Kirchhoff, T; Gaudet, MM; Antoniou, AC; McGuffog, L; Humphreys, MK; Dunning, AM; Bojesen, SE; Nordestgaard, BG; Flyger, H; Kang, D; Yoo, KY; Noh, DY; Ahn, SH; Dork, T; Schurmann, P; Karstens, JH; Hilleman, P; Couch, FJ; Olson, J; Vachon, C; Wang, XS; Cox, A; Brock, I; Elliott, G; Reed, MWR; Burwinkel, B; Meindl, A; Brauch, H; Hamann, U; Ko, YD; Broeks, A; Schmidt, MK; Van ’t Veer, LJ; Braaf, LM; Johnson, N; Fletcher, O; Gibson, L; Peto, J; Turnbull, C; Seal, S; Renwick, A; Rahman, N; Wu, PE; Yu, JC; Hsiung, CN; Shen, CY; Southey, MC; Hopper, JL; Hammet, F; van Dorpe, T; Dieudonne, AS; Hatse, S; Lambrechts, D; Andurilis, IL; Bogdanova, N; Antonenkova, N; Rogov, JI; Prokofieva, D; Bermisheva, M; Khusnutdinova, E; van Asperen, CJ; Tollenaar, Raem; Hooning, MJ; Devilee, P; Margolin, S; Lindblom, A; Milhe, RL; Arias, JI; Zamora, MP; Benitez, J; Severi, G; Baglietto, L; Giles, GG; Spurde, AB; Beesley, J; Chen, XQ; Holland, H; Healey, S; Wang-Gohrke, S; Chang-Claude, J; Mannermaa, A; Kosma, VM; Kauppinen, J; Kataja, V; Aagnarsson, BA; Caligo, MA; Godwin, AK; Nevanlinna, H; Heikkinen, T; Fredericksen, Z; Lindor, N; Nathanson, KL; Domchek, SM; Loman, N; Karlsson, P; Askalnalm, MS; Melin, B; von Wachenfeldt, A; Hogervorst, FBL; Verheus, M (2012) Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. PLoS One, 7 (6). ISSN 1932-6203 DOI: 10.1371/journal.pone.0035706

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DOI: 10.1371/journal.pone.0035706

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Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of 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.


Editor: Ludmila Prokunina-Olsson, National Cancer Institute, National Institutes of Health, United States of America

Received November 16, 2011; Accepted March 20, 2012; Published June 29, 2012

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Funding: Due to the international scale of the collaboration, which included two large consortia, each a consortium of consortia, and a large number of funding sources for each participating center, the description of sources of funding for the study is detailed in Supporting Information, Funding S1. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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

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† These authors contributed equally to this work.
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 one study (MSKCC, see study acronyms in Supporting Information S1) contributed data to these analyses. Data were obtained from all participants. For detailed description, see Supporting Information S1.

Breast Cancer Association Consortium (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 I² 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 \( \text{BRCA1} \) and \( \text{BRCA2} \) 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. This was defined either by the age at interview or age at follow-up depending on the information provided by the participating center. 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 \( \text{BRCA1/2} \) mutation carriers beyond age 80.

All analyses were performed with STATA (Version 10.0).

Results

Description of BCAC Study Population

The mean (±SD) age was 53.1 (±13.1) years for invasive cases, 52.7 (±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).

Figure 1. Forest plot of SNP rs2180341 per-allele odds ratios (ORs) and 95% confidence intervals (CIs) with the risk of breast cancer among studies from Breast Cancer Association Consortium (BCAC) breast cancer cases and controls of European ancestry. Studies are weighted and ranked according to the inverse of the between-study and within study variation of the log odds ratio, which is also represented by the size of the shaded box around the study-specific point estimate. The solid line indicates the OR = 1 and the dashed line indicates the summary OR of all studies. A description of the study acronyms can be found in the Supporting Information S1.

doi:10.1371/journal.pone.0035706.g001
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 ($I^2 = 49.3%$; 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: $I^2 = 0.0%$, 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 ($I^2 = 89.3%$; p = 0.002).

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 0.80–0.99, p = 0.04, Table 2A). The per-allele HR estimate for BRCA2 mutation carriers was 1.02, 95% 0.90–1.16, p = 0.75 (Table 2, 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

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**Table 1.** Summary odds ratios (ORs) and 95% confidence intervals (CIs), adjusted for age and study, for SNP rs2180341 genotypes and breast cancer risk, Breast Cancer Association Consortium (BCAC).

<table>
<thead>
<tr>
<th>Genotype</th>
<th>No. of studies</th>
<th>No. of cases</th>
<th>No. of controls</th>
<th>MAF</th>
<th>Pooled OR$^1$ (95% CI)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Among Women of European Ancestry</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>15,526</td>
<td>18,154</td>
<td>1</td>
<td></td>
<td>1.03 (0.99 – 1.06)</td>
<td>0.13</td>
</tr>
<tr>
<td>AG</td>
<td>10,644</td>
<td>12,142</td>
<td>1.03</td>
<td></td>
<td>(0.99 – 1.06)</td>
<td>0.13</td>
</tr>
<tr>
<td>GG</td>
<td>23</td>
<td>1,780</td>
<td>24.8</td>
<td>1.07</td>
<td>1.06 (0.99 – 1.14)</td>
<td>0.082</td>
</tr>
<tr>
<td>recessive</td>
<td></td>
<td></td>
<td></td>
<td>1.06</td>
<td>(0.99 – 1.14)</td>
<td>0.082</td>
</tr>
<tr>
<td>per allele</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1.03 (1.00 – 1.06)</td>
<td>0.023</td>
</tr>
<tr>
<td><strong>Among Women of Asian Ancestry$^2$</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>1,604</td>
<td>1,228</td>
<td>1</td>
<td></td>
<td>0.99 (0.87 – 1.12)</td>
<td>0.85</td>
</tr>
<tr>
<td>AG</td>
<td>1,041</td>
<td>785</td>
<td>0.99</td>
<td></td>
<td>(0.78 – 1.25)</td>
<td>0.93</td>
</tr>
<tr>
<td>GG</td>
<td>2</td>
<td>191</td>
<td>24.6</td>
<td>0.99</td>
<td>0.99 (0.79 – 1.25)</td>
<td>0.96</td>
</tr>
<tr>
<td>recessive</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>(0.79 – 1.25)</td>
<td>0.96</td>
</tr>
<tr>
<td>per allele</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.99 (0.90 – 1.09)</td>
<td>0.85</td>
</tr>
</tbody>
</table>

$^1$ORs were adjusted for study.

$^2$MAF = minor allele frequency.

Ten studies contributed samples from women self-described as Asian. Two of these studies were conducted in Asian countries and contributed the majority of Asian samples.

doi:10.1371/journal.pone.0035706.t001
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 = 1.05; 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 stratification, 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 substructure on the observed association.

The chance is also a likely explanation of observed heterogeneity 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
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 ascertnements (e.g. prevalence of familial versus sporadic cases or clinical versus population – based ascertainmentes), 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

### 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>OR(^1) (95% CI)</th>
<th>No. of cases</th>
<th>No. of controls</th>
<th>OR(^1) (95% CI)</th>
<th>p for tumor heterogeneity</th>
</tr>
</thead>
<tbody>
<tr>
<td>ER+</td>
<td>AA 6,584 19,554 1</td>
<td>1,930 19,554 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>AG 4,632 13,067 1.04 (1.00 – 1.09) 1,309 13,067 1.01 (0.93 – 1.10)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GG 740 2,079 1.07 (0.97 – 1.18) 186 2,079 0.94 (0.79 – 1.12)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>recessive</td>
<td>1.05 (0.96 – 1.16)</td>
<td>0.93 (0.79 – 1.11)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>per allele</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>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Table 4. Adjusted\(^1\), 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>MAF(^3)</th>
<th>HR (95% CI)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Among BRCA1 Mutation Carriers</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>1,041 934 1</td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AG</td>
<td>582 602 0.87 (0.76 – 1.00) 0.05</td>
<td>0.89 (0.68 – 1.16) 0.4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GG</td>
<td>11 96 106 24.8 0.85 (0.64 – 1.11) 0.23</td>
<td>0.89 (0.80 – 1.00) 0.048</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>recessive</td>
<td>0.89 (0.68 – 1.16) 0.4</td>
<td>0.89 (0.80 – 1.00) 0.048</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>per allele</td>
<td>0.89 (0.68 – 1.16) 0.4</td>
<td>0.89 (0.80 – 1.00) 0.048</td>
<td></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

|          | Among BRCA2 Mutation Carriers | | | | | |
| AA       | 605 528 1 | 1          |              |           |             |         |
| AG       | 384 384 0.97 (0.82 – 1.15) 0.73 | 1.14 (0.86 – 1.56) 0.33 | |
| GG       | 11 68 51 25.2 1.15 (0.84 – 1.56) 0.38 | 1.14 (0.86 – 1.56) 0.33 | |
| recessive| 1.14 (0.86 – 1.56) 0.33 | 1.14 (0.86 – 1.56) 0.33 | |
| per allele | 1.02 (0.90 – 1.16) 0.75 | 1.02 (0.90 – 1.16) 0.75 | |

\(^1\)Adjusted for birth year and study.
\(^2\)Restricted to women of European descent.
\(^3\)MAF = Minor allele frequency.

doi:10.1371/journal.pone.0035706.t003
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-penetrance 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 (PIASA 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 F1 The description of sources of funding for the study in detail.

(DOCX)

Supporting Information F1 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. TT binding site prediction also includes DNA hypersensitivity data. Conserved elements were assessed using placental 46way analysis. r-square values are relative to rs2180341.

(DOC)

Acknowledgments

BCAC: We thank all the participants for taking part in this research.

The KBCP: We thank Mrs Eija Myolainen and Mrs Helena Kemiläinen for their skillful assistance.

The HABCS: We gratefully acknowledge the technical assistance of Marion Haichukiewicz in DNA sample preparation. We furthermore thank Peter Hillemanns, Christof Sohn, Alexander Scharf, Michael Bremer and Johann Hinrich Karstens for their invaluable support in terms of infrastructure and patient samples.

The LMBW: We thank Gillian Peuteman, Dominique Smeets and Sofie Van Soest for technical assistance.

The GC-HBCS study: We are thankful to Bernd Frank for participating in genotyping.

The CARDI-BCS: We thank Anna Gonzalez-Neira, Charo Alonso and Tais Moreno for their technical support.

The ABCS study: The ABCS would like to acknowledge Richard van Hien, Sten Cornelissen, Florida van Leeuwen, Rob Tollenaar and all contributors to the ‘BOSOM’ study, and the support of Dr. H.B. Bueno-Figueroa for the release of control DNA.

The ABCFS: We want to thank Letitia Smith for her contribution to the genotyping for ABCFS. John Hopper is an Australia Fellow of the National Health and Medical Research Council (NHMRC) and Melissa Southey is a NHMRC Senior Research Fellow.

The SBCS: We would like to thank Sue Higham, Helen Cramp and Dan Connley, for their contribution to the SBCS.

The kConFab: ACS/AOCS: The AOCs Management Group (D Bowtell, G Chenevix-Trench, A deFazio, D Gertig, A Green, and PM Webb) gratefully acknowledges the contribution of all the clinical and scientific collaborators (see http://www.aocstudy.org/), the AOCs and the ACS Management Group (A Green, P Parsons, N Hayward, P Webb, D Whiteman) thank all of the project staff, collaborating institutions and study participants.

CIMBA: The Kathleen Cunningham Consortium for Research into Familial Breast Cancer (kConFab): We thank Heather Thorne, Eveline Niedermayer, all the kConFab research nurses and staff, the heads and staff of the Family Cancer Clinics, and the Clinical Follow-Up Study for their contributions to this resource, and the many families who contribute to kConFab.

The AOCs Management Group (D Bowtell, G Chenevix-Trench, A deFazio, D Gertig, A Green, and PM Webb) gratefully acknowledges the contribution of all the clinical and scientific collaborators (see http://www.aocstudy.org/), the AOCs and the ACS Management Group (A Green, P Parsons, N Hayward, P Webb, D Whiteman) thank all of the project staff, collaborating institutions and study participants.

The HERBCS study: We thank Drs. Kristina Attomällä and Carl Blomqvist for their help with the patient data and samples.

The Swedish BRCA1 and BRCA2 study collaborators (SWE-BRCA): Per Karlsson, Margareta Nordling, Anika Bergman and Zakaria Einbeigti, Göteborg University, Hospital: Maria Lindgren, Sigrun Lidgren, Linkoping University Hospital; Ake Borg, Niklas Loman, Hakan Olsson, Ulf Kristoffersson, Helena Järnlund, Karin Henriksson, Lumi University Hospital; Annika Lindholm, Brita Arve, Anna von Wachenfeldt, Annelie Lieljegren, Gisela Barbany-Bustinda and Johanna Kantala, Stockholm, Karolinska University Hospital; Beatrice Melin, Henrik Gronberg, Eva-Lena Statin and Monica Emmanuell, Umeå University Hospital; Hans Elneckrona, Richard Rosenquist Brandell and Niklas Dahl, Uppsala University Hospital.

The Hereditary Breast and Ovarian Cancer Research Group Netherlands (HEBON): HEBON Collaborating Centers: Coordinating center: Netherlands Cancer Institute, Amsterdam: Frans B. L. Hogervorst, Sanne Verhoef; Martijn Verheus, Laura J. van ‘t Vee, Flora E. van Leeuwen, Matti A. Rookus; Erasmus Medical Center, Rotterdam: Margriet Collée, Ans M.W. van den Ouweland, Agnes Jager, Maartje J. Hooning, Madeleine M.A. Tilanus-Linthorst, Leiden University Medical Center: Leonie C. Christi J. van Asperen, Julis T. Wijnen, Maaike P. Vreeswijkstra, Rob A. Tollenaar, Peter Devilee; Radboud University Nijmegen Medical Center, Nijmegen: Marjolijn J. Liitgen, Nicoole Hoogerbrugge; University Medical Center Utrecht, Utrecht: Margreet G. Ausems, Rob B. van der Luijt; Amsterdam Medical Center: Cora M. Aaij, Theo A. van Os; VU University Medical Center, Amsterdam: Johan J.P. Gille, Quinten Wijnhoven; Ferskeef Heijboer; University Hospital Maastricht, Maastricht: Ercan B. Gomez-Garcia, Cees E. van Rosendoel, Marius J. Blok; University Medical Center Groningen University: Jan C. Oosterwijk, Annemarie H van der Horst, Marian J. Maurit, The Netherlands Foundation for the detection of hereditary tumours, Leiden, the Netherlands: Hans F. Vasen.

Epidemiological study of BRCA1 and BRCA2 mutation carriers (EMBRACE): Douglas F. Easton is the PI of the study. EMBRACE Collaborating Centers are: Coordinating center: Netherlands Cancer Institute, Amsterdam: Hans F. Vasen.

EMBRACE Collaborating Centers: Centres for BRCA1 and BRCA2 mutation carriers (EMBRACE): Hans F. Vasen.


Author Contributions

References