

1 **Supplementary Figure and Tables**

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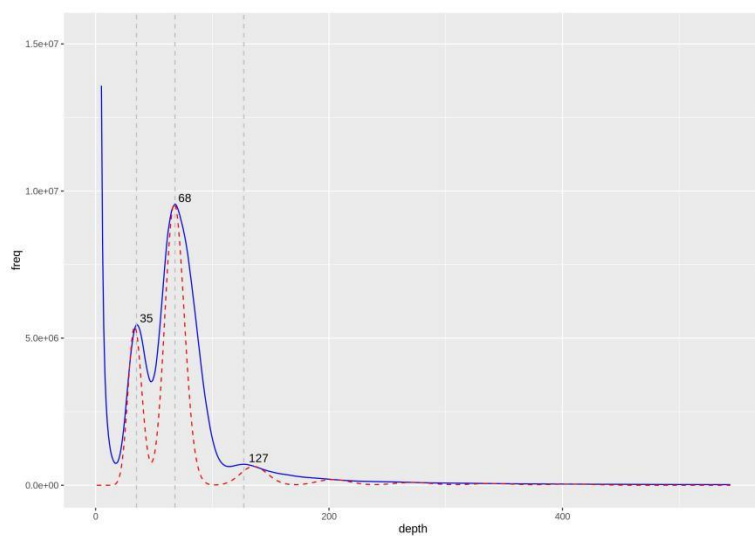
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24		
25	Supplementary Figure 1.	3
26	Supplementary Table 1.	4
27	Supplementary Table 2.	4
28	Supplementary Table 3.	4
29	Supplementary Table 4.	4
30	Supplementary Table 5.	5
31	Supplementary Table 6.	6
32	Supplementary Table 7.	6
33		

Table of Contents

34



35 **Supplementary Figure 1.** The depth-distribution of 19-mers.

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63 **Supplementary Table 1.** WGS-HiFi sequencing statistics.

Total bases (bp)	GC content	A (bp)		T (bp)		G (bp)		C (bp)		
83,637,081,877	37.41(%)	26,133,549,891 (31.25 %)		26,219,012,090 (31.35 %)		15,546,212,226 (18.59 %)		15,738,307,670 (18.82%)		
Total reads	Max. (bp)	Mean (bp)	N10 (bp)	N50 (bp)	N90 (bp)	Min. (bp)	Median (bp)	L10	L50	L90
4,483,876	55,951	18,652	24,854	18,541	15,092	506	17,842	308,620	1,903,166	3,905,712

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66 **Supplementary Table 2.** ONT sequencing statistics.

Total bases (bp)	GC content	A (bp)		T (bp)		G (bp)		C (bp)		
46,941,501,005	37.96 (%)	14,466,215,202 (30.82 %)		14,657,084,477 (31.22 %)		9,206,630,656 (19.61 %)		8,611,570,670 (18.35%)		
Total reads	Max. (bp)	Mean (bp)	N10 (bp)	N50 (bp)	N90 (bp)	Min. (bp)	Median (bp)	L10	L50	L90
1,618,560	522,725	29,002	135,940	64,517	15,632	16	13,233	27,919	239,150	757,838

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69 **Supplementary Table 3.** Hi-C sequencing statistics.

Reads (M)	Bases (G)	Q20 (G)	Q30 (G)	Average length (bp)
832.119	124.818	122.627 (98.2 %)	118.851 (95.2 %)	150

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72 **Supplementary Table 4.** Iso-Seq data statistics.

Total bases (bp)	GC content	A (bp)		T (bp)		G (bp)		C (bp)		
18,726,456,249	42.22 (%)	5,320,606,619 (28.41 %)		5,499,786,293 (29.37 %)		3,940,290,752 (21.04 %)		3,965,772,585 (21.18%)		
Total reads	Max. (bp)	Mean (bp)	N10 (bp)	N50 (bp)	N90 (bp)	Min. (bp)	Median (bp)	L10	L50	L90
16,272,327	111,233	1,150	2,919	1,327	685	87	957	501,408	4,581,631	12,419,299

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75 **Supplementary Table 5.** Summary of the basic features of the estimated genome based on kmer species (a) and kmer individuals (b).

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K-mer	Raw peak	Now node	Low kmer	Now kmer	Coverage	Genome size (Mb)	Heterozygous ratio (%)		Duplication ratio (%)		Error_rate (%)
							a	b	a	b	
19	70	513,743,688	2,301,203,854	77,051,011,277	77.8153	1,043.92	1.075989342	0.236043132	15.1382	62.38115	0.170587465

Supplementary Table 6. Assessment of genome coverage rate.

Data set	Reads mapped	Bases mapped	≥ 1×	≥ 5×	≥10×	≥ 20×
HiFi	98.89 %	98.92 %	100.00 %	99.96 %	99.92 %	98.46 %
Iso-Seq	98.54 %	99.20 %	10.26 %	5.97 %	4.53 %	3.43 %

Supplementary Table 7. Assessment of BUSCO.

Category	Genome		Proteome	
	Number	Ratio	Number	Ratio
Complete BUSCOs	1,595	98.8 %	1595	98.8 %
Complete and single-copy BUSCOs	8	0.5 %	32	2.0 %
Complete and duplicated BUSCOs	1,587	98.3 %	1563	96.8 %
Fragmented BUSCOs	8	0.5 %	5	0.3 %
Missing BUSCOs	11	0.7 %	14	0.9 %
Total BUSCO groups searched	1,614		1614	