Electronic supplement

Demographic mechanisms underpinning genetic assimilation of remnant groups of a large carnivore

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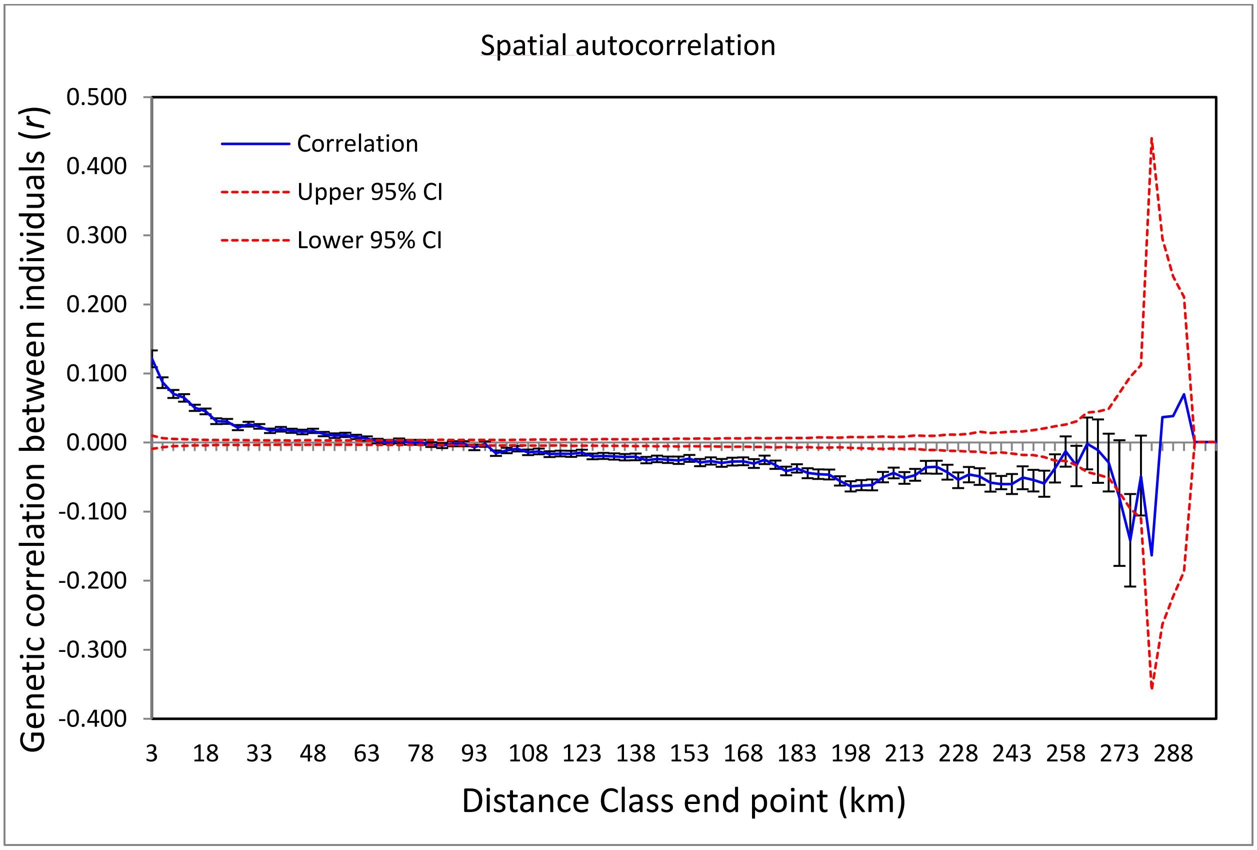
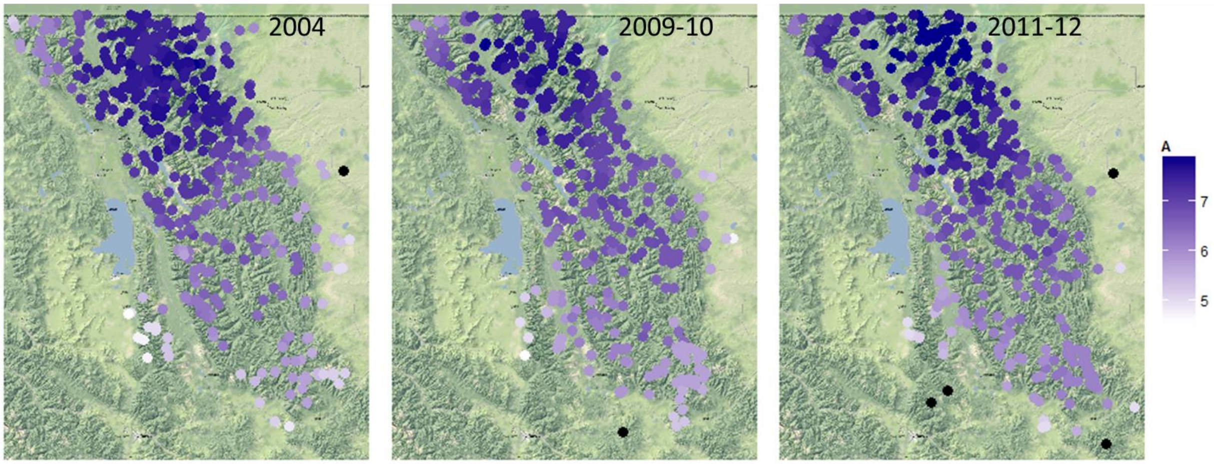
Supplementary Figures

Supplementary figure 1



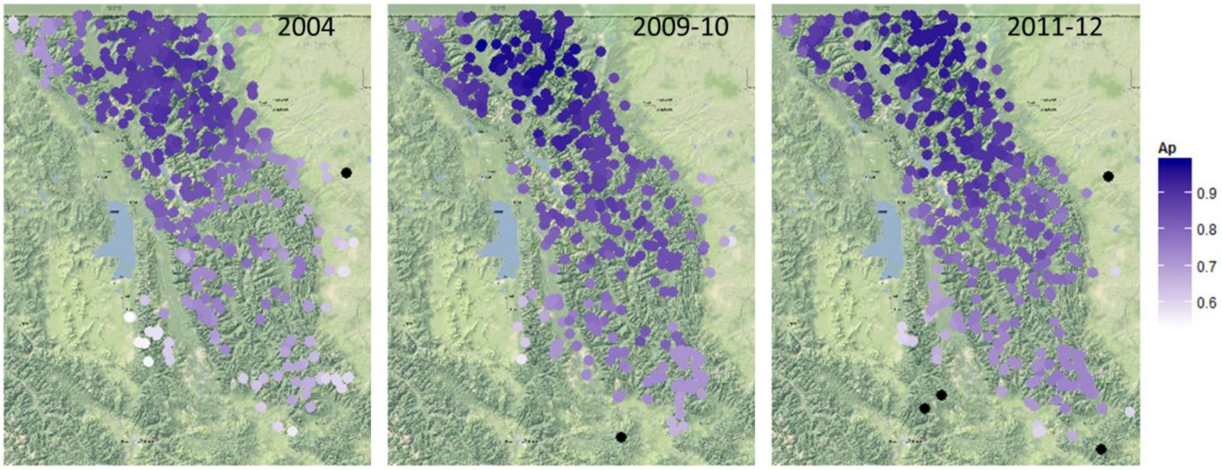
Supplementary figure 1. Correlogram of dataset spatial autocorrelation. Distance bins were in 3 kilometer intervals and showed positive spatial autocorrelation from 3-66 kilometers. The dashed red lines represent the 95% confidence intervals for the null hypothesis that the genetic correlation between individuals is 0. 66 kilometers was subsequently utilized as the neighborhood size.

Supplementary figure 2



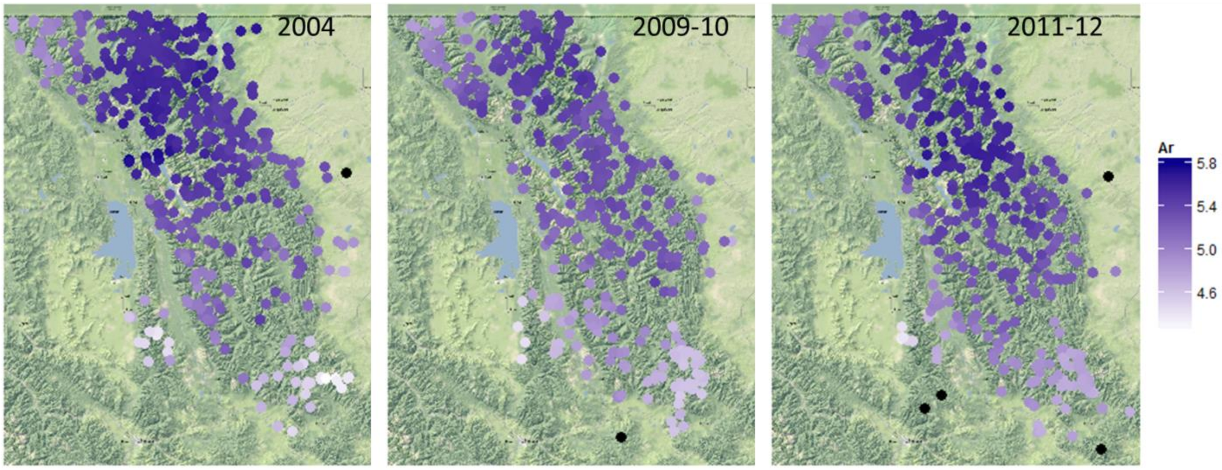
Supplementary figure 2. Number of alleles per locus (A) in the NCDE. Black dots indicate areas with at least one individual that did not have the minimum of 10 individuals in a neighborhood desired to estimate genetic metrics.

Supplementary figure 3



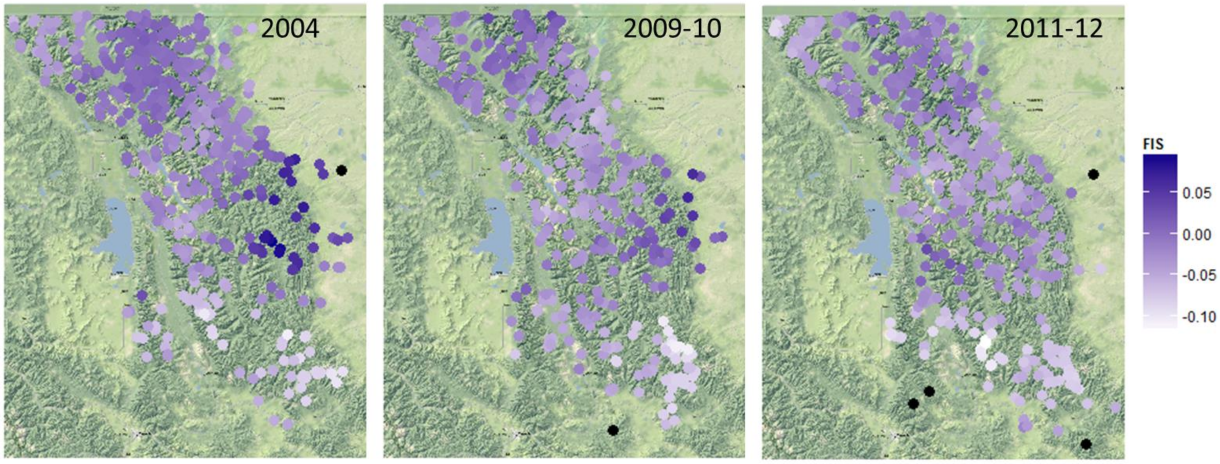
Supplementary figure 3. Genetic neighborhood allelic proportion (A_P) in the NCDE. Black dots indicate areas with at least one individual that did not have the minimum of 10 individuals in a neighborhood desired to estimate genetic metrics.

Supplementary figure 4



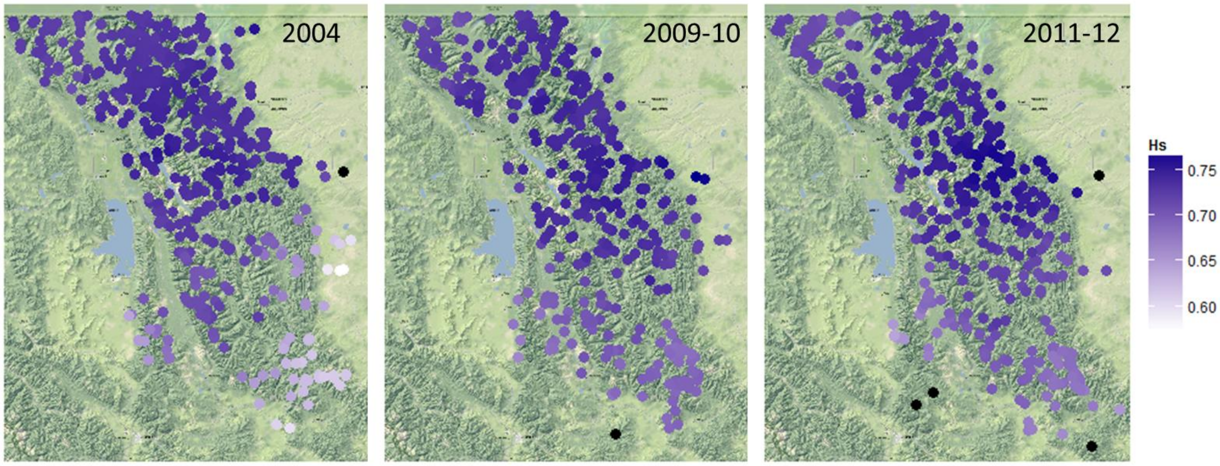
Supplementary figure 4. Allelic richness (A_R) in the NCDE. Black dots indicate areas with at least one individual that did not have the minimum of 10 individuals in a neighborhood desired to estimate genetic metrics.

Supplementary figure 5



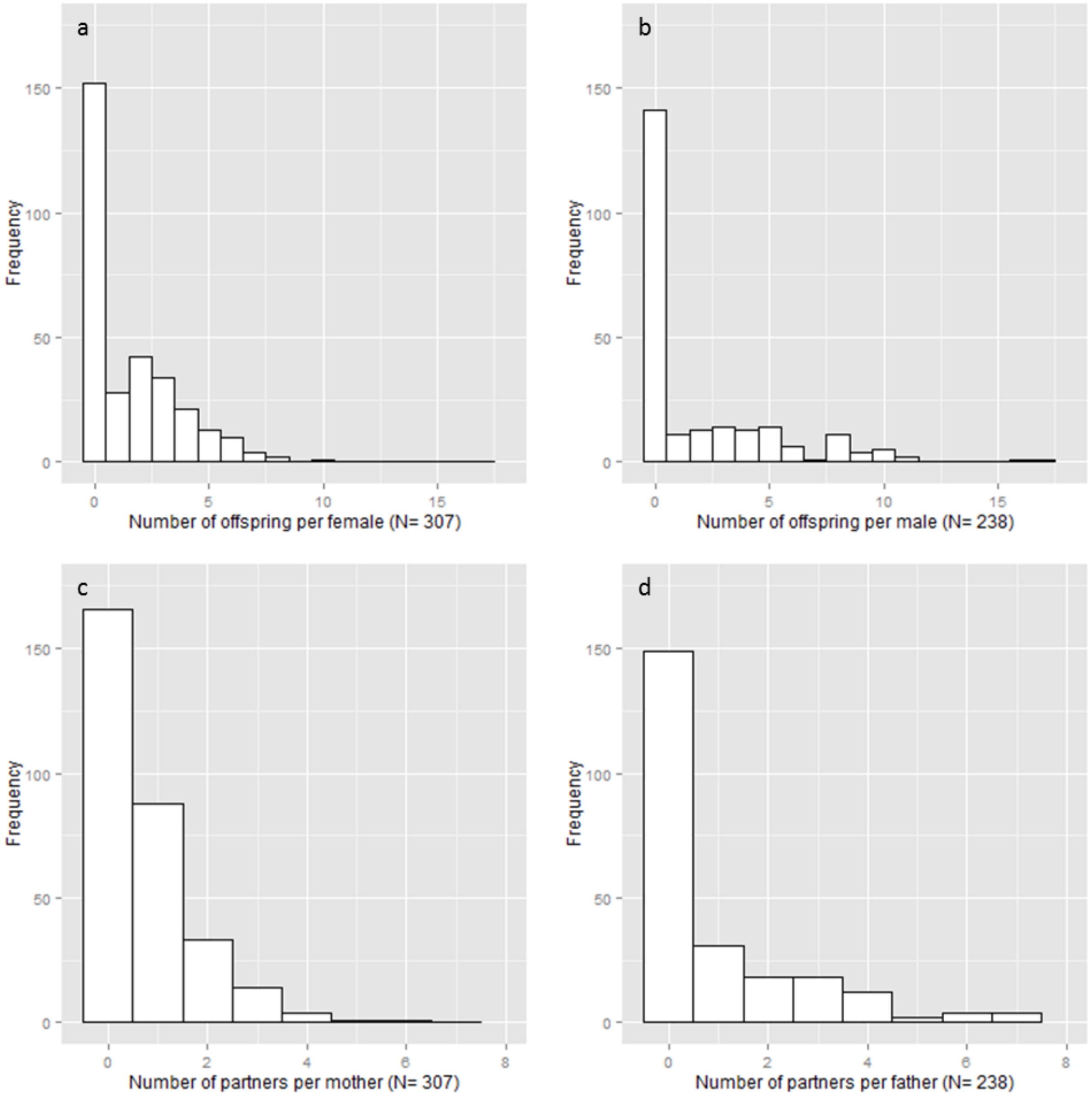
Supplementary figure 5. Inbreeding coefficient (F_{IS}) in the NCDE. Black dots indicate areas with at least one individual that did not have the minimum of 10 individuals in a neighborhood desired to estimate genetic metrics.

Supplementary figure 6



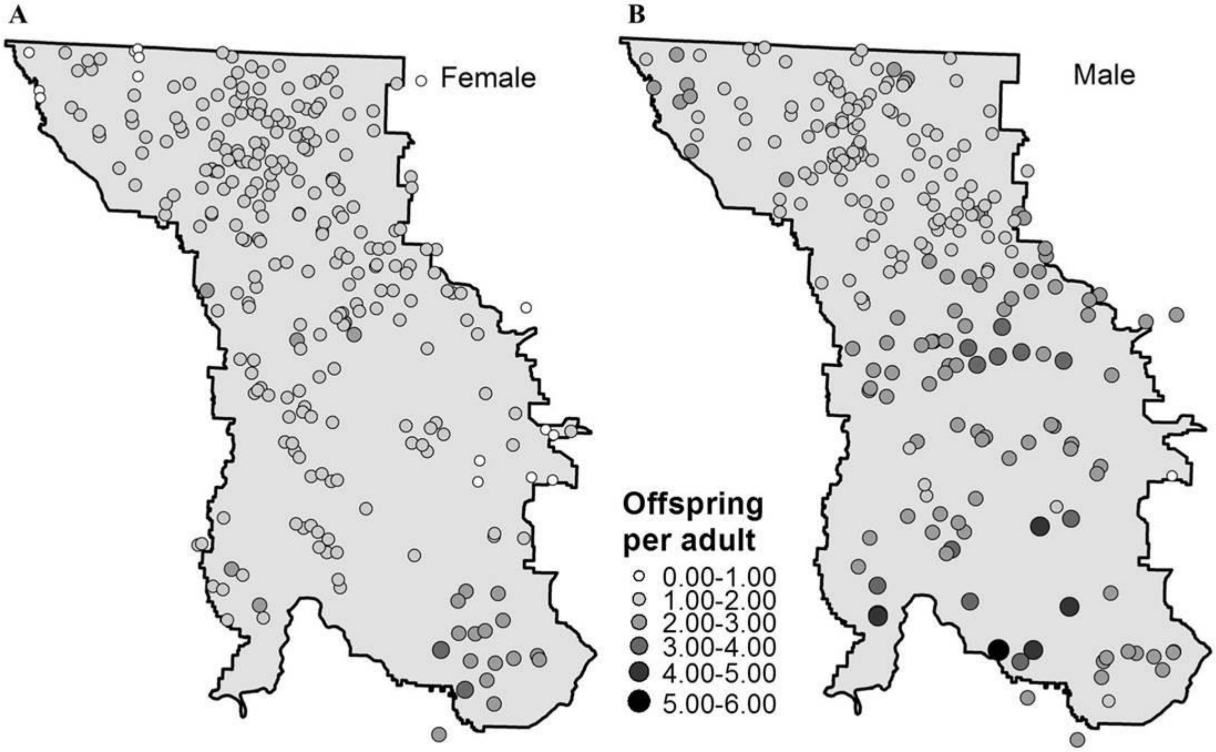
Supplementary figure 6. Nei's genetic diversity (H_S) in the NCDE. Black dots indicate areas with at least one individual that did not have the minimum of 10 individuals in a neighborhood desired to estimate genetic metrics.

Supplementary figure 7



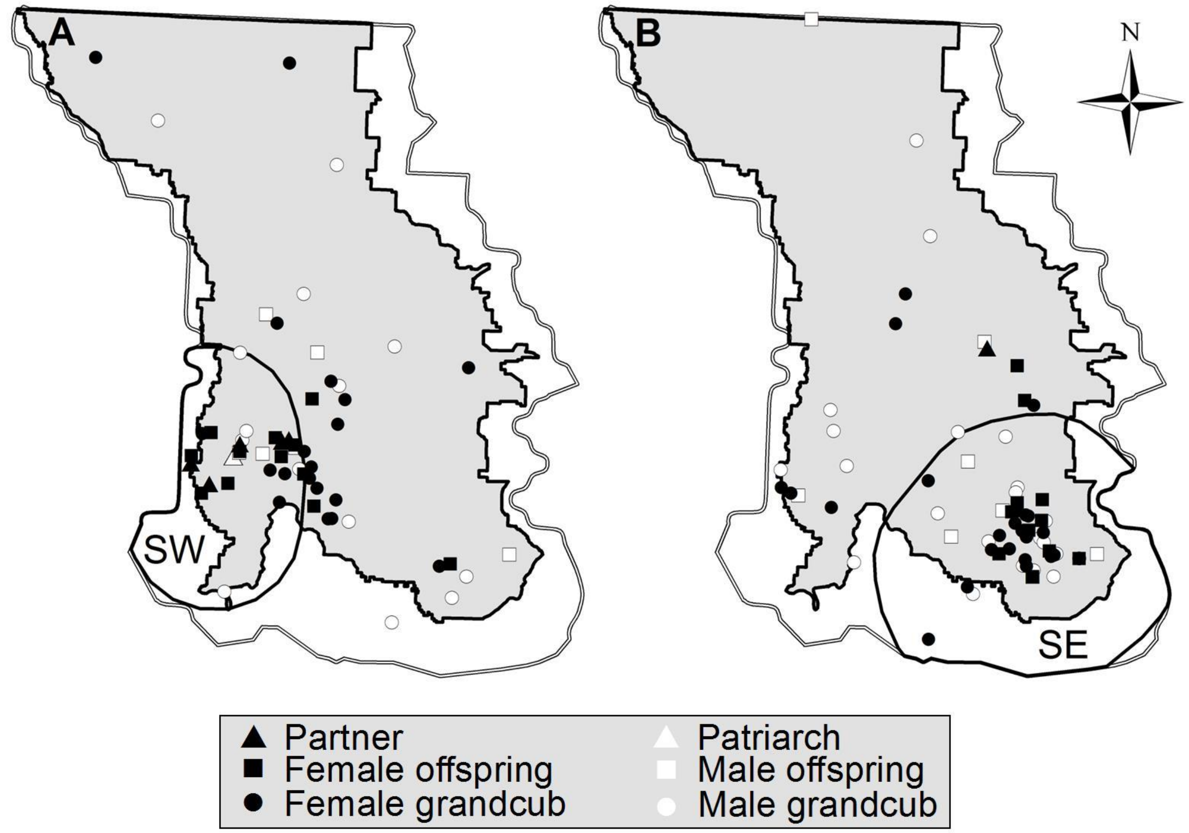
Supplementary figure 7. Histograms of individual reproductive success (a, b) and promiscuity (c, d). Figures show results from samples collected in 2004. Matings between a sampled bear and an inferred bear (undetected) were not included and would increase the estimated number of mates per individual. Some mate pairs were more productive than others; 5 pairings produced 4 offspring each, and 2 pairings produced 5 offspring each (one pair in the SW, one pair in the SE).

Supplementary figure 8



Supplementary figure 8. The average number of offspring per individual within a genetic neighborhood. Large, dark-coloured circles represent high reproductive success, and small, light-coloured circles represent no and low reproductive success.

Supplementary figure 9



Supplementary figure 9. Two generations of descendants of reproductively dominant individuals. Panel a) features the descendants of a sampled male individual in the SW region which had 61 sampled descendants and b) 101 sampled descendants of an inferred male in the SE.

Supplementary Tables

Supplementary table 1, Summary of the number of loci contained in each genotype. Note that for individuals with a single missing allele at a locus, the entire locus was considered missing for this summary.

Number of loci genotyped	Overall count	2004 count
6	1	0
7	116	0
8	5	0
9	57	0
10	2	0
11	74	0
12	4	0
13	1	1
14	46	0
15	15	0
16	144	32
17	1	0
20	1	0
21	1	0
22	4	2
23	6	3
24	637	507

Supplementary table 2. List of loci genotyped along with summary of overall genetic diversity. The first 7 loci (shaded) were used in the spatial genetic diversity analysis because they were consistently typed across all sampling periods.

Locus	Number genotyped	Number of alleles	Observed heterozygosity (H_O)	Expected heterozygosity (H_E)
G10J	1114	6	0.739	0.754
G1A	1115	7	0.735	0.719
G10B	1115	10	0.765	0.772
G1D	1109	12	0.799	0.794
G10H	1110	11	0.650	0.674
G10M	1115	9	0.707	0.712
G10P	1115	7	0.767	0.776
G10C	960	5	0.672	0.652
CXX110	944	8	0.794	0.803
CXX20	858	6	0.577	0.589
G10L	984	6	0.615	0.643
MU50	918	9	0.679	0.720
MU59	882	8	0.634	0.652
G10U	856	7	0.523	0.517
MU23	819	6	0.707	0.706
G10X	807	8	0.468	0.478
REN145.P07	648	4	0.597	0.629
MSUT2	646	6	0.735	0.753
CPH9	644	5	0.632	0.659
MU51	645	6	0.631	0.631
REN144.A06	648	7	0.401	0.383
MU26	644	6	0.643	0.664
D123	650	5	0.340	0.360
D1A	647	6	0.748	0.796

Supplementary table 3. Mean diversity metrics for each region and the core population over time. Allelic richness was calculated within regions only, not between regions.

Region	Allelic richness (AR)	Observed heterozygosity (HO)	Expected heterozygosity (HE)	Inbreeding coefficient (FIS)
EC 2004	6.75	0.69	0.72	0.04
EC 2009-10	6.82	0.74	0.74	0.00
EC 2011-12	6.84	0.76	0.74	-0.02
SE 2004	5.83	0.67	0.64	-0.06
SE 2009-10	5.96	0.73	0.70	-0.05
SE 2011-12	5.90	0.73	0.69	-0.06
SW 2004	5.27	0.70	0.68	-0.04
SW 2009-10	5.41	0.72	0.67	-0.07
SW 2011-12	5.40	0.70	0.67	-0.04
Core (GNP) 2004	7.63	0.73	0.73	0.00
Core (GNP) 2009-10	7.70	0.75	0.74	-0.01
Core (GNP) 2011-12	7.88	0.75	0.74	-0.01