Figure S1: Geographic map and Principal Component Analysis (PCA). Related to Figure 1 and STAR Methods. A. The geographic location of all populations included in the final dataset is reported in the worldwide map [S1–S35]. In details, we analysed 11,607 recipients and 6115 donors. Related to Data S1. Map tiles by Stamen Design, under CC BY 3.0. Data by OpenStreetMap, under ODbL. B. Individual PCA plot for the analysed data.
Figure S2: Refined and raw fineSTRUCTURE trees. Related to STAR Methods. A. Refined fineSTRUCTURE tree composed of 89 homogeneous clusters (as explained in STAR Methods). Each leaf has been labelled according to the corresponding cluster name reported in Data S1, and colored in 20 different macro-groups. B. Dendrogram of donor individuals clustered by fineSTRUCTURE into 370 clusters. Each branch label is in the form X<popA>;Y<popB>, where X and Y are the number of individual for popA and popB in the cluster.
Figure S3: Ancestral mosaic of American populations obtained with NNLS analysis. Related to STAR Methods. Each barplot shows the genetic composition of admixed populations. Only the contribution for the 26 most representative fineSTRUCTURE clusters (proportion of at least 2% in one recipient population) is reported. Map tiles by Stamen Design, under CC BY 3.0. Data by OpenStreetMap, under ODbL.
Figure S4: Heatmaps, UPGMA dendrogram and the European and African relative contribution to the Americas. Related to Figure 1. A. Relative proportion of the main contributing European sources in Americas. Each barplot shows the proportion of a specific ancestry in different American samples. Only populations having relative ancestries proportions ≥2% are shown. The clusters color legend is reported in panel B. B. Relative proportion of the main contributing African sources in the Americas. Each barplot shows the proportion of a specific ancestry in different American samples. Only populations having relative ancestries proportions ≥2% are shown. Map tiles by Stamen Design, under CC BY 3.0. Data by OpenStreetMap, under ODbL. C-D. For each population we have considered the relative contribution of each donor cluster into the total European (C) or African (D) ancestry.
Figure S5: Individual ancestral proportion in 11,607 American individuals from 22 populations as inferred by SOURCEFIND. Related to Figure 1. Only points for ancestry proportion > 5% are shown.
Figure S6: Ancestry-specific effective population size of American populations. Related to Figure 4. A-F. We evaluated the pairwise Pearson correlation of population size trajectories through times for each ancestry using two different time intervals: before (31-60) and after 30 (1-30) generations ago. Circle size refers to the Pearson R2, while crosses indicate non significant comparisons, after Bonferroni correction. G. We combined Identity by Descent and Local Ancestry analysis inference to estimate Ancestry Specific Population size for single continental ancestry. The x-axes show time expressed in years of Common Era. The y-axes show ancestry-specific effective population size (Ne), plotted on a log scale. The lines show estimated ancestry-specific effective population sizes, and ribbons indicate the 95% confidence intervals. Only the population ancestries in which χ2(continent)* N > 50 where χ2 is the proportion of a specific ancestry and N is the total number of chromosomes in the analysed population are represented. H. We combined samples from Colombia, Peru, Mexico and Puerto Rico and inferred the Ancestry Specific Effective Population size as explained in Methods. European and Native American ancestries are reported in blue and yellow, respectively.
**Supplemental References**


