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Gisella Figlioli, Massimo Bogliolo, Irene Catucci, Laura Caleca, Sandra Viz Lasheras, Roser Pujol, Johanna Kiiski, Taru Muranen, Daniel Barnes, Joe Dennis, et al.

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ARTICLE OPEN

The *FANCM*:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer

Gisella Figlioli et al.

Breast cancer is a common disease partially caused by genetic risk factors. Germline pathogenic variants in DNA repair genes *BRCA1*, *BRCA2*, *PALB2*, *ATM*, and *CHEK2* are associated with breast cancer risk. *FANCM*, which encodes for a DNA translocase, has been proposed as a breast cancer predisposition gene, with greater effects for the ER-negative and triple-negative breast cancer (TNBC) subtypes. We tested the three recurrent protein-truncating variants *FANCM*:p.Arg658*, p.Gln1701*, and p.Arg1931* for association with breast cancer risk in 67,112 cases, 53,766 controls, and 26,662 carriers of pathogenic variants of *BRCA1* or *BRCA2*. These three variants were also studied functionally by measuring survival and chromosome fragility in *FANCM*^{-/-} patient-derived immortalized fibroblasts treated with diepoxybutane or olaparib. We observed that *FANCM*:p.Arg658* was associated with increased risk of ER-negative disease and TNBC (OR = 2.44, *P* = 0.034 and OR = 3.79; *P* = 0.009, respectively). In a country-restricted analysis, we confirmed the associations detected for *FANCM*:p.Arg658* and found that also *FANCM*:p.Arg1931* was associated with ER-negative breast cancer risk (OR = 1.96; *P* = 0.006). The functional results indicated that all three variants were deleterious affecting cell survival and chromosome stability with *FANCM*:p.Arg658* causing more severe phenotypes. In conclusion, we confirmed that the two rare *FANCM* deleterious variants p.Arg658* and p.Arg1931* are risk factors for ER-negative and TNBC subtypes. Overall our data suggest that the effect of truncating variants on breast cancer risk may depend on their position in the gene. Cell sensitivity to olaparib exposure, identifies a possible therapeutic option to treat *FANCM*-associated tumors.

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INTRODUCTION

The genetic architecture of inherited breast cancer is complex and involves germline pathogenic variants in high and moderate-risk genes and polygenetic factors. The major high-penetrance breast cancer risk genes include *BRCA1* and *BRCA2*, which are key factors in the DNA double-strand break repair through homologous recombination (HR) and in the inter-strand crosslink (ICL) repair as a part of the Fanconi Anemia (FA) pathway.^{1,2} Recently, based on a prospective cohort of families carrying *BRCA1* or *BRCA2* pathogenic variants, the average cumulative risk by age 80 was estimated to be 72% and 69% for carriers of *BRCA1* and *BRCA2* pathogenic variants, respectively.³ *PALB2* has been previously considered a moderate-risk gene, but the latest estimate of about 44% lifetime risk associated with pathogenic variants may raise this gene to the high-risk group.⁴ Pathogenic variants in moderate-penetrance genes *ATM* and *CHEK2* are also associated with breast cancer, conferring a 20% average lifetime risk.^{5,6} Recently, *BARD1*, *RAD51D*, *BRIP1*, and *RAD51C* have been proposed as risk factors for triple-negative breast cancer (TNBC) with *BARD1* and *RAD51D* conferring high risk, and *BRIP1* and *RAD51C* associated with moderate risk.⁷ Thus, the risk associated with pathogenic variants in each gene may vary by breast tumor subtype.

Many of the *BRCA/FA* pathway genes when altered by biallelic mutations cause FA disease. The *FANCM* gene (FA complementation group M, OMIM #609644) encodes for a translocase, which is a member of the *BRCA/FA* molecular pathway but has been recently disqualified as a disease-causing factor for FA.^{8,9} Some protein-truncating variants in the *FANCM* gene were described as moderate breast cancer risk factors with a greater risk of TNBC. In the Finnish population, *FANCM*:c.5101 C>T (p.Gln1701*,

rs147021911) is relatively frequent and was reported to be associated with breast cancer with odds ratio (OR) of 1.86 with 95% confidence intervals (CIs) = 1.26–2.75. A larger effect was observed in familial cases (OR = 2.11; 95% CI = 1.43–3.32), for estrogen receptor-negative (ER-negative) breast cancer (OR = 2.37; 95% CI = 1.37–4.12) and for TNBC (OR = 3.56; 95% CI = 1.81–6.98).¹⁰ We showed an increased risk (OR = 3.93; 95% CI = 1.28–12.11) of the *FANCM*:c.5791 C>T (rs144567652) truncating variant using familial cases and controls. In vitro analysis showed that this variant causes the skipping of the *FANCM* exon 22 and the creation of a downstream stop codon (p.Gly1906Alafs12*).¹¹ However, in the present study we refer to the *FANCM*:c.5791 C>T base change as to *FANCM*:p.Arg1931*, which is the conventional amino acid annotation (consistent with the stop codon creation according to genetic code). The *FANCM*:p.Arg1931* was also found to be associated with TNBC risk in the Finnish population (OR = 5.14; 95% CI = 1.65–16.0).¹² A burden analysis of truncating variants discovered by a re-sequencing analysis of the entire *FANCM* coding region in German cases and controls confirmed that *FANCM* pathogenic variants had a particularly high risk for TNBC (OR = 3.75; 95% CI = 1.0–12.85).¹³

To study the effect of *FANCM* on breast cancer risk further, we tested three recurrent truncating variants *FANCM*:p.Arg658*, p.Gln1701*, and p.Arg1931*, within the OncoArray Consortium, a collaboration of consortia established to discover germline genetic variants predisposing to different human cancers (e.g., breast, colon, lung, ovary, endometrium and prostate cancers).¹⁴ These three variants were tested for association with breast cancer risk in 67,112 breast cancer cases, 53,766 controls, and 26,662 carriers of pathogenic variants in *BRCA1* or *BRCA2*. We also studied the functional effect of these three variants after their lentiviral transduction into a *FANCM*^{-/-} patient-derived cell line in which

*email: paolo.peterlongo@ifom.eu. A full list of authors and their affiliations appears at the end of the paper.

we measured survival and chromosome fragility after exposure to diepoxybutane (DEB) or the poly (ADP-ribose) polymerase inhibitor (PARPi) olaparib.

RESULTS

Case-control analyses

We analyzed the association of three *FANCM* truncating variants, p.Arg658*, p.Gln1701*, and p.Arg1931*, with breast cancer risk for each variant separately and using a burden analysis. We tested 67,112 invasive breast cancer cases and 53,766 controls collected by the Breast Cancer Association Consortium (BCAC, <http://bcac.ccge.medschl.cam.ac.uk/>) and 26,662 carriers of *BRCA1* or *BRCA2* pathogenic variants collected by the Consortium of Investigators of Modifiers of *BRCA1/2* (CIMBA, <http://cimba.ccge.medschl.cam.ac.uk/>), of whom 13,497 were affected with breast cancer and 13,165 were unaffected.

In the BCAC dataset we assessed the breast cancer risk associated with the *FANCM* variants in a primary overall analysis and in a restricted analysis including only countries in which the variant carrier frequencies were higher than the median of the frequencies. In these analyses we tested association with the variants in all available invasive breast cancer cases or in the ER-positive, ER-negative and TNBC subgroups (Table 1). In the overall analysis, no evidence of association was observed, either with the presence of any *FANCM* variant or with any of the three variants individually. However, *FANCM*:p.Arg658* showed a higher heterozygote frequency in ER-negative breast cancer cases (0.093%) than in controls (0.035%) with a greater than two-fold increased breast cancer risk (OR = 2.44, 95% CI = 1.12–5.34, $P = 0.034$). When only TNBC cases were considered, the association was stronger (OR = 3.79, 95% CI = 1.56–9.18, $P = 0.009$). No association with ER-negative breast cancer or TNBC was seen for p.Gln1701* or p.Arg1931* or for all mutations combined (Table 1). In the country-restricted analyses, we confirmed the association found for p.Arg658* with risk of ER-negative disease and TNBC (OR = 2.31, 95% CI = 1.05–5.07, $P = 0.047$ and OR = 3.56, 95% CI = 1.46–8.69, $P = 0.011$, respectively). The restricted set also provided evidence for an association between p.Arg1931* and ER-negative subgroup (OR = 1.96, 95% CI = 1.24–3.10, $P = 0.006$), though not for TNBC. No significant association was observed for p.Gln1701* with either subgroups (Table 1).

Analyses of carriers of *BRCA1* or *BRCA2* pathogenic variants

We found no evidence of associations for *FANCM*:p.Arg658*, p.Gln1701*, and p.Arg1931* truncating variants with breast cancer risk in carriers of *BRCA1* or *BRCA2* pathogenic variants included in CIMBA (Supplementary Table 1). The p.Arg658* was detected with approximately four-fold higher frequencies in the *BRCA1* affected individuals (0.063%) in comparison to the unaffected (0.013%), and in the *BRCA2* affected individuals (0.071%) in comparison to the unaffected (0.019%). Consistently, hazard ratios (HRs) above two were estimated for *BRCA1* (HR = 2.4, 95% CI = 0.52–11.12) and for *BRCA2* (HR = 2.13, 95% CI = 0.41–11.14) pathogenic variant carriers. The frequencies of p.Gln1701* and p.Arg1931* were not increased in affected versus unaffected individuals carrying *BRCA1* or *BRCA2* pathogenic variants (Supplementary Table 1).

Functional studies

We tested the functional effect of *FANCM*:p.Arg658*, p.Gln1701*, and p.Arg1931* on DNA repair using genetic complementation assays (Fig. 1). These assays were based on the EGF280 cell line derived from immortalized fibroblasts from a patient who lacked the *FANCM* protein due to a homozygous c.1506_1507insTA (p.Ile503*, rs764743944) truncating variant.⁸ Complemented *FANCM*^{-/-} cells were tested for sensitivity to DEB and olaparib

Table 1. Single-variant and burden analyses of *FANCM*:p.Arg658*, p.Gln1701* and p.Arg1931* truncating variants in overall and country-restricted invasive breast cancer cases and controls

Subgroup	Overall					
	Carriers	Non-carriers	Freq %	OR	95% CI	P
<i>FANCM</i> :p.Arg658*						
Controls	19	53,717	0.035	NA		
All cases	31	67,038	0.046	1.26	0.71–2.25	0.430
ER-positive	19	44,516	0.043	1.15	0.61–2.20	0.670
ER-negative	10	10,750	0.093	2.44	1.12–5.34	0.034
TNBC	7	4794	0.146	3.79	1.56–9.18	0.009
<i>FANCM</i> :p.Gln1701*						
Controls	122	53,635	0.229	NA		
All cases	155	66,951	0.232	1.09	0.85–1.38	0.798
ER-positive	97	44,467	0.218	1.02	0.78–1.34	0.893
ER-negative	21	10,748	0.204	0.97	0.61–1.56	0.369
TNBC	10	4794	0.229	1.09	0.57–2.10	0.149
<i>FANCM</i> :p.Arg1931*						
Controls	96	53,633	0.179	NA		
All cases	116	66,968	0.173	1.05	0.80–1.38	0.731
ER-positive	74	44,467	0.166	1.02	0.75–1.38	0.920
ER-negative	27	10,742	0.251	1.52	0.98–2.35	0.070
TNBC	10	4795	0.208	1.29	0.67–2.50	0.461
All variants ^a						
Controls	237	53,455	0.443	NA		
All cases	302	66,736	0.452	1.02	0.86–1.21	0.823
ER-positive	190	44,323	0.427	0.96	0.79–1.16	0.698
ER-negative	58	10,700	0.548	1.23	0.92–1.64	0.154
TNBC	27	4773	0.583	1.32	0.89–1.95	0.167
Subgroup	Country-restricted					
	Carriers	Non-carriers	Freq %	OR	95% CI	P
<i>FANCM</i> :p.Arg658*						
Controls	19	48,887	0.039	NA		
All cases	31	59,540	0.052	1.23	0.69–2.20	0.478
ER-positive	19	39,453	0.048	1.12	0.59–2.15	0.722
ER-negative	10	9613	0.104	2.31	1.05–5.07	0.047
TNBC	7	4283	0.163	3.56	1.46–8.69	0.011
<i>FANCM</i> :p.Gln1701*						
Controls	120	48,506	0.249	NA		
All cases	152	58,919	0.259	1.08	0.85–1.38	0.813
ER-positive	96	38,892	0.246	1.02	0.77–1.34	0.895
ER-negative	21	9558	0.230	0.97	0.60–1.56	0.368
TNBC	10	4197	0.261	1.09	0.56–2.10	0.150
<i>FANCM</i> :p.Arg1931*						
Controls	77	34,988	0.220	NA		
All cases	93	37,903	0.245	1.14	0.84–1.54	0.396
ER-positive	59	25,274	0.233	1.09	0.77–1.53	0.632
ER-negative	25	5920	0.421	1.96	1.24–3.10	0.006
TNBC	10	2614	0.381	1.77	0.91–3.45	0.116
All variants ^b						
Controls	NA					
All cases	NA					
ER-positive	NA					

Table 1 continued

Subgroup	Country-restricted					
	Carriers	Non-carriers	Freq %	OR	95% CI	P
ER-negative	NA					
TNBC	NA					

In bold are indicated the statistically significant results

Freq frequency, OR odds ratio CI confidence interval, P P-value, TNBC triple-negative breast cancer, NA not applicable

^aThe burden analyses were performed by univariate logistic regression

^bThese analyses were not possible in the country-restricted cases and controls as different countries were included for each variant. P-values were from Pearson chi-squared test

by measuring cell survival and chromosome fragility. The FANCM protein was not detectable in the EGF280 fibroblasts. The transduction of these cells with lentiviral vectors carrying wild-type (wt) FANCM cDNA and cDNAs harboring FANCM:p.Gln1701* and p.Arg1931* variants produced, as expected, different C-terminal truncated forms of FANCM. In the EGF280 cells transduced with FANCM:p.Arg658* no visible band was observed on western blot (Fig. 1a and Supplementary Fig. 1). As we lack information on the epitope recognized by the antibody, we could not determine whether the p.Arg658*-derived truncated protein was unstable or if the epitope was lost due to the truncation. We therefore analyzed the mRNA expression of FANCM:p.Arg658* by reverse transcription and digestion of the PCR-amplified cDNAs. The c.1972C > T base substitution causing the p.Arg658* variant was expected to abolish a digestion site for the restriction enzyme *TseI* present in the wt sequence. *TseI*-digestion of wt and mutated cDNAs clearly indicated the presence of a mutated mRNA product in the EGF280 cells transduced with FANCM:p.Arg658* (Fig. 1b and Supplementary Fig. 1).

In the DEB sensitivity-based assay (Fig. 1c), the EGF280 patient-derived cell line showed a high-sensitivity phenotype, that was rescued by expression of the wt FANCM. EGF280 cells expressing FANCM:p.Arg658* failed to rescue DEB sensitivity and showed survival rates overlapping with those of the native EGF280 cells. In comparison, cells expressing FANCM:p.Gln1701* and p.Arg1931* variants showed an intermediate phenotype with survival rates significantly higher than those of EGF280 cells, though significantly lower than those of the cells expressing wt FANCM (Fig. 1c and Supplementary Table 2). These results were confirmed in the chromosome fragility tests where the number of chromatid breaks in cells harboring p.Gln1701* or p.Arg1931* variants was statistically lower than that of EGF280 cells or cells expressing the p.Arg658* and statistically higher than that of cells expressing wt FANCM (Fig. 1d). In the olaparib sensitivity-based assay, the survival rates of the cell lines transduced with the three FANCM truncating variants were not statistically different. Only at higher olaparib concentrations (>5000 nM) the survival rates of these cell lines were significantly lower than that of the wt FANCM cells and higher than that of the EGF280 cells (Fig. 1e and Supplementary Table 3).

DISCUSSION

In this study we investigated the association of the three recurrent FANCM truncating variants p.Arg658*, p.Gln1701*, and p.Arg1931*, with breast cancer risk overall and by tumor subtype. While in non-Finnish Europeans these are the three most common FANCM truncating variants, their carrier frequency is low being 0.033, 0.21 and 0.21%, respectively (<https://gnomad.broadinstitute.org/>).¹⁵ We conducted large case-control studies in 67,112 unselected breast cancer cases, 53,766 controls, and 26,662 carriers of BRCA1 or BRCA2 pathogenic variants. Furthermore, we performed functional

analyses based on a patient-derived FANCM^{-/-} cell line transduced with vectors carrying the three FANCM variants and tested for sensitivity to DEB or olaparib. Our genetic data suggest that FANCM:p.Arg658* is a risk factor for ER-negative and TNBC subtypes with statistically significant ORs of 2.44 and 3.79, respectively. These associations were confirmed when we restricted the analyses to countries with higher carrier frequencies. In these restricted analyses we also found that the p.Arg1931* was associated with breast cancer risk in the ER-negative subtype with statistically significant OR = 1.96. (Table 1). These data, together with previously published genetic studies,^{10–13} confirm that FANCM truncating variants are risk factors for breast cancer, with a stronger association for the ER-negative and TNBC subtypes. Our functional data, obtained in a background of a FANCM null cell line, support these findings showing that all three truncating variants were deleterious; hence, it is expected that, in the heterozygous state, any of these FANCM variants have partial activity. In the functional tests, we also observed that olaparib had a greater effect on survival of the cells harboring any of the FANCM:p.Arg658*, p.Gln1701*, or p.Arg1931* variants with respect to that on EGF280 cells complemented with wt FANCM (Fig. 1e). As this is consistent with previous results,¹⁶ PARP1 inhibition might be a possible therapeutic approach to treat patients with breast tumors associated with germline FANCM pathogenic variants. On the contrary, the DEB sensitivity assays showed that FANCM:p.Arg658* is associated with a stronger impairment of DNA repair activity, compared to p.Gln1701* and p.Arg1931*, possibly reflecting the position of protein truncation (Fig. 1c, d).

FANCM encodes for a key protein of the upstream FA/BRCA pathway mediating the assembly of the FA core complex. This protein is 2048 AA long, possesses in its N-terminal region an intrinsic ATP-dependent DNA translocase activity and, with its central region, recognizes the Bloom's complex, which is also involved in the DNA HR repair. By interacting with its C-terminal binding partner, the FA associated protein 24 (FAAP24), the FANCM protein brings to sites of ICL DNA lesions the FA and the Bloom's complexes initiating HR repair¹⁷ (Fig. 2). We studied FANCM:p.Arg658*, p.Gln1701*, and p.Arg1931* in the same genetic FANCM^{-/-} background and showed that, after exposure to DEB, the N-terminal FANCM:p.Arg658* had a statistically stronger effect on cell survival and chromosome stability (presumably due to less efficient DNA repair activity) than did p.Gln1701* and p.Arg1931*. This also suggests that in human living cells the FANCM:p.Arg658* variant might impair DNA repair more severely than p.Gln1701* and p.Arg1931*. We have shown that in vitro both the p.Gln1701*- and the p.Arg1931*-derived FANCM proteins are expressed and that the p.Arg658*-mRNA is transcribed (Fig. 1a, b). An N-terminus fragment including the first 422 AA of FANCM was shown to be stable when expressed in human cell lines,¹⁷ thus supporting the possibility that the FANCM:p.Arg658*-derived protein may also be expressed and stable. Hence, we hypothesize that the observed difference in survival and chromosome fragility of cells treated with DEB may be attributable to the diverse residual function of the different truncated forms of FANCM. In fact, the p.Gln1701*- and the p.Arg1931*-derived forms are expected to lose the interaction with FAAP24, but to retain the ability of binding other FANCM interacting proteins. Hence, our data suggest that the lack of interaction between FANCM and FAAP24 has a less severe impact on the DNA damage response than when protein truncation occurs upstream the FANCM domains AA 687–1104 and AA 1027–1362 mediating the interaction with the FA core complex and the Bloom's complex, respectively.

Previously published genetic and clinical data support our hypothesis of a position effect. FANCM pathogenic variants were shown to be associated with a moderate risk of developing high-grade serous epithelial ovarian cancer, but p.Arg1931* appeared to confer a lower risk.¹⁸ Moreover, five female breast cancer

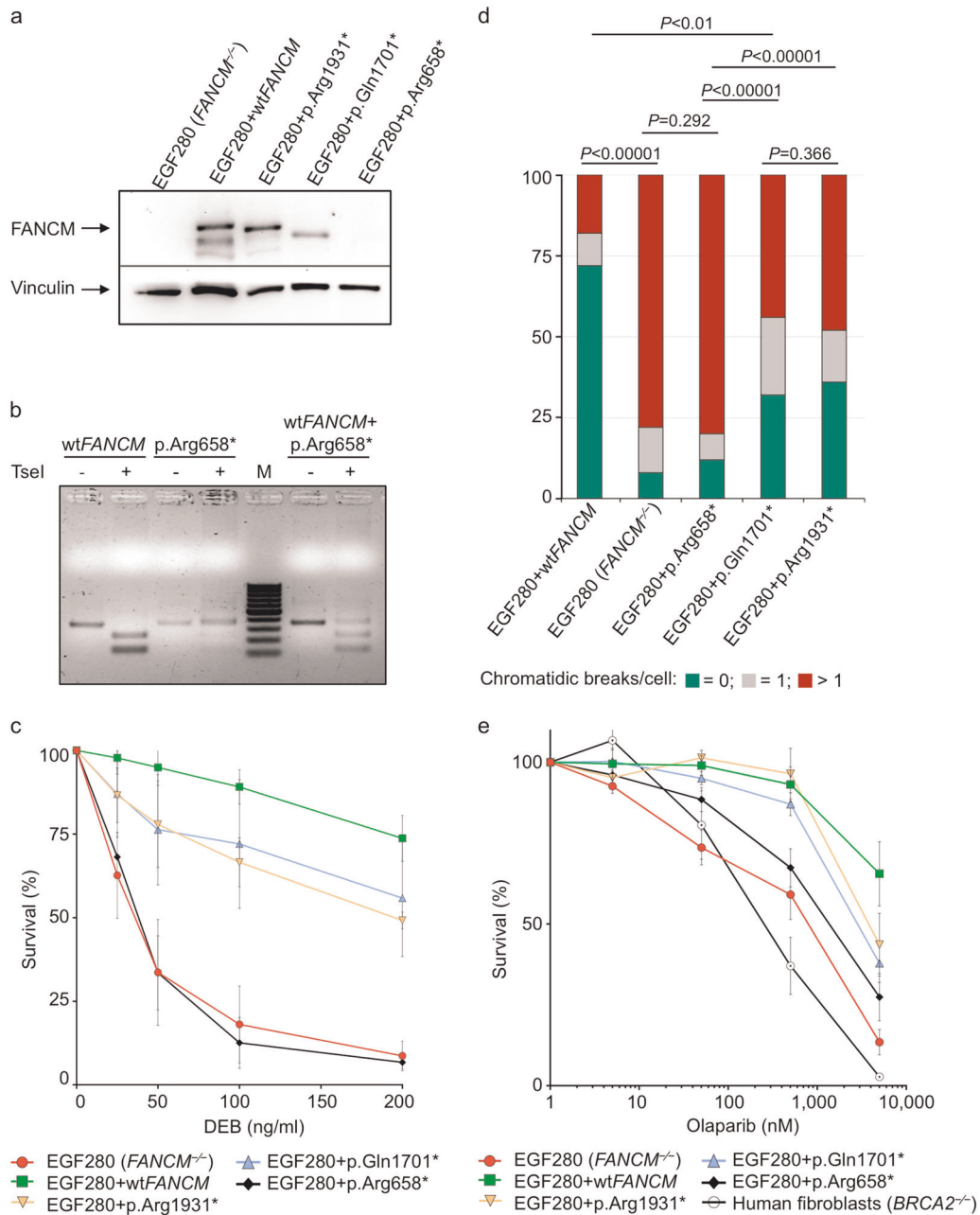


Fig. 1 Functional studies of the *FANCM*:p.Arg658*, p.Gln1701* and p.Arg1931* truncating variants using the patient-derived *FANCM*^{-/-} EGF280 cell line. **a** Western blot showing the FANCM expression in EGF280 cells complemented with lentiviral vectors harboring the three different variants. Bands corresponding to truncated FANCM protein were visible for EGF280 + p.Gln1701* and p.Arg1931*, and no bands were present for the EGF280 + p.Arg658*. **b** Study of the expression of the FANCM protein in EGF280 + p.Arg658*. The c.1972C > T base substitution, causing the p.Arg658* variant abrogates a digestion site for the restriction enzyme *TseI* that is present in the wild-type (wt) cDNA sequence. Total RNA was extracted from EGF280 + wtFANCM and from the EGF280 + p.Arg658* and subjected to reverse transcription. PCR-amplified cDNA products were digested with *TseI*. Digested and undigested cDNAs were loaded. In the first two lanes are shown bands of 386 bp corresponding to uncut wt cDNA, and bands of 257 and 129 bp corresponding to cut wt cDNA. In next two lanes bands of 386 bp indicate that p.Arg658* cDNA was not cut due to the c.1972C > T base substitution abrogating the *TseI* site. In the two lanes after the molecular weight marker (M) undigested and digested products of the two previous PCR products were mixed 1:1 and loaded as a control. **c** Analysis of diepoxybutane (DEB) sensitivity on cell survival. The EGF280 cells expressing p.Arg658* are significantly more sensitive to DEB than the cells expressing p.Gln1701* or p.Arg1931* (*P*-values from Tukey's range test are reported in Supplementary Table 4). EGF280 and EGF280 + wtFANCM are used as controls (*N* = 3; error bars: standard deviation). **d** Chromosome fragility induced by DEB treatment (100 ng/ml). Here, the chromatidic break patterns of the cells expressing wt FANCM, of the cells harboring p.Gln1701* or p.Arg1931* variants, and of the native EGF280 cells or the cells expressing p.Arg658* were statistically different. (*P*-values from chi-squared test; *N* = 2). **e** Analysis of cellular sensitivity to olaparib. Contrarily to what we observed in the DEB sensitivity assays, survival rates of the different complemented cell lines were apparently not different. Human fibroblasts (*BRCA2*^{-/-}) were homozygous for the c.469 A > T (p.Lys157*) truncating variant and were used as a positive control. (*P*-values from Tukey's range test are reported in Supplementary Table 5; *N* = 3; error bars: standard deviation). All blots derive from the same experiment and were processed in parallel

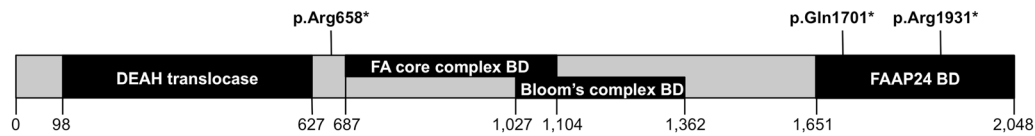


Fig. 2 Schematic diagram of the 2,048 amino acid long FANCM protein. The functional or binding domains (BD) are indicated in black and as reported in Deans and West, 2009. The position of the three FANCM truncating variants c.1972C > T (p.Arg658*), c.5101 C > T (p.Gln1701*) and c.5791 C > T (p.Arg1931*) is also shown

proband carrying homozygous FANCM truncating variants were recently described.⁹ Three of these, two homozygous for p.Gln1701*, and one for p.Arg1931*, developed breast cancer at age 52 years or later and their cells did not demonstrate chromosome fragility. The other two probands were homozygous for p.Arg658* and developed early-onset breast cancer (at age 29 and 32); in addition, one developed several cancers, and the other demonstrated chromosomal fragility.⁹

Due to the rarity of the studied mutations in most populations, estimation of the risks is challenging. Preferably, the cases should be examined in comparison to geographically, ethnically and genetically matched controls. In the Finnish population, p.Gln1701* and p.Arg1931* are reported with carrier frequency of 1.62% and of 0.92%, respectively (<https://gnomad.broadinstitute.org/>).¹⁵ Case-control studies based on the Finnish population showed a strong statistical evidence of association of p.Gln1701* with ER-negative disease, with OR of 2.37 (95% CI = 1.37–4.12, $P = 0.0021$), and with TNBC with ORs of 3.56 (95% CI = 1.81–6.98, $P = 0.0002$),¹⁰ while p.Arg1931* was found associated with TNBC with an OR of 5.14 (95% CI = 1.65–16.0, $P = 0.005$).¹² However, as our 95% CI of risk estimates for TNBC included odds ratios of 2 for both the latter mutations, the published and our results are not mutually exclusive. Risk estimates associated with rare variants may depend on their frequency and the genetic background of the population studied. Hence, pooling the data from multiple outbred and admixed populations as it was done in the present study, may yield different risk estimates than those derived from geographically, ethnically and genetically matched controls, as in the Finnish studies. Indeed, it would have been interesting to test the FANCM variant position effect in the Finnish population, but unfortunately the p.Arg658* is very rare if not absent in this population (<https://gnomad.broadinstitute.org/>).¹⁵

Recent attempts to identify novel, high- to moderate-risk breast cancer-predisposing genes have not been particularly fruitful. However, a few genes have emerged as potential risk factors for ER-negative disease and TNBC, with FANCM, BRIP1, and RAD51C being among those suggested to confer moderate risk of these subtypes. Other predisposing genes increasing the risk of ER-negative and TNBC may also exist. Hence, further gene discovery efforts should take into consideration that risk-associated variants may be associated with specific tumor subtypes and/or variation in risk may depend on the variant position. In addition, we provide evidence that lack of FANCM protein and truncating variants identified in breast cancer patients are associated with increased sensitivity to the PARPi olaparib suggesting a therapeutic opportunity to treat FANCM-associated breast tumors that warrants further investigation. The PARPi sensitivity test may also prove useful for preclinical investigation of further truncating or missense FANCM variants.

In summary, we have shown that FANCM:p.Arg658* is associated with risk of ER-negative breast cancer and TNBC. The outcomes of functional assays testing the DNA repair efficiency in complemented human cells support the hypothesis that breast cancer risk may be greater for N-terminal than C-terminal FANCM truncating variants. Further genetic studies and meta-analyses are warranted to derive more precise risk estimates for the different FANCM variants.

METHODS

Study participants

The individuals included in this study were women of genetically confirmed European ancestry who were originally ascertained in 73 case-control studies from 19 countries participating in the BCAC or in 59 studies enrolling BRCA1 or BRCA2 pathogenic variants carrier from 30 countries participating in the CIMBA.

Ethics

All participating studies, listed in Supplementary Table 4 and Supplementary Table 5, were approved by their ethics review boards and followed national guidelines for informed consent. However, due to the retrospective nature of the majority of the studies, not all participant individuals have provided written informed consent to take part in the present analysis. The Milan Breast Cancer Study Group (MBCSG) was approved by ethics committee from Istituto Nazionale dei Tumori di Milano and Istituto Europeo di Oncologia, in Milan.

The BCAC studies contributed 67,112 invasive breast cancer cases and 53,766 controls. The majority of these studies were population-based, hospital-based or case-control studies nested within population-based cohorts (86%); few were family-clinic-based studies (14%; Supplementary Table 4). For each study subject, information on the disease status and the age at diagnosis or at interview were provided. Data on lifestyle risk factors were available for most subjects and clinical and pathological data were available for most cases. All these data were incorporated in the BCAC dataset (version 10). A total of 44,565 (66%) cases were ER-positive, 10,770 (16%) were ER-negative, and 4,805 (7%) were TNBC; 13,743 (20%) had a positive first-degree family history of breast cancer.

The CIMBA studies contributed 15,679 carriers of a pathogenic BRCA1 variant and 10,983 carriers of a pathogenic BRCA2 variant to this analysis (Supplementary Table 5). Nearly all (98%) of these carriers were ascertained through cancer genetic clinics; few carriers were recruited by population-based sampling of cases or by community recruitment. In some instances, multiple members of the same family were included. For each pathogenic variant carrier, the information on the type of the BRCA1 or BRCA2 variant, disease status, and censoring variables (see below, *Statistical analyses*) were collected and included in the CIMBA database.

Genotyping

Genotyping of FANCM:p.Arg658*, p.Gln1701*, and p.Arg1931* truncating variants was conducted using a custom-designed Illumina genotyping array (the “OncoArray”, Illumina, Inc. San Diego, CA, USA) at six independent laboratories. To ensure consistency of the genotype data, all laboratories used the same genotype-clustering file and genotyped the same set of reference-samples selected from the HapMap project. Samples with a call rate <95% and those with heterozygosity <5% or >40% were excluded. Further details of the genotype-calling and quality control have been described previously.¹⁴ The cluster plots of the three FANCM truncating variants were curated manually to confirm the automatic calls (Supplementary Fig. 2).

Statistical analyses

The BCAC data were analyzed to test the association between FANCM:p.Arg658*, p.Gln1701*, and p.Arg1931* and breast cancer risk. Logistic regression analyses were performed to estimate ORs with 95% CIs for variant carriers versus non-carriers, adjusting for country and the first ten principal components, as previously described.¹⁹ P -values were calculated by applying the likelihood ratio test (LRT) comparing the model containing the variant carrier status as a covariate to a model without the variant carrier status. The primary analyses were performed including all invasive breast cancer cases and controls and subgrouping cases based on tumor hormonal status. We then performed a country-restricted analysis

including the 50% of the countries with the higher variant carrier frequencies. Specifically, we included only countries in which the carrier frequencies in cases and controls combined were higher than the median of the carrier frequencies observed in all countries. Median frequencies were 0.007, 0.114 and 0.163 for p.Arg658*, p.Gln1701* and p.Arg1931* carriers, respectively.

The CIMBA data were analyzed to evaluate the association between each *FANCM* truncating variant and breast cancer risk in carriers of *BRCA1* or *BRCA2* pathogenic variant. A survival analyses framework was applied. Briefly, each variant carrier was followed from the age of 18 years until the first breast cancer diagnosis, or censored as unaffected at ovarian cancer diagnosis, bilateral prophylactic mastectomy, or age at last follow-up. The analyses were performed by modelling the retrospective likelihood of the observed genotypes conditional on the disease phenotype as detailed previously.⁴⁰ All analyses were stratified for country. The per-allele hazard ratio (HR), 95% CIs were estimated separately for each variant. A score test was used to derive *P*-values for the associations. The analyses of the BCAC data were performed using STATA version 15 (StataCorp LLC, College Station, Texas, USA). The analyses of the CIMBA data were carried out using custom-written code in Python and Fortran. All statistical tests were two-sided and *P*-values <0.05 were considered statistically significant.

Cell lines, plasmids, and lentiviral particles production and transduction

The immortalized patient-derived *FANCM*^{-/-} cell line EGF280⁸ was transduced with pLenti CMV rTA3 Blast, a gift from E. Campeau (Addgene plasmid #26429). The doxycycline-inducible lentiviral vector pLVX-TRE3G-FANCM, a gift from N. Ameziane (Vrije Universiteit Medical Center, Amsterdam) was mutated by site-directed mutagenesis using the QuickChange II XL Site-Directed Mutagenesis Kit (Agilent Technologies) and the following PAGE purified mutagenic primers. *FANCM* c.1972C>T primer 1: 5'-GCCTTCTCGGAAGTGCAGTGAAAGTCATCTATCTTTCC-3' and primer 2: 5'-GGAAAAGATAGATGACTTTCACTGCAAGTCCGAGAAGGC-3' for the p.Arg658*; *FANCM* c.5101C>T primer 1: 5'-TAAACAATGGTCC-TATTGTTTGTCTTAAACAGTGCTTGGGT-3' and primer 2: 5'-ACCCAAG-CACTGTTAAGAAGAACAACAATAGGACCATTGTTAA-3' for the p.Gln1701*. Generation of the lentiviral vector containing the *FANCM*:c.5791 C>T (p.Arg1931*) and transduction of the EGF280 cells were already described.¹¹ Expression of exogenous *FANCM* protein was achieved supplementing cell culture medium with doxycycline (1 µg/ml, final concentration). All the cell lines used in this study were routinely checked for mycoplasma contamination using the MycoAlert™ Mycoplasma Detection Kit (Lonza).

Western blot and mRNA expression studies

Cell lysis and western blot assays were performed as previously described.⁸ The following primary antibodies were used: mouse monoclonal anti-FANCM antibody, clone CV5.1 diluted 1:100 (ref: MAB545, MERCK Millipore), mouse monoclonal anti-Vinculin diluted 1:3000 (ref: ab18058, abcam). Western blotting detection was achieved with Luminata™ Classic (Millipore) (Vinculin) and LuminataForte™ (Millipore) (*FANCM*). We used RT PCR to test the expression of the mutant *FANCM*:p.Arg658*. Total RNA was extracted (RNeasy Mini Kit Qiagen) from the wt*FANCM* and *FANCM*:p.Arg658* transduced EGF280 cell lines. Reverse transcription was performed using High-Capacity RNA-to-cDNA Kit (ThermoFisher); a cDNA region corresponding to the *FANCM* sequence containing the amino acid (AA) position Arg658 was amplified by PCR using the forward: 5'-AGTAACAGGCAGGTCCTTCA-3' and reverse: 5'-TGATCTGCCACAGTCTCCA-3' primers. The 386 bp PCR products were then digested with *TseI* restriction enzyme (New England Biolabs) for two hours at 65 °C and analyzed by standard agarose gel electrophoresis.

Cell survival assay

The effect of the different *FANCM* variants on cell survival was measured with a Sulforhodamine B (SRB) assay.²¹ One-thousand cells were seeded in 96-well plates and treated constantly with DEB or PARPi olaparib at the indicated concentrations until untreated cells reached confluency. Cell monolayers were fixed overnight at 4 °C with 75 µl of 20% trichloroacetic acid (TCA). TCA was aspirated, and cells washed with tap water. Once dried, 50 µl of SRB was added to the wells and plates were incubated on a shaker at room temperature for 30 min. The excess of SRB dye was removed by washing repeatedly with 1% acetic acid, the plates were dried for 20 min, and the protein-bound dye was dissolved in 10 mM Tris for OD determination at 492 nm using a microplate reader (Tecan Sunrise™,

Tecan Group Ltd. Männedorf, Switzerland). At least three independent experiments were performed for each cell line and in each experiment, 12 wells were measured per concentration point. These results were statistically analyzed using the Prism (GraphPad) software. Two-Way ANOVA test was used for single comparisons between different cell lines and statistical significance was assessed with the Tukey's range test. A *P*-value < 0.05 was considered statistically significant.

Chromosome fragility test

Chromosome fragility test was performed as previously described.¹¹ Twenty-five metaphases were scored for chromosome breakages using the Metafer Slide Scanning Platform from Metasystems. Results were graphed as distributions of metaphases presenting 0, 1, and >1 chromatid break. Statistical analysis was performed applying chi-squared test.

Reporting summary

Further information on research design is available in the Nature Research Reporting Summary

DATA AVAILABILITY

A subset of the genotype data analysed in this study is publicly available from the dbGaP repository and can be accessed at <https://identifiers.org/dbgap:phs001265.v1.p1> (data generated as part of the BCAC studies) and at <https://identifiers.org/dbgap:phs001321.v1.p1> (data generated as part of the CIMBA studies). The remaining genotype data analysed in this study (and generated as part of the BCAC and CIMBA studies listed in Supplementary Tables 4 and 5 of the related article, respectively) are not publicly available due to restraints imposed by the ethics committees of individual studies, but can be accessed from the corresponding author on reasonable request as described at <https://doi.org/10.6084/m9.figshare.8982296>.²² Additional datasets generated during this study (and supporting Fig. 1 and Supplementary Tables 2 and 3 in the published article) are available on request as described above. The data generated and analyzed during this study are described in the following data record: <https://doi.org/10.6084/m9.figshare.8982296>.²²

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G.F. and M.B. contributed equally to this work as first author. J.S. and P.P. contributed equally to this work as last author. Conceived the study: G.F., M.B., I.C., P.R., H.N., J.S., P.P. Wrote the manuscript: G.F., P.P. Contributed to manuscript writing: M.B., T.A.M., A. J.S., M.H.G., W.K.C., R.L.M., G.C.T., T.D., M.K.S., D.F.E., P.R., H.N. Conceived, designed or obtained financial support for the OncoArray: P.K., J.S., D.F.E., A.C. Data management: D.R., J.D., K.M., M.K.B., G.L., A.M.D., M.L., M.T.P., L.M., M.T.P., A.C.A. Statistical analyses: G.F., J.I.K., H.N., P.P. Functional analyses: M.B., L.C., S.V.L., R.P., J.S. Provided DNA samples and/or phenotypic data: C.M.A., M.A.A., J.A., S.A., C.A.A., B.A.A., T.A., K.A., C.B.A., L.A., H.A.-C., N.N.A., V.A., N.A., K.J.A., B.K.A., E.A., B.A., P.A., J.Az., J.B., R.B.B., D.B., J.B., L.E.B.F., C.J.B., M.W.B., S.B., J.Bar., R.B., M.B., A.M.B., C.B., N.V.B., A.B., S.E.B., B.B., A.Bor., A.F.B., H.B., H.Br., T.B., B.Bu., S.S.B., T.C., A.C., M.A.C., D.C., I.G.C., F.C., J.E.C., J.C.-C., S.J.C., K.B.M.C., C.L.C., A.Co., T.A.C., D.G.C., C.C., K.C., M.B.D., M.dH., P.D., O.D., Y.C.D., G.S. D., N.D., S.M.D., C.M.D., I.d-S-S., K.D., M.D., D.M.E., A.B.E., A.H.E., C.E., M.E., D.G.E., P.A.F., J.F., H.F., W.D.F., T.M.F., E.F., M.G., P.G., M.G.-D., C.G., S.M.G., J.G., M.M.C., J.A.G.-S., M.M.G., S.A.G., G.G.G., G.G., A.K.G., M.S.G., D.E.G., P.Gu., A.G.-B., L.H., C.A.H., N.H., P.H., U.H., P.A. H., A.H., J.H., P.Hi., A.Ho., J.L.H., H.D.H.-III, A.How., C.H., P.J.H., D.J.H., E.N.I., C.I., M.J., A.J., P.J., R.J., W.J., E.M.J., M.E.J., A.Ju., R.K., B.Y.K., E.K., C.M.K., I.K., S.K., P.K., D.L., C.L., L.L.M., J.L., F.L., J.Li., J.T.L., K.H.L., R.N.L., J.Lu., A.M., M.M., S.Ma., J.W.M.P.M., T.M., D.O., N.M., A.Me., U.M., A.Mi., M.Mo., K.L.N., S.L.N., W.G.N., T.N.-D., F.C.N., S.N., L.N.-Z., K.O., E.O., O.I. O., A.F.O., J.E.O., H.O., A.O., L.O., B.P., A.P., J.P., D.P.-K., T.P., N.P., M.A.P., K.P., B.R., J.R., M.U.R., R.R.-M., G.R., H.S.R., V.R., A.R., M.A.R., E.A.R., M.R., V.Ru., M.Ru., E.S., K.S., M.S., M.T. S., R.K.S., M.Sc., C.S., L.S., M.Sh., P.S., X-O.S., J.S., C.F.S., C.So., P.So., M.C.S., J.J.S., L.St., D.S.-L., W.J.T., M.R.T., M.B.T., M.T., J.T., D.L.T., M.Ti., R.A.E.M.T., D.T., M.A.T., T.T., N.T., M.U., C.M. V., E.J.v.R., E.M.v.V., A.V., A.Vi., B.W., J.N.W., C.W., G.W., A.W., X.R.Y., W.Z., A.Z., K.K.Z., A.M. D., M.L., Q.W., L.M., M.T.P. P.D.P.P., F.F., A.E.T., I.L.A., S.J.R., A.J.S., M.H.G., W.K.C., R.L.M., G.C.T., T.D., M.K.S. D.F.E., P.R., E.H., A.C.A., F.J.C., H.N., P.P. All authors read and approved the final version of the manuscript.

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ADDITIONAL INFORMATION

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Correspondence and requests for materials should be addressed to P.P.

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Gisella Figlioli^{1,3,33}, Massimo Bogliolo^{2,3,4,33,33}, Irene Catucci¹, Laura Caleca⁵, Sandra Viz Lasheras², Roser Pujol^{2,3,4}, Johanna I. Kiiski⁶, Taru A. Muranen⁶, Daniel R. Barnes⁷, Joe Dennis⁷, Kyriaki Michailidou^{7,8}, Manjeet K. Bolla⁷, Goska Leslie⁷, Cora M. Aalfs⁹, ABCTB Investigators, Muriel A. Adank¹⁰, Julian Adlard¹¹, Simona Agata¹², Karen Cadoo¹³, Bjarni A. Agnarsson^{14,15}, Thomas Ahearn¹⁶, Kristiina Aittomäki¹⁷, Christine B. Ambrosone¹⁸, Lesley Andrews¹⁹, Hoda Anton-Culver²⁰, Natalia N. Antonenкова²¹, Volker Arndt²², Norbert Arnold²³, Kristan J. Aronson²⁴, Banu K. Arun²⁵, Ella Asseryanis²⁶, Bernd Auber²⁷, Päivi Auvinen^{28,29,30}, Jacopo Azzollini³¹, Judith Balmaña^{32,33}, Rosa B. Barkardottir^{14,34}, Daniel Barrowdale⁷, Julian Barwell³⁵, Laura E. Beane Freeman¹⁶, Charles Joly Beuparant³⁶, Matthias W. Beckmann³⁷, Sabine Behrens³⁸, Javier Benitez^{39,40,41}, Raanan Berger⁴², Marina Bermisheva⁴³, Amie M. Blanco⁴⁴, Carl Blomqvist^{45,46}, Natalia V. Bogdanova^{21,47,48}, Anders Bojesen⁴⁹, Stig E. Bojesen^{50,51,52}, Bernardo Bonanni⁵³, Ake Borg⁵⁴, Angela F. Brady⁵⁵, Hiltrud Brauch^{56,57,58}, Hermann Brenner^{22,58,59}, Thomas Brüning⁶⁰, Barbara Burwinkel^{61,62}, Saundra S. Buys⁶³, Trinidad Caldés⁶⁴, Almuth Caliebe⁶⁵, Maria A. Caligo⁶⁶, Daniele Campa^{38,67}, Ian G. Campbell^{68,69}, Federico Canzian⁷⁰, Jose E. Castelao⁷¹, Jenny Chang-Claude^{38,72}, Stephen J. Chanock¹⁶, Kathleen B. M. Claes⁷³, Christine L. Clarke⁷⁴, Anita Collavoli⁷⁵, Thomas A. Conner⁷⁶, David G. Cox^{77,78}, Cezary Cybulski⁷⁹, Kamila Czene⁸⁰, Mary B. Daly⁸¹, Miguel de la Hoya⁶⁴, Peter Devilee^{82,83}, Orland Diez^{84,85}, Yuan Chun Ding⁸⁶, Gillian S. Dite⁸⁷, Nina Ditsch⁸⁸, Susan M. Domchek⁸⁹, Cecilia M. Dorfling⁹⁰, Isabel dos-Santos-Silva⁹¹, Katarzyna Durda⁷⁹, Miriam Dwek⁹², Diana M. Eccles⁹³, Arif B. Ekcici⁹⁴, A. Heather Eliassen^{95,96}, Carolina Ellberg⁹⁷, Mikael Eriksson⁸⁰, D. Gareth Evans^{98,99}, Peter A. Fasching^{37,100}, Jonine Figueroa^{16,101,102}, Henrik Flyger¹⁰³, William D. Foulkes¹⁰⁴, Tara M. Friebe^{105,106}, Eitan Friedman^{107,108}, Marika Gabrielson⁸⁰, Pragna Gaddam¹⁰⁹, Manuela Gago-Dominguez^{110,111}, Chi Gao¹¹², Susan M. Gapstur¹¹³, Judy Garber¹¹⁴, Montserrat Garcia-Closas¹⁶, José A. García-Sáenz⁶⁴, Mia M. Gaudet¹¹³, Simon A. Gayther¹¹⁶, GEMO Study Collaborators, Graham G. Giles^{87,117,118}, Gord Glendon¹¹⁹, Andrew K. Godwin¹²⁰, Mark S. Goldberg^{121,122}, David E. Goldgar¹²³, Pascal Guénel¹²⁴, Angelica M. Gutierrez-Barrera¹²⁵, Lothar Haeberle¹²⁶, Christopher A. Haiman¹²⁷, Niclas Håkansson¹²⁸, Per Hall^{80,129}, Ute Hamann¹³⁰, Patricia A. Harrington¹³¹, Alexander Hein³⁷, Jane Heyworth¹³², Peter Hillemanns⁴⁸, Antoinette Hollestelle¹³³, John L. Hopper⁸⁷, H. Dean Hosgood III¹³⁴, Anthony Howell¹³⁵, Chunling Hu¹³⁶, Peter J. Hulick^{137,138}, David J. Hunter^{96,112,139}, Evgeny N. Imyanitov¹⁴⁰, KConFab, Claudine Isaacs¹⁴¹, Milena Jakimovska¹⁴², Anna Jakubowska^{79,143}, Paul James^{69,144}, Ramunas Janavicius^{145,146}, Wolfgang Janni¹⁴⁷, Esther M. John¹⁴⁸, Michael E. Jones¹¹⁵, Audrey Jung³⁸, Rudolf Kaaks³⁸, Beth Y. Karlan¹⁴⁹, Elza Khusnutdinova^{43,150}, Cari M. Kitahara¹⁵¹, Irene Konstantopoulou¹⁵², Stella Koutros¹⁶, Peter Kraft^{96,112}, Diether Lambrechts^{153,154}, Conxi Lazaro¹⁵⁵, Loic Le Marchand¹⁵⁶, Jenny Lester¹⁴⁹, Fabienne Lesueur^{157,158,159,160}, Jenna Lilyquist¹⁶¹, Jennifer T. Loud¹⁶², Karen H. Lu¹⁶³, Robert N. Luben¹⁶⁴, Jan Lubinski⁷⁹, Arto Mannermaa^{30,165,166}, Mehdi Manoochehri¹³⁰, Siranoush Manoukian³¹, Sara Margolin^{129,167}, John W. M. Martens¹³³, Tabea Maurer⁷², Dimitrios Mavroudis¹⁶⁸, Noura Mebirouk^{157,158,159,160}, Alfons Meindl⁸⁸, Usha Menon¹⁶⁹, Austin Miller¹⁷⁰, Marco Montagna¹², Katherine L. Nathanson⁸⁹, Susan L. Neuhausen⁸⁶, William G. Newman^{98,99}, Tu Nguyen-Dumont^{171,199}, Finn Cilius Nielsen¹⁷², Sarah Nielsen¹⁷³, Liene Nikitina-Zake¹⁷⁴, Kenneth Offit^{109,175}, Edith Olah¹⁷⁶, Olufunmilayo I. Olopade¹⁷³, Andrew F. Olshan¹⁷⁷, Janet E. Olson¹⁶¹, Håkan Olsson⁹⁷, Ana Osorio^{39,40}, Laura Ottini¹⁷⁸, Bernard Peissel³¹, Ana Peixoto¹⁷⁹, Julian Peto¹⁸⁰, Dijana Plesaska-Karanfiska¹⁴², Timea Pocza¹⁷⁶, Nadege Presneau⁹², Miquel Angel Pujana¹⁸⁰, Kevin Punie¹⁸¹, Brigitte Rack¹⁴⁷, Johanna Rantalala¹⁸², Muhammad U. Rashid^{130,183}, Rohini Rau-Murthy¹⁷⁵, Gad Rennert¹⁸⁴, Flavio Lejbkowitz¹⁸⁴, Valerie Rhenius¹³¹, Atocha Romero¹⁸⁵, Matti A. Rookus¹⁸⁶, Eric A. Ross¹⁸⁷, Maria Rossing¹⁷², Vilijus Rudaitis¹⁸⁸, Matthias Ruebner¹²⁶, Emmanouil Saloustros¹⁸⁹, Kristin Sanden¹⁹⁰, Marta Santamariña^{40,191,192}, Maren T. Scheuner⁴⁴, Rita K. Schmutzler^{193,194}, Michael Schneider¹²⁶, Christopher Scott¹⁶¹, Leigha Senter¹⁹⁵, Mitul Shah¹³¹, Priyanka Sharma¹⁹⁶, Xiao-Ou Shu¹⁹⁷, Jacques Simard³⁶, Christian F. Singer²⁶, Christof Sohn¹⁹⁸, Penny Soucy³⁶, Melissa C. Southey^{171,199}, John J. Spinelli^{200,201}, Linda Steele⁸⁶, Dominique Stoppa-Lyonnet^{202,203,204}, William J. Tapper²⁰⁵, Manuel R. Teixeira^{179,206}, Mary Beth Terry²⁰⁷, Mads Thomassen²⁰⁸, Jennifer Thompson¹³⁷, Darcy L. Thull²⁰⁹, Marc Tischkowitz^{104,210}, Rob A.E.M. Tollenaar²¹¹, Diana Torres^{130,212}, Melissa A. Troester¹⁷⁷, Thérèse Truong¹²⁴, Nadine Tung²¹³, Michael Untch²¹⁴, Celine M. Vachon¹⁶¹, Elizabeth J. van Rensburg⁹⁰, Elke M. van Veen^{98,99}, Ana Vega^{40,191,192}, Alessandra Viel²¹⁵, Barbara Wappenschmidt^{193,194}, Jeffrey N. Weitzel²¹⁶, Camilla Wendt^{129,167}, Greet Wieme⁷³, Alicja Wolk^{128,217}, Xiaohong R. Yang¹⁶, Wei Zheng¹⁹⁷, Argyrios Ziogas²⁰, Kristin K. Zorn²¹⁸, Alison M. Dunning¹³¹, Michael Lush⁷, Qin Wang⁷, Lesley McGuffog⁷, Michael T. Parsons²¹⁹, Paul D. P. Pharoah⁷, Florentia Fostira¹⁵², Amanda E. Toland²²⁰, Irene L. Andrulis^{119,221}, Susan J. Ramus^{222,223}, Anthony J. Swerdlow^{224,225}, Mark H. Greene¹⁶², Wendy K. Chung²²⁶, Roger L. Milne^{87,117,171}, Georgia Chenevix-Trench²¹⁹, Thilo Dörk⁴⁸, Marjanka K. Schmidt^{227,228}, Douglas F. Easton^{7,131}, Paolo Radice⁵, Eric Hahnen^{193,194}, Antonis C. Antoniou⁷, Fergus J. Couch¹³⁶, Heli Nevanlinna⁶, Jordi Surrallés^{2,3,4,229,333} and Paolo Peterlongo^{1,333*}

¹IFOM - the FIRC Institute for Molecular Oncology, Genome Diagnostics Program, Milan, Italy. ²Department of Genetics and Microbiology, Universitat Autònoma de Barcelona, Bellaterra, Barcelona, Spain. ³Center for Biomedical Network Research on Rare Diseases (CIBERER), Madrid, Spain. ⁴Institute of Biomedical Research, Sant Pau Hospital, Barcelona, Spain. ⁵Fondazione IRCCS Istituto Nazionale dei Tumori, Unit of Molecular Bases of Genetic Risk and Genetic Testing, Department of Research, Milan, Italy. ⁶University of Helsinki, Department of Obstetrics and Gynecology, Helsinki University Hospital, Helsinki, Finland. ⁷University of Cambridge, Centre for Cancer Genetic Epidemiology, Department of Public Health and Primary Care, Cambridge, UK. ⁸The Cyprus Institute of Neurology & Genetics, Department of Electron Microscopy/Molecular Pathology and The Cyprus School of Molecular Medicine, Nicosia, Cyprus. ⁹Amsterdam UMC, Ikatie AMC, Department of Clinical Genetics, Amsterdam, The Netherlands. ¹⁰The Netherlands Cancer Institute - Antoni van Leeuwenhoek hospital, Family Cancer Clinic, Amsterdam, The Netherlands. ¹¹Chapel Allerton Hospital, Yorkshire Regional Genetics Service, Leeds, UK. ¹²Veneto Institute of Oncology IOV - IRCCS, Immunology and Molecular Oncology Unit, Padua, Italy. ¹³Memorial Sloan-Kettering Cancer Center, Department of Medicine, New York, NY, USA. ¹⁴Landspítali University Hospital, Department of Pathology, Reykjavik, Iceland. ¹⁵University of Iceland, School of Medicine, Reykjavik, Iceland. ¹⁶National Cancer Institute,

National Institutes of Health, Department of Health and Human Services, Division of Cancer Epidemiology and Genetics, Bethesda, MD, USA. ¹⁷University of Helsinki, Department of Clinical Genetics, Helsinki University Hospital, Helsinki, Finland. ¹⁸Roswell Park Cancer Institute, Buffalo, NY, USA. ¹⁹Nelune Comprehensive Cancer Care Centre, The Bright Alliance Building, Randwick, NSW, Australia. ²⁰University of California Irvine, Department of Epidemiology, Genetic Epidemiology Research Institute, Irvine, CA, USA. ²¹N.N. Alexandrov Research Institute of Oncology and Medical Radiology, Minsk, Belarus. ²²German Cancer Research Center (DKFZ), Division of Clinical Epidemiology and Aging Research, Heidelberg, Germany. ²³University Hospital of Schleswig-Holstein, Campus Kiel, Christian-Albrechts University Kiel, Department of Gynaecology and Obstetrics, and Institute of Clinical Molecular Biology, Kiel, Germany. ²⁴Queen's University, Department of Public Health Sciences, and Cancer Research Institute, Kingston, ON, Canada. ²⁵University of Texas MD Anderson Cancer Center, Department of Breast Medical Oncology, Houston, TX, USA. ²⁶Medical University of Vienna, Dept of OB/GYN and Comprehensive Cancer Center, Vienna, Austria. ²⁷Hannover Medical School, Institute of Human Genetics, Hannover, Germany. ²⁸Kuopio University Hospital, Cancer Center, Kuopio, Finland. ²⁹University of Eastern Finland, Institute of Clinical Medicine, Oncology, Kuopio, Finland. ³⁰University of Eastern Finland, Translational Cancer Research Area, Kuopio, Finland. ³¹Fondazione IRCCS Istituto Nazionale dei Tumori di Milano, Department of Medical Oncology and Hematology, Unit of Medical Genetics, Milan, Italy. ³²Vall d'Hebron Institute of Oncology, High Risk and Cancer Prevention Group, Barcelona, Spain. ³³University Hospital, Vall d'Hebron, Department of Medical Oncology, Barcelona, Spain. ³⁴University of Iceland, BMC (Biomedical Centre), Faculty of Medicine, Reykjavik, Iceland. ³⁵University Hospitals of Leicester NHS Trust, Leicestershire Clinical Genetics Service, Leicester, UK. ³⁶Centre Hospitalier Universitaire de Québec – Université Laval, Research Center, Genomics Center, Québec City, QC, Canada. ³⁷University Hospital Erlangen, Friedrich-Alexander-University Erlangen-Nuremberg, Department of Gynecology and Obstetrics, Comprehensive Cancer Center ER-EMN, Erlangen, Germany. ³⁸German Cancer Research Center (DKFZ), Division of Cancer Epidemiology, Heidelberg, Germany. ³⁹Spanish National Cancer Research Centre (CNIO), Human Genetics Group, Human Cancer Genetics Programme, Madrid, Spain. ⁴⁰Spanish Network on Rare Diseases (CIBERER), Madrid, Spain. ⁴¹Spanish National Cancer Research Centre (CNIO), Genotyping Unit (CEGEN), Human Cancer Genetics Programme, Madrid, Spain. ⁴²Chaim Sheba Medical Center, The Institute of Oncology, Ramat Gan, Israel. ⁴³Ufa Federal Research Center of the Russian Academy of Sciences, Institute of Biochemistry and Genetics, Ufa, Russia. ⁴⁴University of California San Francisco, Cancer Genetics and Prevention Program, San Francisco, CA, USA. ⁴⁵University of Helsinki, Department of Oncology, Helsinki University Hospital, Helsinki, Finland. ⁴⁶Örebro University Hospital, Department of Oncology, Örebro, Sweden. ⁴⁷Hannover Medical School, Department of Radiation Oncology, Hannover, Germany. ⁴⁸Hannover Medical School, Gynaecology Research Unit, Hannover, Germany. ⁴⁹Aarhus University Hospital, Department of Clinical Genetics, Aarhus, Denmark. ⁵⁰Copenhagen University Hospital, Copenhagen General Population Study, Herlev and Gentofte Hospital, Herlev, Denmark. ⁵¹Copenhagen University Hospital, Department of Clinical Biochemistry, Herlev and Gentofte Hospital, Herlev, Denmark. ⁵²University of Copenhagen, Faculty of Health and Medical Sciences, Copenhagen, Denmark. ⁵³IEO, European Institute of Oncology IRCCS, Division of Cancer Prevention and Genetics, Milan, Italy. ⁵⁴Lund University and Skåne University Hospital, Department of Oncology, Lund, Sweden. ⁵⁵London North West University Hospitals NHS Trust, Northwick Park Hospital, North West Thames Regional Genetics Service, Kennedy Galton Centre, Harrow, UK. ⁵⁶Dr. Margarete Fischer-Bosch-Institute of Clinical Pharmacology, Stuttgart, Germany. ⁵⁷University of Tübingen, iFIT-Cluster of Excellence, Tübingen, Germany. ⁵⁸German Cancer Research Center (DKFZ), German Cancer Consortium (DKTK), Heidelberg, Germany. ⁵⁹German Cancer Research Center (DKFZ) and National Center for Tumor Diseases (NCT), Division of Preventive Oncology, Heidelberg, Germany. ⁶⁰Institute for Prevention and Occupational Medicine of the German Social Accident Insurance, Institute of the Ruhr University Bochum, Bochum, Germany. ⁶¹German Cancer Research Center (DKFZ), Molecular Epidemiology Group, C080 Heidelberg, Germany. ⁶²University of Heidelberg, Molecular Biology of Breast Cancer, University Womens Clinic Heidelberg, Heidelberg, Germany. ⁶³Huntsman Cancer Institute, Department of Medicine, Salt Lake City, UT, USA. ⁶⁴Instituto de Investigación Sanitaria San Carlos (IdISSC), Centro Investigación Biomédica en Red de Cáncer (CIBERONC), Medical Oncology Department, Hospital Clínico San Carlos, Madrid, Spain. ⁶⁵University Hospital of Schleswig-Holstein, Campus Kiel, Christian-Albrechts University Kiel, Institute of Human Genetics, Kiel, Germany. ⁶⁶University Hospital of Pisa, Section of Molecular Genetics, Dept. of Laboratory Medicine, Pisa, Italy. ⁶⁷University of Pisa, Department of Biology, Pisa, Italy. ⁶⁸Peter MacCallum Cancer Center, Research Division, Melbourne, VIC, Australia. ⁶⁹The University of Melbourne, Sir Peter MacCallum Department of Oncology, Melbourne, VIC, Australia. ⁷⁰German Cancer Research Center (DKFZ), Genomic Epidemiology Group, Heidelberg, Germany. ⁷¹Instituto de Investigación Sanitaria Galicia Sur (IISGS), Xerencia de Xestión Integrada de Vigo-SERGAS, Oncology and Genetics Unit, Vigo, Spain. ⁷²University Medical Center Hamburg-Eppendorf, Cancer Epidemiology Group, University Cancer Center Hamburg (UCCH), Hamburg, Germany. ⁷³Ghent University, Centre for Medical Genetics, Gent, Belgium. ⁷⁴University of Sydney, Westmead Institute for Medical Research, Sydney, NSW, Australia. ⁷⁵University and University Hospital of Pisa, Section of Genetic Oncology, Dept. of Laboratory Medicine, Pisa, Italy. ⁷⁶Huntsman Cancer Institute, Salt Lake City, UT, USA. ⁷⁷Imperial College London, Department of Epidemiology and Biostatistics, School of Public Health, London, UK. ⁷⁸Cancer Research Center of Lyon, INSERM, U1052 Lyon, France. ⁷⁹Pomeranian Medical University, Department of Genetics and Pathology, Szczecin, Poland. ⁸⁰Karolinska Institutet, Department of Medical Epidemiology and Biostatistics, Stockholm, Sweden. ⁸¹Fox Chase Cancer Center, Department of Clinical Genetics, Philadelphia, PA, USA. ⁸²Leiden University Medical Center, Department of Pathology, Leiden, The Netherlands. ⁸³Leiden University Medical Center, Department of Human Genetics, Leiden, The Netherlands. ⁸⁴Vall d'Hebron Institute of Oncology (VHIO), Oncogenetics Group, Barcelona, Spain. ⁸⁵University Hospital Vall d'Hebron, Area of Clinical and Molecular Genetics, Barcelona, Spain. ⁸⁶Beckman Research Institute of City of Hope, Department of Population Sciences, Duarte, CA, USA. ⁸⁷The University of Melbourne, Centre for Epidemiology and Biostatistics, Melbourne School of Population and Global Health, Melbourne, Victoria, Australia. ⁸⁸Ludwig Maximilian University of Munich, Department of Gynecology and Obstetrics, Munich, Germany. ⁸⁹Perelman School of Medicine at the University of Pennsylvania, Department of Medicine, Abramson Cancer Center, Philadelphia, PA, USA. ⁹⁰University of Pretoria, Department of Genetics, Arcadia, South Africa. ⁹¹London School of Hygiene and Tropical Medicine, Department of Non-Communicable Disease Epidemiology, London, UK. ⁹²University of Westminster, Department of Biomedical Sciences, Faculty of Science and Technology, London, UK. ⁹³University of Southampton, Cancer Sciences Academic Unit, Faculty of Medicine, Southampton, UK. ⁹⁴Friedrich-Alexander University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Institute of Human Genetics, University Hospital Erlangen, Erlangen, Germany. ⁹⁵Harvard Medical School, Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital, Boston, MA, USA. ⁹⁶Harvard T.H. Chan School of Public Health, Department of Epidemiology, Boston, MA, USA. ⁹⁷Lund University, Department of Cancer Epidemiology, Clinical Sciences, Lund, Sweden. ⁹⁸University of Manchester, Division of Evolution and Genomic Medicine, School of Biological Sciences, Faculty of Biology, Medicine and Health, Manchester, UK. ⁹⁹Manchester University NHS Foundation Trust, Manchester Academic Health Science Centre, Manchester Centre for Genomic Medicine, Manchester, UK. ¹⁰⁰University of California at Los Angeles, David Geffen School of Medicine, Department of Medicine Division of Hematology and Oncology, Los Angeles, CA, USA. ¹⁰¹The University of Edinburgh Medical School, Usher Institute of Population Health Sciences and Informatics, Edinburgh, UK. ¹⁰²Cancer Research UK Edinburgh Centre, Edinburgh, UK. ¹⁰³Copenhagen University Hospital, Department of Breast Surgery, Herlev and Gentofte Hospital, Herlev, Denmark. ¹⁰⁴McGill University, Program in Cancer Genetics, Departments of Human Genetics and Oncology, Montréal, QC, Canada. ¹⁰⁵Harvard T.H. Chan School of Public Health, Boston, MA, USA. ¹⁰⁶Dana-Farber Cancer Institute, Boston, MA, USA. ¹⁰⁷Chaim Sheba Medical Center, The Susanne Levy Gertner Oncogenetics Unit, Ramat Gan, Israel. ¹⁰⁸Tel Aviv University, Sackler Faculty of Medicine, Ramat Aviv, Israel. ¹⁰⁹Memorial Sloan-Kettering Cancer Center, Clinical Genetics Research Lab, Department of Cancer Biology and Genetics, New York, NY, USA. ¹¹⁰Instituto de Investigación Sanitaria de Santiago de Compostela (IDIS), Complejo Hospitalario Universitario de Santiago, SERGAS, Genomic Medicine Group, Galician Foundation of Genomic Medicine, Santiago de Compostela, Spain. ¹¹¹University of California San Diego, Moores Cancer Center, La Jolla, CA, USA. ¹¹²Harvard T.H. Chan School of Public Health, Program in Genetic Epidemiology and Statistical Genetics, Boston, MA, USA. ¹¹³American Cancer Society, Epidemiology Research Program, Atlanta, GA, USA. ¹¹⁴Dana-Farber Cancer Institute, Cancer Risk and Prevention Clinic, Boston, MA, USA. ¹¹⁵The Institute of Cancer Research, Division of Genetics and Epidemiology, London, UK. ¹¹⁶Cedars-Sinai Medical Center, The Center for Bioinformatics and Functional Genomics at the Samuel Oschin Comprehensive Cancer Institute, Los Angeles, CA, USA. ¹¹⁷Cancer Council Victoria, Cancer Epidemiology Division, Melbourne, VIC, Australia. ¹¹⁸Monash University, Department of Epidemiology and Preventive Medicine, Melbourne, VIC, Australia. ¹¹⁹Lunenfeld-Tanenbaum Research Institute of Mount Sinai Hospital, Fred A. Litwin Center for Cancer Genetics, Toronto, ON, Canada. ¹²⁰Kansas University Medical Center, Department of Pathology and Laboratory Medicine, Kansas City, KS, USA. ¹²¹McGill University, Department of Medicine, Montréal, QC, Canada. ¹²²McGill University, Division of Clinical Epidemiology, Royal Victoria Hospital, Montréal, QC, Canada. ¹²³Huntsman Cancer Institute, University of Utah School of Medicine, Department of Dermatology, Salt Lake City, UT, USA. ¹²⁴INSERM, University Paris-Sud, University Paris-Saclay, Cancer & Environment Group, Center for Research in Epidemiology and Population Health (CESP), Villejuif, France. ¹²⁵University of Texas MD Anderson Cancer Center, Department of Breast Medical Oncology and Clinical Genetics Program, Houston, TX, USA. ¹²⁶Friedrich-Alexander University Erlangen-Nuremberg, Comprehensive Cancer Center Erlangen-EMN, Department of Gynaecology and Obstetrics, University Hospital Erlangen, Erlangen, Germany. ¹²⁷University of Southern California, Department of Preventive Medicine, Keck School of Medicine, Los Angeles, CA, USA. ¹²⁸Karolinska Institutet, Institute of Environmental Medicine, Stockholm, Sweden. ¹²⁹Södersjukhuset, Department of Oncology, Stockholm, Sweden. ¹³⁰German Cancer Research Center (DKFZ), Molecular Genetics of Breast Cancer, Heidelberg, Germany. ¹³¹University of Cambridge, Centre for Cancer Genetic Epidemiology, Department of Oncology, Cambridge, UK. ¹³²The University of Western Australia, School of Population and Global Health, Perth, WA, Australia. ¹³³Erasmus MC Cancer Institute, Department of Medical Oncology, Family Cancer Clinic, Rotterdam, The Netherlands. ¹³⁴Albert Einstein College of Medicine, Department of Epidemiology and Public Health, Bronx, NY, USA. ¹³⁵University of Manchester, Division of Cancer Sciences, Manchester, UK. ¹³⁶Mayo Clinic, Department of Laboratory Medicine and Pathology, Rochester, MN, USA. ¹³⁷NorthShore

University HealthSystem, Center for Medical Genetics, Evanston, IL, USA. ¹³⁸The University of Chicago Pritzker School of Medicine, Chicago, IL, USA. ¹³⁹University of Oxford, Nuffield Department of Population Health, Oxford, UK. ¹⁴⁰N.N. Petrov Institute of Oncology, St. Petersburg, Russia. ¹⁴¹Lombardi Comprehensive Cancer Center, Georgetown University, Washington, DC, USA. ¹⁴²Macedonian Academy of Sciences and Arts, Research Centre for Genetic Engineering and Biotechnology 'Georgi D. Efreinov', Skopje, Republic of Macedonia. ¹⁴³Pomeranian Medical University, Independent Laboratory of Molecular Biology and Genetic Diagnostics, Szczecin, Poland. ¹⁴⁴Peter MacCallum Cancer Center, Parkville Familial Cancer Centre, Melbourne, VIC, Australia. ¹⁴⁵Vilnius University Hospital Santariskiu Clinics, Hematology, oncology and transfusion medicine center, Dept. of Molecular and Regenerative Medicine, Vilnius, Lithuania. ¹⁴⁶State Research Institute Innovative Medicine Center, Vilnius, Lithuania. ¹⁴⁷University Hospital Ulm, Department of Gynaecology and Obstetrics, Ulm, Germany. ¹⁴⁸Stanford University School of Medicine, Department of Medicine (Oncology) and Stanford Cancer Institute, Stanford, CA, USA. ¹⁴⁹Cedars-Sinai Medical Center, Women's Cancer Program at the Samuel Oschin Comprehensive Cancer Institute, Los Angeles, CA, USA. ¹⁵⁰Bashkir State Medical University, Department of Medical Genetics, Ufa, Russia. ¹⁵¹National Cancer Institute, Radiation Epidemiology Branch, Division of Cancer Epidemiology and Genetics, Bethesda, MD, USA. ¹⁵²National Centre for Scientific Research 'Demokritos', Molecular Diagnostics Laboratory, INRASTES, Athens, Greece. ¹⁵³VIB, VIB Center for Cancer Biology, Leuven, Belgium. ¹⁵⁴University of Leuven, Laboratory for Translational Genetics, Department of Human Genetics, Leuven, Belgium. ¹⁵⁵IDIBELL (Bellvitge Biomedical Research Institute), Catalan Institute of Oncology, CIBERONC, Molecular Diagnostic Unit, Hereditary Cancer Program, Barcelona, Spain. ¹⁵⁶University of Hawaii Cancer Center, Epidemiology Program, Honolulu, HI, USA. ¹⁵⁷Inserm U900, Genetic Epidemiology of Cancer team, Paris, France. ¹⁵⁸PSL University, Paris, France. ¹⁵⁹Institut Curie, Paris, France. ¹⁶⁰Mines ParisTech, Fontainebleau, France. ¹⁶¹Mayo Clinic, Department of Health Sciences Research, Rochester, MN, USA. ¹⁶²National Cancer Institute, Clinical Genetics Branch, Division of Cancer Epidemiology and Genetics, Bethesda, MD, USA. ¹⁶³University of Texas MD Anderson Cancer Center, Department of Gynecologic Oncology and Clinical Cancer Genetics Program, Houston, TX, USA. ¹⁶⁴University of Cambridge, Clinical Gerontology, Department of Public Health and Primary Care, Cambridge, UK. ¹⁶⁵University of Eastern Finland, Institute of Clinical Medicine, Pathology and Forensic Medicine, Kuopio, Finland. ¹⁶⁶Kuopio University Hospital, Imaging Center, Department of Clinical Pathology, Kuopio, Finland. ¹⁶⁷Karolinska Institutet, Department of Clinical Science and Education, Södersjukhuset, Stockholm, Sweden. ¹⁶⁸University Hospital of Heraklion, Department of Medical Oncology, Heraklion, Greece. ¹⁶⁹University College London, MRC Clinical Trials Unit at UCL, Institute of Clinical Trials & Methodology, London, UK. ¹⁷⁰Roswell Park Cancer Institute, NRG Oncology, Clinical Trials Development Division, Buffalo, NY, USA. ¹⁷¹Monash University, Precision Medicine, School of Clinical Sciences at Monash Health, Clayton, VIC, Australia. ¹⁷²Rigshospitalet, Copenhagen University Hospital, Center for Genomic Medicine, Copenhagen, Denmark. ¹⁷³The University of Chicago, Center for Clinical Cancer Genetics, Chicago, IL, USA. ¹⁷⁴Latvian Biomedical Research and Study Centre, Riga, Latvia. ¹⁷⁵Memorial Sloan-Kettering Cancer Center, Clinical Genetics Service, Department of Medicine, New York, NY, USA. ¹⁷⁶National Institute of Oncology, Department of Molecular Genetics, Budapest, Hungary. ¹⁷⁷University of North Carolina at Chapel Hill, Department of Epidemiology, Lineberger Comprehensive Cancer Center, Chapel Hill, NC, USA. ¹⁷⁸University La Sapienza, Department of Molecular Medicine, Rome, Italy. ¹⁷⁹Portuguese Oncology Institute, Department of Genetics, Porto, Portugal. ¹⁸⁰IDIBELL (Bellvitge Biomedical Research Institute), Catalan Institute of Oncology, CIBERONC, ProCURE, Oncobell, Barcelona, Spain. ¹⁸¹Leuven Cancer Institute, University Hospitals Leuven, Multidisciplinary Breast Center, Department of General Medical Oncology, Leuven, Belgium. ¹⁸²Karolinska Institutet, Clinical Genetics, Stockholm, Sweden. ¹⁸³Shaukat Khanum Memorial Cancer Hospital and Research Centre (SKMCH & RC), Department of Basic Sciences, Lahore, Pakistan. ¹⁸⁴Carmel Medical Center and Technion Faculty of Medicine, Clalit National Cancer Control Center, Haifa, Israel. ¹⁸⁵Hospital Universitario Puerta de Hierro, Medical Oncology Department, Madrid, Spain. ¹⁸⁶The Netherlands Cancer Institute, Department of Epidemiology, Amsterdam, The Netherlands. ¹⁸⁷Fox Chase Cancer Center, Biostatistics and Bioinformatics Facility, Philadelphia, PA, USA. ¹⁸⁸Vilnius University, Medical Faculty, Institute of Clinical Medicine, Vilnius, Lithuania. ¹⁸⁹University Hospital of Larissa, Department of Oncology, Larissa, Greece. ¹⁹⁰University of Wisconsin, Cancer Center at ProHealth Care, Waukesha, WI, USA. ¹⁹¹Fundación Pública Galega Medicina Xenómica, Santiago De Compostela, Spain. ¹⁹²Instituto de Investigación Sanitaria de Santiago de Compostela, Santiago De Compostela, Spain. ¹⁹³University Hospital of Cologne, Center for Hereditary Breast and Ovarian Cancer, Cologne, Germany. ¹⁹⁴University of Cologne, Center for Molecular Medicine Cologne (CMMC), Cologne, Germany. ¹⁹⁵The Ohio State University, Clinical Cancer Genetics Program, Division of Human Genetics, Department of Internal Medicine, The Comprehensive Cancer Center, Columbus, OH, USA. ¹⁹⁶University of Kansas Medical Center, Department of Internal Medicine, Division of Oncology, Westwood, KS, USA. ¹⁹⁷Vanderbilt University School of Medicine, Division of Epidemiology, Department of Medicine, Vanderbilt Epidemiology Center, Vanderbilt-Ingram Cancer Center, Nashville, TN, USA. ¹⁹⁸University of Heidelberg, National Center for Tumor Diseases, Heidelberg, Germany. ¹⁹⁹The University of Melbourne, Department of Clinical Pathology, Melbourne, VIC, Australia. ²⁰⁰BC Cancer, Population Oncology, Vancouver, BC, Canada. ²⁰¹University of British Columbia, School of Population and Public Health, Vancouver, BC, Canada. ²⁰²Institut Curie, Service de Génétique, Paris, France. ²⁰³INSERM U830, Department of Tumour Biology, Paris, France. ²⁰⁴Université Paris Descartes, Paris, France. ²⁰⁵University of Southampton, Faculty of Medicine, Southampton, UK. ²⁰⁶University of Porto, Biomedical Sciences Institute (ICBAS), Porto, Portugal. ²⁰⁷Columbia University, Department of Epidemiology, Mailman School of Public Health, New York, NY, USA. ²⁰⁸Odense University Hospital, Department of Clinical Genetics, Odense C, Denmark. ²⁰⁹Magee-Womens Hospital, University of Pittsburgh School of Medicine, Department of Medicine, Pittsburgh, PA, USA. ²¹⁰University of Cambridge, Department of Medical Genetics, Cambridge, UK. ²¹¹Leiden University Medical Center, Department of Surgery, Leiden, The Netherlands. ²¹²Pontificia Universidad Javeriana, Institute of Human Genetics, Bogota, Colombia. ²¹³Beth Israel Deaconess Medical Center, Department of Medical Oncology, Boston, MA, USA. ²¹⁴Helios Clinics Berlin-Buch, Department of Gynecology and Obstetrics, Berlin, Germany. ²¹⁵Centro di Riferimento Oncologico di Aviano (CRO), IRCCS, Division of Functional onco-genomics and genetics, Aviano, Italy. ²¹⁶City of Hope, Clinical Cancer Genetics, Duarte, CA, USA. ²¹⁷Uppsala University, Department of Surgical Sciences, Uppsala, Sweden. ²¹⁸Magee-Womens Hospital, University of Pittsburgh School of Medicine, Pittsburgh, PA, USA. ²¹⁹QIMR Berghofer Medical Research Institute, Department of Genetics and Computational Biology, Brisbane, QLD, Australia. ²²⁰The Ohio State University, Department of Cancer Biology and Genetics, Columbus, OH, USA. ²²¹University of Toronto, Department of Molecular Genetics, Toronto, ON, Canada. ²²²University of NSW Sydney, School of Women's and Children's Health, Faculty of Medicine, Sydney, NSW, Australia. ²²³The Kinghorn Cancer Centre, Garvan Institute of Medical Research, Sydney, NSW, Australia. ²²⁴The Institute of Cancer Research, Division of Genetics and Epidemiology, London, UK. ²²⁵The Institute of Cancer Research, Division of Breast Cancer Research, London, UK. ²²⁶Columbia University, Departments of Pediatrics and Medicine, New York, NY, USA. ²²⁷The Netherlands Cancer Institute - Antoni van Leeuwenhoek Hospital, Division of Molecular Pathology, Amsterdam, The Netherlands. ²²⁸The Netherlands Cancer Institute - Antoni van Leeuwenhoek hospital, Division of Psychosocial Research and Epidemiology, Amsterdam, The Netherlands. ²²⁹Department of Genetics, Sant Pau Hospital, Barcelona, Spain. ²³⁰These authors contributed equally: Gisella Figlioli, Massimo Bogliolo, Jordi Surrallés, Paolo Peterlongo. A full list of consortium members appears at the end of the paper.

ABCTB INVESTIGATORS

Rosemary Balleine²³⁰, Robert Baxter²³¹, Stephen Bray²³², Jane Carpenter⁷⁴, Jane Dahlstrom^{233,234}, John Forbes²³⁵, C. Soon Lee²³⁶, Deborah Marsh²³⁷, Adrienne Morey²³⁸, Nirmala Pathmanathan²³⁹, Rodney Scott^{240,241}, Peter Simpson²⁴², Allan Spigelman²⁴³, Nicholas Wilcken^{244,245}, Desmond Yip^{233,246} and Nikolajs Zeps²⁴⁷

GEMO STUDY COLLABORATORS

Muriel Belotti²⁰², Ophélie Bertrand²⁰², Anne-Marie Birot²⁰², Bruno Buecher²⁰², Sandrine Caputo²⁰², Anais Dupré²⁰², Emmanuelle Fourme²⁰², Marion Gauthier-Villars²⁰², Lisa Golmard²⁰², Marine Le Mentec²⁰², Virginie Moncoutier²⁰², Antoine de Pauw²⁰², Claire Saule²⁰², Nadia Boutry-Kryza^{248,249}, Alain Calender^{248,249}, Sophie Giraud^{248,249}, Mélanie Léone^{248,249}, Brigitte Bressac-de-Paillerets²⁵⁰, Olivier Caron²⁵⁰, Marine Guillaud-Bataille²⁵⁰, Yves-Jean Bignon²⁵¹, Nancy Uhrhammer²⁵¹, Valérie Bonadona²⁴⁹, Christine Lasset²⁴⁹, Pascaline Berthet²⁵², Laurent Castera²⁵², Dominique Vaur²⁵², Violaine Bourdon²⁵³, Catherine Noguès²⁵³, Tetsuro Noguchi²⁵³, Cornel Popovici²⁵³, Audrey Remenieras²⁵³, Hagay Sobol²⁵³, Isabelle Coupier²⁵⁴, Pascal Pujol²⁵⁴, Claude Adenis²⁵⁵, Aurélie Dumont²⁵⁵, Françoise Révillion²⁵⁵, Danièle Muller²⁵⁶, Emmanuelle Barouk-Simonet²⁵⁷, Françoise Bonnet²⁵⁷, Virginie Bubien²⁵⁷, Michel Longy²⁵⁷,

Nicolas Sevenet²⁵⁷, Laurence Gladieff²⁵⁸, Rosine Guimbaud²⁵⁸, Viviane Feillel²⁵⁸, Christine Toulas²⁵⁸, H el ene Dreyfus²⁵⁹, Christine Dominique Leroux²⁵⁹, Magalie Peysselon²⁵⁹, Christine Rebuschung²⁵⁹, Cl ementine Legrand²⁵⁹, Amandine Baurand²⁶⁰, Geoffrey Bertolone²⁶⁰, Fanny Coron²⁶⁰, Laurence Faivre²⁶⁰, Caroline Jacquot²⁶⁰, Sarab Lizard²⁶⁰, Caroline Kientz²⁶¹, Marine Lebrun²⁶¹, Fabienne Prieur²⁶¹, Sandra Fert-Ferrer²⁶², V eronique Mari²⁶³, Laurence V enat-Bouvet²⁶⁴, St ephane B ezieau²⁶⁵, Capucine Delnatte²⁶⁵, Isabelle Mortemousque²⁶⁶, Chrystelle Colas²⁶⁷, Florence Coulet²⁶⁷, Florent Soubrier²⁶⁷, Mathilde Warcoine²⁶⁷, Myriam Bronner²⁶⁸, Johanna Sokolowska²⁶⁸, Marie-Agn es Collonge-Rame²⁶⁹, Alexandre Damette²⁶⁹, Paul Gesta²⁷⁰, Hakima Lallaoui²⁷¹, Jean Chiesa²⁷², Denise Molina-Gomes²⁷³, Olivier Ingster²⁷⁴, Sylvie Manouvrier-Hanu²⁷⁵ and Sophie Lejeune²⁷⁵

KCONFAB

Morteza Aghmesheh²⁷⁶, Sian Greening²⁷⁶, David Amor²⁷⁷, Mike Gattas²⁷⁷, Leon Botes²⁷⁸, Michael Buckley²⁷⁸, Michael Friedlander²⁷⁸, Jessica Koehler²⁷⁸, Bettina Meiser²⁷⁸, Mona Saleh²⁷⁸, Elizabeth Salisbury²⁷⁸, Alison Trainer²⁷⁸, Kathy Tucker²⁷⁸, Yoland Antill²⁷⁹, Alexander Dobrovic²⁷⁹, Andrew Fellows²⁷⁹, Stephen Fox²⁷⁹, Marion Harris²⁷⁹, Sophie Nightingale²⁷⁹, Kelly Phillips²⁷⁹, Joe Sambrook²⁷⁹, Heather Thorne²⁷⁹, Shane Armitage²⁸⁰, Leanne Arnold²⁸⁰, Rosemary Balleine²⁸¹, Rick Kefford²⁸¹, Judy Kirk²⁸¹, Edwina Rickard²⁸¹, Patti Bastick²⁸², Jonathan Beesley²⁸³, Nick Hayward²⁸³, Amanda Spurdle²⁸³, Logan Walker²⁸³, John Beilby²⁸⁴, Christobel Saunders²⁸⁴, Ian Bennett²⁸⁵, Anneke Blackburn²⁸⁶, Michael Bogwitz²⁸⁷, Clara Gaff²⁸⁷, Geoff Lindeman²⁸⁷, Nick Pachter²⁸⁷, Clare Scott²⁸⁷, Adrienne Sexton²⁸⁷, Jane Visvader²⁸⁷, Jessica Taylor²⁸⁷, Ingrid Winship²⁸⁷, Meagan Brennan²⁸⁸, Melissa Brown²⁸⁹, Juliet French²⁸⁹, Stacey Edwards²⁸⁹, Matthew Burgess²⁹⁰, Jo Burke²⁹¹, Briony Patterson²⁹¹, Phyllis Butow²⁹², Bronwyn Culling²⁹², Liz Caldon²⁹³, David Callen²⁹⁴, Deepa Chauhan²⁹⁵, Maurice Eisenbruch²⁹⁵, Louise Heiniger²⁹⁵, Manisha Chauhan²⁹⁶, Alice Christian²⁹⁷, Joanne Dixon²⁹⁷, Alexa Kidd²⁹⁷, Paul Cohen²⁹⁸, Alison Colley²⁹⁹, Georgina Fenton²⁹⁹, Ashley Crook³⁰⁰, Rebecca Dickson³⁰⁰, Michael Field³⁰⁰, Deborah Marsh³⁰⁰, James Cui³⁰¹, Margaret Cummings³⁰², Sarah-Jane Dawson³⁰³, Anna DeFazio^{281,304}, Martin Delatycki³⁰⁵, Tracy Dudding³⁰⁶, Ted Edkins³⁰⁷, Gelareh Farshid³⁰⁸, James Flanagan³⁰⁹, Peter Fong³¹⁰, Laura Forrest³¹¹, David Gallego-Ortega³¹², Peter George³¹³, Grantley Gill³¹⁴, James Kollias³¹⁴, Eric Haan³¹⁵, Stewart Hart³¹⁶, Mark Jenkins³¹⁷, Clare Hunt³¹⁸, Sunil Lakhani^{283,319}, Lara Lipton³²⁰, Liz Lobb²⁹⁵, Graham Mann³²¹, Sue Anne McLachlan³²², Shona O'Connell³²³, Sarah O'Sullivan³²⁴, Ellen Pieper^{311,325}, Bridget Robinson³²⁶, Jodi Saunus^{302,327}, Elizabeth Scott³²⁸, Rodney Scott³²⁹, Andrew Shelling³³⁰, Peter Simpson³⁰², Rachael Williams³³¹ and Mary Ann Young³³²

²³⁰Pathology West ICPMR, Westmead, NSW, Australia. ²³¹Kolling Institute of Medical Research, University of Sydney, Royal North Shore Hospital, Sydney, NSW, Australia. ²³²Pathology North, John Hunter Hospital, Newcastle, NSW 2305, Australia. ²³³Department of Anatomical Pathology, ACT Pathology, Canberra Hospital, Canberra, ACT, Australia. ²³⁴ANU Medical School, Australian National University, Canberra, ACT, Australia. ²³⁵Department of Surgical Oncology, Calvary Mater Newcastle Hospital, Australian New Zealand Breast Cancer Trials Group, and School of Medicine and Public Health, University of Newcastle, Newcastle, NSW, Australia. ²³⁶School of Science and Health, The University of Western Sydney, Sydney, NSW, Australia. ²³⁷Hormones and Cancer Group, Kolling Institute of Medical Research, Royal North Shore Hospital, University of Sydney, Sydney, NSW, Australia. ²³⁸SydPath St Vincent's Hospital, Sydney, NSW, Australia. ²³⁹Department of Tissue Pathology and Diagnostic Oncology, Pathology West, Westmead Breast Cancer Institute, Westmead Hospital, Sydney, NSW, Australia. ²⁴⁰Centre for Information Based Medicine, Hunter Medical Research Institute, Sydney, NSW 2305, Australia. ²⁴¹Priority Research Centre for Cancer, School of Biomedical Sciences and Pharmacy, Faculty of Health, University of Newcastle, Callaghan, NSW, Australia. ²⁴²The University of Queensland, UQ Centre for Clinical Research and School of Medicine, Brisbane, QLD, Australia. ²⁴³Hereditary Cancer Clinic, St Vincent's Hospital, The Kinghorn Cancer Centre, Sydney, NSW 2010, Australia. ²⁴⁴Crown Princess Mary Cancer Centre, Westmead Hospital, Westmead, NSW, Australia. ²⁴⁵Sydney Medical School - Westmead, University of Sydney, Sydney, NSW, Australia. ²⁴⁶Department of Medical Oncology, The Canberra Hospital, Garran, ACT, Australia. ²⁴⁷St John of God Perth Northern Hospitals, Perth, WA, Australia. ²⁴⁸Unit e Mixte de G en etique Constitutionnelle des Cancers Fr equents, Hospices Civils de Lyon, Lyon, France. ²⁴⁹Centre L eon B erard, Lyon, France. ²⁵⁰Institut Gustave Roussy, Villejuif, France. ²⁵¹Centre Jean Perrin, Clermont-Ferrand, France. ²⁵²Centre Fran ois Baclesse, Caen, France. ²⁵³Institut Paoli Calmettes, Marseille, France. ²⁵⁴CHU Arnaud-de-Villeneuve, Montpellier, France. ²⁵⁵Centre Oscar Lambret, Lille, France. ²⁵⁶Centre Paul Strauss, Strasbourg, France. ²⁵⁷Institut Bergoni e, Bordeaux, France. ²⁵⁸Institut Claudius Regaud, Toulouse, France. ²⁵⁹CHU, Grenoble, France. ²⁶⁰CHU, Dijon, France. ²⁶¹CHU, St-Etienne, France. ²⁶²H otel Dieu Centre Hospitalier, Chamb ery, France. ²⁶³Centre Antoine Lacassagne, Nice, France. ²⁶⁴CHU, Limoges, France. ²⁶⁵CHU, Nantes, France. ²⁶⁶CHU Bretonneau, Tours and Centre Hospitalier de Bourges, Bourges, France. ²⁶⁷Groupe Hospitalier Piti e-Salp etri ere, Paris, France. ²⁶⁸CHU Vandoeuvre-les-, Nancy, France. ²⁶⁹CHU, Besan on, France. ²⁷⁰CHU Poitiers, Centre Hospitalier d'Angoul eme and Centre Hospitalier de Niort, Niort, France. ²⁷¹Centre Hospitalier de La Rochelle, La Rochelle, France. ²⁷²CHU Nimes, Car emeau, France. ²⁷³CHI, Poissy, France. ²⁷⁴CHU, Angers, France. ²⁷⁵CHRU, de Lille, France. ²⁷⁶Illawarra Cancer Care Centre Wollongong Hospital, Wollongong, Australia. ²⁷⁷Royal Children's Hospital, Melbourne, VIC, Australia. ²⁷⁸Prince of Wales Hospital, Randwick, NSW, Australia. ²⁷⁹Peter MacCallum Cancer Centre, East Melbourne, VIC, Australia. ²⁸⁰Royal Brisbane and Women's Hospital, Herston, QLD 4029, Australia. ²⁸¹Westmead Hospital, Westmead, NSW, Australia. ²⁸²St George Hospital, Kogarah, NSW, Australia. ²⁸³Queensland Institute of Medical Research, Herston, QLD, Australia. ²⁸⁴Queen Elizabeth Medical Centre, Nedlands, WA, Australia. ²⁸⁵Silverton Place, Brisbane, QLD, Australia. ²⁸⁶Australian National University, Canberra, Australia. ²⁸⁷The Royal Melbourne Hospital, Parkville, VIC, Australia. ²⁸⁸NSW Breast Cancer Institute, Westmead, NSW, Australia. ²⁸⁹University of Queensland, Queensland, QLD, Australia. ²⁹⁰Austin Health, Heidelberg, VIC, Australia. ²⁹¹Royal Hobart Hospital, Hobart, TAS, Australia. ²⁹²Royal Prince Alfred Hospital, Camperdown, NSW, Australia. ²⁹³Garvan Institute of Medical Research, Darlinghurst, NSW, Australia. ²⁹⁴University of Adelaide/Hanson Institute, Rundle Mall, SA, Australia. ²⁹⁵University of Sydney, Sydney, NSW, Australia. ²⁹⁶The Kinghorn Cancer Centre, Sydney, NSW, Australia. ²⁹⁷Wellington Hospital, Wellington, New Zealand. ²⁹⁸St John of God Subiaco Hospital, Subiaco, New Zealand. ²⁹⁹Liverpool Health Service, Liverpool, UK. ³⁰⁰Royal North Shore Hospital, St Leonards, NSW, Australia. ³⁰¹Monash University, Melbourne, VIC, Australia. ³⁰²University of Queensland Medical School, Herston, NSW, Australia. ³⁰³Cambridge University, Cambridge, UK. ³⁰⁴Westmead Institute for Cancer Research, Westmead, NSW, Australia. ³⁰⁵Heidelberg Repatriation Hospital, Heidelberg Heights, VIC, Australia. ³⁰⁶Hunter Area Health Service, Waratah, USA. ³⁰⁷Princess Margaret Hospital for Children, Perth, WA, Australia. ³⁰⁸IMVS, Adelaide, SA, Australia. ³⁰⁹Imperial College London, London, UK. ³¹⁰Auckland City Hospital, Auckland, New Zealand. ³¹¹Parkville Familial Cancer Centre, Melbourne, VIC, Australia. ³¹²The Kinghorn Cancer Centre, Darlinghurst, NSW, Australia. ³¹³Canterbury Health Labs, Christchurch, New Zealand. ³¹⁴Royal Adelaide Hospital, Adelaide, SA, Australia. ³¹⁵Women's and Children's Hospital, North Adelaide, NSW, Australia. ³¹⁶Monash Medical Centre, Bentleigh, VIC, Australia. ³¹⁷University of Melbourne, Melbourne, VIC, Australia. ³¹⁸Monash Medical Centre, Melbourne, VIC, Australia. ³¹⁹The Royal Brisbane & Women's Hospital, Herston, QLD, Australia. ³²⁰Western Hospital, Footscray, VIC, Australia. ³²¹Westmead Millennium Institute, Westmead, NSW, Australia. ³²²St Vincent's Hospital, Fitzroy, VIC, Australia. ³²³Southern Health Familial Cancer Centre, Clayton, VIC, USA. ³²⁴Agnes Walsh House, Subiaco, WA, Australia. ³²⁵Genomic Medicine, Melbourne, VIC, Australia. ³²⁶Christchurch Hospital, Christchurch, New Zealand. ³²⁷Women's Hospital, Herston, QLD, Australia. ³²⁸South View Clinic, Kogarah, NSW, Australia. ³²⁹John Hunter Hospital, New Lambton Heights, NSW 2305, Australia. ³³⁰University of Auckland, Auckland, New Zealand. ³³¹St Vincent's Hospital, Darlinghurst, NSW, Australia. ³³²GenomeOne, Darlinghurst, NSW, Australia.