Variants in *BRCA1/2* in a hospital-based cohort in Chile and national literature review.

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**Supplementary table 1: Positive results in other genes.**

|  |  |
| --- | --- |
| Gene | Individuals |
| *APC* | 1 |
| *ATM* | 17 |
| *ATR* | 1 |
| *AXIN2* | 1 |
| *CDKN2A* | 6 |
| *CHEK2* | 9 |
| *FANCM* | 2 |
| *MSH2* | 4 |
| *MSH3\** | 1 |
| *MSH6* | 2 |
| *MUTYH\** | 4 |
| *NBN* | 1 |
| *NF1* | 1 |
| *PALB2* | 2 |
| *PTEN* | 1 |
| *RAD50* | 3 |
| *RAD51C* | 2 |
| *RAD51D* | 6 |
| *RET* | 2 |
| *TP53* | 6 |
| Total | 72 |

**\***Genes with an autosomal recessive mode of inheritance, considered carriers in manuscript.

**Supplementary Table 2: VUS by gene FALP cohort.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Variant | Cigocity | ACMG classification | Nº Individuals |
| *BRIP1* | c.3411\_3412delTGinsCC (p.Asp1138His) | Heterozygous | VUS | 1 |
| *ABRAXAS1* | c.601A>C (p.Lys201Gln) | Heterozygous | VUS | 1 |
| *ABRAXAS1* | c.272A>T (p.Asn91Ile) | Heterozygous | VUS | 1 |
| *AKT1* | c.7G>A (p.Asp3Asn) | Heterozygous | VUS | 1 |
| *APC* | c.7415C>T (p.Ala2472Val) | Heterozygous | VUS | 1 |
| *APC* | c.2464C>T (p.Leu822Phe) | Heterozygous | VUS | 1 |
| *APC* | c.3629A>T(p.His1210Leu) | Heterozygous | VUS | 1 |
| *APC* | c.1366C>A (p.Leu456Ile) | Heterozygous | VUS | 1 |
| *APC* | c.6017G>A (p.Gly2006Asp) | Heterozygous | VUS | 2 |
| *APC* | c.3629A>T (p.His1210Leu) | Heterozygous | VUS | 1 |
| *APC* | c.6744A>G (Silent) | Heterozygous | VUS | 1 |
| *ATM* | c.2494C>T (p.Arg832Cys) | Heterozygous | VUS | 1 |
| *ATM* | c.1595G>A (p.Cys532Tyr) | Heterozygous | VUS | 1 |
| *ATM* | c.1009C>T (p.Arg337Cys) | Heterozygous | VUS | 1 |
| *ATM* | c.7327C>G(P.aRG2443gLY) | Heterozygous | VUS | 1 |
| *ATM* | c.3136C>T(P.Leu1046Phe) | Heterozygous | VUS | 1 |
| *ATM* | c.404G>A (p.Ala135Tyr) | Heterozygous | VUS | 1 |
| *ATM* | c.3016A>G( P.mET1006Val) | Heterozygous | VUS | 1 |
| *ATM* | c.1595G>A (p.Cys532Tyr) | Heterozygous | VUS | 1 |
| *ATM* | c.8810T>C (p.Val2937Ala) | Heterozygous | VUS | 1 |
| *ATM* | c.2638+6T>C (Intronic) | Heterozygous | VUS | 1 |
| *ATM* | c.8810T>C (p.Val2937Ala) | Heterozygous | VUS | 1 |
| *ATM* | c.3360T>G (p.Phe1120Leu) | Heterozygous | VUS | 1 |
| *ATM* | c.2051A>G (p.Gln684Arg) | Heterozygous | VUS | 1 |
| *ATM* | c.2143C>G (p.Leu715Val | Heterozygous | VUS | 1 |
| *ATM* | c.8850+5A>T (Intronic) | heterozygous | VUS | 1 |
| *ATM* | c.2012T>A (p.Ile671Lys) | heterozygous | VUS | 1 |
| *ATM* | Gain (Exons 62-63) | copy number = 3 | VUS | 1 |
| *ATM* | c.2452A>G (p.Ile818Val) | Heterozygous | VUS | 1 |
| *ATM* | c.9073G>A (p.Val3025Met) | Heterozygous | VUS | 1 |
| *AXIN2* | c.1741C>T(p.Arg581Cys) | Heterozygous | VUS | 1 |
| *AXIN2* | c.1501G>A (p.Gly501Arg) | Heterozygous | VUS | 1 |
| *AXIN2* | c.475G>T (p.Asp159Tyr) | Heterozygous | VUS | 1 |
| *AXIN2* | c.2206C>T (p.Pro736Ser) | Heterozygous | VUS | 1 |
| *AXIN2* | c.1741C>T (p.Arg581Cys) | Heterozygous | VUS | 1 |
| *AXIN2* | c.857G>A (p.Gly286Asp) | Heterozygous | VUS | 1 |
| *AXIN2* | c.1741C>T (p.Arg581Cys) | Heterozygous | VUS | 2 |
| *BAP1* | c.1331C>T (p.Thr444Ile) | Heterozygous | VUS | 1 |
| *BARD1* | c.94G>A (p.Gly32Arg) | Heterozygous | VUS | 1 |
| *BARD1* | c.905A>C (p.Lys302Thr) | Heterozygous | VUS | 1 |
| *BARD1* | c.1028C>T (p.Thr343Ile) | Heterozygous | VUS | 1 |
| *BARD1* | c.1912G>C (p.Ala638Pro) | Heterozygous | VUS | 1 |
| *BARD1* | c.2155A>G(p.Thr719Ala) | Heterozygous | VUS | 1 |
| *BARD1* | c.1268A>G (p.Lys423Arg) | heterozygous | VUS | 1 |
| *BLM* | c.264C>A (p.Asp88Glu) | Heterozygous | VUS | 1 |
| *BMPR1A* | c.749T>C (p.Met250Thr) | Heterozygous | VUS | 1 |
| *BMPR1A* | c.1411C>T (p.Arg471Cys) | Heterozygous | VUS | 1 |
| *BRCA1* | c.1108G>A(pVal370lle) c.2389A>C(p.Lys797Gln | Heterozygous | VUS | 1 |
| *BRCA1* | c.2258G>A(p.Ser753Asn) | Heterozygous | VUS | 1 |
| *BRCA1* | c.3584A>G(p.His1195Arg) | Heterozygous | VUS | 1 |
| *BRCA1* | c.350A>T (p.His117Leu) | Heterozygous | VUS | 1 |
| *BRCA1* | c.3548A>T (p.Lys1183Ile) | Heterozygous | VUS | 1 |
| *BRCA2* | c.9271G>A(p.Val3091lle) | Heterozygous | VUS | 1 |
| *BRCA2* | c.4750G>C (p.Glu1584Gln) | Heterozygous | VUS | 1 |
| *BRCA2* | c.-40G>C (Non-coding) | Heterozygous | VUS | 1 |
| *BRCA2* | c.2274T>G (p.Ser758Arg) | Heterozygous | VUS | 1 |
| *BRCA2* | c.8468A>G (p.Gln2823Arg) | Heterozygous | VUS | 1 |
| *BRCA2* | c.8072C>T (p.Ser2691Phe) | Heterozygous | VUS | 1 |
| *BRCA2* | c.7933A>G (p.Arg2645Gly) | Heterozygous | VUS | 1 |
| *BRCA2* | c.4736C>T (p.Ala1579Val) | Heterozygous | VUS | 1 |
| *BRCA2* | c.2281T>C (p.Tyr761His) | Heterozygous | VUS | 1 |
| *BRCA2* | c.5428G>A (p.Val1810Ile) | Heterozygous | VUS | 1 |
| *BRCA2* | c.8468A>G (p.Gln2823Arg) | Heterozygous | VUS | 1 |
| *BRCA2* | c.4747\_4749delATT (p.lle1583del) | Heterozygous | VUS | 1 |
| *BRCA2* | c.4736C>T (p.Ala1579Val) | Heterozygous | VUS | 1 |
| *BRCA2* | c.2389A>C (p.Lys797Gln) | Heterozygous | VUS | 1 |
| *BRIP1* | c.3651G>T(p.Trp1217Cys) | Heterozygous | VUS | 1 |
| *BRIP1* | c.1153C>A(p.Leu385Met) | Heterozygous | VUS | 1 |
| *BRIP1* | c.2220G>T(p.Gln74Ohis) | Heterozygous | VUS | 1 |
| *BRIP1* | c.1477C>T (p.His493Tyr) | Heterozygous | VUS | 1 |
| *BRIP1* | c.2330G>A (p.Arg777His) | Heterozygous | VUS | 1 |
| *BRIP1* | c.415T>G (p.Ser139Ala) | Heterozygous | VUS | 1 |
| *BRIP1* | c.316C>T (p.Arg106Cys) | Heterozygous | VUS | 1 |
| *BRIP1* | c.82A>G (p.Met28Val) | Heterozygous | VUS | 1 |
| *BRIP1* | c.3571A>G (p.Ile1191Val) | Heterozygous | VUS | 1 |
| *BRIP1* | c.997A>G (p.Lys333Glu) | Heterozygous | VUS | 1 |
| *BUB1B* | c.572C>A (p.Ser191Tyr) | Heterozygous | VUS | 1 |
| *BUB1B* | c.2dup (p.Met1?) | Heterozygous | VUS | 1 |
| *CDC73* | c.917G>A (p.Gly306Asp) | Heterozygous | VUS | 1 |
| *CDH1* | c.44\_46dupTGC (p.Leu15dup) | Heterozygous | VUS | 1 |
| *CDH1* | c.1168G>T (p.Asn390Asp) | Heterozygous | VUS | 2 |
| *CDKN2A* | c.94G>A (p.Gly32Arg) | Heterozygous | VUS | 1 |
| *CEP57* | c.628A>T (p.Met210Leu) | Heterozygous | VUS | 1 |
| *CHEK2* | c.1582G>A(p.Glu528Lys9 | Heterozygous | VUS | 2 |
| *CHEK2* | c.904G>A (p.Glu302Lys) | Heterozygous | VUS | 1 |
| *CHEK2* | c.1505A>G (p.Glu502Gly | Heterozygous | VUS | 1 |
| *CHEK2* | c.1427C>T(p.Thr476Met) | Heterozygous | VUS | 1 |
| *CHEK2* | c.1008G>A (Silent) | Heterozygous | VUS | 1 |
| *CHEK2* | c.246\_260del (p.Asp82\_Glu86del) | Heterozygous | VUS | 1 |
| *CHEK2* | c.46A>C (p.Ser16Arg) | heterozygous | VUS | 1 |
| *DICER1* | c.3388G>A (p.Glu1130Lys) | Heterozygous | VUS | 1 |
| *DICER1* | c.4406T>C(p.Leu1469Pro) | Heterozygous | VUS | 1 |
| *DICER1* | c.3328A>G (p.Ile1110Val) | Heterozygous | VUS | 1 |
| *DICER1* | c.77C>T (p.Pro26Leu) | Heterozygous | VUS | 1 |
| *DICER1* | c.3728T>C (p.Leu1243Pro) | Heterozygous | VUS | 1 |
| *DICER1* | c.5738A>G (p.Lys1913Arg) | Heterozygous | VUS | 2 |
| *DICER1* | c.2228C>A (p.Thr743Lys) | Possibly mosaic | VUS | 1 |
| *DICER1* | c.3380T>G (p.Ile1127Ser) | Heterozygous | VUS | 1 |
| *DICER1* | c.5471G>A (p.Gly1824Glu) | heterozygous | VUS | 1 |
| *DIL3L2* | c.1447C>G (p.Arg483Gly) | Heterozygous | VUS | 1 |
| *EPCAM* | Gain (Entire coding sequence) | copy number = 4 | VUS | 1 |
| *FANCC* | c.395C>G (p.Ala132Gly) | Heterozygous | VUS | 1 |
| *FANCM* | c.1091G>C(p.Cys364ser) | Heterozygous | VUS | 1 |
| *FANCM* | c.4366C>T (p.Arg1456Cys) | Heterozygous | VUS | 2 |
| *FANCM* | c.5669T>C (p.Met1890Thr) | Heterozygous | VUS | 1 |
| *FANCM* | c.1741C>T (p.Arg581Cys) | Heterozygous | VUS | 1 |
| *FANCM* | c.1667A>G (p.Asp556Gly) | Heterozygous | VUS | 1 |
| *FANCM* | c.5228C>A (p.Ser1743Tyr) | Heterozygous | VUS | 1 |
| *FANCM* | c.5893\_5895del (p.Val1965del) | Heterozygous | VUS | 1 |
| *FANCM* | c.6143T>C (p.Ile2048Thr) | Heterozygous | VUS | 1 |
| *FANCM* | c.5792G>A (p.Arg1931Gln) | Heterozygous | VUS | 1 |
| *FANCM* | c.3653A>G (p.Glu1218Gly) | Heterozygous | VUS | 1 |
| *HOXB13* | c.349G>A (p.Gly117Arg) | Heterozygous | VUS | 1 |
| *HOXB13* | c.686G>A (p.Arg229Gln) | Heterozygous | VUS | 1 |
| *KIT* | c.1176C>A (p.Phe392Leu) | Heterozygous | VUS | 1 |
| *KIT* | c.164G>A (p.Arg55Lys) | Heterozygous | VUS | 1 |
| *MEN1* | c.16G>A (p.Ala6Thr) | Heterozygous | VUS | 1 |
| *MLH1* | c.2060G>A(p.Arg687Gln) | Heterozygous | VUS | 1 |
| *MLH1* | c.1270G>A (p.Ala424Thr) | Heterozygous | VUS | 1 |
| *MLH1* | c.2060G>A (p.Arg687Gln) | Heterozygous | VUS | 3 |
| *MLH1* | c.1470G>A (p.Met490Ile) | Heterozygous | VUS | 1 |
| *MLH1* | c.1270G>A (p.Ala424Thr) | Heterozygous | VUS | 1 |
| *MRE11* | c.1715G>A (p.Arg572Gln) | Heterozygous | VUS | 1 |
| *MRE11* | c.1858A>G (p.Ile620Val) | Heterozygous | VUS | 1 |
| *MRE11* | c.274G>A (p.Glu92Lys) | Heterozygous | VUS | 1 |
| *MRE11* | c.1822T>G (p.Ser608Ala) | Heterozygous | VUS | 1 |
| *MRE11* | c.1853T>G (p.Met618Arg) | Heterozygous | VUS | 1 |
| *MSH2* | Gain (Exons 1-10) | copy number = 4 | VUS | 1 |
| *MSH2* | Gain (Exons 11-16) | copy number = 3 | VUS | 1 |
| *MSH2* | c.2572G>A (p.Gly858Arg) | Heterozygous | VUS | 1 |
| *MSH6* | c.1982G>A (p.Gly661Asp) | Heterozygous | VUS | 1 |
| *MSH6* | c.3466A>G (p.Met1156Val) | Heterozygous | VUS | 1 |
| *MSH6* | c.1909C>T (p.Leu637Phe) | Heterozygous | VUS | 1 |
| *MSH6* | c.898C>T (p.Arg300Trp) | Heterozygous | VUS | 1 |
| *MSH6* | c.3316G>C (p.Asp1106His) | Heterozygous | VUS | 1 |
| *MSH6* | c.908T>C (p.Met303Thr) | Heterozygous | VUS | 1 |
| *MSH6* | c.1168G>T (p.Asp390Tyr) | Heterozygous | VUS | 2 |
| *MSH6* | c.2303C>G (p.Pro768Arg) | Heterozygous | VUS | 1 |
| *MSH6* | c.908T>C (p.Met303Thr) | Heterozygous | VUS | 2 |
| *MSH6* | c.451T>A (p.Tyr151Asn) | Heterozygous | VUS | 1 |
| *MSH6* | c.1343G>A (p.Gly448Glu) | Heterozygous | VUS | 1 |
| *MSH6* | c.1844G>C (p.Cys615Ser) | Heterozygous | VUS | 1 |
| *MSH6* | c.3841G>C (p.Glu1281Gln) | Heterozygous | VUS | 1 |
| *MSH6* | c.1312A>G (p.Met438Val) | Heterozygous | VUS | 1 |
| *MUTYH* | c.920G>A (p.Arg307Gln) | Heterozygous | VUS | 1 |
| *MUTYH* | AC.1301C>T(p.Thr434Met) | Heterozygous | VUS | 1 |
| *MUTYH* | c.925C>T(p.Arg309Cys) | Heterozygous | VUS | 1 |
| *MUTYH* | c.1301C>T (p.Thr434Met) | Heterozygous | VUS | 1 |
| *MUTYH* | c.1301C>T (p.Thr434Met) | Heterozygous | VUS | 2 |
| *MUTYH* | c.571C>G (p.Arg191Gly) | Heterozygous | VUS | 1 |
| *MUTYH* | c.1301C>T (p.Thr434Met) | Heterozygous | VUS | 1 |
| *MUTYH* | c.1476+2C>T (Splice donor) | Heterozygous | VUS | 1 |
| *NBN* | c.394A>G(p.lle123Val) | Heterozygous | VUS | 1 |
| *NBN* | c.1412A>G(p.Glu471Gly) | Heterozygous | VUS | 1 |
| *NBN* | c.796C>T (p.Pro266Ser) | Heterozygous | VUS | 2 |
| *NBN* | c.1373A>G (p.Tyr458Cys) | Heterozygous | VUS | 1 |
| *NBN* | Gain (Entire coding sequence) | copy number = 3 | VUS | 1 |
| *NBN* | c.628G>T (p.Val210Phe) | Heterozygous | VUS | 1 |
| *NF1* | c.5668A>G (p.Ile1890Val) | Heterozygous | VUS | 2 |
| *NF1* | c.2032C>G (p.Pro678Ala) | Heterozygous | VUS | 1 |
| *NF1* | c.7150A>G (p.Ile2384Val) | Heterozygous | VUS | 1 |
| *NF1* | c.6579+3A>G (Intronic) | Heterozygous | VUS | 1 |
| *NF1* | c.6943G>A (p.Ala2315Thr) | Heterozygous | VUS | 1 |
| *NF1* | c.4627C>T (p.Leu1543Phe) | Heterozygous | VUS | 1 |
| *NF1* | c.3428A>G (p.His1143Arg) | Heterozygous | VUS | 1 |
| *NF1* | c.643A>T (p.Ser215Cys) | Heterozygous | VUS | 1 |
| *NTHL1* | c.17A>T (p.Glu6Val) | Heterozygous | VUS | 1 |
| *PALB2* | c.127A>G (p.Lys43Glu) | Heterozygous | VUS | 1 |
| *PALB2* | c.2129C>T(p.Thr710Met) | Heterozygous | VUS | 1 |
| *PALB2* | c.2623A>G (p.Met875Val) | Heterozygous | VUS | 1 |
| *PALB2* | c.1772C>A (p.Pro591Gln) | Heterozygous | VUS | 1 |
| *PALB2* | c.3553T>C (p.Tyr1185His) | Heterozygous | VUS | 1 |
| *PALB2* | c.2623A>G (p.Met875Val) | Heterozygous | VUS | 2 |
| *PDGFRA* | c.1099G>A(p.Val367Met) | Heterozygous | VUS | 1 |
| *PDGFRA* | c.3179T>A(p.lle1060Asn) | Heterozygous | VUS | 1 |
| *PHOX2B* | c.833G>T (p.Gly278Val) | Heterozygous | VUS | 1 |
| *PMS2* | c.1465G>A (p.Glu489Lys) | Heterozygous | VUS | 1 |
| *PMS2* | c.1358T>C (p.Met453Thr) | Heterozygous | VUS | 1 |
| *PMS2* | c.1559C>T (p.Ala520Val) | Heterozygous | VUS | 1 |
| *PMS2* | c.1433G>T (p.Ser478Ile) | Heterozygous | VUS | 1 |
| *PMS2* | c.1243G>A (p.Val415Met) | Heterozygous | VUS | 1 |
| *PMS2* | c.2108C>T (p.Thr703Met) | Heterozygous | VUS | 1 |
| *PMS2* | c.1559C>T (p.Ala520Val) | Heterozygous | VUS | 1 |
| *PMS2* | c.452G>A (p.Arg151His) | Heterozygous | VUS | 1 |
| *PMS2* | c.24T>C (Silent) | Heterozygous | VUS | 1 |
| *POLD1* | c.759G>A(Silent9 | Heterozygous | VUS | 1 |
| *POLD1* | c.992G>A(p.Arg331Gln9 | Heterozygous | VUS | 1 |
| *POLD1* | c.523G>T (p.Asp175Tyr) | Heterozygous | VUS | 1 |
| *POLD1* | c.189G>T (p.Glu63Asp) | Heterozygous | VUS | 1 |
| *POLD1* | c.1666G>A (p.Val556Ile) | Heterozygous | VUS | 1 |
| *POLD1* | c.245C>T (p.Pro82Leu) | Heterozygous | VUS | 1 |
| *POLD1* | c.3321G>C (p.Trp1107Cys) | Heterozygous | VUS | 1 |
| *POLD1* | c.661G>T (p.Ala221Ser) | Heterozygous | VUS | 1 |
| *POLD1* | -c.1666G>A (p.Val556Ile) | Heterozygous | VUS | 1 |
| *POLD1* | c.257C>T (p.Ala86Val) | Heterozygous | VUS | 1 |
| *POLE* | c.285G>A (Silent) | Heterozygous | VUS | 1 |
| *POLE* | c.1760A>G (p.Lys587Arg) | Heterozygous | VUS | 1 |
| *POLE* | c.3857G>A (p.Arg1286His) | Heterozygous | VUS | 1 |
| *POLE* | c.1738C>A (p.His580Asn) | Heterozygous | VUS | 1 |
| *POLE* | c.6136G>A (p.Gly2046Arg) | Heterozygous | VUS | 1 |
| *POLE* | c.214T>G (p.Leu72Val) | Heterozygous | VUS | 1 |
| *POLE* | c.3857G>A (p.Arg1286His) | Heterozygous | VUS | 2 |
| *POLE* | c.6674G>A(p.Arg2225His) | Heterozygous | VUS | 1 |
| *POLE* | c.720+3G>A (Intronic) | Heterozygous | VUS | 1 |
| *PTCH1* | c.1414G>T (p.Ala472Ser) | Heterozygous | VUS | 1 |
| *PTCH1* | c.1925C>A (p.Pro642Gln) | Heterozygous | VUS | 1 |
| *PTCH1* | c.1324G>A (p.Val442Met) | Heterozygous | VUS | 1 |
| *PTEN* | c.886T>C (p.Cys296Arg) | Heterozygous | VUS | 1 |
| *RAD50* | c.3508G>A(p.Asp110Asn) | Heterozygous | VUS | 1 |
| *RAD50* | c.670C>T (p.Arg224Cys) | Heterozygous | VUS | 1 |
| *RAD50* | c.2563G>T (p.Asp855Tyr) | Heterozygous | VUS | 1 |
| *RAD50* | c.808A>C (p.Asn270His) | Heterozygous | VUS | 1 |
| *RAD50* | c.586C>T (p.Arg196Cys) | Heterozygous | VUS | 1 |
| *RAD50* | c.1712C>T (p.Pro571Leu) | Heterozygous | VUS | 1 |
| *RAD51C* | c.641G>A (p.Arg214His) | Heterozygous | VUS | 1 |
| *RAD51C* | c.749A>G (p.His250Arg) | Heterozygous | VUS | 1 |
| *RAD51D* | c.557G>A (p.Arg186Gln) | Heterozygous | VUS | 1 |
| *RAD51D* | c.367A>G (p.Asn123Asp) | Heterozygous | VUS | 1 |
| *RAD51D* | c.557G>A (p.Arg186Gln) | heterozygous | VUS | 1 |
| *RECQL* | c.86C>T (p.Thr29Met) | Heterozygous | VUS | 1 |
| *RECQL* | c.1328T>C (p.Met443Thr) | Heterozygous | VUS | 1 |
| *RECQL* | c.86C>T (p.Thr29Met) | Heterozygous | VUS | 1 |
| *RECQL* | c.813T>A (Silent) | Heterozygous | VUS | 1 |
| *RECQL4* | c.821A>G (p.Gln274Arg) | Heterozygous | VUS | 1 |
| *RINT1* | c.1949C>T (p.Pro650Leu) | Heterozygous | VUS | 1 |
| *RINT1* | c.310C>G (p.Arg104Gly) | Heterozygous | VUS | 2 |
| *RINT1* | c.1120C>T (p.Arg374Trp) | Heterozygous | VUS | 1 |
| *RNF43* | c.1948C>T (p.Arg650\*) | Heterozygous | VUS | 1 |
| *RPS20* | c.5C>T (p.Ala2Val) | Heterozygous | VUS | 1 |
| *RUNX1* | c.1197C>A (p.Ser399Arg) | Heterozygous | VUS | 1 |
| *RUNX1* | C122c>T(p.Thr41Met) | Heterozygous | VUS | 1 |
| *SDHB* | c.65G>A (p.Cys22Tyr) | Heterozygous | VUS | 2 |
| *SDHB* | c.589C>T (p.Pro197Ser) | Heterozygous | VUS | 1 |
| *SDHC* | Gain (Exon 1) | copy number = 3 | VUS | 1 |
| *SMAD4* | c.530A>T (p.His177Leu) | Heterozygous | VUS | 1 |
| *SMAD4* | c.642T>G (p.Phe214Leu) | Heterozygous | VUS | 1 |
| *SMARCA4* | c.1593>3A>T(Intronic) | Heterozygous | VUS | 1 |
| *SMARCA4* | c.2066\_2068delAGA(p.Lys689del) | Heterozygous | VUS | 1 |
| *SMARCA4* | c.4395G>T (p.Lys1465Asn) | heterozygous | VUS | 1 |
| *SMARCA4* | c.926G>T (p.Gly309Val) | heterozygous | VUS | 1 |
| *SMARCA4* | c.778A>G (p.Met260Val) | Heterozygous | VUS | 1 |
| *SMARCA4* | c.232T>C (p.Ser78Pro) | Heterozygous | VUS | 1 |
| *SMARCA4* | c.679G>A (p.Ala227Thr) | Heterozygous | VUS | 1 |
| *SMARCA4* | c.3081+6C>T (Intronic) | Heterozygous | VUS | 1 |
| *SMARCA4* | -c.708\_713dup (p.Gly243\_Pro244dup) | Heterozygous | VUS | 1 |
| *STK11* | c.116G>A(p.Arg39His) | Heterozygous | VUS | 1 |
| *STK11* | c.265C>T (p.Pro89Ser) | Heterozygous | VUS | 1 |
| *STK11* | c.1044C>G (p.Asp348Glu) | Heterozygous | VUS | 1 |
| *STK11* | c.374+12G>A (Intronic) | Heterozygous | VUS | 1 |
| *STK11* | c.1108G>A (p.Gly370Arg) | Heterozygous | VUS | 1 |
| *STK11* | c.1171T>G (p.Cys391Gly) | Heterozygous | VUS | 1 |
| *TERT* | c.3332C>T (p.Thr1111Met) | Heterozygous | VUS | 1 |
| *TP53* | c.1136G>T (p.Arg379Leu) | Heterozygous | VUS | 1 |
| *TP53* | c.376-3C>G(Intronic) | Heterozygous | VUS | 1 |
| *TP53* | c.245C>T (p.Pro82Leu) | Heterozygous | VUS | 1 |
| *TSC1* | c.2282A>G (p.Tyr761Cys) | Heterozygous | VUS | 1 |
| *TSC2* | c.5362T>C (p.Tyr1788His) | Heterozygous | VUS | 1 |
| *TSC2* | c.5204T>C (p.Ile1735Thr) | Heterozygous | VUS | 1 |
| *TSC2* | c.2458A>G (p.Ile820Val) | Heterozygous | VUS | 1 |
| *VHL* | c.82G>A(p.Asp28Asn) | Heterozygous | VUS | 1 |
| *WRN* | c.32A>C (p.Gln11Pro) | Heterozygous | VUS | 1 |
| *WRN* | c.2165A>G (p.Asn722Ser) | Heterozygous | VUS | 1 |
| *WRN* | c.513\_514delCAinsTC (p.Thr172Pro) | Heterozygous | VUS | 1 |
| *WRN* | c.1301C>T (p.Thr434Met) | Heterozygous | VUS | 1 |
| *XRCC2* | c.475C>T (p.Arg159Cys) | Heterozygous | VUS | 1 |
| *XRCC2* | c.122-1\_122insATC(p.Gly41delinsAspArg | Heterozygous | VUS | 1 |
| *XRCC2* | c.641G>A (p.Arg214Gln) | Heterozygous | VUS | 1 |
| *XRCC2* | c.753C>G (p.Asn251Lys) | Heterozygous | VUS | 1 |

**Supplementary Table 3: Bivariate inference statistics for test results in female breast cancer patients.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| *Variable* | *N* | *NEGATIVE (N = 372)* | *POSITIVE (N = 90)* | *p-value* |
| **Age** | **460** | **42 (24 - 75)** | **40 (22 - 75)** | **0.6** |
| Missing |  | 2 | 0 |  |
| **Age <50 yrs** | **453** |  |  | **0.3** |
| NO |  | 70 / 367 (19%) | 21 / 86 (24%) |  |
| YES |  | 297 / 367 (81%) | 65 / 86 (76%) |  |
| Missing |  | 5 | 4 |  |
| **Triple-negative** | **430** |  |  | **0.056** |
| NO |  | 276 / 348 (79%) | 57 / 82 (70%) |  |
| YES |  | 72 / 348 (21%) | 25 / 82 (30%) |  |
| Missing |  | 24 | 8 |  |
| ≥**2 primary cancers** | **425** |  |  | **0.022\*** |
| NO |  | 319 / 342 (93%) | 71 / 83 (86%) |  |
| YES |  | 23 / 342 (6.7%) | 12 / 83 (14%) |  |
| Missing |  | 30 | 7 |  |
| **Positive family history** | **437** |  |  | **0.027\*** |
| NO |  | 225 / 351 (64%) | 44 / 86 (51%) |  |
| YES |  | 126 / 351 (36%) | 42 / 86 (49%) |  |
| Missing |  | 21 | 4 |  |
| **Known family variant** | **423** |  |  | **0.023\*** |
| NO |  | 341 / 342 (100%) | 78 / 81 (96%) |  |
| YES |  | 1 / 342 (0.3%) | 3 / 81 (3.7%) |  |
| Missing |  | 30 | 9 |  |
| **Estrogen receptor** | **390** |  |  | **0.2** |
| Negative |  | 96 / 313 (31%) | 29 / 77 (38%) |  |
| Positive |  | 217 / 313 (69%) | 48 / 77 (62%) |  |
| Missing |  | 59 | 13 |  |
| **Progesterone receptor** | **408** |  |  | **0.11** |
| Negative |  | 118 / 331 (36%) | 35 / 77 (45%) |  |
| Positive |  | 213 / 331 (64%) | 42 / 77 (55%) |  |
| Missing |  | 41 | 13 |  |
| **HER2** | **399** |  |  | **0.7** |
| Negative |  | 244 / 323 (76%) | 59 / 76 (78%) |  |
| Positive |  | 79 / 323 (24%) | 17 / 76 (22%) |  |
| Missing |  | 49 | 14 |  |

**Supplementary table 4: Logistic Regression Model.**

|  |  |  |  |
| --- | --- | --- | --- |
| Variable | OR | 95% CI | p-value |
| **<50 years** |  |  | **0.7** |
| NO | — | — |  |
| YES | 1.17 | 0.59, 2.43 |  |
| **Triple negative** |  |  | **>0.9** |
| NO | — | — |  |
| YES | 5,00E+06 | 0.00, Inf |  |
| ≥**2 primary cancers** |  |  | **0.4** |
| NO | — | — |  |
| YES | 1.46 | 0.53, 3.63 |  |
| **Positive family History** |  |  | **0.2** |
| NO | — | — |  |
| YES | 1.46 | 0.81, 2.62 |  |
| **Known family variant** |  |  | **>0.9** |
| NO | — | — |  |
| YES | 41,685,737 | 0.00, NA |  |
| **Estrogen Receptor** |  |  | **0.9** |
| Negative | — | — |  |
| Positive | 1.11 | 0.28, 4.71 |  |
| **Progesterone Receptor** |  |  | **0.5** |
| Negative | — | — |  |
| Positive | 0.71 | 0.27, 2.12 |  |
| **HER2** |  |  | **0.8** |
| Negative | — | — |  |
| Positive | 1.12 | 0.53, 2.28 |  |

**Supplementary Table 5: P/LP *BRCA* Variants reported in Chile: FALP cohort and previous reports.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **BRCA1 (NM\_007294.3)** | | | | | | | |
| **Exon(E)/**  **Intron(I)** | **Variant (HGVS)** | **Effect on amino acid** | **Variant type** | **Nº Chilean families** | **Chilean reference** | **Other population (s)** |
| E2 | c.66dupA | p.Glu23Argfs\*18 | Frameshift | 1 | Gómez et al. (2022) | Argentina, USA hispanic (PMID: 35867948) |
| E2 | c.68\_69del | p.Ser23Cysfs\*39 | Frameshift | 8 | Gallardo et al. (2006); Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); Adaniel et al. (2019), Gómez et al. (2022) | Ashkenazi-Jewish, Global (PMID: 29446198) |
| E2 | c.70\_73dup | p.Pro25Leufs\*17 | Frameshift | 1 | FALP/Gómez et al. (2022) | Spain (PMID: 28477318) |
| E3 | Gain (Exons 3-7) | p.? | Duplication | 3 | FALP/Gómez et al. (2022) | Similar duplications in UK, France, Korea (PMID: 15475941, 22762150, 28351343) |
| E5 | c.181T>G | p.Cys61Gly | Missense | 5 | Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); Gómez et al. (2022) | Global (PMID: 29446198) |
| E5 | c.187\_188insA | p.Leu63Tyrfs\*3 | Frameshift | 1 | Gallardo et al. (2006), Alvarez et al. (2017) | **Absent from ClinVar, latingen.org and HGMD (other than Chilean report)** |
| E5 | c.211A>G | p.Arg71Gly | Missense | 1 | Alvarez et al. (2017) | Global (PMID: 29446198) |
| I5 | c.212+1G>A | p.? | Splice site | 1 | Adaniel et al. (2019) | Global (PMID: 22798144; PMID: 29446198) |
| E6 | c.303T>A | p.Tyr101\* | Nonsense | 2 | Alvarez et al. (2017); Adaniel et al. (2019) | Sweden, African-American (PMID: 29446198) |
| E6 | c.346del | p.Glu116Asnfs\*3 | Frameshift | 1 | Gómez et al. (2022) | India (PMID: 29470806), USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E7 | c.470\_471del | p.Ser157\* | Nonsense | 2 | Adaniel et al. (2019); Gómez et al. (2022) | Global (PMID: 29446198) |
| E7 | c.514C>T | p.Gln172\* | Nonsense | 1 | FALP | Australia, France, Hong-Kong, Germany, Sweden (PMID: 29446198) |
| E10 | c.885\_888del | p.Asp295Glufs\*2 | Frameshift | 2 | Adaniel et al. (2019); Gómez et al. (2022) | Germany (PMID: 12774040), Norway (PMID: 29339979, PMID: 26350514), Greece (PMID: 24010542) |
| E10 | c.1044T>A | p.Cys348\* | Nonsense | 1 | FALP | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E10 | **c.1504\_1507del** | p.Leu502Serfs\*29 | Frameshift | 3 | Alvarez et al. (2017); Adaniel et al. (2019) | Argentina (PMID: 30103829) |
| E10 | c.1674del | p.Gly559Valfs\*13 | Frameshift | 1 | FALP/Gómez et al. (2022) | Colombia (PMID: 28528518), Germany, Spain, USA (PMID: 29446198) |
| E10 | c.1969C>T | p.Gln657\* | Nonsense | 1 | FALP | Portugal (PMID: 24916970), China (PMID: 30720863) |
| E10 | c.2275C>T | p.Gln759\* | Nonsense | 1 | Gómez et al. (2022) | India (PMID: 22752604), China (PMID: 30702160), USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E10 | c.2386delA | p.Thr796Glnfs\*7 | Frameshift | 1 | Gómez et al. (2022) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E10 | c.2486\_2487del | p.Phe829\* | Nonsense | 4 | Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); FALP | Argentina (PMID: 30103829) |
| E10 | c.2960\_2964del | p.Lys987Ilefs\*3 | Frameshift | 1 | FALP | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E10 | c.3228\_3229delAG | p.Gly1077Alafs\*8 | Frameshift | 1 | Gómez et al. (2022) | USA hispanic (PMID: 35867948) |
| E10 | **c.3331\_3334del** | p.Gln1111Asnfs\*5 | Frameshift | 32 | Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); Adaniel et al. (2019); FALP/Gómez et al. (2022); Alvarez et al. (2022) | Global (PMID: 29446198) |
| E10 | c.3485del | p.Asp1162Valfs\*48 | Frameshift | 1 | FALP | Netherlands, US-American, Finland, Sweden, France, Germany (PMID: 29446198) |
| E10 | c.3627dup | p.Glu1210Argfs\*9 | Frameshift | 1 | Adaniel et al. (2019) | Global (PMID: 29446198) |
| E10 | c.3700\_3704delGTAAA | p.Val1234Glnfs\*8 | Frameshift | 1 | Gómez et al. (2022) | Australia (PMID: 29446198) |
| E10 | c.3710\_3711del | p.Ile1237Thrfs\*6 | Frameshift | 1 | Adaniel et al. (2019) | **Absent from ClinVar, latingen.org and HGMD (other than Chilean report)** |
| E10 | c.3756\_3759del | p.Ser1253Argfs\*10 | Frameshift | 2 | Adaniel et al. (2019); FALP/Gómez et al. (2022) | Global (PMID: 29446198) |
| E10 | **c.3759dup** | p.Lys1254\* | Nonsense | 22 | Alvarez et al. (2017); Adaniel et al. (2019); FALP/Gómez et al. (2022); Alvarez et al. (2022) | US-American, Spain (PMID: 29446198) |
| E10 | **c.3817C>T** | p.Gln1273\* | Nonsense | 10 | Gallardo et al. (2006); Alvarez et al (2017); Adaniel et al. (2019); Gómez et al. (2022) | Global (PMID: 25682074, PMID: 29446198) |
| E10 | c.3841C>T | p.Gln1281\* | Nonsense | 1 | Adaniel et al. (2019) | Belgium, France, Germany, Netherlands, Sweden, US-American (PMID: 29446198) |
| E10 | c.3858\_3861del | p.Ser1286Argfs\*20 | Frameshift | 7 | Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); Gómez et al. (2022) | Singapore (PMID: 26187060), China (PMID: 22970155) |
| E10 | c.3932delA | p.Asn1311Thrfs\*7 | Frameshift | 1 | Gómez et al. (2022) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584), Italy (PMID: 8808710) |
| E10 | c.3968\_3971del | p.Gln1323Argfs\*12 | Frameshift | 2 | Alvarez et al. (2017); Adaniel et al. (2019) | France (PMID: 22762150), UK (PMID: 29446198) |
| E10 | c.4057\_4061del | p.Glu1353\* | Nonsense | 1 | FALP | Danish (PMID: 21318380) |
| E10 | c.4065\_4068del | p. Asn1355Lysfs\*10 | Frameshift | 2 | Alvarez et al. (2017); FALP/Gómez et al. (2022) | Global (PMID: 29446198) |
| E10 | c.4066\_4069del | p.Gln1356Lysfs\*9 | Frameshift | 1 | Gonzalez-Hormazabal et al. (2011) | Canada, Denmark, US-American (PMID: 29446198) |
| E12 | Deletion (Exon 12) / c.4186-?\_4675+?del | p. ? | Frameshift | 3 | FALP/Gómez et al. (2022) | Denmark, France, Germany, Korea, UK, US-American, Australia (PMID: 29446198) |
| E12 | c.4327C>T | p.Arg1443\* | Nonsense | 1 | Gómez et al. (2022) | Brazil, USA hispanic (PMID: 35867948) |
| E13 | Partial Deletion (Exons 13-15) / c.4358-2323\_4968del | p.? | Deletion | 1 | FALP/Gómez et al. (2022) | Korea (PMID:25176351) |
| E14 | c.4485-2A>G | p.? | Splice site | 1 | Gómez et al. (2022) | UK (PMID: 29446198) |
| E14 | c.4675+1G>A | p.? | Splice site | 1 | Gómez et al. (2022) | Brazil (PMID: 35867948) |
| E16 | c.5030\_5033delCTAA | p.Thr1677Ilefs\*2 | Frameshift | 1 | Gómez et al. (2022) | Mexico, USA hispanic (PMID: 35867948) |
| E17 | Deletion (Exons 17-18) /c.5075-?\_5193+?del | p. ? | Deletion | 1 | Gómez et al. (2022) | USA, Austria, Belgium, Canada, Denmark, Germany, Italy (PMID: 29446198) |
| I17 | c.5075-1G>A | p.? | Splice site | 1 | Gonzalez-Hormazabal et al. (2011) | Ashkenazi-Jewish (PMID: 12402332), USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584), USA-UK (PMID: 27433846), Taiwan (PMID: 29566657) |
| E17 | c.5095C>T | p.Arg1699Trp | Missense | 1 | FALP | Global (PMID: 29446198) |
| E17 | c.5123C>A | p.Ala1708Glu | Missense | 2 | Gómez et al. (2022) | México, Brazil, Colombia, Perú, USA hispanic (PMID: 35867948) |
| E17 | c.5136G>A | p.Trp1712\* | Nonsense | 1 | Gómez et al. (2022) | Colombia, USA hispanic (PMID: 35867948) |
| E19 | c.5260G>T | p.Glu1754\* | Nonsense | 1 | Gómez et al. (2022) | Colombia, USA hispanic (PMID: 35867948) |
| E20 | c.5266dup | p.Gln1777ProfsT\*74 | Frameshift | 4 | Alvarez et al. (2017); Adaniel et al. (2019); Gómez et al. (2022) | Ashkenazi-Jewish, Global (PMID: 29446198) |
| E23 | c.5434C>G | p.Pro1812Ala | Missense | 2 | Adaniel et al. (2019); Gómez et al. (2022) | Global (PMID: 29446198) |
|  |  |  |  | Total: 149 |  |  |
| **BRCA2 (NM\_000059.3)** | | | | | | | |
| **Exon(E)/Intron(I)** | **Variant (HGVS nomenclature)** | **Effect on amino acid** | **Variant type** | **Chilean families** | **Reference** | **Other population(s)** |
| E2 | Deletion (Exons 2-4) /c.-39-?\_425+?del | p. ? | Deletion | 1 | Gómez et al. (2022) | **Absent from ClinVar, latingen.org and HGMD** |
| E3 | **c.145G>T** | p.Glu49\* | Nonsense | 11 | Gallardo et al. (2006); Alvarez et al. (2017); Adaniel et al. (2019); FALP/Gómez et al. (2022); Alvarez et al. (2022) | Global (PMID: 29446198) |
| E3 | c.161del | p.Asn54Thrfs\*26 | Frameshift | 1 | Adaniel et al. (2019) | China (PMID: 27257965), UK and France (PMID: 29446198) |
| E11 | c.2808\_2811del | p.Ala938Profs\*21 | Frameshift | 1 | Adaniel et al. (2019) | Global (PMID: 29446198) |
| E11 | c.2830A>T | p.Lys944\* | Nonsense | 1 | FALP/Gómez et al. (2022) | Global (PMID: 29446198) |
| E11 | c.3259dupA | p.Thr1087Asnfs\*12 | Frameshift | 1 | Gómez et al. (2022) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E11 | c.3345del | p.Thr1116Leufs\*3 | Frameshift | 1 | Adaniel et al. (2019) | Palestina (PMID: 28486781) |
| E11 | c.3922G>T | p.Glu1308\* | Nonsense | 1 | Gómez et al. (2022) | Costa Rica, USA hispanic (PMID: 35867948) |
| E11 | c.4211C>A | p.Ser1404\* | Nonsense | 1 | Gómez et al. (2022) | China (PMID: 29580149) |
| E11 | **c.4740\_4741dup** | p.Glu1581Valfs\*37 | Frameshift | 30 | Gallardo et al. (2006); Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); Adaniel et al. (2019); FALP/Gómez et al. (2022); Alvarez et al. (2022) | Brazil (PMID: 23469205), Argentina (PMID: 28947987), Spain (PMID: 29446198) |
| E11 | c.4889C>G | p.Ser1630\* | Nonsense | 1 | Gómez et al. (2022) | USA hispanic (PMID: 35867948) |
| E11 | c.5110\_5113delAGAA | p.Arg1704\* | Nonsense | 1 | Gómez et al. (2022) | USA, Italy (PMID: 29446198) |
| E11 | **c.5146\_5149del** | p.Tyr1716Lysfs\*8 | Frameshift | 28 | Gallardo et al. (2006); Gonzalez-Hormazabal et al. (2011); Alvarez et al. (2017); Adaniel et al. (2019); FALP/Gómez et al. (2022) | Spain, Netherlands, Australia (hispanic) (PMID: 29446198) |
| E11 | c.5439del | p.Val1814\* | Nonsense | 3 | Gonzalez-Hormazabal et al. (2011); FALP (2) | Slovenia (PMID: 22923021), USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E11 | c.5796\_5797delTA | p.His1932Glnfs\*12 | Frameshift | 1 | Gómez et al. (2022) | Italy, USA, Australia, Hungary, France (PMID: 29446198) |
| E11 | c.5946del | p.Ser1982Argfs\*22 | Frameshift | 7 | Gallardo et al. (2006); Gonzalez-Hormazabal et al. (2011); Adaniel et al. (2019); Gómez et al. (2022) | Ashkenazi-Jewish, Global (PMID: 29446198) |
| E11 | c.6024dup | p.Gln2009Alafs\*9 | Frameshift | 3 | Adaniel et al. (2019); FALP/Gómez et al. (2022) | Argentina (PMID: 30103829), Colombia (PMID: 28528518), México (PMID: 25236687), Spain (PMID: 29884136), France, US-American (PMID: 29446198), Israel (PMID: 26687385) |
| E11 | c.6220del | p.His2074Thrfs\*7 | Frameshift | 1 | FALP/Gómez et al. (2022) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E11 | c.6275\_6276del | p.Leu2092Profs\*7 | Frameshift | 3 | Gonzalez-Hormazabal et al. (2011); FALP/Gómez et al. (2022) | Global (PMID: 29446198) |
| E11 | c.6405\_6409del | p.Asn2135Lysfs\*3 | Frameshift | 1 | Adaniel et al. (2019) | Global PMID: 29446198) |
| E11 | c.6445\_6446del | p.Ile2149\* | Frameshift | 1 | FALP/Gómez et al. (2022) | Spain (PMID:11857748, PMID: 26026974), Japan (PMID: 19016756) |
| E11 | c.6468\_6469del | p.Gln2157Ilefs\*18 | Frameshift | 2 | Adaniel et al. (2019); FALP (1) | Global (PMID: 29446198) |
| E11 | c.6469C>T | p.Gln2157\* | Nonsense | 1 | Gómez et al. (2022) | Italy (PMID: 29446198) |
| E11 | c.6629\_6630del | p.Glu2210Glyfs\*14 | Frameshift | 1 | Gallardo et al. (2006); Alvarez et al. (2017) | Spain (PMID: 29446198) |
| E11 | c.6727\_6728insAT | p.Ser2243Tyrfs\*38 | Frameshift | 1 | FALP/Gómez et al. (2022) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E14 | c.7180A>T | p.Arg2394\* | Nonsense | 2 | Gómez et al. (2022) | Brazil (PMID: 35867948) |
| E14 | c.7397dup | p.Ala2467Serfs\*8 | Frameshift | 1 | Alvarez et al. (2017) | **Absent from ClinVar, latingen.org and HGMD** |
| E15 | c.7558C>T | p.Arg2520\* | Nonsense | 1 | Gómez et al. (2022) | Brazil, USA hispanic (PMID: 35867948) |
| E18 | c.8068\_8069del | p.Val2690Phefs\*2 | Frameshift | 4 | Gonzalez-Hormazabal et al. (2011), Adaniel et al. (2019); FALP/Gómez et al. (2022) | China (PMID: 19353265) |
| E18 | c.8168A>G | p.Asp2723Gly | Missense | 1 | Alvarez et al. (2017) | Global (PMID: 29446198) |
| E18 | c.8223\_8224dup | p.Asn2742Argfs\*5 | Frameshift | 1 | Alvarez et al. (2017) | **Absent from ClinVar, latingen.org and HGMD** |
| E19 | c.8426dup | p.Ser2810Glnfs\*2 | Frameshift | 4 | Alvarez et al. (2017); Gómez et al. (2022) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E22 | c.8941G>T | p.Glu2981\* | Nonsense | 1 | Alvarez et al. (2017) | France (PMID: 29446198) |
| E23 | c.8970G>A | p.Trp2990\* | Nonsense | 1 | Gómez et al. (2022) | USA, Italy (PMID: 29446198) |
| E23 | **c.8987T>A** | p.Leu2996\* | Nonsense | 7 | Alvarez et al. (2017); Adaniel et al. (2019); FALP/ Gómez et al. (2022); Alvarez et al. (2022) | Argentina (PMID: 30103829) |
| E23 | c.9097delA | p.Thr3033Leufs\*29 | Frameshift | 1 | Gómez et al. (2022) | China (PMID: 29752822), Malasya (PMID: 28993434), Korea (PMID: 25863477), Portugal (PMID: 24916970), Netherlands (PMID: 16683254), Germany (PMID: 11802209), USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E25 | c.9262del | p.Ala3088Profs\*16 | Frameshift | 1 | Gonzalez-Hormazabal et al. (2011) | USA/Denmark/Norway/ Sweden (WECARE cohort, PMID: 20104584) |
| E25 | **c.9382C>T** | p.Arg3128\* | Nonsense | 3 | Alvarez et al. (2017); Adaniel et al. (2019); Gómez et al. (2022) | Global (PMID: 29446198) |
|  |  |  |  | Total: 132 |  |  |

Variants in bold correspond to founder variants reported by Alvarez et al., 2017