

Table S1: Statistics of the ONT sequencing data

	Raw ONT reads	Longest reads
Number of runs	2 MinION + 18 PromethION	
Cumulative size	1,074 Gb	510 Gb
# of reads	120,883,721	11,654,667
Coverage (17Gb)	63 X	30 X
N50 (bp)	24,651	45,077
Coverage (>50Kb)	14.1 X	14.1 X

Table S2: BNG Optical map

	DLE-1 genome map
Genome map number	1,053
Total Genome Map Length (Mbp)	14,947
Genome Map N50 (Mbp)	37.5

Table S3: Raw long-read assemblies

	SMARTDeNovo	Redbean	Flye
Subset of reads used	Longest - 30X	Longest - 30X	Longest - 30X
Cumulative size	14,155,561,280	29,695,324,870	13,050,586,822
# contigs	21,197	646,779	14,205
longest contig (bp)	13,367,134	957,564	18,693,219
minimal size (bp)	34,696	1,157	50,033
N50 (L50)	1,142,720 (3,758)	76,231 (107,967)	1,775,593 (2,165)
N90 (L90)	322,974 (12,488)	21,181 (397,125)	471,502 (7,566)
Restitution time (h)	408	168	1,032
IT	8 nodes with 32-core and 1.5Tb	1 node of 64-core and 3Tb	1 node of 64-core and 3Tb

Table S4: Hybrid assemblies obtained using ONT and BNG data

		SMARTDeNovo	Flye
Scaffolds	Cumulative size	14,272,571,061	14,204,637,528
	# scaffolds	4,255	4,135
	longest scaffold (bp)	253,607,211	252,437,931
	N50 (L50)	48,460,876 (79)	49,688,204 (77)
	N90 (L90)	7,877,958 (378)	8,121,250 (362)
	% of unknown bases	1.81%	5.99%
Contigs	Cumulative size	14,014,403,266	13,330,835,323
	# contigs	14,241	15,282
	longest contig (bp)	15,116,800	19,215,531
	N50 (L50)	2,144,699 (1,963)	1,662,574 (2,131)
	N90 (L90)	595,732 (6,672)	440,639 (8,204)
	BUSCO (n=4,896)	Complete : 97.0% Duplicated : 87.3% Fragmented : 0.4% Missing : 2.6%	Complete : 96.7% Duplicated : 86.6% Fragmented : 0.4% Missing : 2.9%

Table S5: Impact of the polishing

		SMARTDeNovo raw	SMARTDeNovo polished with long reads	SMARTDeNovo polished with short reads
BUSCO (n=4,896)	Complete	83.0%	96.7%	96.6%
	Duplicated	32.5%	83.1%	87.0%
	Fragmented	2.4%	0.6%	0.6%
	Missing	14.6%	2.7%	2.8%
IBSPs (n=5.76 M)	Aligned	80.4%	92.9%	93.4%
	Perfectly aligned	7.0%	28.0%	58.9%

Table S6: Statistics of the ONT reads obtained with two different versions of the guppy basecaller

	Guppy 3.3	Guppy 3.6
Number of runs	2 MinION + 18 PromethION Selection of the longest reads (30X)	
Cumulative size	510 Gb	510 Gb
# of reads	11,731,678	11,654,667
Coverage (17Gb)	30 X	30 X
N50 (bp)	44,797	45,077
Coverage (>50Kb)	13.9 X	14.1 X

Table S7: Long-read assemblies with ONT reads obtained with two different versions of the guppy basecaller

	SMARTDeNovo	SMARTDeNovo
Subset of reads used	Guppy 3.3 Longest - 30X	Guppy 3.6 Longest - 30X
Cumulative size	13,975,909,499	14,155,561,280
# contigs	26,167	21,197
longest contig (bp)	6,593,358	13,367,134
minimal size (bp)	33,360	34,696
N50 (L50)	899,898 (4,685)	1,142,720 (3,758)
N90 (L90)	247,425 (15,801)	322,974 (12,488)

Figure S1. Coverage of individual chromosomes with Illumina short-reads. Coverage was computed using 100 kb windows.

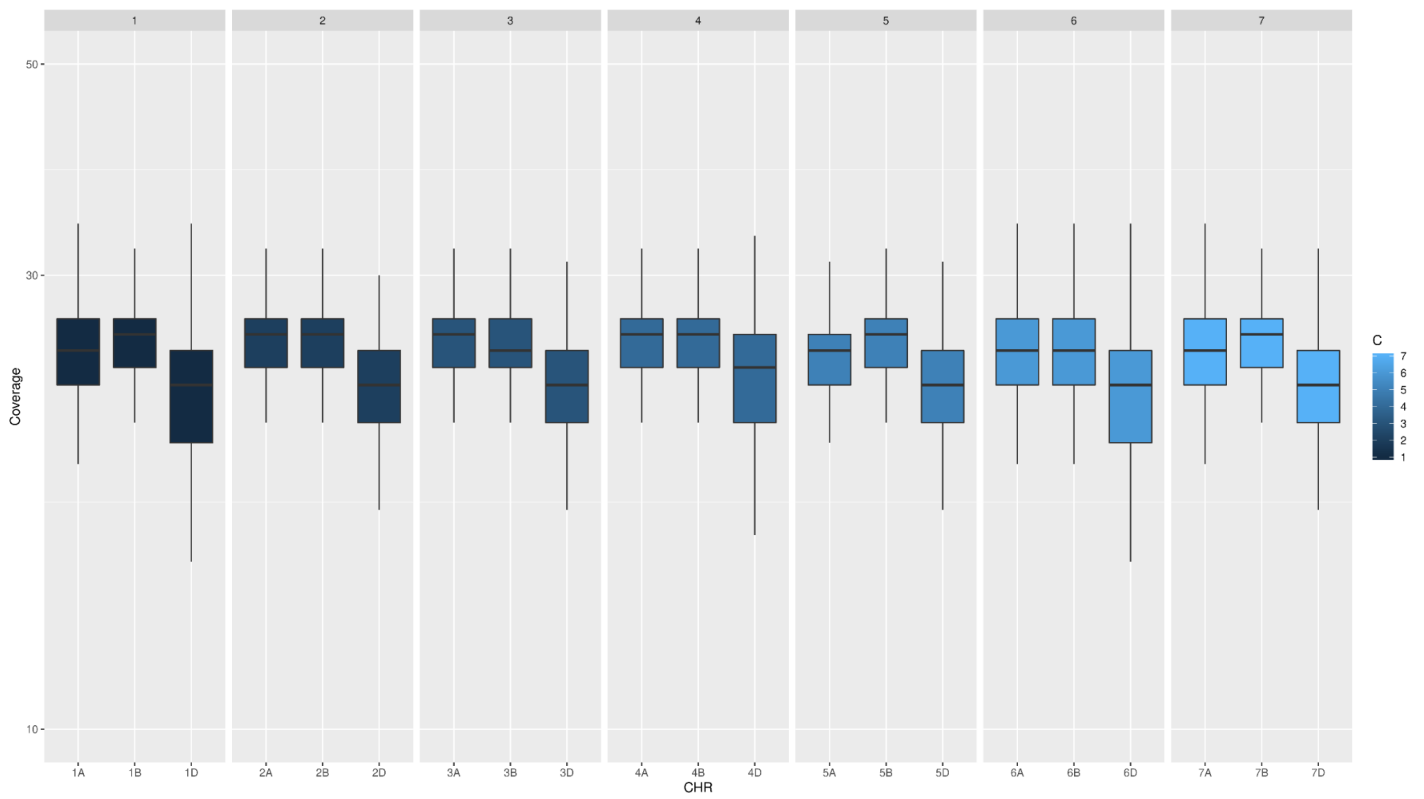


Figure S2. Coverage of individual chromosomes with ONT long-reads. Coverage was computed using 100 kb windows.

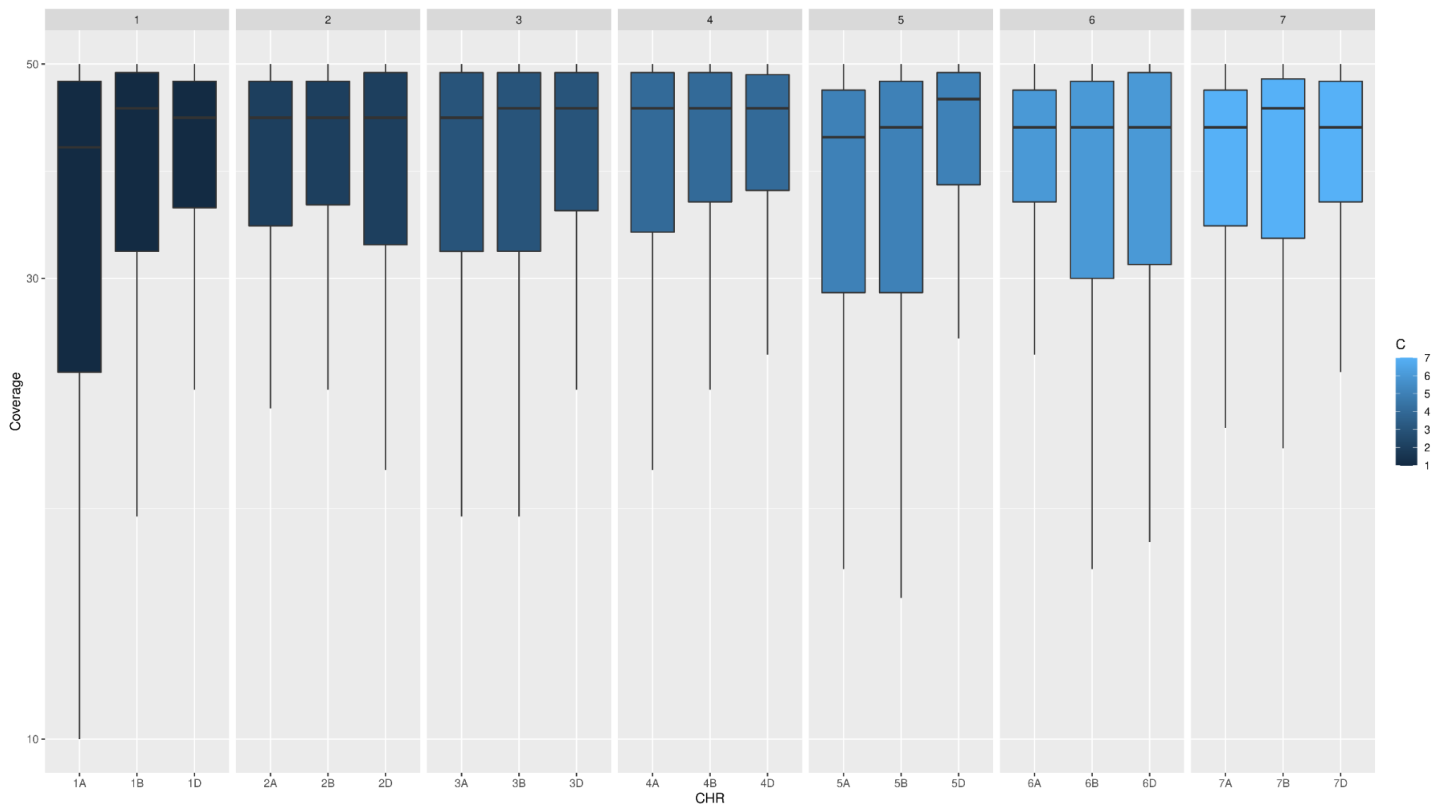


Figure S3. Number of gaps per Mbp in Chinese Spring and Renan genome assemblies.

