Table S.1. Information about microsatellite primer sequences used for the analysis of Balkan chamois population genetics.

Multiplex sets	Locus	Size range (bp)	Accession no.	C (µL)	*Na*	References
SET 1	OarFCB20	80-104	L20004	0.3	5	Buchanan et al. 1994,
	OarFCB304	130-146	L01535	0.3	8	Buchanan & Crawford 1993
	SR-CRSP-5	154-174	L22197	0.2	9	Arevalo et al. 1994
	SY84	170-180	AY725829	0.3	5	An et al. 2005
	CSSM66	193-255	AF232764	0.3	7	Barendse et al. 1994
	ETH10	205-213	Z22739	0.3	2	Toldo et al. 1993
SET 2	SY434	83-101	AY725834	0.3	7	An et al. 2005
	SR-CRSP-11	112-132	-	0.2	7	Kogi et al. 1995
	TGLA53	132-156	GQ368903	0.3	3	Barendse et al. 1994
	BOBT24	148-176	-	0.3	8	Buitkamp et al. 1996
SET 3A	BM1258	101-129	G18385	0.2	10	Bishop et al. 1994
	SR-CRSP-9	124-132	L22000	0.3	7	Bhebhe et al. 1994
	ILSTS030	152-180	L37212	0.3	6	Kemp et al. 1995
	ETH225	138-150	Z14043	0.3	6	Steffen et al. 1993
SET 3B	SR-CRSP-6	140-150	L22198	0.3	2	Bhebhe et al. 1994
	NRAMP1	196-218	AF005380	0.4	3	Matthews & Crawford 1998
				TOTAL	95	
				AVERAGE	5.94	

C – primer concentration (in microliter), stock solution was 100 µM; Na - total number of alleles for each locus

Table S.2. Locus/population matrix containing null alleles identified by the FreeNA software. Null allele frequencies were estimated using the EM algorithm. Frequencies with values higher than $r \geq 0.20$ were indicated.

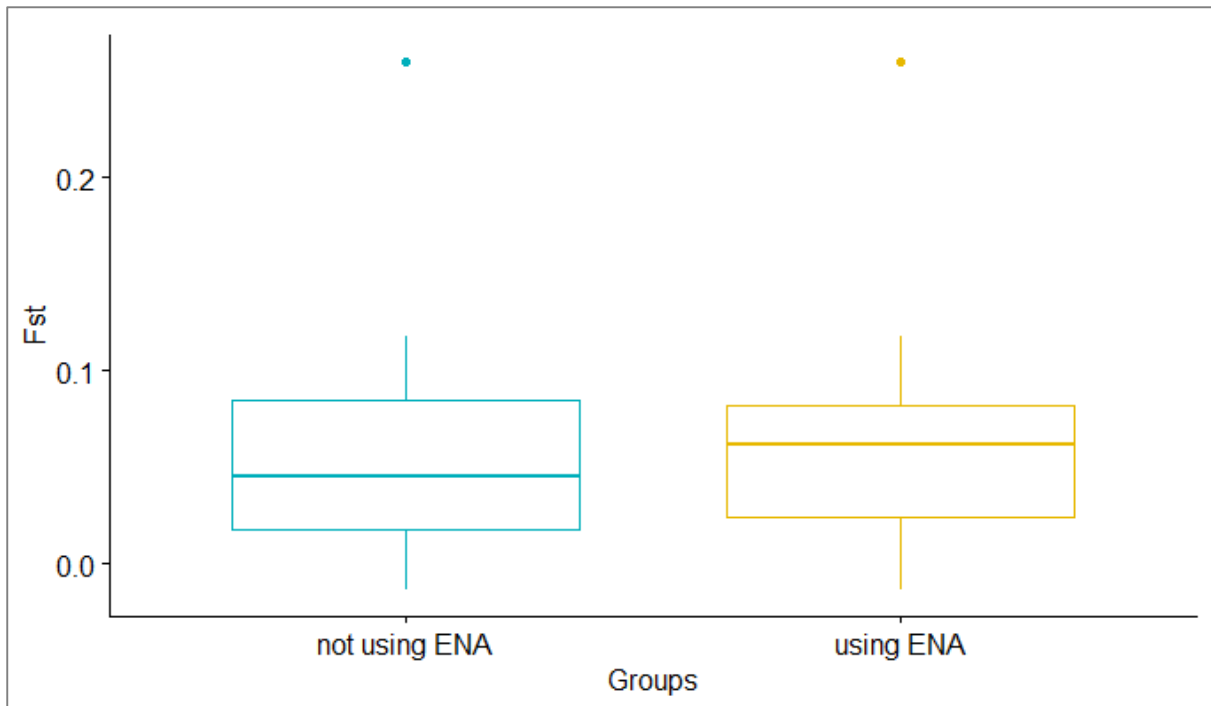|	Populations				
Locus	**PRENJ**	**ČVRSNICA**	**ČABULJA**	**BIOKOVO**	**Total**
OarFCB20	-	-	-	-	0
OarFCB304	-	-	-	-	0
SR-CRSP-5	-	-	-	-	0
SY84	-	-	-	-	0
CSSM66	-	-	-	-	0
ETH10	0.209	-	-	-	1
SY434	0.203	-	-	-	1
SR-CRSP-11	-	-	-	-	0
TGLA53	-	0.203	0.268	-	2
BM1258	-	-	-	-	0
SR-CRSP-9	-	-	-	-	0
ILSTS30	-	-	-	-	0
ETH225	-	-	-	-	0
SR-CRSP-6	0.213	0.276	-	-	2
BOBT24	-	-	-	-	0
NRAMP1	-	-	-	-	0
Total	**3**	**2**	**1**	**0**	**6**

Figure S.1. The comparison of two groups of F_{ST} values (original pairwise F_{ST} values and ENA-corrected pairwise F_{ST} values) using the Wilcoxon Two Sample test.
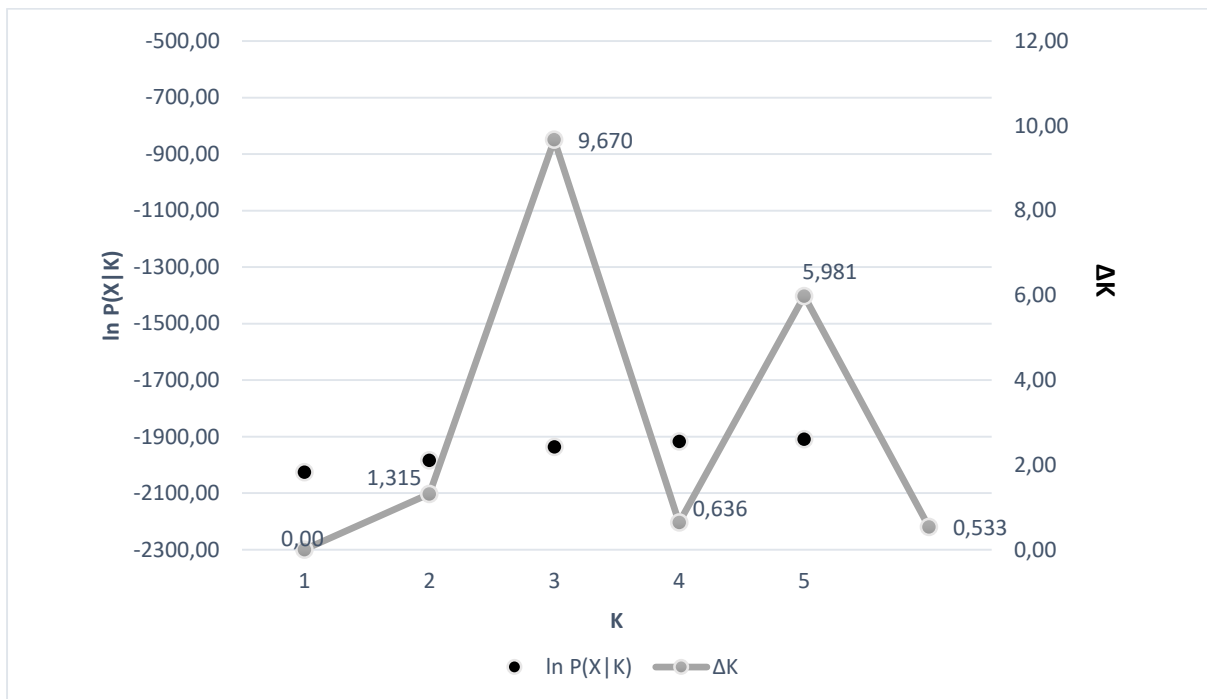

Figure S.2. Evanno method (Evanno et al. 2005) for selecting the representative number of clusters (K).
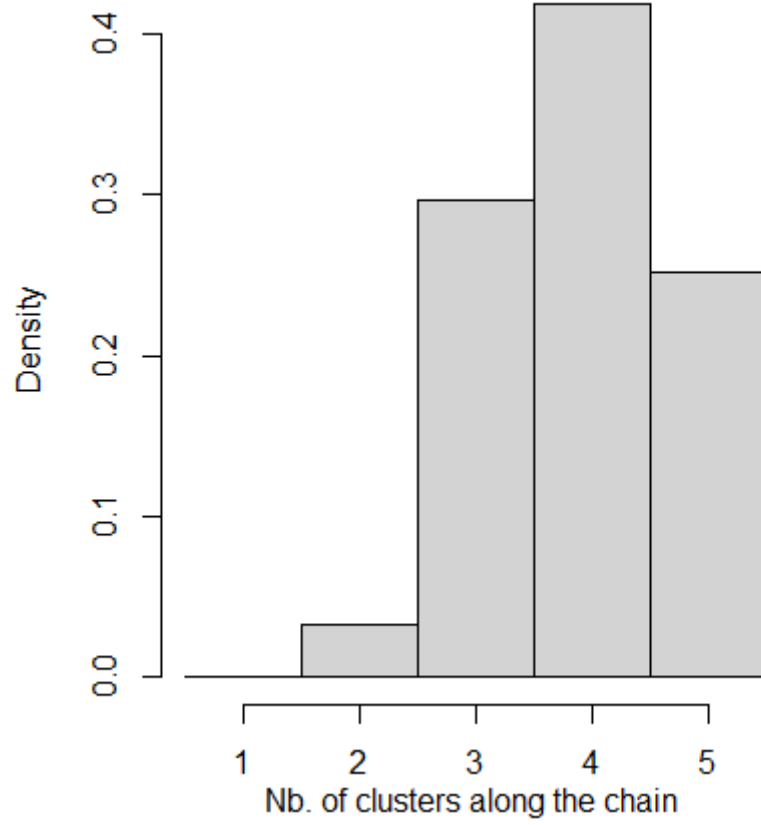
Figure S.3. Number of clusters along the MCMC chain for spatial analysis performed with the GENELAND software.