Table S1: Genetic variability at 12 autosomal short tandem repeat (STR) loci in reference wolves, wolves sampled in the study area, reference dogs, and dogs sampled in the study; corresponding numbers of individuals are in parenthesis (N). **Na**: average observed number of alleles per locus; **Ne**: expected number of alleles per locus; **Np**: number of private alleles; **Ho**: observed heterozygosity; **uHe**: unbiased expected heterozygosity; **PIC:** polymorphic information content; **F_{IS}**: inbreeding coefficient; ***p***: probability to obtain F_{IS}-values higher or lower than those observed after 10000 random permutations of alleles in each population computed by GENETIX (corresponding standard deviation values are in parentheses).

Group (N)	Na		Ne		Np	Ho		uHe		PIC		F_{IS}		*p*
Reference wolves (190)	5.25	(2.45)	2.76	(1.10)	7	0.54	(0.22)	0.57	(0.21)	0.52	(0.20)	-0.035	(0.32)	0.004
Wolves in study area (28)	3.83	(1.19)	2.43	(0.88)	0	0.53	(0.25)	0.53	(0.22)	0.47	(0.20)	-0.088	(0.33)	0.012
Reference dogs (89)	8	(4.73)	3.73	(2.19)	34	0.58	(0.13)	0.66	(0.16)	0.62	(0.17)	0.120	(0.09)	0.000
Dogs in study area (10)	4.67	(1.30)	3.17	(1.42)	1	0.64	(0.20)	0.67	(0.15)	0.59	(0.14)	0.064	(0.23)	0.123

Supplementary Information

From predation to management: monitoring wolf distribution and understanding depredation patterns from attacks on livestock

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