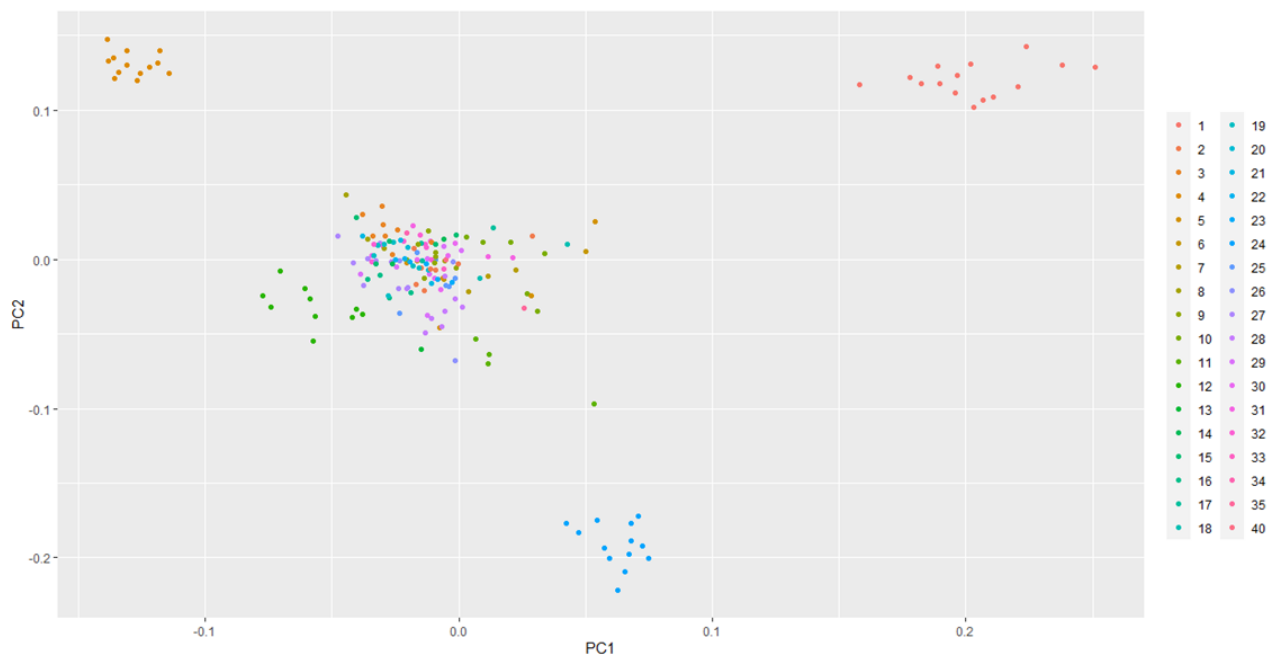
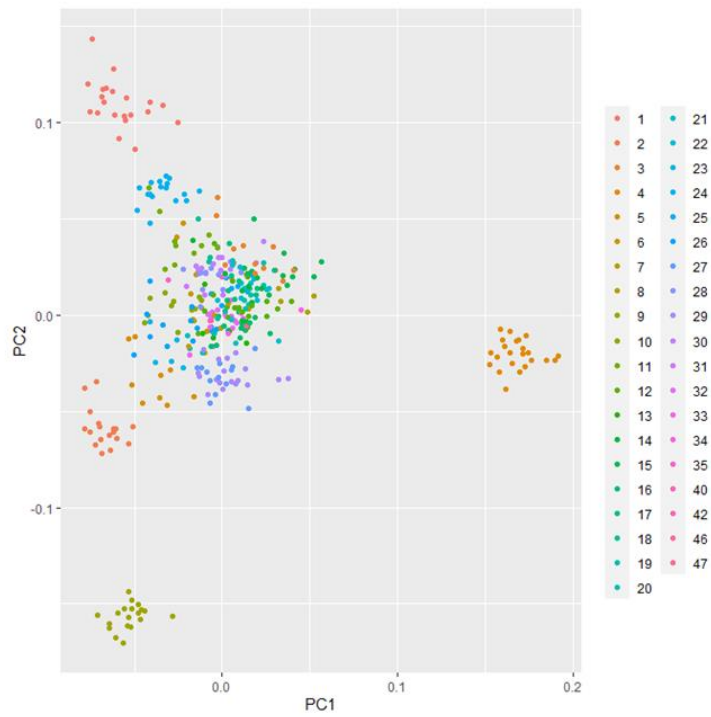


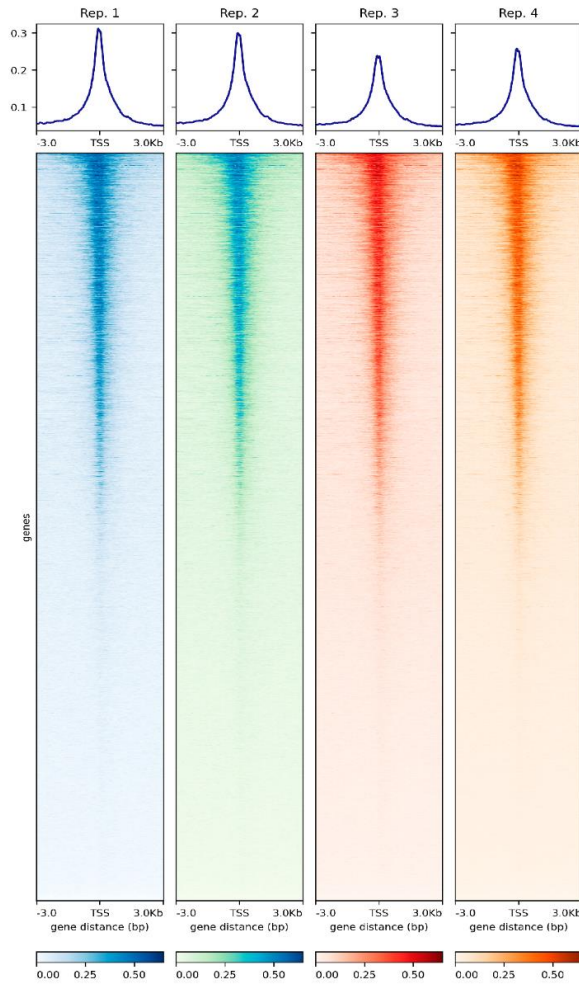


Supplementary Figure 1. Principal Component Analysis plot highlighting sires using 192 animals of a Nellore cattle populations.

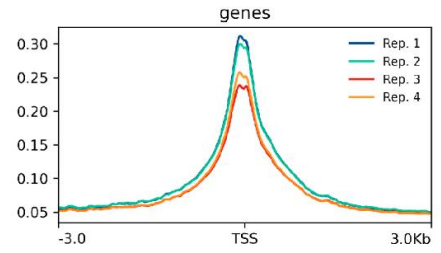


Supplementary Figure 2. Principal Component Analysis plot highlighting sires using 374 animals of a Nellore cattle populations.

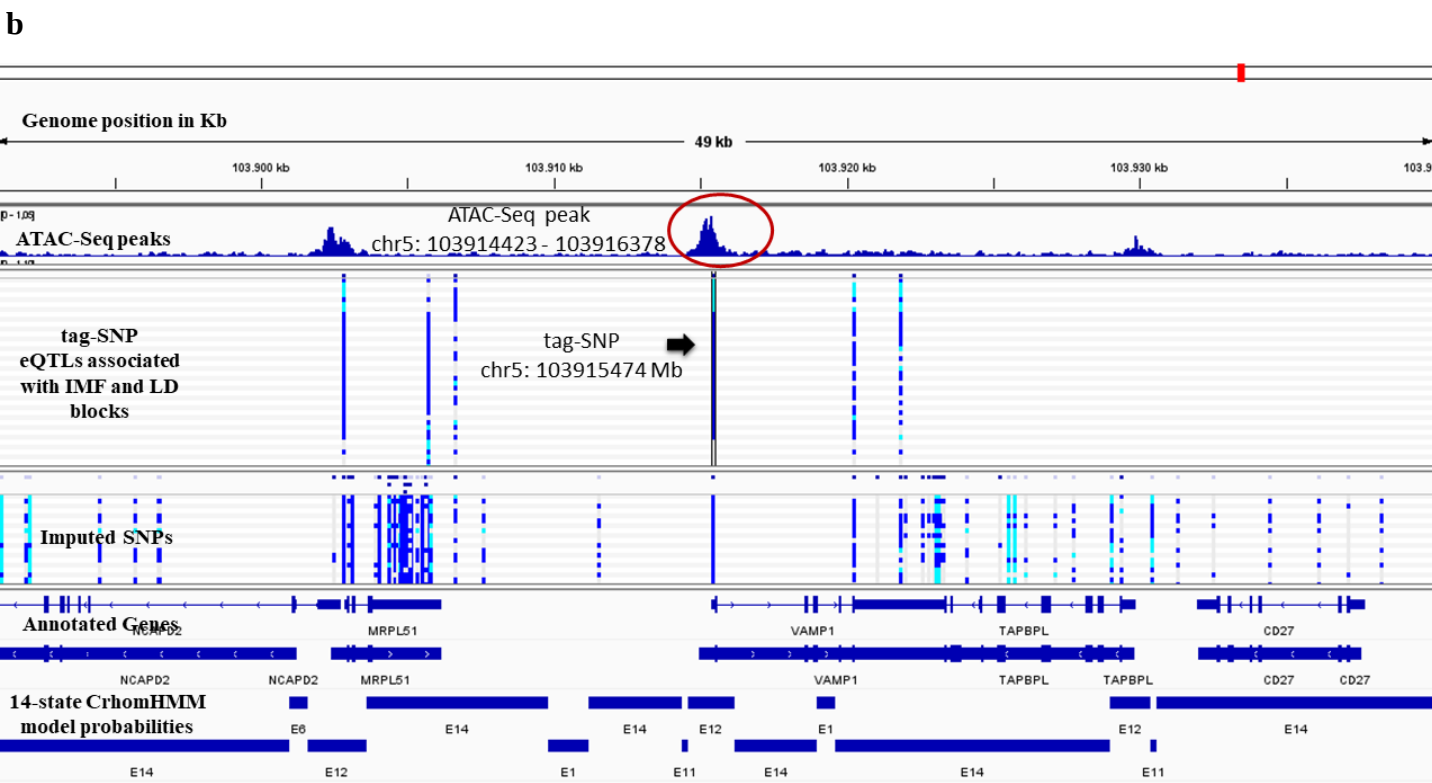
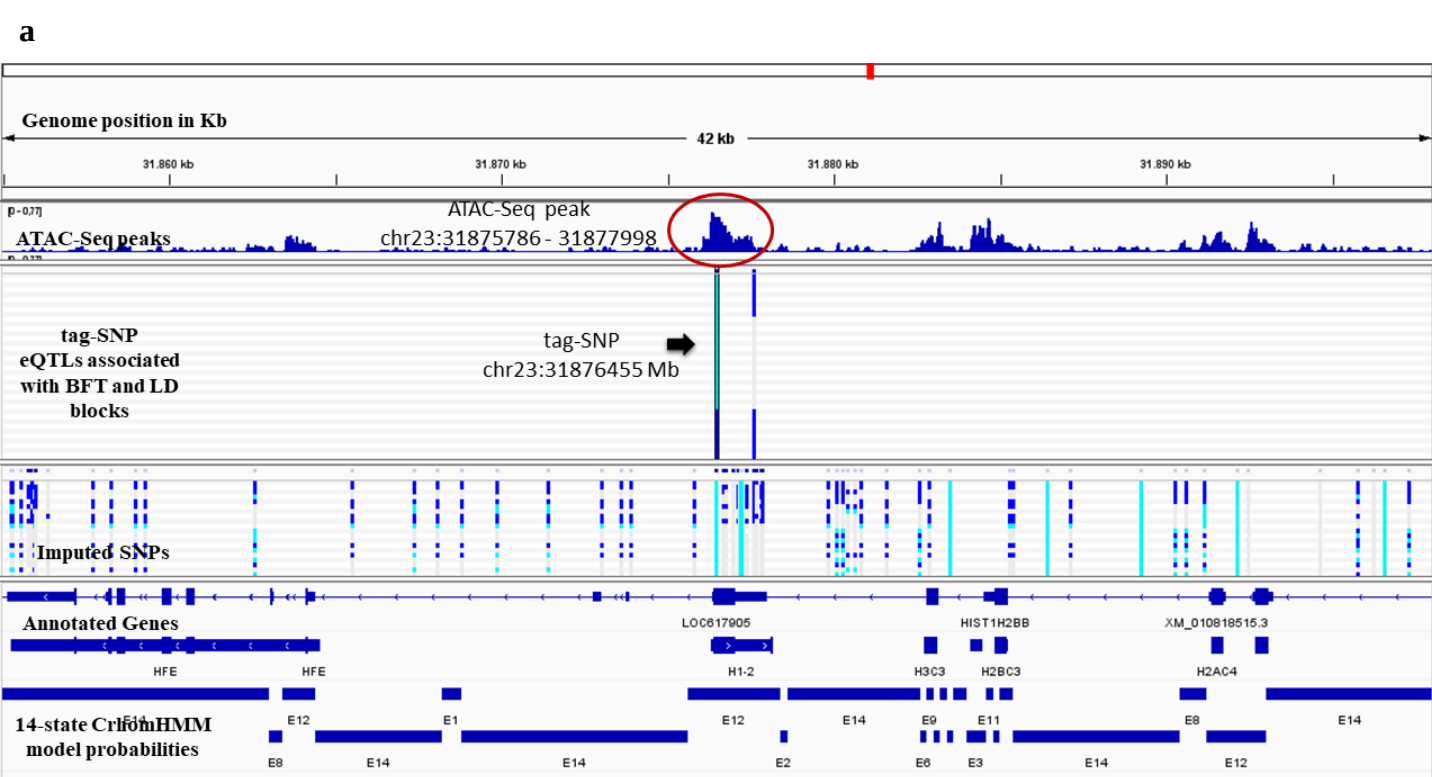
a



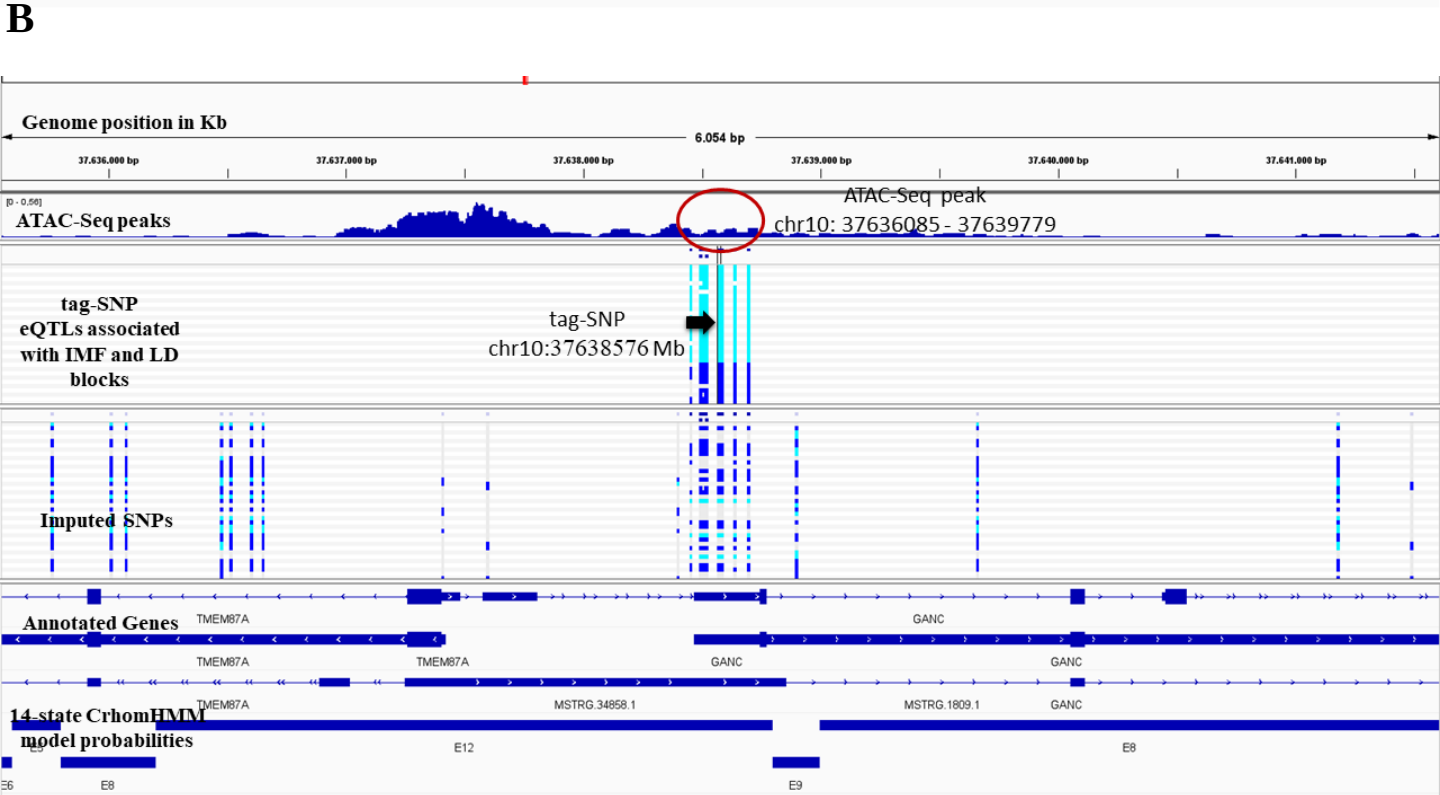
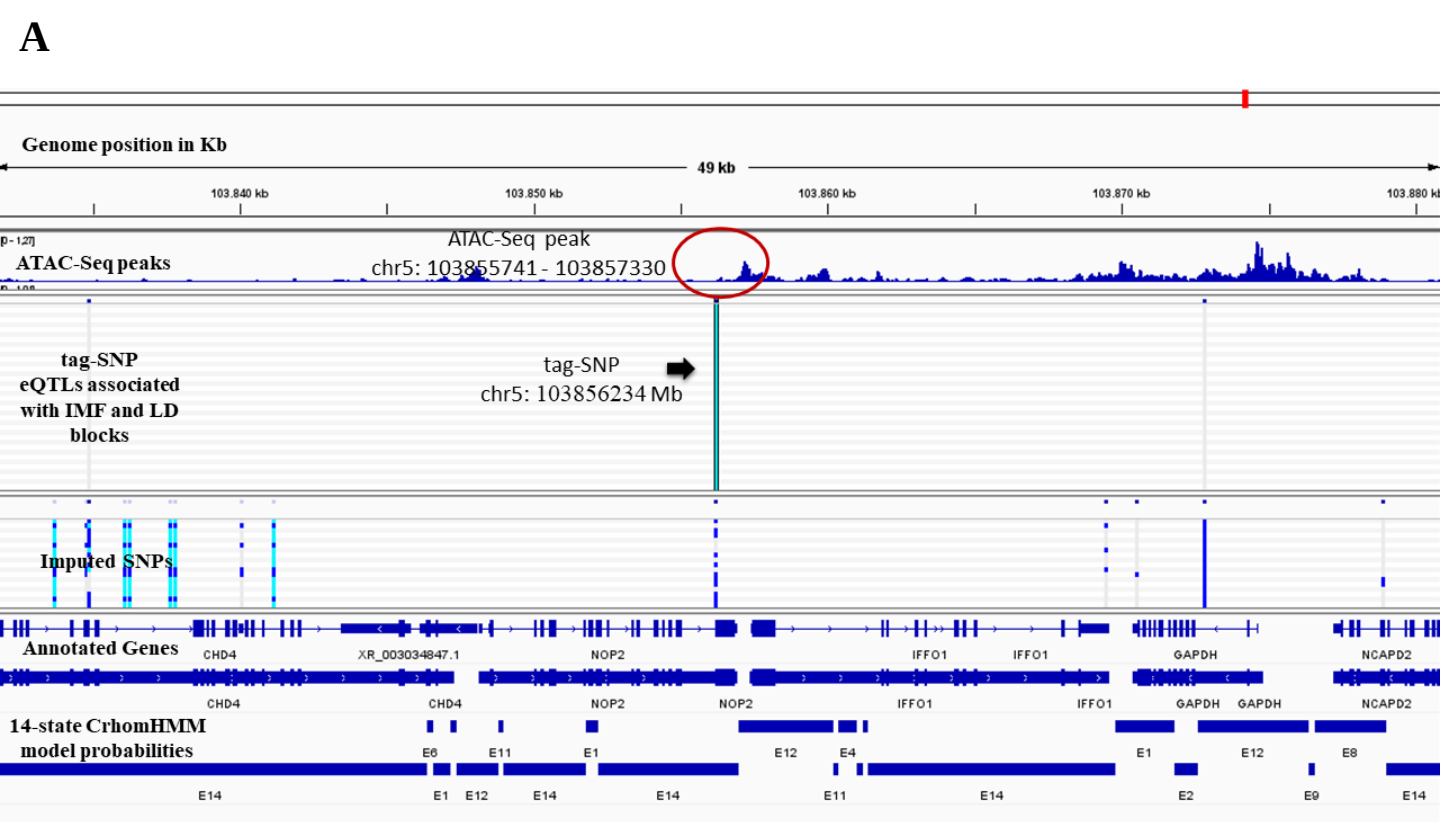
b



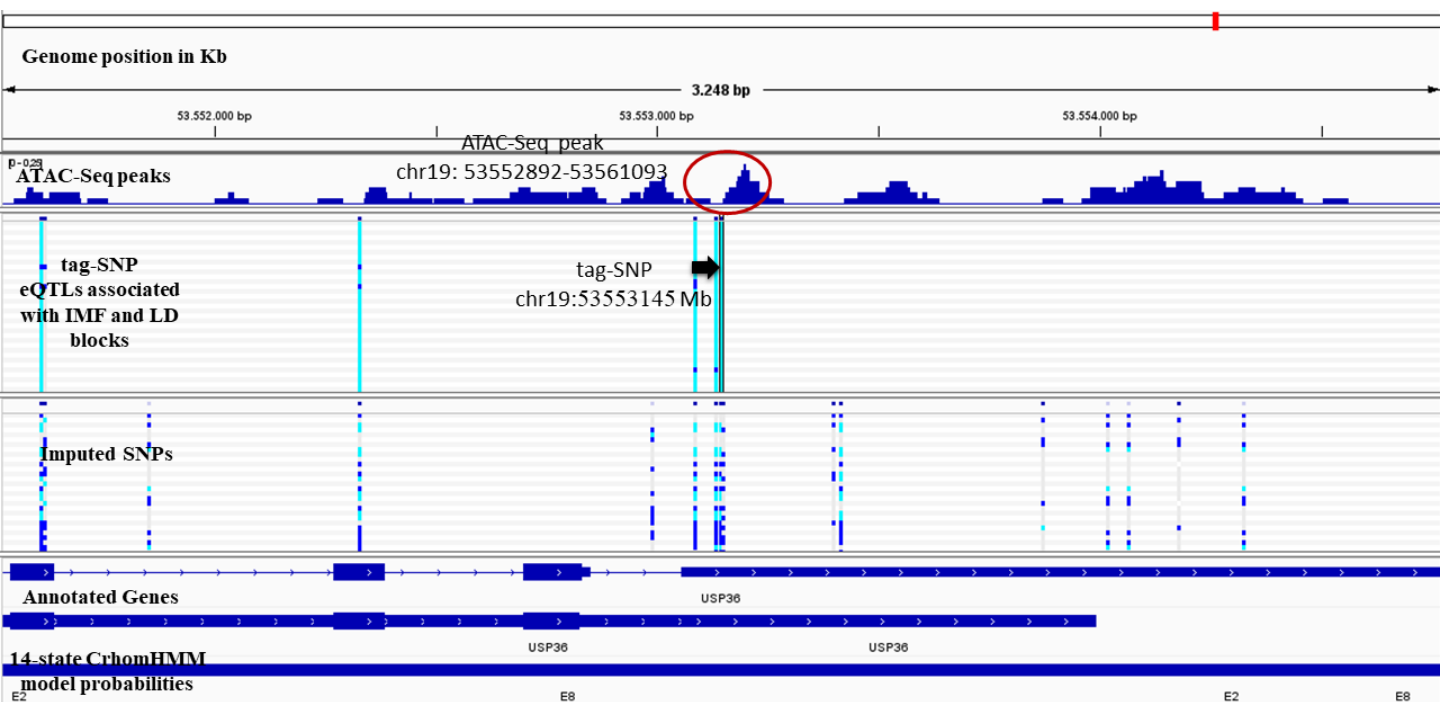
Supplementary figure 3. Analysis of ATAC-seq in bovine muscle. (A) ATAC-seq heatmap signals overlapping TSS of four replicates analyzed. (B) The line plot depicts the overlap of all replicates on TSS. Both signals were plotted based on FRIP score (Y-axis).



Supplementary Figure 4. Visualization of the genome location of eQTLs by IGV software. (A) The SNP rs208816180 is highlighted as “tag-SNP” with an arrow; the ATAC-Seq Peak is highlighted in a red circle; the 14-state ChromHMM model probabilities for cattle muscle were attained from Kern et al. (2021), the E12 state predicts an Insulator. (B) The SNP rs721933457 is highlighted as “tag-SNP” with an arrow; the ATAC-Seq Peak is highlighted in a red circle; the 14-state ChromHMM model probabilities for cattle muscle were attained from Kern et al. (2021), the E12 state predicts an Insulator.



Supplementary Figure 5. Visualization of the genome location of eQTLs by IGV software. (A) The SNP rs523028000 is highlighted as “tag-SNP” with an arrow; the ATAC-Seq Peak is highlighted in a red circle; the 14-state ChromHMM model probabilities for cattle muscle were attained from Kern et al. (2021), the E14 state predicts a low signal. (B) The SNP rs469481754 is highlighted as “tag-SNP” with an arrow; the ATAC-Seq Peak is highlighted in a red circle; the 14-state ChromHMM model probabilities for cattle muscle were attained from Kern et al. (2021), the E12 state predicts an Insulator.



Supplementary Figure 6. Visualization of the genome location of rs456412241 by IGV software. The SNP rs456412241 is highlighted as “tag-SNP” with an arrow; the ATAC-Seq Peak is highlighted in a red circle; the 14-state ChromHMM model probabilities for cattle muscle were attained from Kern et al. (2021), the E8 state predicts an active enhancer.