Supplemental Material

BRCA2 Polymorphisms and Breast Cancer Susceptibility: a Multi-Tools Bioinformatics Approach

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Table 1. List of deleterious missense SNPs in the BRCA2 gene using consensus bioinformatics tool.

rs-id	Variant ID	AA Position	SIFT	PolyPhen-2	PHD-SNP	Predict SNP	SNAP	ClicVar/Varsome
rs80358597	13-32890631-T-G	F12V	D	D	D	D	D	VUS
rs1370260227	13-32890653-G-T	C19F	D	D	D	D	D	VUS
rs774521832	13-32893214-A-G	D23G	D	D	D	D	D	VUS
rs80358961	13-32893219-G-A	G25R	D	D	D	D	D	VUS
rs397508045	13-32893238-G-T	W31L	D	D	D	D	D	VUS
rs1566215918	13-32893367-T-C	L74P	D	D	D	D	D	VUS
rs28897701	13-32893369-G-C	A75P	D	D	D	D	D	Benign
rs774152844	13-32893427-C-A	P94H	D	D	D	D	D	Benign
rs80358660	13-32899312-T-G	L139R	D	D	D	D	D	VUS
rs587782795	13-32900240-C-G	P143R	D	D	D	D	D	VUS
rs80358726	13-32900405-C-A	P168T	D	D	D	D	D	Benign
rs80358761	13-32900658-T-C	I180T	D	D	D	D	D	VUS
rs1334767632	13-32906574-T-C	L320P	D	D	D	D	D	VUS
rs80358412	13-32906798-T-G	W395G	D	D	D	D	D	VUS
rs398122730	13-32907348-G-A	G578D	D	D	D	D	D	VUS
rs397507275	13-32907371-A-G	K586E	D	D	D	D	D	VUS
rs772156559	13-32907390-A-G	Y592C	D	D	D	D	D	VUS
rs587780646	13-32907453-T-G	L613R	D	D	D	D	D	Benign
rs80358479	13-32907504-C-T	T630I	D	D	D	D	D	Benign
rs759389988	13-32910885-T-G	L798R	D	D	D	D	D	Benign
rs80358530	13-32911263-A-T	N924I	D	D	D	D	D	Benign
rs141702094	13-32911590-A-T	D1033V	D	D	D	D	D	VUS
rs558973276	13-32911842-T-C	I1117T	D	D	D	D	D	VUS
rs532871047	13-32911857-G-A	G1122E	D	D	D	D	D	VUS

Table 2. Prediction of the molecular mechanism by mutpred2

Mutation	MutPred2 score	Predicted molecular mechanism (P-value)
F12V	0.544	Altered Disordered interface (P = 0.03) Altered Transmembrane protein (P = 0.04)
C19F	0.777	Altered Disordered interface (P = 0.03) Loss of Relative solvent accessibility (P = 0.01) Altered Transmembrane protein (P = 0.04)
D23G	0.672	Altered Disordered interface (P = 0.03) Loss of Relative solvent accessibility (P = 0.02)
G25R	0.686	Altered Disordered interface (P = 0.03) Gain of Intrinsic disorder (P = 0.05) Gain of Helix (P = 0.03)
W31L	0.779	Gain of Intrinsic disorder (P = 0.03) Altered Disordered interface (P = 0.03) Altered Ordered interface (P = 0.01)
L74P	0.511	Gain of Intrinsic disorder (P = 0.03) Altered Disordered interface (P = 0.03) Loss of Helix (P = 0.03)
P168T	0.581	-
I180T	0.519	Gain of Intrinsic disorder (P = 0.03) Altered Disordered interface (P = 0.03) Altered Metal binding (P = 0.01) Altered Ordered interface (P = 01)
Y592C	0.609	Altered Disordered interface (P = 0.03) Altered Metal binding (P = 0.01) Altered Ordered interface (P = 0.02) Altered DNA binding (P = 0.01) Loss of Methylation at K589 (P = 0.01)
D1033V	0.641	Altered Stability (P = 0.04) Loss of Acetylation at K1032 (P = 0.03)
F1219V	0.694	-
G1529R	0.693	Loss of Acetylation at K1530 (P = 0.03) Altered Disordered interface (P = 0.02) Altered DNA binding (P = 0.02)
A2231P	0.739	Gain of Intrinsic disorder (P = 0.04) Loss of Ubiquitylation at K2232 (P = 0.05) Loss of Methylation at K2232 (P = 0.03)
H2324P	0.647	Altered Disordered interface (P = 0.05) Altered Metal binding (P = 0.05)
C2332R	0.702	Gain of Helix (P = 0.02) Gain of Strand (P = 0.04)
G2596R	0.769	Loss of Loop (P = 0.03) Loss of B-factor (P = 0.04)
C2605Y	0.506	Altered Transmembrane protein (P = 0.01) Altered Transmembrane protein (P = 0.02)