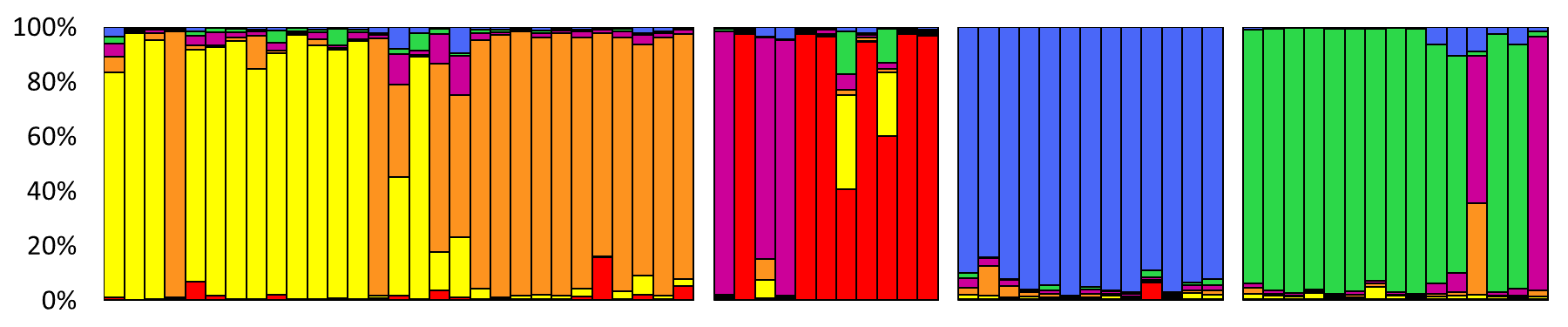
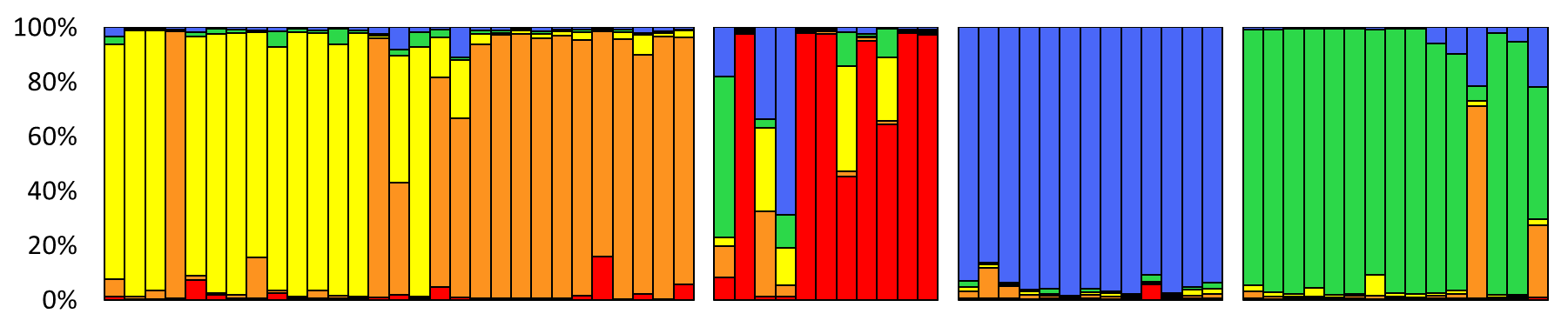
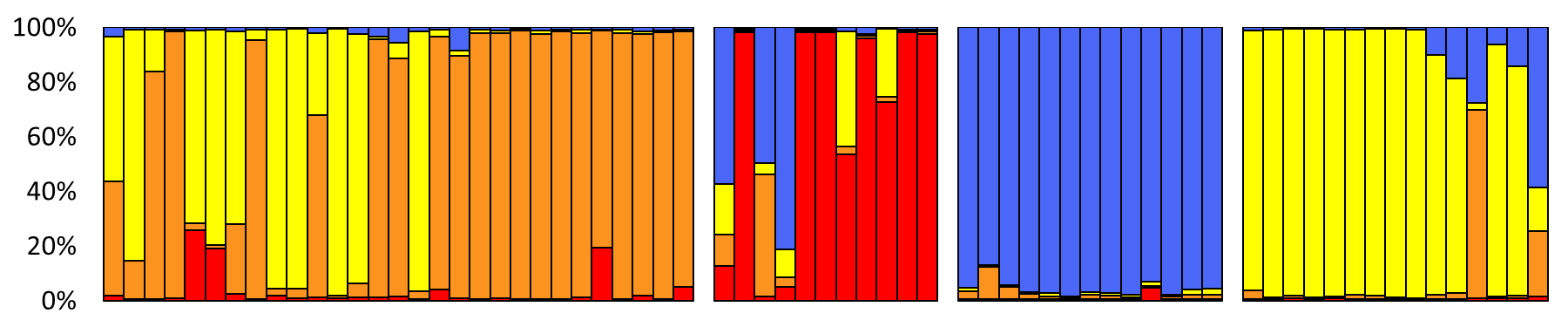
**Table S1. Primer sequences for microsatellites and cytochrome-*b* region for species identification.**

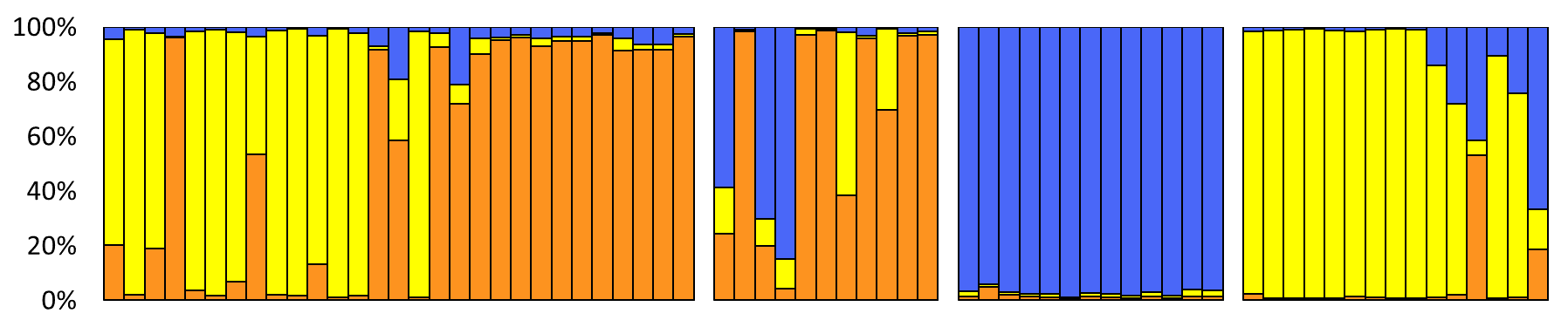
|  |  |  |
| --- | --- | --- |
| Name | Fluorescent label1 | Primer sequences (5’ to 3’) |
| FH2001 | VIC | F – TCCTCCTCTTCTTTCCATTG  R – TGAACAGAGTTAAGGATAGACACG |
| FH2010 | PET | F – AAATGGAACAGTTGAGCATGC  R – CCCCTTACAGCTTCATTTTCC |
| FH2062 | NED | F – GGCTTCTGGAGACAGGCAT  R – CAGAACGCTGTCAGCCCTT |
| FH2096 | FAM | F – CCGTCTAAGAGCCTCCCAG  R – GACAAGGTTTCCTGGTTCCA |
| FH2137 | NED | F – GCAGTCCCTTATTCCAACATG  R – CCCCAAGTTTTGCATCTGTT |
| FH2140 | PET | F – GGGGAAGCCATTTTTAAAGC  R – TGACCCTCTGGCATCTAGGA |
| PEZ19 | FAM | F – GACTCATGATGTTGTGTATC  R – TTTGCTCAGTGCTAAGTCTC |
| ScatID | none | F – TATGCCTGATTCTACAGAT  R – TAGTATAGTCCTCGTCC |

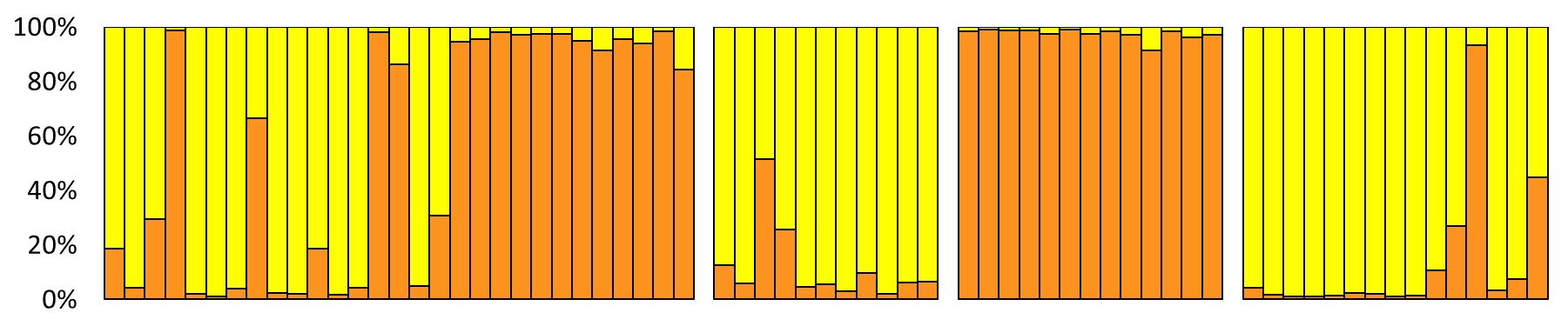
1On forward primer











BFS

CHWP

CNP

NEP

**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 (Peakall and Smouse 2006, 2012). All mean estimates are greater than zero (p < 0.0001).