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Appendix 1–4

Appendix 1. Supplementary figures and tables	2
Appendix 2. Result using volume of intersection (VI)	8
Appendix 3. Distances between random locations	11
Appendix 4. Genetic analysis	13

Appendix 1

Supplementary figures and tables

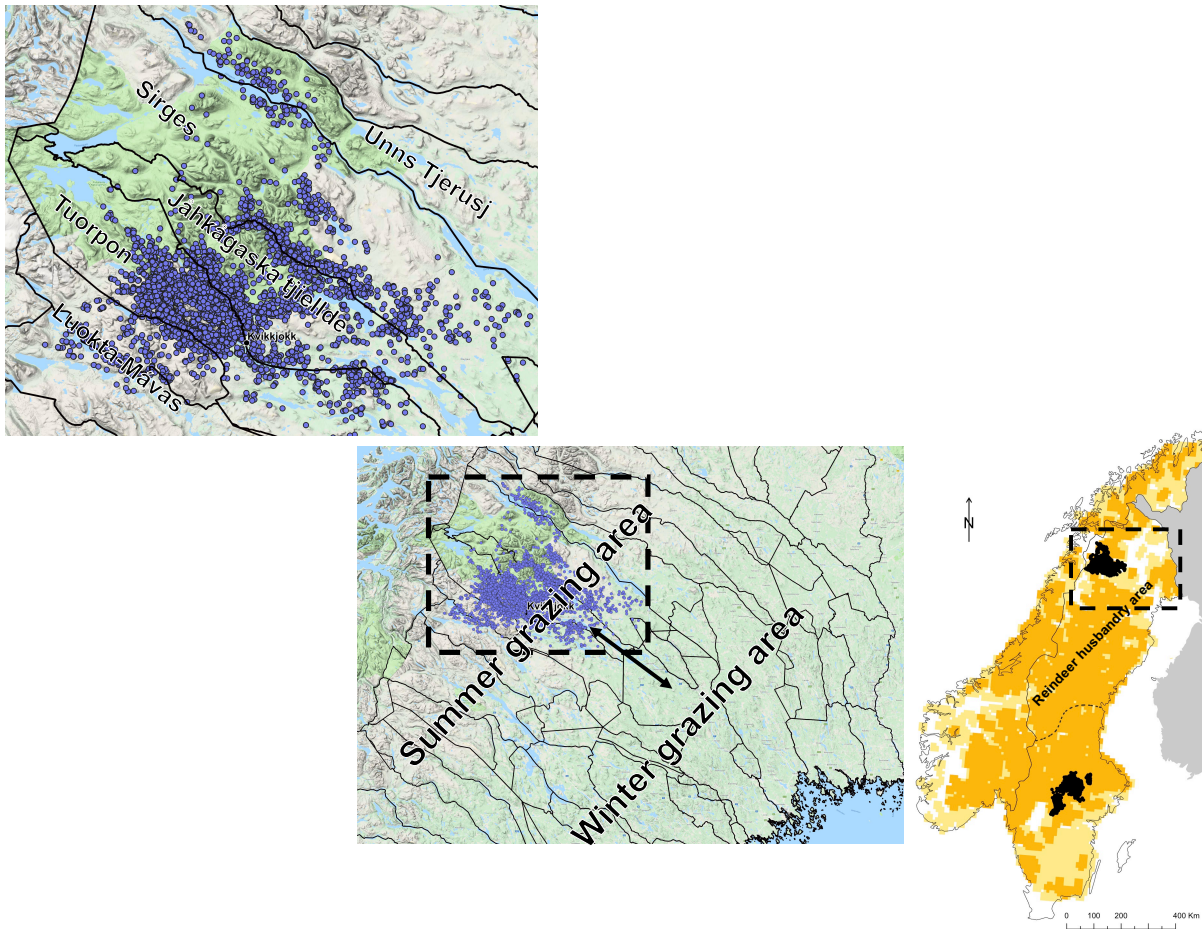


Figure A1. Approximately northern half of Sweden (above dashed line in lower right panel) is designated reindeer husbandry area, used by indigenous Sámi herders. The reindeer husbandry area is divided into 51 separate reindeer herding districts, and our northern study area is located within the summer grazing areas of four of these districts (i.e. Sirges, Jåhkågaska tjiellde, Tuorpon and Loukta-Mavas, upper left panel, blue dots are all lynx VHF and GPS locations included in this study). These four herding districts, as well as the surrounding districts to the north and south, move their reindeer herds between summer grazing areas in alpine areas in the northwest and winter grazing areas in the boreal forest in the southeast, following traditional migration routes and the yearly cycle of the reindeer. The reindeer herds reaches the summer grazing areas in each district in the study area for calving in early summer, during autumn the herds are gathered and moved into the winter grazing areas, 100–300 south east of the study area (middle panel) (Bjärvall et al. 1990, Danell et al. 2006).

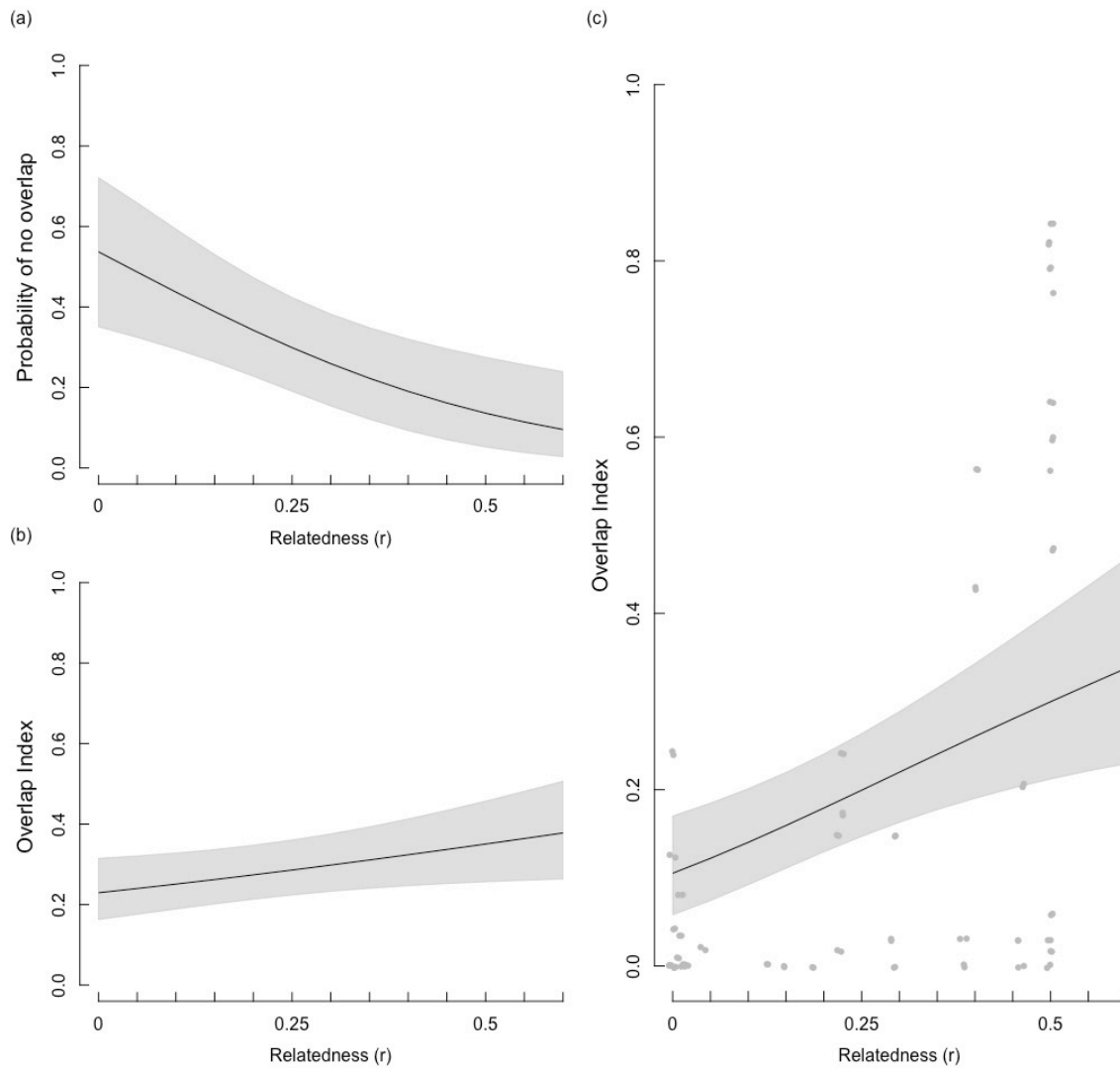


Figure A2. Model predictions (lines) with 95% credible intervals (grey shading) for the northern study area of the linear effect of relatedness on the probability for non-overlapping home ranges (a; Bernoulli model), overlap index >0 (b; Beta model) and the combined model (c; see Fig. 2b in main text). Grey dots are raw data (dots are slightly jittered to show overlapping values).

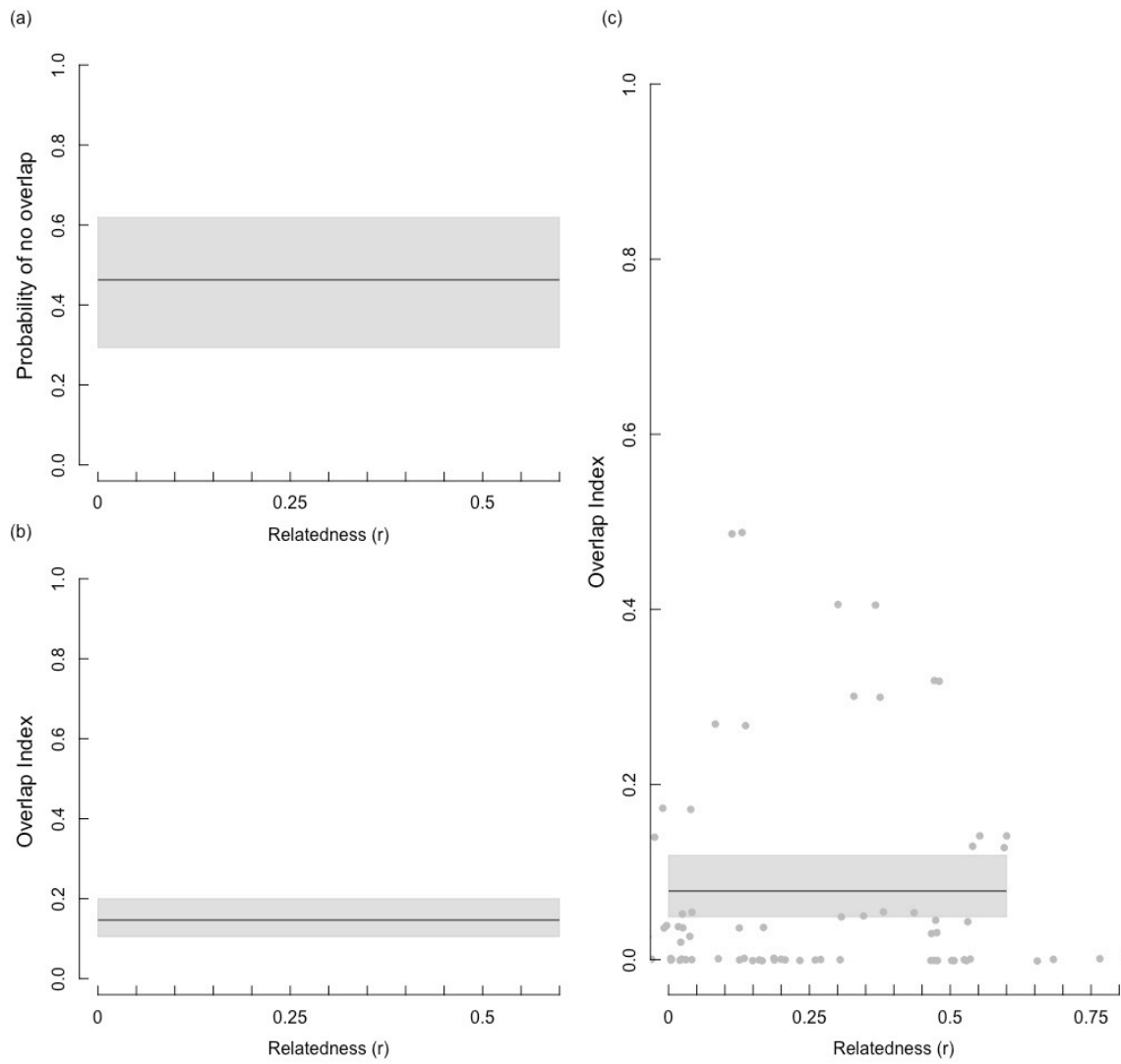


Figure A3. Model predictions (lines) with 95% credible intervals (grey shading) for the southern study area of the linear effect of relatedness on the probability for non-overlapping home ranges (a; Bernoulli model), overlap index >0 (b; Beta model) and the combined model (c; see fig. 2a in main text). Grey dots are raw data (dots are slightly jittered to show overlapping values).

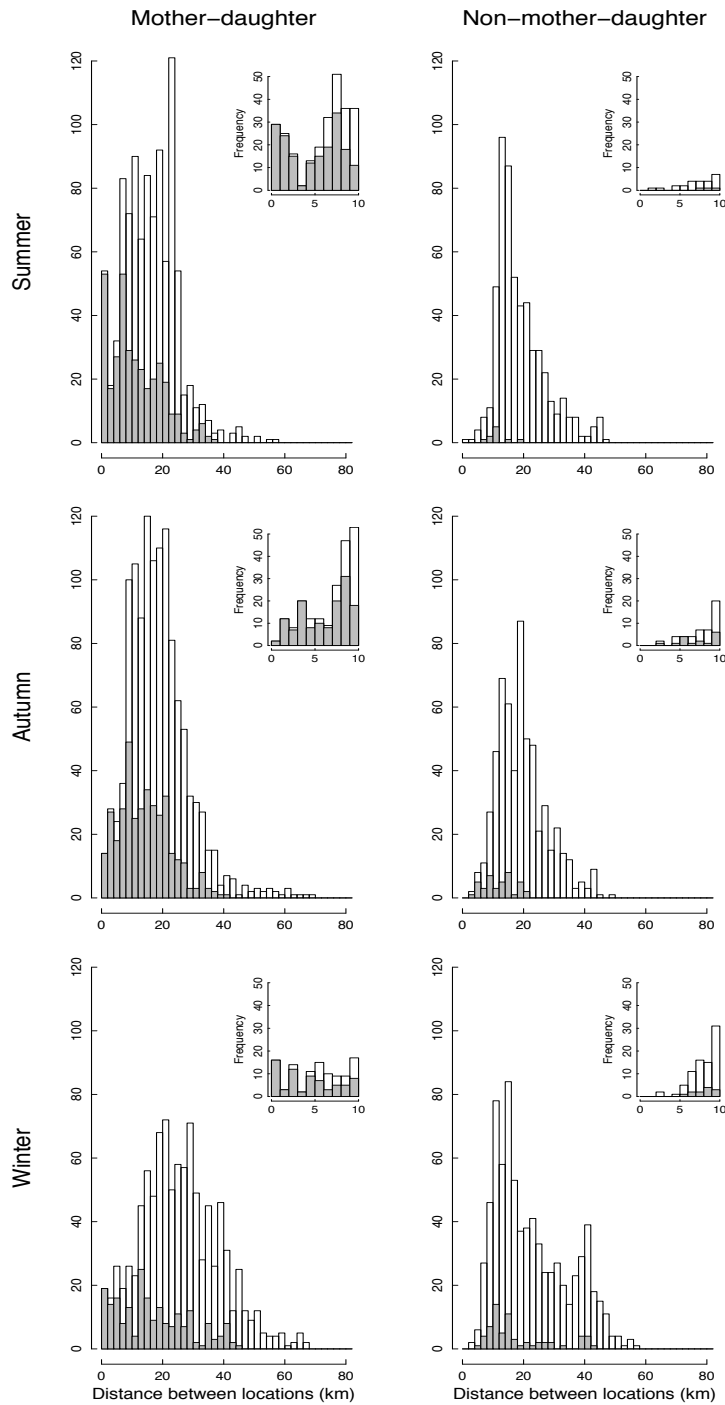


Figure A4. Histogram showing the distribution of distances between simultaneous GPS-locations for neighbouring mother–daughters (left) and non-mother–daughters (right) females in the northern study area during the summer, autumn and winter seasons. Grey shading indicates distances where at least one individual in the pair was within the home range overlap area. The insets in the upper right corner of each figure shows histograms of all distances ≤ 10 km in 1 km intervals.

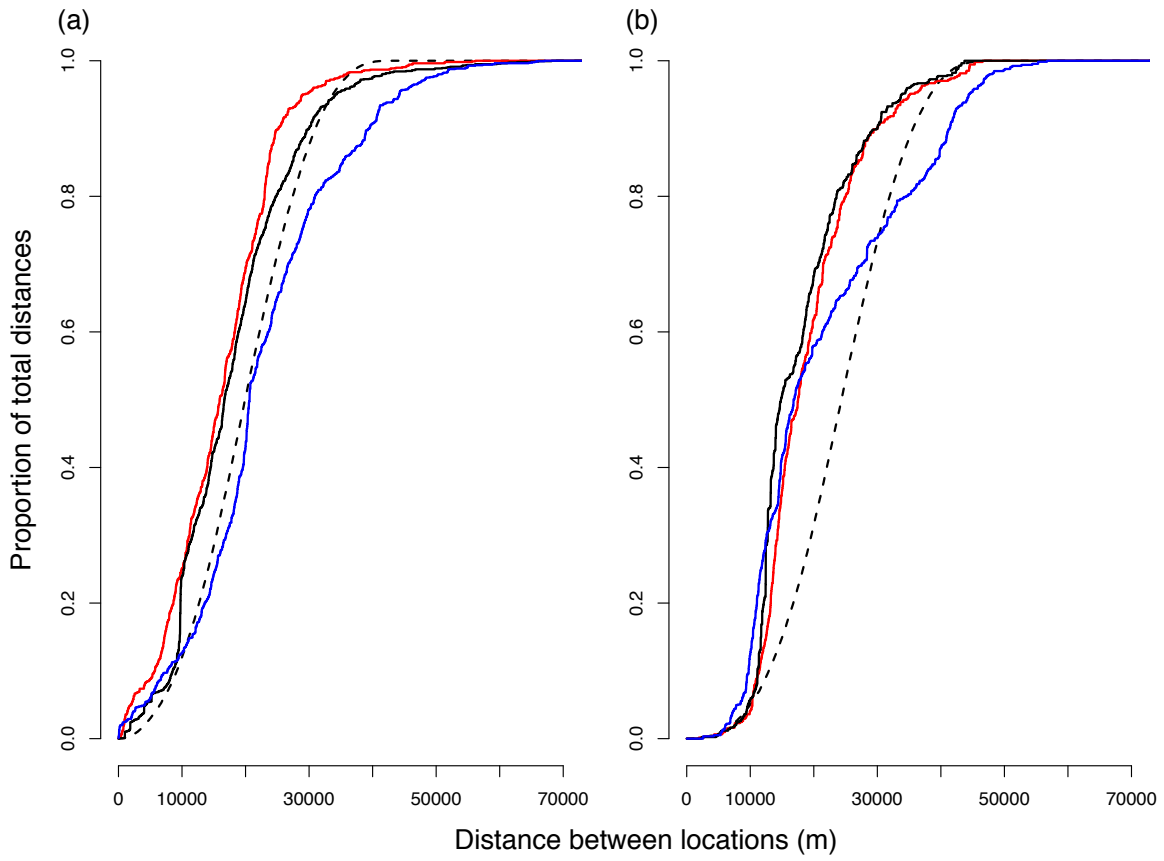


Figure A5. Cumulative distribution of distances between simulated random locations (dashed) and distances between simultaneous locations for mother-offspring (a) and non-mother offspring (b) relationship categories during summer (red line), autumn (black line) and winter (blue line).

Table A1. Posterior mean (SD) parameter estimates and 95% Credible Interval for both overlap index models included in the zero-inflated beta regression (i.e. Bernoulli model for the probability of no home range overlap and Beta model for amount of home range overlap).

	Bernoulli model		Beta model	
	Estimate (SD)	95% CRIs	Estimate (SD)	95% CRIs
North				
Intercept	0.15 (0.40)	-0.62; 0.95	-1.21 (0.22)	-1.64; -0.79
Relatedness	-4.04 (1.4)	-6.86; -1.46	1.19 (0.57)	0.07; 2.31
South				
Intercept	-0.16 (0.34)	-0.88; 0.49	-1.76 (0.19)	-2.14; -1.39

North: $\sigma_\alpha = 0.32$, $\sigma_\beta = 0.17$, $\sigma = 0.25$

South: $\sigma_\alpha = 0.63$, $\sigma_\beta = 0.22$, $\sigma = 0.13$

References for Appendix 1

- Björvall, A. et al. 1990. Renar och rovdjur [Reindeer and predators]. – Tryckindustri. ISBN 91-620-1056-6, in Swedish.
- Danell, A. C. et al. 2006. Space use by Eurasian lynx in relation to reindeer migration. – Can. J. Zool. 84: 546–555.

Appendix 2

Result using volume of intersection (VI)

Table A2. Models used to evaluate the effect of genetic relatedness on home range overlap (volume of intersection) for neighboring pairs of female lynx in the northern and southern study areas.

Related-ness was included as a linear and quadratic explanatory variable in the zero-one inflated beta regression in JAGS and compared to the intercept only model using the Watanabe–Aikaike information criterion (WAIC). The focal individual for each overlap measurement is included as group level effect on the intercept in each model.

Model	WAIC	Δ WAIC	parameters
North			
Intercept only	26.8	11.5	4.6
Linear	15.3	0.0	6.6
Quadratic	17.6	2.3	8.4
South			
Intercept only	-129.1	1.4	6.6
Linear	-129.7	0.8	9.1
Quadratic	-130.5	0.0	10.4

Table A3. Within (a) and between (b) study area comparison of volume of intersection (VI). In (a), probability (Pr) of higher VI for each genealogical relationship category compared to all less or equally related categories and the estimated difference (VI diff) with 95% credible intervals. In (b), probability of higher VI in the northern compared to the southern study area ($Pr(N>S)$) for each relationship category, and the estimated difference with 95% credible intervals. Relationship categories are; mother–daughter (MD), full siblings (FS), half siblings (HS), and unrelated (U).

(a) Within study area comparison					(b) Between study area comparison		
	North		South				
	Pr	VI diff (CRI)	Pr	VI diff (CRI)		$Pr(N>S)$	VI diff (CRI)
Category					Category		
MD>FS	88%	0.07 (-0.05-0.17)	67%	0.01 (-0.05-0.05)	MD	100%	0.15 (0.08-0.23)
MD>HS	100%	0.117 (0.04-0.20)	67%	0.008 (-0.03-0.05)	FS	96%	0.09 (-0.01-0.21)
MD>U	100%	0.12 (0.05-0.19)	26%	-0.009 (-0.04-0.02)	HS	90%	0.04 (-0.02-0.11)
FS>HS	82%	0.05 (-0.05-0.17)	45%	-0.003 (-0.05-0.06)	U	76%	0.04 (-0.02-0.11)
FS>U	86%	0.05 (-0.04-0.17)	22%	-0.02 (-0.06-0.04)			
HS>U	55%	0.004 (-0.05-0.07)	17%	-0.02 (-0.05-0.02)			

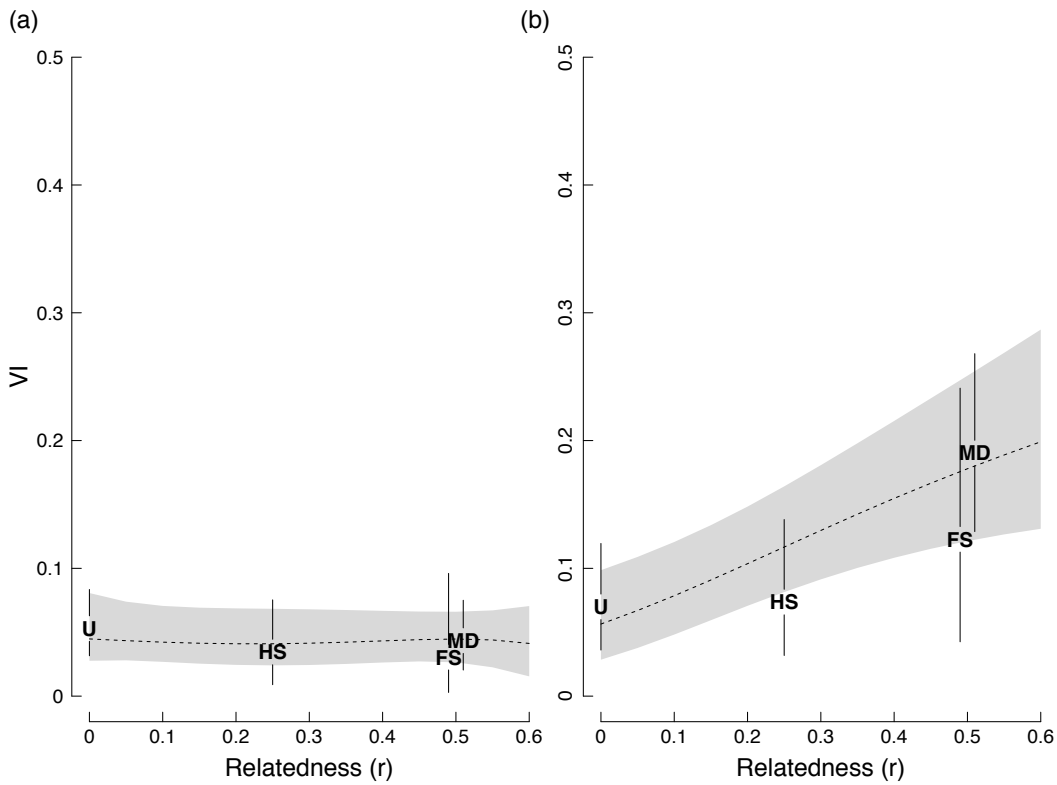


Figure A6. Model predictions (dashed lines) with associated 95% credible intervals (shaded areas) for the effect of genetic relatedness on female lynx home range overlap (volume of intersection, VI) in the southern (a) and northern (b) study areas, from the highest ranked model in Table A2.1. Additionally, the predicted overlap values for each genealogical relationship category is shown at corresponding relatedness values (unrelated: U at $r = 0$, half-siblings: HS at $r = 0.25$, full-siblings: FS at $r = 0.5$, and mother-daughter: MD at $r = 0.5$) with associated 95% CRIs (vertical lines).

Appendix 3

Distances between random locations

Random locations for neighboring females were generated within circles with the same size and overlap as lynx home ranges. To generate random locations uniformly distributed within a circle we used the following code in R, where r corresponds to the average home range radius for female lynx monitored with GPS collars in the northern study area.

```
for(i in 1:5000)

  theta[i]=2*pi* runif(1,0,1) #select random angle between 0 and 2π
  R[i] = r*sqrt(runif(1,0,1)) #selecting a random distance between 0 and r

  # convert to Cartesian coordinates
  x[i]=R[i]*cos(theta[i])
  y[i]=R[i]*sin(theta[i])
}
```

To generate random locations for the neighboring individual we used the same procedure and shifted all x-coordinated with the distance d . To calculate d we used the equation for a circle segment area (figure S3.1)

$$A_{segment} = \frac{r^2}{2}(\theta - \sin\theta)$$

where

$$\theta = 2\arccos\left(\frac{d}{2r}\right)$$

Since the overlap area between the two circles equals two circle segment areas we solved d from the following equation:

$$OA = r^2 \left(2\arccos\left(\frac{d}{2r}\right) - \sin\left(2\arccos\left(\frac{d}{2r}\right)\right) \right)$$

where OA corresponds to the average home range area overlap and r the average home range radius for mother–offspring (20%) or non-mother–offspring (FS, HS and U pooled, 5%) kinship categories.

To calculate distances between simulated locations we randomly selected 50 000 combinations of locations from each circle and calculated the distances between them, for each relatedness category.

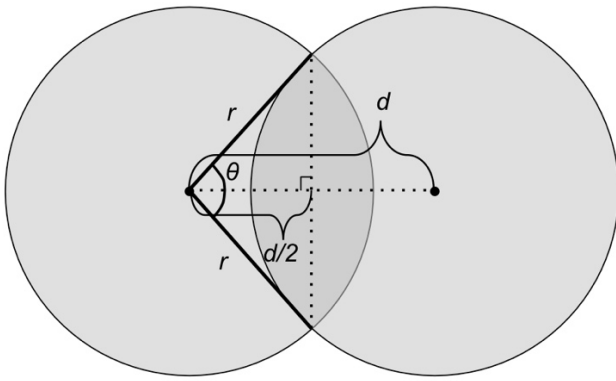


Figure A7. To simulate random locations for the neighboring individual we generated 5000 locations within the average home range radius for female lynx in the northern study area. To generate random locations for a neighboring individual the same procedure was repeated with the shifted distance d , resulting in the 20% area overlap (darker grey area) for mother–daughter and 5% area overlap for non-mother–daughter kinship categories.

Appendix 4

Genetic analysis

Genomic DNA from blood, tissue and hair samples was isolated using standard phenol/chloroform–isoamylalcohol extraction. Genetic samples were initially incubated in 300–500 μl SET-buffer (0.15 M NaCl, 0.05 M TRIS, 0.001 M EDTA), 10 μl Sodium dodecyl sulphate (20%) and 13 μl Proteinase K (10 mg μl^{-1}) at 55°C followed by separation of lysed cell material from DNA using 500 μl phenol and 500 μl chloroform:isoamyl alcohol (24:1) solution. Genomic DNA was precipitated using two volumes ethanol-sodium acetate solution (9 parts 95% ethanol and one part 3M sodium acetate). After removal of the ethanol solution the precipitated DNA was solved in distilled water.

DNA samples were genotyped on 17 microsatellite loci located on the autosomal genome; FCA001, FCA008, FCA031, FCA043, FCA045, FCA090, FCA126, FCA149, FCA272, FCA275, FCA391, FCA506, FCA559, FCA567, FCA573, F026, F115 (Menotti-Raymond and Obrien 1995, Menotti-Raymond et al. 1999). Markers were amplified in a multiplex PCR (Table A1 in appendix) setup using Qiagen Multiplex PCR Kit following the manufacturer's instructions with 20 ng template DNA and 0.2 μM of each primer. Amplification was done with a temperature profile of 95°C for 30 s, followed by 32–35 cycles with 95°C for 30 s, 55°C for 90 s and 72°C for 60 s, and ending with 60° for 30 min. Fragments were separated and visualized by capillary electrophoresis using an ABI3730XL DNA Analyzer (Applied Biosystems) at SciLifelab (Uppsala University, Uppsala, Sweden). Genotyping was performed using the software package Genemapper 5.0 (Applied Biosystems).

Calculations and significance tests of F_{ST} were conducted using GenalEx v6.5 (Peakall and Smouse 2012) using 9999 permutations. We used Microchecker (van Oosterhout et al. 2004) to identify possible null alleles and the analyses indicated that null alleles may be present at FCA506 (binomial test: $p < 0.001$) in the north, as suggested from a general excess of homozygotes for most alleles. In order to avoid erroneous relationship classification (Dakin and Avis 2004, Wagner et al. 2006), FCA506 was omitted from the north. All relatedness estimates were done separately for lynx from the northern and southern study areas because of significant differentiation between lynx in the two areas ($F_{ST} = 0.031$, $p < 0.001$).

We calculated the maximum likelihood estimates of relatedness between lynx using the program ML-RELATE (Kalinowski et al. 2006). The existence of close genealogical relationships (i.e. half siblings (HS), full siblings (FS) or parent–offspring (PO)) was tested by likelihood ratio tests using the maximum likelihood estimates, based on 10 000 randomizations and the 95% confidence interval.

Table A4. Marker loci used to calculate pairwise relatedness presented together with the multiplex group they were run in. The genetic diversity in the south and north is presented for each locus, including the number of alleles (A), mean expected heterozygosity (H_E) and the fixation index (F_{IS}). One significant F_{IS} -value is indicated with *** indicating $p < 0.001$.

Locus	Multiplex	South			North		
		A	H_E	F_{IS}	A	H_E	F_{IS}
F026	1	7	0.785	-0.092	7	0.803	0.080
F115	1	3	0.522	-0.210	5	0.665	0.055
FCA001	1	3	0.566	-0.002	6	0.502	0.107
FCA506	1	4	0.565	0.040	6	0.742	0.299***
FCA391	2	4	0.562	0.025	4	0.670	0.135
FCA559	2	4	0.713	0.165	6	0.772	0.057
FCA008	3	3	0.398	0.042	5	0.587	-0.185
FCA043	3	2	0.436	-0.037	4	0.527	0.106
FCA090	3	2	0.475	-0.001	3	0.519	0.064
FCA031	4	1	0.000	-	2	0.074	-0.040
FCA045	4	2	0.228	0.059	4	0.529	-0.044
FCA149	4	2	0.232	0.265	3	0.288	0.119
FCA126	5	4	0.617	0.019	6	0.615	-0.043
FCA272	5	3	0.553	-0.018	4	0.603	0.000
FCA275	5	3	0.367	0.016	7	0.632	-0.016
FCA567	5	4	0.619	-0.105	5	0.594	0.207
FCA573	5	3	0.634	0.118	3	0.613	0.127
Average		3.18	0.487	0.018	3.94	0.530	0.040

References for Appendix 4

- Dakin, E. E. and Avis, J. C. 2004. Microsatellite null alleles in parentage analysis. – *Heredity* 93: 504–509.
- Kalinowski, S.T. et al. 2006. ML-RELATE: a computer program for maximum likelihood estimation of relatedness and relationship. – *Mol. Ecol.* 6: 576–579.
- Menotti-Raymond, M. and O'Brien, S. J. 1995. Evolutionary conservation of 10 microsatellite loci in 4 species of Felidae. – *J. Hered.* 86: 319–322.
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- Peakall, R. and Smouse, P. E. 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research-an update. – *Bioinformatics* 28: 2537-2539.
- Wagner, A. P. et al. 2006. Estimating relatedness and relationships using microsatellite loci with null alleles. – *Heredity* 97: 336–345.