

Supplemental Table 1. Summary of SNP Selection, Quality Control, and Inclusion.

Locus	SNPs Selected from HapMap as tagging SNPs	SNPs Selected for Assay as putatively functional	Total number Genotyped	Failed HWE*	MAF <1%*	Genotyping Failure >20%*	Selected For Analysis*
<i>ATM</i>	5	2	7	0/0	2/2	0/1	5/5
<i>BRIP1</i>	24	9	33	2/0	3/4	9/9	8/8
<i>BARID1</i>	20	9	29	0/0	5/7	6/6	8/8
<i>CTIP</i>	10	1	11	0/0	3/3	1/1	7/7
<i>MRE11</i>	17	2	19	4/0	5/5	1/2	7/7
<i>NBS1</i>	10	5	15	7/0	2/2	1/1	6/3
<i>RAD50</i>	4	1	5	0/0	1/1	1/1	4/4
<i>RAD51</i>	5	5	10	0/1	3/3	2/3	5/4
<i>TOPBP1</i>	9	4	13	1/0	3/4	1/1	6/5

*Results for *BRCA1/BRCA2*. SNPs could fail quality control by more than one criterion