

University of Groningen

## BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer

Shimelis, Hermela; Mesman, Romy L. S.; Von Nicolai, Catharina; Ehlen, Asa; Guidugli, Lucia; Martin, Charlotte; Calleja, Fabienne M. G. R.; Meeks, Huong; Hallberg, Emily; Hinton, Jamie

*Published in:*  
Cancer Research

*DOI:*  
[10.1158/0008-5472.CAN-16-2568](https://doi.org/10.1158/0008-5472.CAN-16-2568)

**IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.**

*Document Version*  
Publisher's PDF, also known as Version of record

*Publication date:*  
2017

[Link to publication in University of Groningen/UMCG research database](#)

*Citation for published version (APA):*

Shimelis, H., Mesman, R. L. S., Von Nicolai, C., Ehlen, A., Guidugli, L., Martin, C., Calleja, F. M. G. R., Meeks, H., Hallberg, E., Hinton, J., Lilyquist, J., Hu, C., Aalfs, C. M., Aittomaki, K., Andrulis, I., Anton-Culver, H., Arndt, V., Beckmann, M. W., Benitez, J., ... NBCS Collaborators (2017). BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, 77(11), 2789-2799. <https://doi.org/10.1158/0008-5472.CAN-16-2568>

### Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

### Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

*Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.*

## BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer



Hermela Shimelis<sup>1</sup>, Romy L.S. Mesman<sup>2</sup>, Catharina Von Nicolai<sup>3</sup>, Asa Ehlen<sup>3</sup>, Lucia Guidugli<sup>4</sup>, Charlotte Martin<sup>5</sup>, Fabienne M.G.R. Calléja<sup>2</sup>, Huong Meeks<sup>6</sup>, Emily Hallberg<sup>7</sup>, Jamie Hinton<sup>7</sup>, Jenna Lilyquist<sup>7</sup>, Chunling Hu<sup>1</sup>, Cora M. Aalfs<sup>8</sup>, Kristiina Aittomäki<sup>9</sup>, Irene Andrulis<sup>10,11</sup>, Hoda Anton-Culver<sup>12</sup>, Volker Arndt<sup>13</sup>, Matthias W. Beckmann<sup>14</sup>, Javier Benitez<sup>15,16</sup>, Natalia V. Bogdanova<sup>17,18</sup>, Stig E. Bojesen<sup>19,20,21</sup>, Manjeet K. Bolla<sup>22</sup>, Anne-Lise Borresen-Dale<sup>23,24</sup>, Hiltrud Brauch<sup>25,26,27</sup>, Paul Brennan<sup>28</sup>, Hermann Brenner<sup>13,27,29</sup>, Annegien Broeks<sup>30</sup>, Barbara Brouwers<sup>31,32</sup>, Thomas Brüning<sup>33</sup>, Barbara Burwinkel<sup>34,35</sup>, Jenny Chang-Claude<sup>36,37</sup>, Georgia Chenevix-Trench<sup>38</sup>, for kConFab/AOCS Investigators, Ching-Yu Cheng<sup>39</sup>, Ji-Yeob Choi<sup>40,41</sup>, J. Margriet Collée<sup>42</sup>, Angela Cox<sup>43</sup>, Simon S. Cross<sup>44</sup>, Kamila Czene<sup>45</sup>, Hatef Darabi<sup>45</sup>, Joe Dennis<sup>22</sup>, Thilo Dörk<sup>18</sup>, Isabel dos-Santos-Silva<sup>46</sup>, Alison M. Dunning<sup>47</sup>, Peter A. Fasching<sup>14,48</sup>, Jonine Figueroa<sup>49,50</sup>, Henrik Flyger<sup>51</sup>, Montserrat García-Closas<sup>50</sup>, Graham G. Giles<sup>52,53</sup>, Gord Glendon<sup>10</sup>, Pascal Guénel<sup>54</sup>, Christopher A. Haiman<sup>55</sup>, Per Hall<sup>45</sup>, Ute Hamann<sup>56</sup>, Mikael Hartman<sup>57,58</sup>, Frans B. Hogervorst<sup>30</sup>, Antoinette Hollestelle<sup>59</sup>, John L. Hopper<sup>53</sup>, Hidemi Ito<sup>60,61</sup>, Anna Jakubowska<sup>62</sup>, Daehee Kang<sup>40,41,63</sup>, Veli-Matti Kosma<sup>64,65,66</sup>, Vessela Kristensen<sup>23,24,67</sup>, for NBCS Collaborators, Kah-Nyin Lai<sup>68,69</sup>, Diether Lambrechts<sup>70,71</sup>, Loic Le Marchand<sup>72</sup>, Jingmei Li<sup>45</sup>, Annika Lindblom<sup>73</sup>, Artitaya Lophatananon<sup>74</sup>, Jan Lubinski<sup>62</sup>, Eva Machackova<sup>75</sup>, Arto Mannermaa<sup>64,65,66</sup>, Sara Margolin<sup>76</sup>, Frederik Marme<sup>34,77</sup>, Keitaro Matsuo<sup>61,78</sup>, Hui Miao<sup>57</sup>, Kyriaki Michailidou<sup>22,79</sup>, Roger L. Milne<sup>52,53</sup>, Kenneth Muir<sup>74,80</sup>, Susan L. Neuhausen<sup>81</sup>, Heli Nevanlinna<sup>82</sup>, Janet E. Olson<sup>7</sup>, Curtis Olswold<sup>7</sup>, Jan J.C. Oosterwijk<sup>83</sup>, Ana Osorio<sup>15,16</sup>, Paolo Peterlongo<sup>84</sup>, Julian Peto<sup>46</sup>, Paul D.P. Pharoah<sup>22,47</sup>, Katri Pylkäs<sup>85,86</sup>, Paolo Radice<sup>87</sup>, Muhammad Usman Rashid<sup>56,88</sup>, Valerie Rhenius<sup>47</sup>, Anja Rudolph<sup>36</sup>, Suleeporn Sangrajang<sup>89</sup>, Elinor J. Sawyer<sup>90</sup>, Marjanka K. Schmidt<sup>30</sup>, Minouk J. Schoemaker<sup>91,92</sup>, Caroline Seynaeve<sup>59</sup>, Mitul Shah<sup>47</sup>, Chen-Yang Shen<sup>93,94</sup>, Martha Shrubsole<sup>95</sup>, Xiao-Ou Shu<sup>95</sup>, Susan Slager<sup>7</sup>, Melissa C. Southey<sup>96</sup>, Daniel O. Stram<sup>55</sup>, Anthony Swerdlow<sup>91,92</sup>, Soo H. Teo<sup>68,69</sup>, Ian Tomlinson<sup>97</sup>, Diana Torres<sup>56,98</sup>, Thérèse Truong<sup>54</sup>, Christi J. van Asperen<sup>8</sup>, Lizet E. van der Kolk<sup>30</sup>, Qin Wang<sup>22</sup>, Robert Winqvist<sup>85,86</sup>, Anna H. Wu<sup>55</sup>, Jyh-Cherng Yu<sup>99</sup>, Wei Zheng<sup>95</sup>, Ying Zheng<sup>100</sup>, Jennifer Leary<sup>101</sup>, Logan Walker<sup>102</sup>, Lenka Foretova<sup>75</sup>, Florentia Fostira<sup>103</sup>, Kathleen B.M. Claes<sup>104</sup>, Liliana Varesco<sup>105</sup>, Setareh Moghadasi<sup>8</sup>, Douglas F. Easton<sup>22,47</sup>, Amanda Spurdle<sup>106</sup>, Peter Devilee<sup>2</sup>, Harry Vrieling<sup>2</sup>, Alvaro N.A. Monteiro<sup>107,108</sup>, David E. Goldgar<sup>109</sup>, Aura Carreira<sup>3</sup>, Maaike P.G. Vreeswijk<sup>2</sup>, and Fergus J. Couch<sup>1,71</sup>

### Abstract

Breast cancer risks conferred by many germline missense variants in the *BRCA1* and *BRCA2* genes, often referred to as variants of uncertain significance (VUS), have not been established. In this study, associations between 19 *BRCA1* and 33 *BRCA2* missense substitution variants and breast cancer risk were investigated through a breast cancer case-control study using genotyping data from 38 studies of predominantly European ancestry (41,890 cases and 41,607 controls) and nine studies of Asian ancestry (6,269 cases and 6,624 controls). The *BRCA2* c.9104A>C, p.Tyr3035Ser (OR = 2.52; *P* = 0.04), and *BRCA1* c.5096G>A, p.Arg1699Gln (OR = 4.29; *P* = 0.009) variant were associated with moderately increased risks of

breast cancer among Europeans, whereas *BRCA2* c.7522G>A, p.Gly2508Ser (OR = 2.68; *P* = 0.004), and c.8187G>T, p.Lys2729Asn (OR = 1.4; *P* = 0.004) were associated with moderate and low risks of breast cancer among Asians. Functional characterization of the *BRCA2* variants using four quantitative assays showed reduced *BRCA2* activity for p.Tyr3035Ser compared with wild-type. Overall, our results show how *BRCA2* missense variants that influence protein function can confer clinically relevant, moderately increased risks of breast cancer, with potential implications for risk management guidelines in women with these specific variants. *Cancer Res*; 77(11); 2789–99. ©2017 AACR.

Shimelis et al.

<sup>1</sup>Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, Minnesota. <sup>2</sup>Department of Human Genetics, Leiden University Medical Center, Leiden, the Netherlands. <sup>3</sup>Genotoxic Stress and Cancer, Institut Curie, Orsay, France. <sup>4</sup>Department of Human Genetics, University of Chicago, Chicago, Illinois. <sup>5</sup>Research Center, Institut Curie, Orsay, France. <sup>6</sup>Cancer Control and Population Sciences, University of Utah, Salt Lake City, Utah. <sup>7</sup>Department of Health Sciences Research, Mayo Clinic, Rochester, Minnesota. <sup>8</sup>Department of Clinical Genetics, Leiden University Medical Center, Leiden, the Netherlands. <sup>9</sup>Department of Clinical Genetics, Helsinki University Hospital, University of Helsinki, Helsinki, Finland. <sup>10</sup>Lunenfeld-Tanenbaum Research Institute of Mount Sinai Hospital, Toronto, Canada. <sup>11</sup>Department of Molecular Genetics, University of Toronto, Toronto, Canada. <sup>12</sup>Department of Epidemiology, University of California Irvine, Irvine, California. <sup>13</sup>Division of Clinical Epidemiology and Aging Research, German Cancer Research Center (DKFZ), Heidelberg, Germany. <sup>14</sup>Department of Gynaecology and Obstetrics, University Hospital Erlangen, Friedrich-Alexander University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Erlangen, Germany. <sup>15</sup>Human Cancer Genetics Program, Spanish National Cancer Research Centre, Madrid, Spain. <sup>16</sup>Centro de Investigación en Red de Enfermedades Raras (CIBERER), Valencia, Spain. <sup>17</sup>Department of Radiation Oncology, Hannover Medical School, Hannover, Germany. <sup>18</sup>Gynaecology Research Unit, Hannover Medical School, Hannover, Germany. <sup>19</sup>Copenhagen General Population Study, Herlev and Gentofte Hospital, Copenhagen University Hospital, Herlev, Denmark. <sup>20</sup>Department of Clinical Biochemistry, Herlev and Gentofte Hospital, Copenhagen University Hospital, Herlev, Denmark. <sup>21</sup>Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark. <sup>22</sup>Department of Public Health and Primary Care, University of Cambridge, Cambridge, United Kingdom. <sup>23</sup>Department of Cancer Genetics, Institute for Cancer Research, Oslo University Hospital Radiumhospitalet, Oslo, Norway. <sup>24</sup>K.G. Jebsen Center for Breast Cancer Research, Institute of Clinical Medicine, Faculty of Medicine, University of Oslo, Oslo, Norway. <sup>25</sup>Dr. Margarete Fischer-Bosch-Institute of Clinical Pharmacology, Stuttgart, Germany. <sup>26</sup>University of Tübingen, Tübingen, Germany. <sup>27</sup>German Cancer Consortium (DKTK), German Cancer Research Center (DKFZ), Heidelberg, Germany. <sup>28</sup>International Agency for Research on Cancer, Lyon, France. <sup>29</sup>Division of Preventive Oncology, German Cancer Research Center (DKFZ) and National Center for Tumor Diseases (NCT), Heidelberg, Germany. <sup>30</sup>Netherlands Cancer Institute, Antoni van Leeuwenhoek Hospital, Amsterdam, the Netherlands. <sup>31</sup>Laboratory of Experimental Oncology, Department of Oncology, University Hospitals Leuven, Leuven, Belgium. <sup>32</sup>Department of General Medical Oncology, Leuven Cancer Institute, University Hospitals Leuven, Leuven, Belgium. <sup>33</sup>Institute for Prevention and Occupational Medicine of the German Social Accident Insurance, Institute of the Ruhr University Bochum, Bochum, Germany. <sup>34</sup>Department of Obstetrics and Gynecology, University of Heidelberg, Heidelberg, Germany. <sup>35</sup>Molecular Epidemiology Group, German Cancer Research Center (DKFZ), Heidelberg, Germany. <sup>36</sup>Division of Cancer Epidemiology, German Cancer Research Center (DKFZ), Heidelberg, Germany. <sup>37</sup>University Cancer Center Hamburg (UCCH), University Medical Center Hamburg-Eppendorf, Hamburg, Germany. <sup>38</sup>Department of Genetics, QIMR Berghofer Medical Research Institute, Brisbane, Australia. <sup>39</sup>Singapore Eye Research Institute, National University of Singapore, Singapore, Singapore. <sup>40</sup>Department of Biomedical Sciences, Seoul National University College of Medicine, Seoul, Korea. <sup>41</sup>Cancer Research Institute, Seoul National University, Seoul, Korea. <sup>42</sup>Department of Clinical Genetics, Erasmus University Medical Center, Rotterdam, the Netherlands. <sup>43</sup>Sheffield Cancer Research, Department of Oncology and Metabolism, University of Sheffield, Sheffield, United Kingdom. <sup>44</sup>Academic Unit of Pathology, Department of Neuroscience, University of Sheffield, Sheffield, United Kingdom. <sup>45</sup>Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden. <sup>46</sup>Department of Non-Communicable Disease Epidemiology, London School of Hygiene and Tropical Medicine, London, United Kingdom. <sup>47</sup>Department of Oncology, University of Cambridge, Cambridge, United Kingdom. <sup>48</sup>Department of Medicine, Division of Hematology and Oncology, David Geffen School of Medicine, University of California at Los Angeles, Los Angeles, California. <sup>49</sup>Usher Institute of Population Health Sciences and Informatics, The University of Edinburgh Medical School, Edinburgh, United Kingdom. <sup>50</sup>Division of Cancer Epidemiology and Genetics, National Cancer Institute, Rockville, Maryland. <sup>51</sup>Department of Breast Surgery, Herlev and Gentofte Hospital, Copenhagen University Hospital, Herlev, Denmark. <sup>52</sup>Cancer Epidemiology Centre, Cancer Council Victoria, Melbourne, Australia. <sup>53</sup>Centre for Epidemiology and Biostatistics, Melbourne School of Population and Global Health, The University of Melbourne, Melbourne, Australia. <sup>54</sup>Cancer & Environment Group, Center for Research in Epidemiology and Population Health (CESP), INSERM, University Paris-Sud, University Paris-Saclay, Villejuif, France. <sup>55</sup>Department of Preventive Medicine, Keck School of Medicine, University of Southern California, Los Angeles, California. <sup>56</sup>Molecular Genetics of Breast Cancer, German Cancer Research Center (DKFZ), Heidelberg, Germany. <sup>57</sup>Saw Swee Hock School of Public Health, National University of Singapore, Singapore, Singapore. <sup>58</sup>Department of Surgery, National University Health System, Singapore, Singapore. <sup>59</sup>Department of Medical Oncology, Family Cancer Clinic,

Erasmus MC Cancer Institute, Rotterdam, the Netherlands. <sup>60</sup>Division of Epidemiology and Prevention, Aichi Cancer Center Research Institute, Nagoya, Japan. <sup>61</sup>Department of Epidemiology, Nagoya University Graduate School of Medicine, Nagoya, Japan. <sup>62</sup>Department of Genetics and Pathology, Pomeranian Medical University, Szczecin, Poland. <sup>63</sup>Department of Preventive Medicine, Seoul National University College of Medicine, Seoul, Korea. <sup>64</sup>Cancer Center of Eastern Finland, University of Eastern Finland, Kuopio, Finland. <sup>65</sup>Institute of Clinical Medicine, Pathology and Forensic Medicine, University of Eastern Finland, Kuopio, Finland. <sup>66</sup>Imaging Center, Department of Clinical Pathology, Kuopio University Hospital, Kuopio, Finland. <sup>67</sup>Department of Clinical Molecular Biology, Oslo University Hospital, University of Oslo, Oslo, Norway. <sup>68</sup>Cancer Research Initiatives Foundation, Subang Jaya, Selangor, Malaysia. <sup>69</sup>Breast Cancer Research Unit, Cancer Research Institute, University Malaya Medical Centre, Kuala Lumpur, Malaysia. <sup>70</sup>Vesalius Research Center, Leuven, Belgium. <sup>71</sup>Laboratory for Translational Genetics, Department of Oncology, University of Leuven, Leuven, Belgium. <sup>72</sup>University of Hawaii Cancer Center, Honolulu, Hawaii. <sup>73</sup>Department of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm, Sweden. <sup>74</sup>Division of Health Sciences, Warwick Medical School, Warwick University, Coventry, United Kingdom. <sup>75</sup>Department of Cancer Epidemiology and Genetics, Masaryk Memorial Cancer Institute, Brno, Czech Republic. <sup>76</sup>Department of Oncology - Pathology, Karolinska Institutet, Stockholm, Sweden. <sup>77</sup>National Center for Tumor Diseases, University of Heidelberg, Heidelberg, Germany. <sup>78</sup>Division of Molecular Medicine, Aichi Cancer Center Research Institute, Nagoya, Japan. <sup>79</sup>Department of Electron Microscopy/Molecular Pathology, The Cyprus Institute of Neurology and Genetics, Nicosia, Cyprus. <sup>80</sup>Institute of Population Health, University of Manchester, Manchester, United Kingdom. <sup>81</sup>Department of Population Sciences, Beckman Research Institute of City of Hope, Duarte, California. <sup>82</sup>Department of Obstetrics and Gynecology, Helsinki University Hospital, University of Helsinki, Helsinki, Finland. <sup>83</sup>Department of Genetics, University of Groningen, Groningen, the Netherlands. <sup>84</sup>IFOM, The FIRC (Italian Foundation for Cancer Research) Institute of Molecular Oncology, Milan, Italy. <sup>85</sup>Laboratory of Cancer Genetics and Tumor Biology, Cancer and Translational Medicine Research Unit, Biocenter Oulu, University of Oulu, Oulu, Finland. <sup>86</sup>Laboratory of Cancer Genetics and Tumor Biology, Northern Finland Laboratory Centre Oulu, Oulu, Finland. <sup>87</sup>Unit of Molecular Bases of Genetic Risk and Genetic Testing, Department of Preventive and Predictive Medicine, Fondazione IRCCS (Istituto Di Ricovero e Cura a Carattere Scientifico) Istituto Nazionale dei Tumori (INT), Milan, Italy. <sup>88</sup>Department of Basic Sciences, Shaikat Khanum Memorial Cancer Hospital and Research Centre, Lahore, Pakistan. <sup>89</sup>National Cancer Institute, Bangkok, Thailand. <sup>90</sup>Research Oncology, Guy's Hospital, King's College London, London, United Kingdom. <sup>91</sup>Division of Genetics and Epidemiology, The Institute of Cancer Research, London, United Kingdom. <sup>92</sup>Division of Breast Cancer Research, The Institute of Cancer Research, London, United Kingdom. <sup>93</sup>School of Public Health, China Medical University, Taichung, Taiwan. <sup>94</sup>Taiwan Biobank, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan. <sup>95</sup>Division of Epidemiology, Department of Medicine, Vanderbilt-Ingram Cancer Center, Vanderbilt University School of Medicine, Nashville, Tennessee. <sup>96</sup>Department of Pathology, The University of Melbourne, Melbourne, Australia. <sup>97</sup>Wellcome Trust Centre for Human Genetics and Oxford NIHR Biomedical Research Centre, University of Oxford, Oxford, United Kingdom. <sup>98</sup>Institute of Human Genetics, Pontificia Universidad Javeriana, Bogota, Colombia. <sup>99</sup>Department of Surgery, National Taiwan University Hospital, Taipei, Taiwan. <sup>100</sup>Shanghai Municipal Center for Disease Control and Prevention, Shanghai, China. <sup>101</sup>Westmead Millennium Institute for Medical Research, University of Sydney, Sydney, Australia. <sup>102</sup>Department of Pathology, University of Otago, Christchurch, New Zealand. <sup>103</sup>Molecular Diagnostics Laboratory, Institute of Radioisotopes and Radiodiagnostic Products (IRRP), Athens, Greece. <sup>104</sup>Center for Medical Genetics, Ghent University Hospital, Ghent, Belgium. <sup>105</sup>Unit of Hereditary Cancers, IRCCS AOU San Martino, Genova, Italy. <sup>106</sup>Department of Genetics and Computational Biology, QIMR Berghofer Medical Research Institute, Brisbane, Australia. <sup>107</sup>Cancer Epidemiology Program, H. Lee Moffitt Cancer Center and Research Institute, Tampa, Florida. <sup>108</sup>Department of Oncologic Science, University of South Florida, Tampa, Florida. <sup>109</sup>Huntsman Cancer Institute and Department of Dermatology, University of Utah, Salt Lake City, Utah.

**Note:** Supplementary data for this article are available at Cancer Research Online (<http://cancerres.aacrjournals.org/>).

H. Shimelis, R.L.S. Mesman, C. Von Nicolai, A. Ehlen, D.E. Goldgar, A. Carreira, M.P. G. Vreeswijk, and F.J. Couch contributed equally to this article.

**Corresponding Author:** Fergus J. Couch, Mayo Clinic, Stabile 2-42, 200 First Street SW, Rochester, MN 55905. Phone: 507-284-3623; Fax: 507-538-1937; E-mail: couch.fergus@mayo.edu

doi: 10.1158/0008-5472.CAN-16-2568

©2017 American Association for Cancer Research.

## Introduction

Mutation screening of the *BRCA1* and *BRCA2* genes has resulted in the discovery of thousands of unique germline *BRCA1* and *BRCA2* variants. Many pathogenic variants of *BRCA1* or *BRCA2* resulting in truncation of these proteins, along with a small number of pathogenic missense variants, have been associated with high risks of breast cancer with cumulative risks of 55% to 85% by age 70 (1). In contrast, the influence on cancer risk of many rare variants of uncertain significance (VUS), accounting for between 2% and 10% of results from genetic testing, is not known (2–4). As a result, carriers of VUS in these predisposition genes cannot benefit from cancer risk management strategies for women with pathogenic mutations.

Clinical classification of *BRCA1* and *BRCA2* VUS has been largely based on probability-based models, which incorporate likelihood ratios associated with family history of cancer, cosegregation of variants with breast and ovarian cancer within families, tumor histopathology, and prior probabilities of pathogenicity associated with cross-species amino acid sequence conservation (5, 6). While over 200 *BRCA1* and *BRCA2* variants have been classified as pathogenic or neutral/nonpathogenic using a multifactorial likelihood model (7–10), many VUS remain because of limited availability of families segregating the variants. Clinical classification of VUS in *BRCA1* and *BRCA2* has been further complicated by the identification of variants with partial effects on protein function (5, 11, 12). However, to date, only the *BRCA1* c.5096G>A, p.Arg1699Gln (R1699Q) variant has been associated with a reduced cumulative risk of breast cancer (24% by age 70; ref. 13). R1699Q has also been associated with lower penetrance relative to the pathogenic c.5095C>T, p.Arg1699Trp (R1699W) variant in the same residue. In this study, the influence of 52 missense variants in *BRCA1* and *BRCA2* on breast cancer risk was investigated using the iCOGS breast cancer case–control project (14). In addition, the impact of the *BRCA2* c.9104A>C, p.Tyr3035Ser (Y3035S), c.7522G>A, p.Gly2508Ser (G2508S), and c.8187G>T, p.Lys2729Asn (K2729N) variants on *BRCA2* function were evaluated relative to known pathogenic and neutral variants using biochemical, cell-based homology–directed repair (HDR), and *in vivo* embryonic stem (ES) cell–based assays. The combination of these genetic and functional studies show that missense variants in the DNA-binding domain of *BRCA2* with partial effects on protein function can confer moderate risks of breast cancer.

## Materials and Methods

### Participants

Breast cancer cases and controls from 38 studies of predominantly European ancestry (41,890 cases with invasive disease and 41,607 controls) and nine studies of Asian ancestry (6,269 cases and 6,624 controls) from the Breast Cancer Association Consortium were used for genotyping (Supplementary Table S1). All studies were approved by local ethics committees and institutional review boards.

### Variant selection

Missense substitution variants from *BRCA1* ( $n = 19$ ) and *BRCA2* ( $n = 33$ ) were selected by ENIGMA for inclusion on the iCOGS genotyping array based on frequency in the ENIGMA database (Supplementary Tables S2; ref. 15). Variants are defined by Human Genome Variant Society (HGVS) nomenclature and

are based on RefSeq transcripts (*BRCA1*: NM\_007294.3; *BRCA2*: NM\_000059.3).

### Genotyping

Genotyping was conducted using the custom Illumina Infinium array (iCOGS; ref. 14). DNA samples containing each of the variants were included in iCOGS genotyping as positive controls and were used to inform genotype calling. Genotypes were called with the GenCall algorithm. Descriptions of sample and genotype quality control have been published previously (14, 16). Cluster plots for rare variants for this study were manually evaluated relative to positive control samples.

### Statistical analysis

**Case–control analysis.** The association of each variant with breast cancer risk was assessed using unconditional logistic regression, adjusting for study (categorical). Analyses were restricted to either Caucasian or Asian women. Cases selected for iCOGS based on personal or family history of breast cancer were excluded to obtain unbiased OR estimates for the general population. The significance of associations ( $P$  values) was determined by the likelihood ratio test comparing models with and without carrier status as a covariate. Because this study was focused on estimating breast cancer risk associated with each variant, analyses were not adjusted for multiple testing. Moderate risk of breast cancer was defined as OR from 2.0 to 5.0 and high risk of breast cancer was defined as OR > 5.0.

**Segregation analysis.** Risks of breast cancer were assessed using pedigrees based on the likelihood of the observed pedigree genotypes conditional on the pedigree phenotypes and the genotype of the index case. The primary analysis calculated the penetrance for breast cancer in carriers of the p.Y3035S variant assuming a constant relative risk with age. A second analysis allowed for a similar pattern of age specific effects as for population-based pathogenic *BRCA2* variants and calculated the optimal cumulative penetrance at 75% of pathogenic *BRCA2* variants. The age-specific HR, by decade, was assumed to be a constant multiple of the population-based estimates for *BRCA2* pathogenic mutations, with cumulative penetrance reestimated at each trial value of the multiplier. This provided for a similar pattern of age-specific effects as in *BRCA2*, but allowed testing of different penetrance values and only required estimation of a single parameter. Models were fitted under maximum likelihood theory using a modified version of the LINKAGE genetic analysis package (17). Noncarriers were assumed to be at population risks with incidence rates taken from cancer registry data obtained from Cancer Incidence in Five Continents, VIII (IARC, Lyon, France) and risk ratios (RR, the age-specific breast cancer incidence rate in carriers divided by the relevant population rate) were estimated. Reported breast cancers with unknown age at diagnosis were excluded from all analyses. Cancers other than breast (including ovarian cancer) were treated as unaffected at the age of their cancer diagnosis.

### Cell lines

V-C8 cells were a kind gift from Dr. M.Z. Zdzienicka (Department of Molecular Cell Genetics, Nicolaus-Copernicus-University, Bydgoszcz, Poland). 293T cells were obtained from ATCC (CRL-3216). Cells were authenticated by short tandem repeat analysis using the kit GenePrint10 kit (Promega). All the cell lines used in

Shimelis et al.

this study were routinely checked for mycoplasma contamination using the MycoProbe Mycoplasma Detection Set (R&D Systems). Cells were limited to 6 weeks in culture.

### Homology-directed repair assay

The homology-directed repair (HDR) assay for evaluating the influence of variants in the BRCA2 DNA-binding domain (DBD) on BRCA2 homologous recombination DNA repair activity has been described previously (11). Full-length human BRCA2 wild-type and mutant cDNA expression constructs were coexpressed with an I-Sce1-expressing plasmid in *Brca2*-deficient V-C8 cells, stably expressing the DR-GFP reporter plasmid. Homologous recombination-dependent repair of I-Sce1 induced DNA double strand breaks were quantified by FACS of GFP-positive cells after 72 hours. Two independent clones of each variant were evaluated in the HDR assay on three separate occasions. Equivalent expression of wild-type and mutant BRCA2 proteins was confirmed by Western blot analysis of anti-Flag-M2 (Sigma F1804) antibody immunoprecipitates from V-C8 cell lysates.

### Purification of full-length wild-type and mutated BRCA2 protein

Wild-type and mutant human BRCA2 cDNAs were cloned into the C-terminal MBP-GFP-tagged pCMV1 expression plasmids and purified as described previously (18, 19). Briefly, 10 × 15-cm plates of HEK293 cells were transiently transfected using TurboFect (Thermo Scientific) following the manufacturer's specifications and harvested 30 hours posttransfection. Cell extracts were bound to amylose resin (NEB), and the protein was eluted with 10 mmol/L maltose. The eluate was further purified by ion exchange using BioRex 70 resin (Bio-Rad) and step eluted at 250 mmol/L, 450 mmol/L, and 1 mol/L NaCl (18, 19). Each fraction was tested for nuclease contamination. The 1 mol/L NaCl fractions were used for the DNA-binding assay because they were free of nuclease contamination.

### Electrophoretic mobility shift assay

The single-stranded DNA (ssDNA) substrate (oAC423) used for DNA binding was obtained from Sigma and purified by PAGE. Purified wild-type or mutated BRCA2 at concentrations 0, 1, 5, 10, 20 nmol/L was mixed with the ssDNA oligonucleotide oAC423 167-mer (0.2 μmol/L nt), labeled with <sup>32</sup>P at the 5' end, in a buffer containing 25 mmol/L TrisAcO (pH 7.5), 1 mmol/L MgCl<sub>2</sub>, 2 mmol/L CaCl<sub>2</sub>, 1 mmol/L DTT, 1 mmol/L ATP, 100 μg/mL BSA, and incubated for 60 minutes at 37°C. Reaction products were resolved by 6% PAGE, imaged on a Typhoon PhosphorImager (Amersham Biosciences), and analyzed with Image Quant software. The relative amount of product was calculated as labeled complex divided by the total labeled input DNA in each lane. The protein-free lane defined the value of 0% complex.

oAC423: 5'-CTGCTTTATCAAGATAATTTTTGACTCATCAG-AAATATCCGTTTCCTATATTT

ATTCCATTATGTTTTATTCATTTACTTATTCTTTATGTTTCATTT-TTTATATCCTTTACTTTATTTTCTCTGTTTATTCATTTACTTTATTTT-GTATTATCCCTTATCTTATTTA-3'.

### Embryonic stem cell complementation

Selected BRCA2 variants were functionally analyzed on the basis of the ability of human BRCA2 to complement the lethality of mouse *Brca2* deficiency (20, 21). BRCA2 exons containing VUS were generated by mutagenesis PCR and engineered into a human

BRCA2 (hBRCA2) bacterial artificial chromosome (BAC) by Red/ET BAC recombineering in DH10B *E.coli*. BAC DNA was transfected into mES cells containing a conditional mouse *Brca2* allele and a disrupted *Brca2* allele (*Brca2*<sup>-loxP</sup>), and the DR-GFP construct integrated at the *pim1* locus. hBRCA2-containing cells were selected by G418. Per variant, two independent BAC transfections were performed and G418-resistant clones from each BAC transfection were pooled and evaluated for BRCA2 activity using functional assays. In the mES cell HDR assay, cells were transfected with an I-Sce1 expression vector, pCMV-RED-ISce, and GFP-positive cells were quantified by flow cytometry 48 hours after transfection. mES cells were also treated with varying doses of PARP inhibitor (KU-0058948, AstraZeneca) and viable cells were quantified after 48 hours. Cell survival was calculated as the fraction of treated surviving mES cells relative to the cell count of untreated surviving cells per cell line.

### ES cell functional assays

After Cre-recombinase transfection, *mBrca2*-depleted cells were selected for restoration of the HPRT minigene using hypoxanthine-aminopterin-thymidine (HAT)-containing medium. HAT-resistant clones were pooled and evaluated for BRCA2 activity using functional assays. In the mES cell HDR assay, cells were transfected with an I-Sce1 expression vector, pCMV-RED-ISce, and GFP-positive cells were quantified by flow cytometry 48 hours after transfection. mES cells were also treated with varying doses of PARP inhibitor (KU-0058948, AstraZeneca) and viable cells were quantified after 48 hours. Cell survival was calculated as the fraction of treated surviving mES cells relative to the cell count of untreated surviving cells per cell line.

## Results

### Association of BRCA1 and BRCA2 variants with breast cancer risk

A total of 19 BRCA1 and 33 BRCA2 variants encoding missense substitutions and the known pathogenic BRCA1 protein truncating variant c.4327C>T, p.Arg1443Ter (R1443X) were genotyped for 48,159 breast cases and 48,231 controls from the Breast Cancer Association Consortium on the iCOGS custom genotyping array (Supplementary Table S1). Among the BRCA1 variants, 12 have been classified as Class 1-neutral, 6 as Class 3-uncertain, and 2 as Class 5-pathogenic, by the quantitative multifactorial likelihood model that the ENIGMA consortium (www.enigmaconsortium.org) uses for expert panel review of BRCA1 and BRCA2 variants for ClinVar (<http://www.ncbi.nlm.nih.gov/clinvar>) and BRCA Exchange (<http://brcaexchange.org>; Supplementary Table S2). Among the Class 3 variants, BRCA1 c.5207T>C, p.Val1736Ala (V1736A) is known to disrupt BRCA1 activity (22), and both V1736A and c.5363G>A, p.Gly1788Asp (G1788D) are annotated as pathogenic by multiple sources in the ClinVar database. Among the BRCA2 variants, 25 have been classified as Class 1-neutral or Class 2-likely neutral, 6 are Class 3-uncertain, and two [c.8167G>C, p.Asp2723His (D2723H); c.9154C>T, p.Arg3052Trp (R3052W)] have been classified as Class 5-pathogenic using the same multifactorial likelihood model (Supplementary Table S2). Among these, 18 are located in the DNA-binding domain (amino acids 2460–3170).

The BRCA1 R1443X truncating pathogenic variant was associated with high risk of breast cancer (OR = 8.3, *P* = 0.045) in the Caucasian case-control analysis in iCOGS (Table 1; Supplementary Table S3), consistent with what has been estimated for truncating pathogenic BRCA1 variants. Among the missense variants, c.5096G>A, p.Arg1699Gln (R1699Q) was associated with a moderate risk of breast cancer (OR = 4.29, *P* = 0.009; Table 1; Supplementary Table S3). This result was lower than expected for

**Table 1.** Variants in *BRCA1* and *BRCA2* significantly associated with breast cancer risk in a case-control analysis

Gene	Sequence variants <sup>a</sup>			Protein change	Caucasian			Asian				
	HGVs DNA	HGVs Protein	Case, n = 41,890		Control n = 41,607	OR <sup>b</sup>	95% CI	P	Case, n = 6,629	Control, n = 6,624	OR <sup>c</sup>	95% CI
BRCA1	c.2521C>T	p.A19841Trp	160	207	0.81	0.66-1.00	0.045	1	0	—	—	—
	c.4327C>T	p.Arg1443Ter	9	1	8.3	1.05-16.0	0.045	1	1	1.5	0.09-25.75	0.76
	c.5096G>A	p.Arg1699Gln	16	4	4.3	1.43-12.85	0.009	0	0	ND	ND	—
BRCA2	c.4258G>T	p.Asp1420Tyr	657	749	0.86	0.77-0.96	0.005	6	8	1.01	—	0.99
	c.7522G>A	p.Gly2508Ser	0	0	ND	—	—	31	12	2.7	1.37-5.23	0.004
	c.8149G>T	p.Ala2717Ser	137	185	0.8	0.62-0.96	0.02	0	0	ND	—	—
	c.8187G>T	p.Lys2729Asn	3	1	2.8	0.29-27.64	0.368	164	128	1.4	1.12-1.78	0.004
	c.9104A>C	p.Tyr3035Ser	18	7	2.5	1.05-6.05	0.038	3	0	ND	—	—
	c.9292T>C	p.Tyr3098His	14	20	0.7	0.35-1.38	0.304	0	0	ND	—	—

Abbreviations: CI, confidence interval; ND, not determined.

<sup>a</sup>Nucleotide numbering in the reference sequences of BRCA1: NM\_007294.3; BRCA2: NM\_000059.3.<sup>b</sup>Adjusted for 6 European ancestry principal components.<sup>c</sup>Adjusted for two Asian ancestry principal components.

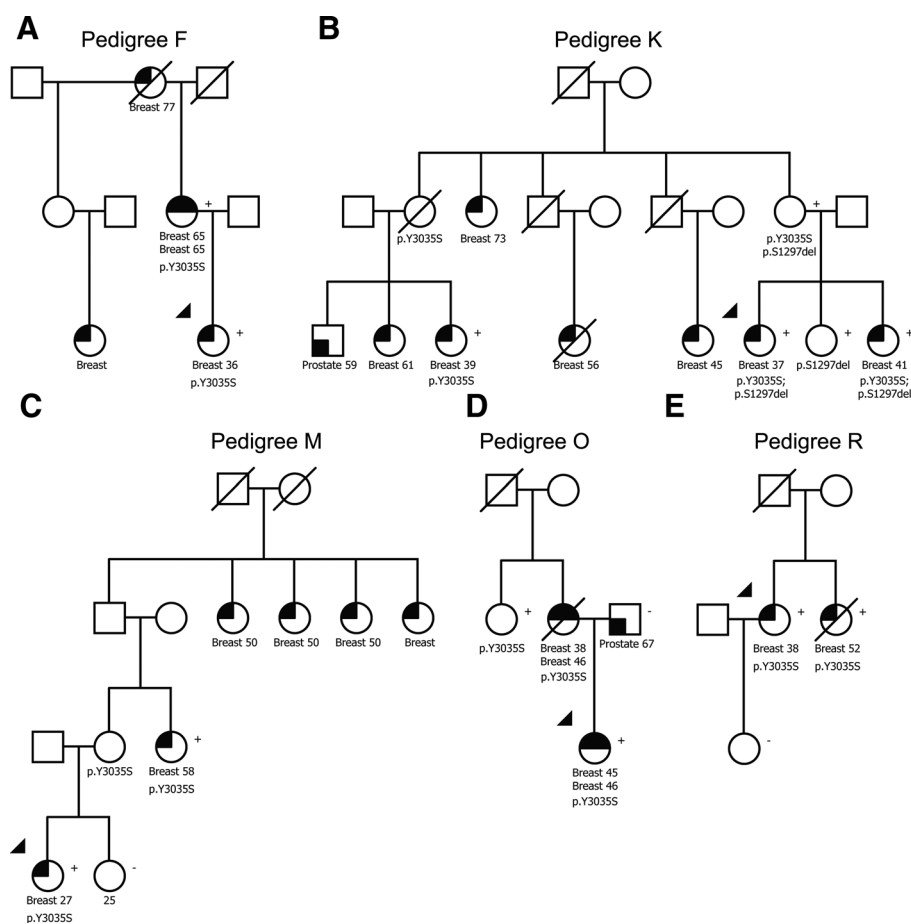
pathogenic *BRCA1* variants, but consistent with the moderate penetrance of this variant estimated from family-based studies (13). Several *BRCA1* variants including the known pathogenic c.5123C>A, p.Ala1708Glu (A1708E); the c.5207T>C, p.Val1736Ala (V1736A); and c.5363G>A, p.Gly1788Asp (G1788D) variants that are identified as pathogenic in ClinVar were not observed in sufficient numbers of cases and controls to allow for estimation of breast cancer risks (Supplementary Tables S2 and S3). Three *BRCA2* variants were statistically significantly associated with increased breast cancer risk ( $P < 0.05$ ) for Caucasian or Asian women. *BRCA2* c.7522G>A, p.Gly2508Ser (G2508S) was observed in 31 cases and 12 controls in the Asian studies (OR = 2.68,  $P = 0.004$ ), but not in any Caucasians, *BRCA2* c.8187G>T, p.Lys2729Asn (K2729N) was observed in 164 cases and 128 controls in the Asian studies (OR = 1.41,  $P = 0.004$ ), and *BRCA2* c.9104A>C, p.Tyr3035Ser (Y3035S) was observed in 18 cases and 7 controls in the Caucasian studies (OR = 2.52,  $P = 0.038$ ; Table 1; Supplementary Table S3). In addition, the *BRCA2* c.4258G>T, p.Asp1420Tyr (D1420Y; OR = 0.86,  $P = 0.005$ ) and c.8149G>T, p.Ala2717Ser (A2717S; OR = 0.77,  $P = 0.02$ ) were negatively associated with risk for Caucasian women (Table 1; Supplementary Table S3). None of the remaining *BRCA2* variants, including the Class 5 pathogenic *BRCA2* variants, c.8167G>C, p.Asp2723His (D2723H) and c.9154C>T, p.Arg3052Trp (R3052W), were observed in enough cases and controls for estimation of breast cancer risk (Supplementary Table S3). Thus, for the first time *BRCA2* variants encoding missense alterations (G2508S, K2729N, and Y3035S) have been associated with moderately (OR < 5.0) increased risks of breast cancer.

To assess further the association with breast cancer for the *BRCA2* G2508S and Y3035S potentially clinically relevant moderate risk variants, pedigrees for segregation analysis were collected through the ENIGMA consortium. Nineteen pedigrees with the Y3035S variant were collected (Fig. 1; Supplementary Fig. S1; Supplementary Table S4). Only one pedigree was obtained for G2508S, suggesting this variant is rare in the Caucasian population. Segregation studies of Y3035S, assuming the relative risk was constant with age, indicated an association with breast cancer risk [risk ratio (RR) = 14.8; 95% CI, 2.4-20.0; Supplementary Table S4]. A second analysis, allowing for a similar pattern of age-specific effects as for population-based pathogenic *BRCA2*-truncating variants, estimated the optimal cumulative penetrance for Y3035S at 0.75 of known pathogenic truncating *BRCA2* variants, and yielded a similar risk ratio for breast cancer (Supplementary Table S4). Y3035S cooccurred with a pathogenic *BRCA2* variant (S1882X) in Pedigree G (Supplementary Fig. S1). Cooccurrence with S1298del in Pedigree K (Fig. 1) was not informative because S1298del is a VUS. Together, the case-control study and the pedigree analysis suggest that Y3035S is associated with moderately increased breast cancer risk.

#### Cell-based HDR analysis of *BRCA2* variants

Inactivation or depletion of *BRCA2* has been associated with deficient HDR of DNA double strand breaks (23), which can be quantified with a cell-based HDR GFP reporter assay (24). This assay has shown 100% sensitivity and specificity for known pathogenic missense variants in the *BRCA2* DNA-binding domain and has been used for characterization of *BRCA2* VUS (8, 11, 25). In this study, the impact of the G2508S, A2717S, K2729N, and Y3035S missense variants on *BRCA2* HDR activity was assessed relative to the D2723H and R3052W known pathogenic and the

Shimelis et al.

**Figure 1.**

BRCA2 p.Y3035S segregates with breast cancer in high-risk families. **A-E**, individual pedigrees containing the Y3035S variant. Upper black quadrants reflect breast cancer status. Type of cancer and age at diagnosis are displayed. Variant status is indicated by "Y3035S." +, mutation positive; -, mutation negative reflects results of genetic testing.

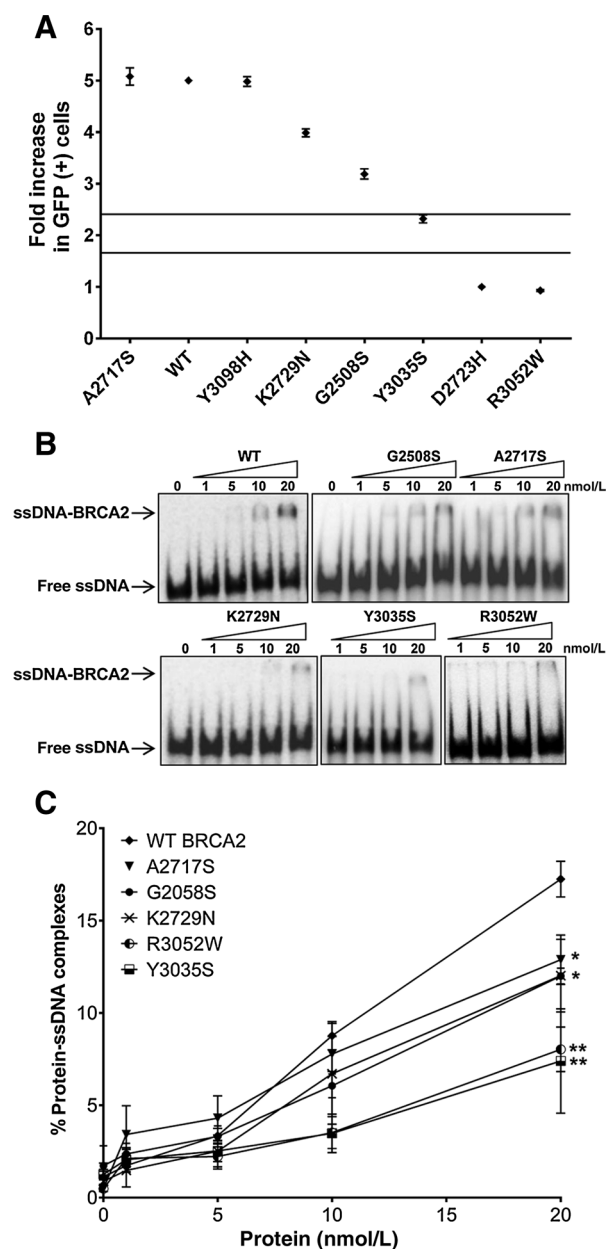
c.9292T>C p.Tyr3098His (Y3098H) known neutral BRCA2 variants (11, 26). D1420Y was not evaluated because the variant is not located in the BRCA2 DBD. All wild-type and mutant BRCA2 proteins displayed equivalent levels of expression relative to  $\beta$ -actin by Western blot analysis (Supplementary Fig. S2). The D2723H and R3052W Class 5 pathogenic variants (11) showed substantial loss of BRCA2 HDR activity (Fig. 2A; Table 2). In contrast, BRCA2 Y3035S showed intermediate levels (2.3-fold relative to D2723H; Fig. 2A; Table 2) of BRCA2 HDR activity. This was outside the thresholds for known pathogenic and neutral missense variants (HDR fold-change <1.66 and >2.41, respectively, that equate to 99% probabilities of pathogenicity and neutrality (11). This intermediate functional effect was consistent with the moderate risk of breast cancer (OR = 2.52,  $P = 0.038$ ) observed in the iCOGS case-control study (Table 1) and the estimated 0.75-fold penetrance of pathogenic BRCA2 variants from segregation studies (Supplementary Table S4). This is the first evidence that reduced BRCA2 function is associated with an intermediate or moderate risk of breast cancer.

In contrast, BRCA2 G2508S exhibited 3.2-fold HDR activity relative to D2723H (Fig. 2A; Table 2). While reduced relative to wild-type activity, this level of HDR activity was associated with >99% probability of neutrality. Similarly, BRCA2 K2729N showed reduced HDR activity relative to the wild-type protein (Fig. 2A; Table 2), which was consistent with a mild influence on breast cancer risk (OR = 1.41,  $P = 0.004$ ) in the Asian population, and >99% probability of neutrality (Fig. 2A). Together, these results

show that the HDR assay is calibrated relative to levels of cancer risk, with minor functional effects for variants associated with low- or modest risks of breast cancer such as c.9976A>T, p.Lys3326Ter (K3326X; OR = 1.28; ref. 27) and K2729N (OR = 1.41), more substantial functional effects for the intermediate risk Y3035S (OR = 2.52), and strong effects for known pathogenic variants such as D2723H and R3052W (Fig. 2A). Thus, the HDR assay may predict the level of risk associated with any BRCA2 DBD variant.

#### ssDNA-binding activity of BRCA2 variants

BRCA2 directly binds to ssDNA and recruits RAD51 to ssDNA at sites of DNA damage during homologous recombination DNA repair (18, 28). Hence, ssDNA binding is integral to the homologous recombination activity of BRCA2. On this basis, an *in vitro* biochemical assay was used to examine the influence of the BRCA2 variants on BRCA2 ssDNA-binding activity. Full-length wild-type and mutant human BRCA2 proteins tagged with (N-terminal) GFP and maltose-binding protein (MBP; GFP-MBP-BRCA2) were expressed and purified to near homogeneity (Supplementary Fig. S3) as described previously (18, 19). Full-length BRCA2 protein expression was confirmed by Western blotting using an antibody against the C-terminus of BRCA2 (Supplementary Fig. S3). The ssDNA-binding activity of full-length wild-type and mutant BRCA2 proteins was evaluated using an EMSA. The wild-type protein bound to ssDNA with a yield of approximately 18% at the maximum attainable concentration of BRCA2 protein (Fig. 2B and C; Table 2), consistent with previous results (18),

**Figure 2.**

**A**, HDR and ssDNA-binding activity of BRCA2 p.Y3035S is reduced. **A**, Activity of BRCA2 missense variants is shown as HDR fold change with SE (of three independent measures of duplicates) on a scale of 1–5. Solid lines represent 99.9% and 0.1% probability of pathogenicity. **B**, Representative EMSA of DNA–protein complexes formed by mixing increasing concentrations (0, 5, 10, 20 nmol/L) of purified BRCA2 wild-type and mutant proteins with ssDNA. **C**, Quantitation of the DNA–protein complex formation shown in **B**. Error bars, SE derived from at least three independent experiments. Statistical difference between wild-type (WT) and mutant BRCA2 protein–DNA complex formation was determined by two-sample *t* test. \*, *P* < 0.05; \*\*, *P* < 0.001.

whereas the R3052W pathogenic control exhibited 2-fold reduced protein–ssDNA complex formation (~8%; Fig. 2B and C; Table 2). Likewise, the Y3035S variant exhibited 2-fold reduced complex formation compared with the wild-type protein (Fig.

2B and C; Table 2). In contrast, G2508S, A2717S, and K2729N showed only partially reduced (~12%–13%) protein–ssDNA complex formation (Fig. 2B and C; Table 2). These findings are consistent with predictions from the crystal structure of the BRCA2 DBD, where Y3035S is predicted to impair DNA binding, similarly to R3052W, because of proximity to DNA in the ssDNA–BRCA2 complex (Supplementary Fig. S4; ref. 26). Overall, the results suggest that the reduction in HDR activity observed for Y3035S (Fig. 2A) is due to a defective ssDNA-binding activity.

#### Mouse embryonic stem cell–based functional analysis of BRCA2 missense variants

Functional complementation of murine (*m*) *Brca2*-null ES cell lethality by human (*h*) BRCA2 variants (20, 21) has been used to characterize BRCA2 VUS. Wild-type human BRCA2 expression rescues *Brca2*-deficient ES cells from lethality, whereas ES cells expressing known pathogenic forms of BRCA2 fail to survive (20). In addition, several variants have shown partial or reduced ES cell survival relative to wild-type BRCA2. Surviving cells expressing these variants have shown moderate defects in HDR assays and sensitivity to cisplatin or a PARP inhibitor (29). In this study, two independent pools of BAC clones for each of *hBRCA2* G2508S, A2717S, D2723H, K2729N, Y3035S, and R3052W were tested for complementation of *mBrca2* deficiency and HDR activity. Cells expressing *hBRCA2* D2723H or R3052W pathogenic variants did not survive after disrupting endogenous *mBrca2* expression and were not included in the downstream functional analysis. Instead, we included mES cells expressing the W31C variant as a negative control. This variant conferred a severe defect in HDR activity because of disruption of the BRCA2–PALB2 interaction (30).

BRCA2 W31C, G2508S, A2717S, K2729N, and Y3035S BACs rescued the lethality of the *mBrca2*-deficient ES cells, suggesting at least partial functional complementation of *mBrca2* deficiency. HDR activity of surviving cells was assessed using the DR-GFP reporter assay. BRCA2 W31C showed only 14% (*P* < 0.001) activity, whereas BRCA2 Y3035S, G2508S, and K2729N variants displayed 50% (*P* = 0.002), 55% (*P* = 0.007), and 70% (*P* = 0.02) of wild-type HDR activity, respectively (Fig. 3A; Table 2). In contrast, HDR activity in cells expressing A2717S was not significantly different to wild-type protein (Fig. 3A; Table 2). The sensitivity of wild-type and mutant BRCA2-expressing ES cells to PARP inhibitor (KU-0058948) was evaluated to determine whether the reduction in HDR associated with some of the variants was sufficient to confer sensitivity to PARP inhibitor. Sensitivity was evaluated by counting viable cells after 48 hours of exposure to different doses of drug. Wild-type BRCA2, G2508S, and A2717S did not show sensitivity to PARP inhibitor, whereas W31C expressing cells showed significant sensitivity (Fig. 3B; Table 2). K2729N and Y3035S resulted in partial rescue of ES cell sensitivity (Fig. 3B; Table 2). Collectively, the ES cell HDR activity of the variants showed high concordance with the ORs from the case–control study, with Y3035S displaying partially deficient BRCA2 activity. In contrast, the level of HDR activity did not correlate well with different levels of PARP inhibitor sensitivity, although Y3035S was partially sensitive to PARP inhibitor, consistent with the results from other assays.

#### Discussion

In this study, associations between 52 *BRCA1* and *BRCA2* missense variants and breast cancer risk were evaluated using a



Shimelis et al.

**Table 2.** Summary of functional effects of each *BRCA2* variant measured by four independent assay

Variants	OR	V-C8 HDR Assay Fold-change ± SE	Protein-DNA binding % protein complexes at 20 nmol/L	ES Cells HDR assay Relative HR ± SE	PARP Inhibitor response % survival at 125 nmol/L ± SE	Overall impact
Wild-type	N/A	5.00	17.47 ± 0.01	1.00	105 ± 11	(+) Wildtype
Y31C	N/A	N/A	N/A	0.14 ± 0.06	46 ± 11	(-) Deleterious
G2508S	2.7	3.19 ± 0.10	12.00 ± 0.43	0.56 ± 0.10	99 ± 3	(-) Mild effect
A2717S	0.8	5.08 ± 0.17	12.88 ± 1.89	0.85 ± 0.20	90 ± 14	(+) Neutral
D2723H	N/A	1.00	N/A	N/A	N/A	(-) Deleterious
K2729N	1.4	3.99 ± 0.08	12.12 ± 1.96	0.70 ± 0.11	81 ± 15	(-) Mild effect
Y3035S	2.5	2.32 ± 0.08	7.39 ± 2.83	0.50 ± 0.15	80 ± 11	(-) Moderate effect
R3052W	N/A	0.93 ± 0.02	8.03 ± 2.09	N/A	N/A	(-) Deleterious
Y3098H	0.7	4.98 ± 0.09	N/A	N/A	N/A	(+) Neutral

NOTE: N/A, not applicable; SE, standard error of the mean.

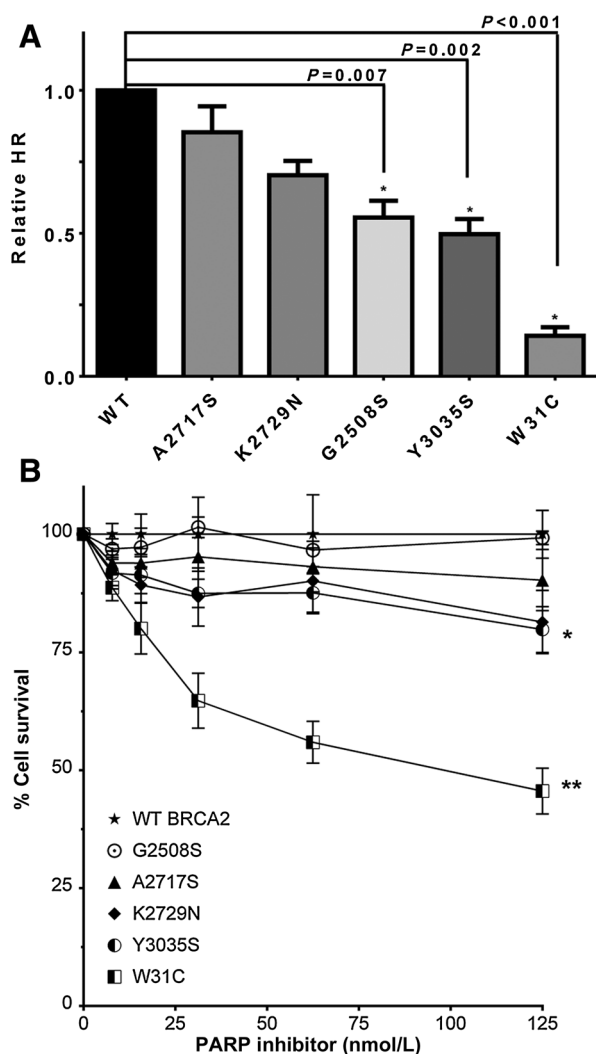
large breast cancer case-control study. To our knowledge, this is the largest case-control study conducted to establish the clinical relevance and estimate the risks of individual rare *BRCA1* and *BRCA2* variants encoding missense substitutions. The case-control analysis showed that *BRCA1* c.5096G>A, R1699Q (OR = 4.29) and *BRCA2* c.9104A>C, Y3035S (OR = 2.52) were associated with moderately increased breast cancer risks for Caucasian women (Table 1), whereas *BRCA2* c.7522G>A, G2508S (OR = 2.68) and c.8187G>T, K2729N (OR = 1.41) were associated with increased risks for Asian women. This is the first study to estimate low to moderate risks of breast cancer for specific *BRCA1* and *BRCA2* missense variants.

The moderate risk of breast cancer associated with the *BRCA1* R1699Q variant (OR = 4.29) was consistent with previous findings from segregation analyses of breast cancer families, which estimated that R1699Q was associated with a cumulative risk of breast or ovarian cancer by age 70 years of 24% relative to the pathogenic R1699W variant and *BRCA1* truncating variants (13). Similarly the quantitative ENIGMA multifactorial likelihood prediction model based on family data and sequence conservation yielded a posterior probability of pathogenicity for R1699Q of only 0.79 (13). Consistent with these findings, *BRCA1* R1699Q protein has shown only partial protein function in HDR and other *in vitro* experiments (12, 13). Thus, the case-control study and functional studies are consistent in identifying R1699Q as a moderate risk variant in *BRCA1*.

*BRCA2* Y3035S was associated with increased risk of disease (OR = 2.52) for Caucasian women. While the numbers of cases and controls with the Y3035S variant were small, the moderate risk estimate is supported by family data showing partial cosegregation with breast cancer, and one pedigree in which *BRCA2* Y3035S cooccurred with *BRCA2* c.5645C>A p.Ser1882Ter (S1882X; Supplementary Fig. S1). Several sequence-based *in silico* prediction models including MetaLR, MetaSVM, Vest3, and A-GVGD (prior probability of pathogenicity of 0.66; Supplementary Table S2) predicted Y3035S as deleterious. In addition, the missense substitution is predicted as likely deleterious by a protein likelihood ratio model based on sequence analysis (31). Analyses of splicing defects using Minigene-based assays have shown no influence on RNA splicing (32), suggesting that the increased risks are not due to abnormal splicing. Importantly, functional analysis of Y3035S using multiple independent assays consistently revealed partial activity. Y3035S showed intermediate *BRCA2* HDR activity in VC8 cells, failed to restore HDR activity in ES cells (Fig. 3A), and only partially rescued sensitivity to PARP inhibition in ES cells (Fig. 3B). Similarly, Y3035S showed significantly reduced ssDNA complex formation (Fig. 2B and C)

consistent with the location of Y3035 in the crystal structure of the *BRCA2* DBD (Supplementary Fig. S4; ref. 28). Together, the functional studies indicate that Y3035S is a hypomorphic *BRCA2* variant. Overall the case-control association study and functional analyses provide the first evidence that a hypomorphic *BRCA2* missense variant can confer a moderate risk of breast cancer. However, Y3035S is consistently reported as "likely benign" and "benign" in the ClinVar public database. As this database is widely used by researchers and clinicians, this underappreciation of moderate risks of breast cancer associated with this variant has the potential to impact patient care. Further prospective studies are required to estimate age-dependent risks of cancer and to inform management protocols for carriers of this and other hypomorphic *BRCA2* variants.

The *BRCA2* G2508S (OR = 2.68,  $P = 0.004$ ) variant was associated with a moderate risk of breast cancer in Asian women, but could not be evaluated in the Caucasian population (Table 1). The variant was predicted neutral by a protein likelihood prediction model (31), but was predicted deleterious by other *in silico* prediction models including MetaLR, MetaSVM, Vest3, and A-GVGD (prior probability of pathogenicity of 0.66; Supplementary Table S2). However, the HDR V-C8 cell-based assay showed only mildly reduced activity similar to K2729N (OR = 1.41) and p. K3326X (OR = 1.28; ref. 27), which are both classified as neutral (Fig. 2A). Likewise, the impact of G2508S on ssDNA binding was limited and most similar to K2729N (Fig. 2B and C). Although G2508S only partially rescued HDR activity in ES cells (Fig. 3A), the variant completely rescued sensitivity to PARP inhibition in ES cells similar to wild-type *BRCA2* (Fig. 3B). Thus, the functional results suggest a limited impact on *BRCA2* activity. As the variant has only been detected in the East Asian population (33, 34), one possibility is that genetic and environmental modifiers in the Asian population account in part for the influence of the variant on breast cancer risk and the discrepancy between the case-control and functional study results. Further studies are needed to resolve this issue, but for now the breast cancer risks associated with this variant must be treated with caution. *BRCA2* K2729N (OR = 1.41,  $P = 0.004$ ) is also common in Asians, but rare in Caucasians (34). This variant has previously been classified as neutral by the multifactorial likelihood classification model (8). Consistent with these findings, functional analysis of K2729N showed only a minor influence on HDR function (8, 11; Fig. 2A) and ssDNA binding (Fig. 2B), and substantial rescue of ES cell-based HR (Fig. 3A) and ES cell drug sensitivity (Fig. 3B). The mild defect in HR function correlated well with the low risk of breast cancer (OR = 1.41,  $P = 0.004$ ) associated with the K2729N variant in the Asian case-control study.



**Figure 3.** HR efficiency and PARP inhibitor sensitivity of mES cells expressing *hBRCA2* variants. **A**, GFP expression from the DR-GFP reporter was analyzed as a measure of HR activity. The percentage GFP-positive cells for each variant was normalized to wild-type (WT) *hBRCA2*-expressing cells. Results represent the mean of three independent experiments, with two independent pools of BAC clones tested per variant. Error bars, SE of three independent experiments. \*, statistical significance. **B**, Relative cell survival compared with untreated cells was determined by cell count after 48-hour exposure to PARP inhibitor KU-0058948. Data represent the mean of three experiments using two independent pools of BAC clones. \*,  $P < 0.05$ ; \*\*,  $P < 0.001$ .

This study contains the first evidence that a biochemical assay using purified full-length BRCA2 protein can be used to assess the DNA-binding capacity of missense variants in the BRCA2 DBD. While purification of wild-type full-length BRCA2 protein to near homogeneity has previously been described (18, 19), in this study, the functional integrity of purified mutant BRCA2 proteins was assessed for the first time in a quantitative ssDNA-binding assay. Full-length proteins were used to limit potentially inaccurate interpretation of effects from partial protein fragments. The correlation of the ssDNA binding assay and HDR activity and the

structural inspection of the DNA-binding domain suggest that the reduction in HDR activity may result from a defect in ssDNA binding. The study also showed that the influence of *BRCA2* variants on HDR activity does not fully predict the response to PARP inhibitor in ES cells (Fig. 3A and B). These findings suggest that only large reductions in HDR activity (<50%) will result in PARP inhibitor sensitivity. Whether tumors associated with these missense variants are sensitive to PARP inhibitor remains to be determined.

Many unique missense variants and VUS in *BRCA1* and *BRCA2* have been reported in the Clinvar database but no validated high-throughput methods for clinical classification of missense variants in these genes have been established. Current methods of classification rely heavily on family data. This study highlights the potential for incorporating results from functional assays in the variant classification process, especially when family data is scarce. In particular, evaluation of missense variants in the BRCA2 DBD is possible with the cell-based HDR assay (11). Importantly, HDR results for variants with low or moderate levels of risk [K3326X (OR = 1.28; ref. 27), K2729N (OR = 1.41), Y3035S (OR = 2.52)], suggest that the HDR assay can be calibrated to differentiate between variants with high, moderate, or low breast cancer risks (Fig. 2A). Additional studies that combine the HDR assay data with family-based and sequence-based models may result in classification of certain *BRCA2* VUS as moderate breast cancer risk missense variants. ES cell complementation assays have also been used to identify inactivating missense variants in the BRCA2 DBD (14, 20, 29, 35), although the assay needs to be validated relative to known pathogenic and neutral *BRCA2* variants before the results can be incorporated into VUS classification models.

In summary, this study establishes for the first time the existence of *BRCA2* missense variants that are associated with moderate risks of breast cancer. Only through the very large iCOGS case-control association study was it possible to define the *BRCA2* missense variant (Y3035S) as a moderate risk pathogenic variant for breast cancer (OR = 2.52,  $P = 0.038$ ). Functional studies showed consistent partial or hypomorphic activity associated with Y3035S, suggesting that other *BRCA2* variants with partial protein activity should be evaluated for moderate risks of breast cancer. Given that the age-related and lifetime risks of breast and ovarian cancer associated with moderate risk variants are likely to be substantially lower than for known pathogenic missense and truncating *BRCA2* variants, risk management guidelines for individuals with these mutations may need to be redefined. Because Y3035S appears to confer similar risks of breast cancer as *CHEK2* or *ATM*-inactivating mutations, perhaps individuals carrying Y3035S or other moderate risk *BRCA2* variants may benefit from following management guidelines similar to individuals with *CHEK2* and *ATM* variants rather than individuals with high-risk pathogenic *BRCA2* variants. However, further studies are needed to establish accurate risks of cancer associated with hypomorphic, moderate risk *BRCA2* variants before any modifications are considered. Ongoing efforts are focused on estimating cancer risks associated with additional selected hypomorphic/intermediate function variants through segregation studies in families, with the goal of calibrating the functional results with levels of cancer risk.

#### Disclosure of Potential Conflicts of Interest

L. Guidugli is an assistant laboratory technical director at Ambry Genetics. P.A. Fasching has received speakers bureau honoraria from Novartis, Pfizer,

Shimelis et al.

Roche, and Celgene. No potential conflicts of interest were disclosed by the other authors.

### Authors' Contributions

**Conception and design:** H. Shimelis, R.L.S. Mesman, N. Bogdanova, J.-Y. Choi, J.L. Hopper, D. Kang, A. Mannermaa, R.L. Milne, D.O. Stram, D.F. Easton, A.B. Spurdle, P. Devilee, A.N. Monteiro, A. Carreira, M.P.G. Vreeswijk, F.J. Couch  
**Development of methodology:** R.L.S. Mesman, C. Von Nicolai, A. Ehlen, C. Martin, F.M.G.R. Calleja, J.L. Hopper, D. Kang, D.O. Stram, H. Vrieling, D.E. Goldgar, A. Carreira, F.J. Couch

**Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.):** R.L.S. Mesman, C. Von Nicolai, A. Ehlen, L. Guidugli, F.M.G.R. Calleja, E. Hallberg, J. Hinton, C. Hu, C.M. Aalfs, K. Aittomaki, I.L. Andrulis, H. Anton-Culver, M.W. Beckmann, J.J. Benitez, N. Bogdanova, S.E. Bojesen, A.-L. Borresen-Dale, H. Brauch, P. Brennan, H. Brenner, A. Broeks, B. Brouwers, T. Bruning, B. Burwinkel, J. Chang-Claude, C.-Y. Cheng, J.-Y. Choi, J.M. Collée, A. Cox, S.S. Cross, K. Czene, T. Dork, I. dos Santos Silva, A.M. Dunning, P.A. Fasching, J.D. Figueroa, H. Flyger, M. Garcia-Closas, G.G. Giles, G. Glendon, P. Guenel, C.A. Haiman, P. Hall, M. Hartman, F.B.L. Hogervorst, A. Hollestelle, J.L. Hopper, H. Ito, A. Jakubowska, V. Kristensen, K.-N. Lai, D. Lambrechts, L.L. Marchand, J. Li, A. Lindblom, A. Lophatananon, J. Lubinski, A. Mannermaa, S. Margolin, F. Marme, K. Matsuo, H. Miao, R.L. Milne, K. Muir, S.L. Neuhause, H. Nevanlinna, J.E. Olson, J.C. Oosterwijk, A. Osorio, P. Peterlongo, J. Peto, P.D.P. Pharoah, K. Pylkäs, P. Radice, M.U. Rashid, V. Rhenius, A. Rudolph, S. Sangrajrang, E.J. Sawyer, M.K. Schmidt, M.J. Schoemaker, C.M. Seynaeve, M. Shah, C.-Y. Shen, M.J. Shrubsole, X.-O. Shu, M.C. Southey, A.J. Swerdlow, S.H. Teo, I. Tomlinson, D. Torres, C.J. van Asperen, R. Winqvist, A.H. Wu, J.-C. Yu, W. Zheng, Y. Zheng, J. Leary, L.C. Walker, L. Foretova, F. Fostira, K. Claes, L. Varesco, S. Moghadasi, D.F. Easton, A.B. Spurdle, P. Devilee, F.J. Couch

**Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** H. Shimelis, R.L.S. Mesman, C. Von Nicolai, L. Guidugli, H. Meeks, M.W. Beckmann, C.-Y. Cheng, J. Dennis, J.D. Figueroa, P. Hall, M. Hartman, D. Lambrechts, K. Matsuo, K. Michailidou, C. Olsowid, J.C. Oosterwijk, M.U. Rashid, C.-Y. Shen, M.C. Southey, A.N. Monteiro, D.E. Goldgar, M.P.G. Vreeswijk, F.J. Couch

**Writing, review, and/or revision of the manuscript:** H. Shimelis, R.L.S. Mesman, L. Guidugli, H. Meeks, J. Hinton, J. Lilyquist, C.M. Aalfs, K. Aittomaki, I.L. Andrulis, H. Anton-Culver, V. Arndt, N. Bogdanova, M.K. Bolla, A.-L. Borresen-Dale, H. Brauch, H. Brenner, A. Broeks, B. Burwinkel, J. Chang-Claude, J.M. Collée, A. Cox, S.S. Cross, K. Czene, H. Darabi, T. Dork, I. dos Santos Silva, A.M. Dunning, P.A. Fasching, J.D. Figueroa, H. Flyger, M. Garcia-Closas, G.G. Giles, G. Glendon, U. Hamann, M. Hartman, A. Hollestelle, J.L. Hopper, A. Jakubowska, D. Kang, V.-M. Kosma, V. Kristensen, K.-N. Lai, D. Lambrechts, L.L. Marchand, J. Li, A. Lindblom, J. Lubinski, A. Mannermaa, S. Margolin, K. Matsuo, K. Michailidou, R.L. Milne, S.L. Neuhause, J.E. Olson, J.C. Oosterwijk, J. Peto, P.D.P. Pharoah, P. Radice, A. Rudolph, E.J. Sawyer, M.K. Schmidt, M.J. Schoemaker, C.M. Seynaeve, M.J. Shrubsole, S.L. Slager, M.C. Southey, A.J. Swerdlow, T. Truong, C.J. van Asperen, L.E. van der Kolk, R. Winqvist, A.H. Wu, W. Zheng, L.C. Walker, L. Foretova, F. Fostira, K. Claes, L. Varesco, S. Moghadasi, D.F. Easton,

A.B. Spurdle, P. Devilee, H. Vrieling, A.N. Monteiro, D.E. Goldgar, A. Carreira, M.P.G. Vreeswijk, F.J. Couch

**Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):** R.L.S. Mesman, L. Guidugli, F.M.G.R. Calleja, E. Hallberg, J. Hinton, J. Lilyquist, H. Anton-Culver, V. Arndt, M.W. Beckmann, M.K. Bolla, A.-L. Borresen-Dale, H. Brauch, A. Broeks, B. Burwinkel, H. Darabi, T. Dork, P.A. Fasching, G.G. Giles, P. Guenel, U. Hamann, F.B.L. Hogervorst, J.L. Hopper, D. Lambrechts, A. Lindblom, K. Matsuo, H. Miao, M.U. Rashid, V. Rhenius, A. Rudolph, M.K. Schmidt, M. Shah, M.C. Southey, D. Torres, T. Truong, C.J. van Asperen, Q. Wang, J.-C. Yu, Y. Zheng, L. Foretova, F.J. Couch  
**Study supervision:** J.L. Hopper, M.U. Rashid, M.K. Schmidt, X.-O. Shu, S.L. Slager, M.C. Southey, D.F. Easton, P. Devilee, A. Carreira, M.P.G. Vreeswijk, F.J. Couch

**Other (protein expression in human cell lines and purification):** C. Martin  
**Other (molecular genetics analysis in the Czech high-risk population, pedigrees and segregation analysis in affected Czech families):** E. Machackova  
**Other (revision of manuscript only, not writing):** M.J. Schoemaker

### Acknowledgments

We thank Shyam Sharan for the PI2F7 conditional mBrca2 knockout mES cell line and Maria Jasin for the DR-GFP-targeting construct.

### Grant Support

This work was supported in part by NIH grants CA116167, CA176785, CA192393, an NIH specialized program of research excellence (SPORE) in breast cancer to the Mayo Clinic (P50 CA116201), the Breast Cancer Research Foundation (to F.C. Couch), the ATIP-AVENIR CNRS/INSERM Young Investigator grant 201201, EC-Marie Curie Career Integration grant CIG293444, Institute National du Cancer/NCA-DGOS\_8706 (to A. Carreira), the Dutch Cancer Society KWF (UL2012-5649 to M.P.G. Vreeswijk), the Australian National Health and Medical Research Council (ID#1010719), and The Cancer Council Queensland (ID#1086286 to A. Spurdle). BCAC data management was funded by Cancer Research UK (C1287/A10118 and C1287/A12014) and by the European Community's Seventh Framework Programme under grant agreement 223175 (HEALTH-F2-2009-223175 to D.F. Easton). Funding for the iCOGS infrastructure came from: the European Community's Seventh Framework Programme under grant agreement no. 223175 (COGS; HEALTH-F2-2009-223175 to P. Hall), Cancer Research UK (C1287/A10118, C1287/A10710, C12292/A11174, C1281/A12014, C5047/A8384, C5047/A15007, C5047/A10692 to D.F. Easton), the NIH (CA128978 to F.J. Couch), and Post-Cancer GWAS initiative (1U19 CA148537, C.A. Haiman; 1U19 CA148065, D.F. Easton; and 1U19 CA148112 - the GAME-ON initiative to T.A. Sellers), the Canadian Institutes of Health Research (CIHR) for the CIHR Team in Familial Risks of Breast Cancer (to I. Andrulis), and the Breast Cancer Research Foundation (to F.J. Couch).

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked *advertisement* in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received September 19, 2016; revised November 14, 2016; accepted March 3, 2017; published OnlineFirst March 10, 2017.

### References

- Antoniou A, Pharoah PD, Narod S, Risch HA, Eyfjord JE, Hopper JL, et al. Average risks of breast and ovarian cancer associated with BRCA1 or BRCA2 mutations detected in case Series unselected for family history: a combined analysis of 22 studies. *Am J Hum Genet* 2003;72:1117-30.
- Quiles F, Fernandez-Rodriguez J, Mosca R, Feliubadalo L, Tornero E, Brunet J, et al. Functional and structural analysis of C-terminal BRCA1 missense variants. *PLoS One* 2013;8:e61302.
- Radice P, De Summa S, Caleca L, Tommasi S. Unclassified variants in BRCA genes: guidelines for interpretation. *Ann Oncol* 2011;22Suppl 1:i18-23.
- Lindor NM, Goldgar DE, Tavtigian SV, Plon SE, Couch FJ. BRCA1/2 sequence variants of uncertain significance: a primer for providers to assist in discussions and in medical management. *Oncologist* 2013;18:518-24.
- Goldgar DE, Easton DF, Deffenbaugh AM, Monteiro AN, Tavtigian SV, Couch FJ. Integrated evaluation of DNA sequence variants of unknown clinical significance: application to BRCA1 and BRCA2. *Am J Hum Genet* 2004;75:535-44.
- Vallee MP, Francy TC, Judkins MK, Babikyan D, Lesueur F, Gammon A, et al. Classification of missense substitutions in the BRCA genes: a database dedicated to Ex-UVs. *Hum Mutat* 2012;33:22-8.
- Easton DF, Deffenbaugh AM, Pruss D, Frye C, Wenstrup RJ, Allen-Brady K, et al. A systematic genetic assessment of 1,433 sequence variants of unknown clinical significance in the BRCA1 and BRCA2 breast cancer-predisposition genes. *Am J Hum Genet* 2007;81:873-83.
- Farrugia DJ, Agarwal MK, Pankratz VS, Deffenbaugh AM, Pruss D, Frye C, et al. Functional assays for classification of BRCA2 variants of uncertain significance. *Cancer Res* 2008;68:3523-31.
- Lee MS, Green R, Marsillac SM, Coquelle N, Williams RS, Yeung T, et al. Comprehensive analysis of missense variations in the BRCT domain of BRCA1 by structural and functional assays. *Cancer Res* 2010;70:4880-90.
- Lindor NM, Guidugli L, Wang X, Vallee MP, Monteiro AN, Tavtigian S, et al. A review of a multifactorial probability-based model for classification of

- BRCA1 and BRCA2 variants of uncertain significance (VUS). *Hum Mutat* 2012;33:8–21.
11. Guidugli L, Pankratz VS, Singh N, Thompson J, Erding CA, Engel C, et al. A classification model for BRCA2 DNA binding domain missense variants based on homology-directed repair activity. *Cancer Res* 2013;73:265–75.
  12. Lovelock PK, Spurdle AB, Mok MT, Farrugia DJ, Lakhani SR, Healey S, et al. Identification of BRCA1 missense substitutions that confer partial functional activity: potential moderate risk variants? *Breast Cancer Res* 2007; 9:R82.
  13. Spurdle AB, Whaley PJ, Thompson B, Feng B, Healey S, Brown MA, et al. BRCA1 R1699Q variant displaying ambiguous functional abrogation confers intermediate breast and ovarian cancer risk. *J Med Genet* 2012;49: 525–32.
  14. Michailidou K, Hall P, Gonzalez-Neira A, Ghoussaini M, Dennis J, Milne RL, et al. Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nat Genet* 2013;45:353–61.
  15. Spurdle AB, Healey S, Devereau A, Hogervorst FB, Monteiro AN, Nathanson KL, et al. ENIGMA—evidence-based network for the interpretation of germline mutant alleles: an international initiative to evaluate risk and clinical significance associated with sequence variation in BRCA1 and BRCA2 genes. *Hum Mutat* 2012;33:2–7.
  16. Pharoah PD, Tsai YY, Ramus SJ, Phelan CM, Goode EL, Lawrenson K, et al. GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nat Genet* 2013;45:362–70.
  17. Lathrop GM, Lalouel JM, Julier C, Ott J. Strategies for multilocus linkage analysis in humans. *Proc Natl Acad Sci U S A* 1984;81:3443–6.
  18. Jensen RB, Carreira A, Kowalczykowski SC. Purified human BRCA2 stimulates RAD51-mediated recombination. *Nature* 2010;467:678–83.
  19. Martinez JS, von Nicolai C, Kim T, Ehlen A, Mazin AV, Kowalczykowski SC, et al. BRCA2 regulates DMC1-mediated recombination through the BRC repeats. *Proc Natl Acad Sci U S A* 2016;113:3515–20.
  20. Kuznetsov SG, Liu P, Sharan SK. Mouse embryonic stem cell-based functional assay to evaluate mutations in BRCA2. *Nat Med* 2008;14:875–81.
  21. Hendriks G, Morolli B, Calleja FM, Plomp A, Mesman RL, Meijers M, et al. An efficient pipeline for the generation and functional analysis of human BRCA2 variants of uncertain significance. *Hum Mutat* 2014; 35:1382–91.
  22. Domchek SM, Tang J, Stopfer J, Lilli DR, Hamel N, Tischkowitz M, et al. Biallelic deleterious BRCA1 mutations in a woman with early-onset ovarian cancer. *Cancer Discov* 2013;3:399–405.
  23. Moynahan ME, Chiu JW, Koller BH, Jasin M. Brca1 controls homology-directed DNA repair. *Mol Cell* 1999;4:511–8.
  24. Wu K, Hinson SR, Ohashi A, Farrugia D, Wendt P, Tavtigian SV, et al. Functional evaluation and cancer risk assessment of BRCA2 unclassified variants. *Cancer Res* 2005;65:417–26.
  25. Couch FJ, Rasmussen LJ, Hofstra R, Monteiro AN, Greenblatt MS, de Wind N. Assessment of functional effects of unclassified genetic variants. *Hum Mutat* 2008;29:1314–26.
  26. Lovelock PK, Wong EM, Sprung CN, Marsh A, Hobson K, French JD, et al. Prediction of BRCA1 and BRCA2 mutation status using post-irradiation assays of lymphoblastoid cell lines is compromised by inter-cell-line phenotypic variability. *Breast Cancer Res Treat* 2007;104:257–66.
  27. Meeks HD, Song H, Michailidou K, Bolla MK, Dennis J, Wang Q, et al. BRCA2 polymorphic stop codon K3326X and the risk of breast, prostate, and ovarian cancers. *J Natl Cancer Inst* 2016;108:djv315. doi:10.1093/jnci/djv315.
  28. Yang H, Jeffrey PD, Miller J, Kinnucan E, Sun Y, Thoma NH, et al. BRCA2 function in DNA binding and recombination from a BRCA2-DSS1-ssDNA structure. *Science* 2002;297:1837–48.
  29. Biswas K, Das R, Eggington JM, Qiao H, North SL, Stauffer S, et al. Functional evaluation of BRCA2 variants mapping to the PALB2-binding and C-terminal DNA-binding domains using a mouse ES cell-based assay. *Hum Mol Genet* 2012;21:3993–4006.
  30. Xia B, Sheng Q, Nakanishi K, Ohashi A, Wu J, Christ N, et al. Control of BRCA2 cellular and clinical functions by a nuclear partner, PALB2. *Mol Cell* 2006;22:719–29.
  31. Karchin R, Agarwal M, Sali A, Couch F, Beattie MS. Classifying Variants of Undetermined Significance in BRCA2 with protein likelihood ratios. *Cancer Inform* 2008;6:203–16.
  32. Thery JC, Krieger S, Gaildrat P, Revillion F, Buisine MP, Killian A, et al. Contribution of bioinformatics predictions and functional splicing assays to the interpretation of unclassified variants of the BRCA genes. *Eur J Hum Genet* 2011;19:1052–8.
  33. Bodian DL, McCutcheon JN, Kothiyal P, Huddleston KC, Iyer RK, Vockley JG, et al. Germline variation in cancer-susceptibility genes in a healthy, ancestrally diverse cohort: implications for individual genome sequencing. *PLoS One* 2014;9:e94554.
  34. Lek M, Karczewski KJ, Minikel EV, Samocha KE, Banks E, Fennell T, et al. Analysis of protein-coding genetic variation in 60,706 humans. *Nature* 2016;536:285–91.
  35. Biswas K, Das R, Alter BP, Kuznetsov SG, Stauffer S, North SL, et al. A comprehensive functional characterization of BRCA2 variants associated with Fanconi anemia using mouse ES cell-based assay. *Blood* 2011;118: 2430–42.

# Cancer Research

The Journal of Cancer Research (1916–1930) | The American Journal of Cancer (1931–1940)

## ***BRCA2* Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer**

Hermela Shimelis, Romy L.S. Mesman, Catharina Von Nicolai, et al.

*Cancer Res* 2017;77:2789-2799. Published OnlineFirst March 10, 2017.

**Updated version** Access the most recent version of this article at:  
doi:[10.1158/0008-5472.CAN-16-2568](https://doi.org/10.1158/0008-5472.CAN-16-2568)

**Supplementary Material** Access the most recent supplemental material at:  
<http://cancerres.aacrjournals.org/content/suppl/2017/03/10/0008-5472.CAN-16-2568.DC1>

**Cited articles** This article cites 35 articles, 11 of which you can access for free at:  
<http://cancerres.aacrjournals.org/content/77/11/2789.full#ref-list-1>

**Citing articles** This article has been cited by 1 HighWire-hosted articles. Access the articles at:  
<http://cancerres.aacrjournals.org/content/77/11/2789.full#related-urls>

**E-mail alerts** [Sign up to receive free email-alerts](#) related to this article or journal.

**Reprints and Subscriptions** To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at [pubs@aacr.org](mailto:pubs@aacr.org).

**Permissions** To request permission to re-use all or part of this article, contact the AACR Publications Department at [permissions@aacr.org](mailto:permissions@aacr.org).