Supplementary Table 3 Genotyping quality of the XRCC2 SNPs in Sheffield (SBCS) study

SNPs	Position[†]	Concordance rate	Call Rate	Common/Rare[‡]	MAF[‡]	HWE[‡,§]
rs3218556[*]	151974534	100	94.7	C/T	0.04	0.7011
rs3218536	151976940	98.9	98.1	G/A	0.09	0.1098
rs3218534[*]	151977928	99.3	95.9	C/T	0.45	1.0000
rs3218501	151982850	100	98.8	C/G	0.04	1.0000
rs3218499	151983072	98.9	98	G/C	0.23	0.1758
rs3218455	151991349	98.9	98	T/C	0.10	0.0001
rs3111465	151993408	99	87.2	G/A	0.05	0.7479
rs3094406	151993798	99.4	82.3	C/G	0.09	0.4271
rs3218408	151998549	99.2	97.9	T/G	0.23	0.2024
rs3218400	152000622	99.6	99	C/A	0.10	0.7415
rs2106776	152003857	98.9	82.8	C/T	0.45	0.7479
rs3218374	152005067	97.5	97.8	C/G	0.46	0.2288

[*] genotyping was done by TaqMan

[†] NCBI genome build 36.1

[‡] Common/Minor: common and rare allele in controls; MAF: minor allele frequency in controls; HWE: Hardy-Weinberg equilibrium

[§] empirical p values based on 10,000 permutations