Supplementary Material 4

Performance of parentage analysis and pedigree assignments of wolf samples in Southern Carpathians, Romania

Parentage analysis was done in program Colony. We allowed for a locus-specific probability of allelic dropout error on each locus (between 0.017 and 0.073) and 0.004 probability of a false allele. We performed 3 independent runs using full-likelihood, medium precision and long run. While the first analyses were run assuming monogamy, the results didn't provide correct pedigree assignments. When analysis was run using a polygamy assumption, the results and their interpretation improved. We checked the performance of the Colony run using traceplots of MCMC chains, with converged at the same likelihood level (Figure S1) indicating decent convergence.
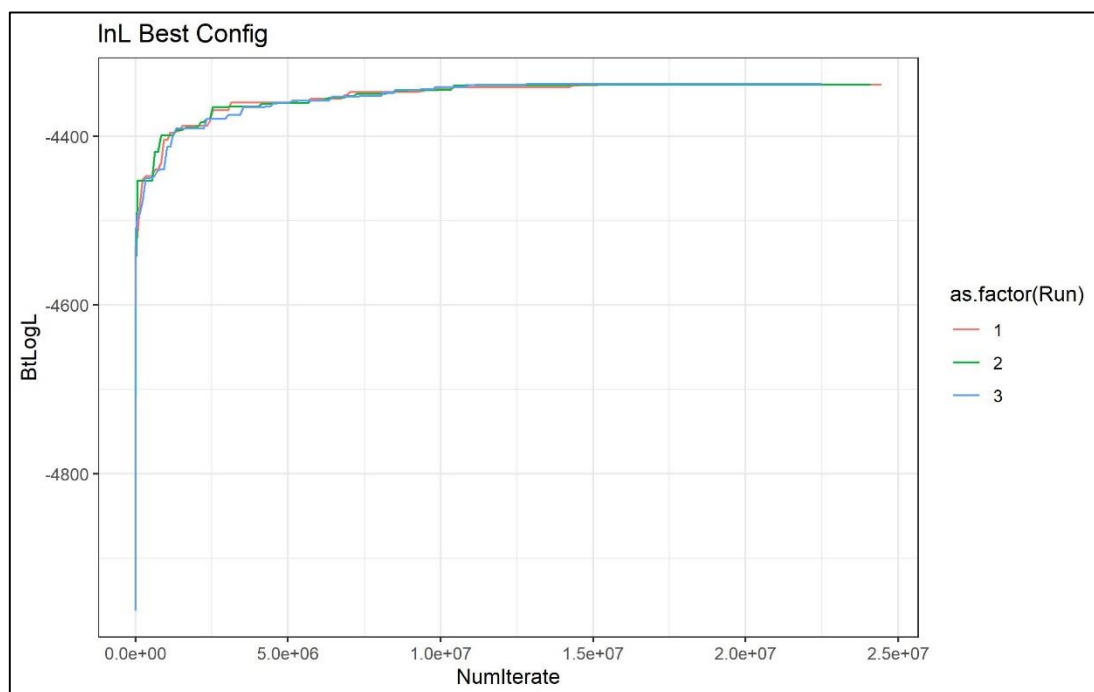

Figure S1. Traceplot of three MCMC Chains used for parentage analysis in Colony software.

We checked the stability of the parentage assignments also with traceplot, where all MCMC chains didn't converge completely because of the presence of hybrid affected the estimates because of several single-parent-offspring pairs, which can go either way in different estimates. This later was probably the case since two of the three runs converge perfectly, and one not (Figure S2).
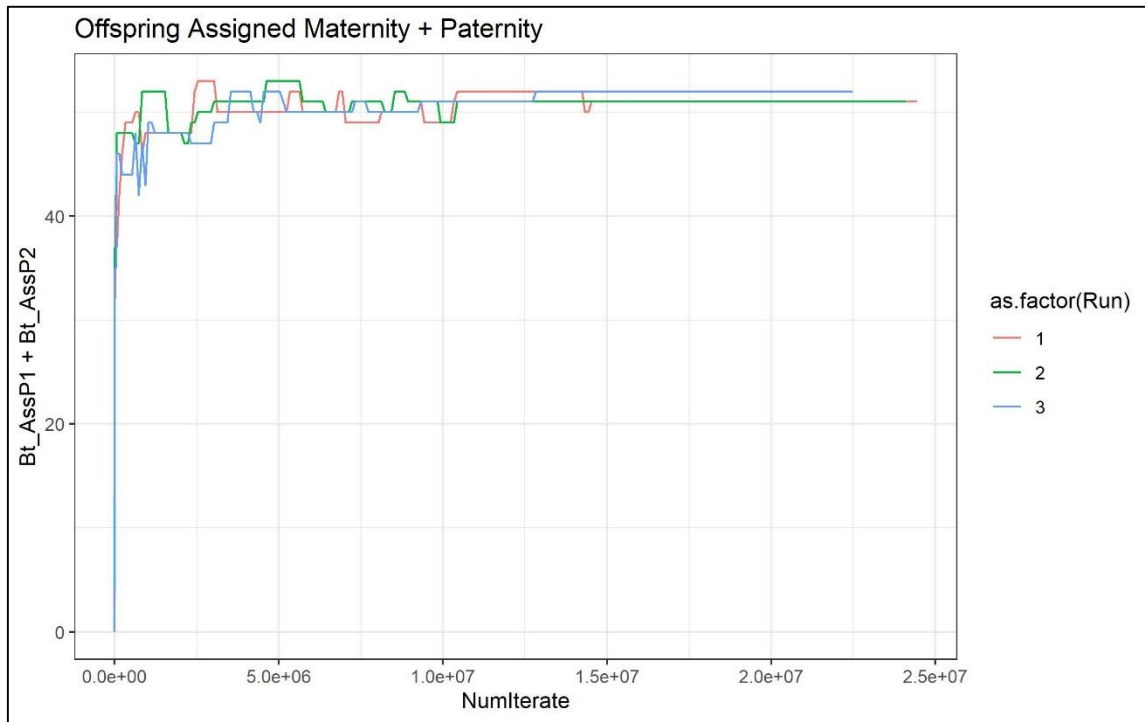
Figure S2. Stability of parentage assignments using three MCMC Chains.