Supplemental Table S10. Accuracy statistics for imputation of the South Asian (SAS) specific variant genotypes from The GTEx Project using the 1000 Genomes panel as the reference. MAF range and mean/median/standard deviation (S.D) of genotype R2 are shown in the columns.

POPULATION	PROTOCOL	MAF	MEAN R2	MEDIAN	S.D.
SAS	Central	[0,0.001]	0.154609	0	0.341588
SAS	Unphased (No augment)	[0,0.001]	0.157327	0	0.335179
SAS	Unphased (Augmented)	[0,0.001]	0.157273	0	0.336651
SAS	Phased (Augmented)	[0,0.001]	0.152381	0	0.332141
SAS	Phased (No augment)	[0,0.001]	0.140565	0	0.321699
SAS	RESHAPE	[0,0.001]	0.123509	0	0.309102
SAS	Central	(0.001,0.01]	0.479895	0.4992	0.40532
SAS	Unphased (No augment)	(0.001,0.01]	0.440218	0.4402	0.3835
SAS	Unphased (Augmented)	(0.001,0.01]	0.460837	0.4771	0.388
SAS	Phased (Augmented)	(0.001,0.01]	0.461197	0.4968	0.389677
SAS	Phased (No augment)	(0.001,0.01]	0.426098	0.3968	0.383502
SAS	RESHAPE	(0.001,0.01]	0.431724	0.372	0.407559
SAS	Central	(0.01,0.05]	0.771782	0.886	0.268082
SAS	Unphased (No augment)	(0.01,0.05]	0.725174	0.8235	0.281305
SAS	Unphased (Augmented)	(0.01,0.05]	0.745684	0.8515	0.277714
SAS	Phased (Augmented)	(0.01,0.05]	0.743893	0.8414	0.27374
SAS	Phased (No augment)	(0.01,0.05]	0.711469	0.8063	0.286332
SAS	RESHAPE	(0.01,0.05]	0.746392	0.8661	0.288528
SAS	Central	(0.05,1]	0.941082	0.9835	0.118021
SAS	Unphased (No augment)	(0.05,1]	0.906981	0.95795	0.138324
SAS	Unphased (Augmented)	(0.05,1]	0.924604	0.9717	0.129182
SAS	Phased (Augmented)	(0.05,1]	0.927896	0.9714	0.122263
SAS	Phased (No augment)	(0.05,1]	0.895611	0.95315	0.150576
SAS	RESHAPE	(0.05,1]	0.933615	0.9817	0.130184