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Supplemental information

Subsistence transition preceded population turnover in the eastern Colombian Andes

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SUPPLEMENTAL FIGURE TITLES and LEGENDS

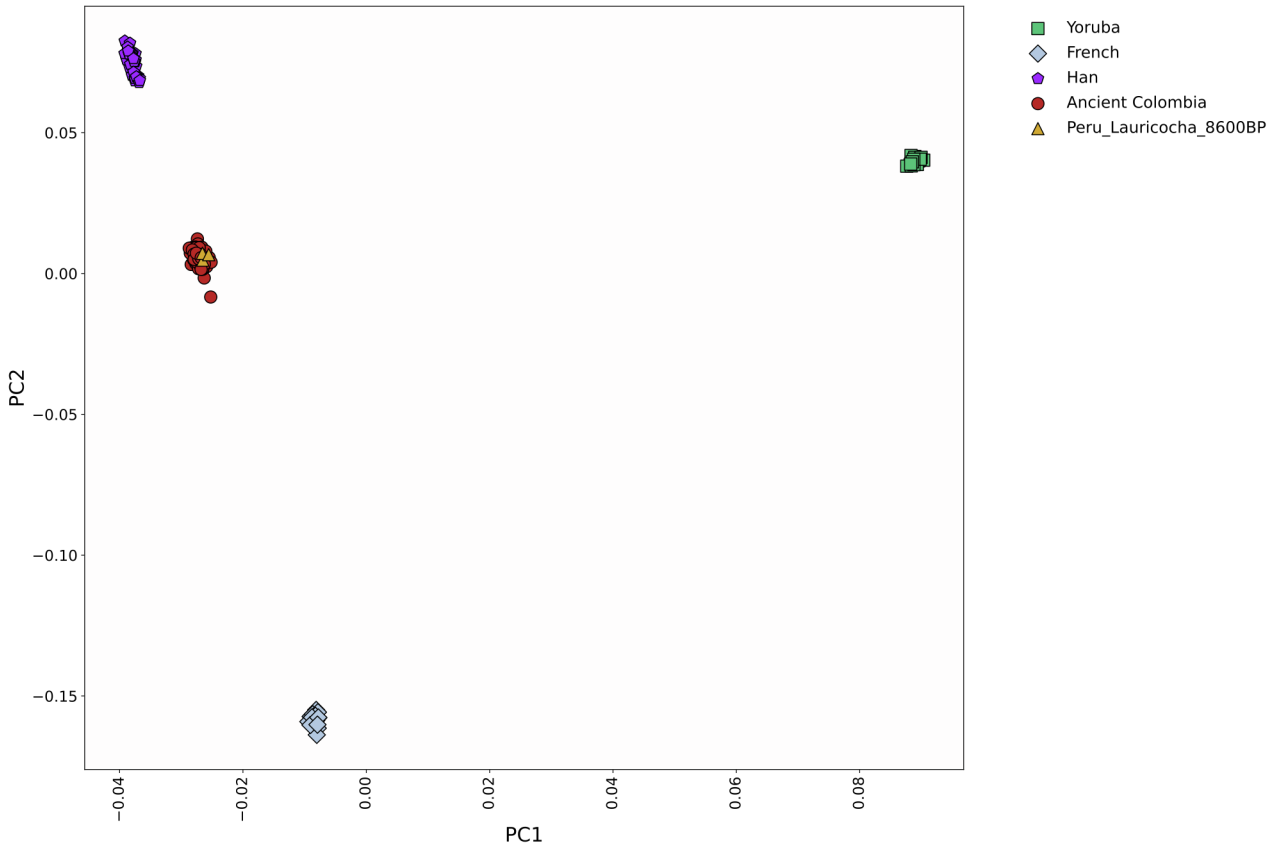


Figure S1. Worldwide PCA with eigenvectors computed using present-day Yoruba, French, and Han Chinese individuals, related to STAR Methods. All ancient individuals were projected, including the 212 from Colombia newly reported in this work. Peru_Lauricocha_8600BP is used here to represent unadmixed Indigenous American ancestry.

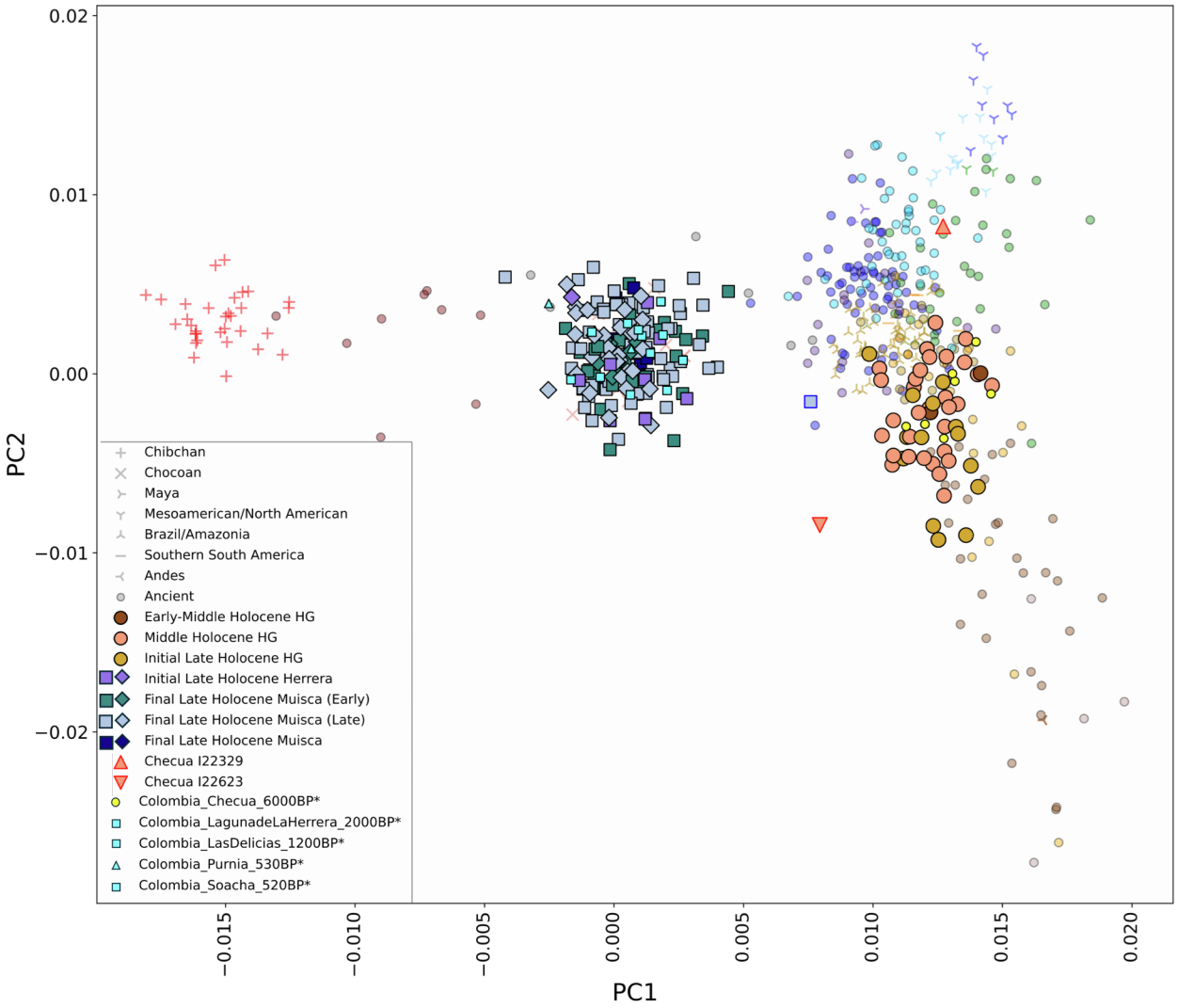


Figure S2. Principal component analysis (PCA) showing ancient individuals from the Altiplano Cundiboyacense projected onto axes of genetic variation defined by present-day American populations with reference data in color, related to Figure 2A. Newly reported data and published ancient Colombian data[37] are represented by large and small colored symbols, respectively. An asterisk next to a sample name in the legend indicates an individual published in ref.[37]. A red outline identifies two individuals who appear as outliers on the PCA reflecting low coverage (<15K SNPs) and a blue outline indicates a PCA outlier of sufficient coverage (>15K SNPs). For the Herrera-Muisca cluster, a square symbol indicates an individual is from a site in the southern department of Cundinamarca, a diamond indicates an individual is from a site in the northern department of Boyacá, and a triangle indicates an individual is from the department of Santander.

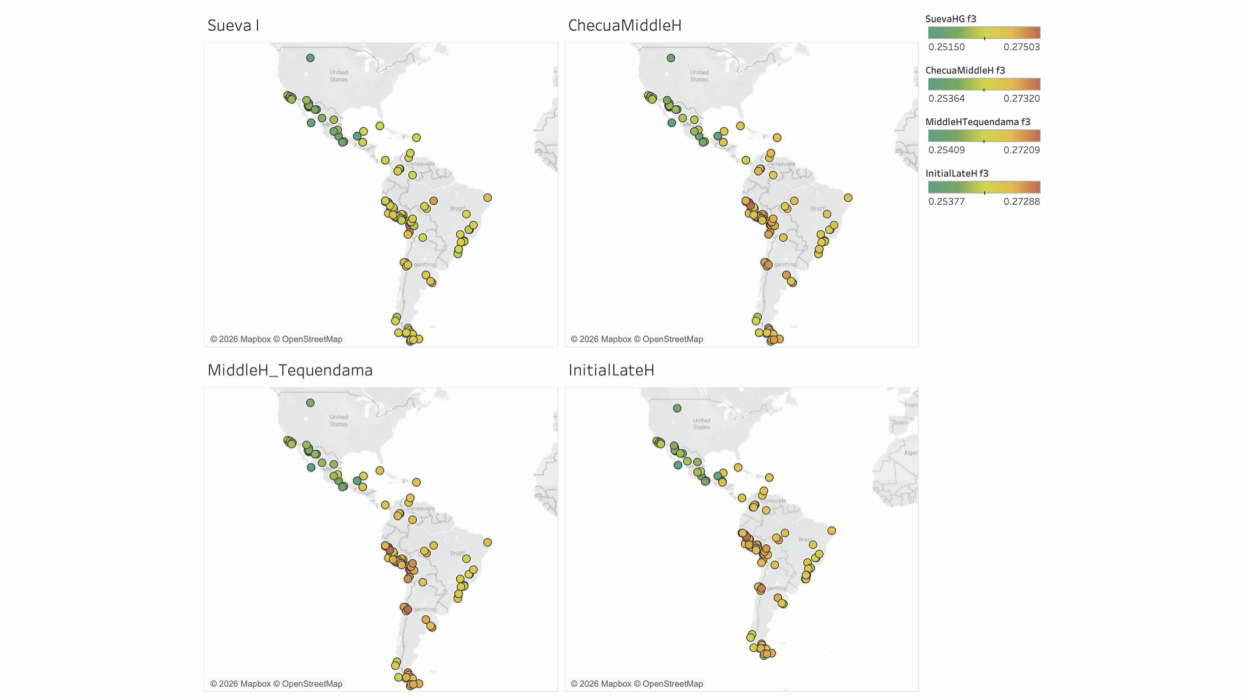


Figure S3. Outgroup-f3 heatmaps showing shared genetic drift between Indigenous American groups and four pre-Herrera Period sub-clades: Sueva I, Checua Middle Holocene, Middle Holocene and Tequendama, and Initial Late Holocene. Each point represents an individual or population plotted at its geographic location (some points jittered slightly for visualization), colored by the magnitude of the f_3 value, with warmer colors indicating greater shared drift. Color scales are shown separately for each panel. Basemaps are from OpenStreetMap/Mapbox. Related to Figure 2C and **Data S2, Table 11**.

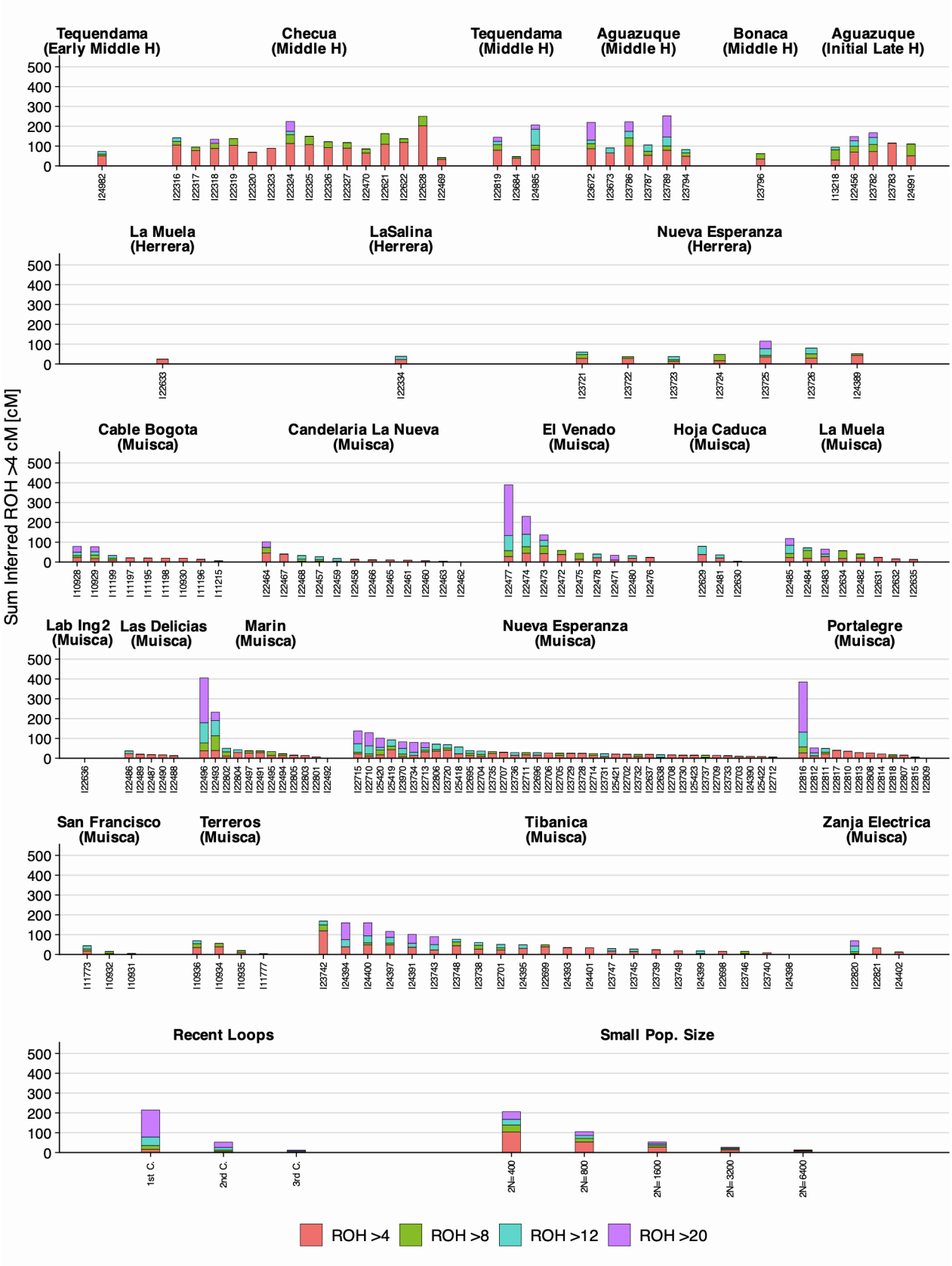

Tequendama (Early Middle H)
Checua (Middle H)
Tequendama (Middle H)
Aguazuque (Middle H)
Bonaca (Middle H)
Aguazuque (Initial Late H)
La Muela (Herrera)
LaSalina (Herrera)
Nueva Esperanza (Herrera)
Cable Bogota (Muisca)
Candelaria La Nueva (Muisca)
El Venado (Muisca)
Hoja Caduca (Muisca)
La Muela (Muisca)
Lab Ing2 (Muisca)
Las Delicias (Muisca)
Marin (Muisca)
Nueva Esperanza (Muisca)
Portalegre (Muisca)
San Francisco (Muisca)
Terreros (Muisca)
Tibanica (Muisca)
Zanja Electrica (Muisca)
Recent Loops
Small Pop. Size
Sum Inferred ROH >4 cM [cM]
0
100
200
300
400
500
1st C.
2nd C.
3rd C.
2N=400
2N=800
2N=1600
2N=3200
2N=6400
ROH >4
ROH >8
ROH >12
ROH >20

Figure S4. ROH calls for 181 ancient Colombian individuals, related to STAR Methods. We depict inferred ROH for individuals from hunter-gatherer/early subsistence transition contexts (top row), Herrera Period contexts (second row), and Muisca Period contexts (third through fifth rows). The legend (bottom row) shows analytical expectations calculated using previously-reported formulas[137] for recent parental relatedness (top right; C represents cousin) and varying population sizes (top left), as well as a color legend for four ROH length categories. Each vertical bar in this figure represents one ancient individual.

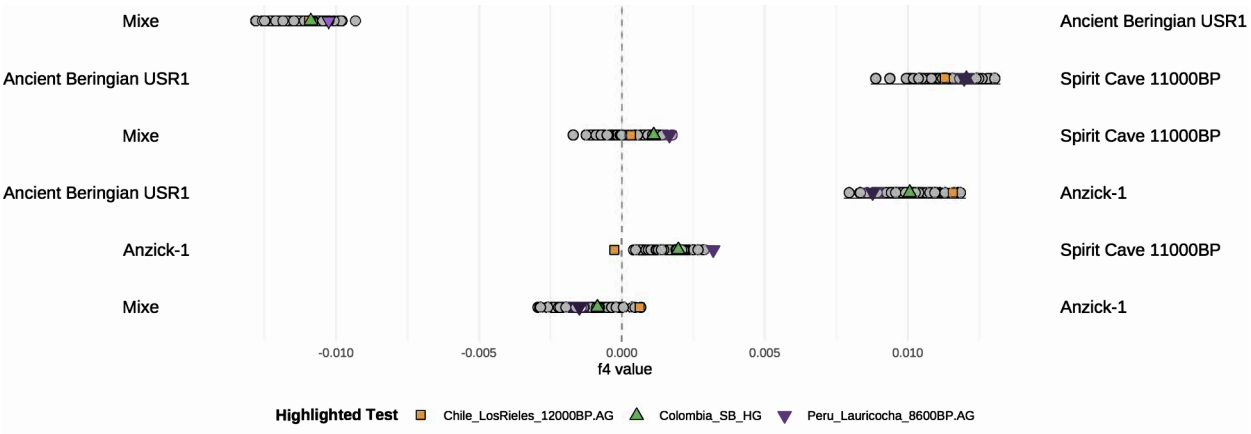


Figure S5. f_4-statistics of the form f_4(Yoruba, *IndigenousAmerican_Test*; *DeepAncient1*, *DeepAncient2*), related to STAR Methods. Colombia_SB_HG (plotted as a green triangle) shows no evidence of ancestry related to Spirit Cave 11000BP or UPopA (proxied here by Mixe) beyond the range observed among other ancient Central and South American populations. Chile_LosRieles_12000BP (orange square) and Peru_Lauricocha_8600BP (purple upside-down triangle) are highlighted for comparison because previous work has identified the former as showing especially strong Anzick-1-related affinity, whereas the latter lacks this specific Anzick-1-related signal[52]. The vertical dashed line marks zero.

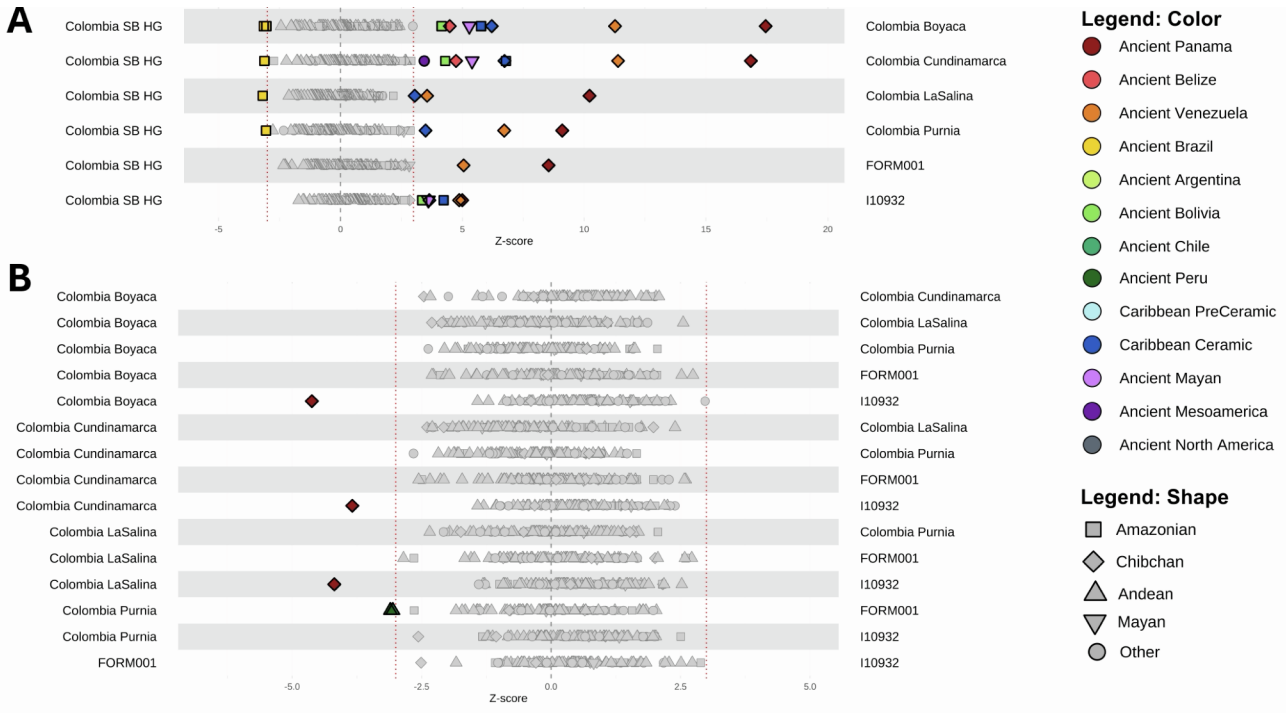


Figure S6. Differences in allele sharing patterns between the ancient people of the Altiplano Cundiboyacense (2M dataset), related to STAR Methods. A) We use the statistic f_4(Yoruba, *IndigenousAmerican_Test*; Colombia_SB_HG; *Colombia_HerreraMuisca*) to explore differences in allele sharing between hunter-gatherers/early subsistence transition contexts and Herrera-Muisca Period people of the Altiplano Cundiboyacense. Data are in **Data S2, Table 16**. B) We use the statistic f_4(Yoruba, *IndigenousAmerican_Test*; *Colombia_HerreraMuisca1*; *Colombia_HerreraMuisca2*) to explore differences in allele sharing between the Herrera-Muisca Period people of the Altiplano Cundiboyacense. Data are in **Data S2, Table 5.** In both panels, red dotted lines denote |Z|=3. Points associated with |Z|<3 are in gray, while those |Z|>3 are in color, with the legend on the right. The first and second affinity we used to assign the color and shape (respectively) of each *Test* population are included in the supplementary data tables. Only tests based on >50K SNPs are plotted.

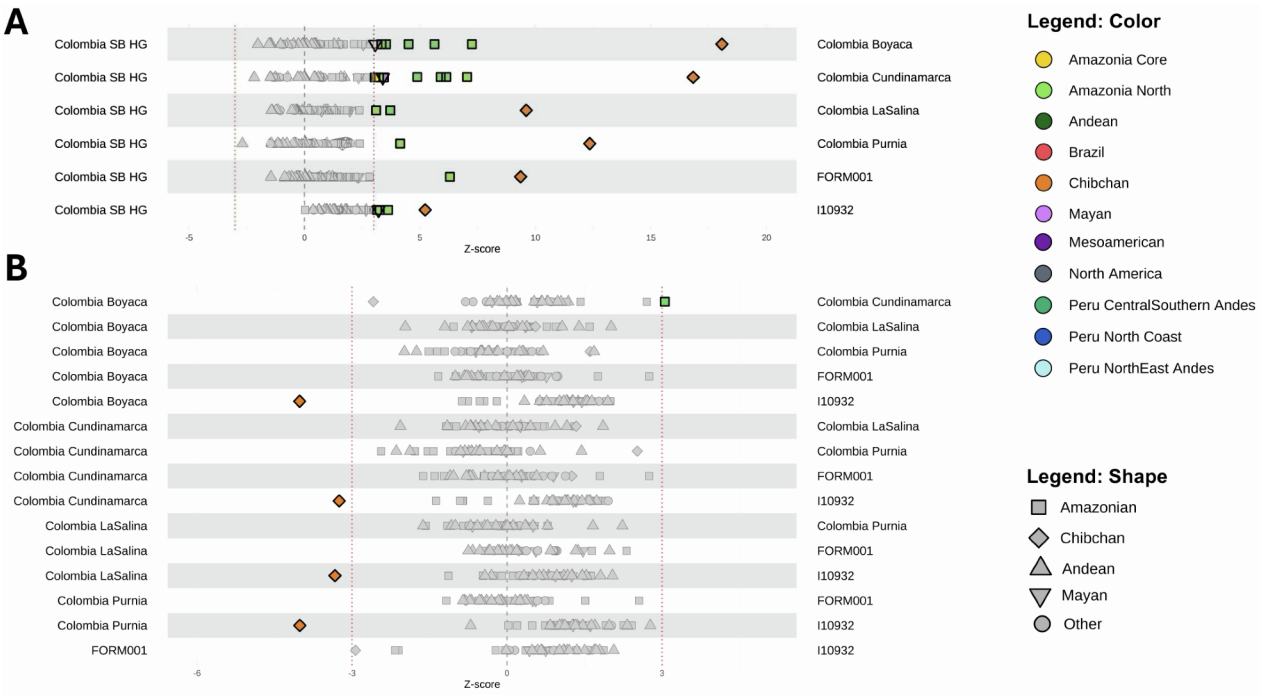


Figure S7. Differences in allele sharing patterns between the people of the Altiplano Cundiboyacense (2M.HO dataset), related to STAR Methods. A) We use the statistic f_4(Yoruba, *Test_HO*; Colombia_SB_HG; *Colombia_HerreraMuisca*) to explore differences in allele sharing between hunter-gatherers/early subsistence transition contexts and Herrera-Muisca Period people of the Altiplano Cundiboyacense. Data are in **Data S2, Table 17.** B) We use the statistic f_4(Yoruba, *Test_HO*; *Colombia_HerreraMuisca1*; *Colombia_HerreraMuisca2*) to explore differences in allele sharing between Herrera-Muisca Period people of the Altiplano Cundiboyacense. Data are in **Data S2, Table 6.** In both panels, red dotted lines denote |Z|=3. Points associated with |Z|<3 are in gray, while those |Z|>3 are in color, with the legend on the right. The first and second affinity we used to assign the color and shape (respectively) of each *Test* population are included in the supplementary data tables. Only tests based on >50K SNPs are plotted.

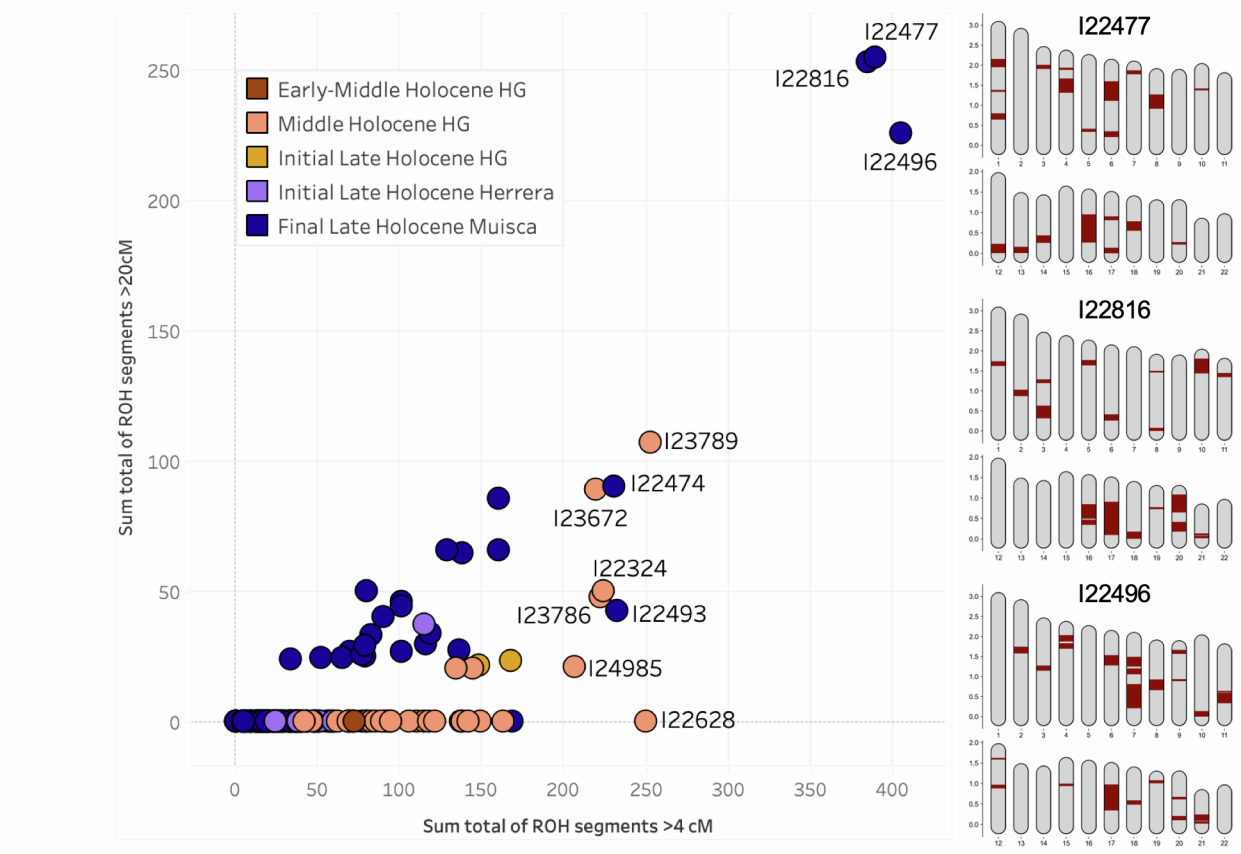


Figure S8. Runs of homozygosity (ROH) across individuals from the Altiplano Cundiboyacense analyzed to identify the offspring of consanguineous unions, related to STAR Methods. Left: plot of sum total of ROH segments >4cM (x-axis) against sum total of ROH segments >20cM (y-axis) for 181 individuals with sufficient coverage. Each point represents one individual, color coded by time period. Eleven individuals with >200cM ROH >4cM are labeled. Data are in **Data S2, Table 12**. On the right, we show karyotypes for three Muisca Period individuals with very high levels of ROH >20cM, indicating consanguinity. Gray outlines represent autosomes and red shaded sections indicate ROH segments.

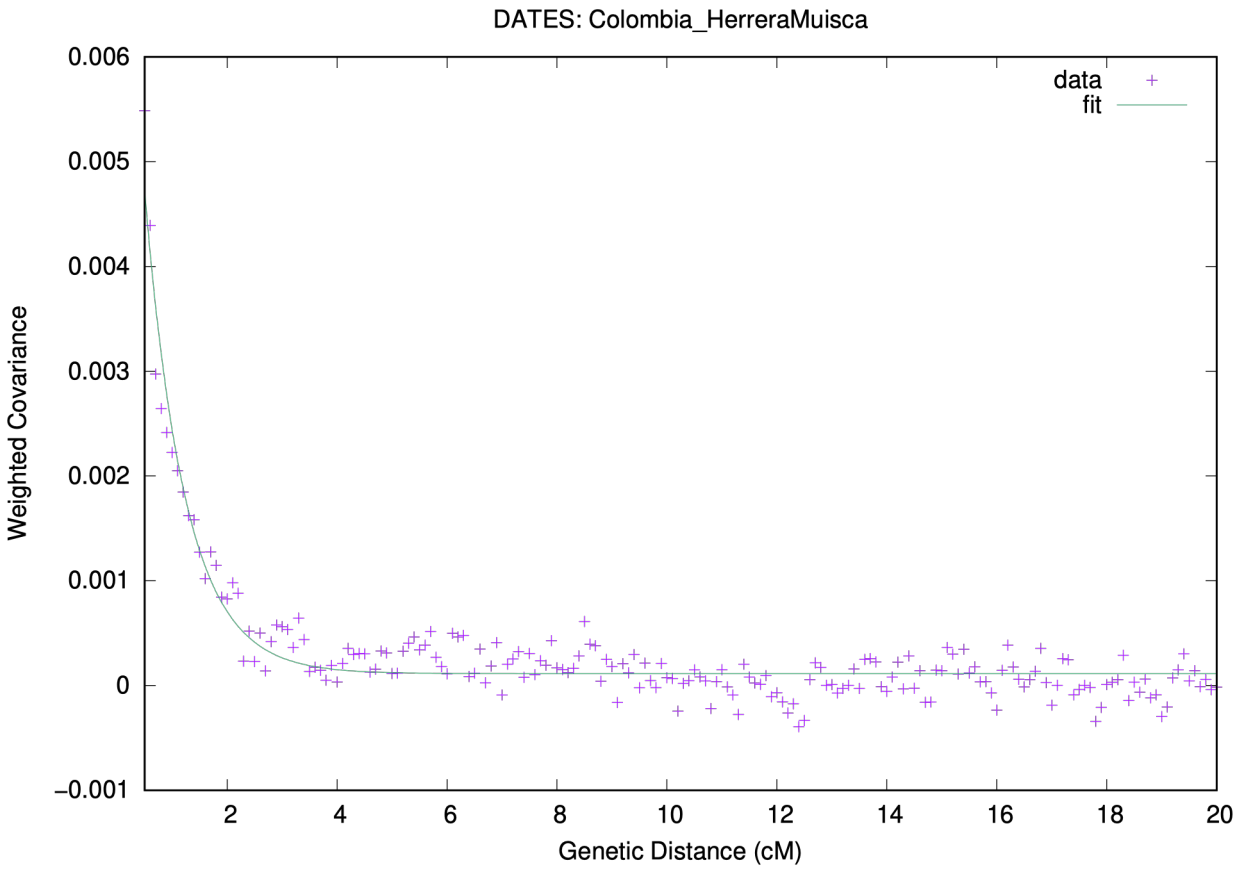


Figure S9. Ancestry covariance decay curve for Herrera-Muisca Period people (target) inferred using a set of pooled ancient and modern Chibchan-related individuals as one reference group and Amazonian-related individuals as a second reference group, related to STAR Methods. Weighted ancestry covariance is shown as a function of genetic distance (cM). Purple crosses represent the observed data, and the solid line shows the best-fitting exponential decay model used by DATES to infer admixture timing. The average date of admixture is estimated at 136 ± 15 generations before the target individuals lived. We observe a strong ancestry covariance decay consistent with admixture, with high statistical support (Z = 9.0). Data are in **Data S2, Table 26**.