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HUMAN GENETICS

Interbreeding between Neanderthals and modern humans was strongly sex biased

Alexander Platt[1]*†, Daniel N. Harris[1]†, Sarah A. Tishkoff[1,2]*

Sex biases in admixture and other demographic processes are recurrent features throughout human evolution. For admixture between Neanderthals and anatomically modern humans (AMHs), sex bias has been proposed as an explanation for the relative lack of Neanderthal ancestry in modern human X chromosomes compared with that in modern human autosomes. By observing a 62% relative excess of AMH ancestry in Neanderthal X chromosomes, we characterized the interbreeding between the two groups as predominantly male Neanderthals with female AMHs. Analytic and numerical modeling presents mate preference as a more parsimonious cause of the sex bias than purely demographic processes with differential patterns of male and female migration.

One of the notable features evident in alignments of Neanderthal genomes to those of modern humans is the presence of "Neanderthal deserts" within modern human genomes: genomic regions where Neanderthal alleles are conspicuously rare in the modern human (and ancient modern human) gene pool. These comprise several megabases scattered throughout the autosomes as well as most of the X chromosome (*1*–*4*). A recent autosomal genomics study showed a correlation between Neanderthal deserts in the modern human genome with regions of the Altai Neanderthal genome that lacked introgression from early modern humans, suggesting that these shared deserts represent genomic incompatibility loci resulting from incipient speciation between the two groups (*5*). This observation leaves two broad categories of hypotheses regarding the Neanderthal deserts across the modern human X chromosomes: (i) The lack of Neanderthal loci amongst the X chromosomes in the modern human gene pool is a result of natural selection preferentially removing Neanderthal alleles from the X chromosome (*6*–*9*), or (ii) the contribution of Neanderthal X chromosomes was reduced from the very beginning (*10*) and represents an original interbreeding that was biased toward male Neanderthals and female anatomically modern humans (AMHs).

To resolve these hypotheses, we need to understand the evolutionary fate of AMH alleles within the Neanderthal population. Although we do not have any Neanderthal genomes that postdate the admixture 45 to 49 thousand years ago (ka) (*3*, *4*) that introduced Neanderthal ancestry to the modern human gene pool, we do have data from an earlier introgression event ~250 ka that led to the Altai Neanderthal genome exhibiting AMH ancestry (*5*, *11*, *12*). If the characteristic phenomenon that led to the lack of Neanderthal X chromosomes in the modern human gene pool was conserved across AMH-Neanderthal interbreeding events, then the different proposed mechanisms lead to radically different predictions regarding the patterns of AMH introgression in Neanderthal X chromosomes. We used the natural experiment provided by early AMH gene flow into Neanderthals to systematically test these predictions as outlined in Table 1.

To characterize AMH introgression in Neanderthals, we used the local introgression identification tool IBDmix (*13*) to compare a reference panel of genomes from 73 women from three modern human sub-Saharan African populations, which were previously shown to contain <0.1% Neanderthal ancestry [the !Xoo and Ju|'hoansi, Khoesan forager populations from Botswana, and the Chabu, foragers from southwest Ethiopia who speak an unclassified language related to Nilo-Saharan (*5*)], with Neanderthal genomes. We primarily focused on the Altai Neanderthal, a female specimen with the oldest high-quality Neanderthal genome sequence [dated to 122 ka (*14*, *15*)] and likely simplest admixture history (*11*) but also considered the female Neanderthal specimens from Chagyrskaya [dated to 80 ka (*16*)] and Vindija [dated to 52 ka (*15*) as well.

Analysis of natural selection against genomic incompatibilities

For autosomal regions of AMH genomes where Neanderthal alleles are missing from the modern human gene pool ("archaic deserts"), homologous Neanderthal regions typically lack AMH introgressed alleles (*5*). This mutual pattern is consistent with standard models of speciation (*17*–*20*) where alleles acquire population-specific interactions with other loci in their genomes and produce deleterious effects when placed in the context of the other population's genomic background. In this scenario, the archaic deserts would be regions of the genome with increased probability of lineage-specific nucleotide substitutions causing hybrid incompatibilities (*21*). Across species with hemizygotic X chromosomes, it is common for protein-coding regions on X chromosomes to diverge more quickly between isolated populations, as selection can act more readily on variants that would otherwise be hidden as recessive [e.g., (*22*–*27*)]. If this "faster X effect" had enriched diverging AMH and Neanderthal X chromosomes for reproductive incompatibilities, then we would expect to find not only a lack of Neanderthal alleles in modern human X chromosomes but a lack of AMH alleles in Neanderthal X chromosomes as well.

Taking the ratio of total AMH introgressed regions to the total size of the genome accessible to IBDmix analysis, we calculated that the Altai Neanderthal's X chromosomes contain significantly elevated proportions of AMH ancestry compared with the autosomes (1.62-fold higher, positional resampling $P = 0.0046$; Fig. 1). The Chagyrskaya and Vindija Neanderthals also have X:autosome introgression ratios significantly above 1 (positional resampling $P = 0.0001$ and $P < 0.0001$, respectively) (fig. S1). This result indicates that there is no strong selection against gene flow between AMH and Neanderthals specific to the X chromosome and that the lack of Neanderthal alleles in the modern human gene pool is not simply the result of excess incompatibility loci on the X chromosome. The historical effective population size of the Altai Neanderthals and their ancestors is not a substantial factor in this conclusion, as genetic drift does not alter the expectation of allele frequencies in average across loci (*28*, *29*).

Analysis of natural selection against elevated Neanderthal mutational load

It has been hypothesized that the larger population size of early AMH compared with that of Neanderthals allowed the early AMH to more effectively purge the population of mildly deleterious mutations and that the accumulation of this greater mutational load in Neanderthals led to their alleles being selectively disfavored compared with those found in AMH [e.g. (*9*, *10*, *30*)]. This phenomenon would predict that natural selection would also enrich the Neanderthal genome for AMH alleles at functionally important loci. Harris *et al.* (*5*) showed that this was not the case in Neanderthal autosomes, where protein-coding regions are less likely to carry AMH alleles than other regions, and we found a similar pattern in the X chromosome. As shown in Table 2, introgressed regions in the Altai Neanderthal X chromosome on average contain smaller proportions of protein-coding exons, transcription factor binding sites, and enhancers than the background rate of the

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Table 1. Hypothetical causes of lack of Neanderthal X chromosomes in modern human populations. We considered four hypotheses explaining the observed lack of Neanderthal ancestry in modern human X chromosomes. Each produces a distinct prediction for the pattern of AMH introgression in Neanderthals.

Class of driving phenomenon	Mechanism	Prediction	Support from data
Natural selection. The AMH X chromosome initially had Neanderthal ancestry levels comparable to that of AMH autosomes, but natural selection favored AMH X chromosomes with less Neanderthal ancestry.	Genomic incompatibility with accelerated functional divergence on the X chromosome (faster X effect)	Increased selection against introgressing alleles will leave the Neanderthal X chromosome with less AMH ancestry than Neanderthal autosomes. This is the pattern seen in specific autosomal regions where AMH lack Neanderthal ancestry.	**Rejected.** Neanderthal X chromosomes contain more AMH ancestry than Neanderthal autosomes.
	AMH X chromosome advantage or mutational load	Neanderthal X chromosomes will preferentially retain AMH alleles at functionally important loci.	**Rejected.** Neanderthal X chromosomes have preferentially retained AMH alleles in nonfunctional regions.
*Sex-biased admixture. Bias favoring female AMH and male Neanderthals during initial admixture introduced relatively fewer copies of Neanderthal X chromosomes to the AMH gene pool than it did Neanderthal autosomes.	Sex-biased demographic processes	Purely demographic models with sex-biased migration patterns can explain relative X and autosome introgression levels without explicit mate preference.	**Possible.** Without mating preference, the relative level of AMH ancestry on Neanderthal X chromosomes can only be reached through complex demographic models with multiple stages of distinctly biased admixture.
	*Ancestry-specific mating preference	*Consistent mate preference patterns can explain relative X and autosome introgression levels.	***Plausible.** Either "general preference for males with Neanderthal ancestry" or "general preference for females with AMH ancestry" is sufficient to explain all observations.

*The hypothesis offering the most parsimonious explanation.

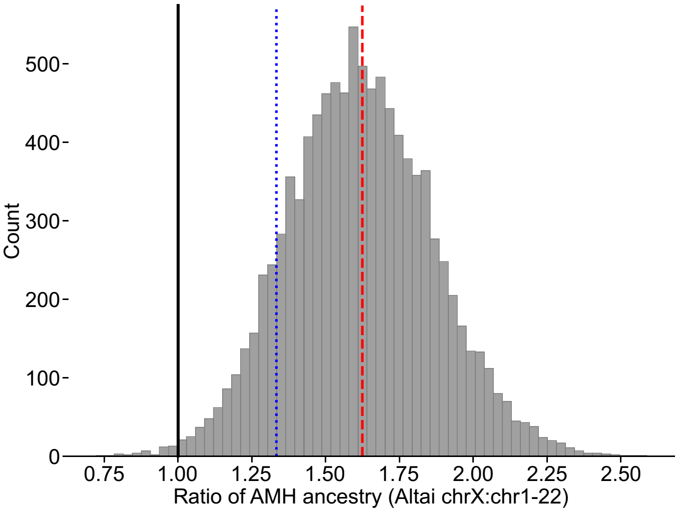

Fig. 1. Ratio of proportion of AMH introgressions in Neanderthal X chromosomes to AMH introgression in Neanderthal autosomes. By resampling AMH introgressions from 300 10-Mb autosomal windows and 16 X chromosome (chrX) windows, we made 10,000 pseudoreplicas of introgressed Neanderthal genomes. The red dashed line indicates the ratio observed in the true Altai genome. Selection against gene flow on the X chromosome would predict a value < 1 (solid black line). Simple sex-biased demographic models can only explain ratios up to 4:3 (blue dotted line).

chromosome. These and comparable results derived from the Vindija and Chagyrskya Neanderthals (table S1) indicate that the excess AMH ancestry found on the Neanderthal X chromosome is preferentially located outside of the most functional parts of the genome, not within them, and that the Neanderthal X chromosomes did not suffer from sufficient mutational load to cause them to be generally deleterious compared with AMH X chromosomes. Although there was indeed selection against gene flow of functional alleles similar to that found in the autosomes, this was not likely sufficient to drive the broad lack of Neanderthal ancestry in the modern human X chromosome gene pool.

Analysis of sex-biased demographic processes

Humans, as is common for mammals, have often been observed to have different demographic and dispersal processes for males and females, leading to sex-biased patterns of admixture [e.g. (*31*–*37*)]. A patrilocal scenario in which female AMHs are more likely than males to relocate to their mate's population of origin would by itself lead to a relative excess of AMH introgression on the Neanderthal X chromosome compared with that on the Neanderthal autosomes, even without any particular individual mate preference. However, as shown in Fig. 1, we estimate that the relative excess of Neanderthal X chromosome AMH ancestry is 1.62. Even the most extreme form of simple sex-biased demographic admixture, one with exclusively female migration (leading to all interbreeding females being AMH), would only result in a ratio of 4:3 (1.33) [(*38*, *39*), Fig. 2A, and supplementary text]. Furthermore, the composition of Neanderthal Y chromosomes indicates there was at least some interbreeding between male AMH and female Neanderthals (*40*).

Not only is it not possible to elevate the X:autosome introgression ratio over 4:3 with only a single sex-biased introgression, it is also not possible to elevate the X:autosome introgression ratio over 4:3 with repeated female AMH migration into Neanderthal populations (Fig. 2B and supplementary text). To get ratios higher than this through purely demographic processes would require at least a two-phase process with distinct sex biases at each phase, such as an initial female-majority AMH migration into one Neanderthal population followed by a female-majority migration from the first Neanderthal population into a second Neanderthal population who comprise the ancestors of the Altai individual (Fig. 2C and supplementary text).

For sex-biased demographic processes to then also account for the lack of Neanderthal X chromosomes in the modern human gene pool would further require the later migration into AMH to be the inverse: a matrilocal scenario with preferentially male Neanderthal relocation into- AMH populations to lower the AMH X:autosome ratio of Neanderthal ancestry.

Analysis of ancestry-specific mating preference

Even in the absence of sex-biased migration patterns, a simple model of mate preference is sufficient to explain the elevated X:autosome AMH introgression ratio in Neanderthals (Fig. 2D). Numerical simulations

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Table 2. Analysis of functional annotations within X chromosome introgressed regions. The X chromosome introgressed regions of the Altai Neanderthal are depleted of functionally annotated elements.

Genome	X chromosome introgressed regions[a]	Annotation	Relative composition[b]	Resampling *P* value[c]
Altai	338	Exons	0.83	0.27
		Transcription factor binding sites	0.81	0.1
		Enhancers	0.74	0.007
		Combined	0.59	$<1 \times 10^{-5}$

[a] Number of introgressed elements.

[b] Relative average proportion of each introgressed region corresponding to a particular functional annotation compared with the total (masked) X chromosome. Numbers less than one indicate a relative depletion of functional elements.

[c] Proportion of 100,000 resampling-with-replacement replicate sets of introgressed regions with average relative compositions greater than one.

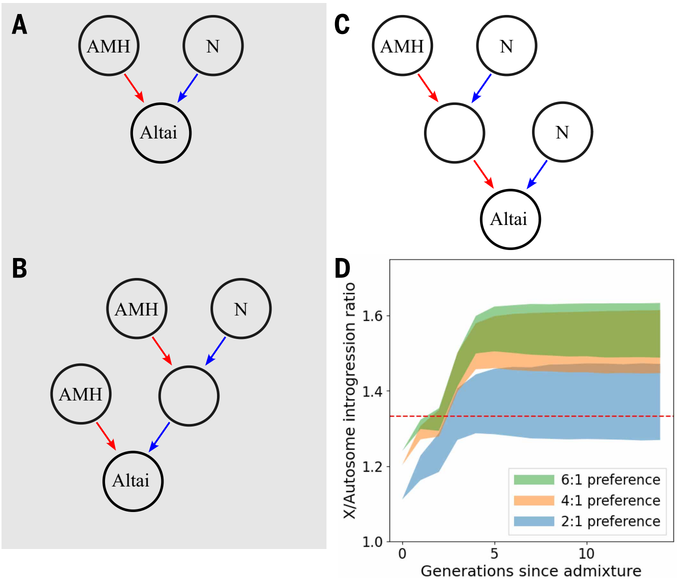

Fig. 2. Evaluation of mechanisms of sex-biased admixture. (**A** to **C**) Diagrams of purely demographic processes. Circles indicate populations, and AMH and N designate unadmixed AMHs and Neanderthals, respectively. Altai represents the population from which the Altai individual is descended. Red and blue arrows represent female- and male-majority contributions, respectively. (**D**) The middle 95% from 2500 numerical simulations of generation-by-generation Neanderthal X:autosome AMH introgression ratios, starting with an initial 5% admixture proportion at generation zero biased toward introgressing females. Subsequent generations include a bias favoring pairs of male Neanderthals with hybrid females over female Neanderthals with hybrid males. The gray shading behind panels (A) and (B) indicates that the models were unable to explain observed Neanderthal X:autosome AMH introgression ratios over 4:3.

indicate that a preference for AMH females or females of predominantly AMH ancestry over AMH males or males of predominantly AMH ancestry could have quickly driven the Neanderthal X:autosome AMH introgression ratio to greater than 4:3 shortly after a simple introgression event. This phenomenon can be seen across a wide spectrum of model parameters and implementation details (fig. S2). The same direction of preference also explains the direction of deviation of Neanderthal X:autosome introgression ratio in modern humans (fig. S3), though the effect captured by these simulations is not as extreme. Mate preference is therefore a parsimonious mechanism for explaining the sex bias that we inferred in the AMH-Neanderthal admixture process, but it does not exclude the possibility of demographic sex biases playing an important role. The rapidity with which mating preference alters the introgression proportion is consistent with the observation that Neanderthal deserts appear on the X chromosomes of even the earliest Eurasian AMH genomes (*3*).

Although we rejected both broad natural selection limiting X chromosome gene flow between AMH and Neanderthals and broad selection favoring functional AMH X chromosome alleles as sufficient hypotheses for driving the observed patterns of AMH-Neanderthal introgression, we did not rule out more complicated scenarios combining selection and sex biases, such as natural selection acting as a modifying force on top of the strong signature left by sex bias. Furthermore, although we showed mate preference to be a parsimonious explanation for sex bias over purely demographic models, they are not mutually exclusive; differential migration and mate preference may all have been at play simultaneously. Indeed, the depletion of AMH introgression in putatively functional parts of the Neanderthal X chromosome (compared with the chromosome as a whole), and the extreme lack of Neanderthal introgression in AMH X chromosomes suggests that something such as the faster X hypothesis may well be supplementing the bias in mate preference. In addition to evolutionary and demographic forces driving chromosomal-scale patterns in genomic composition, individual loci may have experienced distinctive forces shaping the apportioning of their diversity, including instances of adaptive introgression and other forms of natural selection [e.g., (*41*–*43*)]. Neutral demographic processes, including deep structure of early modern humans as proposed by Ragsdale *et al.* (*44*), do not provide a mechanism for differential introgression rates between autosomes and X chromosomes. However complex a demography may be, if males and females follow the same patterns and natural selection is not generating a chromosome-specific filter for or against gene flow, then both the X chromosome and the autosomes will, on average, receive the same amount of introgression [e.g., (*9*, *45*, *46*)]. Fundamentally, the patterns that we observed in AMH-Neanderthal divergence and hybridization follow traditional processes of speciation and were likely colored by a persistent preference for pairings between males of predominantly Neanderthal ancestry and females of predominantly AMH ancestry over the reverse. The bias that we inferred seems to have remained consistent across admixture events separated by 200,000 years. Although we do not know what drove the biases in either event, the potential for preferences in mate choice to persist across time and space have been documented in both human and animal studies [e.g., (*47*–*52*)].

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REFERENCES AND NOTES

1. L. Skov *et al.*, *Nature* **582**, 78–83 (2020).
2. B. Vernot *et al.*, *Science* **352**, 235–239 (2016).
3. L. N. M. Iasi *et al.*, *Science* **386**, eadq3010 (2024).
4. A. P. Sümer *et al.*, *Nature* **638**, 711–717 (2025).
5. D. N. Harris *et al.*, *Curr. Biol.* **33**, 4905–4916.e5 (2023).
6. B. Y. Kim, C. D. Huber, K. E. Lohmueller, *PLOS Genet.* **14**, e1007741 (2018).
7. M. Steinrücken, J. P. Spence, J. A. Kamm, E. Wieczorek, Y. S. Song, *Mol. Ecol.* **27**, 3873–3888 (2018).
8. A. B. Wolf, J. M. Akey, *PLOS Genet.* **14**, e1007349 (2018).
9. I. Juric, S. Aeschbacher, G. Coop, *PLOS Genet.* **12**, e1006340 (2016).
10. E. T. Chevy, E. Huerta-Sánchez, S. Ramachandran, *PLOS Genet.* **19**, e1010399 (2023).
11. L. Li, T. J. Comi, R. F. Bierman, J. M. Akey, *Science* **385**, eadi1768 (2024).
12. M. J. Hubisz, A. L. Williams, A. Siepel, *PLOS Genet.* **16**, e1008895 (2020).
13. L. Chen, A. B. Wolf, W. Fu, L. Li, J. M. Akey, *Cell* **180**, 677–687.e16 (2020).
14. K. Prüfer *et al.*, *Nature* **505**, 43–49 (2014).
15. K. Prüfer *et al.*, *Science* **358**, 655–658 (2017).
16. F. Mafessoni *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **117**, 15132–15136 (2020).
17. H. A. Orr, *Genetics* **144**, 1331–1335 (1996).
18. T. Dobzhansky, *Genetics and the Origin of Species* (Columbia Univ. Press, 1937).

19. W. Bateson, *Darwin and Modern Science*, A. C. Steward, Ed. (Cambridge Univ. Press, 1909), pp. 85–101.
20. H. J. Muller, *New Systematics*, J. Huxley, Ed. (The Clarendon Press, 1940), pp. 185–268.
21. H. A. Orr, M. Turelli, *Evolution* **55**, 1085–1094 (2001).
22. J. Bechsgaard *et al.*, *Mol. Biol. Evol.* **36**, 1281–1293 (2019).
23. A. Kousathanas, D. L. Halligan, P. D. Keightley, *Genetics* **196**, 1131–1143 (2014).
24. D. Garrigan, S. B. Kingan, A. J. Geneva, J. P. Vedanayagam, D. C. Presgraves, *Genome Biol. Evol.* **6**, 2444–2458 (2014).
25. V. Avila *et al.*, *Genome Biol. Evol.* **6**, 2968–2982 (2014).
26. J. E. Mank, B. Vicoso, S. Berlin, B. Charlesworth, *Evolution* **64**, 663–674 (2010).
27. B. Charlesworth, J. A. Coyne, N. H. Barton, *Am. Nat.* **130**, 113–146 (1987).
28. K. M. Lee, G. Coop, *Genetics* **207**, 1591–1619 (2017).
29. W. J. Ewens, *Mathematical population genetics: Theoretical introduction* (Springer, **vol. 27**, 2004).
30. K. Harris, R. Nielsen, *Genetics* **203**, 881–891 (2016).
31. A. Koenig, C. Borries, *Evol. Anthropol.* **21**, 108–112 (2012).
32. E. D. Gunnarsdóttir *et al.*, *Nat. Commun.* **2**, 228 (2011).
33. J. Eriksson *et al.*, *Mol. Ecol.* **15**, 939–949 (2006).
34. C. J. Holden, R. Mace, *Proc. Biol. Sci.* **270**, 2425–2433 (2003).
35. H. Oota, W. Settheetham-Ishida, D. Tiwawech, T. Ishida, M. Stoneking, *Nat. Genet.* **29**, 20–21 (2001).
36. M. Stoneking, *Nat. Genet.* **20**, 219–220 (1998).
37. C. R. Ember, *Behav. Sci. Res.* **10**, 199–227 (1975).
38. A. Goldberg, N. A. Rosenberg, *Genetics* **201**, 263–279 (2015).
39. J. M. Lind *et al.*, *Hum. Genet.* **120**, 713–722 (2007).
40. M. Petr *et al.*, *Science* **369**, 1653–1656 (2020).
41. G. Greenbaum *et al.*, *Nat. Commun.* **10**, 5003 (2019).
42. D. Enard, D. A. Petrov, *Cell* **175**, 360–371.e13 (2018).
43. F. Racimo, S. Sankararaman, R. Nielsen, E. Huerta-Sánchez, *Nat. Rev. Genet.* **16**, 359–371 (2015).
44. A. P. Ragsdale *et al.*, *Nature* **617**, 755–763 (2023).
45. A. Sedghifar, Y. Brandvain, P. Ralph, G. Coop, *Genetics* **201**, 243–261 (2015).
46. P. Verdu, N. A. Rosenberg, *Genetics* **189**, 1413–1426 (2011).
47. M. R. Cunningham, A. R. Roberts, A. P. Barbee, P. B. Druen, C.-H. Wu, *J. Pers. Soc. Psychol.* **68**, 261–279 (1995).
48. D. I. Perrett, K. A. May, S. Yoshikawa, *Nature* **368**, 239–242 (1994).
49. D. I. Perrett *et al.*, *Nature* **394**, 884–887 (1998).
50. G. Rhodes *et al.*, *Perception* **30**, 611–625 (2001).
51. A. P. Møller, R. Thornhill, *Am. Nat.* **151**, 174–192 (1998).
52. C. L. Apicella, A. C. Little, F. W. Marlowe, *Perception* **36**, 1813–1820 (2007).
53. D. N. Harris, danharris-lab/Neanderthal_NHR_Manuscript: Code for Harris et al (2023) and Platt et al (). Release v1.0.0, Zenodo (2025); https://doi.org/10.5281/zenodo.17944780.
54. D. N. Harris, A. Platt, S. A. Tishkoff, Neanderthal_Sex_Bias_2025. Version v1, Zenodo (2026); https://doi.org/10.5281/zenodo.17944925.

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SUPPLEMENTARY MATERIALS

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Editor's summary

Although a low level of Neanderthal ancestry is present in most humans, these regions are not uniformly distributed. A handful of regions in the autosome are entirely devoid of such ancestry in essentially all living humans, and the X chromosome is strongly depleted across its sequence. Platt *et al*. modeled the possible demographic processes and selection that could have produced this pattern. They found that these patterns are most consistent with Neanderthal contributions to human populations being heavily male biased. The concurrent additional depletion in functional regions on the X chromosome suggests that the effects of this skew may have been strengthened by negative selection on Neanderthal variants. —Corinne Simonti

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