

RESEARCH ARTICLE SUMMARY

HUMAN EVOLUTION

Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes

PingHsun Hsieh, Mitchell R. Vollger, Vy Dang, David Porubsky, Carl Baker, Stuart Cantsilieris, Kendra Hoekzema, Alexandra P. Lewis, Katherine M. Munson, Melanie Sorensen, Zev N. Kronenberg, Shwetha Murali, Bradley J. Nelson, Giorgia Chiatante, Flavia Angela Maria Maggiolini, H el ene Blanch e, Jason G. Underwood, Francesca Antonacci, Jean-Fran ois Deleuze, Evan E. Eichler*

INTRODUCTION: Characterizing genetic variants underlying local adaptations in human populations is one of the central goals of evolutionary research. Most studies have focused on adaptive single-nucleotide variants that either arose as new beneficial mutations or were introduced after interbreeding with our now-extinct relatives, including Neanderthals and Denisovans. The adaptive role of copy number variants (CNVs), another well-known form of genomic variation generated through deletions or duplications that affect more base pairs in the genome, is less well understood, despite evidence that such mutations are subject to stronger selective pressures.

RATIONALE: This study focuses on the discovery of introgressed and adaptive CNVs that

have become enriched in specific human populations. We combine whole-genome CNV calling and population genetic inference methods to discover CNVs and then assess signals of selection after controlling for demographic history. We examine 266 publicly available modern human genomes from the Simons Genome Diversity Project and genomes of three ancient hominins—a Denisovan, a Neanderthal from the Altai Mountains in Siberia, and a Neanderthal from Croatia. We apply long-read sequencing methods to sequence-resolve complex CNVs of interest specifically in the Melanesians—an Oceanian population distributed from Papua New Guinea to as far east as the islands of Fiji and known to harbor some of the greatest amounts of Neanderthal and Denisovan ancestry.

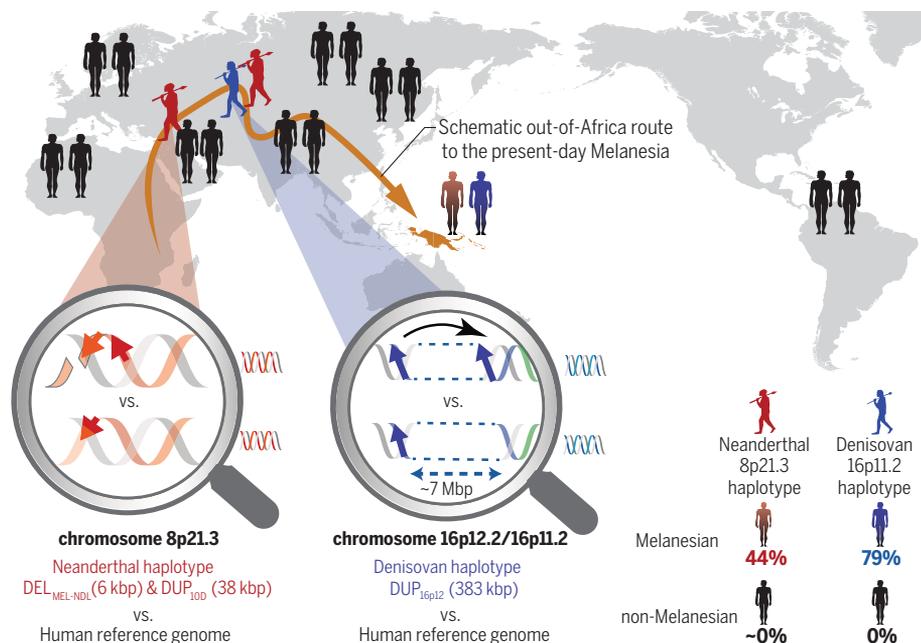
RESULTS: Consistent with the hypothesis of archaic introgression outside Africa, we find a significant excess of CNV sharing between modern non-African populations and archaic hominins ($P = 0.039$). Among Melanesians, we observe an enrichment of CNVs with potential signals of positive selection ($n = 37$ CNVs), of which 19 CNVs likely introgressed from archaic hominins. We show that Melanesian-stratified CNVs are significantly associated with signals of positive selection ($P = 0.0323$). Many map near or within genes associated with metabolism (e.g., *ACOT1* and *ACOT2*), development and cell cycle or signaling (e.g., *TNFRSF10D* and *CDK11A* and *CDK11B*), or immune response (e.g., *IFNLRI*). We characterize two of the largest and most complex CNVs on chromosomes 16p11.2 and 8p21.3 that introgressed from Denisovans and Neanderthals, respectively, and are absent from most other human populations. At chromosome 16p11.2, we sequence-resolve a large duplication of >383 thousand base pairs (kbp) that originated from Denisovans and introgressed into the ancestral Melanesian population 60,000 to 170,000 years ago. This large duplication occurs at high frequency (>79%) in diverse Melanesian groups, shows signatures of positive selection, and maps adjacent to *Homo sapiens*-specific duplications that predispose to rearrangements associated with autism. On chromosome 8p21.3, we identify a Melanesian haplotype that carries two CNVs, a ~6-kbp deletion, and a ~38-kbp duplication, with a Neanderthal origin and that introgressed into non-Africans 40,000 to 120,000 years ago. This CNV haplotype occurs at high frequency (44%) and shows signals consistent with a partial selective sweep in Melanesians. Using long-read sequencing genomic and transcriptomic data, we reconstruct the structure and complex evolutionary history for these two CNVs and discover previously undescribed duplicated genes (*TNFRSF10D1*, *TNFRSF10D2*, and *NPIP16*) that show an excess of amino acid replacements consistent with the action of positive selection.

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CONCLUSION: Our results suggest that large CNVs originating in archaic hominins and introgressed into modern humans have played an important role in local population adaptation and represent an insufficiently studied source of large-scale genetic variation that is absent from current reference genomes. ■



Large adaptive-introgressed CNVs at chromosomes 8p21.3 and 16p11.2 in Melanesians. The magnifying glasses highlight structural differences between the archaic (top) and reference (bottom) genomes. Neanderthal (red) and Denisovan (blue) haplotypes encompassing large CNVs occur at high frequencies in Melanesians (44 and 79%, respectively) but are absent (black) in all non-Melanesians. These CNVs create positively selected genes (*TNFRSF10D1*, *TNFRSF10D2*, and *NPIP16*) that are absent from the reference genome.

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Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes

PingHsun Hsieh¹, Mitchell R. Vollger¹, Vy Dang¹, David Porubsky¹, Carl Baker¹, Stuart Cantsilieris^{1*}, Kendra Hoekzema¹, Alexandra P. Lewis¹, Katherine M. Munson¹, Melanie Sorensen¹, Zev N. Kronenberg^{1†}, Shwetha Murali^{1,2}, Bradley J. Nelson^{1‡}, Giorgia Chiatante³, Flavia Angela Maria Maggolini³, H el ene Blanch e⁴, Jason G. Underwood^{1,5}, Francesca Antonacci³, Jean-Fran ois Deleuze^{4,5}, Evan E. Eichler^{1,2§}

Copy number variants (CNVs) are subject to stronger selective pressure than single-nucleotide variants, but their roles in archaic introgression and adaptation have not been systematically investigated. We show that stratified CNVs are significantly associated with signatures of positive selection in Melanesians and provide evidence for adaptive introgression of large CNVs at chromosomes 16p11.2 and 8p21.3 from Denisovans and Neanderthals, respectively. Using long-read sequence data, we reconstruct the structure and complex evolutionary history of these polymorphisms and show that both encode positively selected genes absent from most human populations. Our results collectively suggest that large CNVs originating in archaic hominins and introgressed into modern humans have played an important role in local population adaptation and represent an insufficiently studied source of large-scale genetic variation.

Upon migration out of their ancestral homeland, our ancestors likely experienced pressure to adapt to new environments. Genomic surveys with single-nucleotide variants (SNVs) have provided evidence for local genetic adaptations (1–4) and the acquisition of variants introgressed from other hominins and subsequently under positive selection in modern humans (5–7). Copy number variants (CNVs) are a form of structural variation, including deletions, duplications, and multi-allelic CNVs, that are >50 base pairs (bp) in length and affect at least five times as many base pairs as SNVs per diploid human genome (8–10). When compared with the relative abundance of SNVs, structural variants are three times as likely to be associated with a genome-wide association signal and 50 times as likely to be associated with expressed quantitative trait loci (eQTL) (11). Although larger CNVs are generally deleterious and associated with disease, examples of adaptive CNVs in humans have been documented (12–15). However, relatively little is known about the ex-

tent to which CNVs contribute to the genetic basis of local adaptation and, more importantly, whether CNVs introgressed from other hominins may have been targets of adaptive selection.

In this work, we systematically searched for genome-wide evidence for selective and archaic introgressed CNVs among Melanesian genomes. Melanesia, a subregion of Oceania, is characterized by island populations distributed across the Bismarck Archipelago and Bougainville Island, just to the east of New Guinea. Melanesians have likely developed adaptations to diet (16), infectious diseases (17), and body size (18) as a result of the tropical island environment. In addition, Melanesians have been relatively isolated over most of their history (>50,000 years), with major influences from populations to the west occurring only during the past 3000 years (19, 20). Melanesians also carry some of the greatest amounts of ancestry from both known archaic hominins, Denisovans (3 to 5%) (21–23) and Neanderthals (1 to 3%) (24), allowing for insights into the role of introgression in human evolution.

An excess of archaic hominin CNVs in non-African populations

We began by constructing a database of 5135 archaic CNVs (table S1) from previous sequence read-depth analyses of genomes of three ancient hominins—a Denisovan (25), a Neanderthal (26) from the Altai Mountains in Siberia, and a Neanderthal from Croatia (24). We compared these archaic genomes to a diversity panel of 17 high-coverage modern human genomes from the Simons Genome Diversity

Project (SGDP) (24). We genotyped these CNVs in 249 genomes from the SGDP panel (27) and 72 nonhuman great ape genomes (28) and then parsimoniously classified CNV events as lineage-specific or shared with modern humans and other ape species. We found that 2684 of the 5135 CNV loci in modern humans are copy number polymorphic in the archaic genomes [i.e., at least one of the three archaic genomes has a copy number estimate not equal to 2]; of these, 142 CNVs are likely derived relative to the 72 nonhuman primate genomes, which are fixed at a diploid copy number (CN2) for these loci. We defined a CNV as hominin specific if it is fixed in CN2 among all nonhuman primate samples and is variable in copy number in at least one hominin sample. Among the 402 hominin-specific CNVs (table S2), 13% (51 of 402) of the CNVs are specifically shared between the three Eurasian archaic hominins and non-African samples. The amount of shared CNVs between the archaic and non-African samples is unlikely under a null expectation ($P = 0.039$, 100,000 permutation simulations; fig. S1). Despite the small sample size of three archaic genomes, our result is consistent with recent evidence for archaic admixture found in Eurasia and suggests that some of the shared CNVs might result from archaic introgression.

Discovery of single-nucleotide and population-stratified CNVs

We performed a more comprehensive computational analysis to discover and assess patterns of single-nucleotide and structural variation in the SGDP populations (29). We identified population-stratified CNVs and then tested for selection and introgression by using SNVs from the diploid sequence flanking population-stratified CNVs (29). Using five CNV callers, we discovered 368,256 autosomal CNVs, of which 93.5% were identified by a single CNV caller (fig. S2 and table S3). We focused on a conserved call set of 19,211 CNVs constructed by applying a variety of quality control filters (fig. S3) (29). We used orthogonal single-nucleotide polymorphism microarray data to determine an overall validation rate of 83.5% (68.2% for duplications and ~100% for deletions) (table S4) (29).

To identify population-stratified CNVs, we applied three statistics quantifying the differences in copy number between a focal population and all the other SGDP samples: V_{ST} , Mann-Whitney U (MWU), and D_{median} (29). After removing admixed individuals (fig. S4), we grouped the remaining SGDP samples ($n = 249$ individuals) into eight focal populations: sub-Saharan Africans ($n = 33$), Native Americans ($n = 20$), East Asians ($n = 47$), Europeans ($n = 51$), Melanesians ($n = 16$), Middle Easterners ($n = 22$), South Asians ($n = 38$), and Siberians ($n = 22$) (29). We found little to no

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correlation between the focal population sample size and the number of stratified CNVs identified by V_{ST} ($r = -0.16$, $P = 0.699$) and MWU test ($r = -0.19$, $P = 0.638$) compared with those obtained by the D_{median} test ($r = -0.73$, $P = 0.039$) (fig. S5). In addition, there is a strong correlation between the Bonferroni P values of the MWU and V_{ST} tests ($r = -0.65$, $P < 2 \times 10^{-16}$); however, 233 CNVs have $V_{ST} > 0.1$ but with MWU Bonferroni's $P > 0.05$, indicating that the two tests are complementary. To conservatively identify stratified CNVs in a focal population, we used the following criteria: (i) $V_{ST} > 0.1$, (ii) Bonferroni P value of the MWU test < 0.05 , and (iii) $D_{median} > 0.5$ (fig. S6). Although the number varied by population (table S5), we observed more stratified CNVs per population than expected by chance ($P < 0.0105$, 10,000 nonparametric permutation simulations) (29), suggesting that the enrichment of stratified CNVs is unlikely to be the result of sampling errors. Because Melanesians share the most introgressed alleles with archaic lineages (an estimated 2 to 4% from both Denisovan and Neanderthal), we focused on this population for a more detailed investigation of introgressed and selected CNVs.

Tests for selective and archaic introgressed CNVs in Melanesians

We considered two possible origins for the population-stratified CNVs: The events could have arisen de novo or, alternatively, could have introgressed from other hominins and then subsequently risen to high frequency by the action of natural selection or demographic processes, including drift. To distinguish between these hypotheses, we applied a variety of population genetic statistics that use both allele frequency and linkage disequilibrium information of SNVs flanking the CNVs for additional evidence of archaic hominin introgression and/or signatures of positive selection (29). Potential biases on the test statistics owing to population history were controlled through coalescent simulations on the basis of the inferred best-fit demographic models for Melanesians. We define the significance of each test as the fraction of simulations with test statistic values greater than or equal to the observed value in the real data (29). A test for a window is significant if its P value is < 0.05 . Among the models we tested (table S6), our best-fit model (fig. S7; log-likelihood = $-103,386$) estimates that the ancestors of Africans and non-Africans diverged $\sim 74,000$ years ago [95% confidence interval (CI): 73,321 to 75,199 years ago], followed by Melanesian–East Asian divergence $\sim 52,000$ years ago (95% CI: 51,450 to 52,591 years ago), consistent with recent reports (19). Our demographic model confirms moderately high gene flow from East Asians to Melanesians [95% CI for $N_{AMH} * m_{MEL-EA} = 1.109$ to $1.128 > 1$ (N_{AMH} , effective population

size of anatomically modern humans; m_{MEL-EA} , migration rate from East Asia to Melanesia); table S7]. This finding is notable because there is evidence for East Asian gene flow into Melanesians, especially in the lowland groups, which constitute approximately one-third of our Melanesian sample set (19, 20).

Our coalescent simulations (fig. S8 and table S8) (29) generally recapitulated the empirical variation pattern of SNVs (fig. S9A) and demonstrated the utility of our approach to identify non-neutrally evolved loci (fig. S9, B and C). We used these parametric coalescent simulations to estimate significance of selection and introgression at individual loci. Among Melanesians, we identified signatures of positive selection at 37 distinct CNV loci [$P < 0.05$, population branch statistic (PBS)] (2) (Fig. 1) and signals of introgression [f_D test (30) at 24 and 28 CNV loci using Neanderthal and Denisovan genomes as archaic references, respectively]. Notably, more than 51% of the selective CNV candidates (19 of 37 CNVs) also have introgression signals at the flanking diploid sequences (Table 1 and tables S9 and S10)—an observation that is highly unlikely ($P = 0.0004$, 10,000 nonparametric permutations). However, we hypothesize that this strong correlation is likely driven by the association between population-stratified CNVs and selection signals at their flanking sequences, because our analysis shows that Melanesian-stratified CNVs are significantly associated with selective signals ($P = 0.0323$, 10,000 nonparametric permutations) but not with archaic introgression signals ($P = 0.2282$, 10,000 nonparametric permutations) (fig. S10).

Among the adaptive introgressed CNV candidates, many map near or within genes associated with metabolism (e.g., *ACOT1* and *ACOT2*), development and cell cycle or cell signaling (e.g., *TNFRSF10D*, *CDK11A*, and *CDK11B*), or immune response (e.g., *IFNLRI*); however, the patterns are complex. For example, whereas the *ACOT1* locus harbors a deletion polymorphism common in East Asians (31, 32), we find a ~ 30 -kbp duplication of *ACOT1* in only 12 SGDP samples, including three Melanesians, thus indicating a multi-allelic CNV (figs. S11 and S12). *ACOT1* is involved in regulating cellular balance between free fatty acids and acyl-CoAs, which are critical for energy expenditure and neuronal function (31). Although the *ACOT1* deletion allele is common across populations, we found that $> 84\%$ of Melanesians retain the *ACOT1* sequences (fig. S12). Furthermore, the major Melanesian haplotype occurs at a much lower frequency in other populations ($< 11\%$) and shows extended haplotype homozygosity (EHH), a signature of positive selection (figs. S11, S13, and S14). Although a similar EHH pattern was observed in other non-Africans, most individuals in those populations carry a different allele at the core

(figs. S11 and S14). Notably, the introgression signal in Melanesians at this region is located on the minor haplotype, not the major haplotype where we observe the strongest signature of selection (figs. S13 and S14). The core SNVs (rs4903119 and rs8015976; fig. S11) on the major haplotype are also associated with eQTL differences in *ACOT1*, *ACOT2*, and the adjacent gene, *HEATR4* (GTEx Portal accessed on 24 June 2019; <https://gtexportal.org>), although additional work will be required to fully define these associations and their potential biological consequences.

It is also noteworthy that our analysis identified CNVs and structural variants with strong signals of selection that have been observed in other human populations (table S9) (29). For example, we identify a deletion-linked haplotype at the *APOBEC3A* and *APOBEC3B* locus that is fixed in Melanesians but relatively rare in other populations (figs. S15 to S19). This deletion allele has been reported at high frequency among Oceanians (32) and is associated with the risk of HIV-1 acquisition (33) as well as breast and ovarian cancers in some Eurasian populations (34). At another immunity-related locus, the alpha-defensin (*DEFB1-T1*) gene family, we find that 87.5% of Melanesians have more *DEFB1-T1* copies than other populations (figs. S20 to S23). They also carry a distinctive haplotype that is rare elsewhere (figs. S23 to S25). This locus is one of the most structurally dynamic regions in the human genome, where recurrent rearrangements have occurred during primate evolution and have been associated with diseases such as immunoglobulin A nephropathy (35, 36). At chromosome 17q21.31, we observe signals of selection and introgression. A large inversion and recurrent duplications in this region have been associated with positive selection and predisposition to disease in Europeans (37, 38). Among Melanesians, we find a nearly fixed haplotype (97%) that is more reminiscent of the ancestral haplotype, which is devoid of both the large inversion and the duplication alleles (figs. S26 to S28). The Melanesian haplotype shows multiple signals of positive selection, including significantly negative Tajima's D (-2.14 , $P = 0.007$), low nucleotide diversity ($\pi < 4.3 \times 10^{-5}$, $P = 0.042$), and elevated EHH across this region (figs. S29 to S32).

Although each of these loci will require more detailed investigation, we focus here on two of the largest and most complex copy number polymorphisms discovered among the Melanesians. Given that the DNA of the Melanesian genomes in the SGDP panel comes from cell lines, which are subject to somatic artifacts, we designed and performed experiments using additional blood-derived Melanesian DNA samples for several CNVs (fig. S33), as well as the two most complex CNV loci reported here, to safeguard against cell line artifacts.

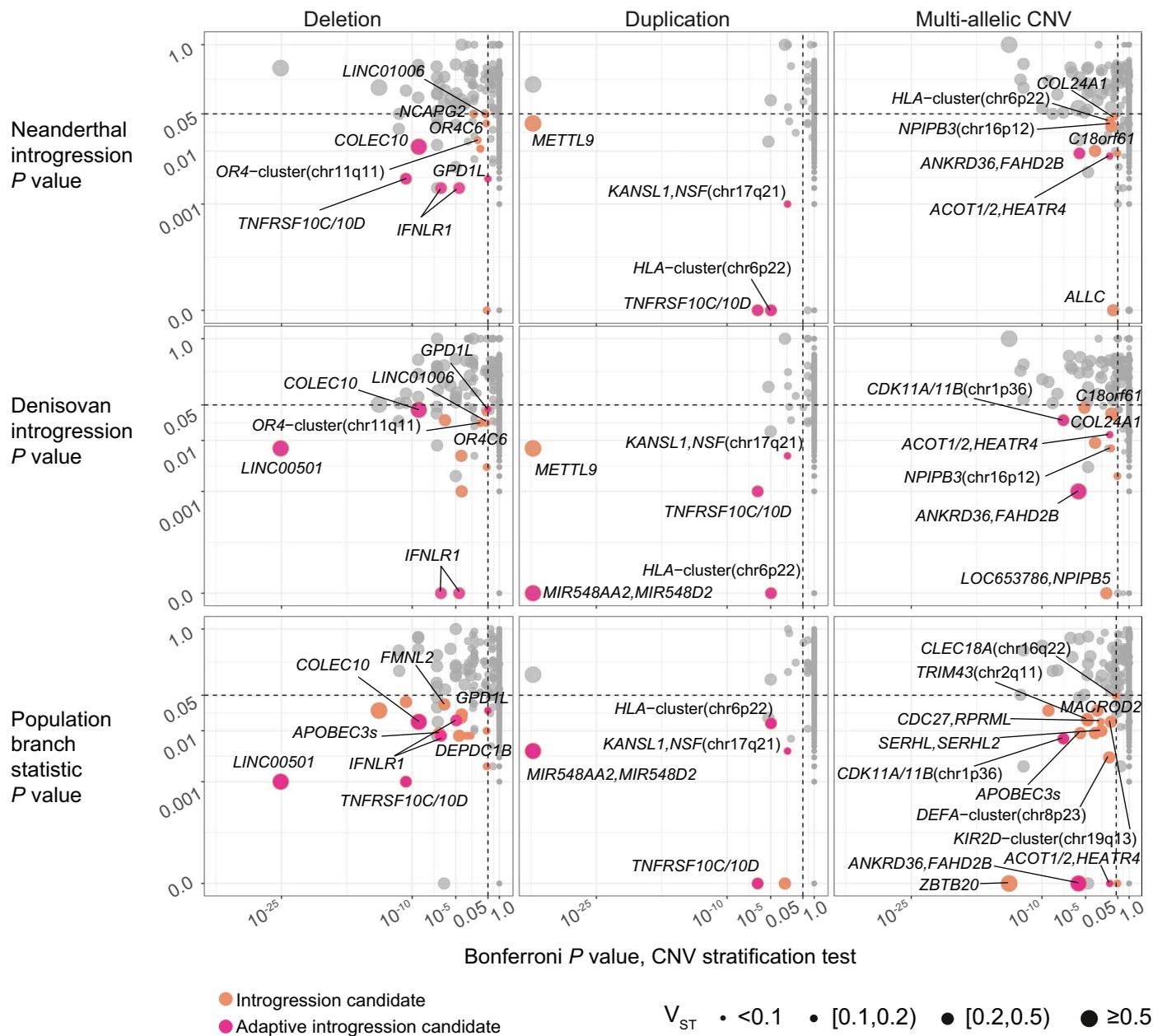


Fig. 1. Candidates for introgressed archaic and selective CNVs. Joint distributions of P values for CNV stratification (x axis, Mann-Whitney U), archaic introgression (f_D statistic, top two rows), and positive selection (population branch statistic, bottom row) tests. The archaic reference sequences used in the calculations of f_D are Neanderthals (top row) and Denisovans (middle row), respectively. CNVs that show signatures of both positive selection and archaic introgression (red circles) are distinguished from loci that show signatures of introgression only (orange circles).

Adaptive introgression of the Melanesian–Denisovan–specific duplication at chromosome 16p11.2

The top two Melanesian-stratified CNVs ($P = 2.5 \times 10^{-32}$) are a 5-kbp (chr16:21,596,722–21,601,720) duplication variant and a 73.5-kbp (chr16:22,710,041–22,783,558) duplication variant (fig. S34) originating from chromosome 16p12.2. Both events are largely restricted to Melanesians and the Denisovan archaic genome (Fig. 2A) and are thought to be involved in a single >225-kbp complex duplication (DUP_{16p12})

introgressed from the Denisovan genome (9). This region has been difficult to correctly sequence and assemble, and only recently has the sequence structure of the ancestral locus (>1.1 Mbp) been correctly resolved [KV880768.1, National Center for Biotechnology Information (NCBI) BioProject: PRJNA31257; fig. S35] (39). Unless otherwise stated, we use this patch of sequence to define the ancestral locus.

By using a series of polymerase chain reaction (PCR)–restriction digest assays to genotype an independent set of 242 blood-derived

DNA samples from diverse Melanesians across eight different population groups (Fig. 2B and table S11), we confirmed that this duplication allele is present at high frequency in Melanesians. Although DUP_{16p12} is present at high frequency in all groups [allele frequency (AF) > 0.79], introgression is nearly complete among lowland populations of West and East New Britain, Papua New Guinea (Fig. 2B and table S11). Leveraging paralogous sequence variants that distinguish the duplicated loci, we applied the f_D statistic and found significant signals for

Table 1. Top candidates for adaptive introgressed CNVs in Melanesians. *P* values for selection and introgression scans are calculated from coalescent simulations. Only loci with selection test *P* values <0.01 are listed. Variant type is determined with respect to the human reference genome. The introgression statistic (f_D) is calculated separately for Neanderthals (NDL) and Denisovans (DNS). mCNV, multi-allelic CNV; DUP, bi-allelic duplication; DEL, bi-allelic deletion. V_{ST} is a measurement of copy number stratification. See tables S9 and S10 for all candidates.

Locus	Size (bp)	Type	Median CN (Melanesians)	Median CN (all others)	V_{ST}	<i>P</i> value selection (PBS)	<i>P</i> value, introgression (f_D) archaic ref: NDL	<i>P</i> value, introgression (f_D) archaic ref: DNS	Genes within 30 kbp
chr2:97699365-97907043	207,678	mCNV	48.722	39.147	0.487	<0.001*	0.009*	0.001*	ANKRD36, FAHD2B
chr8:22886278-23003689†	117,411	DUP	4.054	3.257	0.272	<0.001*	0.003*	0.055	TNFRSF10D/10C
chr14:73990658-74053946	63,288	mCNV	3.997	2.968	0.149	<0.001*	0.008*	0.013*	ACOT1/2, HEATR4
chr3:177002637-177011375	8738	DEL	0.984	1.905	0.702	0.001*	0.363	0.007*	LINC00501
chr8:22981867-22988907	7040	DEL	1.160	2.163	0.428	0.001*	<0.001*	0.001*	TNFRSF10D/10C
chr16:22710041-22783558††	73,517	DUP	3.935	1.969	0.923	0.004*	0.179	<0.001*	MIR548AA2, MIR548D2
chr17:44170850-45157111	986,261	DUP	2.079	3.311	0.172	0.004*	0.001*	0.005*	KANSL1, NSF(chr17q21)
chr1:1568057-1683771	115,714	mCNV	3.291	4.306	0.298	0.007*	0.053	0.025	CDK11A/11B(chr1p36)
chr1:24520349-24523673	3324	DEL	0.790	1.898	0.353	0.008*	0.002*	<0.001*	IFNL1

*Significant test result.

†Newly identified genes: *TNFRSF10D1* and *TNFRSF10D2*.

††Newly identified gene: *NPIP16*.

archaic introgression at both loci ($P < 0.033$ and < 0.001 ; Fig. 1, Table 1, and table S10) using Denisovans, but not Neanderthals ($P = 0.178$; fig. S36), as the source of admixture.

Because the elevated PBS and Tajima's *D* at 16p12.2 (fig. S37) are driven by paralogous sequence variants that are not fully resolved, we sought to further investigate evidence for selection of DUP_{16p12} at its true genomic integration site. We performed a series of fluorescence in situ hybridization (FISH) experiments using probes tiled along the short arm of chromosome 16 in Melanesian cell lines (Fig. 2C, figs. S38 and S39, and tables S12 and S13) (29). Our data localized the derived Melanesian duplication to chromosome 16p11.2 between genomic coordinates of 28.93 and 30.09 Mbp (Fig. 2D). In addition, we generated long-read, high-coverage (75×) whole-genome sequences from a Melanesian individual (HGDP00550; cell line from the HGDP-CEPH panel) who carries the DUP_{16p12} variant. Using the long-read data, we further narrowed the insertion location of this duplication to a 200-kbp interval (29.48 to 29.68 Mbp) adjacent to an *NPIP* (nuclear pore-interacting protein) core duplcon (fig. S40) (29). This is a complex region of >500 kbp of segmental duplication where a *Homo sapiens*-specific duplication emerged ~280,000 years ago and, as a result, predisposes the region to recurrent structural rearrangements associated with autism and developmental delay (15, 40).

To sequence-resolve the DUP_{16p12} copy number polymorphism, we generated a Melanesian large-insert bacterial artificial chromosome (BAC) library (GM10539). From these BACs, we constructed two haplotypes of 222 and 133 kbp, partially confirming the structure of DUP_{16p12} (9) (fig. S41 and S42). To fully assemble the entire locus ab initio, we used the haplotypes

as the initial seeds to pull down long-read Melanesian whole-genome sequence data and iteratively applied the Segmental Duplication Assembler method (41) (fig. S43 and table S14). The procedure generated a ~1.8-Mbp sequence contig spanning more than 900 kbp of complex segmental duplications (Fig. 3A). We confirmed the organization and sequence accuracy (99.86%) for 220 kbp of this assembly for which we have finished BAC sequences derived from an unrelated Melanesian sample (fig. S44). Notably, the sequence-resolved assembly shows that the actual length of DUP_{16p12} duplication polymorphism is ~383 kbp, which is longer than previously thought (9). Sequence and phylogenetic analyses suggest that the variant originated from a series of complex structural changes involving duplication, deletion, and inversion events ~0.5 to 2.5 million years ago (Mya) within the Denisovan ancestral lineage, which subsequently inserted into chromosome 16p11.2 (chr16:29,640,235-29,640,459) between 0.2 to 0.5 million years ago (Fig. 3B, figs. S45 and S46, and table S15).

Within the sequence immediately flanking the 16p11.2 duplication block near the DUP_{16p12} insertion breakpoint, we observe significantly elevated PBS ($P < 0.012$) and f_D ($P < 0.021$, archaic = Denisovan) values (Fig. 2D). Once again, the introgression signal at 16p11.2 is absent when Neanderthals are used as the archaic reference [$P(f_D; \text{archaic} = \text{Neanderthal}) > 0.193$; fig. S47], consistent with a Denisovan origin. To infer the timing of the introgression event, we constructed DUP_{16p12} haplotypes for the Denisovan and Melanesian genomes by remapping the short-read data to the assembled Melanesian contig and KV880768.1 in addition to the human reference. We reconstructed the phylogeny of DUP_{16p12} using ~10-kbp sequen-

ces, where at least five high-quality Denisovan reads are present, and showed that the introgression event likely occurred ~0.06 to 0.17 million years ago (fig. S48).

The Melanesian duplication polymorphism harbors extra copies of segmental duplication sequences that are absent from most human populations, including an additional member of the *NPIP* family (42). To explore the *NPIP* coding potential at this locus, we generated full-length nonchimeric (FLNC) transcript data using Melanesian (GM10539 and GM10541) fibroblast cell lines (29). We identified FLNC transcripts that maintain the same open reading frame (ORF) and encode a previously unidentified member of the *NPIP* family, *NPIP16* (1206 amino acids), mapping exclusively to this duplication polymorphism (Fig. 3C). This Melanesian copy shows elevated pairwise dN/dS ratios (i.e., the number of nonsynonymous substitutions per nonsynonymous site to the number of synonymous substitutions per synonymous site) when compared with other closely related *NPIP* genes (RefSeq release 109) (figs. S49 and S50). Using a phylogenetic branch site test (43), we identified 32 sites as likely positively selected, including a cluster of 28 amino acid differences that occur in the last exon of *NPIP16* (Fig. 3C). Multiple sequence alignment analyses reveal that this cluster is due to two indel events of a repeat motif (GAGCGTCTGCGGG). The first indel upstream of the cluster alters the frame, whereas the second indel located downstream subsequently restores the original *NPIP* frame. These compensatory mutations resulted in a novel sequence at the C terminus of *NPIP16* (fig. S51), as opposed to the other four amino acid replacement events. Notably, at 30 of the 32 sites where there is sequence coverage (more than five reads), the

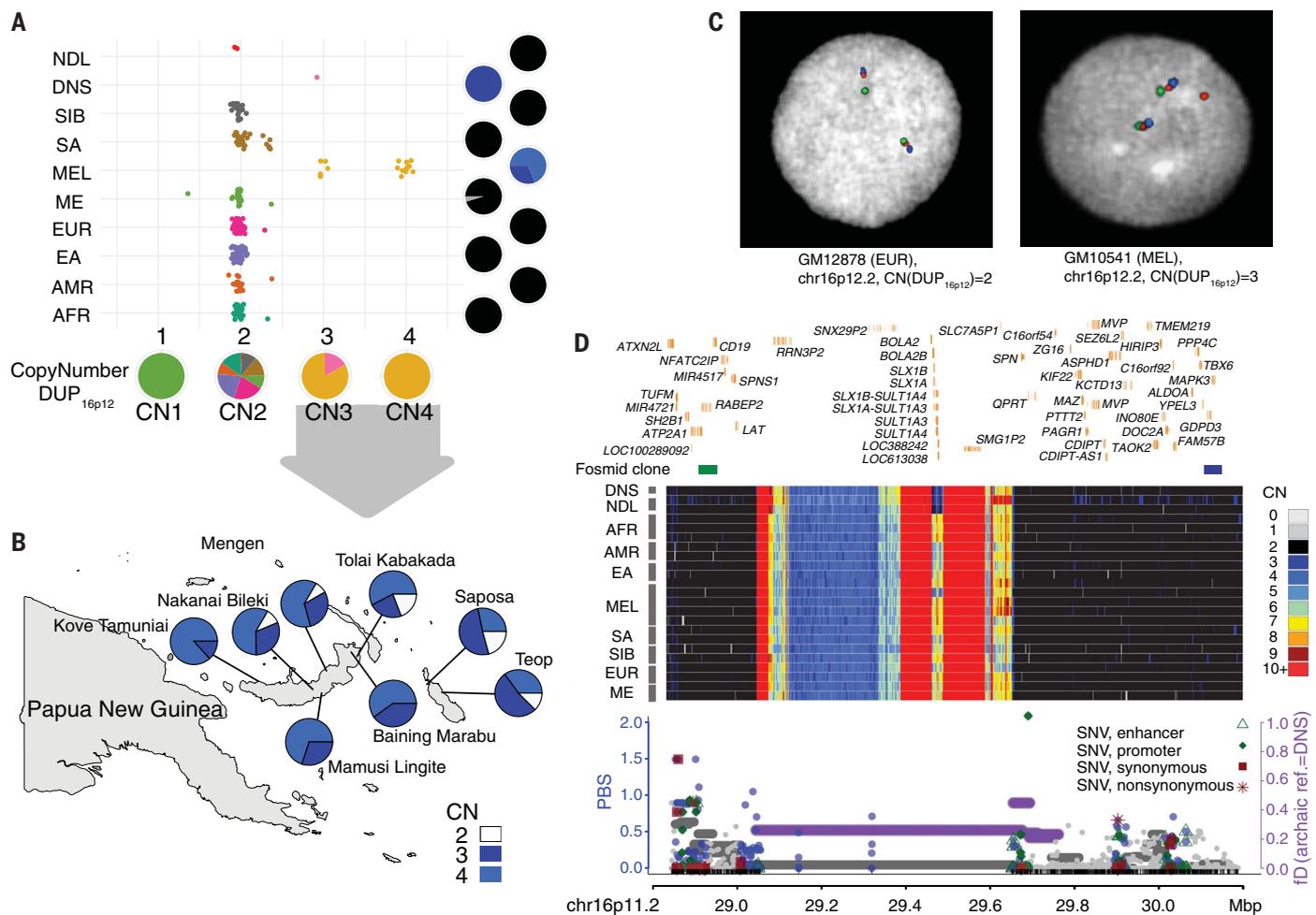


Fig. 2. Evidence for adaptive Denisovan introgression of the chromosome 16p12.2 duplication at 16p11.2 in Melaneseans. (A) Copy number (CN) estimates of DUP_{16p12} for the SGDP populations and three archaic samples. Pie charts indicate the CN frequency of populations (right) and the population fraction of CN genotypes (bottom). NDL, Neanderthals; DNS, Denisovans; SIB, Siberians; SA, South Asians; MEL, Melaneseans; ME, Middle Easterners; EUR, Europeans; EA, East Asians; AMR, Native Americans; AFR, sub-Saharan Africans. (B) Geographic distribution for the DUP_{16p12} duplication genotypes of 242 independent blood-derived DNA samples from Melaneseans. The CN color scheme matches that in (D). (C) FISH experiments using fosmid clones from 16p12.2 confirm an additional copy of DUP_{16p12} (red fosmid clone, 174222_ABC10_2_1_000044550500_M3 at 16p12.2; table S13; fig. S38) in a

Melanesean cell line (GM10541, CN3) as opposed to a European cell line (GM12878, CN2). (D) (Top) Signals of adaptive introgression in the Melaneseans at 16p11.2—the locus in which the DUP_{16p12} duplication was inserted. The heat map shows the CN distribution at chromosome 16p11.2. Fosmid clones (green: ABC10_000044688200_G16; blue: ABC10_000043626100_E12; table S13) indicate the region where the integration of DUP_{16p12} occurred at the 16p11.2 locus. (Bottom) PBS (left y axis) for SNVs (dots) and f_D [horizontal lines, representing windows of 100 SNVs, computed using Denisovans as the archaic reference, right axis] at DUP_{16p12}. Colored circles (blue) and/or horizontal lines (purple) indicate significant test statistics ($P < 0.05$). Note that introgression signals at both 16p12.2 and 16p11.2 disappear if Neanderthals are used as the archaic reference in the f_D computation (figs. S36 and S47).

Denisovan genome carries the same alleles as in the Melanesean *NPIP6B*, suggesting that most of these events emerged in the Denisovan lineage.

Taken together, our findings suggest that the 383-kbp duplication polymorphism in Melaneseans introgressed from Denisovan-like hominins and that it is likely an adaptive CNV. This helps to explain why this polymorphism has become nearly fixed within the Melanesean populations (>80%) despite its large size, which is typically regarded as selectively disadvantageous (8, 44). Our analyses support a model where the locus on chromosome 16p11.2 served

as an acceptor site for large independent duplication events twice in the recent history of the *Homo* genus—once in the *H. sapiens* lineage and once in the ancestral Denisovan lineage where novel duplicate genes have emerged. Notably, the Melanesean-specific gene *NPIP6B* shows ~3% amino acid divergence and evidence of positive selection despite its recent origin. Introgression has generated an amalgam of these two duplications, creating a massive duplication block (~900 kbp) in Melaneseans and related populations. Given the localization of this duplication polymorphism to the recurrent autism-associated breakpoint region,

we predict that these changes in the genomic architecture and the additional *NPIP6B* homologous segments (orange triangles in Fig. 3; see also table S16) will affect the frequency of recurrent rearrangements associated with autism in these populations.

Introgression of Neanderthal CNVs at chromosome 8p21.3 shows signals of positive selection

Another signal of selection (PBS/ F_{ST}) and introgression ($P < 0.005$) in Melaneseans maps to a 76-kbp region on chromosome 8 (chr8:22, 969,611-23,045,069; Fig. 4, A and B, and

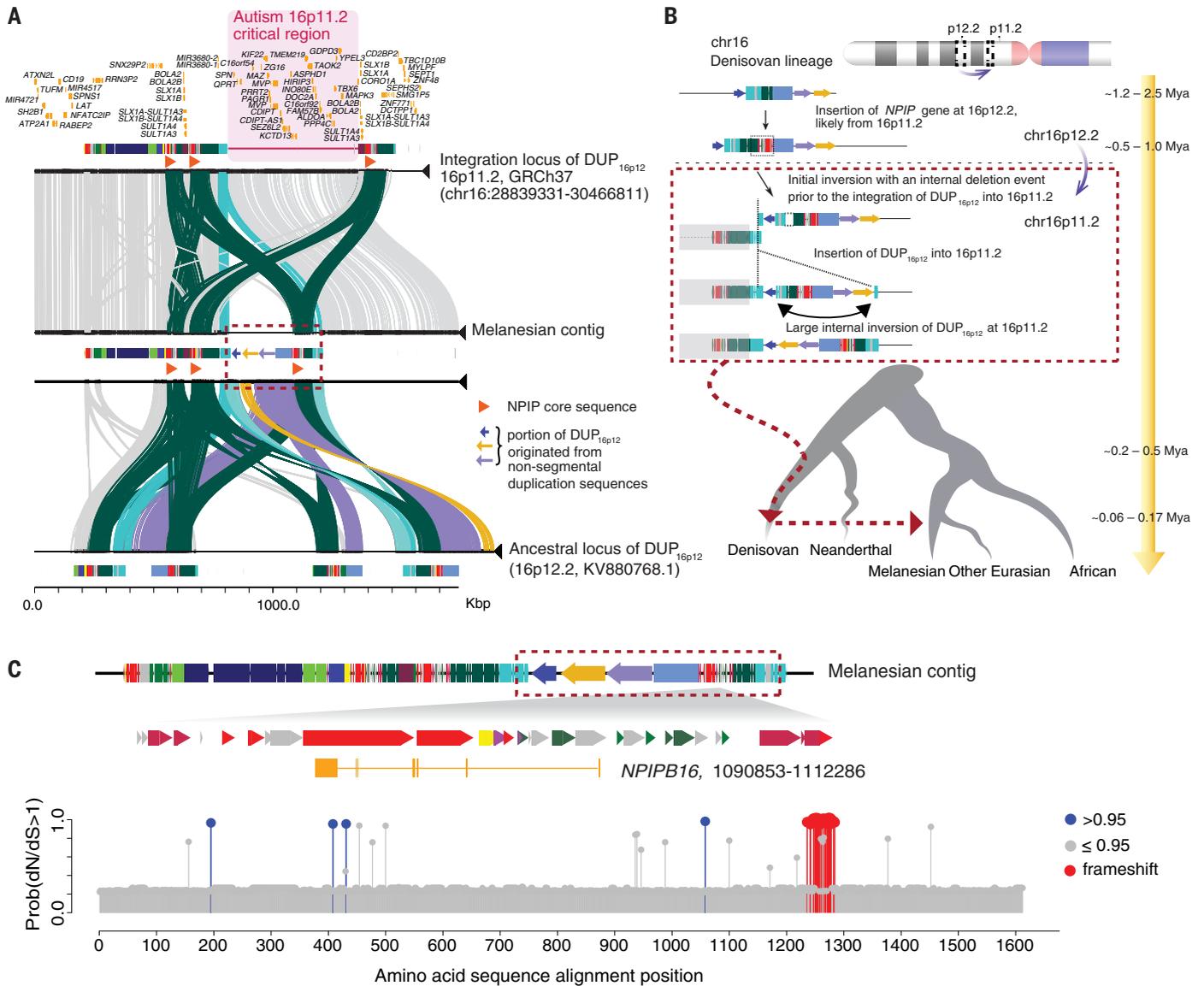


Fig. 3. Reconstruction of the structure and evolutionary history for the Melanesian-Denisovan duplication at chromosome 16p11.2. (A) Structural comparison of chromosome 16p11.2 (human genome reference GRCh37; top), the structure-resolved Melanesian contig (middle) at 16p11.2, and the ancestral locus of DUP_{16p12} at 16p12.2 (KV880768.1; NCBI BioProject: PRJNA31257; bottom). Colored boxes denote annotated human segmental duplications, and lines connecting the sequences show regions of homology. Duplicated segments specific to the Melanesian genome (red dashed box) are indicated if derived from unique (colored arrows) or previous duplication (colored rectangles) sequences. The region of recurrent genome rearrangements associated with autism is highlighted (pink shaded area). (B) Schematic model for the evolution of the DUP_{16p12} duplication. The schematic depicts

structural changes over time, leading to the Melanesian architecture. Evolutionary timing was estimated on the basis of a series of phylogenetic analyses using structure-resolved sequences from 16p12.2 and 16p11.2 loci (31). The absence of intermediate genomes makes the order of some structural changes uncertain. (C) A new member of the *NPIP* gene family, *NPIP*B16 (1206 amino acids), in the Melanesian DUP_{16p12} sequence with predicted sites of positive selection. *dN/dS* analyses show positively selected amino acid substitutions at *NPIP*B16 lineages (blue circles) compared with other *NPIP*B genes. Note that the cluster of massive amino acid changes (red circles) at position 1236 to 1284 (alignment space) is predicted to result from two indel events in the C terminus of *NPIP*B16 as opposed to a series of independent amino acid substitution events (fig. S51).

fig. S52). Within this region, there are two stratified CNVs: a 6-kbp deletion (DEL_{MEL-NDL}, chr8:22,982,302-22,988,251; CNV stratification $P < 8.9 \times 10^{-11}$) and a 31-kbp duplication (DUP_{10D}, chr8:22,991,347-23,022,738; CNV stratification $P < 1.5 \times 10^{-6}$) encompassing *TNFRSF10D* (tumor necrosis factor receptor superfamily 10D). The copy number estimates

of both structural variants (DEL_{MEL-NDL} and DUP_{10D}) are highly correlated among Melanesian samples (Pearson's correlation $r = -0.64$, $P < 0.05$) but not in other SGDP populations (fig. S53). Multiple lines of evidence, including signals of excess heterozygosity, sequence read-depth analyses, and FISH assays, confirm that the duplication variant DUP_{10D} is the major

allele among Melanesians (AF = 0.66) but is also found among a subset of Africans (AF = 0.12) as well as in the three archaic genomes where it is heterozygous (AF = 0.5) (Fig. 4B and figs. S53 to S55). The deletion allele DEL_{MEL-NDL} shows a restricted distribution, as it is observed among Melanesians (AF = 0.437), the two Neanderthals (AF = 1.0), and at low frequency

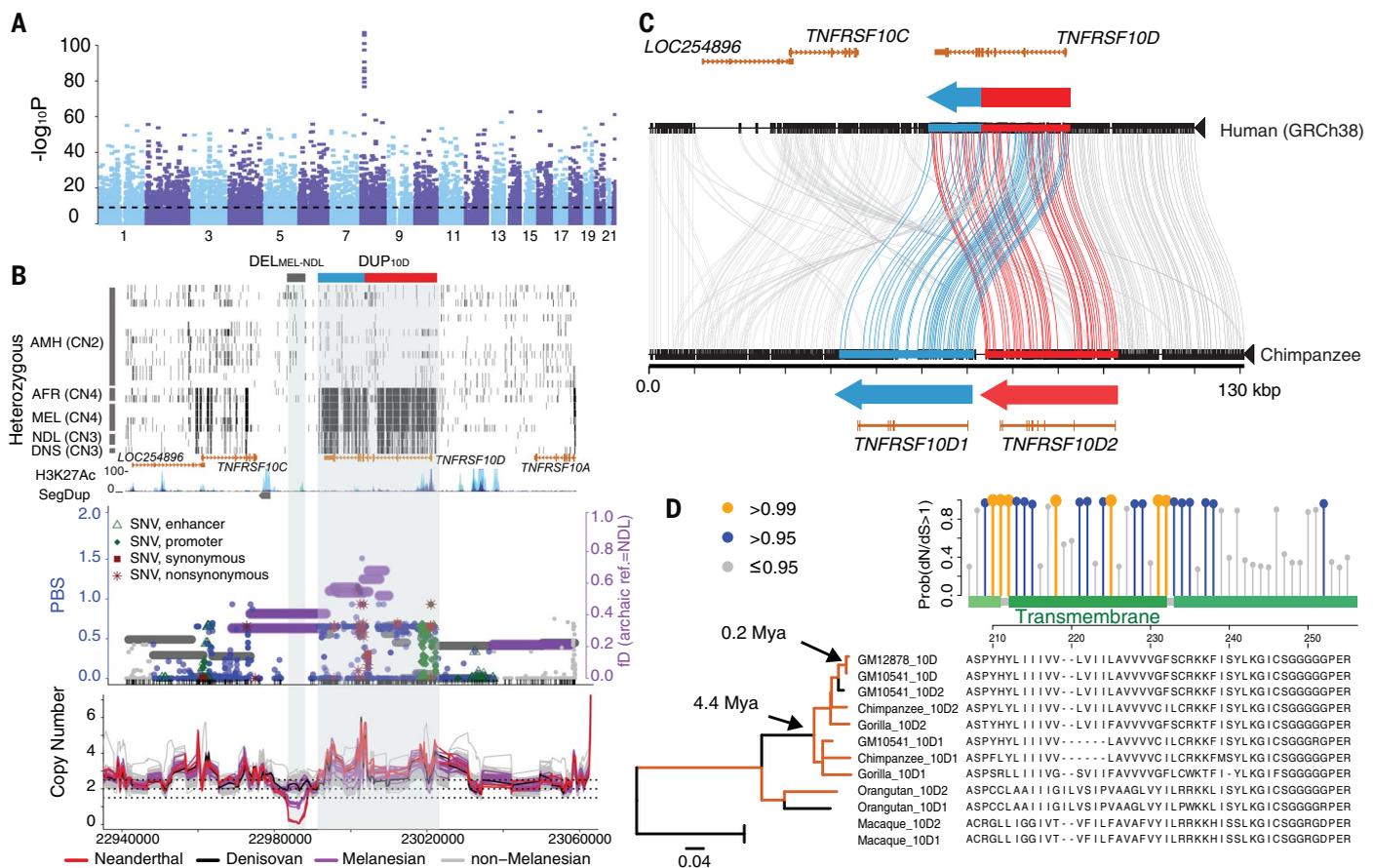


Fig. 4. Highly stratified CNVs at 8p21.3 in Melanesians and evidence for gene duplication and fusion followed by adaptive evolution at the $TNFRSF10D$ locus. (A) Manhattan plot for the P values of window-based F_{ST} test. The horizontal dashed line indicates the genome-wide Bonferroni-corrected significance. (B) (Top) Distribution of heterozygous sites (short black vertical bars) for a subset of the SGDP samples. The gray box at the top shows the location of DEL_{MEL_NDL} , whereas the blue-red box indicates the derived $TNFRSF10D$ form, a fusion of $TNFRSF10D1$ (blue) and $TNFRSF10D2$ (red), as shown in Fig. 3C. (Bottom) Distributions of f_D and PBS statistics, as well as CN trajectories of all samples

among South Asians ($AF = 0.013$). Using a PCR assay, we confirmed the presence of the DEL_{MEL_NDL} deletion allele in two independent sets of cell line and blood-derived Papuan DNA samples (fig. S56 and table S12) (29).

To understand the evolution of DUP_{10D} , we computed its copy number among great apes (28) and samples from the 1000 Genomes Project (1KG) (10). The DUP_{10D} variant is present among all nonhuman primates examined and segregates at low frequencies across the 1KG populations (< 0.025) but is completely absent from others, such as the Europeans (figs. S53 to S55 and S57). We used BACs to sequence the DUP_{10D} locus from chimpanzees, gorillas, orangutans, and rhesus macaques (29). Our sequence comparison analyses showed that all nonhuman ape species share the same tandem organization for the two copies of $TNFRSF10D$ ($TNFRSF10D1$ of 30.3 kbp and

$TNFRSF10D2$ of 33.0 kbp) (Fig. 4C and fig. S58). The absence of the tandem structure from the human reference genome and most extant humans suggests that the single-copy structure of $TNFRSF10D$ emerged specifically in the human lineage.

Using the chimpanzee sequence, we inferred the evolutionary breakpoints at chr8:23,003,123-23,003,255 (GRCh37) partially overlapping the fifth intron and exon of $TNFRSF10D$. We predict that the most common derived form of $TNFRSF10D$ in humans is a product of a nonallelic homologous recombination event between two ancestral genes ($TNFRSF10D1$ and $TNFRSF10D2$). The resulting gene fusion creates a hybrid consisting of the first five exons of $TNFRSF10D2$ and the last four exons of $TNFRSF10D1$. Thus, two-thirds of $TNFRSF10D1$ (~18.4 kbp) and one-third of $TNFRSF10D2$ (~11.9 kbp) are absent from most humans (figs.

across the region. (C) Comparison (Miropeats) of the major human allele versus chimpanzee genome structure, showing the tandem organization of the DUP_{10D} variant and the predicted gene models. (D) Branch-site test of positive selection (dN/dS) using FLNC transcript data shows significant selection signals ($P = 0.005$) compared with the null model and a cluster of positively selected amino acid substitutions at the transmembrane domain of $TNFRSF10D$. Coding-sequence phylogeny shows significant positive selection (orange; dN/dS ratios > 1 ; $P < 0.05$) on specific branches. Note that the orangutan paralogous sequences form a single clade as a result of interlocus gene conversion (fig. S60).

S58 and S59). Bayesian phylogenetic reconstruction of the loci show that two independent duplication events of $TNFRSF10D$ occurred in primate evolution: one in the lineage leading to the Old World monkey and the other in the ancestral lineage of all apes ~27.6 million years ago (95% highest posterior density: 19.9 to 36.1 million years ago; fig. S60). In contrast, we estimate that the gene fusion occurred 1.1 to 1.5 million years ago in the ancestral *Homo* lineage leading to modern humans, Neanderthals, and Denisovans, where it rose to high frequency among most human populations, with the exception of Melanesians.

We assessed the coding potential of the three different $TNFRSF10D$ models by sequencing full-length transcripts from Melanesian (GM10541, CN3), European (GM12878, CN2), and chimpanzee (PanTro, CN4) cell line samples (29). In chimpanzee cells, we identified a six- and a nine-exon

gene model corresponding to *TNFRSF10D1* and *TNFRSF10D2*, respectively (figs. S61 and S62). In contrast, the European CN2 sample possesses only the fusion gene, *TNFRSF10D*, whereas the heterozygous Melanesian sample shows all three gene models, including the two additional models present in chimpanzee (fig. S61). Although ORF analyses indicate that *TNFRSF10D1* carries a premature stop codon in exon 2, which truncates the canonical protein at the 59th amino acid position, a protein with 217 amino acids is still predicted, owing to the use of a second start codon in exon 2 (fig. S62). In contrast, *TNFRSF10D2* maintains an ORF with all nine exons consistent with the annotation in the human reference assembly (ENST00000312584). The more common human fusion gene effectively deletes the *TNFRSF10D1* premature stop codon (fig. S62) and thus restores the canonical ORF.

To further assess the functional importance of the *TNFRSF10D* duplicates, we examined FLNC transcript data from Melanesian (GM10541), European (GM12878), and chimpanzee fibroblast cell lines (29) and inferred orthologous gene models from *TNFRSF10D1* and *TNFRSF10D2* using gorilla, orangutan, and rhesus macaque BAC sequences. We observed a significant excess of amino acid substitutions for the three gene models, especially among the African great ape lineages (fig. S63) (29). Using a branch-site test (43), we find evidence of positive selection for both the fusion gene and the *TNFRSF10D1* copy on the human lineage and, more broadly, for both D1 and D2 in other nonhuman apes ($P = 0.005$; Fig. 4D and figs. S64 and S65). Specifically, we identify a cluster of positively selected sites corresponding to the predicted transmembrane domain of the genes (Fig. 4D and fig. S64).

In contrast to the *TNFRSF10D* duplication, the DEL_{MEL-NDL} variant is absent from all nonhuman apes, suggesting that it is derived (fig. S53). Using a PCR assay (table S17) and seven tagging SNVs [$r^2 > 0.9$ and normalized coefficient of linkage disequilibrium (D') > 0.9 ; table S18], we show that the DEL_{MEL-NDL} variant is largely restricted to the 1KG South Asian populations where it occurs at low frequencies (< 0.07 ; Fig. 5A and figs. S57 and S66). All three Neanderthal genomes, including the low-coverage Mezmaiskaya (24), are homozygous for the DEL_{MEL-NDL} haplotype, suggesting that this deletion is fixed in Neanderthals (table S18). We identify strong Neanderthal introgression signals at DEL_{MEL-NDL} among Melanesians [$P(f_D, \text{archaic} = \text{Neanderthal}) = 0.003$ and $P(S^*) = 0.043$; Fig. 4B and fig. S67], as opposed to Denisovan introgression [$P(f_D, \text{archaic} = \text{Denisovan}) = 0.06$; fig. S68]. Consistent with this, we find that all 15 DEL_{MEL-NDL}-linked SGDP haplotypes are more closely related to the Neanderthal haplotypes than any other human haplotype (fig. S69), forming

a monophyletic clade in both the haplotype network (Fig. 5B) and maximum likelihood estimated phylogenetic tree (log-likelihood = $-21,578$; fig. S70) (31). The time to the most recent common ancestor of the Neanderthal and Melanesian DEL_{MEL-NDL}-linked haplotypes is 40,000 years ago (95% CI: 0 to 122,000 years ago) and that of all human DEL_{MEL-NDL}-linked haplotypes is 120,000 years ago (95% CI: 0 to 241,000 years ago)—both are much younger than the divergence of modern humans and Neanderthals. It is worth noting that the haplotype sharing of the 18.5-kbp sequence between modern humans and Neanderthals is unlikely under a simple model of incomplete lineage sorting (ILS) with reasonable demographic parameters ($P = 0.0403$) (29).

Because the large frequency difference of the DEL_{MEL-NDL} haplotype between Melanesians and other populations can be due to the action of natural selection, we specifically tested this hypothesis. Using the deletion variant as a proxy for the beneficial allele and controlling the age of the variant in coalescent simulations (29), we find that the observed PBS value of the DEL_{MEL-NDL} deletion allele is significantly higher than expected under a null model of neutral evolution (PBS = 0.933, $P = 0.0082$; Fig. 5C). Among Melanesians, the deletion allele is always associated with DUP_{10D}. This 6-kbp deletion corresponds to a histone H3 at lysine 27 (H3K27) acetylation peak (skeletal muscle tissue), which by ChIA-PET (chromatin interaction analysis by paired-end tag) analysis associates with multiple members of the tumor necrosis factor receptor superfamily—a gene family critical for apoptosis (45).

From these observations, we developed a model to account for the recent evolution of this 8p21.3 locus (Fig. 5D). Our data support a copy number reduction of *TNFRSF10D* to create a fusion gene approximately 1.2 to 1.5 million years ago in the ancestral *Homo* lineage. The presence of the ancestral *TNFRSF10D1* and *TNFRSF10D2* in some, but not all, modern human populations likely emerged as a result of ILS. A 6-kbp deletion (DEL_{MEL-NDL}) located ~5 kbp distal to the *TNFRSF10D* locus in a putative regulatory region subsequently originated in the Neanderthal lineage, which then introgressed back into the human lineage $< 120,000$ years ago through contact with ancestral non-Africans. We predict that the unusually high frequency of the DEL_{MEL-NDL}-linked haplotype in Melanesians is a result of natural selection. The ChIA-PET data suggest that this deletion may affect the expression of nearby genes, such as *TNFRSF10C* and *TNFRSF10D* (WashU Epigenome Browser: <https://epigenomegateway.wustl.edu>).

Discussion

Despite the growing body of evidence for adaptive introgression in humans (5–7), the ex-

tent and relative contributions of adaptive introgressed CNVs in human evolution remain largely unexplored. Leveraging sequences from archaic and modern human genomes identifies adaptive introgressed CNV loci, which we resolved and characterized. The enrichment of selective and adaptive introgressed CNVs highlights their potential role in human evolution. Although we cannot rule out potential “hitchhiking” effects due to positive selection acting on nearby genes, the lack of other functional mutations of large effect (i.e., nonsynonymous variants) around our candidate loci suggests that these selection signals are driven by the stratified CNVs identified here and possibly by the genes carried within.

One possible confounding factor in such an analysis is ILS; however, we believe that this has had limited effect for several reasons. First, the time to the most recent common ancestor estimates between the Melanesian and archaic haplotypes at the 16p11.2 and 8p21.3 loci is less than 170,000 years, which is inconsistent with ILS. Second, we account for Melanesian demographic history in determining thresholds of significance for the individual population genetic tests applied here. Finally, tests of positive selection using dN/dS are generally unaffected by ILS (46, 47) and thus cannot account for the signals of positive selection we observe. It should be noted that SNVs that tag the CNV genotypes at the candidate loci of selection in Melanesians are generally specific to Melanesians, with relatively little association in other SGDP populations (9). For example, in the case of the *APOBEC3A* and *APOBEC3B* deletion variant, we find 266 SNVs from the 110-kbp region in almost perfect linkage disequilibrium with the deletion allele in Melanesians, but among other East Asian populations the association is weaker (fig. S19).

Although our limited understanding of genotype–phenotype relationships makes it difficult to predict functional consequences of the CNVs at chromosomes 16p11.2 and 8p21.3, we note that chromosome 16p11.2 harbors adaptive signals associated with human-specific gene duplication expansion that may affect iron regulation in human embryonic development (15). This locus also exhibits an enrichment of complex recurrent structural rearrangements, which predisposes humans to the second most common genetic cause of autism, accounting for ~1% of patients (15, 40). In the case of the 8p21.3 CNVs, the Melanesian DUP_{10D} allele is accompanied by a nearby deletion (DEL_{MEL-NDL}) that originated in Neanderthals and overlaps with known regulatory signals in human skeletal muscle myoblasts (H3K27Ac markers, UCSC Genome Browser). Notably, *TNFRSF10D* has been reported as one of the primate-specific genes preferentially expressed in progenitor cells of the human fetal neocortex (48).

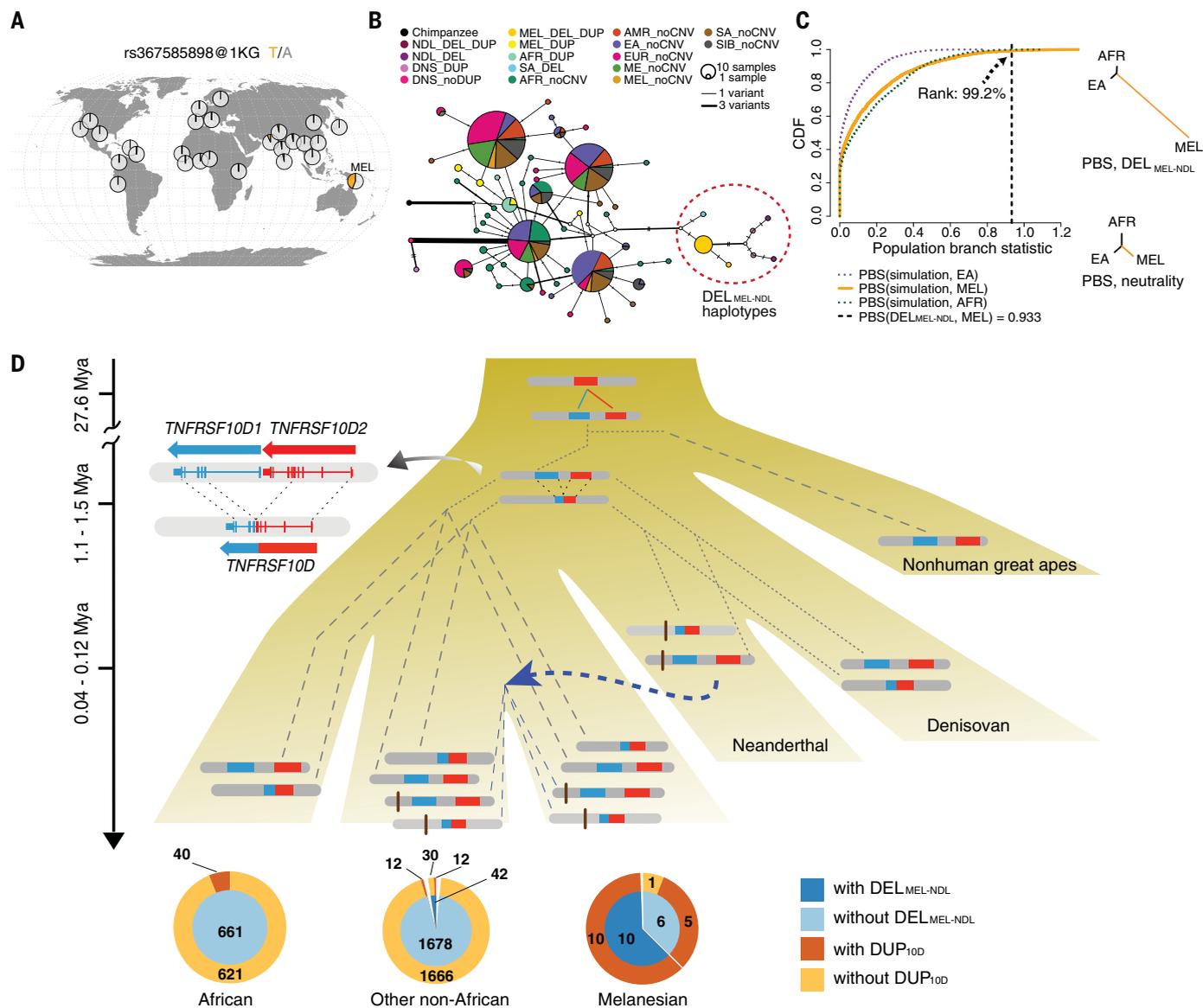


Fig. 5. Complex evolutionary history and evidence of adaptive archaic introgression at 8p21.3 in Melanesians. (A) Geographic distribution of the DEL_{MEL-NDL} tag SNV, rs367585898, using the 1KG data. (B) Median-joint network showing that all deletion-linked haplotypes form a single clade. Colors represent different haplotypes (DEL and DUP refer to DEL_{MEL-NDL} and DUP_{10D}, respectively). Edge width indicates the number of pairwise differences between the joined haplotypes. (C) A highly unusual PBS of DEL_{MEL-NDL} in the Melanesians,

compared with those computed using variants with similar age in neutral coalescent simulations, supports the hypothesis of positive selection favoring this introgressed variant. CDF, cumulative distribution function. (D) (Top) Schematic model for the evolution of the DEL_{MEL-NDL} and DUP_{10D} variants among great ape lineages. Dashed and dotted lines correspond to contemporary and historical lineages, respectively. (Bottom) Pie charts show the numbers of individuals from the 1KG and SGDP panels with or without the two CNVs.

Large genomic gains and losses have the potential to create genes that can affect organismal phenotypes. With our increasing understanding of gene flow between various archaic forms and our ancestors, it is tempting to hypothesize that CNV introgression from other hominins may have played a key role in helping humans migrating out of Africa adapt to new environments by serving as a reservoir of beneficial alleles. In addition, this study highlights the substantial large-scale genetic variation that remains to be characterized in the human population and the need for develop-

ment of additional reference genomes that better capture the diversity of our species and complete our understanding of human genes (11).

Materials and methods summary

We downloaded paired-end Illumina data for 266 fully publicly available human genomes via the SGDP website (27) and called SNVs and indels using the HaplotypeCaller function in Genome Analysis Toolkit (GATK, v3.5). After quality control filtering, these variants were merged with genotypes from the three archaic

genomes (<http://cdna.eva.mpg.de/>) using BCFtools (v1.5). For the SGDP samples, CNV calls were generated using WHAMG, LUMPY (v0.2.13), DELLY2 (v0.7.2), digital comparative genomic hybridization (dCGH), and Genome STRiP (v2.00.1611). We applied only dCGH to the three archaic genomes, owing to the lack of paired-end data in these genomes. Population-stratified CNVs were identified using V_{ST} , MWU, and D_{median} statistics, whereas signals of positive selection and archaic introgression were determined using the PBS, f_D , and S^* statistics (2, 30, 49). Significance of these test

results was determined from coalescent simulations based on the best-fit demographic models inferred from $\partial a \partial i$ (50) and ADMIXTURE (51). Phylogenetic analyses were performed with a combination of RAxML (v8.2.10), BEAST (v2.5.0), and PAML (v14.9). We used FISH, sequencing of BAC clone inserts, and long-read sequencing data to validate CNVs and assess the breakpoints of complex rearrangements. The high-coverage long-read sequence data from the Melanesian sample was generated using PacBio single-molecule, real-time (SMRT) sequencing technology. We followed the Iso-Seq protocol and used PacBio sequencing (52) to generate the FLNC transcript data. Detailed descriptions of materials and methods are available in the supplementary materials (29).

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SUPPLEMENTARY MATERIALS

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Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes

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Adaptive archaic hominin genes

As they migrated out of Africa and into Europe and Asia, anatomically modern humans interbred with archaic hominins, such as Neanderthals and Denisovans. The result of this genetic introgression on the recipient populations has been of considerable interest, especially in cases of selection for specific archaic genetic variants. Hsieh *et al.* characterized adaptive structural variants and copy number variants that are likely targets of positive selection in Melanesians. Focusing on population-specific regions of the genome that carry duplicated genes and show an excess of amino acid replacements provides evidence for one of the mechanisms by which genetic novelty can arise and result in differentiation between human genomes.

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