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Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of \textit{BRCA1}/2

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Abstract

Recently, a locus on chromosome 6q22.33 (rs2180341) was reported to be associated with increased breast cancer risk in the Ashkenazi Jewish (AJ) population, and this association was also observed in populations of non-AJ European ancestry. In the present study, we performed a large replication analysis of rs2180341 using data from 31,428 invasive breast cancer cases and 34,700 controls collected from 25 studies in the Breast Cancer Association Consortium (BCAC). In addition, we evaluated whether rs2180341 modifies breast cancer risk in 3,361 BRCA1 and 2,020 BRCA2 carriers from 11 centers in the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Based on the BCAC data from women of European ancestry, we found evidence for a weak association with breast cancer risk for rs2180341 (per-allele odds ratio (OR) = 1.03, 95% CI 1.00–1.06, p = 0.023). There was evidence for heterogeneity in the ORs among studies (I² = 49.3%; p = 0.004). In CIMBA, we observed an inverse association with the minor allele of rs2180341 and breast cancer risk in BRCA1 mutation carriers (per-allele OR = 0.89, 95%CI 0.80–1.00, p = 0.048), indicating a potential protective effect of this allele. These data suggest that 6q22.33 confers a weak effect on breast cancer risk.


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**Introduction**

Genome-wide association analyses have recently identified multiple loci conferring genetic susceptibility to breast cancer [1,2,3,4]. Due to the low relative risks associated with such loci, however, very large case-control studies are required to confirm these and estimate the associated risks reliably [5,6].

Recently, a putative breast cancer susceptibility locus at chromosome 6q22.33 (tagged by rs2180341) was identified by a two-stage genome-wide association study (GWAS) based on a phase 1 analysis of 299 Ashkenazi Jewish (AJ) controls and 249 AJ kindreds with family history of breast cancer and no known BRCA1 mutation, followed by phase 2 analysis of 979 AJ controls and 950 AJ breast cancer cases [7]. The association signal spanned an approximately 100 kb region with two candidate genes, ECHDC1 and RNF146, mapping to this locus. In a follow-up study, an association was observed in an independent analysis of 1,953 breast cancer cases and 1,467 controls of non-AJ, predominantly European ancestry (per-allele OR 1.18, 95% CI 1.04–1.33, p = 0.0083) with some evidence of a stronger association for ER+ than ER- tumors [8].

Our objective in the current analysis was to further investigate the association of the 6q22.33 locus with breast cancer risk. To this end, we genotyped rs2180341 in 27,950 invasive breast cancer cases and 32,219 controls from 23 case-control studies of primarily European ancestry and 2 studies of Asians included in the Breast Cancer Association Consortium (BCAC). We also evaluated whether rs2180341 was associated with breast cancer risk in BRCA1 or BRCA2 mutation carriers, by genotyping 5,381 mutation carriers from 11 studies in the Consortium of Investigators on Modifiers of BRCA1/2 (CIMBA).

**Materials and Methods**

**Ethics Statement**

Ethics committee approval was obtained for the collection and genetic analysis of all samples, and an informed written consent was obtained from all participants. For detailed description, see Supporting Information S1.

**Breast Cancer Association Consortium (BCAC)**

Twenty-five case-control studies (described in Supporting Information S1) contributed data to these analyses. Data were available on age at study recruitment and ethnicity. Studies were conducted in Europe, North America, and Australia, among women of primarily European descent, and in Southeast Asia. For one study (MSKCC, see study acronyms in Supporting Information S1), we included previously genotyped data from a follow-up analysis reported recently [8]. These data represent an independent group of breast cancer cases and controls of non-AJ European ancestry not used in the prior two-stage GWAS in AJ population [7].

In the current dataset, we excluded breast cancer cases with in situ diagnoses (736 cases). Final analyses included 27,950 invasive breast cancer cases and 32,219 controls of European ancestry, as well as 2,836 invasive breast cancer cases and 2,149 controls of Asian ancestry. All studies received approval from their institutional review committees and participants provided informed consent or were analyzed under specific coding procedures (ABCs).

**Consortium of Modifiers of BRCA1 and BRCA2 (CIMBA)**

Eleven studies (described in Supporting Information S1) from Europe, North America, and Australia contributed samples from carriers to these analyses. Eligible female carriers were aged 18 years or older and had pathogenic mutations in BRCA1 and/or BRCA2. Data were available on year of birth, age at study recruitment, age at cancer diagnosis, age of bilateral prophylactic mastectomy, BRCA1 and BRCA2 mutation description, and ethnicity. Final analyses included 2,776 invasive breast cancer cases and 2,605 unaffected mutation carriers.

**Genotyping**

For most of the BCAC part of the study, the genotyping of rs2180341 was performed by TaqMan allelic discrimination assay using the standard protocol, described previously [8]. For the genotyping of 3 BCAC centers (see Supporting Information S1) and all CIMBA studies, the Sequenom platform was used (Sequenom, San Diego, CA, USA). Briefly, the matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) was used to determine allele-specific primer extension products using Sequenom’s MassARRAY system and iPLEX technology (Sequenom, San Diego, CA, USA). The design of oligonucleotides was carried out according to the guidelines of Sequenom and performed using MassARRAY Assay Design software (version 3.1). Robust quality control criteria, established by BCAC/CIMBA, were applied as detailed in previous consortium studies [9,10,11]. Briefly, the genotyping concordance was verified with internal duplicates and overall data quality was ensured using independent genotyping of CEU samples by each genotyping center. We excluded all samples that failed on two or more of the SNPs genotyped in a particular BCAC/CIMBA genotyping round. All studies met the specified criteria for call rate (>95%), and Hardy-Weinberg Equilibrium (HWE; p≥0.001).

**Statistical Analyses for BCAC**

Study-adjusted, fixed-effects models, weighted for each study by the within- and between-study variances, were used to estimate pooled odds ratios (OR) and 95% confidence intervals (CI). The percent of between-study heterogeneity was estimated using the I^2 statistic [12,13]. ORs for rs2180341 were estimated under the log-additive model (per-allele OR), the recessive model, and the 2 degree of freedom (2 df) model, with the common homozygote as a reference category. Women of non-European ancestry in studies of predominantly European ancestry were excluded from the analysis. Separate estimates for women of Asian ancestry were performed. Analyses stratified on age and estrogen receptor (ER) status among cases were also performed; missing data for each variable were excluded from the respective analyses. The p-values for interaction with age were calculated by comparing the log likelihood estimates of models with and without an interaction term for age and genotype (each coded as an ordinal categorical variable). The p-value for tumor heterogeneity by ER status was based on the comparison of ORs for the ER-positive (ER+) and ER-negative (ER-) tumors.

**Statistical Methods for CIMBA**

Hazard ratios (HRs) and 95% CIs were estimated using a weighted Cox regression approach as described in detail elsewhere [14]. Briefly, to correct for potential bias due to over-sampling of affected carriers the affected and unaffected mutation carriers were differentially weighted such that the observed breast cancer incidences in the mutation carrier dataset agreed with external breast cancer incidences for BRCA1 and BRCA2 mutation carriers. We used a robust variance approach to allow for the dependence among related mutation carriers. We also adjusted for study,
country, ethnicity, and year of birth. Relative risk estimates were calculated separately for \textit{BRCA1} and \textit{BRCA2} mutation carriers. Mutation carriers were censored at the first breast or ovarian cancer or bilateral prophylactic mastectomy. Carriers who developed either cancer were censored at the time of bilateral prophylactic mastectomy only if it occurred more than a year prior to the cancer diagnosis (to avoid censoring at bilateral mastectomies related to diagnosis in which rounded ages were used). The remaining carriers were censored at the age of last observation. Carriers censored at diagnosis of breast cancer were considered affected in the analysis. Carriers with a censoring/last follow-up age older than age 80 were censored at age 80 because there are no reliable cancer incidence rates for \textit{BRCA1}/2 mutation carriers beyond age 80.

All analyses were performed with STATA (Version 10.0).

Results

Description of BCAC Study Population

The mean (\pm SD) age was 53.1 (\pm 13.1) years for invasive cases, 52.7 (\pm 11.8) years for controls. A total of 88.9\% of invasive cases and 92.9\% of controls were of European ancestry. Other women were of Asian ancestry (9.0\% cases and 6.2\% controls) or unknown ancestry (2.1\% cases and 0.9\% controls, respectively).
Among controls of European descent, the minor allele frequency (MAF) of rs2180341 ranged from 22.6% to 28.7% (mean 24.8%; Supporting Information S1). The MAF was similar for controls of Asian descent (24.5%, mean of 2 studies).

Association Between rs2180341 and Risk of Breast Cancer

There was some evidence for an association between the G allele and breast cancer risk (per-allele OR 1.03, 95% CI 1.00–1.06, p = 0.023, Table 1). The highest risk was observed for GG homozygotes (OR = 1.07, 95% CI 1.00–1.15; p = 0.044). Significant between-study heterogeneity (Figure 1) was observed for the per-allele ORs for women of European ancestry (I² = 49.3%; p = 0.004), which was mainly attributable to the strong inverse associations for kConFab/AOCS and HMBCS, and a strong positive association for MSKCC and SBCS. Exclusion of these studies did not alter the overall magnitude of the relative risk estimate and there was no longer evidence of between-study heterogeneity (per-allele OR = 1.03, 95% CI 1.00–1.06, p = 0.034; between-study heterogeneity: I² = 0.0%, p = 0.80).

There was an indication of effect modification by age (p for interaction = 0.044; Table 2); we observed no association in the <40 or 40–49 year age groups, but increased association in the age 50–59 and ≥60 year age groups (OR = 1.05, 95% CI 1.00–1.11 and OR = 1.05, 95% CI 1.00–1.11, respectively). The association in the age group of 50–59 was stronger under the recessive model of analysis (OR = 1.21, 95% CI 1.06–1.38, p = 0.006).

Among women of Asian ancestry, we did not observe an association with overall breast cancer risk and the 6q22.33 locus (Table 1), but there was significant between-study heterogeneity (I² = 89.3%; p = 0.009).

We examined the association of rs2180341 with breast cancer by ER status, which was available from 19 studies that were conducted predominantly among women of European ancestry. There was no significant difference in the per-allele OR for rs2180341 in the risk of ER+ and ER- disease (p for tumor heterogeneity = 0.21; Table 3). However, the per-allele OR estimate for ER+ tumors (OR = 1.04, 95% CI 1.00–1.08) was greater than that for ER- tumors (OR = 0.99, 95% CI 0.93–1.06).

Description of CIMBA Study Population

We also examined the association with rs2180341 in women with BRCA1 or BRCA2 mutations based on data from 2,776 invasive breast cancer cases and 2,605 unaffected carriers. Sixty-two percent of the carriers had a BRCA1 mutation. On average, BRCA1 affected carriers were censored at age 41.0 (±9.3 SD), BRCA1 unaffected carriers at age 43.1 (±12.7 SD), BRCA2 affected carriers at age 44.3 (±13.5 SD), and BRCA2 unaffected carriers at age 45.1 (±13.5 SD). All study subjects were of European descent. Genotype frequencies were in HWE for all studies. Among unaffected carriers, the MAF of rs2180341 ranged from 19.2% to 33.3% (see Supporting Information S1) with a mean of 25.0% (Table 4).

Association Between rs2180341 and Breast Cancer Risk in BRCA1/2 Carriers

The minor allele was statistically significantly associated with a lower breast cancer risk for BRCA1 mutation carriers, (per-allele HR = 0.89, 95% CI 0.80–0.98, p = 0.04, Table 4, Figure 2A). The per-allele HR estimate for BRCA2 mutation carriers was 1.02, 95% 0.90–1.16, p = 0.75 (Table 4, Figure 2B). There was no evidence of between-study heterogeneity for the estimates among BRCA1 (p = 0.15) or BRCA2 (p = 0.19) mutation carriers (see forest plots in Figure 2). ER status was not available for the affected mutation carriers at the time of analysis.

Discussion

While several recent studies on different ancestries reported an association of 6q22.33 with breast cancer risk [15,16], none of the
prior breast cancer GWAS of European populations have
independently identified the 6q22.33 region, possibly due to
limited power in the first stage design of these studies. Noting
that the true magnitude of the effect for 6q22.33 on overall breast
cancer risk is likely to be small, in this report we sought to provide
a more precise estimate of breast cancer risk associated with the
6q22.33 locus in a study of more than 30,000 breast cancer cases
and controls ascertained through the international BCAC. After
restricting the analysis to women of European ancestry, the overall
estimate showed a weak, per-allele association (OR = 1.03; Table 1,
Figure 1), which is smaller than the first replication analysis in non-
AJ European populations (per-allele OR = 1.19) [8]. Findings from
the BCAC study are also consistent with previous observations that
a higher OR was found for minor allele homozygotes. Notably,
there was significant between-study heterogeneity in the BCAC
data, even when the analysis was limited to women of European
ancestry (p = 0.004, Figure 1). For example, while some centers,
(MSKCC, SBCS, or SEARCH) showed comparable effect size
with original observations from AJ GWAS, other centers (e.g.
kConFab, GESBC, HMBCS) yielded risk estimates in the opposite
direction. Such “flip-flop” associations may be due to chance, but
have also been observed in the setting of other known associations,
and may result from local differences in linkage disequilibrium
structure between selected populations, even within the same
ethnicities [17]. Moreover, for two centers ascertained from the
UK population (SBCS and SEARCH) representing a large portion
of the BCAC data (n = 15,478), the magnitude of the association
was more comparable to prior observations in AJ as well as
European ancestry; a per allele OR = 1.09 (95% CI 1.03–1.15;
p = 0.002) was noted in the combined SBCS and SEARCH study
populations compared to OR = 1.18 (95% CI 1.13–1.35, p = 0.008)
in a U.S. study of non-Ashkenazi Caucasians [8]. We hypothesize
that the heterogeneity between studies may largely be attributed to
local population stratification; for example OR estimates observed
in the UK studies differed from those in the Copenhagen (CGPS)
study. While ancestry-informative panels or principal components
from genome-wide scans will need to be incorporated into the
present meta-analysis to quantify potential population stratifica-
tion, such markers were unavailable for the current study. With
the completion of a large ongoing consortia effort on breast cancer
susceptibility (ICOGs) however, this information will be readily
accessible to test the possible confounding effect of the population
substraction on the observed association.

The chance is also a likely explanation of observed heteroge-
neity because individual estimates based on studies with wider
95% confidence intervals, such as kConFab or GESBC, may be
more susceptible to random error [18]. Excluding “outlier” studies
from the present analysis did not alter the magnitude of the OR
estimates, and the statistical significance of the association was only
marginally weaker, suggesting that the observed association is
robust to random error. When pooled with the original AJ GWAS
data [7], the association was stronger (OR = 1.24, 95% CI 1.13–
1.36, p<0.001); however, for the purpose of independent
validation in this study, these original “discovery” data were
excluded from the current analysis.

Another potential concern related to accurate estimate and
adjustment of between-study heterogeneity is the selection of a
statistical model of meta-analysis. In the current study, we report
the results of fixed-effect analysis as opposed to random effect
model. Because of the assumption of low-penetrant effect
uniformly correlated with the response, in the context of the
current meta-analysis of breast cancer case-control studies, the
effect is likely to be similar among the analyzed centers. In
addition, for the small underpowered centers likely subjected to

<table>
<thead>
<tr>
<th>Genotype</th>
<th>N cases</th>
<th>N controls</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>1,917</td>
<td>2,271</td>
<td>1.00 (0.88–1.13)</td>
</tr>
<tr>
<td>AG</td>
<td>442</td>
<td>546</td>
<td>1.04 (0.93–1.16)</td>
</tr>
<tr>
<td>GG</td>
<td>0.95 (0.76–1.19)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>p for interaction</th>
<th>Age 40 years</th>
<th>Age 40–49 years</th>
<th>Age 50–59 years</th>
<th>Age 60 years</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1.00 (0.90–1.07)</td>
<td>1.00 (0.94–1.07)</td>
<td>1.00 (0.95–1.11)</td>
<td>1.00 (0.91–1.11)</td>
</tr>
</tbody>
</table>
random error, overweighing in random model may negatively impact the accuracy of pooled risk assessment. Therefore, a fixed effect model was utilized in the present analysis. A parallel analysis using the random effect models and the results provided were closely similar results (OR = 1.02, 95% CI 0.98–1.06), with the between study heterogeneity of p = 0.005.

We have investigated if other factors also contribute to the heterogeneity of risk estimates observed in this large combined study. As illustrated in the Supporting Information S1, based on the age distribution of cases (median age), we found that the cases from centers with inverse risk estimates were on average 6–17 years younger than the cases from centers showing a susceptible effect. Based on this observation it is possible that the age difference, likely attributable to center ascertainment (e.g. prevalence of familial versus sporadic cases or clinical versus population – based ascertainment), may also influence the 6q22.33 breast cancer risk estimates. For example, one of the outlier studies (kConFab) is predominantly a familial-based ascertainment, with cases and controls on average 17 years younger compared to some other studies. This may suggest that ascertainment differences may possibly contribute to the observed heterogeneity, although the recent BCAC studies on other low-penetrant breast cancer GWAS loci suggest such effects to be marginal. In the present study, however, the age stratified analysis revealed the association of 6q22.33 with breast cancer risk (per-allele ORs = 1.05) in the subsets of breast cancer cases >50 years of age, as shown in Table 3 (p for interaction = 0.044) with the strongest effect in the age group of 50–59 under the recessive model (OR = 1.21, 96% CI 1.06–1.38; p-value = 0.006). This suggests that the breast cancer risk attributed to 6q22.33 allele may be slightly modified by age, and hence some source of potential heterogeneity in the risk estimates may stem from the age distribution related to ascertainment differences between “younger” (e.g. kConFab) and “older” (e.g. MSKCC, SEARCH) studies. While the current study does not provide sufficient power to allow for age-specific meta-analysis, this interaction can be thoroughly examined with expansion of larger datasets.

### Table 3. Association between SNP rs2180341 and breast cancer risk by estrogen receptor (ER) status among cases and controls of European ancestry, Breast Cancer Association Consortium (BCAC).

<table>
<thead>
<tr>
<th>Genotype</th>
<th>No. of cases</th>
<th>No. of controls</th>
<th>OR¹ (95% CI)</th>
<th>No. of cases</th>
<th>No. of controls</th>
<th>OR¹ (95% CI)</th>
<th>p for tumor heterogeneity</th>
</tr>
</thead>
<tbody>
<tr>
<td>ER+</td>
<td>6,584</td>
<td>19,554</td>
<td>1</td>
<td>1,930</td>
<td>19,554</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>4,632</td>
<td>13,067</td>
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<td>1,309</td>
<td>13,067</td>
<td>1.01 (0.93 – 1.10)</td>
<td></td>
</tr>
<tr>
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<td>740</td>
<td>2,079</td>
<td>1.07 (0.97 – 1.18)</td>
<td>186</td>
<td>2,079</td>
<td>0.94 (0.79 – 1.12)</td>
<td></td>
</tr>
<tr>
<td>recessive</td>
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<td></td>
<td>1.05 (0.96 – 1.16)</td>
<td>0.93 (0.79 – 1.11)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>per allele</td>
<td></td>
<td></td>
<td>1.04 (1.00 – 1.08)</td>
<td>0.99 (0.93 – 1.06)</td>
<td>0.21</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

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### Table 4. Adjusted¹, weighted hazard ratios (HRs) and 95% confidence intervals (CIs) for the association between SNP rs2180341 genotype and breast cancer risk, in the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA).²

<table>
<thead>
<tr>
<th>Genotype</th>
<th>No. of Studies</th>
<th>N affected</th>
<th>N unaffected</th>
<th>MAF³</th>
<th>HR (95% CI)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Among BRCA1 Mutation Carriers</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>1,041</td>
<td>934</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>582</td>
<td>602</td>
<td>0.87 (0.76 – 1.00)</td>
<td>1.00</td>
<td>0.05</td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>11</td>
<td>96</td>
<td>106</td>
<td>24.8</td>
<td>0.85 (0.64 – 1.11)</td>
<td>0.23</td>
</tr>
<tr>
<td>recessive</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.89 (0.68 – 1.16)</td>
<td>0.4</td>
</tr>
<tr>
<td>per allele</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.89 (0.80 – 1.00)</td>
<td>0.048</td>
</tr>
<tr>
<td>Among BRCA2 Mutation Carriers</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>AA</td>
<td>605</td>
<td>528</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>384</td>
<td>384</td>
<td>0.97 (0.82 – 1.15)</td>
<td>1.15</td>
<td>0.73</td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>11</td>
<td>68</td>
<td>51</td>
<td>25.2</td>
<td>1.15 (0.84 – 1.56)</td>
<td>0.38</td>
</tr>
<tr>
<td>recessive</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1.14 (0.86 – 1.56)</td>
<td>0.33</td>
</tr>
<tr>
<td>per allele</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1.02 (0.90 – 1.16)</td>
<td>0.75</td>
</tr>
</tbody>
</table>

¹Adjusted for birth year and study.
²Restricted to women of European descent.
³MAF = Minor allele frequency.
doi:10.1371/journal.pone.0035706.t004
rs2180341, and contribute to the observed heterogeneity. While such scenario is possible, recent studies in BCAC have shown that besides ER/PR status, the interaction of low-penetrant alleles from GWAS with other tumor characteristics is weaker [19], thus it is unlikely these would substantially impact the observed heterogeneity. With the small effect of rs2180341 and the current size of the present study it was not possible to test the potential interaction of other tumor clinico-pathological factors. Moreover, for many of the sub-studies used in the current meta-analysis, this information was not available, and hence the reduction of power of such partial analysis may impact the pooled association estimates.

Lastly, our study provides the first estimate of the potential breast cancer modifying effect of 6q22.33 in carriers of BRCA1 mutations. In the 3,361 BRCA1 mutation carriers in CIMBA, we observed a statistically significant inverse association with breast cancer risk (per-allele HR = 0.89, 95% CI 0.80–1.00, p = 0.048, Table 4, Figure 2A). While this finding may be due to random effects, we note that OR estimates less than one were observed in eight of the ten studies. The two remaining studies from this analysis (PISA and EMBRACE) demonstrated HR greater than one. Fluctuations in the study-specific risk estimate may be due to differences in ascertainment bias (e.g., oversampling of familial cases, selection of younger versus older cases or local population differences) between studies. As the majority of BRCA1 cancers are ER-, there is also recent evidence suggesting that E3 ubiquitin-ligases (related family of RNF146, a candidate gene in 6q22.33) and BRCA1 may act in conjunction to regulate ER-mediated pathways in breast cancer tumorigenesis [20,21]. Most interestingly, several recent studies discovered RNF146 to be a critical player in Wnt signaling pathway, providing an evidence for novel biochemical properties of the enzyme in ubiquitination of axin, a critical protein involved in stabilization of beta-catenin [22,23,24]. Besides breast tumorigenesis, this significant observation may suggest a broader role of RNF146 in other types of common cancer.

Hence, further functional analysis is needed to link rs2180341 with tumorigenesis. In our original discovery study, we have demonstrated that rs2180341 tags relatively conserved region of ~100 kb [7]. In the subsequent study [8], our preliminary data indicated a trend of increased expression of RNF146 with the dosage of high-risk allele of rs2180341. While sequencing of the subset of breast tumors did not identify any coding SNPs in RNF146 associated with the risk allele [8], it is likely that there are other non-coding variants correlated with rs2180341 that may explain observed genotype/expression trend. Using the data from recent release of 1000 genomes we have identified several SNPs highly correlated with rs2180341; 2 of them with significantly predictive functional impact on putative transcription binding sites (Supporting Information S1). Interestingly, rs2180341 maps in a histone mark region, identified by CHIP-seq (Supporting Information S1), suggesting potential involvement of these variants in regulation of the expression of nearby genes, including RNF146. In order to provide further biological insight, the more systematic analysis would be needed to test the correlation of RNF146 expression with identified genetic variants in larger subset of breast tumors.

In conclusion, this large study found evidence for a weak overall association between the 6q22.33 locus and sporadic breast cancer risk. Relative risk estimates for rs2180341 were lower in non-AJ Europeans as compared to AJ populations. The study illustrates the difficulties inherent in the reliable estimation of low risk susceptibility alleles – even with a study as large as the current one, in which the overall effect was only marginally significant. It is likely there are many such variants, conferring ORs<1.1, and characterizing such associations with common diseases disease presents a major challenge. It is possible that comprehensive sequencing across the region may identify the true causal variant(s) with stronger effects. If the heterogeneity among studies is due to differences in linkage disequilibrium (LD), fine-scale mapping might also allow identification of more strongly associated variants. The combined effect of these common variants and other as-yet undiscovered rare variants, together with lifestyle risk factors, could provide the basis for risk algorithms for the preventive management of breast cancer.
Supporting Information

Funding Information

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Supporting Information S1 Table A: Summary of the 25 breast cancer case studies used in the BCAC analyses

Table B: Genotype frequency among Caucasian BCAC case and controls, minor allele frequencies (MAF), and Hardy-Weinberg Equilibrium (HWE) by study Table C: Summary of the 11 breast cancer case studies used in the CIMBA analyses Table D: Genotype frequency among CIMBA case and controls, minor allele frequencies (MAF), and Hardy-Weinberg Equilibrium (HWE) by study Table E: Ethics committee approvals (IRB approvals) Table F: SNPs from 6q22.33 with the highest functional impact and highly correlated with rs2180341. Correlated proxies of rs2180341 (r2>0.8) were extracted from latest release of 1000 genomes project on ~300 individuals of European ancestry. The functional impact of all correlated SNPs was assessed using the pipelines of ANNOVAR suite. The functional impact (FI) of each SNP for each of 3 selected categories is defined by FI score. TF binding site prediction also includes DNAI hypersensitivity data. Conserved elements were assessed using placental 46way analysis. r-square values are relative to rs2180341.

(DOCX)

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Author Contributions


References