F:\基因组选择数据\gs_SEQ\图\chr.tiff

**Figure S1.** Imputation accuracy across chromosome. CR, genotype concordance rate which was defined as the proportion of genotypes of imputed variants, which were the same as the whole genome sequencing. AR2, allelic R-squared for consistent variants between imputation and whole genome sequencing. AR2\_ALL, allelic R-squared for all imputed variants. AR2\_ALL>0.15, allelic R-squared for all imputed variants with MAF>0.15.