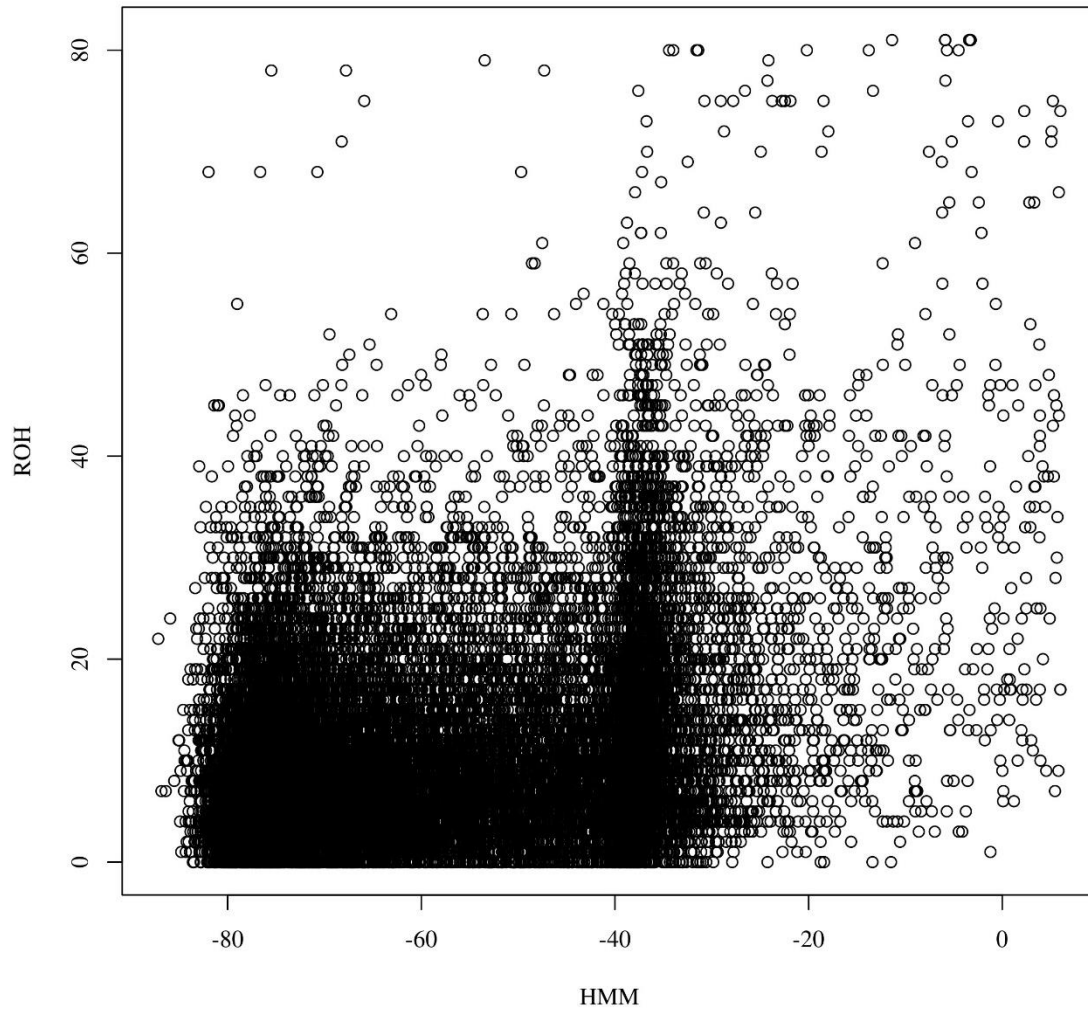


Figure S1. The ROH hotspots scores plot against integrative extended haplotype homozygosity (EHH) scores for ancestral and derived alleles in Holstein population. a. ancestral alleles; b. derived alleles.



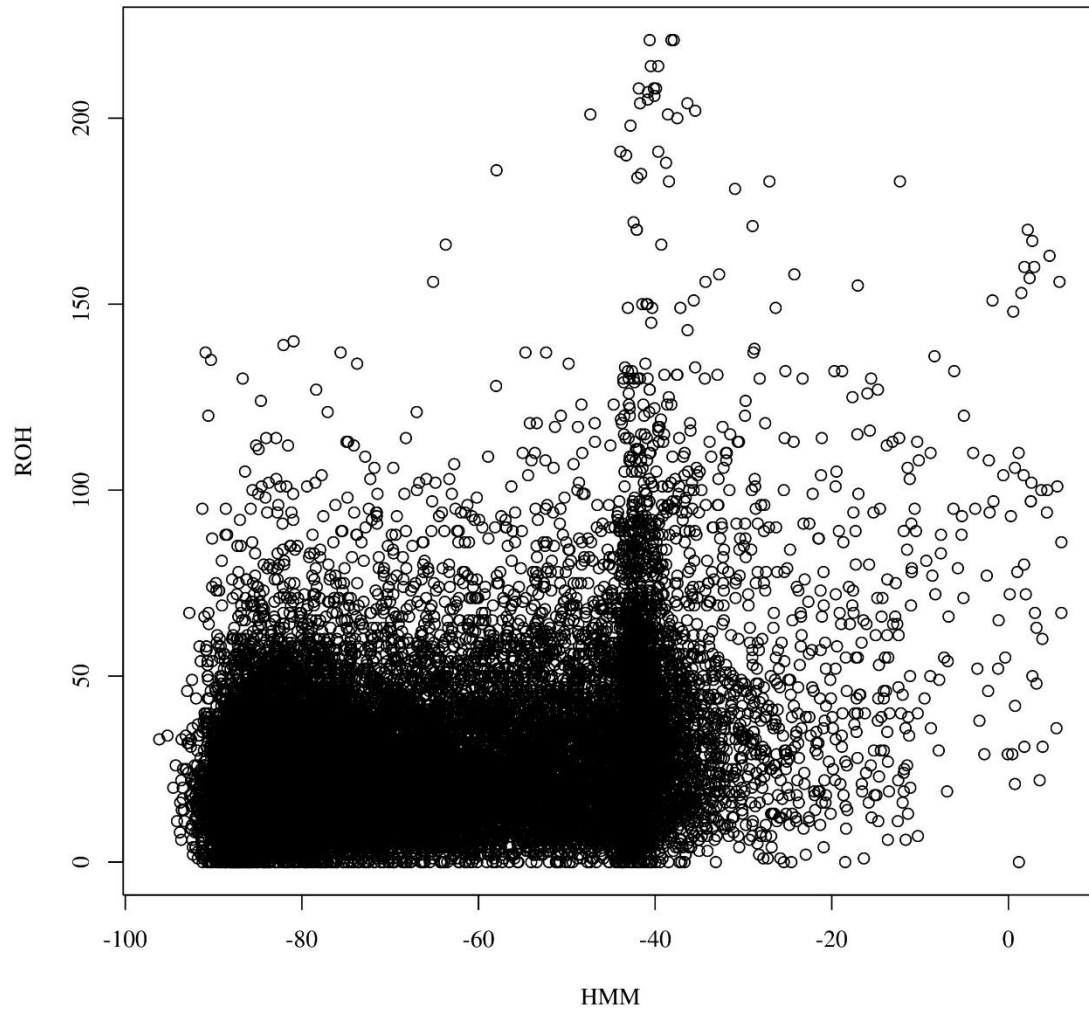
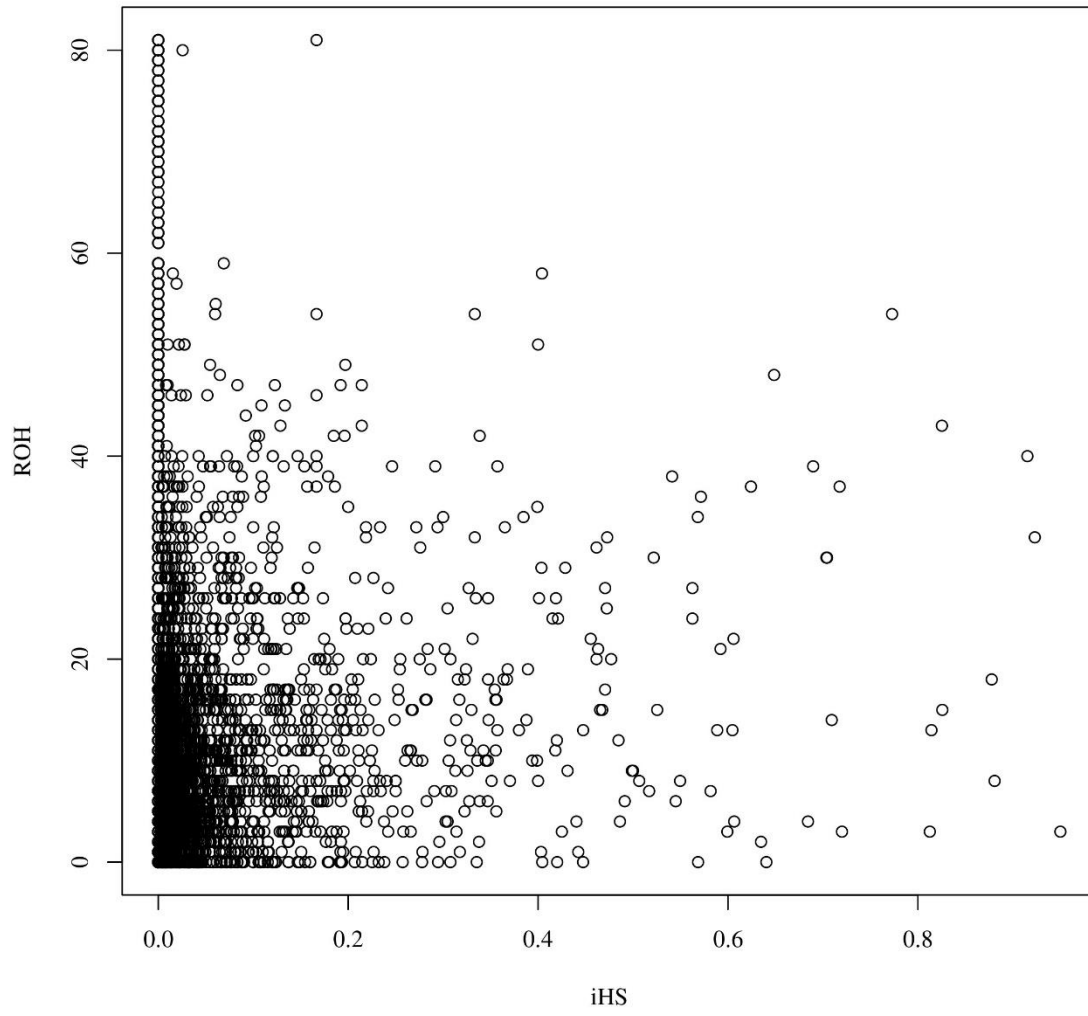


Figure S2. The ROH hotspots scores plot against the posterior probabilities from the hidden Markov model (HMM) measuring hard sweeps for holstein and angus populations. a. Holstein population; b. Angus population.



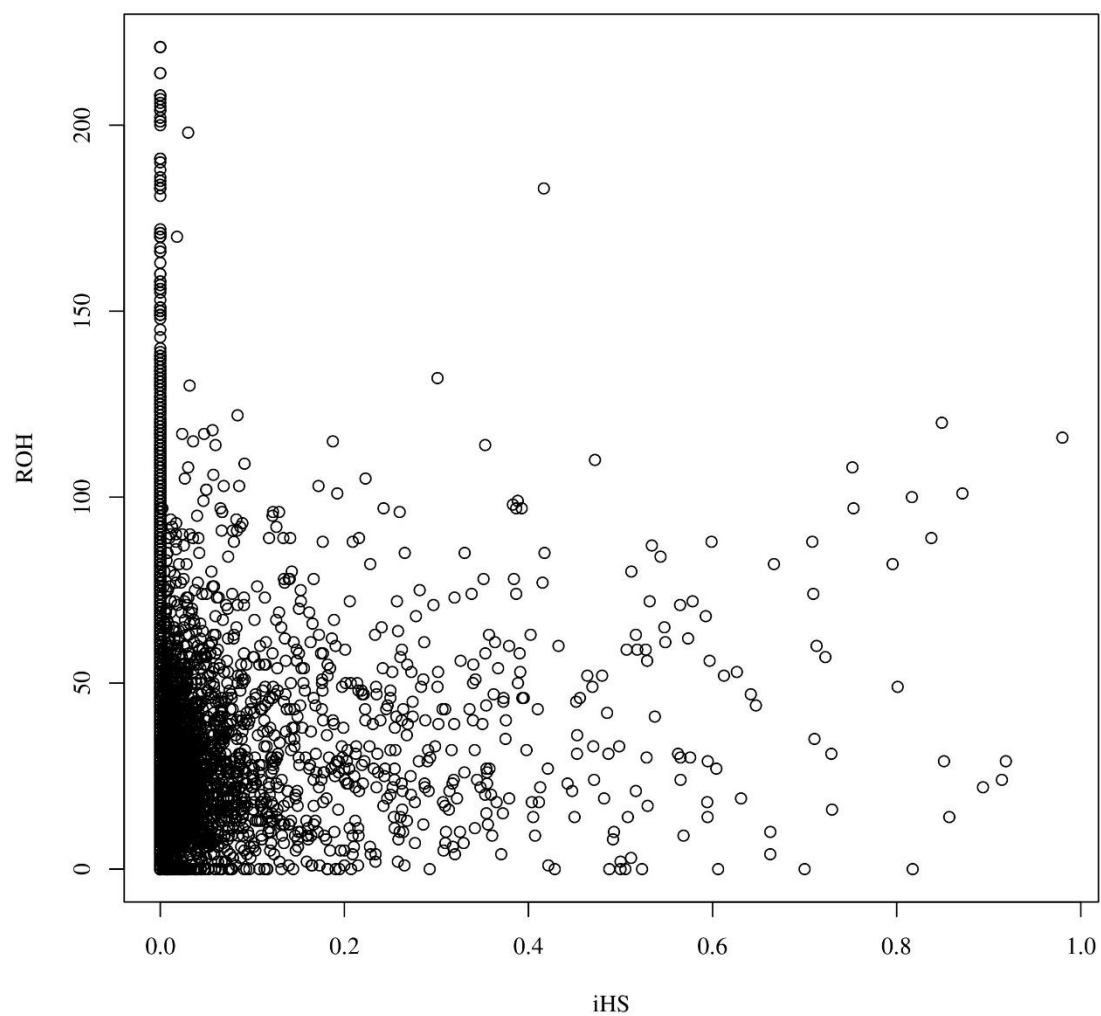


Figure S3. The ROH hotspots scores plot against integrated haplotype scores (iHS) for Holstein and angus populations. a. Holstein population; b. Angus population.

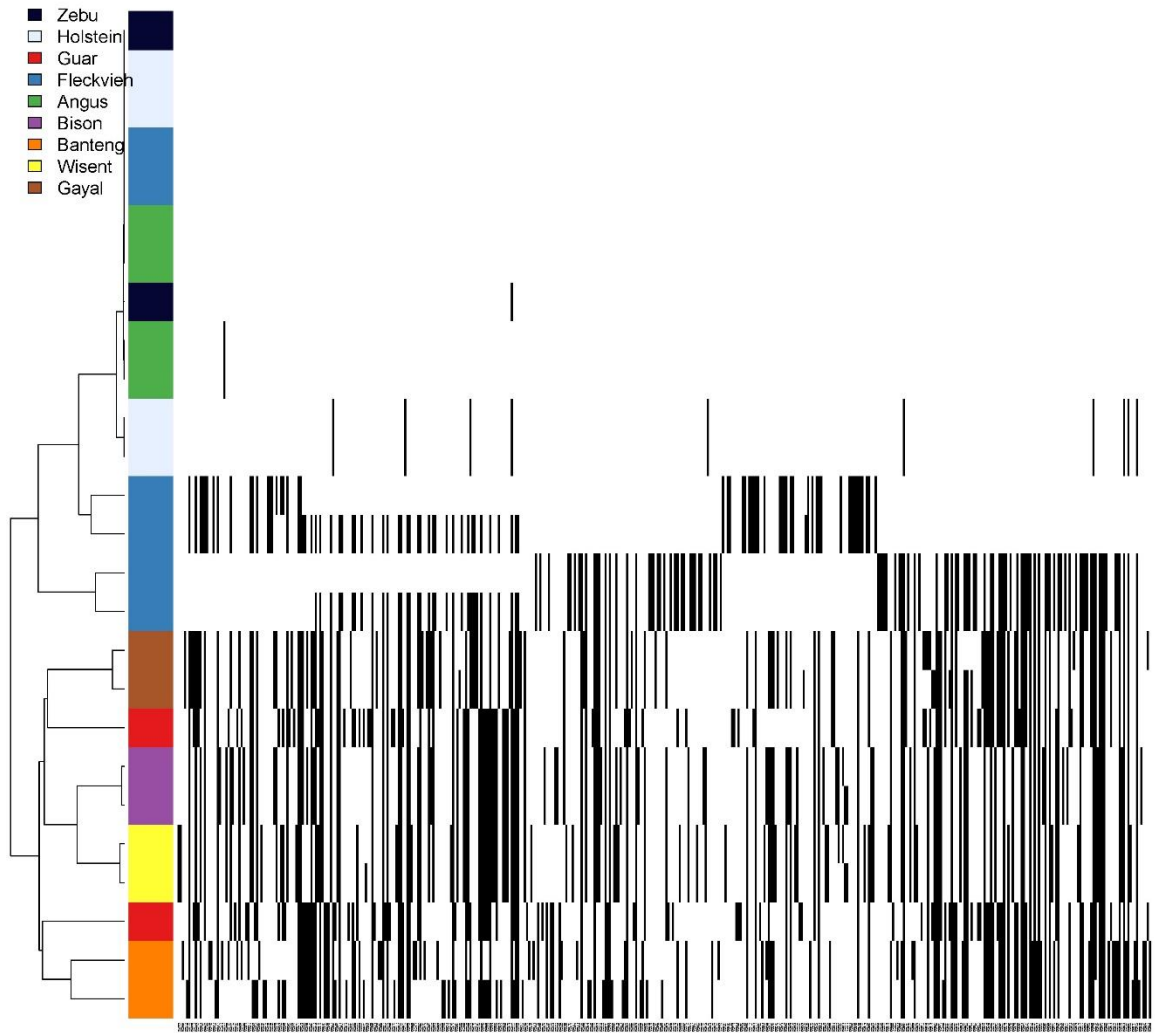


Figure S4. Haplotype structure and phylogenies of haplotypes from an ROH hotspot region containing the *REG3G* gene for *Bos taurus* (Holstein, Angus and Fleckvieh), Zebu (*Bos indicus*), Gaur, Bison, Banteng, Wisent and Gayal. Left panel: the genealogy of *REG3G* haplotypes. Right panel: the haplotype structure around the *REG3G* gene. Colored blocks indicate the origin of haplotypes. The two alleles at each bi-allelic SNP are shown as black or white lines.