Additional D-statistic results

We computed D(P1, P2, Neanderthal, Outgroup) for all pair of individuals (P1,P2) from the Complete Genomics data, as described in the Materials and Methods. The D-statistics were averaged over all combinations of individuals for each given pair of populations. The means and the standard deviations for all twenty-eight pairwise population comparisons are given in Tables S1 and S2. We also show regional comparisons, where some populations are grouped into East Asian, European, or African (Tables S2 and S3). We also computed the admixture rate (f) for each of these combinations (Tables S1-S3) for the data from Analysis A. Where we have results from both Analysis A and Analysis B, we show the results in the text in curly braces, such that the results from the two analyses are given as {Analysis A, Analysis B}.

Comparison between non-Africans and Africans

The averaged D-statistics are consistently positive when comparing African populations and non-African populations (Average D-statistic range = {[0.0429, 0.0891], [0.0530, 0.0750]}, Table S1, Figure S1). These results confirm the previous findings that the non-African populations are more closely related to Neanderthal than African populations (Green et al. 2010). The admixture rate estimated also gives positive values ranging from 0.0191 to 0.0417 (Table S1, Figure S2).

Comparison between Europeans and East Asians (Figure S3-S4)

When we compared the set of D-statistics for the pair (Afr, East Asia) and the pair (Afr, Europe) using Test 1, we find that the D-statistics for the East Asian individuals tend to be higher than the D-statistics for the European individuals (mean difference = {0.0083, 0.0096}, two-tailed p-value = {0.0010, 0.0006}, Table S4). This suggests that East Asians may have a greater signal for genetic admixture with Neanderthals than Europeans. These results are consistent when we consider each African population separately and across both Analysis A and Analysis B. The difference between Europeans and East Asians is always significant using Test 1 (Table S4).

This trend is further supported by the set of positive D-statistics estimated for the pair (Europe, East Asia). The values averaged over each population are given in Table S2. The average D-statistic for the merged East Asian group compared to the merged European group is {0.0110, 0.0131}, which is significantly different from zero (two-tailed p-value = {0.0037, 0.0009}, Table S5).

The f-statistics also show the same trend, with a higher signal between Neanderthals and East Asians, compared to Neanderthals and Europeans. Test 1 shows that the difference in f-statistic of 0.0098 is significant (two-

tailed p-value = 0.0011, Table S7). Test 2 compares Europeans and East Asians directly, and shows that the *f*-statistic

computed is 0.0100, which is significantly different from zero (two-tailed p-value = 0.0072, Table S8).

Gujarati population (Figure S5-S6)

We also studied whether the South Asian population GIH was more similar to the Europeans or the East

Asians in term of admixture from Neanderthal. When compared to the African individuals, the GIH individuals have an

average D-statistic of {0.0712, 0.0656} (Table S3), which is higher than the average D-statistic for Europeans (average

D-statistic for (Afr, Europe) = {0.0644, 0.0604}, Table S3) and lower than the average D-statistic for East Asians

(average D-statistic for (Afr, East Asia) = {0.0727, 0.0699}. The same results are observed when considering each

African population separately (Table S3). We applied both Test 1 and Test 2 to investigate the significance of these

observations. When we use Test 1, we find that the difference in the estimates of *D* for the pair (Afr ,GIH) and the pair

(Afr, East Asia) are significant when comparing against all Africans (two-tailed p-value = {0.0101, 0.0259}, Table S6).

However, the difference in the estimates of *D* for (Afr, GIH) and (Afr, Europe) is not significant (two-tailed p-value =

{0.4232,0.1343}, Table S6). Thus, the average D-statistics found for GIH are closer to the estimates of *D* for the

European samples than for the East Asian samples. When we use Test 2, we find that *D*-statistics for (Europe, GIH) are

not significantly different from 0 (D={0.0035, 0.0067}, p-values = {0.4386, 0.2345}, Table S5). *D* for (GIH, East Asia) are

significantly different from zero in Analysis A (two-tailed p-value=0.0346), but must be taken with caution as the

estimate is not significantly different in Analysis B (two-tailed p-value=0.0867). The results from Test 2 cannot

distinguish if the GIH samples group more closely with East Asians or Europeans, while Test 1 does. Test 1 and Test 2

for the *f*-statistic show similar results (Table S8-S9).

Maasai population (Figure S7-S8)

The Maasai individuals (MKK) seem to share more genetic similarity with Neanderthals than other African

populations. The average D-statistic for (Afr, MKK), with Afr =YRI or LWK, were positive (average D-statistic = {(0.0110,

0.0075), (0.0102, 0.0145)}, Table S2). Using Test 2, the average D-statistic for (YRI+LWK, MKK) is significantly different

from zero (D={0.0123,0.0116}, two-tailed p-value={0.0101, 0.0135}). However, the significant difference from zero is

lost when the Maasai are compared separately to the Yoruba or Luhya, except for the (YRI,MKK) comparison in

Analysis A (two-tailed p-value=0.0418, Table S5). Notably, the (LWK, YRI) pair is not significantly different from zero

(two-tailed p-value = {0.3457, 0.3611}, Table S5).

When we compare the estimates of *D* for the pair (YRI, East Asia) to (MKK, East Asia) using Test 1, the

estimates of *D* for (MKK, East Asia) were significantly different from the estimates of *D* for (YRI, East Asia) by a small

amount (difference = {0.0074, 0.0051}, two-tailed p-value = {0.0054, 0.0352}, Table S4), indicating that the signal of archaic admixture in non-Africans is weaker when we use the MKK as a reference. We also see a significant difference using the Europeans instead of East Asians (two-tailed p-value = {0.0098, 0.0404}, Table S4). A significant difference is also observed when switching between the Maasai and the Luhya as the reference in Analysis A (Table S4), but is above the 0.05 significance threshold in Analysis B. However, again, it is striking to see that there is no significant difference in D-statistics between (YRI, East Asia) and (LWK, East Asia) (two-tailed p-value = {0.1302, 0.1235} for East Asians and {0.1234, 0.1243} for Europeans, Table S4).

The results for the f-statistics show no significant difference between the Maasai and the other two African populations for Test 2 (two-tailed p-value = 0.2021, Table S8). Comparisons of the Maasai separately to the Yoruba and the Luhya show that the main reason for the lack of significance is no significant difference in f when comparing the Yoruba and Maasai (two-tailed p-value = 0.4944 for Europe, 0.4284 for East Asia, Table S7). The estimates of f using the Luhya are, however, significantly different from the estimates using the Maasai for both Europeans (two-tailed p-value = 0.0286, Table S7) and East Asians (two-tailed p-value = 0.0286, Table S7). Test 2 also shows that the Maasai have a significantly greater admixture rate relative to the Luhya (two-tailed p-value = 0.0666, Table S8), but not the Yoruba (two-tailed p-value = 0.4847, Table S8).

Consistency

All the D statistics, f statistics, and p-values of the randomization tests were calculated for two sets of slightly differently prepared data (see Materials and Methods). The results are presented in all tables under the columns *Analysis A* and *Analysis B*. For both analyses, the East Asian populations show a significantly higher estimate of D than the European populations. The two analyses also consistently show the South Asian Gujarati population exhibiting D-statistics closer to the European population than the East Asian populations. Both analyses also show results that suggest the MKK has more shared genetic variants with Neandertals compared to the other African populations. The differences in data preparation, while giving slightly different estimates of D, do not change our conclusions.

The f-statistics also suggest higher admixture into East Asians over Europeans and more similarity in admixture rates between the GIH and Europeans, as compared to GIH and East Asians, but the Maasai genetic similarity is not observed.

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