LIBRARY STATS:

Species/Strain	Assay type	Library number	Name/Description	Indexes	Concentration (ng/µL)
Ammospermophilus harrisii	ATAC-seq	L2005	s_antelope_squirrel_Ammospermophilus_harrisii-Sample2869-	701+501	1.81
Ammospermophilus harrisii	ATAC-seq	L2006	s_antelope_squirrel_Ammospermophilus_harrisii-Sample2869-	701+502	3.46
Mustela nigripes	ATAC-seq	L2007	Black-footed_ferret_Mustela_nigripes-Sample2598-Rep1	701+503	9.58
Mustela nigripes	ATAC-seq	L2008	Black-footed_ferret_Mustela_nigripes-Sample2598-Rep2	701+505	7.36
Microtus agrestis	ATAC-seq	L2009	Field_Vole-Sample2585-Rep1	701+506	17.70
Microtus agrestis	ATAC-seq	L2010	Field_Vole-Sample2585-Rep2	701+507	18.60
Tapirus terrestris	ATAC-seq	L2011	South_American_tapir-Tapirus_terrestris-Sample2876-Rep1	702+501	0.19
Tapirus terrestris	ATAC-seq	L2012	South_American_tapir-Tapirus_terrestris-Sample2876-Rep2	702+502	16.20
Myotis yumanensis	ATAC-seq	L2013	Myotis_yumanensis_S2431_P1_7-9-19_RK-Sample2431-Rep1	702+503	2.18
Myotis yumanensis	ATAC-seq	L2014	Myotis_yumanensis_S2431_P1_7-9-19_RK-Sample2431-Rep2	702+505	6.50
Microtus montanus	ATAC-seq	L2015	Montane_Vole-Sample2587-Rep1	702+506	7.74
Microtus montanus	ATAC-seq	L2016	Montane_Vole-Sample2587-Rep2	702+507	10.20
Macropus rufogriseus	ATAC-seq	L2017	Red_necked_wallaby-Sample2873-Rep1	703+501	0.33
Macropus rufogriseus	ATAC-seq	L2018	Red_necked_wallaby-Sample2873-Rep2	703+502	10.70
Myotis evotis	ATAC-seq	L2019	Myotis_evotis_S2429_P2_7-15-19_0.5M_AO-Sample2429-Rep	703+503	3.74
Myotis evotis	ATAC-seq	L2020	Myotis_evotis_S2429_P2_7-15-19_0.5M_AO-Sample2429-Rep	703+505	6.42
Uromys anak	ATAC-seq	L2021	Giant_Naked_Tailed_Rat-Sample2588-Rep1	703+506	6.88
Uromys anak	ATAC-seq	L2022	Giant_Naked_Tailed_Rat-Sample2588-Rep2	703+507	9.52
Perodicticus potto	ATAC-seq	L2023	West_African_potto-Sample2866-Rep1	704+501	4.24
Perodicticus potto	ATAC-seq	L2024	West_African_potto-Sample2866-Rep2	704+502	1.37
Mustela erminea	ATAC-seq	L2025	Stoat_Mustela_erminea-Sample2591-Rep1	704+503	12.60
Mustela erminea	ATAC-seq	L2026	Stoat_Mustela_erminea-Sample2591-Rep2	704+505	20.00
Cricetulus griseus	ATAC-seq	L2027	Chinese_Hamster_Ovary-Sample2592-Rep1	704+506	5.94
Cricetulus griseus	ATAC-seq	L2028	Chinese_Hamster_Ovary-Sample2592-Rep2	704+507	16.70
Meriones libycus	ATAC-seq	L2029	Libyan_Jird-Sample2884-Rep1	705+501	6.20
Meriones libycus	ATAC-seq	L2030	Libyan_Jird-Sample2884-Rep2	705+502	0.25
Myodes rutilus	ATAC-seq	L2031	backed_vole_Myodes_previously_Clethrionomys_rutilus-Samp	705+503	8.76
Myodes rutilus	ATAC-seq	L2032	backed_vole_Myodes_previously_Clethrionomys_rutilus-Samp	705+505	9.94

LIBRARY STATS:

Species/Strain	Assay type	Library number	Name/Description	Indexes	Concentration (ng/µL)
Ursus americanus	ATAC-seq	L2033	American_Black_Bear-Sample2601-Rep1	705+506	4.14
Ursus americanus	ATAC-seq	L2034	American_Black_Bear-Sample2601-Rep2	705+507	1.93
Carollia perspicillata	ATAC-seq	L2035	Sebas_Short-tailed_Bat-Sample2879-Rep1	706+501	7.54
Carollia perspicillata	ATAC-seq	L2036	Sebas_Short-tailed_Bat-Sample2879-Rep2	706+502	7.30
Muntiacus reevesi	ATAC-seq	L2037	Brinkley_Chinese_muntjac_10-1-2019-Sample2603-Rep1	706+503	3.36
Muntiacus reevesi	ATAC-seq	L2038	Brinkley_Chinese_muntjac_10-1-2019-Sample2603-Rep2	706+505	3.00
Artibeus jamaicensis	ATAC-seq	L2039	Jamaican_fruit_bat-Sample2892-Rep1	707+501	0.83
Artibeus jamaicensis	ATAC-seq	L2040	Jamaican_fruit_bat-Sample2892-Rep2	707+502	4.36
Muntiacus muntjak	ATAC-seq	L2041	JCRB9100_Indian_Muntjac_4_10-4-2019-Sample2604-Rep1	707+503	1.22
Muntiacus muntjak	ATAC-seq	L2042	JCRB9100_Indian_Muntjac_4_10-4-2019-Sample2604-Rep2	707+505	3.64
Ovis canadensis nelsoni	ATAC-seq	L2043	Desert_bighorned_sheep-Sample2891-Rep1	708+501	2.94
Ovis canadensis nelsoni	ATAC-seq	L2044	Desert_bighorned_sheep-Sample2891-Rep2	708+502	7.54
Meriones meridianus	ATAC-seq	L2045	Midday_Gerbil-Sample2582-Rep1	708+503	18.40
Meriones meridianus	ATAC-seq	L2046	Midday_Gerbil-Sample2582-Rep2	708+505	11.90
Eumops auripendulus	ATAC-seq	L2047	Black_bonneted_bat_Shaws_Mastiff_Bat-Sample2880-Rep1	709+501	7.62
Eumops auripendulus	ATAC-seq	L2048	Black_bonneted_bat_Shaws_Mastiff_Bat-Sample2880-Rep2	709+502	12.80
Bassariscus sumichrasti	ATAC-seq	L2049	Cacomistle-Sample2583-Rep1	709+503	2.76
Bassariscus sumichrasti	ATAC-seq	L2050	Cacomistle-Sample2583-Rep2	709+505	15.40
Eulemur macaco	ATAC-seq	L2051	Black_lemur_Eulemur_macaco_rufus-Sample2600-Rep1	710+501	7.90
Eulemur macaco	ATAC-seq	L2052	Black_lemur_Eulemur_macaco_rufus-Sample2600-Rep2	710+502	4.26
Neotoma phenax	ATAC-seq	L2053	Sonoran_Woodrat-Sample2584-Rep1	710+503	5.50
Neotoma phenax	ATAC-seq	L2054	Sonoran_Woodrat-Sample2584-Rep2	710+505	6.56

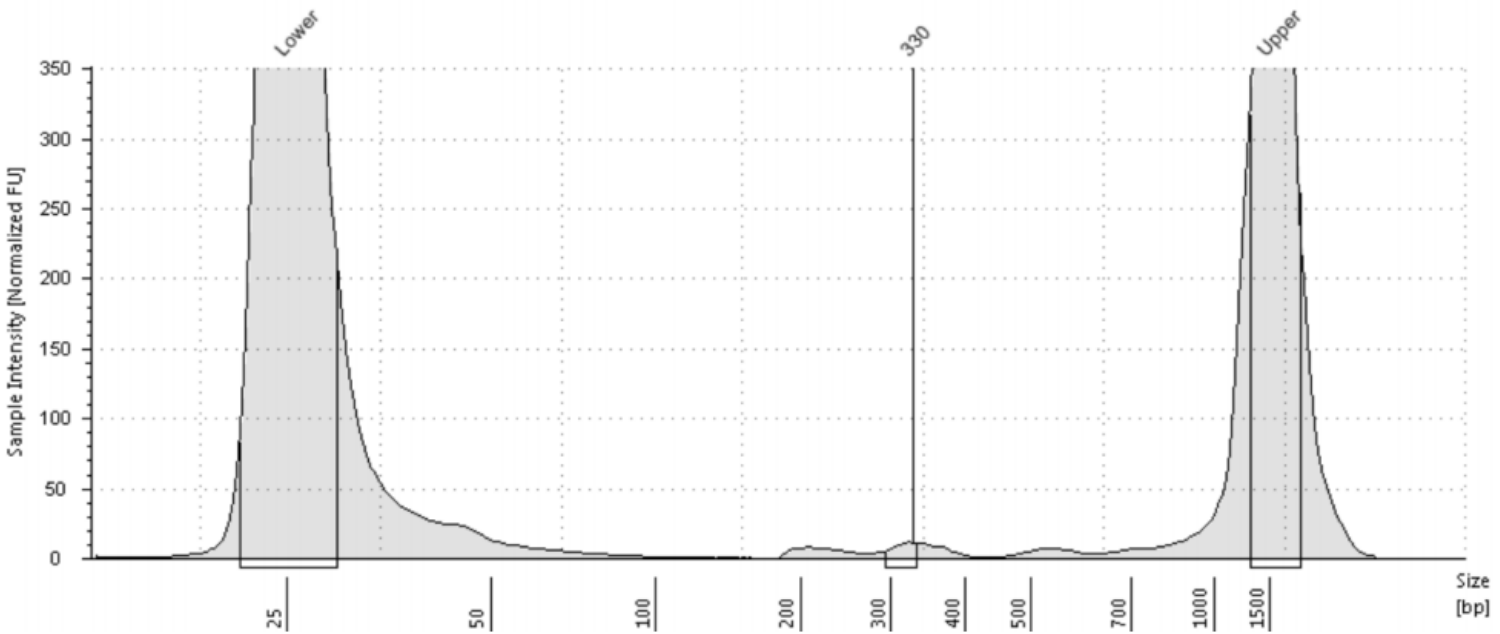
CELL VIABILITY

cells	1	2	3	4	5	6	7	8	9	10	11	12
A	2869 - 0.6m 25%	2876- 0.5m 87	2873- 0.48m 8	2866- 0.5m 86	2884- 0.5m 92%	2879- 0.4m 82%	2892- 0.78m 90	2891- 0.57m 78%	2880- 0.25m 83	2600- 0.48m 90%		
B	2869- 100ul	2876 - 115ul	2873 - 127ul	2866- 120ul	2884- 117ul	2879- 150ul	2892 - 79ul	2891- 106ul	2880-240ul	2600 -125ul		
C	2598- 053m 92%	2431- 0.43m 8	2429- 0.48m 8	2591- 0.39m 8	2596-0.4m 60%	2603-0.79m 78	2604- 1.1m 37%	2582- 1.23m 90%	2583- 0.52m 82	2584- 0.35m 67%		
D	2598-114ul	2431-140ul	2429-127ul	2591-155ul	2596-150ul	2603-77ul	2604-500ul	2582-500ul	2583-115ul	2584-171ul		
E	2585-0.4m 94%	2587- 0.4m 80	2588-0.34m 78	2592- 0.65m 7	2601 - 0.93m 66%							
F	2585-150ul	2587-150ul	2588- 178ul	2592- 94ul	2601- 65ul							
G												
H												

TAPE STATION FRAGMENT DISTRIBUTION

Should be OK

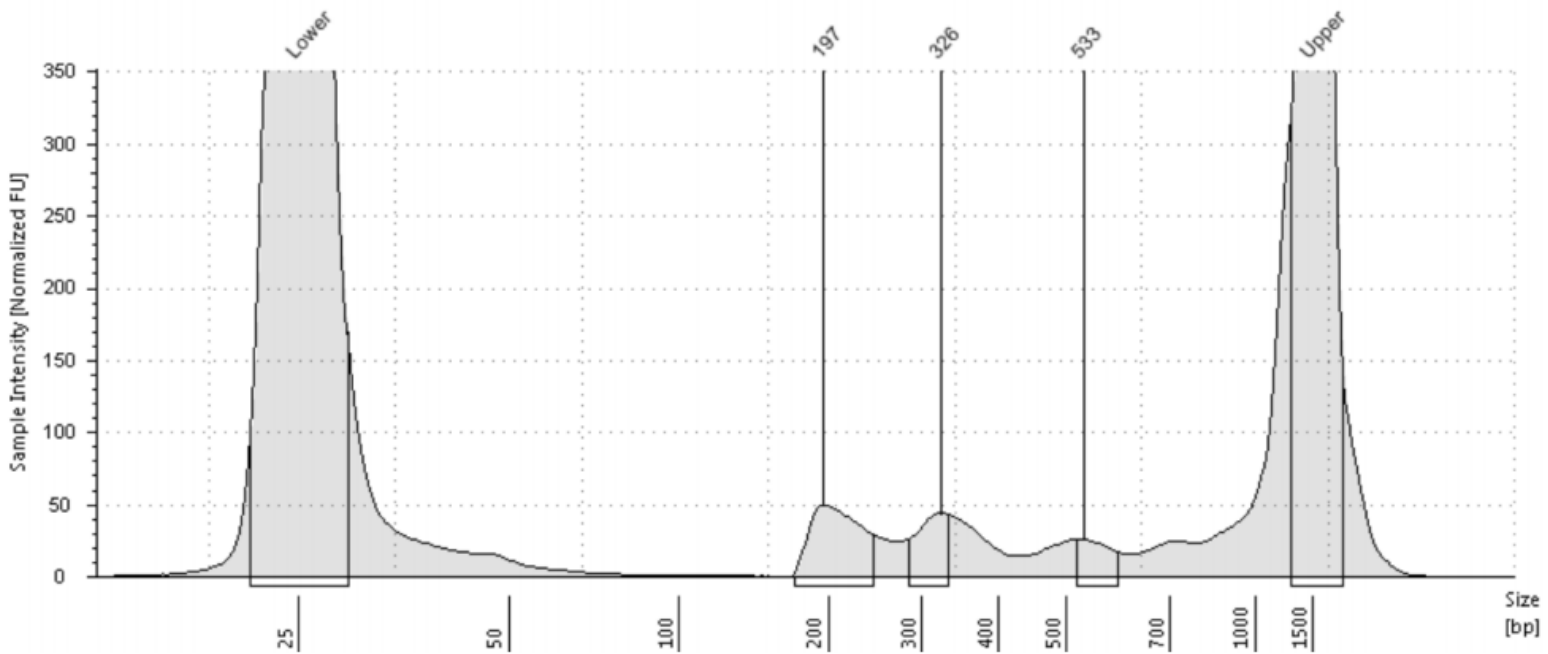
A1: L2005



TAPE STATION FRAGMENT DISTRIBUTION

Should be OK

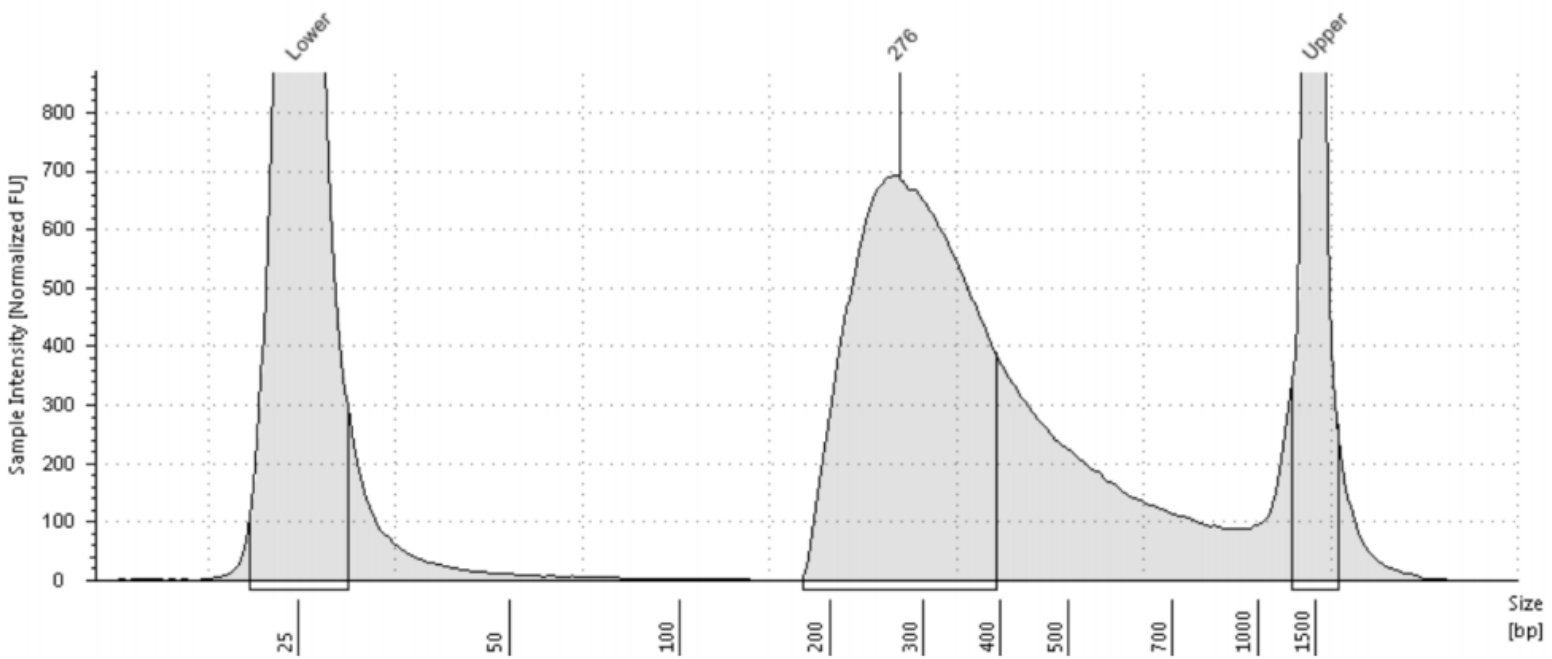
B1: L2006



TAPE STATION FRAGMENT DISTRIBUTION

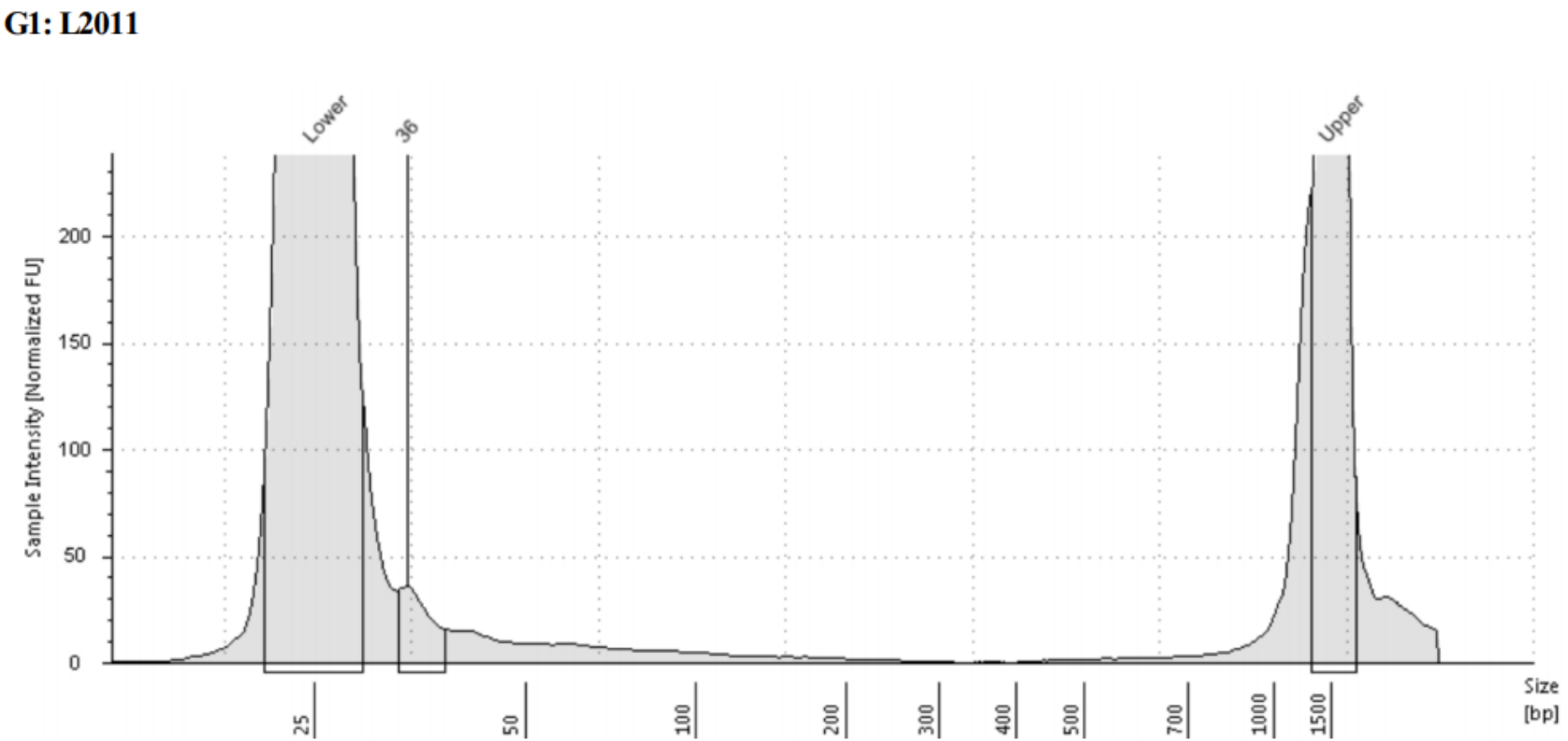
This one is potentially bad

E1: L2009



TAPE STATION FRAGMENT DISTRIBUTION

This one probably has too little DNA

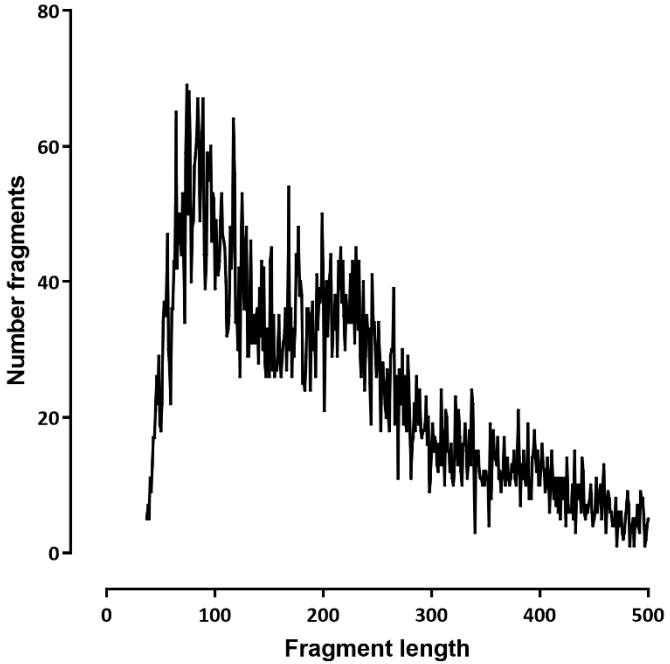


MAPPING STATS

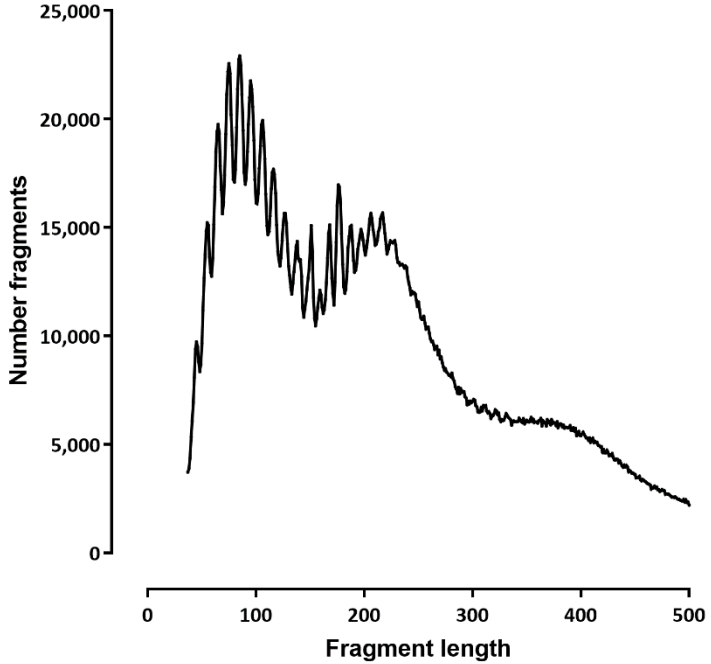
Species	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio	MACS default peaks
Tapirus terrestris	**2x36**	L2011-South_American_tapir-Tapirus_terrestris-Sample2876-Rep1	15,662	23,488		0.98	2,168	0.08	23,170		0
Tapirus terrestris	**2x36**	L2012-South_American_tapir-Tapirus_terrestris-Sample2876-Rep2	6,600,463	9,968,534		0.90	854,662	0.08	9,610,716		45,673
Cricetulus griseus	**2x36**	L2027-Chinese_Hamster_Ovary-Sample2592-Rep1	56,606,065	21,268,679		0.86	2,653,542	0.11	19,720,559		46,834
Cricetulus griseus	**2x36**	L2028-Chinese_Hamster_Ovary-Sample2592-Rep2	39,314,150	7,726,120		0.93	1,314,174	0.15	7,500,608		31,171
Ursus americanus	**2x36**	L2033-American_Black_Bear-Sample2601-Rep1	10,184,712	13,380,064		0.90	1,200,364	0.08	12,589,264		56,237
Ursus americanus	**2x36**	L2034-American_Black_Bear-Sample2601-Rep2	16,649,506	22,321,576		0.90	1,187,528	0.05	20,763,412		66,892
Muntiacus reevesi	**2x36**	L2037-Brinkley_Chinese_muntjac_10-1-2019-Sample2603	7,993,261	7,848,000		0.85	1,207,538	0.13	7,059,064		33,558
Muntiacus reevesi	**2x36**	L2038-Brinkley_Chinese_muntjac_10-1-2019-Sample2603	9,190,403	9,419,274		0.88	1,134,594	0.11	8,542,348		31,245

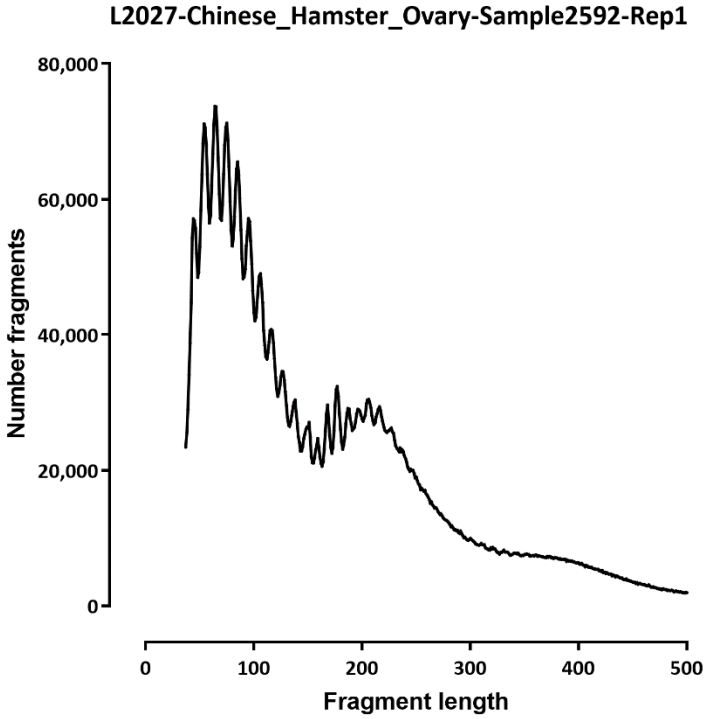
FRAGMENT LENGTH DISTRIBUTION

L2011-South_American_tapir-Tapirus_terrestris-Sample2876-Rep1



L2012-South_American_tapir-Tapirus_terrestris-Sample2876-Rep2

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20,000
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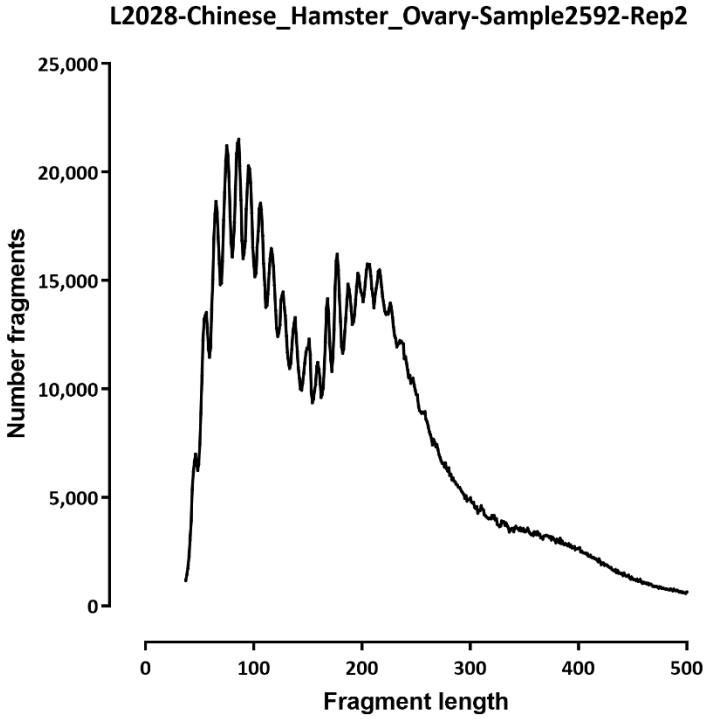
200
300
400
500
Fragment length


L2028-Chinese_Hamster_Ovary-Sample2592-Rep2
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5,000
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Number fragments
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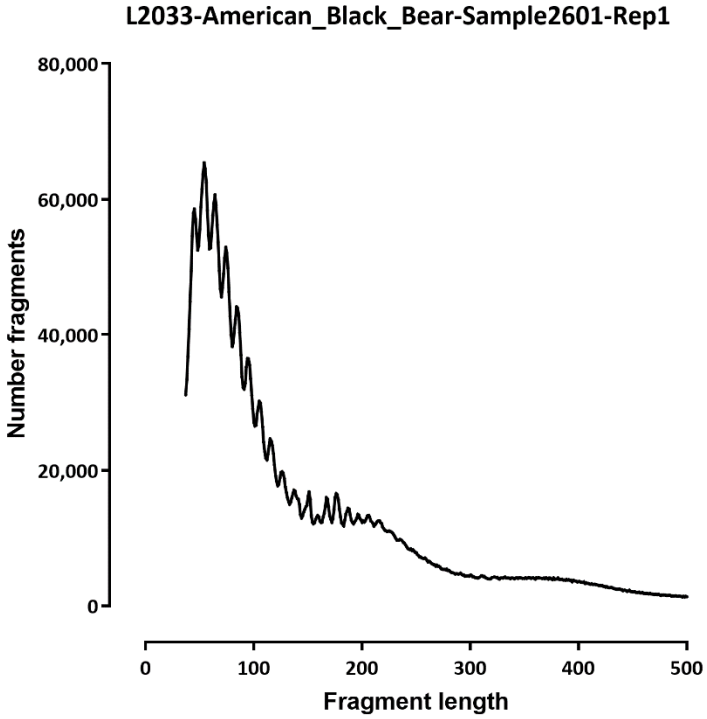
100
200
300
400
500
Fragment length


L2033-American_Black_Bear-Sample2601-Rep1
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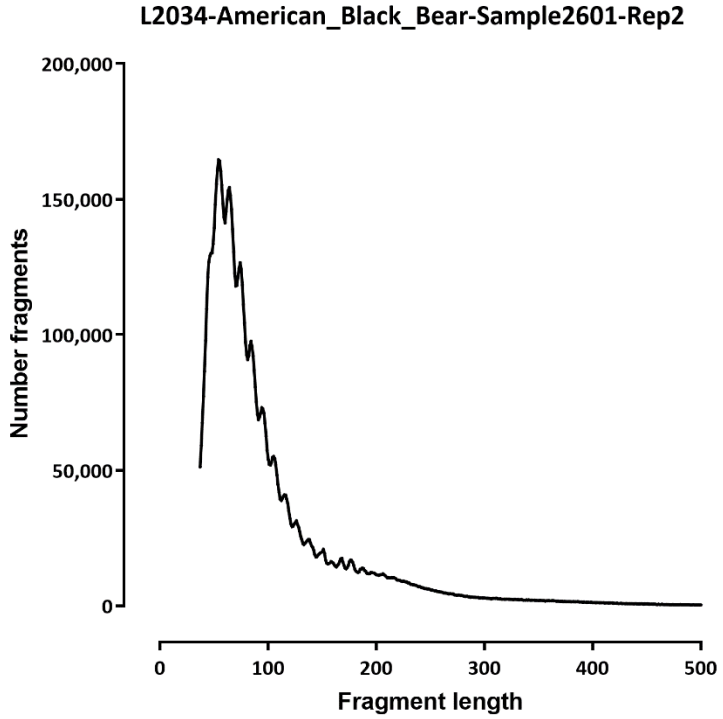
300
400
500
Fragment length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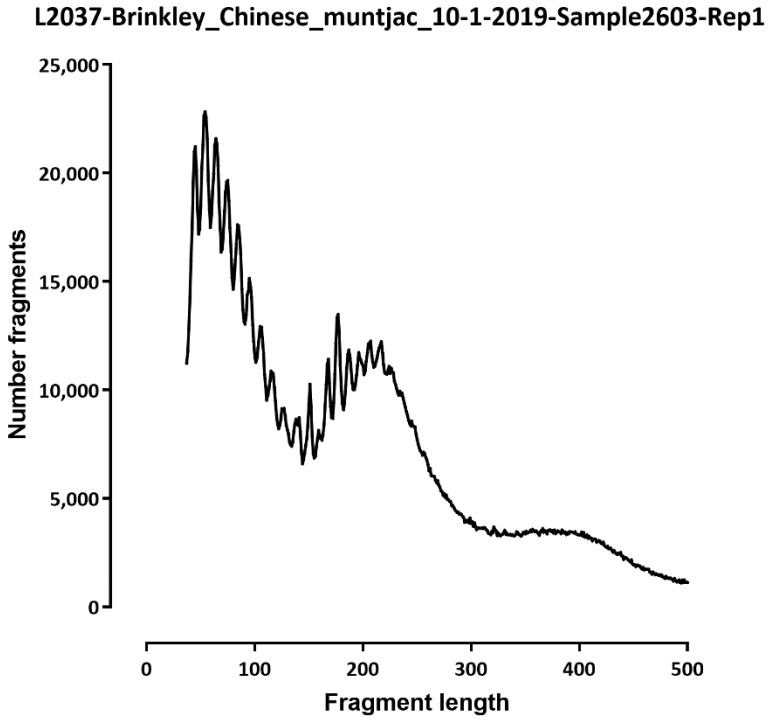
300
400
500
Fragment length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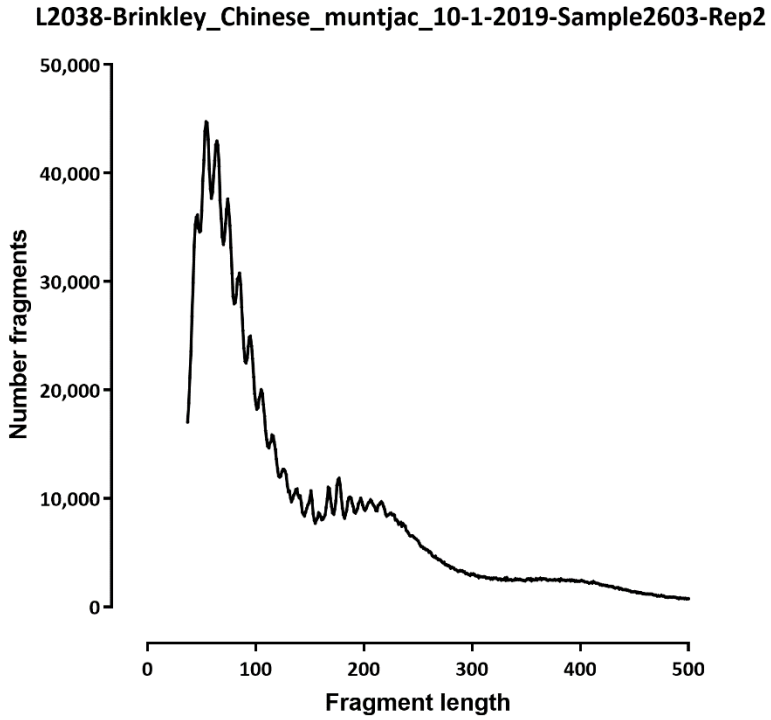
Fragment length


L2038-Brinkley_Chinese_muntjac_10-1-2019-Sample2603-Rep2
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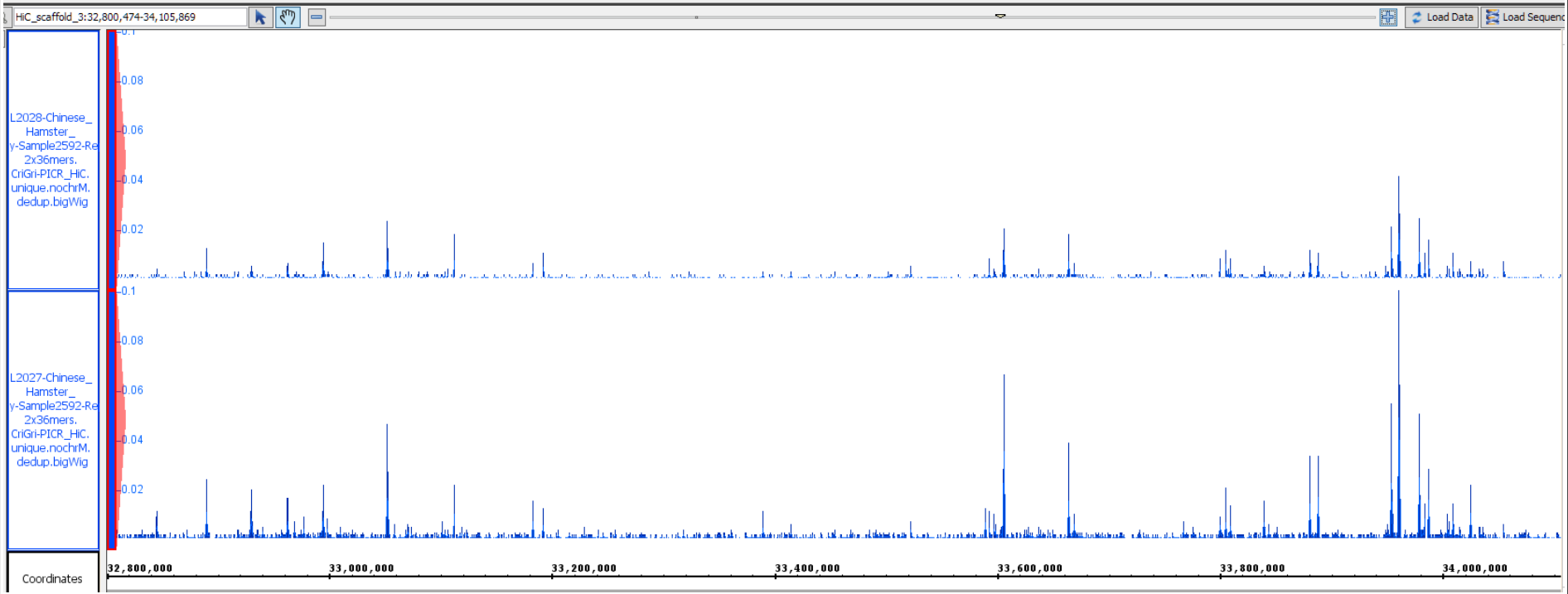
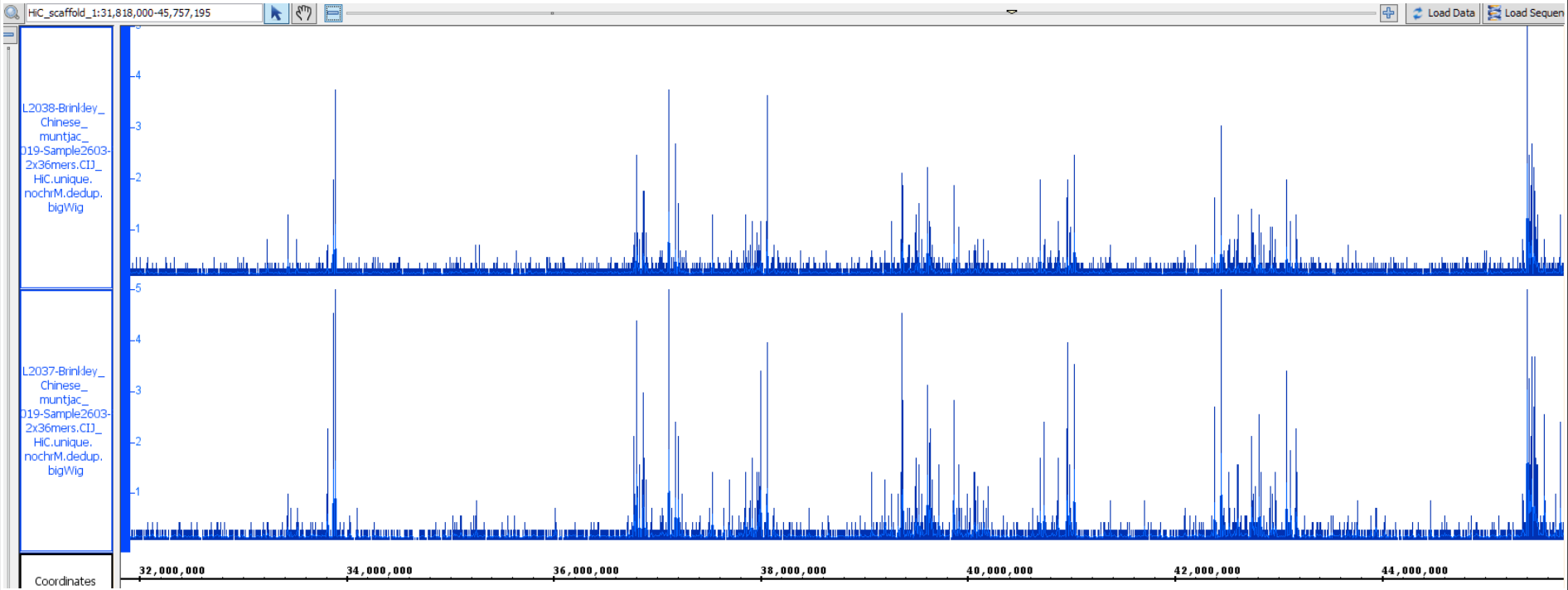
300
400
500
Fragment length

BROWSER SNAPSHOTS

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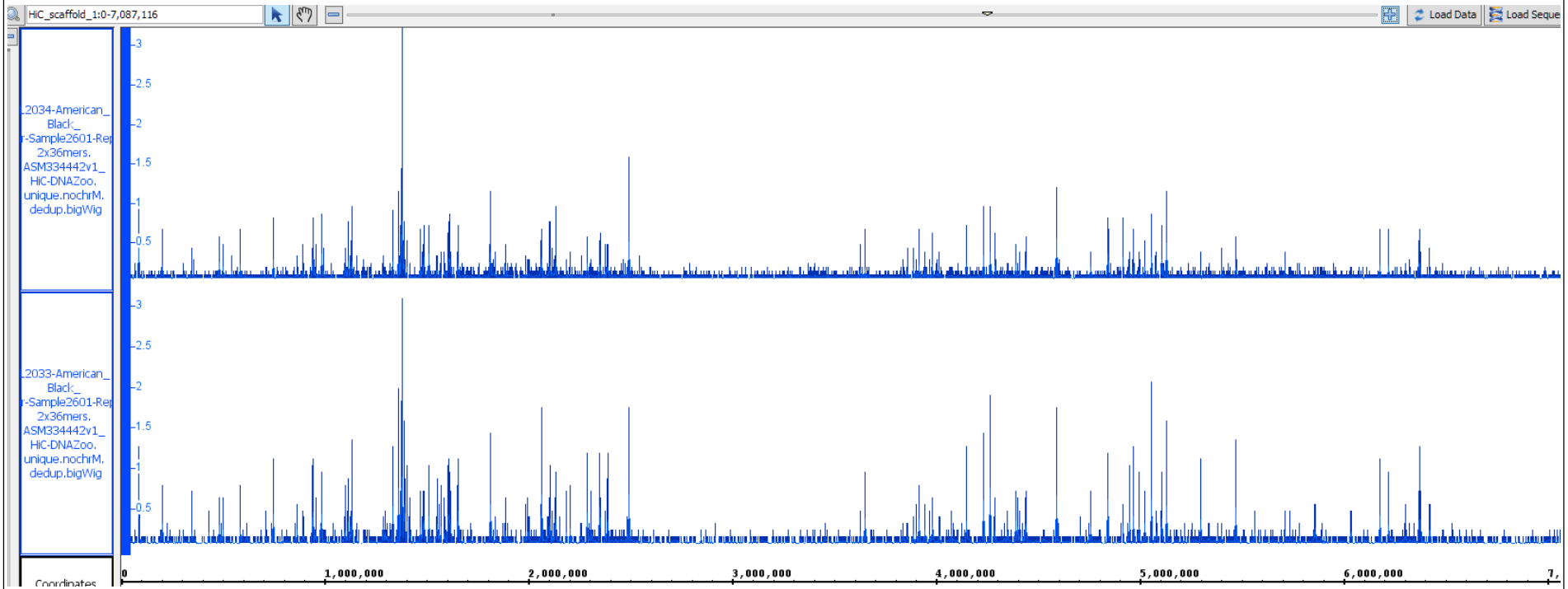
HiC_scaffold_1:0-7,087,116
Load Data
Load Seque
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Black_
r-Sample2601-Rep
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ASM334442v1_
HiC-DNAZoo.
unique.nochrM.
dedup.bigWig
L2033-American_
Black_
r-Sample2601-Rep
2x36mers.
ASM334442v1_
HiC-DNAZoo.
unique.nochrM.
dedup.bigWig
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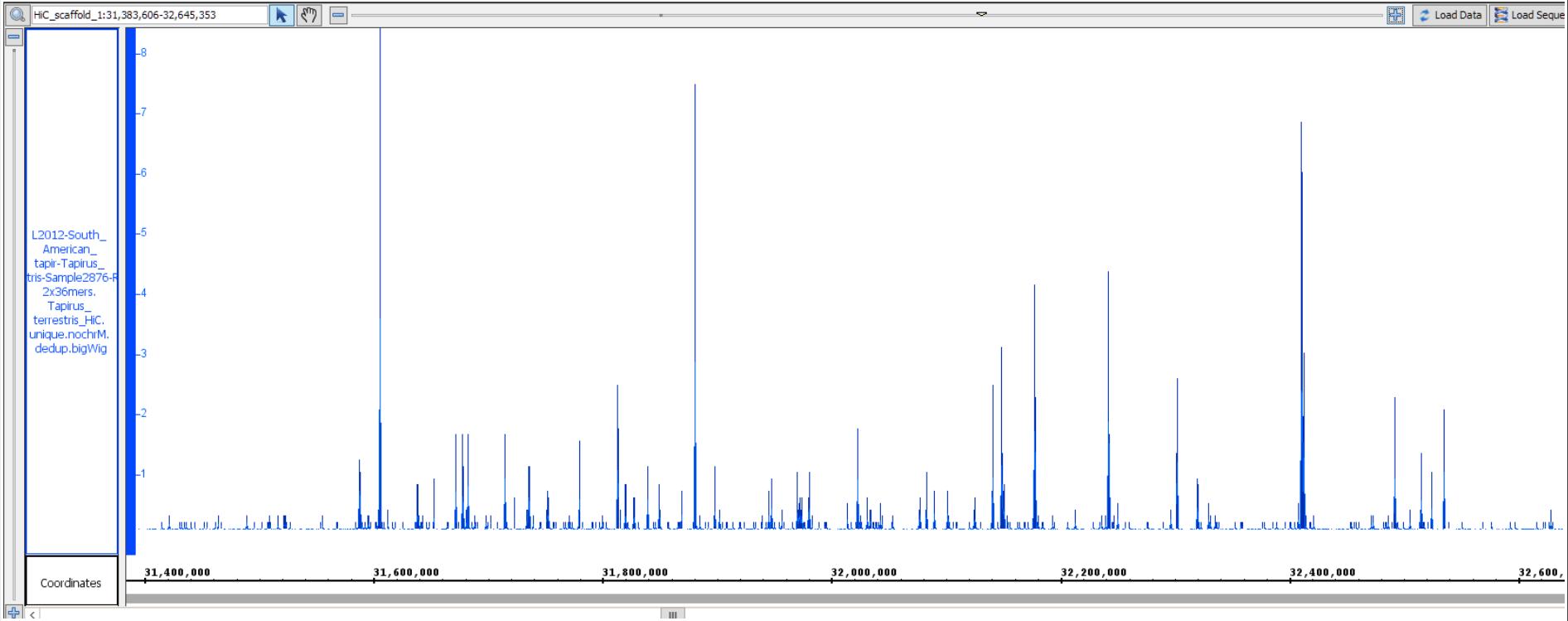
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7
6
5
4
3
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