

Supplementary Material of "Resequencing data provide no evidence for a human bottleneck in Africa during the penultimate glacial period"

- Supplementary table 1: Summary statistics for each marker in the San sample.
- Supplementary table 2: Summary statistics for each marker in the Biaka sample.
- Supplementary table 3: Summary statistics for each marker in the Mandenka sample.
- Supplementary table 4: Posterior probabilities of the different models estimated with the rejection algorithm.
- Supplementary table 5: Posterior P-values of the summary statistics.
- Supplementary table 6: Posterior estimates of the demographic parameters.
- Supplementary figure 1: Posterior distributions of the intensity b of the bottleneck.
- Supplementary figure 2: Mean of the summary statistics as a function of the bottleneck intensity b .
- Supplementary figure 3: Variance of the summary statistics as a function of the bottleneck intensity b .
- Supplementary figure 4: Posterior distribution of the ancestral effective population size N_A .
- Supplementary figure 5: Values of the population-wise summary statistics as a function of the Biaka and San divergence times.

Table 1: Summary statistics for each marker in the San sample.

	sample size	seq. length (bp)	S	D	D^*	H
10qMB119	18	5523	21	-1.157	-0.564	2.248
10qMB127	12	5285	18	-0.392	-0.612	0.303
10qMB128	18	4680	20	-0.248	-0.057	2.301
10qMB85	16	6049	22	-0.512	-1.208	2.65
11pMB20	10	5867	20	-0.859	-1.023	3.556
11pMB23	14	6168	31	0.809	0.937	3.473
12qMB46	18	6567	26	-0.067	-0.359	2.039
13qMB107	6	4484	22	-0.804	-0.705	-1.6
13qMB108	16	5282	19	-0.933	-1.335	-0.417
13qMB31	14	5843	22	-0.592	-0.287	-3.341
13qMB64	18	5764	18	-0.703	1.092	-0.732
13qMB67	18	6058	35	-0.726	-0.93	4
13qMB69	10	6069	16	0.5	0.521	1.422
14qMB85	12	6194	29	-0.721	0.319	-2.788
15qMB35	16	5966	18	0.307	0.465	1.95
16pMB17	18	6781	21	-0.981	0.031	-6.85
16qMB53	18	6168	31	-0.607	-0.855	-5.046
17qMB66	18	5870	15	0.948	0.922	0.549
18pMB7	18	4627	24	-0.213	-0.006	3.791
18qMB34	18	6175	38	0.288	0.367	-1.516
18qMB47	16	5956	20	-0.024	0.906	2.517
18qMB60	16	6195	16	-0.754	-0.423	2.467
18qMB67	16	6482	19	-0.694	-1.647	-0.133
18qMB73	12	5163	32	-0.77	-1.167	1.212
19qMB35	16	5789	26	-0.245	-1.24	0.6
1pMB101	18	6362	37	1.583	0.506	0.837
1pMB4	18	4274	29	-0.357	-1.264	1.595
1pMB81	18	6042	33	-1.191	-2.113	-2.353
20pMB7	18	6797	24	1.306	1.327	2.092
21qMB20	18	5875	22	-0.75	-1.32	-0.941
21qMB23	18	6005	26	0.463	0.887	4.052
2pMB3	16	5610	16	-0.822	-1.141	-0.367
2pMB6	18	5972	31	1.29	0.86	3.686
2qMB114	18	5919	21	-0.365	-0.564	1.542
2qMB134	16	5959	29	0.678	0.38	2.35
2qMB143	16	5470	21	-0.13	0.67	4.383
2qMB221	18	6268	30	-0.528	-1.384	4.209
3qMB148	14	6076	24	-0.911	-1.59	1.846
4pMB27	14	5996	21	-0.453	0.443	2.242
4pMB31	18	6019	14	-0.391	-0.383	-0.941
4qMB105	18	5887	24	-0.187	0.527	4.235
4qMB157	18	8007	45	0.111	0.784	-3.242
4qMB179	18	5912	25	-1.146	-1.734	-1.072
4qMB181	12	4637	18	0.328	0.889	-0.455
5pMB10	16	6455	17	0.079	0.384	-1.15
5pMB31	14	6152	22	-1.134	-1.88	0.571
5pMB35	14	6080	26	-0.074	0.27	1.143
5pMB4	18	4944	9	-0.702	1.499	-0.392
5qMB113	18	6083	24	0.669	1.327	-5.333
5qMB123	18	6035	20	0.186	0.253	-1.464
5qMB128	18	6787	15	-0.916	-0.64	-0.915
6pMB14	16	7163	31	1.009	0.689	-0.767
6pMB45	6	5921	26	0.967	1.331	-1.333
6qMB164	18	5100	15	-0.547	-0.249	1.464
7pMB42	16	6067	16	-0.004	-0.064	-1.567
7pMB8	16	7142	38	-0.564	-0.094	-1.383
7qMB152	16	6008	27	-1.757	-1.595	-0.95
7qMB83	18	6482	18	-0.375	0.416	2.275
8pMB5	16	4759	36	-0.054	0.515	1.283
9pMB8	14	5919	30	-0.047	0.291	4.967
9qMB100	16	6161	24	-0.07	0.06	2.35

Table 2: Summary statistics for each marker in the Biaka sample.

	sample size	seq. length (bp)	S	D	D^*	H
10qMB119	26	5523	17	-0.589	-0.603	1.982
10qMB127	30	5285	19	0.651	-0.076	2.152
10qMB128	28	4680	23	-0.364	-0.343	2.101
10qMB85	26	6049	15	-0.097	-0.459	-0.197
11pMB20	16	5867	25	-0.874	-0.364	2.917
11pMB23	28	6168	41	-0.241	1.469	-0.582
12qMB46	28	6567	26	-0.25	-0.661	1.106
13qMB107	18	4484	20	0.804	0.563	-0.915
13qMB108	28	5282	25	-1.518	-1.642	-2.783
13qMB31	28	5843	31	-0.779	-0.749	-0.635
13qMB64	26	5764	17	-0.645	0.568	-1.44
13qMB67	28	6058	31	-0.201	-0.255	2.317
13qMB69	16	6069	19	-0.129	0.227	1.617
14qMB85	24	6194	36	-0.338	-0.696	3.572
15qMB35	30	5966	28	-0.131	-0.256	4.239
16pMB17	24	6781	34	-0.514	0.023	-3.297
16qMB53	28	6168	26	1.181	0.765	1.725
17qMB66	30	5870	28	0.192	1.389	-4.074
18pMB7	28	4627	17	0.272	0.147	1.794
18qMB34	30	6175	37	-0.541	-0.579	-10.906
18qMB47	24	5956	19	-0.533	-0.67	1.725
18qMB60	26	6195	27	-0.971	-0.791	-0.382
18qMB67	30	6482	18	-0.466	-0.177	-1.315
18qMB73	16	5163	34	-0.767	-0.904	-1.55
19qMB35	16	5789	12	-0.334	-0.173	-0.333
1pMB101	26	6362	47	-0.152	0.729	-9.231
1pMB4	28	4274	27	-0.314	0.26	-1.249
1pMB81	30	6042	50	0.046	-0.4	6.52
20pMB7	28	6797	26	0.181	-1.232	3.217
21qMB20	28	5875	27	-0.453	-0.294	1.55
21qMB23	30	6005	31	-0.322	0.208	4.809
2pMB3	28	5610	27	-0.937	-0.847	-0.222
2pMB6	24	5972	39	-0.35	0.473	-0.587
2qMB114	28	5919	24	-0.387	-1.47	2.857
2qMB134	28	5959	36	-0.009	0.49	0.381
2qMB143	28	5470	27	-0.135	0.26	3.952
2qMB221	24	6268	25	-0.104	-0.649	1.536
3qMB148	26	6076	23	-0.072	0.008	2.535
4pMB27	28	5996	30	-0.643	0.434	0.857
4pMB31	30	6019	29	-1.428	-1.247	-1.848
4qMB105	28	5887	20	-0.252	0.049	1.693
4qMB157	26	8007	62	-0.534	-1.419	-1.526
4qMB179	20	5912	23	0.453	-0.147	3.021
4qMB181	20	4637	30	-0.485	0.332	2.4
5pMB10	26	6455	35	0.131	-0.18	-1.415
5pMB31	26	6152	18	-0.051	-0.48	0.418
5pMB35	28	6080	28	-0.594	-0.216	-1.735
5pMB4	28	4944	12	-1.596	-1.5	0.085
5qMB113	30	6083	34	-0.642	0.37	-11.651
5qMB123	28	6035	26	-1.207	-2.944	-0.058
5qMB128	28	6787	33	-0.699	-0.356	-8.556
6pMB14	24	7163	44	0.197	1.529	-0.449
6pMB45	8	5921	28	1.392	1.231	-0.143
6qMB164	28	5100	11	0.338	1	0.979
7pMB42	20	6067	14	-1.8	-0.869	-8.516
7pMB8	24	7142	39	-0.193	-0.301	-1.819
7qMB152	24	6008	20	0.513	0.457	2.826
7qMB83	28	6482	22	-0.147	0.539	3.212
8pMB5	26	4759	41	-0.697	-1	0.012
9pMB8	28	5919	51	-0.732	-1.595	6.466
9qMB100	28	6161	30	-0.777	-0.835	1.995

Table 3: Summary statistics for each marker in the Mandenka sample.

	sample size	seq. length (bp)	S	D	D^*	H
10qMB119	26	5523	15	0.341	-0.459	1.674
10qMB127	32	5285	20	-0.313	-0.012	0.577
10qMB128	28	4680	22	-0.521	-1.417	3.36
10qMB85	32	6049	15	0.032	-0.576	0.23
11pMB20	20	5867	25	-1.009	-0.786	1.579
11pMB23	24	6168	43	-0.217	-0.797	1.471
12qMB46	28	6567	19	0.486	0.688	1.561
13qMB107	20	4484	12	1.208	0.657	-3.484
13qMB108	26	5282	18	-0.525	0.268	-1.083
13qMB31	30	5843	25	-0.678	-1.709	-0.543
13qMB64	30	5764	16	-0.912	0.016	-1.333
13qMB67	28	6058	32	-0.25	-1.63	2.81
13qMB69	20	6069	23	-0.24	0.138	-0.368
14qMB85	32	6194	30	-0.569	-1.467	0.137
15qMB35	32	5966	24	0.151	-0.013	1.27
16pMB17	26	6781	34	-0.588	-0.913	-6.338
16qMB53	32	6168	26	-0.557	-0.754	-4.931
17qMB66	32	5870	33	-0.365	-0.441	-4.5
18pMB7	28	4627	27	-0.447	-1.124	2.54
18qMB34	28	6175	35	0.235	0.222	-5.905
18qMB47	26	5956	15	0.268	0.4	1.748
18qMB60	30	6195	18	0.158	-0.177	2.952
18qMB67	28	6482	24	0.314	0.659	3.265
18qMB73	18	5163	39	-0.155	0.41	0.288
19qMB35	28	5789	23	-1.059	-0.658	-5.974
1pMB101	22	6362	49	-0.235	0.682	-9.576
1pMB4	24	4274	36	-0.825	-0.075	0.413
1pMB81	30	6042	58	-0.467	-1.527	7.154
20pMB7	28	6797	24	0.289	-0.253	4.217
21qMB20	30	5875	33	0.112	0.079	4.276
21qMB23	32	6005	26	-0.425	-1.051	2.907
2pMB3	28	5610	32	-0.751	-0.668	0.122
2pMB6	26	5972	30	0.017	0.958	0.197
2qMB114	32	5919	22	-0.443	-0.52	3.081
2qMB134	32	5959	38	-0.101	-0.557	-1.911
2qMB143	32	5470	19	-0.714	1.029	-2.597
2qMB221	32	6268	27	0.143	1.066	0.532
3qMB148	32	6076	24	-0.235	-0.329	2.863
4pMB27	28	5996	20	0.053	-0.654	1.545
4pMB31	32	6019	19	-0.907	-0.864	1.129
4qMB105	28	5887	20	0.259	1.454	3.402
4qMB157	30	8007	43	-1.076	-0.602	-14.4
4qMB179	32	5912	29	-0.802	0.055	1.097
4qMB181	24	4637	24	-0.094	-0.458	1.833
5pMB10	26	6455	35	0.708	0.691	-3.631
5pMB31	28	6152	25	-0.859	-1.936	0.455
5pMB35	28	6080	32	-0.437	-0.908	2.122
5pMB4	26	4944	9	-0.824	-1.017	0.628
5qMB113	32	6083	32	0.585	0.989	-3.581
5qMB123	32	6035	25	-0.374	0.676	2.968
5qMB128	28	6787	37	-0.727	0.534	-8.116
6pMB14	20	7163	44	0.431	0.719	0.947
6pMB45	6	5921	29	-1.213	-0.538	-9.067
6qMB164	28	5100	16	-0.585	-1.204	1.344
7pMB42	28	6067	17	0.27	-1.048	-1.693
7pMB8	28	7142	37	-0.816	0.108	-10.349
7qMB152	30	6008	36	-0.852	-0.203	-0.883
7qMB83	28	6482	26	-0.641	-0.947	2.995
8pMB5	24	4759	30	0.127	0.25	-1.304
9pMB8	32	5919	40	0.321	1.442	7.488
9qMB100	28	6161	29	0.197	-0.143	3.783

Table 4: Posterior probabilities of the different models estimated using the proportion of accepted simulations for each model (rejection algorithm).

	High mutation rate			Low mutation rate		
	San	Biaka	Mandenka	San	Biaka	Mandenka
Null	0.55	0.54	0.48	0.64	0.65	0.56
Bottleneck: founder	0.14	0.16	0.20	0.13	0.15	0.20
Bottleneck: fragmentation	0.31	0.30	0.32	0.22	0.20	0.24

Table 5: Posterior two-sided P-values of the summary statistics. S is the number of SNPs, D is the Tajima's D , D^* is the Fu and Li's D^* , H is the Fay and Wu's H , C is Hudson's C , and "Var" denotes the variance. In the posterior check simulations, the P-values are calculated as the probability of obtaining a summary statistic more extreme (on both sides) than the observed value.

San									
	\bar{S}	\bar{D}	\bar{D}^*	\bar{H}	$VarS$	$VarD$	$VarD^*$	$VarH$	\bar{C}
Null, high mut. rate	0.822	0.327	0.619	0.299	0.014	0.701	0.097	0.484	0.681
Founder, high mut. rate	0.457	0.105	0.935	0.169	0.012	0.264	0.033	0.358	0.802
Fragmentation, high mut. rate	0.382	0.509	0.544	0.241	0.122	0.996	0.198	0.788	0.465
Null, low mut. rate	0.167	0.276	0.678	0.232	0.001	0.826	0.113	0.181	0.901
Founder, low mut. rate	0.541	0.225	0.974	0.150	0.001	0.717	0.484	0.191	0.957
Fragmentation, low mut. rate	0.490	0.170	0.990	0.201	0.001	0.990	0.216	0.190	0.971
Biaka									
	\bar{S}	\bar{D}	\bar{D}^*	\bar{H}	$VarS$	$VarD$	$VarD^*$	$VarH$	\bar{C}
Null, high mut. rate	0.693	0.175	0.862	0.763	0.675	0.252	0.996	0.250	0.975
Founder, high mut. rate	0.863	0.044	0.642	0.994	0.454	0.339	0.766	0.306	0.849
Fragmentation, high mut. rate	0.716	0.067	0.749	0.940	0.600	0.098	0.902	0.339	0.784
Null, low mut. rate	0.791	0.020	0.524	0.963	0.335	0.166	0.921	0.466	0.634
Founder, low mut. rate	0.738	0.031	0.739	0.987	0.279	0.209	0.973	0.441	0.706
Fragmentation, low mut. rate	0.667	0.046	0.626	0.900	0.297	0.306	0.914	0.442	0.744
Mandenka									
	\bar{S}	\bar{D}	\bar{D}^*	\bar{H}	$VarS$	$VarD$	$VarD^*$	$VarH$	\bar{C}
Null, high mut. rate	0.673	0.226	0.908	0.314	0.214	0.025	0.991	0.073	0.929
Founder, high mut. rate	0.302	0.226	0.915	0.599	0.110	0.039	0.843	0.082	0.962
Fragmentation, high mut. rate	0.630	0.495	0.585	0.344	0.152	0.006	0.586	0.184	0.978
Null, low mut. rate	0.423	0.175	0.978	0.337	0.118	0.024	0.866	0.092	0.932
Founder, low mut. rate	0.955	0.044	0.452	0.443	0.220	0.028	0.957	0.059	0.914
Fragmentation, low mut. rate	0.601	0.141	0.846	0.339	0.382	0.014	0.865	0.065	0.712

Table 6: Posterior estimates of the demographic parameters.

Null Model						
	$N_0/10^3$	$N_A/10^3$	$T_g/10^3$			
San (low)	230 (71,913)	33 (31,35)	42 (2,92)			
Biaka (low)	81 (19,730)	32 (29,35)	29 (5,90)			
Mandenka (low)	123 (47,757)	32 (28,35)	38 (7,96)			
San (high)	23 (14,99)	11 (9,14)	46 (9,92)			
Biaka (high)	20 (11,127)	12 (9,13)	55 (9,98)			
Mandenka (high)	22 (11,214)	12 (10,15)	31 (6,92)			

Founder model					
	$N_0/10^3$	$T_{dur}/10^3$	$-b$	$N_A/10^3$	$T_g/10^3$
San (low)	159 (48,554)	43 (40,46)	0.11 (0.01,0.41)	33 (32,34)	25 (2,88)
Biaka (low)	108 (31,713)	31 (21,53)	0.13 (0.00,0.44)	32 (30,35)	36 (5,96)
Mandenka (low)	77 (24,523)	37 (20,59)	0.10 (0.00,0.60)	31 (29,34)	31 (2,93)
San (high)	51 (24,211)	28 (21,52)	0.09 (0.00,0.33)	13 (9,18)	15 (4,55)
Biaka (high)	15 (10,91)	33 (20,56)	0.06 (0.00,0.54)	13 (10,15)	63 (3,100)
Mandenka (high)	23 (11,195)	43 (21,59)	0.11 (0.00,0.97)	13 (11,16)	46 (3,99)

Fragmentation model						
	$N_0/10^3$	$T_{dur}/10^3$	$-b$	$N_A/10^3$	$T_g/10^3$	n
San (low)	206 (18,1022)	38 (22,56)	0.14 (0.01,0.57)	33 (30,34)	46 (2,93)	5 (2,9)
Biaka (low)	107 (20,793)	39 (24,54)	0.08 (0.01,0.21)	32 (30,34)	32 (2,100)	6 (2,10)
Mandenka (low)	99 (32,674)	32 (20,59)	0.06 (0.00,0.47)	28 (25,33)	38 (8,96)	5 (2,9)
San (high)	23 (11,231)	38 (21,59)	0.08 (0.00,0.86)	10 (7,14)	47 (5,97)	7 (2,9)
Biaka (high)	18 (9,250)	37 (21,58)	0.23 (0.00,1.31)	12 (9,15)	44 (1,100)	8 (3,10)
Mandenka (high)	25 (20,44)	39 (20,59)	0.12 (0.02,0.84)	12 (9,15)	38 (10,93)	7(2,10)

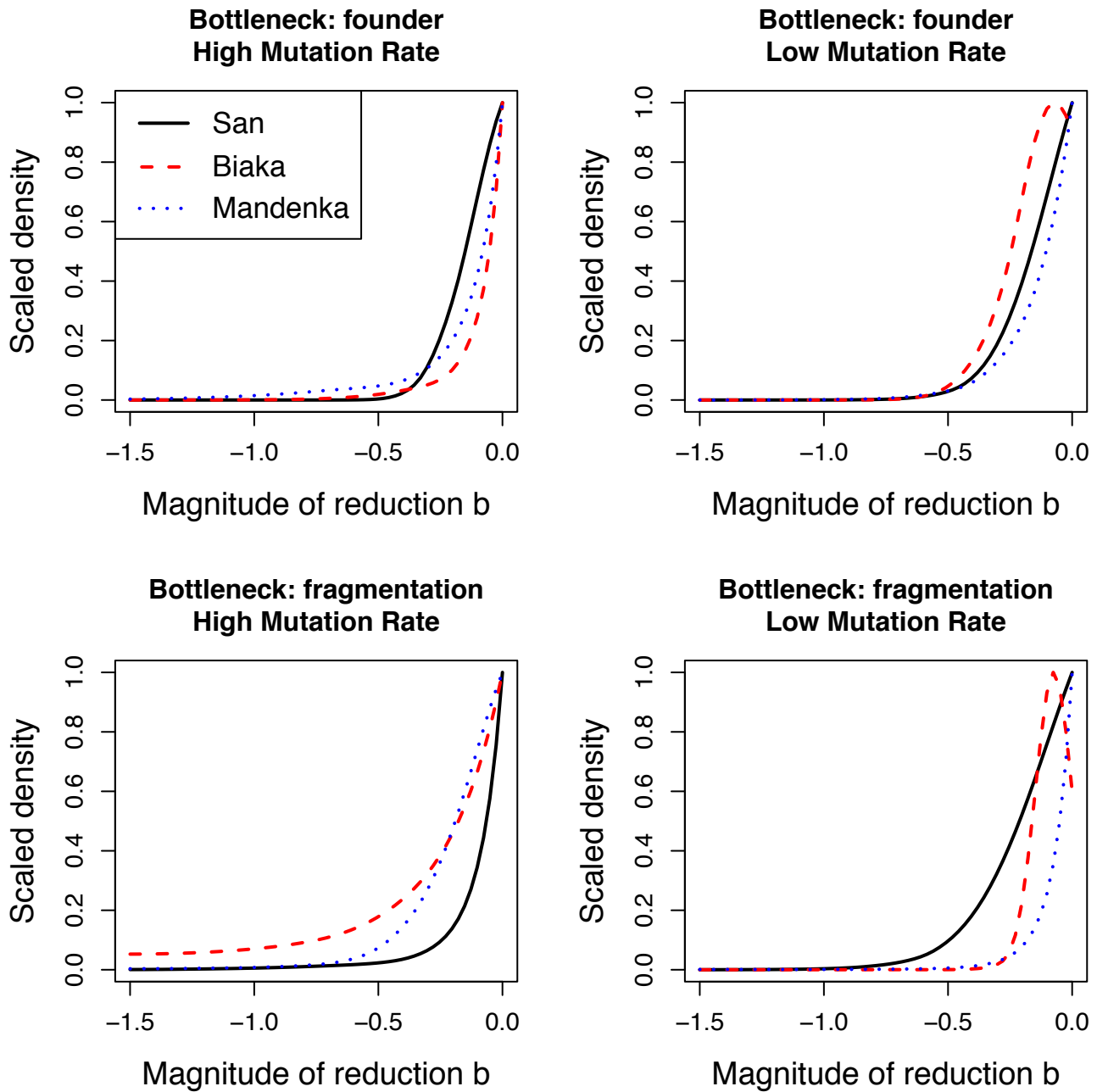


Figure 1: Posterior distributions of the intensity b of the bottleneck for the two bottleneck models and the two mutation rates. The population size N_B during the bottleneck is given by $N_B = N_A \times 10^b$ where N_A is the population size before the bottleneck. There is a 30 fold reduction of population size when $b = -1.5$, a 3 fold reduction of population size when $b = -0.5$ and no reduction in size when $b = 0$.

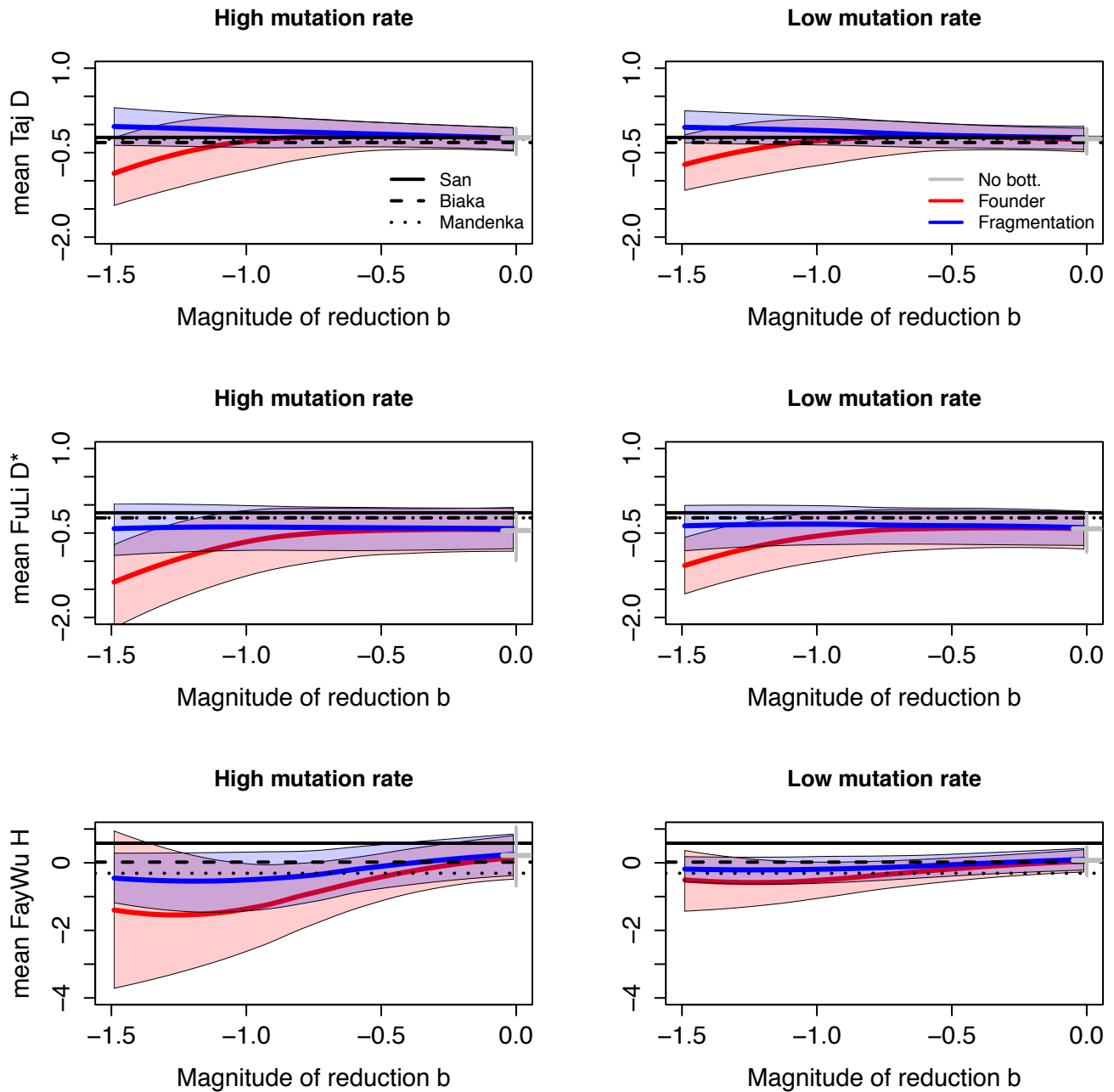


Figure 2: Expected values of the mean (over the 61 loci) Tajima D , Fu and Li D^* , and Fay and Wu's H as functions of the bottleneck intensity. The colored lines represent the expected values and the colored envelopes show the approximate 95% C.I. estimated from non-linear regression. Specifically, the C.I. range from $m(b) - 2\sigma_-(b)$ to $m(b) + 2\sigma_+(b)$ where $\sigma_-(b)$ and $\sigma_+(b)$ are nonlinear estimates of the standard deviation of the negative and positive residuals. The plain, dashed and dotted black horizontal lines correspond to the summary statistics computed for the San, Biaka, and Mandenka samples.

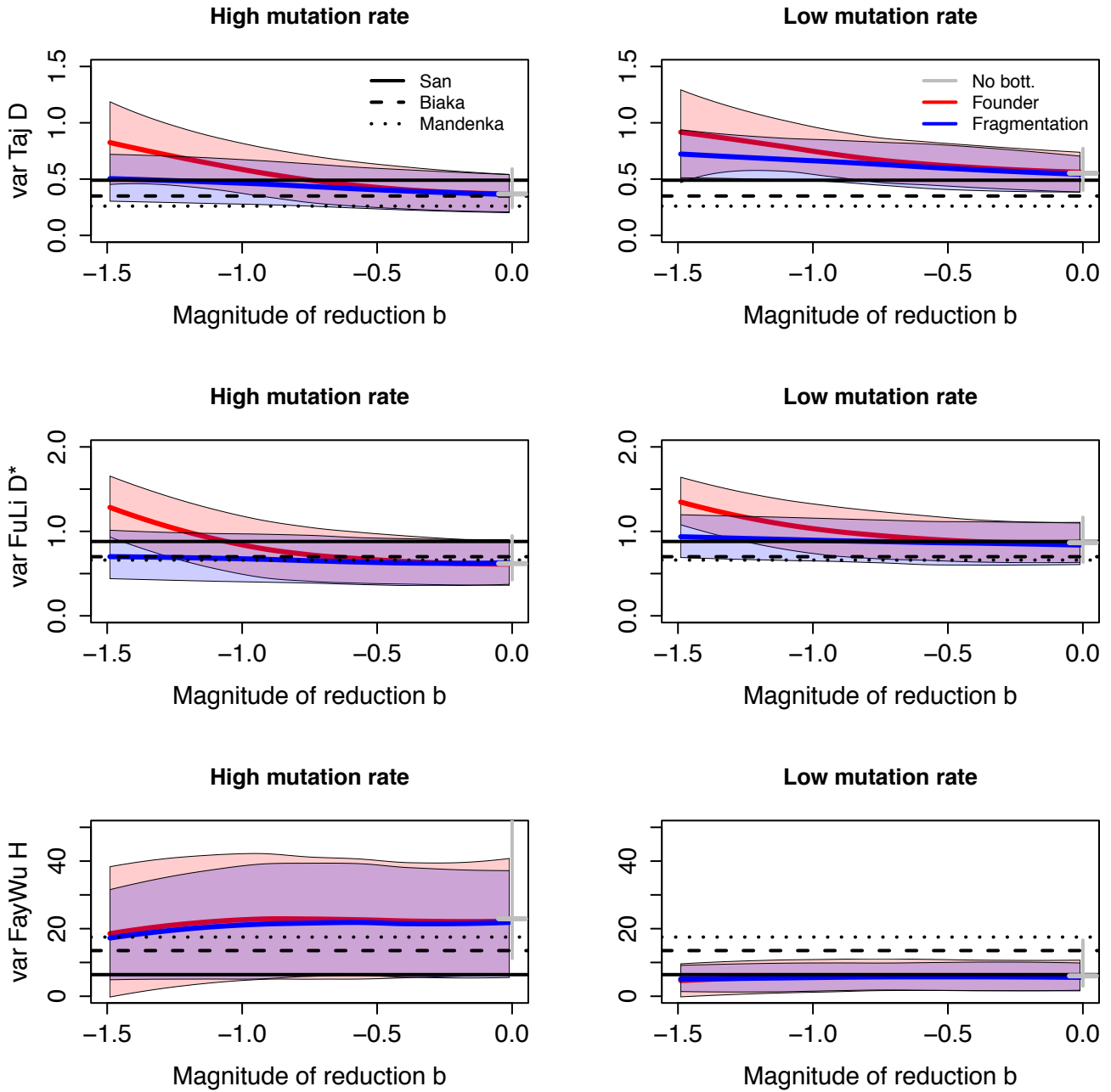


Figure 3: Expected values of the variance (over the 61 loci) of Tajima D , Fu and Li D^* , and Fay and Wu's H as functions of the bottleneck intensity. The colored lines represent the expected values and the colored envelopes show the approximate 95% C.I. estimated from non-linear regression. Specifically, the C.I. range from $m(b) - 2\sigma_-(b)$ to $m(b) + 2\sigma_+(b)$ where $\sigma_-(b)$ and $\sigma_+(b)$ are nonlinear estimates of the standard deviation of the negative and positive residuals. The plain, dashed and dotted black horizontal lines correspond to the summary statistics computed for the San, Biaka, and Mandenka samples.

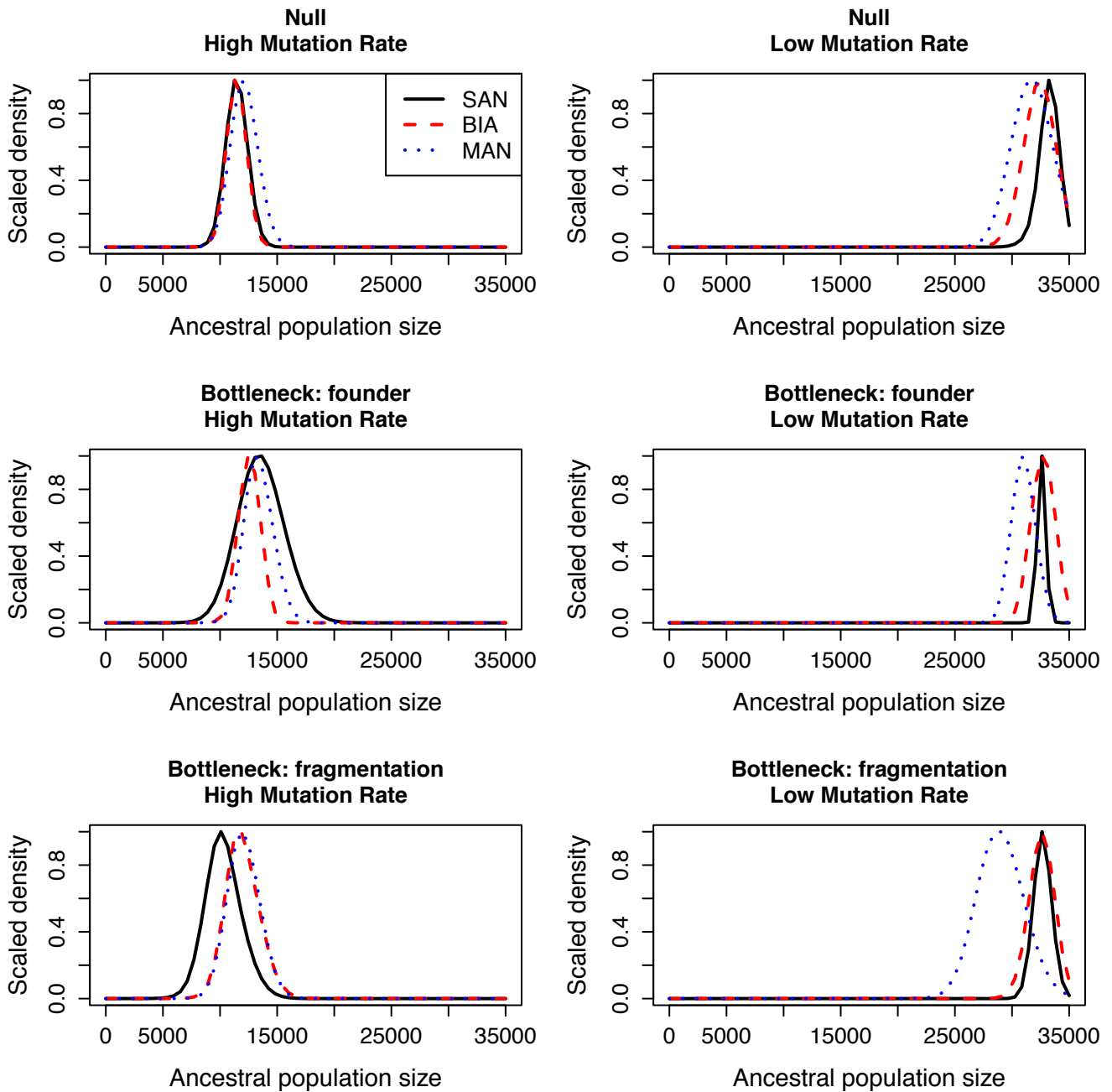


Figure 4: Posterior distribution of the ancestral effective population size N_A .

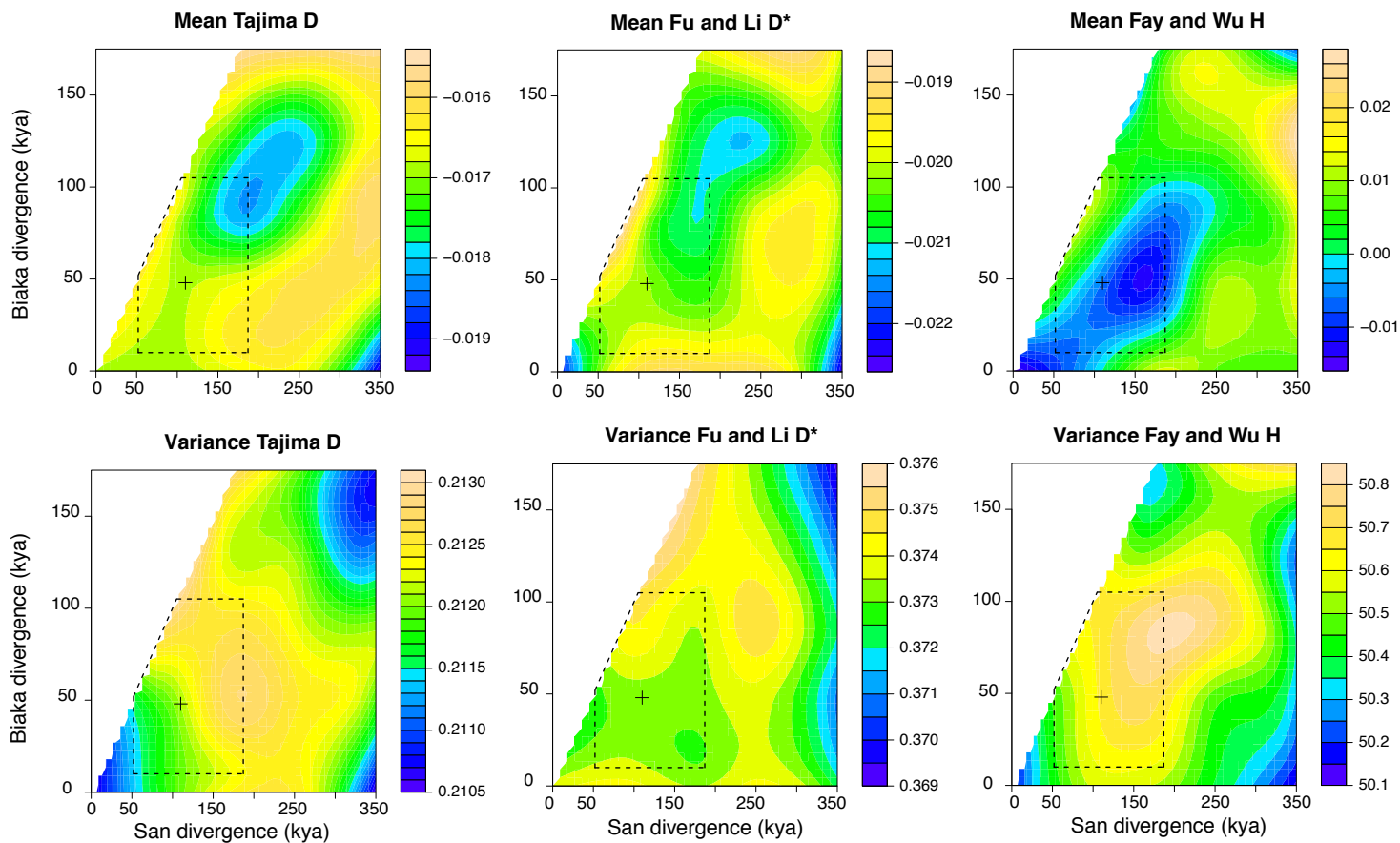


Figure 5: Values of the population-wise summary statistics as a function of the Biaka and San divergence times. The cross corresponds to the point estimate provided by Veeramah et al. (2011) and the dashed lines correspond to their 95% credibility intervals. The simulations of the divergence model were performed assuming a constant effective population size of $N = 14000$ individuals and a mutation rate of $\mu = 2.5 \times 10^{-8}$ /bp/generation.