**Supporting Information**

**Legends to Supplementary Tables**

**Table S1:** Summary of the BRCA1 phosphorylation motifs studied.A list of all BRCA1 phosphorylation sites studied. Bolded phosphorylation site represents *in vivo* phosphorylated residues. \*STK6 score fell below the cut-off value of 5 but since it has previously been shown experimentally (Ouchi, et al., 2004) it is included. \*\* S405 and S1286 were excluded from the study due to wildtype predictions below the score of 5

**Table S2:** Summary of the BRCA2 phosphorylation motifs studied. A list of all BRCA2 phosphorylation sites studied. Bolded phosphorylation site represents *in vivo* phosphorylated residues. \* S206, S384, Y3009 were excluded from the study due to wildtype predictions below the score of 5.

**Table S3:** *BRCA1* and *BRCA2* variants identified in this study to affect biologically characterized phosphorylation sites and were also previously reported in other publications (retrieved from the Leiden Open Variation Database 2.0 (Build 35))

**Table S4:** *BRCA1* and *BRCA2* variants identified in this study to affect biologically uncharacterized phosphorylation sites and were also previously reported in other publications (retrieved from the Leiden Open Variation Database 2.0 (Build 35))

**Table S1**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Phosphorylation Sites** | **BRCA1 Function** | **Kinase (s)** | **Phoshorylation** | **BIC Missense Variants (within 10 nt of motif)** | **NetworKIN 2.0 Beta WT Output (Score>5)** |
| S114 |  |  | Biologically uncharacterized | Y105C, E111A, I124V | S114 - CDK2 - 11.9354 |
| **S308** | Cell Cycle | STK6 | Biologically characterized | E300D, K309T, R315G, S316G | \*S308 - STK6 - 4.1318 |
| S395 |  |  | Biologically uncharacterized | S403F | S395 - CSNK2A2 - 18.6883 S395 - CK2A1 - 18.6883 |
| S398 |  |  | Biologically uncharacterized | S403F, K408E | S398 - CSNK2A2 - 11.7459 S398 - CK2A1 - 11.7459 S398 - TLK1 - 9.4999 |
| S403 |  |  | Biologically uncharacterized | S403F, K408E, D411N, D411E | S403 - CK2A1 - 10.5925 S403 - CSNK2A2 - 10.5925 S403 - CK2A1 - 10.5925 |
| S405\*\* |  |  | Biologically uncharacterized | D411N, D411E | Predictions Score <5 |
| S423 |  |  | Biologically uncharacterized | N417K, N417S, D420Y, E421K, H437P | S423 - CSNK2A2 - 17.8448 S423 - CK2A1 - 17.8448 |
| S451 |  |  | Biologically uncharacterized | E445Q, S454N, I456T, F461L | S451 - TGFBR2 - 7.4107 S451 - ACVR2B - 7.3511 |
| S454 |  |  | Biologically uncharacterized | S454N, I456T, F461L, G462R | S454 - CSNK2A2 - 15.1914 S454 - CK2A1 - 15.1914 |
| **T509** | Transcription, Intracellular Localization | PKB Group | Biologically characterized | K503R, R504H, R504C, R507I, L512F | T509 - PIM2 - 14.0558 T509 - RPS6KP1 - 12.3565 |
| S510 |  |  | Biologically uncharacterized | K503R, R504H, R504C, R507I, L512F | S510 - Pim2 - 11.863 S510 - MOK - 8.9448 |
| S615 |  |  | Biologically uncharacterized | N609S, R612G, A622V | S615 - RP26KB1 - 11.6281 |
| S616 |  |  | Biologically uncharacterized | N609S, R612G, A622V, E624K | S616 - CLK1 - 7.4065 S616 - CLK2 - 7.3988 S616 - PRKCD - 6.1543 S616 - PRKC1 - 6.1357 S616 - PRKCQ - 6.1357 S616 - PRKCZ - 6.1295 S616 - PRKCA - 6.1233 S616 - PRKCG - 6.1109 S616 - RPS6KB1 - 5.7185 |
| T617 |  |  | Biologically uncharacterized | N609S, R612G, A622V, E624K, V621I | T617 - Pim2 - 11.0799 |
| **S632** | Transcription | CDK2 | Biologically characterized | A622V, E624K, V627I, S628R, S632N, P633T, P633S, P634R, P634S, E638K, D642H | S632 - CDK2 - 12.0835 |
| **S694** | Protein Stabilization |  | Biologically characterized | Q687P, D693N, D695Y, D695N, T696A | S694 - RP26KB1 - 9.3335 S694 - PIM2 - 9.1511 |
| S753 |  |  | Biologically uncharacterized | D749Y, R756S, E761A | S753 - CSNK2A2 - 6.2329 S753 - CK2A1 - 6.2329 |
| **S988** | Activation, Intracellular Localization | CHK2 | Biologically characterized | R979C, R979H | Predictions Score <5 |
| **S1143** | DNA Repair |  | Biologically characterized | P1136R, M1137T, S1139I, S1140G, A1142P, S1143F, Q1144H, C1146S, P1150S, D1152N | S1143 - ATM - 12.6322 |
| **S1189** | Molecular Association | ATM, CDK1 | Biologically characterized | V1181I, V1181A, K1183R, S1187N, T1194I, T1196K, T1196I | S1189 - CDK2 - 10.479 S1189 - MAPK14 - 8.324 S1189 - MAPK11 - 8.324 S1189 - MAPK13 - 8.299 S1189 - MAPK8 - 7.6199 S1189 - MAPK10 - 7.6123 S1189 - MAPK9 - 7.6046 |
| **S1191** | Intracellular localization | CDK1 | Biologically characterized | V1181I, V1181A, K1183R, S1187N, T1194I, T1196K, T1196I, Q1200H, Q1200H, G1201S | S1191 - MOK - 7.7417 S1191 - MAPK8 - 7.134 S1191 - MAPK10 - 7.1269 S1191 - MAPK9 - 7.1197 S1191 - MAPK8 - 7.6199 S1191 - MAPK14 - 5.8665 S1191 - MAPK11 - 5.8665 S1191 - MAPK13 - 5.8488 S1191 - CDK2 - 5.7847 S1191 - CDK5 - 5.7794 |
| S1211 |  |  | Biologically uncharacterized | G1201S, R1203Q, G1205R, K1208E, E1214K, S1218C | S1211 - CK2A1 - 20.6567 S1211 - CSNK2A2 - 20.6567 |
| S1212 |  |  | Biologically uncharacterized | R1203Q, G1205R, K1208E, E1214K, S1218C, E1219K, E1219D | S1212 - CSNK2A2 - 8.4757 S1212 - CK2A1 - 8.4757 |
| S1217 |  |  | Biologically uncharacterized | K1208E, E1214K, S1218C, E1219K, E1219D | S1217 - CSNK2A2 - 22.1941 S1217 - CK2A1 - 22.1941 |
| S1218 |  |  | Biologically uncharacterized | K1208E, E1214K, S1218C, E1219K, E1219D | S1218 - CSNK2A2 - 22.3858 S1218 - CK2A1 - 22.3858 |
| S1239 |  |  | Biologically uncharacterized | F1231L, K1233R, N1236K, I1237M, P1238R, P1238L, S1241Y, T1242A, V1247I, T1249S | S1239 - ATM - 15.4434 |
| S1245 |  |  | Biologically uncharacterized | I1237M, P1238R, P1238L, S1241Y, T1242A, V1247I, T1249S, E1250K, K1254E | S1245 - AURKB - 6.2013 S1245 - PAK4 - 5.2138 S1245 - PAK7 - 5.6122 S1245 - PAK2 - 5.1842 S1245 - PAK3 - 5.1581 |
| **S1280** | DNA Repair |  | Biologically characterized | I1275V, A1279T, Q1281P, E1282V, H1283R, H1284R | S1280 - ATM - 11.3997 |
| S1286\*\* |  |  | Biologically uncharacterized | A1279T, Q1281P, E1282V, H1283R, H1284R, A1293D, A1293V | Predictions Score <5 |
| S1328 |  |  | Biologically uncharacterized | K1322I, D1337E | S1328 - RP26KB1 - 9.3335 S1328 - PIM2 - 9.1511 |
| S1330 |  | ATM | Biologically uncharacterized | K1322I, D1337E | S1330 - ATM - 17.5181 |
| S1336 |  |  | Biologically uncharacterized | D1337E, D1344G, E1346K | S1336 - CSNK2A2 - 18.1857 S1336 - Ck2A1 - 18.1857 |
| S1342 |  |  | Biologically uncharacterized | D1337E, D1344G, E1346K, R1347K, R1347G, T1349M, T1349P, E1352K | S1342 - CSNK2A2 - 22.2937 S1342 - CK2A1 - 22.2937 |
|  |  |  |  |  |  |
| **S1387** | Cell Cycle | ATM | Biologically characterized | T1376R, S1377R, V1378I, Q1395R | S1387 - ATM - 17.1378 |
| **S1423** | Cell Cycle, Molecular Association | ATM, ATR | Biologically characterized | E1419Q, H1421Y, H1421R, P1430S, I1432L | S1423 - ATM - 17.6874 |
| **S1457** | Molecular Association | ATM | Biologically characterized | S1448T, S1448G | S1457 - ATM - 17.8914 |
| S1466 |  | ATM | Biologically uncharacterized | N1468H, P1469S, E1470D | S1466 - ATM - 17.3447 |
| **S1497** | Molecular Association | CDK1, CDK2, ATM | Biologically characterized | K1487R, E1494K, R1495K, R1495M, P1502S, R1507T | S1497 - CDK2 - 12.6613 |
| S1499 |  |  | Biologically uncharacterized | K1487R, E1494K, R1495K, R1495M, P1502S, R1507T | GSK3B @ S1499- 5.932 GSK3A @ S1499 - 5.926 |
| **S1524** | Cell Cycle, Molecular Association | ATM, ATR | Biologically characterized | Y1522C, E1527K, I1529V, V1534M | S1524 - ATM - 16.5643 |
| **S1542** | Molecular Association | ATM | Biologically characterized | V1534M, S1542C, P1544L, D1546Y, D1546N, T1550I, L1553M | S1542 - CSNK2A2 -15.1303 S1542 - CK2A1 - 15.1303 |
| S1550 |  |  | Biologically uncharacterized | S1542C, P1544L, D1546Y, D1546N, T1550I, L1553M, D1557H, E1559K, E1559Q | T1550 - NEK2 - 6.7505 |
| **S1572** |  | CK2-A1 | Biologically characterized | T1561I, P1562L, L1564P, I1568V, P1575H, S1577P, D1578G, S1580F | T1572 - CSNK2A2 - 18.7348 T1572 - CK2A1 - 18.7348 |
| S1577 |  |  | Biologically uncharacterized | I1568V, P1575H, S1577P, D1578G, S1580F, A1584S | T1577 - CSNK2A2 - 21.2235 T1577 - CK2A1 - 21.2235 |
| T1700 |  |  | Biologically uncharacterized | T1691K, T1691I, D1692Y, D1692N, D1692H, F1695L, V1696L, C1697R, R1699Q, R1699L, R1699W, G1706A, G1706E, A1708E | T1700 - TGFBR2 - 7.3074 T1700 - ACVR2B - 7.2486 T1700 - PRKD1 - 6.6872 T1700 - PRKCD - 5.5359 T1700 - PRKCI - 5.5191 T1700 - PRKCQ - 5.5191 T1700 - PRKCZ - 5.5136 T1700 - PRKCA - 5.508 T1700 - PRKCG - 5.4968 T1700 - MST2 - 5.4712 |
| T1720 |  | ATM | Biologically uncharacterized | V1713A, V1714G, S1715C, S1715N, S1715R, W1718C, W1718S, T1720A, S1722F, R1726G, N1730S | T1720 - ATM - 12.7702 |
| **Total 44** |  |  | **16 biologically characterized 28 biologically uncharacterized sites** | **Total 191 VUS** |  |

**Table S2**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Phosphorylation Sites** | **BRCA2 Function** | **Kinase (s)** | **Phoshorylation** | **BIC Missense Variants (within 10 nt of motif)** | **NetworKIN 2.0 Beta WT Output (Score>5)** |
| S193 | Cell cycle | PLK1 | Biologically characterized | L184P, E187K, S196I, S196N | S193 - TGFBR2 - 5.2449 S193 - ACVR2B - 5.2026 |
| T203 | Cell cycle | PLK1 | Biologically characterized | S196I, S196N, T207A, V208G, V211L, V211I | S203 - MAP4K4 - 5.0961 S203 - TNIK - 5.0543 |
| S205 | Cell cycle | PLK1 | Biologically characterized | S196I, S196N, T207A, V208G, V211L, V211I | S205 - NEK2 - 5.3174 |
| S206\* | Cell cycle | PLK1 | Biologically characterized | S196I, S196N, T207A, V208G, V211L, V211I | Predictions Score <5 |
| T207 | Cell cycle | PLK1 | Biologically characterized | T207A, V208G, V211L, V211I | T207 - NEK2 - 6.0389 |
| S239 | Cell cycle | PLK1 | Biologically characterized | H236R, D244N, I247T, A248T | S239 - TGFBR2 - 6.2295 S239 - ACVR2B - 6.1794 S239 - PRKCD - 6.1024 S239 - PRKCI - 6.0839 S239 - PRKCQ - 6.0839 S239 - PRKCZ - 6.0777 S239 - PRKCA - 6.0716 S239 - PRKCG - 6.0593 |
| S384\* |  |  | Biologically uncharacterized | P375S, P375L, F376C, S384F | Predictions Score <5 |
| S683 |  |  | Biologically uncharacterized | T675R | S683 - ATM - 17.4843 |
| S755 |  |  | Biologically uncharacterized | P375S, P375L, F376C, S384F | S755 - ATM - 15.9114 |
| S1926 |  |  | Biologically uncharacterized | H1918Y, H1918R, D1923A, D1923V, E1928K, I1929V, N1935S | S1926 - CSNK2A2 - 8.8398 S1926 - CK2A1 - 8.8398 |
| S1943 |  |  | Biologically uncharacterized | N1935S , S1946P, P1947S, V1950I | Predictions Score <5 |
| Y3009\* |  |  | Biologically uncharacterized | E3002K , E3002D, L3011P, T3013I | Predictions Score <5 |
| T3193 |  |  | Biologically uncharacterized | D3188N , P3194Q, T3195A, K3196E, C3198R | T3193 - CDK2 - 13.8792 |
| S3291 | Cell cycle | CDK, ATM | Biologically characterized | P3292L, A3297G | S3291 - CDK2 - 11.3492 S3291 - MAPK11 - 8.4881 S3291 - MAPK13 - 8.4625 S3291 - MAPK14 - 8.4881 |
| **Total 11** |  |  | **7 Biologically characterized 4 Biologically uncharacterized** | **Total 43 VUS** |  |

**Table S3**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Exon** | **Codon** | **Variant as Published** | **DNA Change** | **Protein** | **Reference** | **Assay** | **Assay Result** |
| BRCA1 | 11 | 632 | S632N | [c.1895G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000414%2C0000414%2C0) | p.Ser632Asn | [Fleming et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/12531920) | Evolutionary conservation analysis | Predicted Deleterious |
| BRCA1 | 11 | 632 | S632N | [c.1895G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000415%2C0000415%2C0) | p.Ser632Asn | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Inconclusive |
| BRCA1 | 11 | 632 | S632N | [c.1895G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000416%2C0000416%2C0) | p.Ser632Asn | [Abkevich et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15235020) | Evolutionary conservation analysis | Predicted Neutral |
| BRCA1 | 11 | 1144 | Q1144H | [c.3432G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000638%2C0000638%2C0) | p.Glu1144His | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Inconclusive |
| BRCA2 | 7 | 207 | T207A | [c.619A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA2&action=view&view=0001521%2C0000066%2C0) | p.Thr207Ala | Pettigrew et al. (2007) | Co-localization to predicted ESEs | Predicted Deleterious |

**Table S4**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Exon** | **Codon** | **Variant as Published** | **DNA Change** | **Protein** | **Reference** | **Assay** | **Assay Result** |
| BRCA1 | 11 | 417 | N417S | [c.1250A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000311%2C0000311%2C0) | p.Asn417Ser | [Abkevich et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15235020) | Evolutionary conservation analysis | Predicted Neurtral |
| BRCA1 | 11 | 417 | N417S | [c.1250A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000312%2C0000312%2C0) | p.Asn417Ser | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Inconclusive |
| BRCA1 | 11 | 420 | D420Y | [c.1258G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000313%2C0000313%2C0) | p.Asp420Tyr | [Easton et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17924331) | Multifactorial likelihood-ratio model | Predicted Neurtral |
| BRCA1 | 11 | 420 | D420Y | [c.1258G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000314%2C0000314%2C0) | p.Asp420Tyr | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Inconclusive |
| BRCA1 | 11 | 454 | S454N | [c.1361G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000318%2C0000318%2C0) | p.Ser454Asn | [Abkevich et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15235020) | Evolutionary conservation analysis | Predicted Neurtral |
| BRCA1 | 11 | 609 | N609S | [c.1826A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000400%2C0000400%2C0) | p.Asn609Ser | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Inconclusive |
| BRCA1 | 11 | 612 | R612G | [c.1834A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000401%2C0000401%2C0) | p.Arg612Gly | [Fleming et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/12531920) | Evolutionary conservation analysis | Predicted Deleterious |
| BRCA1 | 11 | 612 | R612G | [c.1834A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000402%2C0000402%2C0) | p.Arg612Gly | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Predicted Deleterious |
| BRCA1 | 11 | 612 | R612G | [c.1834A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000403%2C0000403%2C0) | p.Arg612Gly | [Ramirez et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15001988) | Evolutionary conservation analysis | Predicted Deleterious |
| BRCA1 | 11 | 1201 | G1201S | [c.3601G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000660%2C0000660%2C0) | p.Gly1201Ser | [Salazar et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/15876480) | N/A | N/A |
| BRCA1 | 11 | 1214 | E1214K | [c.3640G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000664%2C0000664%2C0) | p.Glu1214Lys | [Easton et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17924331) | Multifactorial likelihood-ratio model | Predicted Neurtral |
| BRCA1 | 11 | 1214 | E1214K | [c.3640G>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000665%2C0000665%2C0) | p.Glu1214Lys | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Inconclusive |
| BRCA1 | 11 | 1218 | S1218C | [c.3652A>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000666%2C0000666%2C0) | p.Ser1218Cys | [Burk-Herrick et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16518693) | Evolutionary conservation analysis | Predicted Deleterious |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000949%2C0000949%2C0) | p.Phe1695Leu | [Joo et al (2002)](http://www.ncbi.nlm.nih.gov/pubmed/11877378) | Peptide binding ability | As mutant control |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000950%2C0000950%2C0) | p.Phe1695Leu | [Mirkovic et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15172985) | Structure-based prediction (crystallography etc) | Predicted neutral |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000951%2C0000951%2C0) | p.Phe1695Leu | [Williams et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15133503) | Peptide binding ability | As wildtype control |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000952%2C0000952%2C0) | p.Phe1695Leu | [Karchin et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17305420) | Multifactorial likelihood-ratio model | Predicted deleterious |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000953%2C0000953%2C0) | p.Phe1695Leu | [Glover et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16528612) | Peptide binding ability | As wildtype control |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000954%2C0000954%2C0) | p.Phe1695Leu | [Williams et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/14534301) | Bayesian statistics | Predicted neutral |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000955%2C0000955%2C0) | p.Phe1695Leu | [Williams et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/14534301) | Proteolytic degradation | As wildtype control |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000956%2C0000956%2C0) | p.Phe1695Leu | [Abkevich et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15235020) | Evolutionary conservation analysis | Predicted neutral |
| BRCA1 | 18 | 1695 | F1695L | [c.5085T>A](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0002450%2C0001530%2C0) | p.Phe1695Leu | [Lee et al. (2010)](http://www.ncbi.nlm.nih.gov/pubmed/20516115) | Transcription activation/PS/BA/BS | No Functional Effect |
| BRCA1 |  |  |  | + 74 others |  |  |  |  |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000977%2C0000977%2C0) | p.Arg1699Trp | [Glover et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16528612) | Peptide binding ability | As mutant control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000978%2C0000978%2C0) | p.Arg1699Trp | [Mirkovic et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15172985) | Structure-based prediction (crystallography etc) | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000979%2C0000979%2C0) | p.Arg1699Trp | [Nikolopoulos et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17493881) | Peptide binding ability | As mutant control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000980%2C0000980%2C0) | p.Arg1699Trp | [Williams et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/14534301) | Proteolytic degradation | Inconclusive |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000981%2C0000981%2C0) | p.Arg1699Trp | [Williams et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/14534301) | Bayesian statistics | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000982%2C0000982%2C0) | p.Arg1699Trp | [Nikolopoulos et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17493881) | Thermostability assay | As mutant control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000983%2C0000983%2C0) | p.Arg1699Trp | [Shiozaki et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15125843) | Peptide binding ability | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000984%2C0000984%2C0) | p.Arg1699Trp | [Worley et al. (2002)](http://www.ncbi.nlm.nih.gov/pubmed/12496476) | Transcription activation in human cells | As mutant control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000985%2C0000985%2C0) | p.Arg1699Trp | [Gomez-Garcia et al. (2009)](http://www.ncbi.nlm.nih.gov/pubmed/19150617) | Family history | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000986%2C0000986%2C0) | p.Arg1699Trp | [Clapperton et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15133502) | N/A | N/A |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000987%2C0000987%2C0) | p.Arg1699Trp | [Osorio et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17279547) | Multifactorial likelihood-ratio model | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000988%2C0000988%2C0) | p.Arg1699Trp | [Williams et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15133503) | Peptide binding ability | As mutant control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000989%2C0000989%2C0) | p.Arg1699Trp | [Easton et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17924331) | Multifactorial likelihood-ratio model | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000990%2C0000990%2C0) | p.Arg1699Trp | [Williams et al. (2001)](http://www.ncbi.nlm.nih.gov/pubmed/11573086) | Structure-based prediction (crystallography etc) | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000991%2C0000991%2C0) | p.Arg1699Trp | [Vallon-Christersson et al. (2001)](http://www.ncbi.nlm.nih.gov/pubmed/11157798) | Transcription activation in yeast (GAL4-fusions) | As wildtype control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000992%2C0000992%2C0) | p.Arg1699Trp | [Worley et al. (2002)](http://www.ncbi.nlm.nih.gov/pubmed/12496476) | Transcription activation in yeast (GAL4-fusions) | As mutant control |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000993%2C0000993%2C0) | p.Arg1699Trp | [Varma et al. (2005)](http://www.ncbi.nlm.nih.gov/pubmed/16101277) | Structure-based prediction (crystallography etc) | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0002450%2C0001533%2C0) | p.Arg1699Trp | [Lee et al. (2010)](http://www.ncbi.nlm.nih.gov/pubmed/20516115) | Transcription activation/PS/BA/BS | Strong functional effect |
| BRCA1 |  |  |  | + 74 others |  |  |  |  |
| BRCA1 | 18 | 1699 | R1699W | [c.5095C>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0002480%2C0001651%2C0) | p.Arg1699Trp | [Rowling et al. (2010)](http://www.ncbi.nlm.nih.gov/pubmed/20378548) | Thermodynamic stability prediction | Moderately Destabilizing |
| BRCA1 | 18 | 1699 | R1699L | [c.5096G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000994%2C0000994%2C0) | p.Arg1699Leu | [Pettigrew et al. (2005)](http://www.ncbi.nlm.nih.gov/pubmed/16280041) | Evolutionary conservation analysis | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699L | [c.5096G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000995%2C0000995%2C0) | p.Arg1699Leu | [Abkevich et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15235020) | Evolutionary conservation analysis | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699L | [c.5096G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000996%2C0000996%2C0) | p.Arg1699Leu | [Williams et al. (2001)](http://www.ncbi.nlm.nih.gov/pubmed/11573086) | Structure-based prediction (crystallography etc) | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699L | [c.5096G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0000997%2C0000997%2C0) | p.Arg1699Leu | [Mirkovic et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15172985) | Structure-based prediction (crystallography etc) | Predicted deleterious |
| BRCA1 | 18 | 1699 | R1699L | [c.5096G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0002450%2C0001535%2C0) | p.Arg1699Leu | [Lee et al. (2010)](http://www.ncbi.nlm.nih.gov/pubmed/20516115) | Transcription activation/PS/BA/BS | Moderate functional effect |
| BRCA1 |  |  |  | + 74 others |  |  |  |  |
| BRCA1 | 18 | 1699 | R1699L | [c.5096G>T](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0002468%2C0001639%2C0) | p.Arg1699Leu | [Rowling et al. (2010)](http://www.ncbi.nlm.nih.gov/pubmed/20378548) | Thermodynamic stability prediction | not destabilizing |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001111%2C0001111%2C0) | p.Thr1720Ala | [Williams et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/14534301) | Proteolytic degradation | As wildtype control |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001112%2C0001112%2C0) | p.Thr1720Ala | [Williams et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/14534301) | Bayesian statistics | Predicted neutral |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001113%2C0001113%2C0) | p.Thr1720Ala | [Glover et al. (2006)](http://www.ncbi.nlm.nih.gov/pubmed/16528612) | Peptide binding ability | As wildtype control |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001114%2C0001114%2C0) | p.Thr1720Ala | [Phelan et al (2005)](http://www.ncbi.nlm.nih.gov/pubmed/15689452) | Transcription activation in yeast (GAL4-fusions) | Inconclusive |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001115%2C0001115%2C0) | p.Thr1720Ala | [Mirkovic et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15172985) | Structure-based prediction (crystallography etc) | Predicted neutral |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001116%2C0001116%2C0) | p.Thr1720Ala | [McKean-Cowdin et al. (2005)](http://www.ncbi.nlm.nih.gov/pubmed/15726418) | N/A | N/A |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001117%2C0001117%2C0) | p.Thr1720Ala | [Diez et al. (2003)](http://www.ncbi.nlm.nih.gov/pubmed/12955716) | N/A | N/A |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001118%2C0001118%2C0) | p.Thr1720Ala | [Williams et al. (2004)](http://www.ncbi.nlm.nih.gov/pubmed/15133503) | Peptide binding ability | As wildtype control |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0001119%2C0001119%2C0) | p.Thr1720Ala | [Easton et al. (2007)](http://www.ncbi.nlm.nih.gov/pubmed/17924331) | Multifactorial likelihood-ratio model | Predicted neutral |
| BRCA1 | 19 | 1720 | T1720A | [c.5158A>G](http://chromium.liacs.nl/LOVD2/cancer/variants.php?select_db=BRCA1&action=view&view=0002450%2C0001548%2C0) | p.Thr1720Ala | [Lee et al. (2010)](http://www.ncbi.nlm.nih.gov/pubmed/20516115) | Transcription activation/PS/BA/BS | No Functional Effect |
|  |  |  |  | + 74 others |  |  |  |  |