

**Supplemental Table S9.** Accuracy statistics for imputation of the American (AMR) 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.
AMR	Central	[0,0.001]	0.244904	0	0.39185
AMR	Unphased (No augment)	[0,0.001]	0.237338	0	0.377912
AMR	Unphased (Augmented)	[0,0.001]	0.250133	0	0.386338
AMR	Phased (Augmented)	[0,0.001]	0.233264	0	0.375679
AMR	Phased (No augment)	[0,0.001]	0.21651	0	0.366507
AMR	RESHAPE	[0,0.001]	0.194577	0	0.361407
AMR	Central	(0.001,0.01]	0.478059	0.4976	0.378233
AMR	Unphased (No augment)	(0.001,0.01]	0.456549	0.4423	0.359096
AMR	Unphased (Augmented)	(0.001,0.01]	0.468747	0.45785	0.362038
AMR	Phased (Augmented)	(0.001,0.01]	0.470832	0.4825	0.362057
AMR	Phased (No augment)	(0.001,0.01]	0.435708	0.4259	0.35936
AMR	RESHAPE	(0.001,0.01]	0.430598	0.3891	0.382756
AMR	Central	(0.01,0.05]	0.716628	0.83055	0.311186
AMR	Unphased (No augment)	(0.01,0.05]	0.663295	0.7488	0.318089
AMR	Unphased (Augmented)	(0.01,0.05]	0.679138	0.7646	0.318978
AMR	Phased (Augmented)	(0.01,0.05]	0.684375	0.7659	0.311142
AMR	Phased (No augment)	(0.01,0.05]	0.653061	0.72805	0.317512
AMR	RESHAPE	(0.01,0.05]	0.685887	0.7987	0.329716
AMR	Central	(0.05,1]	0.946536	0.9864	0.112344
AMR	Unphased (No augment)	(0.05,1]	0.910134	0.9554	0.132106
AMR	Unphased (Augmented)	(0.05,1]	0.928098	0.9724	0.123985
AMR	Phased (Augmented)	(0.05,1]	0.930965	0.9733	0.12116
AMR	Phased (No augment)	(0.05,1]	0.894911	0.9495	0.149169
AMR	RESHAPE	(0.05,1]	0.940734	0.985	0.124182