Human Mutation

WILEY

SPECIAL ISSUE From Inheritance to Outcome: Germline Mutations
Driving disease progression, prognosis and therapy

REVIEW ARTICLE OPEN ACCESS

A Landscape of Pathogenic Variants and Genetic Counseling in Hereditary Breast Cancer in Latin America and the Caribbean: A Scoping Review

Sebastián Morales[1,2] | Dante Palma-Ruiz[3] | Liliana Zúñiga-Venegas[4,5,6] | Sandra Romero[7] | Ricardo Fernández-Ramires[1,8] | Pablo Alarcón[3,9] | María Teresa Muñoz-Quezada[6,10] | Paula Celis[11] | Romain Boidot[3,12] | Natalia Landeros[3,6,13]

[1]Grupo Chileno de Cáncer Hereditario (GCCH), Santiago, Chile | [2]Centro de Oncología de Precisión, Facultad de Medicina y Ciencias de la Salud, Universidad Mayor, Santiago, Chile | [3]Programa Regional de Cáncer Hereditario, Facultad de Medicina, Universidad Católica del Maule, Talca, Chile | [4]Centro de Investigación de Estudios Avanzados del Maule, Vicerrectoría de Investigación y Post-Grado, Universidad Católica del Maule, Talca, Chile | [5]Facultad de Ciencias de la Salud, Universidad Católica del Maule, Talca, Chile | [6]Centro para la Prevención y el Control del Cáncer (CECAN), Santiago, Chile | [7]Facultad de Ciencias de la Salud y Bienestar Humano, Universidad Tecnológica Indoamérica, Quito, Ecuador | [8]Escuela de Tecnología Médica, Facultad de Medicina y Ciencias de la Salud, Universidad Mayor, Santiago, Chile | [9]Sección Genética Clínica, Hospital Clínico Universidad de Chile, Santiago, Chile | [10]Programa de Epidemiología, Escuela de Salud Pública, Facultad de Medicina, Universidad de Chile, Santiago, Chile | [11]Hospital Regional de Talca (HRT), Talca, Chile | [12]Unit of Molecular Biology, Centre Georges-Francois Leclerc, Dijon, France | [13]Laboratorio de Genómica, Bioinformática y Biosensores Aplicados, Facultad de Medicina, Universidad Católica del Maule, Talca, Chile

Correspondence: Natalia Landeros (nlanderos@ucm.cl)

Received: 24 March 2026 | **Revised:** 3 September 2026 | **Accepted:** 5 October 2026

Guest Editor: Zhijia Xia

Keywords: genetic counseling | health equity | hereditary breast cancer | Latin America and the Caribbean | pathogenic variants | susceptibility

ABSTRACT

Hereditary breast cancer (HBC) accounts for an estimated 15% of breast cancer diagnoses worldwide and is primarily driven by pathogenic variants (PVs) in high- and moderate-penetrance susceptibility genes. Current clinical guidelines recommend genetic counseling and multigene testing for individuals with suspected HBC. However, across Latin America and the Caribbean (LAC), structural inequities persist in access to molecular diagnostics, specialized genetics services, and systematic variant interpretation frameworks, resulting in underdiagnosis, limited representation of regional populations in genomic databases, and asymmetries in the clinical implementation of precision oncology. We systematically reviewed the literature to identify studies reporting pathogenic or likely pathogenic germline variants in HBC susceptibility genes among LAC populations. A total of 120 studies from multiple countries were included. Overall, 202 PVs were identified in *BRCA1* and 199 in *BRCA2*. Furthermore, 180 PVs were identified in 15 high- and moderate-risk genes associated with HBC, whereas 102 PVs were reported in 52 rare susceptibility genes. Our synthesis reveals substantial heterogeneity in the distribution of PVs across countries, recurrent population-specific variants, and a strong predominance of *BRCA1*/2-focused studies, despite growing use of broader genomic testing approaches. Importantly, the availability of genetic counseling and publicly funded testing remains highly uneven, with fragmented implementation and limited integration into national cancer control strategies. Together, these findings highlight a critical gap between the expanding genomic knowledge base and its translation into clinical practice in LAC.

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

Copyright © 2026 Sebastián Morales et al. *Human Mutation* published by John Wiley & Sons Ltd.

1 | Introduction

Breast cancer (BC) is a major public health concern and is the most frequently diagnosed cancer among women worldwide, with incidence and mortality patterns that vary across populations and regions. In 2022, an estimated 2.3 million new cases were reported, accounting for 11.6% of all cancers diagnosed, along with 684,996 deaths, making BC the leading cause of cancer-related mortality in women globally, surpassing lung cancer [1]. BC is a complex, multifactorial disease that arises from the progressive accumulation of genomic and epigenomic alterations [2, 3]. Among established risk factors, family history remains one of the strongest, with up to one quarter of cases showing some degree of familial aggregation. Compared with the general population, women with a first-degree relative diagnosed with BC have a substantially increased lifetime risk [4].

1.1 | Genetic Predisposition for Hereditary Breast Cancer (HBC) Syndrome

HBC is clinically defined by the presence of personal and/or family history patterns, together with molecular evidence based on the identification of germline pathogenic or likely pathogenic variants (PVs) in validated cancer susceptibility genes [5]. HBC may account for up to 25% of all BC cases [6, 7]. Most hereditary cases are attributable to high-penetrance PVs in genes such as *BRCA1* [8], *BRCA2* [9], *CDH1* [10], *PALB2* [11], *PTEN* [12], *STK11* [13], and *TP53* [14]. Additionally, moderate-penetrance genes, including *ATM* [15], *BARD1* [16], *BRIP1* [17], *CHEK2* [18], *NF1* [19], *RAD51C* [20], and *RAD51D* [20], have been consistently implicated in BC susceptibility.

These genes are involved primarily in DNA damage repair pathways and/or cell cycle regulation [21]. Carriers of PVs in *BRCA1* or *BRCA2* face a markedly elevated lifetime risk of BC, reaching up to 87%, as do those with up to 50% risk for ovarian cancer. However, this estimated risk varies according to the specific PVs, family history, ancestry, and geographic context [22]. Despite notable advances in hereditary cancer genomics, the full spectrum and population distribution of PVs are still not fully characterized in ethnically diverse populations, including those of Latin America and the Caribbean (LAC). This knowledge gap is further compounded by limited access to genetic counseling and molecular testing across much of the region.

1.2 | HBC in LAC Populations

LAC includes 43 countries characterized by remarkable cultural, geographic, and genetic diversity. The region represents approximately 8.4% of the global population and accounted for an estimated 1.5 million new cancer cases in 2022 [1], with a steadily increasing cancer burden compared with other regions worldwide [23]. The genetic architecture of LAC populations reflects a complex demographic history shaped by centuries of migration, colonization, and admixture. However, important differences in ancestry exist across the region. Whereas mainland Latin American populations generally exhibit varying proportions of Indigenous American, European (predominantly Iberian and Southern European), and African ancestries, Caribbean populations are characterized by a substantially greater African ancestral contribution resulting from the transatlantic slave trade, together with European and, to a lesser extent, Indigenous ancestries [24]. These distinct ancestry patterns have contributed to differences in allele frequencies, founder effects, and the distribution of PVs among populations, underscoring the importance of considering population genetic structure when investigating HBC susceptibility across LAC [24].

Compared with high-income countries such as the United States of America and Western Europe, marked disparities in BC incidence and mortality exist across regions [25, 26]. Although the overall BC incidence in LAC is lower than that in more developed regions, mortality rates are disproportionately high, largely reflecting delayed diagnosis, limited access to specialized care, and structural constraints within public health systems [27, 28]. Argentina and Uruguay represent notable exceptions, exhibiting higher incidence rates that have been attributed, in part, to greater European ancestry contributions [29]. In 2020, Argentina and Uruguay reported the highest age-standardized BC incidence rates in the region (73.1 and 65.1 per 100,000, respectively), whereas Bolivia reported the lowest (25.5 per 100,000) [25]. The mortality rates followed a similar pattern, with Uruguay (20.1 per 100,000) and Argentina (18.9 per 100,000) having the highest values, whereas Bolivia had the lowest.

In several LAC countries, including Peru, Colombia, and Mexico, approximately 50% of BC cases are diagnosed at advanced stages, substantially reducing survival and increasing healthcare costs [27]. The proportion of young women diagnosed with BC in LAC is nearly double that reported in more developed regions, and the prevalence of triple-negative BC, an aggressive subtype with limited targeted treatment options, is greater [27]. These patterns suggest that a substantial fraction of BC patients in LAC would meet the current criteria for hereditary cancer genetic testing [30, 31]. Nevertheless, access to genetic testing to identify PV and oncological genetic counseling remains highly uneven and is frequently restricted to the private sector.

Available evidence confirms that *BRCA1* and *BRCA2* testing can identify PVs in LAC women, although detection rates vary considerably across populations and ancestral backgrounds, particularly among nonwhite populations [32]. Given the pronounced genetic heterogeneity of the region, integrating this diversity into risk assessment models, testing criteria for genetic studies, and prevention strategies is essential. This scoping review, therefore, examines the extent to which published evidence has moved beyond the *BRCA1-centric* and *BRCA2*-centric paradigms by expanding the use of multigene panels tailored to the regional mutational landscapes. In this context, systematic mapping of the genes analyzed, the reported PVs, and the organization of genetic counseling services is necessary to assess the current scope of multigene testing in the region and to identify gaps in the available evidence.

2 | Methods

2.1 | Study Design

We conducted a scoping review to map and describe published evidence on germline PVs in high- and moderate-risk BC susceptibility genes in LAC populations, including *ATM*, *BARD1*,

BRIP1, *CDH1*, *CHEK2*, *EPCAM*, *MLH1*, *MSH2*, *MSH6*, *NF1*, *PALB2*, *PMS2*, *PTEN*, *RAD51C*, *RAD51D*, *STK11*, and *TP53*, to identify gaps relevant to the implementation of genomic medicine in HBC. The review followed core methodological principles for scoping reviews and was reported in accordance with relevant items from the PRISMA extension for scoping reviews (PRISMA-ScR), where applicable [33].

2.2 | Information Sources and Search Strategy

An expanded literature search was performed in PubMed and SciELO, covering the period from January 1, 2000, to November 2025, and publications in English, Portuguese, or Spanish were considered. The search strategy combined four conceptual blocks: (1) HBC, (2) germline variants, (3) geographical descriptors for LAC, and (4) high- and moderate-risk genes recommended by clinical guidelines for HBC testing. The full PubMed search strategy is provided in File S1.

Before the search strategy was finalized, an initial set of potentially relevant studies was assembled through unstructured searches and expert knowledge within the author team. The final search strategy was calibrated to maximize the retrieval of this preidentified corpus and to ensure the sensitivity and completeness of evidence capture, which is consistent with the exploratory and mapping aims of scoping reviews. Among the 120 studies included in the review, 98 were retrieved through structured database searches, and 22 were identified through alternative sources (earlier unstructured searches, manual screening of reference lists, and expert recommendations). These identification pathways are presented in the PRISMA flow diagram for scoping reviews (Figure 1).

2.3 | Eligibility Criteria

We considered original research articles, clinical series, single case reports, and publications from clinical consortia or registries reporting germline variants in high- or moderate-risk cancer susceptibility genes among individuals with BC from LAC. Consistent with the scoping review design, no restrictions were applied regarding study design, sample size, or clinical setting to capture the breadth of available evidence.

We excluded studies if they (1) included BC patients not selected according to hereditary cancer criteria as the main study population; (2) reported only somatic variants in the selected genes; or (3) were reviews, meta-analyses, editorials, commentaries, or letters without primary genetic data. Systematic reviews and meta-analyses were not included as primary evidence; however, their reference lists were screened to identify additional eligible primary studies.

2.4 | Study Selection

All records retrieved from the database searches were imported into a reference management tool, and duplicates were removed. Titles and abstracts were independently screened by two reviewers to assess potential relevance according to the eligibility criteria. The full texts of records deemed potentially eligible by at least one reviewer were obtained and evaluated in detail. The same eligibility criteria and selection process were applied to studies identified through alternative sources (nonstructured searches, citation chasing, and expert suggestions). Discrepancies between reviewers were resolved by

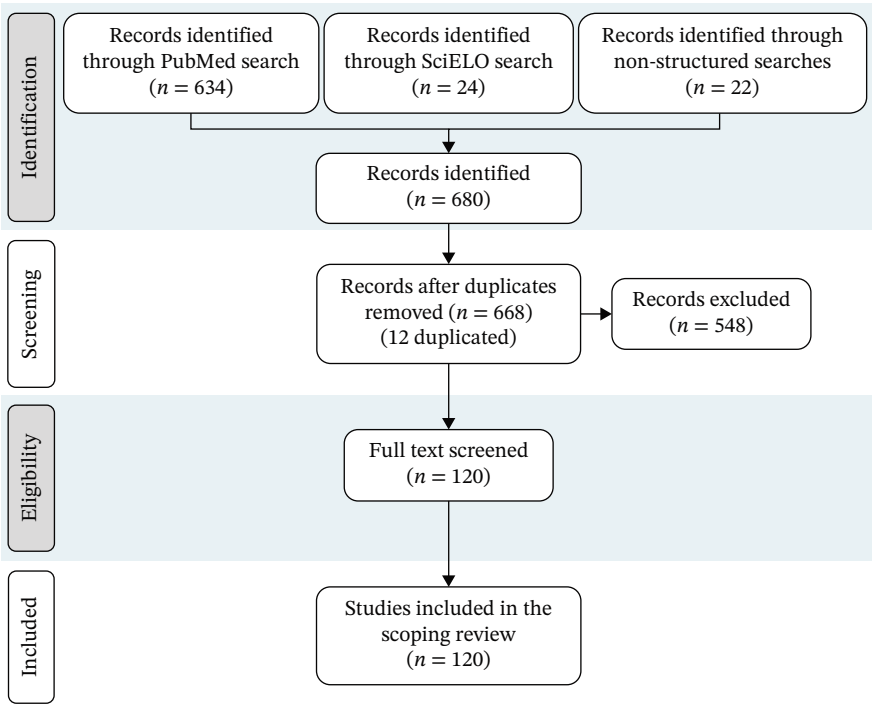


FIGURE 1 | PRISMA extension for scoping reviews (PRISMA-ScR) flow diagram. The figure summarizes the identification, screening, and inclusion of studies reporting germline pathogenic/likely pathogenic variants in high- and moderate-risk breast cancer susceptibility genes in Latin America and the Caribbean. A total of 680 records were identified (PubMed, $n = 634$; SciELO, $n = 24$; nonstructured searches, $n = 22$). After the removal of 12 duplicates, 668 records were screened by title and abstract, and 120 studies were included following full-text assessment.

discussion and, when necessary, by consultation with a third reviewer.

2.5 | Data Charting and Synthesis

For each included study, the following key characteristics were charted via a standardized extraction form: study design, country or countries represented, period of data collection, clinical criteria used to define HBC, genes and panels analyzed, sequencing or genotyping methods, spectrum and frequency of detected germline/likely PVs, ancestry-related information when reported, and any description of genetic counseling or testing pathways.

Given the heterogeneity of the study design, gene panels, and reporting practices across countries and time periods, we did not conduct a formal risk-of-bias assessment or quantitative meta-analysis. The findings were synthesized descriptively, organizing the evidence into thematic domains aligned with the review objective: (i) overall distribution of germline PVs in high- and moderate-risk genes across LAC, (ii) country-specific patterns, (iii) evidence on founder or recurrent variants and ancestral background, and (iv) organization of hereditary cancer services, testing pathways, and identified knowledge gaps.

2.6 | Harmonization and Classification of Variants

All pathogenic and likely PVs reported in the original publications were independently reviewed and selected. Variant nomenclature was standardized according to the recommendations of the Human Genome Variation Society (www.HGVS.org/varnomen), the international standard for sequence variant description in clinical and research genomics. Additionally, corresponding dbSNP identifiers (rsIDs), when available, were retrieved from public variant databases and incorporated to facilitate variant traceability and cross-study comparison. Subsequently, the clinical interpretation of the variants was verified according to current ACMG/AMP guidelines, using public databases and peer-reviewed classifications [34]. Only variants currently classified as pathogenic or likely pathogenic were included in Tables 1, 2, 3 and 4. Variants originally reported as pathogenic or likely pathogenic in the source publications but currently classified as variants of uncertain significance were excluded from this review. This harmonization process reduced redundancy arising from nomenclature differences and minimized duplicate counts of variants reported in studies.

3 | Results

3.1 | PVs in Susceptibility Genes in the Latin American Population With HBC

The identification of PVs associated with hereditary cancers has significant clinical implications for carrier patients and their relatives [28]. Through genetic counseling, these findings facilitate enhanced surveillance and follow-up of both affected patients and healthy carrier relatives, who are at increased risk of developing cancer [28, 146]. Currently, the LAC population remains underrepresented in international genomic databases. The prevalence and impact of PVs in the main genes associated with BC in the region are not yet fully understood [28].

As this scoping review did not include a quantitative meta-analysis, the raw PV counts per country presented in Figure 2 and throughout this section should not be interpreted as directly comparable measures of biological variant diversity across countries. Countries contributing a larger number of studies, larger cohorts, or broader multigene testing panels are expected to report proportionally more PVs regardless of the underlying prevalence of HBC in that population. Apparent differences between countries may therefore reflect disparities in testing intensity, panel breadth, and research funding rather than true differences in the frequency or diversity of PVs.

The Brazilian population represents the most studied population in LAC in the context of HBC. Despite these advances, considerable barriers persist in its nationwide implementation. In the public health system, access to genetic counseling is limited by the availability of human and financial resources. Services are often concentrated in large urban centers, making access difficult for populations in remote regions. Additionally, the lack of integration of genetic testing into public health system clinical protocols delays the diagnosis and proper management of hereditary syndromes such as HBC, hereditary ovarian cancer, or Lynch syndrome. Recent studies have highlighted disparities in coverage, showing a greater proportion of patients in the private sector accessing these services than in the public sector [147].

In the Brazilian population, 91 PVs were identified for *BRCA1* (Figure 2A), and 85 PVs were identified for *BRCA2* (Figure 2B). In *BRCA1*, the most recurrent PVs include c.68_69delAG [35–39], c.3331_3334del [35, 38–41, 50, 75–78, 90–92, 104], c.5266dupC [35, 37, 39–41, 50, 65, 77–80, 90–102], and c.211A>G [37–40, 75–80]. In *BRCA2*, frequently identified PVs include c.9382C>T [38, 39, 65, 78, 90, 91, 104, 110], c.2808_2811del [39, 41, 65, 77, 78, 90–92, 98, 110], and c.6405_6409del [38, 39, 41, 78, 79, 90, 94, 97, 110]. In addition to affecting *BRCA* genes, Brazil has a unique founder effect on *TP53*, where the p.Arg337His variant has been consistently reported at high prevalence [38, 65, 75–80, 91, 94, 95, 102, 130–138]. Additionally, PVs have been described in other high- and moderate-risk genes (Figure 2C), including *CHEK2* (e.g., c.1100delC, c.846+1G>C, and p.Arg-117Gly) [75, 77–80, 94, 95, 102, 104, 121, 129] and c.1187G>A *in MUTYH* [38, 77–79, 94, 95]. Despite advances in integrating genetic counseling into the public health system, challenges remain, particularly with respect to unequal access between urban and remote areas. The coexistence of founder variants and marked molecular heterogeneity underscore the importance of implementing multigene panels adapted to the Brazilian mutational landscape to improve prevention and clinical management.

The Chilean population has an admixed genetic background, with predominant European and Amerindian ancestry components and smaller African contributions, with regional variation in admixture proportions [148]. This population structure should be considered when interpreting the distribution of germline variants and allele frequencies reported

TABLE 1 | Pathogenic or likely pathogenic variants of the *BRCA1* gene reported in patients with hereditary breast cancer from two or more countries in Latin America and the Caribbean.

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80357914	c.68_69del	p.Glu23fs	Brazil	[35–41]
			Chile	[42–49]
			Argentina	[50–54]
			Mexico	[50, 55–57]
			Colombia	[58]
			Bahamas	[59, 60]
			Uruguay	[61]
			Peru	[62–64]
rs28897696	c.5123C>A	p.Ala1708Glu	Brazil	[38, 65, 66]
			Colombia	[50, 58, 67–71]
			Mexico	[49, 56, 57, 72, 73]
			Venezuela	[50]
			Argentina	[54]
			Peru	[63, 64]
			Guatemala	[74]
rs80357382	c.211A>G	p.Arg71Gly	Brazil	[37–40, 75–81]
			Argentina	[50, 51, 54, 72, 82, 83]
			Mexico	[49, 50, 55, 56, 73, 84, 85]
			Chile	[43]
			Peru	[64]
			Guatemala	[74]

(Continues)

TABLE 1 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs41293455	c.4327C>T	p.Arg1443Ter	Brazil	[77, 86]
			Mexico	[49, 55, 56, 72]
			Trinidad and Tobago	[59, 87]
			Guatemala	[74]
			Argentina	[54]
			Peru	[64]
rs80357868	c.3756_3759del	p.Ser1253fs	Chile	[42]
			Brazil	[39, 88]
			Guatemala	[89]
			Barbados	[70]
			Peru	[63]
			Mexico	[57]
rs80357906	c.5266dup	p.Gln1756fs	Brazil	[35, 37, 39–41, 50, 65, 77–81, 88, 90–103]
			Argentina	[50, 52–54]
			Mexico	[56]
			Chile	[42, 43]
			Peru	[64]
rs41293463	c.5324T>G	p.Met1775Arg	Bahamas	[59, 60]
			Colombia	[69]
			Trinidad and Tobago	[59]
			Cayman Islands	[59]
rs80357724	c.798_799del	p.Ser267fs	Brazil	[39, 77, 81, 95]
			Argentina	[51]
			Mexico	[56]
			Guatemala	[74]
			Peru	[64]

(Continues)

TABLE 1 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80357701	c.3331_3334del	p.Gln1111fs	Brazil	[35, 38–41, 50, 75–78, 81, 88, 90–92, 103, 104]
			Chile	[42–44, 47]
			Colombia	[50, 67, 71, 72, 105]
			Trinidad and Tobago	[59]
rs80358042	c.212+1G>A	—	Guatemala	[72, 74, 89]
			Colombia	[71]
			Chile	[42]
			Mexico	[56]
rs80358086	c.4986+6T>C	—	Bahamas	[59, 60]
			Brazil	[78]
			Peru	[50]
			Trinidad and Tobago	[59]
rs387906563	c.815_824dup	p.Thr276fs	Peru	[62, 64, 106]
			Guatemala	[74]
			Mexico	[57, 85]
			Bahamas	[59]
rs80357580	c.5030_5033del	p.Thr1677fs	Argentina	[51]
			Mexico	[50]
			Brazil	[90]
rs28897672	c.181T>G	p.Cys61Gly	Chile	[43, 44, 47, 48]
			Brazil	[37, 38, 90, 98]
			Argentina	[50, 51, 82]
rs80357892	c.3365_3366del	p.Thr1122fs	Barbados	[59]
			Jamaica	[59]
			Trinidad and Tobago	[59]

(Continues)

TABLE 1 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80357123	c.5251C>T	p.Arg1751Ter	Brazil	[39, 41, 75, 78, 90, 92, 98]
			Mexico	[73]
			Peru	[64]
rs55770810	c.5095C>T	p.Arg1699Trp	Brazil	[41]
			Mexico	[56]
			Peru	[64]
rs80357579	c.3770_3771del	p.Glu1257fs	Brazil	[95]
			Colombia	[58]
			Mexico	[57]
rs80357208	c.3817C>T	p.Gln1273Ter	Chile	[42, 43, 45, 107]
			Brazil	[39]
rs80356936	c.303T>A	p.Tyr101Ter	Chile	[42, 43]
			Brazil	[39]
rs80357389	c.4484G>T	p.Arg1495Met	Brazil	[37, 41, 92, 99, 103]
			Peru	[64]
rs80357954	c.1088del	p.Asn363fs	Peru	[64]
			Brazil	[41, 90]
rs80356898	c.1687C>T	p.Gln563Ter	Brazil	[37–41, 50, 79, 90, 92, 94, 95, 102]
			Argentina	[54]
rs80357887	c.470_471del	p.Leu156_Ser157insTer	Brazil	[39, 40, 75, 77, 78, 81, 90]
			Chile	[42]
rs80359876	c.4964_4982del	p.Ser1655fs	Brazil	[78, 81, 90]
			Argentina	[54]
rs80357729	c.3627dup	p.Glu1210fs	Chile	[42]
			Argentina	[51]

(Continues)

TABLE 1 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80357842	c.3858_3861del	p.Ser1286fs	Mexico	[55, 56, 84]
			Chile	[43, 47]
rs80357520	c.3759_3760del	p.Lys1254fs	Mexico	[49, 55, 56]
			Peru	[62]
rs886037993	c.1961_1962del	p.Lys654fs	Brazil	[65]
			Peru	[62, 64]
rs80357933	c.1912del	p.Glu638fs	Brazil	[90]
			Colombia	[105]
rs80357714	c.1380dup	p.Phe461fs	Brazil	[65]
			Colombia	[105]
rs886039955	c.1504_1507del	p.Leu502fs	Chile	[42, 43]
			Argentina	[51]
rs80357136	c.3403C>T	p.Gln1135Ter	Brazil	[35]
			Costa Rica	[108]
rs11571658	c.6275_6276del	p.Leu2092fs	Chile	[47, 107]
			Colombia	[67, 71]
rs80358027	c.4357+1G>C	—	Bahamas	[59, 60]
			Brazil	[78, 90, 92]
rs80357848	c.3764dup	p.Asn1255fs	Brazil	[90]
			Trinidad and Tobago	[59]
rs80357867	c.5177_5180del	p.Arg1726fs	Brazil	[41, 94]
			Trinidad and Tobago	[59]
rs80357635	c.3228_3229del	p.Gly1077fs	Brazil	[41, 92, 97, 109]
			Bahamas	[59]
rs398122674	c.3599_3600del	p.Gln1200fs	Chile	[44]
			Cayman Islands	[59]

(Continues)

TABLE 1 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80357695	c.2389_2390del	p.Glu797fs	Brazil	[99]
			Trinidad and Tobago	[87]
rs80356991	c.427G>T	p.Glu143Ter	Brazil	[95]
			Argentina	[51]
rs41293465	c.5503C>T	p.Arg1835Ter	Colombia	[105]
			Brazil	[37]
rs80357508	c.4065_4068del	p.Asn1355fs	Chile	[43]
			Mexico	[56, 57]
rs62625307	c.3598C>T	p.Gln1200Ter	Brazil	[41, 94]
			Mexico	[49]
rs80357812	c.2766del	p.Val923fs	Trinidad and Tobago	[87]
			Peru	[64]
rs80357064	c.190T>C	p.Cys64Arg	Argentina	[54]
			Brazil	[39, 78]
rs398122670	c.2901_2902dup	p.Pro968fs	Argentina	[54]
			Peru	[64]
rs80357893	c.2910dup	p.His971fs	Brazil	[41]
			Peru	[64]

Abbreviations: —, intronic variant; HGVS, Human Genome Variation Society; NR, not reported or not available in the ClinVar/dbSNP at the time of publication.

TABLE 2 | Pathogenic or likely pathogenic variants of the *BRCA2* gene reported in patients with HBC from two or more countries in Latin America and the Caribbean.

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80359550	c.5946del	p.Ser1982fs	Chile	[42–44, 47]
			Brazil	[41, 92, 97, 104, 110]
			Peru	[63, 106]
			Costa Rica	[108]
			Argentina	[52, 53]
rs80359351	c.2808_2811del	p.Ala938Profs	Brazil	[39, 41, 65, 77, 78, 90–92, 98, 110]
			Colombia	[67, 69, 71, 105]
			Peru	[62]
			Chile	[42]
			Argentina	[52, 53]
			Nicaragua	[111]
rs80359554	c.6024dup	p.Gln2009fs	Colombia	[58, 71, 112]
			Chile	[42]
			Mexico	[56, 85]
			Brazil	[39, 102]
			Argentina	[54]
			Peru	[64]
rs80359212	c.9382C>T	p.Arg3128Ter	Brazil	[38, 39, 65, 78, 90, 91, 104, 110]
			Chile	[42, 43]
			Trinidad and Tobago	[59, 87]
			Guatemala	[74]
rs80359507	c.5351dup	p.Asn1784fs	Uruguay	[113]
			Brazil	[41]
			Paraguay	[114]
			Argentina	[53, 54, 83]

(Continues)

TABLE 2 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs80359277	c.1310_1313del	p.Lys437fs	Bahamas	[59, 60]
			Brazil	[88, 94]
			Barbados	[59]
			Peru	[64]
rs80359604	c.658_659del	p.Val220fs	Brazil	[79, 90]
			Peru	[64]
			Guatemala	[89]
			Mexico	[85]
rs80359584	c.6405_6409del	p.Asn2135fs	Brazil	[38, 39, 41, 78, 79, 81, 90, 94, 97, 110]
			Chile	[42]
			Mexico	[84]
rs80359406	c.3860del	p.Asn1287fs	Uruguay	[113]
			Colombia	[69, 71]
			Brazil	[75, 103]
rs80358824	c.5909C>A	p.Ser1970Ter	Brazil	[79]
			Haiti	[59]
			Trinidad and Tobago	[59]
rs80359479	c.5073dup	p.Trp1692fs	Peru	[69]
			Brazil	[90, 94]
			Cayman Islands	[59]
rs80357832	c.2806_2809del	p.Lys936fs	Colombia	[72]
			Guatemala	[74]
			Mexico	[56]
rs80359577	c.6373del	p.Thr2125fs	Barbados	[59]
			Trinidad and Tobago	[87]
			Haiti	[59]

(Continues)

TABLE 2 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs568027879	c.632-3C>G	—	Barbados	[59]
			Colombia	[71]
			Dominican Republic	[59]
rs864622401	c.4740_4741dup	p.Glu1581fs	Chile	[42, 43, 98, 107]
			Argentina	[53]
			Brazil	[39]
rs80358972	c.7480C>T	p.Arg2494Ter	Puerto Rico	[115]
			Mexico	[84]
			Brazil	[39]
rs864622200	c.8987T>A	p.Leu2996Ter	Chile	[42, 43]
			Argentina	[83]
			Mexico	[85]
rs80359527	c.5681dup	p.Tyr1894Ter	Argentina	[83]
			Paraguay	[114]
			Brazil	[41, 90, 104]
rs80359741	c.9026_9030del	p.Tyr3009fs	Peru	[64]
			Brazil	[91]
			Argentina	[54]
rs80358981	c.7558C>T	p.Arg2520Ter	Jamaica	[116]
			Colombia	[71]
			Mexico	[57]
rs80359380	c.3264dup	p.Gln1089fs	Brazil	[104, 110]
			Mexico	[56, 73]
rs80359537	c.5796_5797del	p.His1932fs	Venezuela	[117]
			Argentina	[52]

(Continues)

TABLE 2 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs1555282054	c.1760del	p.Thr587fs	Colombia	[72]
			Argentina	[72]
rs28897743	c.7007G>A	p.Arg2336His	Mexico	[72]
			Brazil	[41, 95]
rs397507637	c.2701del	p.Ala902fs	Brazil	[37, 110]
			Colombia	[68, 112]
rs80358547	c.2T>G	p.Met1Arg	Brazil	[38, 39, 41, 66, 75, 77, 81, 88, 90, 110]
			Argentina	[72]
rs80359283	c.1389_1390del	p.Val464fs	Uruguay	[113]
			Brazil	[75][75]
rs41293513	c.8168A>G	p.Asp2723Gly	Mexico	[55, 118]
			Chile	[43]
rs80358435	c.145G>T	p.Glu49Ter	Chile	[42, 43]
			Mexico	[56, 73]
rs80358638	c.3922G>T	p.Glu1308Ter	Argentina	[72]
			Puerto Rico	[115, 119]
rs80359303	c.1763_1766del	p.Asn588fs	Colombia	[69, 71, 112]
			Trinidad and Tobago	[59, 87]
rs1131692274	c.1736T>G	p.Leu579Ter	Barbados	[59]
			Haiti	[59]
rs80359264	c.1138del	p.Ser380fs	Brazil	[39, 41, 90, 92, 95]
			Argentina	[83]
rs80356991	c.427G>T	p.Glu143Ter	Argentina	[83]
			Brazil	[95]
rs276174854	c.5146_5149del	p.Tyr1716fs	Chile	[42, 43]
			Mexico	[85]

(Continues)

TABLE 2 | (CONTINUED)

rsID	HGVS nucleotide change	HGVS amino acid change	Country	Reference
rs276174813	c.1796_1800del	p.Thr598_Ser599insTer	Brazil	[81, 110]
			Puerto Rico	[119]
rs80359152	c.9004G>A	p.Glu3002Lys	Mexico	[73]
			Brazil	[41, 120]
rs80359598	c.6486_6489del	p.Lys2162fs	Puerto Rico	[115]
			Mexico	[56]
rs80358452	c.1670T>G	p.Leu557Ter	Argentina	[52]
			Brazil	[39]
rs80359525	c.5616_5620del	p.Lys1872fs	Colombia	[58]
			Brazil	[39]
rs397507954	c.8023A>G	p.Ile2675Val	Brazil	[90]
			Peru	[64]
rs397507422	c.9235del	p.Val3079fs	Guatemala	[89]
			Peru	[64]
rs80359505	c.5303_5304del	p.Leu1768fs	Costa Rica	[108]
			Peru	[64]
rs80359803	c.8754G>A	p.Glu2918Ter	Mexico	[56]
			Peru	[64]
rs397507952	c.8021dup	p.Ile2675fs	Peru	[64]
			Argentina	[82]
rs45580035	c.9154C>T	p.Arg3052Trp	Mexico	[57]
			Brazil	[81, 88]

Abbreviations: —, intronic variant; HGVS, Human Genome Variation Society; NR, not reported or not available in the ClinVar/dbSNP at the time of publication.

TABLE 3 | Pathogenic or likely pathogenic variants found in other high- and moderate-penetrance genes in the population of Latin Americans and the Caribbean with hereditary breast cancer.

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
ATM	rs786204433	c.5644C>T	p.Arg1882Ter	Brazil	1/2000	[127]
				Brazil	2/157	[62]
	rs377349459	c.7913G>A	p.Trp2638Ter	Brazil	1/219	[54]
				Brazil	1/1682	[52]
				Brazil	1/173	[45]
	rs587779834	c.3802del	p.Glu1267_ Val1268insTer	Brazil	2/370	[55]
				Brazil	4/1663	[40]
				Brazil	1/701	[49]
	rs730881294	c.8264_8268del	p.Tyr2755fs	Brazil	1/173	[45]
				Colombia	1/197	[121]
	rs1060501627	c.4906C>T	p.Gln1636Ter	Brazil	1/370	[55]
				Brazil	2/1156	[65]
	rs786204543	c.640del	p.Ser214fs	Brazil	2/157	[62]
				Brazil	1/1663	[40]
	rs80159221	c.1236-2A>G	—	Brazil	1/701	[49]
				Brazil	1/1682	[52]
	rs746235533	c.67C>T	p.Arg23Ter	Brazil	1/370	[55]
	rs587779815	c.1339C>T	p.Arg447Ter	Brazil	1/370	[55]
	rs780619951	c.2413C>T	p.Arg805Ter	Brazil	1/701	[49]
	rs1057516250	c.2999del	p.Asn1000fs	Brazil	1/370	[55]
	rs2135801723	c.4575dup	p.Pro1526fs	Brazil	1/701	[49]
	rs864622164	c.4741dup	p.Ile1581fs	Brazil	1/370	[55]
	rs2547093815	c.6099dup	p.Arg2034fs	Brazil	1/126	[76]
	rs786203421	c.7000_7003del	p.Tyr2334fs	Brazil	1/17	[150]
	rs879254036	c.8292_8293del	p.Ser2764fs	Brazil	1/701	[49]
	rs587782847	c.9047_9057del	p.Lys3016fs	Brazil	1/701	[49]
	rs587781558	c.2921+1G>A	—	Brazil	2/701	[49]
	rs748840480	c.901+1G>A	—	Brazil	2/1156	[65]
	rs2080473458	c.2140del	p.Thr714fs	Brazil	2/1156	[65]
	rs1060501543	c.6729_6730delAA	p.Glu2245fs	Brazil	2/1156	[65]
	rs876658899	c.3510dup	p.Gln1171fs	Colombia	1/197	[121]
	rs1057517025	c.7767del	p.Lys2589fs	Colombia	1/197	[121]
	rs1555137917	c.8419-2A>C	—	Colombia	1/197	[121]
	rs121434219	c.9139 C>T	p.Arg3047Ter	Colombia	1/197	[121]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
	rs864622490	c.3663G>A	p.Trp1221	Mexico	1/53	[126]
	rs786202148	c.2839-3_2839delinsGATACTA	—	Mexico	1/53	[126]
	rs786204726	c.8876_8879del	p.Asp2959fs	Mexico	1/205	[111]
	rs864622669	c.8872_8873del	p.Phe2958fs	Mexico	1/222	[92]
	NR	c.7702_7703del	p.Arg2568fs	Mexico	1/27	[125]
	rs587781658	c.2284_2285del	p.Leu762fs	Guatemala	1/664	[123]
	rs762083530	c.4852C>T	p.Arg1618Ter	Guatemala	1/664	[123]
	rs202206540	c.6154G>A	p.Glu2052Lys	Chile	1/315	[81]
	rs587781347	c.1402_1403del	p.Lys468fs	Peru	1/130	[115]
	rs587782554	c.6404dup	p.Arg2136fs	Cayman Islands	1/664	[112]
BARD1	rs1057517589	c.176_177del	p.Glu59fs	Brazil	2/219	[54]
				Brazil	4/1663	[40]
				Brazil	1/1682	[52]
				Brazil	1/355	[48]
	rs730881425	c.2279C>A	p.Ser760Ter	Brazil	1/355	[48]
	rs587781948	c.1921C>T	p.Arg641Ter	Brazil	1/173	[45]
	rs1559387024	c.1758del	p.Ser586fs	Brazil	1/2000	[127]
	rs2469268815	c.2215dup	p.Tyr739fs	Brazil	1/17	[150]
	rs1259296823	c.2229dup	p.Asn744Ter	Colombia	1/197	[121]
	rs730881411	c.448C>T	p.Arg150Ter	Guatemala	1/664	[123]
BRIP1	rs137852986	c.2392C>T	p.Arg798Ter	Brazil	1/173	[45]
				Brazil	2/701	[49]
	rs780020495	c.1741C>T	p.Arg581Ter	Brazil	1/173	[45]
	rs786202941	c.2097+1G>C	—	Brazil	1/173	[45]
	rs775735278	c.1510del	p.Ile504fs	Brazil	1/105	[57]
	rs1555601203	c.1940G>A	p.Trp647Ter	Brazil	1/701	[49]
	rs587781655	c.918+1G>A	—	Brazil	1/701	[49]
	rs2144114210	c.2714del	p.Asn905fs	Colombia	1/197	[121]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
CDH1	NR	c.1528dup	p.Ala510Glyfs*27	Argentina	1/255	[90]
	rs1555516200	c.1565+2dup	—	Chile	1/315	[81]
	rs876660393	c.2296-2A>G	—	Mexico	1/205	[111]
	NR	c.790C>T	p.Gln264Ter	Brazil	1/701	[49]
CHEK2	rs28909982	c.349A>G	p.Arg117Gly	Brazil	2/219	[54]
				Brazil	1/105	[57]
				Brazil	4/355	[48]
				Brazil	1/167	[61]
				Brazil	1/1682	[52]
				Brazil	1/52	[151]
				Brazil	4/701	[49]
				Colombia	1/197	[121]
				Argentina	2/255	[90]
	rs864622149	c.846+1G>C	—	Brazil	1/219	[54]
				Brazil	1/370	[55]
				Brazil	1/1682	[52]
				Brazil	3/355	[48]
				Colombia	1/197	[121]
				Argentina	1/255	[90]
	rs555607708	c.1100delC	p.Thr367fs	Brazil	1/370	[55]
				Brazil	1/120	[60]
				Brazil	1/59	[152]
				Brazil	1/7	[148]
				Brazil	1/12	[153]
				Brazil	4/1663	[40]
				Brazil	1/1682	[52]
				Brazil	2/701	[49]
				Chile	1/315	[81]
	rs17879961	c.470T>C	p.Ile157Thr	Brazil	1/1682	[52]
				Mexico	1/205	[111]
	rs137853011	c.1283C>T	p.Ser428Phe	Chile	1/315	[81]
				Brazil	1/105	[57]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
	rs587782471	c.707T>C	p.Leu236Pro	Mexico	14/1045	[154]
				Mexico	1/205	[111]
				Mexico	21/1285	[155]
	rs142763740	c.1427C>T	p.Thr476Met	Argentina	1/255	[90]
				Colombia	1/197	[121]
	rs587782401	c.319+2T>A	—	Brazil	1/219	[54]
				Brazil	2/1156	[65]
	rs730881701	c.409C>T	p.Arg137Ter	Brazil	2/701	[49]
	rs786203229	c.593-1G>T	—	Brazil	1/219	[54]
	rs764884641	c.846+4_846+7del	—	Brazil	1/379	[55]
	rs1555915295	c.1008+2T>G	—	Brazil	1/219	[54]
	rs876659250	c.1459C>T	p.Gln487Ter	Brazil	1/370	[55]
	rs137853007	c.433C>T	p.Arg145Trp	Brazil	4/1663	[40]
	rs200928781	c.1169A>C	p.Tyr390Ser	Argentina	1/255	[90]
	rs1555913672	c.1209_1233del	p.Tyr404fs	Argentina	1/255	[90]
	rs587782070	c.279G>A	p.Trp93Ter	Argentina	1/255	[90]
	NR	c.1151delT	p.Ser383_ Leu384insTer	Mexico	1/327	[125]
	rs2146004773	c.664_676del	p.Met222fs	Mexico	1/115	[147]
	NR	c.1237_1238insG	p.Leu413fs	Mexico	1/115	[147]
	rs1601719328	c.1344del	p.Pro449fs	Chile	1/315	[81]
	rs587782245	c.591del	p.Val198fs	Colombia	1/197	[121]
	rs200917541	c.546C>A	p.Tyr139Ter	Guatemala	1/664	[123]
MLH1	rs147542208	c.2080G>T	p.Glu694Ter	Guatemala	1/664	[123]
	rs63751448	c.794G>A	p.Arg265His	Brazil	1/52	[151]
	rs63751615	c.676C>T	p.Arg226Ter	Mexico	1/300	[125]
MSH2	rs587779075	c.1165C>T	p.Arg389Ter	Colombia	1/222	[92]
	rs193922376	c.942+3A>T	—	Colombia	1/197	[121]
	rs63750780	c.1552C>T	p.Gln518Ter	Colombia	1/85	[102]
	rs587779139	c.2152C>T	p.Gln718Ter	Brazil	1/382	[124]
	NR	c.1894_1898del	NR	Brazil	1/382	[124]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
MSH6	rs876658881	c.1519dup	p.Arg507fs	Brazil	1/219	[54]
				Brazil	1/701	[49]
	NR	c.3980_3981insTCAG	p.Leu1330Valfs*12	Mexico	1/341	[156]
	rs1553333127	c.3766dup	p.Tyr1256fs	Colombia	1/197	[121]
	rs1060502891	c.3254del	p.Thr1085fs	Colombia	1/222	[92]
NF1	rs760703505	c.4600C>T	p.Arg1534Ter	Guatemala	1/664	[123]
	rs760949880	c.4245T>A	p.Asn1415Lys	Colombia	1/197	[121]
	rs137854562	c.3721C>T	p.Arg1241Ter	Colombia	1/197	[121]
PALB2	rs1060502760	c.355del	p. Gln119fs	Brazil	1/173	[45]
				Brazil	2/355	[48]
				Brazil	1/1682	[52]
				Brazil	1/102	[131]
				Brazil	1/370	[55]
	rs587776527	c.3256C>T	p.Arg1086Ter	Chile	1/315	[81]
				Brazil	1/1682	[52]
				Colombia	1/197	[121]
				Mexico	1/222	[92]
	rs180177100	c.1240C>T	p.Arg414Ter	Brazil	1/370	[55]
				Brazil	2/355	[48]
				Brazil	1/1682	[52]
				Brazil	1/102	[131]
				Brazil	2/1156	[65]
				Argentina	1/1905	[77]
				Colombia	1/85	[102]
	rs1060502734	c.1671_1674del	p.Ile558fs	Brazil	1/370	[55]
				Brazil	2/355	[48]
				Brazil	1/1682	[52]
				Brazil	2/173	[45]
	rs587781840	c.2964del	p.Val989insTer	Chile	1/315	[81]
				Argentina	4/1905	[77]
				Brazil	1/701	[49]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
	rs876659571	c.2288_2291del	p.His762_ Leu763insTer	Chile	1/48	[82]
				Colombia	4/197	[121]
				Colombia	1/222	[92]
	rs180177136	c.3350+4A>G	—	Brazil	1/701	[49]
				Argentina	1/1905	[77]
				Dominican Republic	2/61	[112]
	rs730881884	c.43G>T	p.Glu15Ter	Jamaica	1/183	[112]
				Jamaica	1/179	[145]
				Argentina	1/1905	[77]
	rs375699023	c.1042C>T	p.Gln348Ter	Argentina	4/1905	[77]
				Brazil	1/1682	[52]
				Brazil	2/355	[48]
	rs180177110	c.2257C>T	p.Arg753Ter	Brazil	1/126	[76]
				Brazil	1/1682	[52]
				Argentina	/1905	[77]
	rs764509489	c.2336C>G	p.Ser779Ter	Argentina	2/1905	[77]
				Mexico	1/115	[147]
	rs747148023	c.2411_2412del	p.Ser804fs	Mexico	1/115	[147]
				Mexico	3/1045	[154]
	rs587776416	c.2167_2168del	p.Met723fs	Mexico	9/1045	[154]
				Mexico	5/1285	[155]
	rs587776413	c.1571C>G	p.Ser524Ter	Trinidad and Tobago	2/298	[112]
				Trinidad and Tobago	4/76	[128]
	rs587782680	c.2052delC	p.Arg686fs	Jamaica	1/183	[112]
				Jamaica	1/179	[145]
	rs1021662947	c.3166C>T	p.Gln1056Ter	Jamaica	1/183	[112]
				Jamaica	1/179	[145]
	rs1555460445	c.2218C>T	p.Gln740Ter	Chile	1/315	[81]
				Argentina	5/1905	[77]
	rs515726123	c.509_510del	p.Arg170fs	Peru	1/130	[115]
				Mexico	1/53	[126]
	rs515726126	c.758_759insT	p.Ser254fs	Jamaica	1/179	[145]
	rs118203997	c.1653T>A	p.Tyr551Ter	Argentina	3/112	[93]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
	NR	c.2283_2284ins	NR	Argentina	1/112	[93]
	rs878855123	c.7G>T	p.Glu3Ter	Argentina	3/1905	[77]
	rs180177102	c.1592del	p.Leu531fs	Argentina	1/1905	[77]
	rs770996884	c.2566C>T	p.Gln856Ter	Argentina	6/1905	[77]
	NR	c.2872_2875del	p.Gln958TyrfsTer3	Argentina	1/1905	[77]
	NR	c.1959T>A	p.Cys653Ter	Argentina	1/1905	[77]
	rs1597079711	c.3062_3063dup	p.Met1022fs	Argentina	1/1905	[77]
	rs1555458828	c.3124dup	p.Thr1042fs	Argentina	1/1905	[77]
	rs864622498	c.93dup	p.Leu32fs	Brazil	1/355	[48]
	rs587776425	c.3426dup	p.Leu1143fs	Brazil	1/355	[48]
	rs587782443	c.226del	p.Ile76fsTer	Brazil	1/701	[49]
	rs1057520653	c.1438A>T	p.Lys480Ter	Brazil	1/701	[49]
	rs180177103	c.1633G>T	p.Glu545Ter	Brazil	1/701	[49]
	rs995629797	c.2730T>A	p.Tyr910Ter	Brazil	1/701	[49]
	rs1060502726	c.2711G>A	p.Trp904Ter	Brazil	2/1156	[65]
	rs864622138	c.3271C>T	p.Gln1091Ter	Brazil	2/1156	[65]
	rs587782566	c.3350+5G>A	—	Brazil	2/1156	[65]
	rs1967002667	c.1002C>A	p.Tyr334Ter	Barbados	1/92	[112]
	rs180177091	c.751C>T	p.Gln251Ter	Barbados	1/92	[112]
	rs587776424	c.3426_3429del	p.Leu1142fs	Guatemala	3/664	[123]
	rs180177143	c.172_175del	p.Gln60fs	Guatemala	1/664	[123]
	rs180177132	c.3113G>A	p.Trp1038Ter	Peru	1/130	[115]
	rs864622301	c.860dup	p.Ser288fs	Chile	1/315	[81]
	rs180177135	c.3323delA	p.Tyr1108fs	Haiti	1/75	[112]
	rs753153576	c.2748+1G>T	—	Nicaragua	1/39	[142]
PMS2	rs760228510	c.631C>T	p.Arg211Ter	Brazil	4/355	[48]
	rs121434629	c.137G>T	p.Ser46Ile	Brazil	1/701	[49]
	rs201451115	c.1939A>T	p.Lys647Ter	Brazil	1/701	[49]
	rs1782958183	c.1855del	p.Asp619fs	Colombia	1/197	[121]
	rs786203954	c.354 -1G>A	—	Colombia	1/197	[121]
PTEN	rs786204862	c.493-1G>T	—	Mexico	1/327	[125]
	rs1554898056	c.264T>G	p.Tyr88Ter	Brazil	1/382	[124]
	rs606231170	c.564T>G	p.Tyr188Ter	Brazil	1/701	[49]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
RAD51C	rs770637624	c.709C>T	p.Arg237Ter	Brazil	2/219	[54]
				Brazil	1/370	[55]
				Brazil	1/701	[49]
				Brazil	3/1682	[52]
				Peru	1/130	[115]
	rs1555602141	c.890_899del	p.Leu297fs	Brazil	1/355	[48]
				Brazil	1/52	[151]
				Brazil	1/1682	[52]
				Brazil	1/701	[49]
	rs730881931	c.404+2T>C	—	Mexico	1/327	[125]
			—	Peru	1/130	[115]
	rs587781995	c.905-2_905-1delAG	—	Argentina	1/112	[93]
	rs201529791	c.656T>A	p.Leu219Ter	Trinidad and Tobago	1/298	[112]
				Trinidad and Tobago	2/76	[128]
	rs1057517812	c.561_562del	p.His187fs	Colombia	1/197	[121]
	NR	NR	p.Ala173fs	Mexico	1/115	[147]
RAD51D	rs587780104	c.694C>T	p.Arg232Ter	Brazil	1/219	[54]
				Brazil	1/355	[48]
				Brazil	3/1682	[52]
				Brazil	1/370	[55]
	rs387906843	c.556C>T	p.Arg186Ter	Colombia	3/197	[121]
				Brazil	1/105	[57]
	rs786203137	c.94_95del	p.Val32fs	Colombia	5/197	[121]
	rs561425038	c.1A>G	p.Met1Val	Argentina	1/255	[90]
	NR	c.404G>A	p.Cys135Tyr	Chile	1/315	[81]
	rs148690585	c.216C>A	p.Tyr72Ter	Chile	1/315	[81]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
TP53	rs121912664	c.1010G>A	p.Arg337His	Brazil	6/219	[54]
				Brazil	6/237	[67]
				Brazil	5/95	[44]
				Brazil	1/102	[131]
				Brazil	26/1663	[40]
				Brazil	6/239	[67]
				Brazil	8/1682	[52]
				Brazil	2/28	[68]
				Brazil	1/101	[47]
				Brazil	1/105	[57]
				Brazil	3/120	[60]
				Brazil	1/173	[45]
				Brazil	6/45	[69]
				Brazil	42/348	[70]
				Brazil	2/54	[71]
				Brazil	5/370	[55]
				Brazil	2/167	[61]
				Brazil	1/44	[129]
				Brazil	3/123	[72]
				Brazil	2/180	[73]
				Brazil	2/1156	[65]
				Brazil	1/83	[74]
				Brazil	61/163	[75]
				Brazil	1/701	[49]
	rs11540652	c.743G>A	p.Arg248Gln	Brazil	1/701	[49]
				Brazil	2/1663	[40]
				Brazil	1/83	[74]
	rs28934575	c.733G>A	p.Gly245Ser	Brazil	1/219	[54]
				Brazil	2/1663	[40]
				Brazil	1/1682	[52]
	rs55863639[+]	c.375G>A	p.Thr125=	Peru	1/84	[95]
				Brazil	1/701	[49]
	rs28934578	c.524G>A	p.Arg175His	Mexico	1/115	[147]
				Nicaragua	1/39	[142]

(Continues)

TABLE 3 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Reference
	rs28934576	c.818G>A	p.Arg273His	Brazil	1/95	[44]
				Colombia	1/197	[121]
	rs876660754	c.517G>A	p.Val173Met	Bahamas	1/247	[112]
				Mexico	1/78	[157]
	rs985033810	c.731G>A	p.Gly244Asp	Guatemala	1/664	[123]
				Guatemala	1/801	[130]
	rs587782620	c.427G>A	p.Val143Met	Brazil	1/54	[59]
	rs587782529	c.1009C > T	p.Arg337Cys	Brazil	1/83	[74]
	rs11540652	c.743G>C	p.Arg248Pro	Brazil	1/355	[48]
	rs1555526001	c.534C>A	p.His178Gln	Brazil	1/126	[76]
	rs786201057	c.374C>T	p.Thr125Met	Brazil	1/701	[49]
	rs28934574	c.844C>T	p.Arg282Trp	Mexico	1/78	[157]
	NR	c.291del	p.Pro98fs	Mexico	1/78	[157]
	NR	c.273dupG	p.Pro92Afs*57	Mexico	1/78	[157]
	rs121912662	c.1031T>C	p.Leu344Pro	Guatemala	1/664	[123]
	rs397516434	c.644C>A	p.Ala215Asp	Guatemala	1/664	[123]
	rs730882025	c.646G>A	p.Val216Met	Guatemala	1/664	[123]
	rs121912651	c.742C>T	p.Arg248Trp	Argentina	2/255	[90]
	rs1131691022	c.1024del	p.Arg342fs	Chile	1/48	[82]
	rs483352697	c.587G>C	p.Arg196Pro	Mexico	2/53	[126]
	rs587782144	c.473G>T	p.Arg158Leu	Colombia	1/197	[121]

Abbreviations: —, intronic variant; HGVS, Human Genome Variation Society; NR, not reported or not available in the ClinVar/dbSNP at the time of publication.
[+]Note on *TP53* c.375G>A (p.Thr125=): This synonymous variant lies at the last nucleotide of exon 4, the canonical 5′ splice donor site of intron 4. RNA-based and functional studies have shown that it disrupts normal splicing, generating aberrant transcripts predicted to undergo nonsense-mediated decay, with consequent loss of p53 transactivation activity [158–160]; It cosegregates with disease in an affected family, is absent from gnomAD population databases, and is classified as pathogenic in ClinVar.

across Chilean studies. Access to genetic counseling is limited, with approximately 35 clinical geneticists practicing nationwide, corresponding to approximately one-third of the recommended ratio per population [149]. A study by Acevedo et al. [150] reported that only 15% of BC patients meeting the NCCN criteria for genetic testing were evaluated, with lower rates observed in public hospitals. These findings indicate limited concordance with international recommendations and point to the absence of standardized national guidelines. In Santiago, a high-risk breast and ovarian cancer program at a private clinic reported that 20.3% of the 315 patients studied had PV, of which 9.5% carried PV in genes such as *RAD51C*, *RAD51D*, *ATM*, *PALB2*, *CHEK2*, and *CDH1* [42] (Figure 2C). The Arturo López Pérez Foundation, which manages approximately 10% of the total BC cases in the country, reported a PV prevalence of 23.5% (170 individuals), with 40% involving genes encoding *BRCA1/2*, including *APC*, *ATM*, *ATR*, *AXIN2*, *CDKN2A*, *CHEK2*, *FANCM*, *MSH2*, *MSH6*, *NBN*, *NF1*, *PALB2*, *PTEN*, *RAD50*, *RAD51C*, *RAD51D*, *RET*, and *TP53* [149]. At the regional level, the Regional Hereditary Cancer Program aimed at decentralizing oncological genetic counseling and molecular diagnostics. This initiative provides additional evidence on the feasibility of delivering oncological genetic services outside the metropolitan area [107]. Overall, studies conducted in Chile have identified 28 PVs in *BRCA1* and 21 in *BRCA2*, with c.68_69delAG being the most frequently reported PV in the *BRCA1* variant. PVs have also been described in *ATM*, *CHEK2*, *CDH1*, *MUTYH*, *PALB2*, and *TP53* [42–46].

The Argentine population is a mixture of European ancestry, mainly from Spain and Italy, with an Amerindian component present to varying degrees in more than 50% of individuals [82]. A total of 37 PVs have been reported in *BRCA1* (Figure 2A), and 39 PVs have been reported in *BRCA2* (Figure 2B), many of which are shared with other LAC and European populations. In *BRCA1*, recurrent PVs include c.68_69delAG [51–53, 151],

TABLE 4 | Pathogenic or likely pathogenic variants found in rare genes in the population of Latin Americans and the Caribbean with hereditary breast cancer.

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Ref.
AIP	NR	c.619del	p.Ala207ProfsTer8	Colombia	1/197	[121]
ATR	rs1453839157	c.3043C>T	p.Arg1015Ter	Brazil	1/157	[62]
AXIN2	rs978837790	c.1908-2A>G	—	Guatemala	1/664	[123]
BCAR1	rs1597262107	c.12+2T>C	—	Brazil	1/52	[151]
BLM	rs2505534228	c.3220_3221insG	p.Thr1074fs	Mexico	1/115	[147]
	rs886051551	c.2206dup	p.Tyr736fs	Mexico	1/341	[156]
	rs587783037	c.3415C>T	p.Arg1139Ter	Colombia	1/197	[121]
	rs747341586	c.2268del	p.Asp757fs	Brazil	2/355	[48]
BUB1B	rs200884355	c.199C>T	p.Arg67Ter	Colombia	2/197	[121]
CDKN2A	rs104894099	c.176T>G	p.Val59Gly	Argentina	1/255	[90]
	rs1800586	c.194-3653G>T	—	Colombia	2/197	[121]
	rs1060501266	c.458-105A>G	—	Colombia	1/197	[121]
CEP57	rs1166323407	c.915_925dup	p.Leu309fs	Colombia	1/197	[121]
CLTCL1	rs199652160	c.988G>A	p.Glu330Lys	Mexico	1/115	[147]
CTNNA1	rs2150032416	c.1206_1207insCC	p.Val403fs	Brazil	1/52	[151]
CYP21A2	rs770199817	c.850A>G	p.Met284Val	Mexico	1/341	[156]
DICER1	rs1421729263	c.4252G>T	p.Glu1418Ter	Brazil	1/355	[48]
	rs2543344129	c.308-2A>G	—	Mexico	1/205	[111]
DCLRE1C	rs786205456	c.403G>A	p.Gly135Arg	Colombia	1/222	[92]
DROSHA	rs2150052710	c.1498G>T	p.Glu500Ter	Brazil	1/52	[151]
ERCC2	rs762309206	c.594+2_594+5del	—	Mexico	1/341	[156]
	rs144564120	c.2150C>G	p.Ala717GLy	Mexico	1/341	[156]
ERCC3	rs56116802	c.657+1G>A	—	Mexico	1/327	[125]
	rs34295337	c.325C>T	p.Arg109Ter	Mexico	1/341	[156]
	NR	c.1129C>T	p.Gln377Ter	Mexico	1/327	[125]
	rs770925947	c.1762dup	p.Glu588fs	Brazil	1/701	[49]
ERCC5	057518813	c.2929_2930del	p.Leu977fs	Colombia	1/197	[121]
EXT2	rs753973135	c.1506G>A	p.Trp502Ter	Mexico	1/115	[147]
FAH	rs80338898	c.782C>T	p.Pro261Leu	Mexico	1/341	[156]
FAM175A	rs764429803	c.1011delA	p.Ala338fs	Brazil	1/173	[45]
FANCA	rs140180549	c.2778+1G>C	—	Colombia	1/197	[121]
	rs1184639006	c.718C>T	p.Gln240Ter	Colombia	1/197	[121]
FANCC	rs374176091	c.673G>T	p.Glu225Ter	Mexico	1/327	[125]
FANCD2	rs766567785	c.2444G>A	p.Arg815Gln	Colombia	1/197	[121]

(Continues)

TABLE 4 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Ref.
FANCE	rs775076977	c.1111C>T	p.Arg371Trp	Mexico	1/341	[156]
FANCM	NR	c.1360_1361insAACAAAGTTA	p.E455Qfs*2	Colombia	1/222	[92]
	rs1888737946	c.4054A>T	p.Lys1352Ter	Colombia	1/197	[121]
	NR	c.5766_5769del	p.Thr1923fs	Brazil	1/173	[45]
FH	rs1057517734	c.1108+1G>T	—	Guatemala	1/664	[123]
FLCN	rs80338682	c.1285del	p.His429fs	Colombia	1/197	[121]
HERPUD1	rs2144823719	c.584_585delTT	p.Phe195fs	Brazil	2/52	[151]
KRAS	rs2141481712	c.461A>G	p.Asp154Gly	Brazil	1/52	[151]
LCP1	rs1376923782	c.1122C>A	p.Tyr374Ter	Brazil	1/52	[151]
LIG4	rs780879476	c.613del	p.Ser205fs	Mexico	1/327	[125]
	rs759838407	c.1512_1513dup	p.Arg505fs	Mexico	1/327	[125]
MEN1	rs794728622	c.669+1G>T	—	Brazil	2/355	[48]
	rs1060499981	c.1328C>A	p.Ser443Tyr	Mexico	1/341	[156]
MITF	rs149617956	c.1273G>A	p.Glu425Lys	Colombia	1/197	[121]
	rs760273611	c.1A>G	p.Met1Val	Brazil	1/52	[151]
MRE11	rs876659145	c.315-2A>G	—	Brazil	1/52	[161]
MUTYH	rs36053993	c.1187G>A	p.Gly396Asp	Brazil	2/219	[54]
				Brazil	1/105	[57]
				Brazil	5/370	[55]
				Brazil	10/701	[49]
				Brazil	4/1663	[40]
				Mexico	3/205	[111]
				Brazil	1/1682	[52]
				Chile	1/48	[82]
				Puerto Rico	1/48	[162]
				Mexico	6/1285	[155]
	rs587778536	c.1147del	p.Leu383fs	Argentina	1/222	[92]
				Brazil	1/701	[49]
				Brazil	1/52	[161]
				Brazil	1/370	[55]
				Brazil	1/355	[48]

(Continues)

TABLE 4 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Ref.
	rs34612342	c.536A>G	p.Tyr179Cys	Colombia	1/222	[92]
				Brazil	1/382	[124]
				Brazil	4/1663	[40]
				Brazil	1/1682	[52]
				Brazil	7/701	[49]
	rs587780078	c.1218_1219dup	p.Glu382fs	Guatemala	2/664	[123]
				Mexico	2/53	[126]
	rs372267274	c.305-1G>C	—	Brazil	1/219	[54]
	rs587780751	c.933+3A>C	—	Brazil	1/219	[54]
	rs587778541	c.1437_1439delGGA	p.Glu480del	Brazil	1/370	[55]
	rs34126013	c.721C>T	p.Arg241Trp	Brazil	2/701	[49]
	rs200495564	c.649C>T	p.Arg217Cys	Brazil	1/701	[49]
	rs587780749	c.652G>T	p.Val218Phe	Brazil	1/701	[49]
	NR	c.1228_1229insGG	p.Glu410fs	Colombia	1/222	[92]
	rs36053993	c.1103G>A	p.Gly368Asp	Colombia	1/197	[121]
	rs1064796630	c.604C>T	p.Gln202Ter	Colombia	1/197	[121]
NBN	rs587776650	c.657_661del	p.Lys219fs	Argentina	1/255	[90]
	rs759232053	c.1515del	p.Glu505fs	Colombia	1/197	[121]
	rs1586088924	c.598del	p.Tyr197fs	Mexico	1/327	[125]
	rs587781969	c.1142delC	p.Pro381fs	Brazil	2/1156	[65]
	rs767454740	c.156_157del	p.Ser53fs	Brazil	1/173	[45]
	NR	c.1688delinsAC	p.Leu563TyrfsTer15	Brazil	1/701	[49]
NSD1	NR	NR	p.Ser2424fs	Mexico	1/115	[147]
NTHL1	rs150766139	c.268C>T	p.Gln82Ter	Brazil	1/355	[48]
	rs749908882	c.115+1G>A	—	Brazil	1/701	[49]
	rs779757251	c.526-1G>A	—	Brazil	1/701	[49]
PDGFB	rs397515633	c.445C>T	p.Arg149Ter	Colombia	1/222	[92]
PLK2	rs772701630	c.1004dup	p.Leu335fs	Brazil	1/52	[151]
RAD50	rs786201897	c.2517dup	p.Asp840fs	Brazil	1/355	[48]
	rs750586158	c.3598C>T	p.Arg1200Ter	Colombia	1/197	[121]
RECQL4	rs34134064	c.1166_1167del	p.Cys389fs	Brazil	1/219	[54]
	rs386833845	c.1573del	p.Cys525fs	Brazil	1/701	[49]
	rs746636748	c.1048_1049del	p.Arg350fs	Colombia	1/197	[121]
	rs1176959485	c.2885+1G>T	—	Mexico	1/327	[125]
RIPK1	rs2113726155	c.1802_1805delGTGC	p.Cys601fs	Brazil	1/52	[151]

(Continues)

TABLE 4 | (CONTINUED)

Genes	rsID	HGVS nucleotide change	HGVS amino acid change	Country	Number of carriers/ number of patients analyzed	Ref.
RTEL1	rs398123017	c.2920C>T	p.Arg974Ter	Mexico	1/341	[156]
	NR	c.3222delG	p.Gly1075Alafs*9	Mexico	1/341	[156]
	rs201540674	c.3791G>A	p.Arg1264His	Mexico	1/341	[156]
SBDS	rs113993993	c.258+2T>C	—	Colombia	1/197	[121]
	rs113993993	c.258+2T>C	—	Mexico	1/341	[156]
SDHA	rs1173940446	c.554dup	p.Ala186fs	Brazil	1/355	[48]
	rs587782077	c.667del	p.Asp223fs	Mexico	1/205	[111]
	rs1175771583	c.699del	p.Val234fs	Brazil	1/701	[49]
SDHB	rs786202100	c.166_170del	p.Pro56fs	Mexico	1/327	[125]
	rs587782077	c.667del	p.Asp223fs	Colombia	1/197	[121]
	rs398122805	c.423+1G>A	—	Guatemala	1/664	[123]
	rs74315370	c.136C>T	p.Arg46Ter	Guatemala	1/664	[123]
SLC34A2	rs1714268814	c.113-2A>G	—	Brazil	1/52	[151]
SLX4	NR	c.4828delT	p.Ser1610fs	Brazil	1/173	[45]
	rs2040576239	c.2972_2973del	p.Gln991fs	Brazil	1/701	[49]
SUFU	rs587776579	c.71dup	p.Ala25fs	Brazil	1/355	[48]
WRN	rs17847577	c.1105C>T	p.Arg369Ter	Argentina	1/222	[92]
	rs1163988347	c.504+1G>A	—	Colombia	1/197	[121]
	rs757968518	c.896dup	p.Ile300fs	Mexico	1/327	[125]
XPC	rs1450238352	c.1103_1104del	p.Gln368fs	Colombia	1/197	[121]

Abbreviations: —, intronic variant; HGVS, Human Genome Variation Society; NR, not reported or not available in the ClinVar/dbSNP at the time of publication.

c.211A>G [50, 51, 72, 82, 83], c.3331_3334del [50, 52, 53], c.5266dupC [50, 52, 53], and c.181T>G [50, 51, 82]. Frequently reported *BRCA2* variants include c.5946delT [52, 53, 121, 129], c.2808_2811del [52, 53], c.6024dup [54], c.5351dup [53, 54, 83], and c.9026_9030del [54]. Additional PVs have been reported in moderate-risk genes such as *CHEK2* (p.Arg117Gly, c.846+1G>C, c.1100delC) [52], as well as in *PALB2* (c.1653T>A) [83] and *RAD51C* (c.905-2_905-1delAG) [83]. The recurrence of several variants also reported in European cohorts is consistent with the ancestral composition of the Argentine population and provides context for the observed variant spectrum in this setting.

The Peruvian population has a high incidence of BC, and the spectrum of germline PVs remains poorly characterized, largely owing to the limited access to genetic testing within the public health system. Available studies report 37 PVs for *BRCA1* (Figure 2A) and 25 PVs for *BRCA2* (Figure 2B), with c.5946delT being the most frequently described *BRCA2* variant, also observed in other LAC countries. PVs have additionally been identified in *ATM*, *PALB2*, *RAD51C*, and *TP53*. Zavaleta et al. [139] identified 14 PVs for *TP53* among HBC patients from a low-income rural region in northern Peru associated with Li–Fraumeni syndrome. These results highlight the need to urgently implement genetic testing and counseling in public hospitals/centers located in low-income cities to provide early diagnosis and personalized treatment to cancer patients [106].

The Uruguayan population is predominantly of European descent (80% and 90%), primarily of Spanish origin, with different genetic contributions from Amerindian (10%) and African (6%) ancestry, largely resulting from historical admixture, particularly between Amerindian women and European men [152]. To date, only two studies have reported germline variants in *BRCA1* and *BRCA2*. Delgado et al. [113] analyzed 42 families with breast and/or ovarian cancer and identified seven truncating PVs, five for *BRCA2* (4359ins6, 5579insA, 3829insTdel35, 4088delA, and 1617delAG) (Figure 2A) and two for *BRCA1* (5583insT and 2687T>G) (Figure 2B) [113]. A subsequent study in Uruguayan Ashkenazi Jewish families specifically screened three founder variants commonly reported in Jewish individuals (*BRCA1* (c.68_69del and (c.5266dup) and *BRCA2* (c.5946del) and identified the *BRCA1* c.68_69delAG variant in three unrelated families [61].

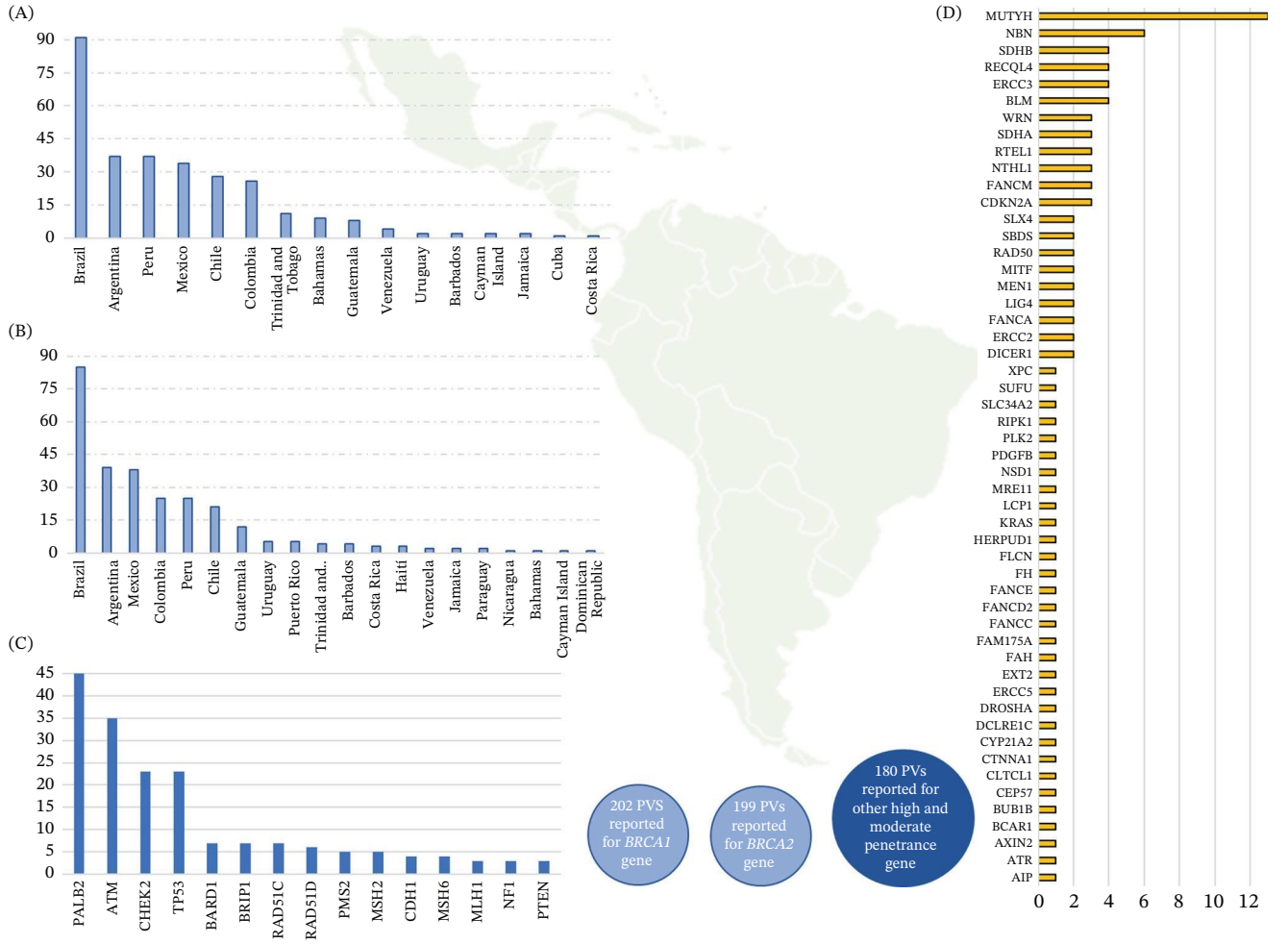


FIGURE 2 | Pathogenic germline variants associated with hereditary breast cancer in Latin America and the Caribbean. (A) Distribution of pathogenic variants (PVs) identified in the *BRCA1* gene, grouped by country. (B) Pathogenic variants reported by country for the *BRCA2* gene. (C) Total number of variants in high- and moderate-risk genes other than *BRCA1/2*, according to NCCN guidelines. (D) Number of pathogenic variants reported in rare genes associated with BC. The counts represent the raw number of pathogenic variants reported in the included studies by country; they are not normalized by the number of genes analyzed per study, the test panel used, or the number of individuals analyzed; therefore, they do not represent true biological diversity.

The Colombian population is characterized by substantial genetic diversity resulting from admixture among Amerindians, Afrodescendants, and European ancestors [153]. Research indicates that Colombian women under 40 years of age have a greater BC risk than women in the United States do [154]. Genetic testing is frequently performed abroad, increasing the cost and limiting access within the health system [58]. Torres et al. developed a low-cost PCR-based assay, the "Colombia Profile," designed to detect founder PVs in *BRCA1* and *BRCA2* [67]. In Colombia, 26 PVs have been reported for *BRCA1* and 25 for *BRCA2* (Figure 2A,B), with *BRCA1* c.5123C>A being described as a recurrent variant. In addition to those in *BRCA1/2*, PVs have been identified in other susceptibility genes, including *CHEK2*, *PALB2*, *MUTYH*, *MSH2*, *MSH6*, *BRIP1*, *BARD1*, and *TP53*, indicating substantial genetic heterogeneity in HBC within the Colombian population.

In the Venezuelan population, BC is frequently diagnosed at advanced stages, and delays in treatment are associated with elevated mortality rates. However, evidence on germline PVs in this population is scarce. To date, four cases of PVs have been reported in *BRCA1* (c.5123C>A, c.951_952insA, c.4603G>T, and c.5277+1G>A), and two cases have been reported in *BRCA2* (c.5796_5797del and c.3036_3039del) (Figure 2A,B). No studies have reported PVs in other genes associated with HBC in this population.

The Mexican population has a high incidence of BC among young women [155]. Studies indicate that women living in socioeconomically disadvantaged areas, particularly in the United States–Mexico border region, have lower access to mammographic screening, contributing to delayed diagnosis. Limited health insurance coverage further restricts access to genetic testing for the identification of PVs [156]. In Mexico, 34 PVs have been reported for *BRCA1* and 38 for *BRCA2* (Figure 2A,B), with the *BRCA1* c.68_69del variant being one of the most recurrent in several regions. PVs have also been described in *TP53*, *PALB2*, *MLH1*, *MUTYH*, *CHEK2*, *CDH1*, and *ATM*.

Our search revealed that fewer than half of the countries in LAC (20 of 44) reported germline PVs identified in patients with HBC, with Brazil contributing the largest number of studies. In contrast, no eligible studies were identified for countries such

as Ecuador, Panama, El Salvador, Bolivia, Honduras, Suriname, Guyana, or Belize, where PV reports were limited to BC patients not selected according to hereditary criteria. Overall, the included studies identified a total of 202 PVs for *BRCA1*, 48 of which were reported in two or more countries within the region (Table 1). For *BRCA2*, 199 PVs were documented, of which 46 were observed in at least two countries (Table 2). Variants reported exclusively in a single country accounted for 154 in *BRCA1* and 153 in *BRCA2*, as detailed in Tables S1 and S2.

3.2 | PVs in the Caribbean Population With HBC

In Puerto Rico, mitochondrial DNA analyses have revealed mixed maternal ancestry, with contributions from Native Americans (61.3%), sub-Saharan Africans (27.2%), and Western Eurasians (11.5%) [157]. Access to genetic testing for hereditary cancer remains limited and is largely restricted to specialized centers in San Juan. In this context, Dutil et al. [115] characterized the HBC profile in the Puerto Rican population, reporting PVs mainly in *BRCA2*, with p.Glu1308Ter (rs80358638) identified as a recurrent variant. PVs have also been reported in other predisposition genes, such as *MUTYH* (rs36053993, c.1187G>A) [115, 119].

Genetic studies of Guatemalan populations have revealed an average of 92% Amerindian ancestry in Mayan individuals and 8% European ancestry, whereas mestizos are estimated to constitute 55% Amerindian ancestry and 41% European ancestry [158]. To date, only one study has described the profile of PVs in Guatemalan individuals with HBC. Ren et al. evaluated 664 BC cases, where 45 PVs were identified in 73 subjects (11%); eight variants were the most recurrent, in *BRCA1* (c.799delT, c.212+1G>A, and c.5123C>A), *BRCA2* (c.8363G>A and c.2414delC), *CHEK2* (c.546C>A), *PALB2* (c.3426_3429del), and *MUTYH* (c.1218_1219dup). In addition, nine rare PVs were reported in low- or unknown-penetrance genes, including AXIN2, FH, MLH1, MUTYH, NF1, and SDHB [74].

In Cuba, the annual incidence of BC is estimated at 40 per 100,000 women, which is lower than the reported rates in the United States (92 per 100,000 among white women and 83 per 100,000 among black women) [159]. Only one study has assessed germline PVs in Cuban patients, analyzing 307 BC patients. Eight women carried a PV, seven in *BRCA2* (2.3%) and only one in *BRCA1*. Most carriers had early-onset disease (diagnosis before 50 years of age) or a first- or second-degree relative with BC [159].

The Caribbean region comprises an archipelago of island nations with a combined population exceeding 40 million, predominantly of African ancestry, with additional genetic contributions from indigenous, Asian, Indian, European, and Middle Eastern populations [59]. A multicenter study by George et al. [59] analyzed 1018 Caribbean-born individuals diagnosed with invasive breast and/or ovarian cancer via a 30-gene panel. The PV frequency varies substantially across countries: 28% (70 of 247) in the Bahamas, 17% in Barbados (*BRCA1*, *BRCA2*, or *PALB2)*, 6.5% in the Cayman Islands (*BRCA1*, *BRCA2*, or *ATM)*, 6.6% in Dominica (*BRCA2* and *PALB2)*, 6.7% in Haiti (*BRCA1*, *BRCA2*, or *PALB2)*, and 5.5% in Jamaica, with PVs occurring primarily in *BRCA1*, *BRCA2*, *PALB2*, and *NBN* [59].

In Bahamas, approximately 172 new cases of BC are diagnosed annually, with a mean age at diagnosis of 42 years. This population has one of the highest reported prevalence rates of PVs worldwide, reaching 23%, primarily in individuals with variants in the *BRCA1* or *BRCA2* genes [160].

Trinidad and Tobago, a twin-island nation in the southern Caribbean, has also been studied. An initial investigation revealed PVs in 49 of the 214 patients (23%) with unselected BCs. The frequency of *BRCA1* variants was greater among women diagnosed before 50 years of age (33%), those with a first-degree relative affected by BC or ovarian cancer (41%), and those with bilateral BC (58%). The most prevalent variant was BRCA1 c.4357+1G>A (IVS13+1G>A), with a frequency of 30% [60, 161]. In another study of 76 high-risk families undergoing genetic counseling and testing for *BRCA1*, *BRCA2*, *PALB2*, and *RAD51C*, PVs were identified in 35 families. The most frequent variants were *BRCA1* c.2766delA (8.6%) and c.2138C>A (5.7%), *BRCA2* c.4327C>T (11%), c.4945_4947delAGAinsTTTT (17%), and c.6373_6375delACCinsG (11%). Variants were also reported in *PALB2* c.1571C>G (p.Ser524Ter, 11.4%), and 5.7% had the c.656T>A (p.Leu219Ter) variant in *RAD51C* [87].

3.3 | PVs in Other High- and Moderate-Penetrance Genes in the Population of LAC With HBC

PVs in genes beyond *BRCA1* and *BRCA2*, such as *PTEN* (Cowden syndrome), *TP53* (Li–Fraumeni syndrome), *STK11* (Peutz–Jeghers syndrome), and *CDH1* (hereditary diffuse gastric cancer), remain comparatively undercharacterized in LAC populations [162]. The NCCN international guidelines (Version 1.2026) recommend that individuals with suspected HBC undergo multigene testing that includes high- and moderate-risk genes. Nevertheless, among the studies included in this review, only 59 reported PVs in these genes. Table 3 summarizes the NCCN-listed genes and the corresponding PVs reported in LAC populations. Across 15 genes, 180 PVs were identified. The highest number of PVs was reported in *PALB2* ($N = 45$), *ATM* ($N = 35$), *CHEK2* ($N = 23$), and *TP53* ($N = 23$). For *TP53*, p.Arg337His (rs121912664) was reported in 17 studies but exclusively in the Brazilian population.

3.4 | Identification of PVs in Rare Genes in LAC Populations With HBC

Beyond established HBC predisposition genes, Table 4 summarizes the reported rare genes. Overall, 102 PVs were identified across 52 rare genes, reported in only 15 of the included genes. Most variants were reported in studies from Brazil ($N = 41$), Mexico ($N = 30$), and Colombia ($N = 27$). The most prevalent variant in LAC was *MUTYH* c.1187G>A (p.Gly396Asp), reported in studies from Brazil, Chile, Puerto Rico, and Mexico. These findings support expanding the range of genes evaluated in LAC genetic studies to characterize the regional genomic architecture of HBC.

4 | Discussion

An important finding of the present review is that the HBC landscape in LAC differs substantially from that described in

predominantly European populations. Although several recurrent *BRCA1* and *BRCA2* PVs are shared across countries, a large proportion of variants identified appear to be population-specific, reflecting the complex demographic history, admixture patterns, and founder effects that characterize the region [72]. Importantly, individuals who met HBC criteria also carried PVs in numerous cancer susceptibility genes beyond *BRCA1* and *BRCA2*. Although the contribution of some of these genes to BC risk remains incompletely characterized, their recurrent identification across independent studies suggests that the genetic architecture of HBC in LAC extends beyond currently established high- and moderate-penetrance genes (as shown in Table 4).

The marked mutational heterogeneity observed across LAC is accompanied by the presence of population-specific founder variants that have substantially shaped HBC susceptibility in certain countries. The most notable example is the *TP53* p.Arg337His variant in Brazil, which represents one of the best characterized founder effects in LAC [163]. Haplotype analyses have demonstrated a common ancestral origin, likely associated with Portuguese–Iberian ancestry, and the variant is estimated to occur in approximately 0.3% of the population in southern Brazil. This founder effect has contributed significantly to the burden of HBC and Li-Fraumeni syndrome in the country [130, 164, 165]. The unusually high regional prevalence of *TP53* p.Arg337His has also motivated neonatal screening initiatives in southern Brazil, primarily aimed at the early detection of pediatric adrenocortical tumors in carriers. These experiences illustrate how the identification of highly prevalent founder variants can support the development of region-specific surveillance and precision medicine strategies [166]. Similarly, in Colombia, *BRCA1* c.5123C>A (p.Ala1708Glu) has been repeatedly identified among hereditary breast and ovarian cancer families and is recognized as one of the major Colombian founder variants [68]. Together, these findings demonstrate how local founder effects have contributed to shaping the current distribution of HBC susceptibility PVs across different LAC populations.

Beyond country-specific founder variants, the regional variant spectrum has also been influenced by historical migration processes and population admixture. Several PVs identified across LAC correspond to founder mutations originally described in Jewish populations, providing additional evidence of the complex demographic history that has shaped HBC susceptibility in the region [167]. Notably, the *BRCA1* c.68_69delAG (185delAG), *BRCA1* c.5266dupC (5382insC), and *BRCA2* c.5946delT (6174delT) variants, which represent the three classical Ashkenazi Jewish founder mutations, have been reported in multiple LAC countries, including Argentina, Brazil, Chile, Mexico, Peru, Colombia, and Uruguay. Likewise, the *BRCA1* c.211A>G (p.Arg71Gly), initially described as a founder mutation in Sephardic Jewish populations, has also been recurrently reported throughout the region. The widespread distribution of these variants likely reflects historical migration events; subsequent admixture among Indigenous American, European, and African populations; and local founder effects. These observations highlight the importance of considering ancestry and population history when designing genetic testing strategies and interpreting HBC risk in LAC population.

The genetic landscape observed in LAC shares several characteristics with other historically underrepresented populations, including African and South Asian populations. Similar to these regions, HBC studies in LAC reveal substantial genetic heterogeneity, population-specific PVs, and limited representation in international genomic databases. This underrepresentation reflects a broader imbalance in human genomics research. Until recently, approximately 78% of individuals included in genome-wide association studies were of European ancestry. In contrast, only 10% were of Asian ancestry, 2% of African ancestry, and approximately 1% of Hispanic or Latin American ancestry [168]. Consequently, clinically relevant PVs identified in LAC populations may be absent, underrepresented, or insufficiently characterized in widely used reference databases. These findings reinforce the need to expand genomic studies in diverse populations to improve variant interpretation, refine HBC risk assessment, and ensure equitable implementation of precision oncology worldwide.

In LAC, the clinical utility of identifying germline PVs is increasingly clear—enabling tailored surveillance, risk-reducing options in selected contexts, and targeted therapies such as PARP inhibitors for eligible patients. However, translation into improved outcomes is constrained by limited access to testing, counseling, and high-cost therapeutics, which remain disproportionately available through private insurance or participation in clinical trials. Strengthening referral pathways and integrating germline testing into oncology care are therefore necessary preconditions for the equitable delivery of precision prevention and treatment [169]. In carriers of germline variants in *BRCA1* or *BRCA2*, risk-reducing surgeries such as prophylactic salpingo-oophorectomy are recommended, as they are associated with increased cancer-specific and overall survival [26]. Carrying variants in other genes, such as *PTEN* or *TP53*, is also a factor that should be considered for this type of surgery. However, there are other hereditary cancer genes for which these preventive procedures are not indicated because evidence has shown that they do not improve survival [169, 170].

Identification of *BRCA1/2* PVs has direct therapeutic implications because PARP inhibitors such as olaparib and talazoparib have demonstrated clinical benefit in selected patients with germline *BRCA*-associated BC. However, despite these advances, access to both genetic testing and targeted therapies remains limited in many LAC countries, restricting the implementation of precision oncology across the region [26, 171].

One option to make new medicines available in LAC countries is through participation in clinical trials. Clinical options include patients with BC in LAC who have PVs in the *BRCA1/2* genes of PARP inhibitor therapies such as Velaparib NCT01506609 [172], NCT02163694 [173], NCT02595905; Talazoparib NCT01945775; and Olaparib NCT02000622, NCT06065059. Further studies focusing on variants in DNA repair genes are needed to study their role as new predictive markers for the response to PARP inhibitors and immunotherapy. The lack of access to high-cost medications is a complex issue in LAC that involves not only economic issues but also political and ethical issues. The sustainability of health systems in these countries is becoming a global threat [171]. Among the anticancer drugs launched worldwide, fewer than

half are available in countries such as Mexico, Brazil, or Chile, the main countries in the region. They are normally accessible only to a privileged minority of the LAC population enrolled in private insurance programs [171].

Several limitations should be considered when interpreting the findings of this review. First, although hereditary breast and ovarian cancer syndrome (HBOC) is commonly considered a unified clinical entity, the present review focused primarily on HBC because the available literature from LAC predominantly reports PVs identified in BC cohorts. Consequently, ovarian cancer-associated PVs were not systematically evaluated, and the findings may not fully capture the complete HBOC genetic landscape across the region. Second, despite the inclusion of evidence from 20 countries, several LAC countries remain underrepresented or lack eligible studies altogether. This limited geographic representation may underestimate the true genetic diversity of HBC susceptibility variants within the region and restrict the generalizability of the findings.

Finally, the results of this review have important implications for the design of HBC testing strategies in LAC. Although *BRCA1* and *BRCA2* remain the most frequently altered genes, PVs were consistently identified across multiple countries in other clinically actionable susceptibility genes, including *TP53*, *PALB2*, *ATM*, *CHEK2*, *RAD51C*, *RAD51D*, and *CDH1*. These findings suggest that *BRCA1/2*-only testing may fail to identify a substantial proportion of HBC predisposition in the region. Therefore, multigene panel testing approaches that incorporate both high- and moderate-penetrance genes may provide greater diagnostic yield and clinical utility. Furthermore, the presence of recurrent founder variants in specific populations highlights the opportunity to develop cost-effective regional testing strategies that combine targeted screening of locally prevalent PVs with broader multigene panel analysis when appropriate.

5 | Conclusion

This review demonstrates that, in LAC countries, advances in the genomic characterization of HBC have outpaced the capacity of health systems to deliver equitable genetic testing and counseling, perpetuating a persistent gap between discovery and implementation. Although a high degree of PV heterogeneity has been documented across the region, current approaches to treating hereditary cancer remain fragmented and insufficient.

Limited coverage of genetic testing within public health systems, shortages of trained oncological genetic counseling professionals, and the absence of integrated national policies for genomic cancer care collectively drive profound inequities in diagnosis, prevention, and access to precision oncology. Although *BRCA1* and *BRCA2* remain the most extensively studied genes in HBC, the evidence synthesized in this review reveals a lower number of reported PVs in other HBC susceptibility genes, such as *PALB2*, *TP53*, *ATM*, and *CHEK2*, despite their clinical implications. These findings underscore the need to move beyond the BRCA-centric model toward the implementation of multigene panels that reflect the regional mutational landscape. Achieving equitable precision oncology for HBC in LAC countries will require coordinated effort that extends beyond expanding genomic research in underrepresented populations, integrating germline testing into routine oncology care, strengthening referral pathways, investing in specialized training, and fostering regional collaborative networks, which are essential steps to translate genomic knowledge into meaningful clinical benefit. Addressing these structural and implementation barriers is critical to closing existing gaps and enabling truly personalized, evidence-based care for individuals and families affected by HBC across the region.

Nomenclature

AMP	Association for Molecular Pathology
BC	breast cancer
FDA	Food and Drug Administration
GC	genetic counseling
HBC	hereditary breast cancer
HGVS	Human Genome Variation Society
LAC	Latin America and the Caribbean
NCCN	National Comprehensive Cancer Network
PARP	poly(ADP–ribose) polymerase
PVs	SSpathogenic or likely pathogenic variants

Author Contributions

Conception: Natalia Landeros. Design of the work: Natalia Landeros and Romain Boidot. Acquisition and analysis of data: Natalia Landeros, Dante Palma-Ruiz, Sandra Romero, and Sebastián Morales. Interpretation of data: Natalia Landeros, Liliana Zúñiga-Venegas, and Dante Palma-Ruiz. Original draft preparation: Natalia Landeros, Sebastián Morales, Dante Palma-Ruiz, Ricardo Fernández-Ramires, Pablo Alarcón, and Sandra Romero. Writing, review, and editing: Natalia Landeros, Liliana Zúñiga-Venegas, María Teresa Muñoz-Quezada, Paula Celis, and Romain Boidot. Funding acquisition: Natalia Landeros. All authors have read and agreed to the published version of the manuscript. Sebastián Morales and Dante Palma-Ruiz contributed equally to this work as first authors.

Acknowledgments

We thank the breast cancer oncology patients in LAC for participating in the studies presented in this review.

Funding

This study is funded by the Fondo de Innovación para la Competitividad FIC-R, Gobierno Regional del Maule (40.058.811-0), the Fondo Nacional de Desarrollo Científico y Tecnológico (No. 1262233), and the National Agency for Research and Development (ANID)—FONDAP-CECAN (152220002).

Ethics Statement

The authors have nothing to report.

Consent

The authors have nothing to report.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

References

1. F. Bray, M. Laversanne, H. Sung, et al., "Global Cancer Statistics 2022: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries," *CA: a Cancer Journal For Clinicians* 74, no. 3 (2024): 229–263, https://doi.org/10.3322/caac.21834.

2. J. Iranzo, I. Martincorena, and E. V. Koonin, "Cancer-Mutation Network and the Number and Specificity of Driver Mutations," *Proceedings of the National Academy of Sciences* 115, no. 26 (2018): E6010–E6019, https://doi.org/10.1073/pnas.1803155115.

3. J. R. Pon, and M. A. Marra, "Driver and Passenger Mutations in Cancer," *Annual Review of Pathology: Mechanisms of Disease* 10, no. 1 (2015): 25–50, https://doi.org/10.1146/annurev-pathol-012414-040312.

4. N. Landeros, I. Castillo, and R. Pérez-Castro, "Preclinical and Clinical Trials of New Treatment Strategies Targeting Cancer Stem Cells in Subtypes of Breast Cancer," *Cells* 12, no. 5 (2023): 720, https://doi.org/10.3390/cells12050720.

5. C. Sessa, J. Balmaña, S. L. Bober, et al., "Risk Reduction and Screening of Cancer in Hereditary Breast-Ovarian Cancer Syndromes: ESMO Clinical Practice Guideline," *Annals of Oncology* 34, no. 1 (2023): 33–47, https://doi.org/10.1016/j.annonc.2022.10.004.

6. A. Yoshimura, I. Imoto, and H. Iwata, "Functions of Breast Cancer Predisposition Genes: Implications for Clinical Management," *International Journal Of Molecular Sciences* 23, no. 13 (2022): 7481, https://doi.org/10.3390/ijms23137481.

7. K. Kast, K. Rhiem, B. Wappenschmidt, et al., "Prevalence of BRCA1/2 Germline Mutations in 21401 Families With Breast and Ovarian Cancer," *Journal Of Medical Genetics* 53, no. 7 (2016): 465–471, https://doi.org/10.1136/jmedgenet-2015-103672.

8. Y. Miki, J. Swensen, D. Shattuck-Eidens, et al., "A Strong Candidate for the Breast and Ovarian Cancer Susceptibility Gene BRCA1," *Science* 266, no. 5182 (1994): 66–71, https://doi.org/10.1126/science.7545954.

9. R. Wooster, S. L. Neuhausen, J. Mangion, et al., "Localization of a Breast Cancer Susceptibility Gene, BRCA2, to Chromosome 13q12-13," *Science* 265, no. 5181 (1994): 2088–2090, https://doi.org/10.1126/science.8091231.

10. A. Girardi, F. Magnoni, E. Vicini, A. Kouloura, C. La Vecchia, and P. Veronesi, "CDH1 Germline Mutations in Families With Hereditary Lobular Breast Cancer," *European Journal of Cancer Prevention* 31, no. 3 (2022): 274–278, https://doi.org/10.1097/CEJ.0000000000000688.

11. A. C. Antoniou, S. Casadei, T. Heikkinen, et al., "Breast-Cancer Risk in Families With Mutations in PALB2," *New England Journal of Medicine* 371, no. 6 (2014): 497–506, https://doi.org/10.1056/NEJMoa1400382.

12. D. Liaw, D. J. Marsh, J. Li, et al., "Germline Mutations of the PTEN Gene in Cowden Disease, an Inherited Breast and Thyroid Cancer Syndrome," *Nature Genetics* 16, no. 1 (1997): 64–67, https://doi.org/10.1038/ng0597-64.

13. A. Hemminki, D. Markie, I. Tomlinson, et al., "A Serine/Threonine Kinase Gene Defective in Peutz-Jeghers Syndrome," *Nature* 391, no. 6663 (1998): 184–187, https://doi.org/10.1038/34432.

14. D. Malkin, F. P. Li, L. C. Strong, et al., "Germ Line p53 Mutations in a Familial Syndrome of Breast Cancer, Sarcomas, and Other Neoplasms," *Science* 250, no. 4985 (1990): 1233–1238, https://doi.org/10.1126/science.1978757.

15. A. Renwick, D. Thompson, S. Seal, et al., "ATM Mutations That Cause Ataxia-Telangiectasia Are Breast Cancer Susceptibility Alleles," *Nature Genetics* 38, no. 8 (2006): 873–875, https://doi.org/10.1038/ng1837.

16. S. De Brakeleer, J. De Grève, R. Loris, et al., "Cancer Predisposing Missense and Protein truncatingBARD1mutations in non-BRCA1orBRCA2breast Cancer Families," *Human Mutation* 31, no. 3 (2010): E1175–E1185, https://doi.org/10.1002/humu.21200.

17. S. Seal, D. Thompson, A. Renwick, et al., "Truncating Mutations in the Fanconi Anemia J Gene BRIP1 Are Low-Penetrance Breast Cancer Susceptibility Alleles," *Nature Genetics* 38, no. 11 (2006): 1239–1241, https://doi.org/10.1038/ng1902.

18. T. Huzarski, C. Cybulski, W. Domagała, et al., "Pathology of Breast Cancer in Women With Constitutional CHEK2 Mutations," *Breast Cancer Research And Treatment* 90, no. 2 (2005): 187–189, https://doi.org/10.1007/s10549-004-3778-2.

19. V. Reinhold, A. Saarinen, E. Suominen, S. Syrjänen, and M. Kankuri-Tammilehto, "Severe Untreated Scoliosis and Early Onset Breast Cancer in a Patient With Neurofibromatosis Associated With a Nonsense Variant of NF1 Gene," *Orthopedic Research and Reviews* 15 (2023): 183–189, https://doi.org/10.2147/ORR.S415978.

20. M. Vuorela, K. Pylkäs, J. M. Hartikainen, et al., "Further Evidence for the Contribution of the RAD51C Gene in Hereditary Breast and Ovarian Cancer Susceptibility," *Breast Cancer Research And Treatment* 130, no. 3 (2011): 1003–1010, https://doi.org/10.1007/s10549-011-1677-x.

21. Y. Sun, T. J. McCorvie, L. A. Yates, and X. Zhang, "Structural Basis of Homologous Recombination," *Cellular and Molecular Life Sciences* 77, no. 1 (2020): 3–18, https://doi.org/10.1007/s00018-019-03365-1.

22. C. A. Ossa, and D. Torres, "Founder and Recurrent Mutations in BRCA1 and BRCA2 Genes in Latin American Countries: State of the Art and Literature Review," *Oncologist* 21, no. 7 (2016): 832–839, https://doi.org/10.1634/theoncologist.2015-0416.

23. E. Cazap, L. M. de Almeida, S. Arrossi, et al., "Latin America and the Caribbean Code Against Cancer: Developing Evidence-Based Recommendations to Reduce the Risk of Cancer in Latin America and the Caribbean," *Journal of Global Oncology* 5 (2019): 1–3, https://doi.org/10.1200/JGO.19.00032.

24. S. J. Serrano-Gomez, M. C. Sanabria-Salas, and L. Fejerman, "Breast Cancer Health Disparities in Hispanics/Latinas," *Current Breast Cancer Reports* 12, no. 3 (2020): 175–184, https://doi.org/10.1007/s12609-020-00370-3.

25. L. Brignoni, M. Cappetta, V. Colistro, et al., "Genomic Diversity in Sporadic Breast Cancer in a Latin American Population," *Genes* 11, no. 11 (2020): 1272, https://doi.org/10.3390/genes11111272.

26. C. H. Barrios, T. Reinert, and G. Werutsky, "Access to High-Cost Drugs for Advanced Breast Cancer in Latin America, particularly trastuzumab," *Ecancermedicalscience* 13 (2019): 898, https://doi.org/10.3332/ecancer.2019.898.

27. E. Cazap, "Breast Cancer in Latin America: A Map of the Disease in the Region," *American Society of Clinical Oncology Educational Book* 38 (2018): 451–456, https://doi.org/10.1200/EDBK_201315.

28. J. S. Herzog, Y. Chavarri-Guerra, D. Castillo, et al., "Genetic Epidemiology of BRCA1- and BRCA2-Associated Cancer Across Latin America," *NPJ Breast Cancer* 7, no. 1 (2021): 107, https://doi.org/10.1038/s41523-021-00317-6.

29. L. M. de Almeida, S. Cortés, M. Vilensky, et al., "Socioeconomic, Clinical, and Molecular Features of Breast Cancer Influence Overall Survival of Latin American Women," *Frontiers In Oncology* 12 (2022): 845527, https://doi.org/10.3389/fonc.2022.845527.

30. C. Villarreal-Garza, C. Aguila, M. C. Magallanes-Hoyos, et al., "Breast Cancer in Young Women in Latin America: An Unmet, Growing Burden," *Oncologist* 18, no. 12 (2013): 1298–1306, https://doi.org/10.1634/theoncologist.2013-0321.

31. C. Villarreal-Garza, J. E. Bargallo-Rocha, E. Soto-Perez-de-Celis, et al., "Real-World Outcomes in Young Women With Breast Cancer Treated With Neoadjuvant Chemotherapy," *Breast Cancer Research And Treatment* 157, no. 2 (2016): 385–394, https://doi.org/10.1007/s10549-016-3811-2.

32. M. J. Hall, J. E. Reid, L. A. Burbidge, et al., "BRCA1 and BRCA2 Mutations in Women of Different Ethnicities Undergoing Testing for Hereditary Breast-Ovarian Cancer," *Cancer* 115, no. 10 (2009): 2222–2233, https://doi.org/10.1002/cncr.24200.

33. A. C. Tricco, E. Lillie, W. Zarin, et al., "PRISMA Extension for Scoping Reviews (PRISMA-ScR): Checklist and Explanation," *Annals Of Internal Medicine* 169, no. 7 (2018): 467–473, https://doi.org/10.7326/M18-0850.

34. S. Richards, N. Aziz, S. Bale, et al., "Standards and Guidelines for the Interpretation of Sequence Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology," *Genetics in Medicine* 17, no. 5 (2015): 405–424, https://doi.org/10.1038/gim.2015.30.

35. V. F. Esteves, L. C. Thuler, L. C. Amêndola, et al., "Prevalence of BRCA1 and BRCA2 Gene Mutations in Families With Medium and High Risk of Breast and Ovarian Cancer in Brazil," *Brazilian Journal of Medical and Biological Research* 42, no. 5 (2009): 453–457, https://doi.org/10.1590/S0100-879X2009000500009.

36. C. V. Dillenburg, I. C. Bandeira, T. V. Tubino, et al., "Prevalence of 185delAG and 5382insC mutations in BRCA1, and 6174delT in BRCA2 in women of Ashkenazi Jewish origin in southern Brazil," *Genetics And Molecular Biology* 35, no. 3 (2012): 599–602, https://doi.org/10.1590/S1415-47572012000400009.

37. R. C. Brianese, K. D. M. Nakamura, F. G. D. S. Almeida, et al., "BRCA1 Deficiency Is a Recurrent Event in Early-Onset Triple-Negative Breast Cancer: A Comprehensive Analysis of Germline Mutations and Somatic Promoter Methylation," *Breast Cancer Research And Treatment* 167, no. 3 (2018): 803–814, https://doi.org/10.1007/s10549-017-4552-6.

38. R. S. C. Guindalini, D. V. Viana, J. P. F. W. Kitajima, et al., "Detection of Germline Variants in Brazilian Breast Cancer Patients Using Multigene Panel Testing," *Scientific Reports* 12, no. 1 (2022): 4190, https://doi.org/10.1038/s41598-022-07383-1.

39. P. Mazzonetto, F. Milanezi, M. D'Andrea, et al., "BRCA1 and BRCA2 Germline Mutation Analysis From a Cohort of 1267 Patients at High Risk for Breast Cancer in Brazil," *Breast Cancer Research and Treatment* 199, no. 1 (2023): 127–136, https://doi.org/10.1007/s10549-023-06892-5.

40. R. M. Freitas, P. Medeiros, M. R. Guerra, and M. T. Bustamante-Teixeira, "Hereditary Breast Cancer," *Mastology* 31 (2021): 1–9, https://doi.org/10.29289/2594539420210041.

41. B. Alemar, C. Gregório, J. Herzog, et al., "BRCA1 and BRCA2 Mutational Profile and Prevalence in Hereditary Breast and Ovarian Cancer (HBOC) Probands From Southern Brazil: Are International Testing Criteria Appropriate for This Specific Population?," *PLoS One* 12, no. 11 (2017): e0187630, https://doi.org/10.1371/journal.pone.0187630.

42. C. Adaniel, F. Salinas, J. M. Donaire, et al., "Non-*BRCA1/2* Variants Detected in a High-Risk Chilean Cohort With a History of Breast and/or Ovarian Cancer," *Journal of Global Oncology* 5 (2019): 1–14, https://doi.org/10.1200/JGO.18.00163.

43. C. Alvarez, T. Tapia, E. Perez-Moreno, et al., "BRCA1andBRCA 2founder mutations account for 78% of germline carriers among hereditary breast cancer families in Chile," *Oncotarget* 8, no. 43 (2017): 74233–74243, https://doi.org/10.18632/oncotarget.18815.

44. L. Jara, S. Ampuero, E. Santibáñez, et al., "BRCA1 and BRCA2 Mutations in a South American Population," *Cancer Genetics And Cytogenetics* 166, no. 1 (2006): 36–45, https://doi.org/10.1016/j.cancergencyto.2005.08.019.

45. M. Gallardo, A. Silva, L. Rubio, et al., "Incidence of BRCA1 and BRCA2 Mutations in 54 Chilean Families With Breast/Ovarian cancer, genotype–phenotype correlations," *Breast Cancer Research And Treatment* 95, no. 1 (2006): 81–87, https://doi.org/10.1007/s10549-005-9047-1.

46. L. Jara, S. Ampuero, L. Seccia, et al., "Frequency of the 185delAG Mutation in the BRCA1 Gene in Chilean Healthy Women With Family History of Breast Cancer," *Revista medica de Chile* 130, no. 10 (2002): 1113–1123.

47. P. Gonzalez-Hormazabal, S. Gutierrez-Enriquez, D. Gaete, et al., "Spectrum of BRCA1/2 Point Mutations and Genomic Rearrangements in High-Risk Breast/Ovarian Cancer Chilean Families," *Breast Cancer Research And Treatment* 126, no. 3 (2011): 705–716, https://doi.org/10.1007/s10549-010-1170-y.

48. L. Jara, S. Ampuero, E. Santibáñez, et al., "Molecular Analysis of the Eighteen Most Frequent Mutations in the BRCA1 Gene in 63 Chilean Breast Cancer Families," *Biological Research* 37, no. 3 (2004): 469–481, https://doi.org/10.4067/S0716-97602004000300011.

49. C. Villarreal-Garza, J. N. Weitzel, M. Llacuachaqui, et al., "The Prevalence of BRCA1 and BRCA2 Mutations Among Young Mexican Women With Triple-Negative Breast Cancer," *Breast Cancer Research And Treatment* 150, no. 2 (2015): 389–394, https://doi.org/10.1007/s10549-015-3312-8.

50. T. R. Rebbeck, T. M. Friebel, E. Friedman, et al., "Mutational Spectrum in a Worldwide Study of 29,700 Families With BRCA1 or BRCA2 Mutations," *Human Mutation* 39, no. 5 (2018): 593–620, https://doi.org/10.1002/humu.23406.

51. A. R. Solano, G. M. Aceto, D. Delettieres, et al., "BRCA1 And BRCA2 Analysis of Argentinean Breast/Ovarian Cancer Patients Selected for Age and Family History Highlights a Role for Novel Mutations of Putative South-American Origin," *Springerplus* 1, no. 1 (2012): 20, https://doi.org/10.1186/2193-1801-1-20.

52. A. R. Solano, P. G. Mele, F. S. Jalil, N. C. Liria, E. J. Podesta, and L. G. Gutiérrez, "Study of the Genetic Variants in BRCA1/2 and Non-BRCA Genes in a Population-Based Cohort of 2155 Breast/Ovary Cancer Patients, Including 443 Triple-Negative Breast Cancer Patients, in Argentina," *Cancers* 13, no. 11 (2021): 2711, https://doi.org/10.3390/cancers13112711.

53. A. R. Solano, N. C. Liria, F. S. Jalil, et al., "BRCA1 and BRCA2 Mutations Other Than the Founder Alleles Among Ashkenazi Jewish in the Population of Argentina," *Frontiers in Oncology* 8 (2018): 323.

54. F. C. Cardoso, S. Goncalves, P. G. Mele, et al., "BRCA1 and BRCA2 Mutations and Clinical Interpretation in 398 Ovarian Cancer Patients: Comparison With Breast Cancer Variants in a Similar Population," *Human Genomics* 12, no. 1 (2018): 39, https://doi.org/10.1186/s40246-018-0171-5.

55. J. C. Fernández-Lopez, S. Romero-Córdoba, R. Rebollar-Vega, et al., "Population and Breast Cancer Patients' Analysis Reveals the Diversity of Genomic Variation of the BRCA Genes in the Mexican Population," *Human Genomics* 13, no. 1 (2019): 3, https://doi.org/10.1186/s40246-018-0188-9.

56. O. Millan Catalan, A. D. Campos-Parra, R. Vázquez-Romo, et al., "A Multi-Center Study of *BRCA1* and *BRCA2* Germline Mutations in Mexican-Mestizo Breast Cancer Families Reveals Mutations Unreported in Latin American Population," *Cancers* 11, no. 9 (2019): 1246, https://doi.org/10.3390/cancers11091246.

57. D. C. Pérez-Ibave, M. L. Garza-Rodríguez, M. F. Noriega-Iriondo, et al., "Identification of Germline Variants in Patients With Hereditary Cancer Syndromes in Northeast Mexico," *Genes* 14, no. 2 (2023): 341, https://doi.org/10.3390/genes14020341.

58. A. M. Cock-Rada, C. A. Ossa, H. I. Garcia, and L. R. Gomez, "A Multi-Gene Panel Study in Hereditary Breast and Ovarian Cancer in Colombia," *Familial Cancer* 17, no. 1 (2018): 23–30, https://doi.org/10.1007/s10689-017-0004-z.

59. S. H. L. George, T. Donenberg, C. Alexis, et al., "Gene Sequencing for Pathogenic Variants Among Adults With Breast and Ovarian Cancer in the Caribbean," *JAMA Network Open* 4, no. 3 (2021): e210307, https://doi.org/10.1001/jamanetworkopen.2021.0307.

60. T. Donenberg, J. Lunn, D. Curling, et al., "A High Prevalence of BRCA1 Mutations Among Breast Cancer Patients From the Bahamas,"

Breast Cancer Research And Treatment 125, no. 2 (2011): 591–596, https://doi.org/10.1007/s10549-010-1156-9.

61. C. Castillo, N. Artagaveytia, L. Brignoni, et al., "Population-Based Screening of Uruguayan Ashkenazi Jews for Recurrent BRCA1 and BRCA2 Pathogenic Sequence Variants," *Molecular Genetics & Genomic Medicine* 10, no. 6 (2022): e1928, https://doi.org/10.1002/mgg3.1928.

62. J. Abugattas, M. Llacuachaqui, Y. S. Allende, et al., "Prevalence of *BRCA1* and *BRCA2* Mutations in Unselected Breast Cancer Patients From Peru," *Clinical Genetics* 88, no. 4 (2015): 371–375, https://doi.org/10.1111/cge.12505.

63. Y. Chávarri-Guerra, C. A. Marcum, C. B. Hendricks, et al., "Breast Cancer Associated Pathogenic Variants Among Women 61 Years and Older With Triple Negative Breast Cancer," *Journal Of Geriatric Oncology* 12, no. 5 (2021): 749–751, https://doi.org/10.1016/j.jgo.2020.11.008.

64. Y. Ferreyra, G. Rosas, A. M. Cock-Rada, et al., "Landscape of germline BRCA1/BRCA2 variants in breast and ovarian cancer in Peru," *Frontiers in Oncology* 13 (2023): 1227864, https://doi.org/10.3389/fonc.2023.1227864.

65. F. C. Silva, B. C. Lisboa, M. C. Figueiredo, et al., "Hereditary Breast and Ovarian Cancer: Assessment of Point Mutations and Copy Number Variations in Brazilian Patients," *BMC Medical Genetics* 15, no. 1 (2014): 55, https://doi.org/10.1186/1471-2350-15-55.

66. T. R. Nagy, S. Maistro, G. Encinas, et al., "Germline and Somatic Mutations in Postmenopausal Breast Cancer Patients," *Clinics* 76 (2021): e2837, https://doi.org/10.6061/clinics/2021/e2837.

67. D. Torres, M. U. Rashid, F. Gil, et al., "High Proportion of BRCA1/2 Founder Mutations in Hispanic Breast/Ovarian Cancer Families From Colombia," *Breast Cancer Research And Treatment* 103, no. 2 (2007): 225–232, https://doi.org/10.1007/s10549-006-9370-1.

68. E. Vargas, R. de Deugd, V. E. Villegas, et al., "Prevalence of BRCA1 and BRCA2 Germline Mutations in Patients of African Descent With Early-Onset and Familial Colombian Breast Cancer," *Oncologist* 27, no. 2 (2022): e151–e157, https://doi.org/10.1093/oncolo/oyab026.

69. D. C. Sierra-Díaz, A. Morel, D. J. Fonseca-Mendoza, et al., "Germline Mutations of breast Cancer Susceptibility Genes Through Expanded Genetic Analysis in Unselected Colombian Patients," *Human Genomics* 18, no. 1 (2024): 68, https://doi.org/10.1186/s40246-024-00623-7.

70. E. Vargas, D. M. Torres Lopez, R. de Deugd, et al., "Low Prevalence of the Four Common Colombian Founder Mutations inBRCA1and-BRCA2in Early-Onset and Familial Afro-Colombian Patients with Breast Cancer," *Oncologist* 24, no. 7 (2019): e475–e479, https://doi.org/10.1634/theoncologist.2018-0346.

71. M. C. Sanabria-Salas, A. L. Rivera-Herrera, M. C. Manotas, et al., "Building a Hereditary Cancer Program in Colombia: Analysis of Germline Pathogenic and Likely Pathogenic Variants Spectrum in a High-Risk Cohort," *European Journal of Human Genetics* 33, no. 7 (2025): 913–929, https://doi.org/10.1038/s41431-025-01807-y.

72. J. Oliver, R. Quezada Urban, C. A. Franco Cortés, et al., "Latin American Study of Hereditary Breast and Ovarian Cancer LACAM: A Genomic Epidemiology Approach," *Frontiers in Oncology* 9 (2019): 1429, https://doi.org/10.3389/fonc.2019.01429.

73. Z. Nahleh, S. Otoukesh, A. K. Dwivedi, et al., "Clinical and Pathological Characteristics of Hispanic BRCA-Associated Breast Cancers in the American-Mexican Border City of El Paso, TX," *American Journal Of Cancer Research* 5, no. 1 (2015): 466–471.

74. M. Ren, A. Orozco, K. Shao, et al., "Germline Variants in Hereditary Breast Cancer Genes Are Associated With Early Age at Diagnosis and Family History in Guatemalan Breast Cancer," *Breast Cancer Research And Treatment* 189, no. 2 (2021): 533–539, https://doi.org/10.1007/s10549-021-06305-5.

75. G. E. S. Felix, R. S. C. Guindalini, Y. Zheng, et al., "Mutational Spectrum of Breast Cancer Susceptibility Genes Among Women Ascertained in a Cancer Risk Clinic in Northeast Brazil," *Breast Cancer Research and Treatment* 193, no. 2 (2022): 485–494, https://doi.org/10.1007/s10549-022-06560-0.

76. G. E. Felix, C. Abe-Sandes, T. M. Machado-Lopes, et al., "Germline Mutations in BRCA1, BRCA2, CHEK2 and TP53 in Patients at High-Risk for HBOC: Characterizing a Northeast Brazilian Population," *Human Genome Variation* 1, no. 1 (2014): 14012, https://doi.org/10.1038/hgv.2014.12.

77. J. P. Faria, J. G. Assumpção, M. L. de Oliveira, and F. C. Soardi, "Spectrum of Germline Pathogenic Variants in Brazilian Hereditary Breast/Ovarian Cancer Cases," *Breast Cancer Research and Treatment* 207, no. 3 (2024): 615–624, https://doi.org/10.1007/s10549-024-07383-x.

78. J. M. de Oliveira, N. B. Zurro, A. V. C. Coelho, et al., "The Genetics of Hereditary Cancer Risk Syndromes in Brazil: A Comprehensive Analysis of 1682 Patients," *European Journal of Human Genetics* 30, no. 7 (2022): 818–823, https://doi.org/10.1038/s41431-022-01098-7.

79. G. Bandeira, K. Rocha, M. Lazar, et al., "Germline Variants of Brazilian Women With Breast Cancer and Detection of a Novel Pathogenic ATM Deletion in Early-Onset Breast Cancer," *Breast Cancer* 28, no. 2 (2021): 346–354, https://doi.org/10.1007/s12282-020-01165-1.

80. J. P. B. Cassoli, Í. Fernandes, L. Carvalho, et al., "Frequency of Deleterious Germline Variants in HER2-Low Breast Cancer Patients Using a Hereditary Multipanel Gene Testing," *Current Issues In Molecular Biology* 46, no. 8 (2024): 7976–7985, https://doi.org/10.3390/cimb46080471.

81. C. M. Carvalho, L. D. C. Braga, L. M. Silva, A. M. Chami, and A. L. D. Silva Filho, "Germline Mutations Landscape in a Cohort of the State of Minas Gerais, Brazil, in Patients Who Underwent Genetic Counseling for Gynecological and Breast Cancer," *Revista Brasileira de Ginecologia e Obstetrícia/RBGO Gynecology and Obstetrics* 45, no. 2 (2023): 74–81, https://doi.org/10.1055/s-0042-1757956.

82. A. R. Solano, F. C. Cardoso, V. Romano, et al., "Spectrum of BRCA1/2 Variants in 940 Patients From Argentina Including Novel, Deleterious and Recurrent Germline Mutations: Impact on Healthcare and Clinical Practice," *Oncotarget* 8, no. 36 (2017): 60487–60495, https://doi.org/10.18632/oncotarget.10814.

83. R. Cerretini, G. Mercado, J. Morganstein, et al., "Germline Pathogenic Variants in BRCA1, BRCA2, PALB2 and RAD51C in Breast Cancer Women From Argentina," *Breast Cancer Research And Treatment* 178, no. 3 (2019): 629–636, https://doi.org/10.1007/s10549-019-05411-9.

84. R. Quezada Urban, C. E. Díaz Velásquez, R. Gitler, et al., "Comprehensive Analysis of Germline Variants in Mexican Patients With Hereditary Breast and Ovarian Cancer Susceptibility," *Cancers* 10, no. 10 (2018): 361, https://doi.org/10.3390/cancers10100361.

85. D. V. Juárez, J. A. Olvera, A. N. Ramos, et al., "Prevalencia de Mutación Germinal de BRCA en Mujeres Jóvenes con Cáncer de Mama: Experiencia de un Centro Privado de Tercer Nivel," *Anales Médicos de la Asociación Médica del Centro Médico ABC* 66, no. 4 (2021): 249–257, https://doi.org/10.35366/102924.

86. J. Z. Pereira, J. G. Carneiro, M. S. Vieira, et al., "Frequency of Germline Genetic Variants in Women With a Personal or Family History of Breast Cancer From Brazil," *Molecular Biology Reports* 49, no. 10 (2022): 9509–9520, https://doi.org/10.1007/s11033-022-07840-0.

87. T. Donenberg, S. George, J. Ali, et al., "A Clinically Structured and Partnered Approach to Genetic Testing in Trinidadian Women With Breast Cancer and Their Families," *Breast Cancer Research And Treatment* 174, no. 2 (2019): 469–477, https://doi.org/10.1007/s10549-018-5045-y.

88. N. M. Cipriano, A. M. de Brito, E. S. de Oliveira, et al., "Mutation Screening of *TP53*, *CHEK2* and *BRCA* Genes in Patients at High Risk for Hereditary Breast and Ovarian Cancer (HBOC) in Brazil," *Breast Cancer* 26, no. 3 (2019): 397–405, https://doi.org/10.1007/s12282-018-00938-z.

89. J. M. Godinez Paredes, I. Rodriguez, M. Ren, et al., "Germline Pathogenic Variants Associated With Triple-Negative Breast Cancer in US Hispanic and Guatemalan Women Using Hospital and Community-Based Recruitment Strategies," *Breast Cancer Research And Treatment* 205, no. 3 (2024): 567–577, https://doi.org/10.1007/s10549-024-07300-2.

90. G. C. Fernandes, R. A. Michelli, H. C. Galvão, et al., "Prevalence of BRCA1/BRCA2 Mutations in a Brazilian Population Sample At-Risk for Hereditary Breast Cancer and Characterization of Its Genetic Ancestry," *Oncotarget* 7, no. 49 (2016): 80465–80481, https://doi.org/10.18632/oncotarget.12610.

91. E. da Costa, S. Silva Carvalho, N. M. Cury, et al., "Germline Variants in DNA Repair Genes Associated With Hereditary Breast and Ovarian Cancer Syndrome: Analysis of a 21 Gene Panel in the Brazilian Population," *BMC Medical Genomics* 13, no. 1 (2020): 21, https://doi.org/10.1186/s12920-019-0652-y.

92. B. Alemar, J. Herzog, C. Brinckmann Oliveira Netto, et al., "Prevalence of Hispanic BRCA1 and BRCA2 Mutations Among Hereditary Breast and Ovarian Cancer Patients From Brazil Reveals Differences Among Latin American Populations," *Cancer Genetics* 209, no. 9 (2016): 417–422, https://doi.org/10.1016/j.cancergen.2016.06.008.

93. I. P. Ewald, P. Izetti, F. R. Vargas, et al., "Prevalence of the BRCA1 Founder Mutation c.5266dupin Brazilian Individuals At-Risk for the Hereditary Breast and Ovarian Cancer Syndrome," *Hereditary Cancer in Clinical Practice* 9, no. 1 (2011): 12, https://doi.org/10.1186/1897-4287-9-12.

94. R. L. Sandoval, A. C. R. Leite, D. M. Barbalho, et al., "Germline molecular data in hereditary breast cancer in Brazil: Lessons from a large single-center analysis," *PLoS One* 16, no. 2 (2021): e0247363, https://doi.org/10.1371/journal.pone.0247363.

95. D. Barbalho, R. Sandoval, E. Santos, et al., "Novel Insights From the Germline Landscape of Breast Cancer in Brazil," *Frontiers in Oncology* 11 (2022): 743231, https://doi.org/10.3389/fonc.2021.743231.

96. R. M. Dufloth, S. Carvalho, J. K. Heinrich, et al., "Analysis of BRCA1 and BRCA2 Mutations in Brazilian Breast Cancer Patients With Positive Family History," *Sao Paulo Medical Journal* 123, no. 4 (2005): 192–197, https://doi.org/10.1590/S1516-31802005000400007.

97. M. C. Gomes, M. M. Costa, R. Borojevic, et al., "Prevalence of BRCA1 and BRCA2 Mutations in Breast Cancer Patients From Brazil," *Breast Cancer Research And Treatment* 103, no. 3 (2007): 349–353, https://doi.org/10.1007/s10549-006-9378-6.

98. D. M. Carraro, M. A. Koike Folgueira, B. C. Garcia Lisboa, et al., "Comprehensive Analysis of BRCA1, BRCA2 and TP53 Germline Mutation and Tumor Characterization: A Portrait of Early-Onset Breast Cancer in Brazil," *PLoS One* 8, no. 3 (2013): e57581, https://doi.org/10.1371/journal.pone.0057581.

99. A. R. de Souza Timoteo, A. M. Gonçalves, L. A. P. Sales, et al., "A Portrait of Germline Mutation in Brazilian At-Risk for Hereditary Breast Cancer," *Breast Cancer Research And Treatment* 172, no. 3 (2018): 637–646, https://doi.org/10.1007/s10549-018-4938-0.

100. E. C. da Costa, F. R. Vargas, A. S. Moreira, et al., "Founder Effect of the BRCA1 5382insC Mutation in Brazilian Patients With Hereditary Breast Ovary Cancer Syndrome," *Cancer Genetics And Cytogenetics* 184, no. 1 (2008): 62–66, https://doi.org/10.1016/j.cancergencyto.2008.03.011.

101. E. S. de Oliveira, B. L. Soares, S. Lemos, et al., "Screening of the BRCA1 Gene in Brazilian Patients With Breast and/or Ovarian Cancer Via High-Resolution Melting Reaction Analysis," *Familial Cancer* 15, no. 2 (2016): 173–181, https://doi.org/10.1007/s10689-015-9858-0.

102. T. B. C. Megid, M. C. Barros-Filho, J. P. Pisani, and M. I. Achatz, "Double Heterozygous Pathogenic Variants Prevalence in a Cohort of Patients With Hereditary Breast Cancer," *Frontiers in Oncology* 12 (2022): 873395, https://doi.org/10.3389/fonc.2022.873395.

103. D. R. da Silva Fontinele, A. Ribeiro, R. E. da Costa, M. K. da Silva Magalhães, and S. C. Vieira, "Genetic Testing for Hereditary Predisposition to Breast Cancer in the Real World: Initial Experience," *Breast Disease* 41, no. 1 (2022): 249–254, https://doi.org/10.3233/BD-210082.

104. A. C. L. V. Gifoni, M. A. C. Gifoni, C. M. Wotroba, et al., "Hereditary Breast Cancer in the Brazilian State of Ceará (The CHANCE Cohort): Higher-Than-Expected Prevalence of Recurrent Germline Pathogenic Variants," *Frontiers in Oncology* 12 (2022): 932957, https://doi.org/10.3389/fonc.2022.932957.

105. I. Briceño-Balcázar, A. Gómez-Gutiérrez, N. A. Díaz-Dussán, M. C. Noguera-Santamaría, D. Díaz-Rincón, and M. C. Casas-Gómez, "Mutational Spectrum in Breast Cancer Associated BRCA1 and BRCA2 genes in Colombia," *Colombia Médica* 48, no. 2 (2017): 58–63, https://doi.org/10.25100/cm.v48i2.1867.

106. J. Buleje, M. Guevara-Fujita, O. Acosta, et al., "Mutational Analysis ofBRCA1andBRCA2genes in Peruvian families With Hereditary Breast And Ovarian Cancer," *Molecular Genetics & Genomic Medicine* 5, no. 5 (2017): 481–494, https://doi.org/10.1002/mgg3.301.

107. N. Landeros, L. Vargas-Roig, S. Denita, et al., "Regional Hereditary Cancer Program in Chile: A Scalable Model of Genetic Counseling and Molecular Diagnosis to Improve Clinical Outcomes for Patients With Hereditary Cancer Across Latin America," *Biological Research* 57, no. 1 (2024): 99, https://doi.org/10.1186/s40659-024-00579-x.

108. G. A. Gutiérrez Espeleta, M. Llacuachaqui, L. García-Jiménez, et al., "*BRCA1* and *BRCA2* Mutations Among Familial Breast Cancer Patients From Costa Rica," *Clinical Genetics* 82, no. 5 (2012): 484–488, https://doi.org/10.1111/j.1399-0004.2011.01774.x.

109. I. P. Ewald, S. L. Cossio, E. I. Palmero, et al., "*BRCA1* and *BRCA2* Rearrangements in Brazilian Individuals With Hereditary Breast and Ovarian Cancer Syndrome," *Genetics And Molecular Biology* 39, no. 2 (2016): 223–231, https://doi.org/10.1590/1678-4685-gmb-2014-0350.

110. E. I. Palmero, D. M. Carraro, B. Alemar, et al., "The Germline Mutational Landscape of BRCA1 and BRCA2 in Brazil," *Scientific Reports* 8, no. 1 (2018): 9188, https://doi.org/10.1038/s41598-018-27315-2.

111. J. F. Martínez González, M. G. M. Rosario, M. Corriols Molina, and J. R. Silva Arrechavala, "Genetic Mutations Associated With Hereditary Breast Cancer in Nicaraguan Women," *Revista Torreón Universitario* 29 (2021): 112–119.

112. D. Torres, J. L. Bermejo, M. U. Rashid, et al., "Prevalence and Penetrance of *BRCA1* and *BRCA2* Germline Mutations in Colombian Breast Cancer Patients," *Scientific Reports* 7, no. 1 (2017): 4713, https://doi.org/10.1038/s41598-017-05056-y.

113. L. Delgado, G. Fernández, G. Grotiuz, S. Cataldi, A. González, and N. Lluveras, "BRCA1 and BRCA2 Germline Mutations in Uruguayan Breast and Breast-Ovarian Cancer Families. Identification of Novel Mutations and Unclassified Variants," *Breast Cancer Research And Treatment* 128, no. 1 (2011): 211–218, https://doi.org/10.1007/s10549-010-1320-2.

114. M. M. González, D. P. Dressler Sanabria, and L. N. Talavera Stefani, "Variantes patogénicas en BRCA2 en Mujeres con Cáncer de Mama del Hospital Día Oncológico de Encarnación- Paraguay, período 2023," *Revista Brasileira de Cancerologia* 71, no. 2 (2025): e184962, https://doi.org/10.32635/2176-9745.RBC.2025v71n2.4962.

115. J. Dutil, J. L. Colon-Colon, J. L. Matta, R. Sutphen, and M. Echenique, "Identification of the Prevalent *BRCA1* and *BRCA2* Mutations in the Female Population of Puerto Rico," *Cancer Genetics* 205, no. 5 (2012): 242–248, https://doi.org/10.1016/j.cancergen.2012.04.002.

116. J. Lerner-Ellis, T. Donenberg, H. Ahmed, et al., "A High Frequency of PALB2 Mutations in Jamaican Patients With Breast Cancer," *Breast Cancer Research And Treatment* 162, no. 3 (2017): 591–596, https://doi.org/10.1007/s10549-017-4148-1.

117. K. Lara, N. Consigliere, J. Pérez, and A. Porco, "*BRCA1* and *BRCA2* Mutations in Breast Cancer Patients From Venezuela,"

Biological Research 45, no. 2 (2012): 117–130, https://doi.org/10.4067/S0716-97602012000200003.

118. L. Gómez-Flores-Ramos, A. L. Barraza-Arellano, A. Mohar, et al., "Germline Variants in Cancer Genes From Young Breast Cancer Mexican Patients," *Cancers* 14, no. 7 (2022): 1647, https://doi.org/10.3390/cancers14071647.

119. H. J. Diaz-Zabala, A. P. Ortiz, L. Garland, et al., "A Recurrent *BRCA2* Mutation Explains the Majority of Hereditary Breast and Ovarian Cancer Syndrome Cases in Puerto Rico," *Cancers* 10, no. 11 (2018): 419.

120. E. I. Palmero, B. Alemar, L. Schüler-Faccini, et al., "Screening for Germline *BRCA1*, *BRCA2*, *TP53* and *CHEK2* Mutations in Families At-Risk for Hereditary Breast Cancer Identified in a Population-Based Study From Southern Brazil," *Genetics and Molecular Biology* 39, no. 2 (2016): 210–222, https://doi.org/10.1590/1678-4685-gmb-2014-0363.

121. R. Gomes, P. D. S. Spinola, A. C. Brant, et al., "Prevalence of Germline Variants in Consensus Moderate-to-High-Risk Predisposition Genes to Hereditary Breast and Ovarian Cancer in BRCA1/2-Negative Brazilian Patients," *Breast Cancer Research and Treatment* 185, no. 3 (2021): 851–861, https://doi.org/10.1007/s10549-020-05985-9.

122. G. T. Torrezan, F. G. D. S. de Almeida, M. C. P. Figueiredo, et al., "Complex Landscape of Germline Variants in Brazilian Patients With Hereditary and Early Onset Breast Cancer," *Frontiers in Genetics* 9 (2018): 161, https://doi.org/10.3389/fgene.2018.00161.

123. P. S. Felicio, R. S. Grasel, N. Campacci, et al., "Whole-Exome Sequencing of Non-*BRCA*1/*BRCA*2 Mutation Carrier Cases at High-Risk for Hereditary Breast/Ovarian Cancer," *Human Mutation* 42, no. 3 (2021): 290–299, https://doi.org/10.1002/humu.24158.

124. J. Abud, P. Koehler-Santos, P. Ashton-Prolla, J. C. Prolla, and Study Group on Hereditary Breast and Colorectal Cancer, "CHEK2 1100DELC Germline Mutation: A Frequency Study in Hereditary Breast and Colon Cancer Brazilian Families," *Arquivos de Gastroenterologia* 49, no. 4 (2012): 273–278, https://doi.org/10.1590/S0004-28032012000400008.

125. C. A. B. Duarte, C. A. Dos Santos, C. D. D. de Oliveira, C. C. Spautz, L. M. Sumita, and S. M. Nakatani, "Hereditary Breast Cancer Next-Generation Sequencing Panel Evaluation in the South Region of Brazil: A Novel *BRCA2* Candidate Pathogenic Variant Is Reported," *Molecular Genetics & Genomic Medicine* 12, no. 8 (2024): e2504, https://doi.org/10.1002/mgg3.2504.

126. J. N. Weitzel, S. L. Neuhausen, A. Adamson, et al., "Pathogenic and Likely Pathogenic Variants in *PALB2*, *CHEK2*, and Other Known Breast Cancer Susceptibility Genes Among 1054 BRCA-Negative Hispanics With Breast Cancer," *Cancer* 125, no. 16 (2019): 2829–2836, https://doi.org/10.1002/cncr.32083.

127. D. Aguilar, M. L. Garza-Rodríguez, C. E. Muñiz-Garza, et al., "Los Olvidados: Non-BRCA Variants Associated With Hereditary Breast Cancer in Mexican Population," *Breast Cancer Research* 27, no. 1 (2025): 7, https://doi.org/10.1186/s13058-024-01957-9.

128. C. E. Díaz-Velásquez, R. Gitler, A. Antoniano, et al., "Evaluation of Genetic Alterations in Hereditary Cancer Susceptibility Genes in the Ashkenazi Jewish Women Community of Mexico," *Frontiers in Genetics* 14 (2023): 1094260, https://doi.org/10.3389/fgene.2023.1094260.

129. A. Gonzalez, F. Del Greco, L. Vargas-Roig, et al., "PALB2 Germline Mutations in a Multi-Gene Panel Testing Cohort of 1905 Breast-Ovarian Cancer Patients in Argentina," *Breast Cancer Research and Treatment* 194, no. 2 (2022): 403–412, https://doi.org/10.1007/s10549-022-06620-5.

130. E. C. Hahn, C. M. Bittar, F. S. L. Vianna, et al., "TP53 p.Arg337His Germline Mutation Prevalence in Southern Brazil: Further Evidence for Mutation Testing in Young Breast Cancer Patients," *PLoS One* 13, no. 12 (2018): e0209934, https://doi.org/10.1371/journal.pone.0209934.

131. N. M. Cury, V. E. Ferraz, and W. A. Silva, "TP53 p.R337H Prevalence in a Series of Brazilian Hereditary Breast Cancer Families," *Hereditary Cancer In Clinical Practice* 12, no. 1 (2014): , https://doi.org/10.1186/1897-4287-12-8.

132. E. I. Palmero, L. Schüler-Faccini, M. Caleffi, et al., "Detection of R337H, a Germline TP53 Mutation Predisposing to Multiple Cancers, in Asymptomatic Women Participating in a Breast Cancer Screening Program in Southern Brazil," *Cancer Letter* 261, no. 1 (2008): 21–25, https://doi.org/10.1016/j.canlet.2007.10.044.

133. K. C. Andrade, K. M. Santiago, F. P. Fortes, L. I. Mambelli, A. F. Nóbrega, and M. I. Achatz, "Early-Onset Breast Cancer Patients in the South and Southeast of Brazil Should Be Tested for the TP53 p.R337H Mutation," *Genetics And Molecular Biology* 39, no. 2 (2016): 199–202, https://doi.org/10.1590/1678-4685-gmb-2014-0343.

134. J. Giacomazzi, M. S. Graudenz, C. A. Osorio, et al., "Prevalence of the TP53 p.R337H Mutation in Breast Cancer Patients in Brazil," *PLoS One* 9, no. 6 (2014): e99893, https://doi.org/10.1371/journal.pone.0099893.

135. J. G. Assumpção, A. L. Seidinger, M. J. Mastellaro, et al., "Association of the Germline TP53 R337H Mutation With Breast Cancer in Southern Brazil," *BMC Cancer* 8, no. 1 (2008): 357, https://doi.org/10.1186/1471-2407-8-357.

136. T. S. Corrêa, P. F. Asprino, E. S. C. de Oliveira, et al., "TP53 p.R337H Germline Variant Among Women at Risk of Hereditary Breast Cancer in a Public Health System of Midwest Brazil," *Genes* 15, no. 7 (2024): 928, https://doi.org/10.3390/genes15070928.

137. P. F. F. da Silva, R. M. Goveia, T. B. Teixeira, et al., "TP53 Pathogenic Variants in Early-Onset Breast Cancer Patients Fulfilling Hereditary Breast and Ovary Cancer and Li-Fraumeni-Like Syndromes," *Biomolecules* 12, no. 5 (2022): 640, https://doi.org/10.3390/biom12050640.

138. R. L. Sandoval, N. Polidorio, A. C. R. Leite, et al., "Breast Cancer Phenotype Associated With Li-Fraumeni Syndrome: A Brazilian Cohort Enriched by TP53 p.R337H Carriers," *Frontiers in Oncology* 12 (2022): 836937, https://doi.org/10.3389/fonc.2022.836937.

139. E. Zavaleta, N. Solis, M. I. Palacios, et al., "Genetic Characterization in High-Risk Individuals From a Low-Resource City of Peru," *Cancers* 14, no. 22 (2022): 5603, https://doi.org/10.3390/cancers14225603.

140. L. N. Gallardo-Alvarado, M. T. Tusié-Luna, M. I. Tussié-Luna, et al., "Prevalence of Germline Mutations in the *TP53* Gene in Patients With Early-Onset Breast Cancer in the Mexican Population," *BMC Cancer* 19, no. 1 (2019): 118, https://doi.org/10.1186/s12885-019-5312-2.

141. S. G. Warneford, L. J. Witton, M. L. Townsend, et al., "Germ-Line Splicing Mutation of the p53 Gene in a Cancer-Prone Family," *Cell Growth And Differentiation* 3, no. 11 (1992): 839–846.

142. J. M. Varley, C. Attwooll, G. White, et al., "Characterization of Germline *TP53* Splicing Mutations and Their Genetic and Functional Analysis," *Oncogene* 20, no. 21 (2001): 2647–2654, https://doi.org/10.1038/sj.onc.1204369.

143. E. M. Pinto, K. N. Maxwell, H. Halalsheh, et al., "Clinical and Functional Significance of TP53 Exon 4-Intron 4 Splice Junction Variants," *Molecular Cancer Research* 20, no. 2 (2022): 207–216, https://doi.org/10.1158/1541-7786.MCR-21-0583.

144. R. S. Grasel, P. S. Felicio, A. E. de Paula, et al., "Using Co-Segregation and Loss of Heterozygosity Analysis to Define the Pathogenicity of Unclassified Variants in Hereditary Breast Cancer Patients," *Frontiers in Oncology* 10 (2020): 571330, https://doi.org/10.3389/fonc.2020.571330.

145. J. Dutil, J. K. Teer, V. Golubeva, et al., "Germline Variants in Cancer Genes in High-Risk Non-BRCA Patients From Puerto Rico," *Scientific Reports* 9, no. 1 (2019): 17769, https://doi.org/10.1038/s41598-019-54170-6.

146. D. Fanale, A. Pivetti, and D. Cancelliere, "BRCA1/2 Variants of Unknown Significance in Hereditary Breast and Ovarian Cancer (HBOC) Syndrome: Looking for the Hidden Meaning," *Critical Reviews*

in Oncology/Hematology 172 (2022): 103626, https://doi.org/10.1016/j.critrevonc.2022.103626.

147. M. I. Achatz, M. Caleffi, R. Guindalini, R. M. Marques, A. Nogueira-Rodrigues, and P. Ashton-Prolla, "Recommendations for Advancing the Diagnosis and Management of Hereditary Breast and Ovarian Cancer in Brazil," *JCO Global Oncology* 6 (2020): 439–452, https://doi.org/10.1200/JGO.19.00170.

148. S. Morales-Pison, P. Gonzalez-Hormazabal, J. C. Tapia, et al., "Heritable Genomic Diversity in Breast Cancer Driver Genes and Associations With Risk in a Chilean Population," *Biological Research* 55, no. 1 (2022): 20, https://doi.org/10.1186/s40659-022-00384-4.

149. F. J. Martin, I. M. Saffie, M. A. Hurtado, et al., "Variants In Brca1/2 In A Hospital-Based Cohort In Chile And National Literature Review," *Ecancermedicalscience* 18 (2024): 1683, https://doi.org/10.3332/ecancer.2024.1683.

150. F. Acevedo, B. Walbaum, M. Camus, et al., "Access Disparities and Underutilization of Germline Genetic Testing in Chilean Breast Cancer Patients," *Breast Cancer Research and Treatment* 199, no. 2 (2023): 363–370, https://doi.org/10.1007/s10549-023-06909-z.

151. N. Landeros, R. Hasbún, P. Alarcón, et al., "Descentralización Del Asesoramiento Genético Oncológico Y Diagnóstico Molecular En Chile: Programa Regional De Cáncer Hereditario," *Revista Médica Maule* 41, no. 1 (2026): 5–11.

152. M. Sans, F. M. Salzano, and R. Chakraborty, "Historical Genetics in Uruguay: Estimates of Biological Origins and Their Problems," *Human Biology* 69, no. 2 (1997): 161–170.

153. W. Rojas, M. V. Parra, O. Campo, et al., "Genetic Make Up and Structure of Colombian Populations by Means of Uniparental and Biparental DNA Markers," *AMerican Journal Of Physical Anthropology* 143, no. 1 (2010): 13–20, https://doi.org/10.1002/ajpa.21270.

154. J. Olaya, J. Sanjuan, D. Torres-Lopez, et al., "Sociodemographic, Clinical, and Variation Outcomes for Breast Cancer and Breast Cancer-Related Mutations in a Ten-Year Cohort From Neiva, Huila, Colombia," *Cureus* 14, no. 12 (2022): e32257, https://doi.org/10.7759/cureus.32257.

155. C. Villarreal-Garza, A. Platas, M. Miaja, et al., "Young Women With Breast Cancer in Mexico: Results of the Pilot Phase of the Joven & Fuerte Prospective Cohort," *JCO Global Oncology* 6 (2020): 395–406, https://doi.org/10.1200/JGO.19.00264.

156. J. J. Salinas, R. Roy, A. K. Dwivedi, and N. K. Shokar, "Hereditary Breast Cancer Risk Analysis in Uninsured Mexican-Origin Women Living in the U.S.-Mexico Border Region," *Hispanic Health Care International* 17, no. 3 (2019): 118–124, https://doi.org/10.1177/1540415319837850.

157. J. C. Martínez-Cruzado, G. Toro-Labrador, J. Viera-Vera, et al., "Reconstructing the Population History of Puerto Rico by Means of mtDNA Phylogeographic Analysis," *American Journal Of Physical Anthropology* 128, no. 1 (2005): 131–155, https://doi.org/10.1002/ajpa.20108.

158. J. Söchtig, V. Álvarez-Iglesias, A. Mosquera-Miguel, M. Gelabert-Besada, A. Gómez-Carballa, and A. Salas, "Genomic Insights on the Ethno-History of the Maya and the 'Ladinos' From Guatemala," *BMC Genomics* 16, no. 1 (2015): 131, https://doi.org/10.1186/s12864-015-1339-1.

159. R. C. Rodriguez, A. A. Esperon, R. Ropero, et al., "Prevalence of BRCA1 and BRCA2 Mutations in Breast Cancer Patients From Cuba," *Familial Cancer* 7, no. 3 (2008): 275–279, https://doi.org/10.1007/s10689-008-9187-7.

160. M. R. Akbari, T. Donenberg, J. Lunn, et al., "The Spectrum of BRCA1 and BRCA2 Mutations in Breast Cancer Patients in the Bahamas," *Clinical Genetics* 85, no. 1 (2014): 64–67, https://doi.org/10.1111/cge.12132.

161. T. Donenberg, H. Ahmed, R. Royer, et al., "A Survey of *BRCA1*, *BRCA2*, and *PALB2* Mutations in Women With Breast Cancer in Trinidad and Tobago," *Breast Cancer Research And Treatment* 159, no. 1 (2016): 131–138, https://doi.org/10.1007/s10549-016-3870-4.

162. C. A. Ossa Gomez, M. I. Achatz, M. Hurtado, et al., "Germline Pathogenic Variant Prevalence Among Latin American and US Hispanic Individuals Undergoing Testing for Hereditary Breast and Ovarian Cancer: A Cross-Sectional Study," *JCO Global Oncology* 8, no. 8 (2022): e2200104, https://doi.org/10.1200/GO.22.00104.

163. E. M. Pinto, and G. P. Zambetti, "What 20 Years of Research Has Taught Us About the *TP53* p.R337H Mutation," *Cancer* 126, no. 21 (2020): 4678–4686, https://doi.org/10.1002/cncr.33143.

164. S. Garritano, F. Gemignani, E. I. Palmero, et al., "Detailed Haplotype Analysis at the TP53 Locus in p.R337H Mutation Carriers in the Population of Southern Brazil: Evidence for a Founder Effect," *Human Mutation* 31, no. 2 (2010): 143–150, https://doi.org/10.1002/humu.21151.

165. D. D. Paskulin, J. Giacomazzi, M. I. Achatz, et al., "Ancestry of the Brazilian *TP53* c.1010G>A (p.Arg337His, R337H) Founder Mutation: Clues From Haplotyping of Short Tandem Repeats on Chromosome 17p," *PLoS One* 10, no. 11 (2015): e0143262, https://doi.org/10.1371/journal.pone.0143262.

166. G. Custódio, G. A. Parise, N. Kiesel Filho, et al., "Impact of Neonatal Screening and Surveillance for the *TP53* R337H Mutation on Early Detection of Childhood Adrenocortical Tumors," *Journal of Clinical Oncology* 31, no. 20 (2013): 2619–2626, https://doi.org/10.1200/JCO.2012.46.3711.

167. J. Dutil, V. A. Golubeva, A. L. Pacheco-Torres, H. J. Diaz-Zabala, J. L. Matta, and A. N. Monteiro, "The Spectrum of *BRCA1* and *BRCA2* Alleles in Latin America and the Caribbean: A Clinical Perspective," *Breast Cancer Research and Treatment* 154, no. 3 (2015): 441–453, https://doi.org/10.1007/s10549-015-3629-3.

168. G. Sirugo, S. M. Williams, and S. A. Tishkoff, "The Missing Diversity in Human Genetic Studies," *Cell* 177, no. 1 (2019): 26–31, https://doi.org/10.1016/j.cell.2019.02.048.

169. M. B. Daly, R. Pilarski, M. B. Yurgelun, et al., "NCCN Guidelines Insights: Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic, Version 1.2020," *Journal of the National Comprehensive Cancer Network* 18, no. 4 (2020): 380–391, https://doi.org/10.6004/jnccn.2020.0017.

170. S. Bertozzi, A. P. Londero, A. Xholli, et al., "Risk-Reducing Breast and Gynecological Surgery for BRCA Mutation Carriers: A Narrative Review," *Journal of Clinical Medicine* 12, no. 4 (2023): 1422, https://doi.org/10.3390/jcm12041422.

171. R. Ruiz, K. Strasser-Weippl, D. Touya, et al., "Improving Access to High-Cost Cancer Drugs in Latin America: Much to Be Done," *Cancer* 123, no. 8 (2017): 1313–1323, https://doi.org/10.1002/cncr.30549.

172. H. S. Han, V. Diéras, M. Robson, et al., "Veliparib With Temozolomide or Carboplatin/Paclitaxel Versus Placebo With Carboplatin/Paclitaxel in Patients With *BRCA1/2* Locally Recurrent/Metastatic Breast Cancer: Randomized Phase II Study," *Annals of Oncology* 29, no. 1 (2018): 154–161, https://doi.org/10.1093/annonc/mdx505.

173. S. Stodtmann, D. Eckert, R. Joshi, et al., "Exposure-Response Model With Time-Varying Predictors to Estimate the Effects of Veliparib in Combination With Carboplatin/Paclitaxel and as Monotherapy: Veliparib Phase 3 Study in BRCA-Mutated Advanced Breast Cancer (BROCADE3) Trial," *Journal of Clinical Pharmacology* 62, no. 10 (2022): 1236–1246, https://doi.org/10.1002/jcph.2061.

174. R. E. da Costa, F. T. de Oliveira, A. L. Araújo, and S. C. Vieira, "Pathogenic Variants in BRCA1/2 Genes Among Patients With Triple-Negative Breast cancer," *Mastology* 31 (2021): 1–5, https://doi.org/10.29289/2594539420210032.

175. F. Vaca-Paniagua, R. M. Alvarez-Gomez, V. Fragoso-Ontiveros, et al., "Full-Exon Pyrosequencing Screening of BRCA Germline Mutations in Mexican Women With Inherited Breast and Ovarian Cancer," *PLoS One* 7, no. 5 (2012): e37432, https://doi.org/10.1371/journal.pone.0037432.

176. P. Ruiz-Flores, O. M. Sinilnikova, M. Badzioch, et al., "BRCA1 and BRCA2 Mutation Analysis of Early-Onset and Familial Breast Cancer Cases in Mexico," *Human Mutation* 20, no. 6 (2002): 474–475, https://doi.org/10.1002/humu.9084.

177. R. M. de Freitas, G. Alves, M. R. Guerra, et al., "Overview of Germline Variants in the BRCA2 Gene in Cohort of Brazilian Women With a High Risk of Hereditary Breast Cancer," *Mastology* 32 (2026): , https://doi.org/10.29289/2594539420220003.

178. A. L. Calderón-Garcidueñas, P. Ruiz-Flores, R. M. Cerda-Flores, and H. A. Barrera-Saldaña, "Clinical Follow Up of Mexican Women With Early Onset of Breast Cancer and Mutations in the BRCA1 and BRCA2 Genes," *Salud publica de Mexico* 47, no. 2 (2005): 110–115, https://doi.org/10.1590/S0036-36342005000200004.

179. N. Llinás-Quintero, E. Cabrera-Florez, G. Mendoza-Fandiño, G. Matute-Turizo, E. M. Vasquez-Trespalacios, and L. J. Gallón-Villegas, "Synchronous Ovarian and Breast Cancers With a Novel Variant in BRCA2 Gene: A Case Report," *Case Reports in Oncological Medicine* 2019 (2019): 6958952, https://doi.org/10.1155/2019/6958952.

Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Supporting Information.** File S1: Search strategy Search strategy used in PubMed. Table S1: Pathogenic variants present in the BRCA1 gene identified in a single Latin America and the Caribbean country. Table S2: Pathogenic variants present in the BRCA2 gene identified in a single Latin American and Caribbean country.