

1 **Modeling of African population history using f -statistics can be highly biased** 2 **and is not addressed by previously suggested SNP ascertainment schemes**

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19

20 **Abstract**

21 f -statistics have emerged as a first line of analysis for making inferences about demographic
22 history from genome-wide data. These statistics can provide strong evidence for either
23 admixture or cladality, which can be robust to substantial rates of errors or missing data. f -
24 statistics are guaranteed to be unbiased under “SNP ascertainment” (analyzing non-
25 randomly chosen subsets of single nucleotide polymorphisms) only if it relies on a
26 population that is an outgroup for all groups analyzed. However, ascertainment on a true
27 outgroup that is not co-analyzed with other populations is often impractical and uncommon
28 in the literature. In this study focused on practical rather than theoretical aspects of SNP
29 ascertainment, we show that many non-outgroup ascertainment schemes lead to false
30 rejection of true demographic histories, as well as to failure to reject incorrect models. But
31 the bias introduced by common ascertainment schemes such as the 1240K panel is mostly limited to
32 situations when more than one sub-Saharan African and/or archaic human groups

33 (Neanderthals and Denisovans) or non-human outgroups are co-modelled, for example, f_4 -
34 statistics involving one non-African group, two African groups, and one archaic group.
35 Analyzing panels of SNPs polymorphic in archaic humans, which has been suggested as a
36 solution for the ascertainment problem, cannot fix all these problems since for some classes
37 of f -statistics it is not a clean outgroup ascertainment, and in other cases it demonstrates
38 relatively low power to reject incorrect demographic models since it provides a relatively
39 small number of variants common in anatomically modern humans. And due to the paucity
40 of high-coverage archaic genomes, archaic individuals used for ascertainment often act as
41 sole representatives of the respective groups in an analysis, and we show that this approach
42 is highly problematic. By carrying out large numbers of simulations of diverse demographic
43 histories, we find that bias in inferences based on f -statistics introduced by non-outgroup
44 ascertainment can be minimized if the derived allele frequency spectrum in the population
45 used for ascertainment approaches the spectrum that existed at the root of all groups being
46 co-analyzed. Ascertaining on sites with variants common in a diverse group of African
47 individuals provides a good approximation to such a set of SNPs, addressing the great
48 majority of biases and also retaining high statistical power for studying population history.
49 Such a “pan-African” ascertainment, although not completely problem-free, allows
50 unbiased exploration of demographic models for the widest set of archaic and modern
51 human populations, as compared to the other ascertainment schemes we explored.

52

53 **Introduction**

54 Archaeogenetics has achieved remarkable progress in the last decade (Skoglund and
55 Mathieson 2018, Stoneking et al. 2023), with genome-wide data for thousands of ancient
56 humans now being published each year. No region of the world is now inaccessible to
57 archaeogenetic research, although isolation of enough authentic DNA from skeletons
58 excavated in tropical and sub-tropical areas (Lipson et al. 2018) or from Pleistocene
59 individuals (Hajdinjak et al. 2021) remains a challenge. For generating usable archaeogenetic
60 data from Africa, targeted enrichment of human DNA on dedicated single nucleotide
61 polymorphism (SNP) capture panels is almost always necessary. A majority of ancient DNA
62 studies on African populations (Skoglund et al. 2017, van de Loosdrecht et al. 2018,
63 Prendergast et al. 2019, Lipson et al. 2020, Wang et al. 2020, Sirak et al. 2021, Lipson et al.

64 2022) relied on a SNP capture panel usually termed "1240K" (Fu et al. 2015, Mathieson et al.
65 2015), and some studies on Upper Paleolithic humans relied on a supplementary panel
66 ("1000K", comprising transversion polymorphisms found in two Yoruba individuals and
67 transversion polymorphisms in the Altai Neanderthal genome) or on its union with 1240K
68 (Fu et al. 2015, Hajdinjak et al. 2021). The 1240K panel was constructed of the following
69 elements: all SNPs on the Human Origins array (itself composed of 13 sub-panels, each
70 ascertained as heterozygous in a single high-coverage human genome, Patterson et al.
71 2012), all SNPs on the Illumina 650Y array, all SNPs on the Affymetrix 50k XBA array, and
72 smaller numbers of SNPs chosen for other purposes (Fu et al. 2015). The 1240K capture
73 panel is now used routinely for analyzing thousands of ancient humans across the world
74 (Skoglund and Mathieson 2018, Olalde and Posth 2020), and successor panels including the
75 full set of 1240K sites are now available (Rohland et al. 2022).

76 Bergström *et al.* (2020), relying on high-quality genomic data for present-day humans,
77 showed that f_4 -statistics including three sub-Saharan African groups and one non-African
78 group, or four sub-Saharan African (hereafter "African") groups can be biased when
79 computed on common SNP panels such as Illumina MEGA, the panel used by Li *et al.* (2008),
80 and the Affymetrix Human Origins array (Patterson et al. 2012). An influence of
81 ascertainment on common population genetic analyses (*ADMIXTURE*, F_{ST}) was also
82 demonstrated. However, the bias in f_4 -statistics including archaic humans and apes was not
83 explored.

84 Bergström *et al.* (2020) found that selecting approximately 1.3M SNPs polymorphic in
85 the group composed of high-coverage archaic human genomes (the Altai and Vindija
86 Neanderthals, the "Denisova 3" Denisovan) effectively eliminated the biases affecting f_4 -
87 statistics calculated on anatomically modern humans (AMH) and including 3 or 4 sub-
88 Saharan African groups. A similar approach (selecting ca. 814K transversion sites variable
89 between the Altai Neanderthal and Denisovan) was proposed by Skoglund *et al.* (2017). A
90 SNP capture reagent relying on this principle, the *myBaits Expert Human Affinities Kit*
91 "Ancestral 850K" module, became available in 2021 from Daicel Arbor Biosciences
92 (<https://arborbiosci.com/genomics/targeted-sequencing/mybaits/mybaits-expert/mybaits-expert-human-affinities/>). This module targets approximately 850K biallelic transversion
93 SNPs (autosomal and X-chromosomal) ascertained as polymorphic in the group composed
94 of high-coverage archaic human genomes: the Altai (Prüfer et al. 2014), Vindija (Prüfer et al.
95

96 2017), and Chagyrskaya Neanderthals (Mafessoni et al. 2020), as well as the “Denisova 3”
97 Denisovan genome (Meyer et al. 2012). This set of variable sites was shown to yield nearly
98 unbiased F_{ST} values for pairs composed of an African and a non-African group within the
99 Simons Genome Diversity Panel (SGDP) dataset (Mallick et al. 2016), in contrast to the
100 1240K panel (see a technical note on manufacturer’s website: [https://arborbiosci.com/wp-](https://arborbiosci.com/wp-content/uploads/2021/03/Skoglund_Ancestral_850K_Panel_Design.pdf)
101 [content/uploads/2021/03/Skoglund_Ancestral_850K_Panel_Design.pdf](https://arborbiosci.com/wp-content/uploads/2021/03/Skoglund_Ancestral_850K_Panel_Design.pdf)).

102 These recommendations are motivated by a theoretical property of f -statistics: if a SNP
103 is the result of a single historical mutation and there has not been natural selection, the
104 statistics are expected to be unbiased if SNPs are either unascertained or ascertained as
105 polymorphic in a population that is an outgroup for all populations being analyzed
106 (Patterson et al. 2012, Wang and Nielsen 2012), and the results in Bergström *et al.* (2020)
107 and in the technical note published on the Daicel Arbor Biosciences product page are
108 consistent with this theoretical property of outgroup ascertainment. The problematic case is
109 non-outgroup ascertainment, that is ascertainment on a population that is co-analyzed with
110 others. A series of papers explored non-outgroup ascertainment affecting measures of
111 population divergence on simulated data and real data for humans and domestic animals
112 (Nielsen and Signorovitch 2003, Nielsen 2004, Nielsen et al. 2004, Clark et al. 2005, Guillot
113 and Foll 2009, Albrechtsen et al. 2010, Wang and Nielsen 2012, Lachance and Tishkoff 2013,
114 McTavish and Hillis 2015, Malomane et al. 2018, Geibel et al. 2021). However, D - and f -
115 statistics which have more robustness than other allele frequency-based statistics in many
116 cases (Patterson et al. 2012), were not considered in those studies. Limited exploration of
117 non-outgroup ascertainment schemes was performed on simulated data in publications
118 introducing the D - and f -statistics, with the conclusion that biases are not noticeable in
119 practice (Durand et al. 2011, Patterson et al. 2012).

120 The existing recommendations for a bias-free SNP enrichment panel also rely on the
121 assumption that archaic humans are nearly perfect outgroups with respect to all AMH, and
122 the low-level archaic admixture in non-Africans (Green et al. 2010, Reich et al. 2010) does
123 not contribute major bias. However, evidence is accumulating that supports archaic
124 admixture in Africans (Chen et al. 2020, Hubisz et al. 2020), and, according to some models,
125 "super-archaic" ancestry (i.e., symmetrically related to Neanderthals, Denisovans, and AMH)
126 may reach 19% in the common ancestor of AMH (Durvasula and Sankararaman 2020).
127 Moreover, for outgroup ascertainment to be unbiased from the theoretical perspective, the

128 outgroup (or a closely related population) should not be then co-analyzed with other
129 populations (Patterson et al. 2012, Wang and Nielsen 2012), and the individuals used for
130 ascertainment should not be used as sole representatives of the respective groups.
131 However, given the paucity of high-coverage archaic genomes (Meyer et al. 2012, Prüfer et
132 al. 2014, 2017, Mafessoni et al. 2020) and the usefulness of archaic or African outgroups for
133 calculation of f_4 - and D -statistics and for testing of admixture models (Maier et al. 2022
134 preprint), these recommendations are often ignored in published f -statistic, *qpAdm*,
135 *qpGraph*, and *TreeMix* analyses (e.g., Skoglund et al. 2017, Lipson et al. 2020, 2022,
136 Hajdinjak et al. 2021, Kılınç et al. 2021, Yaka et al. 2021). For instance, archaic individuals are
137 co-analyzed with anatomically modern humans on archaic-ascertained SNPs (Skoglund et al.
138 2017, Hajdinjak et al. 2021) or a Yoruba group is co-analyzed with non-Africans on Yoruba-
139 ascertained SNPs (Kılınç et al. 2021, Yaka et al. 2021).

140 Since outgroup ascertainment that is “clean” from the theoretical point of view is rarely
141 used in practice, and since the statistical power of outgroup ascertainment to reject
142 incorrect models of population history was not investigated, it is reasonable to examine the
143 performance of archaic ascertainment and common SNP panels such as 1240K in situations
144 that are often encountered in practice. A technical development important for the work
145 reported here is the *ADMIXTOOLS 2* package (Maier et al. 2022 preprint), which extends the
146 functionality of the original *ADMIXTOOLS* package (Patterson et al. 2012), enabling
147 bootstrap resampling for most tools and a rapid algorithm for finding optima in complex
148 admixture graph topology spaces. The *ADMIXTOOLS 2* package also makes calculating
149 millions of f_4 -statistics and fitting tens of thousands of admixture graphs to data a routine
150 task. These developments, taken together, allow us to explore biased f -statistics more
151 systematically and provide more informed guidelines for future studies.

152

153 **Results**

154 1. Empirical analyses: exploration of the effect of ascertainment bias on real data

155 We assembled a set of diploid autosomal genotype calls for 352 individuals (Suppl. Table 1)
156 sequenced at high coverage (Mallick et al. 2016; Fan et al. 2019), including mostly present-
157 day individuals from the Simons Genome Diversity Project (SGDP), several high-coverage
158 ancient genomes with diploid genotype calls (Lazaridis et al. 2014, Fu et al. 2014), and three

159 archaic human genomes: the “Denisova 3” Denisovan (Meyer et al. 2012), Vindija (Prüfer et
160 al. 2017) and Altai Neanderthals (Prüfer et al. 2014). Relying on this "SGDP+archaic" dataset,
161 we explored a wide array of ascertainment schemes: 1) A/T and G/C SNPs (henceforth
162 “AT/GC”) that are, unlike the other mutation classes, unaffected by biased gene conversion
163 (Pouyet et al. 2018), and are also unaffected by deamination ancient DNA damage; 2)
164 random thinning of the unascertained or "AT/GC" sets down to the size approximately equal
165 to that of the 1240K SNP panel if missing data are not allowed on a given population set; 3)
166 the 1240K panel (Fu et al. 2015); 4) the 1000K panel composed of 997,780 SNPs comprising
167 all transversion polymorphisms found in two African (Yoruba) individuals sequenced to high
168 coverage and transversion polymorphisms found in the Altai Neanderthal genome (Fu et al.
169 2015); 5) the union of the 1000K and 1240K panels termed 2200K (Hajdinjak et al. 2021); 6)
170 various components of the 1240K panel (the sites included in the Illumina 650Y and/or
171 Human Origins SNP arrays, sites included exclusively in one of them, and the remaining
172 sites); 7) the largest Human Origins sub-panels – panel 4 ascertained as sites heterozygous
173 in a single San individual, panel 5 ascertained as sites heterozygous in a single Yoruba
174 individual, their union (panels 4+5), and panel 13 including sites where a randomly chosen
175 San allele is derived relative to the Denisovan (Patterson et al. 2012); 8) all sites
176 polymorphic in a group uniting three high-coverage archaic genomes: the “Denisova 3”
177 Denisovan, the Altai and Vindija Neanderthals (this ascertainment scheme is similar to those
178 proposed by Bergström *et al.* 2020 and in the technical note published on the Daicel Arbor
179 Biosciences product page); 9) transversion sites variable in the group comprising these three
180 high-coverage archaic genomes; 10) restricting to SNPs that have high minor allele
181 frequency (MAF > 5%) in the whole "SGDP+archaic" dataset, i.e. high global MAF; 11)
182 restricting to SNPs having high global MAF combined with taking A/T and G/C SNPs only; 12)
183 restricting to SNPs that have > 5% MAF in a selected African or non-African continental
184 meta-population, irrespective of their frequency in the other meta-populations (there are
185 nine such meta-populations in our dataset, and thus nine different ascertainments, see
186 Suppl. Table 1); 13) restricting to SNPs that have > 5% MAF in a selected continental meta-
187 population, A/T and G/C SNPs only. For a list of SGDP-derived SNP sets explored in this study
188 and their sizes in terms of groups, individuals, and SNPs see Suppl. Table 2.

189 To investigate the influence of ascertainment on the ranking of admixture graph models
190 according to their fits to data, we analyzed real data, considering sets of five populations

191 and generated all possible admixture graph topologies with two admixture events (32,745
192 distinct topologies with no fixed outgroup; we considered graphs of this complexity as it was
193 unfeasible to work with exhaustive collections of more complex graphs). First, we tested
194 three combinations of groups (Suppl. Fig. 1). Admixture graph residuals on all sites, on a
195 random subset of them approximately equal to the size of the 1240K set, and on AT/GC
196 sites, are tightly correlated (R for a linear model ~ 1). Residuals of graph models including
197 non-Africans only are also highly correlated on all sites and 1240K sites ($R = 0.95-0.99$,
198 Suppl. Fig. 1). In contrast, the worst f_4 -statistic residuals (WR) for graphs including one
199 archaic human, three African groups, and one African group with ca. 60% of non-African
200 ancestry (Fan et al. 2019) are poorly correlated on all sites and 1240K sites ($R = 0.31-0.35$).
201 Thus, admixture graph fit rankings are severely affected by the 1240K ascertainment if
202 certain population combinations are involved. We considered the possibility that this case
203 of poor correlation was driven by admixture graph topologies that were obviously
204 inconsistent with the data – that is, topologies could be shown to be inconsistent with the
205 data based on gold standard SNP sets without ascertainment bias. However, the lack of
206 strong correlation for some combinations of populations is not just driven by graphs with
207 poor fits to the data. For example, WRs of admixture graphs that are well-fitting the data
208 ($WR < 2.5$ SE) on a random subsample of 840,000 sites have worst residuals ranging from
209 nearly 0 SE to about 10 SE (Suppl. Fig. 1) on ca. 845,000 sites included in the 1240K panel.
210 Rejecting a model that fits the data on unascertained data runs the risk of rejecting the true
211 model, as we show on simulated data in the next section. The converse problem also
212 applies: some admixture graphs are well-fitting ($WR < 2.5$ SE) on the 1240K sites but fit a
213 random sample of sites poorly ($WR > 5$ SE, Suppl. Fig. 1).

214 Next, we explored the same exhaustive set of admixture graph topologies including five
215 groups and two admixture events on the wider collection of ascertainment listed above
216 and on a wider collection of populations. Twelve combinations of five groups including up to
217 two archaic humans, up to five African groups, and up to five non-African groups were
218 tested. In Suppl. Fig. 2 we compare various ways of looking on the effects of ascertainment,
219 using a population quintuplet "Denisovan, Khomani San, Mbuti, Dinka, Mursi" as an
220 example. In Table 1 we focus on the fraction of topologies that are rejected under
221 ascertainment ($WR > 3$ SE) but accepted on all sites ($WR < 3$ SE) as a metric appropriate for
222 quantifying the most serious effects of ascertainment bias, namely the probability of

223 rejecting the true model. In the supplementary materials, we also show alternative
224 measures: a metric reflecting the statistical power of ascertainment, namely the fraction of
225 topologies that are accepted under a given ascertainment ($WR < 3 SE$) but rejected on all
226 sites ($WR > 3 SE$) (Suppl. Table 3), and R^2 of a linear trend for admixture graph WR (Suppl.
227 Figs. 3 and 4, Suppl. Table 4) or log-likelihood (LL) scores (Suppl. Figs. 3 and 4, Suppl. Table
228 5).

229 Although we recognize that there can be no strict rule for classifying ascertainment into
230 biased and unbiased ones since they form a continuum, for high-throughput analysis a
231 classifier is useful. Moreover, fits of admixture graphs vary even in the absence of
232 ascertainment bias, due to random site sampling effects (Fig. 1, Suppl. Fig. 2), as was shown
233 in previous work (Maier et al. 2022 preprint). In this study, we considered a SNP set biased if
234 a metric (such as the fraction of topologies rejected under ascertainment but accepted on
235 all sites) was above (or below, as appropriate) the 2.5th percentile of this metric's
236 distribution across 200 sets of randomly sampled SNPs equal to the size of the 1240K set for
237 a given population combination.

238 Inspecting the key metric of ascertainment performance (the fraction of topologies that
239 are rejected under ascertainment but accepted on all sites), we found only three site
240 sampling schemes that were classified as unbiased for all the population quintuplets tested:
241 the A/T and G/C mutation classes, Human Origins panel 4, and the union of Human Origins
242 panels 4 and 5 (Table 1). However, due to the low number of sites in the latter two panels,
243 the union of Human Origins panels 4 and 5, and especially panel 4, lack power to reject
244 admixture graph models as compared to the 1240K panel and to the A/T and G/C mutation
245 classes, as we show in Suppl. Table 3. Thus, the only ascertainment scheme that is problem-
246 free according to both metrics is a random one: taking the A/T and G/C mutation classes.

247 Among the population quintuplets tested, "Altai Neanderthal, Ju|'hoan North, Biaka,
248 Yoruba, Agaw" (Fig. 1, Suppl. Fig. 3a) and "Altai Neanderthal, Ju|'hoan North, Luhya,
249 Palestinian, Spanish" (Suppl. Fig. 3b) are most susceptible to ascertainment bias (Table 1). A
250 very similar quintuplet "Altai Neanderthal, ancient South African hunter-gatherers, Biaka,
251 Yoruba, Agaw" is encountered within more complex admixture graph models that occupy a
252 central place in Lipson *et al.* (2020, 2022) based on 1240K data (see an investigation of bias
253 affecting the admixture graphs from these studies in Suppl. Text 1 and Suppl. Figs. 5 and 6).
254 As explored below on real and simulated data, a class of f_4 -statistics that are strongly

255 affected by non-random ascertainment underlies admixture graphs for both problematic
256 population quintuplets: $f_4(\text{African X, archaic; African Y, non-African})$. On the other hand,
257 population sets including no archaic human were virtually unbiased (Table 1), but some
258 ascertainment schemes showed limited power to reject admixture graph models in these
259 cases (Suppl. Table 3).

260 Archaic ascertainment has been suggested in the literature (Skoglund et al. 2017,
261 Bergström et al. 2020) as a way to reduce ascertainment bias, however this approach is
262 guaranteed to work only if the outgroup or a related group is not included itself in
263 admixture graphs or f -statistics, and if individuals used for ascertainment are not sole
264 representatives of the respective groups in an analysis. Indeed, our practical-oriented
265 analysis showed that archaic ascertainment is biased in the case of the most problematic
266 population quintuplet "Altai Neanderthal, Ju|'hoan North, Biaka, Yoruba, Agaw" (Table 1);
267 in fact, the archaic ascertainment approach is by far the most biased scheme for population
268 sets including both Neanderthal and Denisovan individuals (Table 1, see also results on
269 simulated data below), and in our analysis it also emerged as the scheme with the lowest
270 statistical power to reject admixture graph models (Suppl. Table 3).

271 If we combine both key bias metrics (the fraction of topologies rejected under
272 ascertainment but accepted on all sites, and the fraction of topologies accepted under
273 ascertainment but rejected on all sites), the 1240K and archaic ascertainment are out-
274 performed by many ascertainment schemes, and most notably by the following: 1) the
275 union of Human Origins panels 4 and 5; 2) the 2200K panel, which combines various kinds of
276 ascertainment such as the 1240K panel, ascertainment on two Yoruba individuals, and on
277 the Altai Neanderthal (Fu et al. 2015); and 3) restricting to variants that are common in the
278 African meta-population in SGDP (Suppl. Table 1), optionally followed by removal of all
279 mutation classes except for A/T and G/C (Table 1). R^2 of a linear trend for admixture graph
280 WR is a metric that in some cases is informative in a way that the fractions of
281 rejected/accepted topologies are not. As illustrated in Fig. 1, R^2 may differ substantially
282 across ascertainment schemes while the fractions of topologies rejected under
283 ascertainment but accepted on all sites or *vice versa* stay nearly constant across most
284 ascertainment schemes (Table 1, Suppl. Table 3). Considering R^2 for admixture graph WR,
285 restricting to variants that are common in a diverse set of African groups (we term this
286 ascertainment scheme "pan-African" or "African MAF" for convenience) emerges as the

287 least biased form of ascertainment (Suppl. Table 4). We note that conclusions of this sort
288 are not quantitative since our collection of 12 population quintuplets, although diverse, is
289 just a small sample from the vast set of all possible population combinations. However,
290 exploring all possible combinations is infeasible, and we consider our approach to be useful
291 as a practical guide for assessing the performance of ascertainment schemes when
292 admixture graphs including archaic humans, Africans, and non-Africans are fitted to genetic
293 data.

294

295 2. Simulation studies confirm the qualitative patterns from exploration of empirical data

296 A major limitation of our empirical analyses of ascertainment bias is that fitting a model
297 with two admixture events is almost certainly inadequate for the histories relating various
298 sets of populations being analyzed. Thus, it is almost certain that all fitted models will be
299 wrong. When we fit wrong models, we have no guarantee that the (incorrect) admixture
300 graph fit to the data will give the same signal of deviation for different SNP ascertainments.
301 Different SNP ascertainments including random ascertainments will simply be sensitive to
302 different aspects of the deviations between the wrong model and the true history. Thus,
303 while the poor correlation between model fits on all sites and under different SNP
304 ascertainment schemes for combinations of archaic humans, sub-Saharan Africans, and
305 non-Africans is a potential signal of bias in analyses, it is valuable to analyze data where the
306 truth is known, as is the case for simulations, to provide clear evidence that typical
307 ascertainment schemes can cause false-positive inferences about history.

308 Using *msprime v.1.1.1* (Baumdicker et al. 2022), we simulated genetic data (a diploid
309 genome composed of three 100 Mb chromosomes with recombination) that reproduce the
310 F_{ST} values (Suppl. Fig. 7a) observed when comparing AMH groups, AMH and archaic
311 humans, and AMH and chimpanzee (Fischer et al. 2006). Ten independent simulations were
312 performed under the same parameters and under a topology (Fig. 2a) that in most
313 important aspects conforms to commonly discussed models of the relationships between
314 anatomically modern and archaic humans (Prüfer et al. 2014, Durvasula and Sankararaman
315 2020). We either simulated or omitted the Neanderthal gene flow to the ancestors of non-
316 Africans (via an unsampled proxy group).

317 We tested several non-outgroup ascertainment schemes: 1) ascertainment on
318 heterozygous sites in a randomly selected individual from the “African 2” group (Fig. 2a, this
319 ascertainment follows the scheme used for generating some of the 12 panels of sites
320 comprising the Human Origins SNP array (Patterson et al. 2012)); 2) ascertainment on
321 heterozygous sites in four randomly selected individuals, one per each “AMH” group (we
322 consider the resulting SNP set to be qualitatively similar to the whole Human Origins SNP
323 set); 3) archaic ascertainment (sites polymorphic in a group composed of one “Denisovan”
324 individual and one individual per each “Neanderthal” group; the same individuals were
325 subsequently used for calculating f -statistics); 4) “African MAF ascertainment”, that is
326 restricting to sites with MAF > 5% in the union of two “African” groups; 5) similar MAF-
327 based ascertainment on two “non-African” groups or 6) on all four “AMH” groups.

328 First, we fitted the correct admixture graph as often practiced in the literature (e.g.,
329 Lipson et al. 2020, 2022): including the outgroup, one “archaic” individual, and all “AMH”
330 groups. Human Origins-like ascertainment (one panel) always leads to rejection of the
331 correct model, both in the absence and in the presence of the Neanderthal gene flow to
332 non-Africans, with WR ranging from 3.4 to 8.8 SE (Fig. 2b). Another form of Human Origins-
333 like ascertainment (four panels) is less problematic but led to rejection of the correct model
334 (WR > 3 SE) in 9 of 30 cases (in the presence of the Neanderthal gene flow to non-Africans),
335 with WR up to 4.6 SE. Only the archaic and African MAF non-outgroup ascertainments (in
336 the presence of the Neanderthal gene flow to non-Africans) did not lead to rejection of
337 these simplified graph topologies, known to be correct since we simulated them. However,
338 when the full simulated model (with the Neanderthal gene flow to non-Africans) including
339 the outgroup and three “archaic” lineages is fitted to the data, all non-outgroup
340 ascertainment schemes become problematic, except for African MAF ascertainment (Fig.
341 2b).

342 We also investigated effects of ascertainment on model ranking using the same
343 approach as that applied to real data. All possible graph topologies with two admixture
344 events (32,745) were fitted to population quintuplets of the following composition: “d or n1
345 or n2”, “a1”, “a2”, “na1”, “na2”. The fractions of topologies rejected/accepted under
346 ascertainment but accepted/rejected on all sites (and the bias classifier) were then used to
347 reveal simulation iterations and ascertained schemes that demonstrated biased model fits
348 (Suppl. Table 6). When no Neanderthal/non-African gene flow was simulated, only the non-

349 African MAF ascertainment emerged as problematic (at least half of simulation iterations for
350 at least one population quintuplet were classified as affected by bias) according to the
351 fraction of topologies rejected under ascertainment but accepted on all sites (Suppl. Table
352 6). When the Neanderthal to non-African gene flow was simulated, all ascertainment
353 schemes, except for the Human Origins-like ascertainment (four panels), emerged as
354 problematic according to the same metric (Suppl. Table 6). Summarizing these results on
355 model ranking and on fits of the true model, we note that the Human Origins-like
356 ascertainment (four panels) is relatively problem-free, unlike archaic ascertainment, MAF-
357 based ascertainments, and Human Origins-like ascertainment (one panel), but it still led to
358 rejection of the true model more often than on all sites or on random site subsamples (Fig.
359 2b).

360 Next, we explored non-outgroup ascertainment schemes that are similar to those
361 presented in Fig. 2b but are based on randomly chosen groups (see Methods for details) and
362 were applied to SNP sets resulting from simulated genetic histories in the form of random
363 admixture graphs. Graphs of four complexity classes including 9 or 10 populations and 4 or
364 5 admixture events were simulated using *msprime v.1.1.1*. Only simulations where pairwise
365 F_{ST} for groups were in the range characteristic for anatomically modern and archaic humans
366 were selected for further analysis, resulting in 20 random topologies per graph complexity
367 class, each including an outgroup (see examples of the simulated histories and F_{ST}
368 distributions in Suppl. Fig. 8). Fits of the true admixture graph (WR) including an outgroup
369 were compared on all sites and on ascertained SNP sets for each topology and
370 ascertainment iteration (Fig. 2c). We note that our simulation setup generated groups
371 sampled at different dates in the past (from 0 to ca. 40,000 generations) or, in other words,
372 groups that have experienced widely different levels of genetic drift with respect to the root
373 (Fig. 2d).

374 As illustrated by distributions of true admixture graph WRs in Fig. 2c, ‘blindly’
375 ascertaining on individuals or sets of groups randomly sampled across the graph almost
376 guarantees rejecting the true historical model by a wide margin. Ascertainment on sites
377 polymorphic in randomly composed sets of three individuals (one individual per group) and
378 restricting to variants common (MAF > 5%) in randomly composed sets of four populations
379 are two forms of ascertainment that are especially problematic (Fig. 2c). Human Origins-like
380 ascertainments (one or four panels) often yield acceptable fits of the simulated graph (WR <

381 3 SE), although median WR of the true graphs equals 4.6 SE for these ascertainment
382 schemes across all graph topologies and all (non-root and non-outgroup) populations used
383 for ascertainment (Fig. 2c).

384 An illuminating result is that F_{ST} between the population used for Human Origins-like
385 non-outgroup ascertainment and the root influences WR of the true graph: all
386 ascertainment with the corresponding $F_{ST} < 0.12$ produce relatively unbiased fits of true
387 graphs ($WR < 4$ SE, see Fig. 2d). In other words, ascertainment on heterozygous sites in a
388 single individual taken from a population that is not an outgroup and is co-analyzed with
389 other populations, but is genetically close to the root of the simulation, is relatively
390 unbiased, unlike ascertainment on a single individual from a more drifted “present-day”
391 population. We directly illustrate this effect by comparing results on outgroups co-analyzed
392 with other populations that are more or less drifted with respect to the root (with effective
393 population sizes differing by two orders of magnitude) (Fig. 2c,d). Co-analyzing the
394 individual used for ascertainment with other groups does not produce biased results if that
395 individual is a part of a wider population of 10 individuals. However, if that individual is the
396 only representative of its group for model fitting, WRs are inflated drastically (Fig. 2c). We
397 also illustrate the difference between true outgroup ascertainment, when an outgroup is
398 not co-modelled with the other groups, and ascertainment on an outgroup that is included
399 in the fitted model (Fig. 2f), which the kind of ascertainment shown in Fig. 2c and
400 elsewhere. The former form of ascertainment is expected to be unbiased even for a highly
401 drifted outgroup (Fig. 2f), while the latter is not (Patterson et al. 2012, Wang and Nielsen
402 2012).

403 Genetic distance from the root is a noisy proxy for the similarity of derived allele
404 frequency (DAF) spectra of the root population and the population used for ascertainment.
405 In Fig. 2e we show DAF spectra across all simulated populations used for Human-Origins-like
406 non-outgroup ascertainment, but only for variants that are polymorphic in the respective
407 root population sample of 10 diploid individuals. These results demonstrate that for the
408 correct admixture graph to fit ascertained data well ($WR < 4$ SE, Fig. 2e), non-outgroup
409 ascertainment should be based on a population where the derived allele frequency
410 spectrum of sites that were polymorphic at the root is preserved relatively well (see a more
411 extensive version of this plot in Suppl. Fig. 9). We note that some ascertainment may be
412 unbiased with respect to the true graph but may have low power due to the paucity of sites

413 with high MAF in “present-day” populations. Indeed, ascertainment on the root itself or on
414 groups genetically close to the root (such as outgroups with a large effective size) are
415 unbiased (Fig. 2c,d), but on average demonstrated lower power to reject incorrect
416 admixture graph models as compared to single-panel Human Origins-like ascertainment on
417 more drifted groups (Suppl. Fig. 10).

418 These results on randomized ascertainment schemes (not to be confused with random
419 site sampling) and simulated histories in the form of random admixture graphs show that
420 ascertainment on groups that are highly drifted with respect to the root of the groups being
421 co-analyzed is problematic. Thus, if proper outgroup ascertainment is impractical (if an
422 outgroup shares few polymorphisms with the other populations analyzed, or if an outgroup
423 is needed for constraining the analysis), unascertained or randomly sampled sets of sites
424 should be treated as a gold standard for admixture graph inference. The 1240K
425 ascertainment is much more complex (Fu et al. 2015, Mathieson et al. 2015) than the
426 ascertainment schemes explored on simulated data, but its effects are possibly
427 intermediate between the effects of a MAF-based ascertainment (since all common SNP
428 panels are more or less depleted for rare variants) and ascertainment on heterozygous sites
429 in single individuals from several groups (since approximately half of the 1240K sites are
430 derived from the Human Origins SNP array, Fu et al. 2015). Thus, we expect an accurate
431 admixture graph including at least one archaic human, at least two African groups, and at
432 least one non-African group (Fig. 2a) to fit the data poorly under the 1240K ascertainment.

433 Finally, we checked if non-outgroup ascertainment could bias the simplest cladality tests
434 in the absence of gene flow. A tree of four groups conforming to the f_4 -statistic (A, B; C, O)
435 was simulated using *msprime v.1.1.1*, with a tree depth of 4,000 or 40,000 generations (Fig.
436 3a). All the groups had a uniform effective population size of 100,000 diploid individuals,
437 except for a 10x to 10,000x size reduction immediately after the A-B divergence (1,999 or
438 9,995 generations in the past). While the dramatic drop in the effective population size of
439 group A yields a complex shape of the derived allele frequency spectrum in {A, B} (Martin
440 and Amos 2021), two of three ascertainment schemes explored here (Human Origins-like
441 ascertainment on one group and MAF-based ascertainment, but not removal of the derived
442 end of the allele frequency spectrum; see Methods) increase the noise in the f_4 -statistic (A,
443 B; C, O), but do not shift the statistic away from its expectation at 0 (Suppl. Fig. 11). These
444 results confirm an observation by Patterson et al. (2012) that in the case of perfect trees

445 SNP non-outgroup ascertainment does not lead to false rejection of cladality. However, as
446 demonstrated in Fig. 2, non-outgroup ascertainment is generally problematic in the case of
447 complex demographic histories with multiple admixture events.

448

449 3. An overview of f_4 -statistic biases caused by non-outgroup ascertainment

450 We explored various classes of f_4 -statistics exhaustively to obtain a "bird's-eye view" on
451 ascertainment biases that was previously difficult to do due to technical challenges in
452 calculating millions of f -statistics (Bergström *et al.* 2020). Another motivation for this
453 analysis was the fact that it is unfeasible to explore fits of large collections of admixture
454 graphs on thousands of population sets, ascertainment schemes and random site
455 subsamples. However, if an exhaustively sampled class of f -statistics is demonstrated to be
456 unbiased, all admixture graph fits based on those statistics are expected to be unbiased too.

457 We used the standard deviation of residuals from a linear trend for f_4 -statistic Z-scores
458 on all sites and under ascertainment (termed "residual SE" for brevity and expressed in the
459 same units as Z-scores) as a single statistic for summarizing results, and we note that it
460 reflects both bias introduced by ascertainment and variance generated by random site
461 sampling. In Suppl. Table 7 and Suppl. Figs. 12 and 13 we show residual SE values for a
462 collection of 27 exhaustively sampled f_4 -statistic classes and for the large collection of
463 ascertainment schemes that was used for exploring effects of ascertainment on admixture
464 graph fits in section 1. The f_4 -statistic classes explored can be described concisely as
465 African(all SGDP populations) $_x$;archaic $_y$;chimpanzee $_1$, African(unadmixed with West
466 Eurasians) $_x$;archaic $_y$;Mediterranean/Middle Eastern (abbreviated as Med/ME) $_z$,
467 African(unadmixed with West Eurasians) $_x$;East Asian $_y$ ($y>0$), American $_x$;European $_y$;Papuan $_z$.
468 Here, x , y , and z stand for the number of groups in the population quadruplet; thus,
469 "African $_3$;East Asian $_1$ " would mean three Africans and one East Asian. All possible distinct f_4 -
470 statistics composed of those "ingredients" were considered.

471 The effect of ascertainment schemes varies dramatically across the classes of f_4 -
472 statistics, but ascertainment schemes based on one or two African individuals (Human
473 Origins sub-panels 4, 5, 13, 4 and 5 combined), on the three archaic individuals (either all
474 sites or transversions only), and components of the 1240K panel such as Illumina650Y
475 emerged as the worst-performing when results across all the f_4 -statistic classes were
476 considered (Suppl. Table 7, Suppl. Fig. 12). Ascertainment schemes based on a global MAF

477 threshold or on a MAF threshold in a single non-African continental meta-population, and
478 the 1000K and 2200K panels are similar in their effects to the 1240K ascertainment (Suppl.
479 Table 7, Suppl. Fig. 12). We recognize that there is a continuum between unbiased and
480 biased ascertainment schemes, and that for nearly all schemes and f_4 -statistic classes a
481 majority of statistics remain unaffected by ascertainment, but for describing our results in a
482 concise way and for partially factoring out effects of SNP panel size, we applied the criterion
483 similar to that employed above for admixture graph fits: residual SE for an f_4 -statistic class is
484 higher than the 97.5th percentile across 200 randomly thinned datasets matching the 1240K
485 panel in size. According to this criterion, the 1240K ascertainment is problematic in the case
486 of the following nine f_4 -statistic classes (Suppl. Table 7): 1) African₄, 2) African₃;Med/ME₁, 3)
487 African₃;East Asian₁, 4) African₃;archaic₁, 5) African₃;chimpanzee₁, 6)
488 African₂;archaic₁;Med/ME₁, 7) African₂;archaic₁;chimpanzee₁, 8) archaic₃;Med/ME₁, 9)
489 archaic₃;African₁, and unproblematic for the remaining 18 classes exhaustively explored in
490 this analysis. Unlike all the other classes explored here (Suppl. Table 7, Suppl. Fig. 12), the
491 class of statistics African₂;archaic₁;Med/ME₁, specifically statistics of the form f_4 (African X,
492 archaic; African Y, non-African), is substantially biased under all non-random types of
493 ascertainment (Fig. 4a). The classes African₃;X are problematic under all ascertainment
494 schemes except for the pan-African ascertainment (Suppl. Table 7, see an example in Fig.
495 4b), and the class African₄ is problematic under all ascertainment schemes except for the
496 1000K, 2200K, and pan-African ascertainment (Suppl. Table 7). Scatterplots underlying these
497 residual SE estimates are also shown in Fig. 5 (for some of the most problematic classes
498 highlighted above) and in Suppl. Figs. 14-16 (for all classes). Importantly, the classes of
499 statistics most affected by ascertainment (African₂;archaic₁;Med/ME₁,
500 African₂;archaic₁;chimpanzee₁, African₃;X, and African₄) are often relevant for fitting
501 admixture graph models of African population history (see Suppl. Text 1). However, for most
502 classes that were classified as problematic, except for African₂;archaic₁;Med/ME₁,
503 African₂;archaic₁;chimpanzee₁, and African₃;X, residuals remain below 1 SE for a great
504 majority of f_4 -statistics (Suppl. Table 7 and Suppl. Fig. 12), and thus these statistics are
505 probably not problematic in practice.

506 Results very similar to those presented above were obtained with a different metric: R^2
507 of a linear model for f_4 -statistics themselves (Suppl. Table 8), instead of residual SE of a
508 linear model for f_4 -statistic Z-scores (Suppl. Table 7). For additional details on f_4 -statistic

509 classes see Suppl. Text 2 (and Suppl. Figs. 13-16), and for a dissection of effects of
510 ascertainment on few selected f_4 -statistics see Suppl. Text 3 (and Suppl. Tables 9-12).

511 In contrast, statistics including non-Africans only, or one or two African groups and non-
512 Africans (see an example in Figs. 4c and 5), are unproblematic under the 1240K, 2200K, pan-
513 African and other MAF-based ascertainment (but demonstrate increased variance due to
514 paucity of sites with high MAF under some other ascertainment types such as Human
515 Origins panels 4&5 and archaic ascertainment, Suppl. Table 7).

516 Pan-African ascertainment (restricting to variants common across 68 African individuals
517 unadmixed with West Eurasians, or across 94 African individuals, Suppl. Table 1), emerged
518 as the best-performing non-outgroup ascertainment scheme. Unlike the other
519 ascertainment schemes explored in this study, this type of ascertainment demonstrates a
520 bias only in the case of the (African X, archaic; African Y, non-African) class of f_4 -statistics
521 (when only statistics with $|Z| < 15$ SE on all sites were considered, Suppl. Table 7, Suppl. Fig.
522 12). Another class of f_4 -statistics is biased under this ascertainment scheme when all
523 statistics are considered: $f_4(\text{non-African X, archaic; African, non-African Y})$ (Suppl. Fig. 12),
524 and pan-African ascertainment is unbiased in the case of the other 25 classes of f_4 -statistics
525 explored in this study (Suppl. Table 7, Suppl. Fig. 12), which also translates into downstream
526 analyses such as fits of admixture graph models (Fig. 1, Table 1, Suppl. Fig. 3, Suppl. Tables
527 3-5).

528

529 **Discussion**

530 f -statistics (Patterson et al. 2012) form a foundation for a range of methods (*qpWave*,
531 *qpAdm*, *qpGraph*) that are used widely for studying population genetic history of humans
532 and other species (see, for instance, Bergström et al. 2020b, Librado et al. 2021). Here, we
533 focused on f_4 -statistics, which are used as standalone tests for cladality (Reich et al. 2009,
534 Patterson et al. 2012) and underlie the *qpAdm* method for fitting admixture models (Haak et
535 al. 2015, Harney et al. 2021). The other f -statistics (f_2 and f_3) can be defined as special cases
536 of f_4 -statistics [$f_2(A, B) = f_4(A, B; A, B)$ and $f_3(A; B, C) = f_4(A, B; A, C)$], and are subject to the
537 same kinds of biases. The existence of bias in the case of non-outgroup ascertainment was
538 recognized in a publication introducing a suite of methods relying on f -statistics (Patterson
539 et al. 2012), but its effects on large collections of f_4 -statistics or on fits of diverse admixture

540 graph models were not explored in that study and in subsequent studies. Since usage of
541 archaic or African outgroups is often unavoidable for calculation of f_4 - and D -statistics and
542 for construction of admixture graph or *qpAdm* models (e.g., Skolgund et al. 2017, Lipson et
543 al. 2020, 2022, Hajdinjak et al. 2021, Kılınc et al. 2021, Yaka et al. 2021), unbiased
544 ascertainment on an outgroup that is not co-analyzed with other populations (as illustrated
545 on simulated data in Fig. 2f) is uncommon in practice. And frequently used SNP panels such
546 as 1240K were built using very complex forms of non-outgroup ascertainment. Therefore, in
547 this study we focused on practical rather than theoretical aspects of the ascertainment bias
548 problem and considered forms of non-outgroup ascertainment that are common in the
549 literature on archaeogenetics of humans, including ascertainment on a phylogenetic
550 outgroup co-analyzed with other populations.

551 The present analysis showed that f_4 -statistics of specific types are affected by
552 ascertainment bias. The most striking example we found is a class of statistics $f_4(\text{African X,}$
553 $\text{archaic; African Y, non-African})$. All statistics in this class are strongly biased in the same
554 direction under the 1240K ascertainment (Suppl. Fig. 15) and under all other non-random
555 ascertainment schemes explored on real (Suppl. Table 7, Suppl. Fig. 12d) and simulated data
556 (Suppl. Fig. 7b). In contrast, all f_4 -statistic classes we explored including one or two African
557 groups and non-Africans, or non-Africans only, turned out to be unbiased under the 1240K
558 ascertainment (Suppl. Table 7, Suppl. Fig. 12). Thus, numerous studies relying on fitting
559 *qpAdm* and/or admixture graph models including one African group and various non-
560 Africans are probably minimally affected by ascertainment bias, as we also demonstrated on
561 exhaustive collections of simple admixture graphs for few population quintuplets (Fig. 1,
562 Table 1, Suppl. Fig. 1, Suppl. Tables 3-5). When these classes of methods are applied to
563 African population history, the situation is different, however. As we demonstrated, the
564 1240K panel emerges as biased when fits of simple admixture graphs including five African
565 groups or one or two archaic and three or four African groups are considered (Fig. 1, Table
566 1, Suppl. Fig. 1, Suppl. Tables 3-5). We also demonstrated that the 1240K ascertainment
567 affects fits of more complex admixture graphs including in all cases chimpanzee and Altai
568 Neanderthal, and also four or six African groups and one or two groups with substantial
569 non-African ancestry (Supp. Text 1, Suppl. Figs. 5 and 6). We expect fits of many other
570 admixture graphs for Africans beyond those tested in this study to be affected by the 1240K
571 ascertainment since the f_4 -statistic classes $\text{African}_2; \text{archaic}_1; \text{non-African}_1$,

572 African₂;archaic₁;chimpanzee₁, and African₃;X are substantially biased under this
573 ascertainment (Suppl. Table 7). These effects were reproduced on simulated data when
574 accurate graphs including “chimpanzee”, one “archaic” lineage, and several “African” and
575 “non-African” lineages were fitted to the data ascertained in various ways (Fig. 2b).

576 In line with theoretical expectations, f_4 -statistics including AMH groups only are largely
577 unbiased under archaic ascertainment (Skoglund et al. 2017, Bergström et al. 2020,
578 technical note published on the Daicel Arbor Biosciences product page). However, as
579 compared to other SNP panels of similar size, archaic ascertainment increases variance in
580 nearly all f_4 -statistic classes of the types non-African₃;X and non-African₄ (Suppl. Table 7,
581 Suppl. Figs. 12-14). Increased variance in these cases can be explained by the low
582 information content of an archaically ascertained panel: unlike the other non-random
583 ascertainment schemes we tested, archaic ascertainment preserves most sites with nearly
584 fixed ancestral variants and leads to just a moderate enrichment for common variants (DAF
585 between 5% and 95%), especially if DAF is based on non-Africans (Suppl. Text 3, Suppl. Fig.
586 7d, Suppl. Table 10). Thus, the archaically ascertained panel includes a relatively small
587 number of variants that are common in AMH and especially in non-Africans (Suppl. Table
588 10), and that increases the noise level. This elevated noise level in f -statistics under archaic
589 ascertainment translates to reduced power to reject admixture graph models based on
590 these f -statistics (Fig. 1, Table 1, Suppl. Fig. 1, Suppl. Tables 3-5). This effect was also
591 reproduced on simulated data (Suppl. Fig. 10). If archaic humans are included in an f -
592 statistic or an admixture graph, archaic ascertainment is no longer guaranteed to be
593 unbiased (see Fig. 2 c,d), and indeed due to the existence of the Neanderthal to non-African
594 gene flow it fails to fix the bias affecting the most problematic class of statistics f_4 (African X,
595 archaic; African Y, non-African), as demonstrated on simulated data in Suppl. Figs. 7b and
596 17.

597 Many ascertainment schemes such as the 1240K, 2000K, Illumina 650Y panels and MAF-
598 based ascertainment on non-Africans skew average DAF across populations in the
599 quadruplet since these panels are enriched for derived variants common in non-Africans vs.
600 Africans and in AMH vs. archaic humans (Suppl. Text 3, Suppl. Table 10). Overrepresentation
601 of derived variants in certain groups of the quadruplet skews f_4 -statistics. We conclude that
602 two ascertainment schemes most often used for studies of African population history
603 (1240K and archaic ascertainment) are not optimal for various reasons: overrepresentation

604 of derived variants common in non-Africans in the former case and a small number of
605 variants common in AMH in the latter case.

606 We found that there exists a non-outgroup ascertainment scheme that is less biased
607 than the other schemes we tested: restricting to variants that are common in a diverse
608 collection of African groups. This scheme demonstrated a bias only in the case of the
609 $f_4(\text{African X, archaic; African Y, non-African})$ and $f_4(\text{non-African X, archaic; African, non-}$
610 $\text{African Y})$ classes of f_4 -statistics among the 27 classes investigated (Suppl. Table 7, Suppl.
611 Figs. 12, 14, and 17). This scheme does not favor derived variants common in non-Africans
612 and supplies many variants common in both Africans and non-Africans (Suppl. Table 10).
613 While for many f_4 -statistic classes and admixture graphs, the difference in performance of
614 the pan-African and archaic ascertainment schemes is small (Table 1, Suppl. Figs. 3, 4, and
615 12, Suppl. Tables 3-5 and 7), the pan-African scheme is applicable when Neanderthals and
616 Denisovans are co-analyzed (Suppl. Figs. 3 and 4), while archaic ascertainment generates
617 extreme shifts in f_4 -statistics in this case (Fig. 2b, Suppl. Fig. 18). The pan-African scheme is
618 also effective for analyses focused on non-Africans, demonstrating no elevated noise level
619 typical for archaic ascertainment (Suppl. Table 7, Suppl. Table 3). Thus, pan-African
620 ascertainment is the most widely applicable scheme among those explored in this study.
621 According to our results on collections of admixture graphs (Table 1) and on f_4 -statistic
622 classes (Suppl. Table 7), a similar form of ascertainment, namely combining sites
623 heterozygous in a single San and a single Yoruba individual (Human Origins panels 4 & 5) is
624 also largely unbiased, with the exception of statistics of the form $f_4(\text{African X, archaic;}$
625 $\text{African Y, non-African})$. However, this ascertainment is also more noisy due to the low
626 number of sites available.

627 As we demonstrated on simulated data, for a non-outgroup ascertainment to be
628 unbiased it should be based on a population where the derived allele frequency spectrum of
629 sites that were polymorphic at the root is preserved relatively well (Fig. 2e) (however, such
630 an ascertainment usually has relatively low statistical power for rejection of incorrect
631 admixture graph models, see Suppl. Fig. 10). We note that the group where ascertainment
632 was performed was co-modelled with the other groups, as is often done in practice. In the
633 light of these results, archaic ascertainment's sub-optimal performance as a non-outgroup
634 ascertainment is due to the fact that Denisovans and Neanderthals have had a low long-
635 term effective population size (Mafessoni et al. 2020), and thus are highly drifted with

636 respect to the root. Moreover, it is often unavoidable that individuals used for archaic
637 ascertainment are used as sole representatives of the respective groups analyzed, and that
638 is also problematic (Fig. 2c). Africans, in contrast, have had much higher effective population
639 sizes (Mafessoni et al. 2020), and we propose that restricting to variants common in a
640 diverse set of African genomes is much more reliable (than archaic ascertainment or
641 ascertainment on a single African population or individual) for preserving the spectrum of
642 variants that existed at the root of archaic and anatomically modern humans. At the same
643 time, pan-African ascertainment supplies enough variants that are common in non-Africans,
644 making it also relatively powerful statistically for analyses focused on non-Africans.

645 An enrichment approach is powerful for large-scale ancient DNA research in Africa due
646 to DNA preservation issues in the hot climate (Skoglund et al. 2017). We did not test a range
647 of allele frequency cut-offs or counts of individuals for pan-African ascertainment, and we
648 do not propose a list of sites for a new DNA enrichment panel. However, our results imply
649 that an effective approach for designing such a panel, which would also be useful for human
650 archaeogenetic studies worldwide, would be to combine selection of the A/T and G/C
651 mutation types with depletion of variants rare in Africa. Frequencies of alleles at A/T and
652 G/C loci are not affected by biased gene conversion (its rate depends on population
653 heterozygosity, Pouyet et al. 2018), and these loci are not hypermutable, and are not
654 affected by deamination damage in ancient DNA. As we demonstrated, restricting to A/T
655 and G/C sites does not bias f_4 -statistics (Suppl. Table 7, Suppl. Figs. 12 and 16, Suppl. Table
656 10) or admixture graph fits (Table 1, Suppl. Tables 3-5). Another reason for taking AT/GC
657 sites only is simply reducing the number of sites since enrichment reagents have limited
658 capacity, and this ascertainment scheme with a 5% MAF threshold yields about 1.6 million
659 variable sites on the “SGDP+archaic” dataset.

660

661 **Methods**

662 *1. Simulating genetic data*

663 *1.1 Simulating the relationships of AMH and archaic humans with msprime v.0.7.4*

664 Twenty-two chromosomes matching the size of the human chromosomes in the *hg19*
665 assembly were simulated with a flat recombination rate (2×10^{-8} per nt per generation) and
666 a flat mutation rate, 1.25×10^{-8} per nt per generation (Scally & Durbin 2012). The standard

667 coalescent simulation algorithm was used (Kelleher et al. 2016), and diploid genomes were
668 assembled from these independently simulated 22 haploid chromosomes. Although this
669 approach does not recapitulate the linkage disequilibrium pattern in real human genomes,
670 it does not make a difference for simulating allele frequencies in deeply divergent groups
671 since chromosome histories become quickly independent in the past (Nelson et al. 2020).

672 The following groups were simulated: chimpanzee (“Chimp”, one individual sampled at
673 the end of the simulation), the Vindija Neanderthal (“Neanderthal”, one individual sampled
674 2,000 generations or 50,000 years in the past, considering a generation time of 25 years),
675 the high-coverage Denisovan “Denisova 3” (“Denisovan”, one individual sampled 2,000
676 generations in the past), five African groups (10 individuals per group sampled at “present”)
677 and three non-African groups (10 individuals per group sampled at “present”). Five classes
678 of simulated topologies are shown in Suppl. Fig. 17b; for a full list of simulation parameters
679 and their values see Suppl. Table 13. Only one simulation iteration was performed for each
680 combination of parameters.

681 We applied archaic ascertainment to the simulated data: restricting to sites polymorphic
682 in the group composed of two “archaic” individuals, “Denisovan” and “Neanderthal” (this
683 scheme reproduces the archaic ascertainment applied to real data, the “SGDP+archaic”
684 dataset, in Suppl. Figs. 17a and 18a). For calculating f -statistics on unascertained and
685 ascertained SNP sets, the software package *ADMIXTOOLS 2* (Maier et al. 2022 preprint) was
686 used. Since there was no missing data and all individuals were diploid, we first calculated all
687 possible f_2 -statistics for 4 Mbp-sized genome blocks (with the “*maxmiss=0*”,
688 “*adjust_pseudohaploid=FALSE*”, and “*minac2=FALSE*” settings), and then used them for
689 calculating f_4 -statistics as linear combinations of f_2 -statistics. This protocol was used for
690 generating the results shown in Suppl. Figs. 17c and 18c.

691

692 *1.2 Simulating the relationships of AMH and archaic humans with msprime v.1.1.1*

693 More realistic simulations were performed with *msprime v.1.1.1* which allows accurate
694 simulation of recombination and of multi-chromosome diploid genomes relying on the
695 Wright-Fisher model (Nelson et al. 2020, Baumdicker et al. 2022). We simulated three
696 chromosomes (each 100 Mb long) in a diploid genome by specifying a flat recombination
697 rate (2×10^{-8} per nt per generation) along the chromosome and a much higher rate at the
698 chromosome boundaries ($\log_e 2$ or ~ 0.693 per nt per generation, see

699 <https://tskit.dev/msprime/docs/stable/ancestry.html#multiple-chromosomes>). A flat
700 mutation rate, 1.25×10^{-8} per nt per generation (Scally & Durbin 2012), and the binary
701 mutation model were used. To maintain the correct correlation between chromosomes, the
702 discrete time Wright-Fischer model was used for 25 generations into the past, and deeper in
703 the past the standard coalescent simulation algorithm was used (as recommended by
704 Nelson et al. 2020).

705 The following groups were simulated: chimpanzee (“c”, one individual sampled at the
706 end of the simulation), the Altai Neanderthal (“n1”, one individual sampled 3,790
707 generations in the past), the Vindija Neanderthal (“n2”, one individual sampled 1,700
708 generations in the past), the high-coverage Denisovan “Denisova 3” (“d”, one individual
709 sampled 1,700 generations in the past), two African groups (“a1” and “a2”, 10 individuals
710 per group sampled at “present”) and two non-African groups (“na1” and “na2”, 10
711 individuals per group sampled at “present”). The topology, dates and some effective
712 population sizes are shown in Fig. 2a; for a full list of simulation parameters see Suppl. Table
713 13. Ten simulation iterations were performed for each combination of parameters, and two
714 combinations were tested: with or without the Neanderthal to non-African gene flow.

715 Upon assessing genetic distances across the simulated groups using F_{ST} , the following
716 ascertainment schemes were applied:

- 717 1. restricting to sites that are heterozygous in a randomly selected individual from the
718 “a2” group (this scheme simulates the generation of one Human Origins SNP panel,
719 Patterson et al. 2012);
- 720 2. taking heterozygous sites from one randomly selected individual per “AMH”
721 population (“a1”, “a2”, “na1”, “na2”) and merging these SNP sets (this scheme
722 simulates the generation of the whole Human Origins SNP array, Patterson et al.
723 2012);
- 724 3. restricting to sites having high minor allele frequency (> 5%) in the union of “African”
725 groups “a1” and “a2” (this scheme simulates the MAF ascertainment on Africans);
- 726 4. restricting to sites having high minor allele frequency (> 5%) in the union of “non-
727 African” groups “na1” and “na2” (this scheme simulates the MAF ascertainment on a
728 non-African continental meta-population);

- 729 5. restricting to sites having high minor allele frequency (> 5%) in the union of all
730 “AMH” groups “a1”, “a2”, “na1”, and “na2” (this scheme simulates the global MAF
731 ascertainment);
- 732 6. restricting to sites polymorphic in the group composed of three “archaic” individuals,
733 “d”, “n1”, and “n2” (this scheme simulates the archaic ascertainment applied to the
734 “SGDP+archaic” dataset throughout this study).

735

736 *1.3 Simulating random admixture graphs and simple trees with msprime v.1.1.1*

737 Genetic histories in the form of random admixture graphs were simulated using the
738 *msprime v.1.1.1* settings described above. We simulated admixture graphs of four
739 complexity classes: the graphs included 8 or 9 non-outgroup populations, one outgroup (all
740 sampled at leaves), and 4 or 5 pulse-like admixture events. Demographic events were
741 separated by date intervals ranging randomly between 1,500 and 8,000 generations, with
742 an upper bound on the tree depth at 40,000 generations. To be more precise, demographic
743 events were not placed in time entirely randomly, but were tied to one or few other events
744 of the same “topological depth” within the graph, as illustrated by examples of the
745 simulated topologies in Suppl. Fig. 8. The same principle was applied to the sampling dates
746 for non-root groups, which were tied to other demographic events such as divergence and
747 admixture of other populations. The random graph topologies and simulated parameter
748 sets were generated using the *random_sim* function from the *ADMIXTOOLS 2* package:
749 https://uqrmaie1.github.io/admixtools/reference/random_sim.html

750 Outgroups facilitate automated exploration of graph topology space. Outgroup branches
751 diverged from the other populations at 40,000 generation in the past and had a large
752 constant effective population size of 100,000 diploid individuals. Other effective population
753 sizes were constant along each edge and were picked randomly from the range of 2,000-
754 40,000 diploid individuals. Admixture proportions for all admixture events varied randomly
755 between 10% and 40%. The root of the simulation and the root of all non-outgroup
756 populations were sampled, and the other populations were sampled at branch tips
757 exclusively. This setup generates groups sampled at widely different dates in the past (from
758 0 to ca. 40,000 generations) or, in other words, located at various genetic distances from
759 the root (Fig. 2d). The outgroup population was sampled at the “present” of the simulation.
760 Sample sizes for all populations were identical: 10 diploid individuals with no missing data.

761 For subsequent analyses we selected only simulations where pairwise F_{ST} for groups
762 were in the range characteristic for anatomically modern and archaic humans (in each
763 simulation there was at least one F_{ST} value below 0.15; see Suppl. Fig. 8). In this way, 20
764 random topologies were simulated per complexity class. Each topology was simulated only
765 once, and 80 simulations were generated in total (see examples of the topologies and
766 respective F_{ST} distributions in Suppl. Fig. 8). Another set of simulations was prepared with
767 the same topologies and parameters, except for the effective population size on the
768 outgroup branch which was set at 1,000 diploid individuals instead of 100,000.

769 The following ascertainment schemes were applied to the outcomes of these randomized
770 simulations: 1) ascertainment on sites heterozygous in a single randomly selected individual
771 (this Human Origins-like ascertainment was repeated for all simulated groups including the
772 outgroup and root groups, generating 920 ascertained datasets); 2) unions of four such
773 Human Origins-like SNP panels, with only one individual per group considered (10 random
774 sets of four groups excluding the outgroup and root groups were explored per topology,
775 generating 800 ascertained datasets); 3) ascertainment on sites polymorphic in a group
776 composed of three randomly selected individuals, with only one individual per group
777 considered (10 random sets of three groups excluding the outgroup and root groups were
778 explored per topology, generating 800 ascertained datasets); and 4) MAF ascertainment, that
779 is restricting to sites having MAF > 5% in random meta-groups (10 random sets of four groups
780 excluding the outgroup and root groups were explored per topology, generating 800
781 ascertained datasets). Group sets used for each ascertainment were recorded. Genetic
782 distances (F_{ST}) were calculated for all populations (including the outgroup and the last
783 common ancestor of all non-outgroup populations) vs. the root sample (Fig. 2d).

784 Alternatively, simple trees were simulated using the *msprime v.1.1.1* settings described
785 above. A tree of four groups conforming to the f_4 -statistic (A, B; C, O) was simulated using
786 *msprime v.1.1.1*, with a tree depth of 4,000 generations (Suppl. Fig. 11). All the groups had a
787 uniform effective population size of 100,000 diploid individuals, except for a bottleneck
788 happening immediately after the A-B divergence (at 1,999 generations in the past) and lasting
789 until the end of the simulation. The following bottleneck classes were simulated: no
790 bottleneck (control), 10x, 100x, 1,000x, and 10,000x reduction in effective population size.
791 For each bottleneck class, 20 independent simulations were performed. All the samples were
792 drawn at “present”: sample sizes were 25, 25, 25 and 10 for populations A, B, C and O,

793 respectively (except for the 10,000x bottleneck class since group A included 10 individuals
794 only in that case). Three ascertainment schemes were tested for the simulated trees: 1)
795 ascertainment on sites heterozygous in a single randomly selected individual (this Human
796 Origins-like ascertainment was repeated for all simulated groups, including group O); 2)
797 restricting to sites having MAF > 5% (or 10%, or 2.5%) in the union of groups A and B
798 composed of 50 diploid individuals; and 3) removal of sites with *derived* allele frequency >
799 95% (or 90%, or 97.5%) in the union of groups A and B. The latter ascertainment scheme was
800 added since the ascertainment schemes we tested on real data deplete the derived end of
801 the allele frequency spectrum more than the ancestral end (Suppl. Tables 10-12).

802 For calculating f -statistics and fitting admixture graphs to unascertained and ascertained
803 SNP sets, the *ADMIXTOOLS 2* (Maier et al. 2022 preprint) software package was used. Since
804 there was no missing data and all individuals were diploid, we first calculated all possible f_2 -
805 statistics for 4 Mbp-sized genome blocks (with the “*maxmiss=0*”,
806 “*adjust_pseudohaploid=FALSE*”, and “*minac2=FALSE*” settings) and then used them for
807 calculating f_4 -statistics as linear combinations of f_2 -statistics or for fitting admixture graphs
808 (with the “*numstart=100*” and “*diag=0.0001*” settings). This calculation protocol was used
809 for generating the results shown in Figs. 2 and in Suppl. Figs. 7-11. When true admixture
810 graphs were fitted to ascertained data, full population samples of 10 individuals were used
811 by default, and in some cases, as indicated in the figure legends, the individual used for
812 ascertainment was used as the only representative of the respective population. Outgroups
813 were included in the fitted graphs; in other words, they were co-analyzed with the other
814 groups. Outgroups were not co-modelled with the other populations in Fig. 2f only.

815 For assessing the power of ascertained simulated datasets to reject incorrect admixture
816 graph models, we first generated a set of such incorrect graphs per each simulated
817 topology. For that purpose, an algorithm for finding well-fitting topologies (*findGraphs* from
818 the *ADMIXTOOLS 2* package) was started on non-ascertained data 300 times, seeded by
819 random graphs containing either the simulated number of admixture events (n , 100 runs),
820 or $n-1$ events (100 runs), or $n+1$ events (100 runs). For a list of settings for the *findGraphs*
821 algorithm see Maier *et al.* (2022 preprint). Thousands of diverse graphs explored by
822 *findGraphs* in the process of topology optimization were generated in this way for each
823 simulated graph, and 100 poorly fitting graphs were randomly picked from a subset of these

824 graphs having LL scores between 70 and 300. This subset of graphs was then fitted to all
825 ascertained datasets derived from the same simulated admixture graph.

826

827 2. Constructing the set of real data

828 We used the *cteam-lite* dataset described in Mallick *et al.* 2016, composed of the full SGDP
829 set (300 high-coverage genomes from present-day populations), the chimpanzee genome
830 (pseudo-haploid genotype calls, see
831 <http://hgdownload.cse.ucsc.edu/goldenPath/panTro2/bigZips/>), and the Altai Neanderthal,
832 “Denisova 3” Denisovan, Ust’-Ishim, WHG Loschbour, and LBK Stuttgart ancient genomes
833 (see SI section 3 in that study). We supplemented *cteam-lite* by 44 present-day African
834 genomes sequenced using the SGDP protocols by Fan *et al.* (2019), the Vindija
835 Neanderthal’s genome (Prüfer *et al.* 2017), and the genome of an ancient African forager
836 individual I10871 sequenced by Lipson *et al.* (2020) (Suppl. Table 1). Sites polymorphic in
837 this set of 352 individuals were extracted from the *cteam-lite* files of the “hetfa” format
838 using the *cpoly* tool (Mallick *et al.* 2016): alleles were grouped into derived and ancestral
839 (polarized) according to the chimpanzee genome; missing data and heterozygous sites were
840 allowed. For each genome, we used individual base quality masks included in *cteam-lite* or
841 constructed using the same protocol for other genomes (Vindija Neanderthal and Fan *et al.*
842 2019): minimum base quality was set by default at 1, as recommended in SI section 3 in
843 Mallick *et al.* 2016, which discarded lowest-quality regions marked as “0”, “?”, or “N”. The
844 individual I10871 was not included in most analyses in this study (except for the complex
845 admixture graphs in Suppl. Text 1) due to its relatively high rate of deamination errors.

846 The resulting dataset prior to missing data removal and ascertainment includes
847 94,691,841 autosomal sites (Suppl. Table 2). To keep the polarity of alleles, all data
848 manipulations and ascertainments were performed using *PLINK v.2.0 alpha* (Chang *et al.*
849 2015). For calculating f_4 -statistics, sets of continental-level meta-populations were selected
850 (e.g., Africans and East Asians or Africans and archaic humans) and then f_4 -statistics were
851 calculated for all possible combinations of populations in the resulting subset of the
852 “SGDP+archaic” dataset, with no missing data (at the population level) allowed *within the*
853 *selected subset*. This was done to avoid potential biases associated with data missing non-
854 randomly across groups. Alternatively, f_4 -statistics were drawn randomly from a certain

855 class of statistics, and no missing data (at the population level) were allowed in the resulting
856 *population quadruplets*.

857

858 *3. Influence of ascertainment on fits of admixture graphs to real data*

859 First, we fitted all possible graphs including two admixture events (32,745 distinct
860 topologies with no fixed outgroup) for three combinations of groups: 1) one archaic
861 individual, three African groups, and one African group with substantial West Eurasian-
862 related ancestry (Altai Neanderthal, Ju|'hoan North, Biaka, Yoruba, and Agaw, respectively);
863 2) five deeply divergent ancient and present-day non-African groups (Ust'-Ishim, Papuan,
864 Onge, LBK Stuttgart, Even); and 3) five deeply divergent present-day non-African groups
865 (Papuan, Onge, Palestinian, Even, Mala). These three sets of simple graphs were fitted to all
866 sites, AT/GC sites, and 1240K sites (no missing data were allowed at the group level within
867 these sets of five populations); 5,000 best-fitting models were selected according to the LL
868 score on all sites and WRs of those models were compared across SNP sets (Suppl. Fig. 1).

869 Next, we explored the same exhaustive set of admixture graph topologies including five
870 groups and two admixture events on the wider collection of ascertainment. Twelve
871 combinations of five groups including up to two archaic humans, up to five African groups,
872 and up to five non-African groups were tested. To ensure fair comparison across at least a
873 subset of population combinations, as a starting point for generating ascertained site sets
874 we used either 11,706,773 sites (with no missing data at the group level) polymorphic in a
875 set of 48 archaic and African groups composed of a total of 97 individuals; or 10,051,585
876 such sites in a set of 59 archaic, African, European, and Middle Eastern groups composed of
877 a total of 120 individuals; or 5,296,653 such sites in a set of 51 Papuan, Native American,
878 European, Anatolian, and Caucasian groups composed of a total of 112 individuals (Suppl.
879 Tables 1 and 2).

880 We examined the fits of these collections of admixture graphs from different
881 perspectives. (1) We considered just 5,000 topologies that are best-fitting on the
882 unascertained site set (Suppl. Figs. 1-3) or all 32,745 topologies tested (Suppl. Fig. 4). (2) We
883 also considered alternative admixture graph fit metrics, LL or WR. LL as a fit metric (see left-
884 hand panels in Suppl. Figs. 3 and 4) is more accurate than WR, but difficult to compare
885 across population sets. Finally, instead of R or R^2 of a linear trend as a measure of
886 correlation of admixture graph fits (Fig. 1, Suppl. Figs. 1-4) we considered the fraction of all

887 possible models of a certain complexity that are rejected under ascertainment ($WR > 3 SE$)
888 but accepted on all sites ($WR < 3 SE$), or *vice versa*.

889

890 4. Automated inference of fitting admixture graphs on real data

891 The 12-population admixture graph published by Lipson et al. 2020 (and later used as a
892 skeleton graph in Lipson et al. 2022) and simpler 7- and 10-population intermediate graphs
893 presented in the former study were revisited by Maier *et al.* (2022 preprint), and thousands
894 of alternative well-fitting graphs of the same complexity were found using the *find_graphs*
895 function from the *ADMIXTOOLS 2* package
896 (<https://uqrmaie1.github.io/admixtools/articles/graphs.html>). Maier *et al.* used the 1240K
897 dataset only, and in the current study we re-fitted the admixture graphs found by the
898 algorithm on the 1240K SNP panel to the AT/GC and unascertained datasets derived from
899 “SGDP+archaic” and also repeated automated admixture graph inference on these two
900 additional SNP sets. Advantages and pitfalls of automated admixture graph inference are
901 described in detail in Maier *et al.*, along with justifications for the specific protocol used in
902 that study, and here we used protocols identical to those employed by Maier *et al.* We first
903 calculated all possible f_2 -statistics for 4 Mbp-sized genome blocks (with the “*maxmiss=0*”,
904 “*adjust_pseudohaploid=FALSE*”, and “*minac2=2*” settings, see Maier *et al.* 2022 for details
905 on the settings) and then used them for fitting admixture graphs (with the “*numstart=100*”
906 and “*diag=0.0001*” settings) and for automated admixture graph inference with the
907 *find_graphs* function (see the Methods section in Maier *et al.* for a complete list of
908 arguments for this function). Only one topology constraint was used at the graph space
909 exploration step: chimpanzee was assigned as an outgroup.

910

911

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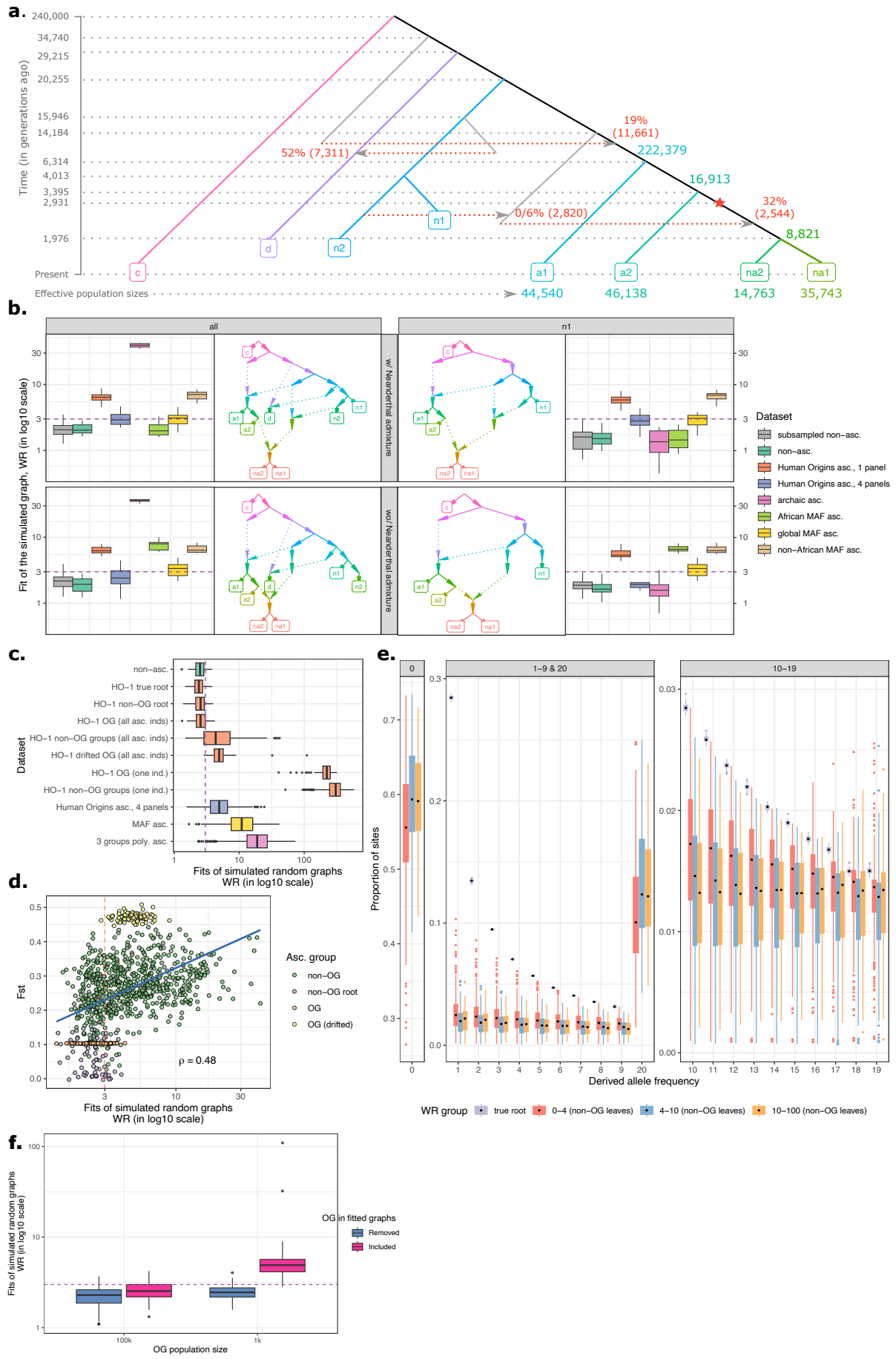
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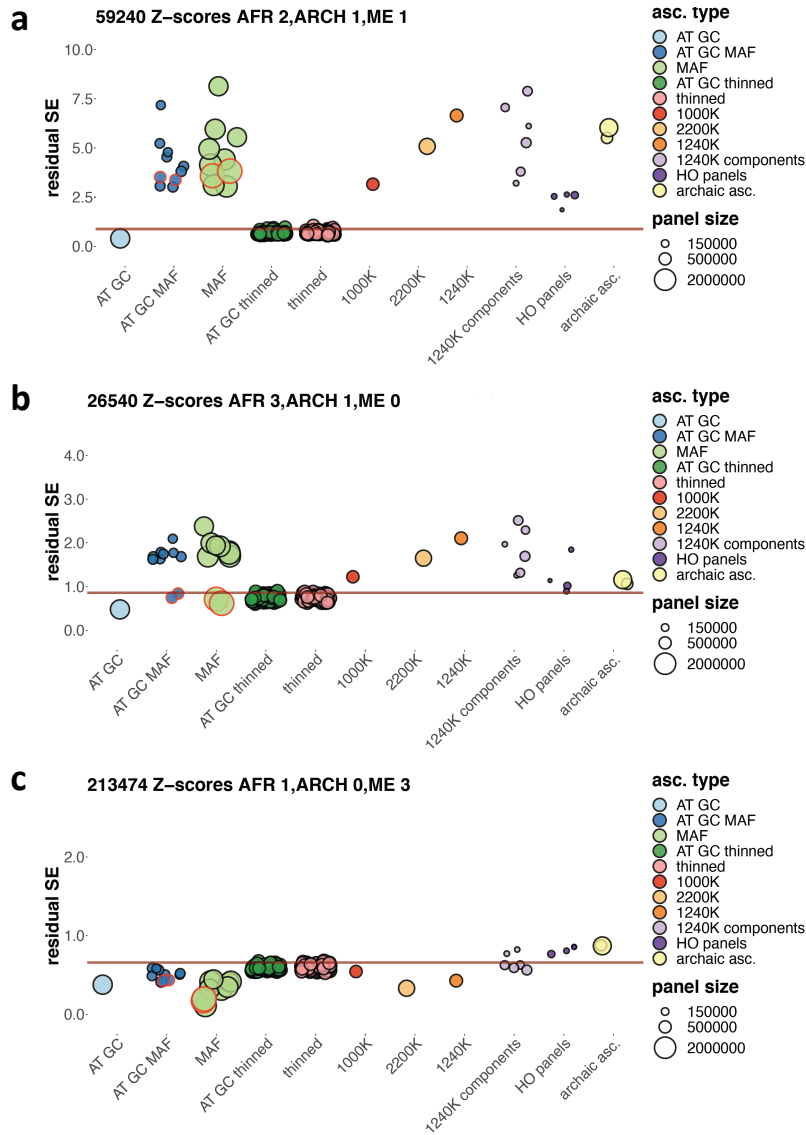
1266 distinct admixture graph topologies. Few examples of admixture graphs whose fits are affected by
1267 ascertainment are also shown beside the scatterplots.



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1270 **Fig. 2.** Exploring the influence of non-outgroup ascertainment on fits of admixture graphs on
1271 simulated data. Results are presented for two topologies (with or without the Neanderthal to non-
1272 African gene flow) and for eight types of SNP sets: 1) 10 sets of randomly selected variable sites
1273 matching the average size of the “Human Origins, one panel” set, 500K sites; 2) unascertained sites
1274 (on average 5.55M polymorphic sites without missing data); 3) Human Origins-like ascertainment,
1275 one panel based on the “a2” group (500K sites on average across simulation iterations); 4) Human
1276 Origins-like ascertainment, a union of four panels based on randomly selected individuals from four
1277 groups (“a1”, “a2”, “na1”, and “na2”, 1.34M sites on average); 5) archaic ascertainment (1.05M sites
1278 on average); 6) “African MAF ascertainment”, that is removal of sites with MAF < 5% in the union of
1279 “a1” and “a2” groups (1.85M sites on average); 7) similar MAF ascertainment on the union of “a1”,
1280 “a2”, “na1”, “na2” (1.62M sites on average); 8) similar MAF ascertainment on the union of “na1”
1281 and “na2” groups (1.48M sites on average). (a) The simulated topology, with dates of demographic
1282 events and sampling dates (in generations) shown on the y-axis or next to gene flows. The
1283 Neanderthal to non-African gene flow was simulated either at 0% (by omitting the “n2” to ghost
1284 AMH gene flow) or as shown in the figure. Effective population sizes of archaic groups are omitted
1285 for clarity. The out-of-Africa bottleneck is marked with a star. (b) Boxplots illustrating the effects of
1286 various ascertainment schemes on fits (WR) of the correct admixture graphs. The dashed line on the
1287 logarithmic scale marks a threshold often used in the literature for classifying models into fitting and
1288 non-fitting ones—3 standard errors—and the observation that common ascertainment schemes
1289 consistently produce much higher Z-scores than this threshold provides unambiguous evidence that
1290 ascertainment bias can profoundly compromise admixture graph fitting. The topologies fitted to the
1291 data are shown beside the boxplots. In the panels on the right, simple graphs including only one
1292 archaic lineage are fitted (“n1” used as an example, but very similar results were obtained for the
1293 “n2” and “d” groups). In the panels on the left, results for the full simulated model fitted to the data
1294 are shown. (c) Ascertainment bias was also explored across 80 simulated genetic histories in the
1295 form of random admixture graphs. WR of the correct admixture graph was used as a measure of
1296 bias. WRs for non-ascertained data and four ascertainment schemes are summarized with boxplots:
1297 1) Human Origins-like ascertainment, one panel; 2) Human Origins-like ascertainment, four panels;
1298 3) MAF-based ascertainment (restricting to common variants) in random sets of four populations; 4)
1299 ascertainment on sites polymorphic in random sets of three individuals (one individual sampled per
1300 population). Human Origins-like ascertainment on single individuals was performed on the true root
1301 or the root of non-outgroup populations, on non-outgroup populations, or on more or less drifted
1302 outgroups (having effective population sizes of 100,000 or 1,000 diploid individuals, respectively) co-
1303 modelled with the other populations (abbreviated as “OG”). Alternatively, the same individual that
1304 was used for ascertainment acted as the only representative of its group for model fitting. (d)
1305 correct admixture graphs under the Human Origins-like ascertainment (one panel) are guaranteed
1306 to be well-fitting (WR < ca. 4 SE) if F_{ST} between the whole population sample used for ascertainment
1307 vs. the sample at the root of the simulation is below 0.12. (e) Derived allele frequency spectra
1308 (derived allele count in a sample of 20 chromosomes vs. proportion of sites) across simulated root
1309 and non-outgroup populations grouped according to the level of ascertainment bias. The spectra
1310 were calculated for sites polymorphic in the root population sample of 20 chromosomes.
1311 Populations are binned by WR of the true graph fitted to sites heterozygous in a single individual
1312 randomly drawn from that population (single-panel Human Origins-like ascertainment). The
1313 boxplots summarize DAF across all simulated graphs. DAF bins are shown in three separate panels
1314 with different y-axis ranges: 0 derived alleles; 1 to 9 and 20 derived alleles; 10 to 19 derived alleles.
1315 (f) Illustration of the principle that outgroup ascertainment is expected to be unbiased only if an
1316 outgroup (abbreviated as “OG”) is not co-analyzed with the other populations. Human Origins-like
1317 ascertainment (one panel) was performed on more or less drifted outgroups (having effective
1318 population sizes of 100,000 or 1,000 diploid individuals, respectively) that were then either included
1319 in the fitted true admixture graphs or removed from them. WRs of these graphs are summarized
1320 with boxplots on the y-axis. The dashed horizontal line corresponds to WR = 3 SE.

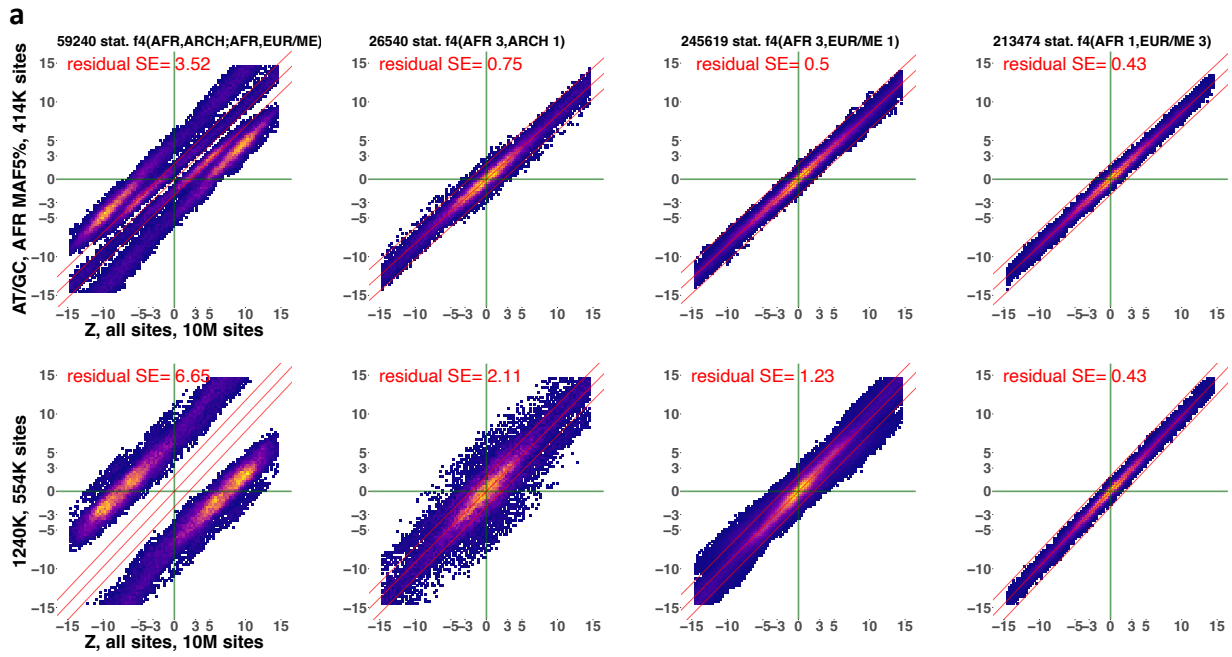


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1323 **Fig. 4.** Variance in f_4 -statistic Z-scores resulting from ascertainment and random site subsampling
 1324 expressed as standard deviations of residuals of a linear model (expressed in the same units as f_4 -
 1325 statistic Z-scores). Results are shown for three classes of f_4 -statistics: f_4 (African X, archaic; African Y,
 1326 Mediterranean/Middle Eastern), f_4 (African X, African Y; African Z, archaic) (expressed in another
 1327 notation as African₃;archaic₁), and f_4 (African, Med/ME X; Med/ME Y, Med/ME Z) (expressed in
 1328 another notation as African₁;Mediterranean/Middle Eastern₃). Results for ascertainment on variants
 1329 common in Africans (either those having no detectable West Eurasian ancestry according to Fan et
 1330 al. (2019) or on all Africans in the SGDP dataset) are circled in red. Residual SE values for f_4 -statistic
 1331 Z-scores lying not far from 0 (absolute Z-scores on all sites < 15) are plotted. The 97.5% percentiles
 1332 of all the thinned replicates combined, including those on all sites and AT/GC sites, are marked by
 1333 the brown lines. Size of the SNP panels is coded by point size, and the broad ascertainment types are
 1334 coded by color according to the legend. Thirty eight site subsampling schemes were explored: 1)
 1335 AT/GC mutation classes; 2) AT/GC mutation classes and restricting to common variants based on a
 1336 global MAF threshold of 5% or on the same threshold applied to one of nine continental-scale
 1337 groups; 3) the same procedure repeated on all sites; 4) random thinning of the AT/GC dataset to the
 1338 1240K SNP count for a given combination of groups (no missing data allowed), results for 100
 1339 thinning replicates are shown; 5) random thinning of all sites to the 1240K SNP count, results for 100
 1340 thinning replicates are shown; 6) the 1000K, 1240K, and 2200K enrichment panels (2200K = 1240K +

1341 1000K); 7) major components of the 1240K panel: sites included in the Illumina 650Y and/or Human
1342 Origins SNP arrays, sites included exclusively in one of them, and remaining sites; 8) the largest
1343 Human Origins sub-panels (4, 5, 13) or their union (4+5); 9) restricting to sites polymorphic in a
1344 group composed of the three high-coverage archaic individuals (either all such sites or transversions
1345 only).

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Fig. 5. Scatterplots illustrating the effects of two ascertainment schemes on Z-scores of f_4 -statistics of four classes including African and/or archaic and/or Mediterranean/Middle Eastern groups. Only statistics of the form $f_4(\text{African } X, \text{ archaic}; \text{ African } Y, \text{ non-African})$ were considered in the class African₂;archaic₁;Med/ME₁. The f_4 -statistic classes were selected to represent severe ascertainment bias (leftmost panels), moderate level of bias (two middle panels) and no bias (rightmost panels). The ascertainments selected are 1240K (the most widely used SNP enrichment panel) and the new “pan-African” scheme proposed in this study to mitigate ascertainment bias for nearly all f_4 -statistic classes. For results on other f_4 -statistic classes see Suppl. Fig. 14, and results for a wider range of ascertainment schemes are summarized in Suppl. Figs. 12 and 13. Class labels and numbers of statistics plotted are shown above the panels. Instead of individual points, heatmaps illustrating point density are shown. Z-scores on all sites (10 million sites, as indicated on the x-axes) are compared to Z-scores on ascertained datasets on the y-axes. Ascertainment types and site counts are shown on the y-axes. All plots include only statistics with absolute Z-scores below 15 on all sites. A linear model fitted to the data and lines representing ± 2 SE are shown in red. Residual SE values for those linear trends are shown in each plot in red.

percentage of models rejected on asc. but accepted on all sites		arch 2, afr 3	arch 1, afr 4	arch 1, afr 3, nafr 1	arch 1, afr 2, nafr 2	afr 5	afr 4, nafr 1	afr 4, nafr 1	afr 3, nafr 2	afr 1, nafr 4	nafr 5	nafr 5	nafr 5	number of biased pop. sets, both metrics	number of biased pop. sets, both metrics	
ascertainment type	further details on the ascertainment	min. size of the SNP panel*	max. size of the SNP panel*	Denisovan, Dinka, Yoruba	Denisovan, Khomani San, Mbuti, Dinka	Altai, Ju hoan North, Luhya, Spanish	Mbuti, Baka, Laka, Fulani, Bantu Tswana	Khomani San, Bakola, Igbo, Mursi, Aari	Bedzan, Cameroon SMA, Esan, Mozabite, Masai	Mbuti, Biaka, Ngumba, LBK, Iranian	Luo, Bedouin B, Jordanian, Abkhasian, Sardinian	Australian, Quechua, Mayan, Lezgin, French	Papuan, Chipewyan, Eskimo Naukan, Finnish, Sardinian	Karitiana, Cree, Eskimo Sireniki, Hungarian, Icelandic	number of biased pop. sets	number of biased pop. sets, both metrics
A>T and G>C mutations		805,042	1,757,840	0.000%	0.009%	0.000%	0.003%	0.000%	0.000%	0.000%	0.311%	0.000%	0.000%	0.000%	0	0
1240K panel		501,429	663,239	0.015%	1.017%	7.974%	5.528%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	3	4
components of the 1240K panel	illumina610-Quad sites	256,277	304,292	0.012%	0.015%	7.992%	5.528%	0.000%	0.000%	0.000%	0.000%	0.021%	0.000%	0.000%	2	3
	sites exclusive to illumina610-Quad	183,680	216,478	0.000%	0.012%	7.974%	5.528%	0.000%	0.000%	0.000%	0.000%	0.061%	0.000%	0.000%	3	4
	sites included in both illumina610-Quad and HumanOrigins	72,597	87,814	0.018%	0.000%	7.971%	5.528%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	2	6
	HumanOrigins sites	244,922	354,460	0.000%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.009%	0.000%	0.000%	0.000%	1	3
	sites exclusive to HumanOrigins	171,249	266,646	0.003%	0.000%	6.883%	0.000%	0.000%	0.000%	0.000%	0.003%	0.000%	0.000%	0.000%	1	2
1240K, other sites	67,096	92,301	0.000%	0.003%	7.952%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	4	
the largest panels included in the HumanOrigins array	panel 13 based on a San individual and Denisovan	67,557	89,655	0.003%	0.168%	6.993%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	6
	panel 4 based on a San individual	52,862	94,493	0.000%	0.000%	0.000%	0.000%	0.003%	0.000%	0.012%	0.000%	0.000%	0.000%	0.000%	0	4
	panel 5 based on a Yoruba individual	44,674	73,180	0.724%	0.000%	5.250%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	2	8
	panels 4 and 5	46,701	157,126	0.015%	0.000%	0.000%	0.000%	0.000%	0.000%	0.006%	0.000%	0.000%	0.000%	0.000%	0	1
other enrichment panels	1000K: transversions in 2 Yoruba ind. and in Altai Neand.	364,079	590,775	0.000%	0.000%	6.890%	0.000%	0.000%	0.000%	0.000%	0.012%	0.000%	0.000%	0.000%	1	2
	2200K = 1000K + 1240K	814,915	1,190,758	0.015%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.012%	0.000%	0.000%	0.000%	1	1
archaic ascertainment	transitions and transversions	525,014	1,555,781	10.484%	0.000%	6.899%	0.009%	0.000%	0.000%	0.003%	0.021%	0.000%	0.000%	0.000%	2	8
	transversions	165,249	484,675	10.484%	0.000%	6.880%	0.003%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	2	8
MAF ascertainment	global, >5% MAF	2,129,201	2,511,335	0.000%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.003%	0.000%	0.000%	0.000%	1	2
	>5% MAF in Africans unadmixed with non-Africans	2,045,769	3,231,875	1.032%	0.003%	6.932%	0.000%	0.000%	0.000%	0.015%	0.006%	0.000%	0.000%	0.000%	2	2
	>5% MAF in all Africans	2,109,808	3,120,326	0.037%	0.003%	6.929%	0.000%	0.000%	0.000%	0.000%	0.009%	0.000%	0.000%	0.000%	1	1
	>5% MAF in Native Americans	1,513,207	1,764,715	0.015%	0.000%	7.992%	5.195%	0.000%	0.000%	0.003%	0.000%	0.000%	0.000%	0.000%	2	3
	>5% MAF in Central Asians and Siberians	1,843,262	2,150,675	0.018%	0.000%	7.974%	0.000%	0.000%	0.000%	0.244%	0.006%	0.000%	0.000%	0.000%	1	2
	>5% MAF in East Asians	1,723,831	2,020,860	0.000%	0.000%	7.992%	5.528%	0.000%	0.000%	0.003%	0.003%	0.000%	0.000%	0.000%	2	3
	>5% MAF in Europeans	1,885,336	2,192,571	0.000%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.003%	0.000%	0.000%	0.000%	1	2
	>5% MAF in Middle Eastern groups	2,018,884	2,306,319	0.006%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	1
	>5% MAF in Papuans and Aboriginal Australians	1,515,022	1,791,390	1.032%	0.000%	7.995%	5.528%	0.000%	0.000%	0.244%	0.311%	0.000%	0.000%	0.000%	3	4
	>5% MAF in South Asians	1,908,459	2,235,024	0.000%	0.000%	7.968%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	2
AT/GC mutation types + MAF ascertainment	global, >5% MAF	323,296	378,287	0.000%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	2
	>5% MAF in Africans unadmixed with non-Africans	309,172	486,906	0.003%	0.000%	6.929%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	1
	>5% MAF in all Africans	319,053	470,070	0.003%	0.006%	6.929%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	1
	>5% MAF in Native Americans	229,939	266,113	0.000%	0.000%	7.974%	6.114%	0.000%	0.000%	0.049%	0.318%	0.000%	0.000%	0.000%	2	3
	>5% MAF in Central Asians and Siberians	280,103	324,245	0.000%	0.000%	7.974%	0.000%	0.000%	0.000%	0.253%	0.049%	0.000%	0.000%	0.000%	2	3
	>5% MAF in East Asians	261,857	304,567	0.000%	0.000%	7.992%	0.000%	0.000%	0.000%	0.003%	0.324%	0.000%	0.000%	0.000%	1	2
	>5% MAF in Europeans	285,723	330,244	0.000%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.003%	0.000%	0.000%	0.000%	1	3
	>5% MAF in Middle Eastern groups	306,450	347,536	0.003%	0.000%	7.952%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	3
	>5% MAF in Papuans and Aboriginal Australians	230,124	272,093	1.029%	0.000%	8.001%	5.528%	0.000%	0.000%	0.244%	0.324%	0.000%	0.000%	0.000%	3	4
	>5% MAF in South Asians	289,739	336,996	0.000%	0.000%	6.948%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	0.000%	1	3
* the SNP counts correspond to sites polymorphic in larger collections of groups from which the analyzed population quintuplets were taken, see Suppl. Table X.		number of biased asc. =>		6	1	33	9	0	0	1	0	1	0	0		
		number of biased asc., both metrics =>		6	2	61	9	0	6	10	0	5	0	9	3	

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Table 1. Performance of ascertainment schemes explored across 12 population quintuplets and assessed as the fraction of all possible admixture graph topologies that are rejected under ascertainment ($WR > 3 SE$) but accepted on all sites ($WR < 3 SE$). We also applied the binary classifier to determine if the ascertainment produces unbiased or biased results (the latter highlighted in bold and underlined text). The numbers of population quintuplets or ascertainment schemes affected by bias (according to the fraction of topologies that are rejected under ascertainment but accepted on all sites, or according to this metric and the fraction of topologies that are accepted under ascertainment but rejected on all sites) are shown in the two rightmost

1371 columns and in two bottom rows, respectively. The composition of the population sets is shown above the table in an abbreviated way: *arch*, archaic
1372 humans, followed by the number of archaic groups; *afr*, Africans; *nafr*, non-Africans or Africans with substantial non-African admixture (Fan et al. 2019).
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