

Additional file 2. Supplementary figures

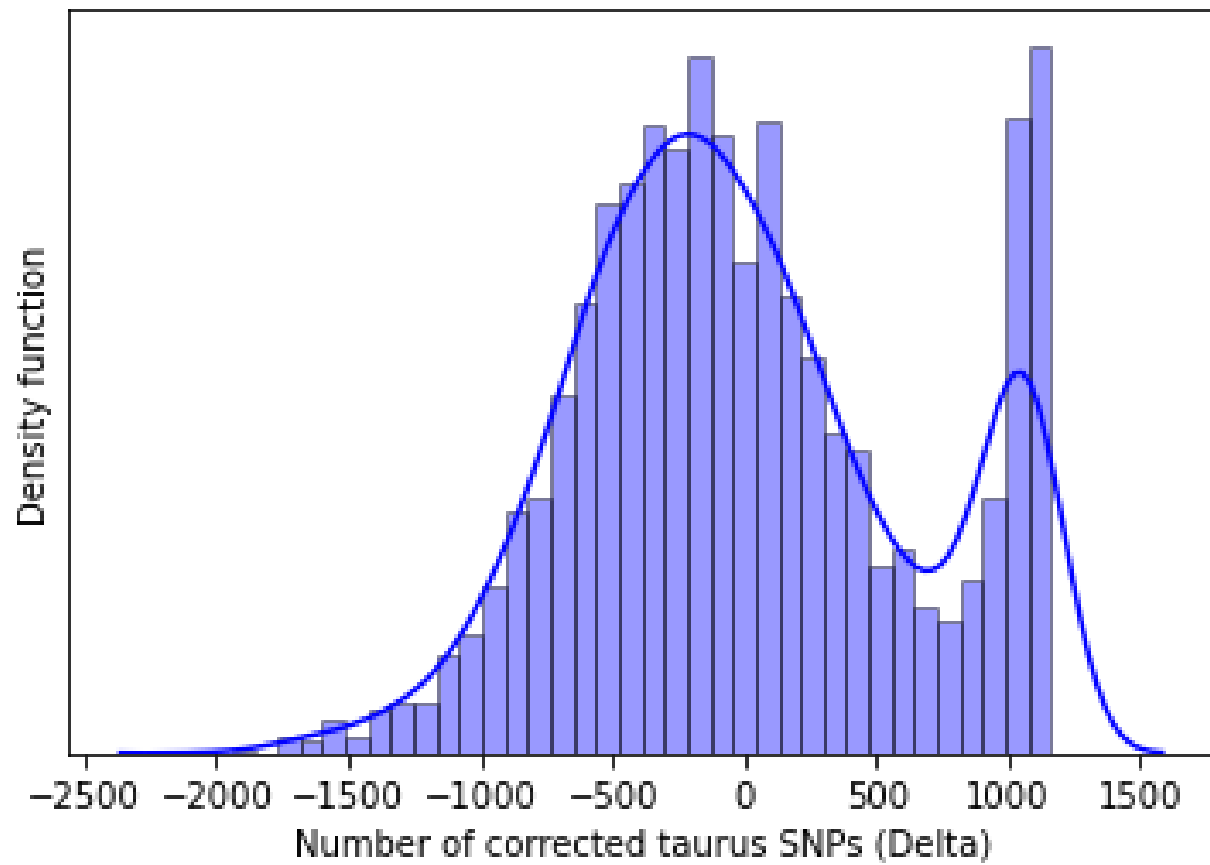


Figure S1. Density function of Δ values. Delta values were calculated as subtraction of mean nearly fixed alternative alleles (NFAA) sites across chromosome from the actual NFAA sites in each respective scanning window of *B. taurus* individuals

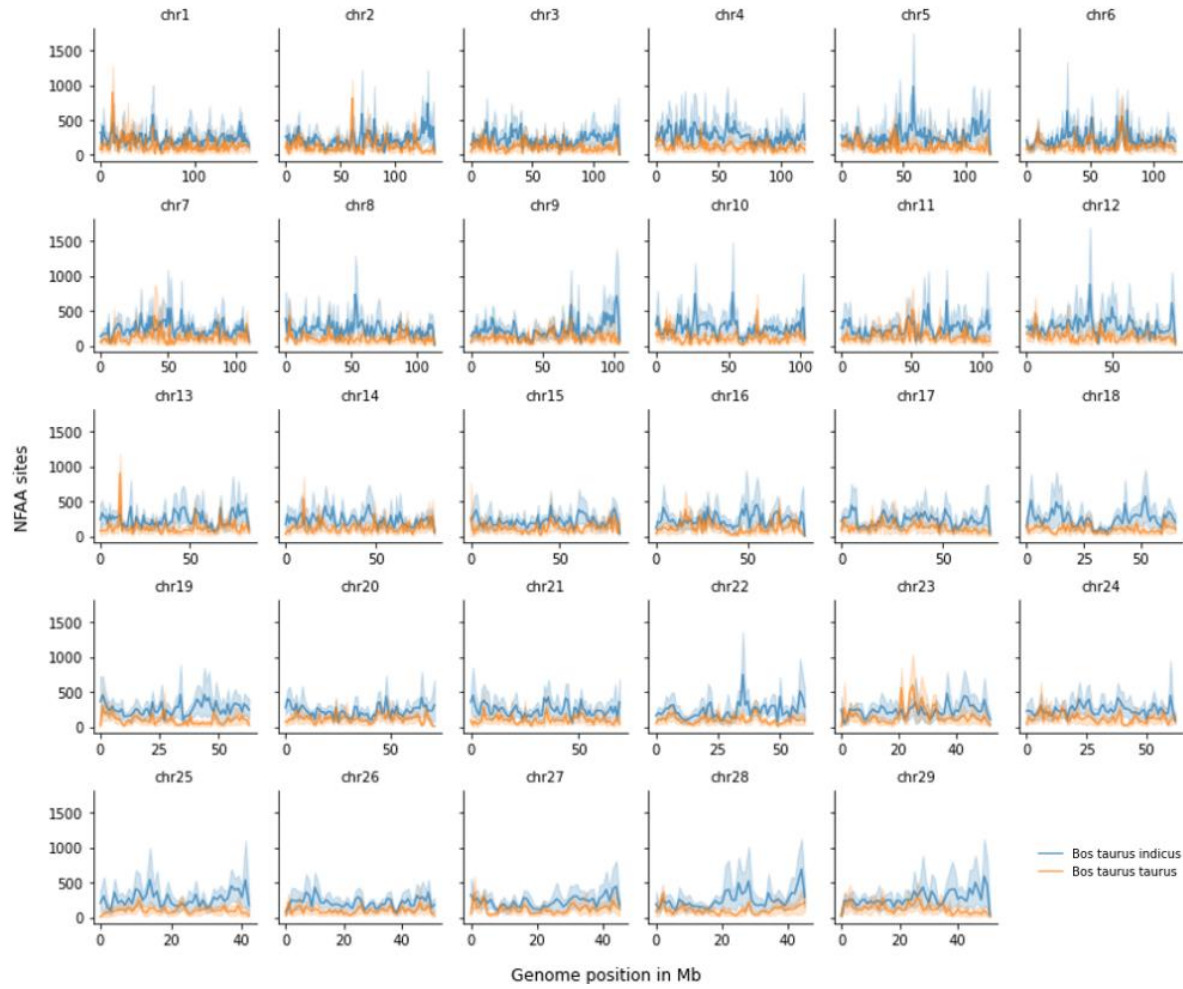


Figure S2. Re-creation of figure 2 from the main text when considering Bohai as taurine (Distribution of the number of SNV with an alternative allele frequency of 0.95 or higher (i.e., nearly fixed alternative allele-NFAA) using ARS_UCD1.2 as the reference genome (1 Mb scanning windows). Main lines with blue and orange colours are the average of NFAA from individuals representing groups of *Bos taurus indicus* and *Bos taurus taurus*. While the shadowed-colours of blue and orange are the actual NFAA for each single breed of *Bos taurus indicus* and *Bos taurus taurus*, respectively)

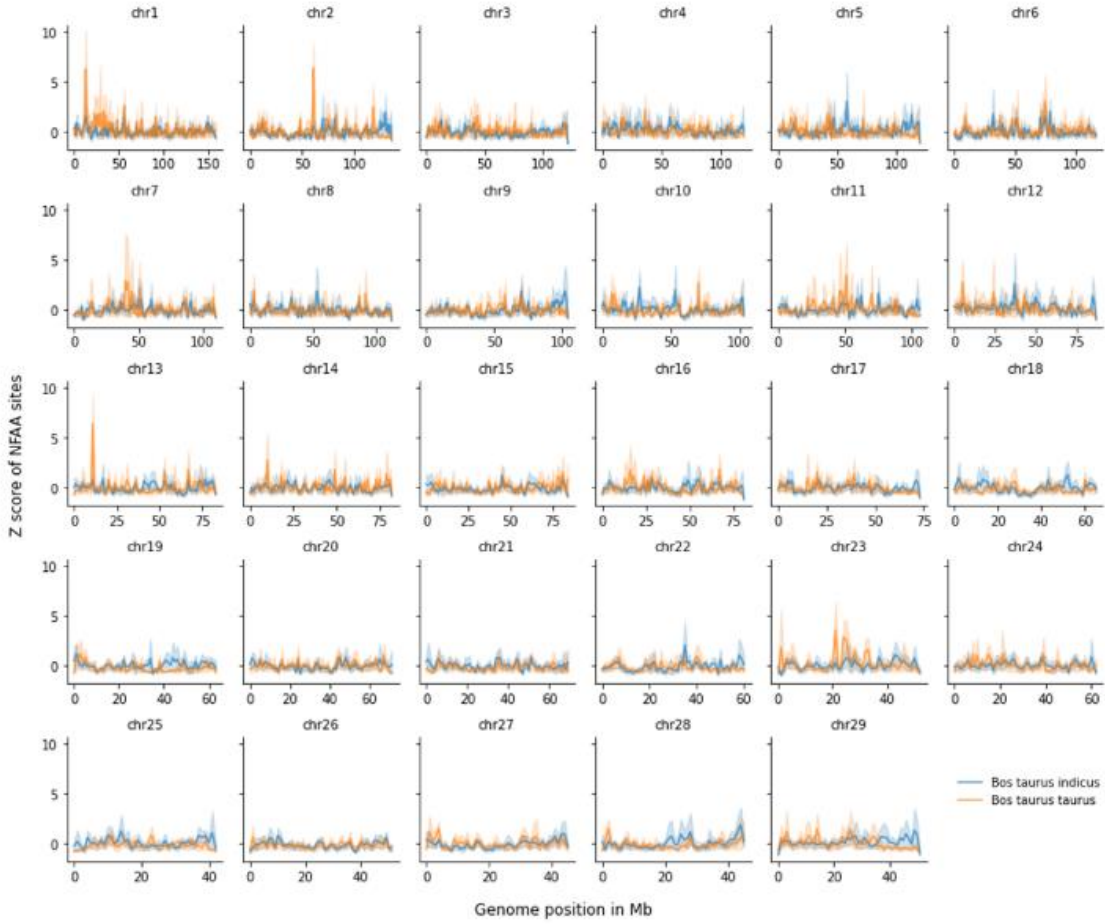


Figure S3. Z-score transformation of the number of SNV with alternative allele frequency of 0.95 or higher (i.e., nearly fixed alternative allele-NFAA) using ARS_UCD1.2 as the reference sequence (1 Mb scanning windows)

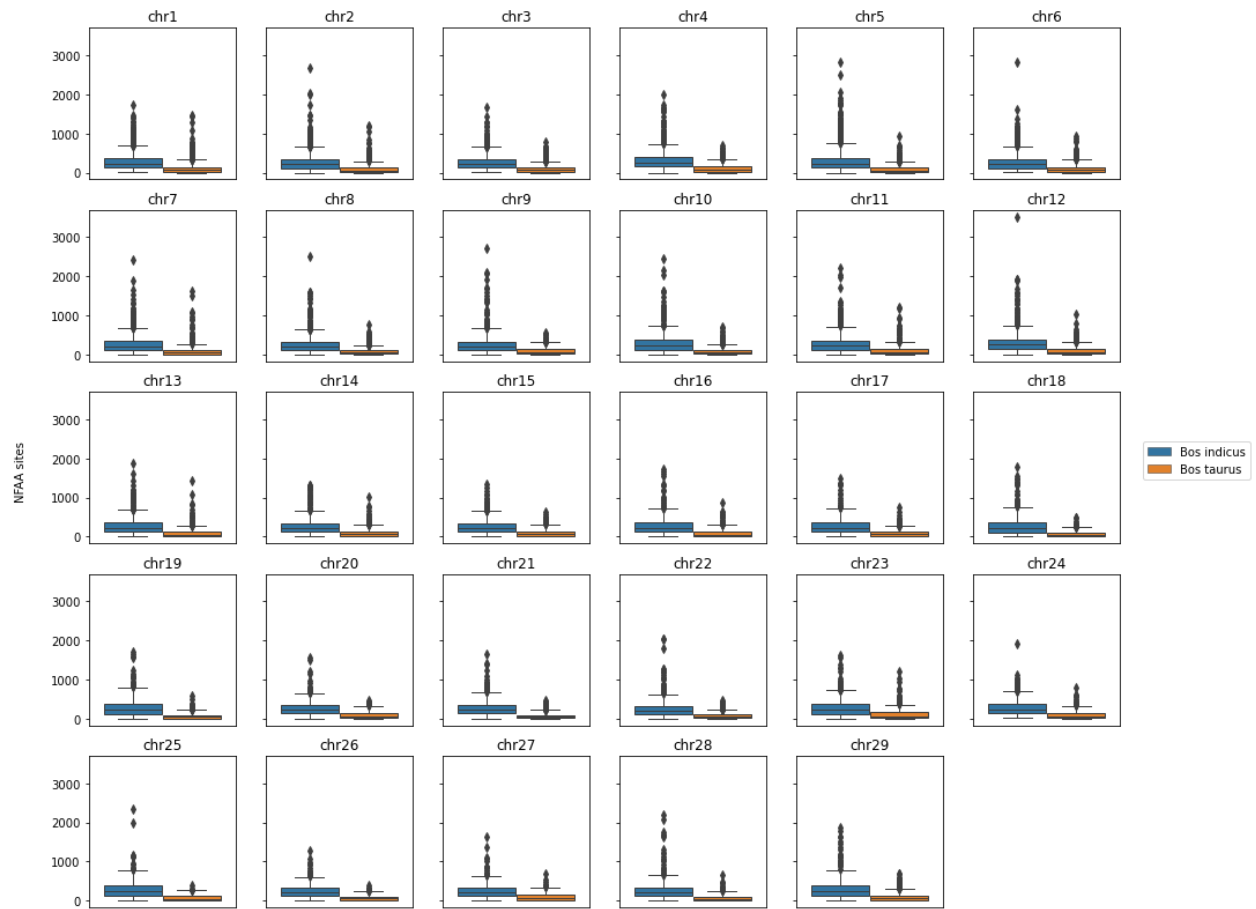


Figure S4. Boxplot of the number of SNV with alternative allele frequency of 0.95 or higher (i.e., nearly fixed alternative allele-NFAA) using ARS_UCD1.2 as the reference sequence (1 Mb scanning windows)

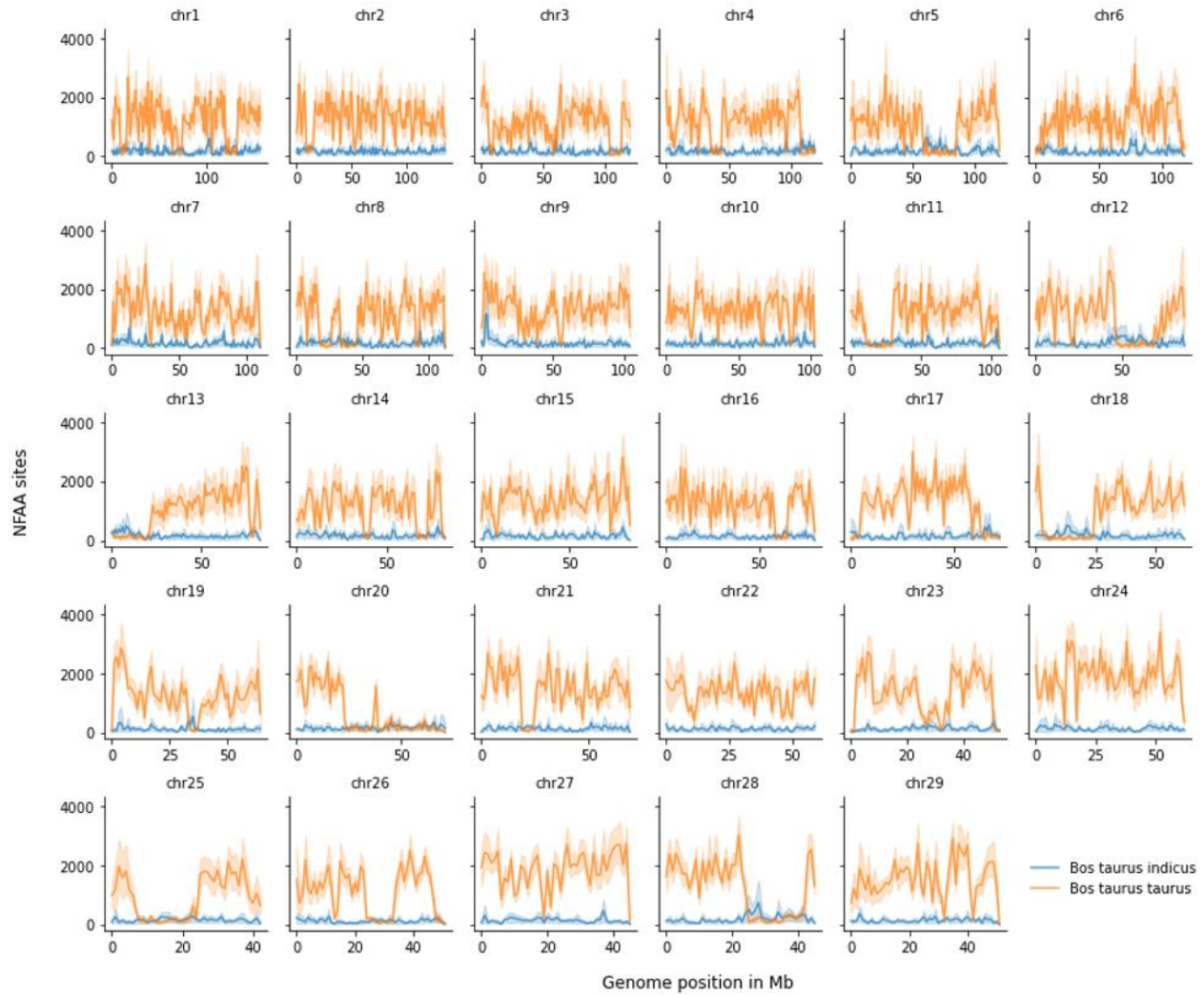


Figure S5. Re-creation of figure 3 from the main text when considering Bohai as taurine (Distribution of the number of SNV with an alternative allele frequency of 0.95 or higher (i.e., nearly fixed alternative allele-NFAA) using UOA_Brahman_1 as the reference genome (1 Mb scanning windows). Main lines with blue and orange colours are the average of NFAA from individuals representing groups of *Bos taurus indicus* and *Bos taurus taurus*. While the shadowed-colours of blue and orange are the actual NFAA for each single breed of *Bos taurus indicus* and *Bos taurus taurus*, respectively)

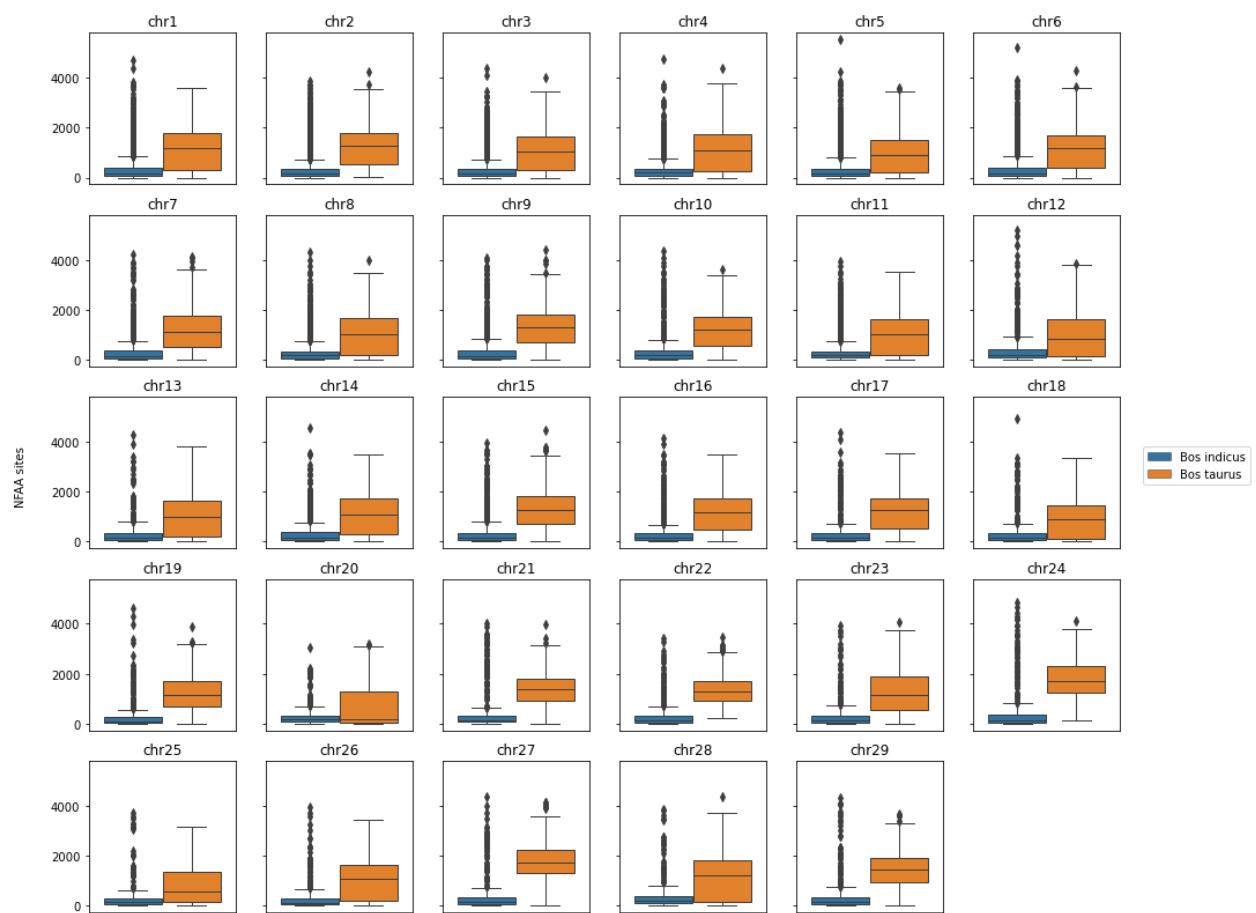


Figure S6. Boxplot of the number of SNV with alternative allele frequency of 0.95 or higher (i.e., nearly fixed alternative allele-NFAA) using UOA_Brahman_1 as the reference sequence (1 Mb scanning windows)

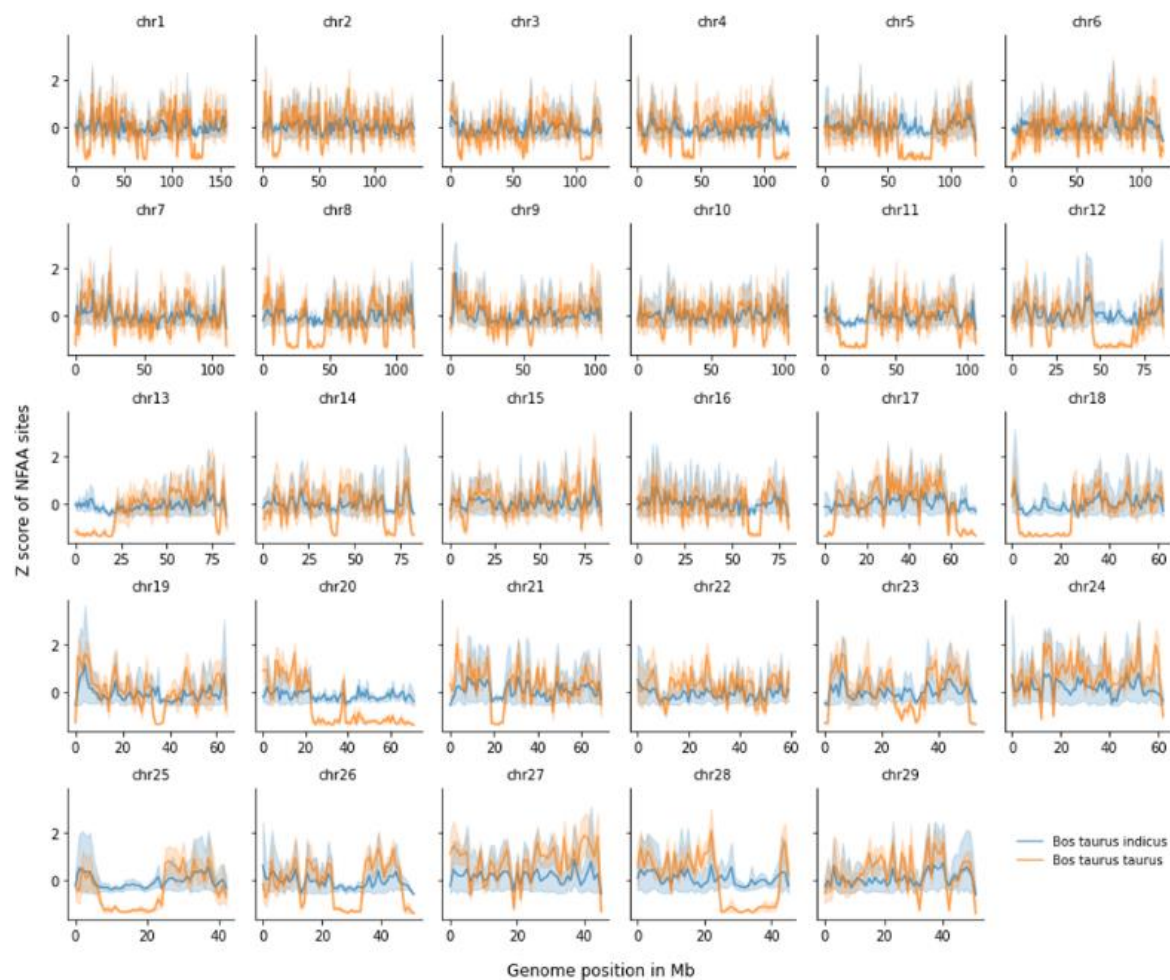


Figure S7. Z-score transformation of the number of SNV with alternative allele frequency of 0.95 or higher (i.e., nearly fixed alternative allele-NFAA) using UOA_Brahman_1 as the reference sequence (1 Mb scanning windows)

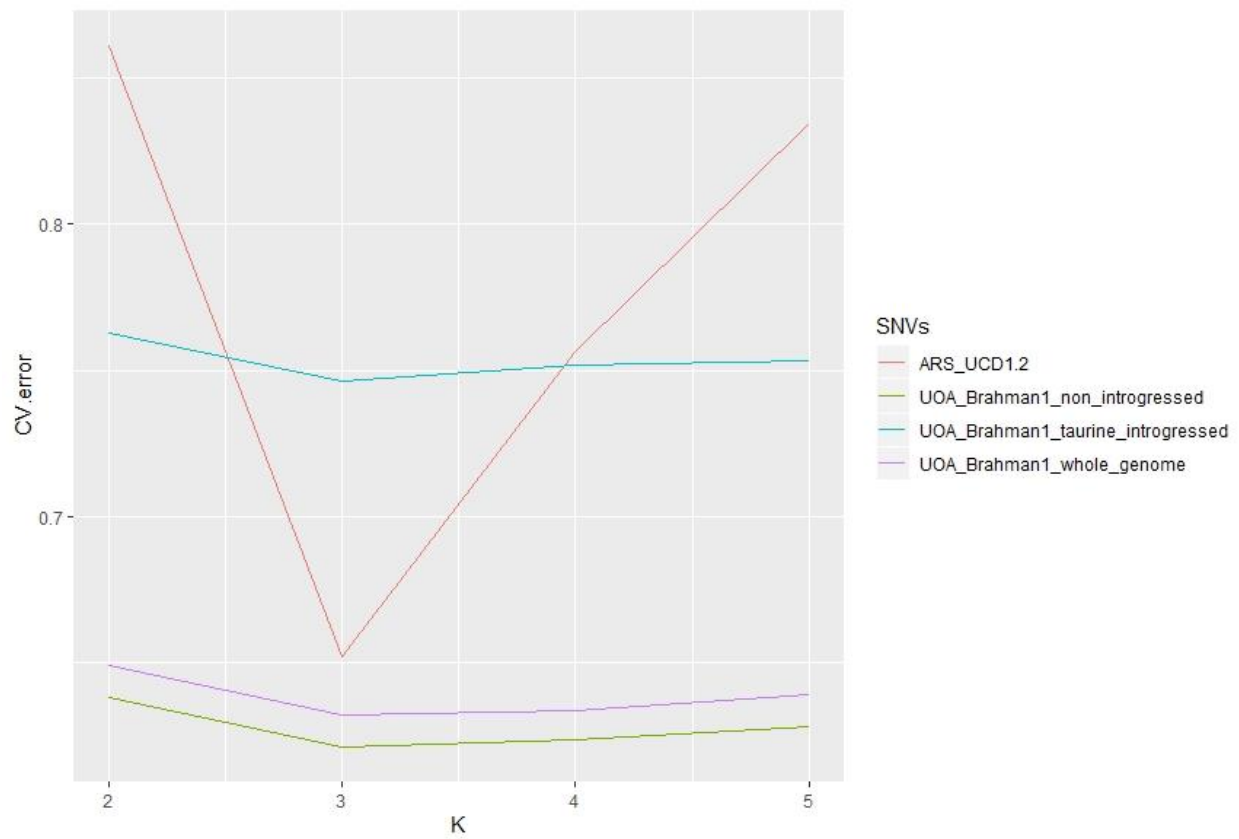


Figure S8. Cross-validation error for admixture analysis using $K = 2$ to 5 using SNVs derived from whole genome, putative taurine-introgressed, non-introgressed of UOA_Brahman_1, and ARS_UCD1.2