was not associated with gene expression changes of TFAP2A in breast cancer tissues in The Cancer Genome Atlas (TCGA) data; this analysis might not be informative since expression of TFAP2A in invasive breast tissue is low [26,27]. Using the TCGA data and a 1 Mb window, expression changes with genotypes of rs9348512 were observed for GCNT2, the gene encoding the enzyme for the blood group I antigen glucosaminyl (N-acetyl) transferase 2. GCNT2, recently found to be overexpressed in highly metastatic breast cancer cell lines [30] and basal-like breast cancer [31], interacts with TGF-β to promote epithelial-to-mesenchymal transition, enhancing the metastatic potential of breast cancer [31]. An assessment of alterations in expression patterns in normal breast tissue from BRCA2 mutation carriers by genotype are needed to further evaluate the functional implications of rs9348512 in the breast tumorigenesis of BRCA2 mutation carriers.

To determine whether the breast cancer association with rs9348512 was limited to BRCA2 mutation carriers, we compared results to those in the general population genotyped by BCAC and to BRCA1 mutation carriers in CIMBA. No evidence of an associations between rs9348512 and breast cancer risk was observed in the general population (OR = 1.00, 95% CI 0.98–1.02, P = 0.74) [14], nor in BRCA1 mutation carriers (HR = 0.99, 95% CI 0.94–1.04, P = 0.75) [13]. Stratifying cases by ER status, there was no association observed with ER-subtypes in either the general population or among BRCA1 mutation carriers (BCAC: ER positive P = 0.89 and ER negative P = 0.60; CIMBA BRCA1: P = 0.49 and P = 0.99, respectively). For the two SNPs associated with breast cancer with P < 10^{-5}, neither rs619373, located in FGF13 (Xq26.3), nor rs184577, located in CYP1B1-AS1 (2p22-p21), was associated with breast cancer risk in the general population [14] or among BRCA1 mutation carriers [13]. The narrow CIs for the overall associations in the general population and in BRCA1 mutation carriers rule out associations of magnitude similar to those observed for BRCA2 mutation carriers. The consistency of the association in the discovery and replication stages and by country, the strong quality control measures and filters, and the clear cluster plot for rs9348512 suggest that our results constitute the discovery of a novel breast cancer susceptibility locus specific to BRCA2 mutation carriers rather than a false positive finding. Replicating this SNP in an even larger population of BRCA2 mutation carriers would be ideal, but not currently

![Figure 1. Associations between SNPs in the region surrounding rs9348512 on chromosome 6 and breast cancer risk. Results based on imputed and observed genotypes. The blue spikes indicate the recombination rate at each position. Genotyped SNPs are represented by diamonds and imputed SNPs are represented by squares. Color saturation indicates the degree of correlation with the SNP rs9348512. doi:10.1371/journal.pgen.1003173.g001](image-url)
possible because we know of no investigators with appropriate data and germline DNA from BRCA2 mutation carriers who did not contribute their mutation carriers to iCOGS. However, CIMBA studies continue to recruit individuals into the consortium.

rs9348512 (6p24) is the first example of a common susceptibility variant identified through GWAS that modifies breast cancer risk specifically in BRCA2 mutation carriers. Previously reported BRCA2-modifying alleles for breast cancer, including those in FGF2, TOX3, MAP3K1, LSP1, 8q24, ESR1, ZNF365, 3p24, 12q24, 5p12, 11q13 and the newly identified BRCA2 modifier locus at 6p24. The figure shows the risks at the 5th and 95th percentiles of the combined genotyped distribution as well as minimum, maximum and average risks.
doi:10.1371/journal.pgen.1003173.g002

**Figure 2. Predicted breast cancer risks for BRCA2 mutation carriers by the combined SNP profile distributions.** Based on the known breast cancer susceptibility loci at FGF2, TOX3, 12p11, 5q11, CDKN2A/B, LSP1, 8q24, ESR1, ZNF365, 3p24, 12q24, 5p12, 11q13 and the newly identified BRCA2 modifier locus at 6p24. The figure shows the risks at the 5th and 95th percentiles of the combined genotyped distribution as well as minimum, maximum and average risks.

### Supporting Information

**Figure S1** Cluster plots for SNPs (A.) rs9348512, (B.) rs619373, and (C.) rs184577. (TIF)

**Figure S2** Multidimensional scaling plots of the top two principal components of genomic ancestry of all eligible BRCA2 iCOGS samples plotted with the HapMap CEU, ASI, and YRI samples: (A.) samples from Finland and BRCA2 617delIT carriers highlighted, and (B.) samples, indicated in red, with >19% non-European ancestry were excluded. (TIF)

**Figure S3** Quantile–quantile plot comparing expected and observed distributions of P-values. Results displayed (A) for the complete sample, (B) after excluding samples from the GWAS discovery stage, and (C) for the complete sample and a set of SNPs from the iCOGS array that were selected independent from the results of the BRCA2 mutation carriers. (TIF)

**Figure S4** Manhattan plot of P-values by chromosomal position for 18,086 SNPs selected on the basis of a previously published genome-wide association study of BRCA2 mutation carriers. Breast cancer associations results based on 4,330 breast cancer cases and 3,881 unaffected BRCA2 carriers. (TIF)

**Figure S5** Forest plot of the country-specific, per-allele hazard ratios (HR) and 95% confidence intervals for the association between breast cancer and rs9348512 genotypes. (TIF)

**Figure S6** Forest plot of the country-specific, per-allele hazard ratios (HR) and 95% confidence intervals for the association with breast cancer for (A.) rs619373 and (B.) rs184577 genotypes. (TIF)

**Table S1** Quality control filtering steps for BRCA2 mutation carriers and SNPs on the COGs array. (DOC)

**Table S2** Description of breast cancer affected and unaffected BRCA2 carriers included in the final analysis of the COGs array SNPs. (DOC)

**Table S3** Breast cancer hazards ratios (HR) and 95% confidence intervals (CI) for all SNPs with P<10⁻⁵ in a 500 Mb region around rs9348512 on 6p24 among BRCA2 mutation carriers. (DOC)

**Table S4** Associations with SNPs at 6p24, FGF13 and 2p22 and breast and ovarian cancer risk using a competing risk analysis model. (DOC)

### Acknowledgments

**iCOGS:** We acknowledge the contributions of Kyriaki Michailidou, Jonathan Tyrer, and Ali Amin Al Olama to the iCOGS genotyping quality control process.

**Consortium of Modifiers of BRCA1/2 Associations (CIMBA):** The authors would like to acknowledge the contribution of the staff of the genotyping unit under the supervision of Dr. Sylvie LaBoissière as well as Frédéric Robidoux from the McGill University and Génome Québec Innovation Centre.

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**Breast Cancer Association Consortium (BCAC):** We thank all the individuals who took part in these studies and all the researchers,
Clinicians, technicians, and administrators who have enabled this work to be carried out.

Amsterdam Breast Cancer Study (ABCs): We thank Annegien Broeks, Sten Cornelissen, Richard van Hien, Linde Braaf, Senno Verhoef, Laura van’t Veer, Emiel Rutgers, Ellen van der Schoot, and Femke Atuma.

Bavarian Breast Cancer Cases and Controls (BBCGs): We thank Lothar Haeberle, Sonja Oeser, Silke Lanfruth, and Reiner Strick.

British Breast Study (BBS): We thank Eileen Williams, Elaine Ryder-Mills, and Kara Sargus.

Breast Cancer Registry (BCFR): Samples from the NC-BCFR were processed and distributed by the Coriell Institute for Medical Research. We wish to thank members and participants in the Breast Cancer Registry for their contributions to the study. The ABCFs would like to also thank Maggie Angelakos, Judi Maskill, and Gillian Dilley. The content of this manuscript does not necessarily reflect the views or policies of the National Cancer Institute or any of the collaborating centers in the BCFR, nor does mention of trade names, commercial products, or organizations imply endorsement by the U.S. Government or the BCFR.


Breast Cancer in Galway Genetic Study (BIGGS): We thank Niall McInerney, Gabrielle Colleran, Andrew Rowan, and Angela Jones.

BRCA-gene mutations and breast cancer in South African women (BMBSA): We wish to thank the families who contribute to the BMBSA study.

Beckman Research Institute of the City of Hope (BRICOH): We thank Greg Wilhote, Yuan Chun Ding, Linda Steele, and Marie Pinto for their work in participant enrollment and biospecimen and data management.

Breast Cancer Study of the University Clinic Heidelberg (BSUCH): We thank Peter Bugert, Medical Faculty Mannheim.

Copenhagen General Population Study (CGPS): We appreciate the staff and participants of the Copenhagen General Population Study. For the excellent technical assistance, we thank Dorthe Uldall Andersen, Maria Birna Arnadottir, Anne Bank, and Dorte Kjeldga˚rd Hansen.

Spanish National Cancer Centre (CNIO): We wish to thank Alicia Barroso, Rosario Alonso, and Guillermo Pita for their assistance.

Spanish National Cancer Centre Breast Cancer Study (CNIO-BCS): We thank Charo Alonso, Guillermo Pita, Nuria Alvarez, Daniel Herrero, Primitiva Menéndez, José Ignacio Arias Pérez, Pilar Zamora, the Human Genotyping-CEGEN Unit (CNIO).

Genetic Study of BRCA1 & BRCA2 Mutation Carriers (EMBRACE): Additional cases were recruited in the context of the VERDI study. We thank Hartwig Ziegler, Sarah Durr, and Volker Herrmann.

German Consortium of Hereditary Breast and Ovarian Cancer (GC-HBOC): We are very thankful to all family members who participated in this study; Wolfram Heirich, Center Leipzig, and Dieter Schäfer, Center Frankfurt, for providing DNA samples; and Juliane Kohler for excellent technical assistance; as well as Heide Hellebrand, Sabine Eugster, and GG-HBOC.

Genetic Modifiers of Cancer Risk in BRCA1/2 Mutation Carriers (GEMO): National Cancer Genetics Network «UNICANCER Genetic Groups», France. We wish to thank all the GEMO collaborating groups for their contribution to this study. GEMO Collaborating Centers are: Coordinating Centers, Unité Mixte de Généétique Constitutionnelle des Cancers Fréquents, Hospices Civils de Lyon - Centre Léon Bérard, & Equipe «Génomique du cancer du sein», Centre de Recherche en Cancérologie, C. Seymour, O. Similokou, Sylvie Mazoyer, Francesca Damiola, Laura Barjhoux, Carole Verny-Pierre, Sophie Giraud, Mélanie Léonie; and Service de Généétique Oncologique, Institut Curie, Paris: Dominique Stoppa-Lyonnet, Marion Gauthier-Villars, Bruno Buecher, Claude Houdayer, Virginie Moncoutier, Muriel Belotti, Carole Tirapo, Antoine de Pauw. Institut Gustave Roussy, Villejuif: Brigitte Bressac-de-
Paillerets, Olivier Caron, Centre Jean Perrin, Clermont-Ferrand; Yves-Jean Bignon, Nancy Uiharhammer, Centre Léon Bérard, Lyon; Christine Lasset, Valérie Bonadona, Sandrine Handallou, Centre François Baclesse, Caen; Agnès Hardouin, Pascale Berthet, Institut Paoli Calmettes, Marseille; Hagay Sobol, Violaine Bourdon, Tetsuro Noguchi, Audrey Remenieras, François Esinger, CHU Arnaud-de-Villeneuve, Montpellier; Isabelle Goupier, Pascal Pujol, Centre Oscar Lambret, Lille; Jean-Philippe Peyrat, Joëlle Fournier, François Révillou, Philippe Vermin, Claude Ast and staff of the Family Cancer Clinic, Centre Léon Bérard, St. Cloud; Etienne Rouleau, Rosette Leducque, Liliane Demange, Catherine Nougues, Centre Paul Strauss, Strasbourg; Danièle Muller, Jean-Pierre Fricker, Institut Bergonié, Bordeaux; Emmanuelle Barouk-Simonet, Françoise Bonnet, Virginie Bubien, Nicolas Sevetin, Michel Longy. Institut Claudius Regaud, Toulouse; Christine Toutas, Rosine Guimbaud, Laurence Gladieff, Viviane Feillé, CHU Grenoble; Dominique Leroux, Hélène Dreyfus, Christine Rebschlag, Magalie Peysselon, CHU Dijon; Fanny Coron, Laurence Grivé, CHU St-Etiene; Fabienne Prieur, Marine Lebrun, Caroline Kientz. Hôtel Dieu Centre Hospitalier, Chambéry; Sandra Fert Ferrer, Centre Antoine Lacassagne, Nice; Marc Frémy, CHU Limoges; Laurence Vénat-Bouvet. CHU Nancy; Capucine Delmatte, CHU Bretonneau, Tours; Isabelle Mortemousque. Groupe Hospitalier Pitie-Salpêtrière, Paris; Florence Coulet, Chrystelle Colas, Florent Solain, CHU Vandoeuvre-les-Nancy; Johanna Sokolowska, Myriam Bronner, Creighton University, Omaha, USA; Henry T Lynch, Carrie L Snyder.

Gene Environment Interaction and Breast Cancer in Germany (GENICA): The GENICA network: Dr. Margarete Fischer-Bosch-Institute of Clinical Pharmacology, Stuttgart, and University of Tubingen, Germany; [C], Hiltrud Brauch, Department of Internal Medicine, Evangelische Krankenhaus Bonn, Germany [Yon-Dschun Ko, Christian Baisch], Institute of Pathology, University of Bonn, Bonn, Germany [Hand-Peter Fischer], Molecular Genetics of Breast Cancer, Deutsches Krebsforschungszentrum (DKFZ), Heidelberg, Germany [UH]; and Institute for Prevention and Occupational Medicine of the German Social Accident Insurance (IPA), Bochum, Germany [Thomas Bruening, Beate Pesch, Sylvia Rabstein, Anne Spichenker, VH].

Hospital Clinico San Carlos (HCSC): We acknowledge Alicia Tosar for her technical assistance.

Helsinki Breast Cancer Study (HEBCS): HEBCS would like to thank Drs. Kristiina Aittomäki, Carl Blomqvist and Kirsimari Aaltonen, for their contributions to this resource, and the many families who contribute to iConFab.

Interdisciplinary HEalth Research Internal Team Breast Cancer Susceptibility (INHERIT): We would like to thank Dr. Martine Dumont and Martine Tranchant for sample management and skillful technical assistance.

Kuopio Breast Cancer Project (KBCP): We thank Eija Myöhänen and Helena Kemilainen.

Kathleen Cunningham Consortium for Research into Familial Breast Cancer [kConFab/AOCS]: We thank Heather Thorne, Eveline Niedermayr, all the iConFab research nurses and staff, the heads and staff of the Family Cancer Clinics, and the Clinical Follow Up Study for their contributions to this resource, and the many families who contribute to iConFab.

Leuven Multidisciplinary Breast Centre (LMBG): We thank Giliam Peuteman, Dominiek Smeets, Thomas Van Brussel, and Kathleen Corthouts.

Mammary Carcinoma Risk Factor Investigation (MARIE): We thank Dieter Flech-Jayus, Rebecca Hein, Stefan Nickel, Mulabebit Gelin, Sabine Behrens, and Ursula Elber.

Milan Breast Cancer Study Group (MBCSG): We thank Daniela Zaffaroni of the Fondazione Istituto Nazionale Tumori, Milan, Italy and the personnel of the CGT laboratory at IFOM-IEO Campus, Milan, Italy.

Montreal Gene-Environment Breast Cancer Study (MTLGBCS): We thank Marine Tranchant (Cancer Genomics Laboratory, CRCHUQ, Montreal), Ivanne Turgeon, and Bea Hegny (McGill University Health Center, Royal Victoria Hospital; McGill University) for DNA extraction, sample management, and skillful technical assistance.

General Hospital Vienna (MUV): We thank the study staff and participants.

National Israeli Cancer Control Center (NICCC): We wish to thank the NICCC National Familial Cancer Consultation Service team led by Sara Dishon, the lab team led by Dr. Flavio Lejbkowicz, and the research field operations team led by Dr. Mina Pinchev.

Oulu Breast Cancer Study (OBCS): We thank Katri Pykal, Arja Jukkola-Vuorinen, Mervi Grip, Salla Kauppila, Meeri Otsukka, and Kari Mononen.

Ontario Cancer Genetics Network (OCGN): We thank the study staff and participants.

University Medical Centre Breast Cancer Study (ORIGO): We thank E. Krol-Warmerdam, and J. Blom for patient accrual, administering questionnaires, and managing clinical information. The LUMC survival data were retrieved from the Leiden hospital-based cancer registry system (ONCDOC) with the help of Dr. J. Molenaar.

The Ohio State University Comprehensive Cancer Center (OSUCCG): Kevin Sweet, Caroline Craven, and Michelle O’Conor were instrumental in accrual of study participants, ascertainment of medical records, and database management. Samples were processed by the OSU Human Genomics Sample Bank.

Odense University Hospital (OUH): We thank the study staff and participants.

Università di Pisa (PBCS): We thank the study staff and participants.

The U.S. National Cancer Institute Polish Breast Cancer Study (SWE-BRCA): We thank the study collaborators: Drs. Louise Brinton, Mark Sherman, Stephen Chanocek, Neolina Szeszenia-Dabrowska, Beata Peplonska, and Witold Zatonksi, as well as Pui Chio and Michael Stagner, for their data management support.

Rotterdam Breast Cancer Study (RBCS): We thank Petra Bos, Jannet Blom, Ellen Crepin, Elisabeth Huijskens, Annette Heemskerk, and the Erasmus MC Family Cancer Clinic.

Sheffield Breast Cancer Study (SBCS): We thank Sue Higham, Helen Cramp, and Dan Crockford.

South East Asian Breast Cancer Association Study (SEABASS): We would like to thank Yap Cheng Har, Nur Aishah Mohd Taib, Phua Sze Yee, Norhashimah Hassan, and all the research nurses, research assistants, and doctors involved in the MyBeCa Study for assistance in patient recruitment, data collection, and sample preparation. In addition, we thank Philip Isu, Sng Jen-Hwei, and Sharifah Nor Akmal for contributing samples from the Singapore Breast Cancer Study and the HUKM-HKL Study respectively.

Study of Epidemiology and Risk Factors in Cancer Heredity (SEARCH): We thank the SEARCH and EPIC teams.

Sheba Medical Centre (SMC): SMC team wishes to acknowledge the assistance of the Meirav Comprehensive breast cancer center at the Sheba Medical Center for assistance in this study.

Swedish Breast Cancer Study (SWE-BRCA): Swedish scientists participating as SWE-BRCA collaborators are: from Lund University and University Hospital: Åke Borg, Håkan Olsson, Helena Jernström, Karin Henriksson, Katja Harbst, Maria Soller, Niklas Loman, Ulf Kristoffersson; from Gothenburg Sahlgrenska University Hospital: Anna Ofvelhorn, Margreta Nordling, Per Karlsson, Zakaria Einbeigi; from Stockholm and Uppsala University Hospitals: Charlotte Nilsson, Staffan Arheden, Maria Soller, Jörgen Bergstrom, Edvard Elomaa, and Tomas Gyllensten; from Umeå University Hospital: Katrin Dyrlund, Carolin Ljungroth, and Staffan Arheden; from Karolinska University Hospital: Tomas Johansson, Per Karlsson, and Pia Svedmyr; from Sahlgrenska University Hospital, Sweden: Johanna Rantala; from Uppsala University: Helena Cronqvist, Gro Ström, and Carin Andersson; and from University Hospital of Lund, Sweden: Lennart Nilsson, Anna Lagerstroem, and Magnus Gyllensten.

The University of Chicago Center for Clinical Cancer Genetics and Global Health (UCHICAGO): We wish to thank

GWAS of BRCA2 Mutation Carriers
Cecilia Zvosec, Qun Niu, physicians, genetic counselors, research nurses and staff of the Cancer Risk Clinic for their contributions to this resource, and the many families who contribute to our program.

University of California Los Angeles (UCLA): We thank Joyce Selden MSGC and Lorna Kwan MPH for assembling the data for this study.

University of California San Francisco (UCSF): We would like to thank Ms. Salmina Chan for her data management and the following genetic counselors for participant recruitment: Beth Crawford, Nicola Stewart, Julie Mak, and Kate Lamvik.

United Kingdom Breakthrough Generations Study (UKBGs): We thank Breakthrough Breast Cancer and the Institute of Cancer Research for support of the Breakthrough Generations Study, and the study participants, study staff, and the doctors, nurses, and other health care providers and health information sources who have contributed to the study.

United Kingdom Familial Ovarian Cancer Registries (UKFOCR): We thank Simon Gaylor, Susan Ramus, Carole Pye, Patricia Harrington, and Eva Wozniak for their contributions towards the UKFOCR.

Victorian Familial Cancer Trials Group (VFCTG): We acknowledge Geoffrey Lindeman, Marion Harris, Martin Delatycki of the Victorian Familial Cancer Trials Group. We thank Sarah Sawyer and Rebecca Driessen for assembling this data and Ella Thompson for performing all DNA amplification.

Author Contributions


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