

Table S2. Akaike Information Criterion (AIC) scores for fitted clines under different models using the R package HZAR (Derryberry et al. 2014) for the individual transects. Bold values in blue indicate the best-fit model from the 15-model comparison. Q is the proportion of ancestry estimated by STRUCTURE based on microsatellite loci. Values for Q and mtDNA of the Italian transect are from Schultze et al. (2020).

	Rhine transect			Alpine transect			Italian transect		
	AIC (Q)	AIC (mtDNA)	AIC (morphology)	AIC (Q)	AIC (mtDNA)	AIC (morphology)	AIC (Q)	AIC (mtDNA)	AIC (morphology)
Null model	43.82	61.26	145.91	58.78	75.98	126.69	45.97	47.08	189.6
Model 1	8.86	9.54	6.97	8.68	19.42	8.54	7.81	7.38	38.40
Model 2	7.91	n/a	n/a	7.85	n/a	n/a	6.79	n/a	n/a
Model 3	12.16	13.20	11.69	11.69	24.17	11.24	11.19	12.12	42.20
Model 4	17.24	17.75	15.57	16.28	27.15	15.21	14.79	14.38	46.14
Model 5	16.77	n/a	n/a	16.12	n/a	n/a	14.92	n/a	n/a
Model 6	22.90	24.70	20.85	20.88	33.10	20.74	20.99	21.96	50.78
Model 7	n/a	n/a	n/a	n/a	n/a	n/a	11.97	9.41	n/a
Model 8	12.55	14.23	11.20	11.96	23.69	10.83	9.51	n/a	42.02
Model 9	17.44	18.84	16.41	16.17	28.52	16.11	14.93	17.16	46.41
Model 10	12.63	12.54	11.19	11.93	23.69	12.83	11.68	11.96	42.44
Model 11	11.71	n/a	n/a	11.69	n/a	n/a	11.22	n/a	n/a
Model 12	17.22	18.57	15.98	16.21	28.43	15.91	16.06	17.18	46.25
Model 13	12.32	14.23	11.19	11.99	23.69	11.10	9.99	11.30	42.34
Model 14	12.36	n/a	n/a	11.69	n/a	n/a	10.00	n/a	n/a
Model 15	17.42	18.43	16.12	16.01	28.61	15.77	15.05	17.18	46.28