

Supplemental tables

Table S1: Human populations used in analyses, with the geographic locations that were used.

Population	latitude	longitude
IDMT (Mentawai) ¹	0.3S	98.4E
IDJV (Javanese) ¹	7.3S	110.4E
IDSB (Kambera) ¹	9.8S	120.0E
IDSO (Manggarai) ¹	8.6S	120.1E
IDRA (Manggarai) ¹	8.7S	120.5E
IDLA (Lamaholot) ¹	8.3S	123.0E
IDLE (Lembata) ¹	8.3S	124.6E
IDAL (Alorese) ¹	8.3S	124.7E
Papuan ²	4.0S	143.0E
Mongola ³	48.0N	119.0E
Hazara ³	33.0N	69.5E
Turkish ³	39.0N	35.2E
Uygur ³	44.0N	81.0E
Uzbekistani ³	41.4N	64.6E
Kashmiri Pandit ⁴	34.22N	75.5E
Pathan ²	32.35N	69.72E
Kshatriya ⁵	27.56N	78.65E
Kanjar ⁵	26.45N	80.32E
Brahmin (UP) ⁵	26.02N	83.18E
Brahmin ⁴	25.45N	82.41E
Kshatriya (UP) ⁵	24.45N	82.41E
Kshatriya ⁴	27.56N	78.65E
Dharkar ⁵	25.44N	83.10E
Chamar ⁵	25.37N	83.04E
Sindhi ²	24.27N	68.70E
Bhil ⁴	23.02N	72.40E
Madiga ⁴	17.58N	79.35E
Mala ⁴	17.22N	78.29E
Velama ⁵	17.05N	79.27E
Vysya ⁴	14.41N	77.39E
Kallar ⁵	10.99N	78.22E

¹ THE HUGO PAN-ASIAN SNP CON-SORTIUM (2009);

² LI *et al.* (2008);

³ HELLENTHAL *et al.* (2014);

⁴ METSPALU and ROMERO (2011);

⁵ MOORJANI *et al.* (2013)

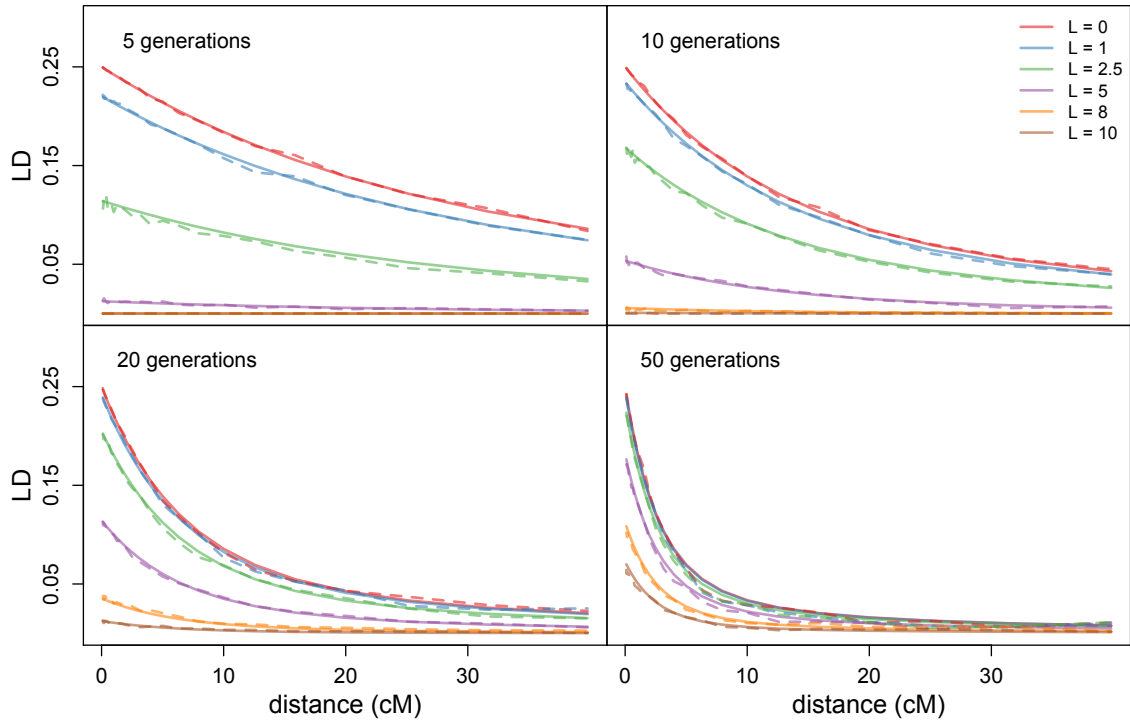
Table S2: Estimated parameters, under the exponential model (Eq. 11) for the Indonesian populations used in our analysis (sum of squares fit). Here, each population has been fit independently

Population	% Asian	Timing	Constant(Multiplicative)	Constant (Additive)	\mathcal{L}
IDAL	44.4	29.1	3.01e-04	2.47e-06	13732.60
IDJV	99.8	665.2	2.68e-2	5.80e-29	12138.46
IDLA	61.6	60.9	7.85e-04	2.016e-08	12505.03
IDLE	58.6	40.7	5.18e-04	6.22e-07	14097.24
IDRA	77.5	106.0	1.45e-03	2.80e-07	11188.83
IDSB	78.7	94.9	1.22e-03	8.16e-13	14042.64
IDSO	66.7	33.5	4.57e-04	5.81e-06	16442.91

Table S3: Estimated parameters, under the exponential model (Eq. 11) for the Central Asian populations used in our analysis (sum of squares fit). Here, each population has been fit independently

Population	% Mongola	Timing (gens)	Constant (Mult.)	Constant (Add.)	\mathcal{L}
Hazara	55.0	25	3.8e-04	1.7e-05	347.1
Turkey	2.2	30	1.2e-04	1.8e-06	436.6
Uygur	55.2	24	3.3e-04	2.3e-05	509.8
Uzbekistan	42.3	20	3.1e-04	2.8e-05	393.5

Figure S1: LD decay curves for populations of increasing distance L from zone and increasing age of contact zone. Solid lines represent analytic predictions and dotted lines represent the output of simulations *under the model* as described in the methods.



Supplemental figures

Figure S2: Exponential fits (Eq. 11) to ancestry-LD in populations sampled at locations (L) from a 50-generation old contact zone. Solid lines represent predicted LD under our contact zone model, and dashed lines the best exponential fit. The estimated timing for each population is shown in parentheses.

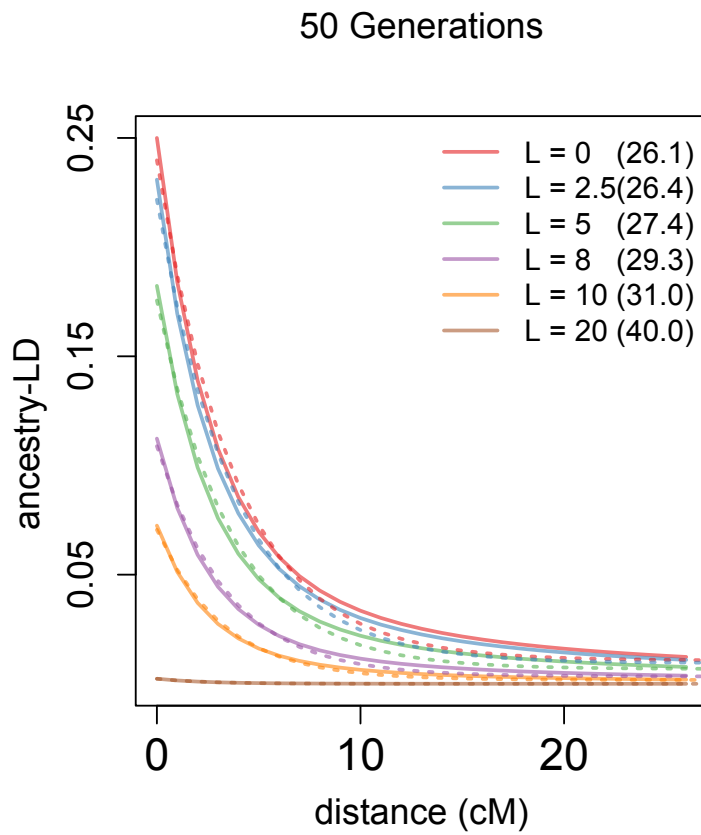


Figure S3: Fits to decay for all Indonesian populations used in analysis, described in Table S1 using the best fit parameters as described in the main text. Grey points are estimates generated by ALDER, and black curves are expected LD under the estimated parameters.

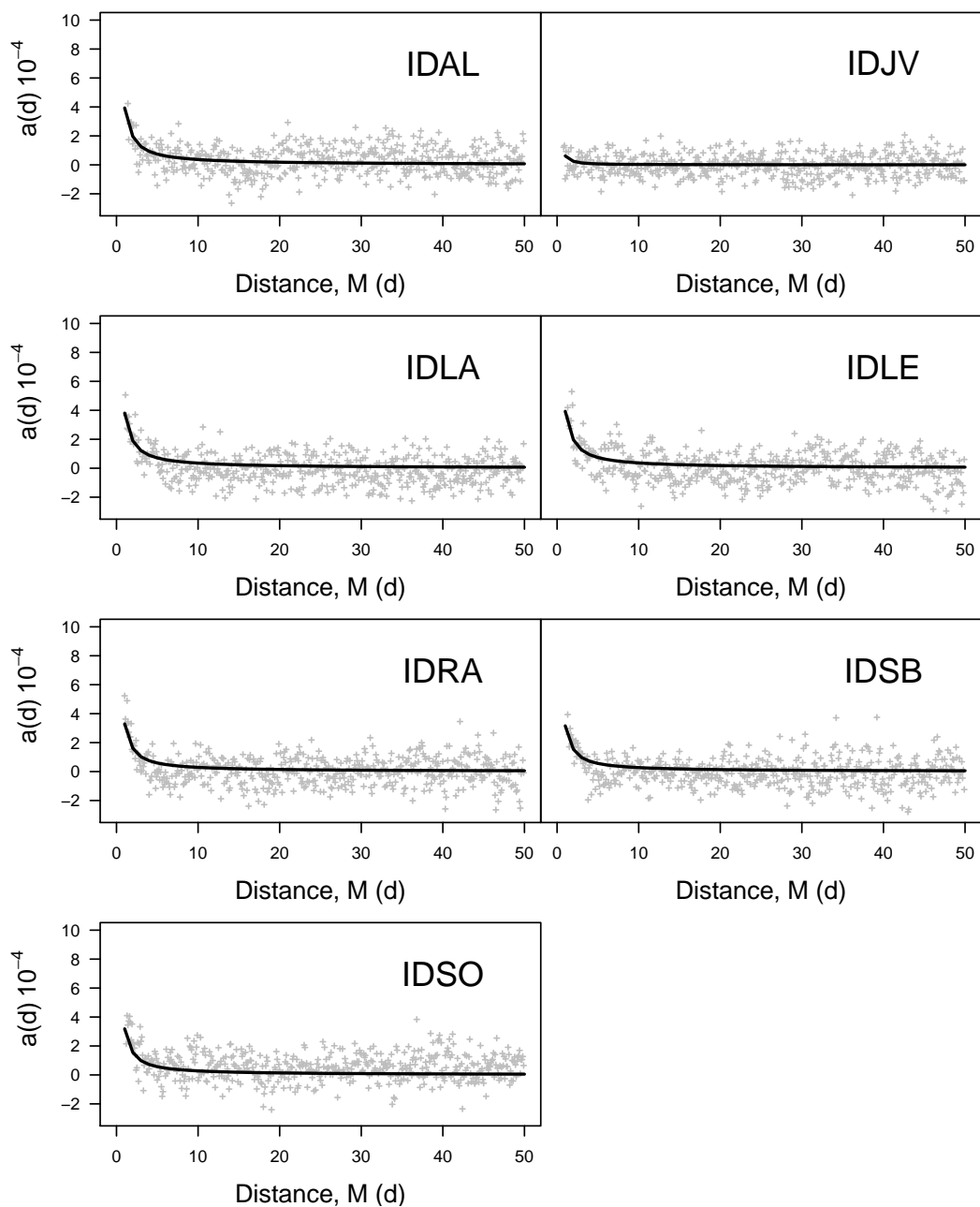


Figure S4: Fits to decay for all Indian populations used in analysis, described in Table S1 using the best fit parameters as described in the main text. Grey points are estimates generated by ALDER, and black curves are expected LD under the estimated parameters. Blue names indicate Indo-European populations, and red labels Dravidian.

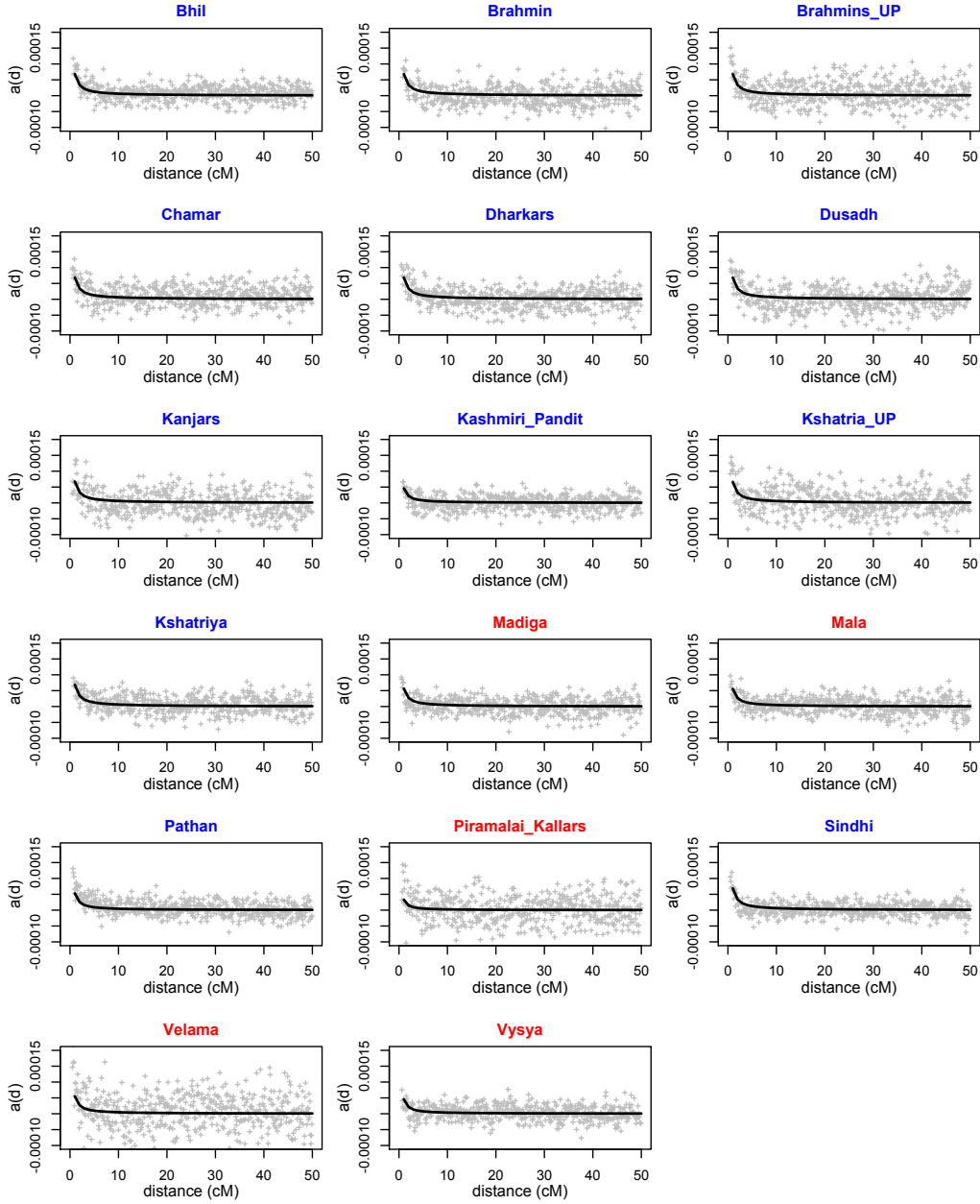


Figure S5: Profile likelihood surfaces for fits to the Indo-European and Dravidian subsets of the population. Blue asterisk indicates parameters giving best fit.

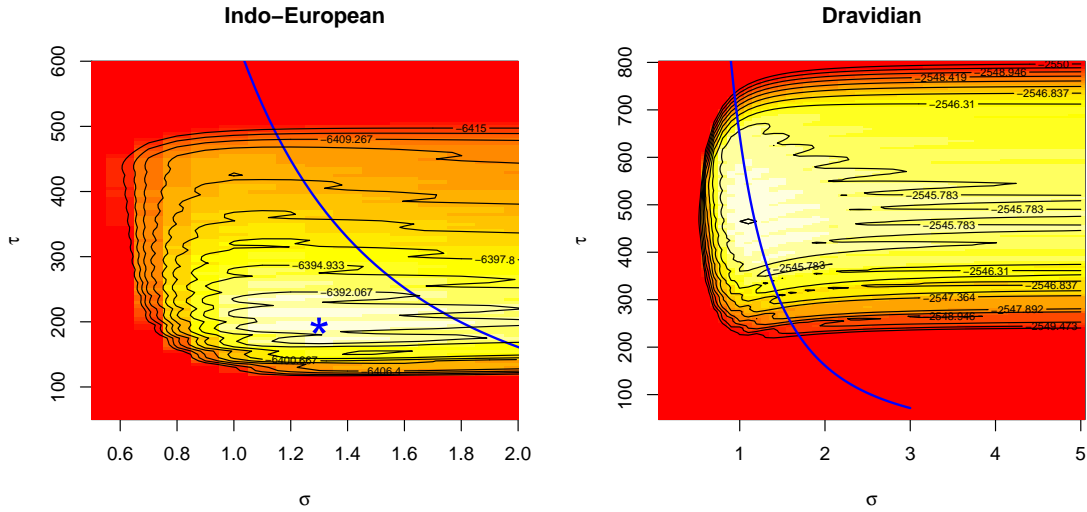


Figure S6: Best-fit curves for each population when fit is made to the set of three Asian populations used in our analysis (Hazara omitted). Grey points are estimates generated by ALDER, and black curves are expected LD under the estimated parameters.

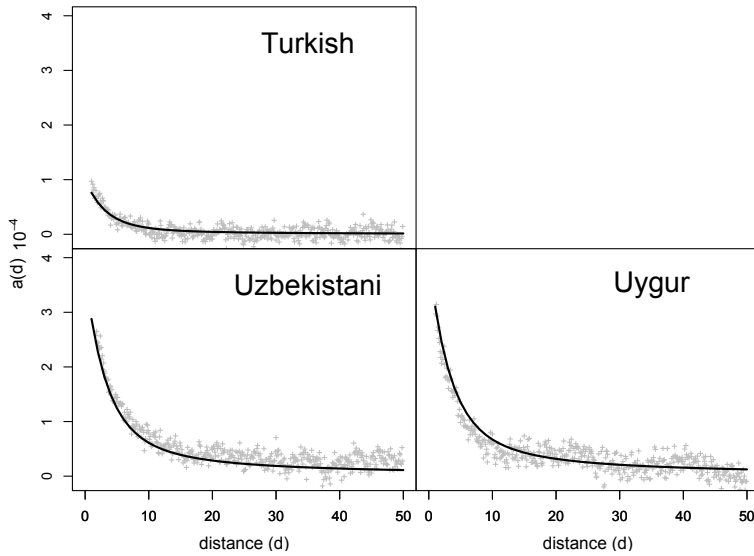


Figure S7: Best-fit curves for each population when the fit is made to the set of the four Central Asian populations used in our analysis. Grey points are estimates generated by ALDER, and black curves are expected LD under the estimated parameters.

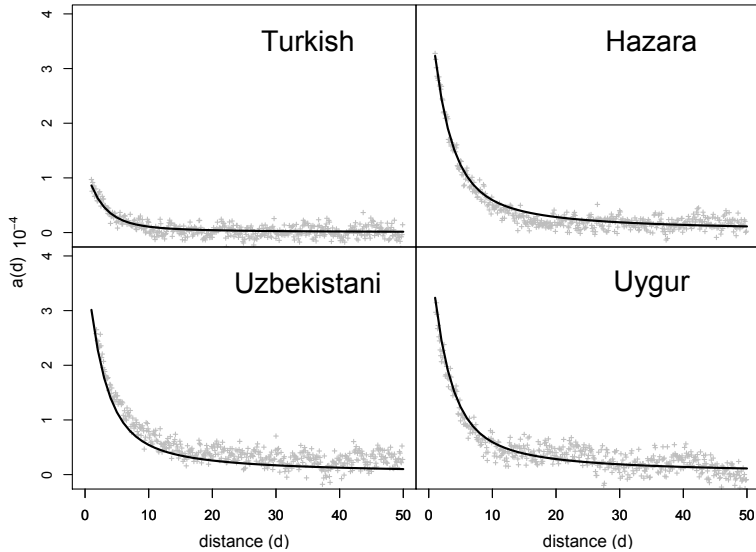
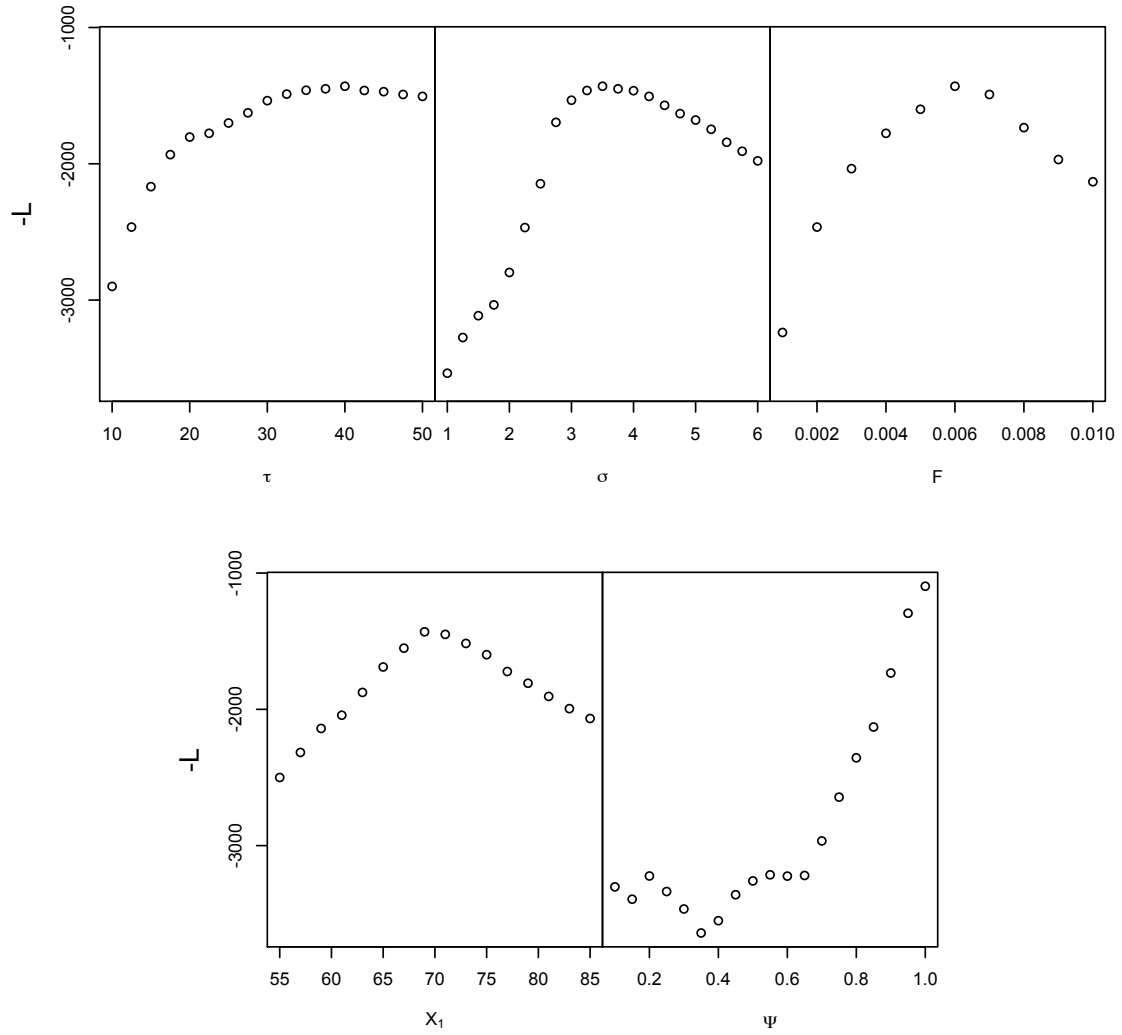


Figure S8: Profile likelihood curves for the five parameters fitted to the Central Asian populations under the invasion-pulse model, showing that the best fit is to a model with cline center at approximately $67^\circ E$ and $\Psi = 1$. This is roughly equivalent to the original model of secondary contact.



References

- HELLENTHAL, G., G. B. J. BUSBY, G. BAND, J. F. WILSON, C. CAPELLI, D. FALUSH, and S. MYERS, 2014 A genetic atlas of human admixture history. *Science* **343**: 747–51.
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