

S7 Table. TMB and SNV according to HR-DDR gene aberration

	Aberration detected			Aberration undetected			p-value
	No.	Mean	SD	No.	Mean	SD	
TMB							
<i>ARID1A</i>	7	12.32	3.83	62	12.23	5.75	0.969
<i>ATM</i>	4	10.42	1.00	65	12.35	5.72	0.505
<i>ATRX</i>	4	11.6	6.09	65	5.58	5.58	0.814
<i>BLM</i>	7	13.17	4.99	62	12.13	5.66	0.645
<i>BRCA1</i>	16	9.32	4.32	53	13.12	5.63	0.016*
<i>BRCA2</i>	20	12.17	4.51	49	12.27	5.99	0.974
<i>BRIP1</i>	11	14.72	3.38	58	11.76	5.79	0.107
<i>FANCA</i>	4	16.62	2.69	65	11.97	5.60	0.105
<i>FANCG</i>	3	24.26	11.03	66	11.69	4.66	0.186
<i>NBN</i>	5	8.17	2.19	64	12.56	5.63	0.09
<i>PALB2</i>	5	10.01	4.60	64	12.41	5.63	0.357
<i>RAD50</i>	5	10.69	3.09	64	12.36	5.71	0.523
SNV							
<i>ARID1A</i>	7	29.71	44.46	62	15.94	5.88	0.444
<i>ATM</i>	4	14.25	5.12	65	17.52	15.33	0.674
<i>ATRX</i>	4	48.25	55.13	65	15.43	5.57	0.319
<i>BLM</i>	7	18.14	8.32	62	17.24	15.55	0.881
<i>BRCA1</i>	16	15.06	5.35	53	18.02	16.77	0.492
<i>BRCA2</i>	20	21.9	26	49	15.47	6.01	0.287
<i>BRIP1</i>	11	18.64	6	58	17.09	16.1	0.755
<i>FANCA</i>	4	23	7.35	65	16.98	15.24	0.438
<i>FANCG</i>	3	22	6.08	66	17.12	15.2	0.584
<i>NBN</i>	5	16.8	8.87	64	17.38	15.35	0.935
<i>PALB2</i>	5	41.8	49.63	64	15.42	5.75	0.3
<i>RAD50</i>	5	13	3.08	64	17.67	15.44	0.505

HR-DDR, homologous recombination DNA damage repair; SD, standard deviation; SNV, single-nucleotide variant; TMB, tumor mutation burden.