

Figure S6: Multidimensional scaling (MDS) analysis of the Native American data. The results of MDS analysis on the original microsatellite data are shown by colored points, with the x-axis corresponding to the first principal coordinate and the y-axis corresponding to the second principal coordinate. The results of MDS analysis on one set of imputed microsatellite data are displayed with gray points, Procrustes-transformed to best match the results from the original data (*Stat. Appl. Genet. Mol. Biol.* 13: 9, 2010). Each pair of corresponding points is connected by a gray line. The allele-sharing distance matrices calculated from the original data, averaging across loci and ignoring loci for which one or both individuals was missing, and from one set of imputed data (after correcting for allelic dropout) were used as the input to the *cmdscale* function in R.