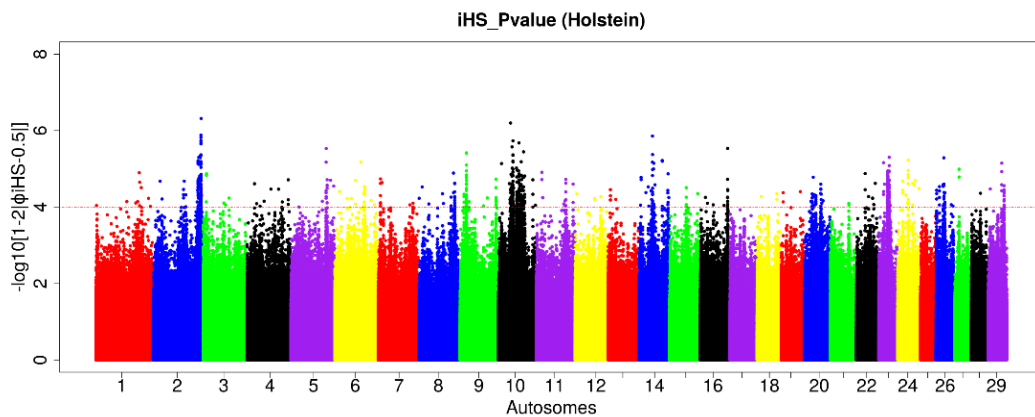
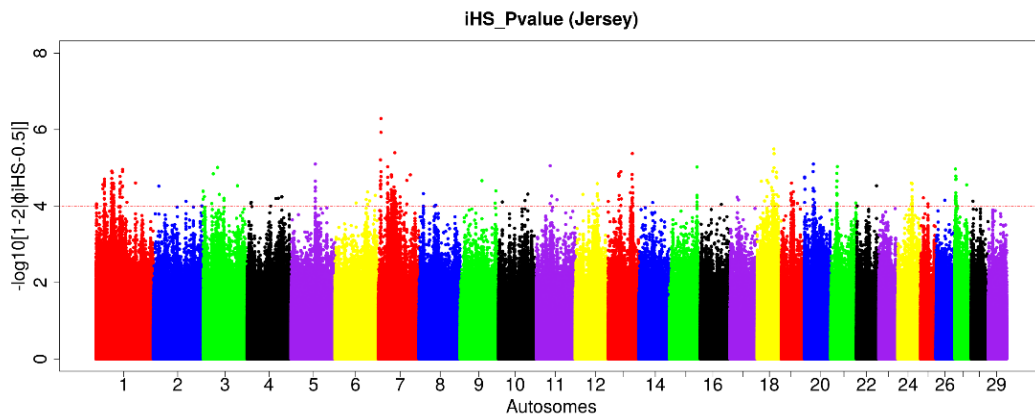


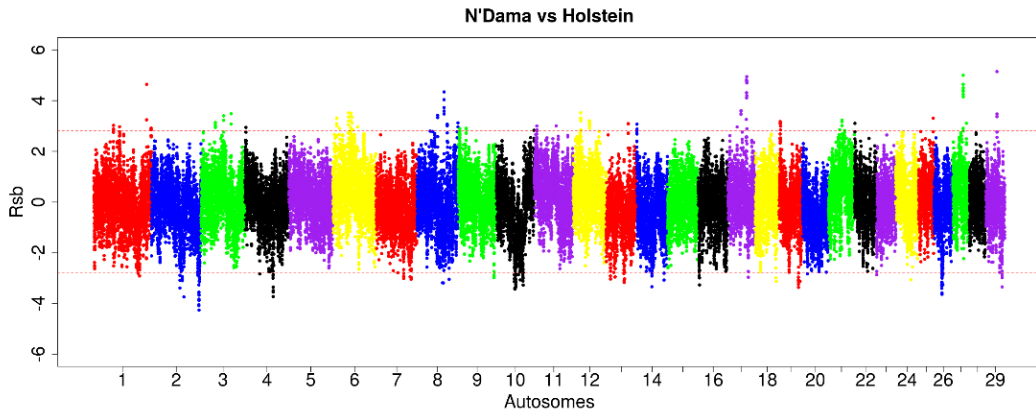
Supplementary Figure S1 | Manhattan plot of the genome-wide distribution of *iHS* scores for the autosomes in N'Dama cattle. The red dash line indicates the threshold of $P < 0.0001$ (equivalent of $-\log(iHS) > 4$) at which windows are considered under selection



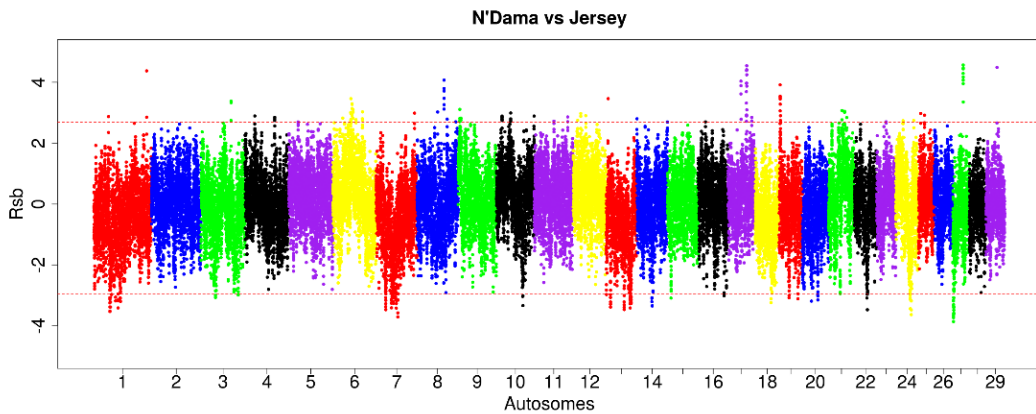
Supplementary Figure S2 | Manhattan plot of the genome-wide distribution of *iHS* scores for the autosomes in Holstein cattle. The red dash line indicates the threshold of $P < 0.0001$ (equivalent of $-\log(iHS) > 4$) at which windows are considered under selection



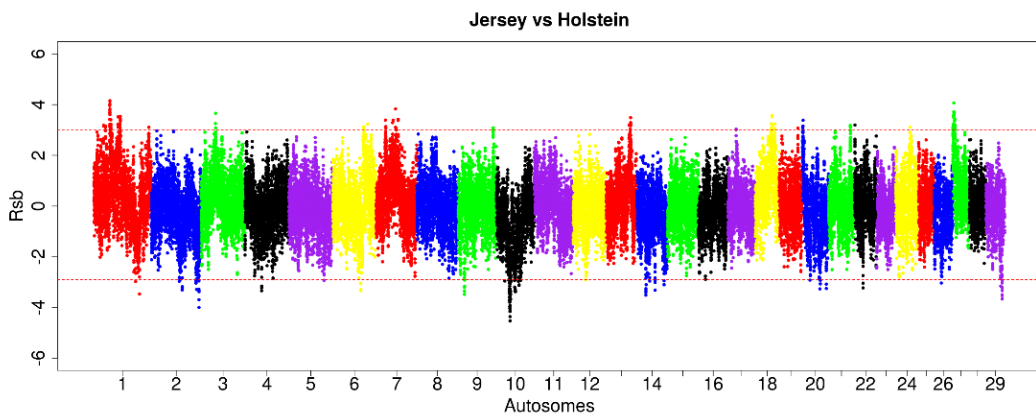
Supplementary Figure S3 | Manhattan plot of the genome-wide distribution of *iHS* scores for the autosomes in Jersey cattle. The red dash line indicates the threshold of $P < 0.0001$ (equivalent of $-\log(iHS) > 4$) at which windows are considered under selection



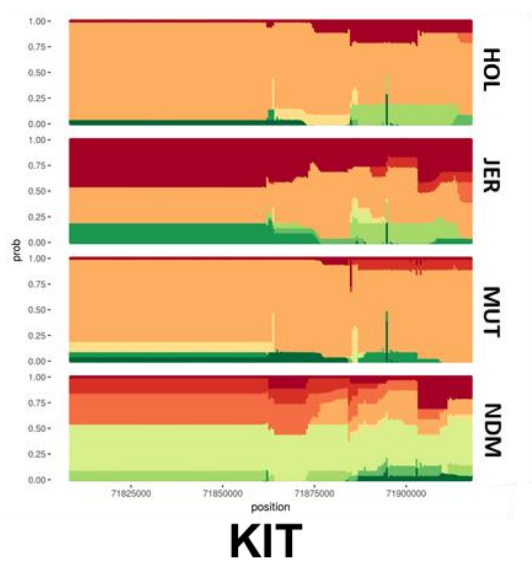
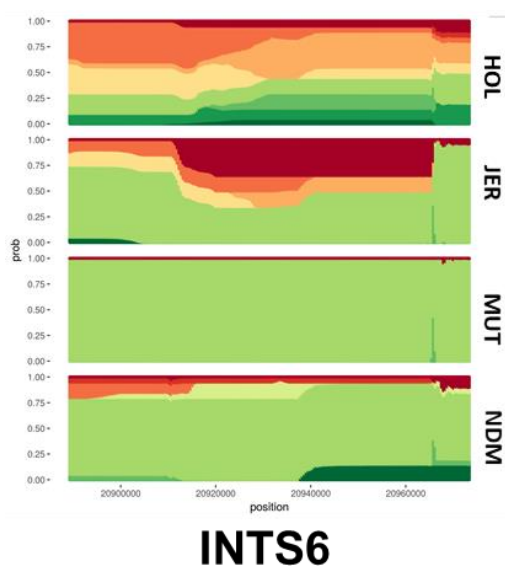
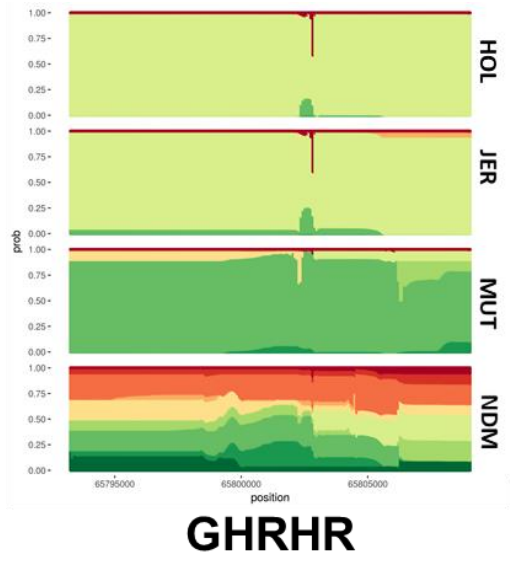
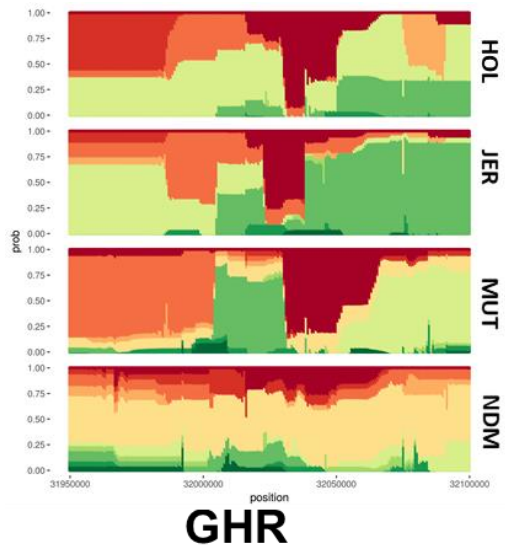
Supplementary Figure S4 | Manhattan plot of the genome-wide distribution of *Rsb* N'Dama - Holstein. Red dash lines are the threshold of the windows in the top 0.5% *Rsb* scores



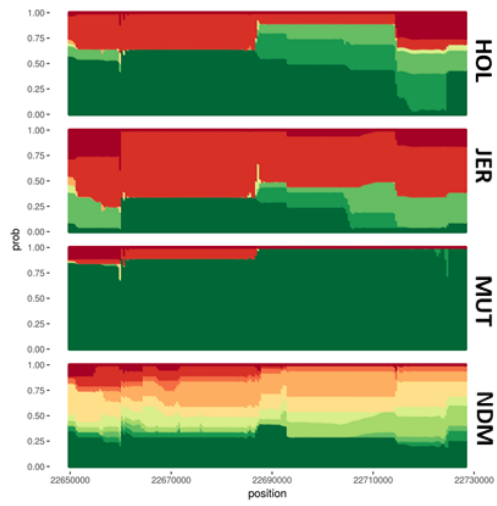
Supplementary Figure S5 | Manhattan plot of the genome-wide distribution of *Rsb* N'Dama - Jersey. Red dash lines are the threshold of the windows in the top 0.5% *Rsb* scores



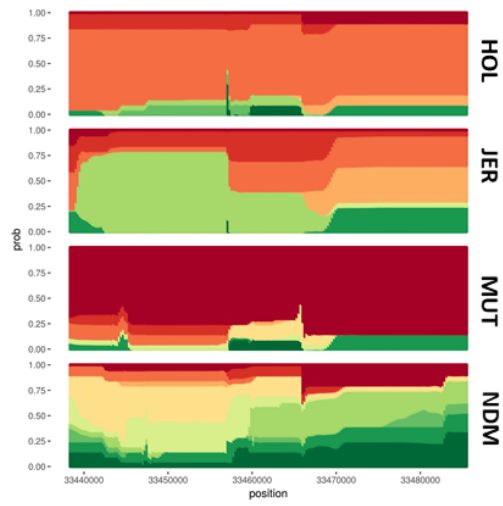
Supplementary Figure S6 | Manhattan plot of the genome-wide distribution of *Rsb* Jersey - Holstein. Red dash lines are the threshold of the windows in the top 0.5% *Rsb* scores



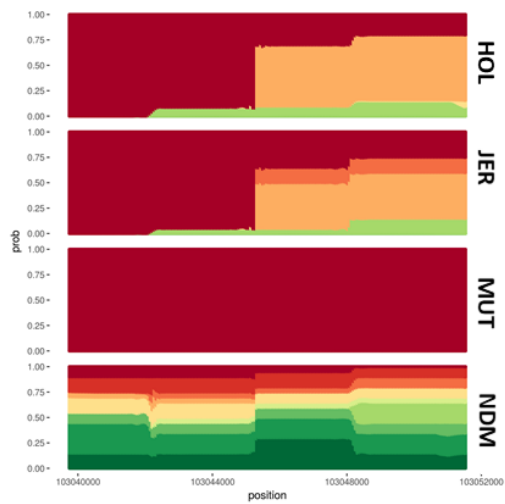
Supplementary Figure S7 | Haplotype diversity for African and European taurine breeds in genomic regions of four candidate genes between Muturu and other taurine breeds



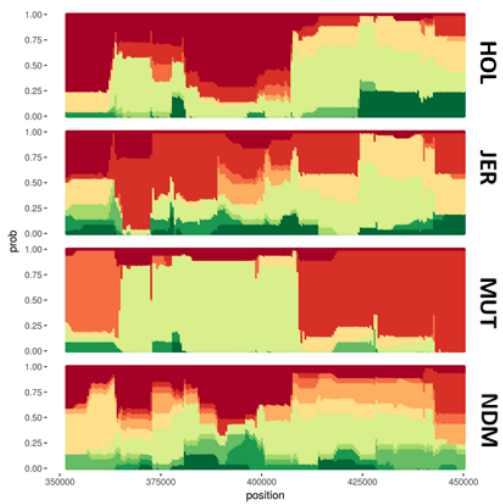
OLA1



NPC1



GFI1B



RCAN1

Supplementary Figure S8 | Haplotype diversity for four taurine breeds in genomic regions of four Muturu candidate genes detected following Rsb comparison test between Muturu and three other *Bos taurus* breeds.