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Breast cancer risk genes: association analysis in more than 113,000 women

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Citation

Dorling, L., Carvalho, S., Allen, J., Gonzalez-Neira, A., Luccarini, C., Wahlstrom, C., ... Easton, D. F. (2021). Breast cancer risk genes: association analysis in more than 113,000 women. *New England Journal Of Medicine*, 384(5), 428-439. doi:10.1056/NEJMoa1913948

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Note: To cite this publication please use the final published version (if applicable).

ORIGINAL ARTICLE

Breast Cancer Risk Genes — Association Analysis in More than 113,000 Women

Breast Cancer Association Consortium*

ABSTRACT

BACKGROUND

Genetic testing for breast cancer susceptibility is widely used, but for many genes, evidence of an association with breast cancer is weak, underlying risk estimates are imprecise, and reliable subtype-specific risk estimates are lacking.

METHODS

We used a panel of 34 putative susceptibility genes to perform sequencing on samples from 60,466 women with breast cancer and 53,461 controls. In separate analyses for protein-truncating variants and rare missense variants in these genes, we estimated odds ratios for breast cancer overall and tumor subtypes. We evaluated missense-variant associations according to domain and classification of pathogenicity.

RESULTS

Protein-truncating variants in 5 genes (*ATM*, *BRCA1*, *BRCA2*, *CHEK2*, and *PALB2*) were associated with a risk of breast cancer overall with a P value of less than 0.0001. Protein-truncating variants in 4 other genes (*BARD1*, *RAD51C*, *RAD51D*, and *TP53*) were associated with a risk of breast cancer overall with a P value of less than 0.05 and a Bayesian false-discovery probability of less than 0.05. For protein-truncating variants in 19 of the remaining 25 genes, the upper limit of the 95% confidence interval of the odds ratio for breast cancer overall was less than 2.0. For protein-truncating variants in *ATM* and *CHEK2*, odds ratios were higher for estrogen receptor (ER)-positive disease than for ER-negative disease; for protein-truncating variants in *BARD1*, *BRCA1*, *BRCA2*, *PALB2*, *RAD51C*, and *RAD51D*, odds ratios were higher for ER-negative disease than for ER-positive disease. Rare missense variants (in aggregate) in *ATM*, *CHEK2*, and *TP53* were associated with a risk of breast cancer overall with a P value of less than 0.001. For *BRCA1*, *BRCA2*, and *TP53*, missense variants (in aggregate) that would be classified as pathogenic according to standard criteria were associated with a risk of breast cancer overall, with the risk being similar to that of protein-truncating variants.

CONCLUSIONS

The results of this study define the genes that are most clinically useful for inclusion on panels for the prediction of breast cancer risk, as well as provide estimates of the risks associated with protein-truncating variants, to guide genetic counseling. (Funded by European Union Horizon 2020 programs and others.)

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*A complete list of collaborators and investigators is provided in the Supplementary Appendix, available at NEJM.org.

Dr. Dorling, Dr. Carvalho, and Mr. Allen and Drs. Teo, Devilee, and Easton contributed equally to this article.

This article was published on January 20, 2021, at NEJM.org.

N Engl J Med 2021;384:428-39.

DOI: 10.1056/NEJMoa1913948

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GENETIC TESTING FOR CANCER SUSCEPTIBILITY is an established part of medical practice. Until recently, testing was performed mainly in patients with a strong family history of cancer and involved a limited number of genes known to be associated with a high risk of cancer or with specific cancer syndromes. With the advent of affordable sequencing, testing with larger panels of genes has become possible. However, for many genes on such panels, evidence of an association with cancer is often weak and accurate estimates of the cancer risks associated with variants are often not available.¹

To better define the set of genes associated with breast cancer risk, we designed a panel consisting of 34 known or suspected breast cancer susceptibility genes, including genes provided on commercial panels. Using this panel, we sequenced germline DNA from more than 60,000 women with breast cancer and more than 53,000 controls participating in studies of the Breast Cancer Association Consortium (BCAC).² We used these data to estimate the risks of breast cancer overall and tumor subtypes associated with germline protein-truncating variants and rare missense variants in these genes.

METHODS

STUDIES

We included samples from women with breast cancer and unaffected controls participating in 44 BCAC studies (Tables S1 and S2 in the Supplementary Appendix, available with the full text of this article at NEJM.org). All the studies were approved by the relevant ethics review boards and used appropriate consent procedures. Overall, 30 studies did not select patients or controls on the basis of family history (population-based studies); the remaining 14 studies oversampled patients with a family history of breast cancer (family-based studies). After all quality-control steps were taken, 53,461 controls and 60,466 women with an invasive tumor (54,624 [90.3%]), in situ tumor (4187 [6.9%]), or tumor of unknown invasiveness (1655 [2.7%]) were included in the analyses. Of these, 48,826 patients and 50,703 controls were from population-based studies.

SEQUENCE ANALYSIS

We analyzed a panel of 34 known or suspected breast cancer susceptibility genes (Tables S3 and

S4), including genes provided on commercial panels. Details regarding library preparation, sequencing, variant calling, quality-control procedures, and variant classification are provided in the Supplementary Methods section in the Supplementary Appendix.

STATISTICAL ANALYSIS

The primary analyses were burden analyses in which odds ratios and 95% confidence intervals for breast cancer associated with the presence of any variant in a given category were estimated by means of logistic regression. The two main categories were protein-truncating variants and rare missense variants (i.e., variants with a population frequency of <0.001). Missense-variant associations were evaluated according to domain and classification of pathogenicity. Analyses were also conducted according to tumor subtype, age, and ancestry (European vs. Asian).

We conducted separate analyses for the population-based studies and the family-based studies. The inclusion of studies that oversampled patients with a family history of breast cancer improves the power to detect association³ but leads to biased risk estimates. Therefore, we report risk estimates, 95% confidence intervals, and P values from the population-based studies but also report the results of association tests from all studies when appropriate. For protein-truncating variants in each gene, evidence of an association is also expressed in terms of Bayesian false-discovery probabilities, reflecting both evidence from the data in this study and evidence from previous research.⁴ Absolute risks were calculated by combining age-specific estimated odds ratios with population incidences in the United Kingdom in 2016 as a baseline.^{5,6} Details regarding the statistical analysis are provided in Supplementary Methods.

RESULTS

PROTEIN-TRUNCATING VARIANTS

Risk of Breast Cancer Overall

Protein-truncating variants in 5 genes (*ATM*, *BRCA1*, *BRCA2*, *CHEK2*, and *PALB2*) were associated with a significant risk of breast cancer overall (P<0.0001) (Table 1 and Figs. 1 and 2). For these genes, odds ratios ranged from 2.10 to 10.57. In *CHEK2*, the c.1100delC variant accounted for approximately 80% of the protein-truncating vari-

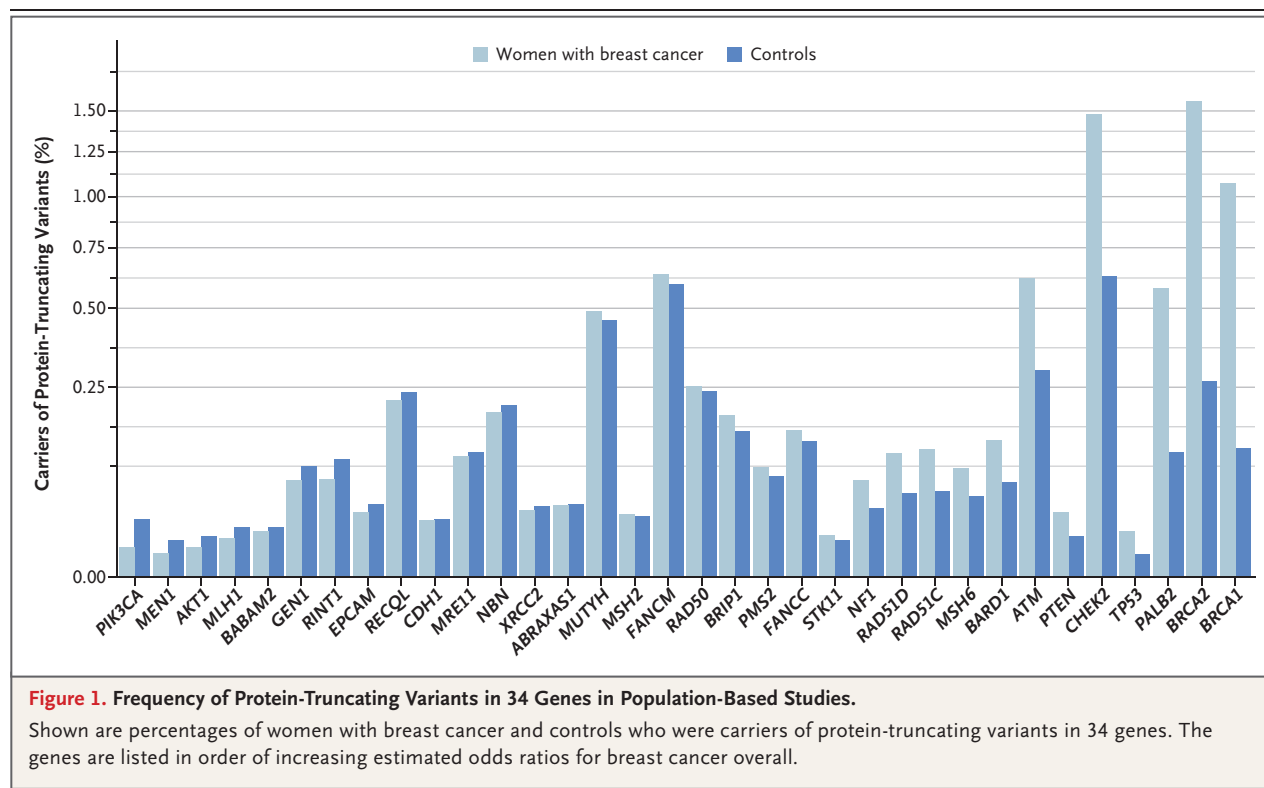
Table 1. Risk of Breast Cancer Overall Associated with Protein-Truncating Variants in 34 Genes in Population-Based Studies and All Studies.*

Gene	Population-Based Studies (48,826 patients and 50,703 controls)†			All Studies (60,466 patients and 53,461 controls)‡		Prior Probability‡	BFDP
	No. of Carriers of Protein- Truncating Variants		Odds Ratio (95% CI)	P Value	P Value		
	Women with Breast Cancer	Controls					
<i>ABRAXAS1</i>	17	19	0.98 (0.50–1.94)	0.96	0.93	0.1	0.98
<i>AKT1</i>	3	6	0.47 (0.12–1.93)	0.29	0.14	0.1	0.94
<i>ATM</i>	294	150	2.10 (1.71–2.57)	9.2×10 ⁻¹³	5.5×10 ⁻²⁰	0.8	1.3×10 ⁻¹⁸
<i>BABAM2</i>	7	9	0.62 (0.23–1.71)	0.36	0.34	0.1	0.95
<i>BARD1</i>	62	32	2.09 (1.35–3.23)	0.00098	0.00011	0.2	0.0076
<i>BRCA1</i>	515	58	10.57 (8.02–13.93)	1.1×10 ⁻⁶²	3.7×10 ⁻⁶⁵	0.99	1.5×10 ⁻⁶⁴
<i>BRCA2</i>	754	135	5.85 (4.85–7.06)	2.2×10 ⁻⁷⁵	8.4×10 ⁻⁷⁷	0.99	3.1×10 ⁻⁷⁶
<i>BRIP1</i>	86	75	1.11 (0.80–1.53)	0.54	0.54	0.2	0.85
<i>CDH1</i>	11	12	0.86 (0.37–1.98)	0.72	0.58	0.2	0.94
<i>CHEK2</i>	704	315	2.54 (2.21–2.91)	3.1×10 ⁻³⁹	3.2×10 ⁻⁶¹	0.99	1.3×10 ⁻⁶⁰
c.1100delC variant	548	245	2.66 (2.27–3.11)	1.1×10 ⁻³³	5.3×10 ⁻⁵³		
Other variants	156	70	2.13 (1.60–2.84)	3.0×10 ⁻⁷	7.4×10 ⁻¹⁰		
<i>EPCAM</i>	14	19	0.73 (0.36–1.49)	0.39	0.13	0.1	0.95
<i>FANCC</i>	71	65	1.26 (0.89–1.79)	0.20	0.20	0.1	0.87
<i>FANCM</i>	302	300	1.06 (0.90–1.26)	0.48	0.28	0.1	0.96
<i>GEN1</i>	31	43	0.66 (0.41–1.06)	0.088	0.18	0.1	0.95
<i>MEN1</i>	2	5	0.37 (0.07–1.97)	0.24	0.64	0.1	0.95
<i>MLH1</i>	5	9	0.58 (0.19–1.77)	0.34	0.55	0.1	0.95
<i>MRE11</i>	48	55	0.88 (0.59–1.32)	0.54	0.34	0.1	0.98
<i>MSH2</i>	13	13	1.06 (0.47–2.36)	0.89	0.80	0.1	0.92
<i>MSH6</i>	39	23	1.96 (1.15–3.33)	0.013	0.021	0.1	0.55
<i>MUTYH</i>	232	231	1.00 (0.83–1.21)	0.99	0.88	0.1	1.00
<i>NBN</i>	90	103	0.90 (0.67–1.20)	0.48	0.65	0.2	0.95
<i>NF1</i>	31	17	1.76 (0.96–3.21)	0.068	0.011	0.2	0.25
<i>PALB2</i>	274	55	5.02 (3.73–6.76)	1.6×10 ⁻²⁶	1.1×10 ⁻³²	0.99	2.9×10 ⁻³²
<i>PIK3CA</i>	3	12	0.21 (0.06–0.75)	0.016	0.19	0.1	0.94
<i>PMS2</i>	40	36	1.16 (0.73–1.85)	0.53	0.37	0.1	0.92
<i>PTEN</i>	14	6	2.25 (0.85–6.00)	0.10	0.0040	0.2	0.14
<i>RAD50</i>	120	121	1.08 (0.83–1.40)	0.57	0.45	0.1	0.95
<i>RAD51C</i>	54	26	1.93 (1.20–3.11)	0.0070	0.00026	0.3	0.0090
<i>RAD51D</i>	51	25	1.80 (1.11–2.93)	0.018	0.0018	0.3	0.044
<i>RECQL</i>	103	120	0.84 (0.64–1.10)	0.21	0.89	0.1	0.95
<i>RINT1</i>	32	49	0.72 (0.46–1.14)	0.17	0.31	0.1	0.96
<i>STK11</i>	6	5	1.60 (0.48–5.28)	0.44	0.50	0.2	0.70
<i>TP53</i>	7	2	3.06 (0.63–14.91)	0.17	0.015	0.8	0.033
<i>XRCC2</i>	15	18	0.96 (0.47–1.93)	0.90	0.81	0.1	0.98

* BFDP denotes Bayesian false-discovery probability, and CI confidence interval.

† The sample sizes reflect totals after quality control. Analyses for genes other than *BRCA1* and *BRCA2* excluded carriers of protein-truncating variants in *BRCA1* and *BRCA2*; therefore, sample sizes were slightly lower in those analyses (47,522 patients and 50,475 controls in population-based studies, and 58,728 patients and 52,976 controls in all studies).

‡ Details regarding the prior probabilities are provided in the Supplementary Methods section in the Supplementary Appendix.



ants. The effect size for this variant (odds ratio, 2.66; 95% confidence interval [CI], 2.27 to 3.11; $P=1.1\times 10^{-33}$ [$P=5.3\times 10^{-53}$ in all studies]) did not differ significantly from the effect size for all other protein-truncating variants in *CHEK2* (odds ratio, 2.13; 95% CI, 1.60 to 2.84; $P=3.0\times 10^{-7}$ [$P=7.4\times 10^{-10}$ in all studies]), with a P value of 0.19 for the difference in the odds ratios.

There was more modest evidence of an association with breast cancer overall for protein-truncating variants in 7 other genes: *BARD1* (odds ratio, 2.09; 95% CI, 1.35 to 3.23; $P=0.00098$ [$P=0.00011$ in all studies]), *RAD51C* (odds ratio, 1.93; 95% CI, 1.20 to 3.11; $P=0.0070$ [$P=0.00026$ in all studies]), *RAD51D* (odds ratio, 1.80; 95% CI, 1.11 to 2.93; $P=0.018$ [$P=0.0018$ in all studies]), *PTEN* (odds ratio, 2.25; 95% CI, 0.85 to 6.00; $P=0.10$ [$P=0.0040$ in all studies]), *NF1* (odds ratio, 1.76; 95% CI, 0.96 to 3.21; $P=0.068$ [$P=0.011$ in all studies]), *TP53* (odds ratio, 3.06; 95% CI, 0.63 to 14.91; $P=0.17$ [$P=0.015$ in all studies]), and *MSH6* (odds ratio, 1.96; 95% CI, 1.15 to 3.33; $P=0.013$ [$P=0.021$ in all studies]) (Table 1). For 4 of these genes (*BARD1*, *RAD51C*, *RAD51D*, and *TP53*), the Bayesian false-discovery probability was less than 0.05 (Table 1).

For the 12 genes that had evidence of an association with breast cancer overall, the effect size for protein-truncating variants did not differ significantly between European women and Asian women (Table S7). Of the remaining 22 genes, all but 3 (*AKT1*, *MSH2*, and *STK11*) had an upper limit of the 95% confidence interval of the odds ratio of less than 2.0 in the population-based studies.

Risk of Tumor Subtypes

Of the 12 genes that had evidence of an association with breast cancer overall, 2 had a stronger association with estrogen receptor (ER)-positive breast cancer than with ER-negative breast cancer: *ATM* (odds ratio, 2.33 [95% CI, 1.87 to 2.91] for ER-positive disease vs. 1.01 [95% CI, 0.64 to 1.59] for ER-negative disease; $P=0.00055$ for the difference) and *CHEK2* (odds ratio, 2.67 [95% CI, 2.30 to 3.11] for ER-positive disease vs. 1.64 [95% CI, 1.25 to 2.16] for ER-negative disease; $P=3.6\times 10^{-5}$ for the difference) (Fig. 2 and Table S8). *CHEK2* also had evidence of an association with ER-negative, non-triple-negative breast cancer (odds ratio, 2.53; 95% CI, 1.75 to 3.67) but not with triple-negative breast cancer (odds ratio, 1.06; 95% CI, 0.63 to 1.76) (Table S9).

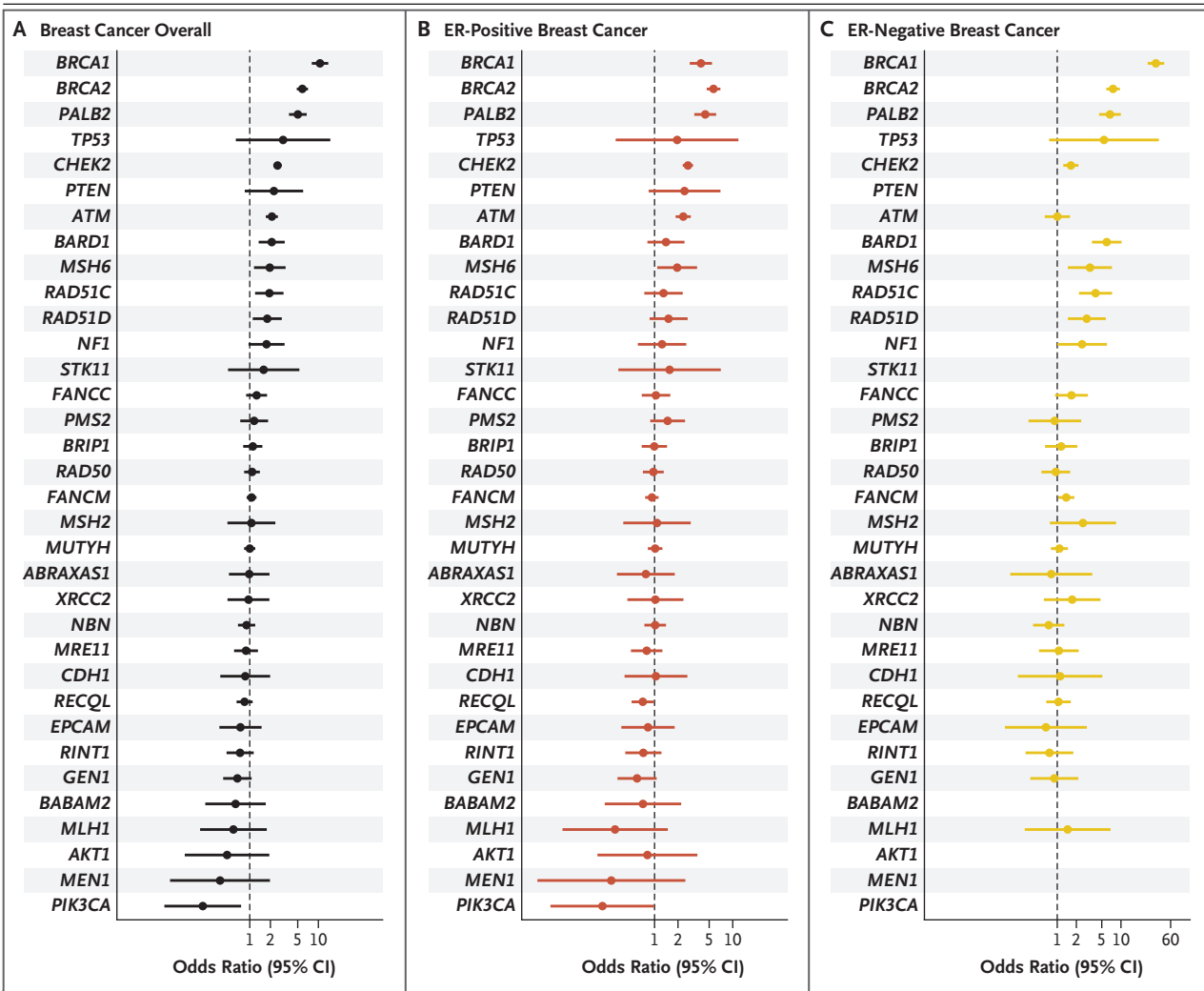


Figure 2. Risk of Breast Cancer Overall and Tumor Subtypes Associated with Protein-Truncating Variants in 34 Genes in Population-Based Studies.

Shown are odds ratios and 95% confidence intervals (CIs) for breast cancer overall (Panel A), estrogen receptor (ER)-positive breast cancer (Panel B), and ER-negative breast cancer (Panel C) associated with protein-truncating variants in 34 genes. The genes are listed in order of decreasing estimated odds ratios for breast cancer overall.

In contrast, for *BARD1*, *BRCA1*, *BRCA2*, *PALB2*, *RAD51C*, and *RAD51D*, odds ratios were higher for ER-negative breast cancer than for ER-positive breast cancer ($P < 0.05$ for all genes). Of these genes, 3 had a stronger association with triple-negative breast cancer than with ER-negative, non-triple-negative breast cancer: *BARD1* ($P = 0.044$), *BRCA1* ($P = 9.6 \times 10^{-17}$), and *BRCA2* ($P = 7.8 \times 10^{-5}$) (Table S8).

Among the genes that had no evidence of an association with breast cancer overall, *FANCM* had some evidence of an association with ER-negative breast cancer ($P = 0.0050$ in all studies) and

FANCC had evidence of an association with triple-negative breast cancer ($P = 0.0021$ in all studies) (Table S9).

For *BRCA1*, *BRCA2*, and *PALB2*, odds ratios were higher for invasive tumors than for in situ tumors. In contrast, for *ATM* and *CHEK2*, odds ratios for invasive tumors and in situ tumors were similar (Table S10).

Age Effects and Absolute Risk

In the population-based studies, odds ratios decreased significantly with increasing age for 6 genes: *BRCA1*, *BRCA2*, *CHEK2*, *PALB2*, *PTEN*, and

TP53 ($P < 0.01$ for all genes) (Tables S11 and S12). Estimated absolute risks of breast cancer were derived by combining age-specific estimated odds ratios with population incidences in the United Kingdom (Fig. 3). For carriers of protein-truncating variants in *BRCA1*, *BRCA2*, and *PALB2*, the estimated absolute risks by 80 years of age exceeded the 30% threshold for high risk, as defined by National Institute for Health and Care Excellence guidelines.⁷ For carriers of protein-truncating variants in *ATM*, *BARD1*, *CHEK2*, *RAD51C*, and *RAD51D*, the estimated absolute risks by 80 years of age were within the 17 to 30% range for moderate risk.

RARE MISSENSE VARIANTS

There was evidence of an association with breast cancer overall for rare missense variants in 6 genes: *CHEK2* (odds ratio, 1.42; 95% CI, 1.28 to 1.58; $P = 2.5 \times 10^{-11}$ [$P = 2.9 \times 10^{-18}$ in all studies]), *ATM* (odds ratio, 1.06; 95% CI, 1.00 to 1.13; $P = 0.051$ [$P = 0.0010$ in all studies]), *TP53* (odds ratio, 1.10; 95% CI, 0.91 to 1.31; $P = 0.32$ [$P = 0.00080$ in all studies]), *BRCA1* (odds ratio, 1.11; 95% CI, 1.02 to 1.20; $P = 0.010$ [$P = 0.027$ in all studies]), *CDH1* (odds ratio, 1.10; 95% CI, 0.98 to 1.23; $P = 0.096$ [$P = 0.042$ in all studies]), and *RECQL* (odds ratio, 1.12; 95% CI, 1.00 to 1.26; $P = 0.047$ [$P = 0.036$ in all studies]) (Table 2). Of these 6 genes, 2 had a stronger association with ER-positive breast cancer than with ER-negative breast cancer (*CHEK2* [$P = 9.1 \times 10^{-5}$] and *CDH1* [$P = 0.012$]) and 1 had a stronger association with ER-negative breast cancer than with ER-positive breast cancer (*BRCA1* [$P = 0.01$]). Odds ratios decreased with increasing age for *BRCA1* ($P = 0.0026$), *CHEK2* ($P = 0.00022$), and *TP53* ($P = 0.00023$).

For missense variants (in aggregate) in *BRCA1*, the risk of breast cancer overall differed according to domain ($P = 3.0 \times 10^{-6}$); there was an increased risk associated with variants located in the regions encoding the RING domain ($P = 1.0 \times 10^{-6}$) and the BRCT1 domain ($P = 0.00020$) (Tables S13 and S14 and Fig. S1A). For missense variants in *CHEK2*, the odds ratios did not vary according to location ($P = 0.52$), such that the risk associated with variants within domains ($P = 4.2 \times 10^{-9}$) was similar to the risk associated with variants outside domains ($P = 0.001$) (Tables S13 and S15 and Fig. S1B). For *ATM*, there was an increased risk associated with variants in the FRAP-ATM-TRRAP (FAT) domain ($P = 0.00019$ in all studies) and the protein kinase domains ($P = 0.00092$ in all stud-

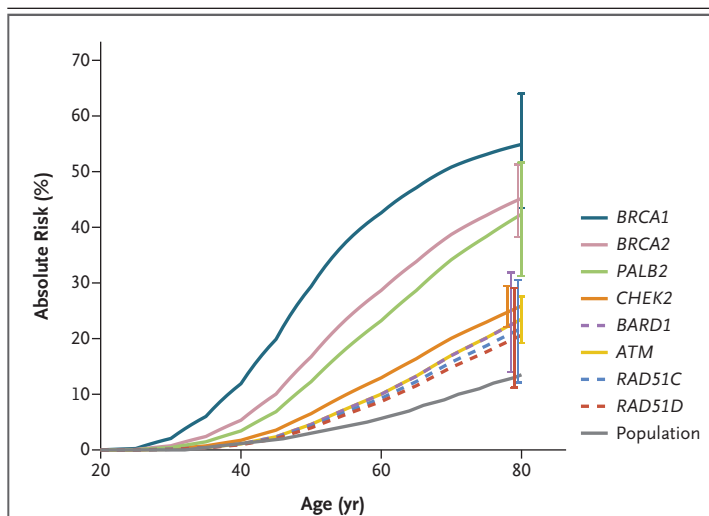


Figure 3. Estimated Absolute Risk of Breast Cancer Associated with Protein-Truncating Variants in 8 Genes.

Shown are absolute risks of breast cancer through 80 years of age associated with protein-truncating variants in 8 genes that had significant evidence of an association with breast cancer overall, on the basis of estimated odds ratios from population-based studies. The absolute risk was not calculated for *TP53* because of the wide 95% confidence interval for the odds ratio and the known association with a substantial risk of childhood cancer. Baseline absolute risks were derived from population incidences in the United Kingdom in 2016.⁶ The I bars indicate 95% confidence intervals.

ies) (Tables S13 and S16 and Fig. S1C). There was no evidence of a risk associated with missense variants in specific domains in *BRCA2* ($P = 0.27$) or *PALB2* ($P = 0.48$) (Tables S13, S17, and S18 and Figs. S1D and S1E).

We specifically examined rare missense variants in *BRCA1*, *BRCA2*, and *TP53* that would be classified as pathogenic according to clinical guidelines. There was clear evidence of an association with breast cancer overall for pathogenic variants (in aggregate) in each gene (odds ratio, 16.11 [95% CI, 5.83 to 44.50] in *BRCA1*, 5.68 [95% CI, 2.62 to 12.29] in *BRCA2*, and 2.91 [95% CI, 1.71 to 4.98] in *TP53*) but not for other missense variants (in aggregate) in each gene (odds ratio, 1.06 [95% CI, 0.98 to 1.15] in *BRCA1*, 0.97 [95% CI, 0.92 to 1.02] in *BRCA2*, and 0.94 [95% CI, 0.77 to 1.14] in *TP53*) (Table S19 and Figs. S2A, S2B, and S2C).

DISCUSSION

This large study, in which we evaluated coding variation in putative breast cancer susceptibility genes, involved more than 60,000 patients and

Table 2. Risk of Breast Cancer Overall Associated with Rare Missense Variants in 34 Genes in Population-Based Studies and All Studies.

Gene	Population-Based Studies (48,826 patients and 50,703 controls)*			All Studies (60,466 patients and 53,461 controls)*	
	No. of Carriers of Rare Missense Variants		Odds Ratio (95% CI)	P Value	P Value
	Women with Breast Cancer	Controls			
<i>ABRAXAS1</i>	233	242	1.04 (0.86–1.25)	0.70	0.40
<i>AKT1</i>	142	156	0.96 (0.76–1.21)	0.72	0.63
<i>ATM</i>	2411	2471	1.06 (1.00–1.13)	0.051	0.0010
<i>BABAM2</i>	167	170	1.01 (0.81–1.26)	0.91	0.63
<i>BARD1</i>	591	616	1.00 (0.89–1.12)	0.94	0.41
<i>BRCA1</i>	1393	1300	1.11 (1.02–1.20)	0.010	0.027
<i>BRCA2</i>	2831	3038	0.98 (0.93–1.04)	0.50	0.58
<i>BRIP1</i>	868	961	0.95 (0.86–1.04)	0.25	0.54
<i>CDH1</i>	682	668	1.10 (0.98–1.23)	0.096	0.042
<i>CHEK2</i>	895	697	1.42 (1.28–1.58)	2.5×10 ⁻¹¹	2.9×10 ⁻¹⁸
<i>EPCAM</i>	290	328	0.97 (0.82–1.14)	0.69	0.43
<i>FANCC</i>	597	620	0.95 (0.85–1.07)	0.42	0.80
<i>FANCM</i>	1434	1566	0.95 (0.88–1.02)	0.17	0.85
<i>GEN1</i>	701	707	1.05 (0.94–1.17)	0.38	0.25
<i>MEN1</i>	109	130	0.86 (0.66–1.12)	0.25	0.81
<i>MLH1</i>	677	711	1.02 (0.91–1.13)	0.78	0.68
<i>MRE11</i>	552	611	0.94 (0.84–1.06)	0.33	0.93
<i>MSH2</i>	908	1024	0.92 (0.84–1.01)	0.093	0.12
<i>MSH6</i>	1088	1155	1.00 (0.92–1.09)	0.98	0.74
<i>MUTYH</i>	659	702	1.00 (0.90–1.12)	1.00	0.58
<i>NBN</i>	665	725	0.95 (0.85–1.06)	0.37	0.71
<i>NF1</i>	816	899	0.94 (0.85–1.03)	0.19	0.53
<i>PALB2</i>	805	892	0.96 (0.87–1.06)	0.39	1.00
<i>PIK3CA</i>	170	205	0.83 (0.67–1.02)	0.080	0.33
<i>PMS2</i>	934	963	0.95 (0.87–1.05)	0.31	0.62
<i>PTEN</i>	68	70	1.08 (0.76–1.53)	0.65	0.48
<i>RAD50</i>	1046	1089	0.99 (0.91–1.08)	0.83	0.44
<i>RAD51C</i>	196	206	0.93 (0.76–1.14)	0.49	0.60
<i>RAD51D</i>	224	212	1.05 (0.86–1.27)	0.64	0.57
<i>RECQL</i>	656	627	1.12 (1.00–1.26)	0.047	0.036
<i>RINT1</i>	732	762	1.01 (0.91–1.12)	0.89	0.18
<i>STK11</i>	114	139	0.83 (0.64–1.07)	0.15	0.16
<i>TP53</i>	257	244	1.10 (0.91–1.31)	0.32	0.00080
<i>XRCC2</i>	207	213	1.03 (0.84–1.25)	0.80	0.53

* The sample sizes reflect totals after quality control. The analysis for each gene excluded carriers of protein-truncating variants in that gene.

53,000 controls, permitting the calculation of risk estimates that are more precise than those obtained previously. We found strong evidence of an association with breast cancer risk (Bayesian false-discovery probability, <0.05) for protein-truncating variants in 9 genes, with a P value of less than 0.0001 for 5 genes (*ATM*, *BRCA1*, *BRCA2*, *CHEK2*, and *PALB2*) and a P value of less than 0.05 for the other 4 genes (*BARD1*, *RAD51C*, *RAD51D*, and *TP53*). We found that, for protein-truncating variants in most of these genes, the odds ratio differed according to breast cancer subtype. Protein-truncating variants in *ATM* and *CHEK2* were more strongly associated with ER-positive disease than with ER-negative disease, a finding consistent with earlier observations,^{5,8} whereas protein-truncating variants in *BARD1*, *BRCA1*, *BRCA2*, *PALB2*, *RAD51C*, and *RAD51D* were more strongly associated with ER-negative disease than with ER-positive disease. None of the other 25 genes in the panel had a Bayesian false-discovery probability of less than 0.10. Of note, 19 genes had an upper limit of the 95% confidence interval of the odds ratio of less than 2.0, with 2.0 representing a proposed threshold for “pathogenic, moderate risk alleles”⁹; we therefore conclude that these genes are not informative for the prediction of breast cancer risk. We confirmed that missense variants in *BRCA1*, *BRCA2*, and *TP53* that would be classified as pathogenic according to clinical guidelines are indeed associated with clinically significant risks. We also found that rare missense variants in *CHEK2* overall, as well as variants in specific domains in *ATM*, are associated with moderate risk.

Our results are broadly consistent with the results of an analysis by Lee et al.,¹⁰ in which the Clinical Genome Resource (ClinGen) clinical validity framework was used (Table S20). Of the 10 genes that were regarded as having definitive evidence of an association with breast cancer risk in that analysis,¹⁰ 7 genes had variants associated with breast cancer risk in our analysis; deleterious variants in the remaining 3 genes (*CDH1*, *PTEN*, and *STK11*) are very rare and confer a predisposition to specific cancer syndromes. Of the 18 genes that were regarded as having moderate, limited, or disputed evidence of an association with breast cancer risk in that analysis, 2 genes (*RAD51C* and *RAD51D*) had protein-truncating variants associated with breast cancer risk in our analysis; 13 of the remaining genes had

an upper limit of the 95% confidence interval of the odds ratio of less than 2.0 (and thus were classified as not conferring moderate or high risk according to our analysis), and the other 3 genes (*MSH2*, *MSH6*, and *NF1*) could not be classified. An association between breast cancer risk and variants in *RAD51C* and *RAD51D* is highly plausible, given that the functions of these genes are related to one another, that both genes had a stronger association with ER-negative breast cancer than with ER-positive breast cancer, and that both genes have evidence of an association with ovarian cancer.¹¹

Association analyses of rare variants are susceptible to bias. Inclusion of studies that oversampled patients with a family history of breast cancer improves the power to detect an association but leads to an upward bias in estimated odds ratios. The expected larger effect size in the family-based studies (as compared with the population-based studies) was seen for protein-truncating variants in all the genes with evidence of an association with breast cancer, except *BRCA1* and *BRCA2*, and was seen for missense variants in *ATM*, *CHEK2*, and *TP53* (Tables S21 and S22). Protein-truncating variants in some of these genes are also associated with other types of cancer. Moreover, testing for cancer susceptibility genes in cancer genetics clinics can lead to a downward bias, because carriers identified through previous testing may be excluded. We observed a depletion of carriers of protein-truncating variants in *BRCA1* and *BRCA2* among women with breast cancer in the family-based studies. Therefore, we regard the estimates from the population-based studies to be the most reliable.

With regard to rare missense variants, the clearest evidence of an association with increased breast cancer risk was for *CHEK2*. For rare missense variants (in aggregate) in *CHEK2*, the odds ratio was approximately 1.4. The association was independent of location, which suggests that a large proportion of missense variants in *CHEK2* confer risk (albeit below the threshold suggested for “pathogenic, moderate risk alleles”⁹). We also found some evidence of an association with risk for rare missense variants (in aggregate) in *ATM*, *BRCA1*, *CDH1*, and *TP53*, with odds ratios of approximately 1.1 (P<0.05) for all genes. Furthermore, we found evidence of an association with risk for missense variants in *BRCA1*, *BRCA2*, and *TP53* that would be classified as pathogenic ac-

ording to standard criteria but not for other missense variants in these genes; the odds ratios for the pathogenic variants (in aggregate) were similar to odds ratios for protein-truncating variants in these genes. For *ATM*, evidence of an association with risk appeared to be restricted to variants located in the regions encoding the phosphatidylinositol 3-kinase and 4-kinase and FAT domains, a finding consistent with previous observations.¹²

The absolute risk estimates for protein-truncating variants in previously established risk genes were broadly consistent with previous estimates, except estimates for *BRCA2* and *TP53*, which were lower than risks reported in previous family-based studies.¹³⁻¹⁵ However, the estimate for *TP53* in this study was based on data from only seven carriers and had a wide confidence interval. The low estimate may reflect the significant early mortality among carriers of protein-truncating variants in *TP53*; alternatively, it is possible that the earlier family-based studies had overestimated the risk.¹⁶ The analysis for *TP53* is further complicated by the possibility of unrecognized somatic mutations in the blood due to age-related clonal hematopoiesis.¹⁷⁻²⁰ The fact that the estimate for *BRCA2* was lower than the estimate for *BRCA1* may reflect the older age distribution in this study, as compared with previous studies, and perhaps a disproportionately large effect of genetic modifiers on risk among *BRCA2* carriers, as compared with *BRCA1* carriers.

Among European women, approximately 6.8% of the patients and 2.0% of the controls had protein-truncating variants in any of the 9 genes associated with breast cancer risk; in addition, 2.2% of the patients and 1.4% of the controls had missense variants in *CHEK2*. The frequency of protein-truncating variants among Asian wom-

en (4.4% of the patients and 1.3% of the controls) was lower than the frequency among European women; this finding is attributable to the much lower frequency of the c.1100delC variant in *CHEK2* among Asian women.

The absolute risk estimates place protein-truncating variants in *BRCA1*, *BRCA2*, and *PALB2* in the high-risk category and place protein-truncating variants in *ATM*, *BARD1*, *CHEK2*, *RAD51C*, and *RAD51D* in the moderate-risk category. These results may guide screening, as well as prevention with risk-reducing surgery or medication, in accordance with national guidelines. However, because breast cancer risk is influenced by other genetic and lifestyle factors, in addition to family history, the incorporation of this information into risk models would be required to give appropriate estimates.²¹

Despite the size of this study, the evidence of an association with breast cancer risk for several of the genes we analyzed (e.g., *FANCM*, *MSH6*, and *NFI*) remains equivocal, and even for the genes that had a clear association with risk, the confidence intervals for the risk estimates are wide. Incorporation of pedigree data and combined analyses with other studies may improve the precision of these estimates. In the meantime, these results may help to guide the clinical reporting of results generated by multigene-panel testing and the counseling of women who are undergoing genetic testing for breast cancer susceptibility.

Supported by the European Union Horizon 2020 research and innovation programs BRIDGES (grant number, 634935) and B-CAST (633784), the Wellcome Trust (v203477/Z/16/Z), and Cancer Research UK (C1287/A16563). Details regarding funding of specific studies are provided in the Supplementary Appendix.

Disclosure forms provided by the authors are available with the full text of this article at NEJM.org.

Requests for individual-level data used in these analyses should be made through the BCAC Data Access Co-ordinating Committee (bcac@medschl.cam.ac.uk).

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