rs2735383, located at a microRNA binding site in the 3’UTR of NBS1, is not associated with breast cancer risk

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may cause genomic instability, cell death and cancer1,2. In fact, mutations in genes involved in DSB repair, such as those encoding proteins involved in the DDR pathway, may cause genomic instability, cell death and cancer1,2. Moreover, when left unrepaired, DSBs can cause the chromosomal instability syndrome Nijmegen breakage syndrome10. In addition, heterozygous carriers of NBS1 mutations can develop cancer specifically10. The functional variant rs2735383, localized in the 3′-untranslated region (UTR) of NBS1, was shown to be associated with increased susceptibility to lung and colorectal cancer. However, the relationship between rs2735383 and susceptibility to breast cancer is not yet clear. Therefore, we genotyped rs2735383 in 1,170 familial non-BRCA1/2 breast cancer cases and 1,077 controls using PCR-based restriction fragment length polymorphism (RFLP-PCR) analysis, but found no association between rs2735383CC and breast cancer risk (OR = 1.214, 95% CI = 0.936–1.574, P = 0.144). Because we could not exclude a small effect size due to a limited sample size, we further analyzed imputed rs2735383 genotypes (r² > 0.999) of 67,640 breast cancer cases and 46,656 controls from the Breast Cancer Association Consortium (BCAC). However, rs2735383CC was not associated with overall breast cancer risk in European (OR = 1.014, 95% CI = 0.969–1.060, P = 0.556) nor in Asian women (OR = 0.998, 95% CI = 0.905–1.100, P = 0.961). Subgroup analyses by age, age at menarche, age at menopause, menopausal status, number of pregnancies, breast feeding, family history and receptor status also did not reveal a significant association. This study therefore does not support the involvement of the genotype at NBS1 rs2735383 in breast cancer susceptibility.

The DNA damage response (DDR) pathway maintains the stability of the human genome via a complex network of pathways integrating signal transduction, regulation of the cell cycle and repair of DNA. Double-strand breaks (DSBs), a particularly severe form of DNA damage, arise as a consequence of cell replication, programmed DNA rearrangements (i.e. meiosis and VDJ recombination) and exposure to carcinogens. When left unrepaired, DSBs may cause genomic instability, cell death and cancer1–2. In fact, mutations in genes involved in DSB repair, but also in the DDR pathway in general, are involved in the etiology of many human cancers. The two major repair pathways that mediate the repair of DSBs are the template-mediated homologous recombination repair pathway and the more error-prone non-homologous end-joining pathway3,4. The MRE11/RAD50/NBS1 complex is an important regulator of DSB repair through these pathways as this complex not only acts as a sensor of DSBs, but also inactivates and activates the ATM protein to the break and activates it5. Activation of ATM, the central mediator of response to DSBs, initiates a cascade of signaling pathways involved in cell cycle checkpoint control, DNA repair and, when necessary, apoptosis by phosphorylation of p53, CHEK2, BRCA1, FANCD2 and NBS1 amongst others6.

The DDR plays an important role in susceptibility to breast cancer. In fact, all of the currently identified high- and moderate-risk breast cancer genes (i.e. BRCA1, BRCA2, CHEK2, ATM, NBS1 and PALB2) are involved in DNA repair7,8. As the majority of familial breast cancer risk is not yet attributable to known risk genes, this makes other genes encoding proteins involved in the DDR pathway attractive candidates for breast cancer susceptibility genes. The recent identification of the early DNA damage response gene MCPH1 as a novel breast cancer susceptibility gene illustrates that this hypothesis still holds5.

In this respect, the NBS1 gene is located at chromosome 8q21 and bi-allelic germline mutations in NBS1 cause the chromosomal instability syndrome Nijmegen breakage syndrome9. In addition, heterozygous carriers of NBS1 mutations are at an increased risk to develop several types of cancer11. The NBS1 c.657del5 founder mutation is the most prevalent mutation implicated in Nijmegen breakage syndrome (i.e. 90%) and has its origin in the Slavic population12. The mutation confers an overall 2.5- to 3-fold increased cancer risk and is associated with increased risk for breast cancer, prostate cancer and lymphoma specifically13. Two other NBS1 mutations implicated in Nijmegen breakage syndrome are p.I171V and p.R215W. Although both mutations associate with an overall cancer risk of 4-fold and 2-fold, respectively, there does not seem to be an increased risk to develop breast cancer specifically13.

Besides the rare Nijmegen breakage syndrome-associated mutations, two common variants in NBS1 (i.e. p.E185Q; rs1805794 and c.2265 + 541G > C; rs2735383) have also been reported to be associated with risks for several cancer types. Recent meta-analyses for rs1805794 have, however, shown that this variant does not associate with breast cancer risk13–16, while associations with lung cancer and urinary system cancer are still inconclusive13,16–18. The functional variant rs2735383, localized in the 3′ UTR of NBS1, has been shown to modulate the binding ability of microRNA-629 in lung cancer cells and microRNA-509-5p in colorectal cancer cells, affect NBS1 transcriptional activity and decrease NBS1 mRNA and NBS1 protein levels19,20. Although rs2735383 has been associated with an increased risk of lung cancer and colorectal cancer19,20, its association with breast cancer risk is yet unclear. For this reason, we assessed whether NBS1 rs2735383 is associated with breast cancer risk in the Rotterdam Breast Cancer Study (RBCS) by RFLP-PCR and in 45 studies of BCAC through imputation of the iCOGS array21.
A previous study had shown that rs2735383 may be associated with breast cancer risk in women >50 years, women with age at menarche >13 years, women with premenopausal status, women with number of abortions ≤2 and women who have breast fed, but not by age at menopause, number of pregnancies and family history. Therefore, to exclude that an association of rs2735383 with breast cancer risk exists in a particular subgroup of women, we analyzed NBS1 rs2735383 and breast cancer risk in the RBCS study. N, number of; MAF, minor allele frequency; OR, odds ratio; CI, confidence interval.

Table 1. Association of NBS1 rs2735383 with breast cancer risk in the RBCS study. N, number of; MAF, minor allele frequency; OR, odds ratio; CI, confidence interval.

<table>
<thead>
<tr>
<th>Ethnicity</th>
<th>Genetic model</th>
<th>N Controls</th>
<th>N Cases</th>
<th>OR (95% CI)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>European</td>
<td>Recessive</td>
<td>40,042</td>
<td>41,915</td>
<td>1.014 (0.969–1.060)</td>
<td>0.556</td>
</tr>
<tr>
<td></td>
<td>Dominant</td>
<td></td>
<td></td>
<td>1.006 (0.978–1.035)</td>
<td>0.684</td>
</tr>
<tr>
<td></td>
<td>Additive</td>
<td></td>
<td></td>
<td>1.000 (0.979–1.021)</td>
<td>0.984</td>
</tr>
<tr>
<td>Asian</td>
<td>Recessive</td>
<td>6,614</td>
<td>5,725</td>
<td>0.998 (0.905–1.100)</td>
<td>0.961</td>
</tr>
<tr>
<td></td>
<td>Dominant</td>
<td></td>
<td></td>
<td>0.995 (0.922–1.074)</td>
<td>0.900</td>
</tr>
<tr>
<td></td>
<td>Additive</td>
<td></td>
<td></td>
<td>0.997 (0.946–1.050)</td>
<td>0.911</td>
</tr>
</tbody>
</table>

Table 2. Association of NBS1 rs2735383 with overall breast cancer risk in the European and Asian BCAC studies. N, number of; MAF, minor allele frequency; OR, odds ratio; CI, confidence interval. *Adjusted for age, study and principal components (PCs). In the European analyses nine PCs were added to the regression model and in the Asian analyses two PCs.

<table>
<thead>
<tr>
<th>Ethnicity</th>
<th>Genetic model</th>
<th>N Controls</th>
<th>N Cases</th>
<th>OR (95% CI)*</th>
<th>P-value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>European</td>
<td>Recessive</td>
<td>40,042</td>
<td>41,915</td>
<td>0.995 (0.922–1.074)</td>
<td>0.900</td>
</tr>
<tr>
<td></td>
<td>Dominant</td>
<td></td>
<td></td>
<td>0.995 (0.922–1.074)</td>
<td>0.900</td>
</tr>
<tr>
<td></td>
<td>Additive</td>
<td></td>
<td></td>
<td>0.997 (0.946–1.050)</td>
<td>0.911</td>
</tr>
</tbody>
</table>

Results

To evaluate the association between NBS1 rs2735383 and breast cancer risk, we analyzed NBS1 rs2735383 by RFLP-PCR in 1,269 non-BRCA1/2 familial breast cancer patients and 1,159 controls from RBCS. Since genetic risk factors are usually enriched in familial/early-onset breast cancer cases, specifically selecting these breast cancer patients improves statistical power. Among the cases, 516 had the GG genotype, 507 had the GC genotype and 114 had the CC genotype (MAF = 0.338). For both cases and controls, the genotypes of rs2735383 were in Hardy-Weinberg equilibrium (HWE). Because rs2735383 CC was associated with an increased risk of lung cancer and colorectal cancer under a recessive genetic model, we analyzed the association of rs2735383 with breast cancer in a similar way. However, rs2735383 was not significantly associated with the risk of breast cancer (OR = 1.21–1.46, P < 0.001), whereas the colorectal cancer risk had been associated with an OR of 1.55 (95% CI = 1.27–1.94, P < 10−4) [13,20]. Here, we do not observe a similar effect size for breast cancer as for lung and colorectal cancer. However, RBCS is underpowered to detect effect sizes smaller than those observed for lung cancer (i.e. OR < 1.28). Therefore, we cannot exclude rs2735383 CC is associated with breast cancer, but confers a smaller risk.

For the overall analysis in Europeans we had 41,915 cases and 40,042 controls available from 36 case-control studies. However, rs2735383 was not associated with breast cancer risk in Europeans, neither under a recessive genetic model (OR = 1.014, 95% CI = 0.969–1.060, P = 0.556; Table 2 and Fig. 1), nor under a dominant (OR = 1.006, 95% CI = 0.978–1.035, P = 0.684; Table 2) or additive model (per allele OR = 1.000, 95% CI = 0.979–1.021, P = 0.984; Table 2). Because the association with increased lung and colorectal cancer risk was observed in the Asian population [13,20], we also performed the same analysis in the nine Asian BCAC studies. In total, we had 5,725 cases and 6,614 controls available for this analysis from nine case-control studies. Also in Asians we did not find any association between rs2735383 and breast cancer risk for either the recessive (OR = 0.998, 95% CI = 0.905–1.100, P = 0.961; Table 2) or additive genetic model (per allele OR = 0.997, 95% CI = 0.946–1.050, P = 0.911; Table 2). These results imply that NBS1 rs2735383 is not associated with an increased risk to develop invasive breast cancer.
Figure 1. Forest plots for the association between rs2735383 and breast cancer risk. (A) for the 36 European BCAC studies and (B) for the nine Asian BCAC studies. Study-specific ORs (squares) were from a recessive genetic model and adjusted by age and PCs. Overall or pooled ORs (diamonds) were from a fixed-effects meta-analysis.
could have easily given rise to false positive findings. Therefore, one should be careful when reporting positive
outcomes.

Subgroup N Controls N Cases MAF Controls MAF Cases OR (95% CI)* P-value*

<table>
<thead>
<tr>
<th>Subgroup</th>
<th>N Controls</th>
<th>N Cases</th>
<th>MAF Controls</th>
<th>MAF Cases</th>
<th>OR (95% CI)*</th>
<th>P-value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 50 years</td>
<td>13,055</td>
<td>13,362</td>
<td>33.76%</td>
<td>33.41%</td>
<td>0.977 (0.899–1.062)</td>
<td>0.581</td>
</tr>
<tr>
<td>&gt; 50 years</td>
<td>26,987</td>
<td>28,553</td>
<td>33.28%</td>
<td>33.38%</td>
<td>1.026 (0.971–1.084)</td>
<td>0.356</td>
</tr>
<tr>
<td>Age at menarche</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 13 years</td>
<td>14,312</td>
<td>13,843</td>
<td>33.72%</td>
<td>33.13%</td>
<td>0.984 (0.914–1.060)</td>
<td>0.677</td>
</tr>
<tr>
<td>&gt; 13 years</td>
<td>8,964</td>
<td>8,095</td>
<td>32.65%</td>
<td>33.63%</td>
<td>1.077 (0.978–1.187)</td>
<td>0.131</td>
</tr>
<tr>
<td>Age at menopause</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 50 years</td>
<td>5,571</td>
<td>7,288</td>
<td>32.79%</td>
<td>33.43%</td>
<td>1.019 (0.906–1.146)</td>
<td>0.755</td>
</tr>
<tr>
<td>&gt; 50 years</td>
<td>3,366</td>
<td>4,262</td>
<td>33.50%</td>
<td>33.24%</td>
<td>0.993 (0.855–1.154)</td>
<td>0.926</td>
</tr>
<tr>
<td>Menopausal status</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Premenopausal</td>
<td>8,974</td>
<td>7,412</td>
<td>33.66%</td>
<td>33.07%</td>
<td>0.981 (0.887–1.085)</td>
<td>0.715</td>
</tr>
<tr>
<td>Postmenopausal</td>
<td>19,648</td>
<td>17,353</td>
<td>33.39%</td>
<td>33.56%</td>
<td>1.007 (0.943–1.075)</td>
<td>0.844</td>
</tr>
<tr>
<td>Number of full-term pregnancies</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤ 2</td>
<td>21,008</td>
<td>19,722</td>
<td>33.53%</td>
<td>33.20%</td>
<td>1.004 (0.942–1.071)</td>
<td>0.893</td>
</tr>
<tr>
<td>&gt; 2</td>
<td>8,258</td>
<td>7,327</td>
<td>33.26%</td>
<td>33.44%</td>
<td>1.032 (0.931–1.144)</td>
<td>0.549</td>
</tr>
<tr>
<td>Breast feeding</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>6,849</td>
<td>6,805</td>
<td>33.36%</td>
<td>33.25%</td>
<td>0.988 (0.884–1.104)</td>
<td>0.828</td>
</tr>
<tr>
<td>Yes</td>
<td>11,947</td>
<td>12,709</td>
<td>33.68%</td>
<td>33.28%</td>
<td>0.978 (0.903–1.060)</td>
<td>0.594</td>
</tr>
<tr>
<td>Family history</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1st degree relative with BC</td>
<td>23,648</td>
<td>4,119</td>
<td>33.21%</td>
<td>32.68%</td>
<td>0.990 (0.884–1.108)</td>
<td>0.859</td>
</tr>
<tr>
<td>Receptor status</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>ER positive</td>
<td>39,699</td>
<td>25,959</td>
<td>33.47%</td>
<td>33.40%</td>
<td>1.021 (0.970–1.075)</td>
<td>0.427</td>
</tr>
<tr>
<td>ER negative</td>
<td>39,618</td>
<td>6,774</td>
<td>33.42%</td>
<td>32.90%</td>
<td>0.991 (0.908–1.082)</td>
<td>0.846</td>
</tr>
<tr>
<td>Triple negative</td>
<td>30,696</td>
<td>2,712</td>
<td>33.10%</td>
<td>32.04%</td>
<td>0.980 (0.847–1.134)</td>
<td>0.788</td>
</tr>
</tbody>
</table>

Table 3. Subgroup analysis of NBS1 rs2735383 and breast cancer risk in the European BCAC studies. N,
number; MAF, minor allele frequency; OR, odds ratio; CI, confidence interval; ER, estrogen receptor; BC, breast
cancer. *Recessive genetic model adjusted for age, study and nine principal components.

individuals or breast cancer patients, we performed subgroup analysis according to age, age at menarche, age at
menopause, menopausal status, number of full-term pregnancies, breast feeding, family history and receptor
status. We did, however, not find any association between the genotype at rs2735383 and the risk of breast cancer
in any of these subgroups for the recessive genetic model (Table 3). Also for the dominant and additive genetic
models we found no association between the genotype at rs2735383 and breast cancer risk that would withstand
multiple testing correction (Supplementary Tables S1 and S2). NBS1 rs2735383 is thus not associated with the risk
for breast cancer, either in the overall analyses or in specific subgroups.

Discussion
The CC genotype of the common variant rs2735383 in the 3'UTR of NBS1 has been shown to be associated with
an increased cancer risk, specifically for lung and colorectal cancer (lung cancer: OR = 1.28, 95% CI = 1.21–1.46,
P < 0.001 and colorectal cancer: OR = 1.55, 95% CI = 1.27–1.94, P < 10^−4)13,20. In the current study, we evaluated
the association of NBS1 rs2735383 with breast cancer risk. We found that the CC genotype of rs2735383 did not
confer an increased breast cancer risk, neither in the overall analyses nor in the subgroup analyses.

In agreement with these results, a small study by Han et al. consisting of 239 premenopausal breast cancer
patients and 477 matched controls from the Nurses’ Health Study II showed that rs2735383 did not associate with
breast cancer risk under an additive genetic model (OR = 0.92, 95% CI = 0.72–1.16, P = 0.469)22. Moreover, the
study of Wu et al. consisting of 450 breast cancer patients and 450 cancer-free controls from the Henan Province
in China also found no association with overall breast cancer risk21. However, after stratification according to
reproductive factors, rs2735383 CC was found to be associated with an increased breast cancer risk for women
≥ 50 years, women with age at menarche ≥ 13 years, women with premenopausal status, women with number of
abortions ≤ 2 and women who have breast fed, but not by age at menopause, number of pregnancies and family
history21. In the current study we therefore also performed subgroup analysis by age, age at menarche, age at
menopause, menopausal status, number of full-term pregnancies, breast feeding, family history and receptor
status, but did not find any association between rs2735383 and risk of breast cancer in any of these subgroups that
would withstand multiple testing correction. We thus could not replicate the earlier positive findings in women
≥ 50 years, women with age at menarche ≥ 13 years, premenopausal women and women who have breast fed. A
possible, but not very likely, explanation for the difference in outcome between the studies may be the European
versus Asian ethnicity. In the current study we chose to perform the subgroup analysis only in the European stud-
ies and not the Asian studies as this made sure that we had sufficient power in the subgroup analysis to identify
smaller effects of rs2735383 on breast cancer risk. In this respect, a more plausible explanation would be that
subgroup analyses, especially in a small study population (i.e. 450 cases and 450 controls in the study of Wu et al.),
could have easily given rise to false positive findings. Therefore, one should be careful when reporting positive
findings from multiple small subgroup comparisons and always use appropriate levels of statistical significance. Unfortunately, in the study from Wu et al. there is no mention of multiple testing correction.

It was found that the rs2735383CC genotype significantly decreased the expression of the NBS1 gene through either binding of microRNA-629 to the 3'-UTR of NBS1 gene in lung cancer cells or the binding of microRNA-509-5p to the 3'-UTR of NBS1 gene in colorectal cancer cells. Since low expression of NBS1 may reduce the efficiency of DSB repair, this way the rs2735383CC genotype likely confers an increased lung and colorectal cancer risk. According to our study, however, the rs2735383CC genotype does not confer an increased breast cancer risk. Considering that in lung and colorectal cancer cells different microRNAs appear to be downregulating NBS1 expression, tissue specific expression of these microRNAs may likely play a role. Besides microRNA-509 and microRNA-629, the C allele at rs2735383 has also been predicted to enhance the binding of microRNA-499 and microRNA-508 to the 3'UTR of NBS1. However, if these microRNAs are not expressed in normal breast tissue, the CC genotype of rs2735383 will not associate with breast cancer risk as NBS1 cannot be downregulated by any of these microRNAs. At least in breast cancer cells, none of these microRNAs, except microRNA-629, are expressed at substantial levels (source: TCGA Research Network: http://cancergenome.nih.gov/). Since microRNAs are often deregulated between normal tissue and cancer tissue, this does not necessarily represent the situation in normal breast cells. Thus, further evaluation of the miRNA expression levels in normal (breast) tissue, but also their correlation with the genotype at rs2735383 should provide more insight for the tissue specificity of rs2735383 and cancer risk.

Importantly, in contrast to lung and colorectal cancer susceptibility, the results of this study do not support the presence of an association (i.e., OR > 1.04 for Europeans and OR > 1.11 for Asians) between the genotype at rs2735383 in the 3'UTR of NBS1 and breast cancer susceptibility.

Materials and Methods

Study population. RBCS cases (N = 1,269) came from the database of the Clinical Genetics Department at Erasmus University Medical Centre in Rotterdam, representing the Southwestern part of the Netherlands. First, we selected families that presented with at least two cases of female breast cancer or at least one case of female breast cancer and one case of ovarian cancer in first- or second-degree relatives. In addition, at least one of these two cases needed to be diagnosed before the age of 60. For each selected family, the youngest breast cancer patient who had been tested for BRCA1 and BRCA2 was then assigned to be the index case and included in RBCS. Furthermore, breast cancer cases were also included if they were diagnosed either before the age of 40 years with unilateral breast cancer or before 50 years of age with bilateral breast cancer and did not report a family history of either breast or ovarian cancer in a first or second degree relative. All index cases and their tested relatives did not carry a BRCA1 or BRCA2 mutation. The median age of the RBCS cases was 44 years (range 18–92 years). RBCS controls (N = 1,159) came from the same database and geographic location as the RBCS cases and included women from cystic fibrosis families who were either spouses of individuals at risk of being carrier of a CFTR mutation or individuals who were tested negative for a CFTR mutation. The median age of the RBCS controls was 41 years (range 10–97 years).

BCAC consists of case-control studies of unrelated women. For the purpose of the current analyses, only studies with participants of European and Asian ancestry were included, resulting in a total of 45 case-control studies (Supplementary Table S3). Studies with participants of African ancestry (i.e., two studies) were not included because power in the analyses would be low due to a relatively low MAF (i.e., 0.123) and small amount of cases (i.e., 1,046). Each study was approved by its relevant governing research ethics committee and all study participants provided written informed consent. The experimental protocol was approved by the Medical Ethical Committee of the Erasmus Medical Center Rotterdam and the study was carried out in accordance with the Code of Conduct of the Federation of Medical Scientific Societies in the Netherlands (http://www.fmwv.nl). Following genotyping on the iCOGS array, quality control exclusions (described below), and analysis-specific exclusions, data from the following women were available for analysis: 47,640 patients with invasive breast cancer and 46,656 controls, totaling 94,296 BCAC participants.

PCR-based RFLP analysis. A 324 bp fragment of the 3'UTR of NBS1 including rs2735383 was amplified in a duplex PCR reaction together with a 713 bp fragment of the LRRC4 gene. Primers for NBS1 and LRRC4 were present in the PCR reaction at a final concentration of 0.25 and 1 μM, respectively, and sequences are available in Supplementary Table S4. The amplified LRRC4 fragment served as an internal digestion control and generated two fragments of 549 and 164 bp upon complete digestion with ScfI (New England Biolabs, Frankfurt am Main, Germany). The 324 bp amplified NBS1 fragment was only digested when the major G allele was present at rs2735383, thereby generating two fragments of 233 and 91 bp. Thus upon successful digestion with ScfI, samples with rs2735383 GG generated four fragments, samples with rs2735383 GC generated five fragments and samples with rs2735383 CC generated three fragments (Fig. 2).

iCOGS genotyping and imputation. Genotyping of BCAC studies was performed previously using the custom iCOGS Illumina Infinium iSelect BeadChip. Briefly, DNA samples from 114,255 BCAC participants were genotyped, along with HapMap2 DNAs for European, African, and Asian populations. Raw intensity data files underwent centralized genotype calling and quality control. The HapMap2 samples were used to identify women with predicted European and Asian ancestry by performing principal component (PC) analysis using a set of over 37,000 unlinked markers. Nine European PCs and two Asian PCs were found to control adequately for residual population stratification in BCAC data. Samples with a low conversion rate, extreme heterozygosity, non-female sex, or one of a first-degree relative pair were excluded. Variants were excluded if they were monomorphic or had a call rate <95% (i.e. when MAF > 0.05) or <99% (i.e. when MAF < 0.05), deviation from HWE (i.e. P < 10–7), or >2% duplicate discordance.
Imputation of genotypes was performed using 1000 Genomes Project data (v3 April 2012 release) as the reference panel\(^{26-27}\). To improve computation efficiency we used a two-step procedure which involved pre-phasing by chromosome and by chunk using SHAPEIT software in the first step\(^{28}\) and imputation of the phased data using IMPUTE version 2 software in the second\(^{29}\). \(NBS1\) rs2735383 was imputed with an imputation \(r^2 > 0.999\) in both Europeans and Asians.

**Statistical analyses.** The association between \(NBS1\) rs2735383 and invasive breast cancer risk was evaluated by logistic regression analysis providing ORs and 95% CIs. In the analyses of BCAC studies, ORs were adjusted for study, age, and PCs. In the analyses of RBCS, ethnicity was not a confounding factor thus reported ORs were unadjusted for PCs. For the European and Asian BCAC studies, we additionally performed study-specific logistic regression analysis adjusting for age and PCs, and pooled the log ORs in a fixed-effects meta-analysis. Subgroup analyses within the European BCAC studies were based on age (i.e. \(\leq 50\) years and >50 years), age at menarche (i.e. \(\leq 13\) years and >13 years), age at menopause (i.e. \(\leq 50\) years and >50 years), menopausal status (i.e. premenopausal and postmenopausal), number of full-term pregnancies (i.e. \(\leq 2\) and >2), breast feeding (i.e. no and yes), first-degree family history of breast cancer and receptor status (i.e. ER positive, ER negative and triple negative). Clinical and demographic characteristics of the BCAC cases are presented in Supplementary Table S5. Association between \(NBS1\) rs2735383 and the clinical and demographic characteristics were evaluated using a \(\chi^2\) test. All \(P\)-values were two-sided and \(P < 0.05\) was considered to be statistically significant after correction for multiple testing by the Bonferroni procedure. Logistic regression analyses were performed using SPSS statistics version 13 (IBM Corporation, Armonk, NY) and fixed-effects meta-analyses using Stata version 13 (StataCorp, College Station, TX).

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