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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, c.1343T>G, 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.

Results For European women, strong evidence of association with breast cancer risk was observed for PALB2 c.1592delT OR 3.44 (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) for African men and 

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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 al12 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 10 11 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.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.4 8–10

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*6) and c.3113 G>A (p.Ile1038fs*4) and the missense variant c.2816T>G (p. Leu939Ile), six rare missense variants in CHEK2: c.349A>G (p.Asp117Gly) and c.1036C>T (p.Arg346Cys) 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.Asp437Tyr) and c.1343T>G (p.Ile448Ser) and ATM c.7271T>G (p.Val242Gly).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 (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.12–23 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.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. 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).

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 Reference(s)</th>
<th>Design‡</th>
<th>Genotyped</th>
</tr>
</thead>
<tbody>
<tr>
<td>PALB2</td>
<td>c.1592delT</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>
</tr>
<tr>
<td></td>
<td>c.2323C&gt;T</td>
<td>p.Gln775*</td>
<td>rs180177111</td>
<td>2815T&gt;G</td>
<td>2816T&gt;G</td>
<td>na</td>
<td>25 26</td>
<td>No</td>
</tr>
<tr>
<td></td>
<td>c.2816T&gt;G</td>
<td>p.Leu939Trp</td>
<td>rs45478192</td>
<td>2.49 (0.45-13.49)‡</td>
<td>95% (43-100)</td>
<td>na</td>
<td>2, 6 20</td>
<td>Yes</td>
</tr>
<tr>
<td></td>
<td>c.3113G&gt;A</td>
<td>p.Trp1038*</td>
<td>rs180177132</td>
<td>1.82 (0.62-5.34)†</td>
<td></td>
<td>na</td>
<td>2</td>
<td>No</td>
</tr>
<tr>
<td></td>
<td>c.3116delA</td>
<td>p.Asn1039Ilefs</td>
<td>rs180177133</td>
<td>1.82 (0.62-5.34)†</td>
<td></td>
<td>na</td>
<td>2</td>
<td>No</td>
</tr>
<tr>
<td></td>
<td>c.3549C&gt;G</td>
<td>p.Tyr1183*</td>
<td>rs180177133</td>
<td>1.82 (0.62-5.34)†</td>
<td></td>
<td>na</td>
<td>2</td>
<td>No</td>
</tr>
<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></td>
<td>C65</td>
<td>11</td>
<td>Yes</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></td>
<td>C65</td>
<td>11</td>
<td>Yes</td>
</tr>
<tr>
<td></td>
<td>c.7150A&gt;G</td>
<td>p.Glu239Lys</td>
<td>rs121908702</td>
<td>1.82 (0.62-5.34)†</td>
<td></td>
<td>C15</td>
<td>11</td>
<td>Yes</td>
</tr>
<tr>
<td></td>
<td>c.1036C&gt;T</td>
<td>p.Arg346Cys</td>
<td>rs121908702</td>
<td>1.82 (0.62-5.34)†</td>
<td></td>
<td>C15</td>
<td>11</td>
<td>Yes</td>
</tr>
<tr>
<td></td>
<td>c.1312G&gt;T</td>
<td>p.Asp434Tyr</td>
<td>rs121908702</td>
<td>1.82 (0.62-5.34)†</td>
<td></td>
<td>C15</td>
<td>11</td>
<td>Yes</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></td>
<td>C15</td>
<td>11</td>
<td>Yes</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></td>
<td>C65</td>
<td>7, 13 23 27</td>
<td>Yes</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.10
‡Able to be measured for measurement on the custom Illumina iSelect genotyping array.21 22
§Breast cancer cases unselected for family history of breast cancer.2
¶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.
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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></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<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>7.1×10⁻⁸⁻⁻⁻</td>
<td>3.44 (1.39 to 8.52)</td>
<td>0.003</td>
</tr>
<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>
</tr>
<tr>
<td>c.3113G&gt;A (p.Trp1038*)</td>
<td>0.00019</td>
<td>0.000101</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>
<td>1.2×10⁻⁴⁻⁻⁻</td>
</tr>
<tr>
<td>CHEK2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>c.349A&gt;G (p.Arg117Gly)</td>
<td>0.00043</td>
<td>0.000103</td>
<td>2.26 (1.29 to 3.95)</td>
<td>0.003</td>
<td>2.03 (1.10 to 3.73)</td>
<td>0.020</td>
</tr>
<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>
</tr>
<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>
</tr>
<tr>
<td>c.1036C&gt;T (p.Arg346Cys)</td>
<td>0.00005</td>
<td>0.000021</td>
<td>5.06 (1.09 to 23.5)</td>
<td>0.017</td>
<td>3.39 (0.68 to 16.9)</td>
<td>0.11</td>
</tr>
<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>
<td>0.62</td>
</tr>
<tr>
<td>c.1343T&gt;G (p.Ile448Ser)¶</td>
<td>0.00002</td>
<td>0</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

| ATM                  |                    |                 |             |             |              |              |
| c.7271T>G (p.Val2424Gly) | 0.00002            | 0.000028        | 11.6 (1.50 to 89.9) | 0.0012       | 11.0 (1.42 to 85.7) | 0.0019        |

†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.

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></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>CHEK2</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>0.00031</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>–</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>0.0011</td>
</tr>
</tbody>
</table>

ATM

| c.7271T>G (p.Val2424Gly) | 0.00004            | 0.00027         | 4.37 (0.52 to 36.4) | 0.17        |

*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=7.1×10⁻⁸⁰⁴); 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=6.9×10⁻⁸⁵), 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).
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>
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<tr>
<td>c.7271T&gt;G (p.Val2424Gly)</td>
<td>0.00009</td>
<td>0.00074</td>
<td>0.92 (0.42 to 1.99)</td>
<td>0.83</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.

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 was observed (p=0.016), 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 9 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 or European 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).

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 by far the largest to take a case-control approach. Consistent with previous reports, PALB2 c.3113G>A (p.Trp1038*) was strongly associated with 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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Align-Grantham Variation Grantham 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 previously been reported; our aim was to more precisely accommodate a multifactorial approach to variant classification.

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.

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Contributors All authors provided DNA samples and/or data and have participated in the Breast Cancer Association Consortium through attendance at regular meetings and planning of the iCOGS experiment. Each author has made substantial contribution through designing and coordinating the studies listed in the supplemental material and therefore have made substantial contributions to the conception or design of this work. Many authors played multiple roles across these activities. Specifically, MCS conceived this study, worked to include the rare variants on iCOGS and drafted the manuscript. RLM led the statistical analysis and drafted the paper. Members of the PALB2 interest group, MCS, DEG, RW, KP, FC, MT, WF, JD, KM, Elvr, TH, HN, JH, TD, KC, JR-F, ZLT, PR, IC, CF, PP, HT, FAO, JGD contributed to the inclusion of the PALB2 rare variants on iCOGS. DFE coordinated the BCAC project and contributed to statistical analysis along with DEG. SVT contributed to the selection of CHEK2 rare variants. GC-T contributed to the data quality related to the calling of the rare genetics variants on iCOGS. MKS, AB, FBH, SV, JC, CS, RJ, FIS, PA, NF, AMB, JP, IDSS, OF, NJ, MBK, EJS, IT, MIK, NM, FM, BB, RY, PG, TT, FM, MS, SB, SFN, HF, JB, MPZ, JIAP, PM, HAC, SN, AZ, CDD, HB, VA, CS, HB, TD, YDK, TAM, KA, CB, NVB, NNA, AL, SM, AM, VK, V-MK, JH, AW, ES, DS, BF, GB, JJ, FC, JR, AR, PS, DS, DJF, SEO, VSP, CP, CM, CAH, BEH, FS, LLM, VK, GW, WA, DLL, SH, SE, PK, JA, XAK, GIG, AMM, AV, MG, SK, FD, RAEMT, CS, AH, MSC, IF, SJ, JL, KC, HD, ME, DME, SR, WIT, SMG, MJH, IWMM, JMC, MTL, PH, JL, JSB, KB, AC, MMWR, CL, CB, AD, UH, DT, HU, TR, AJ, JL, KJ, KD, SS, AET, CBA, DY, AS, AA, NO, MJ, AGP, MRA, NA, DH, DFT, DV, JS, B, PS, RE, KM, FW, HG, JS, NW, MBG, BCT, JDN, FLD, KFC, KTS, JIL, WBS, ST, DIS, JKL, CM, ASK, CC, LCA, KB, JP, JR, MBT, MR, ZKJ, AAAB, SB, SPR, AH, AM, DR, MLN, EV, IV, SL, JAD, MAR, SN, UE, SWG, KOS, LE, GS, FG, JCL, LK, LRG, MTR, RG, MIR, ABR, YMR, RB, FM, RPE, DUK, ANI, AMI, ARN, MON, LMH, AF, EM, D, EH, BP, BB, LB, EBL, BLF, RAW, JMC, MCL, ZCF, KRK, DL, KH, MATH, XW, DAL, FD, MB, AB, ESI, JRM, LA, DW, KLC, ETL, ELP, MS, SBTF, IEV, SB, SHO, LB, BHS, AVVA, KKHA, LAK, LFAGM, TP, YB, ABW, LEK, SDL, NBL, DG, BJ, JG, CMH, LK, SL, NAE, ED, JT, IC, JN, JP, NS, RG, ASW, JHR, VG, WS, HC, XUS, RRT, TS, JRM, SAN, CP, AMM, DF, HYL, IPM, TAS, TAC, YFT, ZCM, AGM, SAG, SBR, UM, AHW, CLP, DDBV, BAAM, UHP, JMI, PW, MG, SC, GGO, SVT, DFE, RLM provided DNA samples and/or phenotypical data. All authors read and approved the final manuscript.

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