

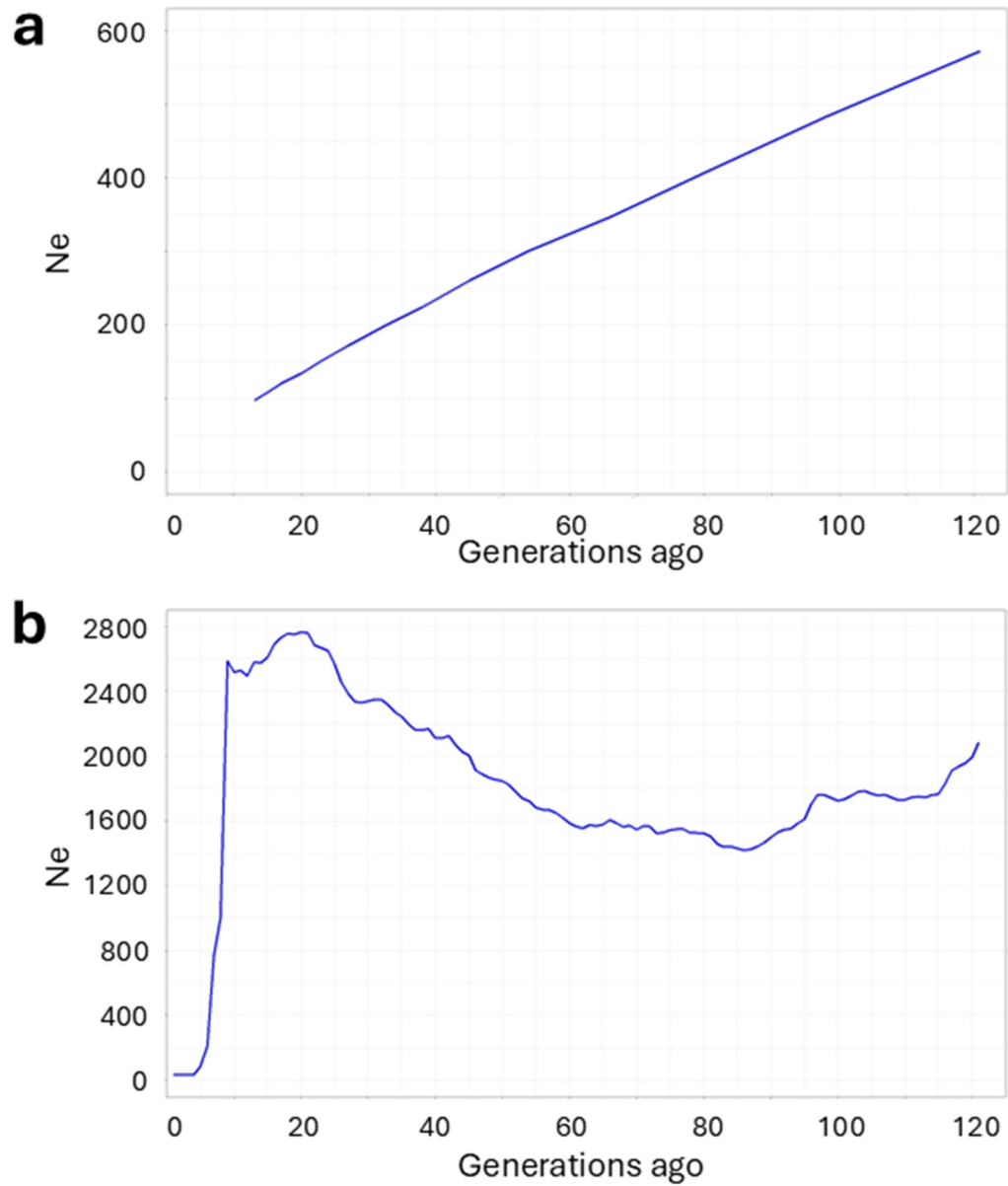


Figure S1. Historical effective population size estimates for Rarámuri Criollo cattle from the Jornada Experimental Range, calculated using the (a) SNeP and (b) GONE software program.

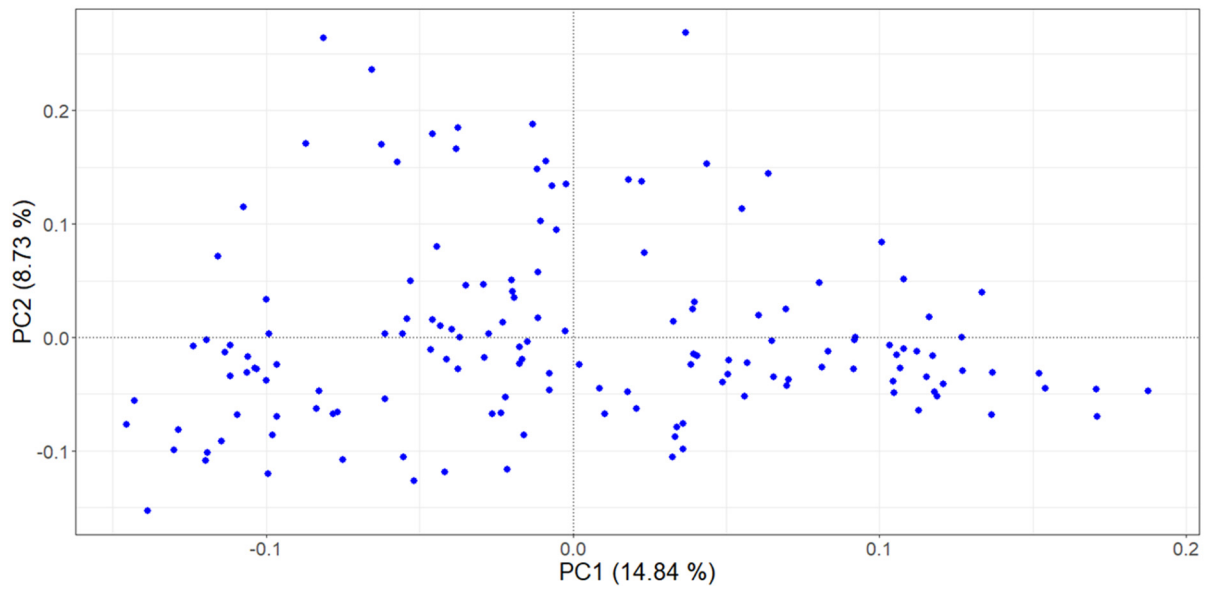


Figure S2. Principal component analysis of Genetic structure of Rarámuri Criollo cattle from the Jornada Experimental Range.

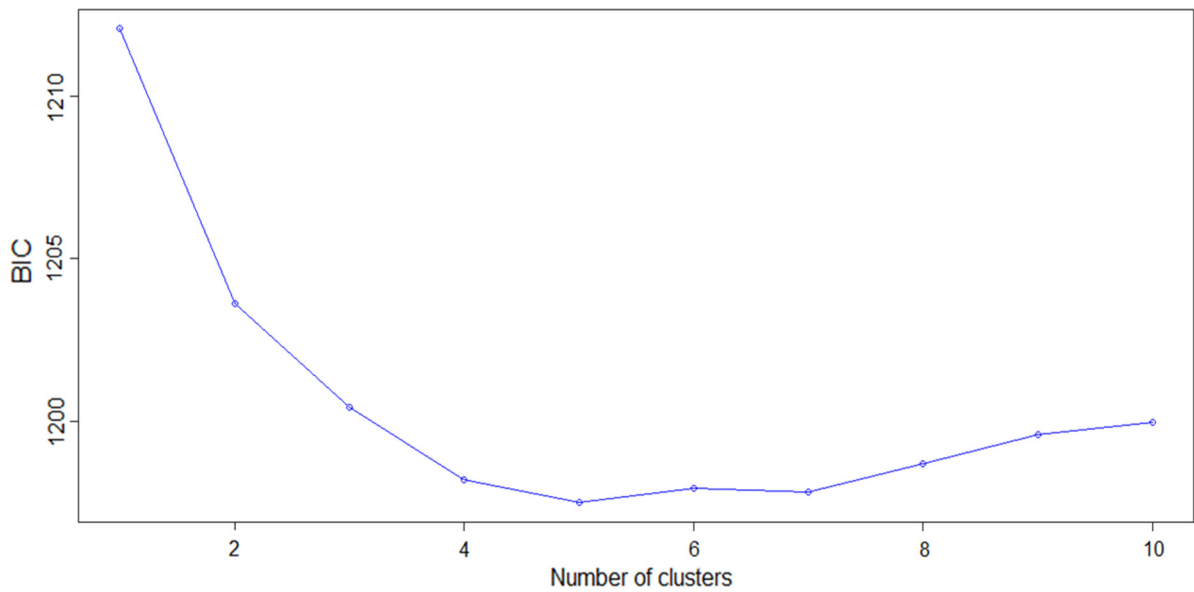


Figure S3. Inference of the number of clusters in Rarámuri Criollo cattle from the Jornada Experimental Range based on K-means algorithm.

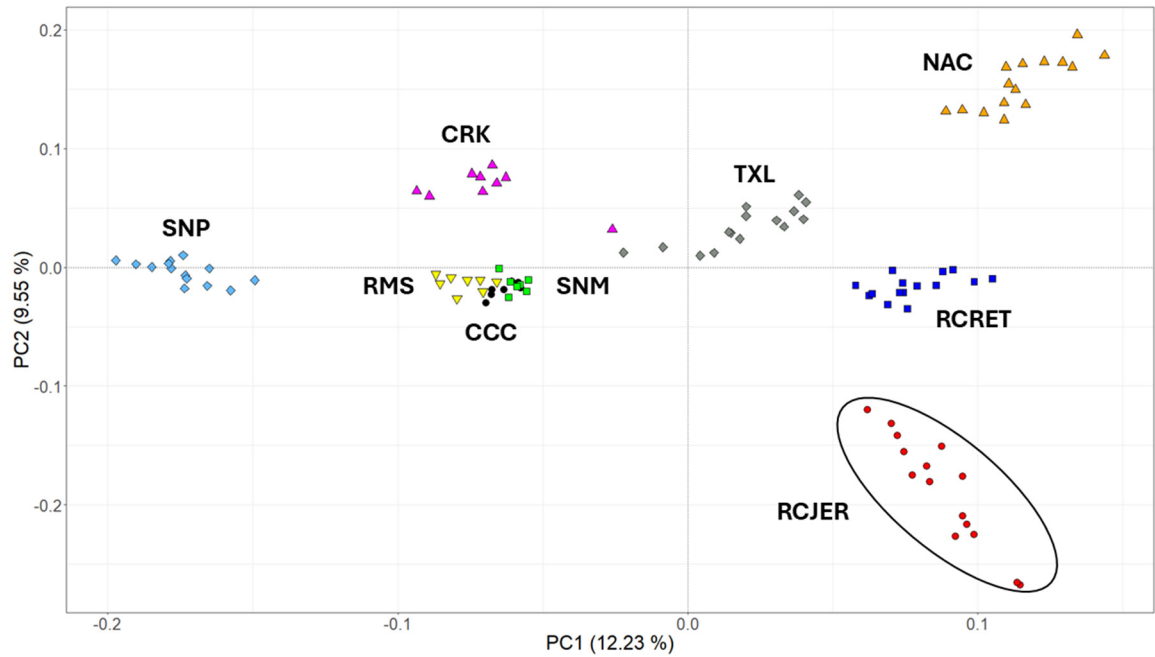


Figure S4. Principal component analysis of nine Criollo cattle populations. Rarámuri Criollo from the Jornada Experimental Range is highlighted with an oval shape. RCJER: Rarámuri Criollo cattle from the Jornada Experimental Range, RCRET: Rarámuri Criollo cattle from the Rancho Experimental Teseachi, TXL: Texas Longhorn, NAC: North American Corriente, CRK: Florida Cracker, SNP: Senepol, CCC: Costeño con Cuernos, RMS: Romosinuano, SNM: San Martinero.

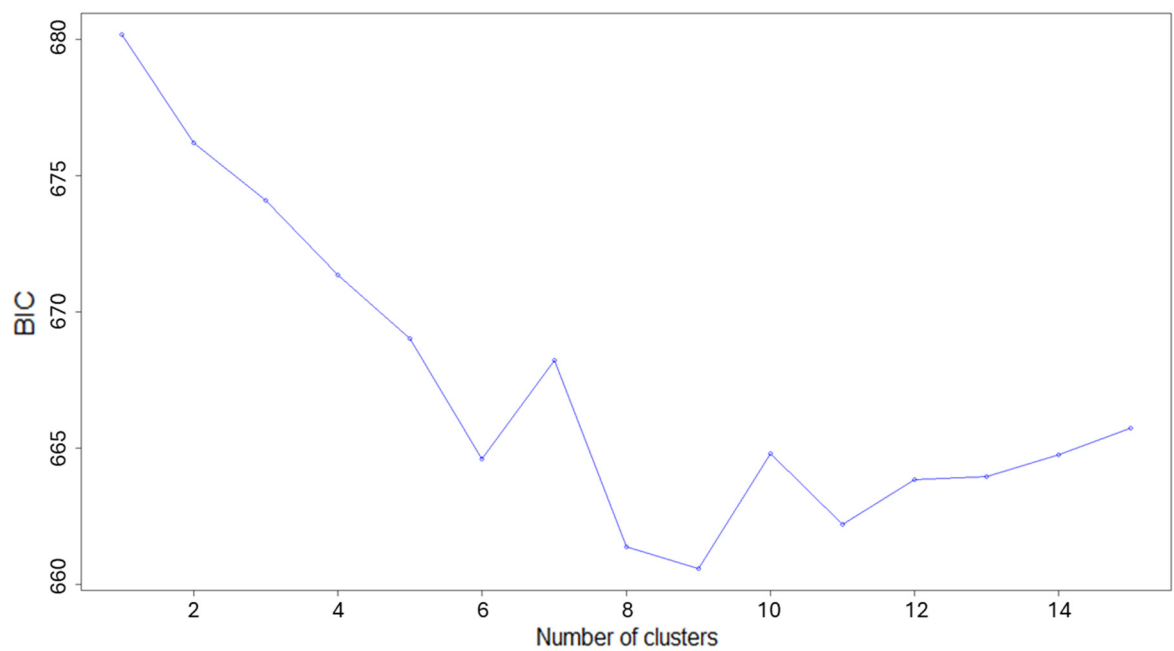


Figure S5. Inference of the number of clusters of nine Criollo cattle populations based on K-means algorithm.

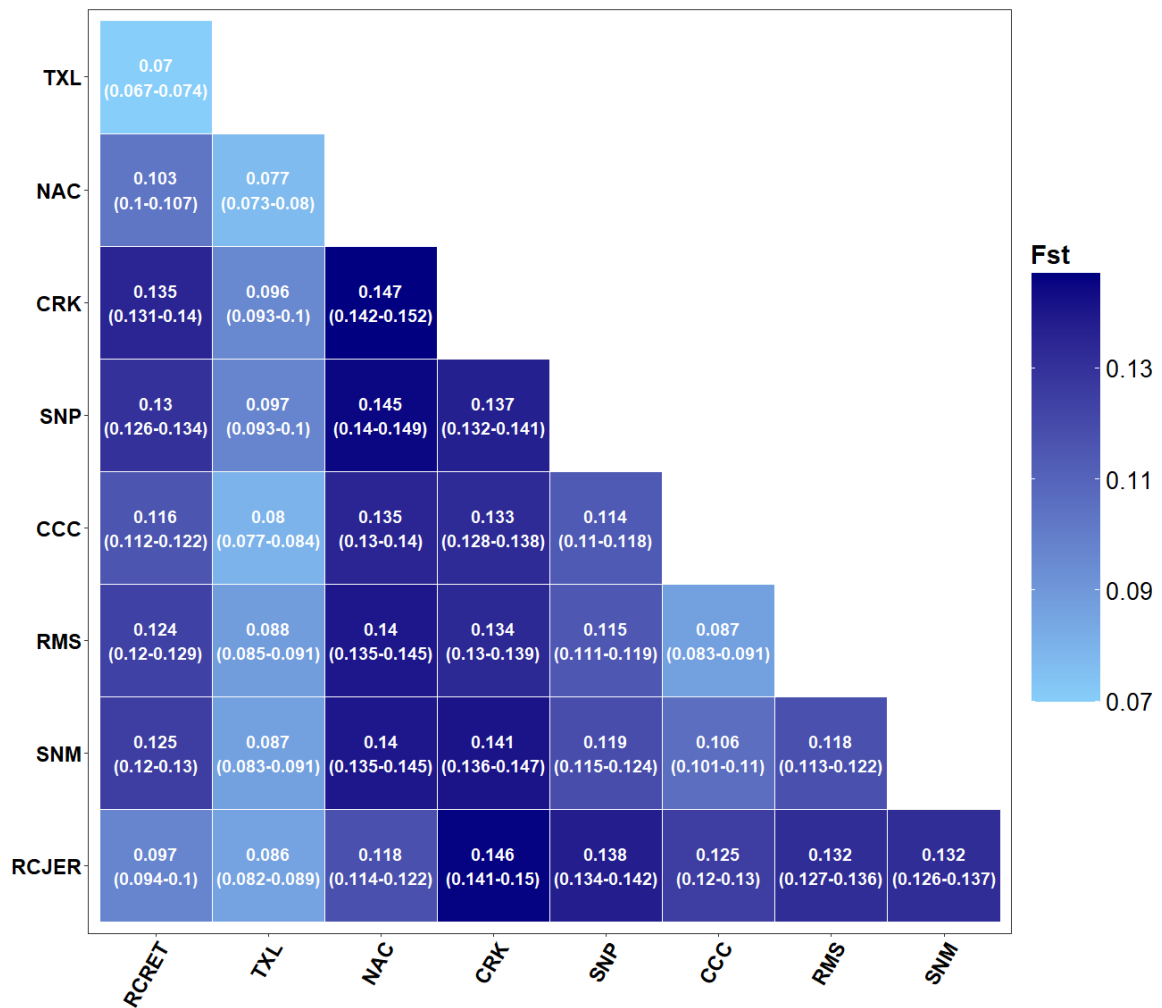


Figure S6. Matrix and heatmap of Fixation Index (F_{ST}) pairwise comparisons among nine Criollo cattle populations. Fixation index followed by a darker blue color indicates greater genetic distance between groups. RCJET: Rarámuri Criollo cattle from the Jornada Experimental Range, RCJET: Rarámuri Criollo cattle from the Rancho Experimental Teseachi, TXL: Texas Longhorn, NAC: North American Corriente, CRK: Florida Cracker, SNP: Senepol, CCC: Costeño con Cuernos, RMS: Romosinuano, SNM: San Martinero.

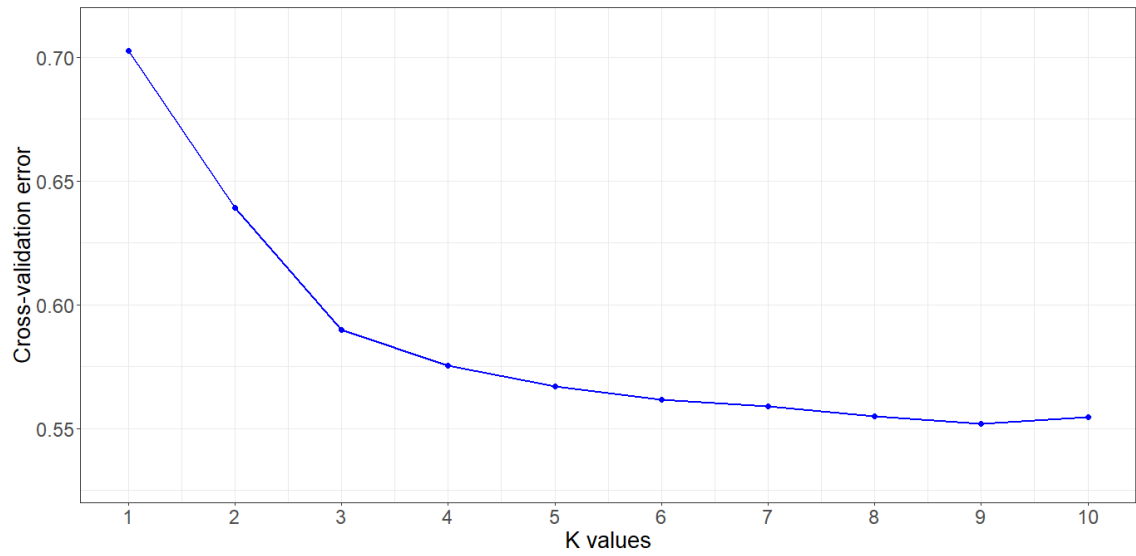


Figure S7. Cross-validation error in the admixture analysis for K varying from 2-10 K = 2 – K =

10.

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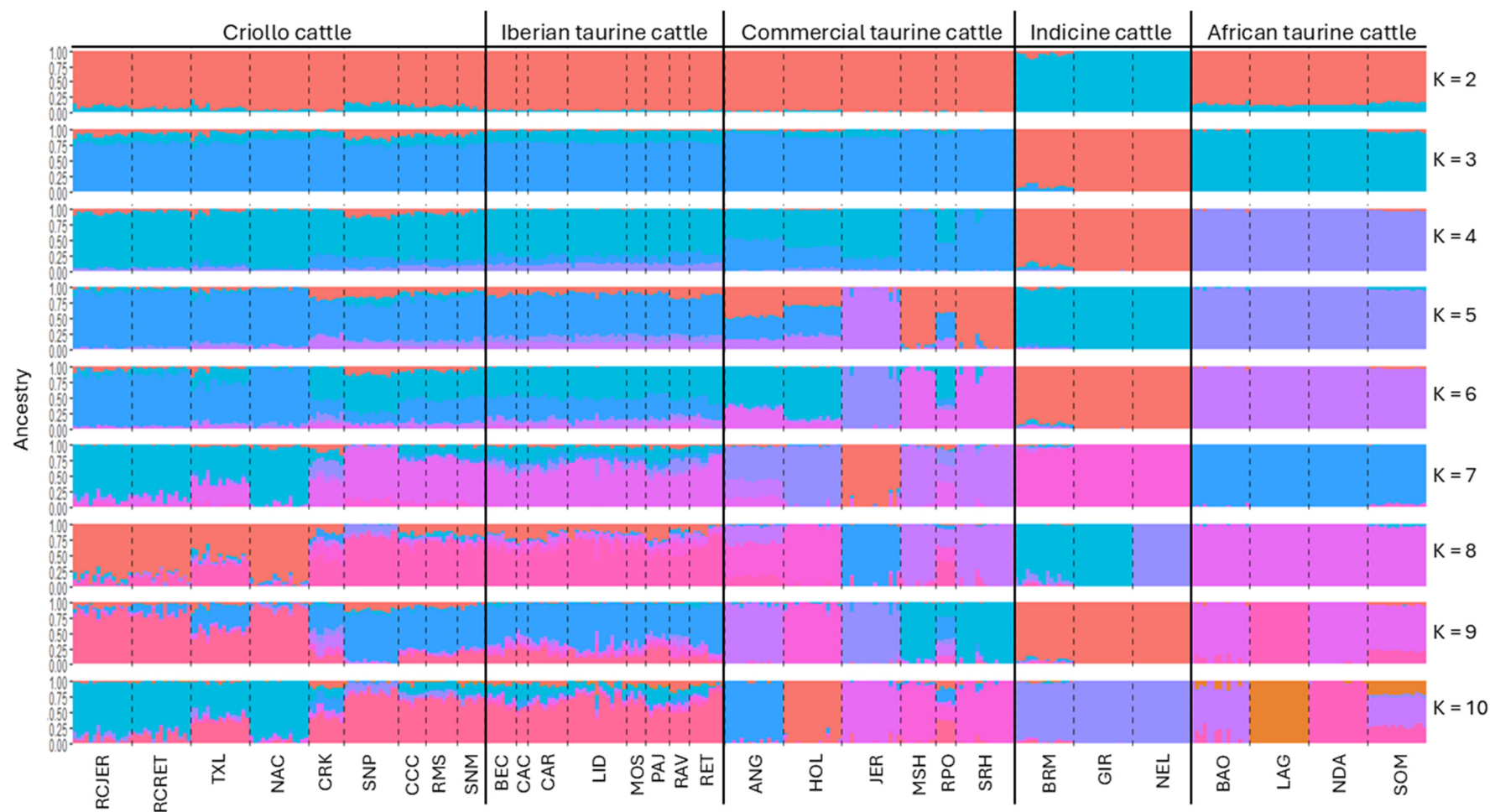
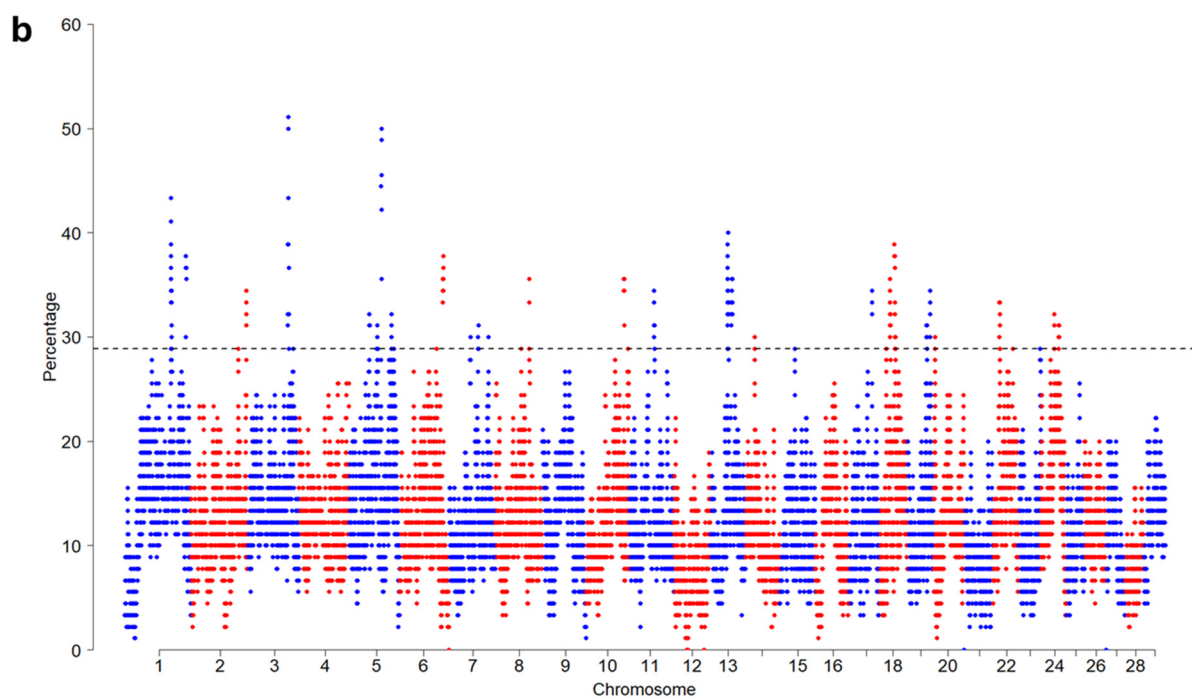
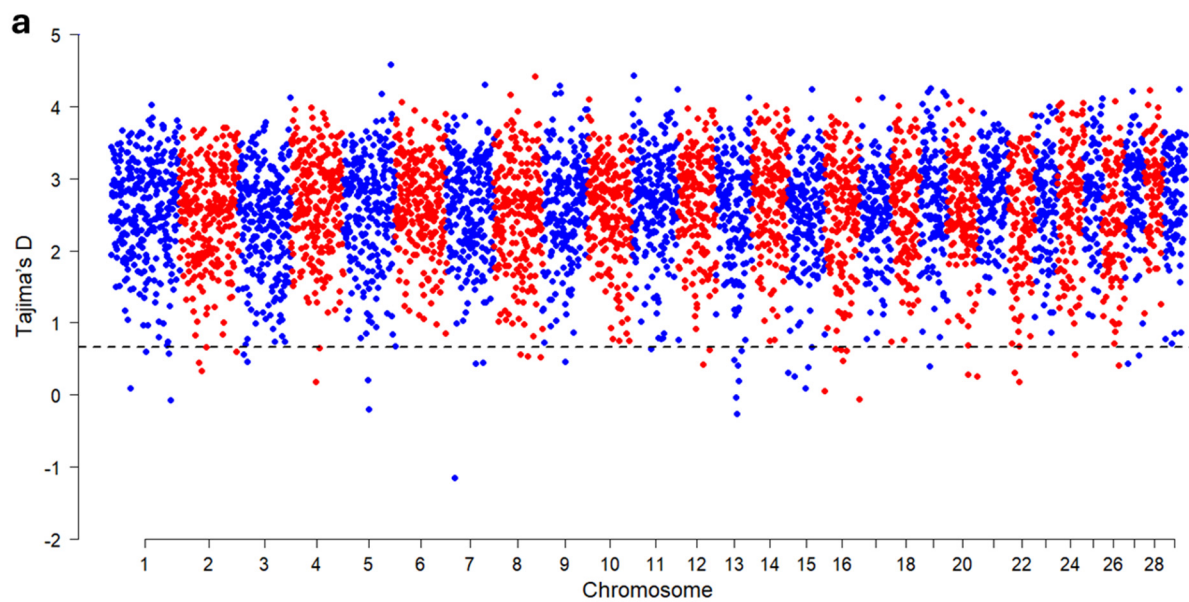


Figure S8. Admixture analysis ($K = 2 - K = 10$) of nine criollo cattle populations compared to other Iberian, commercial, African and Indicine breeds. RCJER: Rarámuri Criollo cattle from the Jornada Experimental Range, RCRET: Rarámuri Criollo cattle from the Rancho Experimental Teseachi, TXL: Texas Longhorn, NAC: North American Corriente, CRK: Florida Cracker, SNP: Senepol, CCC: Costeño con Cuernos, RMS: Romosinuano, SNM: San Martinero, BEC: Berrenda en Colorado, CAC: Cachena, CAR: Cardena Andaluza, LID: Lidia, MOS: Mostrenca, PAJ: Pajuna, RAV: Asturiana de los Valles, RET: Retinta, ANG: Aberdeen Angus, HOL: Holstein, JER: Jersey, MSH: Milking Shorthorn, RPO: Red Poll, SHR: Beef Shorthorn, BAO: Baoule, LAG: Lagune, NDA: N'Dama, SOM: Somba, BRM: Brahman, GIR: Gir, NEL: Nelore.



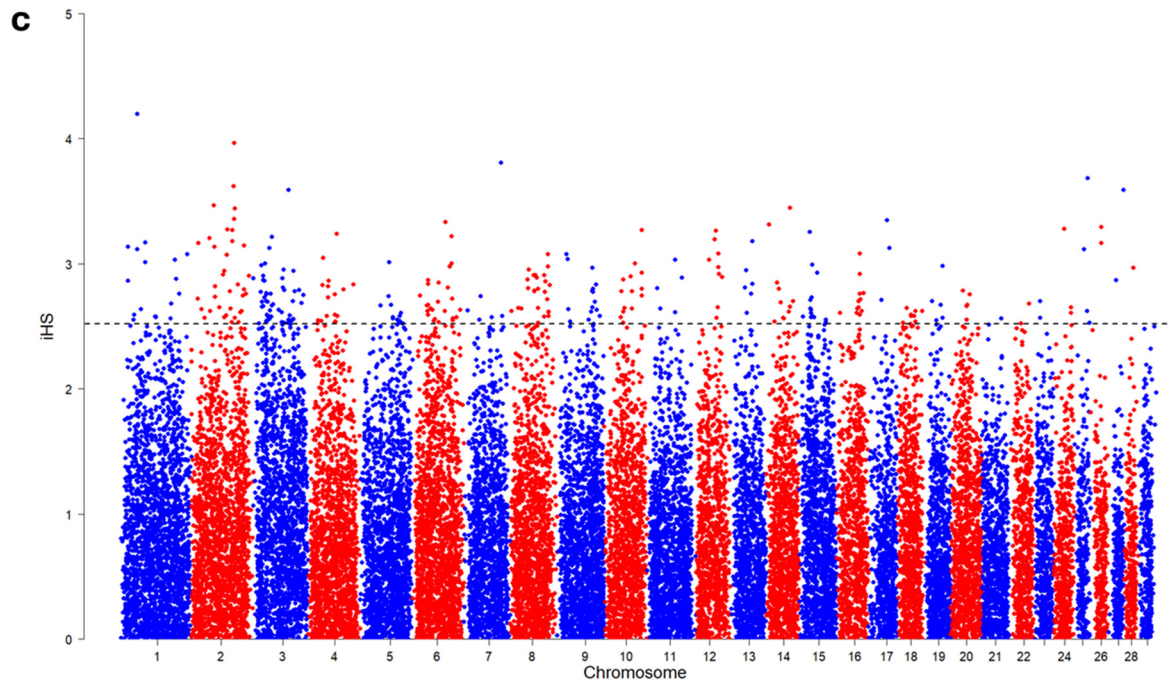
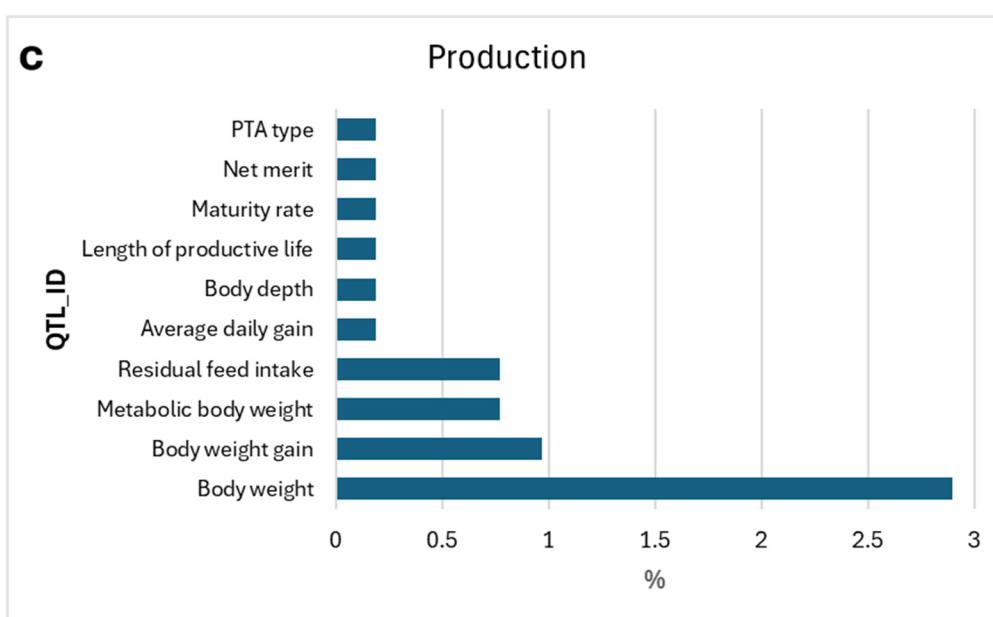
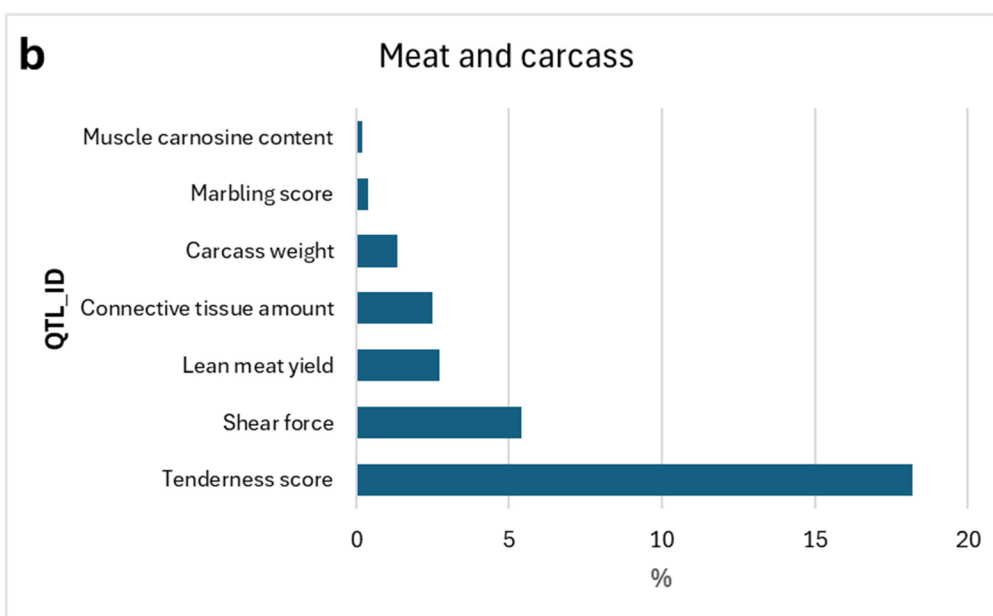
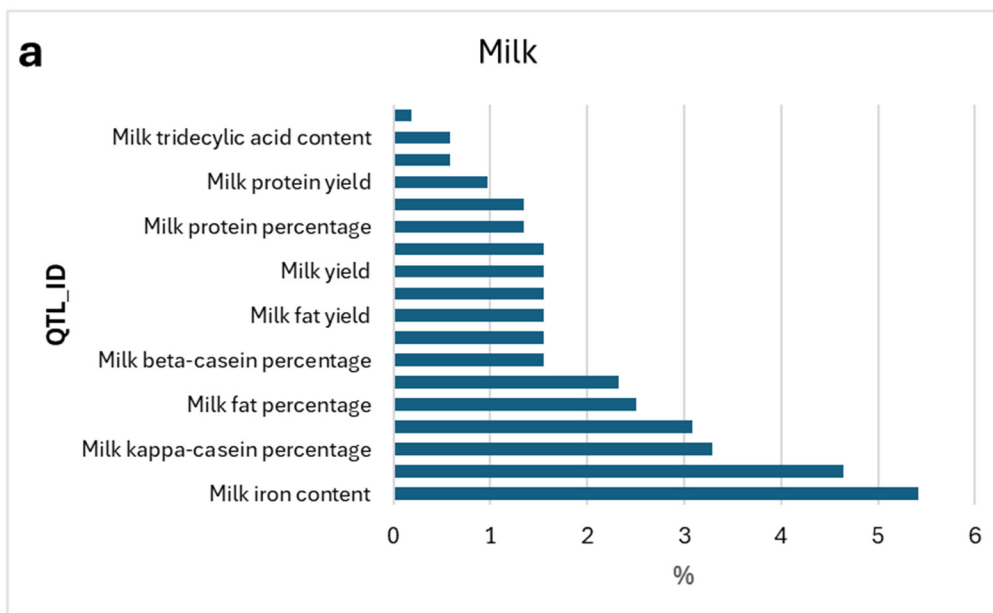


Figure S9. Manhattan plots of genome-wide distribution of selection signatures in Rarámuri Criollo cattle from the Jornada Experimental Range detected using **(a)** Tajima's D statistics, **(b)** runs of homozygosity, and **(c)** integrated Haplotype Scoring. The dotted horizontal line shows the cut-off value to call SNP outliers.



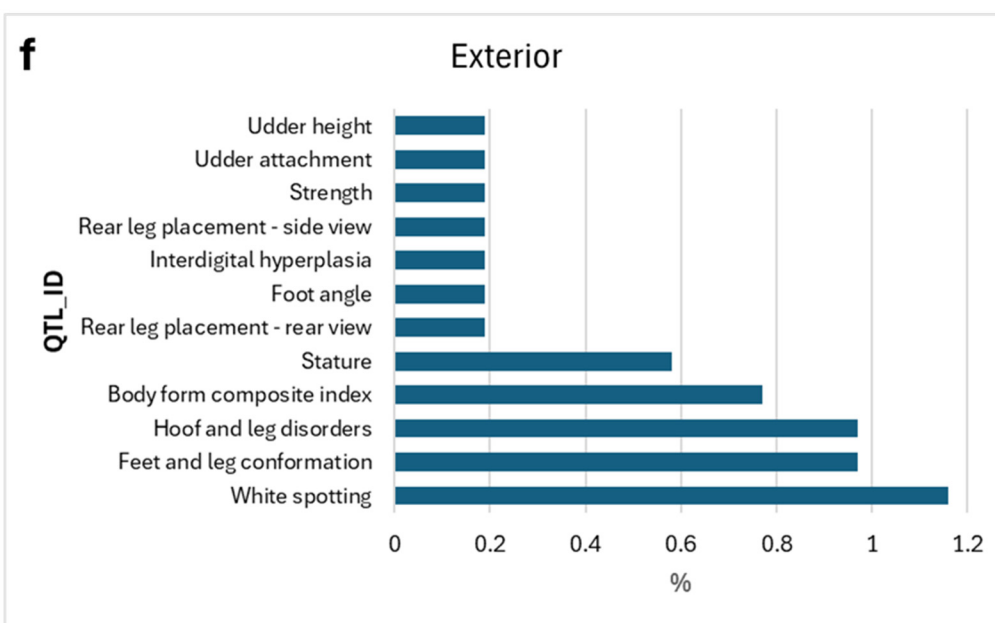
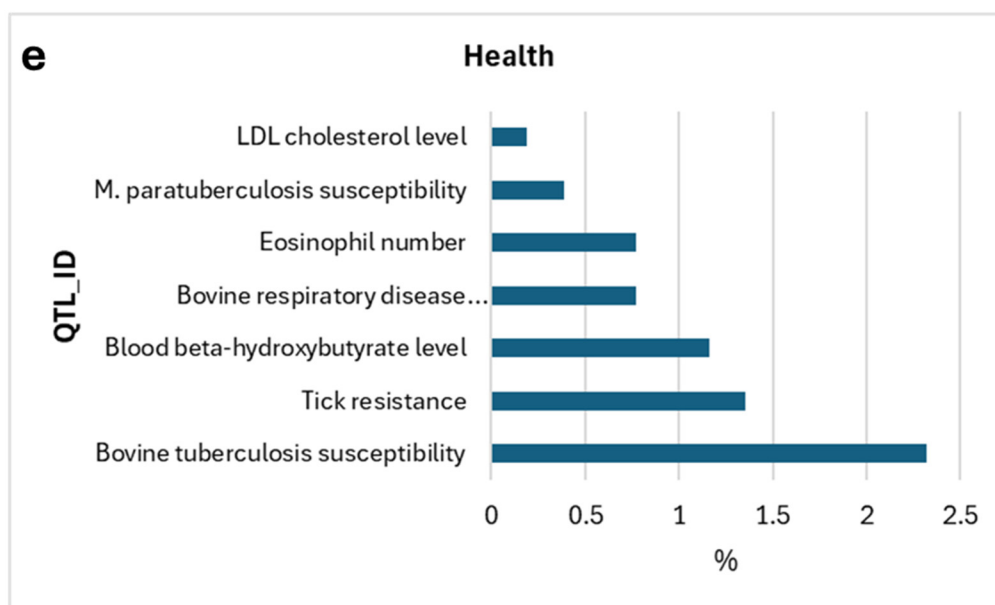
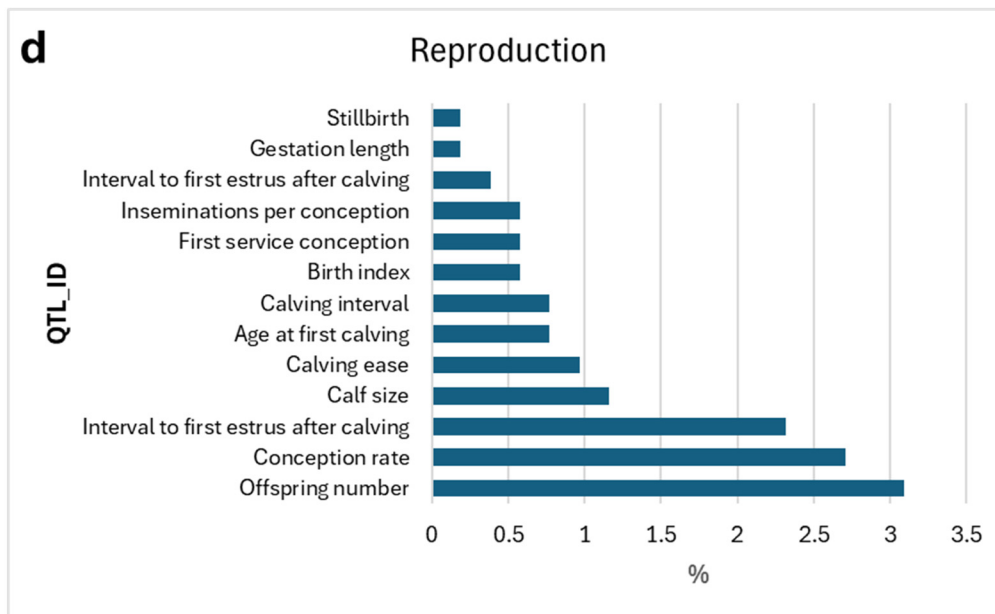


Figure S10. Frequency of QTL presence for **(a)** milk, **(b)** meat and carcass, **(c)** production, **(d)** reproduction, **(e)** health and **(f)** exterior traits in Rarámuri Criollo cattle from the Jornada Experimental Range.