

Gene	Transcript	Chromosome	Position	Protein change	REF	ALT	Reference	Consequence	SIFT score	PhyloP	AF
BRCA1	ENSCAFT00000065506.1	CHR:9	19985052	p.G282S	G	A	Elvers et al 2015	MISSENSE	1.00	-0.44	0.05
BRCA1	ENSCAFT00000065506.1	CHR:9	19986007	p.G600D	G	A	Elvers et al 2015	MISSENSE	0.09	-1.67	0.02
BRCA1	ENSCAFT00000065506.1	CHR:9	19987314	P.C1036R	T	C		MISSENSE	0.29	-0.14	0.03
BRCA1	ENSCAFT00000065506.1	CHR:9	19987956	p.T1250A	A	G	Elvers et al 2015	MISSENSE	1.00	-0.13	0.05
BRCA1	ENSCAFT00000065506.1	CHR:9	19988291		G	A	Borge et al 2011 Illumina 170K Canine HD array (BICF2G630829453)	SYNONYMOUS		0.72	0.67
BRCA1	ENSCAFT00000065506.1	CHR:9	19988343	p.P1379R	G	A		MISSENSE	0.18	0.57	0.05
BRCA1	ENSCAFT00000065506.1	CHR:9	20000085	p.D1521E	C	A		MISSENSE	0.00	1.55	0.04
BRCA1	ENSCAFT00000023190.5	CHR:9	20022197	p.S1743RX	A	AG	Elvers et al 2015	FRAMESHIFT			0.04
BRCA1	ENSCAFT00000023190.5	CHR:9	20022212	p.W1748R	T	C	Elvers et al 2015	MISSENSE		1.23	0.04
BRCA1	ENSCAFT00000065506.1	CHR:9	20024358	p.A1912T	G	A	Elvers et al 2015	MISSENSE	0.04	1.44	0.04

Table S3 a): Summary of the germ-line variants found in the *BRCA1* gene in the 53 individual normal samples in the study. Heat map highlights the SIFT, phyloP scores and allele frequency for each variant. More intense red color denotes lower SIFT score, higher phyloP score and higher allele frequency in the population.

Gene	Transcript	Chromosome	Position	Protein change	REF	ALT	Reference	Consequence	SIFT score	PhyloP	AF
BRCA2	ENSCRAFT0000010309.4	CHR:25	7735412	p.M3332IK	C	CTTT	Yoshikawa et al 2005, Borge et al 2011, Huskey et al 2020, Elvers et al 2015	INSERTION			0.82
BRCA2	ENSCRAFT0000010309.4	CHR:25	7748722	p.N2929D	T	C	Elvers et al. 2015	MISSENSE	0.01	0.04	0.01
BRCA2	ENSCRAFT0000010309.4	CHR:25	7753884		A	G	Elvers et al 2015	SYNONYMOUS		1.06	0.06
BRCA2	ENSCRAFT0000010309.4	CHR:25	7768681		G	A	Yoshikawa et al 2008, Borge et al 2011, Huskey et al 2020, Elvers et al 2015, Lindblad-toh et al. 2005	SYNONYMOUS		3.71	0.12
BRCA2	ENSCRAFT0000010309.4	CHR:25	7768690	p.LL2307L	TAAC	T	Borge et al 2011, Huskey et al 2020, Elvers et al. 2015	IN FRAME DELETION			0.08
BRCA2	ENSCRAFT0000010309.4	CHR:25	7770765	p.C2229F	C	A		MISSENSE	0.35	0.71	0.04
BRCA2	ENSCRAFT0000010309.4	CHR:25	7770789	p.P2221L	G	A	Elvers et al. 2015	MISSENSE	0.00	4.61	0.02
BRCA2	ENSCRAFT0000010309.4	CHR:25	7773147	p.K1435R	T	C	Yoshikawa et al 2008, Huskey et al 2020, Elvers et al. 2015, Lindblad-Toh et al. 2005, Illumina HD SNP TIGRP2P324166	MISSENSE	0.07	1.33	0.25
BRCA2	ENSCRAFT0000010309.4	CHR:25	7773178	p.T1425P	T	G	Yoshikawa et al 2008, Elvers et al. 2015	MISSENSE	0.00	3.66	0.05
BRCA2	ENSCRAFT0000010309.4	CHR:25	7775050	p.K801Q	T	G	Borge et al 2011, Huskey et al 2020, Elvers et al. 2015, Lindblad-Toh et al. 2005, Axelsson et al. 2013	MISSENSE	0.05	0.49	0.27
BRCA2	ENSCRAFT0000010309.4	CHR:25	7775229	p.N741S	T	C	Huskey et al 2020, Elvers et al. 2015	MISSENSE	1.00	1.30	0.98
BRCA2	ENSCRAFT0000010309.4	CHR:25	7775268	p.A728V	G	A	Huskey et al 2020, Elvers et al. 2015	MISSENSE	0.28	-0.18	0.96
BRCA2	ENSCRAFT0000010309.4	CHR:25	7775297		G	T	Huskey et al 2020, Elvers et al. 2015	SYNONYMOUS		0.01	0.91
BRCA2	ENSCRAFT0000010309.4	CHR:25	7775307	p.P715Q	G	T	Huskey et al 2020, Elvers et al. 2015	MISSENSE	1.00	-0.15	0.91
BRCA2	ENSCRAFT0000010309.4	CHR:25	7777317	p.F428L	A	G	Yoshikawa et al 2008, Huskey et al 2020	MISSENSE	0.29	1.43	0.01
BRCA2	ENSCRAFT0000010309.4	CHR:25	7777441	p.C386W	A	C	Yoshikawa et al 2008, Elvers et al. 2015, Axelsson et al. 2013	MISSENSE	1.00	1.99	0.72
BRCA2	ENSCRAFT0000010309.4	CHR:25	7787056	p.H143R	T	C	Yoshikawa et al 2008, Borge et al 2011, Huskey et al 2020, Elvers et al. 2015, Lindblad-Toh et al. 2005, Illumina HD SNP BICF2P918004	MISSENSE	0.27	-0.39	0.11
BRCA2	ENSCRAFT0000010309.4	CHR:25	7787802	p.I103T	A	G	Elvers et al. 2015	MISSENSE	0.22	-0.28	0.05

Table S3 b): Summary of the germ-line variants found in the *BRCA2* gene in the 53 individual normal samples in the study. Heat map highlights the SIFT, phyloP scores and allele frequency for each variant. More intense red color denotes lower SIFT score, higher phyloP score and higher allele frequency in the population.