Supplemental Table S5. Accuracy statistics for imputation of the South Asian (SAS) specific variant genotypes from The 1000 Genomes Project using HRC 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]	0.106589	0	0.227396
SAS	Unphased (No augment)	[0,0.001]	0.083281	0	0.20416
SAS	Unphased (Augmented)	[0,0.001]	0.084377	0	0.205999
SAS	Phased (Augmented)	[0,0.001]	0.077812	0	0.195058
SAS	Phased (No augment)	[0,0.001]	0.070295	0	0.185439
SAS	RESHAPE	[0,0.001]	0.087956	0	0.209785
SAS	Central	(0.001,0.01]	0.469009	0.451	0.304859
SAS	Unphased (No augment)	(0.001,0.01]	0.408368	0.3718	0.294082
SAS	Unphased (Augmented)	(0.001,0.01]	0.422739	0.3817	0.302821
SAS	Phased (Augmented)	(0.001,0.01]	0.404478	0.3729	0.294445
SAS	Phased (No augment)	(0.001,0.01]	0.381179	0.3331	0.289728
SAS	RESHAPE	(0.001,0.01]	0.423889	0.3988	0.297412
SAS	Central	(0.01,0.05]	0.707611	0.7784	0.246036
SAS	Unphased (No augment)	(0.01,0.05]	0.65002	0.6953	0.255904
SAS	Unphased (Augmented)	(0.01,0.05]	0.666112	0.7223	0.257023
SAS	Phased (Augmented)	(0.01,0.05]	0.657885	0.714	0.256216
SAS	Phased (No augment)	(0.01,0.05]	0.625359	0.6661	0.258616
SAS	RESHAPE	(0.01,0.05]	0.667579	0.7306	0.252895
SAS	Central	(0.05,1]	0.928836	0.9721	0.117118
SAS	Unphased (No augment)	(0.05,1]	0.888626	0.9353	0.13393
SAS	Unphased (Augmented)	(0.05,1]	0.908261	0.9542	0.129169
SAS	Phased (Augmented)	(0.05,1]	0.905804	0.9527	0.130917
SAS	Phased (No augment)	(0.05,1]	0.871934	0.925	0.148996
SAS	RESHAPE	(0.05,1]	0.915851	0.962	0.126128