

Table S2. Design, callable bases, and depth summary.

	Ensembl Transcript ID	Ensembl Protein ID	Exon Length	Amplicons	Percent Target Sequence Covered	Percent Callable Bases within Target			Sequence Depth Coverage per Gene		
						Median	Mean	SD	Median	Mean	SD
<i>ATM</i>	ENST00000278616.4	ENSP00000278616.4	9171	135	99.7%	99.2%	98.8%	0.6%	425.2	428.6	99.2
<i>CHEK2</i>	ENST00000328354.6	ENSP00000329178.6	1632	25	100.0%	97.1%	97.0%	0.7%	399.4	404.9	88.7
<i>PALB2</i>	ENST00000261584.4	ENSP00000261584.4	3561	50	97.7%	96.9%	96.9%	0.3%	454.8	460.2	101.9
<i>XRCC2</i>	ENST00000359321.1	ENSP00000352271.1	843	11	100.0%	99.9%	99.6%	1.5%	472.2	481.8	118.6