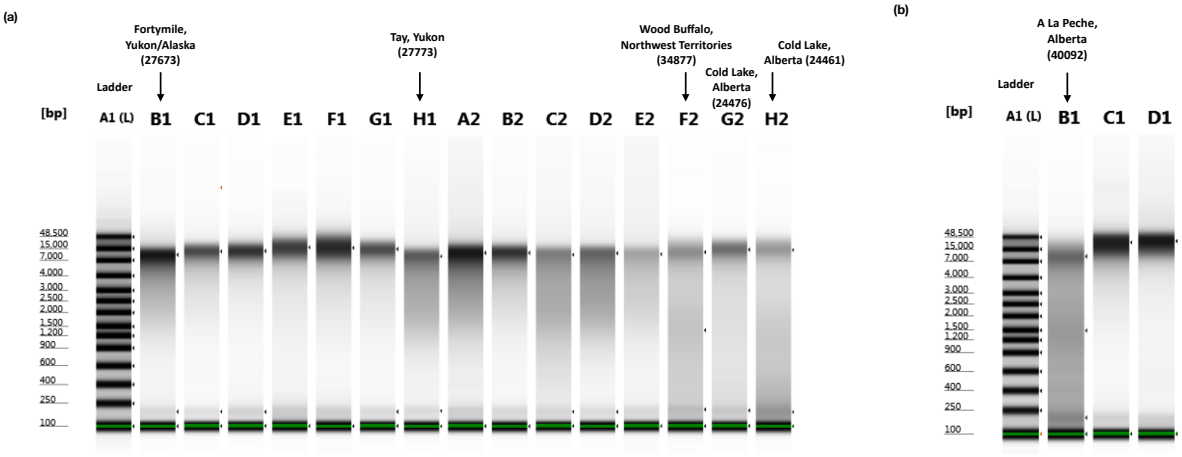
Supplementary Material S1: Microsatellite genotype RFU peak heights for three of the faecal samples. All samples amplified successfully for all 10 microsatellite loci with good RFU scores.

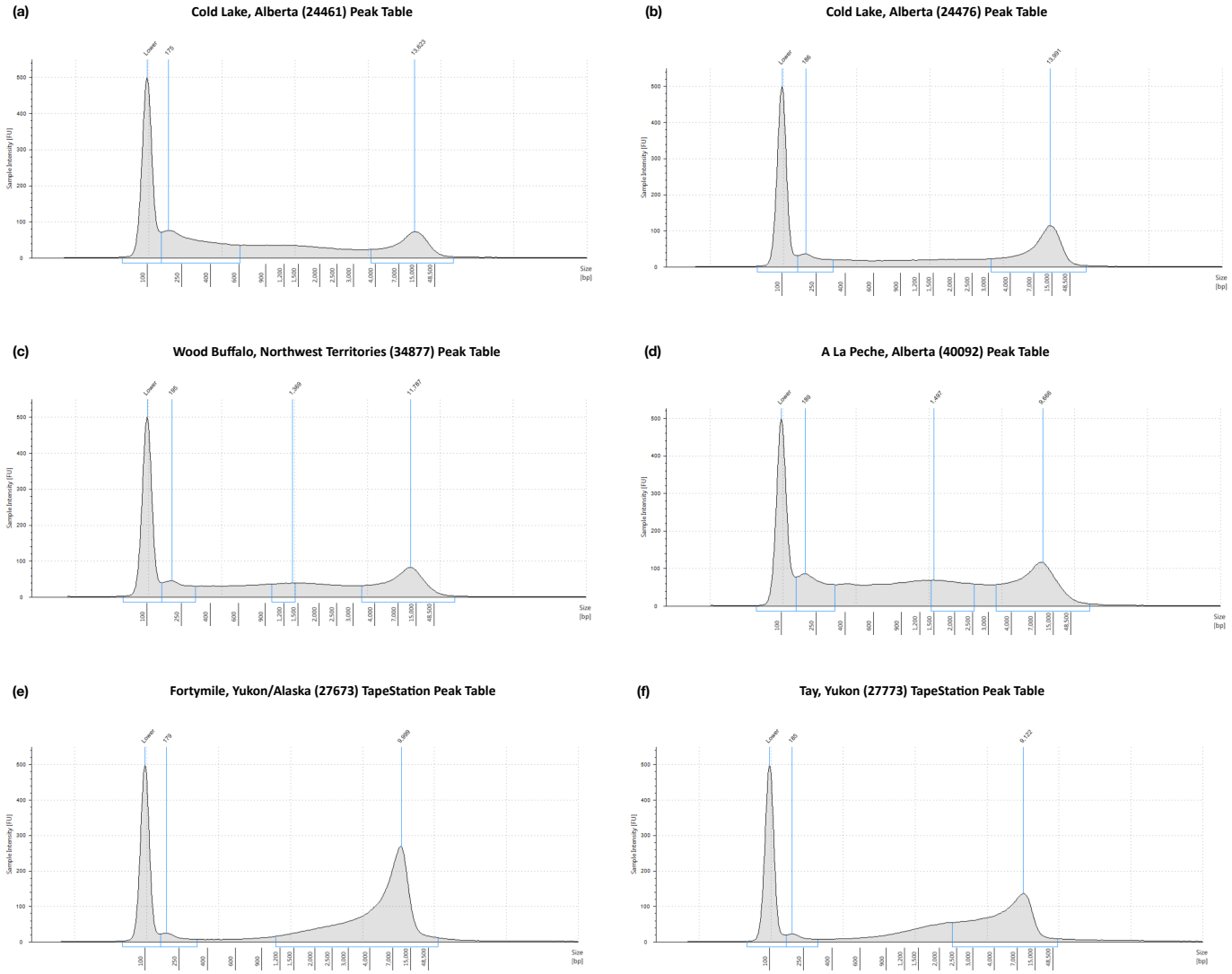
Location and ID	BM888a peak	BM888b peak	FCB193a peak	FCB193b peak	NVHRT16a peak	NVHRT16b peak	OHEQa peak	OHEQb peak	RT1a peak	RT1b peak	RT5a peak	RT5b peak	RT6a peak	RT6b peak	RT7a peak	RT7b peak	RT24a peak	RT24b peak	SexIDa peak	SexIDb peak
Cold Lake, Alberta 24461	16371	16371	7384	5893	4585	2173	1860	1407	3577	2796	5555	4306	4348	4348	7596	7596	4027	696	4515	2956
Cold Lake, Alberta 24476	17847	277	9837	6045	8268	5909	14047	14047	7481	7481	7642	6379	6972	4432	6657	4763	17908	2351	5877	5877
A La Peche, Alberta 40092	16115	15556	14372	10062	9353	9353	9093	9093	2562	2391	10033	7352	3927	2834	5127	4548	5511	5511	8466	4916

Supplementary Material S2: Microsatellite genotype RFU peak heights the remaining faecal sample (34877) and one of the tissue samples (27773). All samples amplified successfully for all 10 microsatellite loci with good RFU scores. The microsatellite loci which are different from the other faecal samples have an asterisk. The other tissue sample was not amplified for microsatellite loci.

Location and ID	BM888a peak	BM888b peak	BM848a peak*	BM848b peak*	MAP2Ca peak*	MAP2Cb peak*	RT30a peak*	RT30b peak*	RT9a peak*	RT9b peak*	RT5a peak	RT5b peak	RT6a peak	RT6b peak	RT7a peak	RT7b peak	RT24a peak	RT24b peak	SexIDa peak	SexIDb peak
Wood Buffalo, Northwest Territories 34877	8517	6780	1930	1930	12979	12979	2692	1651	9953	9953	2783	2193	6804	6804	2188	1425	9953	9953	3627	3627
Tay, Yukon 27773	14989	15359	2436	2436	3302	2713	4335	3072	5605	5605	8186	6706	3214	2089	7289	4485	3890	1214	12743	8317

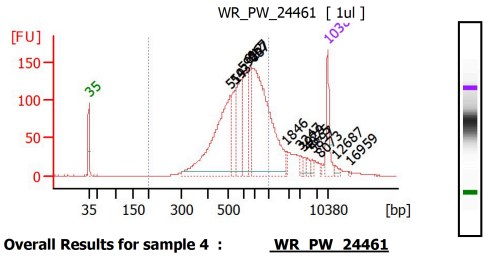


Supplementary Material S3: Gel images of the DNA extractions done by The Centre for Applied Genomics (TCAG) at the Hospital for Sick Children (Toronto, Ontario). Samples included in this study are labelled, with (a) showing the two tissue samples (27673 and 27773) and three of the faecal samples (34877, 24476, and 24461), and (b) showing the other faecal sample (40092). The faecal samples show weaker bands at the larger fragment size than the tissue samples.



Supplementary Material S4: TapeStation plots from The Centre for Applied Genomics (TCAG) at the Hospital for Sick Children (Toronto, Ontario) for the faecal (a-d) and tissue (e-f) samples. The plots show the distribution of fragment sizes for each DNA extract, with the faecal samples vary in their distributions but show more fragments in the middle of the size range.

(a) Cold Lake, Alberta (24461)



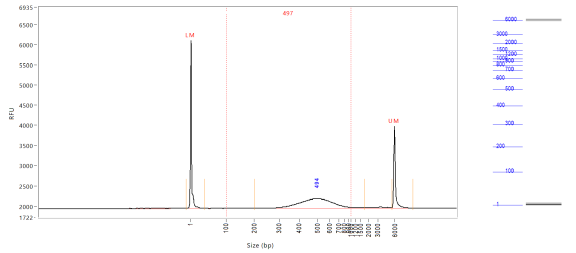
Overall Results for sample 4 : WR_PW_24461

Number of peaks found:	14
Noise:	0.4
Corr. Area 1:	2,368.6

Region table for sample 4 : WR_PW_24461

From [bp]	To [bp]	Corr. Area	% of Total	Average Size [bp]	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
200	1,000	2,368.6	79	612	26.0	1,459.08	3,962.8	

(b) Cold Lake, Alberta (24476)

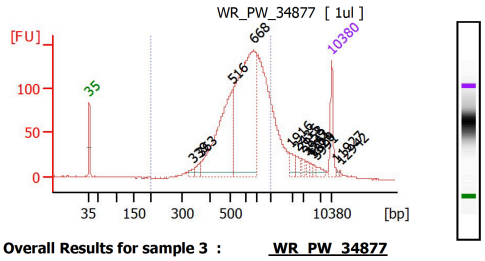


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.1980	0	40	2	219.03	4159	39.652
2	494	2.0278	200	1768	518	33.24	235	33.839
3	6000 (UM)	0.0612	5593	9517	6134	7.71	2021	12.269

TIC:	2.0278	ng/uL
TIM:	6.4418	nmole/L
Total Conc.:	2.1486	ng/uL

Smear Analysis	100 bp to 1000 bp	1.9904 ng/ul	92.6 %Total	6.5885 nmole/L	497 Avg. Size (bp)	23.53 %CV

(c) Wood Buffalo, Northwest Territories (34877)



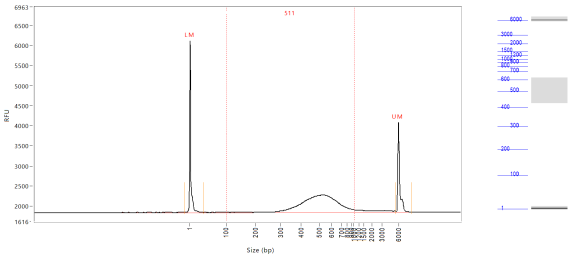
Overall Results for sample 3 : WR_PW_34877

Number of peaks found:	13
Noise:	0.3
Corr. Area 1:	2,318.5

Region table for sample 3 : WR_PW_34877

From [bp]	To [bp]	Corr. Area	% of Total	Average Size [bp]	Size distribution in CV [%]	Conc. [pg/µl]	Molarity [pmol/l]	Color
200	1,000	2,318.5	82	615	25.6	2,036.56	5,486.4	

(d) A La Peche, Alberta (40092)

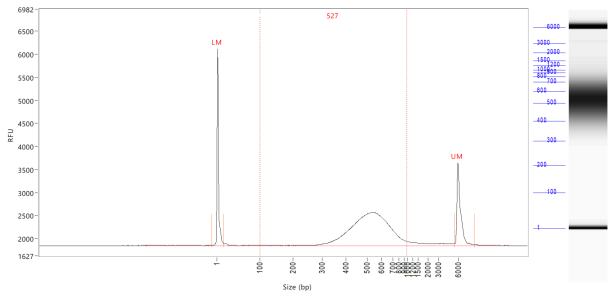


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.1980	0	38	2	210.20	4269	41.510
2	6000 (UM)	0.0677	5593	8412	6126	5.70	2234	14.199

TIC:	0.0000	ng/uL
TIM:	0.0000	nmole/L
Total Conc.:	3.8043	ng/uL

Smear Analysis	100 bp to 1000 bp	3.5179 ng/ul	92.5 %Total	11.3384 nmole/L	511 Avg. Size (bp)	24.08 %CV

(e) Fortymile, Yukon/Alaska (27673)

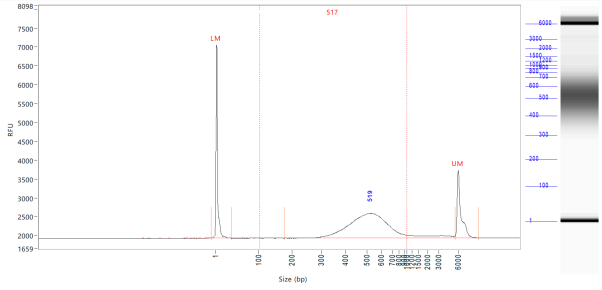


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.1980	0	16	1	247.87	4275	39.608
2	6000 (UM)	0.0871	5492	8562	6231	7.35	1796	17.429

TIC:	0.0000	ng/uL
TIM:	0.0000	nmole/L
Total Conc.:	6.2068	ng/uL

Smear Analysis	100 bp to 1000 bp	5.7890 ng/ul	93.3 %Total	18.0888 nmole/L	527 Avg. Size (bp)	22.56 %CV

(f) Tay, Yukon (27773)

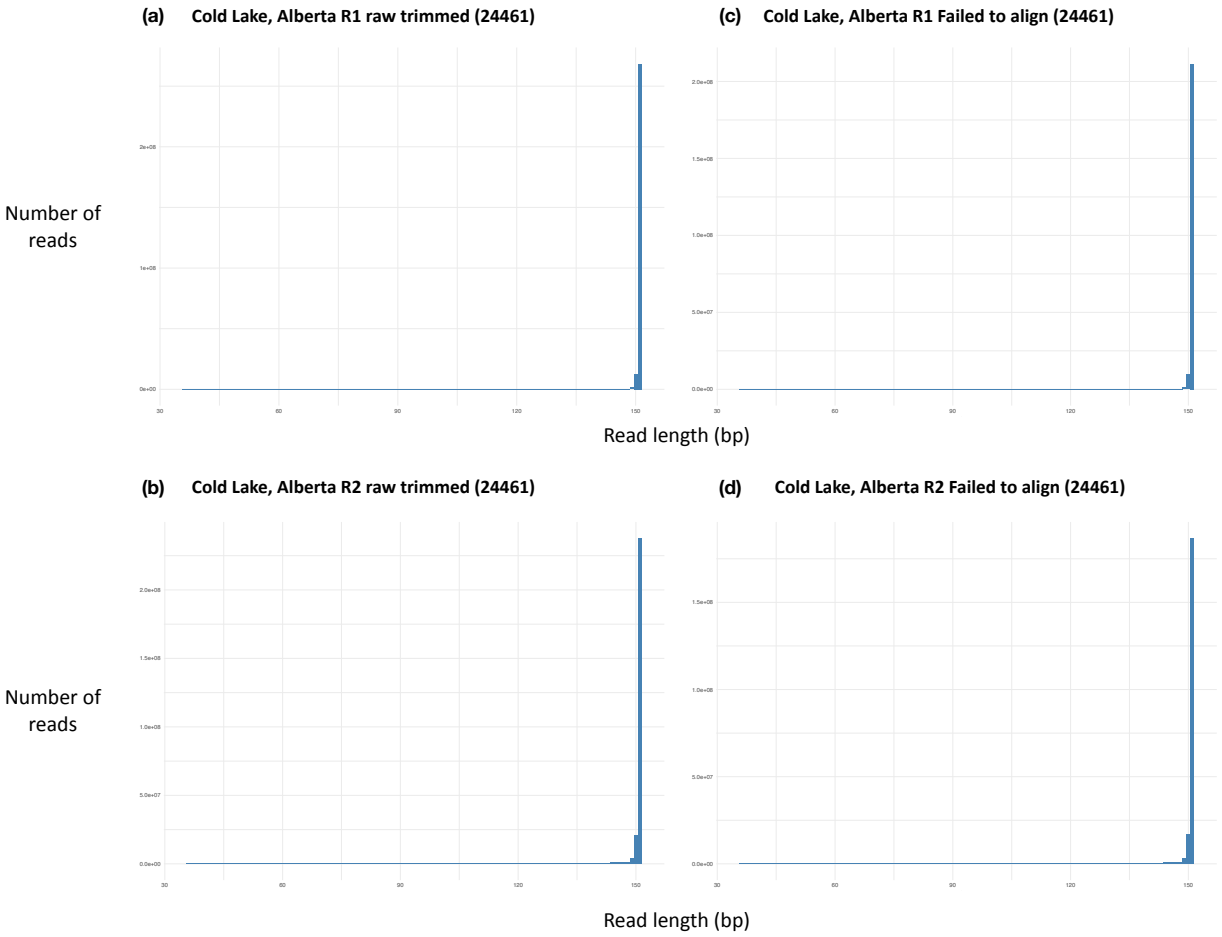


Peak	Size (bp)	Conc. (ng/uL)	From (bp)	To (bp)	Avg. Size (bp)	CV%	RFU	Corr. Peak Area
1	1 (LM)	0.1980	0	37	2	196.65	5141	50.810
2	519	4.3912	175	5492	653	92.78	653	93.895
3	6000 (UM)	0.0731	5492	9165	6321	8.14	1805	18.753

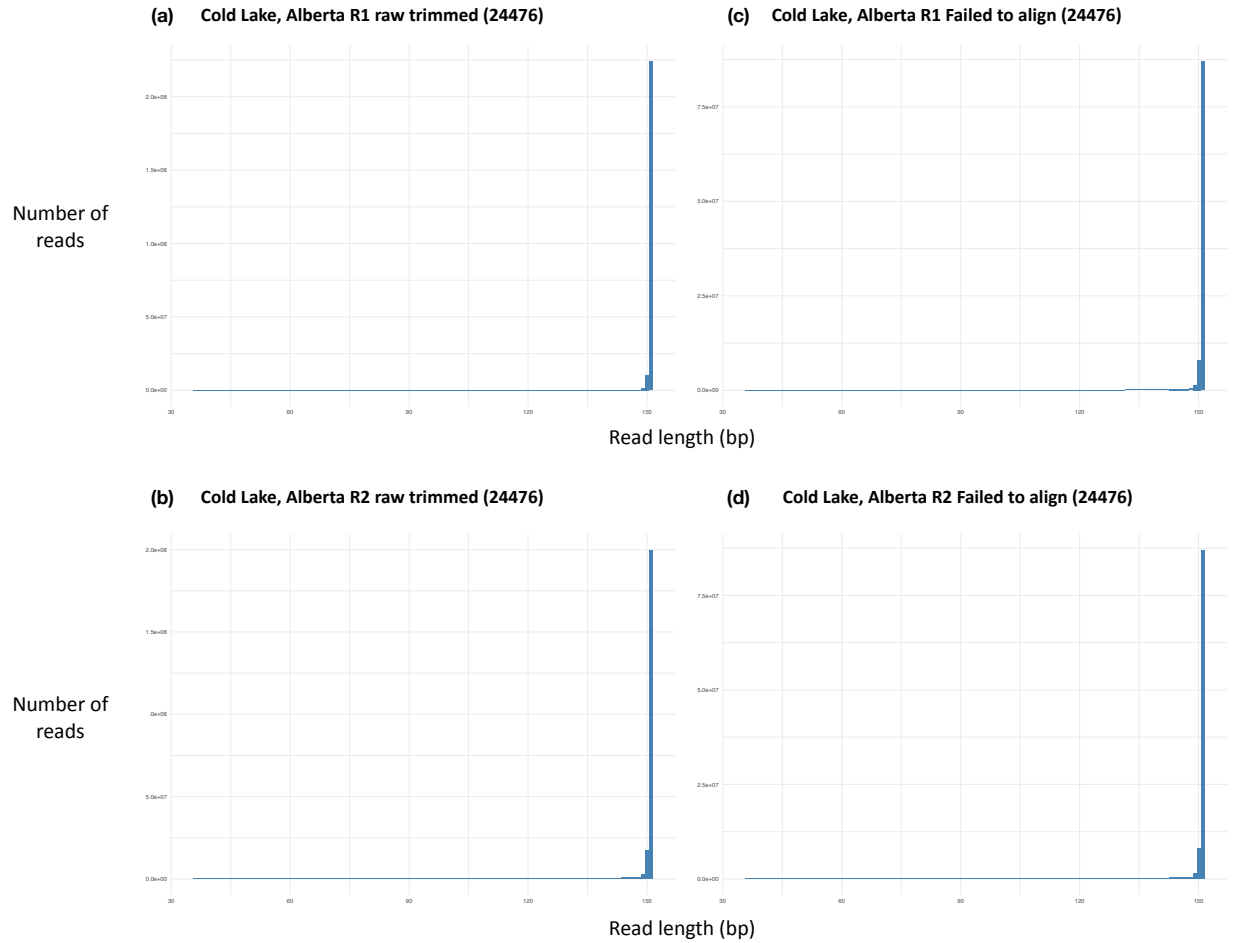
TIC:	4.3912	ng/uL
TIM:	11.0667	nmole/L
Total Conc.:	4.3935	ng/uL

Smear Analysis	100 bp to 1000 bp	4.0875 ng/ul	93.0 %Total	13.0089 nmole/L	517 Avg. Size (bp)	22.03 %CV

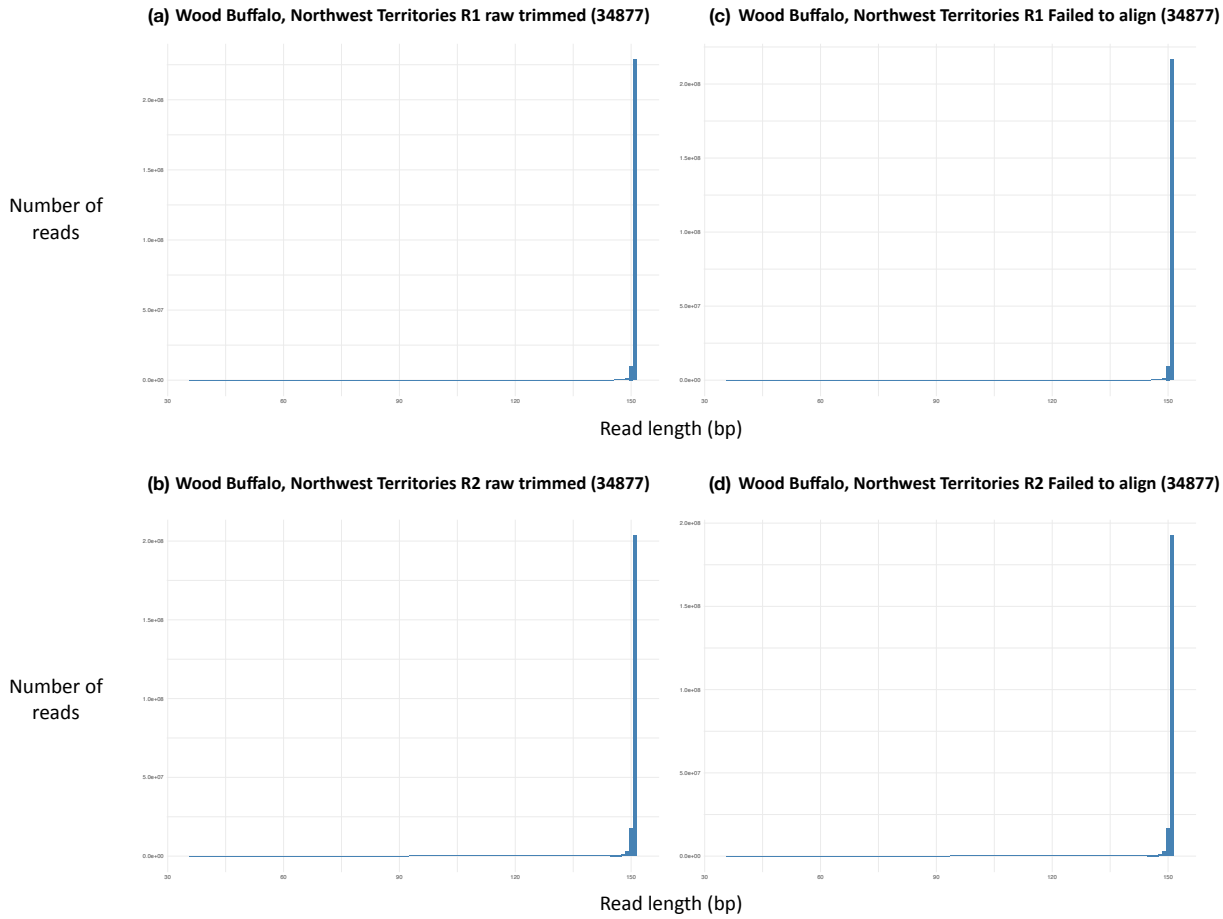
Supplementary Material S5: Fragment Analyzer (b, d, e, f) and Bioanalyzer (a, c) results from The Centre for Applied Genomics (TCAG) at the Hospital for Sick Children (Toronto, Ontario) for the faecal (a-d) and tissue (e-f) samples. The distributions are similar but show lower middle peaks for the faecal samples.



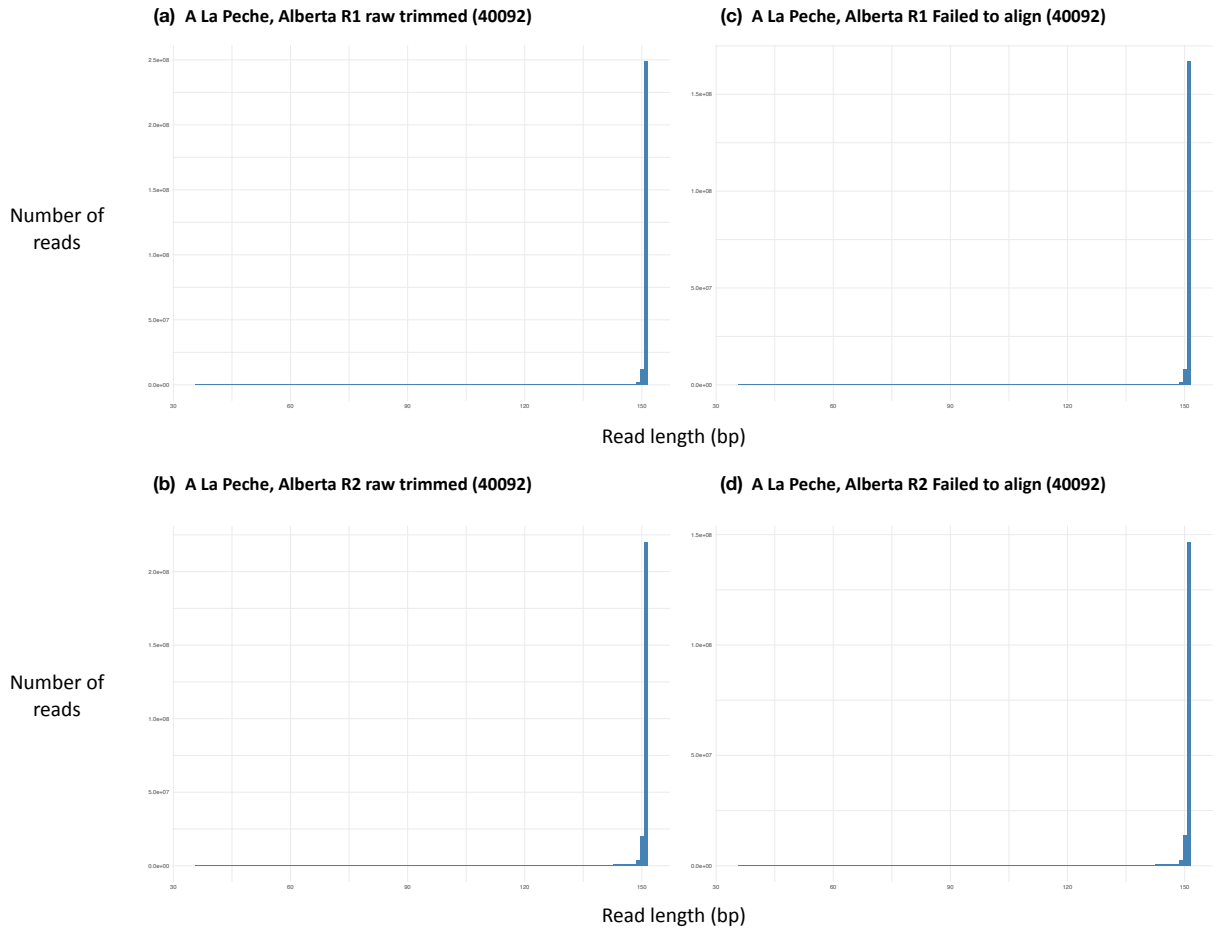
Supplementary Material S6: Distribution of read lengths for the Cold Lake (24461) caribou. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. In both cases, the reads are heavily skewed towards 150 bp.



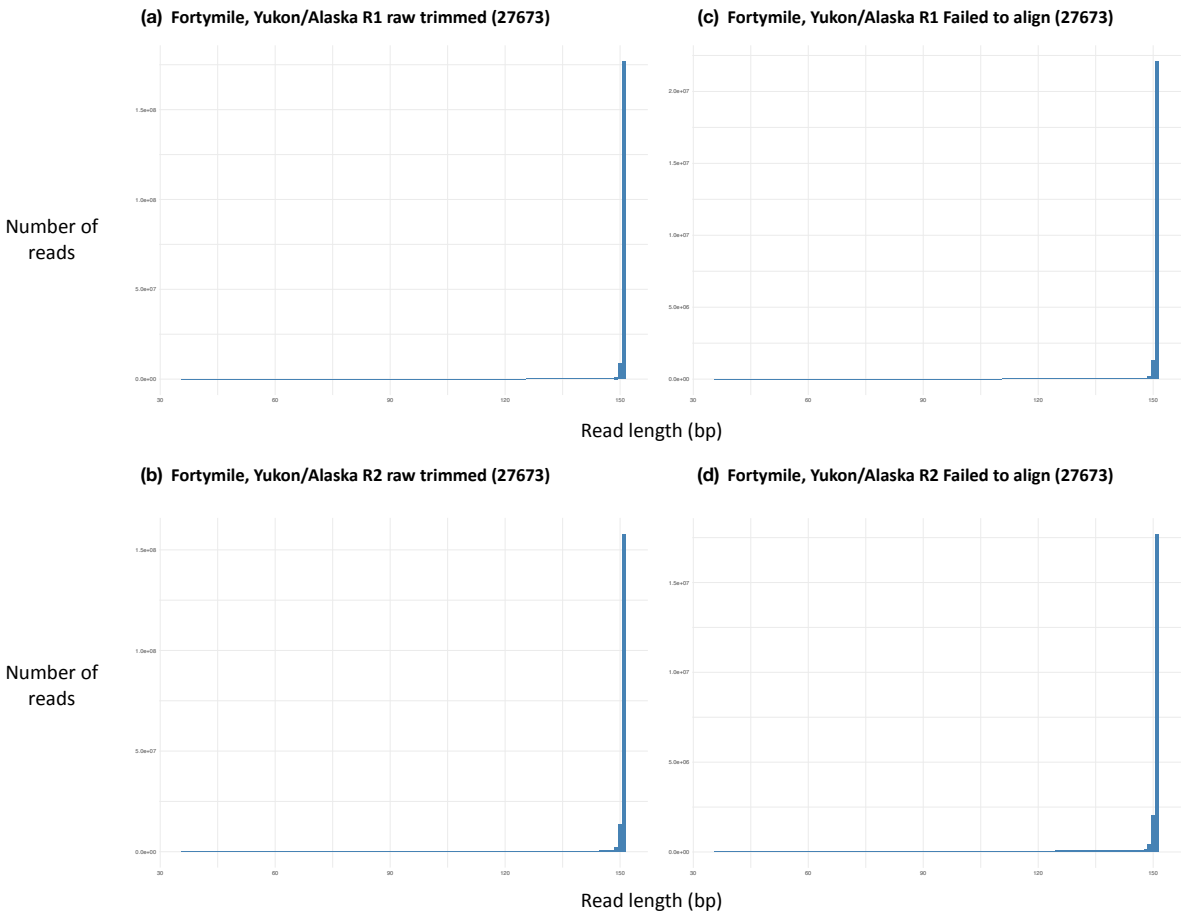
Supplementary Material S7: Distribution of read lengths for the Cold Lake (24476) caribou. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. In both cases, the reads are heavily skewed towards 150 bp.



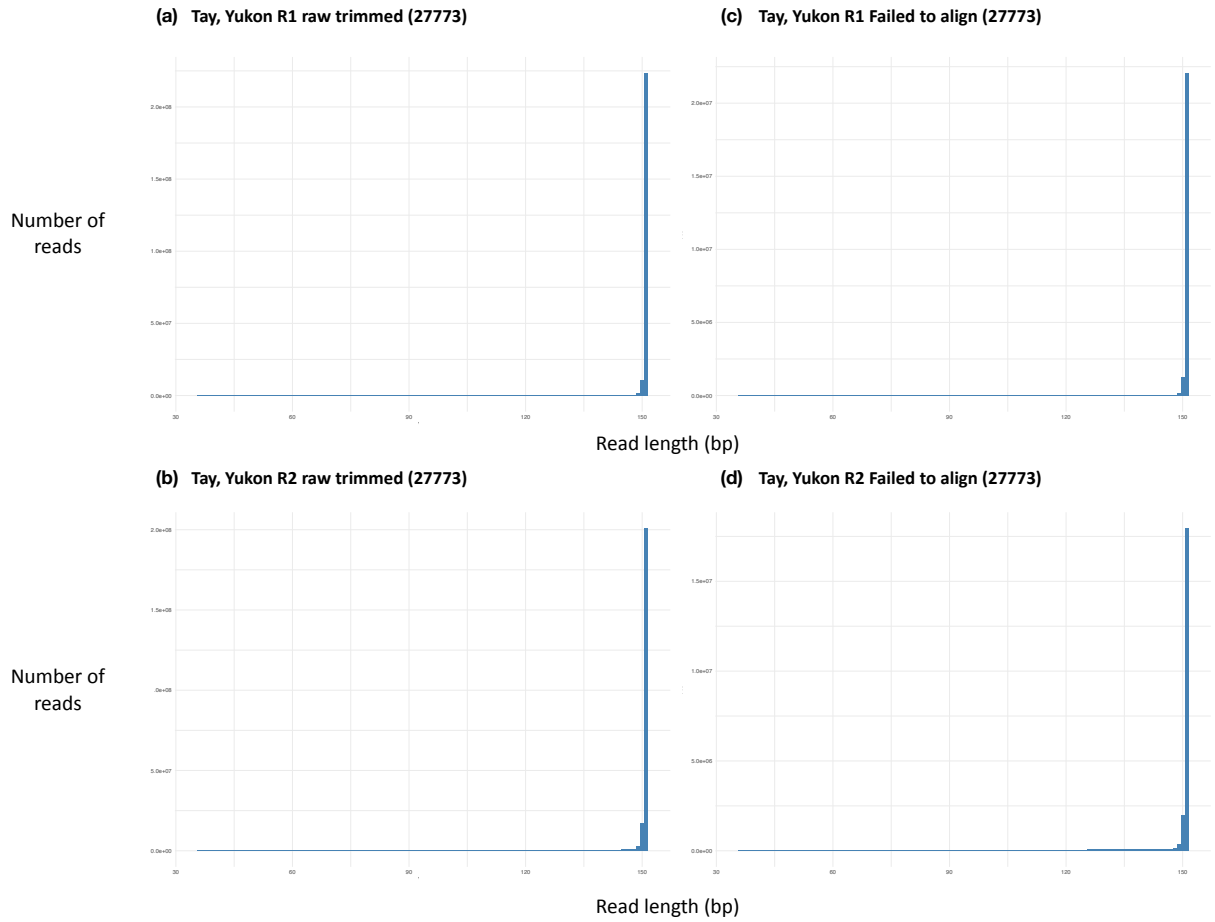
Supplementary Material S8: Distribution of read lengths for the Wood Buffalo (34877) caribou. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. In both cases, the reads are heavily skewed towards 150 bp.



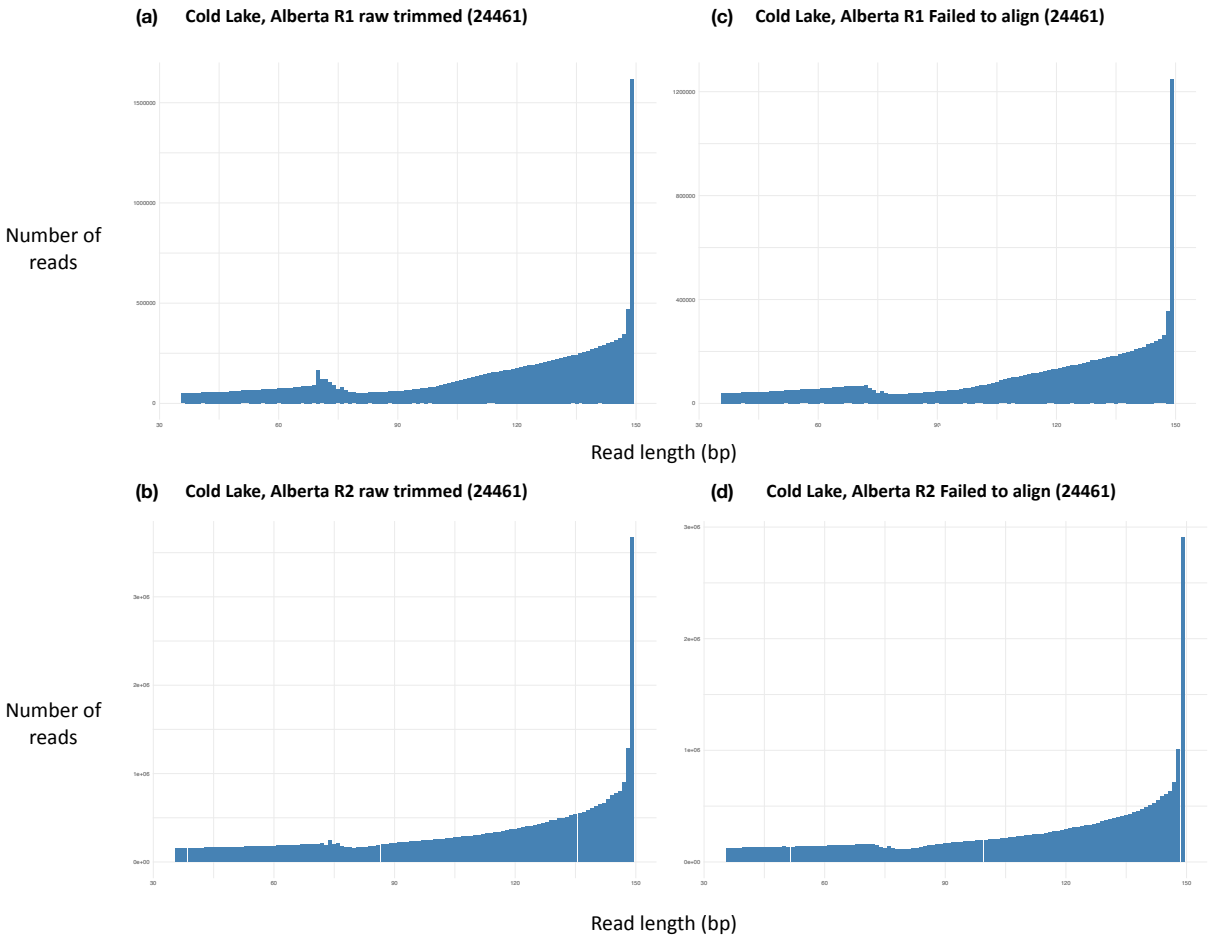
Supplementary Material S9: Distribution of read lengths for the A La Peche (40092) caribou. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. In both cases, the reads are heavily skewed towards 150 bp.



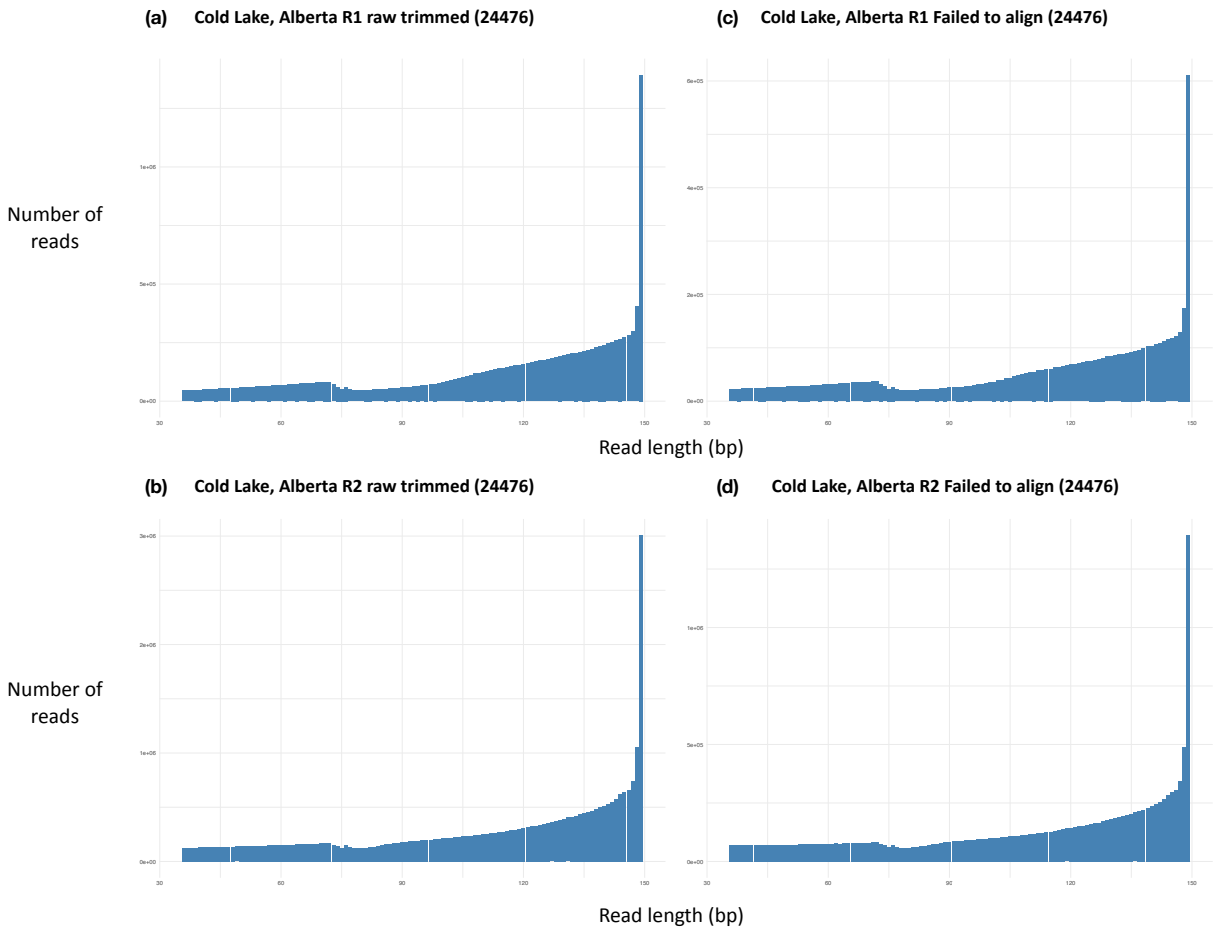
Supplementary Material S10: Distribution of read lengths for the Fortymile (27673) caribou. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. In both cases, the reads are heavily skewed towards 150 bp.



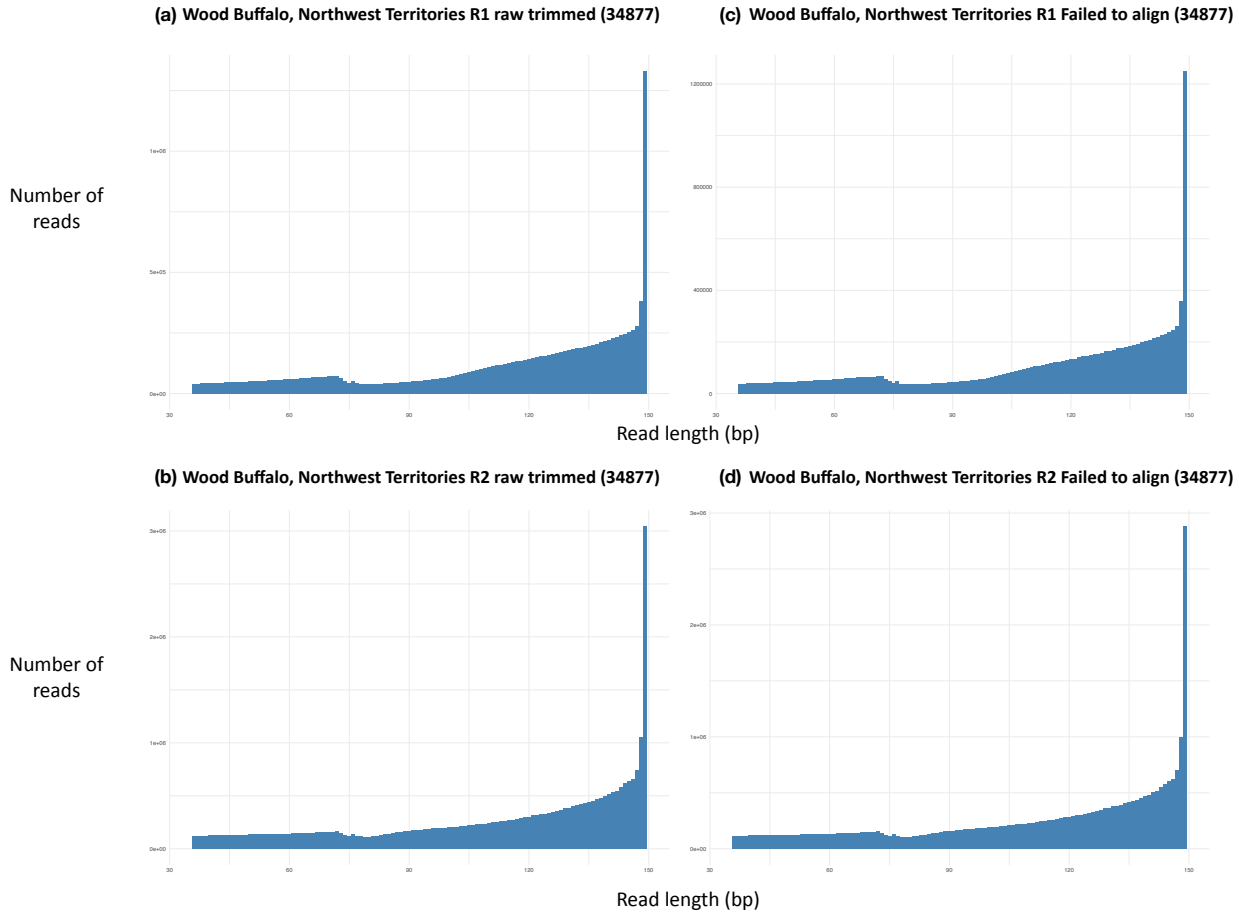
Supplementary Material S11: Distribution of read lengths for the Tay (27773) caribou. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. In both cases, the reads are heavily skewed towards 150 bp.



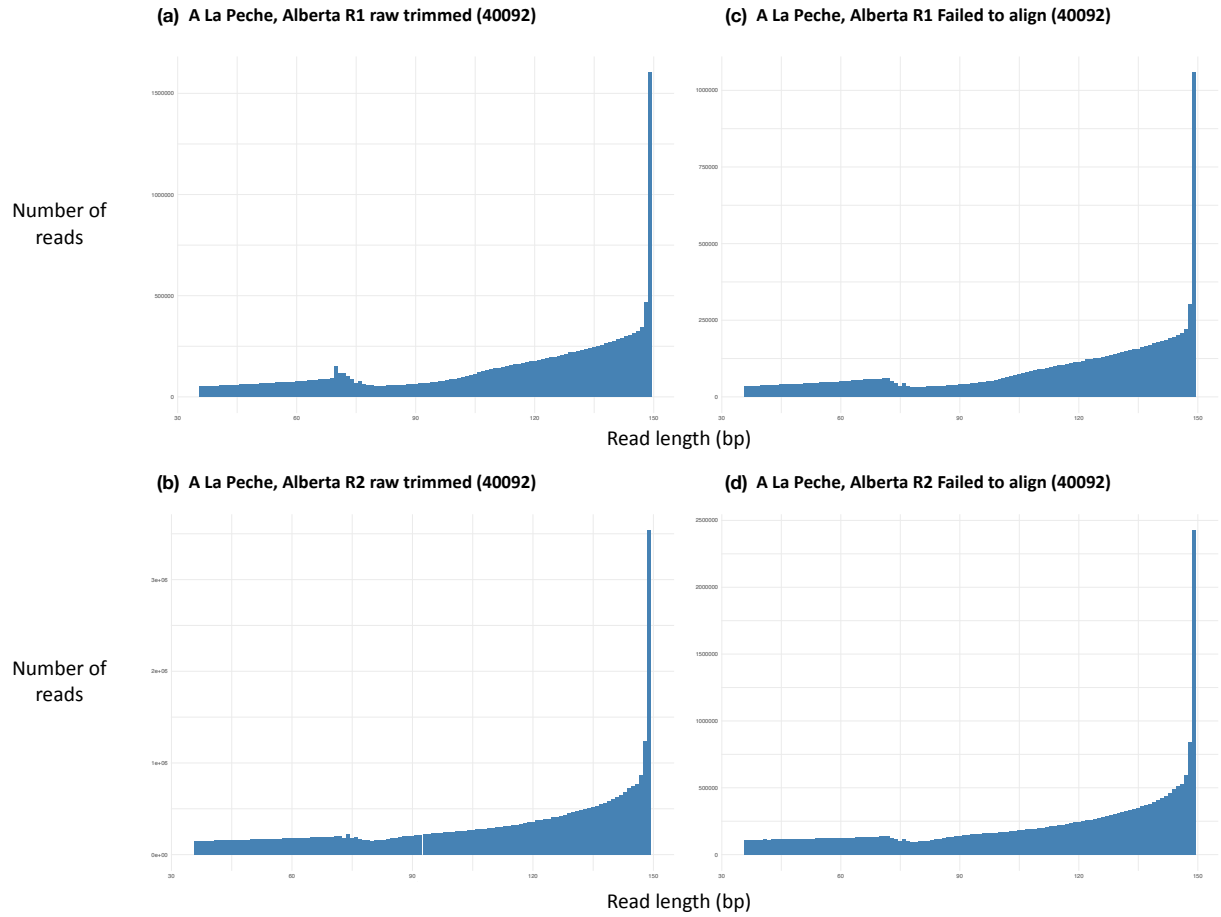
Supplementary Material S12: Distribution of read lengths for the Cold Lake (24461) caribou excluding reads at 150 and 149 bp to focus on the distribution of the short reads. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. The distribution in read length does not change between all raw reads and those which are discarded.



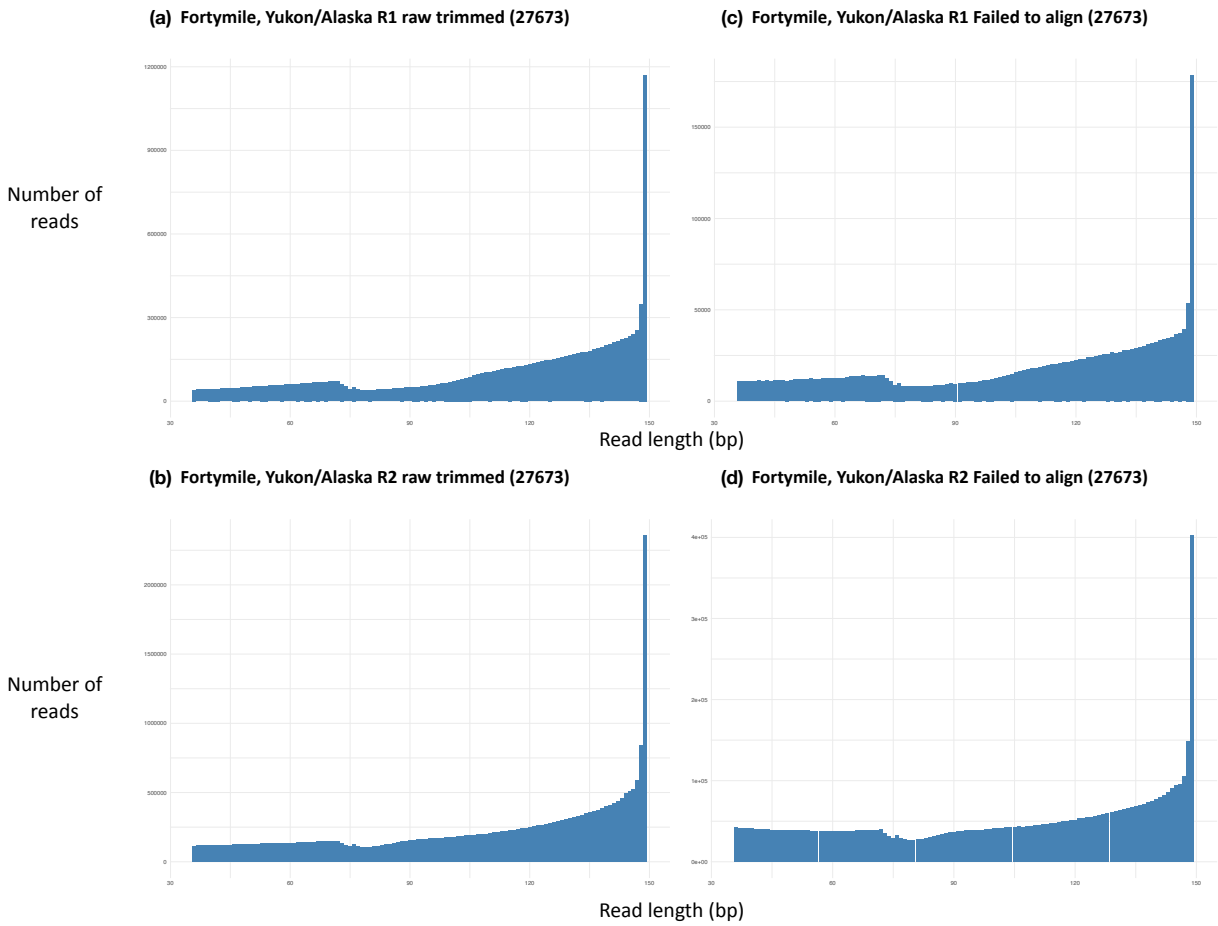
Supplementary Material S13: Distribution of read lengths for the Cold Lake (24476) caribou excluding reads at 150 and 149 bp to focus on the distribution of the short reads. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. The distribution in read length does not change between all raw reads and those which are discarded.



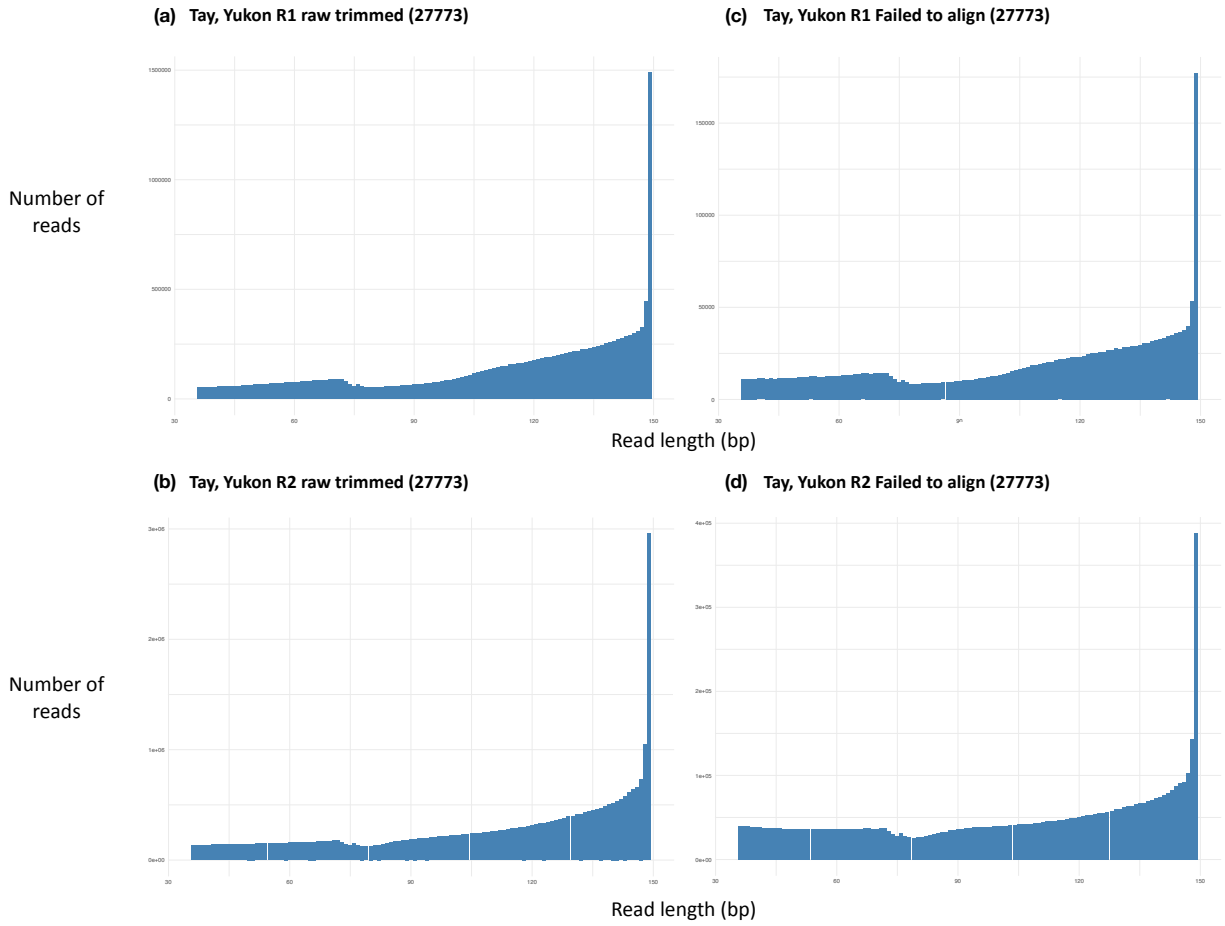
Supplementary Material S14: Distribution of read lengths for the Wood Buffalo (34877) caribou excluding reads at 150 and 149 bp to focus on the distribution of the short reads. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. The distribution in read length does not change between all raw reads and those which are discarded.



Supplementary Material S15: Distribution of read lengths for the A La Peche (40092) caribou excluding reads at 150 and 149 bp to focus on the distribution of the short reads. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. The distribution in read length does not change between all raw reads and those which are discarded.



Supplementary Material S16: Distribution of read lengths for the Fortymile (27673) caribou excluding reads at 150 and 149 bp to focus on the distribution of the short reads. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. The distribution in read length does not change between all raw reads and those which are discarded.



Supplementary Material S17: Distribution of read lengths for the Tay (27773) caribou excluding reads at 150 and 149 bp to focus on the distribution of the short reads. The plots (a) and (b) show the raw reads (after trimming adapter sequences and low quality reads), and (c) and (d) show the reads which failed to align to the reference genome. The distribution in read length does not change between all raw reads and those which are discarded.