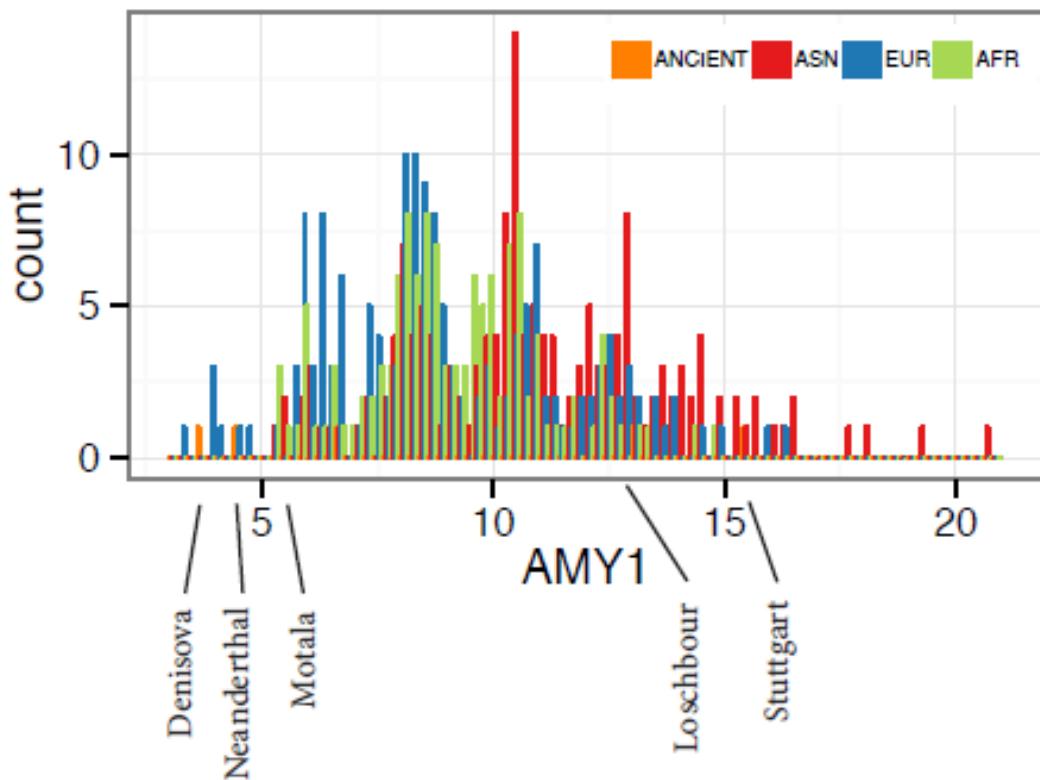


# Extended Data

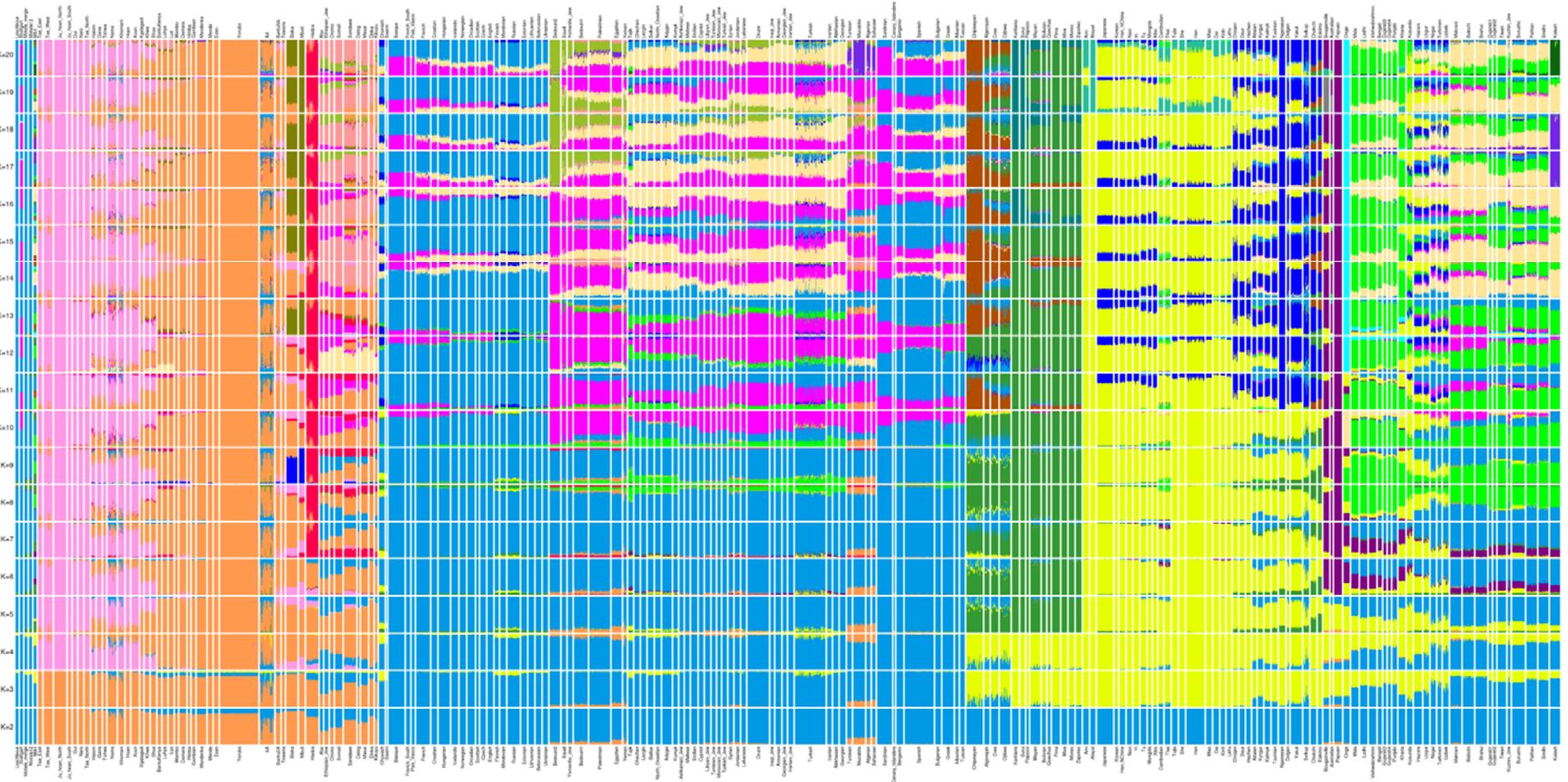
**Extended Data Figure 1: Photographs of analyzed ancient DNA samples.** (A) Loschbour skull; (B) Stuttgart skull, missing the lower right M2 we sampled; (C) excavation at Kanaljorden in Motala, Sweden; (D) Motala 1 in situ.



**Extended Data Figure 2: Amylase CNV analysis.** Distribution of amylase (*AMY1*) copy number inferred for samples from the 1000 Genomes Project compared with ancient genomes: Neanderthal, Denisova, Motala12, Loschbour, and Stuttgart. The relatively high copy number for the pre-agricultural Loschbour sample suggests that high *AMY1* copy number in humans may not entirely be due to selection since the switch to agriculture.

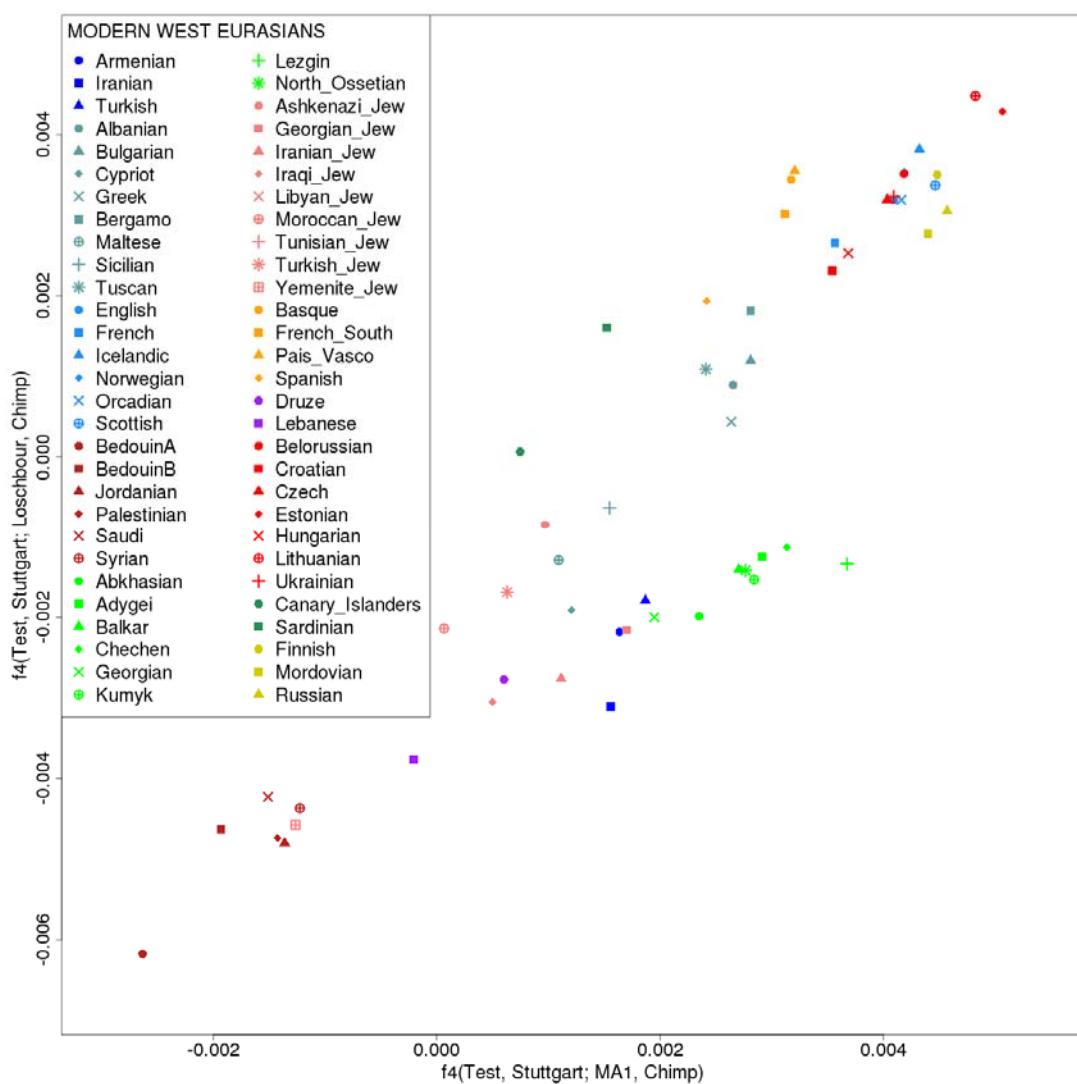


**Extended Data Figure 3: ADMIXTURE analysis (K=2 to K=20).** Ancient samples (Loschbour, Stuttgart, Motala\_merge, Motala12, and MA1) have been placed on the left. The order of the modern populations has been determined by applying hierarchical clustering (as implemented in the function “*hclust*” of R) over the set of admixture coefficients over all K=2 to K=20 runs, with the goal of bringing populations with similar admixture coefficients visually close.



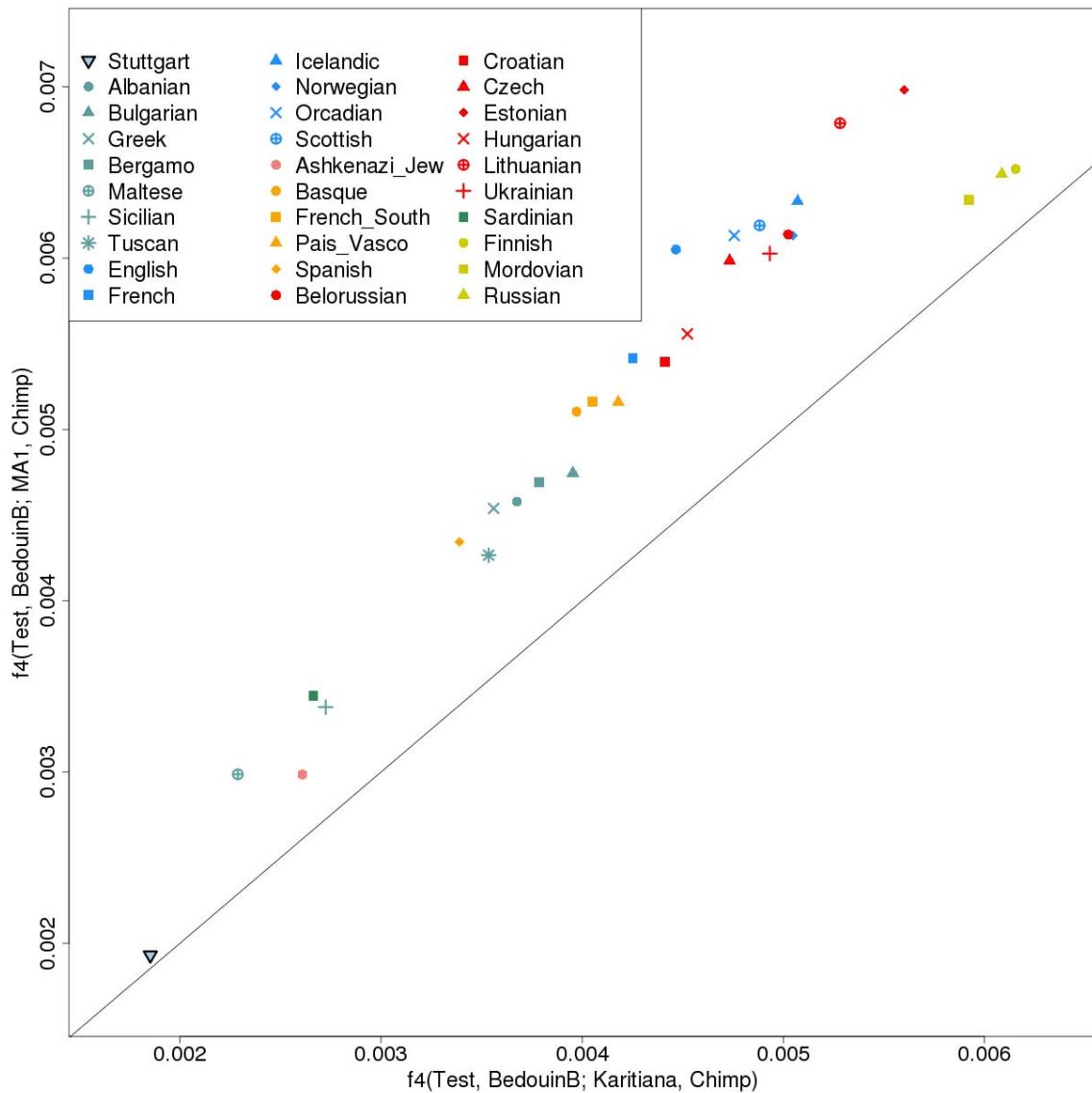
**Extended Data Figure 4: ANE ancestry is present in both Europe and the Near East but WHG ancestry is restricted to Europe, which cannot be due to a single admixture event.**

(x-axis) We computed the statistic  $f_4(\text{Test}, \text{Stuttgart}; \text{MA1}, \text{Chimp})$ , which measures where MA1 shares more alleles with a test population than with Stuttgart. It is positive for most European and Near Eastern populations, consistent with ANE (MA1-related) gene flow into both regions. (y-axis) We computed the statistic  $f_4(\text{Test}, \text{Stuttgart}; \text{Loschbour}, \text{Chimp})$ , which measures whether Loschbour shares more alleles with a test sample than with Stuttgart. Only European populations show positive values of this statistic, providing evidence of WHG (Loschbour-related) gene flow only in Europeans.



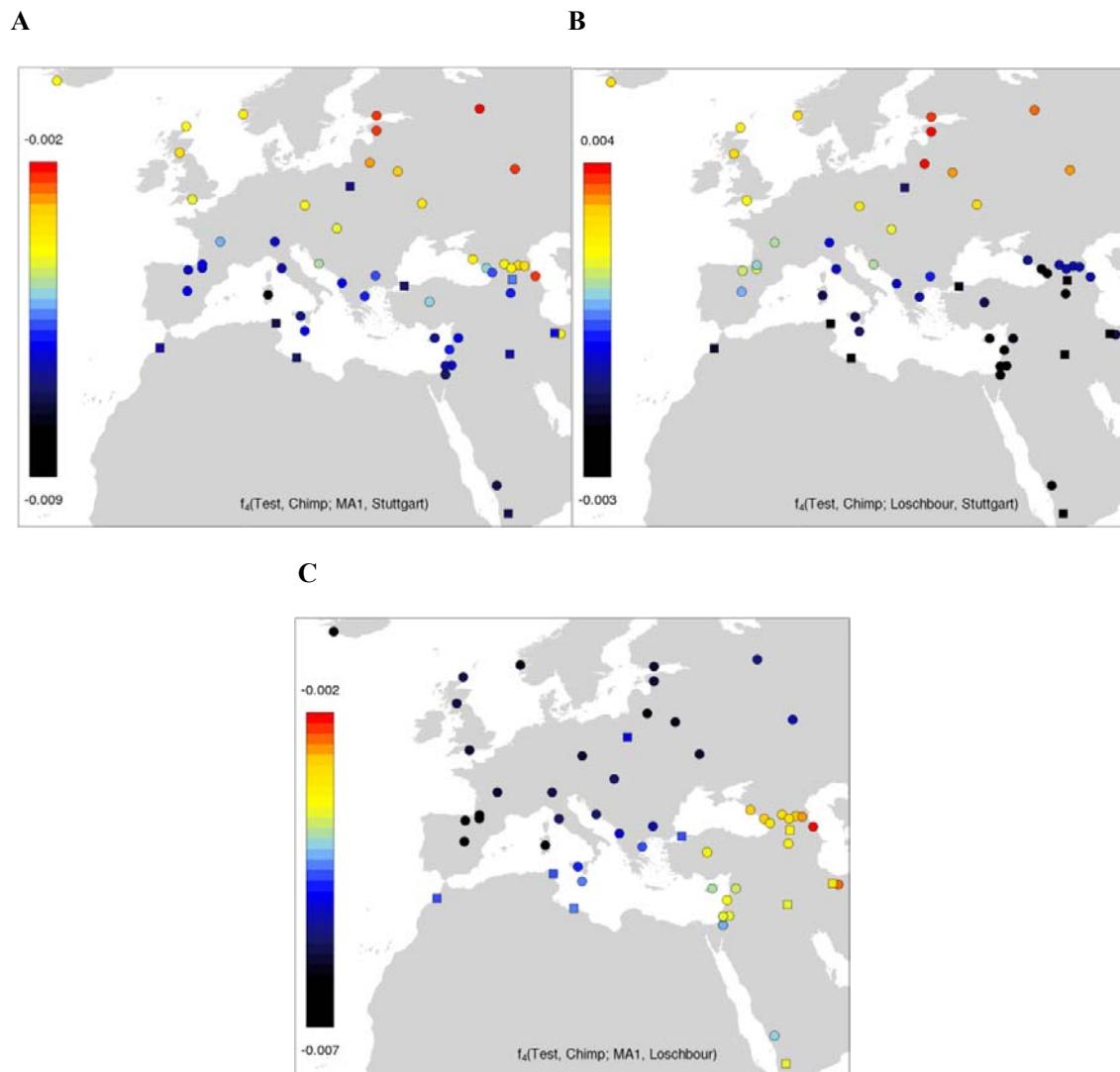
**Extended Data Figure 5: MA1 is the best surrogate for ANE for which we have data.**

Europeans share more alleles with MA1 than with Karitiana, as we see from the fact that in a plot of  $f_4(\text{Test}, \text{BedouinB}; \text{MA1}, \text{Chimp})$  and  $f_4(\text{Test}, \text{BedouinB}; \text{Karitiana}, \text{Chimp})$ , the European cline deviates in the direction of MA1, rather than Karitiana (the slope is  $>1$ ).



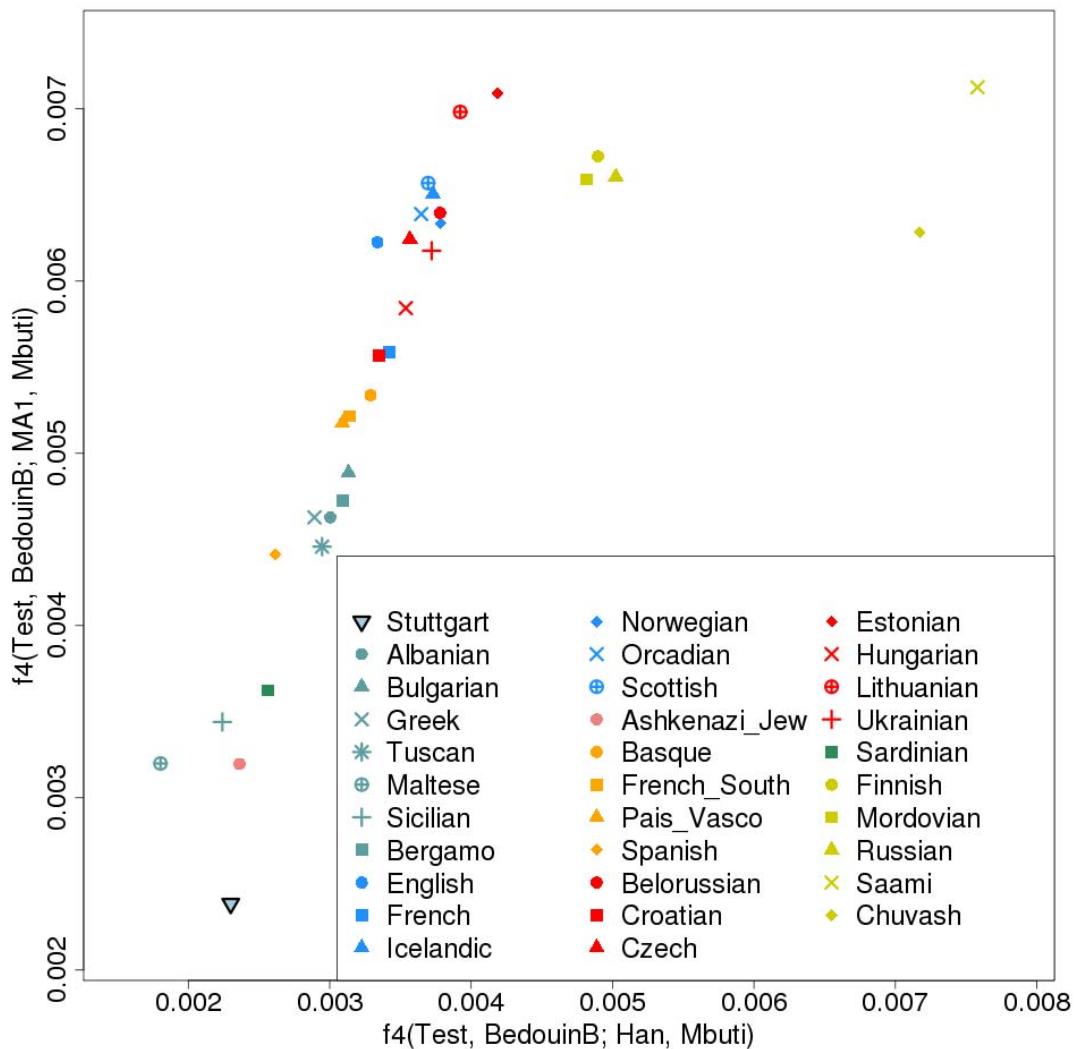
**Extended Data Figure 6: The differential relatedness of West Eurasians to Stuttgart (EEF), Loschbour (WHG), and MA1 (ANE) cannot be explained by two-way mixture.**

We plot on a West Eurasian map the statistic  $f_4(\text{Test}, \text{Chimp}; A_1, A_2)$ , where  $A_1$  and  $A_2$  are a pair of the three ancient samples representing the three ancestral populations of Europe. (A) In both Europe and the Near East/Caucasus, populations from the south have more relatedness to Stuttgart than those from the north where ANE influence is also important. (B) Northern European populations share more alleles with Loschbour than with Stuttgart, as they have additional WHG ancestry than that already present in EEF. (C) We observe a striking contrast between Europe west of the Caucasus and the Near East in degree of relatedness to WHG. In Europe, there is a much higher degree of allele sharing with Loschbour than with MA1, which we ascribe to the 60-80% WHG/(WHG+ANE) ratio in most Europeans that we report in SI12. In contrast the Near East has no appreciable WHG ancestry but some ANE ancestry, especially in the northern Caucasus. (Jewish populations are marked with a square in this figure to assist in interpretation as their ancestry is often anomalous for their geographic regions. We thank Pontus Skoglund for sharing plotting software that we modified to produce these visualizations.



**Extended Data Figure 7: Evidence for Siberian gene flow into far northeastern Europe.**

Some northeastern European populations (Chuvash, Finnish, Russian, Mordovian, Saami) share more alleles with Han Chinese than with other Europeans who are arrayed in a cline from Stuttgart to Lithuanians/Estonians in a plot of  $f_4(\text{Test}, \text{BedouinB}; \text{Han}, \text{Mbuti})$  against  $f_4(\text{Test}, \text{BedouinB}; \text{MA1}, \text{Mbuti})$ .





**Extended Data Table 2: Confirmation of key findings on Human Origins San and Yoruba panels.** We confirm key findings by showing selected  $f$ -statistics on a panel of 151,316 SNPs ascertained in a San individual and 115,577 SNPs ascertained in a Yoruba individual.

Statistic	Interpretation	San panel (n=151,316)		Yoruba panel (n=115,577)		All SNPs (n=594,924)	
		Value	Z	Value	Z	Value	Z
$f_4(\text{Stuttgart, Armenian; Loschbour, Chimp})$	Stuttgart has Mesolithic European admixture	0.0012	2.2	0.0024	3.4	0.0022	4.5
$f_4(\text{Lithuanian, Stuttgart; Loschbour, Chimp})$	Northern European populations have more WHG-related ancestry than Stuttgart	0.0035	6.1	0.0037	5.2	0.0045	9.0
$f_4(\text{French, Stuttgart; MA1, Chimp})$	European populations have more ANE-related ancestry than Stuttgart	0.0026	4.1	0.0028	3.8	0.0036	7.7
$f_4(\text{Lezgin, Stuttgart; MA1, Chimp})$	North Caucasian populations have more ANE-related ancestry than Stuttgart	0.0026	4.1	0.0028	3.5	0.0037	7.5
$f_4(\text{French, Chimp; MA1, Karitiana})$	ANE-related ancestry in Europeans is better represented by MA1 than by Karitiana	0.0021	3.1	0.0019	2.5	0.0021	4.6
$f_4(\text{Loschbour, Stuttgart; Onge, Chimp})$	Eastern non-Africans share more alleles with hunter-gatherers than with Stuttgart	0.0014	2.0	0.0028	3.3	0.0019	3.5
$f_4(\text{Karitiana, Chimp; MA1, Loschbour})$	Karitiana share more alleles with MA1 than with Loschbour	0.0038	4.0	0.0041	3.7	0.0047	7.1
$f_4(\text{Stuttgart, Chimp; Karitiana, Onge})$	West Eurasians share more alleles with Karitiana than other eastern non-Africans	0.0015	2.7	0.0016	2.2	0.0024	5.1

