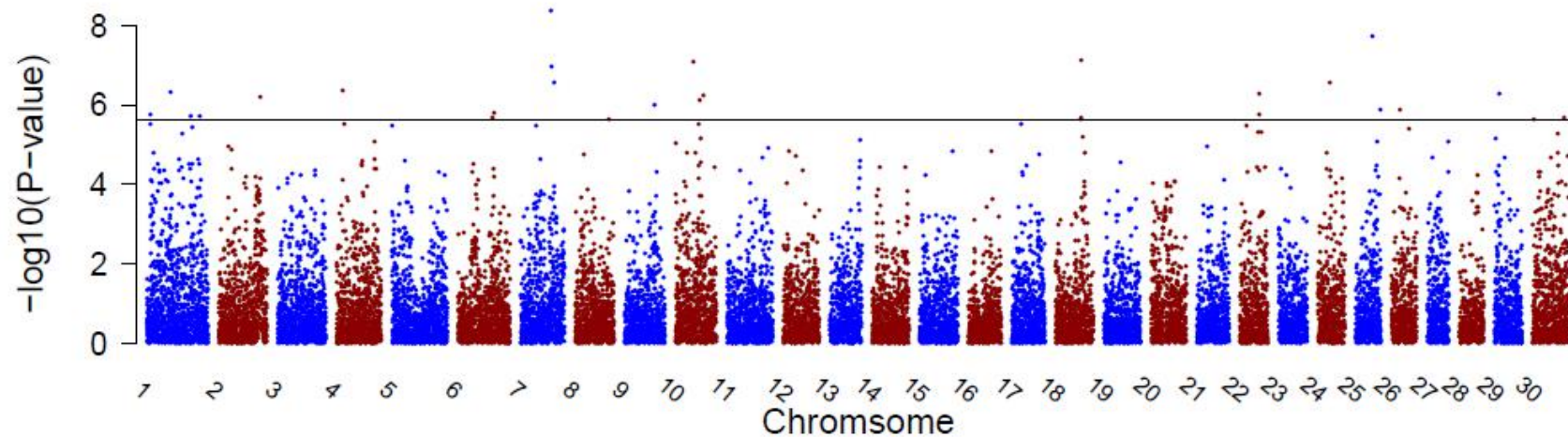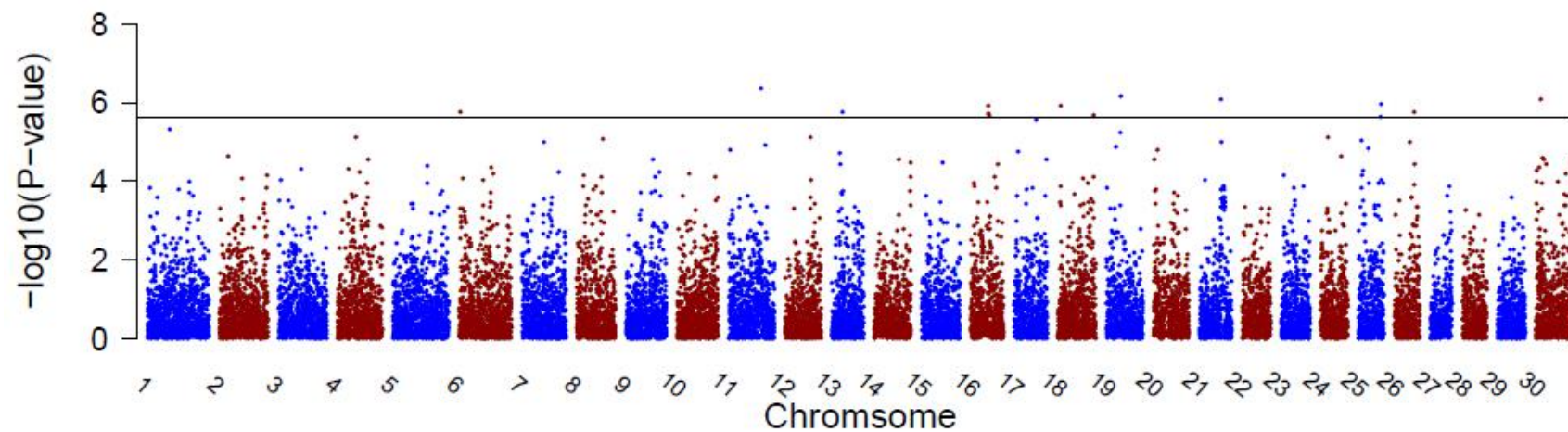**A**

Manhanttan:RA

B

Manhanttan:FS

Figure S1. Genome-wide plots of –log10 (*P*-value) SNP association effects on body confirmation trait of rump angle (RA, A) and final sore (FS, B) obtained by mixed-effect linear regression model (MLM). The scale on the x-axis represents the physical length along each chromosome, wherein chromosome 30 refer to X chromosome, which was considered as an autosome because of overall female cattle in the studied population. The scale on the y-axis is the –log10 (*P*-value) SNP association effects. The solid line represents 5% of genome-wise significance with the corresponding raw *P*-value being equal to 2.42×10^{-6}.