S3 Table. Mutation profile of non-*BRCA1/2* HR-related genes in the *gBRCA1/2p* and *gBRCA1/2w* groups

HR gene	*gBRCA1/2* pathogenicity	Nucleotide change	AA change	Function	VAF (%) or CNV
ARID1A	w	c.4196A>C	Q1399P	Nonsynonymous SNV	58.6
	w	c.4793G>A	R1598H	Nonsynonymous SNV	63.01
	w	c.6791C>G	S2264X	Stopgain SNV	49.8
	w	c.3977_3978insGCA	P1326delinsPQ	Nonframeshift insertion	51.82
	w	c.2465A>G	N822S	Nonsynonymous SNV	64.84
	w	c.908G>C	S303T	Nonsynonymous SNV	56.39
	w	c.3634C>T	Q1212X	Stopgain SNV	3.97
	w	c.5766G>C	L1922F	Nonsynonymous SNV	34.52
ATM	p	c.5369A>G	D1790G	Nonsynonymous SNV	0.96
	w	c.37C>T	R13C	Nonsynonymous SNV	42.92
	w	c.5063T>C	I1688T	Nonsynonymous SNV	76.59
	p	c.818A>G	D273G	Nonsynonymous SNV	32.72
ATRX	w	c.3175G>A	E1059K	Nonsynonymous SNV	27.66
	w	c.6557C>A	S2186Y	Nonsynonymous SNV	3.47
	w	c.853G>C	E285Q	Nonsynonymous SNV	23.69
	w	c.1492A>G	R498G	Nonsynonymous SNV	33.77
	p	c.5974_5976del	1992_1992del	Nonframeshift deletion	41.82
BARD1	w	c.2143C>T	Q715X	Stopgain SNV	74.66
BLM	p	c.178T>A	L60I	Nonsynonymous SNV	81.69
	w	c.178T->A	L60I	Nonsynonymous SNV	41.92
	w	c.2744C>T	A915V	Nonsynonymous SNV	48.94
	w	c.3422A>G	N1141S	Nonsynonymous SNV	42.48
	w	c.635C>T	S212F	Nonsynonymous SNV	3.08
	w	c.1536delA	G512fs	Frameshift deletion	1.16
	p	c.3427G>A	E1143K	Nonsynonymous SNV	46.3
BRIP1	w		AMP	Amp.	5.76
	w		AMP	Amp.	8.42

	p	c.2440C>T	R814C	Nonsynonymous SNV	49.42
	w	c.1267G>C	D423H	Nonsynonymous SNV	3.69
	w	c.3241_3242insT	A1081fs	Frameshift insertion	17.98
	w		AMP	Amp.	5.62
	w	c.2440C>T	R814C	Nonsynonymous SNV	65.17
	w	c.2830C>G	Q944E	Nonsynonymous SNV	40.5
	w	c.2854A>G	I952V	Nonsynonymous SNV	65.51
	w	c.787C>T	L263F	Nonsynonymous SNV	51.3
	w	c.1328G>A	C443Y	Nonsynonymous SNV	47.67
	w		AMP	Amp.	4.66
CHEK2	w	c.751delG	D251fs	Frameshift deletion	30.37
	w	c.546C>A	Y182*	Stopgain SNV	39.93
FANCA	w	c.2546delC	S849fs	Frameshift deletion	22.79
	w	c.913C>T	H305Y	Nonsynonymous SNV	43.93
	w	c.596+2T>C	splicing	Splicing	38.33
	p	c.2395C>T	P799S	Nonsynonymous SNV	50.7
FANCD2	p	c.1318C>T	Q440X	Stopgain SNV	28.61
	w	c.355C>T	R119C	Nonsynonymous SNV	48.53
	w	c.943C>T	R315W	Nonsynonymous SNV	44.87
FANCE	w	c.565G>C	E189Q	Nonsynonymous SNV	2.68
FANCG	p	c.722C>T	P241L	Nonsynonymous SNV	47.33
	w	c.376_377insGTC	L126delinsVL	Nonframeshift insertion	44.82
	p	c.464G>A	R155H	Nonsynonymous SNV	40.93
MRE11A	w	c.1715G>A	R572Q	Nonsynonymous SNV	47.01
NBN	w	c.388C>G	Q130E	Nonsynonymous SNV	2.6
	w		AMP	Amp.	7.9
	p		AMP	Amp.	4.73
	p		AMP	Amp.	4.52
	w		AMP	Amp.	7.36
PALB2	w	c.1873G>A	E625K	Nonsynonymous SNV	1.68
	w	c.3054G>C	E1018D	Nonsynonymous SNV	36.7
	w	c.2608_2609insC	V870fs	Frameshift	39.89

				insertion	
	w	c.3054G>C	E1018D	Nonsynonymous SNV	40.98
	p	c.1379A>G	Q460R	Nonsynonymous SNV	56.28
RAD50	w	c.2165_2166insT	K722fs	Frameshift insertion	16.09
	w	c.3096_3097del	1032_1033del	Frameshift deletion	6.95
	p	c.1094G>A	R365Q	Nonsynonymous SNV	43.85
	w	c.3790C>T	L1264F	Nonsynonymous SNV	45.57
	w	c.353T>C	I118T	Nonsynonymous SNV	38.06
RAD51	w	c.452G>A	R151Q	Nonsynonymous SNV	69.75
RAD51B	w	c.157C>G	L53V	Nonsynonymous SNV	11.18

Amp., amplification; AA, amino acid; CNV, copy number variant; HR, homologous recombination; SNV, single-nucleotide variant; VAF, variant allele frequency.