

# High Levels of Genetic Diversity within Nilo-Saharan Populations: Implications for Human Adaptation

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## Summary

Africa contains more human genetic variation than any other continent, but the majority of the population-scale analyses of the African peoples have focused on just two of the four major linguistic groups, the Niger-Congo and Afro-Asiatic, leaving the Nilo-Saharan and Khoisan populations under-represented. In order to assess genetic variation and signatures of selection within a Nilo-Saharan population and between the Nilo-Saharan and Niger-Congo and Afro-Asiatic, we sequenced 50 genomes from the Nilo-Saharan Lugbara population of North-West Uganda and 250 genomes from 6 previously unsequenced Niger-Congo populations. We compared these data to data from a further 16 Eurasian and African populations including the Gumuz, another putative Nilo-Saharan population from Ethiopia. Of the 21 million variants identified in the Nilo-Saharan population, 3.57 million (17%) were not represented in dbSNP and included predicted non-synonymous mutations with possible phenotypic effects. We found greater genetic differentiation between the Nilo-Saharan Lugbara and Gumuz populations than between any two Afro-Asiatic or Niger-Congo populations. F3 tests showed that Gumuz contributed a genetic component to most Niger-Congo B populations whereas Lugbara did not. We scanned the genomes of the Lugbara for evidence of selective sweeps. We found selective sweeps at four loci (*SLC24A5*, *SNX13*, *TYRP1*, and *UVRAG*) associated with skin pigmentation, three of which already have been reported to be under selection. These selective sweeps point toward adaptations to the intense UV radiation of the Sahel.

## Introduction

The modern humans who migrated out of Africa in the last 100 ka came from only a subset of all African populations. The peoples who remained were more genetically diverse and have continued to diversify in response to changing environmental and disease pressures and admixture events.<sup>1–6</sup> African populations have also migrated and intermixed to create the rich mosaic of genetic and cultural variation that is found today.<sup>7</sup> The paucity of genetic, historical, and archaeological records has led to a heavy dependence on linguistic analysis for classification of African populations, and this strategy has identified four major African language families (Afro-Asiatic, Niger-Congo, Nilo-Saharan, and Khoisan) (Figure 1) and provided evi-

dence for the migration of Bantu speakers out of the Nigeria-Cameroon border region into South and East Africa.<sup>4</sup> The advent of genetic analysis has generally supported the main population groups identified by linguistic analysis but has also revealed admixture between speakers of different language groups and language acquisitions from genetically unrelated groups.<sup>4,6,9</sup>

The Nilo-Saharan family comprises 206 languages spoken by 34 million people (1996 estimate) and is divided into approximately 12 subgroups.<sup>10,11</sup> This family is particularly problematic for linguists because there is only weak evidence for establishing the relationships between the subgroups and some authors treat Nilo-Saharan as a collection of isolated language groups rather than a single family.<sup>11</sup> Some smaller Nilo-Saharan groups (Gumuz, Koman,

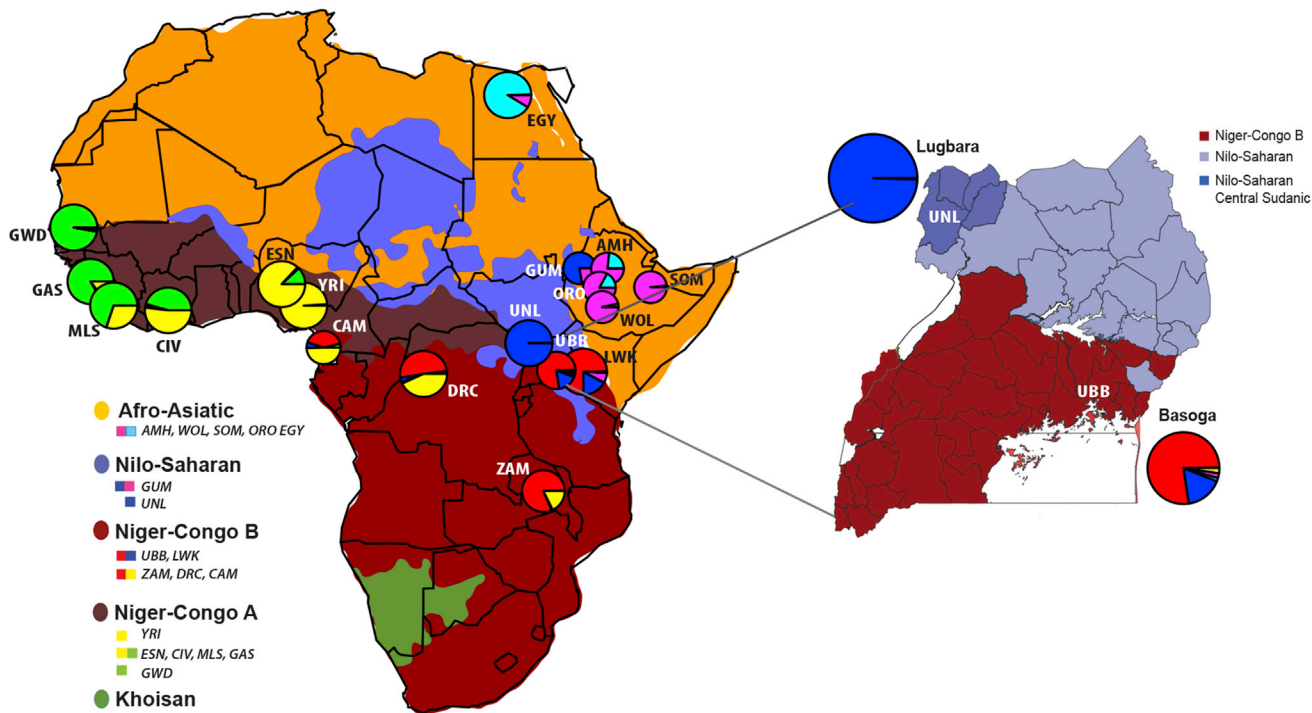
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**Figure 1. Map of Africa Showing the Distribution of Five Major African Linguistic Families, the Locations Where Samples Were Collected, and the Proportions of Different Genetic Components**

The pie chart size is proportional to the sample size and pie chart proportions and colors correspond to the proportions and colors of ADMIXTURE components within that population for  $K = 6$  (Figure 3). Note that the map colors for languages are not associated with pie chart colors. The legend shows first the map color for each major linguistic group and second the major colors (>25% admixture component) of the admixture pie charts for each population in that linguistic group. The linguistic distribution map was compiled from data in Ethnologue and used under the Creative Commons Attribution-ShareAlike 4.0 International License. Our populations were sampled from Guinea (GUI), Côte d’Ivoire (CIV), Cameroon (CAM), Democratic Republic of Congo (DRC), Zambia (ZAM), and Uganda (UNL & UBB), the 1000 Genomes project (Gambia [GWD], Sierra-Leone [MSL], Nigeria [ESN, YRI], Kenya [LWK], Egypt [EGY]), and the African Genome Variation project (Ethiopia [AMH, GUM, ORO, SOM, WOL]). The inset map shows sampling sites in Uganda. The Lugbara (UNL) were from West Nile region that is predominantly occupied by Nilo-Saharan speakers and the Basoga (UBB) were from the southern region, which is occupied by Bantu speaking people. This map was overlaid with pie charts derived from the admixture plot using R tools. The Ugandan map was generated using QGIS3.6 (see [Web Resources](#)) with regional ethnicity classification traced with inference from “Ethnologue languages of Uganda.”<sup>8</sup>

Kadu, Chabu) have been excluded from the Nilo-Saharan family by some authors or treated as early branching distantly related groups by others.<sup>10,12</sup> Genetic data can be used to show how linguistic groups map onto genetically defined human populations.<sup>4</sup> However, genomes have been sequenced from fewer than 100 of the 2,139 African linguistic groups recognized by Ethnologue.<sup>6,13–16</sup> Here we have sequenced the genomes of 50 individuals from the Nilo-Saharan Lugbara population of Northwestern Uganda. The Gumuz is the only other Nilo-Saharan population to be sequenced at this scale and the linguistic evidence for its inclusion in the Nilo-Saharan family is debated.<sup>10,12</sup> For comparison we also sequenced the genomes of 250 individuals from 6 new Niger-Congo populations from Guinea, Côte d’Ivoire, Cameroon, Democratic Republic of Congo, Zambia, and Uganda and also included published data from 13 additional African populations from the 1000 Genomes and African Genome Variation Projects.<sup>2,17</sup> We show that the Lugbara are genetically distinct from all Niger-Congo and Afro-Asiatic populations and from the Gumuz.<sup>2,5</sup> Through this level

of sequencing, we have been able to use the major methods for identification of loci under selection, iHS and xpEHH, which require at least 15 genomes to achieve 80% power.<sup>18</sup> To date, this number of samples has only been sequenced from 7 Niger-Congo, 6 Afro-Asiatic, and a single putative Nilo-Saharan population (Gumuz).<sup>2,16,19</sup> Analyses of Niger-Congo genomes have already identified loci associated with resistance to malaria and human African trypanosomiasis (HAT).<sup>20,21</sup> In the Lugbara we found loci under selection associated with skin pigmentation and hair formation.

## Subjects and Methods

### Study Samples

The samples used for this study were obtained from the TrypanoGEN biobank,<sup>22</sup> the numbers and ethnic groups of the samples from each country are shown in [Table S1](#). Groups of samples that cluster together on the MDS plot and appear similar on the Admixture plots are referred to by the name of the linguistic group unless there were multiple linguistic groups within a cluster, in which case

they are referred to by the country name or abbreviation (Table S1). Ethical approval for the study was provided by the ethics committees of each TrypanoGEN consortium member: Uganda (Vector Control Division Research Ethics Committee (Ministry of Health), Uganda National Council for Science and TechnologyHS 1344), Zambia (The University of Zambia Biomedical Research Ethics Committee: 011-09-13), Democratic Republic of Congo (Minister de la Sante Publique: No 1/2013), Cameroon (Le Comite National d’Ethique de la Recherche pour la Sante Humain: 2013/364/L/CNERSH/SP), Côte d’Ivoire (Ministere de la Sante et de la Lutte Contre le SIDA, Comite National D’Ethique et de la Recherche 2014/No 38/MSLS/CNER-dkn), and Guinea (Comite Consultatif de Deontologie et d’Ethique [CCDE] de l’Institut de Recherche pour le Developpement: 1-22/04/2013). All the participants in the study were guided through the consent forms, and written consent was obtained to collect biological specimens. Study participants provided informed consent for sharing and publishing their anonymized data.

Peripheral blood was collected from the participants at the field sites, frozen, and transported to reference laboratories. DNA was extracted using the whole blood MidiKit (QIAGEN). The DNA was quantified using the Qubit (QIAGEN) and approximately 1 µg was used for sequencing at the University of Liverpool, UK. DNA from Cameroon and Zambia was sequenced at Baylor College, USA.

### Sequencing and SNP calling

300 participants’ DNA samples (Lugbara [UNL], 50; Basoga [UBB], 33; Zambia [ZAM], 41; Democratic Republic of Congo [DRC], 50; Cameroon [CAM], 26; Côte d’Ivoire [CIV], 50; Guinea [GAS], 50) were selected and subjected to whole-genome sequencing (Table S1). The whole-genome sequencing libraries of samples from Guinea, Côte d’Ivoire, Uganda, and DRC were prepared using the Illumina Truseq PCR-free kit and sequenced on the Illumina HiSeq2500 to 10× coverage at the Centre for Genomic Research (University of Liverpool). The samples from Zambia and Cameroon were sequenced on an Illumina X Ten system to 30× at the Baylor College of Medicine Human Genome Sequencing Centre. The sequenced reads were mapped onto the human\_g1k\_v37\_decoy reference genome using BWA.<sup>23</sup> The SNP calling on all the samples was carried out using the genome analysis tool kit GATK v3.4<sup>24</sup> to create a GVCF file for each individual. GVCF files were then merged to create a combined VCF file also using GATK. SnpEff was used for variant annotation.<sup>24</sup> An analysis of copy number variation has been published separately.<sup>25</sup>

From the 1000 Genomes project<sup>16</sup> we obtained variant call files of 50 samples from each of the Esan and Yoruba from Nigeria; Mende from Sierra Leone; Gambian from Western Division of The Gambia; Luhya from Western Kenya; five samples from each of five populations of West Eurasian origin: Utah residents with northern and western European ancestry, Finnish from Finland, British in England and Scotland, Iberian from Spain, Toscani from Italy.

From the African Genome Variation Project<sup>2,26</sup> we extracted 50 Egyptian genome sequences and 24 from each of the following Ethiopian populations: Amhara, Ethiopian Somali, Oromo, Wolayta, and Gumuz. The African Genome Variation datasets were obtained from European Genome-Phenome Archive,<sup>27</sup> EGA: EGAD00001000598, EGA: EGAD00001003296, EGA: EGAD000010001221, under the terms of the Wellcome Sanger Institute (WSI) data access agreement.

### Data Quality Control and Filtering

The data were filtered to minimize batch effects potentially introduced by the presence of samples sequenced at different depths by different labs. For descriptive statistics of the TrypanoGEN dataset all loci were retained. For all other analyses, sites that met any of the following criteria were removed; missing data > 10%, loci with < 3 SNP calls, minor allele frequency (MAF) < 0.01, Hardy-Weinberg equilibrium  $p < 0.001$ . For population analyses, the remaining SNP loci were thinned in order to retain only loci with  $r^2 < 0.1$ . Individuals with >10% missing data were also removed. Data were phased with Shapeit2 v2.r837,<sup>28</sup> which also imputed missing data, prior to combining our data with genomes from the 1000 genomes and African Genome Variation projects using BCftools (v.1.6),<sup>27</sup> retaining only loci that were present in all datasets.

For signatures of selection, the filtered and phased variant call format files were further filtered using VCFtools v.0.1.16<sup>29</sup> to remove loci with MAF < 0.05.

### Multidimensional Scaling Analysis

To infer the population structure based on the underlying genetic variation among the populations, we carried out multidimensional scaling (MDS) using PLINK 1.9<sup>30</sup> and plotted MDS coordinates using R v.3.2.1.<sup>31</sup> The MDS was carried out on our sequence data, which was merged with a maximum of 50 samples from each of the 13 additional populations from Africa and Europe from the 1000 Genomes project<sup>16</sup> and the African Genome Variation project.<sup>2,26</sup>

### Population Admixture

Admixture was tested for 1 to 9 genetic components (K) using ADMIXTURE 1.23<sup>32</sup> with 3 replicate runs for each value of K.

All plausible pairs of available populations that might be sources of the selected East African Populations (UNL, UBB, LWK, GUM, AMH) were tested for evidence of contribution to those populations using the F3 test in AdmixTools<sup>33</sup> and implemented in R using *admixr*.<sup>34</sup>

### Allele Frequency Statistics: In-breeding Coefficient, Tajima D, F<sub>ST</sub>

We followed the workflow of Cadzow et al. for allele frequency statistics.<sup>35</sup> To determine the extent of inbreeding within each of our populations, we measured the inbreeding coefficient,  $F_i$ ,<sup>36</sup> using VCFtools (v.0.01.14).<sup>29</sup> The Tajima D statistic<sup>37</sup> was used to identify regions that did not fit the neutral model of genetic drift and mutation in bins of 3 kb also in VCFtools. The level of population differentiation was estimated with Wright’s  $F_{ST}$ <sup>38</sup> in PLINK v.1.9. The pairwise  $F_{ST}$  matrix was generated between our sequence data, 1000 Genome project,<sup>16</sup> and the African Genome Variation Project populations.<sup>2,26</sup>

### Signatures of Selection

The sequence data were scanned for regions that might be under selection using the Extended Haplotype Homozygosity (EHH) test within and between populations.<sup>39</sup> The SNP were phased using SHAPEIT v.2.2,<sup>28</sup> and the R software package *rehh*<sup>40</sup> was used to calculate two EHH derived statistics: the intra-population integrated Haplotype Score (iHS)<sup>41</sup> and inter-population xpEHH score,<sup>42</sup> that identify SNPs that are under selection in one population but not in another. Only SNPs with a MAF > 0.05 were included in the analysis. We used the method of Voight et al. to

identify the regions of the genome under the strongest selection pressure;<sup>41</sup> the genome was divided into 100 kb bins and the fraction of SNP with  $iHS > 2$  in each bin was obtained. Bins with  $< 20$  SNP were disregarded. The 1% of bins with the highest fraction of SNP with absolute  $iHS > 2$  were considered to be significant.<sup>41</sup> Bins were annotated with the lists of genes that they contained using Biomart. Different types of evidence for signatures of selection were combined using Bedtools v.2.26.0<sup>43</sup> to identify the intersection of the  $iHS$ , with  $xpEHH$  and the allele frequency-based statistics of  $F_{ST}$  and Tajima  $D$ .

## Results

We sequenced the genomes of 50 individuals from the Nilo-Saharan Lugbara population and 250 from 17 linguistic groups from Guinea, Côte d'Ivoire, Cameroon, Democratic Republic of Congo, Uganda, and Zambia (Tables S1 and S2).

The samples from Zambia and Cameroon were sequenced to  $30\times$  coverage while other populations were sequenced to  $10\times$  coverage. The call rate was 97.4% in the  $10\times$  samples and 99.4% in the  $30\times$  samples. The  $30\times$ -sequenced samples had higher proportions of heterozygotes (9.3%) compared with the  $10\times$  sequenced samples (7.5%) and there was a concomitant higher frequency of low Hardy-Weinberg  $p$  values in the  $10\times$  data (Figure S1). There were 38,963,563 raw variants, filtering removed fourteen individuals and 23,017,723 loci leaving 286 samples and 15,945,844 variant loci that were available for population and signatures of selection analyses. Table S3 shows the number of loci removed by each filtering step, most variants were removed from the analysis because of low count or frequency of minor alleles (21,604,569  $MAF < 1\%$  or minor allele count  $\leq 2$ ). The mean call rate after filtering was 99.2% for the  $10\times$  samples and 99.95% for the  $30\times$  samples. The data were phased with Shapeit2, which imputed genotypes at the small number of remaining missing loci. The commonest form of bias in low-coverage data is an excess of singleton variant loci<sup>44</sup> and these were removed by the filtering strategy (Figure S1).

### The Nilo-Saharan Lugbara Population Has a High Proportion of Novel Variation

We observed little evidence of inbreeding within the populations; the majority of the individuals had an inbreeding coefficient ( $F$ ) of less than 0.1 (Figure S2). We classified variants as known if they were present in dbSNP build 150 (20/11/2019) and novel if not. We identified approximately 22 million variant loci in the Lugbara population (Table S4, Figure S3). The frequencies of known and novel variants were similar in all the six Niger-Congo populations (12.9% novel, SE 0.003); however, the Nilo-Saharan Lugbara population from North West Uganda had significantly more novel SNPs (17.1%  $p < 0.001$ ) (Figure S3C), presumably due to an under-representation of Nilo-Saharan populations in previous genomic studies. We assessed the impacts of the variants on function using

$snpEff$ ; 99% of SNP were classified as “modifier,” and these were mainly intergenic; the remaining 1% of SNPs had more informative classifications: low, moderate, or high impact (Table S4, Figures S3B and S3C). Of the 1% of SNP with informative classifications (low, moderate, or high impact), nearly 90% were predicted to have moderate impact in both known and novel variants. The frequency of high-impact variants was twice as high in the novel variants as it was among the known variants (6.3% *cf.* 3.0%). There was a larger proportion of rare alleles ( $MAF < 5\%$ ) in the set of novel SNPs than in the known SNPs (Figure S4), as expected for SNPs that are unique to a specific population or geographic region.

### The Nilo-Saharan Lugbara Population Is Distinct from Other African Populations

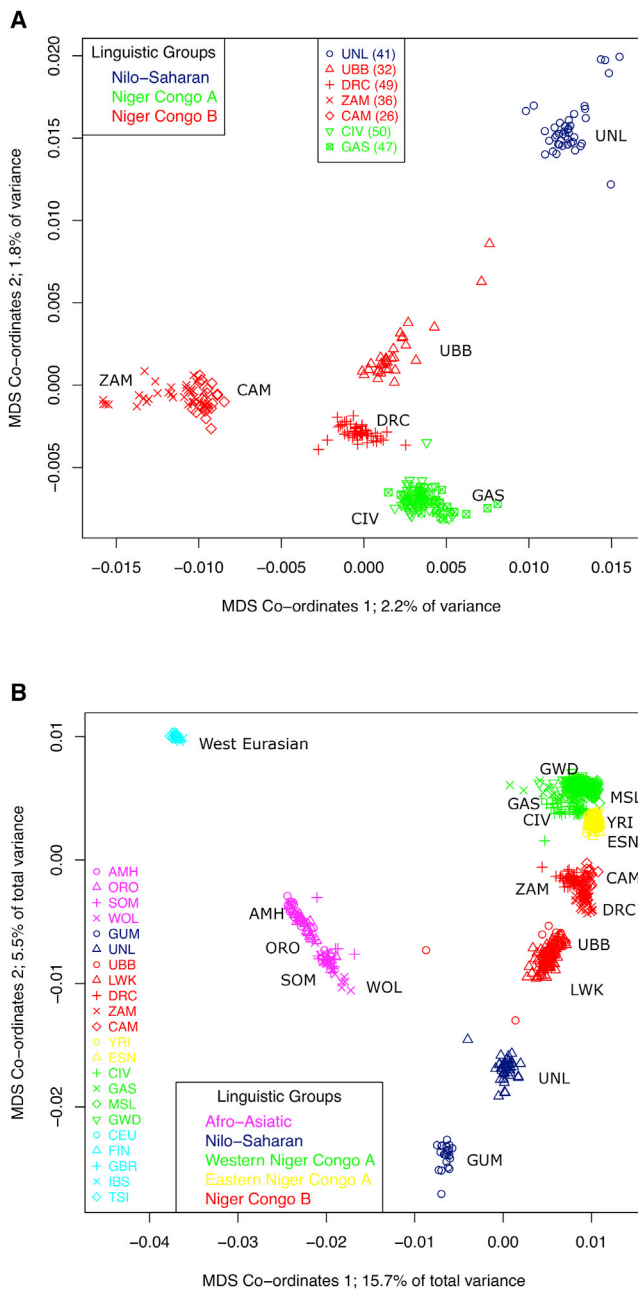
Bi-allelic loci from the 286 TrypanoGEN samples were merged with 1,000 Genomes and African Genome Variation Project data to obtain 10,857,449 loci that were present in all three datasets for population analysis. These were filtered to remove linked loci ( $r^2 > 0.1$ ) yielding a final dataset of 1,465,578 SNP and 731 samples that were used for MDS, Admixture, and F3 analysis.

Multidimensional scaling analysis (Figure 2) showed that samples formed tight geographic groups irrespective of data source or sequence coverage. The exception was the Nilo-Saharan Lugbara population from North West Uganda, which was distinct from both the Nilo-Saharan Gumuz of Ethiopia and the Basoga from southeast Uganda. The two Nilo-Saharan populations were well separated from each other and from the East African Niger-Congo B and the Ethiopian Afro-Asiatic populations. Even when combined with a West Eurasian dataset (Figure S5B), the two putative Nilo-Saharan populations (Lugbara and Gumuz) appeared as divergent from each other as Niger-Congo-A and Niger-Congo-B populations from East and West Africa. This demonstrates that the focus on genetics of Niger-Congo and Afro-Asiatic populations has led to the neglect of the greater diversity within other African populations.

### The Nilo-Saharan Lugbara Show Low Genetic Admixture and High Genetic Distance from Other African Populations

We then used Admixture to analyze the population structure of the same 731 samples used for the MDS analysis. The admixture coefficients of variation were very similar (0.262–0.271) for all numbers of genetic components (K3-9) (Figure S6). Although caution should be used when interpreting Admixture clusters as broad genetic components,<sup>45</sup> remarkably at all values of  $K$  except  $K = 7$  Gumuz and Lugbara shared a single large component, which was also important in Afro-Asiatic samples (at  $K \leq 5$ ) and to a lesser extent in East African Niger Congo B samples (LWK, UBB) (Figure 3).

With  $K > 5$  the Niger-Congo populations separated into an east African cluster of the Ugandan Basoga and Kenyan



**Figure 2. Multidimensional Scaling Analysis of Sequenced Populations**

(A) This study: Guinea (GAS), Côte d'Ivoire (CIV), Cameroon (CAM), Democratic Republic of Congo (DRC), Uganda (Nilotics, UNL, Niger Congo B, UBB), and Zambia (ZAM); seven Soli/Chikunda (Niger-Congo B)-speaking individuals were outliers by MDS and are not shown in this plot but are shown in Figure S5A. (B) This study and African Genome Variation Project Ethiopian samples Amhara (AMH), Welayta (WOL), Oromo (ORO), Ethiopian Somali (SOM), and Gumuz (GUM) and 50 samples from each 1000 Genomes African population Nigeria (ESN, YRI), Gambia (GWD), Mende Sierra Leone (MSL), Kenya (LWK). Colors for each cluster are taken from the color for the dominant genetic component for that cluster in the admixture plot at  $K = 6$ .

Luhya, a central African cluster of the Zambia, Cameroon, and Democratic Republic of Congo, a Nigerian cluster of the Esan and Yoruba, and a far west-African cluster of the

Côte d'Ivoire, Sierra Leone, Guinea, and Gambia populations. We also observed at  $K \geq 8$  a homogeneous group of seven Soli/Chikunda (Niger-Congo B)-speaking individuals within the Zambia population with no admixture with other populations and who were also outliers on the MDS coordinates plot (Figure S5A), the source of this divergent ancestry is unknown.

### F3 Tests of Admixture Hypotheses

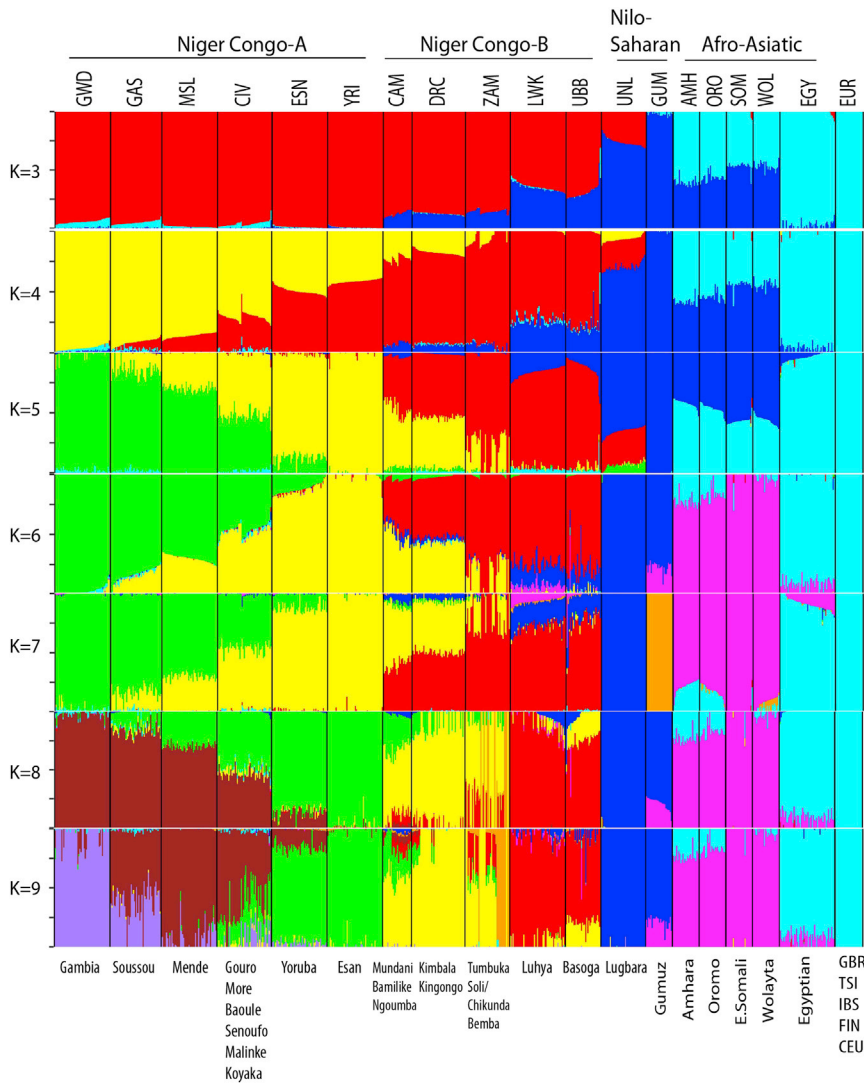
The admixture hypotheses generated by Admixture were tested with the three populations (F3) test implemented with AdmixTools.<sup>33</sup> All possible pairs of 2 West Eurasian (TSI, EGY) and 17 African populations (AMH, ORO, SOM, WOL, DRC, CAM, ZAM, ESN, YRI, GWD, MSL, GUI, CIV, LWK, UBB, GUM, UNL) were tested as possible sources of five East African populations (Afro-Asiatic AMH; Nilo-Saharan GUM and UNL; East African Niger-Congo B UBB and LWK) (Figures 4 and S8).

Pairs of each African population and each West Eurasian population were plausible sources to the Amhara (AMH) population consistent with the Admixture plot which suggests that the Afro-Asiatic populations have a large West Eurasian admixture component as previously reported (Figure S8).

No pairs of populations were jointly source to either of the Nilo-Saharan populations (UNL and GUM) (Figure S8). However, the Gumuz and Lugbara had very different contributions to the ancestry of the Kenyan Luhya (Figure 4), despite sharing apparently similar ancestral components in the Admixture plot (Figure 3). There was evidence that both the Gumuz and Afro-Asiatic populations were plausible sources to the Luhya when paired with most African populations (Zscore  $< -16$  for pairings with Zambia). In contrast there was very little evidence of ancestry from the Lugbara, which were only compatible with the Zambian population as plausible admixture sources, and even there the signal was much weaker (Z score =  $-2.7$ ). The Gumuz but not the Lugbara also contributed to the Ugandan Basoga ancestry (Figure 4) but only when paired with the Zambian population.

These observations are most consistent with the population structure indicated in the Admixture plot at  $K = 6$ . At  $K = 6$  the dominant ancestry component in Lugbara and Gumuz (dark blue in Figure 3) is also shared with the Luhya and Basoga, but this is not consistent with the F3 data. However, a minor component of the Gumuz (pink at  $K = 6$ ), which is not observed in the Lugbara, is also shared with Luhya and Basoga and this is consistent with F3 data, which shows a Gumuz but not Lugbara contribution to these populations. The pink perhaps represents a pre-Bantu expansion East African population that has contributed to the Gumuz, Luhya and Basoga genomes but not the Lugbara.

We obtained pairwise  $F_{ST}$  distances between the Ugandan Lugbara and the other African populations to determine the genetic distance between them (Table S5, Figure S7).  $F_{ST}$  was relatively high (mean  $F_{ST} > 0.015$ )



**Figure 3. Genetic Admixture and Differentiation in Our Data, Selected 1000 Genomes, and AGVP Populations**

Admixture plot (731 samples) for  $K = 3$  to  $K = 9$ . Genome sequences from this study, 1000 Genomes African samples, AGVP Egyptian, Ethiopian, and European populations (GBR, British from England and Scotland; TSI, Toscani in Italy; IBS, Iberian in Spain; FIN, Finnish in Finland; CEU, Utah residents with Northern and Western European ancestry). Three replicates were carried out for each value of  $K$ .

that passed QC, only those with  $MAF > 5\%$  were retained for these analyses, a total of 8,882,525 in the Lugbara and 9,107,514 in the Basoga.

### Signatures of Selection in the Lugbara and Basoga Populations

We compared the regions under selection within the Lugbara and Basoga populations. The Basoga population was selected due to their geographic proximity to the Lugbara (500 km) (Figure 1), the minimally shared genetic ancestry between these two Ugandan populations (Figure 3), and because the Ugandan Basoga can act as representatives of Niger-Congo B populations. Using the phased haplotype dataset of the Lugbara and Basoga populations, the EHH derived integrated haplotype score (iHS) values were calculated using the *rehh3* software for which we observed a normal

distribution of the absolute iHS values (Figure S9). The Manhattan plot (Figure 5) shows 12 regions with extreme iHS ( $|iHS| > 6$ ). However, there were protein-coding genes within 100 kb of only two of these peaks (*ROCK1*, *DCUNID4*). Both genes are involved in diverse ranges of intracellular activities making it difficult to predict a specific effect on phenotype.<sup>46,47</sup> We therefore calculated the frequency of SNP with  $|iHS| > 2$  in 100 kb bins<sup>41</sup> to identify the regions with greatest evidence of selection and that might contain genes associated with known phenotypes (Table S9). The *HLA* region had some of the highest frequencies of SNP with  $|iHS| > 2$  as well as some of the highest values of iHS ( $> 6$ ) and has been found to have signatures of selection previously.<sup>48</sup> A list of genes that are under selection and are also shared between the UNL and UBB populations is shown in Table 1.

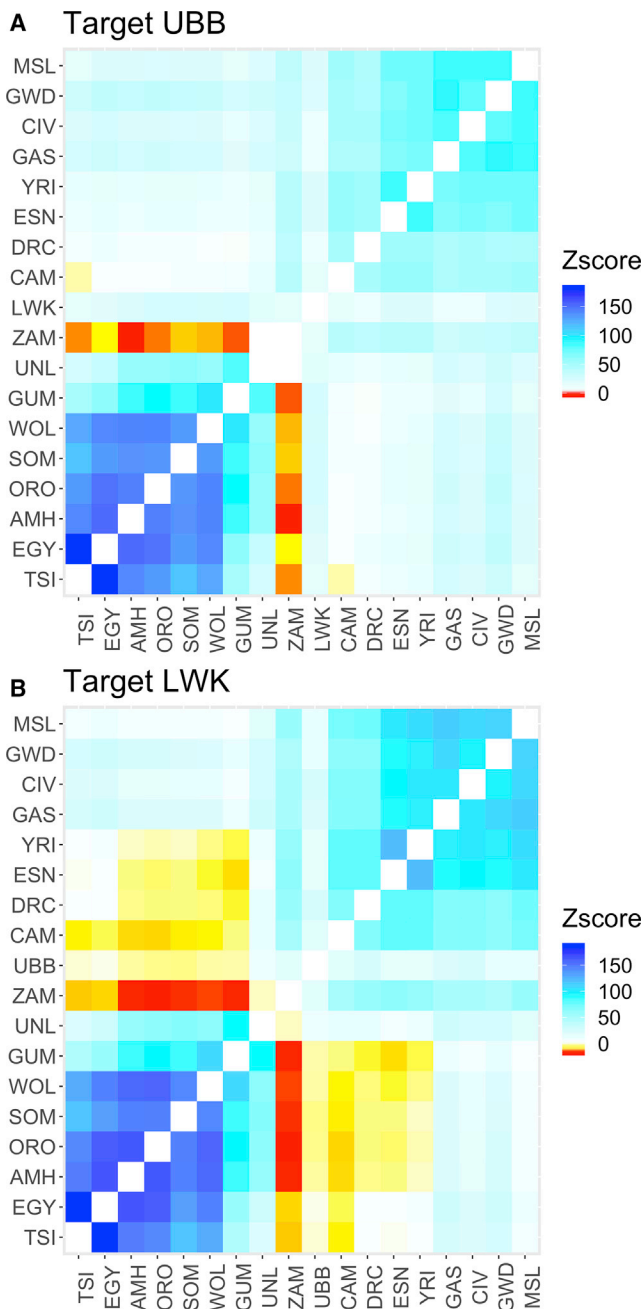
### Signatures of Selection in Nilo-Saharan Lugbara

Given the relative genetic isolation of the Nilo-Saharan Lugbara, we hypothesized that they could have unique genetic adaptations to their environment. We sought to identify those regions of the genomes that were under selection, using the linkage disequilibrium-based models of extended haplotype homozygosity (EHH). Those alleles with extreme EHH were then validated using the allele frequency-based  $F_{ST}$  statistic and Tajima's  $D$ . Of the 15,945,844 variant loci

between the Nilo-Saharan Lugbara samples and the Niger-Congo populations, except for the Uganda Basoga population (mean  $F_{ST} = 0.011$ ) and Kenyan Luhya population (mean  $F_{ST} = 0.012$ ). The Lugbara and Gumuz populations are about 1,000 km apart compared with the approximately 4,000 km, which separates the West and East African Niger-Congo A and B populations. However,  $F_{ST}$  between Niger-Congo A and B (0.008) was lower than between Lugbara and Gumuz ( $F_{ST} = 0.025$ , Table S5), indicating that Lugbara and Gumuz populations have very different histories.

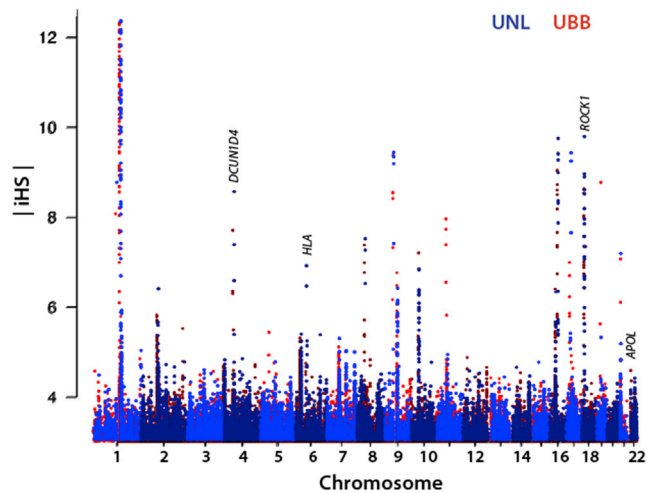
### Signatures of Selection in the Lugbara but Not Basoga Populations

In order to identify SNPs associated with adaptation in the Lugbara population, we identified those selective sweeps in



**Figure 4. F3 Tests of Admixture**  
 (A) Target UBB; Z scores for probability that a pair of populations contributed ancestry to the Uganda Niger Congo B Basoga.  
 (B) Target LWK; Z scores for probability that a pair of populations contributed ancestry to Kenyan Luhya.  
 Heatmap color represents intensity of Z score for probability that a population contributes genetic components to the target. Negative Z scores (yellow to red) are associated with increasingly strong evidence of a contribution and positive scores (cyan to blue) are associated with increasingly strong evidence against a contribution. White squares are inconclusive.

which the signature allele has achieved fixation in the Lugbara population but remains polymorphic in the Basoga population.<sup>69</sup> We first identified loci within the Lugbara population that had extreme iHS values and occurred at a high frequency within a 100 kb window (SNPs having  $iHS > 2.0$



**Figure 5. Genome-wide Signatures of Selection in the Lugbara and Basoga**  
 Manhattan plot showing SNPs with extreme absolute  $iHS$  values ( $|iHS| > 3.0$ ) that occur in the Lugbara (UNL blue) and Basoga (UBB red) populations.

and count  $> 20$ , Table S9). We then identified those that occur only in the UNL population (Table S10). Finally, we identified those genes with extreme  $iHS$  that are highly differentiated between the Lugbara and Basoga populations using high  $F_{ST}$  (top 5% quantile), high Tajima's D, and high cross population EHH ( $xpEHH > 2.5$ ). The three different metrics were combined by ranking genes on each individual metric and then obtaining the sum of the ranks for each gene (Table S11). From this we identified a set of top ranked genes (Table 2) which were highly differentiated between the Lugbara (UNL) and Basoga (UBB) populations. The three highest ranked genes were *NEK4*, which is associated with schizophrenia,<sup>70</sup> *COLQ*, which is most highly expressed in CD8 T cells and CD56 NK cells,<sup>71,72</sup> and *UVRAG*, which is involved in melanosome biogenesis and skin pigmentation<sup>73</sup> and protection against UV radiation (Figure 6).

## Discussion

### SNP Discovery

Africa has the most genetically diverse populations on earth but while there are projects to sequence in excess of 100,000 genomes from populations in Europe,<sup>74</sup> Asia,<sup>75</sup> and the Americas<sup>76</sup> the 1000 Genomes Project is still the single largest dataset for Africa with 661 genome sequences. Not only do African genomes have a greater density of polymorphisms than genomes elsewhere, they also frequently have shorter haplotypes, which require a greater density of markers to phase accurately.<sup>77</sup> To date, most African genome-wide association studies (GWASs) have been undertaken using chips designed for West Eurasian populations. This can severely limit researchers' power to discover loci controlling disease. For example, a GWAS to identify loci regulating severe malaria failed to recapture the sickle cell locus because of limited linkage

**Table 1. The Top 20% of Protein-Coding Genes with Strongest Signatures of Selection in the Lugbara Population**

Chr	Associated Protein-Coding Gene	Associated Effect	Ref.
1	<i>BX842679.1</i> , <b>LYPD8</b> , <b>SDHC</b> , <b>C1orf192</b> , <b>NBPF20</b> , <b>PRDM2</b> , <b>SLC9A1</b> , <b>FAM46B</b> , <i>GFI1<sup>a</sup></i> , <i>GPR89A</i> , <b>PRPF3</b> , <b>ITLN2</b> , <b>F11R</b> , <i>NBPF14</i> , <i>DESI2</i> , <b>PRMT6</b> , <b>FLG<sup>b</sup></b> , <b>XCL2</b> , <i>CENPL</i> , <b>FGGY</b> , <b>PRAMEF10</b> , <b>NROB2</b> , <b>C1orf172</b> , <i>RIMKLA</i> , <b>PPIAL4G</b> , <i>C1orf159</i> , <b>CD48</b>	<sup>a</sup> myeloid leukemia, <sup>b</sup> atopic dermatitis	49,50
2	<b>IRS1<sup>C</sup></b> , <i>RGPDS</i> , <b>PARD3B</b> , <i>PFN4</i> , <i>TPS3I3</i> , <i>DYNC1I2</i> , <b>CH17-132F21.1</b> , <b>C2orf47</b> , <b>SPATS2L</b> , <b>ZNF2</b> , <i>ARHGAP15</i> , <i>VPS54</i> , <b>AC017081.1</b> , <b>RAB3GAP1</b> , <b>MAP3K19</b> , <i>ST3GAL5</i> , <b>RFTN2</b> , <i>ASXL2</i> , <i>GALNT14</i> , <b>AMER3</b> , <b>PROKR1</b>	<sup>c</sup> diabetes	51
3	<i>HACL1</i> , <b>C3orf67</b> , <i>LRRIQ4</i> , <b>FXR1</b> , <b>TMEM45A</b> , <b>TOP2B</b> , <i>ALCAM</i> , <b>IQCB1</b> , <b>GOLGB1</b> , <i>TF<sup>d</sup></i> , <i>FAM162A</i> , <i>WDR5B</i> , <i>ABCF3</i> , <i>VWASB2</i> , <i>RPL24</i> , <i>IQCF3</i> , <i>HTR3E</i> , <i>ACTRT3</i> , <i>FILIP1L</i> , <i>SPSB4</i> , <i>MYNN</i> , <i>COLQ</i> , <b>ABHD14A-ACY1</b> , <i>NEK4</i> , <i>EIF5A2</i> , <i>RPL22L1</i> , <b>CAMK2N2</b> , <b>PSMD2</b> , <b>KCNH8</b> , <i>SFMBT1</i> , <i>TMEM110</i>	<sup>d</sup> anemia	52
4	<b>ABCG2</b> , <i>DCAF4L1</i> , <i>TMEM33</i> , <i>KLHL8</i> , <i>USP46</i> , <b>ERVMER34-1</b> , <i>PAICS</i> , <b>C4orf33</b> , <i>STATH</i> , <i>RXFP1</i> , <i>TECRL</i> , <i>ENPP6</i> , <i>STOX2</i> , <i>ANTXR2</i> , <b>KLHL2</b> , <i>HTN1</i> , <i>HTN3</i> , <b>SCLT1</b> , <b>EIF4E</b> , <b>NDST3<sup>e</sup></b> , <i>C4orf46</i>	<sup>e</sup> schizophrenia	53
5	<i>NR2F1</i> , <i>PARP8</i> , <b>TMEM232</b> , <b>PRELID2</b> , <b>JAKMIP2</b> , <b>PJA2</b> , <b>RP11-1026M7.2</b> , <i>IL9</i> , <i>SLC25A48</i> , <b>TIMD4<sup>f</sup></b> , <b>FAM153B</b> , <i>NNT</i> , <b>RBM27</b> , <b>PLAC8L1</b> , <i>SDHA</i> , <b>MYO10</b> , <b>TTC1</b> , <b>SKP1</b> , <i>MED7</i> , <i>FAM71B</i> , <i>ITK<sup>g</sup></i> , <i>TGFB1</i>	<sup>f</sup> tuberculosis, <sup>g</sup> HIV	54,55
6	<b>SAMD3</b> , <b>TMEM200A</b> , <b>UNC5CL</b> , <b>IPCEF1</b> , <b>OPRM1</b> , <b>EPHA7</b> , <i>PKIB</i> , <i>DDO</i> , <i>METTL24</i> , <b>TULP4</b> , <i>ID4</i> , <b>HLA-DQB1<sup>h</sup></b> , <b>HLA-DQA1</b> , <i>BAI3</i> , <i>COX6A1P2</i> , <i>FGD2</i> , <i>SOX4</i> , <i>MYLK4</i> , <i>WRNIP1</i> , <b>GRIK2</b>	<sup>h</sup> HIV, <sup>h</sup> tuberculosis, <sup>h</sup> diabetes	56–58
7	<i>IGF2BP3</i> , <b>MUC12</b> , <i>MUC3A</i> , <b>NAMPT</b> , <b>AOC1</b> , <b>KCNH2</b> , <b>C7orf62</b> , <b>AC006967.1</b> , <b>RBM48</b> , <b>GATS</b> , <b>PVRIG</b> , <b>GNA12</b> , <b>POM121L12</b> , <b>OR9A2<sup>i</sup></b> , <b>KEL</b> , <b>CARD11</b> , <i>TRPV5</i> , <b>AZGP1</b> , <i>THSD7A</i> , <i>ZNF680</i> , <i>AGR2</i> , <b>CDK6</b> , <i>SERPINE1</i> , <i>ISPD</i>	<sup>i</sup> odor perception	59
8	<b>FAM83A</b> , <b>PRR23D1</b> , <b>LRLE1</b> , <b>ZNF696</b> , <b>STC1</b> , <i>SFRP1</i> , <i>ADCY8</i> , <b>CSMD1</b> , <b>SDR16C5</b> , <i>ZNF705G</i> , <b>DDHD2</b> , <b>PPAPDC1B</b> , <i>PBK</i> , <i>CLN8</i> , <b>COPSS</b>		
9	<b>AL953854.2</b> , <b>BX255923.1</b> , <b>CR769776.1</b> , <b>TPRN<sup>j</sup></b> , <b>SSNA1</b> , <b>CBWD5</b> , <b>AL591479.1</b> , <b>CBWD7</b> , <i>PHF2</i> , <b>C9orf85</b> , <b>BX649567.1</b> , <i>TRMT10B</i> , <i>GRIN1</i> , <b>BRINP1</b> , <b>RP11-195B21.3</b> , <i>AL365202.1</i> , <b>INPP5E</b>	<sup>j</sup> deafness	60
10	<i>BLNK</i> , <b>ZNF37A</b> , <b>FAM21C</b> , <b>AL591684.1</b> , <b>PLEKHS1</b> , <b>CDNF<sup>k</sup></b> , <i>SORCS1</i> , <b>A1CF</b> , <b>ASAH2B</b> , <b>DNAJB12</b> , <b>LARP4B</b> , <i>MALRD1</i> , <i>BLOC1S2</i> , <i>PKD2L1</i> , <i>ANKRD2</i> , <i>UBTD1</i> , <b>ADAM12</b> , <b>AFAP1L2</b> , <b>FANK1</b> , <b>KNDCl</b> , <i>UTF1</i> , <b>MTRNR2L7</b> , <b>C10ORF68</b>	<sup>k</sup> stroke	61
11	<b>SPATA19</b> , <i>MRV11</i> , <b>DPP3</b> , <b>CTD-307407.11</b> , <b>MOGAT2</b> , <b>ANO3</b> , <b>FAM86C1</b> , <b>TREH</b> , <i>DDX6</i> , <i>PGAP2</i> , <i>FADS3</i> , <i>AL356215.1</i> , <b>UBASH3B</b> , <i>UVRAG<sup>l</sup></i> , <b>IFT46</b>	<sup>l</sup> autophagy	62
12	<b>SDR9C7</b> , <b>GALNT9<sup>m</sup></b> , <i>MGAT4C</i> , <b>NTS</b> , <b>SCYL2<sup>m</sup></b> , <i>KCNJ8</i> , <b>AC073528.1</b> , <i>PRPH</i> , <i>TROAP</i> , <i>CLEC6A</i> , <b>LRIG3</b> , <b>TMTC2</b> , <i>HECTD4</i> , <i>SMCO2</i> , <i>AEBP2</i> , <b>LGR5</b> , <i>GAS2L3</i> , <i>CIT</i> , <i>C12orf56</i> , <b>ANO6</b> , <b>CCDC59</b>	<sup>m</sup> neuralblastoma <sup>n</sup> arthrogryposis	63,64

(Continued on next page)



**Table 1. Continued**

Chr	Associated Protein-Coding Gene	Associated Effect	Ref.
13	<b>SLC15A1, DOCK9, THSD1, GPC5, HNRNPA1L2, C1QTNF9B, SPRY2, CKAP2, RFC3, RGCC, VWAS, DZIP1</b>		
14	<b>PPP2R5C, DCAF5, SERPINA6, RP11-796G6.2, TEX22, EGLN3, NPAS3</b>		
15	<b>NDNL2, LMAN1L, FAM219B, MPI, PGPEP1L, CERS3<sup>O</sup>, CKMT1A, CSK<sup>P</sup>, CYP1A2, CORO2B, ITGA11, RAB11A, NEDD4, C2CD4A, FGF7, HDC, C15orf60, DUOX2, CPLX3, BLM, HCN4</b>	<sup>q</sup> ichthyosis, <sup>P</sup> SLE	65,66
16	<b>OTOA, METTL22, TMEM114, CBLN1, USP10, KLHL36, PDILT, UMOD<sup>A</sup>, RP11-20I23.1, GCSH, CTD-2144E22.5, NKD1</b>	<sup>q</sup> kidney disease	67
17	<b>KRTAP4-4, PIK3R5, PIK3R6, MEOX1, MAP2K3, KCNJ12, SLC47A2, LGALS3BP, FLJ45079, NLK, KRT37, KRT38, C17orf82, TBX4, NARF, CLEC10A, ASGR2, IKZF3, AC132872.2, ZNF18, ENGASE, C1QTNF1, FAM211A, ZNF287</b>		
18	<b>ARHGAP28, SLC14A2, MAPRE2, DSEL, KIAA1468, PIGN</b>		
19	<b>TRPM4, RFX1, RLN3, PSG1, ZNF600, ZNF28, NOSIP, RCN3, NFKBID, ARRDC2, DNMT1, EIF3G, CATSPERG, AP3D1, DOT1L, ECSIT, MIER2, AC018755.1, PLEKHJ1, TSHZ3</b>		
20	<b>RIMS4, CPNE1, RP1-309K20.6, WFDC12, FAM182B, ROMO1, NFS1, SPINT4, C20orf166, KCNB1, PTGIS, DLGAP4, AAR2, CST7, SLPI, MAIN4, ARFGEF2, ZSWIM3, ZSWIM1, PANK2</b>		
21	<b>TPTE</b>		
22	<b>KIAA1644, RP1-32I10.10, CHEK2, TTC38, FAM118A, SMC1B, LDOC1L, USP41, APOL4<sup>F</sup>, APOL2<sup>F</sup>, TUBA8, USP18, POLR2F, MICALL1, EIF3L</b>	<sup>F</sup> pathogen immunity	68

Genes are extracted from the protein coding genes in the top 1% of 100 kb iHS Windows (Table S8) with each gene having a mean iHS > 3.0 in the Lugbara population. The genes in bold are those that also have evidence of selection in the Basoga population. Genes with superscripts are those that are associated with the phenotype in the “Associated Effect” Column.

between markers and the functional SNP.<sup>78</sup> Our sequence data from six Niger-Congo populations and the Nilo-Saharan Lugbara have already contributed to the development of an Illumina Omni chip that is enriched for African SNPs and should reduce the number of important loci missed by GWASs in African populations.<sup>79</sup>

### Demographic Inference

In this study, we carried out whole-genome sequencing on populations from six different sub-Saharan African countries, and combined our data with genome sequences from the 1000 Genomes and African Genome Variation projects to better understand the relationship of the Lugbara to neighboring populations. The great diversity of Nilo-Saharan languages meant that they were recognized as belonging to a single family only in 1966 and there is still a debate about whether all these languages share a common root.<sup>80</sup> The Lugbara belong to the large Central Sudanic group of languages, while the Gumuz language

has been hard to classify within the Nilo-Saharan family; the language may be an early branch from the family or it may be a language isolate and not related to Nilo-Saharan languages at all.<sup>12</sup> Genetic evidence has shown that Gumuz speakers are closely related to other Nilo-Saharan speaking groups from West Ethiopia, Sudan, and Sud-Sudan<sup>5</sup> and are well differentiated from neighboring Afro-Asiatic populations (Figure 2 and Table S5A). Our data show that  $F_{ST}$  between the Lugbara and the Gumuz (0.025) exceeds that between African Niger-Congo A and Niger Congo B populations (mean = 0.008, SE 0.0005) and also exceeded that within European, East Asian, and South Asian populations but not the American population in the 1000 Genomes data (Tables S5B and S5C). This is consistent with the relatively large  $F_{ST}$  between the Lugbara and the Gumuz being caused by differences in admixture history as well as isolation.

The two Nilo-Saharan populations also appeared very different in the F3 analyses (Figures 4 and S8). The Gumuz

**Table 2. Top-Ranked Extreme Signatures that Are Highly Differentiated between the Lugbara and Basoga Populations**

Chr	Gene	iHS  Max	iHS  Mean	Frequency iHS > 2	No. of SNPs iHS > 2	TajimaD_mean [UNL]	F <sub>ST</sub> Mean [UNL- UBB]	xpEHH_Max [UNL- UBB]	Rank Score
3	NEK4	3.21	3.35	0.24	48/199	2.05	0.06	4.38	61
3	COLQ	4.15	3.37	0.23	43/189	1.92	0.02	3.58	62
11	UVRAG	4.14	3.31	0.23	72/312	1.73	0.03	3.88	68
7	FAM3C	4.87	3.10	0.19	51/265	2.40	0.04	2.94	70
12	MGAT4C	3.63	3.65	0.23	66/283	1.95	0.02	3.02	77
5	ATP10B	4.31	3.08	0.21	61/291	1.84	0.02	4.60	88
5	TENM2	3.44	3.19	0.34	104/305	1.73	0.01	4.23	90
3	SMIM4	4.04	3.07	0.27	57/208	0.36	0.05	3.57	91
11	DGAT2	4.14	3.26	0.23	72/312	1.45	0.02	2.32	95
5	C5orf30	3.50	3.04	0.17	38/218	2.34	0.05	3.42	101
3	HACL1	4.15	3.98	0.23	43/189	1.03	0.01	1.69	105
3	GNL3	3.21	3.00	0.24	48/199	2.05	0.08	2.67	106
10	CYP2C8	4.43	3.04	0.17	68/404	2.50	0.02	1.19	108
2	ATP5G3	3.70	3.21	0.17	48/279	1.82	0.01	3.32	111
10	PDLIM1	3.68	3.15	0.16	55/337	1.76	0.02	3.03	111
1	WDR3	3.80	3.18	0.15	21/136	1.61	0.01	4.17	113
22	POLR2F	4.99	3.35	0.23	45/200	0.88	0.00	1.26	115
14	TEX22	3.23	3.34	0.15	38/262	2.30	0.02	2.53	117
10	C10orf129	3.68	3.03	0.16	55/337	3.46	0.04	1.86	119
3	DUSP7	3.57	3.17	0.26	43/165	0.12	0.03	1.79	122

Genes were ranked separately for xpEHH,  $F_{ST}$ , and Tajima D. The rank score was obtained by ranking genes separately by Tajima D,  $F_{ST}$ , and xpEHH and then an overall score was obtained by summing the ranks of the three metrics.

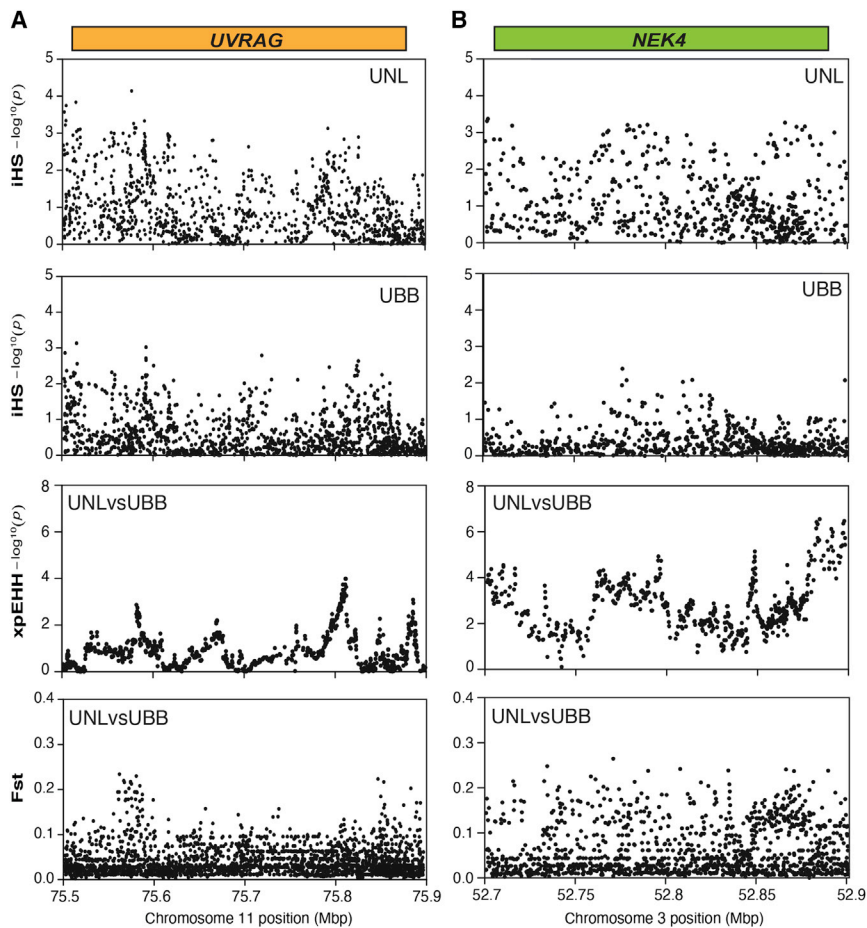
was most similar to the Afro-Asiatics with respect to their African component, in that there was evidence of shared ancestry to the Luhya (Figure 4A) when paired with any Niger-Congo B or Nigerian population and to the Basoga (Figure 4B) when paired with the Zambian population. The Lugbara, in contrast, appeared as a source population for the Basoga and Luhya only when paired with the Zambian population. This difference is surprising given the similarity of the two Nilo-Saharan populations in the admixture plots at most values of K. The patterns of genetic contribution from the Lugbara and Gumuz to the Luhya and Basoga in the F3 data are most consistent with the Admixture data at  $K = 6$  where Gumuz but not Lugbara share a small ancestry component with the Afro-Asiatics. This component (pink) is also present in the Luhya but is marginal in the Basoga (Figure 3;  $K = 6$ ). This component shared between the Gumuz, Basoga, and Luhya may represent an ancient East African population that was present before the Bantu Expansion.

The data are consistent with the Gumuz being genetically members of the Nilo-Saharan family and not an isolate, as some linguists have suggested.<sup>10,12</sup> The large genetic distance between the Lugbara and Gumuz may be indicative of the deep splits within the Nilo-Saharan fam-

ily, which merit much greater efforts to capture. A recent study included 2–4 samples from each of 9 lineages, supports the large genetic diversity within this family, and indicates that this family is a rich source of novel genetic variation.<sup>6</sup> With sequence information from further Nilo-Saharan populations, the genetic relationship of the Lugbara and Gumuz to other members of the family will also be resolved.

### Signatures of Selection

We identified signatures of selection in multiple genes associated with immune responses and other conditions. However, the multiple and diverse functions of individual genes make it hard to predict the specific adaptations or phenotypes that might have driven selection at these loci. Nevertheless, there was a group of genes associated with skin tone and hair form which are plausibly associated with the particularly dark color of the skin of Nilo-Saharanans and the intense UV radiation they experience. *UVRAG* showed the third greatest combined evidence for selection in Lugbara but not Basoga (Table 2). This gene, which is involved in melanine deposition in response to ultraviolet (UV) radiation,<sup>73</sup> has not previously been found under selection. Two other genes involved in skin



**Figure 6. Signatures of Selection Unique to the Uganda Nilotic Lugbara Population** Evidence (iHS, xpEHH, and Tajima D) for differential selection signatures between Lugbara (UNL) and Basoga (UBB) at the *UVRAG* locus on chromosome 11 (A) and the *NEK4* locus on chromosome 3 (B).

suite of traits for adaptation to the harsh conditions of the Sahel where the majority of Nilo-Saharan populations are found.

In conclusion, the Nilo-Saharan language speakers are an under-represented source for discovery of genetic variation. They are more genetically differentiated than the neighboring Afro-Asiatic and Niger-Congo groups but have been much less studied. They have contributed a large component to the genome of Afro-Asiatic speakers<sup>26</sup> and a smaller proportion of the genomes of East African Niger-Congo-B speakers. There is evidence for selection for skin color and hair form, which could be adaptive for the semi-arid Sahel where the majority of Nilo-Saharan populations live. Linguistic evidence suggests that substantial further genetic diversity remains to

pigmentation (*SNX13* and *TYROBP*) were in the top 1% of gene regions under selection in Lugbara and were also under selection in Basoga (Table S8) and a further five genes involved in skin pigmentation (*IRF4*, *TYRP1*, *HERC2*, *SLC24A5*, *OPRM1*) had some evidence of selection (Table S7).<sup>81</sup> Therefore, 7 of the 18 genes previously associated with skin pigmentation by Martin et al.<sup>81</sup> had some evidence of selection in this study.

Nilo-Saharans have some of the darkest skin tones in the world<sup>82</sup> and the Lugbara generally have a darker skin compared to the Basoga.<sup>83</sup> Skin reflectance is correlated with UV radiation<sup>84</sup> and the dark skin tones of the Nilo-Saharans could be an adaptation to the open savannah conditions of the Sahel where there is limited tree and cloud cover and which is predicted by models to be one of the regions of the world with darkest skin pigmentation.<sup>84</sup> *UVRAG* may be an important contributor to the exceptionally dark skin tones of the Nilo-Saharans in conjunction with *SNX13* and *TYROBP* in particular and possibly also *IRF4*, *TYRP1*, *HERC2*, *SLC24A5*, and *OPRM1*.

Hair form is probably related to thermoregulation by helping keep the head cool during exercise.<sup>85</sup> 6 keratin and 16 keratin-associated proteins, which are involved in hair formation, were in 3 regions with evidence of selection on chromosomes 12, 17, and 21 (Table S7) and selection for hair form as well as skin color could be part of a

be discovered within the Nilo-Saharan group, which should be a priority for further genome analysis studies.

#### Data and Code Availability

The datasets generated and/or analyzed during the current study are available from the corresponding author on reasonable request. The sequenced data have been submitted to the EGA by H3ABionet under the study accession number EGA: EGAS00001002602.

#### Supplemental Data

Supplemental Data can be found online at <https://doi.org/10.1016/j.ajhg.2020.07.007>.

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## Declaration of Interests

The authors declare no competing interests.

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## Web Resources

European Genome-phenome Archive (EGA), <https://www.ebi.ac.uk/ega>

QGIS, <https://qgis.org/en/site/>

## References

- Campbell, M.C., Hirbo, J.B., Townsend, J.P., and Tishkoff, S.A. (2014). The peopling of the African continent and the diaspora into the new world. *Curr. Opin. Genet. Dev.* 29, 120–132.
- Gurdasani, D., Carstensen, T., Tekola-Ayele, F., Pagani, L., Tachmazidou, I., Hatzikotoulas, K., Karthikeyan, S., Iles, L., Pollard, M.O., Choudhury, A., et al. (2015). The African Genome Variation Project shapes medical genetics in Africa. *Nature* 517, 327–332.
- Molinaro, L., Montinaro, F., Yelmen, B., Marnetto, D., Behar, D.M., Kivisild, T., and Pagani, L. (2019). West Asian sources of the Eurasian component in Ethiopians: a reassessment. *Sci. Rep.* 9, 18811.
- Tishkoff, S.A., Reed, F.A., Friedlaender, F.R., Ehret, C., Ranciaro, A., Froment, A., Hirbo, J.B., Awomoyi, A.A., Bodo, J.-M., Doumbo, O., et al. (2009). The genetic structure and history of Africans and African Americans. *Science* 324, 1035–1044.
- Pagani, L., Kivisild, T., Tarekegn, A., Ekong, R., Plaster, C., Gallego Romero, I., Ayub, Q., Mehdi, S.Q., Thomas, M.G., Luiselli, D., et al. (2012). Ethiopian genetic diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool. *Am. J. Hum. Genet.* 91, 83–96.
- Fan, S., Kelly, D.E., Beltrame, M.H., Hansen, M.E.B., Mallick, S., Ranciaro, A., Hirbo, J., Thompson, S., Beggs, W., Nyambo, T., et al. (2019). African evolutionary history inferred from whole genome sequence data of 44 indigenous African populations. *Genome Biol.* 20, 82.
- Li, S., Schlebusch, C., and Jakobsson, M. (2014). Genetic variation reveals large-scale population expansion and migration during the expansion of Bantu-speaking peoples. *Proc. Biol. Sci.* 281, 20141448.
- Lewis, M.P., Simons, F.G., and Fenning, D.C. (2016). *Ethnologue: Languages of the World, Nineteenth Edition* (SIL International).
- Hollfelder, N., Schlebusch, C.M., Günther, T., Babiker, H., Hassan, H.Y., and Jakobsson, M. (2017). Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. *PLoS Genet.* 13, e1006976.
- Bender, M.L. (2000). Nilo-Saharan. In *African Languages*, B. Heine and D. Nurse, eds. (Cambridge University Press).
- T. Güldemann, ed. (2018). *The Languages and Linguistics of Africa* (Berlin, Boston: De Gruyter).
- Dimmendaal, G.J. (2008). Language Ecology and Linguistic Diversity on the African Continent. *Lang. Linguist. Compass* 2, 840–858.
- Mallick, S., Li, H., Lipson, M., Mathieson, I., Gymrek, M., Racimo, F., Zhao, M., Chennagiri, N., Nordenfelt, S., Tandon, A., et al. (2016). The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. *Nature* 538, 201–206.
- Hsieh, P., Veeramah, K.R., Lachance, J., Tishkoff, S.A., Wall, J.D., Hammer, M.F., and Gutenkunst, R.N. (2016). Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. *Genome Res.* 26, 279–290.
- Lachance, J., Vernot, B., Elbers, C.C., Ferwerda, B., Froment, A., Bodo, J.-M., Lema, G., Fu, W., Nyambo, T.B., Rebbeck, T.R., et al. (2012). Evolutionary history and adaptation from high-coverage whole-genome sequences of diverse African hunter-gatherers. *Cell* 150, 457–469.
- Auton, A., Brooks, L.D., Durbin, R.M., Garrison, E.P., Kang, H.M., Korbel, J.O., Marchini, J.L., McCarthy, S., McVean, G.A., Abecasis, G.R.; and 1000 Genomes Project Consortium (2015). A global reference for human genetic variation. *Nature* 526, 68–74.
- Abecasis, G.R., Altshuler, D., Auton, A., Brooks, L.D., Durbin, R.M., Gibbs, R.A., Hurles, M.E., McVean, G.A.; and 1000 Genomes Project Consortium (2010). A map of human genome variation from population-scale sequencing. *Nature* 467, 1061–1073.
- Ma, Y., Ding, X., Qanbari, S., Weigend, S., Zhang, Q., and Simianer, H. (2015). Properties of different selection signature statistics and a new strategy for combining them. *Heredity* 115, 426–436.
- Shriner, D., and Keita, S.O.Y. (2016). Migration Route Out of Africa Unresolved by 225 Egyptian and Ethiopian Whole Genome Sequences. *Front. Genet.* 7, 98.
- Cooper, A., Ilboudo, H., Alibu, V.P., Ravel, S., Enyaru, J., Weir, W., Noyes, H., Capewell, P., Camara, M., Milet, J., et al. (2017). *APOL1* renal risk variants have contrasting resistance and susceptibility associations with African trypanosomiasis. *eLife* 6, 56.
- Shriner, D., and Rotimi, C.N. (2018). Whole-Genome-Sequence-Based Haplotypes Reveal Single Origin of the Sickle Allele during the Holocene Wet Phase. *Am. J. Hum. Genet.* 102, 547–556.
- Ilboudo, H., Noyes, H., Mulindwa, J., Kimuda, M.P., Koffi, M., Kaboré, J.W., Ahouty, B., Ngoyi, D.M., Fataki, O., Simo, G., et al.; TrypanoGEN Research Group as members of The H3Africa Consortium (2017). Introducing the TrypanoGEN biobank: A valuable resource for the elimination of human African trypanosomiasis. *PLoS Negl. Trop. Dis.* 11, e0005438.
- Li, H., and Durbin, R. (2009). Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 25, 1754–1760.
- McKenna, A., Hanna, M., Banks, E., Sivachenko, A., Cibulskis, K., Kernysky, A., Garimella, K., Altshuler, D., Gabriel, S., Daly, M., and DePristo, M.A. (2010). The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res.* 20, 1297–1303.
- Nyangiri, O.A., Noyes, H., Mulindwa, J., Ilboudo, H., Kabore, J.W., Ahouty, B., Koffi, M., Asina, O.F., Mumba, D., Ofon, E., et al.; TrypanoGEN Research Group, as members of The H3Africa Consortium (2020). Copy number variation in human genomes from three major ethno-linguistic groups in Africa. *BMC Genomics* 21, 289.

26. Pagani, L., Schiffels, S., Gurdasani, D., Danecek, P., Scally, A., Chen, Y., Xue, Y., Haber, M., Ekong, R., Oljira, T., et al. (2015). Tracing the route of modern humans out of Africa by using 225 human genome sequences from Ethiopians and Egyptians. *Am. J. Hum. Genet.* *96*, 986–991.
27. Li, H. (2011). A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. *Bioinformatics* *27*, 2987–2993.
28. Delaneau, O., Zagury, J.-F., and Marchini, J. (2013). Improved whole-chromosome phasing for disease and population genetic studies. *Nat. Methods* *10*, 5–6.
29. Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., et al.; 1000 Genomes Project Analysis Group (2011). The variant call format and VCFtools. *Bioinformatics* *27*, 2156–2158.
30. Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A.R., Bender, D., Maller, J., Sklar, P., de Bakker, P.I.W., Daly, M.J., and Sham, P.C. (2007). PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am. J. Hum. Genet.* *81*, 559–575.
31. R Core Team (2008). R: A language and environment for statistical computing (Vienna, Austria).
32. Alexander, D.H., Novembre, J., and Lange, K. (2009). Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* *19*, 1655–1664.
33. Patterson, N., Moorjani, P., Luo, Y., Mallick, S., Rohland, N., Zhan, Y., Genschoreck, T., Webster, T., and Reich, D. (2012). Ancient admixture in human history. *Genetics* *192*, 1065–1093.
34. Petr, M., Vernot, B., and Kelso, J. (2019). admixr-R package for reproducible analyses using ADMIXTOOLS. *Bioinformatics* *35*, 3194–3195.
35. Cadzow, M., Boocock, J., Nguyen, H.T., Wilcox, P., Merriman, T.R., and Black, M.A. (2014). A bioinformatics workflow for detecting signatures of selection in genomic data. *Front. Genet.* *5*, 293.
36. Wright, S. (1922). Coefficient of inbreeding and relationship. *Am. Naturalist* *56*, 330–338.
37. Tajima, F. (1989). Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* *123*, 585–595.
38. Wright, S. (1950). Genetical structure of populations. *Nature* *166*, 247–249.
39. Sabeti, P.C., Reich, D.E., Higgins, J.M., Levine, H.Z.P., Richter, D.J., Schaffner, S.F., Gabriel, S.B., Platko, J.V., Patterson, N.J., McDonald, G.J., et al. (2002). Detecting recent positive selection in the human genome from haplotype structure. *Nature* *419*, 832–837.
40. Gautier, M., and Vitalis, R. (2012). rehh: an R package to detect footprints of selection in genome-wide SNP data from haplotype structure. *Bioinformatics* *28*, 1176–1177.
41. Voight, B.F., Kudaravalli, S., Wen, X., and Pritchard, J.K. (2006). A map of recent positive selection in the human genome. *PLoS Biol.* *4*, e72.
42. Tang, K., Thornton, K.R., and Stoneking, M. (2007). A new approach for using genome scans to detect recent positive selection in the human genome. *PLoS Biol.* *5*, e171.
43. Quinlan, A.R., and Hall, I.M. (2010). BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics* *26*, 841–842.
44. Korneliussen, T.S., Moltke, I., Albrechtsen, A., and Nielsen, R. (2013). Calculation of Tajima's D and other neutrality test statistics from low depth next-generation sequencing data. *BMC Bioinformatics* *14*, 289.
45. van Dorp, L., Balding, D., Myers, S., Pagani, L., Tyler-Smith, C., Bekele, E., Tarekegn, A., Thomas, M.G., Bradman, N., and Hellenthal, G. (2015). Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. *PLoS Genet.* *11*, e1005397.
46. Hartmann, S., Ridley, A.J., and Lutz, S. (2015). The Function of Rho-Associated Kinases ROCK1 and ROCK2 in the Pathogenesis of Cardiovascular Disease. *Front. Pharmacol.* *6*, 276.
47. Kim, A.Y., Bommeljé, C.C., Lee, B.E., Yonekawa, Y., Choi, L., Morris, L.G., Huang, G., Kaufman, A., Ryan, R.J.H., Hao, B., et al. (2008). SCCRO (DCUN1D1) is an essential component of the E3 complex for neddylation. *J. Biol. Chem.* *283*, 33211–33220.
48. Meyer, D., and Thomson, G. (2001). How selection shapes variation of the human major histocompatibility complex: a review. *Ann. Hum. Genet.* *65*, 1–26.
49. Möröy, T., and Khandanpour, C. (2019). Role of GFI1 in Epigenetic Regulation of MDS and AML Pathogenesis: Mechanisms and Therapeutic Implications. *Front. Oncol.* *9*, 824.
50. Weidinger, S., Illig, T., Baurecht, H., Irvine, A.D., Rodriguez, E., Diaz-Lacava, A., Klopp, N., Wagenpfeil, S., Zhao, Y., Liao, H., et al. (2006). Loss-of-function variations within the filaggrin gene predispose for atopic dermatitis with allergic sensitizations. *J. Allergy Clin. Immunol.* *118*, 214–219.
51. Rung, J., Cauchi, S., Albrechtsen, A., Shen, L., Rocheleau, G., Cavalcanti-Proença, C., Bacot, F., Balkau, B., Belisle, A., Borch-Johnsen, K., et al. (2009). Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. *Nat. Genet.* *41*, 1110–1115.
52. Miller, J.L. (2013). Iron deficiency anemia: a common and curable disease. *Cold Spring Harb. Perspect. Med.* *3*, a011866–a011866.
53. Lencz, T., Guha, S., Liu, C., Rosenfeld, J., Mukherjee, S., DeRosse, P., John, M., Cheng, L., Zhang, C., Badner, J.A., et al. (2013). Genome-wide association study implicates NDS1 in schizophrenia and bipolar disorder. *Nat. Commun.* *4*, 2739.
54. Huang, L., Ye, K., McGee, M.C., Nidetz, N.F., Elmore, J.P., Limper, C.B., Southard, T.L., Russell, D.G., August, A., and Huang, W. (2020). Interleukin-2-Inducible T-Cell Kinase Deficiency Impairs Early Pulmonary Protection Against *Mycobacterium tuberculosis* Infection. *Front. Immunol.* *10*, 3103.
55. Sims, B., Farrow, A.L., Williams, S.D., Bansal, A., Krendelchikoff, A., Gu, L., and Matthews, Q.L. (2017). Role of TIM-4 in exosome-dependent entry of HIV-1 into human immune cells. *Int. J. Nanomedicine* *12*, 4823–4833.
56. Vyakarnam, A., Sidebottom, D., Murad, S., Underhill, J.A., Easterbrook, P.J., Dagleish, A.G., and Peakman, M. (2004). Possession of human leucocyte antigen DQ6 alleles and the rate of CD4 T-cell decline in human immunodeficiency virus-1 infection. *Immunology* *112*, 136–142.
57. Delgado, J.C., Baena, A., Thim, S., and Goldfeld, A.E. (2006). Aspartic acid homozygosity at codon 57 of HLA-DQ beta is associated with susceptibility to pulmonary tuberculosis in Cambodia. *J. Immunol.* *176*, 1090–1097.
58. Singh, G.C., Ahmed, M., Zaid, M., and Hasnain, S. (2020). Biochemical, serological, and genetic aspects related to gene

- HLA-DQB1 and its association with type 1 diabetes mellitus (T1DM). *Mol. Genet. Genomic Med.* 8, e1147.
59. Malnic, B., Godfrey, P.A., and Buck, L.B. (2004). The human olfactory receptor gene family. *Proc. Natl. Acad. Sci. USA* 101, 2584–2589.
  60. Li, Y., Pohl, E., Boulouiz, R., Schraders, M., Nürnberg, G., Charif, M., Admiraal, R.J.C., von Ameln, S., Baessmann, I., Kandil, M., et al. (2010). Mutations in TPRN cause a progressive form of autosomal-recessive nonsyndromic hearing loss. *Am. J. Hum. Genet.* 86, 479–484.
  61. Joshi, H., McIntyre, W.B., Kooner, S., Rathbone, M., Gabriele, S., Gabriele, J., Baranowski, D., Frey, B.N., and Mishra, R.K. (2020). Decreased Expression of Cerebral Dopamine Neurotrophic Factor in Platelets of Stroke Patients. *J. Stroke Cerebrovasc. Dis.* 29, 104502.
  62. Yang, Y., Quach, C., and Liang, C. (2016). Autophagy modulator plays a part in UV protection. *Autophagy* 12, 1677–1678.
  63. Berois, N., Gattolliat, C.-H., Barrios, E., Capandeguy, L., Douc-Rasy, S., Valteau-Couanet, D., Bénard, J., and Osinaga, E. (2013). GALNT9 gene expression is a prognostic marker in neuroblastoma patients. *Clin. Chem.* 59, 225–233.
  64. Seidahmed, M.Z., Al-Kindi, A., Alsaif, H.S., Miqdad, A., Alabbad, N., Alfifi, A., Abdelbasit, O.B., Alhussein, K., Alsamadi, A., Ibrahim, N., et al. (2020). Recessive mutations in SCYL2 cause a novel syndromic form of arthrogyrosis in humans. *Hum. Genet.* 139, 513–519.
  65. Youssefian, L., Vahidnezhad, H., Saeidian, A.H., Sotoudeh, S., Mahmoudi, H., Daneshpazhooch, M., Aghazadeh, N., Adams, R., Ghanadan, A., Zeinali, S., et al. (2017). Autosomal recessive congenital ichthyosis: CERS3 mutations identified by a next generation sequencing panel targeting ichthyosis genes. *Eur. J. Hum. Genet.* 25, 1282–1285.
  66. Manjarrez-Orduño, N., Marasco, E., Chung, S.A., Katz, M.S., Kirridly, J.F., Simpfendorfer, K.R., Freudenberg, J., Ballard, D.H., Nashi, E., Hopkins, T.J., et al. (2012). CSK regulatory polymorphism is associated with systemic lupus erythematosus and influences B-cell signaling and activation. *Nat. Genet.* 44, 1227–1230.
  67. Lv, L., Wang, J., Gao, B., Wu, L., Wang, F., Cui, Z., He, K., Zhang, L., Chen, M., and Zhao, M.-H. (2018). Serum uromodulin and progression of kidney disease in patients with chronic kidney disease. *J. Transl. Med.* 16, 316.
  68. Smith, E.E., and Malik, H.S. (2009). The apolipoprotein L family of programmed cell death and immunity genes rapidly evolved in primates at discrete sites of host-pathogen interactions. *Genome Res.* 19, 850–858.
  69. Sabeti, P.C., Varilly, P., Fry, B., Lohmueller, J., Hostetter, E., Cotsapas, C., Xie, X., Byrne, E.H., McCarroll, S.A., Gaudet, R., et al.; International HapMap Consortium (2007). Genome-wide detection and characterization of positive selection in human populations. *Nature* 449, 913–918.
  70. Takata, A., Matsumoto, N., and Kato, T. (2017). Genome-wide identification of splicing QTLs in the human brain and their enrichment among schizophrenia-associated loci. *Nat. Commun.* 8, 14519.
  71. Wu, C., Jin, X., Tsueng, G., Afrasiabi, C., and Su, A.I. (2016). BioGPS: building your own mash-up of gene annotations and expression profiles. *Nucleic Acids Res.* 44 (D1), D313–D316.
  72. Campbell, A.R., Regan, K., Bhawe, N., Pattanayak, A., Parihar, R., Stiff, A.R., Trikha, P., Scoville, S.D., Liyanarachchi, S., Kondadasula, S.V., et al. (2015). Gene expression profiling of the human natural killer cell response to Fc receptor activation: unique enhancement in the presence of interleukin-12. *BMC Med. Genomics* 8, 66.
  73. Li, S., Jang, G.-B., Quach, C., and Liang, C. (2019). Darkening with UVRAG. *Autophagy* 15, 366–367.
  74. Sosinsky, A., Ambrose, J., Zarowiecki, M., Mitchell, J., Henderson, S., Murugaesu, N., Hamblin, A., Turnbull, C., Walker, S., Perez-Gil, D., et al. (2019). 100,000 genomes project: Integrating whole genome sequencing (WGS) data into clinical practice. *Ann. Oncol.* 30, vii1.
  75. Gao, Y., Zhang, C., Yuan, L., Ling, Y., Wang, X., Liu, C., Pan, Y., Zhang, X., Ma, X., Wang, Y., et al.; Han100K Initiative (2020). PGG.Han: the Han Chinese genome database and analysis platform. *Nucleic Acids Res.* 48 (D1), D971–D976.
  76. Rutter, J.L., Goldstein, D.B., Denny, J.C., Philip-pakis, A., Smoller, J.W., and Jenkins, G. (2019). The “All of Us” Research Program. *N. Engl. J. Med.* 381, 1–9.
  77. Teo, Y.-Y., Small, K.S., and Kwiatkowski, D.P. (2010). Methodological challenges of genome-wide association analysis in Africa. *Nat. Rev. Genet.* 11, 149–160.
  78. Jallow, M., Teo, Y.-Y., Small, K.S., Rockett, K.A., Deloukas, P., Clark, T.G., Kivinen, K., Bojang, K.A., Conway, D.J., Pinder, M., et al.; Wellcome Trust Case Control Consortium; and Malaria Genomic Epidemiology Network (2009). Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nat. Genet.* 41, 657–665.
  79. Rotimi, C., Abayomi, A., Abimiku, A., Adabayeri, V.M., Adebamowo, C., Adebisi, E., Ademola, A.D., Adeyemo, A., Adu, D., Affolabi, D., et al.; H3Africa Consortium (2014). Research capacity. Enabling the genomic revolution in Africa. *Science* 344, 1346–1348.
  80. Greenberg, J.H. (1966). *The languages of Africa* (Cambridge University Press).
  81. Martin, A.R., Lin, M., Granka, J.M., Myrick, J.W., Liu, X., Sockell, A., Atkinson, E.G., Werely, C.J., Möller, M., Sandhu, M.S., et al. (2017). An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. *Cell* 171, 1340–1353.e14.
  82. Barsh, G.S. (2003). What controls variation in human skin color? *PLoS Biol.* 1, E27.
  83. Roberts, D.F., and Bainbridge, D.R. (1963). Nilotic Physique. *Am. J. Phys. Anthropol.* 21, 341–370.
  84. Chaplin, G. (2004). Geographic distribution of environmental factors influencing human skin coloration. *Am. J. Phys. Anthropol.* 125, 292–302.
  85. Jablonski, N.G., and Chaplin, G. (2014). The evolution of skin pigmentation and hair texture in people of African ancestry. *Dermatol. Clin.* 32, 113–121.