



**Supplemental Fig. S23. Comparison of LD patterns (a and b) and Tajima's  $D$  (c) between selected regions and whole genome.** (a) LD patterns between pairs of homozygous SNPs for selected regions and whole genome. Selected regions had significantly higher LD than the whole genome background across the range of distances separating loci ( $P < 10^{-16}$ , Mann-Whitney  $U$  test). (b) LD in selected regions. In the majority of selected regions, almost all homozygous SNPs showed strong LD (blue bars). After random shuffling of all homozygous SNPs in the genomes of the ten breeds, the strong LD between SNPs in selected regions was completely lost (red bars). These results validated the method used to detect selected regions and are consistent with the hypothesis that these regions were under positive selection pressure during the original derivation of these breeds. (c) Comparison of Tajima's  $D$  in 10 kb windows in the whole genome and in selected regions. Selected regions showed highly negative Tajima's  $D$  values (Median = -1.18) than whole genome (Median = 0) ( $P < 10^{-16}$ , Mann-Whitney  $U$  test), which further support that these regions were positively selected during derivation of these breeds. Tajima's  $D$  was calculated with a custom Perl script using the formula described in original paper<sup>6</sup>.