Supplemental Data

Population Genetic Inference from Personal

Genome Data: Impact of Ancestry and Admixture

on Human Genomic Variation

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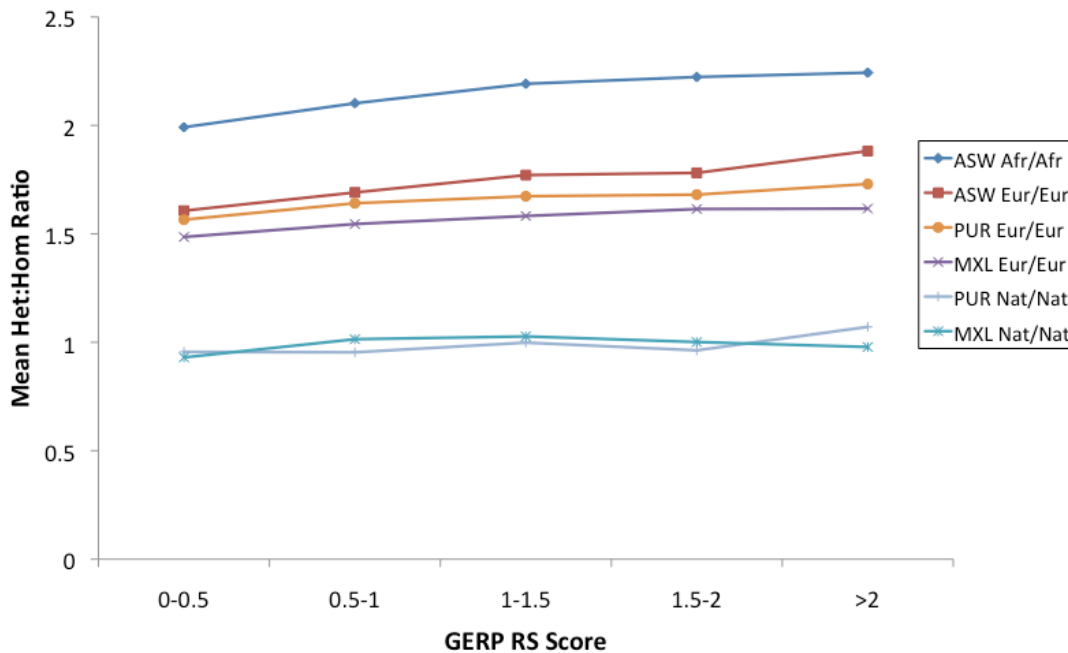

Figure S1. Relationship between Sequence Constraint and Ancestry

The ratio of heterozygous to homozygous variants for each indicated ancestry is shown stratified by the GERP RS score. Higher RS scores indicate stronger evolutionary constraint.
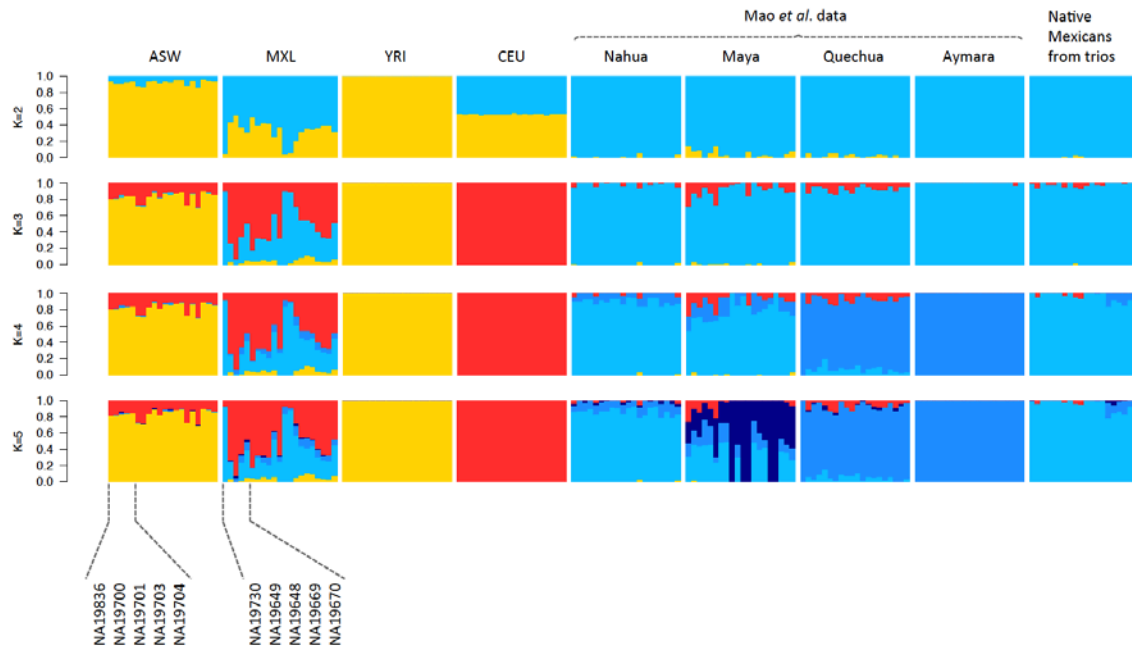
Figure S2. Admixture Analysis and Reference Panel Choice

Admixture deconvolution with PCAdmix requires a phased reference panel. For this study, we used a set of 10 trios sampled from each source population, including Yoruba from Ibadan (YRI), European-Americans from Utah (CEU), and a combined sample of Native American groups from Mexico. The analysis was performed using ADMIXTURE[46] with 352,095 SNPs common to all reference panels, including genotype data from Mao et al.[47]. ASW and MXL individuals with genome sequence data available are indicated.

A
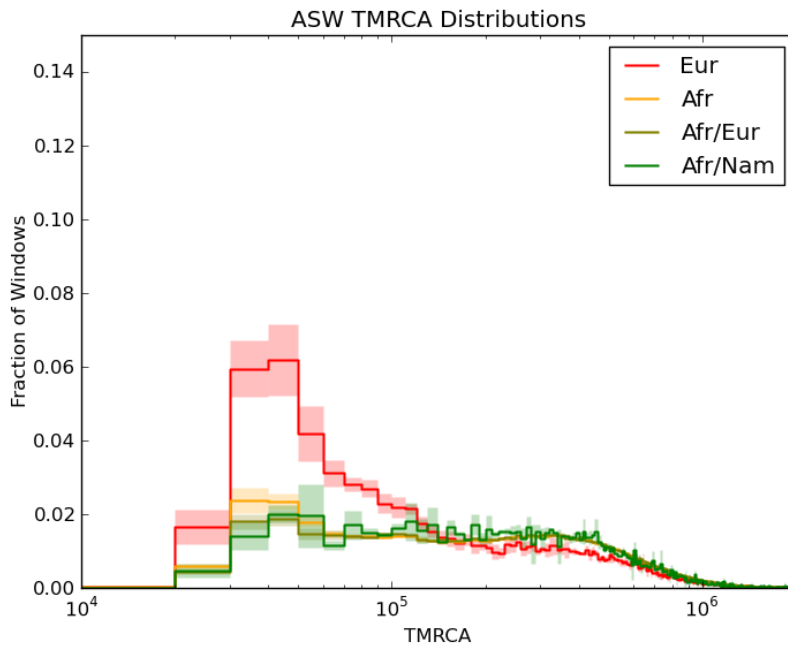
B
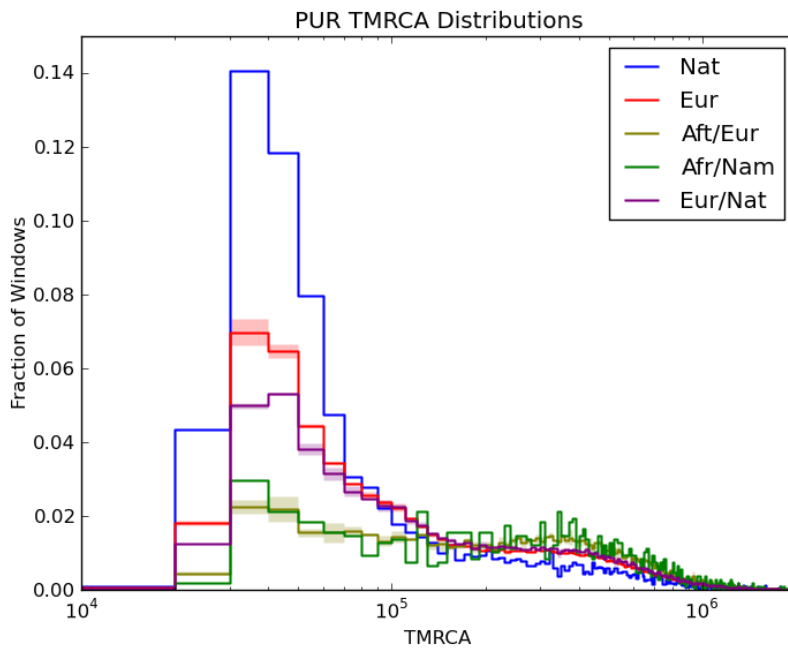
Figure S3. Distribution of Inferred T_{MRCA}

The distribution of inferred T_{MRCA} calculated in 10 kb windows scaled using chimpanzee divergence are shown for (A) ASW and (B) PUR individuals

A

B
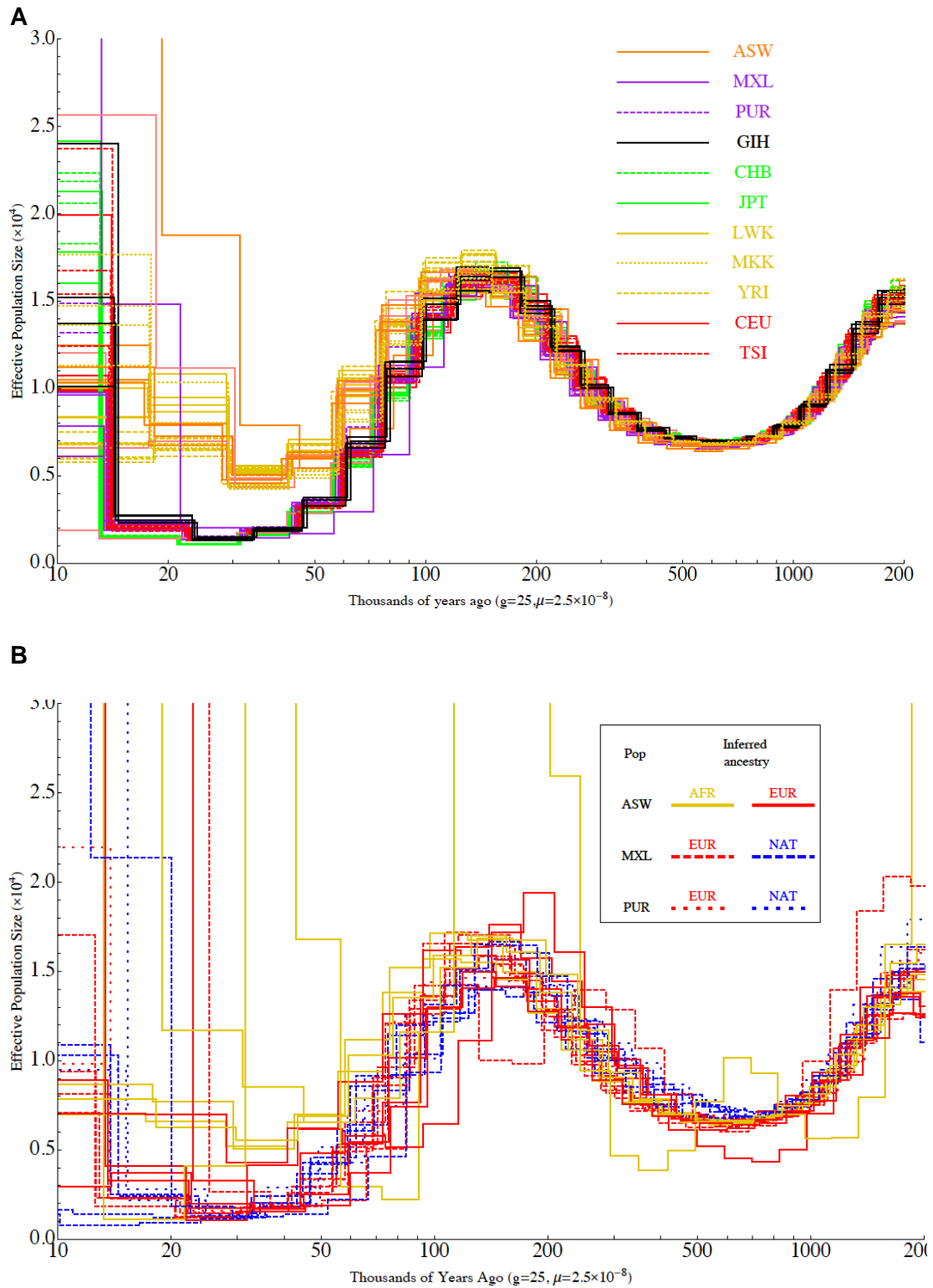
Figure S4. Demographic History Inferred with PSMC

PSMC results are shown for each individual separately for each population (A) and for each inferred ancestry following admixture deconvolution (B).
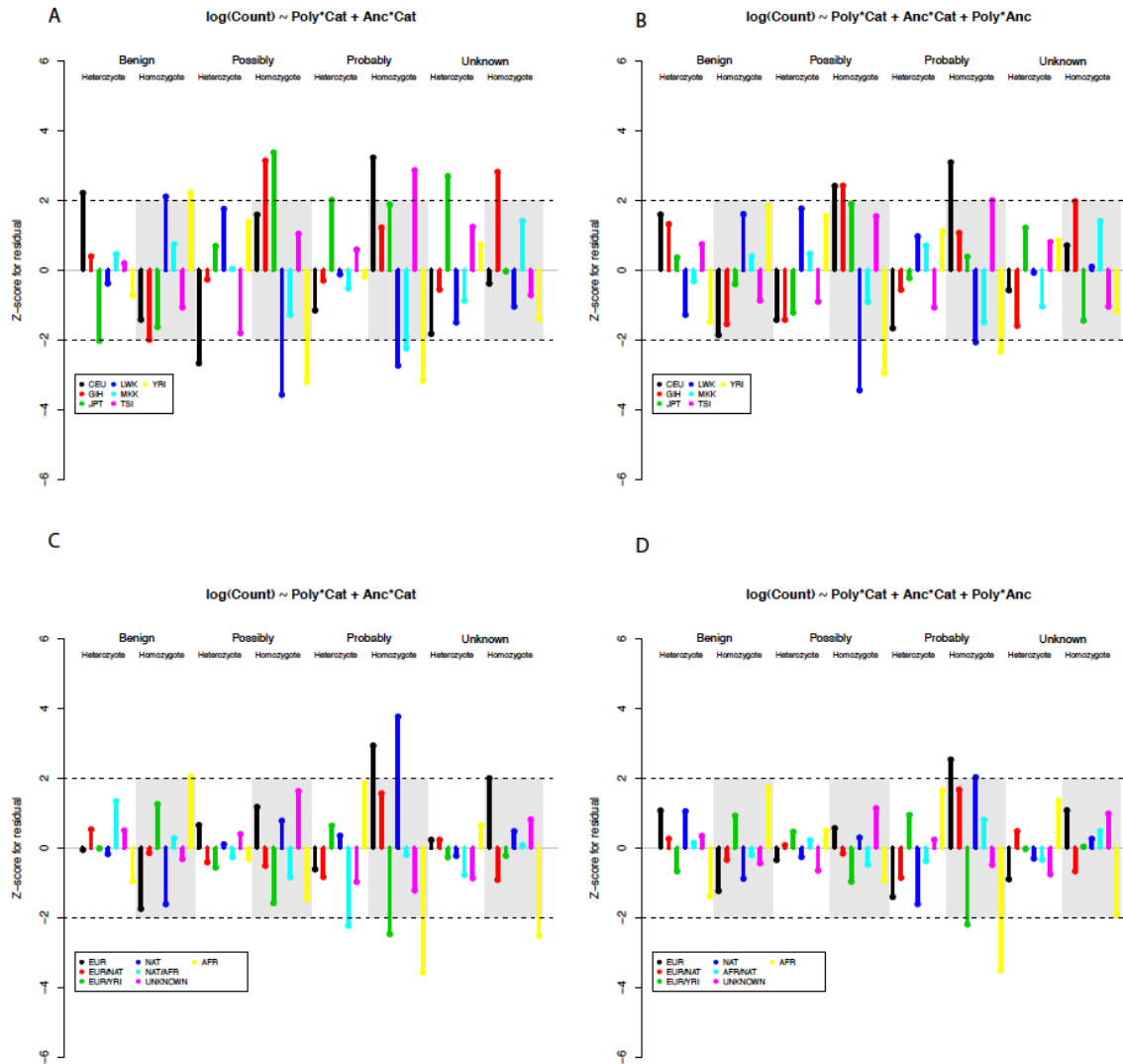
Figure S5. Residuals from Models of PolyPhen Counts

Z score residuals are shown for models of PolyPhen counts that consider pairwise interactions between PolyPhen status, zygosity category, and ancestry for the studied populations (A and B) and for the deconvolved ancestries of admixed individuals (C and D). Analysis was limited to those samples sequenced by Complete Genomics. This significant residuals observed in each case demonstrate the necessity of the PolyPhen*Catetogry*Ancestry interaction term.

Figure S6. Distribution of Counts for PolyPhen Categories

Autosomal variant counts are reported for each population for each PolyPhen prediction and zygosity category. Analysis was limited to those samples sequenced by Complete Genomics.

Table S1. Genotype Concordance

A

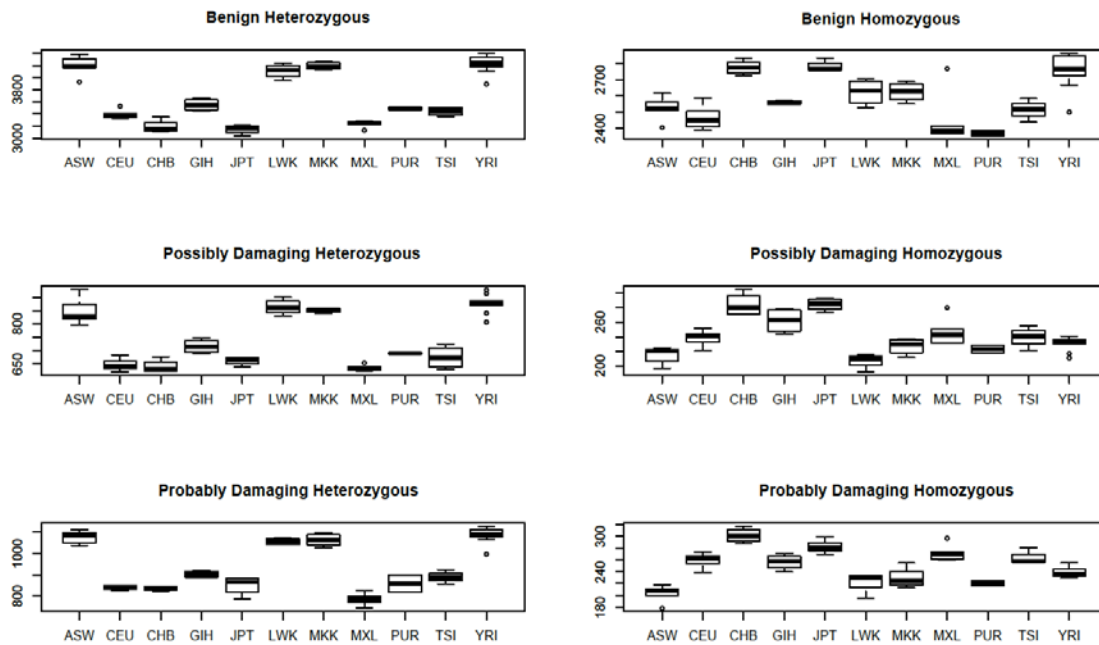| Sample	Population	HomRef	Het	HomAlt
NA19700	ASW	99.95%	99.85%	99.49%
NA19701	ASW	99.95%	99.80%	99.50%
NA19703	ASW	99.95%	99.90%	99.50%
NA19704	ASW	99.95%	99.83%	99.51%
NA06985	CEU	99.92%	98.12%	99.43%
NA06994	CEU	99.98%	98.73%	99.56%
NA07357	CEU	99.98%	99.90%	99.58%
NA18526	CHB	99.98%	99.92%	99.60%
NA18537	CHB	99.97%	99.60%	99.60%
NA18555	CHB	99.97%	99.94%	99.60%
NA18558	CHB	99.95%	99.81%	99.57%
NA20845	GIH	99.97%	99.81%	99.54%
NA20846	GIH	99.97%	99.93%	99.55%
NA20847	GIH	99.97%	99.92%	99.54%
NA20850	GIH	99.97%	99.86%	99.55%
NA18940	JPT	99.96%	99.84%	99.59%
NA18942	JPT	99.97%	99.93%	99.60%
NA18947	JPT	99.97%	99.63%	99.59%
NA18956	JPT	99.97%	99.86%	99.59%
NA21733	MKK	99.94%	99.42%	99.50%
NA19649	MXL	99.97%	99.75%	99.55%
NA19669	MXL	99.97%	99.68%	99.58%
NA19670	MXL	99.97%	99.87%	99.57%
NA20502	TSI	99.97%	99.68%	99.53%
NA20509	TSI	99.97%	99.85%	99.55%
NA20510	TSI	99.97%	99.88%	99.55%
NA18501	YRI	99.95%	99.90%	99.51%
NA18504	YRI	99.95%	99.90%	99.52%
NA18505	YRI	99.95%	99.91%	99.54%
NA18508	YRI	99.96%	99.90%	99.53%
NA18517	YRI	99.95%	99.84%	99.53%
NA19129	YRI	99.96%	99.89%	99.55%
NA19238	YRI	99.95%	99.83%	99.54%
NA19239	YRI	99.96%	99.88%	99.53%
Mean		99.96%	99.75%	99.55%

B

Sample	Population	HomRef	Het	HomAlt
NA19836	ASW	99.94%	98.41%	97.43%
NA19730	MXL	99.94%	98.00%	98.75%
Mean		99.94%	98.21%	98.09%

Genotype concordance is given for subset of samples sequenced by Complete Genomics (A) and SOLiD (B) relative to genotypes from the HapMap Project Phase 3.

Table S2. Sequence Diversity Summary

A

Population	Samples	Callable Bp per Sample	SNPs per Kilobase per Sample	Mean Heterozygosity *10^-3	Novel SNPs per Sample	NonSyn:Syn Allele Count per Sample
YRI	9	2,598,173,495	1.51	0.998	3.8%	0.842
ASW	4	2,578,256,849	1.45	0.981	5.3%	0.842
MKK	4	2,600,975,555	1.47	0.979	7.0%	0.848
LWK	4	2,575,705,972	1.47	0.979	6.7%	0.846
GIH	4	2,609,837,580	1.28	0.784	3.8%	0.857
PUR	2	2,594,712,021	1.26	0.782	3.0%	0.858
TSI	4	2,605,098,621	1.25	0.761	2.9%	0.867
CEU	5	2,597,855,813	1.24	0.755	1.8%	0.864
MXL	4	2,576,042,930	1.21	0.743	3.0%	0.856
CHB	4	2,606,261,347	1.25	0.718	2.8%	0.864
JPT	4	2,601,200,458	1.25	0.717	2.7%	0.866

B

Population	Samples	Callable Bp per Sample	SNPs per Kilobase per Sample	Mean Heterozygosity *10^-3	Novel SNPs per Sample	NonSyn:Syn Allele Count per Sample
ASW						
Afr/Afr	4	1,711,944,548	1.47	0.979	5.9%	0.832
Eur/Eur	4	53,078,411	1.18	0.729	2.7%	0.841
Afr/Eur	4	610,389,450	1.42	0.999	4.1%	0.856
Eur/Nat	2	5,467,801	1.14	0.831	3.4%	0.782
Afr/Nat	4	37,223,156	1.43	1.005	4.5%	0.881
Not assigned	4	162,887,384	1.50	1.025	4.9%	0.884
MXL						
Afr/Afr	3	3,145,648	1.42	0.877	6.2%	0.518
Eur/Eur	4	1,126,011,138	1.18	0.703	2.8%	0.864
Afr/Eur	4	81,605,200	1.34	0.937	4.1%	0.816
Eur/Nat	4	670,517,775	1.24	0.791	3.0%	0.862
Nat/Nat	4	173,058,489	1.17	0.567	3.0%	0.757
Afr/Nat	4	38,004,649	1.31	0.917	4.3%	0.996
Not assigned	4	484,258,654	1.26	0.796	3.2%	0.844
PUR						
Afr/Afr	1	2,370,069	1.52	0.981	3.9%	0.000
Eur/Eur	2	1,667,365,559	1.23	0.751	2.8%	0.865
Afr/Eur	2	119,098,072	1.47	1.036	4.1%	0.865
Eur/Nat	2	308,502,582	1.24	0.794	3.1%	0.907
Nat/Nat	2	23,382,334	1.21	0.582	3.1%	0.668
Afr/Nat	2	10,807,890	1.53	1.080	3.8%	0.622
Not assigned	2	464,370,551	1.29	0.816	3.1%	0.814

C

Population	Callable Bp per Sample	SNPs per Kilobase	Heterozygosity *10^-3	Novel SNPs	NonSyn:Syn Allele Count
ASW (NA19836)	2,465,426,377	1.69	1.129	7.6%	0.870
Afr/Afr	1,470,327,580	1.69	1.118	8.4%	0.842
Eur/Eur	128,032,937	1.37	0.788	5.1%	0.887
Afr/Eur	663,648,162	1.70	1.188	6.3%	0.901
Eur/Nat	5,253,481	1.54	0.868	4.6%	0.278
Afr/Nat	3,081,266	2.01	1.410	7.7%	0.628
Not assigned	195,082,951	1.80	1.245	7.9%	0.971
MXL (NA19730)	2,433,504,691	1.40	0.785	6.3%	0.875
Eur/Eur	21,608,276	1.44	0.899	5.6%	1.045
Afr/Eur	443,987	2.74	1.651	3.5%	0.000
Eur/Nat	341,574,989	1.47	0.921	5.7%	0.864
Nat/Nat	1,707,489,841	1.37	0.730	6.4%	0.877
Afr/Nat	50,849,701	1.55	1.087	7.6%	0.718
Not assigned	311,537,897	1.49	0.880	6.4%	0.899

(A) All samples were sequenced by Complete Genomics. Novel SNPs were determined relative to variants discovered by the 1000 Genomes low-coverage sequencing pilot, limited to genomic positions interrogated by the project.

(B) Sequence variation was recalculated based on the assignment of each genome into diploid source population classifications as indicated. Only individuals having at least 1 MB of each assigned ancestry are included. Only samples sequenced using Complete Genomics technology are shown.

(C) Diversity statistics obtained for NA19836 and NA19730, sequenced using the SOLiD technology.

Table S3. Ancestry Assignment Proportions

Sample Name	Population	Eur/Eur	Nat/Nat	Afr/Afr	Eur/Nat	Afr/Eur	Eur/Nat	Not Assigned
NA19700	ASW	3.5%	0.0%	63.5%	0.0%	27.5%	0.1%	5.4%
NA19701	ASW	0.7%	0.0%	65.1%	0.3%	22.6%	4.8%	6.4%
NA19703	ASW	2.0%	0.0%	70.1%	0.1%	21.1%	0.3%	6.4%
NA19704	ASW	2.0%	0.0%	66.9%	0.0%	23.2%	0.6%	7.3%
NA19836	ASW	5.2%	0.0%	59.6%	0.2%	26.6%	0.1%	8.3%
NA19730	MXL	0.9%	70.2%	0.0%	13.9%	0.0%	2.1%	13.0%
NA19648	MXL	75.9%	0.2%	0.1%	8.4%	1.8%	0.1%	13.6%
NA19649	MXL	45.5%	5.5%	0.0%	23.4%	4.2%	0.4%	20.9%
NA19669	MXL	34.7%	6.2%	0.1%	33.4%	3.0%	1.2%	21.4%
NA19670	MXL	18.3%	14.9%	0.2%	39.0%	3.6%	4.3%	19.6%
HG00731	PUR	70.4%	0.4%	0.0%	9.3%	3.2%	0.4%	16.3%
HG00732	PUR	57.9%	1.4%	0.1%	14.5%	5.9%	0.4%	19.8%

The fraction of the genome of each sample assigned to each ancestral category is listed. Assignment was performed using a 0.9 posterior-probability threshold obtained from the forward-backward algorithm in PCAdmix.

Table S4. Log-Likelihood and Akaike Information Criteria Results for Model Comparison

Data set	Model: log(Counts) ~ ., family=poisson()	AIC	LL	DOF	AIC Difference
All Genomes	Pop*Zyg+Zyg*Poly+Poly*Pop	4137.1	-2010.55	58	
	Population * Zygosity * PolyPhen	3981.065	-1902.53	88	156.03
Admixed with Ancestry Deconvolution	Indiv*Anc+Anc*Zyg+Zyg*Poly+Poly*Anc	3177.209	-1494.604	94	
	Indiv*Anc+Anc*Zyg*Poly	3146.372	-1461.186	112	30.84
	Indiv*Anc+Pop*Zyg+Anc*Zyg*Poly	3089.738	-1430.869	114	56.63

Table S5. Model Coefficients for Individual Sample Analysis by Population

Coefficients	Estimate	Std Error	z value	Pr(>|z|)
(Intercept)	8.3414102	0.0069056	1207.922	<2e-16
PolyphenPossibly	-1.5966446	0.0168253	-94.895	<2e-16
PolyphenProbably	-1.3605904	0.0152838	-89.022	<2e-16
PolyphenUnknown	-2.8336426	0.0293038	-96.699	<2e-16
CategoryHomozygous	-0.5082063	0.0112676	-45.103	<2e-16
AncestryCEU	-0.2134152	0.0103305	-20.659	<2e-16
AncestryCHB	-0.2748887	0.0112319	-24.474	<2e-16
AncestryGIH	-0.1674118	0.0108701	-15.401	<2e-16
AncestryJPT	-0.2883181	0.011279	-25.562	<2e-16
AncestryLWK	-0.0209012	0.010419	-2.006	0.044849
AncestryMKK	-0.0003577	0.0103594	-0.035	0.972454
AncestryMXL	-0.2606157	0.0104677	-24.897	<2e-16
AncestryPUR	-0.1851869	0.013826	-13.394	<2e-16
AncestryTSI	-0.1992014	0.0109743	-18.152	<2e-16
AncestryYRI	0.0063382	0.0086031	0.737	0.461285
PolyphenPossibly:CategoryHomozygous	-0.868716	0.0359889	-24.138	<2e-16
PolyphenProbably:CategoryHomozygous	-1.1603933	0.0360424	-32.195	<2e-16
PolyphenUnknown:CategoryHomozygous	-0.2757196	0.0520977	-5.292	1.21E-07
PolyphenPossibly:AncestryCEU	-0.0586951	0.0255176	-2.3	0.021438
PolyphenProbably:AncestryCEU	-0.035194	0.0230436	-1.527	1.27E-01
PolyphenUnknown:AncestryCEU	-0.0611071	0.0445527	-1.372	0.170198
PolyphenPossibly:AncestryCHB	-0.0084088	0.027426	-0.307	0.759149
PolyphenProbably:AncestryCHB	0.0220992	0.0247242	0.894	0.371413
PolyphenUnknown:AncestryCHB	0.070426	0.0467006	1.508	0.131546
PolyphenPossibly:AncestryGIH	-0.0033246	0.0265067	-0.125	0.900188
PolyphenProbably:AncestryGIH	-0.0085164	0.0241071	-0.353	0.723883
PolyphenUnknown:AncestryGIH	-0.007637	0.0462267	-0.165	0.868781
PolyphenPossibly:AncestryJPT	0.0365496	0.0272236	1.343	0.179411
PolyphenProbably:AncestryJPT	0.0524404	0.024644	2.128	0.033344
PolyphenUnknown:AncestryJPT	0.127658	0.046138	2.767	0.00566
PolyphenPossibly:AncestryLWK	0.0379977	0.025164	1.51	0.131044
PolyphenProbably:AncestryLWK	0.0009034	0.0230552	0.039	0.968744
PolyphenUnknown:AncestryLWK	-0.0304774	0.0445737	-0.684	0.494131
PolyphenPossibly:AncestryMKK	0.0020042	0.0252288	0.079	0.936682
PolyphenProbably:AncestryMKK	-0.011847	0.0229884	-0.515	0.606311
PolyphenUnknown:AncestryMKK	-0.0164082	0.0441505	-0.372	0.71016
PolyphenPossibly:AncestryMXL	-0.0311551	0.0256931	-1.213	0.225288
PolyphenProbably:AncestryMXL	-0.0547753	0.0234589	-2.335	0.019546
PolyphenUnknown:AncestryMXL	-0.0597661	0.0451432	-1.324	0.185528
PolyphenPossibly:AncestryPUR	-0.0236121	0.0339371	-0.696	0.486579
PolyphenProbably:AncestryPUR	-0.0410289	0.0309809	-1.324	0.185395
PolyphenUnknown:AncestryPUR	0.045729	0.0577337	0.792	0.428321
PolyphenPossibly:AncestryTSI	-0.031222	0.0269508	-1.158	0.246669
PolyphenProbably:AncestryTSI	0.0079162	0.0242429	0.327	0.744017
PolyphenUnknown:AncestryTSI	0.0562409	0.0458369	1.227	0.21983
PolyphenPossibly:AncestryYRI	0.0243891	0.0208864	1.168	0.242926
PolyphenProbably:AncestryYRI	0.0015626	0.0190366	0.082	0.934579
PolyphenUnknown:AncestryYRI	0.0341053	0.0363007	0.94	0.347463
CategoryHomozygous:AncestryCEU	0.1916177	0.0163404	11.727	<2e-16
CategoryHomozygous:AncestryCHB	0.3691895	0.0171929	21.473	<2e-16
CategoryHomozygous:AncestryGIH	0.1808956	0.0171811	10.529	<2e-16
CategoryHomozygous:AncestryJPT	0.3844207	0.0172191	22.325	<2e-16
CategoryHomozygous:AncestryLWK	0.0592946	0.016828	3.524	0.000426
CategoryHomozygous:AncestryMKK	0.0391324	0.0167901	2.331	0.01977
CategoryHomozygous:AncestryMXL	0.2364659	0.0164332	14.389	<2e-16

CategoryHomozygous:AncestryPUR	0.1238932	0.0219348	5.648	1.62E-08
CategoryHomozygous:AncestryTSI	0.1955284	0.0172962	11.305	<2e-16
CategoryHomozygous:AncestryYRI	0.0811062	0.0139153	5.829	5.59E-09
PolyphenPossibly:CategoryHomozygous:AncestryCEU	0.1865991	0.0508252	3.671	0.000241
PolyphenProbably:CategoryHomozygous:AncestryCEU	0.3031425	0.0494823	6.126	9.00E-10
PolyphenUnknown:CategoryHomozygous:AncestryCEU	0.1696198	0.0744989	2.277	0.022798
PolyphenPossibly:CategoryHomozygous:AncestryCHB	0.1952388	0.0522948	3.733	1.89E-04
PolyphenProbably:CategoryHomozygous:AncestryCHB	0.2809786	0.0509453	5.515	3.48E-08
PolyphenUnknown:CategoryHomozygous:AncestryCHB	0.0725263	0.0766674	0.946	0.344155
PolyphenPossibly:CategoryHomozygous:AncestryGIH	0.1903419	0.0525991	3.619	2.96E-04
PolyphenProbably:CategoryHomozygous:AncestryGIH	0.2309152	0.0521353	4.429	9.46E-06
PolyphenUnknown:CategoryHomozygous:AncestryGIH	0.2573369	0.0761354	3.38	0.000725
PolyphenPossibly:CategoryHomozygous:AncestryJPT	0.1493586	0.0521799	2.862	4.21E-03
PolyphenProbably:CategoryHomozygous:AncestryJPT	0.1837998	0.0514487	3.572	0.000354
PolyphenUnknown:CategoryHomozygous:AncestryJPT	-0.0023948	0.0765084	-0.031	0.975029
PolyphenPossibly:CategoryHomozygous:AncestryLWK	-0.1115157	0.0542993	-2.054	0.040003
PolyphenProbably:CategoryHomozygous:AncestryLWK	0.0522859	0.0530775	0.985	0.324582
PolyphenUnknown:CategoryHomozygous:AncestryLWK	0.0743105	0.0773473	0.961	0.336684
PolyphenPossibly:CategoryHomozygous:AncestryMKK	0.0174284	0.0533294	0.327	0.743814
PolyphenProbably:CategoryHomozygous:AncestryMKK	0.0956651	0.0527234	1.814	0.069605
PolyphenUnknown:CategoryHomozygous:AncestryMKK	0.1810454	0.0755754	2.396	0.016595
PolyphenPossibly:CategoryHomozygous:AncestryMXL	0.1984679	0.0506148	3.921	8.81E-05
PolyphenProbably:CategoryHomozygous:AncestryMXL	0.3747103	0.0493018	7.6	2.95E-14
PolyphenUnknown:CategoryHomozygous:AncestryMXL	0.1883879	0.074663	2.523	1.16E-02
PolyphenPossibly:CategoryHomozygous:AncestryPUR	0.1242341	0.0679462	1.828	6.75E-02
PolyphenProbably:CategoryHomozygous:AncestryPUR	0.188265	0.0670703	2.807	0.005001
PolyphenUnknown:CategoryHomozygous:AncestryPUR	0.1120045	0.0971163	1.153	0.248786
PolyphenPossibly:CategoryHomozygous:AncestryTSI	0.1445606	0.0536921	2.692	0.007094
PolyphenProbably:CategoryHomozygous:AncestryTSI	0.2566407	0.0519836	4.937	7.94E-07
PolyphenUnknown:CategoryHomozygous:AncestryTSI	0.0337401	0.0780547	0.432	0.665551
PolyphenPossibly:CategoryHomozygous:AncestryYRI	-0.039185	0.0443917	-0.883	3.77E-01
PolyphenProbably:CategoryHomozygous:AncestryYRI	0.0812618	0.0439353	1.85	0.064374
PolyphenUnknown:CategoryHomozygous:AncestryYRI	0.0221431	0.0637828	0.347	0.728468

Table S6. Model Coefficients for Individual Sample Analysis by Deconvolved Ancestry

Coefficients	Estimate	Std Error	z value	Pr(>|z|)
(Intercept)	8.22668291	0.04378088	187.905819	0
IndividualHG00732PUR	-24.564109	1412.97649	-0.0173847	0.98612975
IndividualNA19648MXL	-24.564109	1412.97647	-0.0173847	0.98612975
IndividualNA19649MXL	-24.56411	1412.97643	-0.0173847	0.98612975
IndividualNA19669MXL	-24.564109	1412.97636	-0.0173847	0.98612975
IndividualNA19670MXL	-5.0498685	0.14158031	-35.667872	1.25E-278
IndividualNA19700ASW	-0.3555226	0.04504968	-7.8917906	2.98E-15
IndividualNA19701ASW	-0.4266798	0.0451856	-9.4428269	3.63E-21
IndividualNA19703ASW	-0.2900283	0.04493251	-6.4547542	1.08E-10
IndividualNA19704ASW	-0.3470768	0.04120995	-8.4221605	3.70E-17
AncestryEUR	-0.4767	0.04640445	-10.272721	9.35E-25
AncestryEUR/AFR	-3.5015719	0.07844127	-44.639408	0
AncestryEUR/NAT	-2.3554046	0.05724522	-41.145874	0
AncestryNAT	-6.4071867	0.22561442	-28.398835	2.09E-177
AncestryNAT/AFR	-6.3734686	0.28248045	-22.562512	1.01E-112
AncestryUNKNOWN	-1.8021414	0.03627417	-49.681124	0
PolyphenPossibly	-1.6171629	0.02395205	-67.516675	0
PolyphenProbably	-1.3444317	0.02143442	-62.723027	0
PolyphenUnknown	-2.8286636	0.04126403	-68.550353	0
CategoryHomozygous	-0.4407566	0.01557646	-28.296328	3.83E-176
IndividualHG00732PUR:AncestryEUR	24.3552884	1412.97649	0.01723687	0.98624765
IndividualNA19648MXL:AncestryEUR	24.5472034	1412.97647	0.01737269	0.9861393
IndividualNA19649MXL:AncestryEUR	24.0807833	1412.97643	0.01704259	0.98640264
IndividualNA19669MXL:AncestryEUR	23.8490181	1412.97636	0.01687857	0.98653349
IndividualNA19670MXL:AncestryEUR	3.57526256	0.14488774	24.6760884	1.93E-134
IndividualNA19700ASW:AncestryEUR	-2.9590163	0.08402561	-35.215649	1.15E-271
IndividualNA19701ASW:AncestryEUR	-3.9672401	0.12846756	-30.88126	2.13E-209
IndividualNA19703ASW:AncestryEUR	-3.3417515	0.0941385	-35.498244	5.23E-276
IndividualNA19704ASW:AncestryEUR	-3.420141	0.09751055	-35.074574	1.65E-269
IndividualHG00732PUR:AncestryEUR/AFR	25.6791155	1412.97649	0.01817377	0.98550022
IndividualNA19648MXL:AncestryEUR/AFR	23.9655206	1412.97648	0.01696102	0.98646771
IndividualNA19649MXL:AncestryEUR/AFR	24.9695749	1412.97643	0.01767161	0.98590083
IndividualNA19669MXL:AncestryEUR/AFR	25.0641326	1412.97636	0.01773854	0.98584744
IndividualNA19670MXL:AncestryEUR/AFR	5.46629265	0.16401833	33.3273278	1.55E-243
IndividualNA19700ASW:AncestryEUR/AFR	2.66305416	0.08107336	32.8474635	1.24E-236
IndividualNA19701ASW:AncestryEUR/AFR	2.5584472	0.08163435	31.3403286	1.32E-215
IndividualNA19703ASW:AncestryEUR/AFR	2.37204918	0.08164778	29.052218	1.44E-185
IndividualNA19704ASW:AncestryEUR/AFR	2.62667236	0.07907796	33.2162373	6.28E-242
IndividualHG00732PUR:AncestryEUR/NAT	24.9149577	1412.97649	0.01763296	0.98593166
IndividualNA19648MXL:AncestryEUR/NAT	24.7099258	1412.97647	0.01748785	0.98604742
IndividualNA19649MXL:AncestryEUR/NAT	25.4464564	1412.97643	0.01800912	0.98563158
IndividualNA19669MXL:AncestryEUR/NAT	25.6490309	1412.97636	0.01815248	0.98551721
IndividualNA19670MXL:AncestryEUR/NAT	6.37236575	0.14700497	43.3479622	0
IndividualNA19701ASW:AncestryEUR/NAT	-2.8033832	0.18581666	-15.086823	1.98E-51
IndividualNA19703ASW:AncestryEUR/NAT	-4.7963327	0.45083814	-10.638702	1.97E-26
IndividualHG00732PUR:AncestryNAT	25.5449386	1412.97651	0.01807881	0.98557598
IndividualNA19648MXL:AncestryNAT	23.7168114	1412.97653	0.016785	0.98660814
IndividualNA19649MXL:AncestryNAT	27.1614945	1412.97645	0.01922289	0.9846633
IndividualNA19669MXL:AncestryNAT	27.5210014	1412.97638	0.01947733	0.98446032
IndividualNA19670MXL:AncestryNAT	8.90102879	0.2620614	33.9654321	7.22E-253
IndividualHG00732PUR:AncestryNAT/AFR	24.6382174	1412.97654	0.0174371	0.98608791
IndividualNA19648MXL:AncestryNAT/AFR	24.7717486	1412.97652	0.01753161	0.98601252
IndividualNA19649MXL:AncestryNAT/AFR	25.495668	1412.97647	0.01804394	0.9856038
IndividualNA19669MXL:AncestryNAT/AFR	26.342965	1412.97639	0.0186436	0.98512542
IndividualNA19670MXL:AncestryNAT/AFR	8.40649759	0.31567234	26.6304534	3.01E-156
IndividualNA19700ASW:AncestryNAT/AFR	-2.2094267	1.03872641	-2.1270536	0.03341563
IndividualNA19701ASW:AncestryNAT/AFR	4.04381539	0.28465933	14.2058068	8.43E-46
IndividualNA19703ASW:AncestryNAT/AFR	1.33599688	0.32552885	4.10408128	4.06E-05

IndividualNA19704ASW:AncestryNAT/AFR	1.41971359	0.32394	4.38264362	1.17E-05
IndividualHG00732PUR:AncestryUNKNOWN	24.7103931	1412.97649	0.01748818	0.98604716
IndividualNA19648MXL:AncestryUNKNOWN	24.3690487	1412.97647	0.01724661	0.98623988
IndividualNA19649MXL:AncestryUNKNOWN	24.7473686	1412.97643	0.01751435	0.98602628
IndividualNA19669MXL:AncestryUNKNOWN	24.8570514	1412.97636	0.01759198	0.98596435
IndividualNA19670MXL:AncestryUNKNOWN	5.23605042	0.14115779	37.0935986	3.56E-301
IndividualNA19700ASW:AncestryUNKNOWN	-0.3690557	0.05270311	-7.0025413	2.51E-12
IndividualNA19701ASW:AncestryUNKNOWN	-0.3701103	0.05383834	-6.8744754	6.22E-12
IndividualNA19703ASW:AncestryUNKNOWN	-0.2093766	0.04974379	-4.2091005	2.56E-05
PolyphenPossibly:CategoryHomozygous	-0.8423817	0.04948171	-17.024101	5.44E-65
PolyphenProbably:CategoryHomozygous	-1.1848462	0.04958739	-23.894102	3.53E-126
PolyphenUnknown:CategoryHomozygous	-0.3645623	0.07380695	-4.9394042	7.84E-07
AncestryEUR:PolyphenPossibly	0.01331302	0.03438272	0.38720085	0.69860752
AncestryEUR/AFR:PolyphenPossibly	-0.0217267	0.04208907	-0.5162074	0.60570959
AncestryEUR/NAT:PolyphenPossibly	-0.0301259	0.04407832	-0.6834627	0.49431454
AncestryNAT:PolyphenPossibly	0.03255912	0.109279	0.29794494	0.76574519
AncestryNAT/AFR:PolyphenPossibly	-0.0970103	0.11343077	-0.8552382	0.3924193
AncestryUNKNOWN:PolyphenPossibly	0.00934939	0.04069459	0.22974537	0.81828964
AncestryEUR:PolyphenProbably	-0.0548865	0.0312122	-1.7584955	0.07866323
AncestryEUR/AFR:PolyphenProbably	-0.0267841	0.03770509	-0.7103578	0.47748227
AncestryEUR/NAT:PolyphenProbably	-0.0804027	0.03999555	-2.0102902	0.04440049
AncestryNAT:PolyphenProbably	-0.0673293	0.10163748	-0.6624455	0.50768578
AncestryNAT/AFR:PolyphenProbably	-0.2801294	0.10890095	-2.572332	0.0101016
AncestryUNKNOWN:PolyphenProbably	-0.0682185	0.03717405	-1.8351116	0.06648916
AncestryEUR:PolyphenUnknown	-0.0315017	0.05986622	-0.5262013	0.59874834
AncestryEUR/AFR:PolyphenUnknown	-0.0348042	0.07287297	-0.4776007	0.63293443
AncestryEUR/NAT:PolyphenUnknown	-0.0708143	0.07707059	-0.9188239	0.35818771
AncestryNAT:PolyphenUnknown	0.07712826	0.18422808	0.41865637	0.67546729
AncestryNAT/AFR:PolyphenUnknown	-0.3143636	0.21692661	-1.4491705	0.14728998
AncestryUNKNOWN:PolyphenUnknown	-0.1274034	0.07318181	-1.7409167	0.08169818
AncestryEUR:CategoryHomozygous	0.1438969	0.02194561	6.55697752	5.49E-11
AncestryEUR/AFR:CategoryHomozygous	-0.1922931	0.02835919	-6.7806271	1.20E-11
AncestryEUR/NAT:CategoryHomozygous	-0.008894	0.02846645	-0.3124365	0.75470881
AncestryNAT:CategoryHomozygous	0.802063	0.0593681	13.5100001	1.37E-41
AncestryNAT/AFR:CategoryHomozygous	-0.2393428	0.07630532	-3.1366466	0.00170892
AncestryUNKNOWN:CategoryHomozygous	0.01152875	0.02647133	0.43551846	0.66318614
AncestryEUR:PolyphenPossibly:CategoryHomozygous	0.1444687	0.06755644	2.13848903	0.03247707
AncestryEUR/AFR:PolyphenPossibly:CategoryHomozygous	-0.026642	0.09229069	-0.2886747	0.77283032
AncestryEUR/NAT:PolyphenPossibly:CategoryHomozygous	0.06756771	0.08983601	0.75212281	0.45197721
AncestryNAT:PolyphenPossibly:CategoryHomozygous	0.22435544	0.16540698	1.35638434	0.17497691
AncestryNAT/AFR:PolyphenPossibly:CategoryHomozygous	0.04917538	0.25278356	0.19453551	0.84575659
AncestryUNKNOWN:PolyphenPossibly:CategoryHomozygous	0.15479838	0.08101283	1.91078832	0.05603179
AncestryEUR:PolyphenProbably:CategoryHomozygous	0.34222006	0.06634077	5.15851799	2.49E-07
AncestryEUR/AFR:PolyphenProbably:CategoryHomozygous	0.0207498	0.09174757	0.22616181	0.82107557
AncestryEUR/NAT:PolyphenProbably:CategoryHomozygous	0.38540357	0.0845628	4.55760152	5.17E-06
AncestryNAT:PolyphenProbably:CategoryHomozygous	0.67860582	0.1511677	4.48909267	7.15E-06
AncestryNAT/AFR:PolyphenProbably:CategoryHomozygous	0.38903916	0.24337063	1.59854608	0.1099215
AncestryUNKNOWN:PolyphenProbably:CategoryHomozygous	0.20071041	0.08190015	2.45067201	0.01425898
AncestryEUR:PolyphenUnknown:CategoryHomozygous	0.28834492	0.10024863	2.87629787	0.0040237
AncestryEUR/AFR:PolyphenUnknown:CategoryHomozygous	0.17725189	0.13104957	1.35255604	0.1761975
AncestryEUR/NAT:PolyphenUnknown:CategoryHomozygous	0.17956196	0.13269137	1.35323014	0.17598212
AncestryNAT:PolyphenUnknown:CategoryHomozygous	0.31341091	0.24749679	1.2663231	0.20539743
AncestryNAT/AFR:PolyphenUnknown:CategoryHomozygous	0.47411695	0.36253094	1.30779723	0.19094209
AncestryUNKNOWN:PolyphenUnknown:CategoryHomozygous	0.36193836	0.1213482	2.98264293	0.00285771

Table S7. Model Coefficients for Individual Sample Analysis by Deconvolved Ancestry with Population of Origin Effect on Heterozygosity

Coefficients	Estimate	Std Error	z value	Pr(>|z|)
(Intercept)	8.18638085	0.045094	181.540365	0
IndividualHG00732PUR	-24.58406	1425.49168	-0.017246	0.98624035
IndividualNA19648MXL	-24.63264	1433.91598	-0.0171786	0.98629415
IndividualNA19649MXL	-24.63264	1433.91599	-0.0171786	0.98629415
IndividualNA19669MXL	-24.63264	1433.91592	-0.0171786	0.98629415
IndividualNA19670MXL	-5.0889783	0.14179261	-35.890294	4.33E-282
IndividualNA19700ASW	-0.3150464	0.04633154	-6.7998251	1.05E-11
IndividualNA19701ASW	-0.3862036	0.04646371	-8.3119393	9.42E-17
IndividualNA19703ASW	-0.249552	0.04621762	-5.3994999	6.68E-08
IndividualNA19704ASW	-0.3066005	0.04260748	-7.1959312	6.20E-13
AncestryEUR	-0.4171519	0.04734942	-8.8100742	1.25E-18
AncestryEUR/AFR	-3.4873058	0.07850871	-44.41935	0
AncestryEUR/NAT	-2.2885241	0.05802467	-39.440538	0
AncestryNAT	-6.3161543	0.22577181	-27.975832	3.20E-172
AncestryNAT/AFR	-6.337914	0.28254622	-22.431424	1.94E-111
AncestryUNKNOWN	-1.7547148	0.0368924	-47.563038	0
CategoryHomozygous	-0.4412717	0.01557679	-28.328792	1.53E-176
PolyphenPossibly	-1.6171629	0.02395205	-67.516675	0
PolyphenProbably	-1.3444317	0.02143442	-62.723027	0
PolyphenUnknown	-2.8286636	0.04126403	-68.550353	0
IndividualHG00732PUR:AncestryEUR	24.3752386	1425.49168	0.01709953	0.98635721
IndividualNA19648MXL:AncestryEUR	24.5783957	1433.91598	0.01714075	0.98632433
IndividualNA19649MXL:AncestryEUR	24.1119748	1433.91599	0.01681547	0.98658383
IndividualNA19669MXL:AncestryEUR	23.8802107	1433.91592	0.01665384	0.98671277
IndividualNA19670MXL:AncestryEUR	3.57703344	0.14490305	24.6857015	1.52E-134
IndividualNA19700ASW:AncestryEUR	-2.9560449	0.08403011	-35.178401	4.28E-271
IndividualNA19701ASW:AncestryEUR	-3.9642687	0.1284705	-30.857423	4.45E-209
IndividualNA19703ASW:AncestryEUR	-3.3387801	0.09414252	-35.465166	1.69E-275
IndividualNA19704ASW:AncestryEUR	-3.4171696	0.09751443	-35.042706	5.04E-269
IndividualHG00732PUR:AncestryEUR/AFR	25.6990657	1425.49168	0.01802821	0.98561635
IndividualNA19648MXL:AncestryEUR/AFR	24.0021134	1433.91599	0.01673886	0.98664495
IndividualNA19649MXL:AncestryEUR/AFR	25.0061669	1433.91599	0.01743907	0.98608634
IndividualNA19669MXL:AncestryEUR/AFR	25.1007257	1433.91592	0.01750502	0.98603373
IndividualNA19670MXL:AncestryEUR/AFR	5.47346404	0.16402868	33.3689446	3.87E-244
IndividualNA19700ASW:AncestryEUR/AFR	2.65952117	0.08107896	32.8016173	5.58E-236
IndividualNA19701ASW:AncestryEUR/AFR	2.55491421	0.08163991	31.2949157	5.47E-215
IndividualNA19703ASW:AncestryEUR/AFR	2.36851619	0.08165335	29.006969	5.37E-185
IndividualNA19704ASW:AncestryEUR/AFR	2.62313937	0.07908371	33.1691489	3.00E-241
IndividualHG00732PUR:AncestryEUR/NAT	24.934908	1425.49168	0.01749215	0.986044
IndividualNA19648MXL:AncestryEUR/NAT	24.7452194	1433.91598	0.01725709	0.98623152
IndividualNA19649MXL:AncestryEUR/NAT	25.4817492	1433.91599	0.01777074	0.98582175
IndividualNA19669MXL:AncestryEUR/NAT	25.6843248	1433.91592	0.01791202	0.98570904
IndividualNA19670MXL:AncestryEUR/NAT	6.378238	0.14702119	43.3831192	0
IndividualNA19701ASW:AncestryEUR/NAT	-2.8053585	0.18581939	-15.097233	1.69E-51
IndividualNA19703ASW:AncestryEUR/NAT	-4.798308	0.45083926	-10.643057	1.88E-26
IndividualHG00732PUR:AncestryNAT	25.5648889	1425.4917	0.01793408	0.98569144
IndividualNA19648MXL:AncestryNAT	23.7322284	1433.91604	0.01655064	0.9867951
IndividualNA19649MXL:AncestryNAT	27.1769108	1433.916	0.01895293	0.98487865
IndividualNA19669MXL:AncestryNAT	27.5364188	1433.91594	0.01920365	0.98467865
IndividualNA19670MXL:AncestryNAT	8.8870245	0.26209605	33.9075099	5.16E-252
IndividualHG00732PUR:AncestryNAT/AFR	24.6581676	1425.49173	0.01729801	0.98619887
IndividualNA19648MXL:AncestryNAT/AFR	24.8093928	1433.91603	0.01730184	0.98619581
IndividualNA19649MXL:AncestryNAT/AFR	25.5333115	1433.91602	0.0178067	0.98579306
IndividualNA19669MXL:AncestryNAT/AFR	26.3806095	1433.91595	0.0183976	0.98532167
IndividualNA19670MXL:AncestryNAT/AFR	8.41472043	0.31568224	26.6556663	1.54E-156
IndividualNA19700ASW:AncestryNAT/AFR	-2.2142171	1.03872843	-2.1316612	0.03303471
IndividualNA19701ASW:AncestryNAT/AFR	4.03902501	0.2846667	14.1886106	1.08E-45
IndividualNA19703ASW:AncestryNAT/AFR	1.33120649	0.3255353	4.08928455	4.33E-05

IndividualNA19704ASW:AncestryNAT/AFR	1.41492321	0.32394649	4.36776834	1.26E-05
IndividualHG00732PUR:AncestryUNKNOWN	24.7303434	1425.49168	0.01734864	0.98615848
IndividualNA19648MXL:AncestryUNKNOWN	24.4027	1433.91598	0.01701822	0.98642208
IndividualNA19649MXL:AncestryUNKNOWN	24.7810192	1433.91599	0.01728206	0.9862116
IndividualNA19669MXL:AncestryUNKNOWN	24.8907031	1433.91592	0.01735855	0.98615058
IndividualNA19670MXL:AncestryUNKNOWN	5.24028044	0.14117296	37.1195758	1.36E-301
IndividualNA19700ASW:AncestryUNKNOWN	-0.3690557	0.05270311	-7.0025413	2.51E-12
IndividualNA19701ASW:AncestryUNKNOWN	-0.3701103	0.05383834	-6.8744754	6.22E-12
IndividualNA19703ASW:AncestryUNKNOWN	-0.2093766	0.04974379	-4.2091005	2.56E-05
CategoryHomozygous:populationMXL	0.21908711	0.03076327	7.12171004	1.07E-12
CategoryHomozygous:populationPUR	0.12157065	0.03278784	3.70779659	0.00020907
CategoryHomozygous:PolyphenPossibly	-0.8423817	0.04948171	-17.024101	5.44E-65
CategoryHomozygous:PolyphenProbably	-1.1848462	0.04958739	-23.894102	3.53E-126
CategoryHomozygous:PolyphenUnknown	-0.3645623	0.07380695	-4.9394042	7.84E-07
AncestryEUR:PolyphenPossibly	0.01331302	0.03438272	0.38720085	0.69860752
AncestryEUR/AFR:PolyphenPossibly	-0.0217267	0.04208907	-0.5162074	0.60570959
AncestryEUR/NAT:PolyphenPossibly	-0.0301259	0.04407832	-0.6834627	0.49431454
AncestryNAT:PolyphenPossibly	0.03255912	0.109279	0.29794494	0.76574519
AncestryNAT/AFR:PolyphenPossibly	-0.0970103	0.11343077	-0.8552382	0.3924193
AncestryUNKNOWN:PolyphenPossibly	0.00934939	0.04069459	0.22974537	0.81828964
AncestryEUR:PolyphenProbably	-0.0548865	0.0312122	-1.7584955	0.07866323
AncestryEUR/AFR:PolyphenProbably	-0.0267841	0.03770509	-0.7103578	0.47748227
AncestryEUR/NAT:PolyphenProbably	-0.0804027	0.03999555	-2.0102902	0.04440049
AncestryNAT:PolyphenProbably	-0.0673293	0.10163748	-0.6624455	0.50768578
AncestryNAT/AFR:PolyphenProbably	-0.2801294	0.10890095	-2.572332	0.0101016
AncestryUNKNOWN:PolyphenProbably	-0.0682185	0.03717405	-1.8351116	0.06648916
AncestryEUR:PolyphenUnknown	-0.0315017	0.05986622	-0.5262013	0.59874834
AncestryEUR/AFR:PolyphenUnknown	-0.0348042	0.07287297	-0.4776007	0.63293443
AncestryEUR/NAT:PolyphenUnknown	-0.0708143	0.07707059	-0.9188239	0.35818771
AncestryNAT:PolyphenUnknown	0.07712826	0.18422808	0.41865637	0.67546729
AncestryNAT/AFR:PolyphenUnknown	-0.3143636	0.21692661	-1.4491705	0.14728998
AncestryUNKNOWN:PolyphenUnknown	-0.1274034	0.07318181	-1.7409167	0.08169818
AncestryEUR:CategoryHomozygous	-0.0281547	0.03654461	-0.77042	0.44105081
AncestryEUR/AFR:CategoryHomozygous	-0.2287565	0.02907114	-7.8688526	3.58E-15
AncestryEUR/NAT:CategoryHomozygous	-0.2084227	0.04130079	-5.0464577	4.50E-07
AncestryNAT:CategoryHomozygous	0.58777659	0.06674072	8.80686621	1.29E-18
AncestryNAT/AFR:CategoryHomozygous	-0.3448123	0.07790512	-4.4260548	9.60E-06
AncestryUNKNOWN:CategoryHomozygous	-0.12995	0.03486443	-3.7272956	0.00019355
AncestryEUR:CategoryHomozygous:PolyphenPossibly	0.1444687	0.06755644	2.13848903	0.03247707
AncestryEUR/AFR:CategoryHomozygous:PolyphenPossibly	-0.026642	0.09229069	-0.2886747	0.77283032
AncestryEUR/NAT:CategoryHomozygous:PolyphenPossibly	0.06756771	0.08983601	0.75212281	0.45197721
AncestryNAT:CategoryHomozygous:PolyphenPossibly	0.22435544	0.16540698	1.35638434	0.17497691
AncestryNAT/AFR:CategoryHomozygous:PolyphenPossibly	0.04917538	0.25278356	0.19453551	0.84575659
AncestryUNKNOWN:CategoryHomozygous:PolyphenPossibly	0.15479838	0.08101283	1.91078832	0.05603179
AncestryEUR:CategoryHomozygous:PolyphenProbably	0.34222006	0.06634077	5.15851799	2.49E-07
AncestryEUR/AFR:CategoryHomozygous:PolyphenProbably	0.0207498	0.09174757	0.22616181	0.82107557
AncestryEUR/NAT:CategoryHomozygous:PolyphenProbably	0.38540357	0.0845628	4.55760152	5.17E-06
AncestryNAT:CategoryHomozygous:PolyphenProbably	0.67860582	0.1511677	4.48909267	7.15E-06
AncestryNAT/AFR:CategoryHomozygous:PolyphenProbably	0.38903916	0.24337063	1.59854608	0.1099215
AncestryUNKNOWN:CategoryHomozygous:PolyphenProbably	0.20071041	0.08190015	2.45067201	0.01425898
AncestryEUR:CategoryHomozygous:PolyphenUnknown	0.28834492	0.10024863	2.87629787	0.0040237
AncestryEUR/AFR:CategoryHomozygous:PolyphenUnknown	0.17725189	0.13104957	1.35255604	0.1761975
AncestryEUR/NAT:CategoryHomozygous:PolyphenUnknown	0.17956196	0.13269137	1.35323014	0.17598212
AncestryNAT:CategoryHomozygous:PolyphenUnknown	0.31341091	0.24749679	1.2663231	0.20539743
AncestryNAT/AFR:CategoryHomozygous:PolyphenUnknown	0.47411695	0.36253094	1.30779723	0.19094209
AncestryUNKNOWN:CategoryHomozygous:PolyphenUnknown	0.36193836	0.1213482	2.98264293	0.00285771

Table S8. Model Coefficients for Individual Sample Analysis by Deconvolved Ancestry with Individual Level Terms for Population of Origin Effect on Heterozygosity

Coefficients	Estimate	Std Error	z value	Pr(>|z|)
(Intercept)	8.1973221	0.04547019	180.279049	0
IndividualHG00732PUR	-24.606778	1427.74523	-0.0172347	0.98624937
IndividualNA19648MXL	-24.635852	1432.78439	-0.0171944	0.98628154
IndividualNA19649MXL	-24.649728	1435.00045	-0.0171775	0.98629501
IndividualNA19669MXL	-24.646887	1434.41872	-0.0171825	0.98629103
IndividualNA19670MXL	-5.0939131	0.14217526	-35.828407	3.99E-281
IndividualNA19700ASW	-0.3261112	0.04717485	-6.9128201	4.75E-12
IndividualNA19701ASW	-0.4015771	0.04734311	-8.4822705	2.21E-17
IndividualNA19703ASW	-0.2644298	0.04706581	-5.6182999	1.93E-08
IndividualNA19704ASW	-0.3092605	0.04340144	-7.1255806	1.04E-12
AncestryEUR	-0.4185421	0.04733977	-8.8412379	9.47E-19
AncestryEUR/AFR	-3.4885805	0.07849577	-44.442909	0
AncestryEUR/NAT	-2.2900728	0.05798576	-39.493713	0
AncestryNAT	-6.3134885	0.2258131	-27.958912	5.14E-172
AncestryNAT/AFR	-6.3395088	0.28253111	-22.438268	1.67E-111
AncestryUNKNOWN	-1.7557371	0.03685254	-47.642235	0
CategoryHomozygous	-0.3503891	0.04059954	-8.6303722	6.12E-18
PolyphenPossibly	-1.6171629	0.02395205	-67.516675	0
PolyphenProbably	-1.3444317	0.02143442	-62.723027	0
PolyphenUnknown	-2.8286636	0.04126403	-68.550353	0
IndividualHG00732PUR:AncestryEUR	24.3778616	1427.74523	0.01707438	0.98637728
IndividualNA19648MXL:AncestryEUR	24.5764329	1432.78439	0.01715292	0.98631462
IndividualNA19649MXL:AncestryEUR	24.1129153	1435.00045	0.01680342	0.98659344
IndividualNA19669MXL:AncestryEUR	23.8803752	1434.41872	0.01664812	0.98671734
IndividualNA19670MXL:AncestryEUR	3.57664718	0.14490551	24.6826175	1.64E-134
IndividualNA19700ASW:AncestryEUR	-2.9562956	0.08403277	-35.18027	4.01E-271
IndividualNA19701ASW:AncestryEUR	-3.9646005	0.12847272	-30.859473	4.18E-209
IndividualNA19703ASW:AncestryEUR	-3.3391027	0.09414547	-35.467482	1.56E-275
IndividualNA19704ASW:AncestryEUR	-3.417261	0.09751631	-35.042968	4.99E-269
IndividualHG00732PUR:AncestryEUR/AFR	25.7046979	1427.74524	0.0180037	0.9856359
IndividualNA19648MXL:AncestryEUR/AFR	24.0010563	1432.78439	0.01675134	0.98663499
IndividualNA19649MXL:AncestryEUR/AFR	25.009604	1435.00045	0.01742829	0.98609494
IndividualNA19669MXL:AncestryEUR/AFR	25.1030884	1434.41872	0.01750053	0.98603731
IndividualNA19670MXL:AncestryEUR/AFR	5.47400481	0.16403335	33.3712913	3.58E-244
IndividualNA19700ASW:AncestryEUR/AFR	2.66085519	0.08108654	32.8150045	3.60E-236
IndividualNA19701ASW:AncestryEUR/AFR	2.5568471	0.08164778	31.3155744	2.86E-215
IndividualNA19703ASW:AncestryEUR/AFR	2.37038029	0.08166087	29.0271267	2.99E-185
IndividualNA19704ASW:AncestryEUR/AFR	2.62329875	0.07908698	33.1697914	2.94E-241
IndividualHG00732PUR:AncestryEUR/NAT	24.9398078	1427.74523	0.01746797	0.98606329
IndividualNA19648MXL:AncestryEUR/NAT	24.7439247	1432.78439	0.01726982	0.98622136
IndividualNA19649MXL:AncestryEUR/NAT	25.4845599	1435.00045	0.01775927	0.9858309
IndividualNA19669MXL:AncestryEUR/NAT	25.6861341	1434.41872	0.017907	0.98571305
IndividualNA19670MXL:AncestryEUR/NAT	6.37853596	0.1470249	43.3840522	0
IndividualNA19701ASW:AncestryEUR/NAT	-2.8039542	0.18582036	-15.089597	1.90E-51
IndividualNA19703ASW:AncestryEUR/NAT	-4.7969536	0.45083963	-10.640044	1.94E-26
IndividualHG00732PUR:AncestryNAT	25.5587967	1427.74526	0.01790151	0.98571742
IndividualNA19648MXL:AncestryNAT	23.7278933	1432.78444	0.01656069	0.98678709
IndividualNA19649MXL:AncestryNAT	27.1709702	1435.00047	0.01893447	0.98489338
IndividualNA19669MXL:AncestryNAT	27.5305458	1434.41874	0.01919282	0.98468728
IndividualNA19670MXL:AncestryNAT	8.88420532	0.26214347	33.8906225	9.16E-252
IndividualHG00732PUR:AncestryNAT/AFR	24.6643718	1427.74529	0.01727505	0.98621719
IndividualNA19648MXL:AncestryNAT/AFR	24.8084854	1432.78444	0.01731488	0.98618542
IndividualNA19649MXL:AncestryNAT/AFR	25.5372026	1435.00049	0.01779595	0.98580163
IndividualNA19669MXL:AncestryNAT/AFR	26.3833692	1434.41875	0.01839307	0.98532528
IndividualNA19670MXL:AncestryNAT/AFR	8.4154149	0.31568779	26.6573974	1.47E-156
IndividualNA19700ASW:AncestryNAT/AFR	-2.2125564	1.03872884	-2.1300616	0.03316652
IndividualNA19701ASW:AncestryNAT/AFR	4.04141286	0.28466682	14.196993	9.56E-46
IndividualNA19703ASW:AncestryNAT/AFR	1.3335108	0.32553592	4.09635533	4.20E-05

IndividualNA19704ASW:AncestryNAT/AFR	1.41515777	0.3239478	4.36847476	1.25E-05
IndividualHG00732PUR:AncestryUNKNOWN	24.7343488	1427.74523	0.01732406	0.98617809
IndividualNA19648MXL:AncestryUNKNOWN	24.4011725	1432.78439	0.0170306	0.98641221
IndividualNA19649MXL:AncestryUNKNOWN	24.7831236	1435.00045	0.01727046	0.98622085
IndividualNA19669MXL:AncestryUNKNOWN	24.8918949	1434.41872	0.0173533	0.98615477
IndividualNA19670MXL:AncestryUNKNOWN	5.24033924	0.14117442	37.1196084	1.36E-301
IndividualNA19700ASW:AncestryUNKNOWN	-0.3685999	0.05270641	-6.9934546	2.68E-12
IndividualNA19701ASW:AncestryUNKNOWN	-0.3694222	0.05384206	-6.8612206	6.83E-12
IndividualNA19703ASW:AncestryUNKNOWN	-0.2087152	0.04974759	-4.1954832	2.72E-05
IndividualHG00732PUR:CategoryHomozygous	0.05406411	0.03274214	1.65120864	0.09869598
IndividualNA19648MXL:CategoryHomozygous	0.11231051	0.03281501	3.42253441	0.0006204
IndividualNA19649MXL:CategoryHomozygous	0.14008135	0.03326995	4.21044692	2.55E-05
IndividualNA19669MXL:CategoryHomozygous	0.13488807	0.03359879	4.01467059	5.95E-05
IndividualNA19670MXL:CategoryHomozygous	0.1126836	0.03538804	3.18422813	0.00145141
IndividualNA19700ASW:CategoryHomozygous	-0.090517	0.04222823	-2.1435193	0.03207142
IndividualNA19701ASW:CategoryHomozygous	-0.0778335	0.04250952	-1.830966	0.06710561
IndividualNA19703ASW:CategoryHomozygous	-0.0792875	0.0421834	-1.879589	0.06016412
IndividualNA19704ASW:CategoryHomozygous	-0.1155701	0.04183781	-2.7623352	0.00573895
CategoryHomozygous:PolyphenPossibly	-0.8423817	0.04948171	-17.024101	5.44E-65
CategoryHomozygous:PolyphenProbably	-1.1848462	0.04958739	-23.894102	3.53E-126
CategoryHomozygous:PolyphenUnknown	-0.3645623	0.07380695	-4.9394042	7.84E-07
AncestryEUR:PolyphenPossibly	0.01331302	0.03438272	0.38720085	0.69860752
AncestryEUR/AFR:PolyphenPossibly	-0.0217267	0.04208907	-0.5162074	0.60570959
AncestryEUR/NAT:PolyphenPossibly	-0.0301259	0.04407832	-0.6834627	0.49431454
AncestryNAT:PolyphenPossibly	0.03255912	0.109279	0.29794494	0.76574519
AncestryNAT/AFR:PolyphenPossibly	-0.0970103	0.11343077	-0.8552382	0.3924193
AncestryUNKNOWN:PolyphenPossibly	0.00934939	0.04069459	0.22974537	0.81828964
AncestryEUR:PolyphenProbably	-0.0548865	0.0312122	-1.7584955	0.07866323
AncestryEUR/AFR:PolyphenProbably	-0.0267841	0.03770509	-0.7103578	0.47748227
AncestryEUR/NAT:PolyphenProbably	-0.0804027	0.03999555	-2.0102902	0.04440049
AncestryNAT:PolyphenProbably	-0.0673293	0.10163748	-0.6624455	0.50768578
AncestryNAT/AFR:PolyphenProbably	-0.2801294	0.10890095	-2.572332	0.0101016
AncestryUNKNOWN:PolyphenProbably	-0.0682185	0.03717405	-1.8351116	0.06648916
AncestryEUR:PolyphenUnknown	-0.0315017	0.05986622	-0.5262013	0.59874834
AncestryEUR/AFR:PolyphenUnknown	-0.0348042	0.07287297	-0.4776007	0.63293443
AncestryEUR/NAT:PolyphenUnknown	-0.0708143	0.07707059	-0.9188239	0.35818771
AncestryNAT:PolyphenUnknown	0.07712826	0.18422808	0.41865637	0.67546729
AncestryNAT/AFR:PolyphenUnknown	-0.3143636	0.21692661	-1.4491705	0.14728998
AncestryUNKNOWN:PolyphenUnknown	-0.1274034	0.07318181	-1.7409167	0.08169818
AncestryEUR:CategoryHomozygous	-0.0233921	0.03696362	-0.6328409	0.52683756
AncestryEUR/AFR:CategoryHomozygous	-0.2289011	0.02909863	-7.8663872	3.65E-15
AncestryEUR/NAT:CategoryHomozygous	-0.2064777	0.04137734	-4.990116	6.03E-07
AncestryNAT:CategoryHomozygous	0.59275986	0.06738907	8.79608297	1.42E-18
AncestryNAT/AFR:CategoryHomozygous	-0.3449722	0.07861414	-4.3881705	1.14E-05
AncestryUNKNOWN:CategoryHomozygous	-0.1281572	0.03488536	-3.6736668	0.00023909
AncestryEUR:CategoryHomozygous:PolyphenPossibly	0.1444687	0.06755644	2.13848903	0.03247707
AncestryEUR/AFR:CategoryHomozygous:PolyphenPossibly	-0.026642	0.09229069	-0.2886747	0.77283032
AncestryEUR/NAT:CategoryHomozygous:PolyphenPossibly	0.06756771	0.08983601	0.75212281	0.45197721
AncestryNAT:CategoryHomozygous:PolyphenPossibly	0.22435544	0.16540698	1.35638434	0.17497691
AncestryNAT/AFR:CategoryHomozygous:PolyphenPossibly	0.04917538	0.25278356	0.19453551	0.84575659
AncestryUNKNOWN:CategoryHomozygous:PolyphenPossibly	0.15479838	0.08101283	1.91078832	0.05603179
AncestryEUR:CategoryHomozygous:PolyphenProbably	0.34222006	0.06634077	5.15851799	2.49E-07
AncestryEUR/AFR:CategoryHomozygous:PolyphenProbably	0.0207498	0.09174757	0.22616181	0.82107557
AncestryEUR/NAT:CategoryHomozygous:PolyphenProbably	0.38540357	0.0845628	4.55760152	5.17E-06
AncestryNAT:CategoryHomozygous:PolyphenProbably	0.67860582	0.1511677	4.48909267	7.15E-06
AncestryNAT/AFR:CategoryHomozygous:PolyphenProbably	0.38903916	0.24337063	1.59854608	0.1099215
AncestryUNKNOWN:CategoryHomozygous:PolyphenProbably	0.20071041	0.08190015	2.45067201	0.01425898
AncestryEUR:CategoryHomozygous:PolyphenUnknown	0.28834492	0.10024863	2.87629787	0.0040237
AncestryEUR/AFR:CategoryHomozygous:PolyphenUnknown	0.17725189	0.13104957	1.35255604	0.1761975
AncestryEUR/NAT:CategoryHomozygous:PolyphenUnknown	0.17956196	0.13269137	1.35323014	0.17598212
AncestryNAT:CategoryHomozygous:PolyphenUnknown	0.31341091	0.24749679	1.2663231	0.20539743
AncestryNAT/AFR:CategoryHomozygous:PolyphenUnknown	0.47411695	0.36253094	1.30779723	0.19094209
AncestryUNKNOWN:CategoryHomozygous:PolyphenUnknown	0.36193836	0.1213482	2.98264293	0.00285771

Appendix SA: Assessment of PCAdmix Assignment Accuracy

We assessed the accuracy of ancestral assignments from PCAdmix using a simulation strategy to construct synthetic admixed genomes. These genomes were then analyzed using the PCAdmix ancestry deconvolution pipeline. To create simulated admixed samples, we first simulated ancestry tracks following a forward-time Markovian process. To assess performance over a range of ancestry proportions, we simulated tracks for an African-American like population (having 80% African, 19.5% European, and 0.5% Native American ancestry) and a Mexican-like population (having 1% African, 39% European, and 60% Native American ancestry). We created simulations for both sets for 8 generations and 15 generations of admixture.

A key aspect of PCAdmix inference is the use of phased haplotypes. For our simulations, we employed a leave-one-out strategy. For each simulated admixed individual, we randomly selected one of the 20 samples from each population in the reference panel to serve as a donor. Appropriate haplotypes were then copied from the three donors to create the simulated admixed sample. Local ancestry was then inferred for this synthetic sample using the remaining 19 individuals from each population in the reference panel (Figure 1). This procedure was repeated to analyze 40 simulated individuals for each analysis. In each case, assignment was determined in 100-SNP windows using a posterior probability threshold of 0.9, the same settings as used in other analyses.
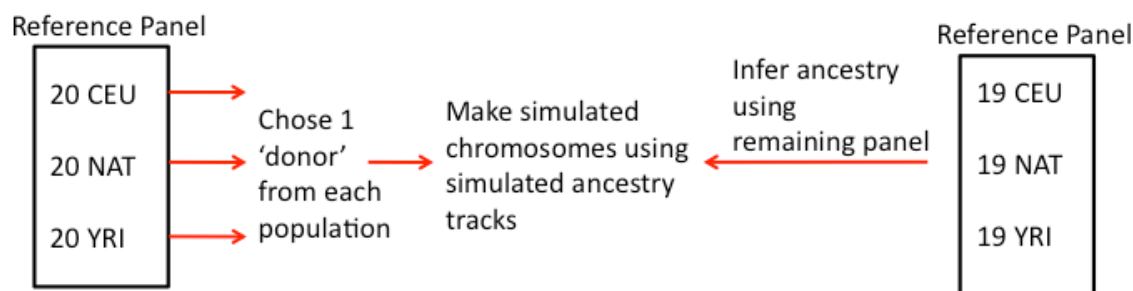

Figure SA1. Strategy for Performing Inference on Simulated Individuals

We find a high degree of concordance with the simulated results (Tables 1 and 2). For example, in the 8-generation ASW simulation, 90.4% of the genome that is truly European in origin is correctly assigned, conversely 96.3% of the genome assigned as European is actually European in origin (Table 4).

Table SA1. Inference Accuracy for 40 Samples Simulated after 8 Generations of Admixture

ASW		Assigned Population			
True Population	Total bp	CEU	NAT	YRI	Not Assigned
CEU	35,320,899,051	90.4%	0.3%	2.5%	6.8%
NAT	1,504,944,467	2.5%	88.5%	2.5%	6.5%
YRI	177,678,675,282	0.7%	0.0%	96.9%	2.4%

ASW		True Population		
Assigned Population	Total bp	CEU	NAT	YRI
CEU	33,181,472,876	96.3%	0.1%	3.6%
NAT	1,482,485,313	7.6%	89.8%	2.6%
YRI	173,056,365,661	0.5%	0.0%	99.5%
Not Assigned	6,784,194,950	35.2%	1.4%	63.4%

MXL		Assigned Population			
True Population	Total bp	CEU	NAT	YRI	Not Assigned
CEU	82,599,113,564	87.4%	2.2%	0.3%	10.1%
NAT	130,102,951,424	4.4%	88.7%	0.3%	6.7%
YRI	1,687,823,717	1.4%	1.0%	92.0%	5.6%

MXL		True Population		
Assigned Population	Total bp	CEU	NAT	YRI
CEU	77,928,323,756	92.7%	7.3%	0.0%
NAT	117,301,794,596	1.6%	98.4%	0.0%
YRI	2,128,568,338	11.7%	15.4%	72.9%
Not Assigned	17,145,832,110	48.7%	50.7%	0.6%

Table SA2. Inference Accuracy for 40 Samples Simulated after 15 Generations of Admixture

ASW True Population	Total bp	Assigned Population CEU	NAT	YRI	Not Assigned
CEU	44,135,452,993	85.7%	0.3%	4.1%	9.9%
NAT	1,404,590,563	5.1%	75.8%	4.5%	14.6%
YRI	168,964,475,244	1.1%	0.0%	95.2%	3.7%

ASW Assigned Population	Total bp	True Population CEU	NAT	YRI
CEU	39,816,473,708	95.0%	0.2%	4.8%
NAT	1,271,986,808	11.5%	83.6%	4.8%
YRI	162,644,740,098	1.1%	0.0%	98.8%
Not Assigned	10,771,318,186	40.4%	1.9%	57.6%

MXL True Population	Total bp	Assigned Population CEU	NAT	YRI	Not Assigned
CEU	81,753,814,956	81.2%	3.6%	0.3%	14.9%
NAT	129,708,890,382	4.5%	85.3%	0.2%	10.0%
YRI	3,041,813,462	2.4%	2.1%	86.9%	8.6%

MXL Assigned Population	Total bp	True Population CEU	NAT	YRI
CEU	72,254,477,759	91.8%	8.0%	0.1%
NAT	113,701,958,954	2.6%	97.3%	0.1%
YRI	3,187,916,645	8.0%	9.0%	83.0%
Not Assigned	25,360,165,442	48.0%	51.0%	1.0%

To assess the effect of reference panel on population inference, we conducted an additional simulation using TSI and LWK to construct simulated genomes while performing inference using CEU and YRI (Figure 2). This results in a modest drop in assignment accuracy.
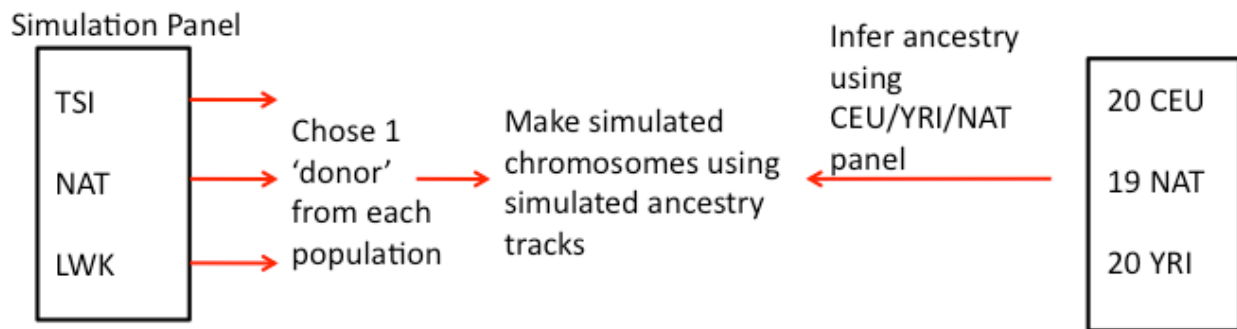

Figure SA2. Inference Strategy Using TSI and LWK to Simulate Admixed Genomes

Table SA3. Inference Accuracy for 15 Generations with TSI or LWK

ASW True Population	Total bp	Assigned Population CEU	NAT	YRI	Not Assigned
CEU	44,135,452,993	83.8%	0.4%	4.2%	11.6%
NAT	1,404,590,563	4.8%	75.9%	4.7%	14.6%
YRI	168,964,475,244	2.3%	0.1%	91.1%	6.5%

ASW Assigned Population	Total bp	True Population CEU	NAT	YRI
CEU	40,954,186,490	90.4%	0.2%	9.5%
NAT	1,334,938,828	12.7%	79.8%	7.5%
YRI	155,907,744,839	1.2%	0.0%	98.8%
Not Assigned	16,307,648,643	31.4%	1.3%	67.4%

MXL True Population	Total bp	Assigned Population CEU	NAT	YRI	Not Assigned
CEU	81,753,814,956	81.2%	3.6%	0.3%	14.8%
NAT	129,708,890,382	4.3%	85.7%	0.2%	9.8%
YRI	3,041,813,462	2.8%	2.4%	84.2%	10.6%

MXL Assigned Population	Total bp	True Population CEU	NAT	YRI
CEU	72,019,115,361	92.2%	7.7%	0.1%
NAT	114,208,290,396	2.6%	97.3%	0.1%
YRI	3,084,716,027	9.2%	7.8%	83.1%
Not Assigned	25,192,397,016	48.0%	50.7%	1.3%

Table SA4. Summary of Ancestry Assignment Accuracy

	8 Generations		15 Generations		15 Generations, TSI/LWK	
	Sensitivity	Positive Predictive Value	Sensitivity	Positive Predictive Value	Sensitivity	Positive Predictive Value
ASW						
CEU	90.4%	96.3%	85.7%	95.0%	83.8%	90.4%
NAT	88.5%	89.8%	75.8%	83.6%	75.9%	79.8%
YRI	96.9%	99.5%	95.2%	98.8%	91.1%	98.8%
MXL						
CEU	87.4%	92.7%	81.2%	91.8%	81.2%	92.2%
NAT	88.7%	98.4%	85.3%	97.3%	85.7%	97.3%
YRI	92.0%	72.9%	86.9%	83.0%	84.2%	83.1%

This table represents a summary of the results represented in Tables 1-3.

As a final analysis, we performed local ancestry deconvolution on samples from the TSI and LWK populations, two groups without expected admixture from continentally distinct populations. We find that less than 2% of their genomes are assigned an incorrect continent of ancestry.

Table SA5. PCAdmix Results for TSI and LWK Individuals

	Assignment			
Panel	CEU	NAT	YRI	Not Assigned
TSI (88 samples)	88.51%	0.41%	0.65%	10.43%
LWK (90 samples)	1.24%	0.04%	94.28%	4.45%

Appendix SB: Statistical Description of the GLM Model

We first consider the case where counts in individuals from a given population are pooled, and where we do not have information about the local ancestry in the genome. The fully saturated model, assuming a logarithmic link function for a Poisson distribution, is then:

$$Log(Counts_{AZP}) = \beta + \beta_A + \beta_Z + \beta_P + \beta_{AZ} + \beta_{AP} + \beta_{ZP} + \beta_{AZP}$$

where the β represent fitting parameters in the model subject to the usual constraints $\beta_A = \beta_Z = \beta_P = \beta_{AZ} = \beta_{AP} = \beta_{ZP} = \beta_{AZP} = 0$ when *either* A=ASW, Z=heterozygous, or P=benign. If the populations have had the same demographic history as the reference genome and polymorphisms are neutral, only β and β_Z would significantly depart from zero. (For example, we'd expect two heterozygous sites for every homozygous nonreference site if the individual and the reference genome were drawn from the same population). Differences in effective population size would lead to significant β_A (i.e., consistently more variation in some genomes than other) and other differences in demographic history, such as recent growth, may lead to significant values for β_{AZ} (i.e., proportionally more homozygous variants in genomes from some populations vs. others). To understand the effect of selection on this model, imagine that all populations are identical and that we have two classes of functional alleles with different selective coefficients. Since selection would keep deleterious alleles at lower frequencies, we expect a significant interaction term β_{ZP} regardless of demographic history. The term β_{AP} represents the fact that populations may bear different levels of deleterious-to-neutral polymorphisms, for example because of differences in effective population sizes. A natural question is then whether linear and pairwise interaction terms will be sufficient to describe the interplay of demography and selection. In other words, a population having experienced a bottleneck is expected to display both proportionally more homozygous nonreference variants, and an increased proportion of deleterious variants. Is the proportion of homozygous deleterious variants in that population simply a product of these two effects?

This model can be fited to either individual level data or to pooled data across individuals, and can be easily modified to account for diverse covariates. When applying this model to an admixed genome *I*, with ancestry proportion p_{AI} from ancestry A, we expect that each diploid ancestry contributes in proportion to the fraction of the genome it covers: $Counts_{IAZP} = p_{AI}Counts_{AZP}$, with $Counts_{AZP}$ the expected genome-wide counts for a genome of uniform ancestry *A*. Using $\beta_{AI} = Log(p_{AI})$, this should be easily accounted for by adding an individual-by-diploid ancestry term to our model:

$$Log(Counts_{IAZP}) = \beta + \beta_I + \beta_{AI} + \beta_A + \beta_Z + \beta_P + \beta_{AZ} + \beta_{AP} + \beta_{ZP} + \beta_{AZP},$$

(where ancestry *A* is now drawn from Eur/Eur, Eur/Nam, Afr/Eur, Nam/Nam, Afr/Nam, Afr/Afr, and I is an individual label). In practice, we optimize β_{AI} with the other parameters to account for possible differences in the ancestral populations.

We find that many of the β_{AZP} are highly significant via comparisons of log-likelihood or using the Akaike Information Criteria (AIC), regardless of whether we analyze admixed or nonadmixed genomes (Figure 7, Figure S5, Tables S4–S6). This is illustrated in Figure S6, which shows more Probably Damaging homozygous mutations in the Out-of-Africa populations vs. the African populations beyond that predicted by the overall higher levels of variation in African genomes. Mathematically, this is seen in the coefficients of the regression model and AIC comparison of models. For Z="Homozygous", P="Probably damaging", we find significant coefficients for different values of A: CEU ($\beta_{AZP} = 0.3031$; p < 1e-9), CHB ($\beta_{AZP} = 0.2809$; p < 5e-8), GIH ($\beta_{AZP}=0.2309$, p <10e-6) JPT ($\beta_{AZP} = 0.183$, p<0.000354) or TSI ($\beta_{AZP}=0.257$, p < 8e-7) indicating that these ancestries increase the odds of being in a homozygous probably damaging state with respect to ASW ancestry and above that which would be

predicted from ancestry, zygosity, or PolyPhen alone (or their pairwise interactions). Similarly, in the admixed genomes, we find that the odds of being in a Z=homozygous and P=probably damaging state are higher for European ancestry ($\beta_{AZP} = 0.3422$, p < 2.49e-07) and Native American ancestry increases the odds ($\beta_{AZP} = 0.6786$, p < 7.15e-06) compared to the African ancestry. Segments of joint European/Native admixed ancestry also increase the relative proportion of homozygous probably damaging counts (β_{AZP}=0.3854, p = 5.17e-06), although a significant effect is not observed for African/European and African/Native American. Model comparison using log-likelihood ratio tests or AIC (Table S4) always favor the model where the degree of homozygosity varies across PolyPhen categories in an ancestry-specific manner (i.e., there is a significant nonzero β_{AZP}) with an improvement in AIC of 30.8 for the comparison of the admixed genomes with ancestry deconvolution and a gain of over 150 for all genomes combined. These observations emphasize the intricate interaction of demography and selection in the generation of world-wide patterns of genomic diversity.