

## Supplementary Material 3

### Hybridization between wild-collected genotypes of wolves and reference dogs in Southern Carpathians, Romania.

We used Bayesian clustering in program STRUCTURE v. 2.3.4 to detect hybrids (Figure S1). We used large-sized domestic dogs from the same sampling area as a reference. We used the population admixture model in STRUCTURE with correlated frequencies and used wild-collected genotypes of wolves and 21 reference dogs sampled in and around the study area in the same run. Structure was run with 105 iterations of burn-in followed by 106 MCMC iteration. We used the population admixture model with correlated frequencies, used wild-collected genotypes and reference dogs in the same run. We explored  $K = 2$ , and used CLUMPAK to interpret results from independent runs.

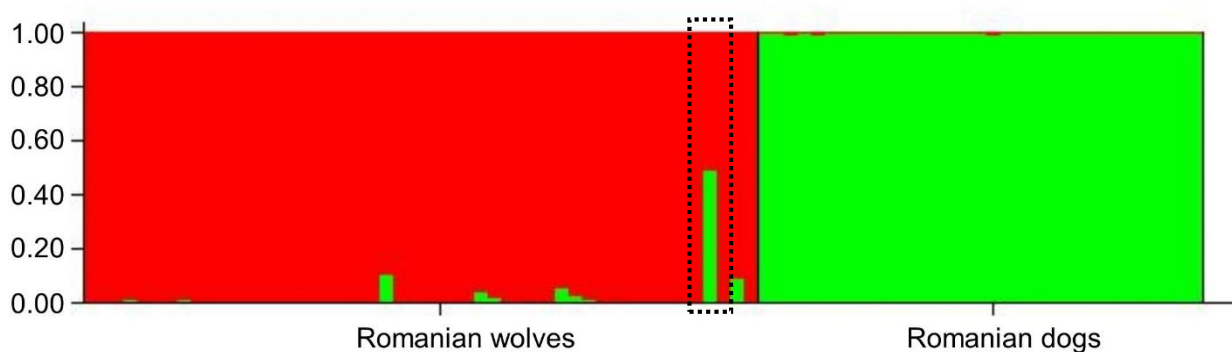


Figure S1. STRUCTURE graph of the wolf / dog hybridization analysis. Genotype EF.15J8, highlighted above and belonging to a male sampled in the wild, has a genetic structure of a typical F1 wolf-dog hybrid.