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Supplementary Information

Fig. S1 Length distribution of CCS reads.

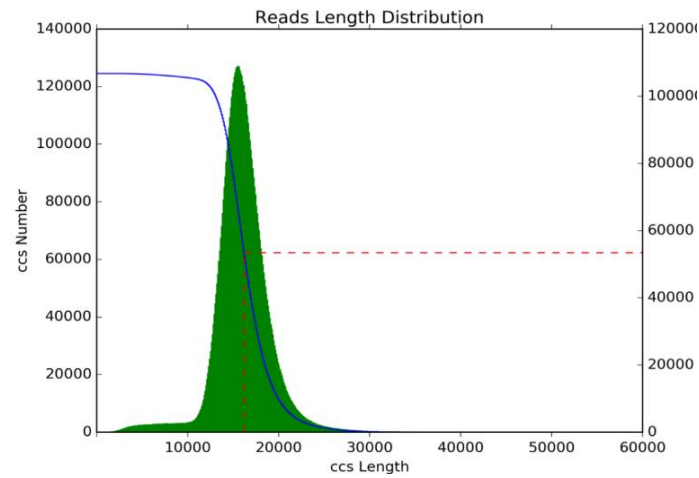


Fig. S2 BUSCO plot of the several sheep genomes. C: Complete BUSCOs; S: Complete and single-copy BUSCOs; D: Complete and duplicated BUSCOs; F: Fragmented BUSCOs; M: Missing BUSCOs; n: Total BUSCO groups searched (BBS: Butuo Black sheep; ARS-UI_Ramb_v2.0: Rambouillet; EFS2: EFS v2.0 ; GD: Guide black fur sheep).

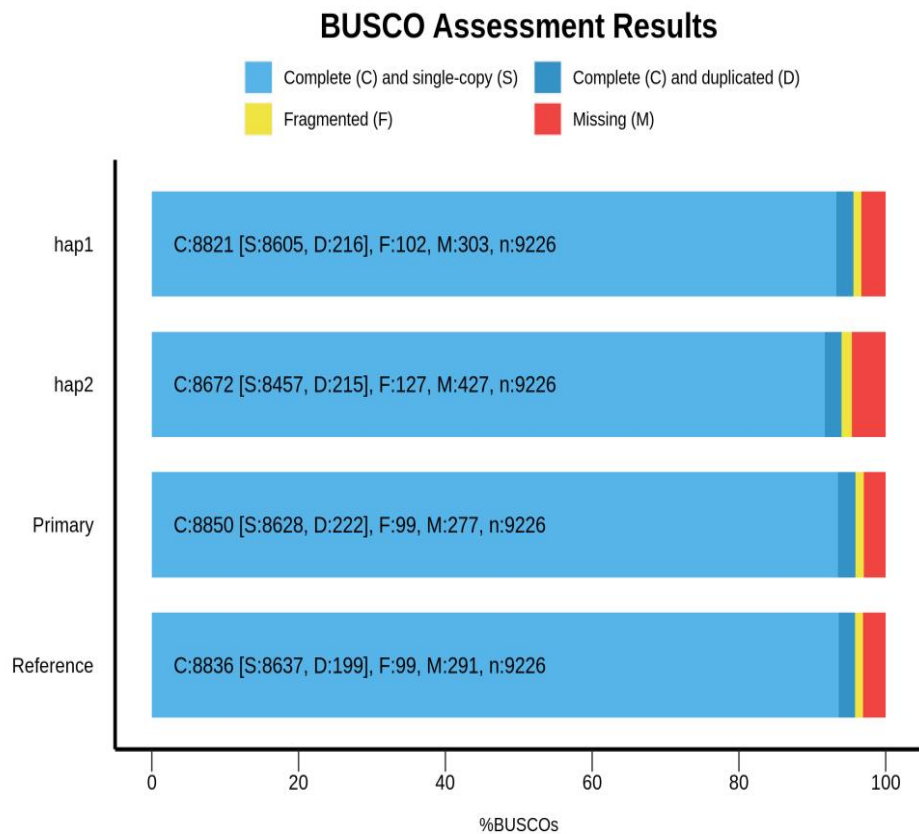


Fig. S3 A circos plot of 27 chromosomes of Butuo Black Sheep genome assembly. (I) chromosomes of the Butuo Black Sheep genome; (II) mRNA density; (III) exon density; (IV) CDS density; (V) gene density; (VI) GC density; (II -VI) were drawn in 1 Mb.

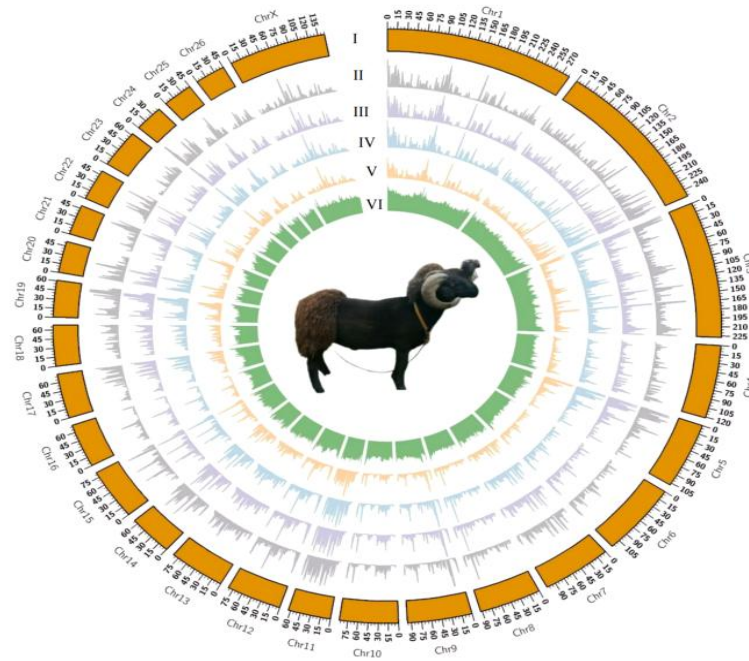


Fig. S4 Comparison of four genomes (BBS: Butuo Black sheep; ARS-UI_Ramb_v2.0: Rambouillet; EFS2: EFS v2.0 ; GD: Guide black fur sheep). a) BUSCO plot of the several sheep genomes. b) Compleasm plot of the several sheep genomes. c) The lengths of genomic chromosomes of the four sheep assemblies.

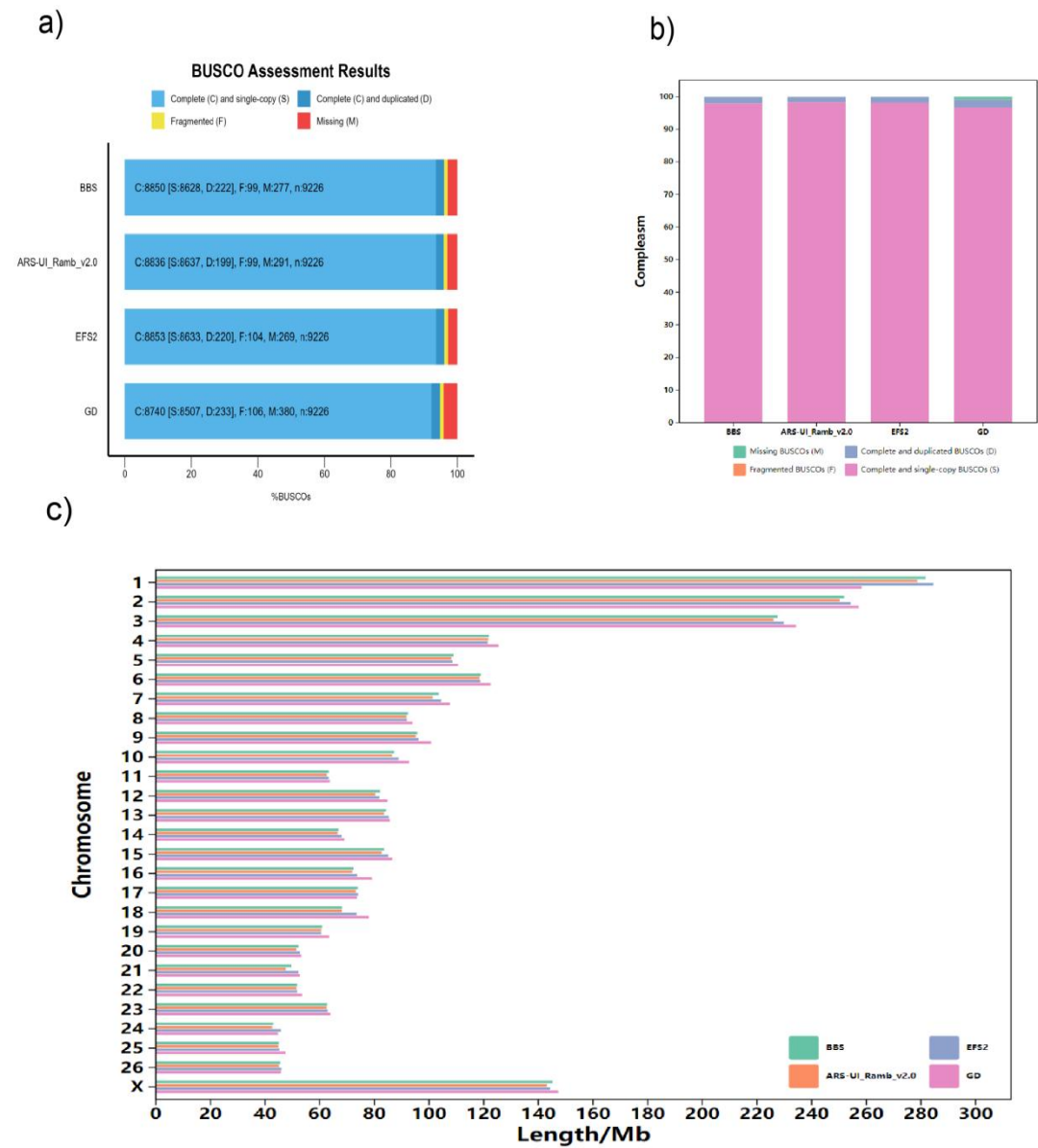


Fig. S5 Boxplot presentation of 50 Butuo Black sheep sequencing yield, Q30 and average depth.

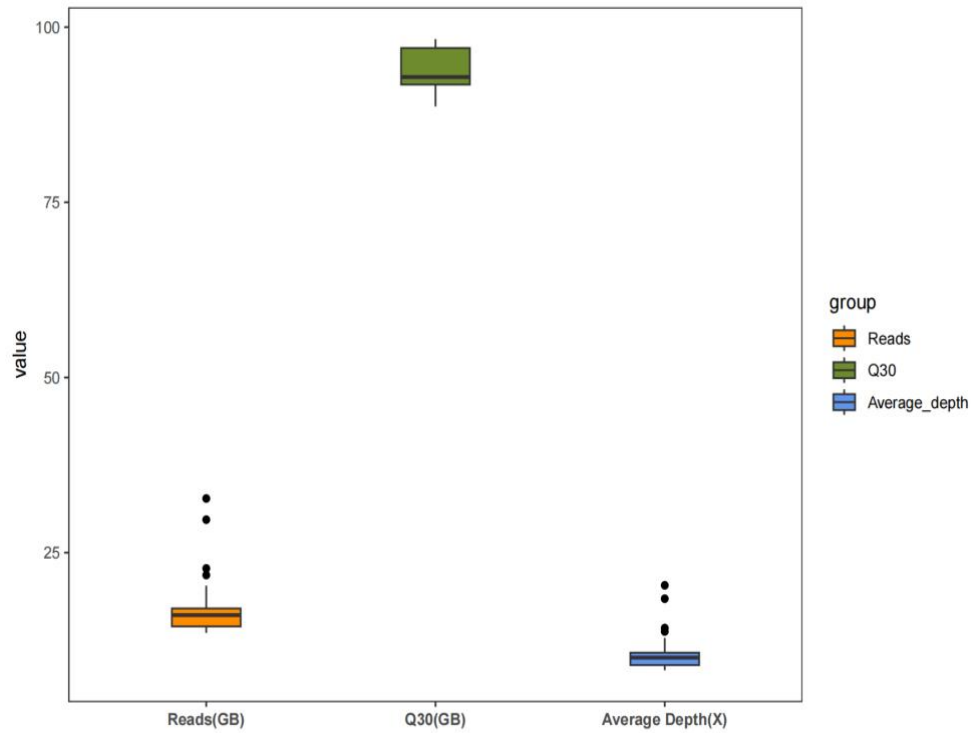


Table S1 Statistics of sequencing data.

Platform	Reads Number	Total bases(bp)	Average length(bp)	N50 length(bp)	Genome depth	GC (%)
PacBio CCS data	6,676,985	106,779,617,087	15,992	16,238	40.68	42.86

Table S2 Comparison of chromosome lengths, gaps and telomere lengths between the BBS and ARS-UI_Ramb_v2.0 genome assemblies.

Chr	ARS-UI_Ramb_v2.0			Assembly		
	Ungapped length(bp)	Gap number	Telomere length(bp)	Ungapped length(bp)	Gap number	Telomere length(bp)
1	278612202	10	174	281641059	8	0
2	250198558	7	34566	251916033	2	3120
3	226087100	4	14730	227516011	2	4228
4	121577099	2	36	121915237	1	0
5	108218288	5	4584	108941064	1	0
6	118468697	2	78	118919893	1	190198
7	101272418	4	18948	103482995	0	0
8	91791871	2	15618	92258836	2	1907
9	95178658	2	5910	95669460	3	3301
10	86457471	4	5946	87269023	17	0
11	62546497	2	10998	63231295	2	1042
12	80403155	1	14898	82049262	7	840
13	83510835	2	24096	84236294	3	2955
14	66515157	3	20664	66882886	0	1620
15	82536637	4	13830	83550907	0	0
16	71896864	1	24	72269533	0	0
17	73166223	2	1422	73936024	1	6602
18	67983460	2	14694	68157210	2	1256
19	60560550	2	72	60857095	1	782
20	51450217	3	16044	52244338	1	0
21	47512694	3	25416	49611285	1	1694
22	51510491	4	22392	51712427	0	2511
23	62439644	2	18936	62714727	0	78
24	42630236	0	120	42954610	2	0
25	44863754	0	24	45025596	1	0
26	45051859	1	8160	45450391	1	0
X	143168225	7	92316	145271243	10	2340
Sum	2628097205	81	384696	263967783 4	69	224474

Table S3 Genome continuity, Base accuracy and Transposable elements (TEs) in the assembled four sheep assembly.

	BBS		ARS-UI_Ramb_v2.0 (GCF_016772045.1)		EFS2 (GCA_033439445.1)		GD (GCA_040259355.1)	
Data	HiFi		Illumina, Pacific Biosciences, Hi-C, Oxford Nanopore		PacBio HiFi, ONT, Hi-C		PacBio Hifi, Hi-C, Illumina	
Long reads coverage	40.68×		75×		49×		98×	
Genome size	2,639,684,734		2,615,649,360		2,726,314,016		2,695,369,666	
Scaffold N50	92.26 Mb		101.3 Mb		104.1 Mb		100.77 Mb	
Scaffold L50	10		8		9		9	
Contig N50	71.45 Mb		43.2 Mb		104.1 Mb		19.22 Mb	
Contig L50	14		24		9		42	
GC percent	43.83		42		44		42.5	
QV	68.3		44.77		69.1		68.7	
DNA	57618268	2.18	57458680	2.20	57771604	2.12	57519235	2.13
LINE	750099235	28.42	745615853	28.51	753361801	27.63	751779737	27.89
SINE	298016237	11.29	296956109	11.35	298959651	10.97	298018944	11.06
LTR	148574225	5.63	126463989	4.83	144217256	5.29	127682172	4.74
Other	0	0.00	0	0.00	0	0.00	0	0.00
Unknown	470951	0.01	484282	0.02	469695	0.02	474805	0.02
Total	1233369485	46.72	1226978913	46.91	1238593904	45.43	1235474893	45.84

Table S4 Statistics of whole-genome sequencing data.

sample	Total number of reads (million)	Total bases (bp)	Q20 (%)	Q30 (%)	GC (%)	Primary mapping rate	Mapping rate	Average Depth	Duplicate (%)
BTB01	229.78	34,355,604,676	96.97	92.09	42.57	99.87	99.93	10.72	12.45
BTB02	209	31,234,851,326	96.7	93.73	42.34	99.86	99.92	9.67	12.75
BTB03	187.68	28,057,742,525	96.3	92.03	42.6	99.86	99.92	8.82	12.35
BTB04	214.17	32,011,563,049	96.69	92.75	42.71	99.88	99.93	9.97	12.6
BTB05	238.03	35,599,835,264	97.27	90.9	42.66	99.87	99.93	11.25	13.1
BTB06	201.96	30,181,514,962	96.56	92.16	42.6	99.86	99.92	9.25	13.05
BTB07	192.79	28,798,134,932	96.41	91.78	42.61	99.87	99.92	8.95	12.7
BTB08	189.15	28,221,755,097	96.36	92.84	42.52	99.87	99.93	8.69	12.5
BTB09	291.89	43,597,105,088	98.59	93.28	42.82	99.91	99.94	13.74	14.1
BTB10	232.77	34,800,769,749	96.57	93.78	42.62	99.86	99.92	10.99	13.3
BTB11	201.38	30,105,491,062	96.27	90.66	42.73	99.86	99.92	9.32	13.55
BTB12	183.88	27,483,616,741	96.19	93.56	42.36	99.86	99.92	8.59	11.9
BTB13	189.61	28,338,198,013	96.49	91.81	42.93	99.85	99.91	8.75	14.25
BTB14	212.48	31,733,912,266	96.79	91.73	42.35	99.86	99.92	9.95	12.25
BTB15	228.25	34,104,283,892	96.9	90.73	42.84	99.88	99.93	10.73	13.4
BTB16	224.37	33,521,823,727	96.6	92.63	42.41	99.87	99.92	10.46	12.05
BTB17	188.29	28,141,526,384	95.94	96.49	42.55	99.86	99.92	8.80	13.05
BTB18	231.33	34,568,295,898	96.83	95.95	42.57	99.87	99.92	10.85	12.85
BTB19	197.4	29,495,112,022	95.96	91.28	42.55	99.85	99.91	9.21	12.55
BTB20	208.61	31,163,423,344	96.37	92.8	42.36	99.86	99.92	9.62	13.7
BTB21	397.71	59,420,440,451	98.39	91.06	42.84	99.9	99.94	18.42	15.7
BTB22	438.13	65,461,622,270	98.56	91.84	42.32	99.91	99.94	20.34	14.6
BTB23	193.68	28,942,753,940	96.04	90.29	42.77	99.87	99.92	8.91	13.55
BTB24	195.4	29,177,488,760	96.57	92.27	42.52	99.86	99.92	9.00	13.2
BTB25	195.48	29,205,361,600	95.7	91.94	42.51	99.86	99.92	9.12	12.75
BTB26	304.47	45,498,667,676	97.97	91.88	42.21	99.9	99.94	14.24	14.75
BTB27	182.05	27,208,982,393	95.83	91.28	42.74	99.86	99.92	8.50	12.8
BTB28	193.58	28,939,990,793	96.22	93.86	42.78	99.86	99.92	9.05	13.15
BTB29	222.73	33,279,759,098	96.79	93.05	42.61	99.87	99.93	10.38	12.85
BTB30	271.48	40,581,529,780	97.1	92.26	42.5	99.89	99.93	12.83	13.5
BTB31	245.94	36,744,694,969	97.2	91.15	42.42	99.88	99.93	11.52	13.15
BTB32	228.56	34,079,021,502	96.84	93.07	42.36	99.88	99.93	10.14	13.1
BTB33	200.31	29,895,223,057	95.78	90.05	42.53	99.86	99.92	8.95	13.75
BTB34	192.98	28,830,296,379	96.24	91.43	42.66	99.86	99.92	8.94	12.55
BTB35	214.11	31,963,032,328	96.32	91.94	42.83	99.85	99.91	9.41	13.65
BTB36	181.9	27,234,204,731	99.24	93.29	42.38	99.9	99.94	8.58	14.1
BTB37	180.88	27,072,474,856	99.38	89.2	42.37	99.91	99.95	8.21	14.7
BTB38	226.15	33,849,284,395	99.12	92.49	42.21	99.91	99.94	10.58	13.75
BTB39	186.41	27,912,894,273	99.13	91.54	42.35	99.9	99.94	8.87	14.2

BTB40	216.07	32,338,904,403	99.24	91.78	42.21	99.91	99.95	10.13	12.85
BTB41	222.04	33,227,287,491	99.35	95.71	42.62	99.92	99.95	10.29	12.4
BTB42	223.91	33,505,586,121	99.25	95.83	42.67	99.87	99.90	10.31	13.7
BTB43	227.11	33,997,936,851	99.15	95.9	42.38	99.9	99.94	10.74	13.25
BTB44	219.01	32,777,847,641	99.19	96.24	42.2	99.9	99.94	10.33	13.45
BTB45	226.46	33,895,714,153	99.19	89.73	42.28	99.91	99.94	10.59	13.65
BTB46	226.23	33,864,055,957	99.12	92.21	42.4	99.9	99.94	10.85	12.8
BTB47	218.01	32,625,462,093	99.28	91.98	42.19	99.91	99.94	10.07	12.6
BTB48	201.91	30,228,192,334	99.21	92.27	42.07	99.91	99.94	9.42	15.7
BTB49	216.42	32,394,317,603	99.26	88.88	42.32	99.91	99.94	10.24	13.05
BTB50	252.1	37,376,568,495	99.37	91.63	42.27	99.92	99.95	10.65	13.9
