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Family groups of brown bears in Sør-Varanger, Norway

Application of SNP and STR markers to reconstruct pedigrees from DNA-samples noninvasively collected 2004-2016

NIBIO REPORT | VOL. 3 | NO. 160 | 2017

Alexander Kopatz[1], Rune Andreassen[2], Daniel Kling[3],
Rolf Randa[4], Kristin Forfang[1], Snorre B. Hagen[1], Hans Geir Eiken[1]

[1]Norwegian Institute of Bioeconomy Research (NIBIO), Svanhovd, Norway
[2]Oslo and Akershus University College of Applied Sciences, Oslo, Norway
[3]Oslo University Hospital, Oslo, Norway
[4]Norwegian Nature Inspectorate (SNO), Kirkenes, Norway

TITTEL/TITLE

Family groups of brown bears in Sør-Varanger, Norway. Application of SNP and STR markers to reconstruct pedigrees from DNA-samples noninvasively collected 2004-2016

FORFATTER(E)/AUTHOR(S)

Alexander Kopatz[1], Rune Andreassen[2], Daniel Kling[3], Rolf Randa[4], Kristin Forfang[1], Snorre B. Hagen[1], Hans Geir Eiken[1]

[1]Norwegian Institute of Bioeconomy Research (NIBIO), Svanhovd, Norway

[2]Oslo and Akershus University College of Applied Sciences, Oslo, Norway

[3]Oslo University Hospital, Oslo, Norway

[4]Norwegian Nature Inspectorate (SNO), Kirkenes, Norway

DATO/DATE:	RAPPORT NR./ REPORT NO.:	TILGJENGELIGHET/AVAILABILITY:	PROSJEKTNR./PROJECT NO.:	SAKSNR./ARCHIVE NO.:
13.12.2017	3/160/2017	Open	10772	17/01812

ISBN:	ISSN:	ANTALL SIDER/ NO. OF PAGES:	ANTALL VEDLEGG/ NO. OF APPENDICES:
978-82-17-02006-6	2464-1162	39	3

OPPDRAGSGIVER/EMPLOYER:	KONTAKTPERSON/CONTACT PERSON:
Fylkesmannen i Finnmark	Alexander Kopatz

STIKKORD/KEYWORDS:	FAGOMRÅDE/FIELD OF WORK:
Relasjoner, familiegrupper, slektskap rekonstruksjon, populasjonsgenetikk	Genetisk overvåkning av rovdyr
Relatedness, family groups, pedigree reconstruction, population genetics	Large carnivore genetic monitoring

SAMMENDRAG/SUMMARY:

Sammendrag

Vi rekonstruerte familieforhold (foreldre-barn og søsken) mellom 154 kjente brunbjørnindivider (*Ursus arctos*) i Sør-Varanger, Norge. Dette ble gjort ved bruk av genetiske data (SNP og STR) fra innsamlede møkk- og hårprøver i området i perioden 2004 til 2016. Slektskap ble testet ved å beregne sannsynlighetsovervekt (likelihood ratios=LRs) i programmet FAMILIAS, en programvare brukt i menneskelig rettsmedisin for å rekonstruere familieforhold. Totalt ble det funnet 65 foreldre-barn-relasjoner og 56 søskenrelasjoner. Av disse var 40 relasjoner (34 foreldre-barn og 6 søsken) ytterligere støttet av uavhengige observasjonsdata fra felten. Ytterligere analyser av de genetiske dataene tydet på at mange av de bjørnene som verken ble klassifisert som foreldre-barn eller søsken kan være mer fjerne slektninger, men en mer detaljert analyse er nødvendig for å kunne trekke slike konklusjoner. Basert på de genetiske dataene ble minimumstallet for unger per år beregnet til å være gjennomsnittlig 4,08 og det gjennomsnittlige antallet var to unger per hunnbjørn og tre unger per hannbjørn. SNP-chipen brukt til genetisk analyse i dette studiet har blitt utviklet for den svenske brunbjørnpopulasjonen, en populasjon som er genetisk forskjellig fra Sør-Varangerpopulasjonen. Våre resultatene viser at det er et behov for videre utvikling av denne SNP-chipen og dens individuelle loci, selv om den har nok styrke til å detektere den tidligere rapporterte subpopulasjonsstrukturen i Sør-Varanger. Observasjonsdataene, innsamlingsinnsatsen og kvaliteten på prøvematerialet for brunbjørnen i Sør-Varanger er enestående og materialet sørger for en unik forskningsplattform for å validere og videreutvikle SNP-chipen til å kunne rekonstruere familiegrupperinger.

Summary

We reconstructed family relationships (parent-child and siblings) among 154 known brown bear individuals (*Ursus arctos*) in Sør-Varanger, Norway. This was done by using genetic data (SNP- and STR) from hair and scat samples collected in the area from 2004 to 2016. The relationship was tested by calculating likelihood ratios (LRs) with the program FAMILIAS, a software applied in human forensics to reconstruct family relationships. Overall, we detected 65 parent-child and 56 sibling relationships. Of these, 40 relationships (34 parent-child and 6 siblings) were further supported by independent observational data from the field. Additional analyses of the genetic data suggested that some of the bears were not classified as either parent-child or siblings and may be more distant relatives, but a more detailed analysis is necessary to draw such conclusions. Based on the genetic data, the minimum number of cubs per year was estimated to be on average 4.08 and the average number was 2 cubs per female and 3 cubs per male. The SNP-chip applied for genetic analysis in this study has been developed on the Swedish brown bear population, a population genetically different from the Sør-Varanger population. Our results show that there is a need for further evaluation of this SNP-chip and its individual loci, although it is has enough power enough to detect the previously reported subpopulation structure in Sør-Varanger. The observational data, sampling effort and quality of the sample material of the brown bears in Sør-Varanger is remarkable and the material provides a unique testing ground to validate and improve the SNP-chip to reconstruct family groups.

LAND/COUNTRY:	Norge/Norway
FYLKE/COUNTY:	Finnmark
KOMMUNE/MUNICIPALITY:	Sør-Varanger
STED/LOKALITET:	Svanvik

GODKJENT /APPROVED	**PROSJEKTLEDER /PROJECT LEADER**
Hans Geir Eiken	Alexander Kopatz
NAVN/NAME	**NAVN/NAME**

Preface

Reconstruction of family groups in wildlife management and research

Quantification of the number of successful reproductions of brown bears (*Ursus arctos*) in an area has become very important to wildlife management of late. This is because a specific maximum number of reproductions may be one of the goals to be achieved in management plans, e.g. to keep a population stable in size. Data about the genetic relatedness among individuals can be used to reconstruct the family structure and pedigree of wild bears living in a specific area such as Sør-Varanger, where a sufficient number of samples has been collected for DNA identification of individuals and where observations of related bears have been recorded by the Norwegian State Nature Inspectorate (SNO) in the field (see also e.g. Schregel et al. 2012; Aarnes et al. 2014; Kopatz et al. 2014). Also, the reconstruction of a family tree of bears in a particular area can also serve as a measure of viability and, once family structure is known, to easier identify immigrating bears from other regions.

Svanvik, 13.12.17

Alexander Kopatz

Content

1 Introduction

Background

Sør-Varanger, including the Pasvik Valley, in Northern Norway houses one of the largest and densest brown bear populations in Norway (Schregel et al. 2012). Since 2004, non-invasive genetic sampling (feces and hairs) has been conducted in Sør-Varanger (see e.g. Smith et al. 2007, Wartiainen et al. 2009; Kopatz et al. 2011, 2012, 2013, 2014, Aarnes et al. 2015, Kopatz et al. 2016). Plus, observations of females with cubs are reported regularly from the region (Wartiainen et al. 2009; Kopatz et al. 2014), but little is known about the number of reproductions and the family structure in this population.

In our 2014 study, we have utilized genetic data from STRs (short tandem repeats) originating from feces and hair samples collected in Sør-Varanger during the period from 2004 to 2014 to investigate female brown bear relationships and sampling localities (see Kopatz et al. 2014). In the same period, personnel from the Norwegian State Nature Inspectorate (SNO) have observed 9 female brown bears with potentially female cubs. Sampling areas of those female brown bears and their potential offspring showed substantial geographical vicinity suggesting overlapping home ranges. Of the 9 female bears initially observed, 6 had produced 10 female cubs, confirmed by genetic methods. The relationship of 3 females with their potential cubs could not be confirmed as of yet because of limited power of the analysis due to a low number of genetic markers used. One additional near-family relationship was identified between two observed female bears; however the type of relationship (parent-child, siblings, etc) could not be determined.

Here, we attempt to reconstruct family groups of the brown bears in Sør-Varanger by adding genetic information retrieved from SNPs (single nucleotide polymorphisms) applying the newly developed SNP-chip for brown bears in Scandinavia. SNPs are usually characterized by high genomic resolution and reproducibility across studies, surveys and laboratories (Norman and Spong 2015), which are some of the reasons the implementation of a SNP-based genetic monitoring of brown bears in Sweden and Norway is currently discussed. We use state-of-the-art approaches as applied in human forensic genetics to reconstruct maternity and paternity as well as to identify unknown family members combining STR and SNP markers. The detected family relationships were compared to the observed family groups made by the Norwegian State Nature Inspectorate (SNO), which are strong, *a priori* assumptions that individuals were close relatives. Further, we determine the minimum number of annual reproductions of the brown bears sampled in the period from 2004 to 2016.

Objectives

The aims of this project are the following:

- To reconstruct the family structure of the bears genetically identified in Sør-Varanger.
- To calculate the minimum number of reproductions per year in Sør-Varanger.
- To calculate the minimum number of cubs per individual female detected.
- To detect immigrating bears into the bear population of Sør-Varanger.

2 Material and Methods

Study area

The study area encompasses the municipality of Sør-Varanger in Finnmark, Northern Norway. The terrestrial area covers 3481.5 km². The area consists of arctic and boreal ecosystems in a mosaic of peat land and forest with Scots pine (*Pinus silvestris*) and downy birch (*Betula pubescens*).

Sampling and data analyses

Since 2004, non-invasive genetic sampling has been conducted in Sør-Varanger, Eastern Finnmark and up to 2016, a total of 158 individual brown bears have been identified with microsatellite or short tandem repeats (STR) markers. Most of the individual brown bears have been genotyped with 8 genetic markers for monitoring purposes, and some with 12 to 15 markers for research already. Further, every identified individual brown bear has been registered with its location and and date; in Sør-Varanger and, as well as neighboring areas in Finland and Russia. We genotyped these 158 brown bears detected in Sør-Varanger using Single Nucleotide Polymorphism markers (SNPs). The panel contained 96 SNPs initially designed to infer relatedness among brown bear individuals in the Swedish brown bear population. At each step, 96 DNA-samples from brown bear was mapped against 96 SNPs using the Fludigm Biomark HD system and GT 96.96 IFC plates. The samples were pre-amplified with specific target primers in regular PCR with 40 cycles to yield a more stable SNP analysis. Pre-amplification products were diluted 1:100 in TE-buffer (1mM TE, 0.1mM EDTA) and loaded onto the IFC plate for SNP analysis using the PCR program for 96.96 GT Fast. Data management was performed in SNP Genotyping Analysis software. Our procedures followed the strict guidelines for forensic examination of animal DNA material (Linacre et al. 2011).

The analyses were performed at NIBIO Svanhovd with the Fluidigm Biomark system using the SNP panel developed on the Swedish brown bear as described in Norman et al. (2013). All genotyping results were quality checked. We used the latest version of the program FAMILIAS 3.2.2 (Egeland and Mostad 2000; Kling et al. 2014), developed for and applied in human forensic research to calculate likelihood ratios (LR) for genetic relationship. The LR shows which pedigree is more likely than others. We analyzed the genotype data for parent-child and sibling relationships. The FAMILIAS software is widely in use worldwide by human forensic laboratories and has been applied to numerous cases e.g. resolving family relations, individual identification after disasters etc. Calculating family relationships requires allele frequency data of the population in question and we deduced this information from the SNP-data. Based on our previous study using STR-markers we used a kinship correction (F_{ST}) of θ=0.09 (Andreassen et al. 2012).

The likelihood ratio (LR), the ratio of the probability of an observed relationship (e.g. parent-child) as reported by SNO against the probability of being unrelated was used as criteria to confirm or reject a family relationship with the program FAMILIAS (Egeland and Mostad 2000; Kling et al. 2014). Since our focus here was to identify parent-child relationships first, we selected a LR=1000 as threshold value to accept these relationships. A LR of 1000 would mean that there is 99.99% probability for the tested relationship against the two individuals being unrelated, based on genetic data only.

Personnel of the Norwegian State Nature Inspectorate (SNO) records regularly brown bears including females with cubs by observation. Such observations can be characterized as strong indication of relatedness of the brown bears observed, since unrelated brown bears tend to roam separately and solitary (Dahle and Swenson 2003; Dahle et al. 2006; Støen et al. 2005 and 2006). Further, family members, especially related female brown bears are known to show overlapping home ranges (Støen et al. 2006; Zedrosser et al. 2007). We compared the results of based on detected, genetic relationships to these observations.

A combination of the obtained results of confirmed parent-child relationships (LR>1000) of the SNP-data and the sampling year of brown bears in Sør-Varanger was used to estimate the minimum number of reproductions in the area. Further, for theses confirmed parent-child relationships, we calculated the average number of offspring for the analyzed female and male brown bears. In another step, we reconstructed potential relationships visually with a dendogram. A dendogram is a tool to visually group genotypes with identical alleles. However, apart from indicating a family relation between certain individuals it does not reveal the particular family relationship.

For comparisons and evaluation of our results, we plotted the number of collected samples and identified individuals across the study period. Further, we determined the population genetic substructure of the brown bears in Sør-Varanger with the program Structure 2.3.4 (Pritchard et al. 2000; 100,000 burnin, 1,000,000 iterations; 10 independent runs for *K*=10) and a factorial-correspondence analysis with Genetix 4.05.2 (Belkhir et al. 1996-2004).

3 Results and Discussion

The stored genetic material was overall of reliable quality. Of the 158 individual brown bears genotyped with the SNP-panel, 7 were removed from further analyses due to low quality data and therefore unreliable genotype results (FI002, FI022, FI047, FI053, FI079, FI090 and FI204).

The forensic assessment resulted in the identification of 65 parent-child relationships and 56 sibling relationships with a LR>1000 (Table A1). Pairs of relationships are presented as Bear 1 and Bear 2, whereas which bear is the parent and which individual the offspring, cannot be answered solely by the genotype data. Here, the observational data, or, if available, age of the brown bears would be necessary. We compared the detected parent-child and sibling relationships with the field observations of 112 relationships, shown as pairs of different brown bears recorded by the wildlife management (Tab. 1a, b and c). Based on a threshold value of LR>1000, overall, we found 40 of the relationships detected by the combined SNP and STR data also supported by direct observation. More specifically, this number can be separated into parent-child relationships where this number was 34, while for siblings the number was 6. A summary of these results are given in tables 1a, b and c. Overall, 21 genetic family groups were identified based on the SNP-data (Table A2). Observed family groups on the other hand were identified to the most extent, although values for LR were below the cut-off value of LR=1000. In comparison to our previous study of female brown bear relationships in the area (Kopatz et al. 2014), the three observed parent-child relationships which could not be confirmed based on genetic methods in our previous study in 2014, two (FI063F-FI129F and FI097F-FI139F) were now confirmed with a high LR (Tab. 1a).

We used the SNP-data of 154 individuals, 65 females and 89 males, for analysis. In order to give an estimate of the annual reproduction, we counted every new parent-child relationship across the sampling period annually detected in blind test of FAMILIAS based on the SNP-data and with a LR>1000 (Fig. 1). The minimum number of cubs per year was on average 4.08 (SD=2.84). Also based on the confirmed parent-child relationships identified in the SNP-data (LR>1000) the average number of offspring was 2 cubs per female and 3 per male. These results can be considered as a conservative, careful estimate, because there might be the probability that not all parents and cubs have been sampled. In a second analysis we used number of identical alleles in individuals to group them in a dendogram. One dendrogram based on genetic data of the observed brown bears (Fig. 2) as well as one dendrogram based on data for the whole data set (Fig. 3). Here, overall, the grouping of the the individuals was very similar to the suggested family groups based on observational data, as indicated by the color (see Tab. 1).

When comparing the LR-values of the family reconstruction based on the SNP-chip with the results based on STRs, it is notable that the values for LR are generally larger when using the SNP-data (Tab. 1 and Tabs. A1 and A3). However, the SNP-chip also led to a number of exclusions and therefore should be validated regarding its performance. This is likely to improve its performance and decrease the number of false exclusions. In our previous studies we used a LR>20 to indicate parent-child relationship. Using both the SNPs and STRs the power of the test will increase, and this allows for an increase of the threshold (LR>1000) that largely excludes false positives.

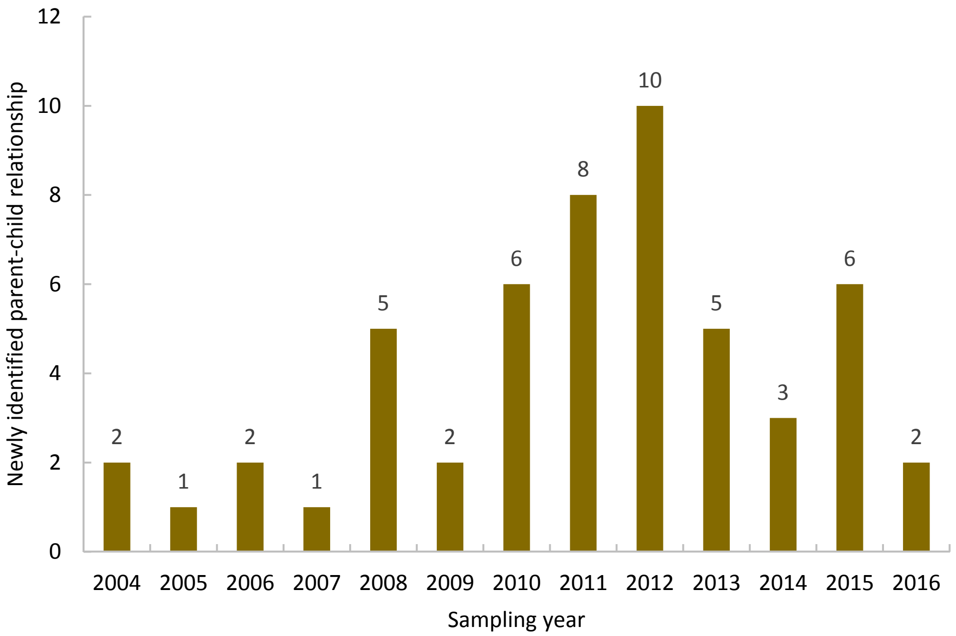

Fig. 1. **The identified parent-child relationships with the highest likelihood ratios (LR>1000) of brown bears in Sør-Varanger, Norway across the sampling period.**

Also, it may be possible that not all brown bears in the area have been sampled. However, when comparing the number of samples collected and individual brown bears identified, the trend appears to be close to saturation (Fig. 4). This means that most brown bears in the area have been sampled and detected. In order to sample all individuals, an excessive, unproportional effort of at least doubling the number of collected samples would be required, as indicated by the saturation curve that close to the plateau (Fig. 4).

Laboratory analyses were performed to the latest standard in animal forensic research at Svanhovd (see Andreassen et al. 2012). The observational recorded data of brown bears was made by wildlife professionals and the samples collected are assumed to be from the observed individuals. Moreover, some individual brown bears have been observed multiple times together. Another reason that some observed relationships were not detected could be the performance of the newly developed SNP-chip, which remained unfeasible to be able to detect some of the strongly indicated relationships with high certainty (LR>1000). Reasons could be that the genetic assessment with the SNP-chip is affected by a smaller number of SNP-loci with undetected alleles (so called *0-alleles*). Therefore, we propose further tests with the SNP-assay compared to STRs and further evaluation for wildlife forensic applications with genetic material from multiple populations in northern Europe, as it has been done earlier for STRs (Andreassen et al. 2012).

The SNP-data seems sensitive enough to distinguish between closer family relationships and unrelated indviduals as well as to detect population genetic substructure. We found the same local genetic structure in the brown bear population of Sør-Varanger as reported previously based on 8 STR-markers (Schregel et al. 2017). Fig 5 shows the bar plot and a factorial-correspondence analysis of all 154 brown bears in this study. Here, it appears, that the genotypes assigned to the second genetic cluster increased over the last years (Fig. 5a) and one individual in particular, FI143M is notably forming an outlier (Fig. 5b). It appears that this individual might be an immigrant from another region. Also here, more investigations and validations of the SNP-chip is required.

Tab. 1. The 112 observed relationship of brown bears as recorded by field observations versus the genetic relationship with the SNP-chip based of forensic reconstruction in the program Familias, separated by relationship: a) confirmed parent-child relationships, b) confirmed sibling relationships, and, c) not confirmed relationships. In addition LRs for the genetic relationshop suggested by STRs is show as well as the summary of both LRs, SNPs and STRs. Genetically confirmed relationships are indicated with "Yes" and its value of the likelihood ratio (LR), ambigious relationships are presented with a question mark (?) and missing and unconfirmed relationships are left blank (-). Missing individuals are marked with an asterisk (*).

a) Confirmed parent-child relationships:

Confirmed (SNPs & STRs)	Confirmed (SNPs)	Bear 1	Bear 2	Genetic Relationship (SNPs)	LR (SNPs)	Genetic Relationship (STRs)	LR (STRs)	LR (SNPs & STRs)	Observed Relationship
Yes	Yes	FI073M	FI138M	Parent-Child	305207.00	Parent-Child	11.03	3365548.11	Parent-Child
Yes	Yes	FI073M	FI139F	Parent-Child	27171.10	Parent-Child	81.24	2207295.93	Parent-Child
Yes	Yes	FI097F	FI139F	Parent-Child	27171.10	Parent-Child	6.06	164548.73	Parent-Child
Yes	Yes	FI133M	FI200M	Parent-Child	24138.30	Parent-Child	12.16	293405.86	Parent-Child
Yes	Yes	FI063F	FI166M	Parent-Child	23874.60	Parent-Child	3.91	93321.28	Parent-Child
Yes	Yes	FI063F	FI129F	Parent-Child	16759.90	Parent-Child	29.96	502072.97	Parent-Child
Yes	Yes	FI019F	FI119F	Parent-Child	8846.55	Parent-Child	3.59	31759.56	Parent-Child
Yes	Yes	FI042F	FI077F	Parent-Child	7266.80	Parent-Child	134.98	980894.46	Parent-Child
Yes	Yes	FI070M	FI167F	Parent-Child	6349.14	Parent-Child	9.59	60878.79	Parent-Child
Yes	Yes	FI097F	FI174F	Parent-Child	5627.68	Parent-Child	4.39	24717.50	Parent-Child
Yes	Yes	FI098F	FI117F	Parent-Child	5338.99	Parent-Child	43.41	231761.28	Parent-Child
Yes	Yes	FI041M	FI106M	Parent-Child	5280.38	Parent-Child	39.62	209225.55	Parent-Child
Yes	Yes	FI019F	FI091M	Parent-Child	4286.11	Parent-Child	6.88	29498.64	Parent-Child
Yes	Yes	FI042F	FI145M	Parent-Child	3856.35	Parent-Child	240.07	925786.23	Parent-Child
Yes	Yes	FI019F	FI121F	Parent-Child	3310.67	Parent-Child	10.33	34213.46	Parent-Child
Yes	Yes	FI149F	FI150F	Parent-Child	2956.43	Parent-Child	40.53	119826.18	Parent-Child
Yes	Yes	FI070M	FI131M	Parent-Child	2904.45	Parent-Child	1.24	3607.94	Parent-Child
Yes	Yes	FI019F	FI092M	Parent-Child	1855.22	Parent-Child	11.82	21930.93	Parent-Child
Yes	Yes	FI040F	FI153M	Parent-Child	1776.89	Parent-Child	27.42	48723.39	Parent-Child
Yes	Yes	FI004F	FI085M	Parent-Child	1733.07	Parent-Child	289.56	501831.22	Parent-Child
Yes	Yes	FI063F	FI192F	Parent-Child	1366.61	Parent-Child	11.23	15351.95	Parent-Child
Yes	Yes	FI042F	FI147F	Parent-Child	1138.04	Parent-Child	24.55	27943.66	Parent-Child
Yes	-	FI063F	FI167F	Parent-Child	941.93	Parent-Child	10.92	10288.99	Parent-Child
Yes	-	FI015M	FI091M	Parent-Child	728.76	Parent-Child	2.98	2174.17	Parent-Child
Yes	-	FI042F	FI136M	Parent-Child	690.37	Parent-Child	91.79	63367.11	Parent-Child
Yes	-	FI077F	FI200M	Parent-Child	609.76	Parent-Child	12.57	7663.70	Parent-Child
Yes	-	FI040F	FI134M	Parent-Child	526.01	Parent-Child	6.17	3244.48	Parent-Child
Yes	-	FI043F	FI111F	Parent-Child	458.46	Parent-Child	3.70	1695.35	Parent-Child
Yes	-	FI097F	FI138M	Parent-Child	353.91	Parent-Child	30.21	10691.53	Parent-Child
Yes	-	FI111F	FI186F	Parent-Child	284.04	Parent-Child	3.80	1080.07	Parent-Child
Yes	-	FI063F	FI131M	Parent-Child	270.73	Parent-Child	36.66	9925.38	Parent-Child
Yes	-	FI015M	FI092M	Parent-Child	221.20	Parent-Child	21.84	4830.88	Parent-Child
Yes	-	FI063F	FI191M	Parent-Child	162.90	Parent-Child	106.95	17422.38	Parent-Child
Yes	-	FI040F	FI120M	Parent-Child	134.47	Parent-Child	15.04	2022.93	Parent-Child

b) Confirmed sibling relationships:

Confirmed (SNPs & STRs)	Confirmed (SNPs)	Bear 1	Bear 2	Genetic Relationship (SNPs)	LR (SNPs)	Genetic Relationship (STRs)	LR (STRs)	LR (SNPs & STRs)	Observed Relationship
Yes	Yes	FI129F	FI131M	Siblings	3123180.00	Siblings	5.28	16489047.43	Siblings
Yes	Yes	FI091M	FI092M	Siblings	573072.00	Parent-Child	14.47	8290346.09	Siblings
Yes	Yes	FI116F	FI118M	Siblings	5048.91	Siblings	75.21	379722.46	Siblings
Yes	Yes	FI136M	FI145M	Siblings	1242.94	Parent-Child	134.75	167481.19	Siblings
Yes	-	FI117F	FI118M	Siblings	587.53	Siblings	18.29	10745.02	Siblings
Yes	-	FI110F	FI111F	Siblings	192.92	Siblings	15.38	2966.40	Siblings

c) Not confirmed relationships:

Confirmed (SNPs & STRs)	Confirmed (SNPs)	Bear 1	Bear 2	Genetic Relationship (SNPs)	LR (SNPs)	Genetic Relationship (STRs)	LR (STRs)	LR (SNPs & STRs)	Observed Relationship
?	?	FI137M	FI176F	Siblings	67255.30	Parent-Child	113.59	-	?
?	Yes	FI145M	FI147F	Parent-Child	19260.20	Siblings	32771.20	-	Parent-Child
?	?	FI098F	FI116F	Siblings	10907.70	Parent-Child	29.50	-	Parent-Child
?	?	FI098F	FI118M	Siblings	1788.99	Parent-Child	32.71	-	Parent-Child
?	-	FI097F	FI102F	Parent-Child	232.99	Siblings	154.07	-	Parent-Child
-	-	FI019F	FI113M	No match	-	Parent-Child	1.01	-	Parent-Child
-	-	FI019F	FI165M	No match	-	Parent-Child	1.55	-	Parent-Child
-	-	FI019F	FI171M	No match	-	Parent-Child	1.69	-	Parent-Child
-	-	FI097F	F114M	No match	-	Parent-Child	3.19	-	Parent-Child
-	-	FI038F	FI106M	No match	-	Parent-Child	5.00	-	Parent-Child
-	-	FI097F	FI140M	No match	-	Parent-Child	5.41	-	Parent-Child
-	-	FI019F	FI054F	No match	-	Parent-Child	6.10	-	Parent-Child
-	-	FI040F	FI073M	No match	-	Parent-Child	6.68	-	Parent-Child
-	-	FI070M	FI166M	No match	-	Parent-Child	9.18	-	Parent-Child
-	-	FI043F	FI110F	No match	-	Parent-Child	9.55	-	Parent-Child
-	-	FI040F	FI135F	No match	-	Parent-Child	9.89	-	Parent-Child
-	-	FI043F	FI161M	No match	-	Parent-Child	10.23	-	Parent-Child
-	-	FI043F	FI109F	No match	-	Parent-Child	15.58	-	Parent-Child
-	-	FI063F	FI187M	No match	-	Parent-Child	16.71	-	Parent-Child
-	-	FI043F	MO046	No match	-	Parent-Child	19.74	-	Parent-Child
-	-	FI040F	FI154M	No match	-	Parent-Child	21.02	-	Parent-Child
-	-	FI040F	FI072F	No match	-	Parent-Child	27.14	-	Parent-Child
-	-	FI111F	FI185M	No match	-	Parent-Child	28.73	-	Parent-Child
-	-	FI007F	FI048M	No match	-	Parent-Child	41.38	-	Parent-Child
-	-	FI004F	FI007F	No match	-	Parent-Child	43.48	-	Parent-Child
-	-	FI043F	FI193M	No match	-	Parent-Child	45.50	-	Parent-Child
-	-	FI019F	FI052M	No match	-	Parent-Child	45.90	-	Parent-Child
-	-	FI043F	FI160F	No match	-	Parent-Child	47.72	-	Parent-Child
-	-	FI017M	FI134M	No match	-	Parent-Child	48.50	-	Parent-Child
-	-	FI043F	FI155M	No match	-	Parent-Child	57.12	-	Parent-Child
-	-	FI007F	FI049M	No match	-	Parent-Child	67.81	-	Parent-Child
-	-	FI004F	FI086F	No match	-	Parent-Child	71.95	-	Parent-Child
-	-	FI017M	FI113M	No match	-	Parent-Child	94.83	-	Parent-Child
-	-	FI007F	FI068M	No match	-	Parent-Child	109.20	-	Parent-Child
-	-	FI008F*	FI010F	-	-	-	-	-	Parent-Child
-	-	FI019F	FI053M*	-	-	-	-	-	Parent-Child
-	-	FI019F	FI40F	No match	-	No match	-	-	Parent-Child
-	-	FI042F	FI146M*	-	-	-	-	-	Parent-Child
-	-	FI043F	FI039F	No match	-	No match	-	-	Parent-Child
-	-	FI097F	FI175F	Siblings	338.85	Siblings	2.78	942.86	Parent-Child
-	-	FI070M	FI129F	Parent-Child	113.52	Parent-Child	2.92	331.06	Parent-Child
?	?	FI187M	FI192F	Parent-Child	1303.58	Siblings	654.60	-	Siblings
?	?	FI052M	FI054F	Parent-Child	1246.88	No match	-	-	Siblings
?	-	FI102F	FI114M	Parent-Child	809.95	Siblings	35.27	-	Siblings
-	-	FI160F	FI161M	No match	-	Parent-Child	1.56	-	Siblings
-	-	FI155M	FI161M	No match	-	Siblings	2.12	-	Siblings
-	-	FI185M	FI186F	No match	-	Siblings	2.52	-	Siblings
-	-	FI119F	FI121F	No match	-	Siblings	7.28	-	Siblings
-	-	FI109F	FI111F	No match	-	Parent-Child	11.12	-	Siblings
-	-	FI109F	FI110F	No match	-	Parent-Child	14.71	-	Siblings
-	-	FI136M	FI147F	No match	-	Siblings	17.40	-	Siblings
-	-	FI187M	FI191M	No match	-	Siblings	34.52	-	Siblings
-	-	FI072F	FI073M	No match	-	Siblings	46.72	-	Siblings
-	-	FI166M	FI167F	No match	-	Siblings	47.52	-	Siblings
-	-	FI155M	FI160F	No match	-	Siblings	67.14	-	Siblings
-	-	FI174F	FI175F	No match	-	Siblings	619.83	-	Siblings

Confirmed (SNPs & STRs)	Confirmed (SNPs)	Bear 1	Bear 2	Genetic Relationship (SNPs)	LR (SNPs)	Genetic Relationship (STRs)	LR (STRs)	LR (SNPs & STRs)	Observed Relationship
-	-	FI085M	FI086F	No match	-	Parent-Child	643.18	-	Siblings
-	-	FI048M	FI049M	No match	-	No match	-	-	Siblings
-	-	FI052M	FI053M*	-	-	-	-	-	Siblings
-	-	FI070M	FI071M	No match	-	No match	-	-	Siblings
-	-	FI136M	FI146M*	-	-	-	-	-	Siblings
-	-	FI138M	FI140M	No match	-	No match	-	-	Siblings
-	-	FI145M	FI146M*	-	-	-	-	-	Siblings
-	-	FI146M*	FI147F	-	-	-	-	-	Siblings
-	-	FI193M	MO046	No match	-	No match	-	-	Siblings
-	Yes	FI131M	FI167F	Siblings	419788.00	No match	-	-	Siblings
-	Yes	FI191M	FI192F	Siblings	2604.10	No match	-	-	Siblings
-	-	FI138M	FI139F	Siblings	288.00	No match	-	-	Siblings
-	-	FI153M	FI154M	Siblings	283.72	Siblings	1.79	507.30	Siblings
-	-	FI165M	FI171M	Siblings	220.19	No match	-	-	Siblings
-	-	FI116F	FI117F	Siblings	147.19	Siblings	1.47	215.67	Siblings

Tab. 2. Overview of field observations (observed) of family groups among the identified brown bears in Sør-Varanger, Norway, and, the reconstructed family relationships based on SNP- and STR-analysis and field observations.

	Relationships		
	All *N*	Parent-Child *N*	Sibling *N*
Observed	112	74	36
Analyzed	105	71	32
Not analyzed	7	3	4
Analyzed	105	71	32
Confirmed with SNPs & STRs	40	34	6
Confirmed with SNPs	29	23	6
Ambigious relationship	10	6	4

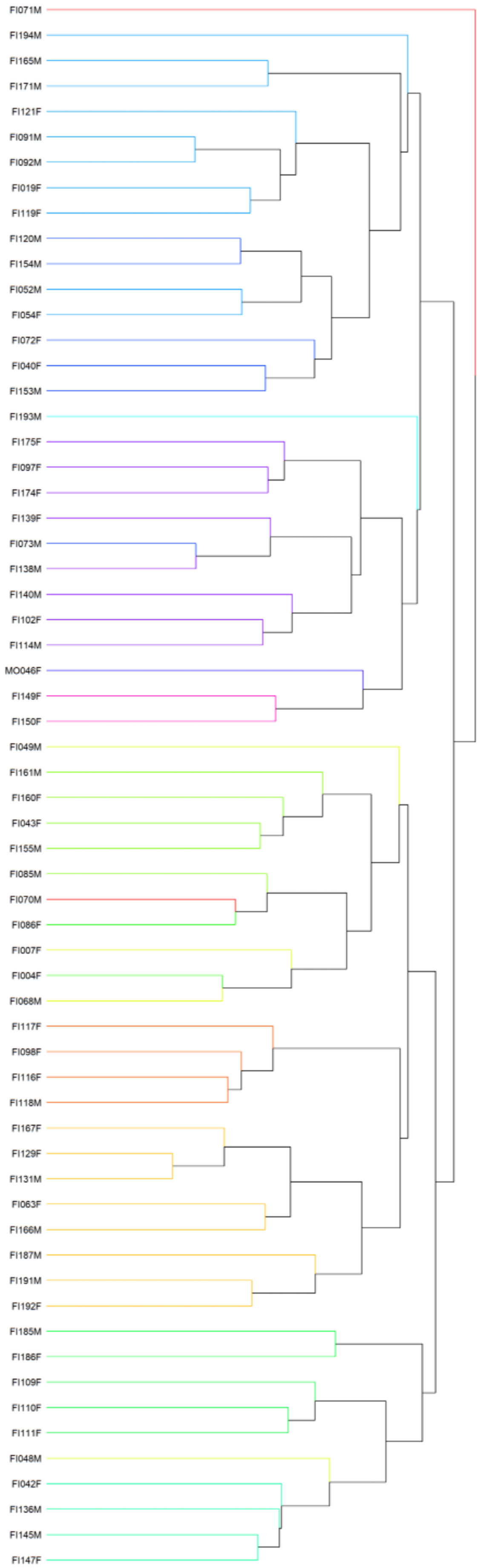

Fig.2. Dendogram of the genetic relationship based on SNP-analysis among observed brown bears in Sør-Varanger. The color represents the family group indicated based on recorded field observations (see Table 1).

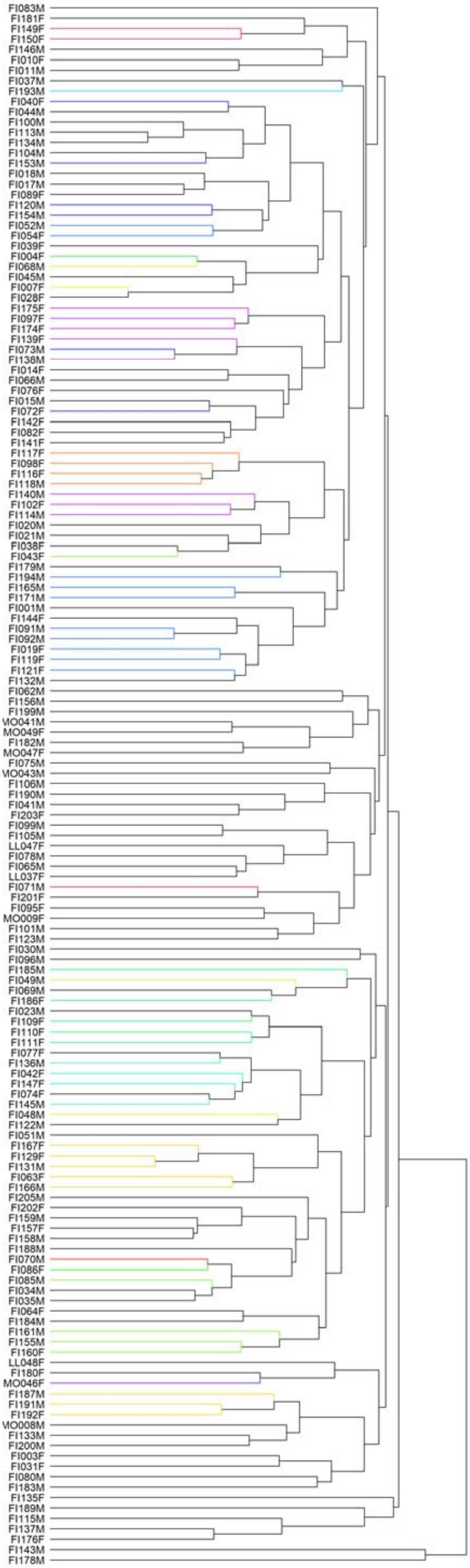

Fig.3. Dendogram of the genetic relationship based on SNP-analysis among all analyzed brown bears in Sør-Varanger. The color represents the family group indicated based on recorded field observations (see Table 1).

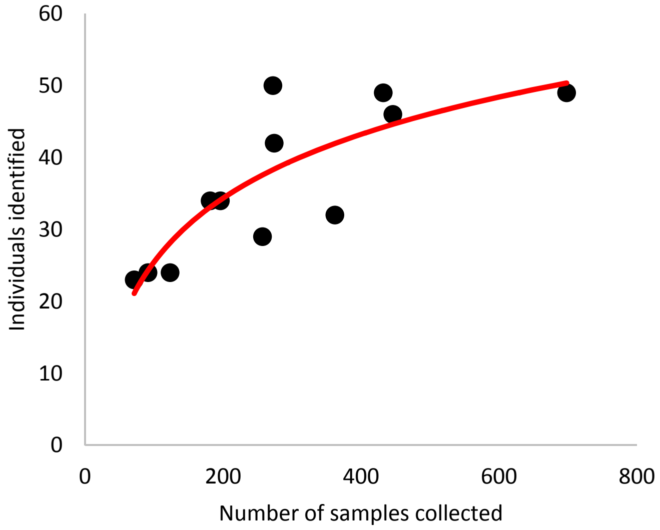

Fig. 4. Number of samples collected against the number of individual brown bears identified annually in Sør-Varanger, Norway for the period from 2005 to 2016.

a)

b)

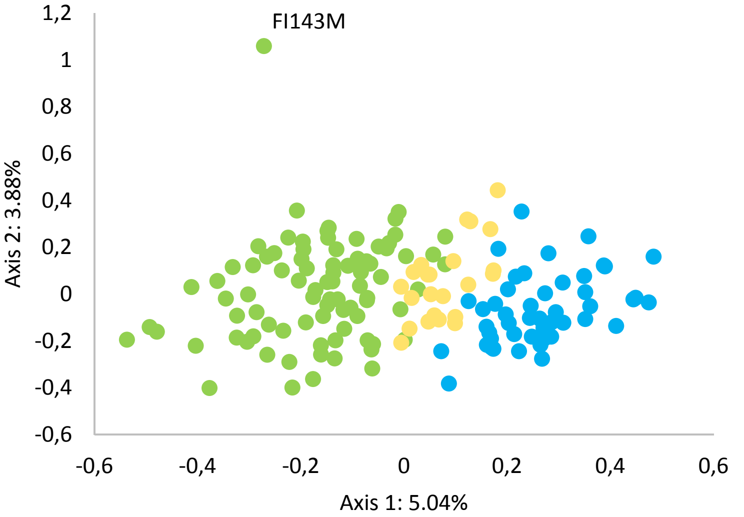

Fig. 5. a) Population structure of individual brown bear genotypes (SNPs) from Sør-Varanger, Norway, 2004 to 2016 for two genetic clusters (*K*=2). Each bar represents one individual partionined into segments, the length of each segment corresponds to the individual, cluster membership value (q_i). Individuals are sorted by sample number from left to right. b) Factorial-correspondence analysis of the same brown bears with the genetic cluster indicated by color: green (cluster 1), blue (cluster 2) and yellow (admixed, unassigned) individuals (q_i<0.7).

4 Concluding Remarks

According to the aims of this study, we can conclude:

- To reconstruct the family structure of the bears genetically identified in Sør-Varanger:
- The dendograms showed that most individuals suggested as close family members by observation data were grouped in a similar manner if using simple allele sharing methods. However, more detailed analysis is necessary to deduce the nature of these relationships (cousins, uncle-nephew etc.). At total of 121 genetic relationships were deteced of which 46 relationships were supported by observation as either parent-child or siblings. However, we do not believe that the genetic analysis disclose all such relationships in the families assumed to live in Sør-Varanger. Further validation of the SNP-chip and its performance is needed to investigate such possible mechanism and thus requires further research and tests.
- To calculate the minimum number of reproductions per year in Sør-Varanger:
- The average was 4 cubs per year. While it remains a challenge to estimate the number of offspring for each year or season, we estimated the number of cubs indirectly by counting each new parent-child relationship during the period. This numbers can be considered as a conservative, minimum estimate.
- To calculate the minimum number of cubs per individual female detected:
- Based on this number and the confirmed parent-child relationships identified in the SNP-data we found that the average number of offspring was 2 cubs per female and 3 per male. Also this numbers can be considered as conservative, minimum estimates.
- To detect immigrating bears into the bear population of Sør-Varanger:
- Population genetic structure seems to be similar to the structure revealed by 8 STRs. Here, based on the SNP-data, one individual in particular, FI143M, forms an outlier, in the factorial-correspondence analysis as well as dendogram. This individual most likely is an immigrant from further away. All other brown bears belong to the same, larger genetic unit. There appeared to be a few other individuals, rather unrelated to the rest of the family groups in Sør-Varanger, forming outliers in the dendogram.

Overall, the observational data, sampling effort and the quality of the sample material of the brown bears in Sør-Varanger is remarkable. After further evaluation and test of the SNP-chip, and potential replacement of some of the SNP-markers, a better assessment of the family structure is to be expected.

5 Acknowledgements

We thank Magne Asheim and Steinar Wikan from the Norwegian State Nature Inspectorate (SNO) and Tore Johan Olsen (Finnmark County Governor’s Office) for the good and fruitful collaboration and Julia Schregel (NIBIO Svanhovd) for laboratory work.

The project was funded by the Finnmark County Governor’s Office, Environmental Department, Norway.

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Appendix

Table A1: Results of 151 SNP-genotypes of brown bears from Sør-Varanger, sampled 2004 to 2016 and their parent-child and sibling with the program FAMILIAS 3.2.2 sorted by the largest likelihood ratio (LR). The ID no. of each brown bear contains the sex as last character (F=female, M=male).

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI007F	FI028F	Siblings	Not observed	11595300.0	NA	80	2	93.13 %	86.25 %	13.75 %	0 %	0.385	0	0	0.54
FI129F	FI131M	Siblings	Siblings	3123180.0	NA	81	1	90.74 %	81.48 %	18.52 %	0 %	0.36	0	0	0.44
FI113M	FI134M	Siblings	Not observed	2051750.0	NA	93	8	91.40 %	82.80 %	17.20 %	0 %	0.36	0	0	0.44
FI007F	FI028F	Parent-Child	Not observed	1666100.0	0	80	2	93.13 %	86.25 %	13.75 %	0 %	0.385	0	0	0.54
FI129F	FI131M	Parent-Child	Siblings	654591.0	0	81	1	90.74 %	81.48 %	18.52 %	0 %	0.36	0	0	0.44
FI091M	FI092M	Siblings	Siblings	573072.0	NA	87	4	89.08 %	79.31 %	19.54 %	1.15 %	0.325	0	0.12	0.42
FI131M	FI167F	Siblings	Not observed	419788.0	NA	90	1	87.78 %	77.78 %	20 %	2.22 %	0.3125	0	0.14	0.39
FI073M	FI138M	Parent-Child	Not observed	305207.0	0	91	16	89.01 %	78.02 %	21.98 %	0 %	0.32	0	0	0.28
FI073M	FI138M	Siblings	Not observed	290165.0	NA	91	16	89.01 %	78.02 %	21.98 %	0 %	0.32	0	0	0.28
FI113M	FI134M	Parent-Child	Not observed	194100.0	0	93	8	91.40 %	82.80 %	17.20 %	0 %	0.36	0	0	0.44
FI115M	FI137M	Parent-Child	Not observed	72231.6	0	91	19	83.52 %	67.03 %	32.97 %	0 %	0.25	0	0	0
FI137M	FI176F	Siblings	Not observed	67255.3	NA	90	19	85.56 %	72.22 %	26.67 %	1.11 %	0.2725	0	0.18	0.27
FI099M	FI105M	Parent-Child	Not observed	46969.5	0	92	17	84.78 %	69.57 %	30.43 %	0 %	0.2925	0	0	0.17
FI099M	FI105M	Siblings	Not observed	30384.4	NA	92	17	84.78 %	69.57 %	30.43 %	0 %	0.2925	0	0	0.17
FI041M	FI203F	Parent-Child	Not observed	28341.0	0	90	9	83.33 %	66.67 %	33.33 %	0 %	0.27	0	0	0.08
FI077F	FI136M	Parent-Child	Not observed	27843.1	0	90	10	85 %	70 %	30 %	0 %	0.2875	0	0	0.15
FI097F	FI139F	Parent-Child	Parent-Child	27171.1	0	90	16	83.33 %	66.67 %	33.33 %	0 %	0.25	0	0	0
FI133M	FI200M	Parent-Child	Not observed	24138.3	0	91	12	82.42 %	64.84 %	35.16 %	0 %	0.2575	0	0	0.03
FI063F	FI166M	Parent-Child	Parent-Child	23874.6	0	87	12	83.91 %	67.82 %	32.18 %	0 %	0.27	0	0	0.08
FI077F	FI145M	Siblings	Not observed	22752.1	NA	89	10	84.83 %	70.79 %	28.09 %	1.12 %	0.2675	0	0.17	0.24
FI104M	FI153M	Parent-Child	Not observed	20094.0	0	91	8	86.26 %	72.53 %	27.47 %	0 %	0.275	0	0	0.1
FI145M	FI147F	Parent-Child	Not observed	19260.2	0	90	6	84.44 %	68.89 %	31.11 %	0 %	0.28	0	0	0.12
FI038F	FI043F	Siblings	Not observed	18520.7	NA	89	5	88.76 %	78.65 %	20.22 %	1.12 %	0.3125	0	0.14	0.39
FI015M	FI072F	Parent-Child	Not observed	18017.0	0	89	3	85.96 %	71.91 %	28.09 %	0 %	0.275	0	0	0.1
FI074F	FI145M	Siblings	Not observed	17824.5	NA	89	10	85.96 %	74.16 %	23.60 %	2.25 %	0.27	0	0.21	0.29
FI071M	FI201F	Parent-Child	Not observed	17432.8	0	90	15	81.67 %	63.33 %	36.67 %	0 %	0.25	0	0	0
FI064F	FI184M	Parent-Child	Not observed	17176.1	0	88	13	82.95 %	65.91 %	34.09 %	0 %	0.265	0	0	0.06
FI063F	FI129F	Parent-Child	Parent-Child	16759.9	0	77	12	85.06 %	70.13 %	29.87 %	0 %	0.285	0	0	0.14
FI077F	FI136M	Siblings	Not observed	15345.5	NA	90	10	85 %	70 %	30 %	0 %	0.2875	0	0	0.15

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI180F	MO046F	Parent-Child	Not observed	15207.3	0	89	21	81.46 %	62.92 %	37.08 %	0 %	0.25	0	0	0
FI129F	FI167F	Siblings	Not observed	14764.1	NA	79	1	86.08 %	73.42 %	25.32 %	1.27 %	0.28	0	0.14	0.26
FI070M	FI086F	Parent-Child	Not observed	13777.2	0	90	1	86.11 %	72.22 %	27.78 %	0 %	0.295	0	0	0.18
FI158M	FI159M	Parent-Child	Not observed	12909.0	0	89	1	87.08 %	74.16 %	25.84 %	0 %	0.3025	0	0	0.21
FI082F	FI141F	Parent-Child	Not observed	12572.6	0	88	3	84.66 %	69.32 %	30.68 %	0 %	0.2625	0	0	0.05
FI158M	FI159M	Siblings	Not observed	12235.0	NA	89	1	87.08 %	74.16 %	25.84 %	0 %	0.3025	0	0	0.21
FI023M	FI109F	Parent-Child	Not observed	12071.9	0	90	6	82.22 %	64.44 %	35.56 %	0 %	0.25	0	0	0
FI070M	FI086F	Siblings	Not observed	11782.7	NA	90	1	86.11 %	72.22 %	27.78 %	0 %	0.295	0	0	0.18
FI098F	FI116F	Siblings	Parent-Child	10907.7	NA	89	5	85.96 %	71.91 %	28.09 %	0 %	0.3025	0	0	0.21
FI034M	FI188M	Parent-Child	Not observed	9977.5	0	90	1	86.11 %	72.22 %	27.78 %	0 %	0.285	0	0	0.14
FI157F	FI158M	Siblings	Not observed	9976.0	NA	87	1	87.36 %	74.71 %	25.29 %	0 %	0.3075	0	0	0.23
FI073M	FI139F	Parent-Child	Not observed	9312.1	0	90	16	83.33 %	66.67 %	33.33 %	0 %	0.25	0	0	0
FI034M	FI035M	Siblings	Not observed	9101.2	NA	90	7	87.22 %	77.78 %	18.89 %	3.33 %	0.2875	0	0.18	0.33
FI019F	FI119F	Parent-Child	Parent-Child	8846.6	0	90	4	85 %	70 %	30 %	0 %	0.28	0	0	0.12
FI145M	FI147F	Siblings	Not observed	7643.0	NA	90	6	84.44 %	68.89 %	31.11 %	0 %	0.28	0	0	0.12
FI017M	FI089F	Siblings	Not observed	7360.1	NA	89	3	88.20 %	77.53 %	21.35 %	1.12 %	0.2875	0	0.18	0.33
FI042F	FI077F	Parent-Child	Not observed	7266.8	0	89	10	81.46 %	62.92 %	37.08 %	0 %	0.25	0	0	0
FI070M	FI085M	Parent-Child	Not observed	6854.1	0	92	1	85.33 %	70.65 %	29.35 %	0 %	0.285	0	0	0.14
FI129F	FI166M	Siblings	Not observed	6583.1	NA	81	1	87.04 %	74.07 %	25.93 %	0 %	0.3	0	0.08	0.28
FI100M	FI113M	Siblings	Not observed	6456.7	NA	92	18	88.59 %	79.35 %	18.48 %	2.17 %	0.2875	0	0.18	0.33
FI070M	FI167F	Parent-Child	Not observed	6349.1	0	90	1	82.78 %	65.56 %	34.44 %	0 %	0.2525	0	0	0.01
FI035M	FI086F	Siblings	Not observed	6241.6	NA	91	1	86.26 %	75.82 %	20.88 %	3.30 %	0.265	0	0.22	0.28
FI023M	FI110F	Parent-Child	Not observed	6233.4	0	90	6	81.67 %	63.33 %	36.67 %	0 %	0.25	0	0	0
FI157F	FI158M	Parent-Child	Not observed	6108.2	0	87	1	87.36 %	74.71 %	25.29 %	0 %	0.3075	0	0	0.23
FI063F	FI129F	Siblings	Parent-Child	5645.8	NA	77	12	85.06 %	70.13 %	29.87 %	0 %	0.285	0	0	0.14
FI097F	FI174F	Parent-Child	Parent-Child	5627.7	0	89	16	83.71 %	67.42 %	32.58 %	0 %	0.27	0	0	0.08
FI098F	FI116F	Parent-Child	Parent-Child	5607.1	0	89	5	85.96 %	71.91 %	28.09 %	0 %	0.3025	0	0	0.21
FI069M	FI186F	Parent-Child	Not observed	5508.1	0	87	14	80.46 %	60.92 %	39.08 %	0 %	0.25	0	0	0
FI098F	FI117F	Parent-Child	Parent-Child	5339.0	0	89	5	82.02 %	64.04 %	35.96 %	0 %	0.25	0	0	0
FI041M	FI106M	Parent-Child	Not observed	5280.4	0	91	9	78.57 %	57.14 %	42.86 %	0 %	0.25	0	0	0
FI034M	FI188M	Siblings	Not observed	5257.0	NA	90	1	86.11 %	72.22 %	27.78 %	0 %	0.285	0	0	0.14
FI116F	FI118M	Siblings	Siblings	5048.9	NA	90	5	86.67 %	73.33 %	26.67 %	0 %	0.28	0	0.19	0.31
FI100M	FI134M	Siblings	Not observed	4910.1	NA	91	18	87.91 %	76.92 %	21.98 %	1.10 %	0.275	0	0.2	0.3
FI041M	FI203F	Siblings	Not observed	4600.3	NA	90	9	83.33 %	66.67 %	33.33 %	0 %	0.27	0	0	0.08
FI015M	FI072F	Siblings	Not observed	4374.5	NA	89	3	85.96 %	71.91 %	28.09 %	0 %	0.275	0	0	0.1

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI017M	FI154M	Parent-Child	Not observed	4358.2	0	91	3	86.81 %	73.63 %	26.37 %	0 %	0.2775	0	0	0.11
FI063F	FI166M	Siblings	Parent-Child	4356.8	NA	87	12	83.91 %	67.82 %	32.18 %	0 %	0.27	0	0	0.08
FI104M	FI153M	Siblings	Not observed	4336.9	NA	91	8	86.26 %	72.53 %	27.47 %	0 %	0.275	0	0	0.1
FI019F	FI091M	Parent-Child	Parent-Child	4286.1	0	89	4	84.83 %	69.66 %	30.34 %	0 %	0.285	0	0	0.14
FI042F	FI145M	Parent-Child	Parent-Child	3856.4	0	90	10	83.33 %	66.67 %	33.33 %	0 %	0.265	0	0	0.06
FI004F	FI068M	Siblings	Not observed	3796.9	NA	85	1	87.06 %	76.47 %	21.18 %	2.35 %	0.27	0	0.21	0.29
FI070M	FI085M	Siblings	Not observed	3780.7	NA	92	1	85.33 %	70.65 %	29.35 %	0 %	0.285	0	0	0.14
FI034M	FI085M	Siblings	Not observed	3512.6	NA	90	1	86.11 %	74.44 %	23.33 %	2.22 %	0.255	0	0.24	0.26
FI074F	FI158M	Parent-Child	Not observed	3450.8	0	87	1	85.63 %	71.26 %	28.74 %	0 %	0.29	0	0	0.16
FI019F	FI119F	Siblings	Parent-Child	3348.8	NA	90	4	85 %	70 %	30 %	0 %	0.28	0	0	0.12
FI019F	FI121F	Parent-Child	Parent-Child	3310.7	0	87	4	84.48 %	68.97 %	31.03 %	0 %	0.28	0	0	0.12
FI070M	FI158M	Parent-Child	Not observed	3184.0	0	89	1	84.27 %	68.54 %	31.46 %	0 %	0.2625	0	0	0.05
FI149F	FI150F	Parent-Child	Parent-Child	2956.4	0	89	20	83.15 %	66.29 %	33.71 %	0 %	0.275	0	0	0.1
FI070M	FI131M	Parent-Child	Not observed	2904.5	0	92	1	82.07 %	64.13 %	35.87 %	0 %	0.25	0	0	0
FI157F	FI159M	Siblings	Not observed	2774.3	NA	88	1	86.93 %	76.14 %	21.59 %	2.27 %	0.265	0	0.22	0.28
FI104M	FI113M	Parent-Child	Not observed	2699.0	0	92	8	85.87 %	71.74 %	28.26 %	0 %	0.265	0	0	0.06
FI070M	FI159M	Parent-Child	Not observed	2650.0	0	91	1	84.07 %	68.13 %	31.87 %	0 %	0.255	0	0	0.02
FI133M	FI200M	Siblings	Not observed	2633.7	NA	91	12	82.42 %	64.84 %	35.16 %	0 %	0.2575	0	0	0.03
FI191M	FI192F	Siblings	Siblings	2604.1	NA	86	12	84.88 %	70.93 %	27.91 %	1.16 %	0.26	0	0.23	0.27
FI074F	FI158M	Siblings	Not observed	2566.4	NA	87	1	85.63 %	71.26 %	28.74 %	0 %	0.29	0	0	0.16
FI019F	FI091M	Siblings	Parent-Child	2496.2	NA	89	4	84.83 %	69.66 %	30.34 %	0 %	0.285	0	0	0.14
FI064F	FI184M	Siblings	Not observed	2368.9	NA	88	13	82.95 %	65.91 %	34.09 %	0 %	0.265	0	0	0.06
FI074F	FI159M	Parent-Child	Not observed	2331.1	0	88	1	82.95 %	65.91 %	34.09 %	0 %	0.25	0	0	0
FI115M	FI137M	Siblings	Not observed	1987.9	NA	91	19	83.52 %	67.03 %	32.97 %	0 %	0.25	0	0	0
FI015M	FI082F	Parent-Child	Not observed	1980.7	0	88	3	82.95 %	65.91 %	34.09 %	0 %	0.25	0	0	0
FI097F	FI174F	Siblings	Parent-Child	1963.6	NA	89	16	83.71 %	67.42 %	32.58 %	0 %	0.27	0	0	0.08
FI021M	FI038F	Siblings	Not observed	1937.7	NA	89	5	84.83 %	70.79 %	28.09 %	1.12 %	0.255	0	0.2	0.22
FI015M	FI089F	Parent-Child	Not observed	1919.4	0	89	3	83.71 %	67.42 %	32.58 %	0 %	0.25	0	0	0
FI019F	FI092M	Parent-Child	Parent-Child	1855.2	0	87	4	83.33 %	66.67 %	33.33 %	0 %	0.265	0	0	0.06
FI098F	FI118M	Siblings	Parent-Child	1789.0	NA	89	5	85.39 %	70.79 %	29.21 %	0 %	0.2925	0	0	0.17
FI040F	FI153M	Parent-Child	Parent-Child	1776.9	0	90	8	83.89 %	67.78 %	32.22 %	0 %	0.2525	0	0	0.01
FI004F	FI085M	Parent-Child	Parent-Child	1733.1	0	89	1	83.15 %	66.29 %	33.71 %	0 %	0.25	0	0	0
FI017M	FI120M	Parent-Child	Not observed	1632.5	0	91	3	83.52 %	67.03 %	32.97 %	0 %	0.25	0	0	0
FI023M	FI147F	Parent-Child	Not observed	1588.2	0	89	6	82.02 %	64.04 %	35.96 %	0 %	0.2525	0	0	0.01
FI133M	FI192F	Parent-Child	Not observed	1582.2	0	89	12	80.90 %	61.80 %	38.20 %	0 %	0.25	0	0	0

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI019F	FI144F	Parent-Child	Not observed	1517.0	0	90	4	82.78 %	65.56 %	34.44 %	0 %	0.2525	0	0	0.01
FI129F	FI166M	Parent-Child	Not observed	1413.3	0	81	1	87.04 %	74.07 %	25.93 %	0 %	0.3	0	0.08	0.28
FI038F	FI098F	Siblings	Not observed	1375.2	NA	88	5	85.23 %	72.73 %	25 %	2.27 %	0.255	0	0.24	0.26
FI063F	FI192F	Parent-Child	Parent-Child	1366.6	0	87	12	79.31 %	58.62 %	41.38 %	0 %	0.25	0	0	0
FI019F	FI121F	Siblings	Parent-Child	1354.7	NA	87	4	84.48 %	68.97 %	31.03 %	0 %	0.28	0	0	0.12
FI149F	FI150F	Siblings	Parent-Child	1330.9	NA	89	20	83.15 %	66.29 %	33.71 %	0 %	0.275	0	0	0.1
FI035M	FI085M	Siblings	Not observed	1309.8	NA	92	1	85.33 %	73.91 %	22.83 %	3.26 %	0.25	0	0.25	0.25
FI187M	FI192F	Parent-Child	Siblings	1303.6	0	89	12	81.46 %	62.92 %	37.08 %	0 %	0.2525	0	0	0.01
FI082F	FI141F	Siblings	Not observed	1300.2	NA	88	3	84.66 %	69.32 %	30.68 %	0 %	0.2625	0	0	0.05
FI041M	FI190M	Siblings	Not observed	1296.2	NA	91	9	82.97 %	67.03 %	31.87 %	1.10 %	0.24	0	0.15	0.11
FI052M	FI054F	Parent-Child	Siblings	1246.9	0	80	11	85.63 %	71.25 %	28.75 %	0 %	0.26	0	0	0.04
FI136M	FI145M	Siblings	Siblings	1242.9	NA	93	10	84.41 %	70.97 %	26.88 %	2.15 %	0.245	0	0.26	0.24
FI040F	FI104M	Parent-Child	Not observed	1189.2	0	89	8	84.27 %	68.54 %	31.46 %	0 %	0.2575	0	0	0.03
FI017M	FI154M	Siblings	Not observed	1175.0	NA	91	3	86.81 %	73.63 %	26.37 %	0 %	0.2775	0	0	0.11
FI098F	FI118M	Parent-Child	Parent-Child	1168.3	0	89	5	85.39 %	70.79 %	29.21 %	0 %	0.2925	0	0	0.17
FI119F	FI132M	Parent-Child	Not observed	1153.9	0	89	4	83.71 %	67.42 %	32.58 %	0 %	0.2525	0	0	0.01
FI042F	FI147F	Parent-Child	Parent-Child	1138.0	0	89	6	82.02 %	64.04 %	35.96 %	0 %	0.25	0	0	0
FI003F	FI004F	Parent-Child	Not observed	1121.9	0	89	1	82.02 %	64.04 %	35.96 %	0 %	0.25	0	0	0
FI040F	FI044M	Parent-Child	Not observed	1116.5	0	89	8	84.27 %	68.54 %	31.46 %	0 %	0.2675	0	0	0.07
FI104M	FI134M	Siblings	Not observed	1104.1	NA	91	8	86.26 %	73.63 %	25.27 %	1.10 %	0.2525	0	0.21	0.22
FI097F	FI139F	Siblings	Parent-Child	1087.8	NA	90	16	83.33 %	66.67 %	33.33 %	0 %	0.25	0	0	0
FI092M	FI144F	Siblings	Not observed	1003.7	NA	87	4	84.48 %	70.11 %	28.74 %	1.15 %	0.245	0	0.26	0.24

Tab. A2: Identified family groups (clusters) with the program FAMILIAS and a likelihood ratio of LR>1000.

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI003F	FI004F	Parent-Child	Not observed	1121.9	0	89	1	82.02 %	64.04 %	35.96 %	0 %	0.25	0	0	0
FI004F	FI068M	Siblings	Not observed	3796.9	NA	85	1	87.06 %	76.47 %	21.18 %	2.35 %	0.27	0	0.21	0.29
FI034M	FI085M	Siblings	Not observed	3512.6	NA	90	1	86.11 %	74.44 %	23.33 %	2.22 %	0.255	0	0.24	0.26
FI035M	FI085M	Siblings	Not observed	1309.8	NA	92	1	85.33 %	73.91 %	22.83 %	3.26 %	0.25	0	0.25	0.25
FI070M	FI085M	Siblings	Not observed	3780.7	NA	92	1	85.33 %	70.65 %	29.35 %	0 %	0.285	0	0	0.14
FI070M	FI085M	Parent-Child	Not observed	6854.1	0	92	1	85.33 %	70.65 %	29.35 %	0 %	0.285	0	0	0.14
FI004F	FI085M	Parent-Child	Parent-Child	1733.1	0	89	1	83.15 %	66.29 %	33.71 %	0 %	0.25	0	0	0
FI035M	FI086F	Siblings	Not observed	6241.6	NA	91	1	86.26 %	75.82 %	20.88 %	3.30 %	0.265	0	0.22	0.28
FI070M	FI086F	Siblings	Not observed	11782.7	NA	90	1	86.11 %	72.22 %	27.78 %	0 %	0.295	0	0	0.18
FI070M	FI086F	Parent-Child	Not observed	13777.2	0	90	1	86.11 %	72.22 %	27.78 %	0 %	0.295	0	0	0.18
FI070M	FI131M	Parent-Child	Not observed	2904.5	0	92	1	82.07 %	64.13 %	35.87 %	0 %	0.25	0	0	0
FI129F	FI131M	Parent-Child	Siblings	654591.0	0	81	1	90.74 %	81.48 %	18.52 %	0 %	0.36	0	0	0.44
FI129F	FI131M	Siblings	Siblings	3123180.0	NA	81	1	90.74 %	81.48 %	18.52 %	0 %	0.36	0	0	0.44
FI070M	FI158M	Parent-Child	Not observed	3184.0	0	89	1	84.27 %	68.54 %	31.46 %	0 %	0.2625	0	0	0.05
FI074F	FI158M	Siblings	Not observed	2566.4	NA	87	1	85.63 %	71.26 %	28.74 %	0 %	0.29	0	0	0.16
FI074F	FI158M	Parent-Child	Not observed	3450.8	0	87	1	85.63 %	71.26 %	28.74 %	0 %	0.29	0	0	0.16
FI157F	FI158M	Parent-Child	Not observed	6108.2	0	87	1	87.36 %	74.71 %	25.29 %	0 %	0.3075	0	0	0.23
FI157F	FI158M	Siblings	Not observed	9976.0	NA	87	1	87.36 %	74.71 %	25.29 %	0 %	0.3075	0	0	0.23
FI070M	FI159M	Parent-Child	Not observed	2650.0	0	91	1	84.07 %	68.13 %	31.87 %	0 %	0.255	0	0	0.02
FI074F	FI159M	Parent-Child	Not observed	2331.1	0	88	1	82.95 %	65.91 %	34.09 %	0 %	0.25	0	0	0
FI157F	FI159M	Siblings	Not observed	2774.3	NA	88	1	86.93 %	76.14 %	21.59 %	2.27 %	0.265	0	0.22	0.28
FI158M	FI159M	Siblings	Not observed	12235.0	NA	89	1	87.08 %	74.16 %	25.84 %	0 %	0.3025	0	0	0.21
FI158M	FI159M	Parent-Child	Not observed	12909.0	0	89	1	87.08 %	74.16 %	25.84 %	0 %	0.3025	0	0	0.21
FI129F	FI166M	Parent-Child	Not observed	1413.3	0	81	1	87.04 %	74.07 %	25.93 %	0 %	0.3	0	0.08	0.28
FI129F	FI166M	Siblings	Not observed	6583.1	NA	81	1	87.04 %	74.07 %	25.93 %	0 %	0.3	0	0.08	0.28
FI070M	FI167F	Parent-Child	Not observed	6349.1	0	90	1	82.78 %	65.56 %	34.44 %	0 %	0.2525	0	0	0.01
FI129F	FI167F	Siblings	Not observed	14764.1	NA	79	1	86.08 %	73.42 %	25.32 %	1.27 %	0.28	0	0.14	0.26
FI131M	FI167F	Siblings	Not observed	419788.0	NA	90	1	87.78 %	77.78 %	20 %	2.22 %	0.3125	0	0.14	0.39
FI034M	FI188M	Siblings	Not observed	5257.0	NA	90	1	86.11 %	72.22 %	27.78 %	0 %	0.285	0	0	0.14
FI034M	FI188M	Parent-Child	Not observed	9977.5	0	90	1	86.11 %	72.22 %	27.78 %	0 %	0.285	0	0	0.14

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI007F	FI028F	Parent-Child	Not observed	1666100.0	0	80	2	93.13 %	86.25 %	13.75 %	0 %	0.385	0	0	0.54
FI007F	FI028F	Siblings	Not observed	11595300.0	NA	80	2	93.13 %	86.25 %	13.75 %	0 %	0.385	0	0	0.54

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI015M	FI072F	Siblings	Not observed	4374.5	NA	89	3	85.96 %	71.91 %	28.09 %	0 %	0.275	0	0	0.1
FI015M	FI072F	Parent-Child	Not observed	18017.0	0	89	3	85.96 %	71.91 %	28.09 %	0 %	0.275	0	0	0.1
FI015M	FI082F	Parent-Child	Not observed	1980.7	0	88	3	82.95 %	65.91 %	34.09 %	0 %	0.25	0	0	0
FI015M	FI089F	Parent-Child	Not observed	1919.4	0	89	3	83.71 %	67.42 %	32.58 %	0 %	0.25	0	0	0
FI017M	FI089F	Siblings	Not observed	7360.1	NA	89	3	88.20 %	77.53 %	21.35 %	1.12 %	0.2875	0	0.18	0.33
FI017M	FI120M	Parent-Child	Not observed	1632.5	0	91	3	83.52 %	67.03 %	32.97 %	0 %	0.25	0	0	0
FI082F	FI141F	Siblings	Not observed	1300.2	NA	88	3	84.66 %	69.32 %	30.68 %	0 %	0.2625	0	0	0.05
FI082F	FI141F	Parent-Child	Not observed	12572.6	0	88	3	84.66 %	69.32 %	30.68 %	0 %	0.2625	0	0	0.05
FI017M	FI154M	Siblings	Not observed	1175.0	NA	91	3	86.81 %	73.63 %	26.37 %	0 %	0.2775	0	0	0.11
FI017M	FI154M	Parent-Child	Not observed	4358.2	0	91	3	86.81 %	73.63 %	26.37 %	0 %	0.2775	0	0	0.11

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI019F	FI091M	Siblings	Parent-Child	2496.2	NA	89	4	84.83 %	69.66 %	30.34 %	0 %	0.285	0	0	0.14
FI019F	FI091M	Parent-Child	Parent-Child	4286.1	0	89	4	84.83 %	69.66 %	30.34 %	0 %	0.285	0	0	0.14
FI019F	FI092M	Parent-Child	Parent-Child	1855.2	0	87	4	83.33 %	66.67 %	33.33 %	0 %	0.265	0	0	0.06
FI091M	FI092M	Siblings	Siblings	573072.0	NA	87	4	89.08 %	79.31 %	19.54 %	1.15 %	0.325	0	0.12	0.42
FI019F	FI119F	Siblings	Parent-Child	3348.8	NA	90	4	85 %	70 %	30 %	0 %	0.28	0	0	0.12
FI019F	FI119F	Parent-Child	Parent-Child	8846.6	0	90	4	85 %	70 %	30 %	0 %	0.28	0	0	0.12
FI019F	FI121F	Siblings	Parent-Child	1354.7	NA	87	4	84.48 %	68.97 %	31.03 %	0 %	0.28	0	0	0.12
FI019F	FI121F	Parent-Child	Parent-Child	3310.7	0	87	4	84.48 %	68.97 %	31.03 %	0 %	0.28	0	0	0.12
FI119F	FI132M	Parent-Child	Not observed	1153.9	0	89	4	83.71 %	67.42 %	32.58 %	0 %	0.2525	0	0	0.01
FI019F	FI144F	Parent-Child	Not observed	1517.0	0	90	4	82.78 %	65.56 %	34.44 %	0 %	0.2525	0	0	0.01
FI092M	FI144F	Siblings	Not observed	1003.7	NA	87	4	84.48 %	70.11 %	28.74 %	1.15 %	0.245	0	0.26	0.24

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI021M	FI038F	Siblings	Not observed	1937.7	NA	89	5	84.83 %	70.79 %	28.09 %	1.12 %	0.255	0	0.2	0.22
FI038F	FI043F	Siblings	Not observed	18520.7	NA	89	5	88.76 %	78.65 %	20.22 %	1.12 %	0.3125	0	0.14	0.39
FI038F	FI098F	Siblings	Not observed	1375.2	NA	88	5	85.23 %	72.73 %	25 %	2.27 %	0.255	0	0.24	0.26
FI098F	FI116F	Parent-Child	Parent-Child	5607.1	0	89	5	85.96 %	71.91 %	28.09 %	0 %	0.3025	0	0	0.21
FI098F	FI116F	Siblings	Parent-Child	10907.7	NA	89	5	85.96 %	71.91 %	28.09 %	0 %	0.3025	0	0	0.21
FI098F	FI117F	Parent-Child	Parent-Child	5339.0	0	89	5	82.02 %	64.04 %	35.96 %	0 %	0.25	0	0	0
FI098F	FI118M	Parent-Child	Parent-Child	1168.3	0	89	5	85.39 %	70.79 %	29.21 %	0 %	0.2925	0	0	0.17
FI098F	FI118M	Siblings	Parent-Child	1789.0	NA	89	5	85.39 %	70.79 %	29.21 %	0 %	0.2925	0	0	0.17
FI116F	FI118M	Siblings	Siblings	5048.9	NA	90	5	86.67 %	73.33 %	26.67 %	0 %	0.28	0	0.19	0.31

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI023M	FI109F	Parent-Child	Not observed	12071.9	0	90	6	82.22 %	64.44 %	35.56 %	0 %	0.25	0	0	0
FI023M	FI110F	Parent-Child	Not observed	6233.4	0	90	6	81.67 %	63.33 %	36.67 %	0 %	0.25	0	0	0
FI023M	FI147F	Parent-Child	Not observed	1588.2	0	89	6	82.02 %	64.04 %	35.96 %	0 %	0.2525	0	0	0.01
FI145M	FI147F	Siblings	Not observed	7643.0	NA	90	6	84.44 %	68.89 %	31.11 %	0 %	0.28	0	0	0.12
FI145M	FI147F	Parent-Child	Not observed	19260.2	0	90	6	84.44 %	68.89 %	31.11 %	0 %	0.28	0	0	0.12
FI042F	FI147F	Parent-Child	Parent-Child	1138.0	0	89	6	82.02 %	64.04 %	35.96 %	0 %	0.25	0	0	0

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI034M	FI035M	Siblings	Not observed	9101.2	NA	90	7	87.22 %	77.78 %	18.89 %	3.33 %	0.2875	0	0.18	0.33

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI040F	FI044M	Parent-Child	Not observed	1116.5	0	89	8	84.27 %	68.54 %	31.46 %	0 %	0.2675	0	0	0.07
FI040F	FI104M	Parent-Child	Not observed	1189.2	0	89	8	84.27 %	68.54 %	31.46 %	0 %	0.2575	0	0	0.03
FI104M	FI113M	Parent-Child	Not observed	2699.0	0	92	8	85.87 %	71.74 %	28.26 %	0 %	0.265	0	0	0.06
FI104M	FI134M	Siblings	Not observed	1104.1	NA	91	8	86.26 %	73.63 %	25.27 %	1.10 %	0.2525	0	0.21	0.22
FI113M	FI134M	Parent-Child	Not observed	194100.0	0	93	8	91.40 %	82.80 %	17.20 %	0 %	0.36	0	0	0.44
FI113M	FI134M	Siblings	Not observed	2051750.0	NA	93	8	91.40 %	82.80 %	17.20 %	0 %	0.36	0	0	0.44
FI104M	FI153M	Siblings	Not observed	4336.9	NA	91	8	86.26 %	72.53 %	27.47 %	0 %	0.275	0	0	0.1
FI104M	FI153M	Parent-Child	Not observed	20094.0	0	91	8	86.26 %	72.53 %	27.47 %	0 %	0.275	0	0	0.1
FI040F	FI153M	Parent-Child	Parent-Child	1776.9	0	90	8	83.89 %	67.78 %	32.22 %	0 %	0.2525	0	0	0.01

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI041M	FI106M	Parent-Child	Not observed	5280.4	0	91	9	78.57 %	57.14 %	42.86 %	0 %	0.25	0	0	0
FI041M	FI190M	Siblings	Not observed	1296.2	NA	91	9	82.97 %	67.03 %	31.87 %	1.10 %	0.24	0	0.15	0.11
FI041M	FI203F	Siblings	Not observed	4600.3	NA	90	9	83.33 %	66.67 %	33.33 %	0 %	0.27	0	0	0.08
FI041M	FI203F	Parent-Child	Not observed	28341.0	0	90	9	83.33 %	66.67 %	33.33 %	0 %	0.27	0	0	0.08

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI042F	FI077F	Parent-Child	Not observed	7266.8	0	89	10	81.46 %	62.92 %	37.08 %	0 %	0.25	0	0	0
FI077F	FI136M	Siblings	Not observed	15345.5	NA	90	10	85 %	70 %	30 %	0 %	0.2875	0	0	0.15
FI077F	FI136M	Parent-Child	Not observed	27843.1	0	90	10	85 %	70 %	30 %	0 %	0.2875	0	0	0.15
FI074F	FI145M	Siblings	Not observed	17824.5	NA	89	10	85.96 %	74.16 %	23.60 %	2.25 %	0.27	0	0.21	0.29
FI077F	FI145M	Siblings	Not observed	22752.1	NA	89	10	84.83 %	70.79 %	28.09 %	1.12 %	0.2675	0	0.17	0.24
FI042F	FI145M	Parent-Child	Parent-Child	3856.4	0	90	10	83.33 %	66.67 %	33.33 %	0 %	0.265	0	0	0.06
FI136M	FI145M	Siblings	Siblings	1242.9	NA	93	10	84.41 %	70.97 %	26.88 %	2.15 %	0.245	0	0.26	0.24

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI052M	FI054F	Parent-Child	Siblings	1246.9	0	80	11	85.63 %	71.25 %	28.75 %	0 %	0.26	0	0	0.04
FI063F	FI129F	Siblings	Parent-Child	5645.8	NA	77	12	85.06 %	70.13 %	29.87 %	0 %	0.285	0	0	0.14
FI063F	FI129F	Parent-Child	Parent-Child	16759.9	0	77	12	85.06 %	70.13 %	29.87 %	0 %	0.285	0	0	0.14
FI063F	FI166M	Siblings	Parent-Child	4356.8	NA	87	12	83.91 %	67.82 %	32.18 %	0 %	0.27	0	0	0.08
FI063F	FI166M	Parent-Child	Parent-Child	23874.6	0	87	12	83.91 %	67.82 %	32.18 %	0 %	0.27	0	0	0.08
FI133M	FI192F	Parent-Child	Not observed	1582.2	0	89	12	80.90 %	61.80 %	38.20 %	0 %	0.25	0	0	0
FI063F	FI192F	Parent-Child	Parent-Child	1366.6	0	87	12	79.31 %	58.62 %	41.38 %	0 %	0.25	0	0	0
FI187M	FI192F	Parent-Child	Siblings	1303.6	0	89	12	81.46 %	62.92 %	37.08 %	0 %	0.2525	0	0	0.01
FI191M	FI192F	Siblings	Siblings	2604.1	NA	86	12	84.88 %	70.93 %	27.91 %	1.16 %	0.26	0	0.23	0.27
FI133M	FI200M	Siblings	Not observed	2633.7	NA	91	12	82.42 %	64.84 %	35.16 %	0 %	0.2575	0	0	0.03
FI133M	FI200M	Parent-Child	Not observed	24138.3	0	91	12	82.42 %	64.84 %	35.16 %	0 %	0.2575	0	0	0.03

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI064F	FI184M	Siblings	Not observed	2368.9	NA	88	13	82.95 %	65.91 %	34.09 %	0 %	0.265	0	0	0.06
FI064F	FI184M	Parent-Child	Not observed	17176.1	0	88	13	82.95 %	65.91 %	34.09 %	0 %	0.265	0	0	0.06

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI069M	FI186F	Parent-Child	Not observed	5508.1	0	87	14	80.46 %	60.92 %	39.08 %	0 %	0.25	0	0	0

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI071M	FI201F	Parent-Child	Not observed	17432.8	0	90	15	81.67 %	63.33 %	36.67 %	0 %	0.25	0	0	0

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI073M	FI138M	Siblings	Not observed	290165.0	NA	91	16	89.01 %	78.02 %	21.98 %	0 %	0.32	0	0	0.28
FI073M	FI138M	Parent-Child	Not observed	305207.0	0	91	16	89.01 %	78.02 %	21.98 %	0 %	0.32	0	0	0.28
FI073M	FI139F	Parent-Child	Not observed	9312.1	0	90	16	83.33 %	66.67 %	33.33 %	0 %	0.25	0	0	0
FI097F	FI139F	Siblings	Parent-Child	1087.8	NA	90	16	83.33 %	66.67 %	33.33 %	0 %	0.25	0	0	0
FI097F	FI139F	Parent-Child	Parent-Child	27171.1	0	90	16	83.33 %	66.67 %	33.33 %	0 %	0.25	0	0	0
FI097F	FI174F	Siblings	Parent-Child	1963.6	NA	89	16	83.71 %	67.42 %	32.58 %	0 %	0.27	0	0	0.08
FI097F	FI174F	Parent-Child	Parent-Child	5627.7	0	89	16	83.71 %	67.42 %	32.58 %	0 %	0.27	0	0	0.08

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI099M	FI105M	Siblings	Not observed	30384.4	NA	92	17	84.78 %	69.57 %	30.43 %	0 %	0.2925	0	0	0.17
FI099M	FI105M	Parent-Child	Not observed	46969.5	0	92	17	84.78 %	69.57 %	30.43 %	0 %	0.2925	0	0	0.17

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI100M	FI113M	Siblings	Not observed	6456.7	NA	92	18	88.59 %	79.35 %	18.48 %	2.17 %	0.2875	0	0.18	0.33
FI100M	FI134M	Siblings	Not observed	4910.1	NA	91	18	87.91 %	76.92 %	21.98 %	1.10 %	0.275	0	0.2	0.3

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI115M	FI137M	Siblings	Not observed	1987.9	NA	91	19	83.52 %	67.03 %	32.97 %	0 %	0.25	0	0	0
FI115M	FI137M	Parent-Child	Not observed	72231.6	0	91	19	83.52 %	67.03 %	32.97 %	0 %	0.25	0	0	0
FI137M	FI176F	Siblings	Not observed	67255.3	NA	90	19	85.56 %	72.22 %	26.67 %	1.11 %	0.2725	0	0.18	0.27

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI149F	FI150F	Siblings	Parent-Child	1330.9	NA	89	20	83.15 %	66.29 %	33.71 %	0 %	0.275	0	0	0.1
FI149F	FI150F	Parent-Child	Parent-Child	2956.4	0	89	20	83.15 %	66.29 %	33.71 %	0 %	0.275	0	0	0.1

Bear 1	Bear 2	Genetic Relationship	Observed Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI180F	MO046F	Parent-Child	Not observed	15207.3	0	89	21	81.46 %	62.92 %	37.08 %	0 %	0.25	0	0	0

Table A3: Results of 154 STR-genotypes of brown bears from Sør-Varanger, sampled 2004 to 2016 and their parent-child and sibling with the program FAMILIAS 3.2.2 with an likelihood ratio (LR) >20 and sorted by the largest LR. The ID no. of each brown bear contains the sex as last character (F=female, M=male).

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI145M	FI147F	Siblings	32771.2	NA	12	1	83.33 %	66.67 %	33.33 %	0 %	0.3875	0	0	0.55
MO041M	MO047F	Siblings	13291.9	NA	8	1	93.75 %	87.50 %	12.50 %	0 %	0.4575	0	0	0.83
FI074F	FI147F	Siblings	10007.4	NA	12	1	83.33 %	66.67 %	33.33 %	0 %	0.3825	0	0	0.53
FI021M	FI043F	Siblings	7979.29	NA	12	1	79.17 %	58.33 %	41.67 %	0 %	0.355	0	0	0.42
FI074F	FI145M	Siblings	5275.74	NA	12	1	79.17 %	58.33 %	41.67 %	0 %	0.3575	0	0	0.43
FI017M	FI054F	Parent-Child	2243.5	0	12	2	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI017M	FI054F	Siblings	2191.02	NA	12	2	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI021M	FI043F	Parent-Child	1764.84	0	12	1	79.17 %	58.33 %	41.67 %	0 %	0.355	0	0	0.42
FI145M	FI147F	Parent-Child	1727.09	0	12	1	83.33 %	66.67 %	33.33 %	0 %	0.3875	0	0	0.55
FI074F	FI147F	Parent-Child	1357.16	0	12	1	83.33 %	66.67 %	33.33 %	0 %	0.3825	0	0	0.53
FI074F	FI145M	Parent-Child	1174.44	0	12	1	79.17 %	58.33 %	41.67 %	0 %	0.3575	0	0	0.43
FI035M	FI086F	Siblings	1011.34	NA	11	2	81.82 %	63.64 %	36.36 %	0 %	0.355	0	0	0.42
FI181F	MO008M	Parent-Child	939.928	0	8	1	62.50 %	25 %	75 %	0 %	0.2525	0	0	0.01
MO041M	MO047F	Parent-Child	742.618	0	8	1	93.75 %	87.50 %	12.50 %	0 %	0.4575	0	0	0.83
FI066M	FI082F	Siblings	706.959	NA	11	1	77.27 %	63.64 %	27.27 %	9.09 %	0.3325	0	0.11	0.44
FI051M	FI063F	Parent-Child	666.474	0	12	6	66.67 %	33.33 %	66.67 %	0 %	0.2675	0	0	0.07
FI187M	FI192F	Siblings	654.604	NA	8	1	75 %	62.50 %	25 %	12.50 %	0.3125	0.100837	0.14	0.39
FI085M	FI086F	Parent-Child	643.182	0	12	2	75 %	50 %	50 %	0 %	0.2925	0	0	0.17
FI035M	FI086F	Parent-Child	641.84	0	11	2	81.82 %	63.64 %	36.36 %	0 %	0.355	0	0	0.42
FI174F	FI175F	Siblings	619.826	NA	8	1	81.25 %	75 %	12.50 %	12.50 %	0.3675	0.100837	0.07	0.54
FI100M	FI113M	Siblings	380.701	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3725	0	0	0.49
FI159M	FI202F	Siblings	335.6	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.365	0	0	0.46
FI004F	FI085M	Parent-Child	289.562	0	12	2	70.83 %	41.67 %	58.33 %	0 %	0.27	0	0	0.08
FI054F	FI091M	Siblings	261.17	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3575	0	0.08	0.51
FI100M	FI120M	Siblings	252.52	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3625	0	0	0.45
FI085M	FI086F	Siblings	246.988	NA	12	2	75 %	50 %	50 %	0 %	0.2925	0	0	0.17
FI042F	FI145M	Parent-Child	240.068	0	12	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI115M	FI137M	Siblings	221.779	NA	8	7	68.75 %	37.50 %	62.50 %	0 %	0.3075	0	0	0.23
FI133M	FI180F	Parent-Child	218.452	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI065M	LL037F	Siblings	215.115	NA	8	1	81.25 %	75 %	12.50 %	12.50 %	0.35	0.100837	0.09	0.49
FI115M	FI137M	Parent-Child	203.497	0	8	7	68.75 %	37.50 %	62.50 %	0 %	0.3075	0	0	0.23
FI072F	FI082F	Parent-Child	203.335	0	12	1	66.67 %	33.33 %	66.67 %	0 %	0.25	0	0	0
FI021M	FI038F	Parent-Child	194.297	0	12	1	66.67 %	33.33 %	66.67 %	0 %	0.2525	0	0	0.01

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI040F	FI044M	Parent-Child	184.835	0	12	1	70.83 %	41.67 %	58.33 %	0 %	0.29	0	0	0.16
FI157F	FI202F	Siblings	184.078	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3575	0	0	0.43
FI072F	FI092M	Siblings	178.349	NA	11	1	72.73 %	54.55 %	36.36 %	9.09 %	0.3	0.0753294	0.16	0.36
FI129F	FI167F	Siblings	170.656	NA	8	1	75 %	50 %	50 %	0 %	0.3325	0	0	0.33
FI017M	FI089F	Parent-Child	166.189	0	12	2	70.83 %	41.67 %	58.33 %	0 %	0.2925	0	0	0.17
FI004F	FI035M	Parent-Child	155.609	0	11	2	72.73 %	45.45 %	54.55 %	0 %	0.2575	0	0	0.03
FI066M	FI092M	Parent-Child	155.106	0	10	1	65 %	30 %	70 %	0 %	0.25	0	0	0
FI097F	FI102F	Siblings	154.072	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.36	0	0	0.44
FI017M	FI104M	Parent-Child	148.52	0	11	1	68.18 %	36.36 %	63.64 %	0 %	0.2575	0	0	0.03
FI051M	FI063F	Siblings	141.998	NA	12	6	66.67 %	33.33 %	66.67 %	0 %	0.2675	0	0	0.07
FI073M	FI100M	Siblings	140.132	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3625	0	0	0.45
FI100M	FI135F	Siblings	139.979	NA	8	1	75 %	50 %	50 %	0 %	0.3375	0	0	0.35
FI042F	FI077F	Parent-Child	134.983	0	12	2	54.17 %	8.33 %	91.67 %	0 %	0.25	0	0	0
FI136M	FI145M	Parent-Child	134.746	0	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI181F	MO008M	Siblings	132.181	NA	8	1	62.50 %	25 %	75 %	0 %	0.2525	0	0	0.01
FI136M	FI145M	Siblings	129.665	NA	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI007F	FI028F	Siblings	128.976	NA	5	2	90 %	80 %	20 %	0 %	0.43	0	0	0.72
FI072F	FI134M	Siblings	122.599	NA	8	1	81.25 %	75 %	12.50 %	12.50 %	0.35	0.100837	0.09	0.49
FI054F	FI100M	Siblings	118.913	NA	8	1	75 %	50 %	50 %	0 %	0.335	0	0	0.34
FI157F	FI202F	Parent-Child	118.378	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3575	0	0	0.43
FI133M	FI192F	Parent-Child	116.717	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI035M	FI085M	Siblings	116.306	NA	11	2	72.73 %	54.55 %	36.36 %	9.09 %	0.275	0.0752032	0.2	0.3
FI092M	FI134M	Siblings	115.75	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3675	0	0	0.47
FI135F	FI153M	Siblings	114.215	NA	8	1	75 %	50 %	50 %	0 %	0.33	0	0	0.32
FI137M	FI176F	Parent-Child	113.585	0	8	7	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI158M	FI159M	Siblings	112.608	NA	8	1	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI159M	FI202F	Parent-Child	112.149	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.365	0	0	0.46
FI007F	FI068M	Parent-Child	109.204	0	12	2	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI017M	FI052M	Parent-Child	108.013	0	12	2	66.67 %	33.33 %	66.67 %	0 %	0.255	0	0	0.02
FI063F	FI191M	Parent-Child	106.954	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI015M	FI142F	Siblings	104.42	NA	7	1	78.57 %	57.14 %	42.86 %	0 %	0.3525	0	0	0.41
FI040F	FI044M	Siblings	102.589	NA	12	1	70.83 %	41.67 %	58.33 %	0 %	0.29	0	0	0.16
FI054F	FI113M	Siblings	101.754	NA	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI017M	FI089F	Siblings	99.8454	NA	12	2	70.83 %	41.67 %	58.33 %	0 %	0.2925	0	0	0.17
FI129F	FI167F	Parent-Child	96.9259	0	8	1	75 %	50 %	50 %	0 %	0.3325	0	0	0.33

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI017M	FI134M	Siblings	96.6316	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.36	0	0	0.44
FI077F	FI143M	Parent-Child	96.044	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.295	0	0	0.18
FI017M	FI113M	Parent-Child	94.8281	0	8	1	75 %	50 %	50 %	0 %	0.315	0	0	0.26
FI004F	FI034M	Parent-Child	94.2077	0	10	2	70 %	40 %	60 %	0 %	0.2875	0	0	0.15
FI042F	FI136M	Parent-Child	91.7877	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.25	0	0	0
FI100M	FI113M	Parent-Child	91.7176	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3725	0	0	0.49
FI104M	FI113M	Siblings	88.7895	NA	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3525	0	0	0.41
FI100M	FI120M	Parent-Child	88.6986	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3625	0	0	0.45
FI054F	FI113M	Parent-Child	86.6802	0	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI017M	FI100M	Siblings	84.5439	NA	8	2	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI073M	FI139F	Parent-Child	81.2369	0	8	1	75 %	50 %	50 %	0 %	0.3075	0	0	0.23
FI004F	FI085M	Siblings	78.6993	NA	12	2	70.83 %	41.67 %	58.33 %	0 %	0.27	0	0	0.08
FI034M	FI035M	Parent-Child	78.0405	0	9	2	72.22 %	44.44 %	55.56 %	0 %	0.295	0	0	0.18
FI044M	FI140M	Parent-Child	77.9764	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI042F	FI074F	Parent-Child	77.443	0	12	2	58.33 %	16.67 %	83.33 %	0 %	0.25	0	0	0
FI147F	FI159M	Parent-Child	77.4026	0	8	1	75 %	50 %	50 %	0 %	0.31	0	0	0.24
FI065M	FI078M	Parent-Child	75.5888	0	12	2	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI116F	FI118M	Siblings	75.2088	NA	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI034M	FI085M	Siblings	73.7846	NA	10	2	70 %	50 %	40 %	10 %	0.265	0.0759067	0.22	0.28
FI120M	FI134M	Siblings	73.6049	NA	8	1	75 %	50 %	50 %	0 %	0.33	0	0	0.32
FI158M	FI159M	Parent-Child	73.0088	0	8	1	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI039F	FI043F	Parent-Child	72.6088	0	12	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI017M	FI113M	Siblings	72.3442	NA	8	1	75 %	50 %	50 %	0 %	0.315	0	0	0.26
FI004F	FI086F	Parent-Child	71.9481	0	12	2	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI051M	FI129F	Parent-Child	71.5152	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.265	0	0	0.06
FI135F	FI153M	Parent-Child	70.5787	0	8	1	75 %	50 %	50 %	0 %	0.33	0	0	0.32
FI054F	FI073M	Siblings	70.3314	NA	12	1	66.67 %	41.67 %	50 %	8.33 %	0.245	0.0673161	0.26	0.24
FI132M	FI204F	Siblings	70.1318	NA	8	1	87.50 %	75 %	25 %	0 %	0.395	0	0	0.58
FI113M	FI154M	Siblings	70.0302	NA	8	1	75 %	62.50 %	25 %	12.50 %	0.3125	0.100837	0.14	0.39
FI007F	FI049M	Parent-Child	67.8139	0	12	2	54.17 %	8.33 %	91.67 %	0 %	0.25	0	0	0
FI116F	FI118M	Parent-Child	67.5135	0	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI097F	FI102F	Parent-Child	67.5089	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.36	0	0	0.44
FI034M	FI086F	Parent-Child	67.3334	0	10	2	65 %	30 %	70 %	0 %	0.25	0	0	0
FI155M	FI160F	Siblings	67.1399	NA	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI077F	FI143M	Siblings	64.0449	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.295	0	0	0.18

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI155M	FI160F	Parent-Child	62.6496	0	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI147F	FI159M	Siblings	62.4755	NA	8	1	75 %	50 %	50 %	0 %	0.31	0	0	0.24
FI113M	FI120M	Siblings	62.0429	NA	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI104M	FI113M	Parent-Child	61.7584	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3525	0	0	0.41
FI070M	FI157F	Siblings	61.6301	NA	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI017M	FI100M	Parent-Child	60.9876	0	8	2	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI100M	FI153M	Parent-Child	60.4295	0	8	1	75 %	50 %	50 %	0 %	0.31	0	0	0.24
FI100M	FI135F	Parent-Child	58.5159	0	8	1	75 %	50 %	50 %	0 %	0.3375	0	0	0.35
FI015M	FI073M	Parent-Child	57.2061	0	11	2	59.09 %	18.18 %	81.82 %	0 %	0.25	0	0	0
FI023M	FI185M	Parent-Child	57.1946	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2675	0	0	0.07
FI043F	FI155M	Parent-Child	57.1249	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.275	0	0	0.1
FI023M	FI175F	Parent-Child	56.0621	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI054F	FI100M	Parent-Child	55.7473	0	8	1	75 %	50 %	50 %	0 %	0.335	0	0	0.34
FI073M	FI139F	Siblings	55.2371	NA	8	1	75 %	50 %	50 %	0 %	0.3075	0	0	0.23
FI004F	FI034M	Siblings	54.9743	NA	10	2	70 %	40 %	60 %	0 %	0.2875	0	0	0.15
FI104M	FI135F	Siblings	54.8421	NA	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI035M	FI070M	Parent-Child	54.7732	0	11	2	72.73 %	45.45 %	54.55 %	0 %	0.265	0	0	0.06
FI104M	FI134M	Siblings	54.505	NA	8	1	75 %	50 %	50 %	0 %	0.3225	0	0	0.29
FI100M	FI154M	Parent-Child	52.8365	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2925	0	0	0.17
FI074F	FI136M	Siblings	52.4543	NA	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI134M	FI135F	Siblings	50.1095	NA	8	1	75 %	50 %	50 %	0 %	0.33	0	0	0.32
FI100M	FI153M	Siblings	49.587	NA	8	1	75 %	50 %	50 %	0 %	0.31	0	0	0.24
FI054F	FI135F	Siblings	48.6666	NA	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI017M	FI134M	Parent-Child	48.4999	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.36	0	0	0.44
FI182M	MO047F	Parent-Child	48.2144	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI104M	FI134M	Parent-Child	48.0165	0	8	1	75 %	50 %	50 %	0 %	0.3225	0	0	0.29
FI043F	FI160F	Parent-Child	47.7235	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI120M	FI134M	Parent-Child	47.6165	0	8	1	75 %	50 %	50 %	0 %	0.33	0	0	0.32
FI166M	FI167F	Siblings	47.518	NA	8	1	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI034M	FI035M	Siblings	47.4339	NA	9	2	72.22 %	44.44 %	55.56 %	0 %	0.295	0	0	0.18
FI072F	FI073M	Siblings	46.7158	NA	12	1	66.67 %	41.67 %	50 %	8.33 %	0.24	0.0673161	0.27	0.23
FI104M	FI135F	Parent-Child	46.075	0	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI019F	FI052M	Parent-Child	45.8979	0	12	1	66.67 %	33.33 %	66.67 %	0 %	0.25	0	0	0
FI023M	FI174F	Parent-Child	45.7986	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI044M	FI193M	Parent-Child	45.4983	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.27	0	0	0.08

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI073M	FI142F	Parent-Child	45.2182	0	8	1	75 %	50 %	50 %	0 %	0.31	0	0	0.24
FI015M	FI142F	Parent-Child	44.7749	0	7	1	78.57 %	57.14 %	42.86 %	0 %	0.3525	0	0	0.41
FI157F	FI159M	Parent-Child	44.5115	0	8	1	75 %	50 %	50 %	0 %	0.3025	0	0	0.21
FI092M	FI144F	Siblings	44.0965	NA	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI015M	FI082F	Parent-Child	43.8693	0	11	2	59.09 %	18.18 %	81.82 %	0 %	0.25	0	0	0
FI004F	FI007F	Parent-Child	43.4768	0	12	2	58.33 %	16.67 %	83.33 %	0 %	0.25	0	0	0
FI098F	FI117F	Parent-Child	43.4092	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI015M	FI066M	Parent-Child	42.6965	0	10	2	55 %	10 %	90 %	0 %	0.25	0	0	0
FI017M	FI082F	Siblings	42.62	NA	12	2	66.67 %	50 %	33.33 %	16.67 %	0.245	0.134632	0.26	0.24
FI104M	FI153M	Siblings	41.5435	NA	8	1	75 %	62.50 %	25 %	12.50 %	0.3	0.100837	0.16	0.36
FI007F	FI048M	Parent-Child	41.3809	0	12	2	58.33 %	16.67 %	83.33 %	0 %	0.25	0	0	0
FI133M	FI187M	Parent-Child	41.2328	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI077F	FI136M	Parent-Child	41.176	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI113M	FI120M	Parent-Child	40.7973	0	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI133M	FI191M	Parent-Child	40.7902	0	8	1	50 %	0 %	100 %	0 %	0.25	0	0	0
FI149F	FI150F	Parent-Child	40.5307	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI070M	FI157F	Parent-Child	39.8009	0	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI004F	FI035M	Siblings	39.777	NA	11	2	72.73 %	45.45 %	54.55 %	0 %	0.2575	0	0	0.03
FI041M	FI106M	Parent-Child	39.6232	0	8	1	62.50 %	25 %	75 %	0 %	0.2575	0	0	0.03
FI073M	FI142F	Siblings	38.9532	NA	8	1	75 %	50 %	50 %	0 %	0.31	0	0	0.24
FI074F	FI159M	Parent-Child	38.9058	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.26	0	0	0.04
FI070M	FI085M	Parent-Child	38.8023	0	12	2	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI021M	FI038F	Siblings	38.5546	NA	12	1	66.67 %	33.33 %	66.67 %	0 %	0.2525	0	0	0.01
FI102F	FI140M	Parent-Child	38.2831	0	8	1	75 %	50 %	50 %	0 %	0.305	0	0	0.22
FI007F	FI028F	Parent-Child	38.1139	0	5	2	90 %	80 %	20 %	0 %	0.43	0	0	0.72
FI054F	FI135F	Parent-Child	37.9716	0	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI073M	FI091M	Siblings	37.3602	NA	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI073M	FI100M	Parent-Child	37.3542	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3625	0	0	0.45
FI100M	FI141F	Parent-Child	36.8962	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.275	0	0	0.1
FI100M	FI154M	Siblings	36.7184	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2925	0	0	0.17
FI063F	FI131M	Parent-Child	36.6614	0	7	1	64.29 %	28.57 %	71.43 %	0 %	0.25	0	0	0
FI092M	FI134M	Parent-Child	36.6514	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3675	0	0	0.47
FI049M	FI069M	Parent-Child	36.212	0	12	2	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI102F	FI140M	Siblings	35.9632	NA	8	1	75 %	50 %	50 %	0 %	0.305	0	0	0.22
FI054F	FI091M	Parent-Child	35.9474	0	8	1	81.25 %	62.50 %	37.50 %	0 %	0.3575	0	0.08	0.51

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI073M	FI141F	Parent-Child	35.8829	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.26	0	0	0.04
FI044M	FI140M	Siblings	35.5333	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI102F	FI114M	Siblings	35.2733	NA	7	1	78.57 %	57.14 %	42.86 %	0 %	0.34	0	0	0.36
FI054F	FI134M	Siblings	34.9989	NA	8	1	75 %	62.50 %	25 %	12.50 %	0.3	0.100837	0.16	0.36
FI187M	FI191M	Siblings	34.5164	NA	8	1	62.50 %	37.50 %	50 %	12.50 %	0.24	0.100837	0.27	0.23
FI017M	FI154M	Parent-Child	34.2476	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI054F	FI104M	Siblings	33.8627	NA	11	1	68.18 %	45.45 %	45.45 %	9.09 %	0.25	0.0753294	0.25	0.25
FI074F	FI136M	Parent-Child	33.5244	0	8	1	75 %	50 %	50 %	0 %	0.32	0	0	0.28
FI023M	FI077F	Parent-Child	33.0721	0	12	2	54.17 %	8.33 %	91.67 %	0 %	0.25	0	0	0
FI098F	FI118M	Parent-Child	32.7098	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI017M	FI104M	Siblings	32.3725	NA	11	1	68.18 %	36.36 %	63.64 %	0 %	0.2575	0	0	0.03
FI147F	FI158M	Parent-Child	32.0615	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.285	0	0	0.14
FI102F	FI138M	Parent-Child	31.5579	0	8	1	75 %	50 %	50 %	0 %	0.3075	0	0	0.23
FI017M	FI135F	Parent-Child	31.0553	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.285	0	0	0.14
FI102F	FI138M	Siblings	30.9425	NA	8	1	75 %	50 %	50 %	0 %	0.3075	0	0	0.23
MO041M	MO049F	Parent-Child	30.5625	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI040F	FI114M	Parent-Child	30.5332	0	7	1	71.43 %	42.86 %	57.14 %	0 %	0.2525	0	0	0.01
FI157F	FI159M	Siblings	30.4762	NA	8	1	75 %	50 %	50 %	0 %	0.3025	0	0	0.21
FI145M	FI159M	Parent-Child	30.4378	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI097F	FI138M	Parent-Child	30.2099	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.27	0	0	0.08
FI182M	MO041M	Parent-Child	30.1043	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI041M	FI203F	Parent-Child	30.1022	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI063F	FI129F	Parent-Child	29.9568	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI045M	FI205M	Parent-Child	29.7379	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.28	0	0	0.12
FI023M	FI122M	Parent-Child	29.5597	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI098F	FI116F	Parent-Child	29.5	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI166M	FI167F	Parent-Child	29.2132	0	8	1	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI072F	FI082F	Siblings	29.0852	NA	12	1	66.67 %	33.33 %	66.67 %	0 %	0.25	0	0	0
FI111F	FI185M	Parent-Child	28.7316	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.295	0	0	0.18
FI147F	FI185M	Parent-Child	28.1406	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2525	0	0	0.01
FI120M	FI141F	Parent-Child	27.8715	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI092M	FI144F	Parent-Child	27.7847	0	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI040F	FI153M	Parent-Child	27.4206	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2525	0	0	0.01
FI066M	FI092M	Siblings	27.3647	NA	10	1	65 %	30 %	70 %	0 %	0.25	0	0	0
FI034M	FI045M	Parent-Child	27.2263	0	10	2	65 %	30 %	70 %	0 %	0.25	0	0	0

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI023M	FI147F	Parent-Child	27.1445	0	12	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI040F	FI072F	Parent-Child	27.1378	0	12	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI045M	FI144F	Parent-Child	27.0255	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.27	0	0	0.08
FI100M	FI134M	Siblings	26.9992	NA	8	1	75 %	50 %	50 %	0 %	0.3275	0	0	0.31
FI069M	FI186F	Parent-Child	26.6003	0	8	1	62.50 %	25 %	75 %	0 %	0.2575	0	0	0.03
FI051M	FI129F	Siblings	26.4068	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.265	0	0	0.06
FI017M	FI052M	Siblings	26.2222	NA	12	2	66.67 %	33.33 %	66.67 %	0 %	0.255	0	0	0.02
FI017M	FI120M	Parent-Child	26.1487	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI113M	FI153M	Parent-Child	25.9493	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.27	0	0	0.08
FI113M	FI135F	Parent-Child	25.926	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.285	0	0	0.14
FI111F	FI185M	Siblings	25.8917	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.295	0	0	0.18
FI141F	FI142F	Siblings	25.8574	NA	8	1	75 %	62.50 %	25 %	12.50 %	0.3	0.100837	0.16	0.36
FI043F	FI155M	Siblings	25.8032	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.275	0	0	0.1
FI021M	FI039F	Parent-Child	25.3951	0	12	1	58.33 %	16.67 %	83.33 %	0 %	0.25	0	0	0
FI034M	FI070M	Parent-Child	25.3433	0	10	2	65 %	30 %	70 %	0 %	0.25	0	0	0
FI155M	MO046F	Parent-Child	24.9014	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.27	0	0	0.08
FI076F	FI205M	Parent-Child	24.5879	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2875	0	0	0.15
FI042F	FI147F	Parent-Child	24.5542	0	12	1	58.33 %	16.67 %	83.33 %	0 %	0.25	0	0	0
FI144F	FI194M	Siblings	24.4945	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.3025	0	0	0.21
FI023M	FI110F	Parent-Child	24.1763	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI064F	FI184M	Parent-Child	24.0954	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.275	0	0	0.1
FI015M	FI076F	Parent-Child	23.7364	0	11	2	54.55 %	9.09 %	90.91 %	0 %	0.25	0	0	0
FI015M	FI089F	Parent-Child	23.2484	0	11	2	54.55 %	9.09 %	90.91 %	0 %	0.25	0	0	0
FI113M	FI134M	Siblings	23.1032	NA	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI121F	FI144F	Siblings	22.7791	NA	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI042F	FI136M	Siblings	22.7095	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.25	0	0	0
FI073M	FI091M	Parent-Child	22.5861	0	8	1	75 %	50 %	50 %	0 %	0.325	0	0	0.3
FI035M	FI070M	Siblings	22.5798	NA	11	2	72.73 %	45.45 %	54.55 %	0 %	0.265	0	0	0.06
FI139F	FI142F	Siblings	22.4579	NA	8	1	68.75 %	50 %	37.50 %	12.50 %	0.255	0.100837	0.24	0.26
FI132M	FI204F	Parent-Child	22.3949	0	8	1	87.50 %	75 %	25 %	0 %	0.395	0	0	0.58
FI023M	FI185M	Siblings	22.1423	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2675	0	0	0.07
FI134M	FI135F	Parent-Child	22.1072	0	8	1	75 %	50 %	50 %	0 %	0.33	0	0	0.32
FI147F	FI158M	Siblings	21.9675	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.285	0	0	0.14
FI015M	FI092M	Parent-Child	21.8396	0	10	2	55 %	10 %	90 %	0 %	0.25	0	0	0
FI139F	FI141F	Parent-Child	21.0459	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0

Bear 1	Bear 2	Genetic Relationship	LR	Inconsistencies	Overlapping markers	Cluster	Shared alleles	IBS=2	IBS=1	IBS=0	Kinship	P(IBD=0)	Kappa0	Kappa2
FI040F	FI154M	Parent-Child	21.0221	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.25	0	0	0
FI017M	FI135F	Siblings	20.9164	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.285	0	0	0.14
FI121F	FI144F	Parent-Child	20.7736	0	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI045M	FI204F	Parent-Child	20.7081	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.295	0	0	0.18
FI077F	FI136M	Siblings	20.577	NA	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI098F	MO009F	Parent-Child	20.5007	0	8	1	56.25 %	12.50 %	87.50 %	0 %	0.25	0	0	0
FI035M	LL047F	Parent-Child	20.2083	0	7	1	64.29 %	28.57 %	71.43 %	0 %	0.25	0	0	0
FI113M	FI134M	Parent-Child	20.1763	0	8	1	75 %	50 %	50 %	0 %	0.3175	0	0	0.27
FI054F	FI154M	Parent-Child	20.1068	0	8	1	62.50 %	25 %	75 %	0 %	0.25	0	0	0
FI072F	FI154M	Parent-Child	20.1058	0	8	1	68.75 %	37.50 %	62.50 %	0 %	0.2775	0	0	0.11
FI090M	FI095F	Siblings	20.0279	NA	8	1	62.50 %	37.50 %	50 %	12.50 %	0.235	0.100837	0.28	0.22

Epilogue

Key words:	Relatedness, family groups, pedigree reconstruction, population genetics, brown bear, Ursus arctos, Norway

NIBIO
NORWEGIAN INSTITUTE OF
BIOECONOMY RESEARCH

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Cover photo: Steinar Wikan. A female brown bear with two cubs in Sør-Varanger.