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Maternal variability of Croatian Spotted goat (*Capra hircus*)

*Ivana Drzaic, Ino Curik, Dinko Novosel, Vlatka Cubric-Curik**

Department of Animal Science, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia

Supplementary Online Material (SOM)

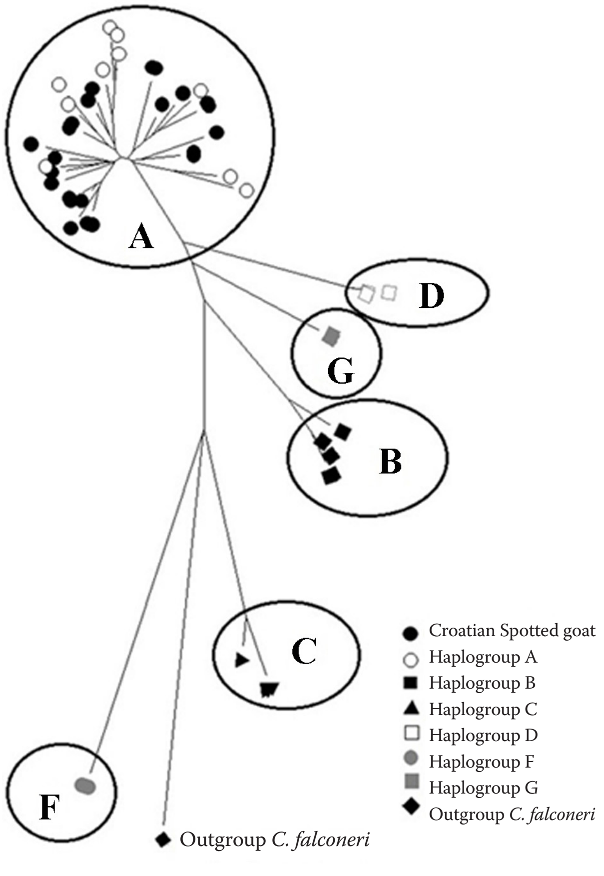

Figure S1. Neighbour-joining tree of goat mtDNA control region sequences. The 28 reference mtDNA haplotypes (480 bp sequences) were used to identify six maternal lineages (A, B, C, D, F and G)

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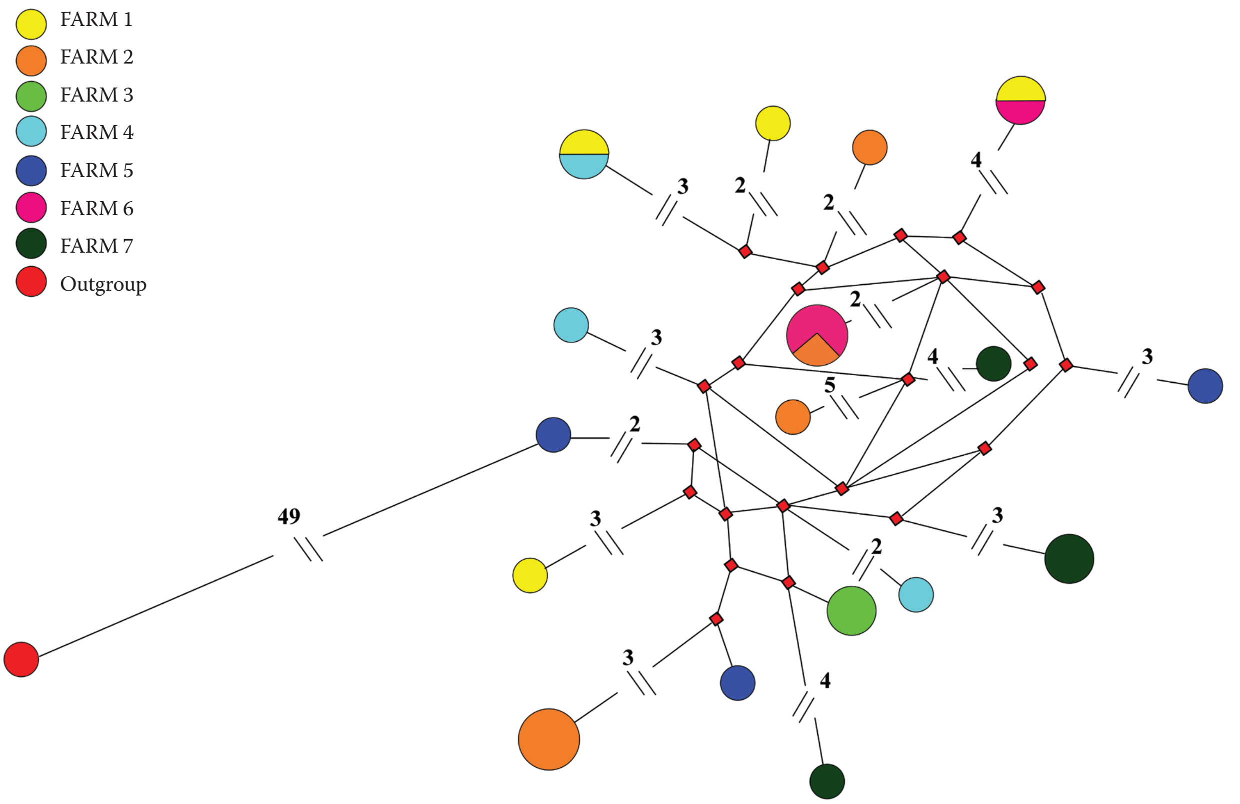

Figure S2. Median joining network of 17 haplotypes (660 bp sequences) in 25 Croatian Spotted goats. Circle size represents the number of individuals included in haplotype

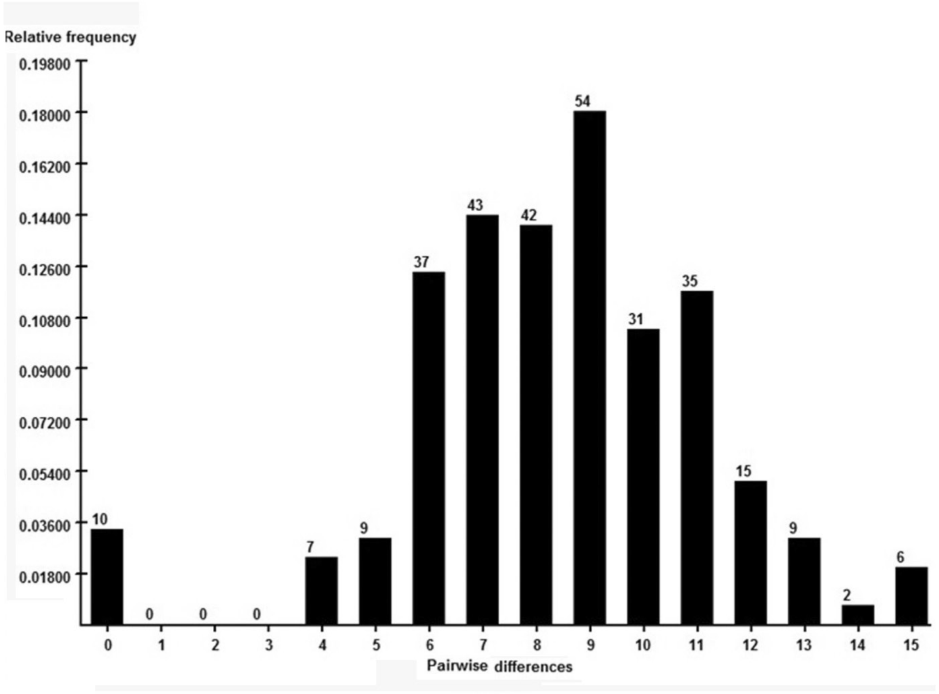

Figure S3. Mismatch distribution of mtDNA haplotypes in Croatian Spotted goats (660 bp sequences)

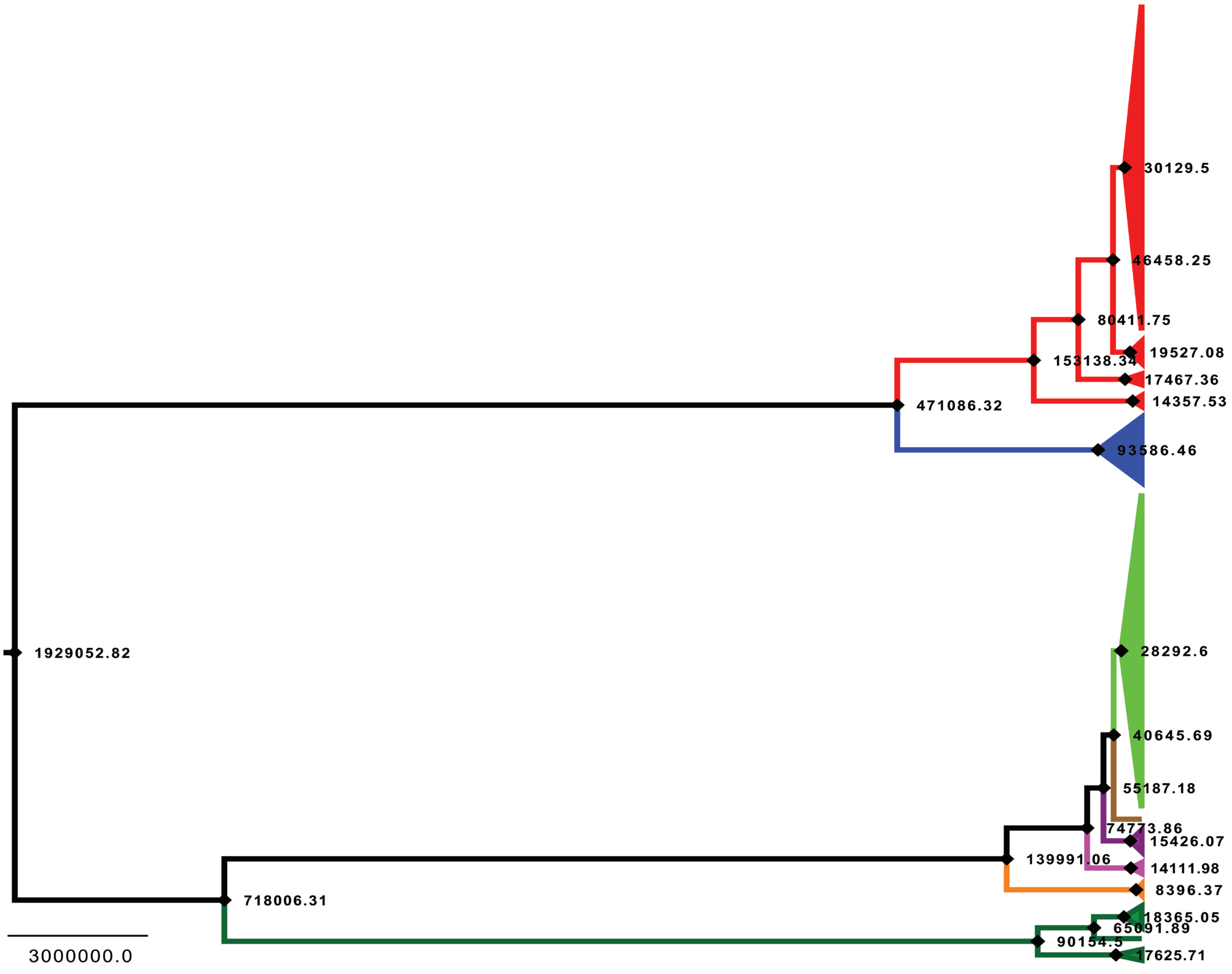

Figure S4. Calibrated phylogenetic tree. Genus *Bos* (Taurine, Aurochses, Romagnola and Indicine cattle) is presented in red colour, genus *Bison* is presented in blue colour, genus *Ovis* is presented in green colour. Goat haplogroup A is presented in light green colour, goat haplogroup C is presented in brown, goat haplogroup D is presented in purple, goat haplogroup B is presented in orange, goat haplogroup G is presented in light purple.

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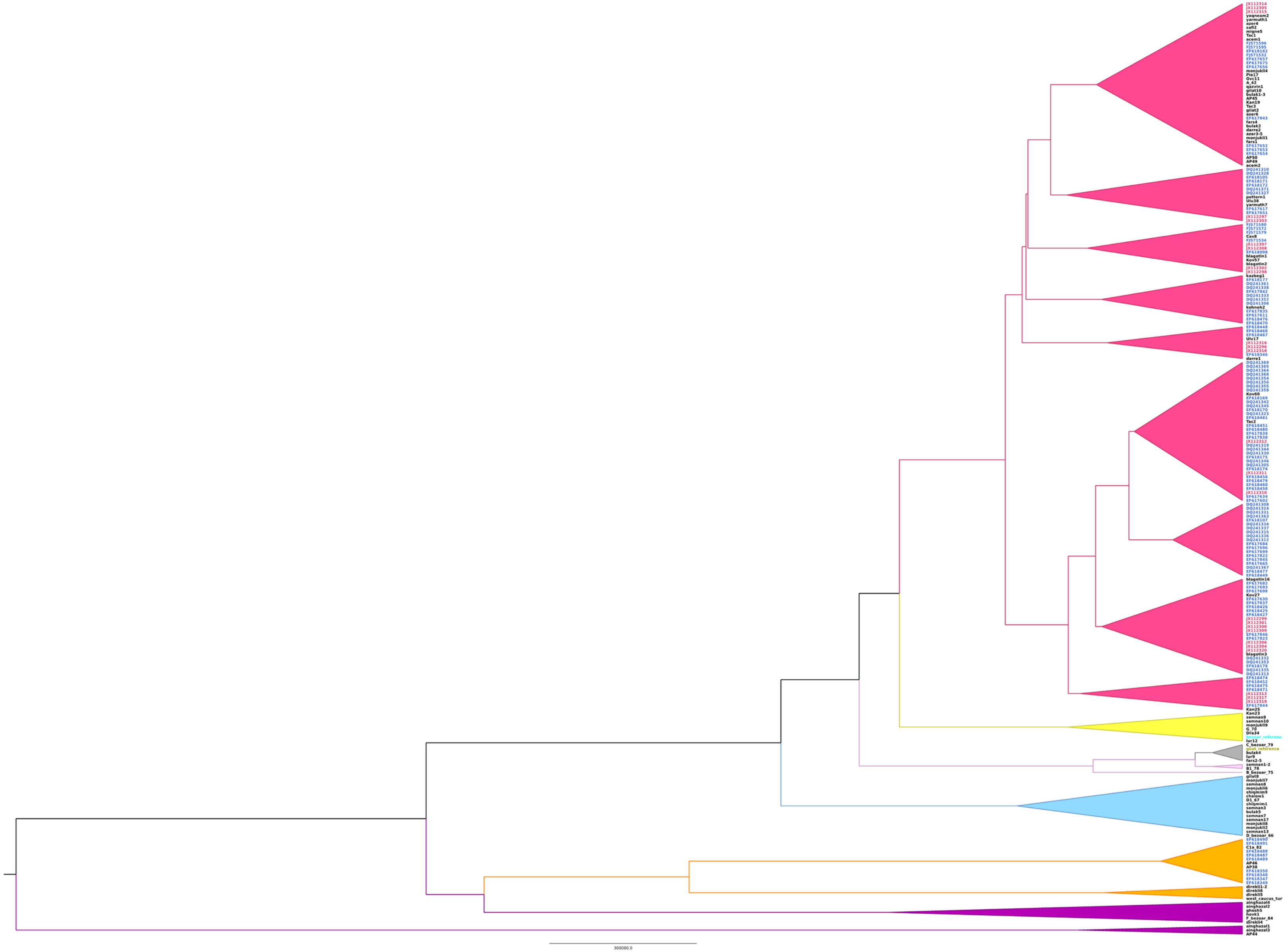

Figure S5. Most common ancestor tree with 85 ancient goat sequences and 152 recent goat sequences. Taxa names of Croatian samples are presented in red colour, taxa names of ancient samples are presented in black colour and taxa names of recent samples from Mediterranean countries are presented in blue colour. Bezoar reference sequence taxa name is presented in turquoise and goat reference sequence taxa name is in yellow. Clades coloured in red represent A haplogroup, clades in yellow represent G haplogroup, clades in grey represent C haplogroup, clades in light pink represent B haplogroup, clades in blue represent D haplogroup, clades in orange represent C1 haplogroup, clades in purple present F haplogroup

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Table S1. AMOVA parameters for goat breeds analyzed in the present study

Country	Breed	Source	*n*	No. of haplotypes	HD ± SD	ND ± SD	Fu's Fs	Tajima's D
Croatia	Croatian Spotted	this study	25	17	0.967 ± 0.019	0.02156 ± 0.002125	–4,403	–0,55107
Italy	Arbi	Vacca et al. 2010	10	9	0.978 ± 0.054	0.02090 ± 0.00214	–1.715	–1.06523
	Argeteta dell' Etna	Naderi et al. 2007	14	13	0.989 ± 0.031	0.01316 ± 0.00159	–6.634	–1.02223
	Bionda dell' Adamello	Naderi et al. 2007	15	15	1.000 ± 0.024	0.01989 ± 0.00177	–7.933	0.01658
	Camoscata alpina	Naderi et al. 2007	11	9	0.945 ± 0.066	0.01791 ± 0.00243	–1.352	–1.13618
	Derivata di Siria	Sardina e al. 2006	9	5	0.806 ± 0.120	0.01338 ± 0.00223	1.720	0.23031
	Grigia Molisana	Naderi et al. 2007	12	9	0.939 ± 0.058	0.01749 ± 0.00180	–0.858	–0.44048
	Girgentana	Sardina et al. 2006	54	22	0.952 ± 0.011	0.02176 ± 0.00427	–1.304	–1.17691
	Maltese	Vacca et al. 2010; Sardina et al. 2006	20	13	0.942 ± 0.034	0.01616 ± 0.00148	–2.014	–0.79269
	Orobica	Naderi et al. 2007	8	7	0.964 ± 0.077	0.01037 ± 0.00220	–0.674	0.03431
	Sarda	Vacca et al. 2010	33	27	0.987 ± 0.011	0.02346 ± 0.00132	–11.341	–0.63250
	Valdostana	Naderi et al. 2007	15	14	0.990 ± 0.028	0.02219 ± 0.00130	–4.891	–0.89016
Albania	Capore	Naderi et al. 2007	15	14	0.990 ± 0.028	0.01726 ± 0.00203	–6.155	–1.20779
	Dukati	Naderi et al. 2007	13	13	1.00 ± 0.030	0.02004 ± 0.00150	–6.118	–0.60280
	Hasi	Naderi et al. 2007	14	13	0.989 ± 0.031	0.01616 ± 0.00143	–5.562	–0.90104
	Mati	Naderi et al. 2007	11	10	0.982 ± 0.046	0.01771 ± 0.00207	–2.823	–1.06931
	Liqenasi	Naderi et al. 2007	12	6	0.864 ± 0.064	0.01942 ± 0.00162	2.739	–0.02343
	Muzhake	Naderi et al. 2007	12	12	1.00 ± 0.034	0.01702 ± 0.06166	–5.943	–0.94451
Austria	Pinzgau	Naderi et al. 2007	13	11	0.974 ± 0.039	0.02525 ± 0.00446	–1.596	–1.04188
	Tauern Pied	Naderi et al. 2007	11	6	0.873 ± 0.071	0.01600 ± 0.00189	1.740	0.59753
Greece	Greece	Naderi et al. 2007	16	13	0.975 ± 0.029	0.01560 ± 0.00332	–4.086	–1.56623
	Skopelos	Naderi et al. 2007	16	12	0.917 ± 0.064	0.00715 ± 0.00130	–6.648	–1.79025
Romania	Austria-Romania	Naderi et al. 2007	8	7	0.964 ± 0.077	0.01914 ± 0.00233	–0.698	–0.44778
	Romania	Naderi et al. 2007	13	13	1.00 ± 0.030	0.02025 ± 0.00178	–6.042	–1.22605
Switzerland	Alpine	Naderi et al. 2007	18	12	0.935 ± 0.041	0.03095 ± 0.00720	0.316	–0.17245
	Grison Striped	Naderi et al. 2007	15	12	0.962 ± 0.040	0.01756 ± 0.00142	–2.730	–0.51594
	Peacock	Naderi et al. 2007	17	10	0.919 ± 0.044	0.01499 ± 0.00195	–0.477	–0.26300
	St. Gallen Booted	Naderi et al. 2007	11	8	0.945 ± 0.054	0.04378 ± 0.00921	1.971	1.21477
Spain	Florida	Naderi et al. 2007	12	11	0.086 ± 0.040	0.02195 ± 0.00189	–2.826	–0.98419
	Verata	Naderi et al. 2007	12	9	0.939 ± 0.058	0.01893 ± 0.00136	–0.653	–0.54655
	Guadarrama	Naderi et al. 2007	13	13	1.00 ± 0.030	0.01763 ± 0.00264	–6.698	–0.93182
Egypt	Baladi	Naderi et al. 2007	18	14	0.974 ± 0.025	0.02253 ± 0.00415	–2.506	–0.85169
	Payoya	Naderi et al. 2007	14	14	1.00 ± 0.027	0.02181 ± 0.00161	–6.540	–0.68799

HD = haplotope diversity, *n* = number of individuals, ND = nucleotide diversity, SD = standard deviation (sequences of 480 bp)