Supplementary Information

Article title: Integrating genomic tools into ex situ conservation management of caribou (*Rangifer tarandus*) in Canada

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Table S1: Results of genetic clustering analysis

GAN	Institution	Genetic cluster	Sample type	Sex	D1	D2
MFL12-00011	YWP	1	Feces	Female	-26.58	2.42
MFL12-00012	YWP	1	Feces	Female	-21.97	1.96
MFL17-00082	YWP	1	Feces	Male	-23.84	2.14
MFL17-00083	YWP	1	Feces	Male	-26.35	2.53
MFL22-00184	YWP	1	Feces	Female	-25.18	2.3
MFL22-00185	YWP	1	Feces	Male	-23.37	2.46
MIG12-28178508	YWP	1	Feces	Female	-24.88	2.47
MIG12-28178510	YWP	1	Feces	Female	-25.81	2.33
NA	YWP	1	Feces	Male	-28.94	2.67
BRV14-00517	GVZ	2	Blood	Female	2.07	-1.85
BRV15-00641	GVZ	2	Blood	Female	2.58	-2.03
BRV15-00641	GVZ	2	Feces	Female	1.72	-1.83
BRV22-02000	GVZ	2	Blood	Female	2.41	-2.04
BRV22-02000	GVZ	2	Feces	Female	1.26	-1.03
DKJ24-05851	APZ	2	Blood	Female	1.73	0.2
KCS17-00218	ZSSF	2	Blood	Female	1.91	-2.1
KCS18-00246	ZSSF	2	Blood	Female	2.34	-1.7
KCS19-00374	ZSSF	2	Blood	Female	0.63	-3.56
KCS20-00456	ZSSF	2	Blood	Female	2.19	-1.89
KCS21-00511	ZSSF	2	Blood	Female	2.75	-1.14
KCS24-00675	ZSSF	2	Blood	Female	3.56	-0.42

LBJ20-11311	CZ	2	Feces	Female	2.11	-1.97
LBJ22-12176	CZ	2	Feces	Female	2.12	-1.97
MIG12-28705488	APZ	2	Blood	Female	1.17	0.1
VDZ17-00246	MHZ	2	Blood	Female	2.13	-1.89
VRM24-00700	BCWP	2	Blood	Male	2.19	-1.89
YVZ18-11797	TZ	2	Feces	Female	1.97	-2.96
YVZ18-11802	TZ	2	Feces	Female	2.78	-4.52
ZHR21-00215	SN	2	Blood	Female	2.26	-1.95
ZHR21-00215	SN	2	Feces	Female	1.99	-1.93
QQW18-00138	RPZ	3	Blood	Female	3.71	-13.4
QQW18-00138	RPZ	3	Feces	Female	3.77	-13.45
QQW18-00139	RPZ	3	Blood	Female	3.71	-13.53
QQW18-00139	RPZ	3	Feces	Female	3.79	-13.61
YVZ18-11801	TZ	3	Blood	Female	4.23	-16.14
YVZ18-11801	TZ	3	Feces	Female	2.99	-9.55
YVZ18-11804	TZ	3	Blood	Female	3.73	-13.29
DKJ12-00824	EVZ	4	Blood	Female	8.53	6.14
DKJ12-00866	EVZ	4	Blood	Male	8.83	6.14
DKJ13-01158	EVZ	4	Blood	Female	9.05	6.36
DKJ13-01159	EVZ	4	Blood	Male	8.71	6.31
DKJ13-01160	APZ	4	Blood	Female	6.57	4.49
DKJ13-01160	APZ	4	Feces	Female	10.01	7.15
DKJ13-01209	EVZ	4	Blood	Male	8.83	6.29
DKJ14-01836	APZ	4	Blood	Female	8.45	5.84
DKJ16-04607	ZSSF	4	Blood	Female	8.96	6.42
DKJ20-05460	APZ	4	Blood	Male	7.5	5.27
DKJ21-05554	APZ	4	Blood	Female	9.69	6.78
DKJ23-05769	APZ	4	Blood	Male	8.72	5.99
DKJ23-05769	ZSSF	4	Blood	Male	8.71	5.99
DKJ23-05773	APZ	4	Blood	Male	9.1	6.45
DKJ23-05773	ZSSF	4	Blood	Male	9.11	6.45
DKJ24-05851	APZ	4	Feces	Female	8.98	5.98
DKJ24-05855	APZ	4	Blood	Male	8.68	6.27
MIG12-28705488	APZ	4	Feces	Female	8.71	5.74

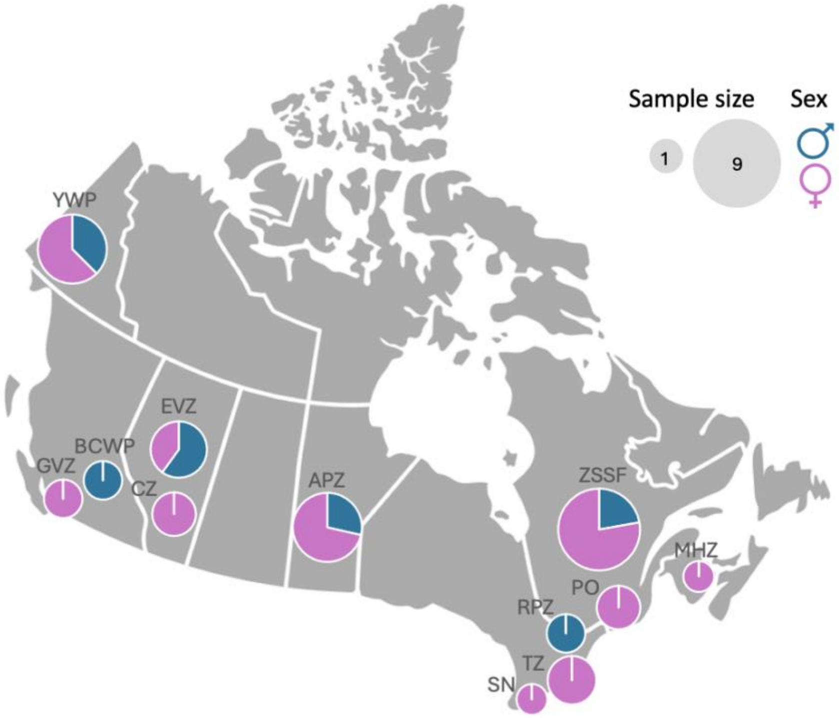

Figure S1. Geographic location of accredited Canadian zoos that provided samples of *Rangifer tarandus* individuals. From west to east Canada: Yukon Wildlife Preserve (YWP), BC Wildlife Park (BCWP), Greater Vancouver Zoo (GVZ), Edmonton Valley Zoo (EVZ), Calgary Zoo (CZ), Assiniboine Park Zoo (APZ), Safari Niagara (SF), Toronto Zoo (TZ), Riverview Park Zoo (RPZ), Zoo Sauvage de Saint-Félicien (ZS), Parc Omega (PO), Magnetic Hill Zoo (MHZ).

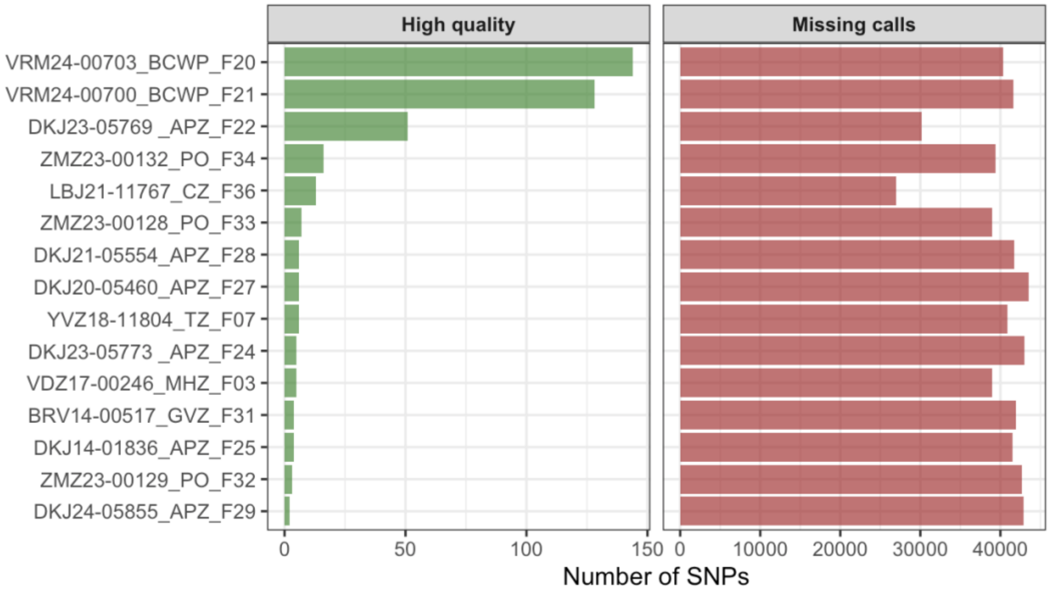

Figure S2. Comparison of number of SNPs of high quality (green) versus those with missing calls (red) of failed samples. These samples were removed from downstream analyses.

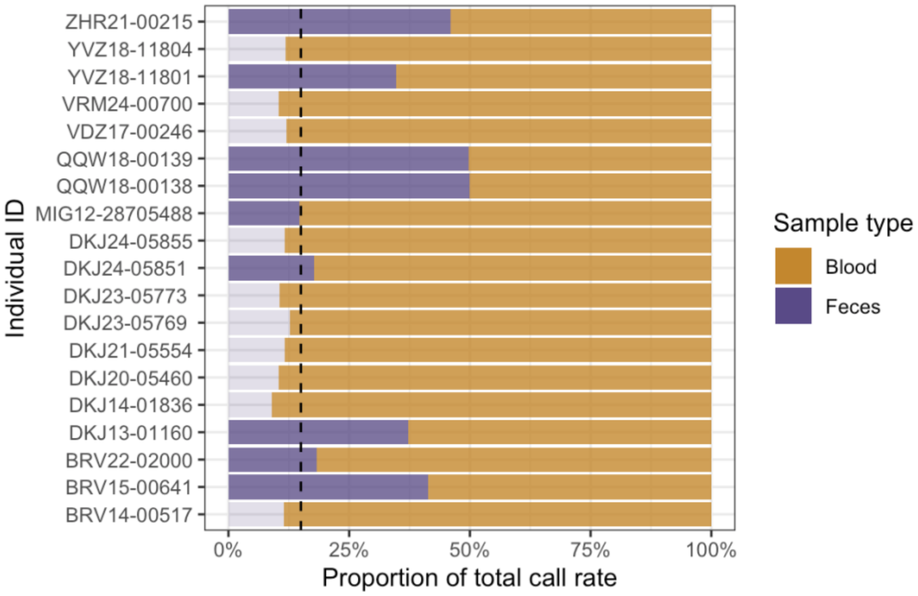

Figure S3. Proportion of total call rates of paired blood-fecal samples (n=19). The vertical dashed line indicates the minimum quality threshold (0.15%). Fecal samples that do not meet the minimum quality control are coloured in light purple (n=9).

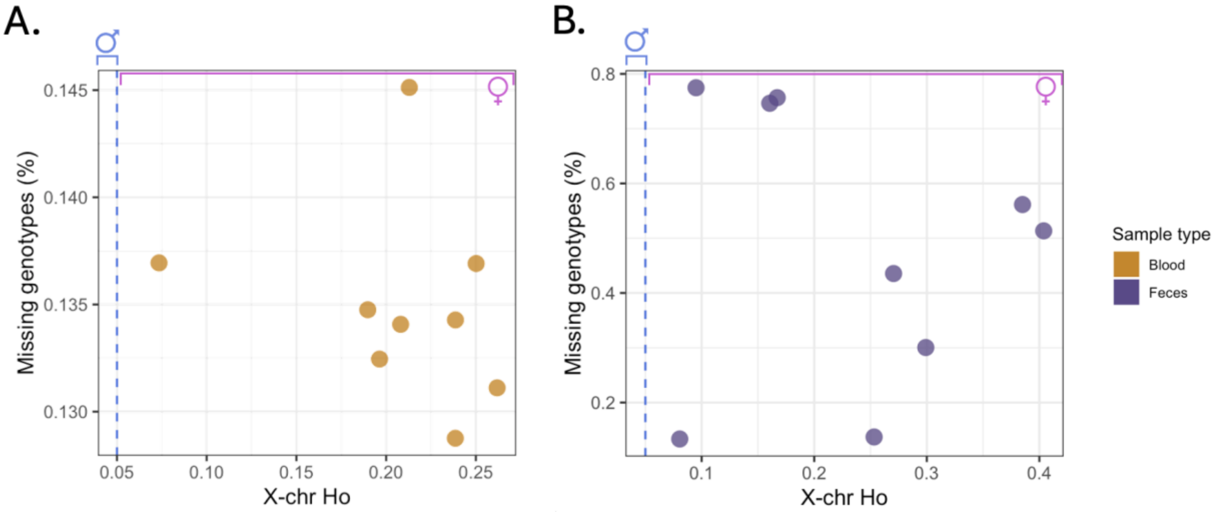

Figure S4. Sex assignment based on observed heterozygosity of SNPs located in the X chromosome for female individuals with paired samples (n=9). The figure shows results of genotype data obtained from whole blood samples (A; dark yellow) and feces (B; purple). The dashed line indicates the threshold used for molecular sex assignment. Samples with H_O values below 0.05 are categorized as males, whereas samples with HO values between 0.05 and 0.5 are categorized as females.

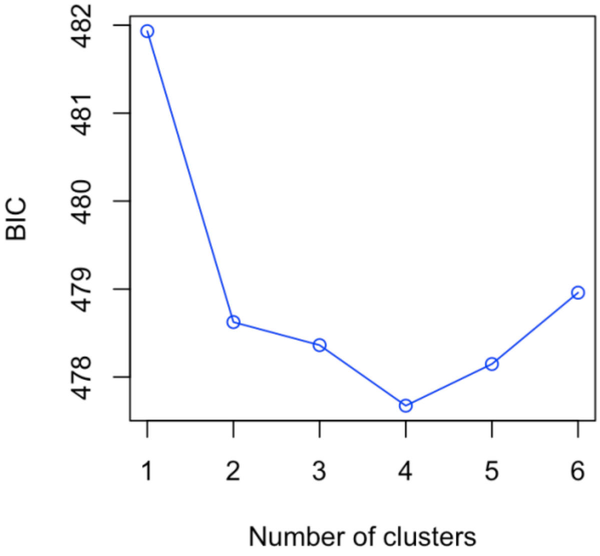

Figure S5. Bayesian Information Criterion (BIC) values for 6 possible genetic clusters in the managed caribou population. The lowest BIC value is chosen as the best number of clusters describing our dataset.

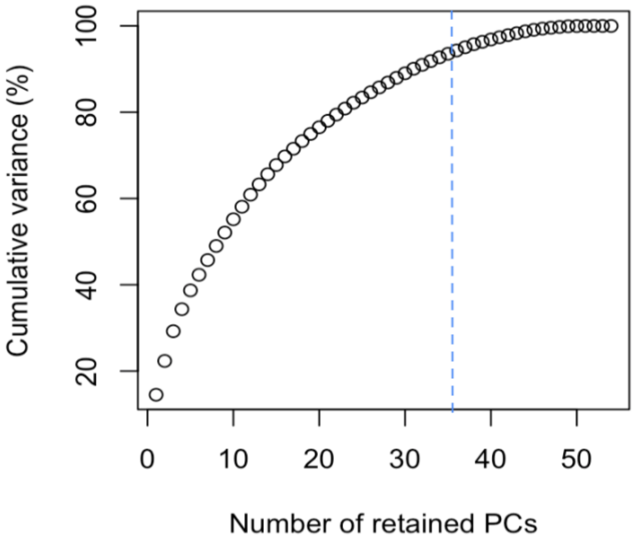

Figure S6. Number of PCs as a function of the cumulative variance for DAPC analysis. The total number of retained PCs was 35 (dashed blue line).

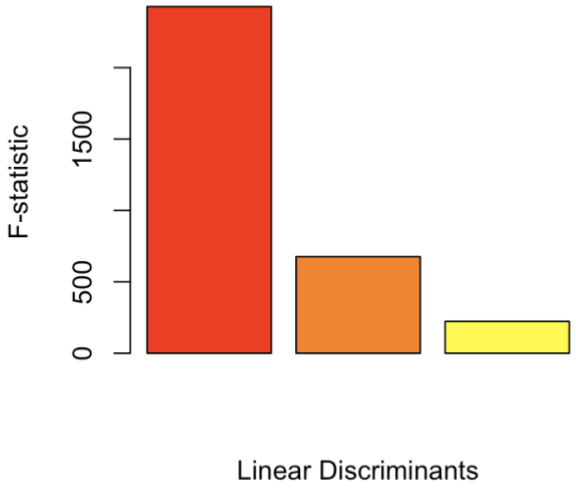

Figure S7. DAPC's eigenvalues for three discriminant functions. Discriminant 1 (red) explained 73% of the variation, Discriminant 2 (orange) explained 20.3% of the variation, and Discriminant 3 (yellow) explained 6.7% of the variation.

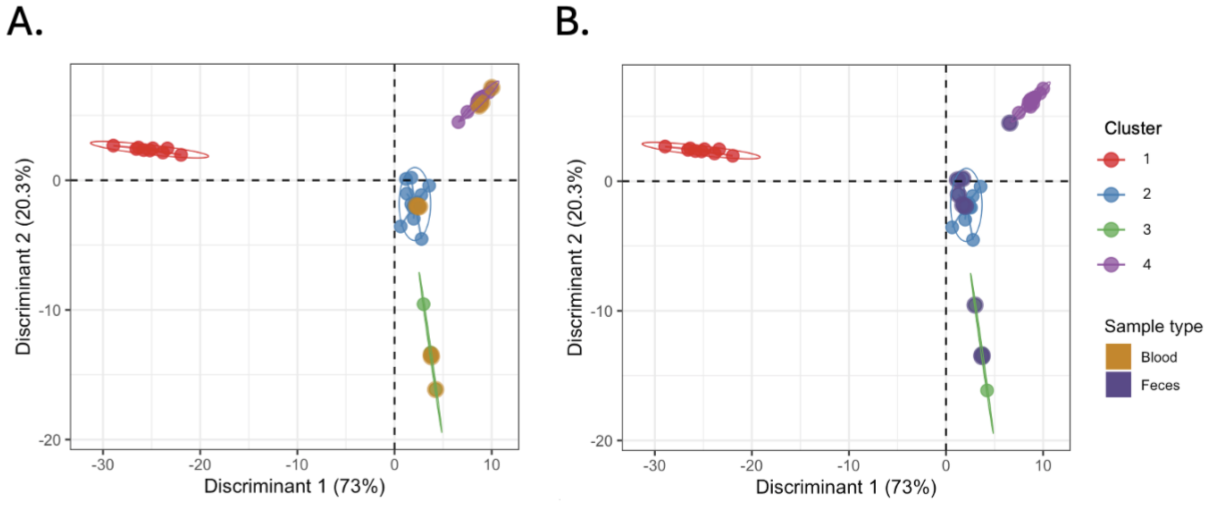

Figure S8. DAPC results comparing the clustering of individuals with paired samples. Genotypes derived from blood (A; dark yellow) and fecal samples (B; purple) consistently assign individuals to the same clusters. Colours represent same genetic groups as in Fig. 3; red: cluster 1, blue: cluster 2, green: cluster 3, and purple: cluster 4.

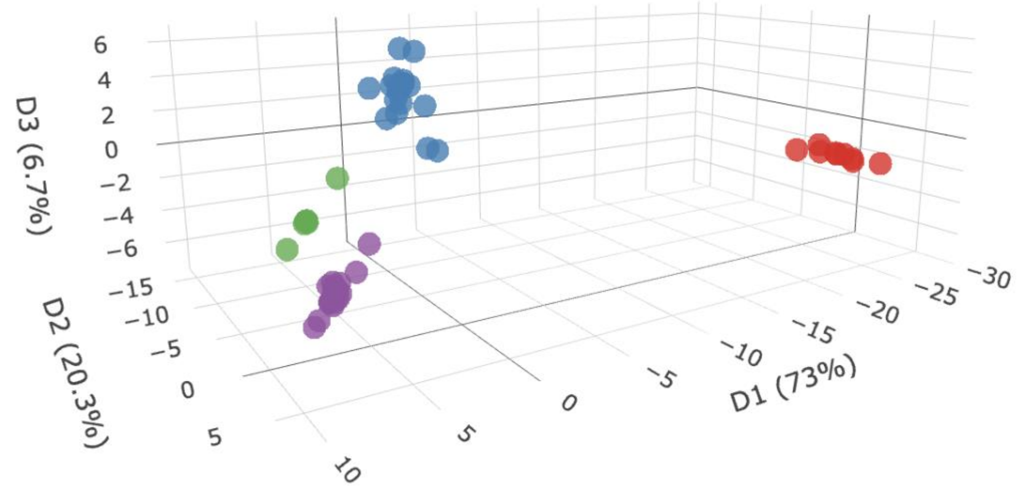

Figure S9. Three-dimensional visualization DAPC results for 4 populations. Colours represent same genetic groups as in Fig. 8; red: cluster 1, blue: cluster 2, green: cluster 3, and purple: cluster 4.

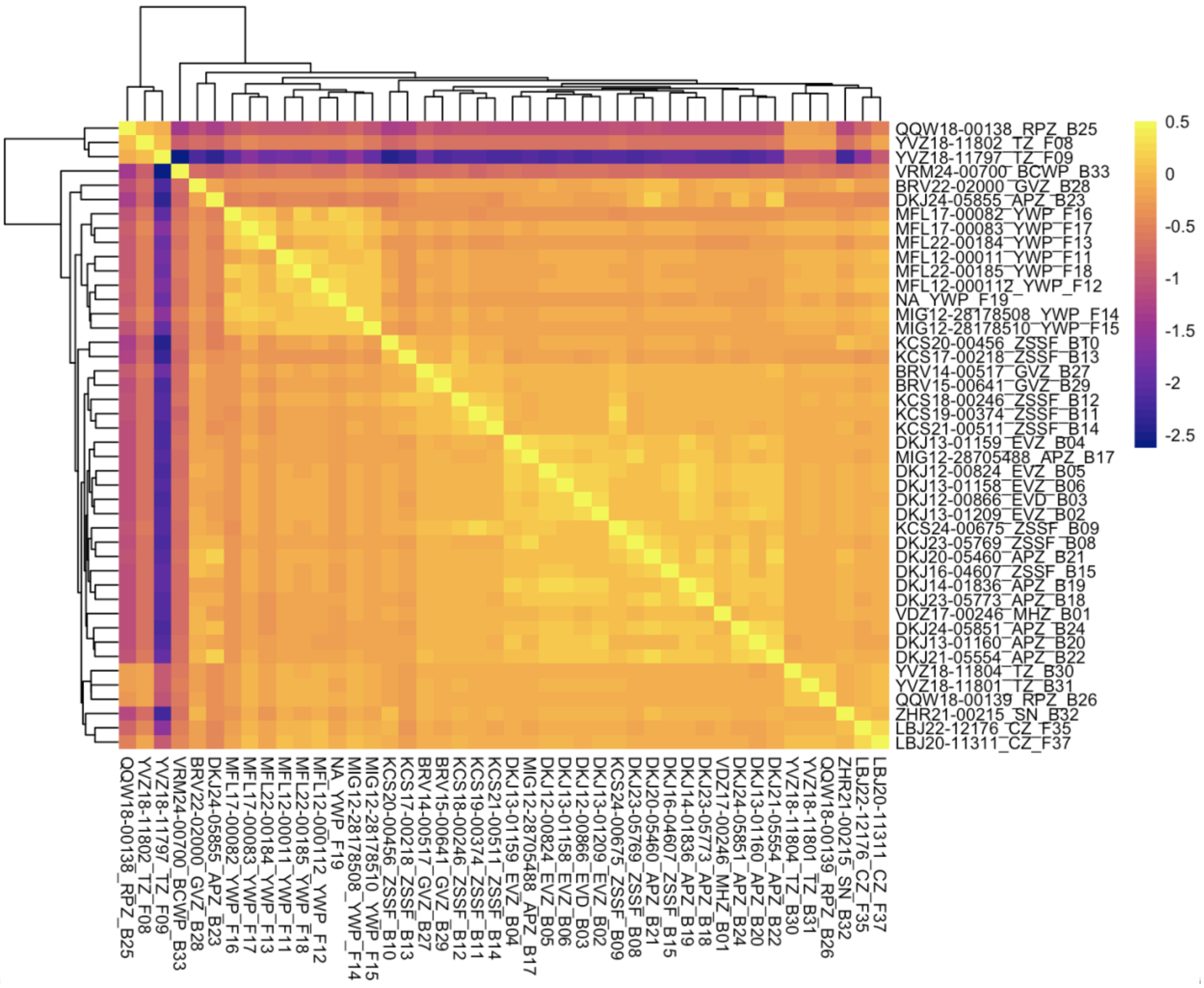

Figure S10. Heatmap showing pairwise kinship estimates among 44 *Rangifer* tarandus individuals.

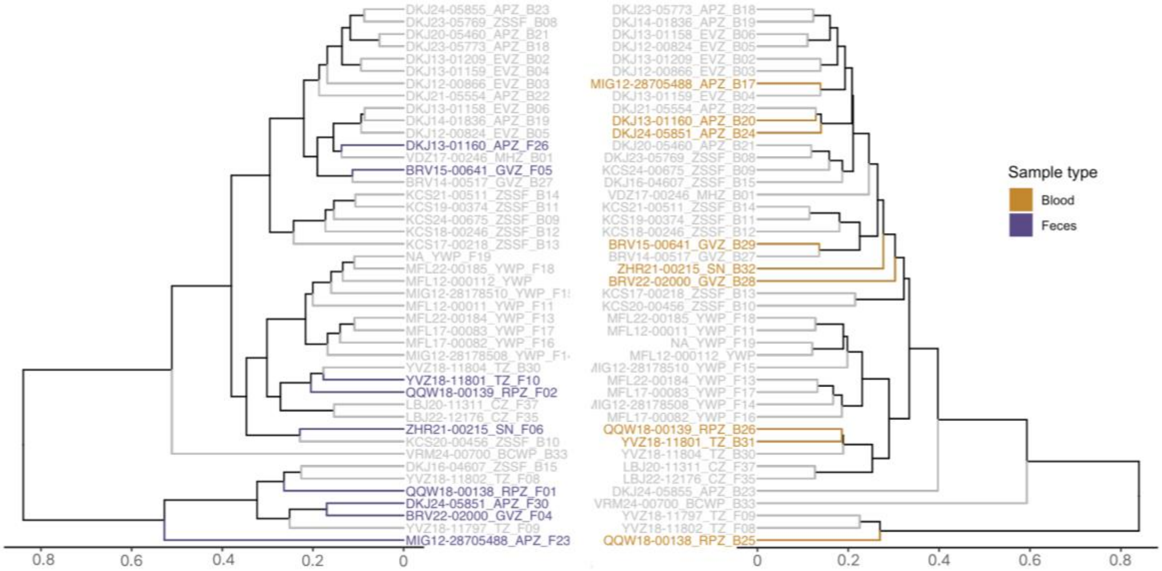

Figure S11. Mirrored cladograms of pairwise kinship between 44 caribou / reindeer housed in Canadian zoos. Individuals with paired samples are highlighted on each cladogram according to their sample type, feces: purple and blood: dark orange. Branch lengths represent genetic distances, which were calculated as 0.5 – kinship. Closely related individuals are clustered together and have shorter branch lengths.

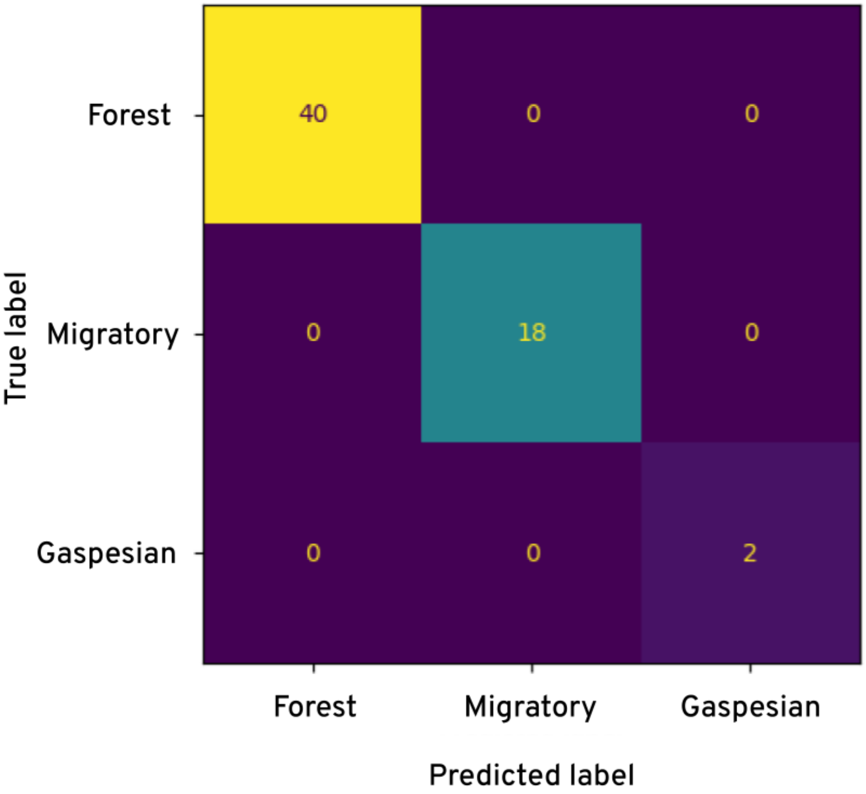

Figure S12. Confusion matrix resulting from the ecotype prediction in the test set using an optimized model based on the multinomial NaiveBayes algorithm. A stratified split was applied to the entire data set, comprising 1,326 samples genotyped for 45,419 SNPs, hence the proportion of each class in the test set represents the overall proportion of each ecotype in the entire data set.