**ORIGINAL ARTICLE**

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


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.7271T>G, ATM c.1592delT, c.2816T>G and c.3113G>A, BRCA2 c.1343T>G, c.349A>G, 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.

Results For European women, strong evidence of association with breast cancer risk was observed for PALB2 c.1592delT OR 11.0 (95% CI 1.29 to 3.95), c.7271T>G OR 11.0 (95% CI 1.29 to 3.95), c.1036C>T OR 5.06 (95% CI 1.09 to 23.5), c.1312G>T OR 2.21 (95% CI 1.06 to 4.63), and c.1343T>G OR 3.03 (95% CI 1.84 to 9.60, p=6.9×10−7). For European men and African men and women, evidence of association with breast cancer risk was observed for ATM c.1592delT OR 3.44 (95% CI 1.39 to 8.52, p=7.1×10−5), PALB2 c.3113G>A OR 4.21 (95% CI 1.53 to 6.03, p=0.0006) for African men and women, and c.1343T>G OR 4.21 (95% CI 1.53 to 6.03, p=0.0006) for African women. We also found evidence of association with prostate 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.1343T>G OR 3.03 (95% CI 1.84 to 9.60, p=6.9×10−7). 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.

Cancer genetics


Reference:

Cancer genetics

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.4–6 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%).6 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, Tatvigian et al.12 estimated an OR of 2.85 (95% CI 0.83 to 8.86) 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.7, 14 15 Le Calvez-Kelm et al.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.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.3–4 3–4 3–5 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.3 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)4 and c.3113 G>A (p.Trp1038*)5 and the missense variant c.2816T>G, (p. Leu939Thr), six rare missense variants in CHEK2: c.349A>G (p.Arg117Gly) and c.1036C>T (p.Arg346Gly) predicted to be deleterious on the basis of evolutionary conservation,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).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.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 (42671 cases and 42164 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 (22301 cases and 22320 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, 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 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 (16287 cases (14542 with invasive disease) and 23491 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.22–23 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.

**Genotyping**

Three PALB2 variants c.2323C>T (p.Gln775*), c.3116delA (p.Asn1039Ilefs) and c.3549C>G (p.Try1183*) 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 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 for assessing 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 0.05.25 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.23 26 All analyses were carried out using Stata: Release V10 (StataCorp, 2008).

**RESULTS**

PALB2

In BCAC, PALB2 c.1592delE (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 (KBGP), Oulu Breast Cancer Study (OBCS) and Karolinska Mammaryography Project for Risk Prediction Breast Cancer (pKARMA); see online supplementary.

<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>
</tr>
</thead>
<tbody>
<tr>
<td>PALB2</td>
<td>c.1592delE</td>
<td>p.Leu531Cysfs</td>
<td>rs1801771102</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>
</tr>
<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>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>c.3116delA</td>
<td>p.Asn1039Ilefs</td>
<td>rs180177132</td>
<td>95% (44-100)</td>
<td>na</td>
<td>2, 6, 20</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td></td>
<td>c.3549C&gt;G</td>
<td>p.Try1183*</td>
<td>rs118203998</td>
<td>na</td>
<td>2</td>
<td>No</td>
<td>No</td>
<td></td>
<td></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>C65</td>
<td>11</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td></td>
<td>c.538C&gt;T</td>
<td>p.Arg180Cys</td>
<td>rs77130927</td>
<td>2.47 (0.45-13.49)†</td>
<td>C5</td>
<td>11</td>
<td>Yes</td>
<td>Yes</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>C15</td>
<td>11</td>
<td>Yes</td>
<td>Yes</td>
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<tr>
<td></td>
<td>c.1036C&gt;T</td>
<td>p.Arg346Cys</td>
<td>na</td>
<td>8.75 (1.06-72.2¶)</td>
<td>C65</td>
<td>11</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td></td>
<td>c.1312G&gt;T</td>
<td>p.Asp438Tyr</td>
<td>na</td>
<td>2.47 (0.45-13.49)†</td>
<td>C5</td>
<td>11</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td></td>
<td>c.1343T&gt;G</td>
<td>p.Ile448Ser</td>
<td>rs17886163</td>
<td>1.82 (0.62-5.34)†</td>
<td>C15</td>
<td>11</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>ATM</td>
<td>c.7271T&gt;G</td>
<td>p.Val2424Gly</td>
<td>rs28904921</td>
<td>52% (28-80)</td>
<td>C65</td>
<td>7, 18, 23, 27</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
</tbody>
</table>

*Human Genome Variation Society (HGVS); reference sequences PALB2, NM_024675.3, NP_078951.2; 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
‡OR estimated based on personal or family history of breast cancer.
§Breast cancer cases unselected for family history of breast cancer.
¶OR estimated in a combined group of C65 CHEK2 variants.11
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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>
</tr>
</thead>
<tbody>
<tr>
<td>PALB2‡</td>
<td>c.1592delT (p.Leu531Cysfs)</td>
<td>0.00014</td>
<td>0.00082</td>
<td>4.52 (1.90 to 10.80)</td>
<td>7.1×10⁻⁸⁻</td>
<td>3.44 (1.39 to 8.52)</td>
</tr>
<tr>
<td></td>
<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>
</tr>
<tr>
<td></td>
<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>6.9×10⁻⁸⁻</td>
<td>4.21 (1.84 to 9.60)</td>
</tr>
<tr>
<td>CHEK2‡</td>
<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>
<td>2.03 (1.10 to 3.73)</td>
</tr>
<tr>
<td></td>
<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>
</tr>
<tr>
<td></td>
<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>
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<tr>
<td></td>
<td>c.1036C&gt;T (p.Arg348Cys)</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></td>
<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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<tr>
<td></td>
<td>c.1343T&gt;G (p.Ile448Ser)</td>
<td>0.00002</td>
<td>0</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>ATM§</td>
<td>c.7271T&gt;G (p.Val2424Gly)</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>
</tr>
</tbody>
</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 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>PALB2</td>
<td>c.1592delT (p.Leu531Cysfs)</td>
<td>0.00018</td>
<td>0.00331</td>
<td>2.06 (0.59 to 7.11)</td>
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<tr>
<td></td>
<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>
</tr>
<tr>
<td></td>
<td>c.3113G&gt;A (p.Trp1038*)</td>
<td>0.00045</td>
<td>0.0027</td>
<td>0.49 (0.18 to 1.36)</td>
</tr>
<tr>
<td>CHEK2‡</td>
<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>
</tr>
<tr>
<td></td>
<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>
</tr>
<tr>
<td></td>
<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>
</tr>
<tr>
<td></td>
<td>c.1036C&gt;T (p.Arg348Cys)</td>
<td>0.00018</td>
<td>0.00022</td>
<td>1.07 (0.28 to 4.07)</td>
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<tr>
<td></td>
<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>
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<td>c.1343T&gt;G (p.Ile448Ser)</td>
<td>0.00002</td>
<td>0</td>
<td>–</td>
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<tr>
<td></td>
<td>c.1343T&gt;G (Africans§)</td>
<td>0.01296</td>
<td>0.057</td>
<td>3.03 (1.53 to 6.03)</td>
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<tr>
<td>ATM§</td>
<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>
</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 S1), giving strong evidence of association with breast cancer risk (p=7.1×10⁻⁸); the OR estimate was 4.32 (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=6.9×10⁻⁸), 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 (table 3 and 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).

**Discussion**

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 far by 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.

The estimates for the two loss-of-function PALB2 variants (c.1592delT and c.3113G>A) were consistent with each other and with estimates based on segregation analysis. 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

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**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>
</tr>
</thead>
<tbody>
<tr>
<td>PALB2</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>CHEK2</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</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>ATM</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>

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

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*Proportion of subjects carrying the variant.
‡ LRT, likelihood ratio test; OR, OR for carriers of the variant versus common-allele homozygotes, adjusted for study and seven principal components.
Cancer genetics

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. Reports of the association of the missense variant I157T, (C15) ATM c.7271T>G because these associations provided those reported previously such as 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 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.

Author 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, 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
15FOM, 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 Franconia, Department of Gynecology and Obstetrics, University Hospital Erlangen, Friedrich-Alexander University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Erlangen, Germany
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