

## Supplemental Information for:

### Genomics, environment and balancing selection in behaviorally bimodal populations: the caribou case

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## Supporting methods

### *Method S1*

RAD protocol for Pool-seq library preparation.

Each of the 18 pooled samples was digested with 20 U SbfI (New England Biolabs®) in final volume of 20 µL. Reactions were first incubated at 37°C for 1 h and denatured at 35°C for 20 min. Each restriction product was ligated to a common adapter with a unique barcode adapter (P1) using T4 Quick ligase (New England Biolabs®) and 100mM ATP (Promega), a Subsequently, each barcoded samples were pooled into a multiplexed library, followed by DNA shearing (Covaris S220) and size selection. Selected fragments were blunt ended using the NEB Quick Blunting Kit (New England Biolabs®) in a final volume of 50 µL, and purified using Ampure XP beads (Beckman Coulter). Additionally, blunt end libraries were followed by A-tailing and P2 adapter ligation. The libraries were enriched and tagged with a second unique barcode during PCR amplification. The library amplification reaction used 10ng of the pooled ligation product, 12.5 µL of 2x Phusion-HF Master Mix (Thermo-scientific), 1.25 µL of 100% DMSO, P1 PCR primer (10nM) and P2 Sanger Index (25nM) in final volume of 25 µL. PCR was initiated at 98°C for 30 s, followed by 12 cycles of 98°C for 10 s and 72°C for 1 min, with a final extension at 72°C for 5 min concluded the reaction. Products were cleaned with Ampure XP beads according to the manufacturer's protocol.

### *Method S2*

Brief description of parameters used is Stacks pipeline (Catchen *et al.* 2013) for the *de novo* assembly.

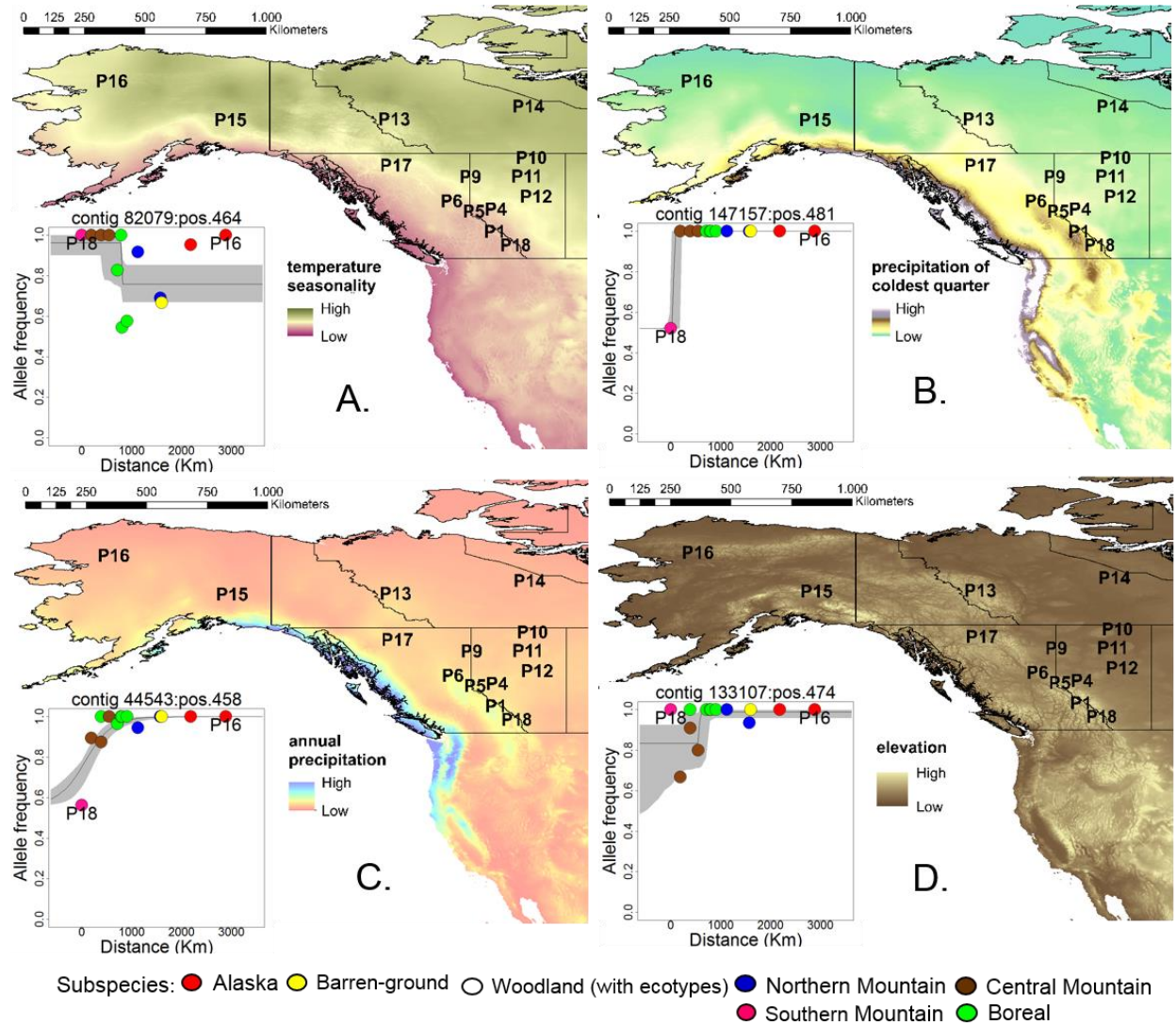
m=minimum depth of coverage required to create a stack (default value=3);  
M=number of mismatches allowed between stacks within individuals (default value=2);  
N=maximum distance allowed to align secondary reads to primary stacks (default value=4);  
n=number of mismatches allowed between stacks between individuals (default value=1);  
max\_locus\_stacks=maximum number of stacks at a single *de novo* locus (default value=3).

Following Mastretta-Yanes *et al.* (2015) we identified the best values to be used for the above parameters: m=3, M=4, N=6, n=3, max\_locus\_stacks=3.

References are in body of paper.

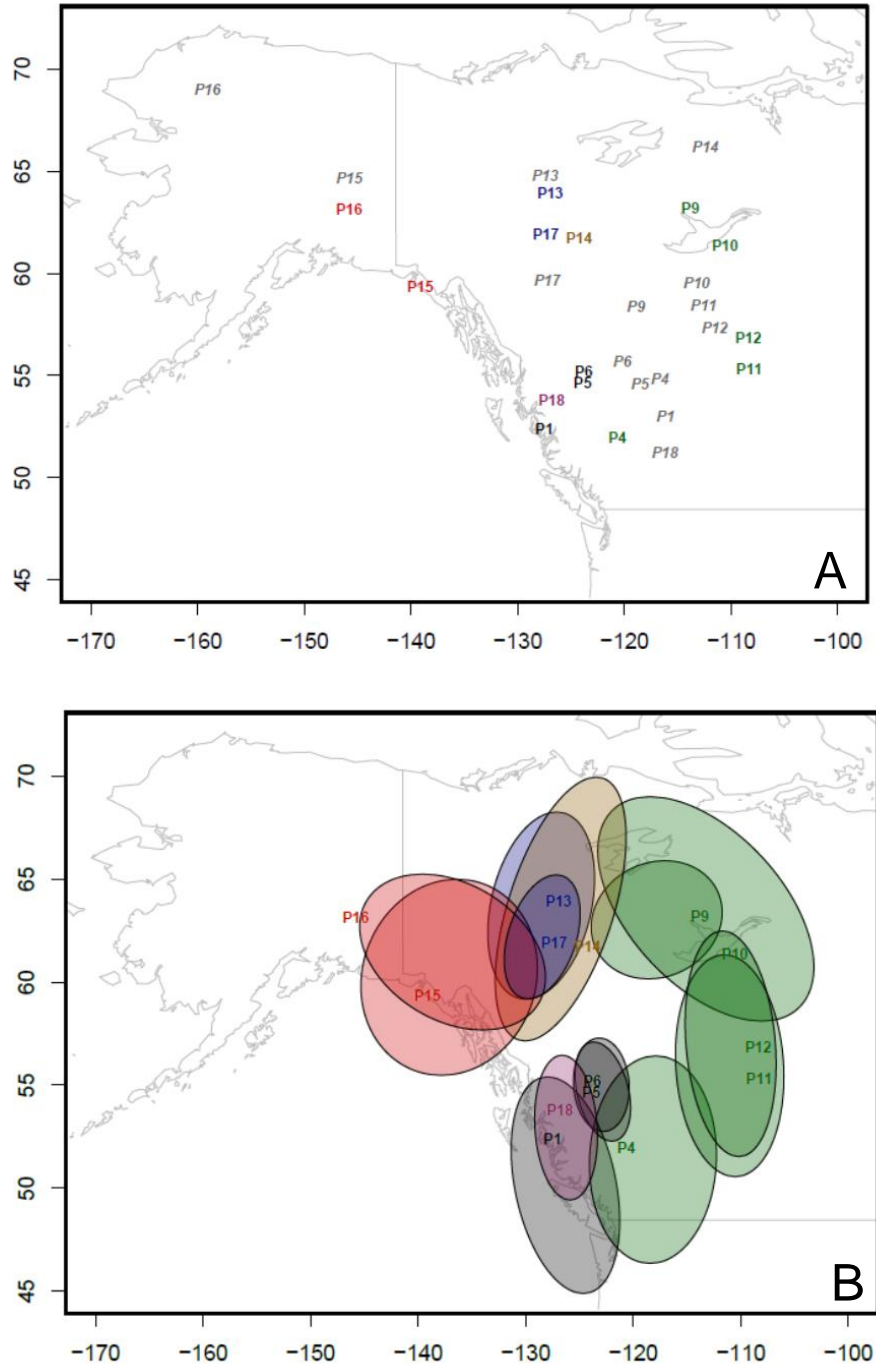
## Supporting figures

Fig. S1



**Fig. S1.** Cline variation of SNPs across caribou populations in western North America. Maps showing the variables associated with the greatest number of SNPs, including, temperature seasonality (n=12, panel A), precipitation of coldest quarter (n=11, panel B), annual precipitation (n=10, panel C) and elevation (n=8, panel D). For each variable, the geographical cline of allele frequency of the SNP with the highest association (highest Bayes Factor) is shown in a cline shape plot. Abbreviated names are used as caribou populations' identifiers and colors represent recognized subspecies and ecotypes.

Fig. S2

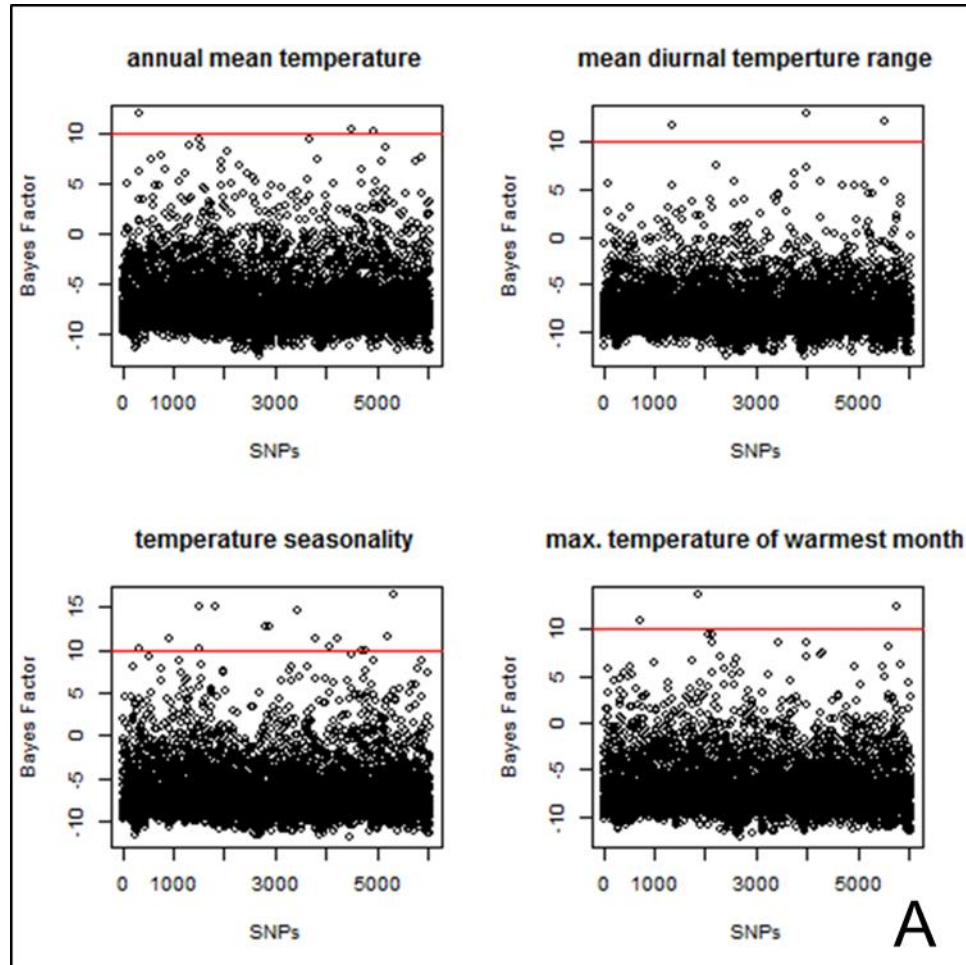


**Fig. S2.** Geogenetic locations of caribou populations. SpaceMix-inferred geogenetic locations of caribou populations based on prior of true sampling sites and populations data (6,041 SNPs) including (A) plot showing in grey geographic locations of caribou populations and, in coded color, geogenetic locations; and (B) plot showing geogenetic locations of caribou populations

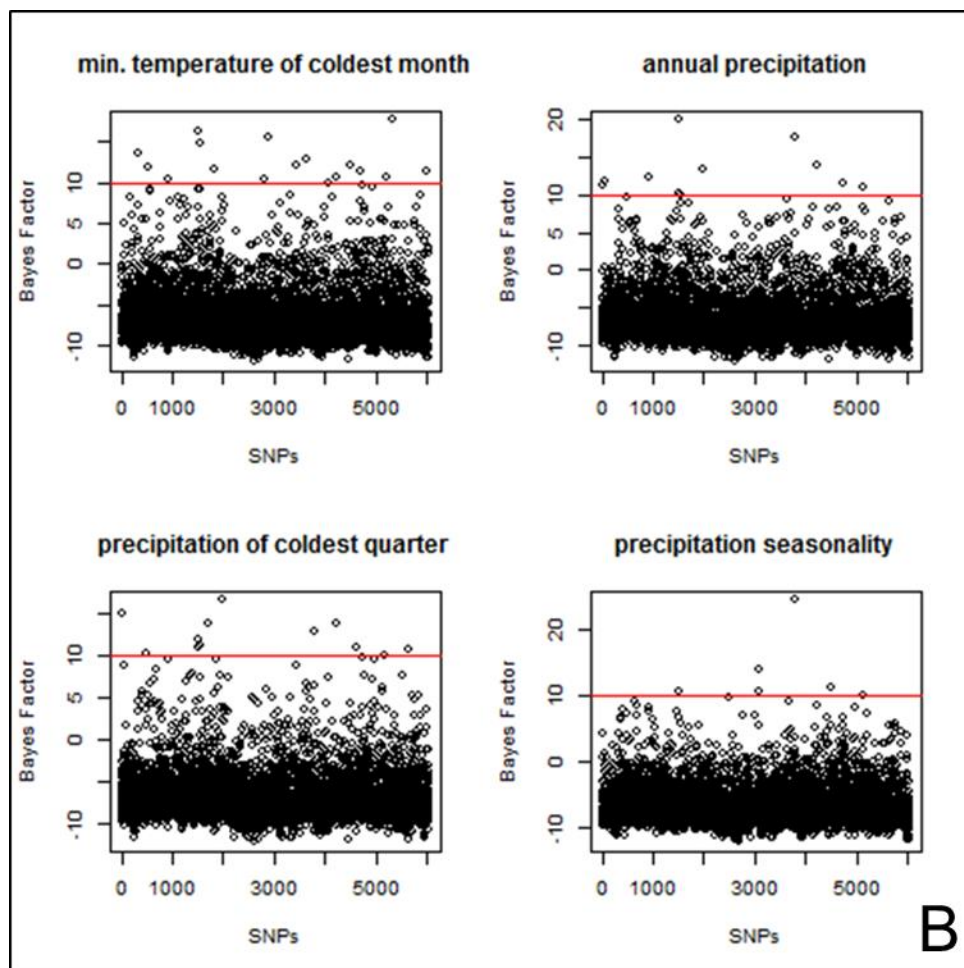
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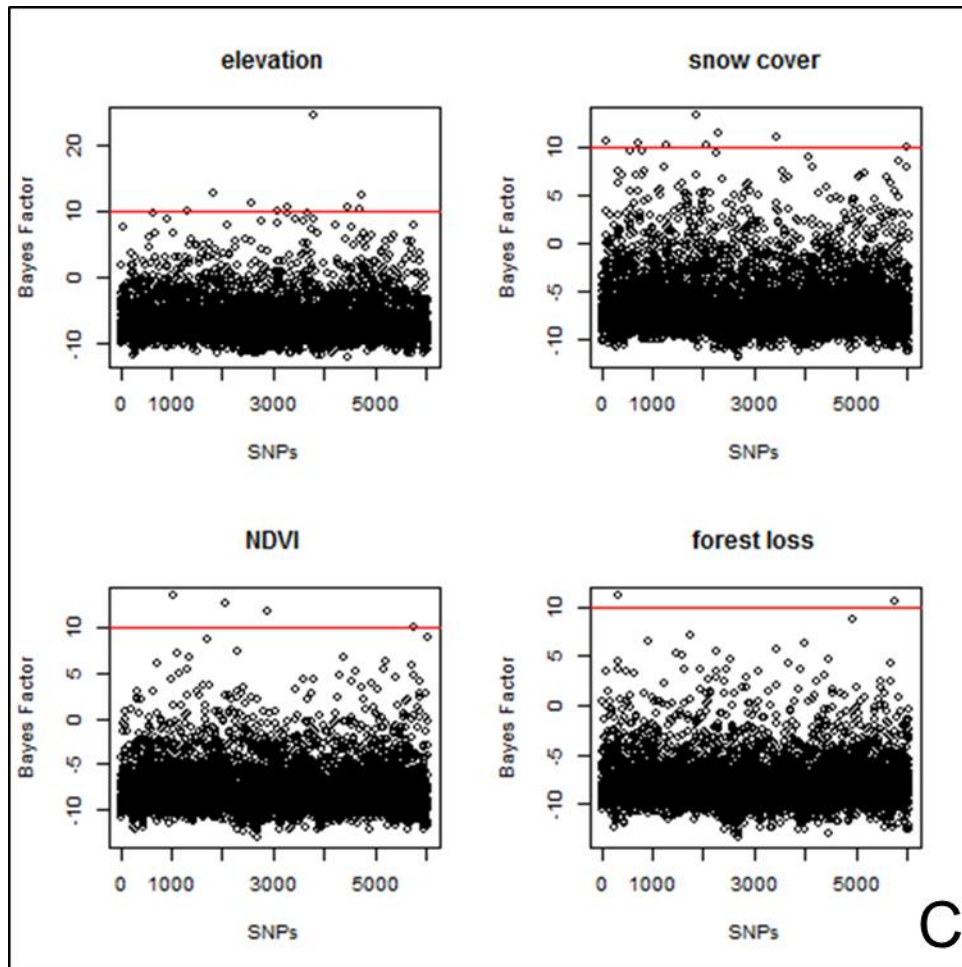
with ellipses, representing the 95% of confidence intervals of geogenetic locations. Abbreviated names are used as caribou populations' identifiers and colors represent recognized subspecies and ecotypes: black= Central Mountain; pink= Southern Mountain; green= Boreal; blue= Northern Mountain; red= Alaskan; yellow= Barren-ground.

*Fig. S3*



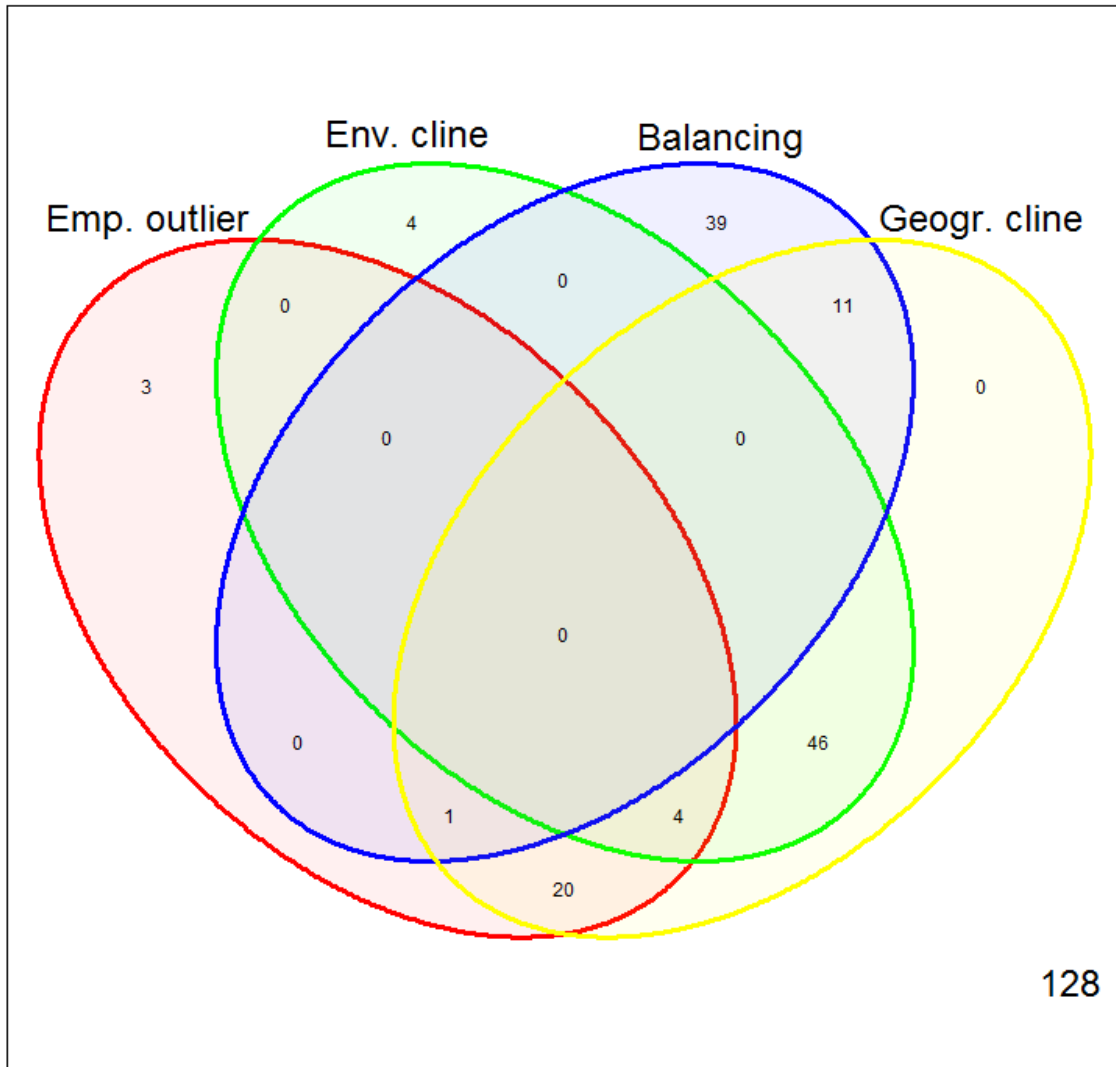






**Fig. S3.** SNPs associated with environmental variables. Manhattan plots of Bayes Factors for (A) annual mean temperature, mean diurnal temperature range, temperature seasonality and maximum temperature of warmest month; (B) minimum temperature of coldest month, annual precipitation, precipitation of coldest quarter and precipitation seasonality (C) elevation, snow cover, Normalized Difference Vegetation Index (NDVI) and percentage of forest loss. The plots show the association (BF) of each SNP (SNPs Id from 1 to 6,041 on x-axis) to environmental variables. SNPs with the strongest association ( $BF > 10$ ) are above the red line.

Fig. S4



**Fig. S4.** Venn diagram showing overlap between the union of our candidate SNPs under selection identified with empirical  $F_{ST}$  approach (red circle), BayPass (green circle), BayeScan (blue circle) and Hzar (yellow circle).



## Supporting tables

Table S1

**Table S1.** Environmental layers used to detect environmental and geographical clines of SNPs in caribou populations distributed across western North America.

Pool	Distance	Long	Lat	BIO1	BIO2	BIO4	BIO5	BIO6	BIO12	BIO19	BIO15	Elev.	SC	NDVI	FL
P18	0.00	-117.428	50.75047	6.73	97.90	7759.86	191.87	139.72	948.43	327.61	28.73	1659.30	60.46	6905.43	2.65
P1	193.11	-117.376	52.4415	24.11	106.44	7839.73	156.03	183.15	636.67	135.91	30.00	2139.81	68.87	3987.31	0.68
P4	388.46	-117.862	54.15304	16.06	124.48	8671.08	204.99	166.21	590.38	98.95	50.48	1154.40	45.12	7455.45	9.99
P5	391.92	-119.608	53.9233	0.25	105.47	8575.03	182.31	171.12	662.28	156.00	26.84	1387.97	55.59	6986.63	5.52
P6	547.46	-121.159	55.00786	0.25	105.47	8575.03	182.31	171.12	662.28	156.00	26.84	1387.97	55.59	6986.63	5.52
P12	717.21	-113.065	56.52481	-6.22	122.65	12603.26	219.78	267.73	462.72	67.91	58.34	563.97	39.89	7510.78	2.61
P9	786.60	-119.962	57.54002	11.77	111.93	12373.78	211.46	257.01	442.48	70.55	49.94	729.59	48.57	7681.91	5.52
P11	806.01	-114.025	57.58873	13.47	117.55	13166.51	218.85	280.45	437.78	67.34	51.46	531.54	44.22	7581.32	5.19
P10	909.54	-114.645	58.6378	30.67	107.72	13414.56	203.63	287.63	428.16	67.17	44.87	696.98	54.11	7057.38	6.30
P17	1122.94	-127.748	58.72726	30.42	114.83	10778.95	181.10	244.81	478.83	104.72	36.85	1224.72	68.30	6680.76	1.29
P13	1572.12	-127.94	63.57859	86.86	107.76	13681.59	170.95	321.86	426.25	69.86	43.77	1334.91	85.24	4727.59	0.30
P14	1601.39	-113.879	64.90676	90.89	87.19	14962.79	168.51	338.49	253.88	36.29	49.75	301.24	80.99	5596.86	2.43
P15	2182.12	-145.107	63.49848	57.67	119.31	13169.62	192.65	289.92	311.10	43.71	69.25	888.56	78.16	6474.55	5.03
P16	2883.38	-157.556	67.568	89.32	85.07	13145.77	143.70	299.90	258.63	37.83	66.00	322.05	83.11	6523.22	0.73

Distance= distance (Km) from Southernmost pool (P18) to Northernmost pool (P16); BIO1=Annual mean temperature (°C x10); BIO2= Mean diurnal temperature range (°C x10); BIO4= Temperature Seasonality (standard deviation \*100); BIO5= Max Temperature of warmest Month (°C x10); BIO6= minimum temperature of coldest month (°C x10); BIO12= annual precipitation (mm); BIO19= precipitation of coldest quarter (mm); BIO15= precipitation seasonality (Coefficient of Variation); Elev. = elevation (m); SC = snow cover; NDVI= Normalized Difference Vegetation Index; FL= % of forest loss.

BIO1, BIO2, BIO4, BIO5, BIO6, BIO12, BIO19, BIO15 were downloaded from wordclim.org and chosen to minimize correlation between variables as in Schweizer *et al.* (2016)

NDVI and snow cover were downloaded from NASA website (Global monthly MODIS /Terra)

Forest loss was downloaded from the Global Forest Change 2000–2014 website

[https://earthenginepartners.appspot.com/science-2013-global-forest/download\\_v1.2.html](https://earthenginepartners.appspot.com/science-2013-global-forest/download_v1.2.html) (Hansen *et al.* 2013).

References in body of paper

Table S2

**Table S2.** Number of raw and filtered reads (obtained after Process\_radtags in Stacks pipeline) for each caribou pool and library.

Library	Pool	N raw reads	N reads after process_rad_tags
Lib 1	P1	3,965,478	2,074,045
Lib 1	P2	2,226,334	1,077,155
Lib 1	P3	1,945,856	969,939
Lib 1	P4	2,386,018	1,232,187
Lib 1	P5	5,302,868	2,600,946
Lib 1	P6	4,415,204	2,097,016
Lib 1	P7	6,424,468	3,049,342
Lib 1	P8	2,907,550	1,359,433
Lib 1	P9	4,184,022	2,073,336
Lib 1	P10	4,305,018	2,411,927
Lib 1	P11	3,880,246	1,993,248
Lib 1	P12	2,786,674	1,428,252
Lib 1	P13	10,721,980	5,258,542
Lib 1	P14	2,724,592	1,264,378
Lib 1	P15	6,361,104	3,045,498
Lib 1	P16	6,257,926	2,908,776
Lib 1	P17	4,931,248	3,313,361
Lib 1	P18	3,745,758	2,123,214
Lib 2	P1	5,497,758	2,599,264
Lib 2	P2	2,476,640	1,159,456
Lib 2	P3	1,400,560	5,72,631
Lib 2	P4	2,218,844	1,106,626
Lib 2	P5	15,580,038	438,578
Lib 2	P6	4,509,978	262,091
Lib 2	P7	7,407,906	352,9251
Lib 2	P8	1,782,180	1,162,333
Lib 2	P9	3,855,052	1,908,270
Lib 2	P10	6,685,102	3,218,078
Lib 2	P11	5,786,136	3,622,911
Lib 2	P12	3,120,500	1,690,264
Lib 2	P13	10,076,182	5,149,739
Lib 2	P14	3,482,546	1,430,794
Lib 2	P15	9,022,090	4,126,736
Lib 2	P16	4,313,936	2,556,921
Lib 2	P17	6,447,456	3,979,919
Lib 2	P18	3,976,528	2,523,181

Table S3

**Table S3.** Estimates of basic population genetic parameters in each caribou pool in western North America.

Pool	N. of mapped read	N. of SNPs <sup>a</sup>	Average heterozygosity <sup>b</sup>	Tajima's $\pi$	Watterson's $\theta$
Pool 1	20,466	13,957	0.398826	0.008195	0.008245
Pool 2	17,844	14,226	0.397497	0.008215	0.008268
Pool 3	16,017	14,245	0.397335	0.008257	0.008312
Pool 4	19,158	14,133	0.398237	0.008255	0.008308
Pool 5	19,732	14,084	0.398163	0.008214	0.008266
Pool 6	19,227	14,134	0.398183	0.008224	0.008277
Pool 7	20,344	14,014	0.398385	0.008201	0.008252
Pool 8	18,897	14,188	0.397905	0.008255	0.008306
Pool 9	19,188	14,062	0.398309	0.008196	0.008271
Pool 10	19,790	14,051	0.398412	0.008222	0.008273
Pool 11	20,156	14,034	0.398461	0.008221	0.008272
Pool 12	17,821	14,154	0.397628	0.008252	0.008305
Pool 13	21,050	13,979	0.398113	0.008203	0.008253
Pool 14	21,149	14,163	0.398214	0.008235	0.008289
Pool 15	20,338	14,015	0.398387	0.008219	0.008269
Pool 16	19,933	14,105	0.398184	0.008228	0.008279
Pool 17	22,184	14,023	0.398543	0.008194	0.008244
Pool 18	19,725	14,077	0.398271	0.008214	0.008265

<sup>a</sup> SNPs identified using PoPoolation, used for average estimation of heterozygosity, Tajima's  $\pi$ , and Watterson's  $\theta$ .

<sup>b</sup> Average expected heterozygosity is the sum of  $[2 \times p \times (1 - p)]$  for all SNPs with the total number of all SNPs identified in each population, where  $p$  is the frequency of the most common allele.

Table S4

**Table S4.** Excel file reporting results of geographic clines analysis conducted with HZAR (see excel file named TableS4). Estimated clines parameters (centre, width and allele frequency at the top and bottom of the clines) are shown for environmentally correlated SNPs (identified with BayPass; C), outlier SNPs (identified with empirical  $F_{ST}$  approach; B) and SNPs under balancing selection (identified with BayeScan; C). AICc values of model I, model II, model III and Null model (no cline variation) are also reported. Finally, selected model is indicated (model with lowest AICc).

Table S5

**Table S5.** Characterization of GO annotations discovered, referred to bovine genome, of SNPs under selection in caribou populations distributed across western North America.

Annotations discovered (n=11) including 2 outliers found with empirical  $F_{ST}$  approach and 9 SNPs found significantly associated to environmental variables in 14 caribou populations.

Contig Name/ associated to	Description	Length	E value	Similarity	GOs/ Enzyme
101413/ BIO12	myomegalin isoform X18	670	1.20E-13	71.93%	GO:0004930; GO:0007186; GO:0016021; GO:0033038; GO:0001580
133107/ altitude	adhesion G -coupled receptor E2 isoform X1	669	5.40E-22	88.14%	GO:0008270; GO:0006384; GO:0008466; GO:0006355; GO:0017025; GO:0000126/ EC:2.4.1.186
141454 BIO19	myomegalin isoform X18	669	1.20E-14	67.69%	GO:0007010; GO:0006384; GO:0032990; GO:0050839; GO:0007157; GO:0007156; GO:0046814; GO:0005215; GO:0002860; GO:0005887; GO:0070062; GO:0005925; GO:0046982; GO:0019064; GO:0044782; GO:0017025; GO:0008270; GO:0042803; GO:0055085; GO:0060370; GO:0030382; GO:0007289; GO:0006355; GO:0008037; GO:0009566; GO:0000126; GO:0004872; GO:0002891; GO:0005102; GO:0009986; GO:0001675; GO:0051654; GO:0042271; GO:0046596; GO:0005915; GO:0033005
144728/ BIO19	mediator of RNA polymerase II transcription subunit 30	193	1.20E-11	75.61%	GO:0019827; GO:0045893; GO:0016592; GO:0004872; GO:0030521; GO:0001104; GO:0006367; GO:0046966; GO:0006357
40198/ BIO6	adhesion G -coupled receptor E2 isoform X1	669	1.30E-19	78.46%	GO:0055085; GO:0016021; GO:0008466; GO:0005215/EC:2.4.1.186
44543/ BIO4 BIO12 BIO19 BIO15 alt	glypican-5 precursor	595	1.20E-12	74.36%	GO:0043395; GO:0005578; GO:0005886; GO:0031225
69096/ -	adhesion G -coupled receptor E2 isoform X1	669	1.90E-11	75.47%	GO:0007010; GO:0032990; GO:0050839; GO:0007157; GO:0008466; GO:0007156; GO:0046814; GO:0005215; GO:0002860; GO:0005887; GO:0070062; GO:0005925; GO:0046982; GO:0019064; GO:0044782; GO:0042803; GO:0055085; GO:0060370; GO:0030382; GO:0007289; GO:0008037; GO:0009566; GO:0004872; GO:0002891; GO:0005102; GO:0009986; GO:0001675; GO:0051654; GO:0042271; GO:0046596; GO:0005915; GO:0033005/ EC:2.4.1.186
75166/ BIO15	WD repeat-containing 60 isoform X1	988	7.80E-31	86.49%	GO:0070062-IEA; GO:0005615-IEA; GO:0005929-IEA
77354 / BIO19	glypican-5 precursor	595	5.20E-13	73.53%	GO:0043395; GO:0005578; GO:0005886; GO:0031225
92872/ BIO19	myomegalin isoform X18	1183	5.10E-10	82.86%	GO:0008270; GO:0006384; GO:0006355; GO:0017025; GO:0000126
95090/ -	adhesion G -coupled receptor E2 isoform X1	669	4.70E-09	69.77%	GO:0055085; GO:0016021; GO:0005215

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Annotations discovered (n=10), under balancing selection (20 outliers found with BayeScan) in 14 caribou populations.

Contig Name	Description	Length	E value	Similarity	GOs/ Enzyme
102803	pregnancy-associated glyco 11	376	2.5E-12	84.13%	GO:0004190; GO:0006508/EC:3.4.23
109390	pregnancy-associated glyco 1-like	380	3.50E-20	67.90%	GO:0005615; GO:0005622; GO:0005887; GO:0045121; GO:0004190; GO:0005068; GO:0042169; GO:0006508; GO:0007169; GO:0007565; GO:0030163; GO:0035556; GO:0050868/EC:3.4.23;
156715	protocadherin gamma-B1	812	8.40E-67	100.00%	GO:0005886; GO:0016021; GO:0005509; GO:0007156
38804	transport Sec23B isoform X1	767	2.00E-19	88.46%	GO:0000139; GO:0030127; GO:0030868; GO:0033116; GO:0048471; GO:0008270; GO:0006886; GO:0006888
47711	membrane FAM159A isoform X2	162	2.60E-14	74.51%	GO:0005578; GO:0005886; GO:0016021; GO:0031225; GO:0043395
50941	60S ribosomal L5	297	5.20E-104	96.97%	GO:0005730; GO:0022625; GO:0003735; GO:0008097; GO:0000027; GO:0006412
6910	adhesion G -coupled receptor E2 isoform X1	669	1.10E-15	71.88%	GO:0000126; GO:0000800; GO:0008270; GO:0017025; GO:0046982; GO:0006355; GO:0006384; GO:0007140; GO:0007143; GO:0009566; GO:0043066; GO:0048808
79834	pregnancy-associated glyco 1-like	377	3.20E-16	76.36%	GO:0005615; GO:0005622; GO:0005887; GO:0045121; GO:0004190; GO:0005068; GO:0042169; GO:0006508; GO:0007169; GO:0007565; GO:0030163; GO:0035556; GO:0050868/ EC:3.4.23
93471	zinc finger 510	284	1.20E-25	80.20%	GO:0005654; GO:0005794; GO:0031965; GO:0034399; GO:0008139; GO:0008536; GO:0008565; GO:0044822; GO:0000059; GO:0000060; GO:0006355; GO:0006607; GO:0006610; GO:0042307; GO:0071230
98859	myomegalin isoform X18	295	3.20E-20	78.95%	GO:0016021; GO:0004930; GO:0033038; GO:0001580; GO:0007186

Annotations discovered (n=12), including 23 outliers found with empirical  $F_{ST}$  in pools of sedentary and migratory caribou individuals.

Contig Name	Description	Length	E value	Similarity	GOs/ Enzyme
102907	membrane FAM159A isoform X2	2.1E-25	595	76.00%	GO:0043395; GO:0016021; GO:0005578; GO:0005886; GO:0031225
107134	myomegalin isoform X18	2.7E-15	669	64.56%	GO:0008270; GO:0006384; GO:0008466; GO:0006355; GO:0017025; GO:0000126/ EC:2.4.1.186
139714	myomegalin isoform X18	3.4E-11	1183	82.05%	GO:0007010; GO:0032990; GO:0050839; GO:0007157; GO:0007156; GO:0046814; GO:0005215; GO:0002860; GO:0005887; GO:0070062; GO:0005925; GO:0046982; GO:0019064; GO:0044782; GO:0042803; GO:0055085; GO:0060370; GO:0030382; GO:0007289; GO:0008037; GO:0009566; GO:0004872; GO:0002891; GO:0005102; GO:0009986; GO:0001675; GO:0051654; GO:0042271; GO:0046596; GO:0005915; GO:0033005
140714	myomegalin isoform X18	6.2E-10	1183	81.58%	GO:0007010; GO:0032990; GO:0050839; GO:0007157; GO:0007156; GO:0046814; GO:0002860; GO:0005887; GO:0070062; GO:0005925; GO:0046982; GO:0019064; GO:0044782; GO:0042803; GO:0060370; GO:0030382; GO:0007289; GO:0008037; GO:0009566; GO:0004872; GO:0002891; GO:0005102; GO:0009986; GO:0001675;

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					GO:0051654, GO:0042271; GO:0046596; GO:0005915; GO:0033005
143028	importin-5	8.9E-09	422	88.24%	GO:0042307; GO:0008565; GO:0005794; GO:0008536; GO:0000059; GO:0008139; GO:0005654; GO:0044822; GO:0006610; GO:0071230; GO:0031965; GO:0000060; GO:0006607; GO:0034399
148437	myomegalin isoform X18	1.9E-09	669	83.33%	GO:0055085; GO:0016021; GO:0005215
150786	myomegalin isoform X18	3.7E-30	295	90.20%	GO:0004930; GO:0007186; GO:0016021; GO:0033038; GO:0001580
37040	sodium potassium calcium exchanger mitochondrial isoform X5	4.7E-09	524	69.39%	GO:0042803, GO:0030061, GO:0032592; GO:0051480, GO:0005432, GO:0005886, GO:0006851, GO:0050796, GO:0042593; GO:0051560; GO:0070588; GO:0005829; GO:0035725
44250	transcription factor IIB 90 kDa subunit isoform X1	5E-15	301	69.57%	GO:0048808, GO:0008270; GO:0006384; GO:0007143; GO:0007140; GO:0000800; GO:0008466, GO:0006355; GO:0009566; GO:0000126; GO:0046982; GO:0043066; GO:0017025/ EC:2.4.1.186
53319	myomegalin isoform X18	1.2E-45	295	94.74%	GO:0008283; GO:0035264; GO:0060463; GO:0060487; GO:0008544; GO:0006366, GO:0090132; GO:0001228; GO:0043565; GO:0007155; GO:0045944; GO:0060324; GO:0005215; GO:0005654; GO:0042733, GO:0004930; GO:0001843; GO:0003208; GO:0043010; GO:0033038; GO:0031490; GO:0060672; GO:0045617; GO:0055085, GO:0007186; GO:0048701; GO:0001580, GO:0007420; GO:0005886; GO:0051973; GO:0044030; GO:0005911; GO:0001161; GO:0016021; GO:0070830
68038	adhesion G-coupled receptor E2 isoform X1	5.5E-12	670	77.08%	GO:0006384; GO:0032592; GO:0005432; GO:0050796; GO:0046982; GO:0051560; GO:0070588; GO:0005829; GO:0017025; GO:0048808; GO:0008270; GO:0042803; GO:0030061; GO:0007143; GO:0007140; GO:0051480; GO:0000800; GO:0006355; GO:0009566; GO:0000126; GO:0005886; GO:0006851; GO:0043066; GO:0042593; GO:0035725
72872	zinc finger 510	1.4E-50	284	84.54%	GO:0042307; GO:0008565; GO:0006355; GO:0005794; GO:0008536, GO:0000059; GO:0008139; GO:0005654, GO:0044822; GO:0006610; GO:0071230; GO:0031965; GO:0000060; GO:0006607; GO:0034399



## Supporting notes

### Note S1

#### Organization of caribou ecotypes

A fundamental step toward caribou management and conservation has been the delineation of caribou DUs (Ray *et al.* 2015; including those used here), in essence ecotypes, based upon concordance of behavioral, morphological, ecological, geographic and/or neutral genetic distinctiveness (COSEWIC 2011). Legislatively, DU's are comparable to the distinct population segment (DPS) under the U.S. Endangered Species Act of 1973. However, some knowledge gaps were identified and further investigation was demanded based upon ecological and genomic traits (COSEWIC 2011). Our population structure analysis supported DU designation with few exceptions, indicating the robust basis of DUs' classification scheme according to COSEWIC, but also highlighted the possibility for refinement. The Little Smoky population (currently considered of Boreal ecotype, isolated and not self-sustaining; Hervieux *et al.* 2013) was grouped together with Central Mountain and Southern Mountain ecotype populations in our study (Fig. 3E), in particular when selected outliers were used (Figs. 3C and 3D). In addition, Jasper and Banff populations of Central Mountain ecotype were genetically close to a population of Southern Mountain ecotype. Interestingly, caribou belonging to the Little Smoky population have characteristics that are intermediate between the Boreal and Mountain ecotypes, as a significant portion of the population has Mountain traits including migration and/or harboring mtDNA haplotypes that did not evolve in the boreal forest (i.e. of BEL lineage; McDevitt *et al.* 2009). The Little Smoky caribou could be either the last remaining population of a transitional ecotype between mountain and boreal ecotypes, or they may be an indication of mountain caribou that have adapted to a boreal forest environment. Overall, our results emphasize the need to consider both differences and intermediate traits among populations and DUs, including the divide between Boreal and Mountain and between Southern and Central Mountain ecotypes.

Other differences were found in ordinate and NJ tree analyses of all SNPs and SNPs under selection (selected outliers, Fig. 3A, B, C, D). Barren-ground caribou (P14) were clearly differentiated when all SNPs were used in PCoA analysis (Fig. 3A). In tree analyses, Barren-ground caribou branched together with Northern Mountain caribou (P13 and P17), whereas in the ordinate analysis that used SNPs under selection they were close to Northern Mountain and Alaska caribou. These patterns were consistent with geographic distance of the Barren-ground caribou from other groups (Fig. 1), whereas in ecological terms the ecotype has known similarities with both Northern Mountain and Alaska caribou, including ability to feed on terrestrial lichens and capacity for long range migrations (Geist 1998; Hummel & Ray 2008). On the other hand, Southern Mountain caribou (P18) were clearly differentiated when SNPs under selection were used in PCoA analysis (Fig. 3C). In NJ tree analyses, Southern Mountain caribou

branched together with Central Mountain caribou (P1, P5 and P6), whereas in the ordinate analysis using all SNPs they were close to Central Mountain and Boreal caribou. These patterns were consistent with geographic proximity of the Southern Mountain caribou to other groups (Fig. 1). However, in ecological terms, which could be reflected in the analysis of SNPs under selection, the Southern Mountain ecotype has unique characteristics, including spending the winter at high elevation and feeding predominantly on arboreal lichens (Geist 1998; Bergerud *et al.* 2007).

## References

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Other references in body of paper