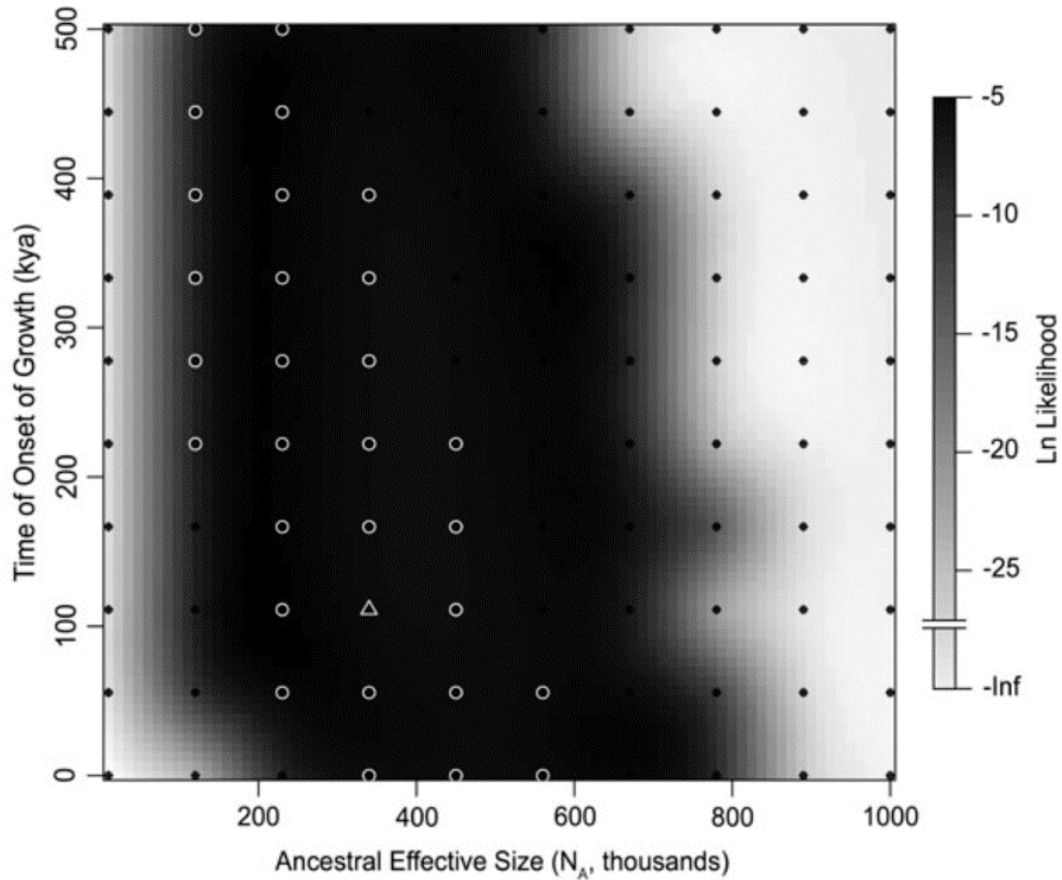


Additional file 1. Log-likelihood surface (N_A versus τ) for the haploid mtDNA control region. Black and white points indicate the grid of sampling locations. Log-likelihoods at these points are known with certainty, whereas log-likelihoods in the intervening space are interpolated. Regions of the parameter space with highest likelihood are shaded black. Only highlighted white points (circles and triangles) fall within the 95% confidence interval. The maximum likelihood estimate (MLE) is indicated by a white triangle. N_0 was set to its value for the MLE.

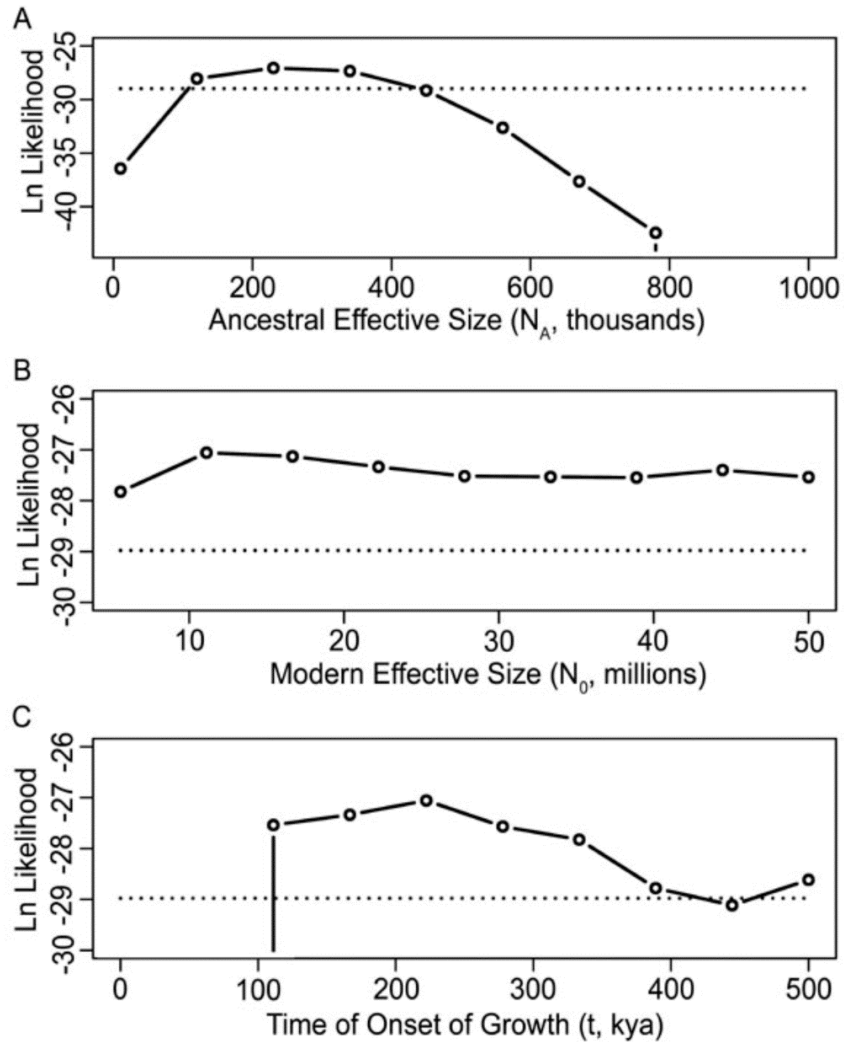


Additional file 2. Log-likelihood surface (N_A versus τ) for the autosomal *RAG2*

locus. Black and white points indicate the grid of sampling locations. Log-likelihoods at these points are known with certainty, whereas log-likelihoods in the intervening space are interpolated. Regions of the parameter space with highest likelihood are shaded black. Only highlighted white points (circles and triangles) fall within the 95% confidence interval. The maximum likelihood estimate (MLE) is indicated by a white triangle. N_0 was set to its value for the MLE.

Additional file 3. Grid points forming the 95% Confidence Interval of the three-dimensional parameter space ranked by likelihood value. The Maximum Likelihood estimate (MLE) is shown in bolded italics, and points within the 95% confidence area that are plotted in Fig. 2 are highlighted.

N_A	N_0	τ (years)	$L^*(\lambda)$	N_A	N_0	τ (years)	$L^*(\lambda)$
230,000	11,118,889	222,223	-27.06	120,000	5,564,444	444,445	-29.11
230,000	16,673,333	222,223	-27.13	120,000	11,118,889	388,889	-29.15
340,000	22,227,778	166,667	-27.34	450,000	50,000,000	111,112	-29.16
230,000	44,445,556	166,667	-27.40	230,000	11,118,889	333,334	-29.21
230,000	22,227,778	166,667	-27.48	120,000	11,118,889	277,778	-29.24
230,000	27,782,222	166,667	-27.52	340,000	16,673,333	222,223	-29.25
230,000	33,336,667	166,667	-27.53	120,000	22,227,778	277,778	-29.35
340,000	50,000,000	111,112	-27.54	340,000	50,000,000	166,667	-29.45
230,000	38,891,111	166,667	-27.55	230,000	16,673,333	277,778	-29.62
230,000	11,118,889	277,778	-27.57	450,000	44,445,556	111,112	-29.67
340,000	16,673,333	166,667	-27.71	450,000	38,891,111	111,112	-29.71
340,000	27,782,222	166,667	-27.74	230,000	5,564,444	444,445	-29.83
340,000	33,336,667	166,667	-27.82	450,000	27,782,222	111,112	-29.86
230,000	5,564,444	333,334	-27.82	450,000	33,336,667	111,112	-29.95
230,000	27,782,222	222,223	-27.91	120,000	22,227,778	222,223	-30.03
230,000	50,000,000	166,667	-27.92	120,000	27,782,222	222,223	-30.04
120,000	11,118,889	333,334	-28.05	120,000	5,564,444	388,889	-30.19
340,000	11,118,889	222,223	-28.10	340,000	22,227,778	222,223	-30.22
340,000	38,891,111	111,112	-28.13	120,000	5,564,444	333,334	-30.23
340,000	38,891,111	166,667	-28.26	120,000	38,891,111	222,223	-30.26
340,000	11,118,889	166,667	-28.28	120,000	33,336,667	277,778	-30.30
230,000	16,673,333	166,667	-28.30	450,000	11,118,889	166,667	-30.31
230,000	22,227,778	222,223	-28.32	340,000	5,564,444	333,334	-30.35
340,000	44,445,556	166,667	-28.37	450,000	16,673,333	166,667	-30.47
340,000	5,564,444	277,778	-28.54	120,000	16,673,333	222,223	-30.48
120,000	5,564,444	500,000	-28.62	120,000	33,336,667	222,223	-30.55
230,000	5,564,444	277,778	-28.65	340,000	11,118,889	277,778	-30.62
340,000	44,445,556	111,112	-28.70	450,000	22,227,778	111,112	-30.63
230,000	5,564,444	388,889	-28.78	230,000	5,564,444	500,000	-30.90
120,000	16,673,333	277,778	-28.86	340,000	27,782,222	222,223	-30.91
230,000	11,118,889	166,667	-29.06	450,000	22,227,778	166,667	-30.93
340,000	33,336,667	111,112	-29.08				



Additional file 4. Profile likelihood curves drawn from the combined likelihood surface for the haploid mtDNA control region and autosomal *RAG2* locus. Dotted lines indicate the 95% confidence interval. Note that there is little power to infer modern effective sizes, and that an onset of growth for all times less than ~100 kya is statistically unlikely.