

Supplementary Information (SI)

Population genetics of caribou in the Alaska-Yukon border region: implications for designation of conservation units and small herd persistence

Conservation Genetics

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Table S1. Pairwise genetic differentiation between caribou herds: Jost's D (Jost 2008; upper right) and $G''st$ (Hedrick 2005; lower left). Both indices range from zero (no difference) to one (total differentiation). Symbols indicate whether D and $G''st$ are statistically significantly greater than zero for each herd pair based on three critical values from adjustments for multiple comparisons.

	Fortymile	Clear Creek	Chisana	Hart River	Klaza	Mentasta	Nelchina	Porcupine	White Mtns
Fortymile	--	0.004	0.128 [#]	0.009	0.125 [#]	0.022	0.026 [#]	0.026 [#]	0.083 [#]
Clear Creek	0.005	--	0.148 [#]	-0.007	0.155 [#]	0.069 [#]	0.046 [#]	0.015	0.095 [#]
Chisana	0.152 [*]	0.175 [*]	--	0.160 [*]	0.176 [*]	0.110 [*]	0.133 [*]	0.146 [*]	0.180 [*]
Hart River	0.010	-0.009	0.188 [*]	--	0.150 [*]	0.060 [*]	0.057 [*]	0.009	0.099 [*]
Klaza	0.149 [*]	0.184 [*]	0.213 [*]	0.177 [*]	--	0.106 [*]	0.16 [*]	0.162 [*]	0.142 [*]
Mentasta	0.026	0.082 [*]	0.132 [*]	0.071 [*]	0.127 [*]	--	-0.010	0.072 [*]	0.088 [*]
Nelchina	0.031 [*]	0.055 [*]	0.159 [*]	0.067 [*]	0.191 [*]	-0.012	--	0.058 [*]	0.099 [*]
Porcupine	0.030 [*]	0.018	0.173 [*]	0.011	0.191 [*]	0.084 [*]	0.068 [*]	--	0.080 [*]
White Mtns	0.097 [*]	0.111 [*]	0.213 [*]	0.116 [*]	0.170 [*]	0.104 [*]	0.117 [*]	0.093 [*]	--

* Genetic differentiation between the two herds is significantly greater than zero using a Bonferroni correction ($p \leq 0.001$) as well as the Benjamini-Yekutieli modified false discovery rate procedure ($p \leq 0.012$) and the Benjamini-Hochberg false discovery rate procedure ($p \leq 0.040$)

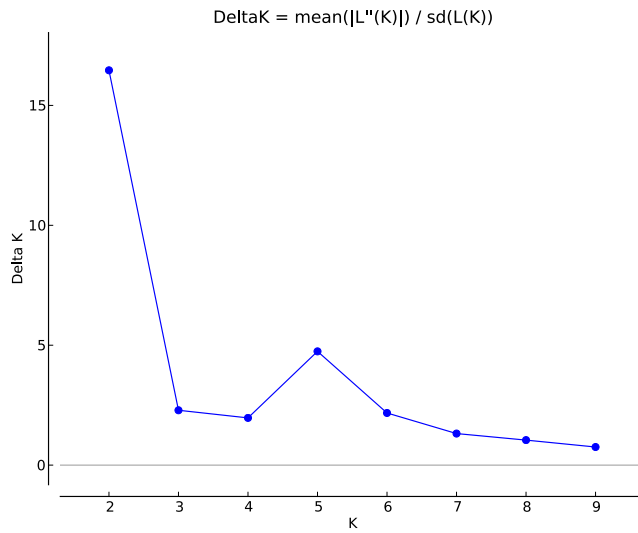


Fig. S1 Rate of change of the $\ln$ probability between values of $K = 1$ -10 (ΔK ; Evanno et al. 2005) identified by STRUCTURE analysis with locpriors. This suggests there are two higher-order genetic clusters within the Alaska-Yukon border herds, though there is a secondary peak at $K = 5$.

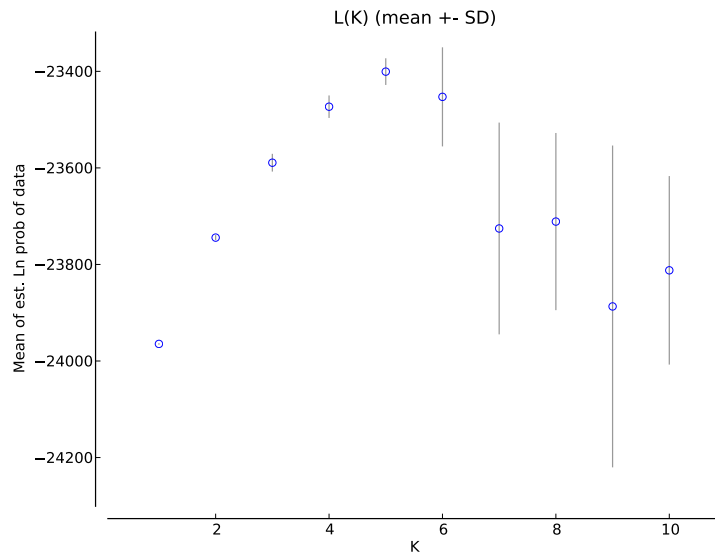


Fig. S2 Mean $\ln$ probability of between one ($K = 1$) to ten ($K = 10$) genetic clusters within the Alaska-Yukon border herds according to STRUCTURE analysis with locpriors. An asymptote and the lowest $\ln$ probability at $K = 5$ suggest there may be additional structure beyond the two main clusters suggested using the ΔK criterion (Evanno et al. 2005).

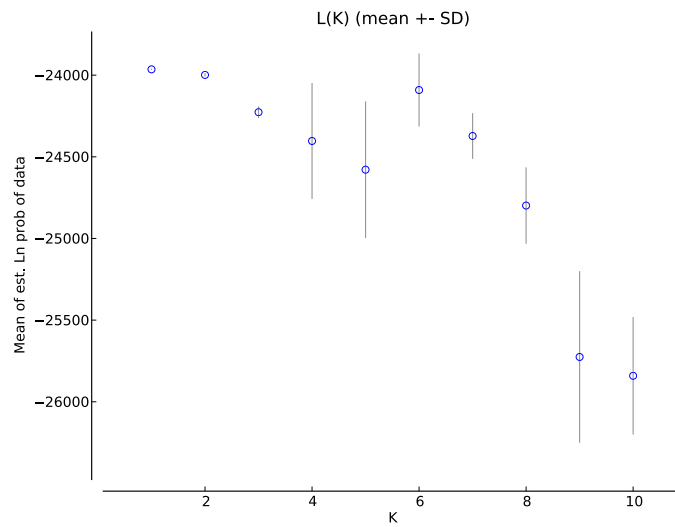


Fig. S3 Mean ln probability of between one ($K = 1$) to ten ($K = 10$) genetic clusters within the Alaska-Yukon border herds according to STRUCTURE admixture analysis (without locpriors). The lowest ln probability is at $K = 1$, though an increase at $K = 6$ suggests a weak signal of additional structure.

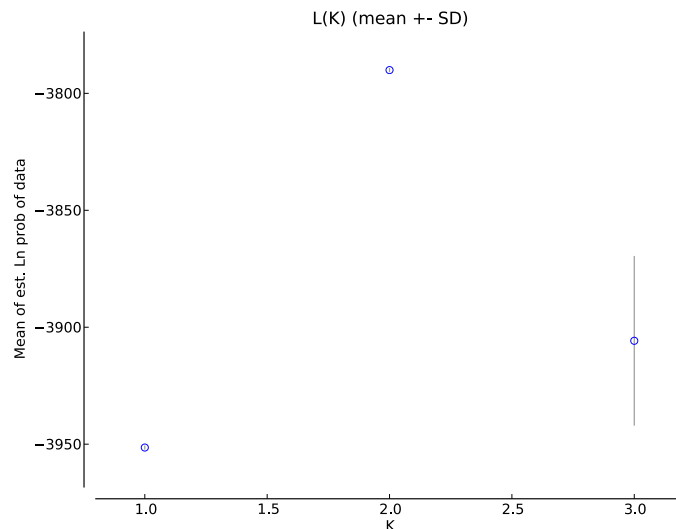


Fig. S4 Mean ln probability of between one ($K = 1$) to three ($K = 3$) genetic clusters within Cluster 1 (the Klaza and Chisana herds) according to STRUCTURE analysis with locpriors. The lowest ln probably at $K = 2$ suggests two clusters.

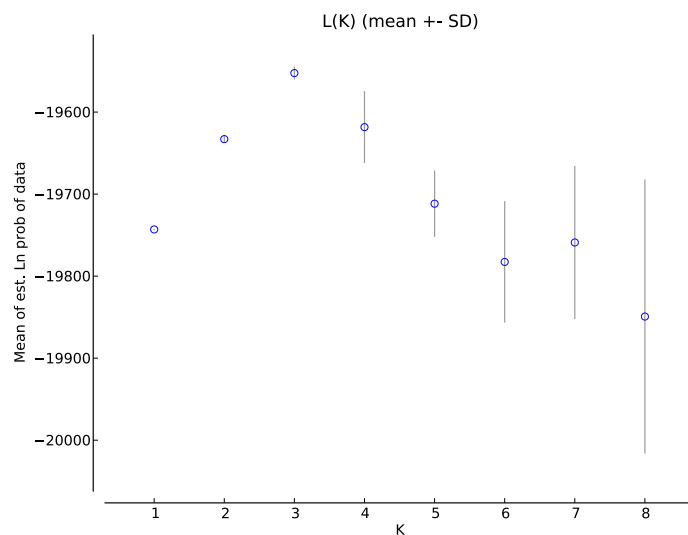


Fig. S5 Mean ln probability of between one ($K = 1$) to eight ($K = 8$) genetic clusters within Cluster 2 (all herds except Chisana and Klaza) according to STRUCTURE analysis with locpriors. The lowest ln probably at $K = 3$ suggests there are three genetic sub-clusters within Cluster 2.

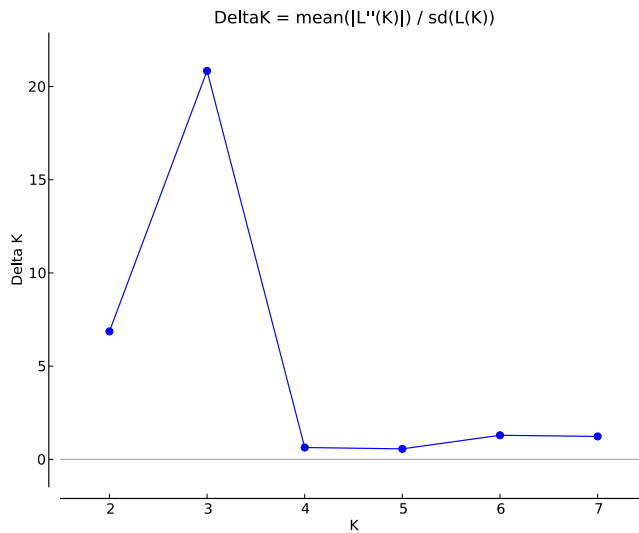


Fig. S6 The rate of change of the ln probability between $K = 1$ -8 (ΔK ; Evanno et al. 2005) in a STRUCTURE analysis of Cluster 2 with locpriors. This suggests there are three genetic sub-clusters within Cluster 2.