Supplementary Information for:

Genome-wide analysis of SNPs is consistent with no domestic dog ancestry in the endangered Mexican wolf (*Canis lupus baileyi*)

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Note: Supplementary Table S1 [Description and summary of the Mexican wolves used in this study, including all results generated on a per-individual basis] has been uploaded as a separate file in the supplemental material.

Table S2. Reproducibility of genotypes across eight replicated Mexican wolves (*Canis lupus baileyi*) on the CanineHD BeadChip.

ID	# Correct	# Errors	Total	Frequency
10	171001	3	171004	0.99998
29	171015	7	171022	0.99996
72	171146	12	171158	0.99993
412	170856	7	170863	0.99996
547	170350	3	170353	0.99998
1038	170666	17	170683	0.99990
66	141798	9936	151734	0.93452
593	160141	178	160319	0.99889
Mean	165871.6	1270.4	167142.0	0.99164
SD	10425.6	3501.9	7238.3	0.02308

Figure S1. Model of demographic history used in the simulations. The four extant populations include North American, or Yellowstone, gray wolves (NAGW), Mexican wolves (MW), domestic dogs (DOG), and European gray wolves (EUGW). Effective population sizes are shown inside each population and divergence times (dotted lines) are provided in years. The three migration bands (red arrows) simulated occurred 'g' generations in the past. See Table 2 (main text) for a complete description of all migration schemes.

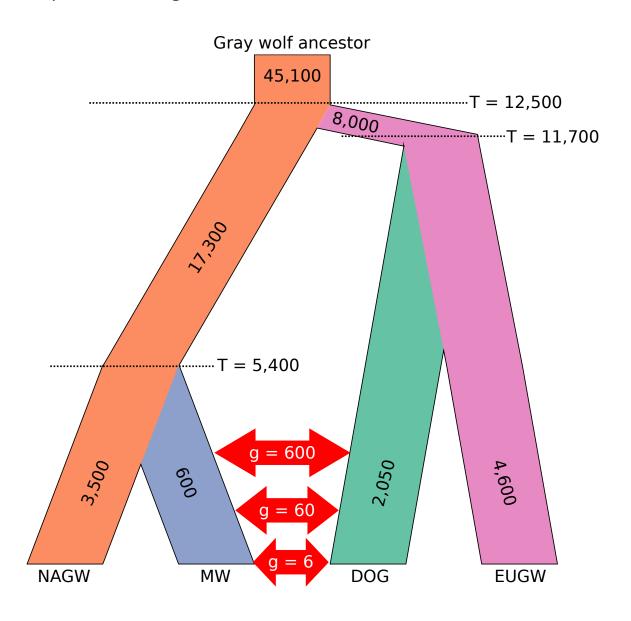


Figure S2. Proportion of North American gray wolf (yellow), European gray wolf (orange), and domestic dog (blue) ancestry in 88 Mexican wolves summed across all chromosomes from the local ancestry fragments inferred using LAMP-LD. Mexican wolves are separated by their captive population of origin, MB = McBride, AR = Aragón, GR = Ghost Ranch, or CL = cross-lineage.

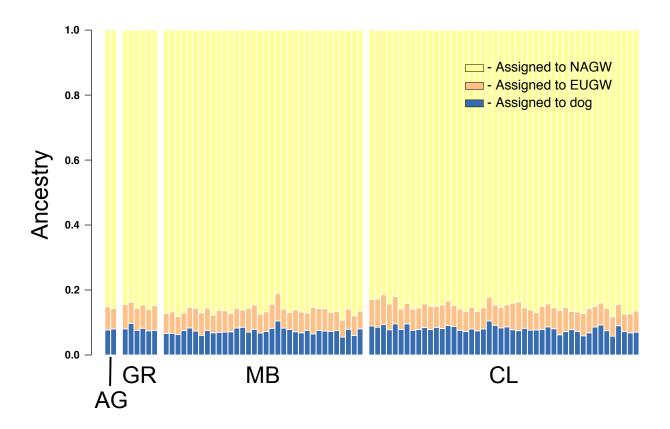


Figure S3. Locations of local ancestry fragments assigned to North American gray wolf (yellow), European gray wolf (orange), or domestic dog (blue) parental populations. Each plot shows an individual Mexican wolf's genome, whose studbook number and population are given.

