Supplemental Table S6. Accuracy statistics for imputation of the East Asian (EAS) 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.
EAS	Central	[0,0.001]	0.070698	0	0.176614
EAS	Unphased (No augment)	[0,0.001]	0.050423	0	0.146257
EAS	Unphased (Augmented)	[0,0.001]	0.052452	0	0.151308
EAS	Phased (Augmented)	[0,0.001]	0.049108	0	0.143034
EAS	Phased (No augment)	[0,0.001]	0.043197	0	0.132062
EAS	RESHAPE	[0,0.001]	0.05516	0	0.154653
EAS	Central	(0.001,0.01]	0.513627	0.5258	0.360618
EAS	Unphased (No augment)	(0.001,0.01]	0.432227	0.3797	0.341158
EAS	Unphased (Augmented)	(0.001,0.01]	0.464234	0.4373	0.353798
EAS	Phased (Augmented)	(0.001,0.01]	0.454174	0.4218	0.350064
EAS	Phased (No augment)	(0.001,0.01]	0.416586	0.3552	0.337149
EAS	RESHAPE	(0.001,0.01]	0.470826	0.4582	0.349601
EAS	Central	(0.01,0.05]	0.837613	0.9311	0.212088
EAS	Unphased (No augment)	(0.01,0.05]	0.749747	0.8631	0.264605
EAS	Unphased (Augmented)	(0.01,0.05]	0.783696	0.8899	0.248312
EAS	Phased (Augmented)	(0.01,0.05]	0.777151	0.885	0.247508
EAS	Phased (No augment)	(0.01,0.05]	0.728637	0.8411	0.270146
EAS	RESHAPE	(0.01,0.05]	0.812009	0.9062	0.224429
EAS	Central	(0.05,1]	0.941314	0.978	0.106541
EAS	Unphased (No augment)	(0.05,1]	0.890911	0.9361	0.133839
EAS	Unphased (Augmented)	(0.05,1]	0.916299	0.9583	0.122016
EAS	Phased (Augmented)	(0.05,1]	0.914611	0.9572	0.124976
EAS	Phased (No augment)	(0.05,1]	0.874837	0.9282	0.149393
EAS	RESHAPE	(0.05,1]	0.93162	0.9708	0.114431