Supplemental Material
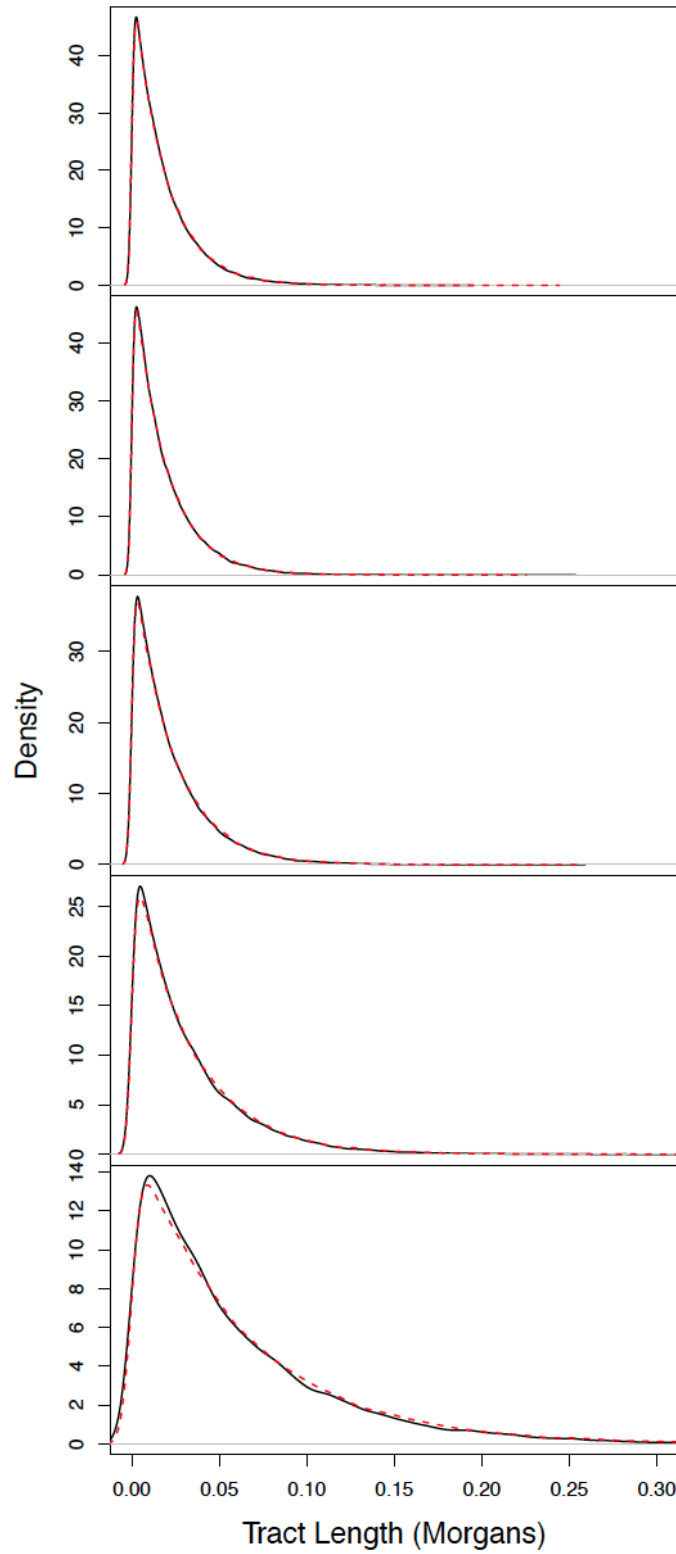
Table S1 Description of summary statistics used to describe admixture models and LAI accuracy.
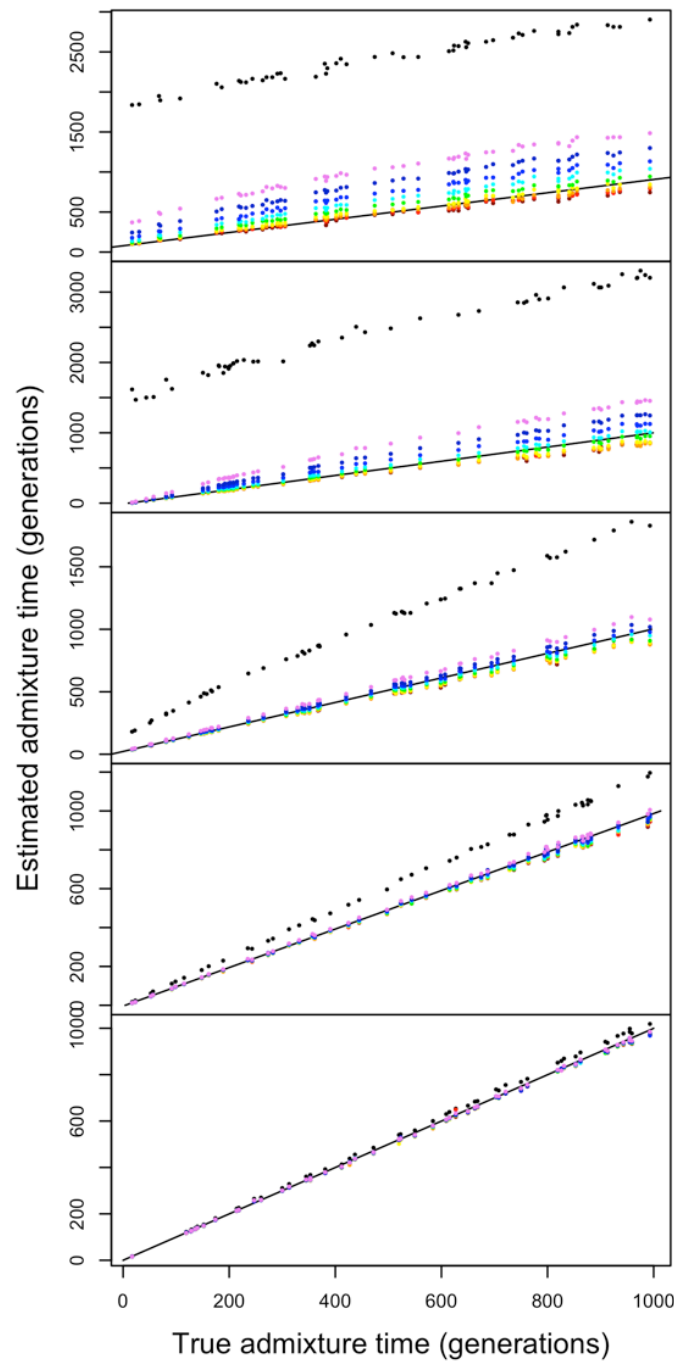
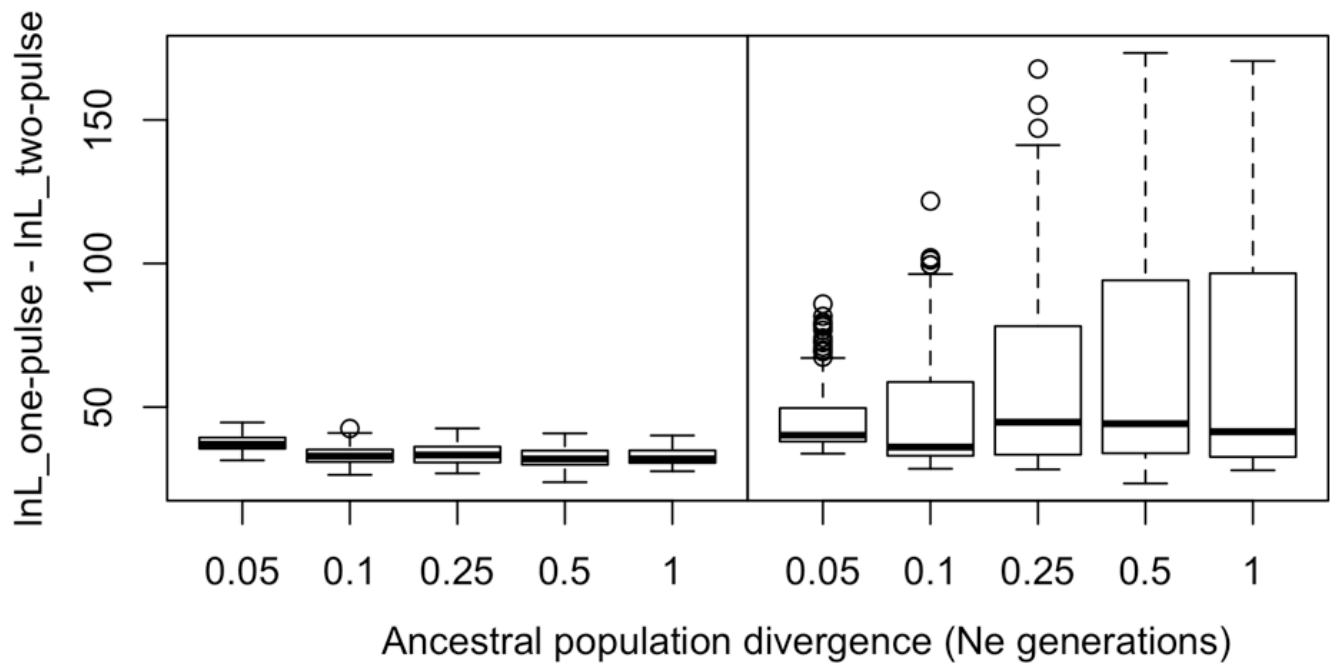| Label	Description
pulse_time	True admixture time simulated using SELAM.
Normalized root mean squared error	across 20 replicate simulations. We normalized each error estimate by the true admixture time or ancestry proportion.
mean_posterior_error	The average distance between the posterior distribution of hidden states and the true state. See **?** for a formal explanation.
accuracy	The proportion of sites where the maximum likelihood estimate of the hidden state is equal to the true ancestry state after LAI.
confident_correct	The proportion of accurate sites where the posterior probability is greater than 0.95 after LAI.

Supplementary Figure S1 Tract length distributions obtained using our tract length model approximation (solid black) and forward-in-time simulation (dashed red). In the model considered, there are five ancestry types $A_1..A_k$ and four admixture pulses occurring at 20, 40, 60, and 80 generations since the present. Each pulse in forward time contributes $\frac{1}{2}$, $\frac{1}{3}$, $\frac{1}{4}$, and $\frac{1}{5}$, respectively, of total resident genetic ancestry. Each simulation had a diploid population size of size 10,000 and we aggregated data from 50 sampled individuals across 100 simulations to produce the full tract length distribution. From top to bottom, respective ancestry tract length distributions correspond A_k, A_1, A_2, A_3, A_4.

Table S2 Simulated and analytical transition rates for a model with five ancestry types, $k = 5$. t_4, t_3, t_2, t_1, and t_0 are 80, 60, 40, 20, and 0 generations since the present, respectively. m_4, m_3, m_2, and m_1 are $\frac{1}{2}$, $\frac{1}{3}$, $\frac{1}{4}$, and $\frac{1}{5}$ respectively.
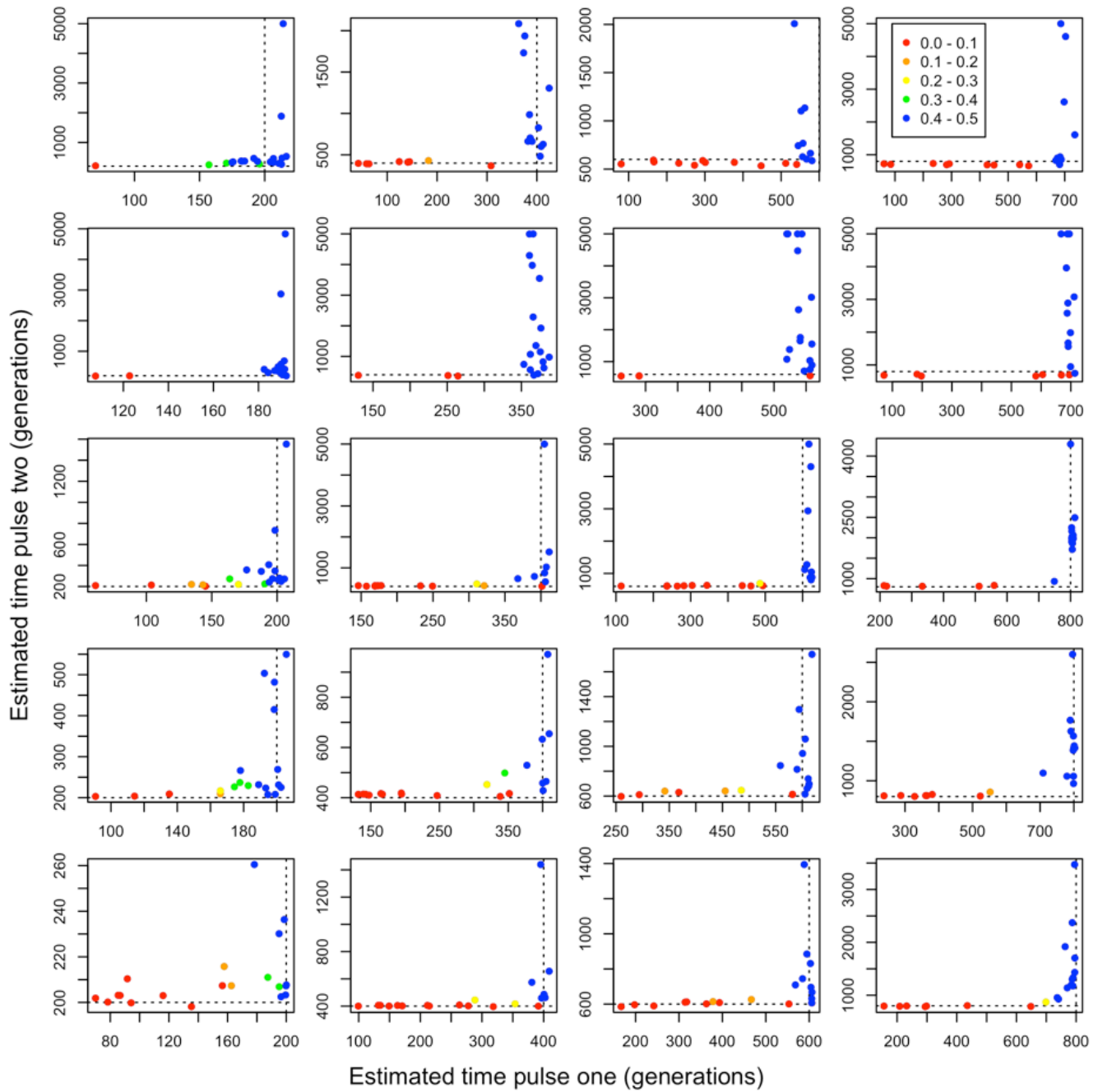
From	To	Rate_Simulation	Rate_Analytical
5	4	25.715	25.625
5	3	15.509	15.645
5	2	9.045	8.991
5	1	4.025	3.998
4	5	25.449	25.625
4	3	15.654	15.645
4	2	8.956	8.991
4	1	3.978	3.998
3	5	15.640	15.645
3	4	15.509	15.645
3	2	8.920	8.991
3	1	4.013	3.998
2	5	9.007	8.991
2	4	9.066	8.991
2	3	9.058	8.991
2	1	3.955	3.998
1	5	3.936	3.998
1	4	4.001	3.998
1	3	3.970	3.998
1	2	4.001	3.998

Supplementary Figure S2 Estimated admixture times for single pulse admixture models with varying levels of genetic divergence between ancestral populations. Specifically, from top to bottom, ancestral populations are 0.05, 0.1, 0.25, 0.5, and 1 N_e generations divergent from one another. LD pruned is 1 (black), 0.9 (violet), 0.8 (dark blue), 0.7 (blue), 0.6 (cyan), 0.5 (green), 0.4 (yellow), 0.3 (orange), 0.2 (red), 0.1 (dark red).

Supplementary Figure S3 The likelihood ratio between two-pulse and single-pulse ancestry models fit to data simulated under a single pulse (left) and a two pulse model (right). The single pulse model included a pulse of 50% of ancestry 50 generations prior to sampling. The two pulse model included a first pulse in forward time of 33% of ancestry 100 generations prior to sampling, and a second pulse in forward time of 25% of ancestry both from ancestry type 1, at time 20 generations prior to sampling. Each boxplot is based on 20 replicate simulations for each level of ancestral population divergence.

Supplementary Figure S4 Two-pulse admixture models fitted using our framework to data generated under a single pulse admixture model. We considered varying levels of population divergence. From top to bottom, the ancestral populations are 0.05, 0.1, 0.25, 0.5, and 1 N_e generation divergent from one another. From left to right, the single admixture pulse occurred 200, 400, 600, and 800 generations prior to sampling and replaced one half of the individuals in the population. Point colors correspond to the proportion of ancestry that is attributable to the second pulse with 0.0-0.1 (red), 0.1-0.2 (orange), 0.2-0.3 (yellow), 0.3-0.4 (green) and 0.4-0.5 (blue). Dashed lines reflect the true admixture time. Note that axes may differ between subplots.

Table S3 Local ancestry inference accuracy statistics of single pulse admixture models fit to two pulse admixture data. Listed statistics are described in Table S1.

divergence	pulse_time	mean_posterior_error	accuracy	confident_correct
0.05	20	0.0086	0.7991	0.2878
0.05	40	0.0071	0.7837	0.2383
0.05	60	0.0060	0.7698	0.1981
0.05	80	0.0053	0.7582	0.1712
0.05	200	0.0004	0.5092	0.0037
0.05	400	0.0002	0.4903	0.0023
0.05	600	0.0002	0.4751	0.001
0.05	800	0.0001	0.4659	0.0016
0.1	20	0.0080	0.9331	0.7713
0.1	40	0.0079	0.9278	0.7471
0.1	60	0.0078	0.9216	0.7221
0.1	80	0.0080	0.91638	0.7019
0.1	200	0.0046	0.6983	0.0999
0.1	400	0.0030	0.676	0.0675
0.1	600	0.0025	0.6621	0.0525
0.1	800	0.0021	0.6504	0.0437
0.25	20	0.0010	1	0.9697
0.25	40	0.0011	0.9902	0.9669
0.25	60	0.001	0.9892	0.9634
0.25	80	0.0013	0.9884	0.9606
0.25	200	0.0093	0.9174	0.7203
0.25	400	0.0093	0.9106	0.6935
0.25	600	0.0092	0.9039	0.6667
0.25	800	0.0094	0.8979	0.6447
0.5	20	0.0002	0.9974	0.9912
0.5	40	0.0002	0.9972	0.9904
0.5	60	0.0003	0.9969	0.9894
0.5	80	0.0003	0.9967	0.98873
0.5	200	0.0035	0.9724	0.9088
0.5	400	0.0037	0.9696	0.8989
0.5	600	0.0039	0.9673	0.8908
0.5	800	0.0041	0.9649	0.8825
1	20	6.0757e-05	0.9993	0.99764
1	40	6.7744e-05	0.9993	0.9974
1	60	7.4457e-05	0.99916	0.99720
1	80	8.0574e-05	0.9991	0.9969
1	200	0.0008	0.9925	0.97535

divergence	pulse_time	mean_posterior_error	accuracy	confident_correct
1	400	0.0009	0.9918	0.97289
1	600	0.0010	0.9909	0.97002
1	800	0.0011	0.9903	0.96794

Table S4 Local ancestry inference accuracy statistics of two pulse admixture model fit to two pulse admixture population. Listed statistics are described in Table S1.
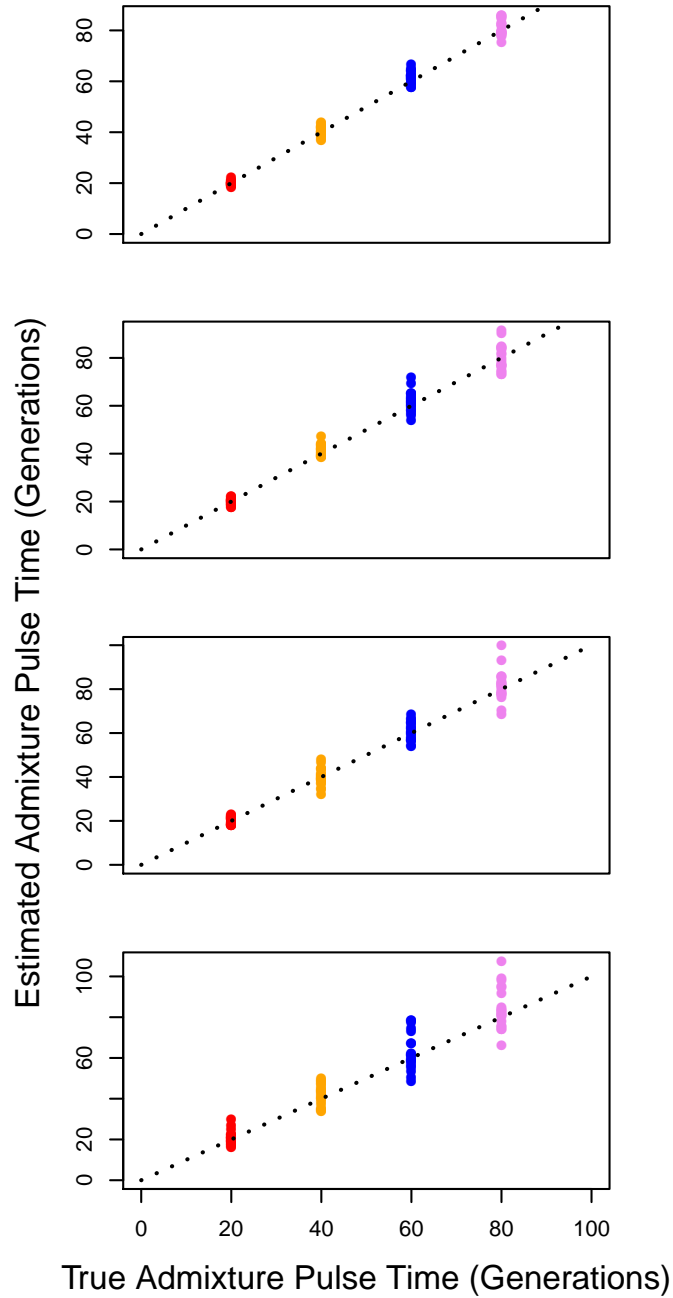
divergence	pulse_time	mean_posterior_error	accuracy	confident_correct
0.05	20	0.0067	0.7978	0.2591
0.05	40	0.0062	0.7825	0.2211
0.05	60	0.0054	0.7686	0.1873
0.05	80	0.0049	0.7572	0.1631
0.05	200	0.0003	0.5093	0.0034
0.05	400	0.0002	0.4902	0.0023
0.05	600	0.0002	0.4753	0.0018
0.05	800	0.0001	0.466	0.0016
0.1	20	0.0074	0.9333	0.7648
0.1	40	0.0077	0.9277	0.7434
0.1	60	0.0078	0.9216	0.7215
0.1	80	0.0080	0.9164	0.7016
0.1	200	0.0037	0.6979	0.0898
0.1	400	0.0029	0.6759	0.0661
0.1	600	0.0025	0.662	0.0525
0.1	800	0.0021	0.6505	0.0438
0.25	20	0.0010	0.991	0.9693
0.25	40	0.0011	0.9902	0.9666
0.25	60	0.0012	0.9892	0.9633
0.25	80	0.0013	0.9884	0.9604
0.25	200	0.0085	0.9175	0.7112
0.25	400	0.0090	0.9105	0.6882
0.25	600	0.0091	0.9039	0.6648
0.25	800	0.0094	0.8979	0.6440
0.5	20	0.0002	0.9974	0.9911
0.5	40	0.0002	0.9972	0.9904
0.5	60	0.0003	0.9969	0.9893
0.5	80	0.0003	0.9967	0.9886
0.5	200	0.0033	0.9724	0.9071
0.5	400	0.0036	0.9696	0.8978
0.5	600	0.0039	0.9673	0.8903
0.5	800	0.0041	0.9648	0.8823
1	20	6.0073e-05	0.9993	0.9976

1	40	6.7661e-05	0.9993	0.9974
1	60	7.4321e-05	0.9992	0.9972
1	80	8.0529e-05	0.9991	0.9969
1	200	0.0008	0.9925	0.9752
1	400	0.0009	0.9918	0.9727
1	600	0.0010	0.9909	0.9698
1	800	0.0011	0.9903	0.9679

Table S5 Local ancestry inference accuracy statistics of two pulse admixture model fit to single pulse admixture population. Listed statistics are described in Table S1.

divergence	pulse_time	mean_posterior_error	accuracy	confident_correct
0.05	20	0.0073	0.9214	0.7125
0.05	40	0.0087	0.8613	0.4809
0.05	60	0.0077	0.8139	0.3124
0.05	80	0.0059	0.7786	0.2135
0.05	100	0.0047	0.7473	0.1505
0.1	20	0.0022	0.9808	0.9345
0.1	40	0.0043	0.9618	0.8655
0.1	60	0. 0059	0.943	0.8001
0.1	80	0.0075	0.9271	0.7422
0.1	100	0.0084	0.9107	0.6803
0.25	20	0.0002	0.9977	0.9921
0.25	40	0.0004	0.9952	0.9838
0.25	60	0.0007	0.9926	0.9749
0.25	80	0.0010	0.9901	0.9663
0.25	100	0.0014	0.9874	0.9576
0.5	20	5.6568e-05	0.9994	0.9976
0.5	40	0.0001	0.9986	0.9952
0.5	60	0.0001	0.9979	0.9927
0.5	80	0.0002	0.9971	0.9903
0.5	100	0.0003	0.9964	0.9877
1	20	1.4541e-05	0.9999	0.9993
1	40	3.2523e-05	0.9997	0.9987
1	60	4.7858e-05	0.9995	0.9980
1	80	6.5332e-05	0.9993	0.9974
1	100	8.6379e-05	0.9991	0.9967
0.05	200	0.0019	0.6507	0.0378
0.05	400	0.0006	0.5599	0.0081
0.05	600	0.0003	0.5119	0.0034
0.05	800	0.0002	0.4847	0.0022

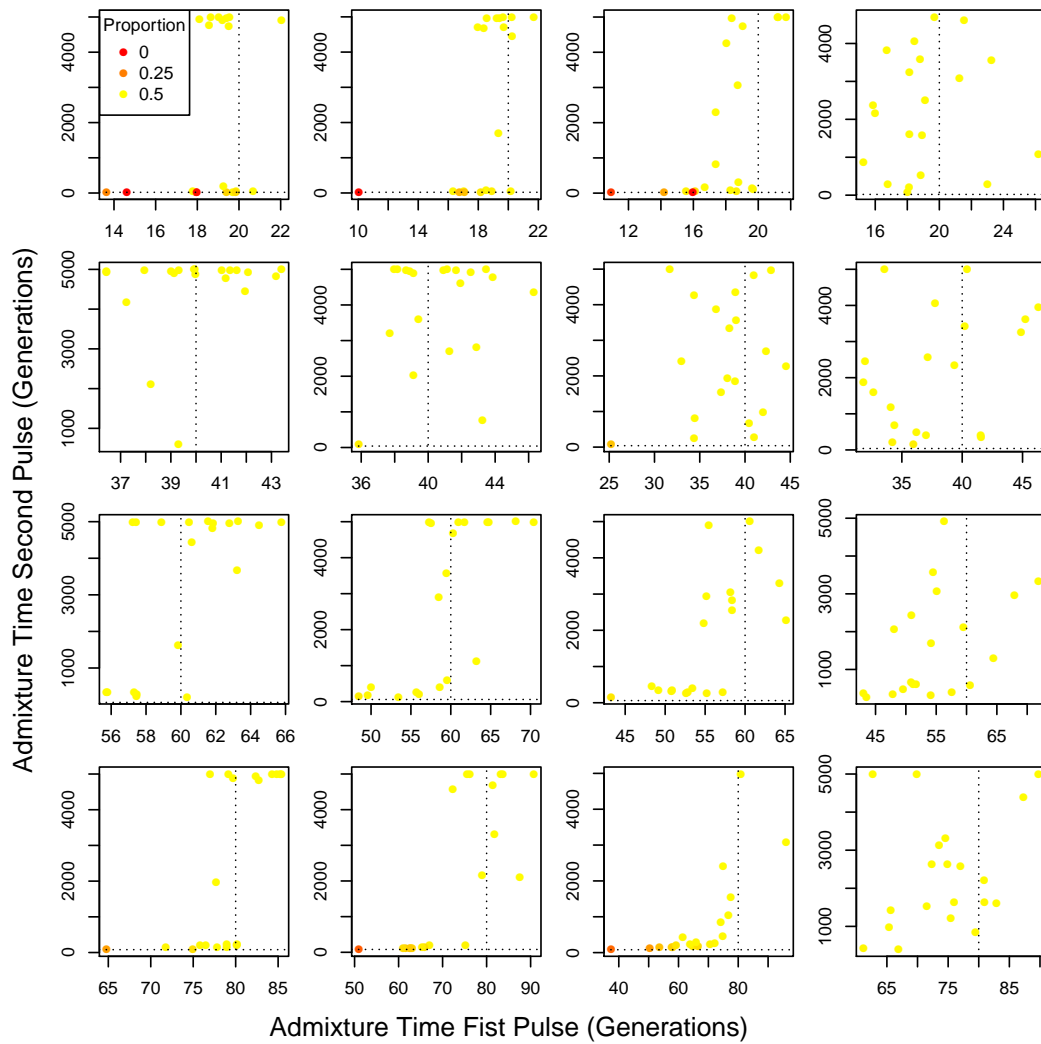|				
0.05	1000	0.0002	0.4605	0.0015
0.1	200	0.0092	0.8468	0.4402
0.1	400	0.0059	0.7638	0.1951
0.1	600	0.0037	0.7085	0.0998
0.1	800	0.0026	0.6709	0.0602
0.1	1000	0.0018	0.6401	0.0379
0.25	200	0.0030	0.9745	0.9131
0.25	400	0.0057	0.9503	0.8301
0.25	600	0.0076	0.9285	0.7533
0.25	800	0.0090	0.9099	0.6880
0.25	1000	0.0096	0.8927	0.6260
0.5	200	0.0008	0.9925	0.9748
0.5	400	0.0017	0.9846	0.9485
0.5	600	0. 0027	0.977	0.9231
0.5	800	0.0036	0.9696	0.8986
0.5	1000	0.0043	0.9626	0.8747
1	200	0. 0001	0.998	0.9933
1	400	0. 0004	0.996	0.9865
1	600	0.0006	0.9939	0.9796
1	800	0.0009	0.9918	0.9727
1	1000	0.0011	0.9897	0.9657

Supplementary Figure S5 Admixture time estimates for single pulse models fitted to single pulse data at varying levels of recombination map perturbation. Rho was modified every 5Mb by multiplying by a scalar chosen at random from a uniform distribution between 1-d and 1+d where d is 0.25, 0.5 0.75 and 1 from top to bottom (See Methods). We simulated single pulse models occurring 20 (red), 40 (orange), 60 (blue), and 80 (pink) generations ago. Note that axes may differ between subplots. Summary statistics of model fitting are reported in Tables S6 and S7.

Table S6 Accuracy statistics of estimated single pulse admixture time fit to data generated under a single pulse model at varying levels of recombination map perturbation. Listed statistics are described in Table S1.
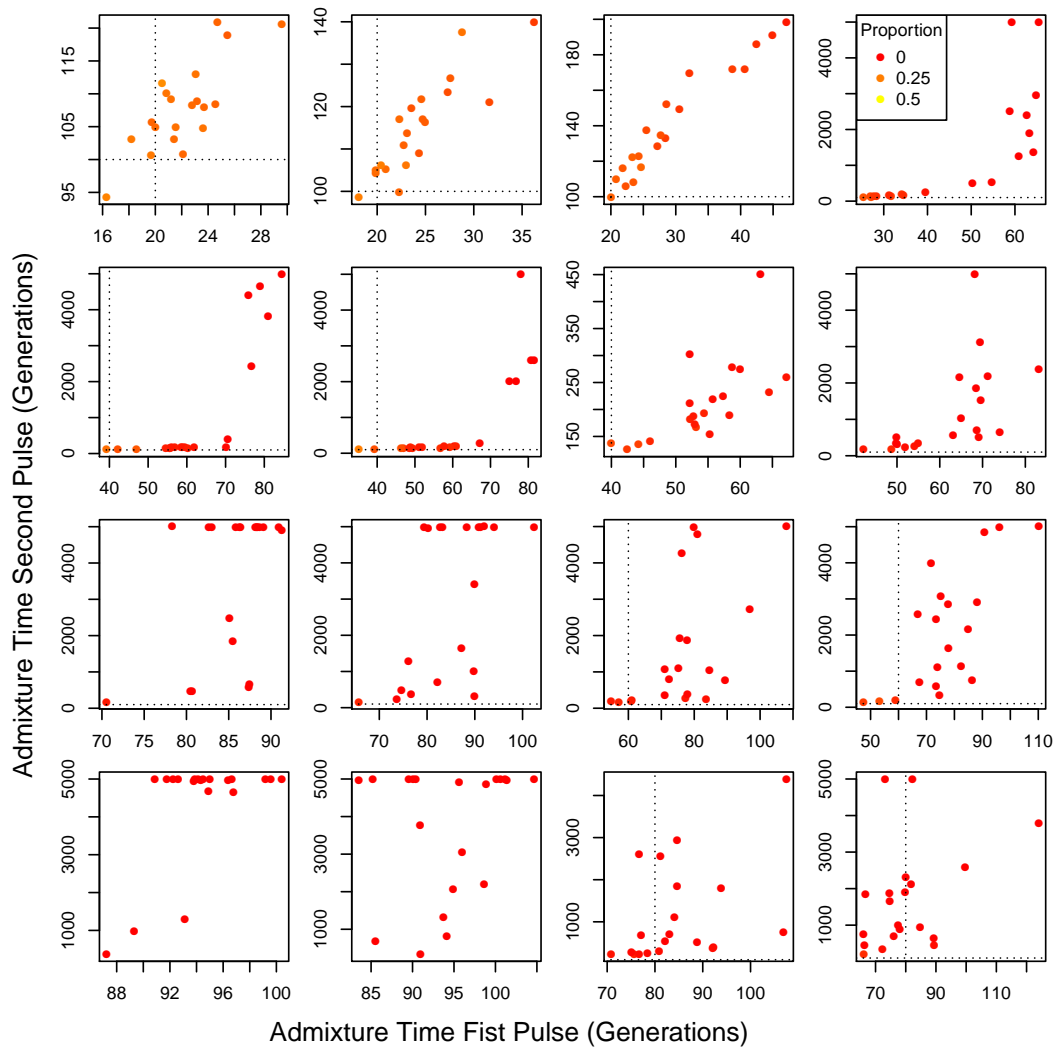
pulse_time	NRMSE_0.25	NRMSE_0.5	NRMSE_0.75	NRMSE_0.25
20	0.0314	0.0522	0.0805	0.1169
40	0.0400	0.0534	0.0739	0.1153
60	0.0401	0.0594	0.0588	0.1186
80	0.0327	0.0554	0.0619	0.1014

Table S7 Local ancestry inference accuracy statistics of single pulse admixture model fit to single pulse admixture population after perturbing recombination rates every 5Mb windowed. Listed statistics are described in Table S1.
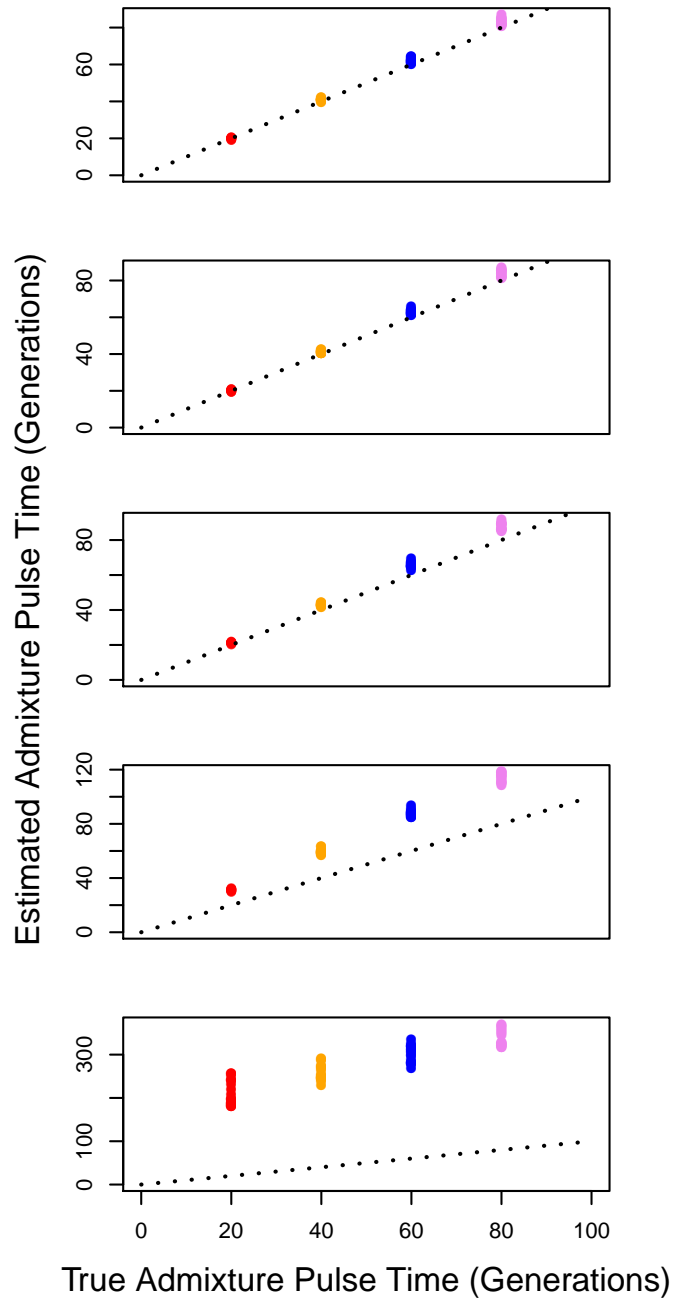
pulse_time	rho_error	mean_posterior_error	accuracy	confident_correct
20	0.25	0.0089	0.9890	0.9837
20	0.5	0.0089	0.9890	0.9837
20	0.75	0.0089	0.9890	0.9837
20	1	0.0089	0.9889	0.9836
40	0.25	0.0140	0.9816	0.9707
40	0.5	0.0141	0.9816	0.9707
40	0.75	0.0141	0.9816	0.9706
40	1	0.0141	0.9816	0.9704
60	0.25	0.0180	0.9755	0.9588
60	0.5	0.0180	0.9755	0.9587
60	0.75	0.0181	0.9754	0.9584
60	1	0.0181	0.9754	0.9583
80	0.25	0.0204	0.9710	0.9485
80	0.5	0.0204	0.9710	0.9484
80	0.75	0.0204	0.9709	0.9482
80	1	0.0205	0.9708	0.9478

Supplementary Figure S6 Admixture time estimates for double pulse models fitted to single pulse data at varying levels of recombination map perturbation. Rho was modified every 5Mb by multiplying by a scalar chosen at random from a uniform distribution between 1-d and 1+d where d is 0.25, 0.5 0.75 and 1 from left to right. For all admixture models considered, the second pulse occurred 100 generations before the present. From top to bottom, the most recent pulse occurred 20, 40, 60, and 80 generations ago. Note that axes may differ between subplots.
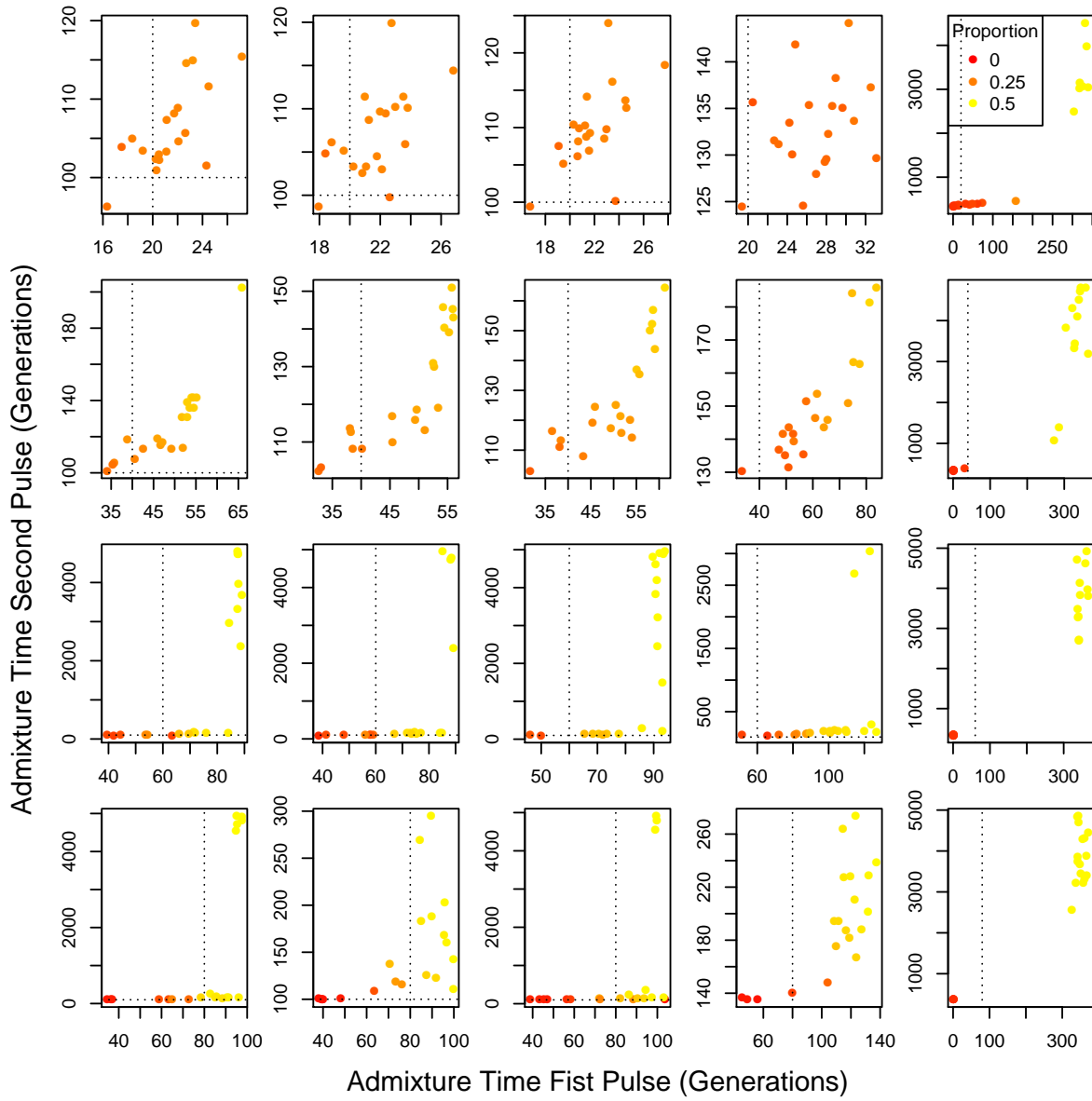
Supplementary Figure S7 Admixture time estimates for double pulse models fitted to double pulse data at varying levels of recombination map perturbation. Rho was modified every 5Mb by multiplying by a scalar chosen at random from a uniform distribution between 1-d and 1+d where d is 0.25, 0.5 0.75 and 1 from left to right. For all admixture models considered, the second pulse occurred 100 generations before the present. From top to bottom, the most recent pulse occurred 20, 40, 60, and 80 generations ago. Note that axes may differ between subplots.
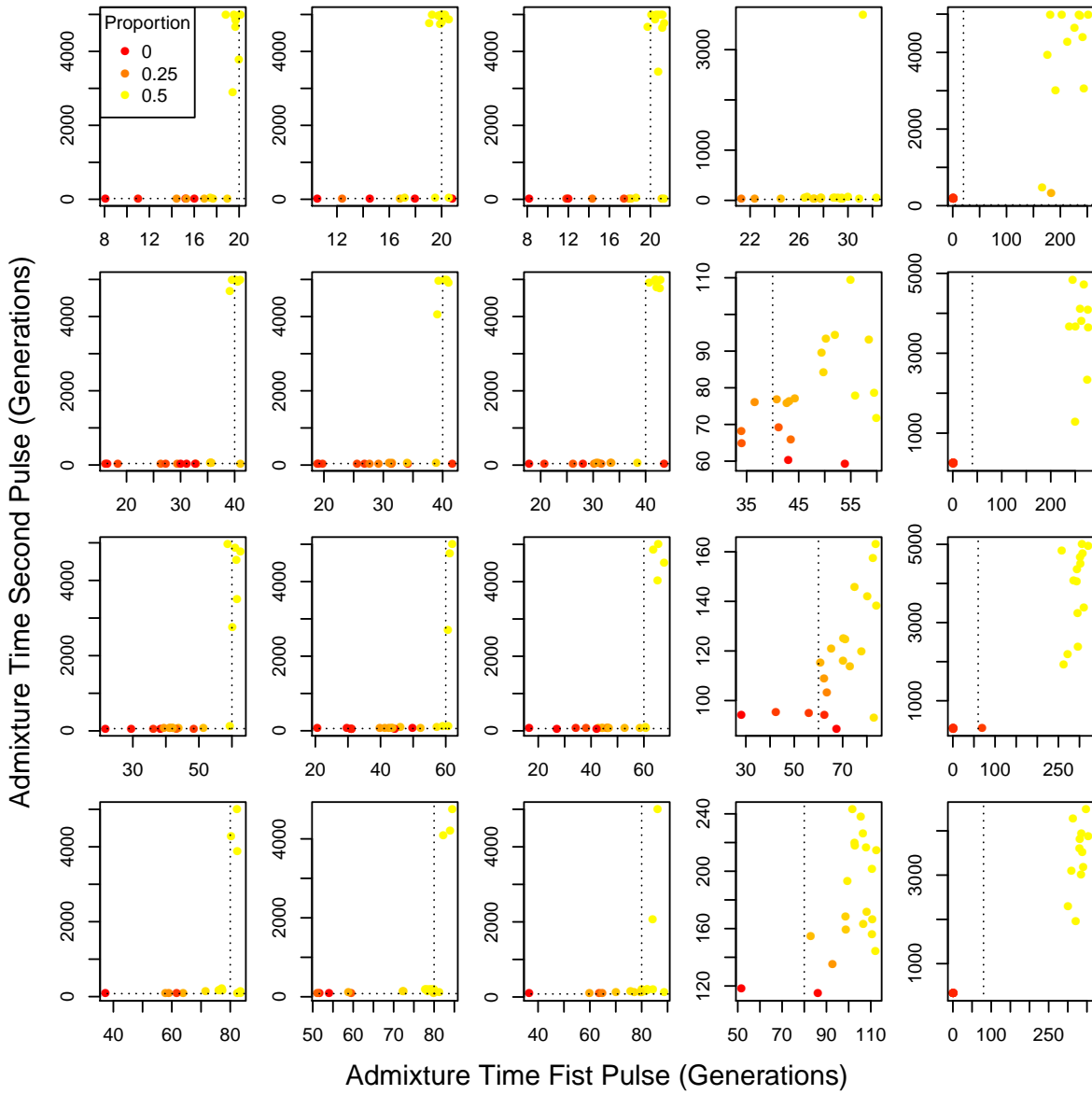
Supplementary Figure S8 Admixture time estimates for varying divergence between the real source population and assumed reference. Here, we applied a single pulse admixture model to single pulse admixture data. From top to bottom, the reference used to estimate the timing of admixture was 0.005, 0.01, 0.02, 0.05, and 0.1 N_e generations diverged from the real source population. We simulated single pulse models occurring 20 (red), 40 (orange), 60 (blue), and 80 (pink) generations ago. Note that axes may differ between subplots. Summary statistics of the model fit are listed in Table S8.

Table S8 Accuracy statistics of single pulse admixture model fit to single pulse admixture population at varying levels of divergence between source and assumed reference. Listed statistics are described in Table S1.

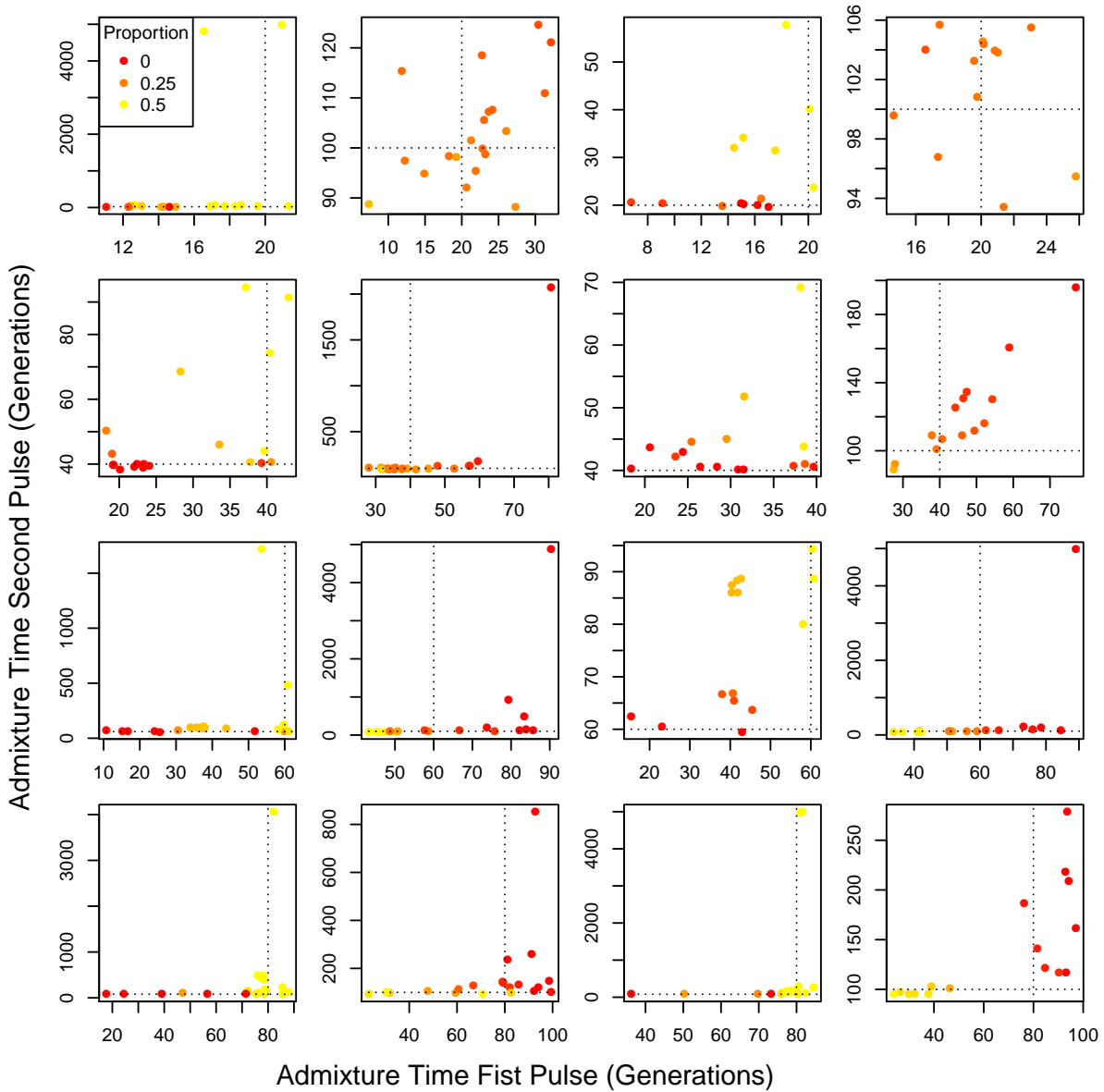| divergence	pulse_time	mean_posterior_error	accuracy	confident_correct
0.005	20	0.0002	0.9977	0.9927
0.005	40	0.0005	0.9952	0.9847
0.005	60	0.0008	0.9926	0.9764
0.005	80	0.0011	0.9901	0.9680
0.01	20	0.0003	0.9974	0.9922
0.01	40	0.0006	0.9948	0.9838
0.01	60	0.0009	0.9921	0.9752
0.01	80	0.0012	0.9894	0.9665
0.02	20	0.0003	0.9969	0.9910
0.02	40	0.0007	0.9939	0.9819
0.02	60	0.0011	0.9906	0.9720
0.02	80	0.0015	0.9875	0.9625
0.05	20	0.0012	0.9919	0.9803
0.05	40	0.0020	0.9860	0.9646
0.05	60	0.0028	0.9805	0.9501
0.05	80	0.0034	0.9754	0.9367
0.1	20	0.0158	0.9180	0.8310
0.1	40	0.0172	0.9077	0.8083
0.1	60	0.0182	0.8996	0.7895
0.1	80	0.0189	0.8929	0.7735

Supplementary Figure S9 Admixture time estimates for two pulse population model fit to two pulse data at varying level of divergence between source and assumed reference. From left to right, the reference used to estimate the timing of admixture was 0.005, 0.01, 0.02, 0.05, and 0.1 N_e generations diverged from the real source population. For all admixture models considered, the second pulse occurred 100 generations before the present. From top to bottom, the most recent pulse occurred 20, 40, 60, and 80 generations ago. Note that axes differ slightly between subplots. Summary statistics of model fit are listed in Table S9.

Supplementary Figure S10 Admixture time estimates for two pulse population model fit to single pulse data at varying level of divergence between source and assumed reference. From left to right, the reference used to estimate the timing of admixture was 0.005, 0.01, 0.02, 0.05, and 0.1 N$_e$ generations diverged from the real source population. From top to bottom, single pulses occurred 20, 40, 60, and 80 generations ago. Note that axes differ slightly between subplots.

Table S9 Accuracy statistics of double pulse admixture model fit to double pulse admixture population at varying levels of divergence between assumed reference and source population. Listed statistics are described in Table S1.

divergence	pulse_time	mean_posterior_error	accuracy	confident_correct
0.005	20	0.0011	0.9910	0.9707
0.005	40	0.0012	0.9902	0.9682
0.005	60	0.0012	0.9893	0.9643
0.005	80	0.0013	0.9883	0.9616
0.01	20	0.0011	0.9903	0.9694
0.01	40	0.0013	0.9894	0.9665
0.01	60	0.0013	0.9885	0.9633
0.01	80	0.0015	0.9875	0.9604
0.02	20	0.0014	0.9887	0.9660
0.02	40	0.0016	0.9876	0.9628
0.02	60	0.0016	0.9865	0.9584
0.02	80	0.0018	0.9853	0.9558
0.05	20	0.0033	0.9772	0.9412
0.05	40	0.0034	0.9755	0.9366
0.05	60	0.0037	0.9739	0.9323
0.05	80	0.0039	0.9721	0.9275
0.1	20	0.0191	0.8904	0.7659
0.1	40	0.0189	0.8900	0.7638
0.1	60	0.0191	0.8887	0.7605
0.1	80	0.0192	0.8854	0.7516

Supplementary Figure S11 Admixture time estimates for varying sample sizes. From top to bottom, panels show admixture scenarios where the most recent pulse occurred 20, 40, 60, and 80 generations in the past, respectively. For all admixture models considered, the second pulse occurred 100 generations before the present. Columns one and two simulate a sample size of 10 individuals, and columns three and four simulate a sample size of 25 individuals. Columns one and three show simulated single pulse models, columns two and four show simulated double pulse models. In all cases we fit a double pulse model to the simulated data. Summary statistics of model fitting for varying sample sizes are reported in Tables S10, S11, S12. Note that axes may differ between subplots.

Table S10 Local ancestry inference accuracy statistics using sample sizes 10 and 25. Listed statistics are described in Table S1.
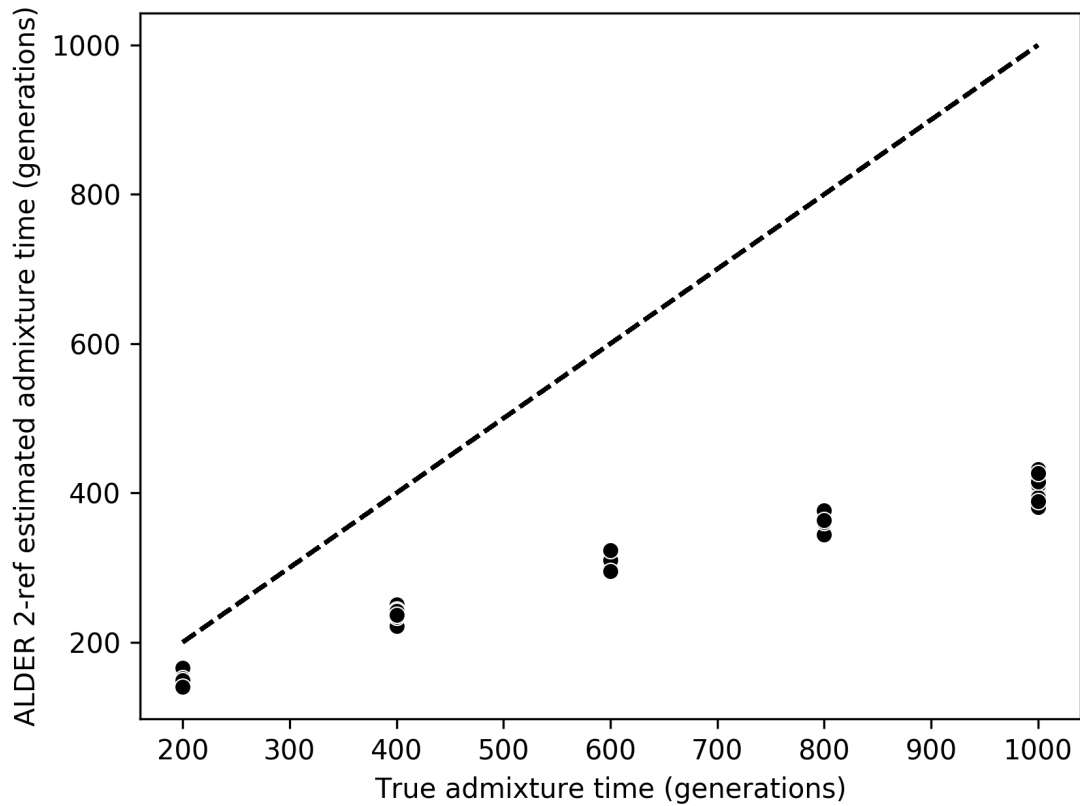
admixture_time	sample_size	mean_posterior_error	accuracy	confident_correct
20	10	0.0010	0.9911	0.9699
20	25	0.0010	0.9907	0.9690
40	10	0.0011	0.9902	0.9668
40	25	0.0011	0.9900	0.9665
60	10	0.0012	0.9890	0.9633
60	25	0.0012	0.9893	0.9639
80	10	0.0012	0.9883	0.9606
80	25	0.0013	0.9883	0.9607

Table S11 Estimated timing of admixture accuracy statistics using sample sizes 10, 25, and 50. Listed parameters are: simulated timing of admixture pulse (pulse_time), the normalized root mean squared error of estimated admixture time computed from 20 simulations for each sample size tested.

pulse_time	NRMSE_10	NRMSE_25	NRMSE_50
20	0.0553	0.9634	0.0251
40	0.0333	0.9806	0.0123
60	0.0313	0.9902	0.0110
80	0.0344	0.9723	0.0217

Table S12 Accuracy statistics of a double pulse model using sample sizes of 10, 25, and 50. Listed statistics are described in Table S1. In addition, we list the normalized root mean squared error of the admixture proportion introduced during t_1 (NRMSE_A_1).

sample_size	NRMSE_t_1	NRMSE_A_1	NRMSE_t_2
10	0.2571	0.2678	0.0573
25	0.0698	0.0909	0.0657
50	0.0531	0.0754	0.0413

Supplementary Figure S12 ALDER's admixture time estimates. We simulated single pulse models occurring 200, 400, 600, 800, and 1000 generations ago (shown left to right). Summary statistics of model fit are listed in Table S14. These results were generated by increasing the maxdis of ALDER to 0 (see Methods).

Table S13 ALDER and Ancestry_HMM NRMSE in estimating timing of single pulse admixture. Listed statistics are described in Table S1. Pulse times greater than 100 were generated by increasing the maxdis of ALDER to 0 (see Methods).

pulse_time	ALDER_normalized_NRMSE	Ancestry_HMM_normalized_NRMSE
20	0.1423	0.0251
40	0.1483	0.0123
60	0.1777	0.0110
80	0.2828	0.0217
100	0.2776	0.0141
200	0.2581	0.0271
400	0.4013	0.0234
600	0.4747	0.0264
800	0.5362	0.0083
1000	0.5933	0.0122

Table S14 ALDER and Ancestry_HMM NRMSE in estimating timing of double pulse admixture. The table lists the timing of the first admixture pulse in backwards time (pulse_time_t_1), the timing of the second admixture pulse in backwards time (pulse_time_t_2), the number of two pulse models fit by ALDER out of 20 replicates (fit_two_pulse), the NRMSE of ALDER's estimated timing of the first pulse (ALDER_NRMSE_t_1), the NRMSE of ALDER's estimated timing of the second pulse (ALDER_NRMSE_t_2, the NRMSE of Ancestry_HMM's estimated timing of the first pulse (Ancestry_HMM_NRMSE_t_1), the NRMSE of Ancestry_HMM's estimated timing of the second pulse (Ancestry_HMM_NRMSE_t_2). Pulse times greater than 100 were generated by increasing the maxdis of ALDER to 0 (see Methods).

pulse_time_t_1	pulse_time_t_2	fit_two_pulse	ALDER_NRMSE_t_1	ALDER_NRMSE_t_2	Ancestry_HMM_NRMSE_t_1	Ancestry_HMM_NRMSE_t_2
20	100	6/20	0.1207	0.1856	0.0307	0.0214
40	100	0/20	N/A	N/A	0.0457	0.0298
60	100	2/20	0.1319	0.1215	0.0235	0.0148
80	100	1/12	0.0206	0.3132	0.0179	0.0115
200	1000	12/20	0.1708	0.6364	0.0090	0.0293
400	1000	2/20	0.6775	0.6521	0.0146	0.0265
600	1000	8/20	0.8417	0.6387	0.0168	0.0127
800	1000	1/20	0.5155	0.5943	0.0242	0.0272