

Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Gene-Environment Interactions

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ABSTRACT: Genes that alter disease risk only in combination with certain environmental exposures may not be detected in genetic association analysis. By using methods accounting for gene-environment ($G \times E$) interaction, we aimed to identify novel genetic loci associated with breast cancer risk. Up to 34,475 cases and 34,786 controls of European ancestry from up to 23 studies in the Breast Cancer Association Consortium were included. Overall, 71,527 single nucleotide polymorphisms (SNPs), enriched for association with breast cancer, were tested for interaction with 10 environmental risk factors using three recently proposed hybrid methods and a joint test of association and interaction. Analyses were adjusted for age, study, population stratification, and confounding factors as applicable. Three SNPs in two independent loci showed statistically significant association: SNPs rs10483028 and rs2242714 in perfect linkage disequilibrium on chromosome 21 and rs12197388 in ARID1B on chromosome 6. While rs12197388 was identified using the joint test with parity and with age at menarche (P -values = 3×10^{-07}), the variants on chromosome 21 q22.12, which showed interaction with adult body mass index (BMI) in 8,891 postmenopausal women, were identified by all methods applied. SNP rs10483028 was associated with breast cancer in women with a BMI below 25 kg/m² (OR = 1.26, 95% CI 1.15–1.38) but not in women with a BMI of 30 kg/m² or higher (OR = 0.89, 95% CI 0.72–1.11, P for interaction = 3.2×10^{-05}). Our findings confirm comparable power of the recent methods for detecting $G \times E$ interaction and the utility of using $G \times E$ interaction analyses to identify new susceptibility loci. *Genet Epidemiol* 38:84–93, 2014. © 2013 Wiley Periodicals, Inc.

KEY WORDS: breast cancer risk; gene-environment interaction; polymorphisms; body mass index; case-control study

Introduction

The risk of breast cancer, the most common malignant disease in women, is known to be influenced by multiple genetic and nongenetic (environmental¹) factors. Among the most important environmental risk factors are reproductive factors, such as parity (the number of births) and age at menarche, but exogenous hormone use, anthropometric factors, such as body height and body mass index (BMI), and several other lifestyle factors are also associated with breast cancer risk [Bakken et al., 2011; Bergström et al., 2001; Clavel-Chapelon, 2002; Collaborative Group on Hormonal Factors in Breast Cancer, 1996; Ewertz et al., 1990; Key et al., 2006; Ursin et al., 1995; van den Brandt et al., 2000]. Nevertheless, one of the strongest risk factors for breast cancer is having a family member with a diagnosis of breast cancer [Pharoah et al., 1997]. Several high-penetrance genes, such as *BRCA1* and *BRCA2*, as well as moderate penetrance genetic risk variants have been identified. Disease-causing mutations in *BRCA1* and *BRCA2* increase breast cancer risk up to 20-fold [Mavaddat et al., 2010; Stratton and Rahman, 2008]. However, due to the low frequency of the high-risk and moderate

risk variants, they account for only about 20% of familial breast cancer. Genetic association analyses have additionally identified a number of common genetic susceptibility variants. Recently, the large-scale Collaborative Oncological Gene-environment Study (COGS) validated 23 of 27 previously established breast cancer loci and identified 41 new loci associated with overall breast cancer risk, 4 additional loci for estrogen receptor negative breast cancer, and 2 loci for *BRCA1* and *BRCA2* mutation carriers [Couch et al., 2013; Garcia-Closas et al., 2013; Gaudet et al., 2013; Michailidou et al., 2013]. All the common genetic loci, taken together, have been estimated to explain about 30% of familial risk [Michailidou et al., 2013]. Gene-gene and gene-environment ($G \times E$) interactions may explain a further part of the remaining familial breast cancer risk [Mavaddat et al., 2010]. Testing for interactions with previously identified common susceptibility variants for breast cancer has led to very few consistent results [Campa et al., 2011; Marian et al., 2011; Milne et al., 2010; Nickels et al., 2013; Prentice et al., 2010, 2009; Rebbeck et al., 2009; Travis et al., 2010].

An agnostic approach to identify $G \times E$ interactions using existing genome-wide association data has been considered a largely untapped potential means to detect new genetic variants associated with disease risk [Thomas et al., 2012]. As the standard case-control approach is known to have low power for detecting multiplicative $G \times E$ interactions, alternative methods with greater power have been developed for testing for $G \times E$ interactions in large-scale association studies [Mukherjee et al., 2012]. For large-scale scans,

Supporting Information is available in the online issue at wileyonlinelibrary.com.

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¹Environmental factors include all factors that are not directly measurable from genomic DNA but could nevertheless be partly genetically determined.

Table 1. Description of the environmental risk factors by case-control status from 23 studies in the BCAC

Risk factor	Category	Cases	Controls	All
Reference age	<i>N</i>	34,475	34,786	69,261
	<i>N</i> premenopausal	13,954	14,532	28,486
	<i>N</i> postmenopausal	20,521	20,254	40,775
	Mean (SD) ^a	56.2 (11.2)	55.5 (11.5)	55.9 (11.4)
Number of births (parity)	<i>N</i> ^b	27,174	28,508	55,682
	Mean (SD) ^a	1.9 (1.3)	2.0 (1.3)	1.9 (1.3)
Age at menarche (menarche)	<i>N</i> ^b	21,942	23,109	45,051
	Mean (SD) ^a	13.1 (1.6)	13.1 (1.6)	13.1 (1.6)
Adult body height (cm, height)	<i>N</i> ^b	24,016	20,178	44,194
	Mean (SD) ^a	164 (6.6)	165 (6.6)	164 (6.6)
BMI (kg/m ² , postmenopausal women, BMI post)	<i>N</i> ^b	4,423	4,468	8,891
	Mean (SD) ^a	25.2 (4.5)	24.8 (4.2)	25.0 (4.4)
BMI (kg/m ² , premenopausal women, BMI pre)	<i>N</i> ^b	1,759	1,446	3,205
	Mean (SD) ^a	24.7 (5.1)	25.5 (5.6)	25.0 (5.4)
Use of oral contraceptives (years, oral contraceptive duration)	<i>N</i> ^b	11,017	11,911	22,928
	Mean (SD) ^a	5.3 (7.0)	5.9 (7.1)	5.6 (7.1)
Estrogen-progesterone therapy (years, postm. women, ^a estrogen-progesterone therapy duration)	<i>N</i> ^b	3,790	4,057	7,847
	Mean (SD) ^a	1.7 (4.3)	1.2 (3.7)	1.4 (4.0)
Estrogen therapy (years, postm. women, ^a estrogen therapy duration)	<i>N</i> ^b	3,876	4,085	7,961
	Mean (SD) ^a	1.3 (4.1)	1.0 (3.5)	1.1 (3.8)
Alcohol consumption (grams per day, alcohol)	<i>N</i> ^b	3,812	4,055	7,867
	Mean (SD) ^a	7.3 (16.0)	6.8 (11.3)	7.1 (13.8)
Family history of breast cancer (famhist)	<i>N</i> ^b	20,108	18,522	38,630
	Yes (%)	4,213 (21%)	1,606 (9%)	5,819 (15%)

^a Women who stopped hormone therapy before diagnosis/interview were assigned 0 years of therapy.

^b *N* is the final sample size for analysis without individuals with unknown values in the variable or any of the adjustment variables.

two-step procedures attempt to gain power through enrichment of possible $G \times E$ interaction after a first screening step for marginal genetic association and/or $G \times E$ correlation [Gauderman et al., 2013; Hsu et al., 2012; Murcay et al., 2011]. Testing jointly for marginal genetic association and $G \times E$ interaction in a two degree of freedom (*df*) test has been shown to achieve good power in gene discovery [Dai et al., 2012; Kraft et al., 2007].

We, therefore, aimed to identify new breast cancer susceptibility loci using about 71,500 single nucleotide polymorphisms (SNPs) enriched for association with breast cancer, by employing different recently proposed methods that account for $G \times E$ interaction in a large pooled dataset from studies participating in the Breast Cancer Association Consortium (BCAC).

Methods

Study Participants

We analyzed primary data from 21 case-control and 2 cohort studies in European populations participating in BCAC (Supplementary Table S1). These studies fulfilled the criteria of comprising individuals of European descent and having at least 200 cases and 200 controls with information on age and at least one of the environmental risk factors of interest. All studies were approved by the relevant ethics committees and informed consent was obtained from all participants. All studies collected data with standardized questionnaires. To reconcile differences in study questionnaires, a multistep harmonization procedure was applied to data submitted by all studies according to a common data dictionary. All time-dependent variables were assessed at reference age, which was

defined as the age at diagnosis for cases and the age at enrolment for controls in cohort studies, and age at diagnosis for cases and age at interview for controls in case-control studies [Nickels et al., 2013]. Menopausal status was defined based on reference age: women aged ≤ 54 years were considered as being premenopausal and women aged > 54 years as being postmenopausal [Nickels et al., 2013]. To calculate adult BMI, we used the variable “usual weight.” For this variable, women were asked for their usual weight in adulthood or their weight a year ago. Participants were excluded from analysis if they were male, were prevalent cases at recruitment in Melbourne Collaborative Cohort Study (MCCS), were not of European descent, or had a missing value for reference age, the specific environmental variable of interest, or the related adjustment variables. The number of women included in analyses therefore varied according to the environmental factor being studied (Table 1).

Genetic Information

Genotyping was carried out in BCAC with the collaboration of three other consortia as part of the COGS. Details of initial SNP selection, genotyping, and quality-control criteria are available in the supplementary material of a recent publication [Michailidou et al., 2013]. Briefly, genotyping of 211,155 SNPs proposed by the four consortia was carried out using an Illumina iSelect genotyping array (iCOGS). Of the 70,862 SNPs proposed by BCAC, 61,240 SNPs had originally been selected from a meta-analysis of nine genome-wide association studies of breast cancer risk, which has led to the discovery of 41 new susceptibility loci for breast cancer [Michailidou et al., 2013]. The remaining SNPs were (i) for fine mapping of

known susceptibility loci, (ii) in selected candidate genes or pathways (iii) potentially related to prognosis, or (iii) associated with cancer-related quantitative traits or other cancers. After genotyping, standard quality-control measures were applied to all SNPs and all samples genotyped. SNPs were excluded from the database if their genotypes were discrepant in more than 2% of the duplicate samples across all consortia using this array. SNPs were also excluded if their call rates were below 95% or if their distribution in controls strongly deviated from Hardy–Weinberg Equilibrium ($P < 10^{-6}$). Study participants were excluded from all analyses if the overall call rate was below 95% or if heterozygosity deviated significantly from that expected in the general population (either lower or higher, $P < 10^{-6}$). We used genotype data of 87,658 SNPs nominated by BCAC as well as SNPs of common interest, for example, because of possible association with breast cancer related traits or other cancer sites, which remained after application of quality-control criteria. The present analysis aimed to identify new breast cancer susceptibility loci by considering $G \times E$ interaction, therefore fine mapping SNPs for the previously identified regions were excluded from analysis, leading to a final number of 71,527 SNPs. Genotype intensity cluster plots were checked manually for SNPs in each new region yielding a statistically significant $G \times E$ interaction using any one of the methods employed and SNPs were eliminated if the clustering was judged to be poor. SNP annotations were checked using HaploReg v2 [Ward and Kellis, 2012], and the UCSC Genome Browser [Meyer et al., 2013]. Information on linkage disequilibrium (LD) structure around identified SNPs was obtained using SNP Annotation and Proxy Search (SNAP) [Johnson et al., 2008].

Statistical Analysis

Ten established environmental risk factors for breast cancer were considered. The specific risk variables were selected based on the marginal effects for these risk factors derived from meta-analyses of the nine population-based studies and included number of full-term pregnancies, age at menarche, adult body height, adult BMI (separately for postmenopausal and premenopausal women), duration of oral contraceptive use, duration of menopausal hormone therapy in current users (separately for estrogen-progesterone therapy and estrogen-only therapy), average daily alcohol intake, and family history of breast cancer in first-degree relatives. All 10 environmental variables were evaluated as continuous variables with the exception of family history of breast cancer.

SNPs were assessed using a log-additive model, in which the SNPs are coded according to the number of minor alleles (0–1–2) and analyzed as continuous variables. All analyses were adjusted for reference age, study, and six principal components (PCs) to account for population stratification, with an additional PC for the study Leuven Multidisciplinary Breast Centre (LMBC). The PCs had initially been derived by analyzing 37,000 uncorrelated SNPs that had been genotyped on the same array for other consortia [Michailidou et al., 2013].

Further adjustment variables or restrictions were applied according to the environmental variables assessed (Supplementary Table S2).

Four recently proposed methods that exploit $G \times E$ interaction to detect new disease-associated SNPs were applied. Three methods were designed to test for $G \times E$ interaction: (i) the hybrid two-step (H2) approach, (ii) a cocktail method (Cocktail), and (iii) a joint screening (EDG \times E) approach [Gauderman et al., 2013; Hsu et al., 2012; Murcray et al., 2011]. The fourth method was designed to test jointly for genetic main effect and $G \times E$ interaction: the $2df$ test [Dai et al., 2012]. The H2, Cocktail, and EDG \times E approaches are two-step approaches, which combine a testing step with a screening step and a multiple testing correction module. All three methods use the same two tests in the screening step. The first test is a marginal test for genetic association, where the association of the SNPs with the disease of interest is tested without inclusion of the environmental factor. The second test in the screening step tests for correlation between the environmental factor and the SNP, where one is used as an explanatory variable for the other. This test is performed in combined cases and controls, and takes advantage of the oversampling of cases as compared with the general population.

The H2 approach sets certain P -value thresholds for SNPs to pass the marginal and the correlation screening step [Murcray et al., 2011]. Only those SNPs that pass at least one of the screening steps are further tested for $G \times E$ interaction. For the screening step for H2, the proposed thresholds of 10^{-5} for the marginal screening step and 10^{-3} for the correlation screening were used. $G \times E$ interaction is tested using the likelihood ratio test to compare the logistic regression models with and without an interaction term, as in standard case-control analysis. The P -value thresholds for the testing step are calculated by dividing the desired P -value level by the number of SNPs that passed the respective screening step. As two screening steps are performed, a weighting factor of 0.5 is applied to both (giving them equal weight) in order to maintain the overall significance level. SNPs that pass both screening steps are assigned the higher P -value.

In the Cocktail approach, the common screening P -value is assigned the P -value of the correlation screening if this P -value is below a predefined threshold (in our case 10^{-3}) [Hsu et al., 2012]. Otherwise, it is assigned the P -value from the marginal screening test. For the testing step, either standard case-control analysis or a case-only analysis is applied depending on the P -values in the screening tests [Hsu et al., 2012]. If the screening P -value corresponds to the P -value from the marginal screening, SNPs are tested with case-only analysis and case-control analysis otherwise. Subsequently, all SNPs are sorted in ascending order by the screening P -value. According to the weighted hypothesis testing, j groups of increasing size are formed by the equation: $size_j = 5 \times 2^{(j-1)}$. All SNPs of j groups are assigned identical alpha thresholds by the formula: $\alpha_j = 0.05/[5 \times 2^{(2j-1)}]$, which ensures that the overall desired alpha level of 0.05 is maintained [Ionita-Laza et al., 2007]. A SNP is considered significant in the Cocktail

approach if the P -value from the testing step is below the alpha threshold for the respective group determined in the screening step.

The EDG \times E approach combines the chi-square values from both screening tests into one value and compares it with the chi-square distribution at 2 df [Gauderman et al., 2013]. Resulting P -values are sorted in ascending order and alpha thresholds for j groups are calculated according to the weighted hypothesis testing approach. In the testing step, the EDG \times E approach uses case-control analysis and the resulting P -values are compared to the thresholds calculated based on the screening step.

The 2 df test jointly tests marginal association and $G \times E$ interaction [Kraft et al., 2007]. We employed the newly proposed procedure to combine the two independent tests for the marginal genetic association and for the $G \times E$ interaction, exploiting the independence between the two tests [Dai et al., 2012]. This is a chi-squared test applied to the sum of the two squared z scores or log P -values. To correct for multiple testing, Bonferroni correction was applied leading to a P -value threshold of about 7×10^{-7} in the present analysis. Dai et al. offered three different options to test for $G \times E$ interaction, of which the standard case-control logistic regression was chosen to avoid biased results due to violation of the $G \times E$ independence assumption in the population [Dai et al., 2012].

For comparison, standard case-control logistic regression (CC) for $G \times E$ interaction with the Bonferroni-corrected P -value threshold of 7×10^{-7} was also applied. To assess study heterogeneity, we estimated odds ratios (OR) for the per-allele genetic main effect and $G \times E$ interaction for each individual study, adjusting for age, and assessed P -values for heterogeneity using a Q-test. Subjects with missing data for a particular SNP or environmental factor were excluded from the respective analysis. We also calculated stratum-specific per-allele ORs for each SNP tested statistically significant using any one of the methods employed. Data preparation and statistical analyses were performed with SAS software (release 9.2) and the R Language and Environment for Statistical Computing, version 2.15.0.

Results

The mean age at recruitment of the study participants was 56 years (Table 1). The sample size and number of studies included for the analyses of the 10 different environmental

variables varied between 3,205 women from 4 studies for BMI among premenopausal women and 55,682 women from 22 studies for the number of full-term pregnancies. The exact numbers by study are shown in Supplementary Table S3.

Overall, three SNPs showing a statistically significant association were detected in the analysis of $G \times E$ interaction between 10 environmental variables and 71,527 SNPs. Not all were detected by all four methods applied and none was detected using the standard CC approach. All three SNPs were found with the 2 df test (Table 2). The latter two of these SNPs were also found to show statistically significant interaction using the other three approaches (Supplementary Tables S4a–c). One SNP is located on chromosome 6 and the other two SNPs are located on chromosome 21q22.12. The latter two SNPs lie in a distance of about 4,000 base pairs, which makes recombination unlikely [Li and Freudenberg, 2009], and are in perfect LD ($r^2 = 1.0$) [Hapmap, 2013]. The SNPs, which were all found to be statistically significantly associated using the 2 df test, have not been identified previously as being associated with breast cancer risk and are not in LD with known susceptibility loci.

The two associated SNPs on chromosome 21q22.12 (rs10483028 and rs2242714) were identified by analyzing interaction with adult BMI in a sample of 8,891 postmenopausal women from seven studies. Considering the $G \times E$ interaction effect (OR = 0.84) was essential for the identification of the two SNPs. The SNP rs10483028 on chromosome 21 showed a decreased effect with increasing BMI, the per-allele ORs being 1.26 (95% CI 1.15–1.38) in women with BMI <25 kg/m², 1.10 (95% CI 0.96–1.26) in women with BMI between 25 kg/m² and 30 kg/m², and 0.89 (95% CI 0.72–1.11) in women with BMI >30 kg/m² (Fig. 1).

SNP rs12197388 on chromosome 6 was identified in interaction analyses with age at menarche and with parity. This SNP did not show a clear $G \times E$ interaction (OR = 1.09) with either risk factor but passed the threshold of the 2 df test (7×10^{-7}) due to its highly significant marginal association ($P < 6 \times 10^{-8}$).

There was little or no evidence for heterogeneity by study in the $G \times E$ interaction ORs for the three identified SNPs. This was also true for the marginal associations of the SNPs with breast cancer risk (Supplementary Table S5 and Supplementary Figure S1 [panel A1–A4]). None of the three identified SNPs had been selected for COGS Illumina iSelect genotyping array (iCOGS) with respect to the environmental factors studied and none was found to be substantially correlated with parity/age at menarche and adult BMI in

Table 2. Significantly associated SNPs with $P < 7 \times 10^{-7}$ in the analysis of multiplicative interaction between 71,527 SNPs and 10 environmental risk factors for breast cancer, using the 2 df test

SNP	Chromosome	Region	Position build 36	Environmental variable	P -value marginal	OR marginal	P -value interaction	OR interaction	P -value 2 df test
rs12197388	6	ARID1B	161630341	Parity	5.69×10^{-8}	1.09	0.37	1.01	2.68×10^{-7}
				Menarche	5.24×10^{-8}	1.09	0.52	0.99	2.99×10^{-7}
rs10483028 ^a	21	21q22.12	35595443	BMI post	1.70×10^{-5}	1.17	3.19×10^{-5}	0.84	1.68×10^{-8}
rs2242714 ^a	21	21q22.12	35599557	BMI post	2.47×10^{-5}	1.16	4.12×10^{-5}	0.84	3.07×10^{-8}

^a These two SNPs were also identified to show statistically significant multiplicative interaction with BMI using the H2, Cocktail, and EDG \times E approaches (see Supplementary Tables S4a–c).

Effect of rs10483028 by strata of usual BMI

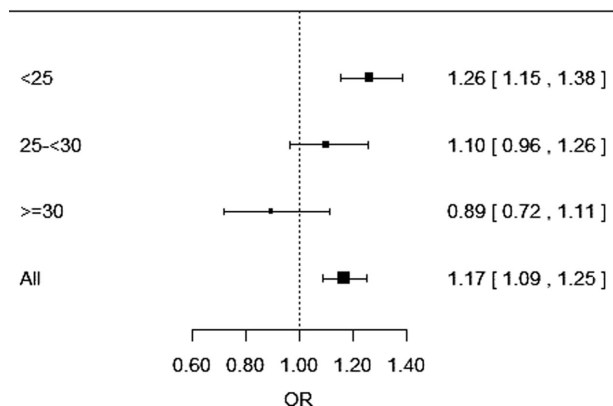


Figure 1. Effect of rs10483028 on breast cancer risk by strata of adult BMI in 8,891 postmenopausal women from BCAC.

postmenopausal women, respectively (Supplementary Table S6).

Discussion

To our knowledge, this is the first large-scale agnostic search for $G \times E$ interaction to identify new susceptibility loci for breast cancer. To gain power, three recently developed two-step approaches for testing for $G \times E$ interaction as well as a joint test for marginal association and $G \times E$ interaction were used. We identified three SNPs representing two genetic loci associated with breast cancer risk.

The two SNPs rs10483028 and rs2242714 on chromosome 21q22.12 showing strong $G \times E$ interaction effects are located outside known genes. Nevertheless, as shown for the region 8q24, these regions might contain enhancer elements, which may affect the expression of genes in the vicinity [Ahmadiyeh et al., 2010]. There are several SNPs in strong LD ($r^2 > 0.8$) with rs10483028 and rs2242714 (Supplementary Figure S3). However, none of them is located in a known regulatory element (Supplementary Figure S4). The *RUNX1* gene is located approximately 300 kb upstream of the two SNPs and has a tumor suppressor role reflected by many somatic mutations in breast tumors. The tumor suppressor activity of *RUNX1* is considered to be mediated in part by antagonism of estrogen signaling [Chimge and Frenkel, 2013]. Recurrent mutations in the *CBFB* transcription factor gene and deletions of its partner *RUNX1* also indicated inactivation of this transcription factor complex in breast cancer [Banerji et al., 2012].

The identified SNP rs12197388 is located on chromosome 6 in an intronic region of *ARID1B*, which belongs to the SWI/SNF chromatin remodeling complex family. SWI/SNF complexes have the ability to enhance or suppress gene transcription by mobilizing nucleosomes [Weissman and Knudsen, 2009]. *ARID1B* has recently been implicated in breast

cancer development through the identification of driver mutations, which confer clonal selective advantage on cancer cells [Stephens et al., 2012]. This gene has been shown to act as a tumor suppressor in pancreatic cancer cell lines [Khursheed et al., 2013]. Mutations in the SWI/SNF complex have also been associated with certain types of syndromes, among those the *ARID1B*-related intellectual disability syndrome [Kosho et al., 2013] as well as with early treatment failure and decreased survival in children with neuroblastoma [Sausen et al., 2013]. Whether rs12197388 potentially influences *ARID1B* function is unclear, as it does not seem to be associated with regulatory elements, and there are no further SNPs in at least moderate LD ($r^2 > 0.6$) with rs12197388 based on data from the 1000 Genomes Project (Supplementary Figure S2).

Our results indicate that accounting for $G \times E$ interaction using two-step/hybrid methods can lead to the identification of new susceptibility loci. All three methods that test only for $G \times E$ interaction identified the two SNPs on chromosome 21 because of a strong interaction between the SNPs and BMI in postmenopausal women but not the SNP rs12197388 on chromosome 6 because of the absence of $G \times E$ interaction. This suggests comparable power of these methods based on empirical evidence, which was also demonstrated by simulation studies [Mukherjee et al., 2012]. The consistency of the results between methods provides some support for the robustness of the finding. The SNP rs12197388, on the other hand, was identified through its marginal effect on breast cancer risk. The association between rs12197388 and breast cancer risk was weaker if all subjects of European descent from BCAC were included, irrespective of the availability of information on the respective environmental risk factors ($OR = 1.05$, $P = 7.2 \times 10^{-5}$). Because the genetic association was not genome-wide statistically significant, rs12197388 was not identified as susceptibility locus for breast cancer in the recent publication [Michailidou et al., 2013]. Restricted to studies that collected information on epidemiologic risks, our finding could be due to chance or through introducing a selection bias that we are currently not able to explain. However, both the marginal association with breast cancer risk of rs12197388 and the estimates for $G \times E$ with number of births and age at menarche were not heterogeneous between studies in the current analysis (Supplementary Figure S1). For the other two SNPs, rs10483028 and rs2242714, which showed statistical interaction with adult BMI in postmenopausal women, the association with breast cancer risk was weaker but still apparent when analyzed in all postmenopausal subjects of European descent in BCAC ($OR = 1.06$, $P\text{-value} = 0.001$).

Large sample sizes, comprising more than 20,000 cases and controls, were available for the present interaction analyses with number of births, age at menarche, and adult body height. However, sample size was moderate for analyses with most of the other risk factors, such as BMI and menopausal hormone therapy. Multiplicative interactions identified to date between environmental risk factors and common breast cancer susceptibility alleles have been weak or at most moderate [Nickels et al., 2013]. An at least fourfold larger sample size has been shown to be necessary for the identification of

$G \times E$ effects of the same order of magnitude as compared to marginal effects [Smith and Day, 1984]. Therefore, statistical power to detect an interaction with the other risk factors was still limited [Hein et al., 2008].

As the present analyses were based on preselected SNPs, the parameters used for the methods, which are designed for genome-wide $G \times E$ detection, might not have been optimal in this setting. The H2 and the Cocktail approach require thresholds for the screening step P -values, which can be arbitrary. For the H2 approach, we used the thresholds for the screening steps, which were proposed by the authors and found to be optimal in most of their simulation configurations [Murcay et al., 2011]. Similarly, for the Cocktail approach we used the threshold that had been originally proposed for the Cocktail I approach [Hsu et al., 2012].

Several studies that contributed to the present analyses were nonpopulation-based. However, selection bias is not expected to influence estimates of $G \times E$ interactions in most circumstances [Morimoto et al., 2003]. We did not observe pronounced differences between results from population-based and nonpopulation-based studies in $G \times E$ interaction analyses (Supplementary Figure S1). In a previous publication on $G \times E$ interactions with known breast cancer SNPs, we also did not observe between-study heterogeneity in interaction ORs. In sensitivity analyses, $G \times E$ estimates were not found to change substantially after restriction to population-based studies only [Nickels et al., 2013]. Differential misclassification would rather have led to an underestimation of interaction effects [Garcia-Closas et al., 1998]. In BCAC, risk factor information is harmonized thoroughly in a standardized fashion. For cases in case-control and cohort studies, the reference time was always time at diagnosis. For controls,

The present analyses were restricted to subjects of European ancestry and adjusted for study to reduce bias due to population stratification. The present results were consistent with previous results on marginal SNP associations from BCAC [Michailidou et al., 2013]. Most of the previously identified breast cancer susceptibility alleles were again detected by application of the $2df$ test, which also considers the marginal genetic association.

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