Supplemental Table S11. Accuracy statistics for imputation of the East Asian (EAS) 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.
EAS	Central	[0,0.001]	0.104799	0	0.29939
EAS	Unphased (No augment)	[0,0.001]	0.110967	0	0.30535
EAS	Unphased (Augmented)	[0,0.001]	0.11277	0	0.307319
EAS	Phased (Augmented)	[0,0.001]	0.106624	0	0.300197
EAS	Phased (No augment)	[0,0.001]	0.092152	0	0.281445
EAS	RESHAPE	[0,0.001]	0.08051	0	0.264959
EAS	Central	(0.001,0.01]	0.423259	0.1648	0.455185
EAS	Unphased (No augment)	(0.001,0.01]	0.378932	0.1141	0.43005
EAS	Unphased (Augmented)	(0.001,0.01]	0.396901	0.1654	0.435286
EAS	Phased (Augmented)	(0.001,0.01]	0.399023	0.1987	0.435486
EAS	Phased (No augment)	(0.001,0.01]	0.362646	0.0045	0.428411
EAS	RESHAPE	(0.001,0.01]	0.383936	0	0.446291
EAS	Central	(0.01,0.05]	0.72632	0.90465	0.342828
EAS	Unphased (No augment)	(0.01,0.05]	0.613577	0.6656	0.351359
EAS	Unphased (Augmented)	(0.01,0.05]	0.653855	0.7488	0.343819
EAS	Phased (Augmented)	(0.01,0.05]	0.662333	0.7628	0.338237
EAS	Phased (No augment)	(0.01,0.05]	0.603952	0.6656	0.352843
EAS	RESHAPE	(0.01,0.05]	0.696481	0.8716	0.35544
EAS	Central	(0.05,1]	0.939134	0.98405	0.121855
EAS	Unphased (No augment)	(0.05,1]	0.897857	0.9512	0.145866
EAS	Unphased (Augmented)	(0.05,1]	0.918886	0.9686	0.134592
EAS	Phased (Augmented)	(0.05,1]	0.921825	0.9683	0.128867
EAS	Phased (No augment)	(0.05,1]	0.884987	0.9462	0.157176
EAS	RESHAPE	(0.05,1]	0.931654	0.9823	0.134589