PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS

A full list of authors and affiliations appears at the end of the article.

Abstract

Background—The rarity of mutations in PALB2, CHEK2 and ATM make it difficult to estimate precisely associated cancer risks. Population-based family studies have provided evidence that at least some of these mutations are associated with breast cancer risk as high as those associated with rare BRCA2 mutations. We aimed to estimate the relative risks associated with specific rare variants in PALB2, CHEK2 and ATM via a multicentre case-control study.

Methods—We genotyped 10 rare mutations using the custom iCOGS array: PALB2 c.1592delT, c.2816T>G and c.3113G>A, CHEK2 c.349A>G, c.538C>T, c.715G>A, c.1036C>T, c.1312G>T, and c.1343T>G and ATM c.7271T>G. We assessed associations with breast cancer risk (42 671 cases and 42 164 controls), as well as prostate (22 301 cases and 22 320 controls) and ovarian (14 542 cases and 23 491 controls) cancer risk, for each variant.

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Competing interests None declared.

Data sharing statement This would vary for each study—each study is listed in the supplemental material.
Results—For European women, strong evidence of association with breast cancer risk was observed for PALB2 c.1592delT OR 3.44 (95% CI 1.39 to 8.52, \( p=7.1 \times 10^{-5} \)), PALB2 c.3113G>A OR 4.21 (95% CI 1.84 to 9.60, \( p=6.9 \times 10^{-8} \)) and ATM c.7271T>G OR 11.0 (95% CI 1.42 to 85.7, \( p=0.0012 \)). We also found evidence of association with breast cancer risk for three variants in CHEK2, c.349A>G OR 2.26 (95% CI 1.29 to 3.95), c.1036C>T OR 5.06 (95% CI 1.09 to 23.5) and c.538C>T OR 1.33 (95% CI 1.05 to 1.67) (\( p \leq 0.017 \)). Evidence for prostate cancer risk was observed for CHEK2 c.1343T>G OR 3.03 (95% CI 1.53 to 6.03, \( p=0.0006 \)) for African men and CHEK2 c.1312G>T OR 2.21 (95% CI 1.06 to 4.63, \( p=0.030 \)) for European men. No evidence of association with ovarian cancer was found for any of these variants.

Conclusions—This report adds to accumulating evidence that at least some variants in these genes are associated with an increased risk of breast cancer that is clinically important.

INTRODUCTION

The rapid introduction of massive parallel sequencing (MPS) into clinical genetics services is enabling the screening of multiple breast cancer susceptibility genes in one assay at reduced cost for women who are at increased risk of breast (and other) cancer. These gene panels now typically include the so-called ‘moderate-risk’ breast cancer susceptibility genes, including PALB2, CHEK2 and ATM.\(^1\)–\(^3\) However, mutations in these genes are individually extremely rare and limited data are available with which to accurately estimate the risk of cancer associated with them.

Estimation of the age-specific cumulative risk (penetrance) of breast cancer associated with specific mutations in these three genes has been limited to those that have been observed more frequently, such as PALB2 c.1592delT (a Finnish founder mutation), PALB2 c.3113G>A and ATM c.7271T>G. These mutations have been estimated to be associated with a 40% (95% CI 17% to 77%), 91% (95% CI 44% to 100%) and 52% (95% CI 28% to 80%) cumulative risk of breast cancer to the age of 70 years, respectively.\(^4\)–\(^7\) These findings, based on segregation analyses in families of population-based case series, indicate that at least some mutations in these ‘moderate-risk’ genes are associated with a breast cancer risk comparable to that of the average pathogenic mutation in BRCA2: 45% (95% CI 31% to 56%).\(^8\) However, such estimates are imprecise and, moreover, may be confounded by modifying genetic variants or other familial risk factors.

Case-control studies provide an alternative approach to estimating cancer risks associated with specific variants. This design can estimate the relative risk directly, without making assumptions about the modifying effects of other risk factors. However, because these variants are rare, such studies need to be extremely large to provide precise estimates.

The clearest evidence for association, and the most precise breast cancer risk estimates, for rare variants in PALB2, CHEK2 and ATM relate to protein truncating and splice-junction variants.\(^9\)–\(^10\) However, studies based on mutation screening in case-control studies, combined with stratification of variants by their evolutionary likelihood suggest that at least some evolutionarily unlikely missense substitutions are associated with a similar risk to those conferred by truncating mutations.\(^11\)–\(^13\) For example, Tavtigian et al\(^12\) estimated an OR of 2.85 (95% CI 0.83 to 4.86) for evolutionarily unlikely missense substitutions in the 3′ third
of ATM, which is comparable to that for truncating variants. Specifically, ATM c.7271C>G has been associated with a more substantial breast cancer risk in several studies.\textsuperscript{7,13} Le Calvez-Kelm et al.\textsuperscript{11} estimated that the ORs associated with rare mutations in CHEK2 from similarly designed studies were 6.18 (95% CI 1.76 to 21.8) for rare protein-truncating and splice-junction variants and 8.75 (95% CI 1.06 to 72.2) for evolutionarily unlikely missense substitutions.\textsuperscript{11}

It is plausible that monoallelic mutations in PALB2, CHEK2 and ATM could be associated with increased risk of cancers other than breast cancer, as has been observed for BRCA1 and BRCA2 and both ovarian and prostate cancers.\textsuperscript{14–17} However, with the exception of pancreatic cancer in PALB2 carriers, there is little evidence to support or refute the existence of such associations, although a few individually striking pedigrees have been observed.\textsuperscript{4,8,18–20}

In this study we selected rare genetic variants on the basis that they had been observed in breast cancer candidate gene case-control screening projects involving PALB2, CHEK2 or ATM. These included three rare variants in PALB2: the protein truncating variants c.1592delT (p.Leu531Cysfs)\textsuperscript{4} and c.3113 G>A (p.Trp1038*)\textsuperscript{6} and the missense variant c.2816T>G, (p. Leu939Trp), six rare missense variants in CHEK2: c.349A>G (p.Arg117Gly) and c.1036C>T (p.Arg346Cys) predicted to be deleterious on the basis of evolutionary conservation,\textsuperscript{11} c.538C>T (p.Arg180Cys), c.715G>A (p.Glu239Lys), c.1312G>T (p.Asp438Tyr) and c.1343T>G (p.Ile448Ser) and ATM c.7271T>G (p.Val2424Gly).\textsuperscript{7} We assessed the association of these variants with breast, ovarian and prostate risk by case-control analyses in three large consortia participating in the Collaborative Oncological Gene-environment Study.\textsuperscript{21,22}

**METHODS**

**Participants**

Participants were drawn from studies participating in three consortia as follows:

The Breast Cancer Association Consortium (BCAC), involving a total of 48 studies: 37 of women from populations with predominantly European ancestry (42 671 cases and 42 164 controls), 9 of Asian women (5795 cases and 6624 controls) and 2 of African-American women (1046 cases and 932 controls). All cases had invasive breast cancer. The majority of studies were population-based or hospital-based case-control studies, but some studies of European women oversampled cases with a family history or with bilateral disease (see online supplementary table S1). Overall, 79% of BCAC cases with known Estrogen Receptor (ER) status (23% missing) are ER-positive. The proportion of cases selected by family history that are ER-positive is 78% (38% missing).

The Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome (PRACTICAL) involving a total of 26 studies: 25 included men with European ancestry (22 301 cases and 22 320 controls) and 3 included African-American men (623 cases and 569 controls). The majority of studies were population-based or hospital-based case-control studies (see online supplementary table S2).
The Ovarian Cancer Association Consortium (OCAC), involving a total of 46 studies. Some studies were case-only and their data were combined with case-control studies from the same geographical region (leaving 36 study groupings). Of these groupings, 33 included women from populations with predominantly European ancestry (16 287 cases (14 542 with invasive disease) and 23 491 controls), 25 included Asian women (813 cases (720 with invasive disease) and 1574 controls), 17 included African-American women (186 cases (150 with invasive disease) and 200 controls) and 29 included women of other ethnic origin (893 cases (709 with invasive disease) and 864 controls). The majority of studies were population-based or hospital-based case-control studies (see online supplementary table S3).

Details regarding sample quality control have been published previously. All study participants gave informed consent and all studies were approved by the corresponding local ethics committees (see online supplementary tables S1–S3).

**Variant selection**

We selected for genotyping 13 rare mutations that had been observed in population-based case-control mutation screening studies. These variants were *PALB2* (c.1592delT, p. Leu531Cysfs; c.2323C>T p.Gln775*; c.2816T>G, p. Leu939Trp; c.3113G>A, p.Trp1038*, c.3116delA, p. Asn1039Ilefs; c.3549C>G, p.Tyr1183*), *CHEK2* (c.349A>G, p.Arg117Gly; c.538C>T, p.Arg180Cys; c.715G>A p.Glu239Lys; c.1036C>T, p.Arg346Cys; c.1312G>T, p.Asp438Tyr; c.1343T>G, p.Ile448Ser) and *ATM* (c.7271T>G, p.Val2424Gly) see table 1. A DNA sample carrying each of these variants was included in a plate of control DNAs that was distributed to each genotyping centre to assist with quality control and genotype calling.

**Genotyping**

Three *PALB2* variants c.2323C>T (p.Gln775*), c.3116delA (p.Asn1039Ilefs) and c.3549C>G (p.Tyr1183*) were unable to be designed for measurement on the custom Illumina iSelect genotyping array and were not considered further (table 1). Genotyping was conducted using a custom Illumina Infinium array (iCOGS) in four centres, as part of a multiconsortia collaboration as described previously. Genotypes were called using Illumina’s proprietary GenCall algorithm and then, for the data generated from the rare variant probes, manually confirmed with reference to the positive control sample. Two per cent of samples were provided in duplicate by all studies and 270 HapMap2 samples were genotyped in all four genotyping centres. Subjects with an overall call rate <95% were excluded. Plates with call rates <90% were excluded on a variant-by-variant basis. Cluster plots generated for all of the 10 rare variants were manually checked to confirm automated calls (see online supplementary figure S1).

**Statistical methods**

The association of each variant with breast, prostate and ovarian cancer risk was assessed using unconditional logistic regression to estimate ORs for carriers versus non-carriers, adjusting for study (categorical). p Values were determined by the likelihood ratio test comparing models with and without carrier status as a covariate. We also applied conditional logistic regression, defining risk sets by study, and found that this made no difference to the
OR estimates, CIs or p values to two significant figures; since model convergence was a problem for this latter regression analysis, all subsequent analyses were based on unconditional logistic regression. For the main analyses of breast cancer risk in European women, we also included as covariates the first six principal components, together with a seventh component specific to one study (Leuven Multidisciplinary Breast Centre (LMBC)) for which there was substantial inflation not accounted for by the components derived from the analysis of all studies. Addition of further principal components did not reduce inflation further. Data from all breast cancer studies were included to assess statistical significance. Data from cases selected for inclusion based on personal or family history of breast cancer were excluded in order to obtain unbiased OR estimates for the general population of white European women (leaving 37 039 cases and 38 260 controls from 32 studies). Multiple testing was adjusted for using the Benjamini-Hochberg procedure to control the false discovery rate, with a significance threshold of 0.05. Reported p values are unadjusted unless otherwise stated. Reported CIs are all nominal. We included two race-specific principal components in each of the main breast cancer analyses of Asian and African-American women. Similar analyses were conducted using the data from PRACTICAL and OCAC, consistent with those used previously. All analyses were carried out using Stata: Release V.10 (StataCorp, 2008).

RESULTS

PALB2

In BCAC, PALB2 c.1592delT (Leu531Cysfs) was only observed in 35 cases and 6 controls, all from four studies from Sweden and Finland (Helsinki Breast Cancer Study (HEBCS), Kuopio Breast Cancer Project (KBCP), Oulu Breast Cancer Study (OBCS) and Karolinska Mammography Project for Risk Prediction Breast Cancer (pKARMA); see online supplementary table S1), giving strong evidence of association with breast cancer risk (p=7.1x10^{-5}); the OR estimate was 4.52 (95% CI 1.90 to 10.8) based on all studies and 3.44 (95% CI 1.39 to 8.52) based on unselected cases and controls (table 2). We also found evidence of heterogeneity by ER status (p=0.0023), the association being stronger for ER-negative disease (OR 6.49 (95% CI 2.17 to 19.4) versus 2.24 (95% CI 1.05 to 7.24) for ER-positive disease).

PALB2 c.3113G>A (p.Trp1038*) was identified in 44 cases and 8 controls from nine BCAC studies. Only one carrier of the variant was of non-European origin. Strong evidence of association with breast cancer risk was observed (p=6.9x10^{-8}), with an estimated OR of 5.93 (95% CI 2.77 to 12.7) based on all studies and 4.21 (95% CI 1.85 to 9.61) based on unselected cases and controls. There was no evidence of a differential association by ER status (p=0.15).

Based on unselected cases, the estimated OR associated with carrying either of these PALB2 variants (c.1592delT or c.3113G>A) was 3.85 (95% CI 2.09 to 7.09).

PALB2 c.2816T>G (p.Leu939Trp) was identified in 150 cases and 145 controls and there was no evidence of association with risk of breast cancer. There was no evidence of
association with risk of prostate or ovarian cancer for any of the three PALB2 variants (see tables 3 and 4).

CHEK2

CHEK2 c.349A>G (p.Arg117Gly) was identified in 44 cases and 18 controls in studies participating in BCAC; all of these women were of European origin. We found evidence of association with breast cancer (p=0.003), with little change in the OR after excluding selected cases (OR 2.03 (95% CI 1.10 to 3.73)).

CHEK2 c.538C>T (p.Arg180Cys) was identified in 158 breast cancer cases and 142 controls in studies of white Europeans. Evidence of association with breast cancer risk (p=0.016) was observed, with an unbiased OR estimate of 1.34 (95% CI 1.06 to 1.70). A consistent OR estimate was observed for Asian women, based on 45 case and 45 control carriers (OR 1.16 (95% CI 0.75 to 1.76)).

CHEK2 c.715G>A (p.Glu239Lys) mutations were identified in 15 cases and 9 controls, all European women participating in BCAC and no evidence of association with risk of breast cancer was observed (p=0.21).

CHEK2 c.1036C>T (p.Arg346Cys) was identified in nine cases from seven studies and two controls from two different studies in BCAC (neither control carrier was from a study that had case carriers), all of European origin. We found evidence of association with breast cancer risk (p=0.017) with reduced OR estimate of 3.39 (95% CI 0.68 to 16.9) after excluding selected cases.

None of the above four CHEK2 variants (CHEK2 c.349A>G (p.Arg117Gly); c.538C>T (p.Arg180Cys); c.715G>A (p.Glu239Lys) and c.1036C>T (p.Arg346Cys)) were found to be associated with an increased risk of prostate or ovarian cancer (tables 3 and 4). CHEK2 variant c.1312G>T (p.Asp438Tyr) was not associated with risk of breast cancer for European women (p=0.91). Variant c.1343T>G (p.Ile448Ser) was not observed in any breast cancer cases of European or Asian origin. It was detected in 48 cases and 29 controls of African origin, giving weak evidence of association (OR 1.52 (95% CI 0.95 to 2.43, p=0.083)). CHEK2 c.1312G>T (p.Asp438Tyr) was identified in 23 cases and 11 controls from PRACTICAL, all European, providing evidence of association with prostate cancer risk (OR 2.21 (95% CI 1.06 to 4.63, p=0.030)). CHEK2 c.1343T>G (p.Ile448Ser) was observed in 35 cases and 11 controls, all African, participating in PRACTICAL and was also associated with an increased risk of prostate cancer (OR 3.03 (95% CI 1.53 to 6.03, p=0.00059)). There was no evidence that these CHEK2 variants were associated with risk of ovarian cancer (table 4).

ATM

ATM c.7271T>G (p.Val2424Gly) was identified in 12 cases and 1 control in studies participating in BCAC, all of European origin, giving evidence of association with breast cancer risk (p=0.0012). The OR estimate based on unselected studies was 11.0 (95% CI 1.42 to 85.7). There was no evidence of association of this variant with prostate or ovarian cancer risk (see tables 3 and 4).
The present report adds to an accumulating body of evidence that at least some rare variants in so-called ‘moderate-risk’ genes are associated with an increased risk of breast cancer that is of clinical relevance.

These findings are presented at a time when detailed information about variants in these genes is becoming more readily available via the translation of diagnostic genetic testing from Sanger sequencing-based testing platforms to MPS platforms that test panels of genes in single assays. The vast majority of information about PALB2, CHEK2 and ATM, variants generated from these new testing platforms is not being used in clinical genetics services due to lack of reliable estimates of the cancer risk associated with individual variants, or groups of variants, in each gene. Previous analyses have been largely based on selected families, relying on data on the segregation of the variant. The present study is by far the largest to take a case-control approach. Consistent with previous reports, PALB2 c.3113G>A (p.Trp1038*), PALB2 c.1592delT (p.Leu531Cysfs) and ATM c.7271T>G (p.Val2424Gly) were found to be associated with substantially increased risk of breast cancer all with associated relative risk estimates of 3.44 or greater.

We found no evidence of association with breast cancer for PALB2 c.2816T>G (p.Leu939Trp), with an upper 95% confidence limit excluding an OR >1.5 which is notable given the Align-Grantham Variation Granthan Deviation (Align-GVGD) score and the observed impact on protein function. The estimate for ATM c.7271T>G (p.Val2424Gly) was also consistent with that found by segregation analysis.

The substantial increased risk of breast cancer associated with ATM c.7271T>G (p.Val2424Gly) could be due to the reduction in kinase activity (with near-normal protein levels) observed for ATM p.Val2424Gly, thus this variant is likely to be acting as a dominant negative mutation.

In contrast, we found no evidence of an association with risk of prostate or ovarian cancer with any of these three variants: however, the confidence limits were wide; based on the upper 95% confidence limit we could exclude an OR of >1.4 for prostate cancer for the loss-of-function PALB2 c.3113G>A and 1.9 for c.1592delT and c.3113G>A combined.

We analysed six rare missense variants in CHEK2. Two of these (CHEK2 c.349A>G (p.Arg117Gly; rs28909982) and c.1036C>T (p.Arg346Cys)) had evidence of a significant impact on the protein based on in silico prediction. We proposed these variants for inclusion in the iCOGS design as they had been identified in 3/1242 cases and 1/1089 controls and 3/1242 cases and 0/1089 controls, respectively, in a population-based case-control mutation screening study of CHEK2. In that study, Le Calvez-Kelm et al, estimated an OR of 8.75 (95% CI 1.06 to 72.2) for variants with an Align-GVGD score C65 (based on nine cases and one control). The current analysis provides confirmatory evidence of this association in a much larger sample (OR 2.18 (95% CI 1.23 to 3.85)) including 40 unselected case and 18 control carriers. The evidence that CHEK2 is a breast cancer susceptibility gene is largely
based on studies of protein truncating variants, in particular CHEK2 1100delC.\textsuperscript{33} Reports of the association of the missense variant I157T, (C15) and breast cancer risk have been conflicting but a large meta-analysis involving 15,985 breast cancer cases and 18,609 controls estimated a modest OR of 1.58 (95% CI 1.42 to 1.75).\textsuperscript{34} We also found evidence (p=0.015) of an association for c.538C>T (Align-GVGD C25); OR 1.34 (95% CI 1.06 to 1.70), a risk comparable to I157T.

The p values reported above have not been adjusted for multiple testing. This was not considered appropriate for the associations with breast cancer risk of PALB2 c.1592delT, c.3113G>A and ATM c.7271T>G because these associations had previously been reported; our aim was to more precisely estimate the associated relative risks. All three associations with breast cancer risk reported for CHEK2 variants remained statistically significant after adjusting for the other tests conducted in relation to breast cancer risk, but not after correcting for all tests for all cancers. Nevertheless, the findings for CHEK2 c.349A>G and c.1036C>T confirmed those reported previously, although collectively. The association observed with CHEK2 c.538C>T requires independent replication.

Do this approach and new data have an impact on clinical recommendations for women and families carrying these rare genetic variants? Although age-specific cumulate risks for cancer are more informative for genetic counselling and clinical management of carriers, our study provides information that is relevant to clinical recommendations. As discussed in Easton \textit{et al.},\textsuperscript{35} a relative risk of 4 will place a woman in a ‘high-risk’ category (in the absence of any other risk factor) and a relative risk between 2 and 4 will place a woman in this category if other risk factors are present. Thus, several of the variants included in this report (PALB2 c.1592delT; c.3113G>A ATM c.7271T>G) would place the carrier in a high-risk group, especially if other risk factors, such as a family history, are present. The high level of breast cancer risk associated with PALB2 c.1592delT and c.3113G>A reported here is consistent with the penetrance estimate reported for a group of loss-of-function mutations in PALB2\textsuperscript{9} and has an advantage in terms of clinical utility that the estimates in this study have been made at a mutation-specific level. Therefore, this work provides important information for risk reduction recommendations (such as prophylactic mastectomy and potentially salpingo-oophorectomy) for carriers of these variants. However, further prospective research is required to characterise these risks and to understand the potential of other risk-reducing strategies such as salpingo-oophorectomy and chemoprevention.

The consistency of the relative risk estimates with those derived through family based studies supports the hypothesis that these variants combine multiplicatively with other genetic loci and familial risk factors; this information is critical for deriving comprehensive risk models. Even with very large sample sizes such as those studied here, however, it is still only possible to derive individual risk estimates for a limited set of variants, and even for these variants the estimates are still imprecise. This internationally collaborative approach also has limited capacity to improve risk estimates for rare variants that are only observed in specific populations. Inevitably, therefore, risk models will depend on combining data across multiple variants, using improved in silico predictions and potentially biochemical/functional evidence to synthesise these estimates efficiently. It will also be necessary
develop counselling and patient management strategies that can accommodate a multifactorial approach to variant classification.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Authors


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Affiliations

1Genetic Epidemiology Laboratory, Department of Pathology, The University of Melbourne, Melbourne, Australia
2Huntsman Cancer Institute, Salt Lake City, UT, USA
3Laboratory of Cancer Genetics and Tumor Biology, Cancer and Translational Medicine Research Unit and Biocenter Oulu, University of Oulu, Nordlab Oulu, Oulu, Finland
4Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, MN, USA
5Department of Medical Genetics and National Institute for Health Research Cambridge Biomedical Research Centre, University of Cambridge, and the Department of Clinical Genetics, East Anglian Regional Genetics Service, Addenbrooke’s Hospital
6Program in Cancer Genetics, Department of Human Genetics and Oncology, Lady Davis Institute, and Research Institute, McGill University Health Centre, McGill University, Montreal, Canada
7Centre for Cancer Genetic Epidemiology, Department of Public Health and Primary Care, University of Cambridge, Strangeways Laboratory, Worts Causeway, Cambridge, UK
8Department of Genetics, University of Pretoria, South Africa
9Department of Obstetrics and Gynecology, University of Helsinki and Helsinki University Central Hospital, Helsinki, Finland
10Centre for Epidemiology and Biostatistics, School of Population and Global Health, The University of Melbourne, Melbourne, Australia
11Gynaecology Research Unit, Hannover Medical School, Hannover, Germany
12Center for Medical Genetics, Ghent University Hospital, De Pintelaan 185, 9000, Ghent, Belgium
13Department of Pathology and Human Oncology and Pathogenesis Program, Memorial Sloan-Kettering Cancer Center, New York, New York, USA
14Unit of Molecular Bases of Genetic Risk and Genetic Testing, Department of Preventive and Predictive Medicine, Fondazione IRCCS Istituto Nazionale dei Tumori (INT), Milan, Italy
15IFOM, the FIRC Institute of Molecular Oncology, Milan, Italy
16Netherlands Cancer Institute, Antoni van Leeuwenhoek hospital, Amsterdam, The Netherlands
17Australian Breast Cancer Tissue Bank, University of Sydney at the Westmead Institute for Medical Research, NSW, Australia
18Centre for Cancer Research, University of Sydney at the Westmead Institute for Medical Research, NSW, Australia
19Division of Molecular Medicine, Pathology North, Newcastle and University of Newcastle, NSW, Australia
20University Breast Center Fraunonia, Department of Gynecology and Obstetrics, University Hospital Erlangen, Friedrich-Alexander University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Erlangen, Germany
21David Geffen School of Medicine, Department of Medicine Division of Hematology and Oncology, University of California at Los Angeles, CA, USA
22Unit of Biostatistics, Department of Gynecology and Obstetrics, University Hospital Erlangen, Friedrich-Alexander University Erlangen-Nuremberg, Erlangen, Germany
23Institute of Human Genetics, University Hospital Erlangen, Friedrich Alexander University Erlangen-Nuremberg, Erlangen, Germany
24Non-communicable Disease Epidemiology Department,
London School of Hygiene and Tropical Medicine, London, UK

Breast Cancer Research Centre, The Institute of Cancer Research, London, UK

Division of Cancer Studies, NIHR Comprehensive Biomedical Research Centre, Guy’s & St. Thomas’ NHS Foundation Trust in partnership with King’s College London, London, UK

Wellcome Trust Centre for Human Genetics and Oxford Biomedical Research Centre, University of Oxford, UK and Oxford NIHR Biomedical Research Centre, Headington, OX3 7LE

Surgery, Lambe Institute for Translational Science, NUIGalway, University Hospital Galway, Galway, Ireland

Department of Obstetrics and Gynecology, University of Heidelberg, Heidelberg, Germany

National Center for Tumor Diseases, University of Heidelberg, Heidelberg, Germany

Molecular Epidemiology Group, German Cancer Research Center (DKFZ), Heidelberg, Germany

Inserm (National Institute of Health and Medical Research), CESP (Center for Research in Epidemiology and Population Health), U1018, Environmental Epidemiology of Cancer, Villejuif, France

University Paris-Sud, UMRS 1018, Villejuif, France

Copenhagen General Population Study, Herlev Hospital, Copenhagen University Hospital, University of Copenhagen, Copenhagen, Denmark

Department of Clinical Biochemistry, Herlev Hospital, Copenhagen University Hospital, University of Copenhagen, Copenhagen, Denmark

Department of Breast Surgery, Herlev Hospital, Copenhagen University Hospital, Copenhagen, Denmark

Human Genetics Group, Human Cancer Genetics Program, Spanish National Cancer Research Centre (CNIO), Madrid, Spain

Centro de Investigación en Red de Enfermedades Raras (CIBERER), Valencia, Spain

Servicio de Oncología Médica, Hospital Universitario La Paz, Madrid, Spain

Servicio de Cirugía General y Especialidades, Hospital Monte Naranco, Oviedo, Spain

Servicio de Anatomía Patológica, Hospital Monte Naranco, Oviedo, Spain

Department of Epidemiology, University of California Irvine, Irvine, California, USA

Beckman Research Institute of City of Hope, Duarte, California, USA

Department of Epidemiology, University of California Irvine, Irvine, California, USA

Cancer Prevention Institute of California, Fremont, California, USA

Division of Clinical Epidemiology and Aging Research, German Cancer Research Center (DKFZ), Heidelberg, Germany

Division of Preventive Oncology, German Cancer Research Center (DKFZ), Heidelberg, Germany

German Cancer Consortium (DKTK), German Cancer Research Center (DKFZ), Heidelberg, Germany

Saarland Cancer Registry, Saarbrücken, Germany

Dr. Margarete Fischer-Bosch-Institute of Clinical Pharmacology, Stuttgart

University of Tübingen, Tübingen, Germany

Institute for Prevention and Occupational Medicine of the German Social Accident Insurance, Institute of the Ruhr University, Bochum (IPA), Germany

Department of Internal Medicine, Evangelische Kliniken Bonn gGmbH, Johanniter Krankenhaus, Bonn, Germany

Department of Obstetrics and Gynecology, University of Helsinki and Helsinki University Central Hospital, Helsinki, Finland

Department of Clinical Genetics, Helsinki University Central Hospital, Helsinki, Finland

Department of Oncology, Helsinki University Central Hospital, Helsinki, Finland

Department of Radiation Oncology, Hannover Medical School, Hannover, Germany

N.N. Alexandrov Research Institute of Oncology and Medical
Radiology, Minsk, Belarus 59Department of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm, Sweden 60Department of Oncology – Pathology, Karolinska Institutet, Stockholm, Sweden 61School of Medicine, Institute of Clinical Medicine, Pathology and Forensic Medicine, and Cancer Center of Eastern Finland, University of Eastern Finland, Kuopio, Finland 62Imaging Center, Department of Clinical Pathology, Kuopio University Hospital, Kuopio, Finland 63School of Medicine, Institute of Clinical Medicine, Oncology, University of Eastern Finland, Kuopio, Finland 64Biocenter Kuopio, Cancer Center of Eastern Finland, Kuopio University Hospital, Kuopio, Finland 65QIMR Berghofer Medical Research Institute, Brisbane, Australia 66Research Department, Peter MacCallum Cancer Centre and The Sir Peter MacCallum Department of Oncology, University of Melbourne, Victoria, Australia 67Vesalius Research Center (VRC), VIB, Leuven, Belgium 68Laboratory for Translational Genetics, Department of Oncology, University of Leuven, Leuven, Belgium 69University Hospital Gasthuisberg, Leuven, Belgium 70Division of Cancer Epidemiology, German Cancer Research Center (DKFZ), Heidelberg, Germany 71Department of Cancer Epidemiology/Clinical Cancer Registry and Institute for Medical Biometrics and Epidemiology, University Clinic Hamburg-Eppendorf, Hamburg, Germany 72Department of Health Sciences Research, Mayo Clinic, Rochester, MN, USA 73Anatomical Pathology, The Alfred Hospital, Melbourne, Australia 74Department of Preventive Medicine, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA 75Epidemiology Program, Cancer Research Center, University of Hawaii, Honolulu, HI, USA 76Department of Genetics, Institute for Cancer Research, Oslo University Hospital, Radiumhospitalet, Oslo, Norway 77Faculty of Medicine (Faculty Division Ahus), University of Oslo (UiO), Norway 78Division of Epidemiology, Department of Medicine, Vanderbilt Epidemiology Center, Vanderbilt-Ingram Cancer Center, Vanderbilt University School of Medicine, Nashville, TN, USA 79Program in Molecular and Genetic Epidemiology, Harvard School of Public Health, Boston, MA, USA 80Department of Epidemiology, Harvard School of Public Health, Boston, MA, USA 81Channing Laboratory, Department of Medicine, Brigham and Women’s Hospital and Harvard Medical School, Boston, MA, USA 82Ontario Cancer Genetics Network, Lunenfeld-Tanenbaum Research Institute of Mount Sinai Hospital, Toronto, Ontario, Canada 83Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada 84Prosserman Centre for Health Research, Lunenfeld-Tanenbaum Research Institute of Mount Sinai Hospital, Toronto, Ontario, Canada 85Division of Epidemiology, Dalla Lana School of Public Health, University of Toronto, Toronto, Ontario, Canada 86Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada 87Laboratory Medicine Program, University Health Network, Toronto, Ontario; Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada 88Department of Oncology, Oulu University Hospital, University of Oulu, Oulu, Finland 89Department of Surgery, Oulu University Hospital, University of Oulu, Oulu, Finland 90Department of Pathology, Oulu University Hospital, University of Oulu, Oulu, Finland 91Department of Surgical Oncology, Leiden University Medical Center, 2300 RC Leiden, The Netherlands
Family Cancer Clinic, Department of Medical Oncology, Erasmus MC-Daniel den Hoed Cancer Centre, Rotterdam, The Netherlands
Division of Cancer Epidemiology and Genetics, National Cancer Institute, Rockville, Maryland, USA
Department of Cancer Epidemiology and Prevention, M. Sklodowska-Curie Memorial Cancer Center & Institute of Oncology, Warsaw, Poland
Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm 17177, Sweden
Faculty of Medicine, University of Southampton (UoS), Southampton UK
Department of Medical Oncology, Family Cancer Clinic, Erasmus MC Cancer Institute, Rotterdam, The Netherlands
Department of Clinical Genetics, Family Cancer Clinic, Erasmus University Medical Center, Rotterdam, The Netherlands
Department of Surgical Oncology, Family Cancer Clinic, Erasmus University Medical Center, Rotterdam, The Netherlands
Human Genetics Division, Genome Institute of Singapore, Singapore
Sheffield Cancer Research, Department of Oncology, University of Sheffield, Sheffield, UK
Centre for Cancer Genetic Epidemiology, Department of Oncology, University of Cambridge, Cambridge, UK
Molecular Genetics of Breast Cancer, German Cancer Research Center (DKFZ), Heidelberg, Germany
Institute of Human Genetics, Pontificia Universidade Javeriana, Bogota, Colombia
Frauenklinik der Stadtklinik Baden-Baden, Baden-Baden, Germany
Institute of Pathology, Städtisches Klinikum Karlsruhe, Karlsruhe, Germany
Department of Genetics and Pathology, Pomeranian Medical University, Szczecin, Poland
Postgraduate School of Molecular Medicine, Warsaw Medical University, Warsaw, Poland
Department of Molecular Virology, Immunology and Medical Genetics, Comprehensive Cancer Center, The Ohio State University, Columbus, OH, USA
Roswell Park Cancer Institute, Buffalo, New York, USA
Molecular Diagnostics Laboratory, IRRP, National Centre for Scientific Research "Demokritos", Aghia Paraskevi Attikis, Athens, Greece
Division of Genetics and Epidemiology, Institute of Cancer Research, London, UK
Division of Breast Cancer Research, Institute of Cancer Research, London, UK
Centre d’innovation Genome Quebec et Université McGill Montreal Quebec, Canada
McGill University, Montreal, Quebec, Canada
Cancer Genomics Laboratory, Centre Hospitalier Universitaire de Quebec Research Center. Laval University, Quebec, Canada
The Institute of Cancer Research, London, SM2 5NG, UK
Royal Marsden NHS Foundation Trust, Fulham, London, SW3 6JJ, UK
University of Warwick, Coventry, UK
Department of Medical Epidemiology and Biostatistics, Karolinska Institute, Stockholm, Sweden
Department of Medical Biochemistry and Genetics, University of Turku, and Tyks Microbiology and Genetics, Department of Medical Genetics, Turku University Hospital, Turku, Finland
Institute of Biomedical Technology/BioMediTech, University of Tampere, Tampere, Finland
Department of Clinical Biochemistry, Herlev Hospital, Copenhagen University Hospital, Herlev Ringvej 75, DK-2730 Herlev, Denmark
Department of Human Genetics University of Utah, Salt Lake City, UT, USA and Department of Clinical Biochemistry, Herlev
Hospital, Copenhagen University Hospital, University of Copenhagen, Copenhagen, Denmark
Cancer Epidemiology Unit, Nuffield Department of Population Health, University of Oxford, Oxford, UK
Surgical Oncology (Uro-Oncology: S4), University of Cambridge, Box 279, Addenbrooke’s Hospital, Hills Road, Cambridge, UK and Cancer Research UK Cambridge Research Institute, Li Ka Shing Centre, Cambridge, UK
Professor of Social Medicine, University of Bristol, Canynge Hall, 39 Whatley Road, Bristol BS8 2PS
Nuffield Department of Surgical Sciences, Old Road Campus Research Building (off Roosevelt Drive), University of Oxford, Headington, Oxford, OX3 7DQ
Cambridge Institute of Public Health, University of Cambridge, Forvie Site, Robinson Way, Cambridge CB2 0SR
Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, Washington, USA
Department of Epidemiology, School of Public Health, University of Washington, Seattle, Washington, USA
International Epidemiology Institute, 1455 Research Blvd., Suite 550, Rockville, MD 20850
Department of Obstetrics, Gynecology and Reproductive Sciences, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA
Department of Urology, University Hospital Ulm, Germany
Institute of Human Genetics University Hospital Ulm, Germany
Brigham and Women’s Hospital/Dana-Farber Cancer Institute, 45 Francis Street-ASB II-3, Boston, MA 02115
Washington University, St Louis, Missouri
International Hereditary Cancer Center, Department of Genetics and Pathology, Pomeranian Medical University, Szczecin, Poland
Division of Genetic Epidemiology, Department of Medicine, University of Utah School of Medicine
Division of Cancer Prevention and Control, H. Lee Moffitt Cancer Center, 12902 Magnolia Dr., Tampa, Florida, USA
Molecular Medicine Center and Department of Medical Chemistry and Biochemistry, Medical University – Sofia, 2 Zdrave St, 1431, Sofia, Bulgaria
Australian Prostate Cancer Research Centre-Qld, Institute of Health and Biomedical Innovation and Schools of Life Science and Public Health, Queensland University of Technology, Brisbane, Australia
Department of Genetics, Portuguese Oncology Institute, Porto, Portugal and Biomedical Sciences Institute (ICBAS), Porto University, Porto, Portugal
University Hospital Erlangen, Department of Gynecology and Obstetrics, Friedrich-Alexander-University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Universitaetsstrasse 21-23, 91054 Erlangen, Germany
University Hospital Erlangen, Institute of Pathology, Friedrich-Alexander-University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Universitaetsstrasse 21-23, 91054 Erlangen, Germany
Laboratory for Translational Genetics, Department of Oncology, University of Leuven, Belgium
Department of Epidemiology, The Geisel School of Medicine at Dartmouth, Lebanon, NH, USA
Department of Epidemiology, The Geisel School of Medicine at Dartmouth, Hannover, NH, USA
Program in Epidemiology, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA, USA
Department of Epidemiology, University of Washington, Seattle, WA, USA
German Cancer Research Center, Division of Cancer Epidemiology, Heidelberg, Germany
Gynecology, University of Ulm, Ulm, Germany
Department of Gynecological Oncology, Roswell Park Cancer Institute, Buffalo, NY
Cancer Epidemiology Program, University of Hawaii Cancer Center, Hawaii, USA
Department of Pathology, Kapiolani Medical Center for Women and Children, John A. Burns School of Medicine, University of Hawaii, Honolulu, Hawaii 96826, USA
Cancer Prevention and Control, Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, Los Angeles, California, USA
Community and Population Health Research Institute, Department of Biomedical Sciences, Cedars-Sinai Medical Center, Los Angeles, California, USA
Department of Gynecology and Obstetrics, Friedrich Schiller University, Jena University Hospital, Jena, Germany
Clinics of Obstetrics and Gynaecology, Hannover Medical School, Hannover, Germany
Department of Pathology, Helsinki University Central Hospital, Helsinki, 00029 HUS, Finland
University of Pittsburgh Department of Obstetrics, Gynecology and Reproductive Sciences and Ovarian Cancer Center of Excellence Pittsburgh PA USA
University of Pittsburgh Department of Epidemiology, University of Pittsburgh Graduate School of Public Health and Womens Cancer Research Program, Magee-Womens Research Institute and University of Pittsburgh Cancer Institute Pittsburgh PA USA
The University of Texas School of Public Health, Houston, TX, USA
Department of Cancer Prevention and Control, Roswell Park Cancer Institute, Buffalo, NY
Department of Gynecology and Gynecologic Oncology, Kliniken Essen-Mitte/Evang. HuysSENS-Stiftung/Knappschaft GmbH, Essen, Germany
Department of Gynecology and Gynecologic Oncology, Dr. Horst Schmidt Kliniken Wiesbaden, Wiesbaden, Germany
Tuebingen University Hospital, Department of Women’s Health, Tuebingen, Germany
Women’s Cancer Program at the Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, Los Angeles, California
Department of Virus, Lifestyle and Genes, Danish Cancer Society Research Center, Copenhagen, Denmark
Department of Obstetrics and Gynecology, Rigshospitalet, Copenhagen, Denmark
Molecular Unit, Department of Pathology, Herlev Hospital, University of Copenhagen, Copenhagen, Denmark
Unit of Medical Genetics, Department of Preventive and Predictive Medicine, Fondazione IRCCS Istituto Nazionale dei Tumori (INT), Milan, Italy
Division of Cancer Prevention and Genetics, Istituto Europeo di Oncologia (IEO), Milan, Italy
Department of Experimental Oncology, Istituto Europeo di Oncologia (IEO), Milan, Italy
University of Kansas Medical Center, Kansas City, KS, USA
Department of Medical Oncology, Mayo Clinic, Rochester, Minnesota, USA
College of Pharmacy and Health Sciences, Texas Southern University, Houston, Texas, USA
Department of Gynecologic Oncology, The University of Texas MD Anderson Cancer Center, Houston, Texas, USA
Department of Epidemiology, The University of Texas MD Anderson Cancer Center, Houston, Texas, USA
Gynecology Service, Department of Surgery, Memorial Sloan-Kettering Cancer Center, New York, NY, USA
Department of Obstetrics and Gynecology, Duke University Medical Center, Durham, North Carolina, USA
Statistical Science, Duke University, Durham, North Carolina, USA 186
Department of Surgery, Duke University Medical Center, Durham, North Carolina, USA 187
Cancer Prevention, Detection & Control Research Program, Duke Cancer Institute, Durham, North Carolina, USA 188
Obstetrics and Gynecology Epidemiology Center, Brigham and Women's Hospital, Boston, Massachusetts, USA 189
Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School
Department of Epidemiology, Harvard TH Chan School of Public Health, Boston, Massachusetts, USA 191
Cancer Prevention and Control Program, Rutgers Cancer Institute of New Jersey, The State University of New Jersey, New Brunswick, NJ, USA 192
Department of Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center, New York, NY, USA 193
Department of Gynecology and Obstetrics, Haukeland University Hospital, Bergen, Norway 194
Centre for Cancer Biomarkers, Department of Clinical Sciences, University of Bergen, Bergen, Norway 195
Radboud university medical center, Department of Gynaecology, Nijmegen, Netherlands 196
Radboud university medical centre, Radboud Institute for Health Sciences, Nijmegen, Netherlands 197
Netherlands Comprehensive Cancer Organisation, Utrecht, Netherlands 198
Department of Obstetrics & Gynecology, Oregon Health & Science University 199
Knight Cancer Institute, Oregon Health & Science University, Portland, Oregon, USA 200
Canada's Michael Smith Genome Sciences Centre, BC Cancer Agency, Vancouver, BC, Canada 201
Department of Biomedical Physiology and Kinesiology, Simon Fraser University, Burnaby, BC Canada 202
Department of Public Health Sciences, College of Medicine, Medical University of South Carolina, SC, USA 203
Hollings Cancer Center, Medical University of South Carolina, SC, USA 204
International Hereditary Cancer Center, Department of Genetics and Pathology, Pomeranian Medical University, Szczecin, Poland 205
Department of Gynecological Surgery and Gynecological Oncology of Adults and Adolescents, Pomeranian Medical University, Szczecin, Poland 206
Gyn Clinic, Rigshospitalet, University of Copenhagen, Denmark 209
Department of Pathology, Rigshospitalet, University of Copenhagen, Denmark 210
Department of Oncology, Rigshospitalet, University of Copenhagen, Denmark 211
Department of Oncology, University of Cambridge, Strangeways Research Laboratory, Cambridge, UK 212
Cancer Genetics Laboratory, Research Division, Peter MacCallum Cancer Centre, St Andrews Place, East Melbourne 213
Institute of Cancer Sciences, University of Glasgow, Wolfson Wohl Cancer Research Centre, Beatson Institute for Cancer Research, Glasgow, UK 214
The Cancer Research UK Clinical Trials Unit, Beatson West of Scotland Cancer Centre, 1053 Great Western Road, Glasgow, G12 0YN 215
Department of Gynaecological Oncology, Glasgow Royal Infirmary 216
Department of Health Research and Policy - Epidemiology, Stanford University School of Medicine, Stanford CA, USA 217
Epidemiology Center, College of Medicine, University of South Florida, Tampa, Florida, USA 218
Public Health Ontario, Toronto, Canada 219
Women’s College Research Institute, University of Toronto, Toronto, Ontario, Canada 220
Department of Cancer Epidemiology, Moffit
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REFERENCES


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Table 1

Rare genetic variants included in the iCOGS array.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Variant</th>
<th>Amino acid</th>
<th>dbSNP rs</th>
<th>OR (95% CI)</th>
<th>Penetrance (95% CI)</th>
<th>Align-GVGD</th>
<th>Reference(s)</th>
<th>Designed</th>
<th>Genotyped</th>
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<tr>
<td>PALB2</td>
<td>c.1592delT</td>
<td>p.Leu531Cysfs</td>
<td>rs180177102</td>
<td>3.94 (1.5–12.1)</td>
<td>40% (17–77)</td>
<td>na</td>
<td>4, 5, 10</td>
<td>Yes</td>
<td>Yes</td>
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<tr>
<td></td>
<td>c.2323C&gt;T</td>
<td>p.Gln775*</td>
<td>rs180177111</td>
<td>na</td>
<td>25.26</td>
<td>No</td>
<td>No</td>
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<td></td>
<td>c.2816T&gt;G</td>
<td>p.Leu939Trp</td>
<td>rs45478192</td>
<td>C55</td>
<td>20</td>
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<td>Yes</td>
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<td></td>
<td>c.3113G&gt;A</td>
<td>p.Tyr1183*</td>
<td>rs180177132</td>
<td>95% (44–100)</td>
<td>40% (17–77)</td>
<td>na</td>
<td>2.4, 20</td>
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<td>c.3116delA</td>
<td>p.Asn1039Ilefs</td>
<td>rs180177133</td>
<td>na</td>
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<td></td>
<td>c.3549C&gt;G</td>
<td>p.Tyr1183*</td>
<td>rs118203998</td>
<td>na</td>
<td>2</td>
<td>No</td>
<td>No</td>
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<tr>
<td>CHEK2</td>
<td>c.349A&gt;G</td>
<td>p.Arg117Gly</td>
<td>rs28909982</td>
<td>8.75 (1.06–72.2)</td>
<td>40% (17–77)</td>
<td>na</td>
<td>11</td>
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<td>Yes</td>
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<td></td>
<td>c.538C&gt;T</td>
<td>p.Arg180Cys</td>
<td>rs77130927</td>
<td>2.47 (0.45–13.49)</td>
<td>40% (17–77)</td>
<td>na</td>
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<tr>
<td></td>
<td>c.715G&gt;A</td>
<td>p.Glu239Lys</td>
<td>rs121908702</td>
<td>1.82 (0.62–5.34)</td>
<td>40% (17–77)</td>
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<td>c.1036C&gt;T</td>
<td>p.Arg346Cys</td>
<td>rs13120793</td>
<td>8.75 (1.06–72.2)</td>
<td>40% (17–77)</td>
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<td></td>
<td>c.1312G&gt;T</td>
<td>p.Asn438Tyr</td>
<td>rs17886163</td>
<td>2.47 (0.45–13.49)</td>
<td>40% (17–77)</td>
<td>na</td>
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<td>c.1343T&gt;G</td>
<td>p.Tyr448Ser</td>
<td>rs17886163</td>
<td>1.82 (0.62–5.34)</td>
<td>40% (17–77)</td>
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<td>Yes</td>
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<tr>
<td>ATM</td>
<td>c.7271T&gt;G</td>
<td>p.Val2424Gly</td>
<td>rs28904921</td>
<td>52% (28–80)</td>
<td>40% (17–77)</td>
<td>na</td>
<td>11</td>
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* Human Genome Variation Society (HGVS); reference sequences PALB2, NM_024675.3, NP_0579851.2; CHEK2, NM_007194.3, NP_009125.1; ATM, NM_000051.3, NP_000042.3.

† Age-specific cumulative risk of breast cancer to age 70 years.5–7

‡ Able to be designed for measurement on the custom Illumina iSelect genotyping array.2122

§ Breast cancer cases unselected for family history of breast cancer.4

¶ OR estimated in a combined group of C65 CHEK2 variants.11

* OR estimated in a combined group of C25 CHEK2 variants.11

‡‡ OR estimated in a combined group of C15 CHEK2 variants.11

na, not available.
Table 2

Summary results from Breast Cancer Association Consortium studies of white Europeans (42 671 invasive breast cancer cases and 42 164 controls)

<table>
<thead>
<tr>
<th>Variant</th>
<th>Frequency Controls</th>
<th>Frequency Cases</th>
<th>OR (95% CI)</th>
<th>LRT p Value</th>
<th>OR (95% CI)</th>
<th>LRT p Value</th>
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<tbody>
<tr>
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<td></td>
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<td></td>
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<tr>
<td>c.1592delT (p.Leu531Cysfs)</td>
<td>0.00014</td>
<td>0.00082</td>
<td>4.52 (1.90 to 10.8)</td>
<td>7.1x10^-5</td>
<td>3.44 (1.39 to 8.52)</td>
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<tr>
<td>c.2816T&gt;G (p.Leu939Trp)</td>
<td>0.00342</td>
<td>0.00352</td>
<td>1.05 (0.83 to 1.32)</td>
<td>0.70</td>
<td>1.03 (0.80 to 1.32)</td>
<td>0.82</td>
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<td>c.3113G&gt;A (p.Trp1038*)</td>
<td>0.00019</td>
<td>0.00101</td>
<td>5.93 (2.77 to 12.7)</td>
<td>6.9x10^-8</td>
<td>4.21 (1.84 to 9.60)</td>
<td>1.2x10^-4</td>
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<tr>
<td><strong>CHEK2</strong></td>
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<tr>
<td>c.349A&gt;G (p.Arg117Gly)</td>
<td>0.00043</td>
<td>0.00103</td>
<td>2.26 (1.29 to 3.95)</td>
<td>0.003</td>
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<tr>
<td>c.538C&gt;T (p.Arg180Cys)</td>
<td>0.00337</td>
<td>0.00370</td>
<td>1.33 (1.05 to 1.67)</td>
<td>0.016</td>
<td>1.34 (1.06 to 1.70)</td>
<td>0.015</td>
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<tr>
<td>c.715G&gt;A (p.Glu239Lys)</td>
<td>0.00021</td>
<td>0.00035</td>
<td>1.70 (0.73 to 3.93)</td>
<td>0.210</td>
<td>1.47 (0.60 to 3.64)</td>
<td>0.40</td>
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<tr>
<td>c.1036C&gt;T (p.Arg346Cys)</td>
<td>0.00005</td>
<td>0.00021</td>
<td>5.06 (1.09 to 23.5)</td>
<td>0.017</td>
<td>3.39 (0.68 to 16.9)</td>
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<tr>
<td>c.1312G&gt;T (p.Asp438Tyr)</td>
<td>0.00078</td>
<td>0.00082</td>
<td>1.03 (0.62 to 1.71)</td>
<td>0.910</td>
<td>0.87 (0.49 to 1.52)</td>
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<td>c.1343T&gt;G (p.Ile448Ser)</td>
<td>0.00002</td>
<td>0</td>
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<td>–</td>
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<td>–</td>
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<td><strong>ATM</strong></td>
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<tr>
<td>c.727T&gt;G (p.Val242Gly)</td>
<td>0.00002</td>
<td>0.00028</td>
<td>11.6 (1.50 to 89.9)</td>
<td>0.0012</td>
<td>11.0 (1.42 to 85.7)</td>
<td>0.0019</td>
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</table>

*Proportion of subjects carrying the variant.
†Excluding women from five studies that selected all cases based on family history or bilateral disease and the subset of selected cases from other studies (based on 34 488 unselected cases and 34 059 controls).
‡CHEK2 c.1343T>G (p.Ile448Ser) was only observed in one control and no cases of white European origin.
§PALB2 c.3113G>A (p.Trp1038*) only observed in the UK, Australia, the USA and Canada. PALB2 c.1592delT (p.Leu531Cysfs) only observed in Finland and Sweden.

LRT, likelihood ratio test; OR, OR for carriers of the variant versus common-allele homozygotes, adjusted for study and seven principal components.
## Table 3
Summary results from the Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome studies for white European men * (22,301 prostate cancer cases and 22,320 controls)

<table>
<thead>
<tr>
<th>Variant</th>
<th>Frequency ‡ Controls</th>
<th>Frequency ‡ Cases</th>
<th>OR (95% CI)</th>
<th>LRT p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>PALB2</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.1592delT (p.Leu531Cysfs)</td>
<td>0.00018</td>
<td>0.00031</td>
<td>2.06 (0.59 to 7.11)</td>
<td>0.24</td>
</tr>
<tr>
<td>c.2816T&gt;G (p.Leu939Trp)</td>
<td>0.00354</td>
<td>0.00381</td>
<td>0.95 (0.69 to 1.29)</td>
<td>0.73</td>
</tr>
<tr>
<td>c.3113G&gt;A (p.Trp1038*)</td>
<td>0.00045</td>
<td>0.00027</td>
<td>0.49 (0.18 to 1.36)</td>
<td>0.16</td>
</tr>
<tr>
<td><strong>CHEK2‡</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.349A&gt;G (p.Arg117Gly)</td>
<td>0.00063</td>
<td>0.00081</td>
<td>1.46 (0.71 to 3.02)</td>
<td>0.30</td>
</tr>
<tr>
<td>c.538C&gt;T (p.Arg180Cys)</td>
<td>0.00341</td>
<td>0.00296</td>
<td>1.02 (0.73 to 1.44)</td>
<td>0.90</td>
</tr>
<tr>
<td>c.715G&gt;A (p.Glu239Lys)</td>
<td>0.00018</td>
<td>0.00027</td>
<td>1.47 (0.41 to 5.35)</td>
<td>0.55</td>
</tr>
<tr>
<td>c.1036C&gt;T (p.Arg346Cys)</td>
<td>0.00018</td>
<td>0.00022</td>
<td>1.07 (0.28 to 4.07)</td>
<td>0.93</td>
</tr>
<tr>
<td>c.1312G&gt;T (p.Asp438Tyr)</td>
<td>0.00049</td>
<td>0.00103</td>
<td>2.21 (1.06 to 4.63)</td>
<td>0.03</td>
</tr>
<tr>
<td>c.1343T&gt;G (p.Ile448Ser)</td>
<td>0</td>
<td>0.00009</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>c.1343T&gt;G (Africans§)</td>
<td>0.019</td>
<td>0.057</td>
<td>3.03 (1.53 to 6.03)</td>
<td>0.001</td>
</tr>
<tr>
<td><strong>ATM</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.7271T&gt;G (p.Val2424Gly)</td>
<td>0.00004</td>
<td>0.00027</td>
<td>4.37 (0.52 to 36.4)</td>
<td>0.17</td>
</tr>
</tbody>
</table>

* For white European men, unless otherwise indicated.

† Proportion of subjects carrying the variant.

‡ CHEK2 c.1343T>G (p.Ile448Ser) was the only CHEK2 variant observed in African men and was identified in two cases and no controls of white European origin.

§ Based on data from 623 and 569 African-American cases and controls, respectively.

LRT, likelihood ratio test; OR, OR for carriers of the variant versus common-allele homozygotes, adjusted for study and seven principal components.
## Table 4

Summary results from the Ovarian Cancer Association Consortium studies for white European women (14,542 invasive ovarian cancer cases and 23,491 controls)

<table>
<thead>
<tr>
<th>Variant</th>
<th>Frequency* Controls</th>
<th>Frequency* Cases</th>
<th>OR (95% CI)</th>
<th>LRT p Value</th>
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<tbody>
<tr>
<td><strong>PALB2</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.1592delT (p.Leu531Cysfs)</td>
<td>0.00004</td>
<td>0.00012</td>
<td>2.50 (0.21 to 29.1)</td>
<td>0.45</td>
</tr>
<tr>
<td>c.2816T&gt;G (p.Leu939Trp)</td>
<td>0.00413</td>
<td>0.00399</td>
<td>0.96 (0.69 to 1.34)</td>
<td>0.81</td>
</tr>
<tr>
<td>c.3113G&gt;A (p.Trp1038*)</td>
<td>0.00034</td>
<td>0.00031</td>
<td>1.34 (0.36 to 4.97)</td>
<td>0.66</td>
</tr>
<tr>
<td><strong>CHEK2</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.349A&gt;G (p.Arg117Gly)</td>
<td>0.00038</td>
<td>0.00031</td>
<td>1.07 (0.32 to 3.60)</td>
<td>0.92</td>
</tr>
<tr>
<td>c.538C&gt;T (p.Arg180Cys)</td>
<td>0.00128</td>
<td>0.00160</td>
<td>1.49 (0.83 to 2.67)</td>
<td>0.18</td>
</tr>
<tr>
<td>c.715G&gt;A (p.Glu239Lys)</td>
<td>0.00021</td>
<td>0.00037</td>
<td>1.47 (0.42 to 5.22)</td>
<td>0.54</td>
</tr>
<tr>
<td>c.1036C&gt;T (p.Arg346Cys)</td>
<td>0</td>
<td>0.00012</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>c.1312G&gt;T (p.Asp438Tyr)</td>
<td>0.00081</td>
<td>0.00074</td>
<td>0.92 (0.42 to 1.99)</td>
<td>0.83</td>
</tr>
<tr>
<td>c.1343T&gt;G (p.Ile448Ser)</td>
<td>0.00009</td>
<td>0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td><strong>ATM</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.7271T&gt;G (p.Val2424Gly)</td>
<td>0</td>
<td>0.00012</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

* Proportion of subjects carrying the variant.
‡ c.1036C>T (p.Arg346Cys) was not observed in any sample.

LRT, likelihood ratio test; OR, OR for carriers of the variant versus common-allele homozygotes, adjusted for study and seven principal components.