Figure S1 Simulated projections with ancestral misidentification. The proportion of sites misidentified is given in the legend. For both models, the population is a constant size of 10,000 and the time of divergence is 400 kya. In part B, there is an additional admixture event of 0.02 from the test to the reference population at 50 kya.
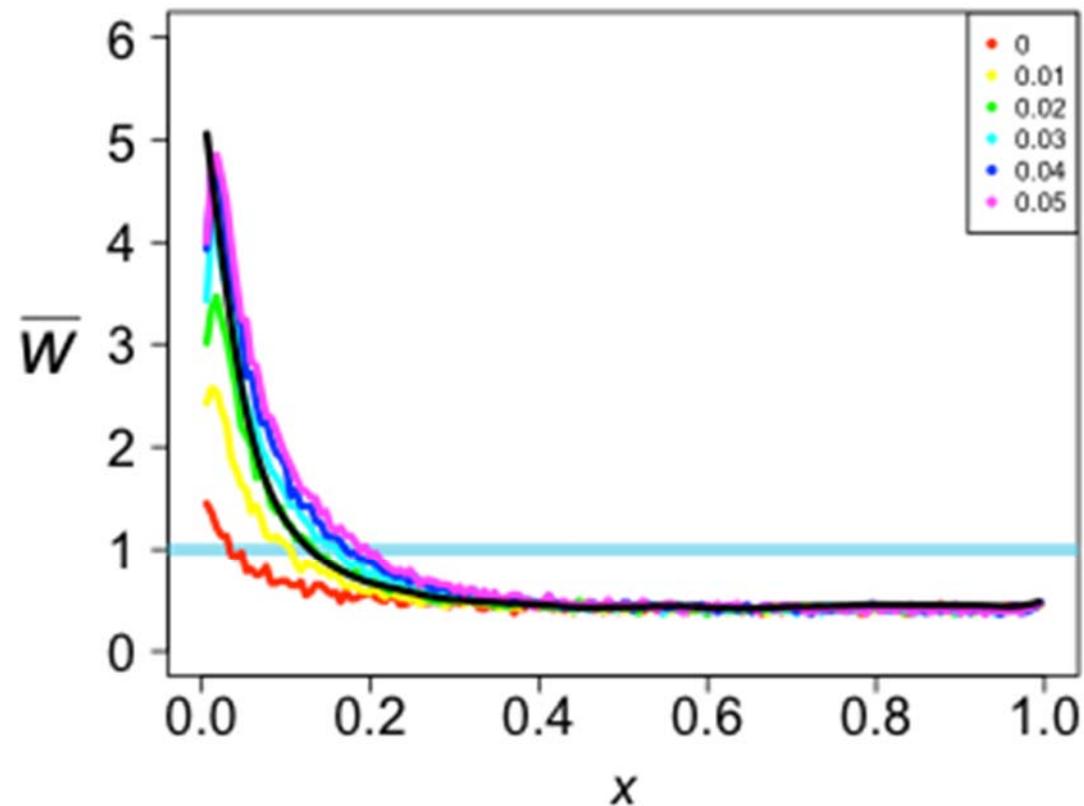
Figure S2   The simulated projections for reference CEU and test Neanderthal for our model when altering the amount of admixture ($f_{NEA\text{-}ANC1}$). The black line is the observed projection.
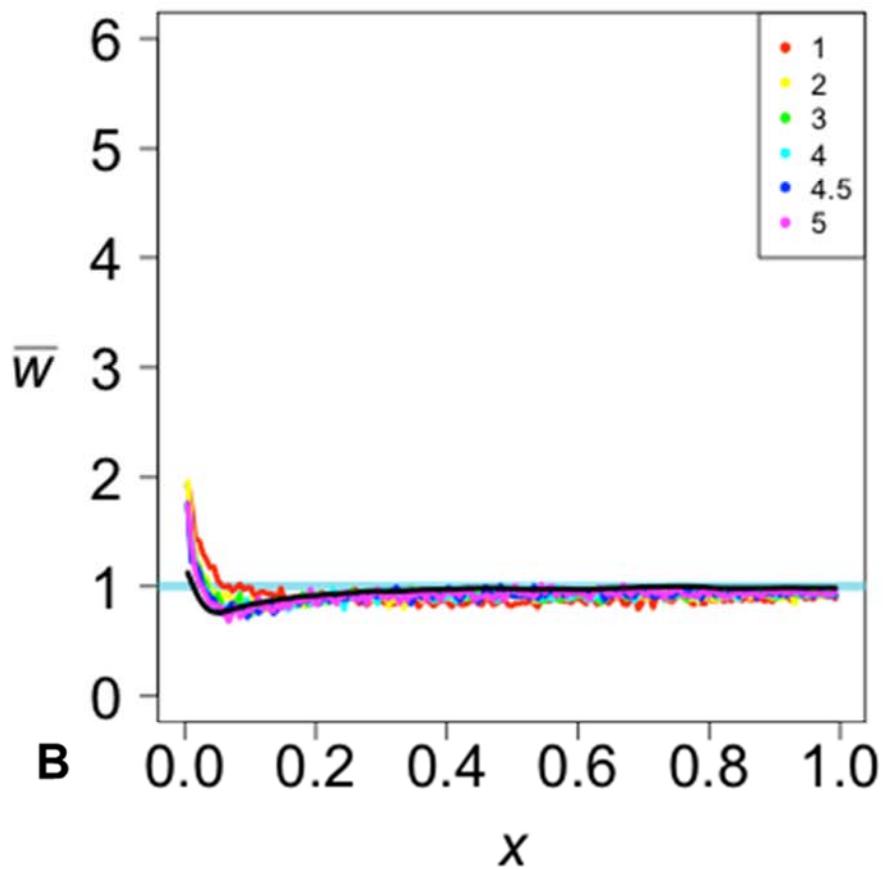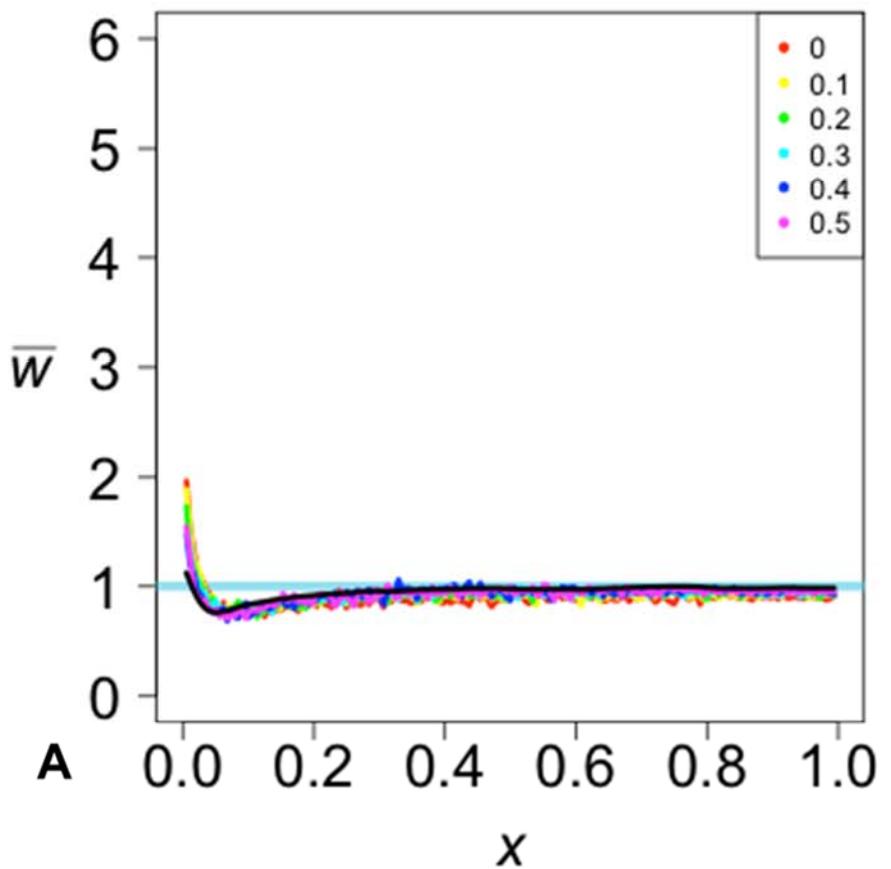
Figure S3 The simulated projections for reference YRI and test French for our model when altering (A) the population increase in the Yoruba population backwards in time (N_{ANC4}/N_{YOR}) and (B) the amount of admixture from Europeans to Yorubans ($f_{ANC1-ANC4}$). The black line is the observed projection.

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Table S1 LSS comparing the observed projections for reference CEU to each other. The diagonals compare that test genome to the $\overline{w}(x)=1$ line.

	Mandenka	Papuan	Han	Yoruba	Mbuti	Dinka	Deni	San	Altai	French
Mandenka	**18.88**	9.02	9.57	0.13	0.70	0.18	15.67	1.28	42.60	19.89
Papuan		**2.79**	0.24	9.36	12.78	7.81	38.52	13.13	87.05	2.85
Han			**2.12**	9.93	13.57	8.29	40.15	13.98	88.61	2.33
Yoruba				**19.28**	0.65	0.22	15.38	1.27	41.66	20.33
Mbuti					**23.97**	1.20	10.39	0.26	36.66	24.90
Dinka						**17.20**	17.79	1.95	44.51	18.20
Deni							**53.26**	8.49	29.67	53.79
San								**23.89**	38.52	24.70
Altai									**112.92**	115.23
French										**0.19**

Table S2   LSS comparing the observed projections for reference CHB to each other. The diagonals compare that test genome to the $\overline{w}(x) = 1$ line.

	Mandenka	Papuan	Han	Yoruba	Mbuti	Dinka	Deni	San	Altai	French
Mandenka	**31.41**	11.67	32.39	0.36	1.06	0.55	18.78	1.82	53.21	6.54
Papuan		**7.05**	7.14	11.82	14.95	11.01	51.02	16.60	108.84	2.93
Han			**0.54**	32.73	36.72	32.27	80.54	37.32	162.00	14.48
Yoruba				**31.67**	1.07	0.52	18.45	1.82	52.67	6.60
Mbuti					**35.56**	1.51	13.03	0.63	49.02	9.59
Dinka						**31.26**	20.65	2.71	53.04	5.65
Deni							**78.26**	10.88	30.14	41.54
San								**36.14**	49.98	11.35
Altai									**158.14**	85.85
French										**13.24**

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Table S3   LSS comparing the observed projections for reference YRI to each other. The diagonals compare that test genome to the $\overline{w}(x)=1$ line.

	Mandenka	Papuan	Han	Yoruba	Mbuti	Dinka	Deni	San	Altai	French
Mandenka	**0.12**	1.02	0.92	0.12	3.64	0.23	28.44	4.72	27.68	0.90
Papuan		**1.46**	0.10	1.33	2.95	0.49	22.50	3.21	21.66	0.12
Han			**1.30**	1.22	2.98	0.41	23.50	3.37	22.58	0.08
Yoruba				**0.10**	4.21	0.36	29.90	5.41	29.22	1.20
Mbuti					**3.96**	3.30	18.20	0.57	15.99	3.03
Dinka						**0.35**	27.07	4.18	26.18	0.39
Deni							**30.78**	13.18	0.57	24.12
San								**5.33**	11.52	3.51
Altai									**29.87**	23.16
French										**1.27**

Table S4   LSS (Least Sum of Squares) comparing our model to the observed projections, altering the amount of admixture from Neanderthals to non-Africans ($f_{NEA-ANC1}$).

	Test Neanderthal		
$f_{NEA-ANC1}$	**CEU**	**CHB**	**YRI**
0	69.51	109.74	3.32
0.01	25.02	41.76	2.51
0.02	7.88	11.34	2.11
0.03	**4.33**	**2.74**	1.34
0.04	7.03	3.91	1.19
0.05	13.34	8.79	**0.95**

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Table S5   LSS comparing our model to the observed projections, altering the population increase in the Yoruba population backwards in time (N_{ANC4}/N_{YOR}) and the amount of admixture ($f_{ANC1-ANC4}$) from Europeans to Yorubans.

	Test French		
N_{ANC4}/N_{YOR}	**YRI**	$f_{ANC1-ANC4}$	**YRI**
1	4.44	0	2.72
2	2.23	0.1	1.89
3	1.51	0.2	1.16
4	1.31	0.3	0.75
4.5	**1.21**	0.4	**0.56**
5	1.32	0.5	0.59