

File S2

iHS is an analytical method and statistic used to scan SNP data for signals of recent positive selection based on the EHH (extended haplotype homozygosity) statistic proposed by Sabeti et al. (2002). The software that calculates the unstandardised iHS statistic is available under request from the developers.

The iHS statistic should have an approximately standard normal distribution at all SNPs under neutral evolution (Voight et al. 2006). Large negative values indicate unusually long haplotypes carrying the derived allele, while large positive values indicate long haplotypes carrying the ancestral allele. Values of $iHS > 2.5$ are considered strong evidence for selection on the ancestral allele, while $iHS < -2.5$ suggests selection on the derived allele. In Table 2 we consider only absolute values of iHS since both large and small (negative) values of the iHS are suggestive of selection.