

Supplementary Figures & Tables

1 Figures

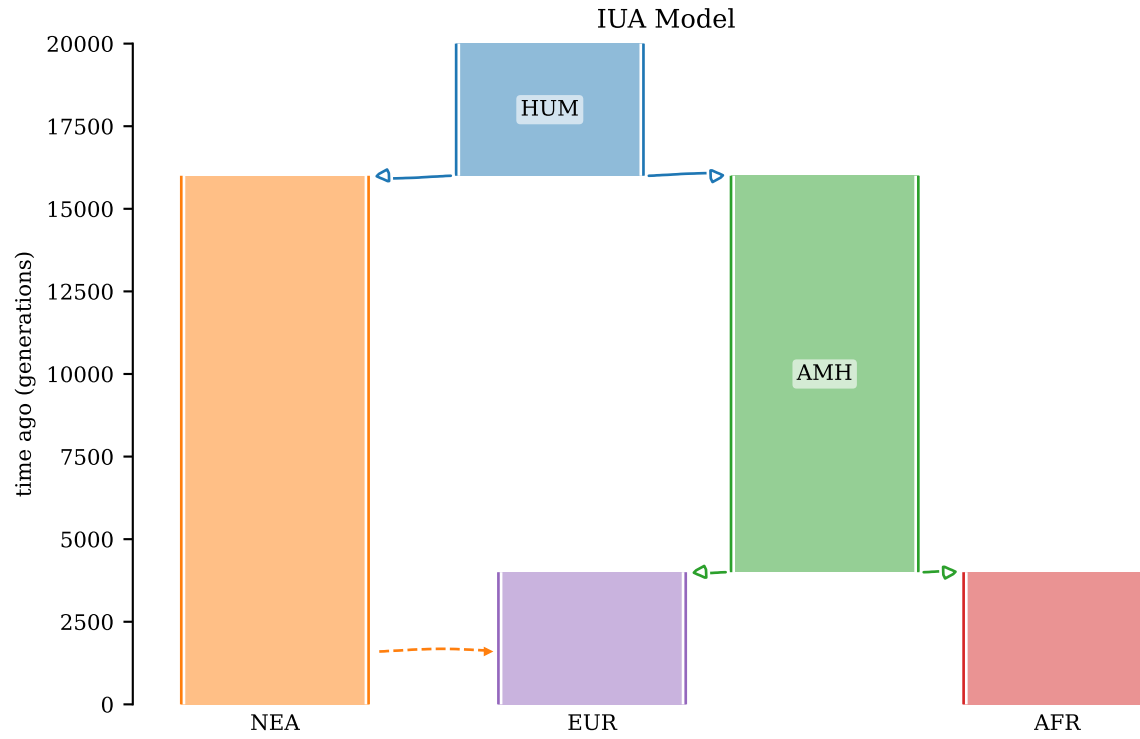


Figure S1: Instantaneous unidirectional admixture (IUA)—based on a simplified version of human evolution from *Racimo et. al., 2017*—used in this study. Solid lines represent divergence events and the dashed line represents a gene flow event.

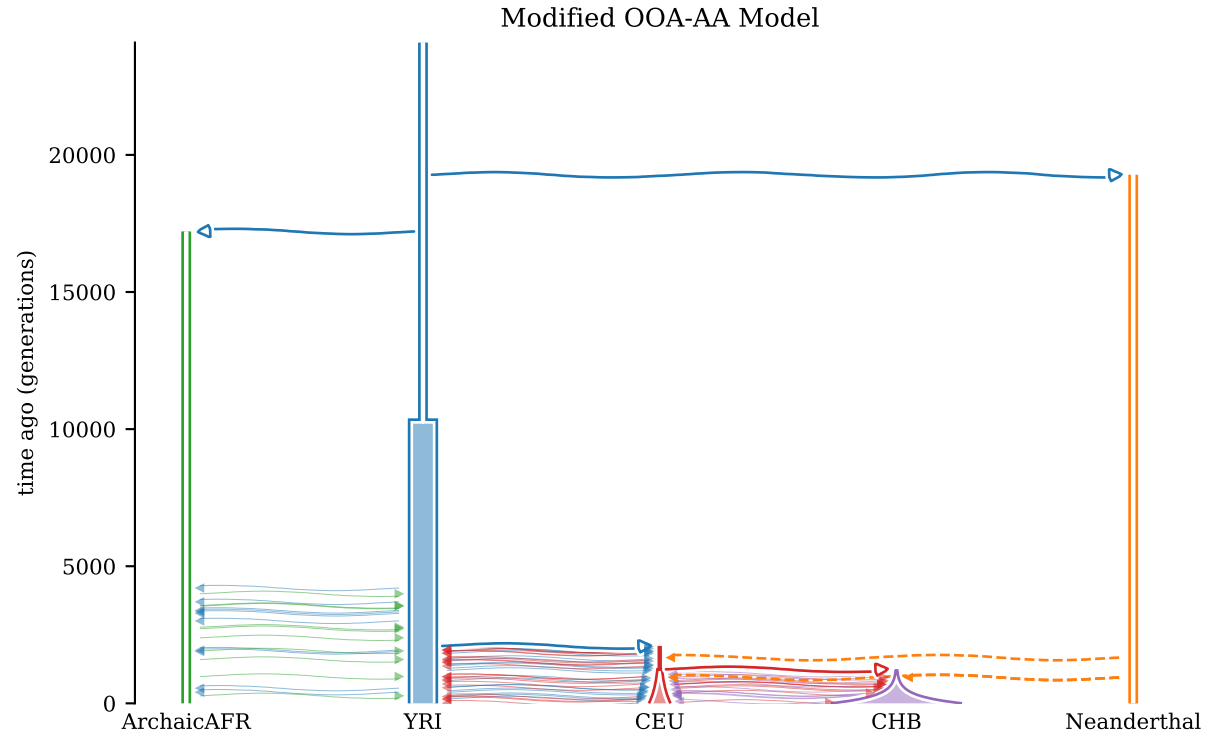


Figure S2: Realistic model of human demography—modified from *Ragsdale and Gravel 2019*—used in this study. Solid lines represent divergence events and dashed lines represents a gene flow events.

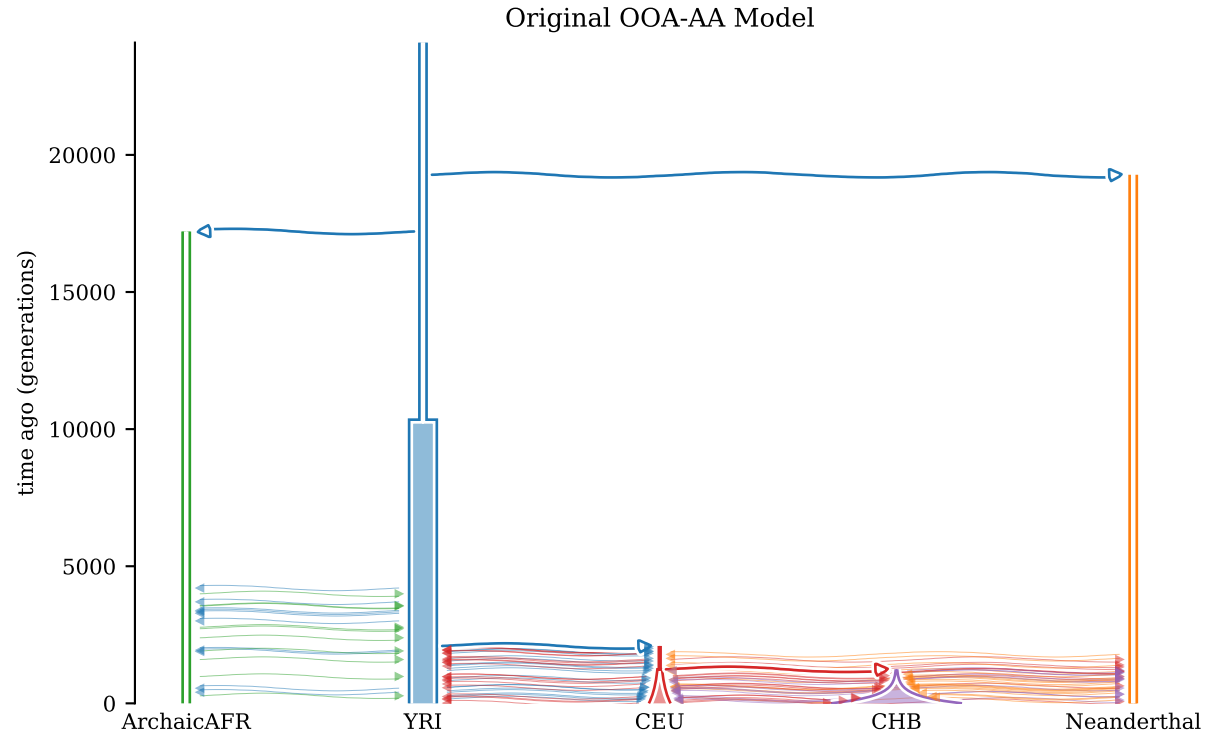


Figure S3: Realistic model of human demography—as originally specified in *Ragsdale and Gravel 2019*—used in this study. Solid lines represent divergence events and dashed lines represents a gene flow events.

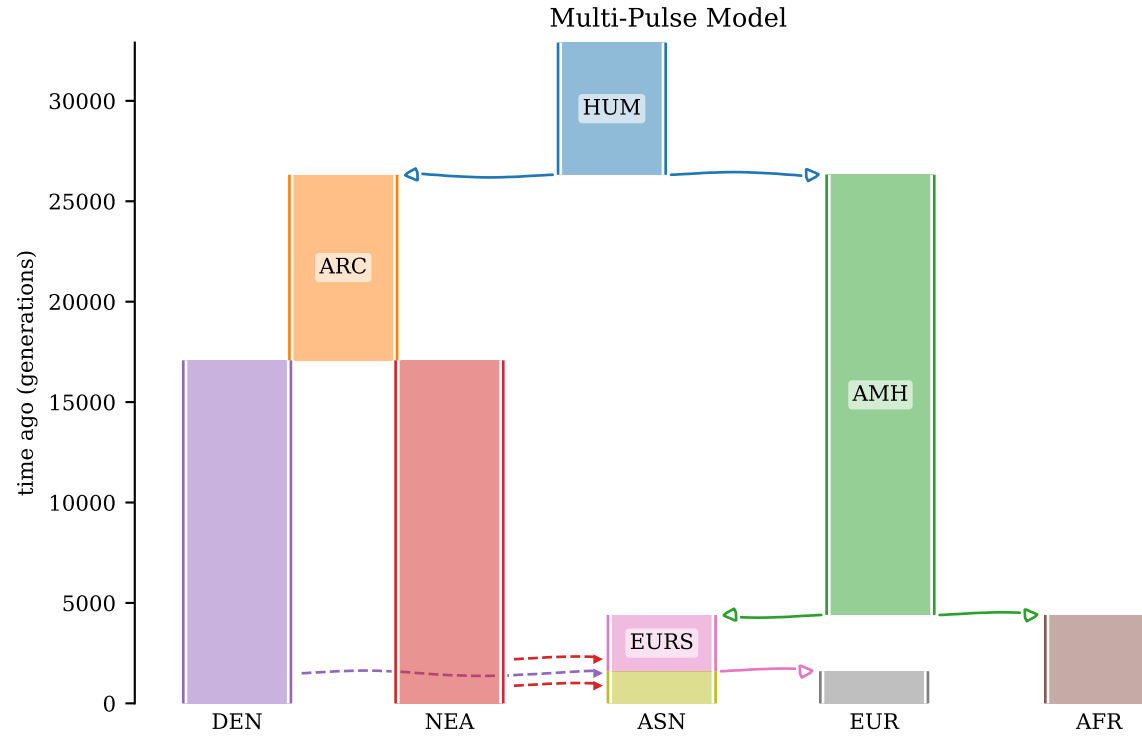


Figure S4: Multi-pulse model of archaic introgression used in this study. Solid lines represent divergence events and dashed lines represents a gene flow events.

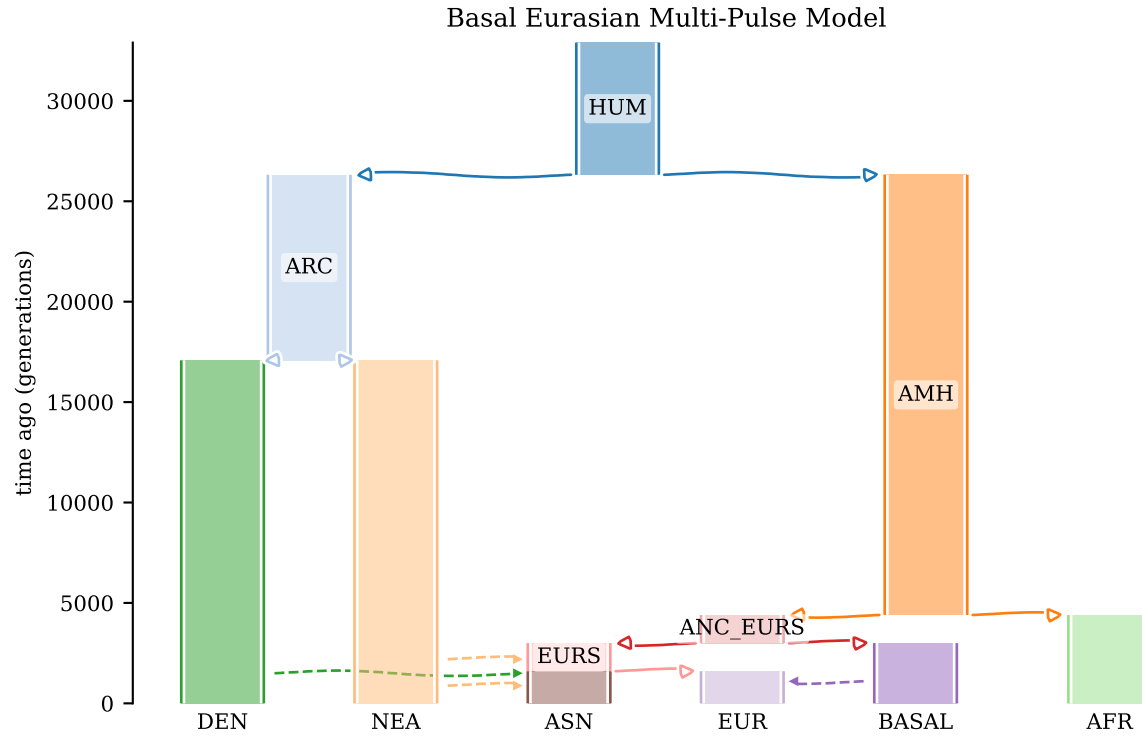


Figure S5: Multi-pulse model of archaic introgression with gene flow from a so called "Basal Eurasian" population used in this study. Solid lines represent divergence events and dashed lines represents a gene flow events.

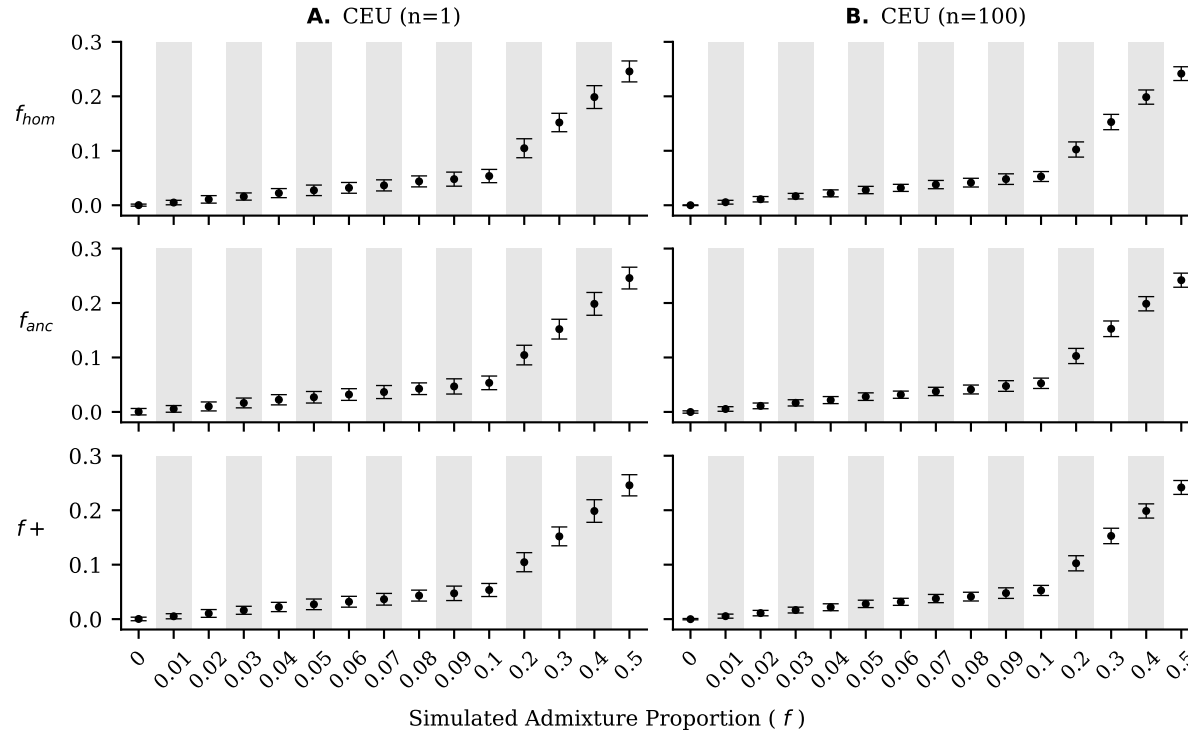


Figure S6: The mean (dots) and standard deviation (error bars) of f_{hom} , f_{anc} , and $f+$ for the CEU population in simulations under a more realistic model of human demography with a sampling scheme of $n = 1$ (panel **A**) and $n = 100$ (panel **B**) genomes from each of the potential recipient populations.

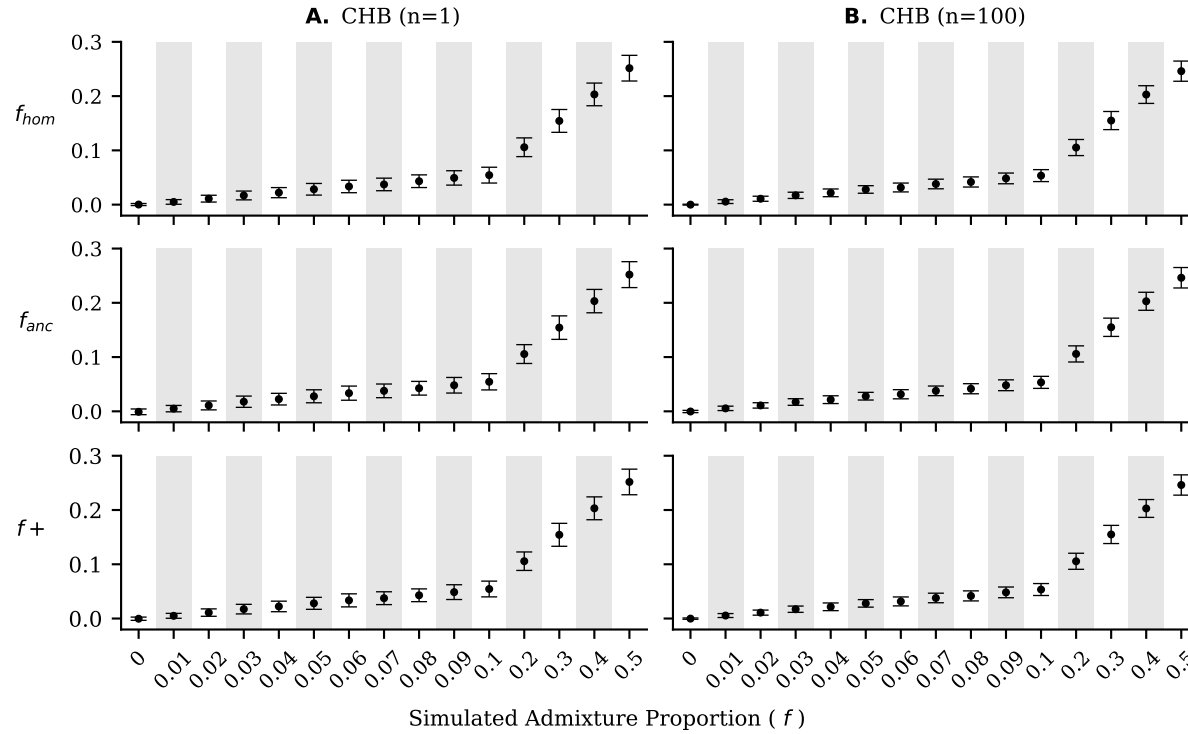


Figure S7: The mean (dots) and standard deviation (error bars) of f_{hom} , f_{anc} , and f_+ for the CHB population in simulations under a more realistic model of human demography with a sampling scheme of $n = 1$ (panel **A**) and $n = 100$ (panel **B**) genomes from each of the potential recipient populations.

2 Tables

	$n = 1$								$n = 100$							
	<i>ABBA</i>		<i>BABA</i>		<i>BAAA</i>		<i>ABAA</i>		<i>ABBA</i>		<i>BABA</i>		<i>BAAA</i>		<i>ABAA</i>	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	5465.17	145.786	5495.06	174.939	30466.83	30466.83	30504.71	360.091	5503.459	99.246	5493.25	89.21	30521.818	30521.818	30510.263	173.3
$f = 0.01$	5717.9	162.822	5482.68	150.028	30691.47	30691.47	30441.17	306.834	5683.277	99.461	5491.361	94.012	30703.991	30703.991	30501.073	174.717
$f = 0.02$	5915.09	207.047	5486.46	134.769	30886.86	30886.86	30489.11	322.086	5918.106	116.926	5475.363	86.416	30892.775	30892.775	30469.369	165.639
$f = 0.03$	6128.35	219.137	5464.9	151.926	31080.67	31080.67	30418.99	330.756	6109.743	133.018	5466.721	87.228	31066.999	31066.999	30430.308	152.027
$f = 0.04$	6344.98	224.19	5457.72	153.123	31252.23	31252.23	30344.05	292.802	6322.632	157.614	5460.399	92.418	31270.053	31270.053	30412.161	148.245
$f = 0.05$	6523.7	272.163	5467.93	165.331	31428.86	31428.86	30371.63	314.048	6525.706	162.207	5462.683	90.809	31430.519	31430.519	30377.307	169.344
$f = 0.06$	6763.24	310.029	5447.03	151.423	31605.59	31605.59	30364.75	299.154	6731.675	168.588	5456.044	80.457	31613.554	31613.554	30330.141	184.834
$f = 0.07$	6979.47	295.38	5444.42	152.392	31835.4	31835.4	30309.45	331.667	6948.888	189.516	5440.227	98.226	31807.404	31807.404	30296.78	177.464
$f = 0.08$	7183.91	295.533	5442.11	154.242	32005.34	32005.34	30260.73	304.602	7162.842	183.305	5436.045	81.119	31959.277	31959.277	30256.61	166.038
$f = 0.09$	7366.55	330.042	5408.98	146.531	32151.19	32151.19	30223.34	309.618	7397.239	207.577	5442.056	89.398	32212.754	32212.754	30258.873	175.291
$f = 0.1$	7574.85	345.14	5438.46	162.725	32376.43	32376.43	30235.37	304.808	7602.723	216.035	5420.829	80.242	32383.078	32383.078	30219.948	164.952
$f = 0.2$	9680.98	392.051	5365.18	154.698	34201.91	34201.91	29883.61	295.968	9737.691	278.78	5373.982	80.579	34282.719	34282.719	29940.206	160.401
$f = 0.3$	11775.45	458.298	5312.79	162.303	36121.95	36121.95	29622.88	286.636	11820.454	323.273	5303.895	71.677	36156.464	36156.464	29614.956	156.411
$f = 0.4$	13808.99	545.123	5239.44	146.509	37905.85	37905.85	29348.76	321.16	13890.801	306.937	5231.154	82.028	37961.395	37961.395	29310.817	139.544
$f = 0.5$	15888.34	571.99	5169.04	160.197	39733.58	39733.58	28999.17	338.799	15973.043	326.765	5178.227	71.947	39825.797	39825.797	29028.167	163.446

Table S1: The mean (μ) and standard deviation (σ) of each allele sharing site pattern between donor and recipient populations from 100 replicate simulations under an IUA model of introgression (see Figure S1) per admixture portion (f).

	$n = 1$								$n = 100$							
	<i>ABBA</i>		<i>BABA</i>		<i>BAAA</i>		<i>ABAA</i>		<i>ABBA</i>		<i>BABA</i>		<i>BAAA</i>		<i>ABAA</i>	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	930.51	64.016	922.82	76.896	21145.85	21145.85	21128.37	422.106	925.594	38.574	924.856	36.317	21172.813	21172.813	21178.431	177.082
$f = 0.01$	1146.04	164.083	950.32	73.325	21308.29	21308.29	21085.87	355.821	1161.299	151.017	941.615	37.937	21347.06	21347.06	21132.82	173.405
$f = 0.02$	1388.87	270.689	962.04	82.514	21449.92	21449.92	21049.05	355.924	1395.229	216.809	958.382	45.624	21492.765	21492.765	21052.189	155.638
$f = 0.03$	1605.62	278.711	971.92	91.535	21665.74	21665.74	21010.99	375.695	1641.213	222.986	981.813	45.752	21649.188	21649.188	20988.938	165.208
$f = 0.04$	1875.73	353.863	995.04	105.142	21745.71	21745.71	20860.5	402.936	1858.153	278.112	993.388	52.834	21770.682	21770.682	20909.659	175.301
$f = 0.05$	2098.58	416.521	1016.95	105.916	21873.99	21873.99	20808.6	339.641	2122.177	302.454	1018.54	59.959	21935.686	21935.686	20825.567	154.587
$f = 0.06$	2301.22	401.378	1038.42	103.689	22059.52	22059.52	20795.22	421.01	2288.618	281.98	1028.601	58.389	22033.893	22033.893	20783.524	185.324
$f = 0.07$	2487.48	422.636	1047.17	118.077	22214.41	22214.41	20770.76	392.179	2553.619	343.669	1055.63	69.962	22227.236	22227.236	20740.811	165.605
$f = 0.08$	2799.79	420.128	1070.04	124.241	22376.21	22376.21	20692.76	387.733	2691.676	343.483	1054.78	59.835	22316.171	22316.171	20689.874	163.512
$f = 0.09$	2980.61	522.222	1092.56	104.837	22497.67	22497.67	20650.51	408.156	2985.191	417.713	1092.76	67.888	22529.64	22529.64	20651.583	186.357
$f = 0.1$	3211.27	489.95	1094.5	133.077	22680.11	22680.11	20573.87	368.508	3166.78	384.45	1088.685	66.258	22644.868	22644.868	20569.972	207.883
$f = 0.2$	5323.67	666.195	1224.73	143.135	24080.39	24080.39	19992.0	371.823	5244.473	586.663	1235.684	84.679	24003.713	24003.713	19979.526	240.193
$f = 0.3$	7260.47	651.261	1355.05	154.912	25267.78	25267.78	19359.9	421.043	7290.452	568.385	1354.797	84.671	25313.556	25313.556	19375.832	250.17
$f = 0.4$	9100.43	769.168	1435.45	184.026	26417.33	26417.33	18760.38	434.491	9092.109	514.219	1429.62	81.405	26440.301	26440.301	18771.175	207.241
$f = 0.5$	10884.17	697.749	1440.74	166.488	27593.89	27593.89	18151.78	410.824	10739.418	482.943	1478.097	80.529	27465.756	27465.756	18190.12	216.318
Original Model	1481.11	276.914	1018.94	80.92	21270.2	21270.2	20808.1	353.2	1533.123	202.111	1025.721	52.224	21370.501	21370.501	20870.248	198.149

Table S2: The mean (μ) and standard deviation (σ) of each allele sharing site pattern between the Neanderthal and CEU populations from 100 replicate simulations under a realistic model of human demography (see Figure S2) per admixture portion (f). Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$								$n = 100$							
	<i>ABBA</i>		<i>BABA</i>		<i>BAAA</i>		<i>ABAA</i>		<i>ABBA</i>		<i>BABA</i>		<i>BAAA</i>		<i>ABAA</i>	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	934.2	69.582	927.17	70.361	21182.93	21182.93	21217.99	431.995	924.622	39.63	925.532	37.311	21185.397	21185.397	21198.106	180.018
$f = 0.01$	1150.93	168.358	953.36	71.185	21321.98	21321.98	21124.25	398.96	1162.986	146.833	943.296	39.222	21369.843	21369.843	21153.123	167.137
$f = 0.02$	1400.73	250.677	963.89	82.524	21485.21	21485.21	21053.76	375.359	1391.294	203.48	961.332	46.067	21515.224	21515.224	21083.225	164.239
$f = 0.03$	1640.96	325.808	971.01	92.789	21691.52	21691.52	20988.08	393.487	1661.809	246.33	982.643	44.592	21675.661	21675.661	20995.167	174.373
$f = 0.04$	1877.06	370.903	1003.47	103.632	21773.5	21773.5	20884.64	425.134	1854.788	298.396	994.304	52.943	21778.46	21778.46	20928.016	188.018
$f = 0.05$	2139.36	445.71	1020.34	106.041	21936.67	21936.67	20840.67	390.708	2126.662	301.511	1022.295	60.3	21957.289	21957.289	20854.561	183.226
$f = 0.06$	2354.81	449.712	1031.17	110.067	22159.67	22159.67	20833.92	360.285	2277.733	348.574	1029.234	59.629	22041.557	22041.557	20798.666	197.698
$f = 0.07$	2517.41	469.168	1045.95	115.556	22258.9	22258.9	20766.76	409.831	2559.627	381.779	1056.793	71.114	22247.489	22247.489	20756.667	199.83
$f = 0.08$	2783.1	459.444	1076.98	133.706	22371.31	22371.31	20690.94	404.079	2704.243	384.563	1056.106	61.491	22342.556	22342.556	20699.08	181.359
$f = 0.09$	3028.03	534.741	1087.47	113.787	22528.24	22528.24	20632.18	412.798	3002.136	416.357	1094.909	69.325	22560.492	22560.492	20664.256	201.644
$f = 0.1$	3240.08	577.808	1092.25	128.416	22731.33	22731.33	20581.91	417.812	3195.566	448.746	1087.617	66.507	22682.428	22682.428	20575.972	221.881
$f = 0.2$	5369.94	656.301	1227.8	145.219	24104.51	24104.51	19971.27	346.689	5352.274	610.597	1230.984	83.52	24090.155	24090.155	19945.377	258.798
$f = 0.3$	7340.65	800.498	1342.61	144.623	25344.41	25344.41	19348.08	426.819	7375.947	657.394	1355.759	90.367	25385.743	25385.743	19360.986	285.147
$f = 0.4$	9262.11	774.945	1421.74	169.275	26558.62	26558.62	18719.97	448.514	9253.655	626.236	1425.363	84.504	26559.397	26559.397	18728.226	251.869
$f = 0.5$	11096.05	874.243	1429.86	178.433	27748.53	27748.53	18069.86	431.316	10898.188	696.852	1470.569	82.449	27582.945	27582.945	18143.087	298.144
Original Model	1512.69	316.969	1015.74	81.989	21342.76	21342.76	20820.99	336.052	1540.101	193.612	1021.449	48.881	21385.526	21385.526	20865.97	206.672

Table S3: The mean (μ) and standard deviation (σ) of each allele sharing site pattern between the Neanderthal and CHB populations from 100 replicate simulations under a realistic model of human demography (see Figure S2) per admixture portion (f). Note that ”Original Model” corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$			$n = 100$		
	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$
$f = 0$	-29.89	-37.88	0.487	10.209	11.556	0.495
$f = 0.01$	235.22	250.3	0.475	191.916	202.918	0.459
$f = 0.02$	428.63	397.75	0.459	442.743	423.406	0.438
$f = 0.03$	663.45	661.68	0.497	643.022	636.691	0.477
$f = 0.04$	887.26	908.18	0.467	862.233	857.893	0.485
$f = 0.05$	1055.77	1057.23	0.498	1063.024	1053.212	0.464
$f = 0.06$	1316.21	1240.84	0.395	1275.631	1283.414	0.471
$f = 0.07$	1535.05	1525.95	0.486	1508.661	1510.623	0.493
$f = 0.08$	1741.8	1744.61	0.496	1726.797	1702.667	0.413
$f = 0.09$	1957.57	1927.85	0.456	1955.183	1953.881	0.495
$f = 0.1$	2136.39	2141.06	0.494	2181.894	2163.13	0.434
$f = 0.2$	4315.8	4318.3	0.496	4363.709	4342.513	0.434
$f = 0.3$	6462.66	6499.07	0.448	6516.559	6541.508	0.426
$f = 0.4$	8569.55	8557.09	0.484	8659.648	8650.578	0.472
$f = 0.5$	10719.3	10734.41	0.479	10794.816	10797.63	0.493

Table S4: Assessing if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero in simulations under an IUA model of introgression (see Figure S1). The rows correspond to the simulated admixture proportions, the columns represent the mean site pattern difference across 100 replicate simulations and the corresponding p -value to assess if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero. After accounting for multiple-comparisons using the Bonferroni correction, a p -value less than 0.00333 is considered significant.

	$n = 1$			$n = 100$		
	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$
$f = 0$	7.69	17.48	0.483	0.738	-5.618	0.469
$f = 0.01$	195.72	222.42	0.443	219.684	214.24	0.472
$f = 0.02$	426.83	400.87	0.45	436.847	440.576	0.483
$f = 0.03$	633.7	654.75	0.464	659.4	660.25	0.496
$f = 0.04$	880.69	885.21	0.491	864.765	861.023	0.48
$f = 0.05$	1081.63	1065.39	0.469	1103.637	1110.12	0.466
$f = 0.06$	1262.8	1264.3	0.497	1260.017	1250.369	0.45
$f = 0.07$	1440.31	1443.65	0.494	1497.99	1486.425	0.435
$f = 0.08$	1729.75	1683.45	0.416	1636.895	1626.297	0.442
$f = 0.09$	1888.05	1847.16	0.413	1892.432	1878.057	0.426
$f = 0.1$	2116.77	2106.24	0.482	2078.096	2074.896	0.483
$f = 0.2$	4098.94	4088.39	0.48	4008.79	4024.187	0.428
$f = 0.3$	5905.42	5907.88	0.496	5935.655	5937.724	0.49
$f = 0.4$	7664.98	7656.95	0.486	7662.49	7669.126	0.47
$f = 0.5$	9443.43	9442.11	0.498	9261.32	9275.636	0.441
Original Model	462.17	462.1	0.5	507.402	500.254	0.469

Table S5: Assessing if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero in the CEU population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions, the columns represent the mean site pattern difference across 100 replicate simulations and the corresponding p -value to assess if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero. After accounting for multiple-comparisons using the Bonferroni correction, a p -value less than 0.003125 is considered significant. Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$			$n = 100$		
	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$
$f = 0$	7.03	-35.06	0.418	-0.909	-12.709	0.442
$f = 0.01$	197.57	197.73	0.5	219.69	216.72	0.485
$f = 0.02$	436.84	431.45	0.49	429.962	432.0	0.491
$f = 0.03$	669.95	703.44	0.443	679.165	680.495	0.494
$f = 0.04$	873.59	888.86	0.47	860.484	850.444	0.45
$f = 0.05$	1119.02	1096.0	0.457	1104.367	1102.728	0.492
$f = 0.06$	1323.64	1325.75	0.496	1248.5	1242.891	0.472
$f = 0.07$	1471.46	1492.14	0.461	1502.834	1490.822	0.444
$f = 0.08$	1706.12	1680.37	0.459	1648.137	1643.475	0.478
$f = 0.09$	1940.56	1896.06	0.41	1907.226	1896.236	0.444
$f = 0.1$	2147.83	2149.42	0.497	2107.949	2106.456	0.492
$f = 0.2$	4142.14	4133.24	0.486	4121.289	4144.779	0.403
$f = 0.3$	5998.04	5996.33	0.497	6020.188	6024.757	0.48
$f = 0.4$	7840.37	7838.65	0.497	7828.291	7831.171	0.489
$f = 0.5$	9666.19	9678.67	0.481	9427.619	9439.857	0.45
Original Model	496.95	521.77	0.451	518.652	519.556	0.496

Table S6: Assessing if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero in the CHB population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions, the columns represent the mean site pattern difference across 100 replicate simulations and the corresponding p -value to assess if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero. After accounting for multiple-comparisons using the Bonferroni correction, a p -value less than 0.003125 is considered significant. Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$			$n = 100$		
	D	D_{anc}	$D+$	D	D_{anc}	$D+$
$f = 0$	0.13	0.07	0.08	0.11	0.08	0.1
$f = 0.01$	0.34	0.27	0.34	0.66	0.5	0.6
$f = 0.02$	0.56	0.39	0.52	0.98	0.88	0.96
$f = 0.03$	0.87	0.63	0.86	1.0	0.98	1.0
$f = 0.04$	0.96	0.89	0.95	1.0	1.0	1.0
$f = 0.05$	0.99	0.92	0.99	1.0	1.0	1.0
$f = 0.06$	1.0	0.95	1.0	1.0	1.0	1.0
$f = 0.07$	1.0	0.97	1.0	1.0	1.0	1.0
$f = 0.08$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.09$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.1$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.2$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.3$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.4$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.5$	1.0	1.0	1.0	1.0	1.0	1.0

Table S7: Statistical power of D , D_{anc} , and $D+$ to detect introgression in simulations under an IUA model of introgression (see Figure S1). The rows correspond to the simulated admixture proportions and the columns represent the proportion of statistically significant replicates from zero at $p\text{-value} < 0.05$ out of 100 replicate simulations.

	$n = 1$			$n = 100$		
	D	D_{anc}	$D+$	D	D_{anc}	$D+$
$f = 0$	0.13	0.11	0.13	0.0	0.0	0.0
$f = 0.01$	0.54	0.25	0.44	0.6	0.2	0.39
$f = 0.02$	0.87	0.46	0.66	1.0	0.54	0.85
$f = 0.03$	1.0	0.78	0.89	1.0	0.9	1.0
$f = 0.04$	1.0	0.88	0.94	1.0	0.98	1.0
$f = 0.05$	1.0	0.93	1.0	1.0	1.0	1.0
$f = 0.06$	1.0	0.98	0.99	1.0	1.0	1.0
$f = 0.07$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.08$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.09$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.1$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.2$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.3$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.4$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.5$	1.0	1.0	1.0	1.0	1.0	1.0
Original Model	0.94	0.52	0.77	1.0	0.98	1.0

Table S8: Statistical power of D , D_{anc} , and $D+$ to detect introgression in the CEU population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent the proportion of statistically significant replicates from zero at $p\text{-value} < 0.05$ out of 100 replicate simulations. Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$			$n = 100$		
	D	D_{anc}	$D+$	D	D_{anc}	$D+$
$f = 0$	0.16	0.07	0.11	0.0	0.0	0.0
$f = 0.01$	0.49	0.26	0.36	0.69	0.18	0.47
$f = 0.02$	0.91	0.54	0.76	0.96	0.5	0.83
$f = 0.03$	0.97	0.77	0.87	1.0	0.9	0.98
$f = 0.04$	1.0	0.86	0.95	1.0	0.93	0.98
$f = 0.05$	1.0	0.91	0.97	1.0	0.99	1.0
$f = 0.06$	1.0	0.97	0.99	1.0	1.0	1.0
$f = 0.07$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.08$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.09$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.1$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.2$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.3$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.4$	1.0	1.0	1.0	1.0	1.0	1.0
$f = 0.5$	1.0	1.0	1.0	1.0	1.0	1.0
Original Model	0.96	0.62	0.85	1.0	1.0	1.0

Table S9: Statistical power of D , D_{anc} , and $D+$ to detect introgression in the CHB population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent the proportion of statistically significant replicates from zero at $p\text{-value} < 0.05$ out of 100 replicate simulations. Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$									$n = 100$								
	D			D_{anc}			$D+$			D			D_{anc}			$D+$		
	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ
$f = 0$	0.0	-0.003	0.02	0.0	-0.001	0.005	0.0	-0.001	0.006	0.0	0.001	0.009	0.0	0.0	0.002	0.0	0.0	0.003
$f = 0.01$	0.019	0.021	0.021	0.004	0.004	0.006	0.006	0.007	0.007	0.019	0.017	0.009	0.004	0.003	0.002	0.006	0.005	0.003
$f = 0.02$	0.038	0.037	0.022	0.007	0.006	0.006	0.012	0.011	0.007	0.038	0.039	0.011	0.007	0.007	0.003	0.012	0.012	0.004
$f = 0.03$	0.056	0.057	0.021	0.011	0.011	0.005	0.018	0.018	0.007	0.056	0.055	0.011	0.011	0.01	0.003	0.018	0.018	0.004
$f = 0.04$	0.073	0.075	0.023	0.014	0.015	0.005	0.024	0.024	0.007	0.073	0.073	0.012	0.014	0.014	0.003	0.024	0.023	0.004
$f = 0.05$	0.09	0.088	0.023	0.017	0.017	0.006	0.029	0.029	0.008	0.09	0.089	0.013	0.017	0.017	0.003	0.029	0.029	0.004
$f = 0.06$	0.106	0.107	0.027	0.021	0.02	0.007	0.035	0.034	0.01	0.106	0.105	0.013	0.021	0.021	0.003	0.035	0.035	0.005
$f = 0.07$	0.122	0.123	0.023	0.024	0.025	0.007	0.041	0.041	0.009	0.122	0.122	0.013	0.024	0.024	0.003	0.041	0.041	0.005
$f = 0.08$	0.137	0.138	0.025	0.028	0.028	0.006	0.046	0.047	0.009	0.137	0.137	0.013	0.028	0.027	0.003	0.046	0.046	0.005
$f = 0.09$	0.152	0.153	0.027	0.031	0.031	0.007	0.052	0.052	0.01	0.152	0.152	0.015	0.031	0.031	0.004	0.052	0.052	0.005
$f = 0.1$	0.166	0.164	0.026	0.035	0.034	0.007	0.057	0.057	0.009	0.166	0.167	0.014	0.035	0.035	0.004	0.057	0.057	0.005
$f = 0.2$	0.287	0.286	0.026	0.067	0.067	0.007	0.109	0.109	0.011	0.287	0.289	0.013	0.067	0.068	0.004	0.109	0.11	0.006
$f = 0.3$	0.379	0.378	0.023	0.099	0.099	0.008	0.157	0.156	0.011	0.379	0.38	0.013	0.099	0.099	0.005	0.157	0.157	0.007
$f = 0.4$	0.452	0.45	0.019	0.128	0.127	0.009	0.2	0.198	0.012	0.452	0.453	0.01	0.128	0.129	0.004	0.2	0.2	0.006
$f = 0.5$	0.511	0.509	0.019	0.157	0.156	0.009	0.24	0.239	0.012	0.511	0.51	0.009	0.157	0.157	0.005	0.24	0.24	0.006

Table S10: Summary of methods to detect introgression in simulations under an IUA model of introgression (see Figure S1). The rows correspond to the simulated admixture proportions and the columns represent the coalescent based expectation (\mathbb{E}), mean (μ), and standard deviation (σ) of metrics to detect introgression from 100 replicate simulations per admixture portion (f).

	$n = 1$						$n = 100$					
	D		D_{anc}		$D+$		D		D_{anc}		$D+$	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	0.005	0.041	0.0	0.006	0.001	0.006	0.0	0.014	-0.0	0.002	-0.0	0.002
$f = 0.01$	0.089	0.071	0.005	0.006	0.009	0.008	0.101	0.055	0.005	0.004	0.01	0.007
$f = 0.02$	0.173	0.09	0.009	0.008	0.018	0.012	0.18	0.059	0.01	0.005	0.019	0.009
$f = 0.03$	0.24	0.076	0.015	0.008	0.028	0.013	0.247	0.052	0.015	0.005	0.029	0.009
$f = 0.04$	0.3	0.079	0.021	0.009	0.039	0.014	0.298	0.055	0.02	0.006	0.038	0.011
$f = 0.05$	0.339	0.074	0.025	0.01	0.047	0.016	0.347	0.049	0.026	0.006	0.048	0.011
$f = 0.06$	0.371	0.078	0.029	0.01	0.055	0.016	0.376	0.046	0.029	0.006	0.054	0.011
$f = 0.07$	0.402	0.07	0.034	0.011	0.062	0.017	0.411	0.041	0.035	0.007	0.064	0.012
$f = 0.08$	0.443	0.061	0.039	0.01	0.073	0.016	0.433	0.043	0.038	0.007	0.07	0.013
$f = 0.09$	0.457	0.069	0.043	0.013	0.079	0.021	0.46	0.045	0.043	0.009	0.08	0.015
$f = 0.1$	0.487	0.067	0.049	0.011	0.089	0.019	0.485	0.041	0.048	0.008	0.087	0.014
$f = 0.2$	0.623	0.051	0.093	0.015	0.161	0.024	0.617	0.028	0.091	0.012	0.159	0.019
$f = 0.3$	0.684	0.038	0.132	0.015	0.222	0.022	0.686	0.019	0.133	0.012	0.222	0.017
$f = 0.4$	0.726	0.039	0.169	0.017	0.275	0.025	0.728	0.015	0.17	0.01	0.275	0.014
$f = 0.5$	0.766	0.03	0.206	0.017	0.325	0.022	0.758	0.013	0.203	0.01	0.32	0.013
Original Model	0.177	0.087	0.011	0.009	0.021	0.014	0.194	0.053	0.012	0.004	0.022	0.008

Table S11: Summary of methods to detect introgression in the CEU population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent the mean (μ) and standard deviation (σ) of metrics to detect introgression from 100 replicate simulations per admixture portion (f). Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$						$n = 100$					
	D		D_{anc}		$D+$		D		D_{anc}		$D+$	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	0.004	0.041	-0.001	0.005	-0.001	0.005	-0.001	0.017	-0.0	0.002	-0.0	0.002
$f = 0.01$	0.09	0.072	0.005	0.006	0.009	0.008	0.101	0.057	0.005	0.004	0.01	0.006
$f = 0.02$	0.178	0.086	0.01	0.008	0.019	0.012	0.178	0.061	0.01	0.005	0.019	0.008
$f = 0.03$	0.247	0.094	0.016	0.01	0.03	0.015	0.251	0.059	0.016	0.006	0.03	0.01
$f = 0.04$	0.294	0.093	0.021	0.01	0.039	0.016	0.295	0.066	0.02	0.007	0.037	0.012
$f = 0.05$	0.344	0.086	0.026	0.011	0.048	0.018	0.346	0.055	0.026	0.006	0.048	0.011
$f = 0.06$	0.382	0.088	0.031	0.012	0.057	0.02	0.372	0.056	0.029	0.008	0.054	0.013
$f = 0.07$	0.405	0.081	0.035	0.012	0.063	0.019	0.41	0.054	0.035	0.008	0.064	0.014
$f = 0.08$	0.436	0.077	0.039	0.012	0.072	0.019	0.433	0.054	0.038	0.008	0.07	0.015
$f = 0.09$	0.465	0.071	0.044	0.013	0.081	0.021	0.461	0.049	0.044	0.009	0.08	0.015
$f = 0.1$	0.489	0.075	0.05	0.013	0.09	0.023	0.488	0.05	0.049	0.01	0.088	0.017
$f = 0.2$	0.625	0.052	0.094	0.015	0.163	0.023	0.624	0.031	0.094	0.013	0.163	0.02
$f = 0.3$	0.688	0.042	0.134	0.018	0.224	0.027	0.688	0.025	0.135	0.014	0.225	0.02
$f = 0.4$	0.733	0.036	0.173	0.018	0.28	0.025	0.732	0.019	0.173	0.013	0.28	0.019
$f = 0.5$	0.771	0.033	0.211	0.019	0.331	0.026	0.762	0.017	0.206	0.015	0.324	0.019
Original Model	0.189	0.081	0.012	0.008	0.023	0.014	0.199	0.052	0.012	0.005	0.023	0.008

Table S12: Summary of methods to detect introgression in the CHB population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent the mean (μ) and standard deviation (σ) of metrics to detect introgression from 100 replicate simulations per admixture portion (f). Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$						$n = 100$					
	f_{hom}		f_{anc}		$f+$		f_{hom}		f_{anc}		$f+$	
	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>
$f = 0$	0.004	0.003	0.006	0.005	0.004	0.003	0.002	0.001	0.002	0.002	0.002	0.001
$f = 0.01$	0.007	0.006	0.008	0.007	0.007	0.006	0.007	0.006	0.007	0.006	0.007	0.006
$f = 0.02$	0.013	0.012	0.014	0.013	0.013	0.012	0.012	0.012	0.013	0.012	0.012	0.012
$f = 0.03$	0.018	0.018	0.019	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018	0.018
$f = 0.04$	0.024	0.024	0.024	0.023	0.024	0.023	0.024	0.024	0.024	0.024	0.024	0.024
$f = 0.05$	0.031	0.03	0.031	0.03	0.031	0.03	0.03	0.03	0.031	0.03	0.031	0.03
$f = 0.06$	0.036	0.036	0.038	0.037	0.037	0.036	0.037	0.036	0.036	0.036	0.036	0.036
$f = 0.07$	0.042	0.042	0.042	0.042	0.042	0.042	0.042	0.042	0.042	0.042	0.042	0.042
$f = 0.08$	0.048	0.048	0.048	0.048	0.048	0.048	0.048	0.048	0.049	0.048	0.048	0.048
$f = 0.09$	0.054	0.054	0.055	0.054	0.054	0.054	0.054	0.054	0.054	0.054	0.054	0.054
$f = 0.1$	0.061	0.06	0.061	0.06	0.061	0.06	0.06	0.06	0.06	0.06	0.06	0.06
$f = 0.2$	0.12	0.12	0.12	0.12	0.12	0.12	0.119	0.119	0.12	0.12	0.12	0.119
$f = 0.3$	0.181	0.18	0.18	0.18	0.18	0.18	0.18	0.179	0.179	0.179	0.179	0.179
$f = 0.4$	0.241	0.241	0.242	0.241	0.241	0.241	0.24	0.24	0.24	0.24	0.24	0.24
$f = 0.5$	0.302	0.301	0.301	0.301	0.301	0.301	0.3	0.3	0.3	0.3	0.3	0.3

Table S13: Statistical power of f_{hom} , f_{anc} , and $f+$ to infer the true admixture proportion in simulations under an IUA model of introgression (see Figure S1). The rows correspond to the simulated admixture proportions and the columns represent either the root-mean-squared-error (*RMSE*) or mean-absolute-error (*MAE*) for each statistic.

	$n = 1$						$n = 100$					
	f_{hom}		f_{anc}		$f+$		f_{hom}		f_{anc}		$f+$	
	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>
$f = 0$	0.002	0.002	0.006	0.005	0.003	0.003	0.001	0.001	0.002	0.002	0.001	0.001
$f = 0.01$	0.007	0.006	0.008	0.006	0.007	0.006	0.006	0.005	0.006	0.005	0.006	0.005
$f = 0.02$	0.012	0.01	0.013	0.011	0.012	0.011	0.01	0.01	0.01	0.01	0.01	0.01
$f = 0.03$	0.016	0.014	0.016	0.014	0.016	0.014	0.014	0.013	0.015	0.013	0.014	0.013
$f = 0.04$	0.02	0.018	0.02	0.018	0.02	0.018	0.019	0.018	0.019	0.018	0.019	0.018
$f = 0.05$	0.025	0.023	0.025	0.023	0.025	0.023	0.023	0.022	0.023	0.022	0.023	0.022
$f = 0.06$	0.03	0.028	0.03	0.028	0.03	0.028	0.029	0.028	0.029	0.028	0.029	0.028
$f = 0.07$	0.035	0.034	0.036	0.033	0.035	0.034	0.033	0.032	0.033	0.032	0.033	0.032
$f = 0.08$	0.038	0.036	0.039	0.037	0.038	0.037	0.039	0.039	0.04	0.039	0.039	0.039
$f = 0.09$	0.044	0.042	0.045	0.043	0.045	0.043	0.043	0.042	0.044	0.042	0.043	0.042
$f = 0.1$	0.048	0.046	0.048	0.047	0.048	0.047	0.048	0.047	0.048	0.047	0.048	0.047
$f = 0.2$	0.097	0.095	0.097	0.096	0.097	0.095	0.099	0.098	0.098	0.097	0.098	0.097
$f = 0.3$	0.149	0.148	0.149	0.148	0.149	0.148	0.148	0.147	0.148	0.147	0.148	0.147
$f = 0.4$	0.202	0.201	0.203	0.202	0.203	0.201	0.202	0.201	0.202	0.201	0.202	0.201
$f = 0.5$	0.255	0.254	0.255	0.254	0.255	0.254	0.259	0.258	0.258	0.258	0.259	0.258
Original Model	0.009	0.007	0.011	0.008	0.01	0.007	0.008	0.007	0.008	0.007	0.008	0.007

Table S14: Statistical power of f_{hom} , f_{anc} , and $f+$ to infer the true admixture proportion in the CEU population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent either the root-mean-squared-error (*RMSE*) or mean-absolute-error (*MAE*) for each statistic. Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$						$n = 100$					
	f_{hom}		f_{anc}		$f+$		f_{hom}		f_{anc}		$f+$	
	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>	<i>RMSE</i>	<i>MAE</i>
$f = 0$	0.002	0.002	0.005	0.004	0.003	0.002	0.001	0.001	0.002	0.002	0.001	0.001
$f = 0.01$	0.007	0.006	0.008	0.006	0.007	0.006	0.006	0.005	0.006	0.005	0.006	0.005
$f = 0.02$	0.011	0.01	0.012	0.01	0.011	0.01	0.01	0.009	0.01	0.009	0.01	0.009
$f = 0.03$	0.015	0.014	0.016	0.013	0.015	0.013	0.014	0.013	0.014	0.013	0.014	0.013
$f = 0.04$	0.02	0.018	0.021	0.018	0.02	0.018	0.02	0.018	0.02	0.019	0.02	0.019
$f = 0.05$	0.024	0.022	0.025	0.023	0.025	0.022	0.023	0.022	0.023	0.022	0.023	0.022
$f = 0.06$	0.029	0.027	0.03	0.027	0.029	0.027	0.03	0.028	0.03	0.029	0.03	0.028
$f = 0.07$	0.035	0.033	0.035	0.032	0.035	0.033	0.033	0.032	0.033	0.032	0.033	0.032
$f = 0.08$	0.039	0.037	0.04	0.037	0.039	0.037	0.039	0.038	0.039	0.038	0.039	0.038
$f = 0.09$	0.043	0.041	0.044	0.042	0.044	0.041	0.043	0.042	0.043	0.042	0.043	0.042
$f = 0.1$	0.048	0.046	0.048	0.046	0.048	0.046	0.048	0.047	0.048	0.047	0.048	0.047
$f = 0.2$	0.096	0.094	0.096	0.094	0.096	0.094	0.096	0.095	0.095	0.094	0.096	0.094
$f = 0.3$	0.147	0.146	0.147	0.146	0.147	0.146	0.146	0.145	0.146	0.145	0.146	0.145
$f = 0.4$	0.198	0.197	0.198	0.197	0.198	0.197	0.198	0.197	0.198	0.197	0.198	0.197
$f = 0.5$	0.25	0.249	0.249	0.248	0.249	0.248	0.255	0.254	0.254	0.254	0.255	0.254
Original Model	0.01	0.007	0.012	0.009	0.011	0.008	0.009	0.007	0.009	0.007	0.009	0.007

Table S15: Statistical power of f_{hom} , f_{anc} , and $f+$ to infer the true admixture proportion in the CHB population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent either the root-mean-squared-error (*RMSE*) or mean-absolute-error (*MAE*) for each statistic. Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$									$n = 100$								
	f_{hom}			f_{anc}			$f+$			f_{hom}			f_{anc}			$f+$		
	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ	\mathbb{E}	μ	σ
$f = 0$	0.0	-0.001	0.004	0.0	-0.001	0.005	0.0	-0.001	0.004	0.0	0.0	0.002	0.0	0.0	0.002	0.0	0.0	0.002
$f = 0.01$	0.004	0.004	0.004	0.004	0.005	0.006	0.004	0.004	0.005	0.004	0.004	0.002	0.004	0.004	0.003	0.004	0.004	0.002
$f = 0.02$	0.008	0.008	0.005	0.008	0.007	0.007	0.008	0.008	0.005	0.008	0.008	0.002	0.008	0.008	0.003	0.008	0.008	0.002
$f = 0.03$	0.012	0.012	0.004	0.012	0.012	0.006	0.012	0.012	0.005	0.012	0.012	0.002	0.012	0.012	0.003	0.012	0.012	0.003
$f = 0.04$	0.016	0.016	0.005	0.016	0.017	0.006	0.016	0.017	0.005	0.016	0.016	0.003	0.016	0.016	0.003	0.016	0.016	0.003
$f = 0.05$	0.02	0.02	0.005	0.02	0.02	0.006	0.02	0.02	0.005	0.02	0.02	0.003	0.02	0.02	0.004	0.02	0.02	0.003
$f = 0.06$	0.024	0.024	0.006	0.024	0.023	0.008	0.024	0.024	0.007	0.024	0.024	0.003	0.024	0.024	0.004	0.024	0.024	0.003
$f = 0.07$	0.028	0.028	0.006	0.028	0.028	0.008	0.028	0.028	0.006	0.028	0.028	0.003	0.028	0.028	0.004	0.028	0.028	0.003
$f = 0.08$	0.032	0.032	0.006	0.032	0.032	0.007	0.032	0.032	0.006	0.032	0.032	0.003	0.032	0.032	0.004	0.032	0.032	0.004
$f = 0.09$	0.036	0.036	0.007	0.036	0.036	0.008	0.036	0.036	0.007	0.036	0.036	0.004	0.036	0.036	0.004	0.036	0.036	0.004
$f = 0.1$	0.04	0.04	0.007	0.04	0.04	0.008	0.04	0.04	0.007	0.04	0.04	0.004	0.04	0.04	0.004	0.04	0.04	0.004
$f = 0.2$	0.08	0.08	0.008	0.08	0.08	0.009	0.08	0.08	0.008	0.08	0.081	0.005	0.08	0.08	0.005	0.08	0.081	0.005
$f = 0.3$	0.12	0.12	0.009	0.12	0.12	0.01	0.12	0.12	0.009	0.12	0.121	0.006	0.12	0.121	0.006	0.12	0.121	0.006
$f = 0.4$	0.16	0.159	0.01	0.16	0.159	0.011	0.16	0.159	0.01	0.16	0.16	0.005	0.16	0.16	0.006	0.16	0.16	0.005
$f = 0.5$	0.2	0.199	0.012	0.2	0.199	0.012	0.2	0.199	0.011	0.2	0.2	0.006	0.2	0.2	0.006	0.2	0.2	0.006

Table S16: Summary of methods to quantify introgression in simulations under an IUA model of introgression (see Figure S1). The rows correspond to the simulated admixture proportions and the columns represent the coalescent based expectation (\mathbb{E}), mean (μ), and standard deviation (σ) of metrics to quantify introgression from 100 replicate simulations per admixture portion (f).

	$n = 1$						$n = 100$					
	f_{hom}		f_{anc}		$f+$		f_{hom}		f_{anc}		$f+$	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	0.0	0.002	0.0	0.006	0.0	0.003	0.0	0.001	-0.0	0.002	-0.0	0.001
$f = 0.01$	0.005	0.004	0.006	0.006	0.005	0.005	0.006	0.003	0.005	0.004	0.005	0.004
$f = 0.02$	0.011	0.007	0.01	0.008	0.01	0.007	0.011	0.005	0.011	0.005	0.011	0.005
$f = 0.03$	0.016	0.007	0.016	0.009	0.016	0.007	0.017	0.005	0.017	0.006	0.017	0.005
$f = 0.04$	0.022	0.008	0.022	0.009	0.022	0.009	0.022	0.006	0.022	0.006	0.022	0.006
$f = 0.05$	0.027	0.01	0.027	0.011	0.027	0.01	0.028	0.007	0.028	0.007	0.028	0.007
$f = 0.06$	0.032	0.01	0.032	0.011	0.032	0.01	0.032	0.007	0.032	0.007	0.032	0.006
$f = 0.07$	0.036	0.01	0.037	0.012	0.036	0.011	0.038	0.008	0.038	0.008	0.038	0.008
$f = 0.08$	0.044	0.01	0.043	0.011	0.043	0.01	0.041	0.008	0.041	0.008	0.041	0.008
$f = 0.09$	0.048	0.013	0.047	0.014	0.047	0.013	0.048	0.01	0.048	0.01	0.048	0.01
$f = 0.1$	0.054	0.012	0.053	0.013	0.053	0.012	0.053	0.009	0.053	0.01	0.053	0.009
$f = 0.2$	0.105	0.017	0.104	0.018	0.105	0.018	0.102	0.014	0.103	0.014	0.103	0.014
$f = 0.3$	0.152	0.017	0.152	0.018	0.152	0.017	0.153	0.014	0.153	0.014	0.153	0.014
$f = 0.4$	0.199	0.021	0.198	0.021	0.199	0.021	0.199	0.013	0.199	0.013	0.199	0.013
$f = 0.5$	0.246	0.019	0.246	0.02	0.246	0.019	0.242	0.013	0.242	0.013	0.242	0.013
Original Model	0.012	0.007	0.012	0.009	0.012	0.008	0.013	0.005	0.013	0.005	0.013	0.005

Table S17: Summary of methods to quantify introgression in the CEU population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent the mean (μ) and standard deviation (σ) of metrics to quantify introgression from 100 replicate simulations per admixture portion (f). Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	$n = 1$						$n = 100$					
	f_{hom}		f_{anc}		$f+$		f_{hom}		f_{anc}		$f+$	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
$f = 0$	0.0	0.002	-0.001	0.005	-0.0	0.003	-0.0	0.001	-0.0	0.002	-0.0	0.001
$f = 0.01$	0.005	0.004	0.005	0.006	0.005	0.005	0.006	0.003	0.005	0.004	0.006	0.004
$f = 0.02$	0.011	0.006	0.011	0.008	0.011	0.007	0.011	0.005	0.011	0.005	0.011	0.005
$f = 0.03$	0.017	0.008	0.018	0.01	0.017	0.009	0.017	0.006	0.017	0.006	0.017	0.006
$f = 0.04$	0.022	0.009	0.022	0.011	0.022	0.01	0.022	0.007	0.021	0.007	0.022	0.007
$f = 0.05$	0.028	0.011	0.028	0.012	0.028	0.011	0.028	0.007	0.028	0.007	0.028	0.007
$f = 0.06$	0.033	0.011	0.033	0.013	0.033	0.012	0.032	0.008	0.031	0.008	0.032	0.008
$f = 0.07$	0.037	0.012	0.038	0.013	0.037	0.012	0.038	0.009	0.038	0.009	0.038	0.009
$f = 0.08$	0.043	0.012	0.043	0.013	0.043	0.012	0.042	0.009	0.042	0.009	0.042	0.009
$f = 0.09$	0.049	0.013	0.048	0.014	0.049	0.014	0.048	0.01	0.048	0.01	0.048	0.01
$f = 0.1$	0.054	0.015	0.054	0.015	0.054	0.015	0.053	0.011	0.053	0.011	0.053	0.011
$f = 0.2$	0.106	0.017	0.106	0.017	0.106	0.017	0.105	0.015	0.106	0.015	0.106	0.015
$f = 0.3$	0.154	0.021	0.154	0.022	0.154	0.021	0.155	0.017	0.155	0.017	0.155	0.017
$f = 0.4$	0.203	0.021	0.203	0.022	0.203	0.021	0.203	0.016	0.203	0.017	0.203	0.016
$f = 0.5$	0.251	0.024	0.252	0.024	0.252	0.024	0.246	0.019	0.246	0.019	0.246	0.019
Original Model	0.013	0.008	0.013	0.009	0.013	0.008	0.013	0.005	0.013	0.005	0.013	0.005

Table S18: Summary of methods to quantify introgression in the CHB population under realistic simulations of human demography (see Figure S2). The rows correspond to the simulated admixture proportions and the columns represent the mean (μ) and standard deviation (σ) of metrics to quantify introgression from 100 replicate simulations per admixture portion (f). Note that "Original Model" corresponds to the results using the original model from *Ragsdale and Gravel 2019* (see Figure S3).

	EUR						ASN					
	$n = 1$			$n = 100$			$n = 1$			$n = 100$		
	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$
$f_{NEA} = 0; f_{DEN} = 0$	1.13	-3.74	0.493	-2.148	0.981	0.49	-23.1	-5.79	0.475	-5.75	-13.134	0.474
$f_{NEA} = 0; f_{DEN} = 0.005$	7.63	-3.41	0.483	3.397	16.614	0.452	76.81	72.92	0.495	71.184	83.656	0.455
$f_{NEA} = 0; f_{DEN} = 0.01$	10.27	25.77	0.477	-4.663	-16.074	0.463	134.88	139.63	0.493	126.192	116.47	0.468
$f_{NEA} = 0; f_{DEN} = 0.015$	8.53	-26.29	0.453	-6.341	-5.129	0.496	208.21	232.71	0.461	198.766	211.171	0.46
$f_{NEA} = 0; f_{DEN} = 0.02$	23.45	40.21	0.473	-1.392	-8.143	0.476	310.77	291.55	0.474	272.539	262.174	0.463
$f_{NEA} = 0.005; f_{DEN} = 0$	177.68	154.06	0.468	174.963	184.513	0.469	401.72	355.71	0.432	358.169	369.07	0.468
$f_{NEA} = 0.005; f_{DEN} = 0.005$	151.68	151.42	0.5	183.871	181.543	0.493	420.86	423.17	0.497	438.172	438.623	0.499
$f_{NEA} = 0.005; f_{DEN} = 0.01$	181.47	147.95	0.452	171.577	155.368	0.445	512.44	488.88	0.465	485.462	477.153	0.471
$f_{NEA} = 0.005; f_{DEN} = 0.015$	194.65	183.37	0.482	187.383	190.038	0.491	588.01	616.88	0.456	574.423	575.571	0.496
$f_{NEA} = 0.005; f_{DEN} = 0.02$	151.4	177.47	0.458	170.253	157.222	0.463	598.77	565.56	0.449	615.728	614.482	0.496
$f_{NEA} = 0.01; f_{DEN} = 0$	348.61	295.65	0.425	361.37	360.53	0.497	708.15	706.5	0.498	729.426	724.445	0.484
$f_{NEA} = 0.01; f_{DEN} = 0.005$	333.47	320.52	0.479	358.112	358.932	0.498	805.86	782.3	0.46	803.604	781.849	0.432
$f_{NEA} = 0.01; f_{DEN} = 0.01$	345.26	360.64	0.475	375.792	386.991	0.465	873.63	872.38	0.498	868.126	876.717	0.474
$f_{NEA} = 0.01; f_{DEN} = 0.015$	365.14	340.59	0.461	359.884	375.163	0.442	925.75	899.36	0.458	918.066	939.6	0.424
$f_{NEA} = 0.01; f_{DEN} = 0.02$	352.47	386.22	0.45	362.348	350.404	0.466	993.27	995.7	0.497	999.34	985.154	0.453
$f_{NEA} = 0.015; f_{DEN} = 0$	525.7	511.52	0.478	509.951	513.517	0.489	1106.77	1108.42	0.498	1066.485	1066.743	0.499
$f_{NEA} = 0.015; f_{DEN} = 0.005$	570.63	525.48	0.432	559.119	570.418	0.461	1180.67	1179.24	0.498	1165.936	1179.591	0.446
$f_{NEA} = 0.015; f_{DEN} = 0.01$	541.25	525.89	0.477	534.657	540.419	0.479	1213.38	1225.37	0.482	1202.914	1194.777	0.472
$f_{NEA} = 0.015; f_{DEN} = 0.015$	532.38	525.03	0.487	550.304	548.61	0.495	1304.08	1325.41	0.467	1276.638	1267.785	0.471
$f_{NEA} = 0.015; f_{DEN} = 0.02$	493.97	506.58	0.481	535.464	539.921	0.486	1348.94	1378.87	0.454	1325.467	1333.965	0.47
$f_{NEA} = 0.02; f_{DEN} = 0$	695.03	684.67	0.483	718.255	716.803	0.495	1448.84	1422.47	0.46	1447.819	1442.411	0.483
$f_{NEA} = 0.02; f_{DEN} = 0.005$	717.56	704.26	0.48	713.221	702.212	0.461	1536.15	1509.74	0.461	1507.578	1510.627	0.49
$f_{NEA} = 0.02; f_{DEN} = 0.01$	752.92	768.5	0.475	749.628	756.473	0.474	1615.03	1600.18	0.48	1611.919	1629.797	0.433
$f_{NEA} = 0.02; f_{DEN} = 0.015$	694.22	708.01	0.481	729.494	716.208	0.457	1616.21	1655.6	0.439	1647.817	1634.883	0.458
$f_{NEA} = 0.02; f_{DEN} = 0.02$	735.42	729.57	0.493	742.87	762.032	0.437	1806.93	1803.72	0.495	1734.26	1745.281	0.464

Table S19: Assessing if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero in the hypothetical European and Asian populations under a multi-pulse model of introgression from Neanderthals and Denisovans (see Figure S4) for all pairwise combinations of admixture proportions (f_{NEA} and f_{DEN}) from 0% to 2%. The rows correspond to the simulated admixture proportions, the columns represent the mean site pattern difference across 100 replicate simulations and the corresponding p -value to assess if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero. After accounting for multiple-comparisons using the Bonferroni correction, a p -value less than 0.002 is considered significant.

	EUR						ASN					
	$n = 1$			$n = 100$			$n = 1$			$n = 100$		
	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$	$ABBA - BABA$	$BAAA - ABAA$	$p - value$
$f_{NEA} = 0; f_{DEN} = 0$	20.41	32.1	0.483	-6.487	14.902	0.429	-0.88	43.98	0.435	-7.365	29.788	0.374
$f_{NEA} = 0; f_{DEN} = 0.005$	29.13	5.53	0.465	-4.662	1.019	0.48	78.32	60.3	0.473	65.714	69.991	0.486
$f_{NEA} = 0; f_{DEN} = 0.01$	-23.97	21.18	0.433	5.839	1.002	0.484	113.22	102.37	0.484	141.515	115.508	0.411
$f_{NEA} = 0; f_{DEN} = 0.015$	-6.94	-20.55	0.479	13.673	9.471	0.484	219.63	186.55	0.453	216.295	211.303	0.481
$f_{NEA} = 0; f_{DEN} = 0.02$	2.11	-9.7	0.48	2.425	21.277	0.446	283.82	264.25	0.472	282.137	288.326	0.482
$f_{NEA} = 0.005; f_{DEN} = 0$	139.01	163.2	0.464	154.998	168.042	0.453	358.62	358.98	0.499	373.579	389.946	0.442
$f_{NEA} = 0.005; f_{DEN} = 0.005$	143.59	149.68	0.491	133.738	118.959	0.45	440.15	462.33	0.465	417.926	404.327	0.454
$f_{NEA} = 0.005; f_{DEN} = 0.01$	129.2	100.53	0.463	134.032	144.062	0.462	509.87	476.26	0.456	486.115	494.417	0.472
$f_{NEA} = 0.005; f_{DEN} = 0.015$	140.21	109.42	0.456	149.708	151.293	0.494	584.32	604.06	0.471	568.648	564.759	0.488
$f_{NEA} = 0.005; f_{DEN} = 0.02$	149.03	171.9	0.464	140.381	140.525	0.5	649.73	659.92	0.487	619.205	622.525	0.489
$f_{NEA} = 0.01; f_{DEN} = 0$	305.63	339.3	0.456	295.404	292.712	0.491	765.68	779.31	0.483	731.528	729.959	0.495
$f_{NEA} = 0.01; f_{DEN} = 0.005$	276.31	269.7	0.49	295.794	291.864	0.486	790.26	767.4	0.467	796.144	789.836	0.477
$f_{NEA} = 0.01; f_{DEN} = 0.01$	260.29	248.33	0.479	299.015	314.712	0.447	857.58	848.71	0.488	868.268	883.897	0.449
$f_{NEA} = 0.01; f_{DEN} = 0.015$	297.87	300.06	0.496	290.962	284.05	0.474	930.87	934.52	0.494	926.772	915.821	0.459
$f_{NEA} = 0.01; f_{DEN} = 0.02$	300.64	318.05	0.474	287.159	298.565	0.458	1005.36	975.48	0.459	1004.375	1038.56	0.391
$f_{NEA} = 0.015; f_{DEN} = 0$	418.29	451.18	0.451	460.899	463.85	0.49	1144.69	1170.89	0.464	1116.882	1117.64	0.498
$f_{NEA} = 0.015; f_{DEN} = 0.005$	408.56	428.37	0.47	432.525	439.239	0.478	1141.79	1131.85	0.485	1147.234	1143.431	0.488
$f_{NEA} = 0.015; f_{DEN} = 0.01$	434.95	401.08	0.454	430.956	441.178	0.466	1184.71	1173.34	0.483	1198.455	1208.898	0.463
$f_{NEA} = 0.015; f_{DEN} = 0.015$	493.5	481.98	0.485	419.808	423.074	0.489	1322.54	1283.41	0.44	1260.104	1262.36	0.493
$f_{NEA} = 0.015; f_{DEN} = 0.02$	435.12	455.33	0.469	444.705	447.39	0.49	1368.13	1338.17	0.452	1352.822	1343.623	0.467
$f_{NEA} = 0.02; f_{DEN} = 0$	571.4	566.62	0.492	585.948	570.366	0.446	1429.72	1449.12	0.47	1471.65	1467.111	0.483
$f_{NEA} = 0.02; f_{DEN} = 0.005$	589.33	545.78	0.435	560.738	577.273	0.443	1561.06	1534.65	0.458	1503.25	1515.064	0.461
$f_{NEA} = 0.02; f_{DEN} = 0.01$	599.1	561.22	0.443	557.286	563.83	0.477	1588.19	1547.05	0.439	1560.229	1564.305	0.486
$f_{NEA} = 0.02; f_{DEN} = 0.015$	596.92	613.3	0.475	570.059	549.534	0.428	1664.67	1645.85	0.47	1624.164	1619.687	0.484
$f_{NEA} = 0.02; f_{DEN} = 0.02$	636.11	622.51	0.479	608.509	590.207	0.435	1739.12	1768.77	0.452	1742.161	1730.27	0.46

Table S20: Assessing if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero in the hypothetical European and Asian populations under a multi-pulse model of introgression from Neanderthals and Denisovans with an additional pulse of gene flow from a so called "Basal Eurasian" population (see Figure S5) for all pairwise combinations of admixture proportions (f_{NEA} and f_{DEN}) from 0% to 2%. The rows correspond to the simulated admixture proportions, the columns represent the mean site pattern difference across 100 replicate simulations and the corresponding p -value to assess if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero. After accounting for multiple-comparisons using the Bonferroni correction, a p -value less than 0.002 is considered significant.

	$ABBA - BABA$	$BAAA - ABAA$	$p - value$
CEU	13960.242	14314.081	0.402
FIN	14240.051	16109.465	0.14
GBR	13621.099	14726.33	0.277
IBS	13375.0	15011.692	0.202
TSI	13279.486	14338.346	0.256
CHB	16789.359	19883.155	0.101
CHS	16618.8	20871.371	0.059
CDX	16470.989	20108.935	0.023
JPT	16341.356	19786.279	0.054
KHV	16281.626	19061.303	0.07
BEB	14977.07	18427.163	0.039
GIH	14534.204	17736.437	0.064
ITU	14647.108	17299.304	0.05
PJL	14412.208	16719.917	0.057
STU	14312.333	17161.294	0.053
CLM	13233.394	14108.734	0.301
MXL	13875.812	15756.422	0.145
PEL	14777.082	16675.824	0.125
PUR	11820.096	12472.481	0.335

Table S21: Assessing if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero for $((YRI, P2), \textit{Altai Neanderthal})$ trios in the 1000 genomes project. Rows represent the $P2$ population for the trio results and the columns the columns represent the mean site pattern difference across trios and the corresponding p -value to assess if $(ABBA - BABA) - (BAAA - ABAA)$ significantly differs from zero. After accounting for multiple-comparisons using the Bonferroni correction, a p -value less than 0.0026 is considered significant.

	D		D_{anc}		$D+$		f_{hom}		f_{anc}		$f+$	
	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ	μ	σ
CEU	0.041	0.004	0.01	0.001	0.016	0.002	0.012	0.001	0.012	0.002	0.012	0.001
FIN	0.041	0.003	0.011	0.001	0.017	0.002	0.012	0.001	0.013	0.002	0.012	0.001
GBR	0.04	0.004	0.01	0.001	0.016	0.002	0.011	0.001	0.012	0.002	0.012	0.001
IBS	0.039	0.003	0.011	0.002	0.016	0.002	0.011	0.001	0.012	0.002	0.012	0.001
TSI	0.039	0.004	0.01	0.002	0.016	0.002	0.011	0.001	0.012	0.002	0.011	0.001
CHB	0.049	0.004	0.014	0.002	0.021	0.002	0.014	0.001	0.016	0.002	0.015	0.001
CHS	0.048	0.004	0.015	0.002	0.021	0.002	0.014	0.001	0.017	0.002	0.015	0.002
CDX	0.048	0.003	0.014	0.001	0.021	0.002	0.014	0.001	0.016	0.002	0.015	0.001
JPT	0.047	0.003	0.014	0.002	0.021	0.002	0.014	0.001	0.016	0.002	0.015	0.001
KHV	0.047	0.003	0.014	0.001	0.02	0.001	0.014	0.001	0.015	0.002	0.015	0.001
BEB	0.044	0.003	0.013	0.002	0.019	0.002	0.013	0.001	0.015	0.002	0.014	0.001
GIH	0.042	0.003	0.013	0.002	0.019	0.002	0.012	0.001	0.014	0.002	0.013	0.001
ITU	0.043	0.003	0.012	0.001	0.018	0.001	0.012	0.001	0.014	0.001	0.013	0.001
PJL	0.042	0.003	0.012	0.001	0.018	0.002	0.012	0.001	0.013	0.002	0.013	0.001
STU	0.042	0.004	0.012	0.002	0.018	0.002	0.012	0.001	0.014	0.002	0.013	0.001
CLM	0.039	0.005	0.01	0.002	0.016	0.002	0.011	0.001	0.011	0.002	0.011	0.001
MXL	0.04	0.004	0.011	0.001	0.017	0.002	0.012	0.001	0.013	0.002	0.012	0.001
PEL	0.043	0.004	0.012	0.002	0.018	0.002	0.012	0.001	0.013	0.002	0.013	0.001
PUR	0.035	0.005	0.009	0.002	0.014	0.002	0.01	0.001	0.01	0.002	0.01	0.002

Table S22: The mean (μ) and standard deviation (σ) of all introgression metrics for ((YRI, P2), Altai Neanderthal) trios in the 1000 genomes project where rows represents the respective P2 population for the trio results.

	Site Pattern Counts				Site Pattern Differences		Detection Metrics						Quantification Metrics					
	<i>ABBA</i>	<i>BABA</i>	<i>BAAA</i>	<i>ABAA</i>	<i>ABBA - BABA</i>	<i>BAAA - ABAA</i>	<i>D</i>	<i>p - value</i>	<i>D_{anc}</i>	<i>p - value</i>	<i>D+</i>	<i>p - value</i>	<i>f_{hom}</i>	σ	<i>f_{anc}</i>	σ	<i>f+</i>	σ
CEU	178686.455	164683.266	710638.497	695172.877	14003.189	15465.62	0.041	0.0	0.011	0.0	0.017	0.0	0.013	0.002	0.013	0.002	0.013	0.002
FIN	179031.036	164668.561	710965.968	693572.578	14362.474	17393.39	0.042	0.0	0.012	0.0	0.018	0.0	0.013	0.002	0.015	0.002	0.014	0.001
GBR	178557.14	164879.991	710566.718	694572.368	13677.149	15994.35	0.04	0.0	0.011	0.0	0.017	0.0	0.012	0.002	0.014	0.002	0.013	0.002
IBS	178070.734	164607.78	709977.626	693780.074	13462.954	16197.552	0.039	0.0	0.012	0.0	0.017	0.0	0.012	0.002	0.014	0.002	0.013	0.001
TSI	178060.36	164743.257	710026.979	694487.596	13317.104	15539.384	0.039	0.0	0.011	0.0	0.017	0.0	0.012	0.002	0.013	0.002	0.013	0.002
CHB	181002.098	164195.934	712256.723	691202.309	16806.164	21054.414	0.049	0.0	0.015	0.0	0.022	0.0	0.015	0.002	0.018	0.002	0.017	0.002
CHS	180875.077	164219.927	712291.95	690251.844	16655.15	22040.106	0.048	0.0	0.016	0.0	0.022	0.0	0.015	0.002	0.019	0.002	0.017	0.002
CDX	180749.697	164233.596	712372.16	691096.065	16516.101	21276.095	0.048	0.0	0.015	0.0	0.022	0.0	0.015	0.002	0.018	0.002	0.017	0.002
JPT	180807.724	164447.848	712199.429	691255.526	16359.876	20943.903	0.047	0.0	0.015	0.0	0.021	0.0	0.015	0.002	0.018	0.002	0.016	0.002
KHV	180684.322	164336.497	712244.409	692051.098	16347.825	20193.311	0.047	0.0	0.014	0.0	0.021	0.0	0.015	0.002	0.017	0.002	0.016	0.002
BEB	179409.557	164398.409	711619.425	692038.09	15011.148	19581.335	0.044	0.0	0.014	0.0	0.02	0.0	0.013	0.001	0.017	0.002	0.015	0.001
GIH	178956.411	164389.555	711067.865	692115.643	14566.856	18952.223	0.042	0.0	0.014	0.0	0.019	0.0	0.013	0.001	0.016	0.002	0.015	0.001
ITU	179084.768	164362.731	711261.704	692726.341	14722.036	18535.362	0.043	0.0	0.013	0.0	0.019	0.0	0.013	0.001	0.016	0.001	0.015	0.001
PJL	178926.57	164445.326	711200.889	693279.051	14481.244	17921.838	0.042	0.0	0.013	0.0	0.019	0.0	0.013	0.001	0.015	0.001	0.014	0.001
STU	178819.539	164423.601	710873.484	692550.773	14395.938	18322.711	0.042	0.0	0.013	0.0	0.019	0.0	0.013	0.001	0.016	0.001	0.014	0.001
CLM	177906.744	164638.873	709986.837	694691.111	13267.871	15295.726	0.039	0.0	0.011	0.0	0.016	0.0	0.012	0.001	0.013	0.001	0.013	0.001
MXL	178805.656	164842.313	710971.409	694089.274	13963.343	16882.135	0.041	0.0	0.012	0.0	0.018	0.0	0.013	0.001	0.015	0.001	0.014	0.001
PEL	179596.91	164775.627	711624.143	693882.313	14821.283	17741.831	0.043	0.0	0.013	0.0	0.019	0.0	0.013	0.002	0.015	0.002	0.014	0.002
PUR	176552.434	164690.52	708663.714	694972.186	11861.914	13691.528	0.035	0.0	0.01	0.0	0.015	0.0	0.011	0.001	0.012	0.001	0.011	0.001

Table S23: All site pattern counts and estimates of introgression metrics calculated from derived allele frequencies among non-African populations in the 1000 Genome’s Project. All *p-values* and standard deviations (σ) were calculated from a bootstrapped distribution consisting of 1000 bootstrapped replicates. After accounting for multiple-comparisons using the Bonferroni correction, a *p-value* less than 0.0026 is considered significant.

	Site Pattern Counts				Site Pattern Differences		Detection Metrics				Quantification Metrics							
	<i>ABBA</i>	<i>BABA</i>	<i>BAAA</i>	<i>ABAA</i>	<i>ABBA - BABA</i>	<i>BAAA - ABAA</i>	<i>D</i>	<i>p-value</i>	<i>D_{anc}</i>	<i>p-value</i>	<i>D+</i>	<i>p-value</i>	<i>f_{hom}</i>	σ	<i>f_{anc}</i>	σ	<i>f+</i>	σ
((Dingo, Basenji), Israeli Wolf), Golden Jackal)	186412.0	154645.0	413597.0	370899.0	31767.0	42698.0	0.093	0.0	0.054	0.0	0.066	0.0	0.051	0.004	0.065	0.005	0.058	0.004

Table S24: All site pattern counts and estimates of introgression metrics from single whole-genome sequences for the trio ((Dingo, Basenji), Israeli Wolf) where the Golden Jackal was used to polarize ancestral states. All *p-values* and standard deviations (σ) were calculated from a bootstrapped distribution consisting of 1000 bootstrapped replicates. A *p-value* less than 0.05 is considered significant.