Supplemental Table S4. Accuracy statistics for imputation of the American (AMR) 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.
AMR	Central	[0,0.001]	0.254797	0	0.353762
AMR	Unphased (No augment)	[0,0.001]	0.209501	0	0.326248
AMR	Unphased (Augmented)	[0,0.001]	0.206551	0	0.327434
AMR	Phased (Augmented)	[0,0.001]	0.189747	0	0.312348
AMR	Phased (No augment)	[0,0.001]	0.176936	0	0.303706
AMR	RESHAPE	[0,0.001]	0.205978	0	0.327213
AMR	Central	(0.001,0.01]	0.462817	0.4451	0.301277
AMR	Unphased (No augment)	(0.001,0.01]	0.399879	0.35585	0.293552
AMR	Unphased (Augmented)	(0.001,0.01]	0.405254	0.3717	0.295375
AMR	Phased (Augmented)	(0.001,0.01]	0.392346	0.3456	0.293841
AMR	Phased (No augment)	(0.001,0.01]	0.374043	0.3327	0.289655
AMR	RESHAPE	(0.001,0.01]	0.41068	0.3742	0.300782
AMR	Central	(0.01,0.05]	0.670967	0.7083	0.257047
AMR	Unphased (No augment)	(0.01,0.05]	0.606	0.6157	0.268162
AMR	Unphased (Augmented)	(0.01,0.05]	0.619931	0.6379	0.26883
AMR	Phased (Augmented)	(0.01,0.05]	0.609523	0.6242	0.268876
AMR	Phased (No augment)	(0.01,0.05]	0.582363	0.5872	0.269671
AMR	RESHAPE	(0.01,0.05]	0.623651	0.6425	0.267179
AMR	Central	(0.05,1]	0.932173	0.9757	0.117025
AMR	Unphased (No augment)	(0.05,1]	0.889763	0.93665	0.134085
AMR	Unphased (Augmented)	(0.05,1]	0.911638	0.958	0.128531
AMR	Phased (Augmented)	(0.05,1]	0.907852	0.956	0.132184
AMR	Phased (No augment)	(0.05,1]	0.869298	0.9248	0.150083
AMR	RESHAPE	(0.05,1]	0.920465	0.9668	0.126425