Supplemental Figure S3: Mean correlation R² and IQS between true and imputed genotypes for duoHMM+IMPUTE, IMPUTE+IMPUTE, SHAPEIT+IMPUTE, duoHMM+minimac, MaCH+minimac, and SHAPEIT+minimac: (A) R2 for EUR and (B) R² for AFR, using the random selection strategy. The first/second of a pair of programs in the key indicates phasing/imputation functions. Computation of the mean of R2 and IQS is based on a second randomly generated set of all 100 genetic datasets with a sample size of 960 subjects, each having 7,954 SNPs for EUR and 10,891 SNPs for AFR.