

Table S1. Primer sequences for microsatellites and cytochrome-*b* region for species identification.

Name	Fluorescent label ¹	Primer sequences (5' to 3')
FH2001	VIC	F – TCCTCCTCTTCTTTCCATTG R – TGAACAGAGTTAAGGATAGACACG
FH2010	PET	F – AAATGGAACAGTTGAGCATGC R – CCCCTTACAGCTTCATTTTCC
FH2062	NED	F – GGCTTCTGGAGACAGGCAT R – CAGAACGCTGTCAGCCCTT
FH2096	FAM	F – CCGTCTAAGAGCCTCCCAG R – GACAAGGTTTCCTGGTTCCA
FH2137	NED	F – GCAGTCCCTTATTCCAACATG R – CCCCAAGTTTTGCATCTGTT
FH2140	PET	F – GGGGAAGCCATTTTAAAGC R – TGACCCTCTGGCATCTAGGA
PEZ19	FAM	F – GACTCATGATGTTGTGTATC R – TTTGCTCAGTGCTAAGTCTC
ScatID	none	F – TATGCCTGATTCTACAGAT R – TAGTATAGTCCTCGTCC

¹On forward primer

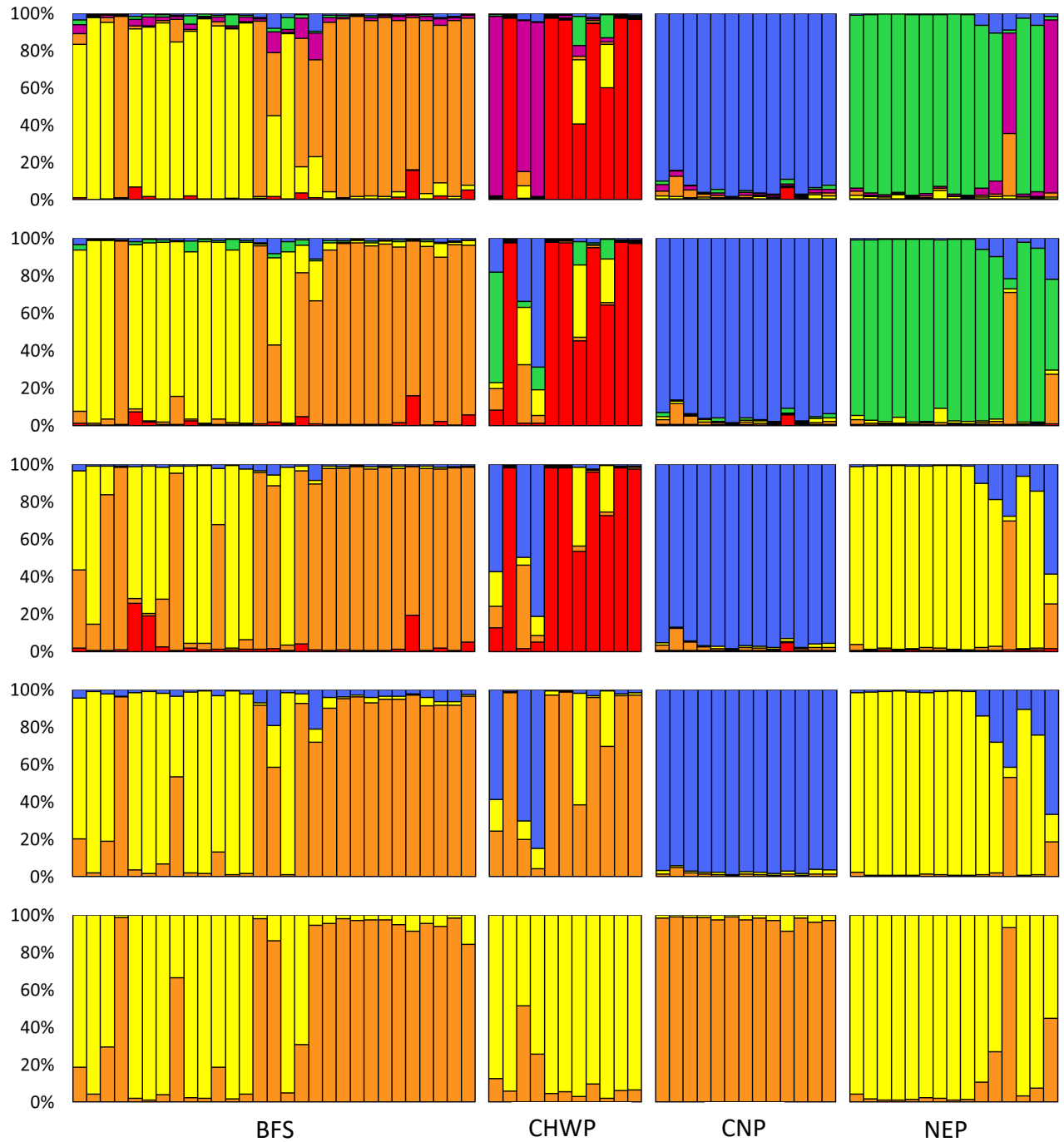


Figure S1. Genetic assignments from STRUCTURE, showing different levels of K . From top to bottom: $K=6$, $K=5$, $K=4$, $K=3$, and $K=2$. Our best fitting model is $K=5$ (see Figure 2 in main manuscript). Plots are aligned and averaged across 5 replicates.

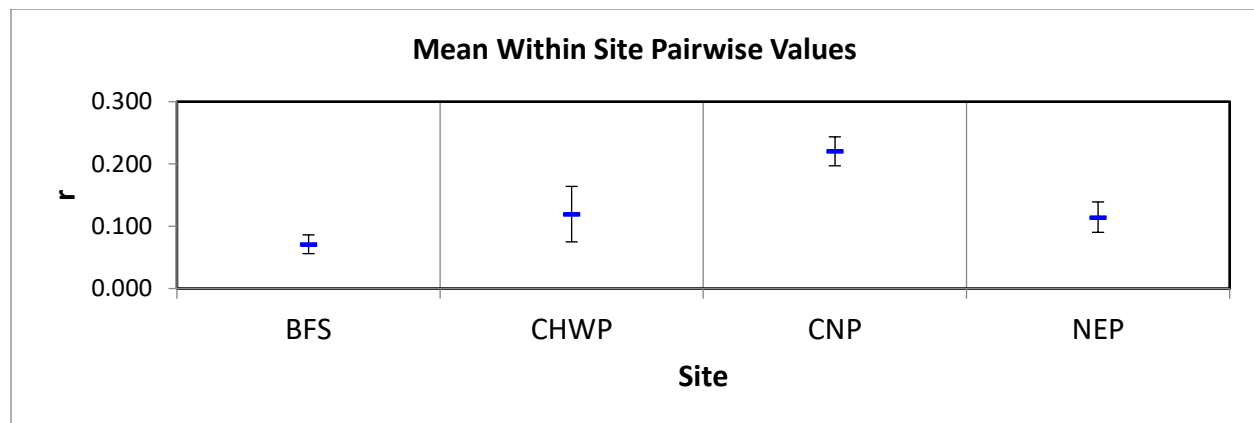


Figure S2. Mean within-site pairwise relatedness. Mean pairwise relatedness of coyotes (Lynch & Ritland estimator) within the four sites. The ranges of values come from 9,999 random permutations and 10,000 bootstraps in GenAlEx [31]. (Peakall and Smouse 2006, 2012). All mean estimates are greater than zero ($p < 0.0001$).