

Supplementary Methods

Selective signatures associated with phenotypic traits based on SNPs.

We compared the 133 commonly selected regions associated with different phenotypes (e.g., production, morphological and physiological traits) by XP-CLR, π -ratio and iHS analyses as well as the 95 commonly selected regions by XP-CLR, π -ratio and HKA analyses with previously mapped QTLs. We found that 30 of the selective sweeps by XP-CLR, π -ratio and iHS and 43 of the selective sweeps by XP-CLR, π -ratio and HKA overlapped with known QTLs⁶⁹, which are associated with a number of traits such as reproduction, milk, growth, meat and carcass, fat deposition in the tails and wool fineness (Supplementary Table S5, Supplementary Data S43 and S44). Specifically, for XP-CLR, π -ratio and iHS, the number of QTLs (shorter than 100 Mb) overlapping for traits such as reproduction, milk, growth, meat and carcass, fat deposition in the tails are 3 (permutation test, $P < 0.01$), 1 (permutation test, $P < 0.05$), 20 (permutation test, $P < 0.001$), 7 (permutation test, $P < 0.05$), respectively (Supplementary Table S5 and Supplementary Data S43). For XP-CLR, π -ratio and HKA, the overlapping numbers of QTLs (shorter than 100 Mb) for the above traits are 1 (permutation test, $P < 0.001$), 4 (permutation test, $P < 0.001$), 32 (permutation test, $P < 0.001$) and 2 (permutation test, $P < 0.05$), respectively (Supplementary Table S5 and Supplementary Data S44).