Supplemental Methods

Single-SNP measures of genetic diversity

Missingness was estimated as the proportion of SNPs that could not be called. From the Yellowstone National Park wolves in the dataset (n=19), known pedigree relationships were used to calibrate identity by state (IBS) or similarity scores (vonHoldt et al. 2008) to identify closely related individuals. A minimum score of IBS>0.8 indicated a relatedness status of half-siblings and values below this level were used for identifying a set of unrelated wild canids for subsequent analyses.

SNPs were excluded based on high pairwise genotypic associations (r^2) using `PLINK` (Purcell et al. 2007) to obtain a set of unlinked SNPs for two different datasets either including all canids (dogs, wolves, coyotes) or just for a subset of canids (wolves and coyotes).

Assessing appropriate K values in `STRUCTURE` analyses

To choose an appropriate K value for presentation we evaluated likelihood values, the parameter Δ (Evanno et al. 2005) and assessed if clusters were biologically realistic (as emphasized in the `STRUCTURE` manual). We initially analyzed the 300 sample dataset for K=2 through 12 and observed a maximum likelihood value at K=8 (Supplemental Fig. S7A) but results through K=10 were biologically informative (Fig. 4). The variability among replicates for K>10 was very high (Supplemental Fig. S7A) and likelihood values decreased precipitously so that no additional biologically informative resolution was observed (see discussion in Pritchard et al. 2000). The parameter Δ maximized at K=3 corresponding to the three canid species of gray wolf, coyote and dog (Supplemental Fig. S7A). To confirm the signal of admixture found in North American canids (coyotes, gray wolves, and red wolves), we calculated the 90% probability intervals (PI) for the membership of an individual to clusters at K=3, as this resolves dogs, coyotes and gray wolves.

All analyses demonstrated a primary partition between New and Old World wolves; consequently, we also performed separate `STRUCTURE` analyses to enhance resolution within each of these two groupings (see discussion in Pritchard et al. 2000). Likelihood values increased until K=7 for both analyses (Supplemental Fig. S7B,C). The parameter Δ was maximal at this value in European wolves and at K=4 in North American wolves. However, we continued to observe biological informative clusters until K=7 in North American wolves (Fig. 4) and hence present results for K=7 for both areas.

Linkage disequilibrium analysis

We used `PLINK` (--r2 --ld-window 99999 --ld-window-r2 0 --maf 0.15) excluding SNPs with MAF<15%. Inter-SNP distances (Kb) were binned into the following classes: 1.25, 2.5, 3.75, 5, 7.5, 10, 15, 20, 30, 40, 60, 80, 115, 150, 212.5, 275, 387.5, 500, 737.5, 975 and 1000Kb. Genotypic associations were averaged for each inter-SNP distance class. Because LD estimates in particular are sensitive to sample size, we explored the trend of LD with sample size for a reduced random sample of 3, 6 and 10 individuals for each population (Supplemental Fig. S6)

Modeling ancestry and timing of admixture

We followed previous studies that utilized subsets of ancestry informative markers (AIMs) that are diagnostic of parental populations to enhance haplotype assignment (Tian et al. 2006; Price et al. 2007; Rosenberg et al. 2010). For the analysis using the western wolf and western coyote as the ancestral reference populations, we first performed a sensitivity analysis in `SABER` to examine the effect of SNP diagnostic power (coyote-wolf pairwise F_{ST} value) paired with chromosomal spacing density. We ranked all 48,036 SNPs by pairwise western coyote/western gray wolf F_{ST} values and established datasets containing the highest rank F_{ST} SNPs for each chromosome at a range of spacing densities from 1 SNP per 70Kb to 1 SNP per 2.5Mb. We found that an average SNP density greater than ~1 SNP per 750Kb (corresponding to SNPs with F_{ST} values < 0.40) resulted in decreasing average block size estimates and unstable τ estimates. Consequently, we selected a subset of 3,102 SNPs and 7,083 SNPs with F_{ST} ≥ 0.4 for analysis with two and three ancestral reference populations, respectively.

We also evaluated initial prior values for the number of generations to the composite admixture event, τ (τ = 1, 10, 100, 1000 and 10000 generations) using the combined analysis option for all 38 autosomes for the four groups: Great Lakes wolves, red wolves, northeastern coyotes and midwestern/southern coyotes. For all groupings, admixture time estimates were consistent for initial setting values of τ = 1, 10 and 100, but varied extensively at higher τ values of 1000 and 10000. We selected τ = 100 as the best-fit initial parameter estimate for final analysis of admixed samples, estimates of ancestry block assignments and sizes, and τ.

Among the Great Lakes wolves, red wolves and Algonquin wolves analyzed by the two-ancestor model, we found two Great Lakes wolves that did not show any assignment to coyote or joint ancestry. These two individuals also had high assignment to the non-admixed Rocky Mountains Forest and Atlantic Forest wolf populations, respectively, in `STRUCTURE`. Additionally, the three Isle Royale National Park wolves are admixed with coyotes to the same extent as the mainland Great Lakes wolves (~15%), but with larger τ estimates likely as a result of the significant level of inbreeding in this population (see main text and Supplemental Table S6).

We separately analyzed the ancestry of the wolves from Northern Quebec (n=10) as a possible ancestral population and individually to evaluate if they were admixed to any extent. Using the western coyote and western wolf as ancestral populations, we found the Northern Quebec wolves to have 100% wolf assignment. When the Northern Quebec wolves were used as an ancestral reference population, ancestry assignments from `SABER` of the admixed canids were comparable with regard to the fraction of gray wolf and coyote ancestry, and estimates of τ are generally within a few percent (Supplemental Tables S5 and S7). Overall, the length of assigned haplotype blocks is less (but with the same between-species ratios) when Northern Quebec wolves are used as an ancestral population, which may reflect the dominance of western gray wolves in the F_{ST} rankings used to choose the top ranking SNPs for the analysis.

Additionally, we repeated the analyses for the northeastern and midwestern/southern admixed coyote populations assuming three ancestral populations (dogs, western coyotes, and western gray wolves). The same ancestral western gray wolf and western coyote individuals were used as for the two-ancestor model above, with the addition of an ancestral dog reference population consisting of 12 dogs from 12 modern breeds (American Cocker Spaniel, Basset Hound, Beagle, Border Collie, Collie, Doberman Pinscher, Golden Retriever, Greyhound, Giant Schnauzer, Scottish Terrier, Standard Poodle, and Whippet). As before, we selected subsets of SNPs that had F_{ST} values >0.40 for three pairwise comparisons: between western gray wolves and western coyotes, western gray wolves and dogs, and western coyotes and dogs which resulted in a final SNP density of ~1 SNP per 750Kb for 7,083 AIM SNPs across all 38 canid chromosomes.

Finally, since chromosomes with very few ancestry blocks are likely to bias the timing estimates (Tang et al. 2006), we exercised caution in interpreting small differences in admixture timing. We also note that estimating τ assumes a simple model of admixture followed by population isolation and does not necessarily capture the complexity of intermittent gene flow or backcrossing events discussed here (Tang et al. 2006).

Literature Cited

Evanno G, Regnaut S, Goudet J. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol Ecol* **14**: 2611-2620.

Fain SR, Straughan DJ, Taylor BF. 2010. Genetic outcomes of wolf recovery in the Western Great Lakes states. *Conserv Genet* DOI: 10.1007/s10592-010-0068-x.

Ferrell R, Morizot D, Horn J, Carley C. 1980. Biochemical markers in a species endangered by introgression: the red wolf. *Biochem Genet* **18**: 39-49.

Freeman R, Shaw J. 1979. Hybridization in Canis (Canidae) in Oklahoma. *Southwest Nat* **24**: 485-500.

Kays R, Curtis A, Kirchmann JJ. 2010. Rapid adaptive evolution of northeastern coyotes via hybridization with wolves. *Biol Letters* **6**: 89-93.

Koblmüller S, Nord M, Wayne RK, Leonard JA. 2009. Origin and status of the Great Lakes wolf. *Mol Ecol* **18**: 2313-2326.

Kyle CJ, Johnson AR, Patterson BR, Wilson PJ, Grewal SK, White BN. 2006. Genetic nature of eastern wolves: Past, present and future. *Conserv Genet* **7**: 273-287.

Lehman N, Eisenhawer A, Hansen K, Mech LD, Peterson RO, Gogan PJP, Wayne RK. 1991. Introgression of coyote mitochondrial DNA into sympatric North American gray wolf populations. *Evolution* **45**: 104-119.

Leonard JA, Wayne RK. 2008. Native Great Lakes wolves were not restored. *Biol Letters* **4**: 95-98.

Lindblad-Toh K, Wade C, Mikkelsen TS, Karlsson EK, Jaffe DB, Kamal M, Clamp M, Chang JL, Kulbokas EJ, Zody MC, et al. 2005. Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature* **438**: 803-819.

McCarley H. 1962. The taxonomic status of wild canids (Canidae) in the south central United States. *Southwest Nat* **7**: 227-235.

Mech LD, Federoff N. 2002. α-1 antitrypson polymorphism and systematics of eastern North American wolves. *Can J Zoolog* **80**: 961-963.

Mengel RM. 1971. A study of dog-coyote hybrids and implications concerning hybridization in Canis. *J Mammal* **52**: 316-336.

Nowak RM. 1979. *North American Quaternary Canis*. Monograph of the Museum of Natural History, University of Kansas.

Nowak RM. 2002. The original status of wolves in eastern North America. *Southeast Nat* **1**: 95-130.

Nowak RM. 2009. Taxonomy, morphology, and genetics of wolves in the Great Lakes region of the United States. Recovery of Gray Wolves in the Great Lakes (Eds. Wydeven AP, et al.), pp. 233-250. Springer, New York, New York.

Paradiso J. 1968. Canids recently collected in east Texas, with comments on the taxonomy of the red wolf. *Am Midl Nat* **80**: 529-535.

Price AL, Patterson N, Yu F, Cox DR, Waliszewska A, McDonald GJ, Tandon A, Schirmer C, Neubauer J, Bedoya G, et al. 2007. A genomewide admixture map for Latino populations. *Am J Hum Genet* **80**: 1024-1036.

Pritchard J, Stephens M, Donnelly P. 2000. Inference of population structure using multilocus genotype data. *Genetics* **155**: 945-959.

Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, et al. 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am J Hum Genet* **81**: 559-575.

Reich D, Wayne RK, Goldstein DB. 1999. Genetic evidence for a recent origin by hybridization of red wolves. *Mol Ecol* **8**: 139-144.

Rosenberg NA, Huang L, Jewett EM, Szpiech Z, Jankovic I, Boehnke M. 2010. Genome-wide association studies in diverse populations. *Nat Rev Genet* **11**: 356-366.

Roy M, Geffen E, Smith D, Ostrander EA, Wayne RK. 1994. Patterns of differentiation and hybridization in North American wolflike canids, revealed by analysis of microsatellite loci. *Mol Biol Evol* **11**: 553-570.

Roy MS, Geffen E, Smith D, Wayne RK. 1996. Molecular genetics of pre-1940 red wolves. *Conserv Biol* **10**: 1413-1424.

Rutledge L, Garroway CJ, Loveless KM, Patterson BR. 2010a. Genetic differentiation of eastern wolves in Algonquin Park despite bridging gene flow between coyotes and grey wolves. *Heredity* DOI: 10.1038/hdy.2010.6.

Rutledge L, Bos K, Pearce R, White BN. 2010b. Genetic and morphometric analysis of sixteenth century *Canis* skull fragments: implications for historic eastern and gray wolf distribution in North America. *Conserv Genet* **11**: 1273-1281.

Tang H, Coram M, Wang P, Zhu X, Risch N. 2006. Reconstructing genetic ancestry blocks in admixed individuals. *Am J Hum Genet* **79**: 1-12.

Tian C, Hinds DA, Shigeta R, Kittles R, Ballinger DG, Seldin MF. 2006. A genomewide single-nucleotide-polymorphism panel with high ancestry information for African American admixture mapping. *Am J Hum Genet* **79**: 640-649.

vonHoldt B, Stahler D, Smith DW, Earl DA, Pollinger JP, Wayne RK. 2008. The genealogy and genetic viability of reintroduced Yellowstone grey wolves. *Mol Ecol* **17**: 252-274.

vonHoldt B, Pollinger JP, Lohmueller KE, Han E, Parker HG, Quignon P, Degenhardt JD, Boyko AR, Earl DA, Auton A, et al. 2010. Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. *Nature* **464**: 898-902.

Wayne RK, Jenks S. 1991. Mitochondrial DNA analysis implying extensive hybridization of the endangered red wolf *Canis rufus*. *Nature* **351**: 565-568.

Wheeldon T, White B. 2009. Genetic analysis of historic western Great Lakes region wolf samples reveals early Canis lupus/Canis lycaon hybridization. *Biol Letters* **5**: 101-104.

Wilson P, Grewal S, Lawford ID, Heal JNM. 2000. DNA profiles of the eastern Canadian wolf and the red wolf provide evidence for a common evolutionary history independent of the gray wolf. *Can J Zoolog* **78**: 2156-2166.

Wilson GA, Rannala B. 2003. Bayesian inference of recent migration rates using multilocus genotypes. *Genetics* **163**: 1177-1191.

Wilson PJ, Grewal SK, Mallory FF, White BN. 2009. Genetic characterization of hybrid wolves across Ontario. *J Hered* **100**: S80-S89.

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Plot of 10 principal components for all canids for the 48K SNP dataset.

Supplemental Figure S2. Principal component analysis of the 48K SNP dataset: Old and New World wolves (**A**); Old World wolves (**B**); North American wolves (**C**); and all coyotes (**D**). Abbreviations: AL, Alabama; BC, British Columbia; CA, California; CT, Connecticut; IL, Illinois; IRNP, Isle Royale National Park; LA, Louisiana; OH, Ohio; MB, Manitoba; MS, Mississippi; NH, New Hampshire; NY, New York; QC, Quebec; UT, Utah; VA, Virginia; VT, Vermont; and WA, Washington.

Supplemental Figure S3. PCA plots for the 48K SNP dataset: Old and New World wolves (**A**); Old World wolves (**B**); North American wolves (**C**); coyotes (**D**); North American canids (**E**); and North American canids excluding Mexican wolves (**F**).

Supplemental Figure S4. Principal component analysis of 710 SNPs ascertained by comparing dog genome sequence with that of wolf or coyote (see vonHoldt et al 2010).

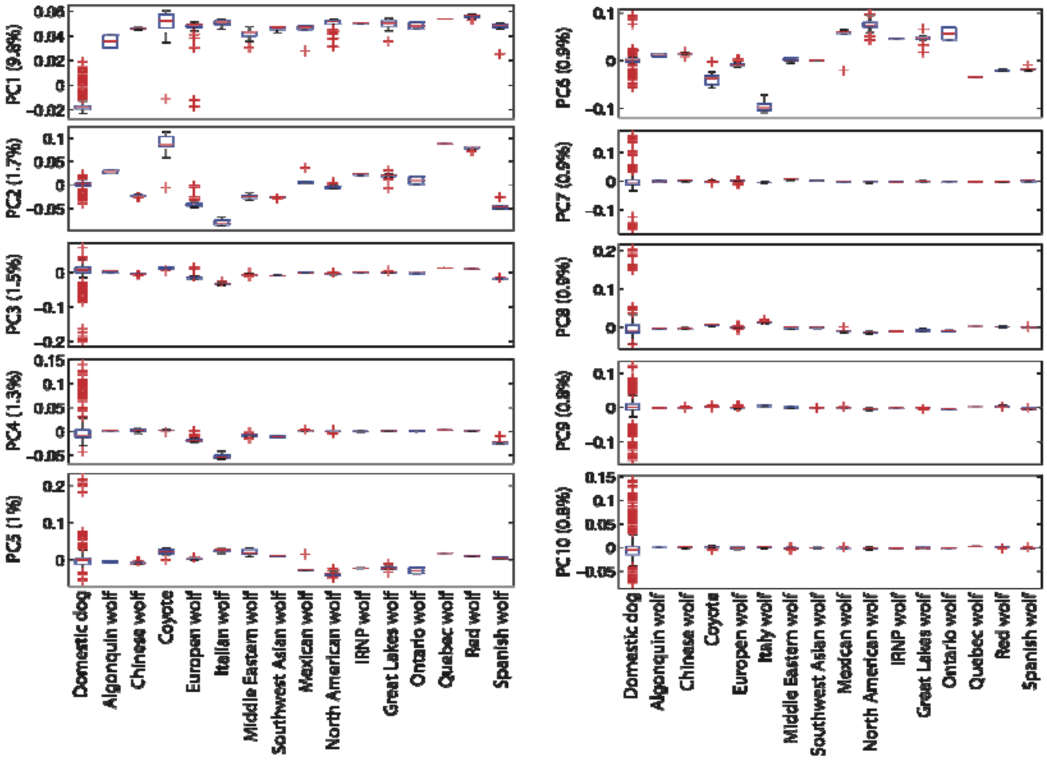
Supplemental Figure S5. Neighbor-joining cladograms (**A**) and phylograms (**B**) utilizing the 48K SNP dataset for non-admixed wolf (**left**) and coyote populations (**right**). Bootstrap support >95% of 1,000 replicates are indicated as dots on branches. Branch colors either represent habitats in North American wolves (light blue, coastal forest; green, temperate forest; red, rocky mountain forest; purple, tundra/taiga; brown, aridlands) or localities. Outgroups are the coyote (**left**) and a golden jackal (**right**). (Lindblad-Toh et al. 2005).

Supplemental Figure S6. Average decay of LD (genotypic association, r^2) with increasing inter-SNP distance (Kb) for all North American canid populations with a random sampling of 10 (top), 6 (middle), and 3 (lower) individuals per population. If a population size was smaller than these sample sizes, it was excluded.

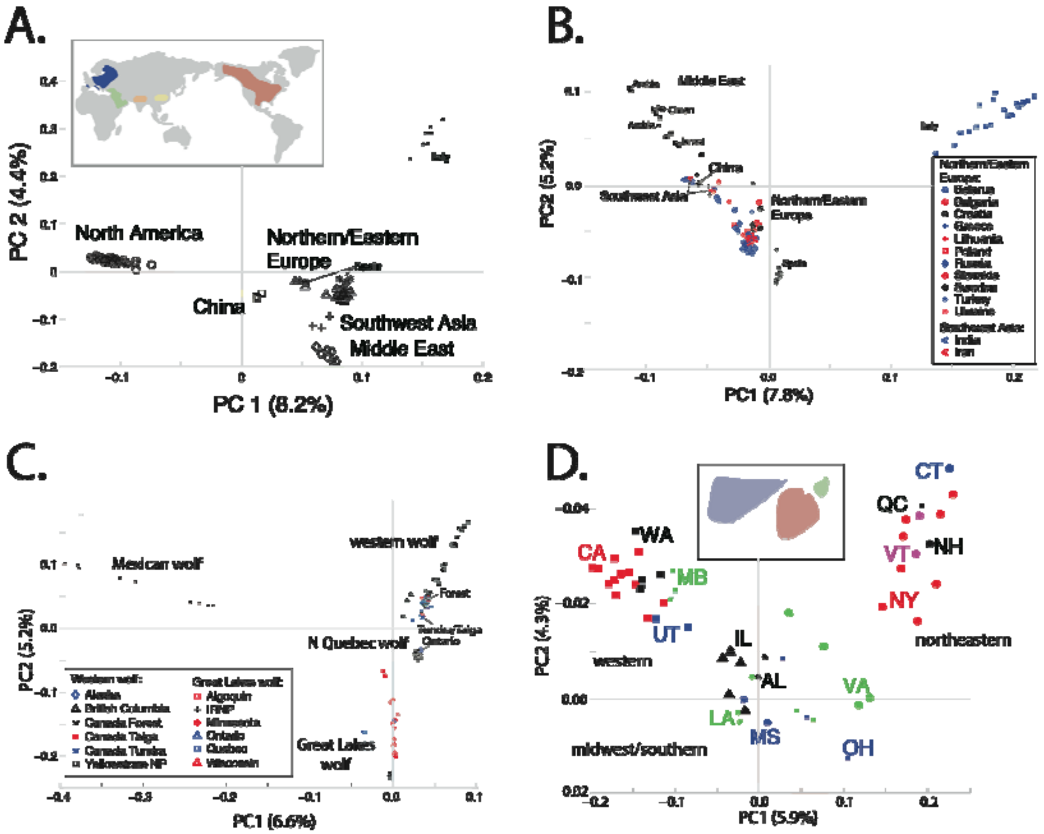
Supplemental Figure S7. Plot of log likelihood (red line) and delta K (blue line) (Evanno et al. 2005): complete dataset in Figure 4 (**A**); North American gray wolves (**B**); and Eurasian gray wolves (**C**).

Supplemental Figure S8. Histogram of ancestry block sizes, mean block size, genome-wide ancestry (%), and number of generations since admixture.

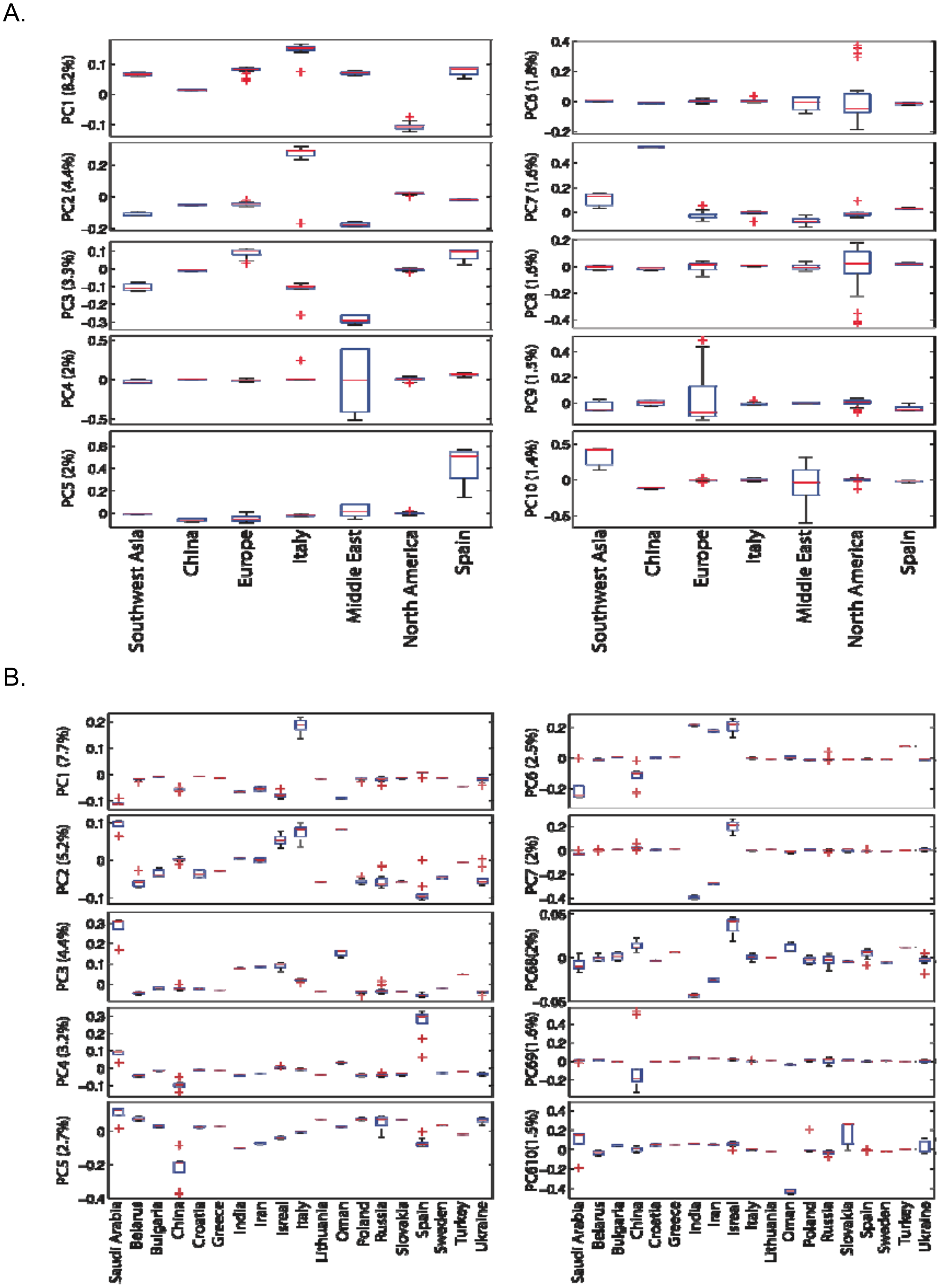
Supplemental Figure S1.



Supplemental Figure S2.

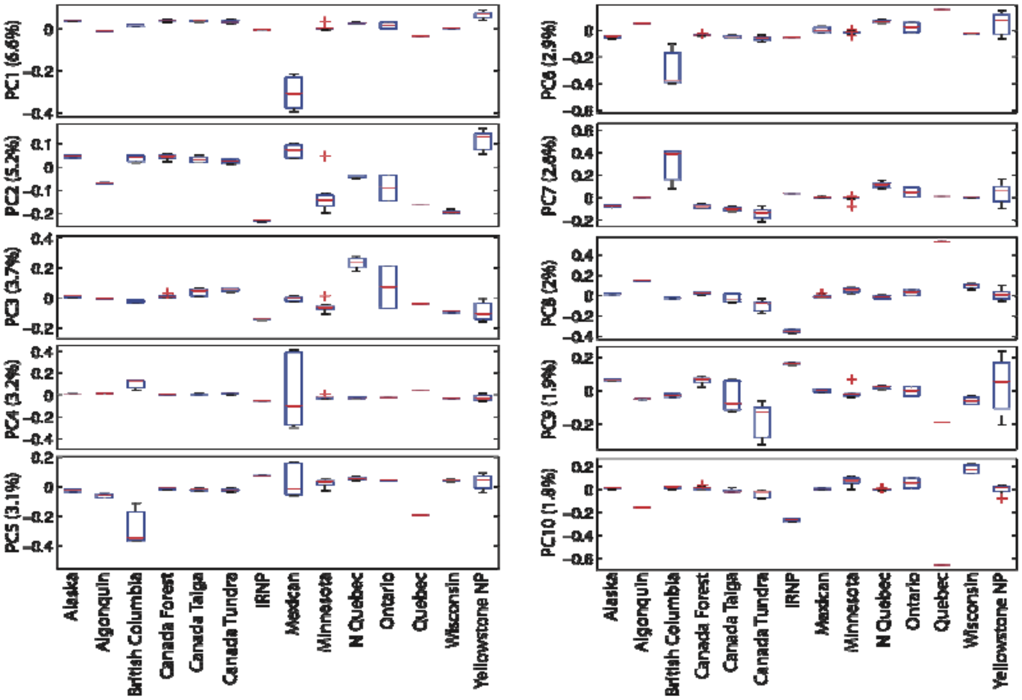


Supplemental Figure S3.

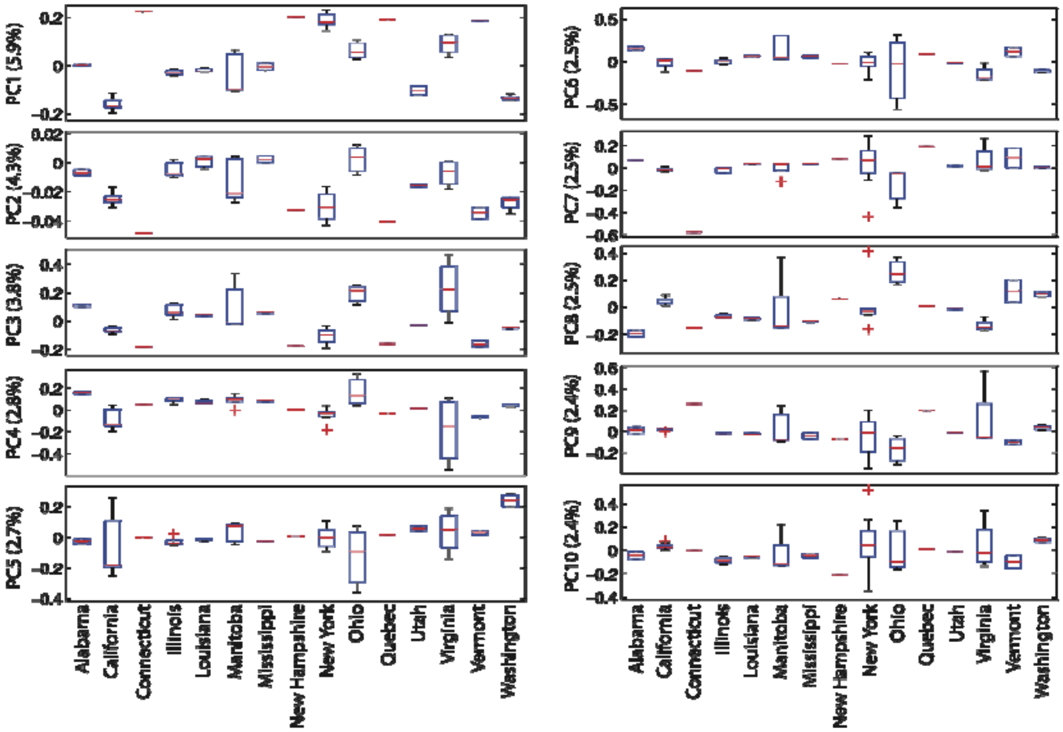


Supplemental Figure S3 (*continued*).

C.

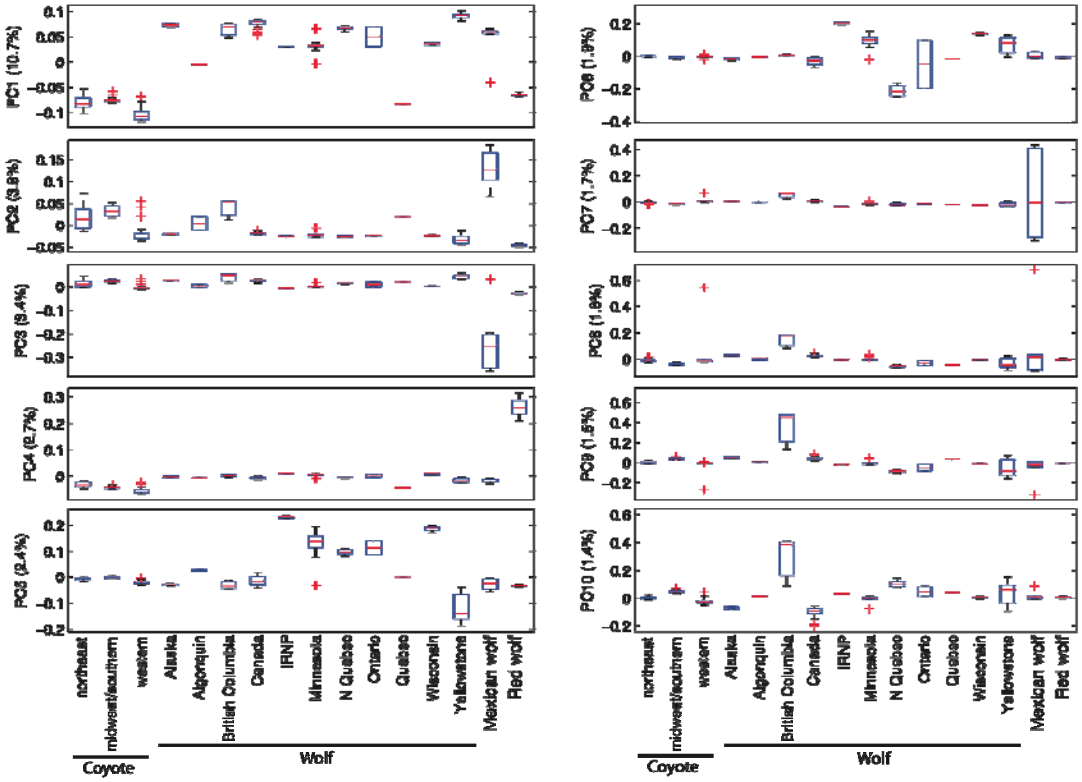


D.

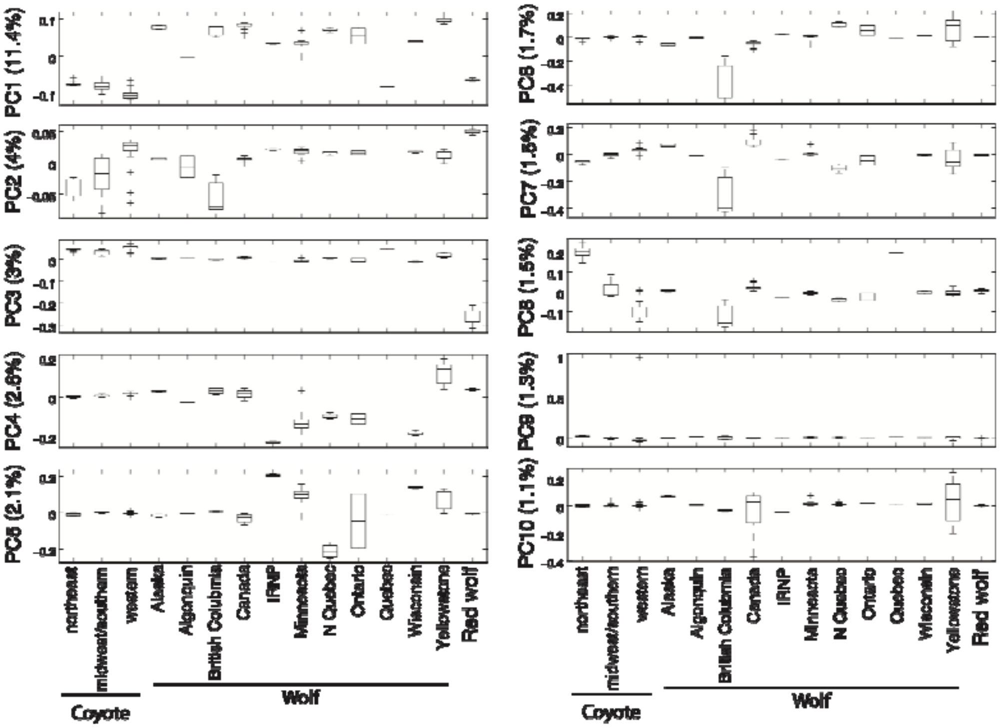


Supplemental Figure S3 (*continued*).

E.



F.



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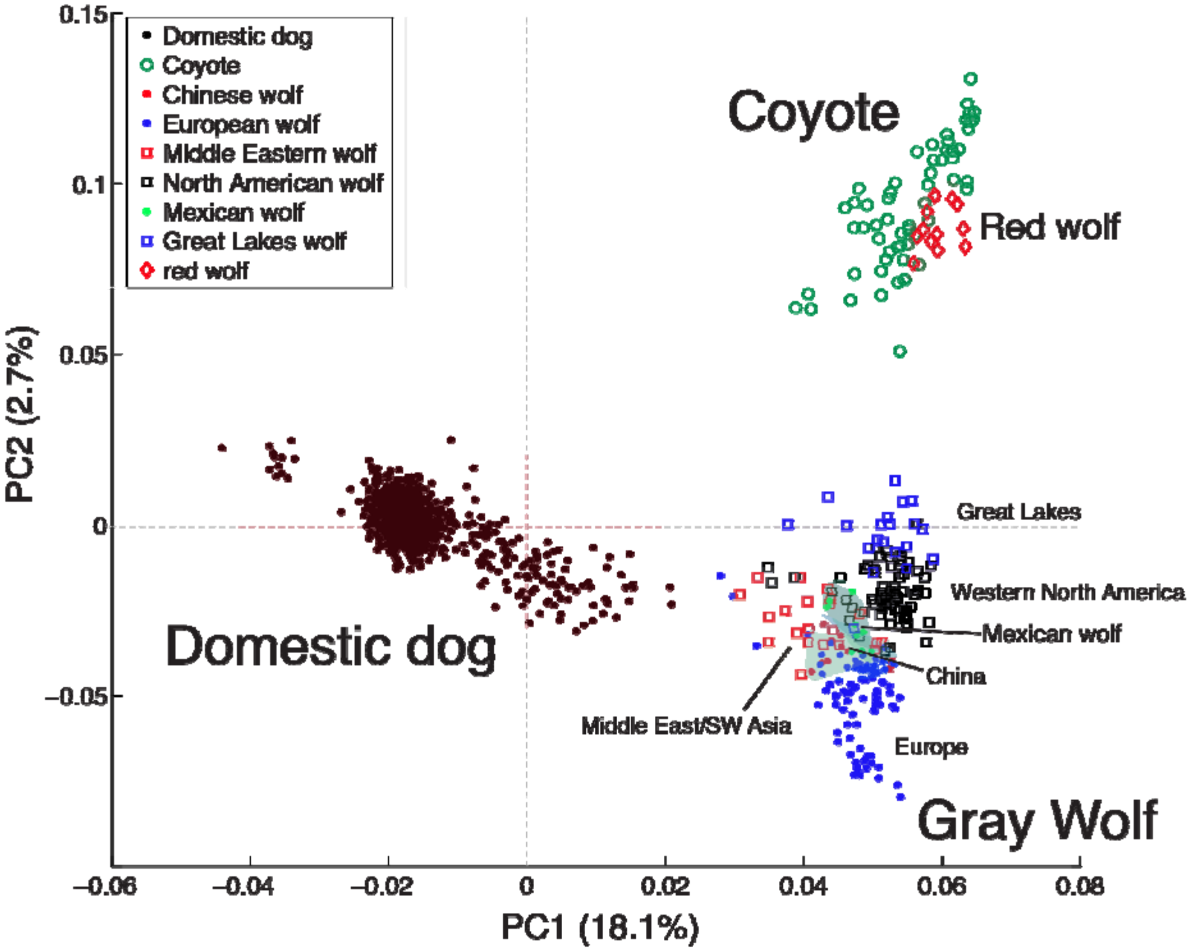
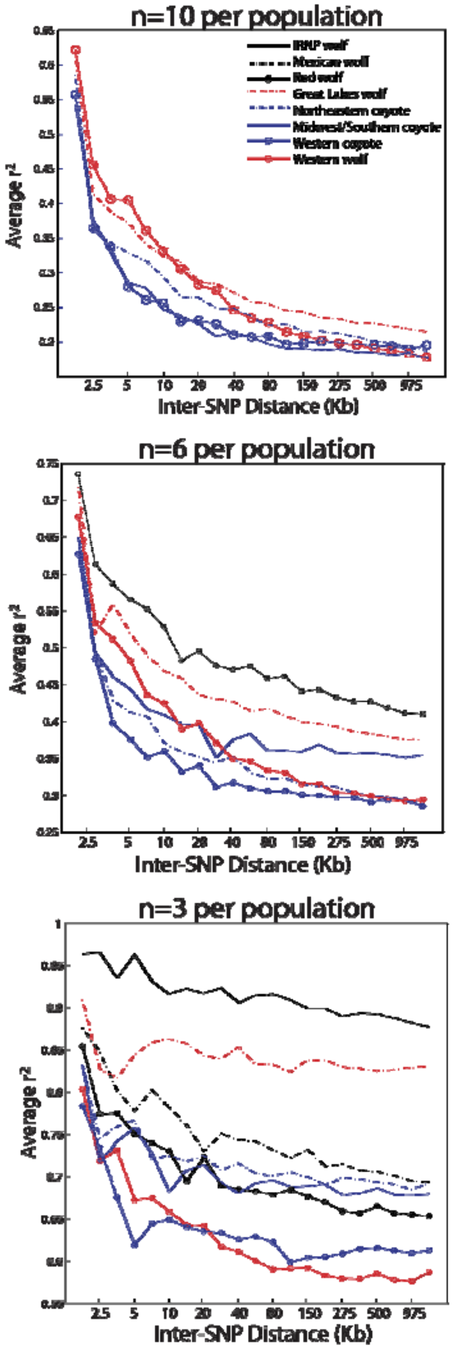


Supplemental Figure S5.

Supplemental Figure S6.



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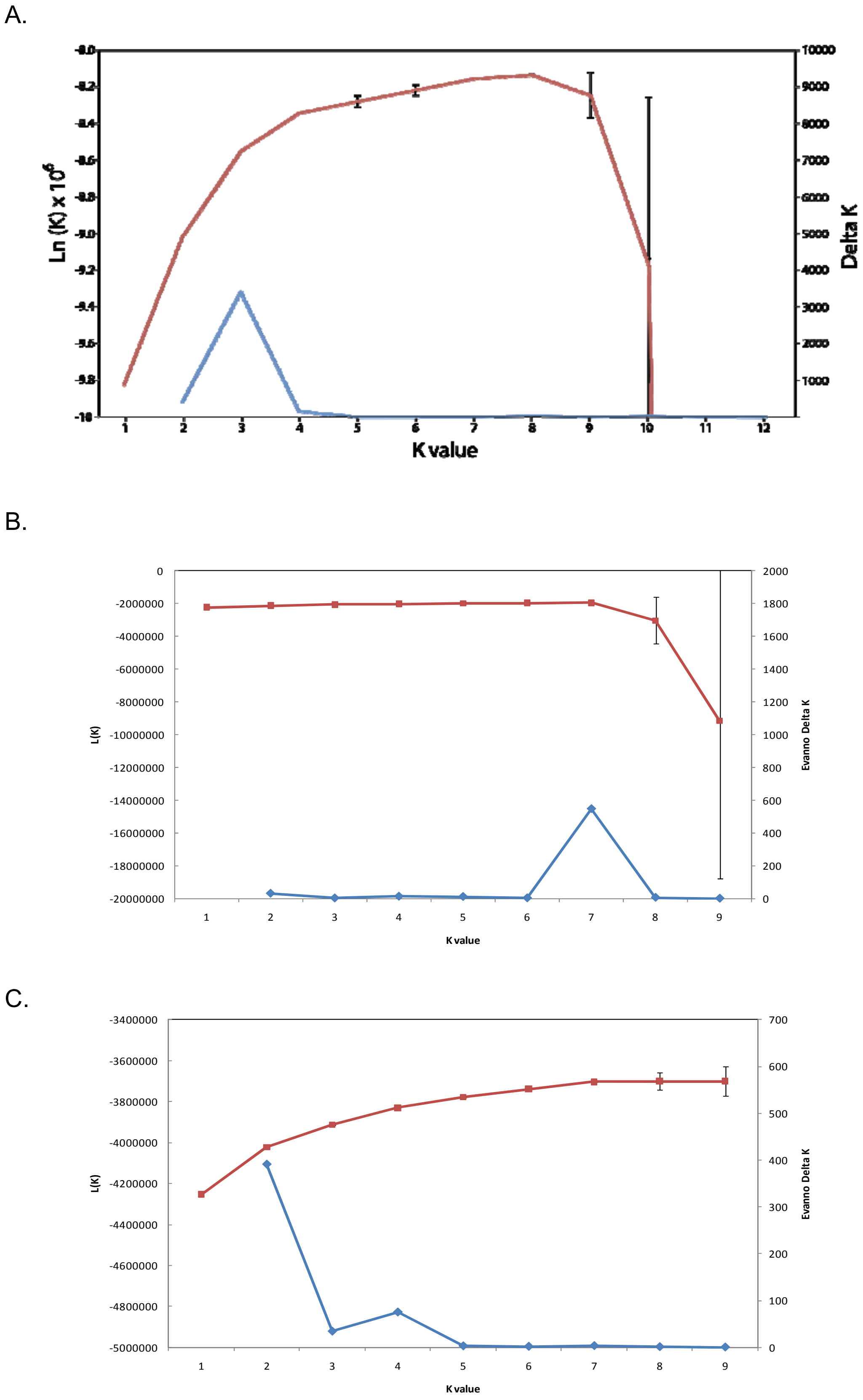

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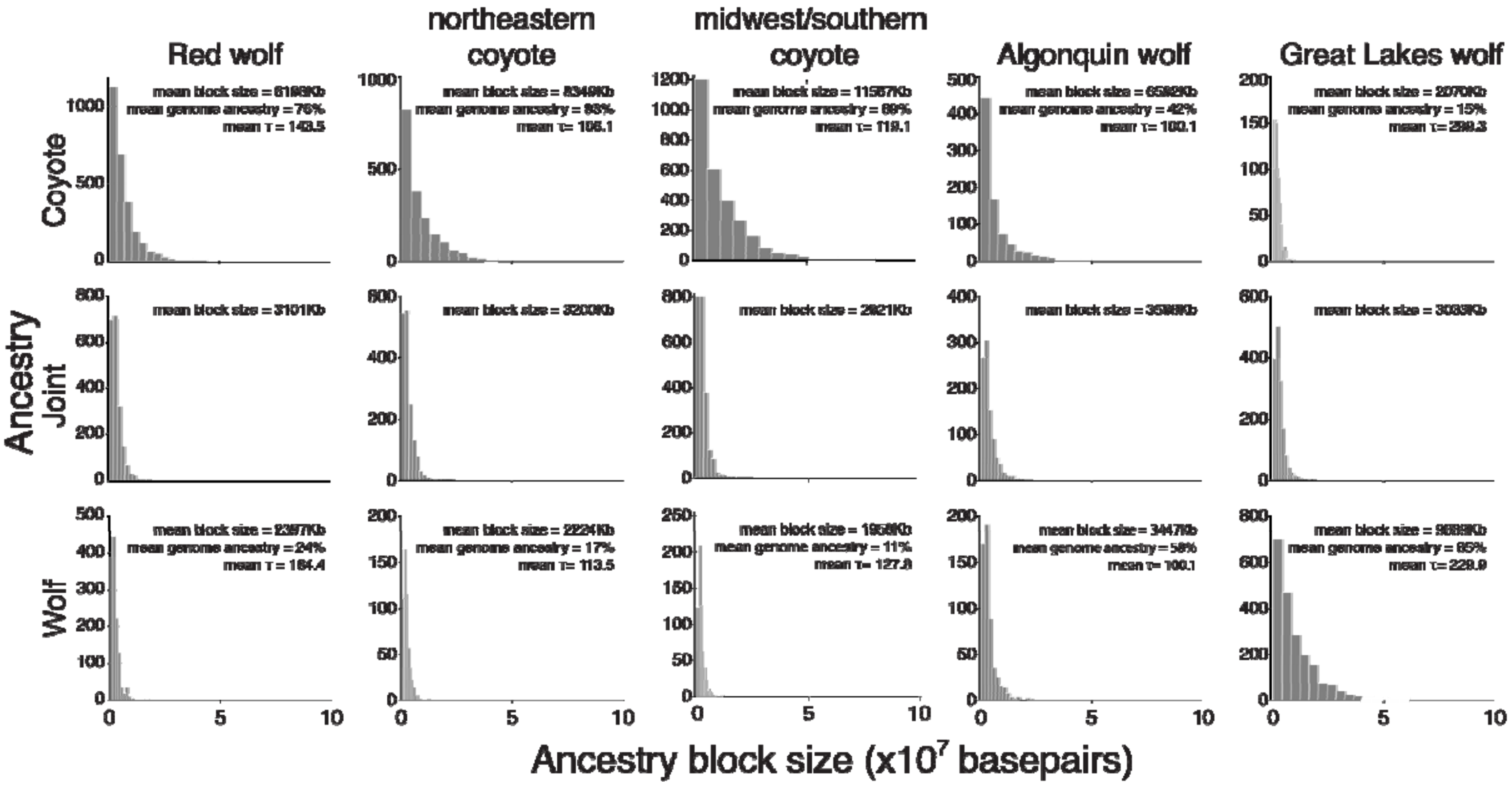

Supplemental Table S1. Summary of taxonomic investigations of the red wolf (**A**) and Great Lakes wolf (**B**).

A.

Reference*	Year	Approach	Taxonomic Conclusion	Hybridization**
Red wolf				
1	1937	morphology	Unique species – gray wolf ancestry	Recent, minor
2	1962	morphology	Unique species, one subspecies is coyote-red wolf hybrid	Recent, hybrid swam
3	1967	morphology	Subspecies of gray wolf	Recent, hybrid swam
4	1968	morphology	Subspecies of coyote	Recent, hybrid swam
5	1970	Review of data	Gray wolf-coyote hybrid	Recent, hybrid swam
6,7	1971,1978	Brain morphology	Unique species – gray wolf ancestry	-
8,9	1974,1978	morphology	Unique species – gray wolf ancestry	Recent, hybrid swam
10	1977	morphology	Unique species	Recent, hybrid swam
11	1979	morphology	Unique species – gray wolf ancestry	Recent, extensive
12-15	1979,1992,2002,2009	morphology	Unique species – gray wolf ancestry	Recent, extensive
16	1980	morphology	Unique species	Recent, hybrid swam
17	1991	mtDNA	Gray wolf – coyote hybrid	Recent, hybrid swam
18,19	1994,1996	mtDNA, microsatellites	Gray wolf – coyote hybrid	Recent, hybrid swam
20	1998	microsatellites	Unique species – coyote ancestry	Recent
21	1999	microsatellites	Gray wolf – coyote hybrid	Ancient/recent, hybrid swam
22-24	2000,2006,2008	mtDNA, microsatellites	Hybrid species, possibly conspecific w/ coyotes	Recent, extensive
25	2002	protein electrophoresis	Unique species – coyote ancestry	Recent, extensive
26	2002	MHC	Closely related to coyotes	Recent

Supplemental Table S1 (*continued*).

B.

Reference*	Year	Approach	Taxonomic Conclusion	Hybridization**
Great Lakes wolf				
1	1937	morphology	Gray wolf subspecies	Minor
27	1971	morphology	Gray wolf subspecies	Recent
28	1975	morphology	Gray wolf-coyote hybrid	Recent, extensive
29	1985	morphology	Gray wolf subspecies	Recent, extensive
18,30	1991,1994	mtDNA, microsatellites	Gray wolf – coyote hybrid	Recent, hybrid swam
22-24,31,32	2000, 2003, 2006, 2008, 2009	mtDNA, microsatellites	Unique species likely conspecific with red wolf – coyote ancestry	Recent, extensive
13,14	2002, 2009	morphology	Gray wolf subspecies	Recent, extensive
25	2002	protein electrophoresis	Gray wolf species or subspecies	Ancient
33	2008	mtDNA	-	Ancient/recent, hybrid swam
34,35	2008, 2010	Body size, review	Unique species	Recent, extensive
36	2010	morphology, mtDNA	--	Recent, hybrid swam
37	2009	mtDNA, microsatellites	Gray wolf subspecies	Ancient/recent, extensive
38-41	2009, 2010	morphology, ancient and recent mtDNA	Unique species – coyote ancestry	Ancient/recent, extensive
42	2009	mtDNA, microsatellites	Unique species – coyote ancestry	Ancient/recent, extensive
43	2010	mtDNA, microsatellites	Unique species	Ancient/recent, extensive

*We have cited multiple references in some rows to represent efforts of specific research groups, and in cases where data and analyses overlap considerably. However, many authors are often shared between papers in different rows.

**Hybridization with gray wolves, coyotes or both species. Recent, <500 years; Extensive, reported from multiple localities or a large geographic area; hybrid swam, hybridization throughout most of the population and/or the term specifically used by authors to describe the population.

Literature Cited: 1. Goldman 1937; 2. McCarley 1962; 3. Lawrence and Bossert 1967; 4. Paradiso 1968; 5. Mech 1970; 6. Atkins and Dillon 1971; 7. Atkins 1978; 8. Gipson et al. 1974; 9. Gipson 1978; 10. Elder and Hayden 1977; 11. Freeman and Shaw 1979; 12. Nowak 1979; 13. Nowak 2002; 14. Nowak 2009; 15. Nowak 1992; 16. Ferrell et al. 1980; 17. Wayne and Jenks 1991; 18. Roy et al. 1994; 19. Roy et al. 1996; 20. Bertorelle and Excoffier 1998; 21. Reich et al. 1999; 22. Wilson et al. 2000; 23. Kyle et al. 2006; 24. Kyle et al. 2008; 25. Mech and Federoff 2002; 26. Hedrick et al. 2002; 27. Mengel 1971; 28. Kolenosky and Stanfield 1975; 29. Schmitz and Kolenosky 1985; 30. Lehman et al. 1991; 31. Wilson et al. 2009; 32. Wilson and Rannala 2003; 33. Leonard and Wayne 2008; 34. Mech and Paul 2008; 35. Mech 2010; 36. Kays et al. 2010; 37. Koblmüller et al. 2009; 38. Rutledge et al. 2009; 39. Rutledge et al. 2010a; 40. Rutledge et al. 2010b; 41. Rutledge et al. 2010c; 42. Wheeldon and White 2009; and 43. Fain et al. 2010.

Supplemental Table S2. Number (N) of domestic and wild canids genotyped on the canine SNP array.

Common Name		N	Populations*
Canis familiaris	domestic dog	912	Worldwide
Canis aureus	golden jackal	2	Kenya, Africa
Canis mesomelas	black-backed jackal	6	South (2) and East (4) Africa
Canis adustus	side-striped jackal	1	Kenya, Africa
Canis simensis	Ethiopian wolf	4	Ethiopia, Africa
Canis rufus	red wolf	12	Captive colony
Canis latrans	*coyote*	57	
	midwestern/southern	19	Alabama (2), Illinois (5), Louisiana (3), Mississippi (2), Ohio (3), Virginia (4)
	northeastern	13	Connecticut (1), New Hampshire (1), New York (8), Quebec (1), Vermont (2)
	western	25	Alaska (2), California (12), Manitoba (5), Utah (2), Washington (4)
Canis lupus	*gray wolf*	208	
	Western and eastern North America	3	Alaska
		10	North Quebec
		18	Yellowstone NP
		26	Canada
		3	British Columbia
	Great Lakes	19	Isle Royale NP (3), Algonquin NP (2), Minnesota (11), southern Quebec (1), Ontario (2), and Wisconsin (4)
	Balkans, eastern and northern Europe	57	Belarus (7), Bulgaria (3), Croatia (3), Greece (1), Lithuania (1), Poland (8), Russia (18), Slovakia (3), Sweden (2), and Ukraine (11)
		20	Italy
		10	Spain
	Middle East	16	Israel (8), Oman (3), and Saudi Arabia (5)
	southwest Asia	6	India (3), Iran (2), and Turkey (1)
	China	10	
	Mexican wolf	10	Aragon (2), Ghost Ranch (3) and Studbook (5) lineages

*sample size per population is indicated in parentheses

Supplemental Table S3. F_{ST} for the 48K SNP dataset in North American canids (**A**), North American wolf populations (**B**), and Old World wolf populations (**C**; boxed areas represent Middle East, *upper left*, and Europe, *lower right*).

A.

Group	midwestern/ southern coyote	northeastern coyote	western wolf	Great Lakes wolf	Mexican wolf	Red wolf
western coyote	0.03	0.05	0.14	0.11	0.18	0.10
midwestern/southern coyote		0.02	0.12	0.08	0.15	0.08
northeastern coyote			0.11	0.08	0.15	0.09
western wolf				0.05	0.10	0.12
Great Lakes wolf					0.11	0.11
Mexican wolf						0.18
Red wolf						

B.

Group	BC	Canada	N Quebec	Yellowstone	Algonquin	IRNP	Minnesota	Ontario	Wisconsin
Alaska	0.07	0.01	0.06	0.03	0.04	0.10	0.04	0.00	0.06
British Columbia		0.06	0.11	0.08	0.10	0.16	0.08	0.07	0.10
Canada			0.05	0.03	0.03	0.07	0.05	0.01	0.05
N Quebec				0.08	0.05	0.11	0.07	0.00	0.08
Yellowstone					0.05	0.10	0.07	0.03	0.08
Algonquin						0.12	0.01	0.00	0.04
IRNP							0.04	0.09	0.07
Minnesota								0.02	0.00
Ontario									0.01

Supplemental Table S3 (continued).

C.

Group	India	Iran	Israel	Oman	Turkey	Belarus	Bulgaria	Croatia	Greece	Italy	Lithuania	Poland	Russia	Slovakia	Spain	Sweden	Ukraine	China
Saudi Arabia	0.16	0.13	0.10	0.08	0.09	0.12	0.13	0.14	0.12	0.21	0.11	0.12	0.11	0.14	0.17	0.13	0.11	0.12
India		0.01	0.09	0.12	0.14	0.09	0.11	0.11	0.16	0.19	0.15	0.09	0.07	0.12	0.15	0.14	0.06	0.08
Iran			0.05	0.07	0.11	0.05	0.06	0.02	0.13	0.16	0.13	0.05	0.04	0.09	0.13	0.13	0.01	0.05
Israel				0.06	-0.02	0.07	0.06	0.07	0.01	0.18	0.00	0.07	0.07	0.08	0.13	0.05	0.06	0.08
Oman					-0.03	0.07	0.06	0.03	0.00	0.20	-0.01	0.08	0.08	0.09	0.15	0.07	0.05	0.08
Turkey						-0.03	-0.05	-0.17	0.00	0.10	0.00	-0.03	-0.02	0.00	0.06	0.08	-0.08	-0.03
Belarus							0.01	0.04	-0.04	0.15	-0.06	0.01	0.00	0.02	0.09	0.01	0.00	0.05
Bulgaria								-0.02	-0.07	0.15	-0.06	0.01	0.01	0.02	0.10	0.03	-0.02	0.04
Croatia									-0.17	0.21	-0.18	0.04	0.06	0.02	0.14	-0.01	0.00	0.06
Greece										0.09	0.00	-0.04	-0.02	0.00	0.06	0.08	-0.09	-0.02
Italy											0.09	0.14	0.12	0.16	0.16	0.11	0.14	0.16
Lithuania												-0.06	-0.04	-0.01	0.05	0.07	-0.11	-0.03
Poland													0.01	0.01	0.09	0.01	0.00	0.05
Russia														0.02	0.08	0.00	0.01	0.05
Slovakia															0.11	0.05	-0.01	0.05
Spain																0.08	0.08	0.12
Sweden																	-0.02	0.03
Ukraine																		0.04

Supplemental Table S4. Analysis of molecular variation for groupings of coyote and wolf populations (df = degrees of freedom, SS = sum of squares; *$p<0.05$; **$p<0.001$).

Groupings[‡]	Grouping tested	df	SS	Variance component	Percent of variation	Fixation Index
1. All wolves: (Old World wolves)(North American wolves)	Among groups	1	1.7	0.01*	4.7	$F_{ST} = 0.19$
	Among populations within groups	5	2.3	0.02**	14.2	
	Within populations	202	21.3	0.11**	81.1	
2. Old World wolves: (China)(Europe)(Middle East, SW Asia)	Among groups	2	1.0	0.01*	6.0	$F_{ST} = 0.27$
	Among populations within groups	15	3.6	0.03**	21.0	
	Within populations	95	8.8	0.09**	73.0	
3. Old World wolves: (Italy)(Spain)(SW Asia)(China)	Among groups	3	1.7	0.01	9.0	$F_{ST} = 0.39$
	Among populations within groups	2	0.3	0.04*	30.2	
	Within populations	39	3.0	0.08**	60.8	
4. North American wolves: (Western)(Great Lakes)(Mexican wolf)	Among groups	2	0.9	0.01**	10.4	$F_{ST} = 0.24$
	Among populations within groups	8	1.4	0.02**	13.8	
	Within populations	60	5.3	0.09**	75.8	
5. North American canids: (BC, N Quebec, Great Lakes, Mexican wolf, red wolf)(coyotes)	Among groups	1	1.2	0.01	10.4	$F_{ST} = 0.30$
	Among populations within groups	6	2.2	0.02**	19.1	
	Within populations	106	8.6	0.08**	70.5	
6. North American canids: (BC, N Quebec, Great Lakes, Mexican wolf)(coyotes, red wolf)	Among groups	1	1.3	0.02*	14.0	$F_{ST} = 0.31$
	Among populations within groups	6	2.1	0.02**	16.9	
	Within populations	106	8.6	0.08**	69.1	

[‡] Groupings: *Old World wolves:* 1. Belarus, 2. Bulgaria, 3. Croatia, 4. Italy, 5. Poland, 6. Russia, 7. Slovakia, 8. Spain, 9. Sweden, 10. Ukraine, 11. Saudi Arabia, 12. Oman, 13. Israel, 14. India 15. Iran, 16. Turkey, 17. China; [Europe: 1-10] [Middle East: 11-13] [SW Asia: 14-16]; *North American wolves:* 18. Alaska, 19. British Columbia, 20. Canada Forest, 21. Canada Tundra, 22. North Quebec, 23. Yellowstone NP, 24. Algonquin, 25. IRNP, 26. Minnesota, 27. Quebec, 28. Ontario, 29. Wisconsin [western: 18-23] [Great Lakes: 24-29]; 30. Mexican wolf; *Coyotes:* 31. western, 32. midwestern/southern, 33. northeastern; and 34. Red wolf.

Supplemental Table S5. Haplotype block size (standard error, SE), generations since admixture (τ) and genome-wide ancestry per individual. Joint indicates an assignment to both coyote and wolf ancestry.

Individual	Coyote block (Kb)	Joint block (Kb)	Wolf block (Kb)	Coyote τ	Wolf τ	Coyote Ancestry (%)	Wolf Ancestry (%)
Reference populations							
western coyote (n=12)						100	0
western gray wolf (n=12)						0	100
Algonquin wolf							
1	2783.5	4547.3	3466.3	125	125	44.1	55.9
2	3032.8	3291.8	4446.1	75.2	75.2	39.7	60.3
Average (SE)	6592.2 (280)	3597.5 (100)	3446.9 (134)	100.1 (24.9)	100.1 (24.9)	41.9 (2.2)	58.1 (2.2)
Red wolf							
1	6470.3	3125.9	2612.2	148.9	192.8	76.8	23.2
2	6542.3	3243.0	2510.1	128.1	161.5	77.2	22.8
3	6183.7	2815.6	2549.7	124.9	156.3	75.3	24.7
4	6131.6	3534.8	2367.4	135.8	173.8	74.3	25.7
5	6286.3	3420.5	2502.3	128.5	162.3	74.9	25.1
6	6330.0	2680.0	2292.0	148.6	192.6	78.1	21.9
7	5739.0	3084.4	2416.6	140.3	180.5	75.1	24.9
8	5970.2	3180.8	2248.3	155.9	202.9	75.3	24.7
9	6449.2	3132.5	2379.9	133.6	170.3	76.2	23.8
10	6044.2	2978.2	2226.5	157.8	205.3	76.9	23.1
11	6162.7	2820.5	2600.0	146.5	189.5	76.2	23.8
12	6123.6	2933.6	2103.4	178.7	233.7	77.7	22.3
Average (SE)	6197.5 (115)	3101.3 (52)	2396.9 (49)	143.5 (4.5)	184.4 (6.5)	76.1 (0.3)	23.9 (0.3)
Great Lakes wolf							
1	2066.9	3241.2	8459.0	254.5	194.5	15.7	84.3
2	2139.2	2883.0	9731.4	355.7	273.9	14.3	85.7
3	2006.2	3348.6	9482.4	272.7	208.3	14.4	85.6
4	2151.8	3324.4	9245.6	394.9	304.6	15.7	84.3

5	1710.8	3041.2	1014.0	277.4	212.7	13.4	86.6
6	1837.8	2983.8	9581.2	341.1	262.6	14.2	85.8
7	2180.9	2871.9	9358.9	341.8	262.8	14.6	85.4
8	2163.1	3132.1	1028.4	271.5	207.6	14.6	85.4
9	1870.8	2818.3	9725.5	243.9	186.5	14.8	85.2
10	2340.2	2939.8	1052.1	197.9	152.3	14.1	85.9
11	2162.5	2838.4	9340.6	417.6	322.2	13.9	86.1
12	2136.4	2924.6	10744.8	222.9	170.7	14.0	86.0
13	1387.0	2178.1	4884.7	102.7	100.8	19.5	80.5
14	1408.9	1683.9	6538.1	231.5	177.3	13.5	87.0
15	1383.3	1789.6	6968.6	166.8	131.3	13.7	86.3
16	1420.3	1560.1	5827.9	489.9	378.8	15.5	84.5
17	1602.8	1445.9	6199.2	435.8	336.7	16.2	83.8
18	1483.1	1809.0	5693.4	323.5	248.0	16.7	83.3
Average (SE)	1735.5 (35)	2541.2 (45)	8016.3 (135)	296.7 (24)	229.5 (18)	14.9 (0.3)	85.1 (0.4)

Supplemental Table S6. Analysis of genome-wide ancestry for the admixed coyote populations assuming three non-admixed ancestral populations.

Individual	Location/ Population	Coyote τ	Wolf τ	Dog τ	Coyote Ancestry (%)	Wolf Ancestry (%)	Dog Ancestry (%)
Reference populations							
domestic dog (n=12)					0	0	100
western coyote (n=12)					100	0	0
western gray wolf (n=12)					0	100	0
northeastern coyote							
1	New York	41.3	109.5	12.7	80.2	7.0	12.8
2	Quebec	111.9	64.7	11.4	81.8	9.4	8.8
3	Vermont	220.8	60.1	11.4	84.5	9.6	5.9
4	Vermont	54.5	64.0	15.2	84.2	8.3	7.5
5	New York	81.8	48.5	17.0	82.0	6.6	11.4
6	Connecticut	149.7	74.3	14.5	81.1	6.9	12.0
7	New York	52.6	87.9	17.4	84.1	10.7	5.2
8	New York	71.7	142.0	21.3	82.8	6.5	10.7
9	New York	147.2	88.4	11.1	83.7	10.0	6.3
10	New York	63.3	50.6	19.6	82.3	6.4	11.3
11	New York	125.8	129.4	16.5	80.0	9.7	10.3
12	New York	24.5	71.5	10.5	81.1	8.6	10.3
13	New Hampshire	101.9	123.1	24.1	80.6	13.1	6.3
Average (SE)		95.9 (15.2)	50.6 (11.6)	15.6 (1.2)	82.2 (0.4)	8.7 (0.6)	9.1 (0.7)
midwestern/southern coyote							
1	Illinois	200.1	595.6	17.9	92.7	1.3	6.0
2	Illinois	45.6	145.2	16.3	94.5	1.4	4.1
3	Illinois	113.9	173.1	38.3	96.3	0.4	3.3
4	Illinois	94.2	91.9	21.0	93.0	1.1	5.9
5	Illinois	101.0	221.6	8.3	97.8	0.3	1.9
6	Virginia	17.9	66.4	9.3	80.7	2.4	16.9
7	Virginia	89.6	93.5	11.4	83.1	2.9	14.0
8	Virginia	46.2	138.5	12.0	86.0	2.3	11.7
9	Virginia	75.6	43.7	7.2	90.2	1.0	8.8
10	Alabama	101.1	147.2	18.4	90.8	3.8	5.4

11	Alabama	7.6	89.6	14.7	89.8	2.1	8.1
12	Louisiana	96.2	114.3	10.1	92.5	5.2	2.3
13	Louisiana	193.7	118.0	7.4	93.5	4.2	2.3
14	Louisiana	65.2	138.1	14.4	90.6	6.4	3.0
15	Mississippi	19.4	205.4	12.5	92.1	5.0	2.9
16	Mississippi	7.0	39.0	12.5	90.4	2.1	7.5
17	Ohio	63.1	78.6	20.4	90.4	0.9	8.7
18	Ohio	31.8	86.4	15.9	84.9	1.6	13.5
19	Ohio	62.6	72.3	9.4	81.8	1.5	16.7
Average (SE)		75.4 (12.5)	139.9 (27.8)	14.6 (1.6)	90.1 (1.1)	2.4 (0.4)	7.5 (1.1)

Supplemental Table S7. Haplotype block size (standard error, SE), generations since admixture (τ) and genome-wide ancestry per individual. Joint indicates an assignment to both western coyote and Northern Quebec gray wolf ancestry.

Individual	Coyote block (Kb)	Joint block (Kb)	Wolf block (Kb)	Coyote τ	Wolf τ	Coyote Ancestry (%)	Wolf Ancestry (%)
Reference populations							
western coyote (n=12)						100	0
Northern Quebec gray wolf (n=12)						0	100
Algonquin wolf							
1	1732	2367	2221	100.0	100.1	43.2	56.8
2	1788	1907	2791	74.8	74.9	39.5	60.5
Average (SE)	1760 (28)	2137 (230)	2506 (285)	87.4 (12.6)	87.4 (12.6)	41.4 (1.9)	58.7 (1.9)
Red wolf							
1	4643	1997	1768	135.0	172.4	78.2	21.8
2	4618	1777	1654	133.7	170.5	79.0	21.0
3	4163	1861	1703	121.1	149.9	76.4	23.6
4	4345	1899	1816	135.5	173.2	76.9	23.1
5	4381	1923	1705	127.8	161.1	77.1	22.9
6	4303	2028	1517	148.5	192.4	78.1	21.9
7	4230	2020	1686	124.1	155.1	76.2	23.8
8	4498	1812	1615	152.0	197.3	77.2	22.8
9	4569	1804	1839	129.8	164.3	78.0	22.0
10	4182	1917	1452	154.2	200.3	78.1	21.9
11	4406	1799	1649	135.5	173.3	77.4	22.6
12	4582	2017	1585	161.3	210.3	78.5	21.5
Average (SE)	4410 (49)	1905 (27)	1666 (33)	138.2 (3.7)	176.7 (5.5)	77.6 (0.3)	22.4 (0.9)
Great Lakes wolf							
1	1298	1739	6062	378.7	290.1	14.5	85.5
2	1390	1599	6476	416.3	321.5	13.8	86.2
3	1447	1743	6468	393.5	302.1	13.7	86.3

4	1404	1663	6122	379.9	291.9	15.0	85.0
5	1306	1750	6535	289.0	221.3	13.4	86.6
6	1184	1637	5860	478.9	371.3	13.8	86.2
7	1219	1602	5872	408.2	315.2	14.1	85.9
8	1376	1791	6627	268.4	205.1	13.5	86.5
9	1193	1725	6214	345.7	265.7	13.9	86.1
10	1320	1375	5979	240.6	183.8	13.8	86.2
11	1299	1640	6905	353.1	271.5	13.0	87.0
12	1348	1703	6847	257.9	197.3	14.1	85.9
13	1444	2136	4733	137.2	114.3	20.2	79.8
14	1321	1646	6972	235.7	180.3	12.5	87.5
15	1324	1837	6463	217.2	166.5	14.1	85.9
16	1421	1625	6070	445.5	343.3	15.2	84.8
17	1559	1580	6322	416.8	321.0	15.7	84.3
18	1411	1847	6049	339.4	260.6	15.8	84.2
Average (SE)	1348 (23)	1702 (36)	6254 (121)	333.4 (21.7)	256.8 (16.6)	14.5 (0.4)	85.6 (0.4)