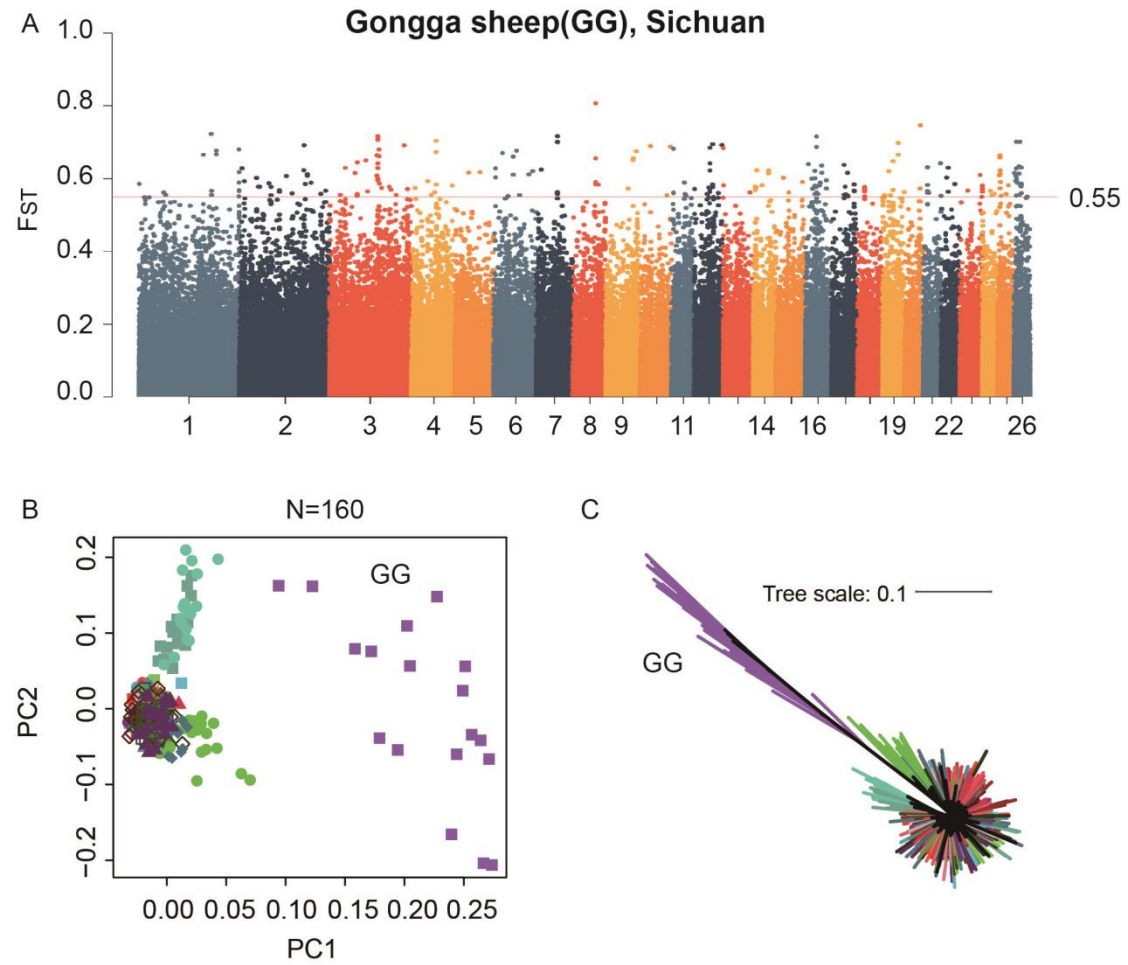
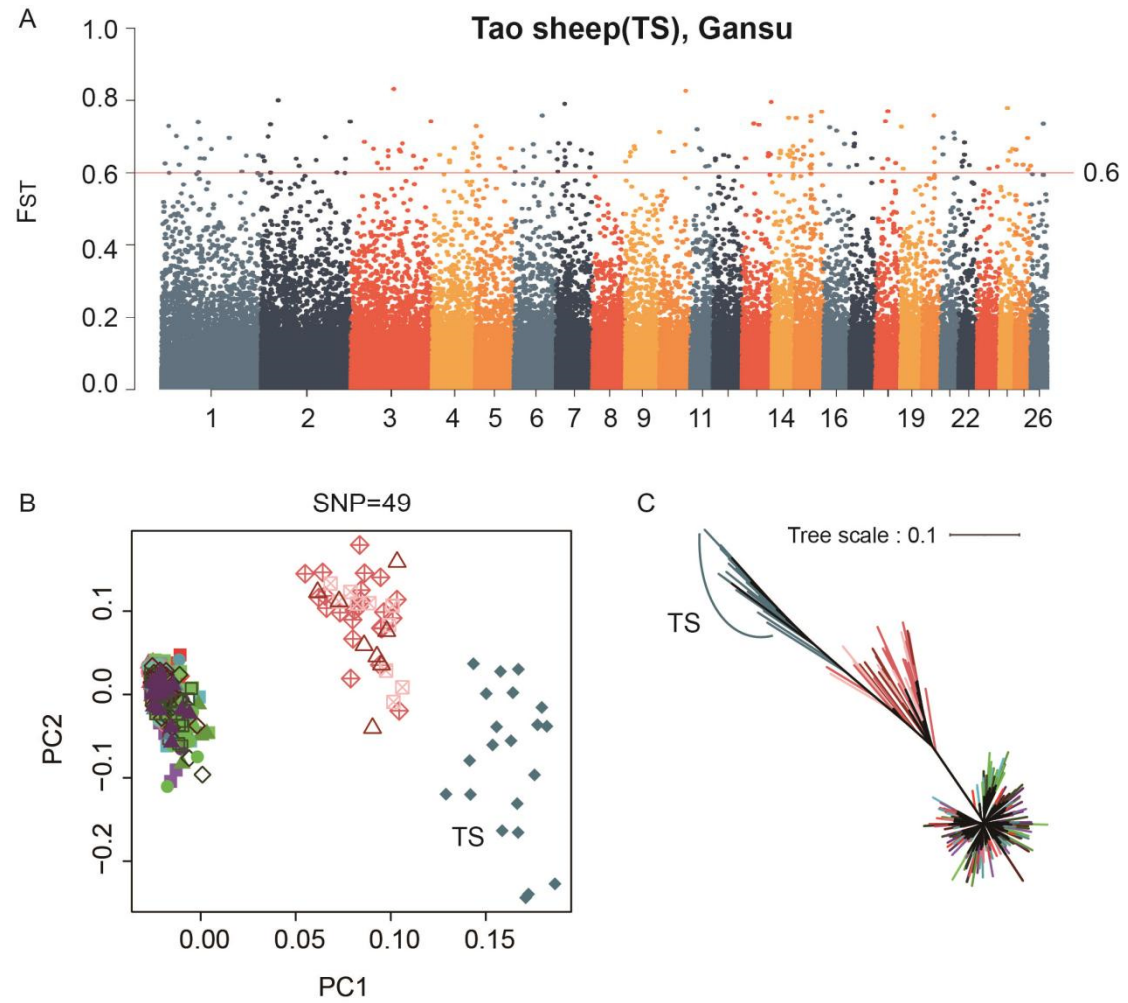


Supplementary Figure S1. Construction of specific SNP genetic marker sets in Qinghai black Tibetan sheep (HZ). (A) Genome wide distribution of F_{ST} values in Qinghai black Tibetan sheep. The significance threshold of selection signature was set to 0.6 for each individual test and is indicated with red horizontal full lines.(B) Principal component analysis and (C) NJ tree analysis of 104 SNPs distinguishing Heizang sheep (HZ) sheep. The green solid square represents HZ sheep in PCA plots. The color of HZ sheep in the Neighbor-Joining tree was as the same as that in the PCA plots.



Supplementary Figure S2. Construction of specific SNP genetic marker sets in Sichuan Gongga Tibetan sheep (GG). (A) Genome wide distribution of F_{ST} values in Sichuan Gongga Tibetan sheep. The significance threshold of selection signature was set to 0.55 for each individual test and is indicated with red horizontal full lines. (B) Principal component analysis and (C) NJ tree analysis of 160 SNPs distinguishing Gongga sheep (GG) sheep. The color of GG sheep in the Neighbor-Joining tree was as the same as that in the PCA plots.



Supplementary Figure S3. Construction of specific SNP genetic marker sets in Gansu Tao sheep (TS). (A) Genome wide distribution of F_{ST} values in Gansu Tao sheep. The significance threshold of selection signature was set to 0.55 for each individual test and is indicated with red horizontal full lines. (B) Principal component analysis and (C) Neighbor-Joining tree (NJ) tree analysis of 49 SNPs distinguishing Tao sheep (TS). The color of TS sheep in the NJ tree was as the same as that in the PCA plots.