

Table S4. Tally of variants by primary annotation category and frequency.

Total Number of Variants Discovered by Gene and Type											
	Canonical Splice*	Frame Shift*	Inframe	Intronic	Missense	Regulatory	Splice Site	Stop Gained*	Synonymous	UTR	Total
ATM	10	25	4	230	324	6	43	24	119	0	785
CHEK2	2	6	0	40	77	8	11	7	11	3	165
PALB2	0	18	1	28	125	11	8	16	48	0	255
XRCC2	2	4	0	0	34	13	1	5	8	1	68
Total	14	53	5	298	560	38	63	52	186	4	1273

Variants Classified as Common (Carrier Frequency >0.1%) by Gene and Type											
	Canonical Splice*	Frame Shift*	Inframe	Intronic	Missense	Regulatory	Splice Site	Stop Gained*	Synonymous	UTR	Total
ATM	0	0	0	10	25	0	4	0	11	0	50
CHEK2	0	1	0	0	4	0	0	0	1	0	6
PALB2	0	0	0	2	7	0	0	0	4	0	13
XRCC2	0	0	0	0	2	0	0	0	0	1	3
Total	0	1	0	12	38	0	4	0	16	1	72

Variants Classified as Rare (Carrier Frequency <0.1%) by Gene and Type											
	Canonical Splice*	Frame Shift*	Inframe	Intronic	Missense	Regulatory	Splice Site	Stop Gained*	Synonymous	UTR	Total
ATM	10	25	4	220	299	6	39	24	108	0	735
CHEK2	2	5	0	40	73	8	11	7	10	3	159
PALB2	0	18	1	26	118	11	8	16	44	0	242
XRCC2	2	4	0	0	32	13	1	5	8	0	65
Total	14	52	5	286	522	38	59	52	170	3	1201

*Truncating variants