

ERGA Assembly Report

v23.09.27_beta

Tags: ERGA-Satellite

ToLID	ddCitColo1
Species	<i>Citrullus colocynthis</i>
Class	Magnoliopsida
Order	Cucurbitales
Haploid Number	12 (source: direct)
Ploidy	2
Sex	NA

Data profile

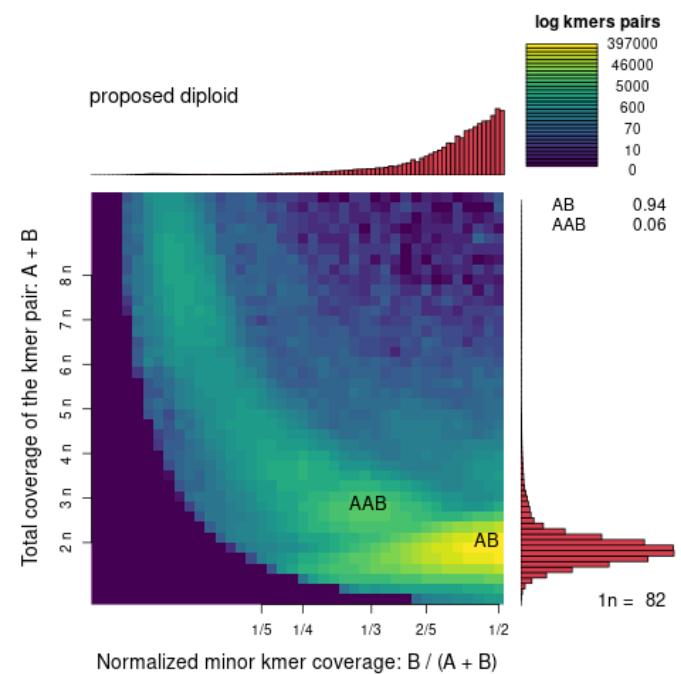
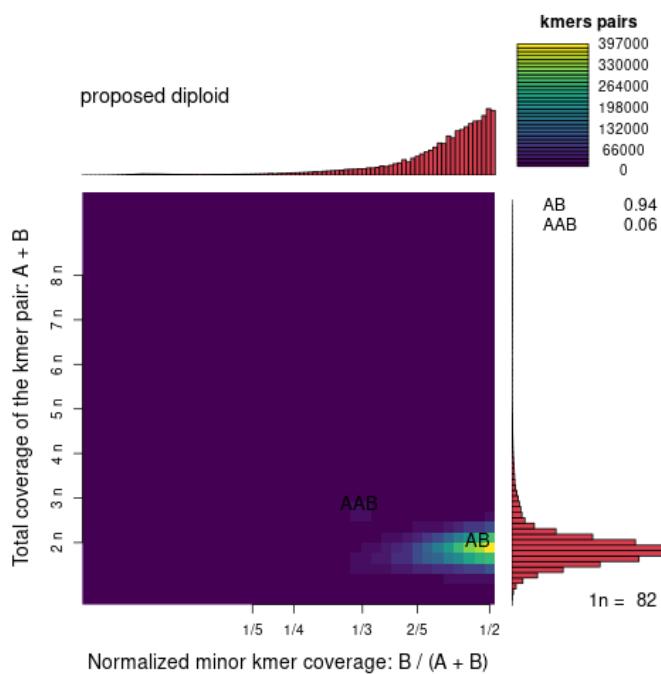
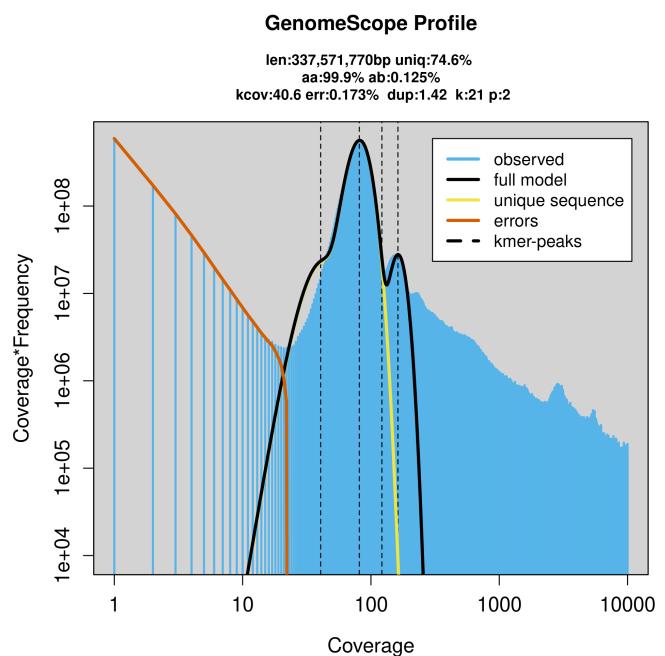
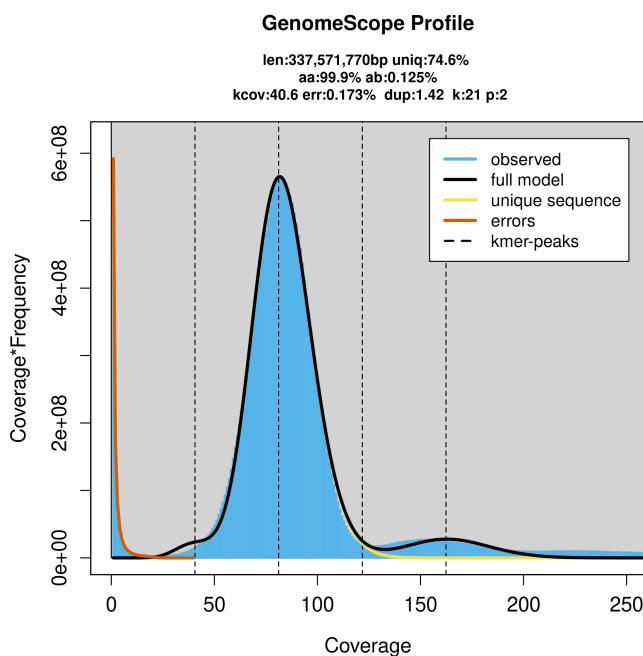
Data	Coverage
PacBio-HiFi	85x
HiC	120x

Pipeline summary

Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.18.9-r527
YaHS	1.2a.1

Genome profiling

Estimated Haploid Length	337,117,689
Heterozygosity rate	0.114815%
Kmer coverage	40.59
Proposed ploidy	2

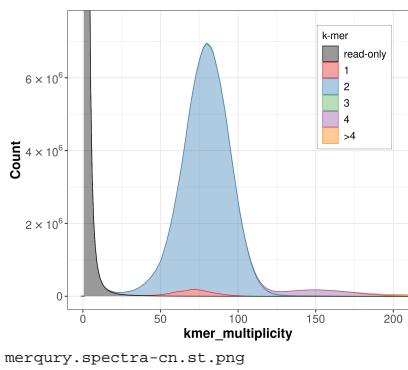
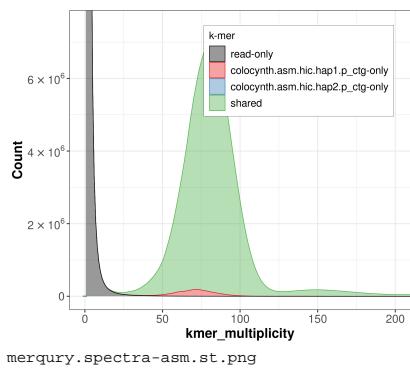
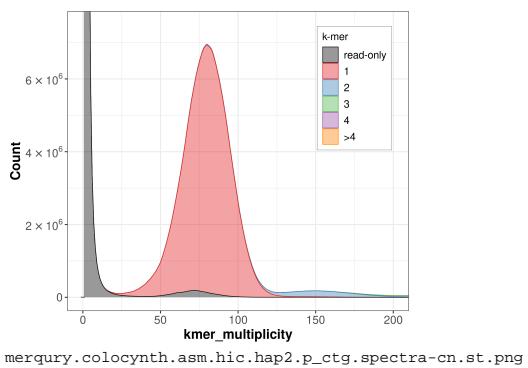
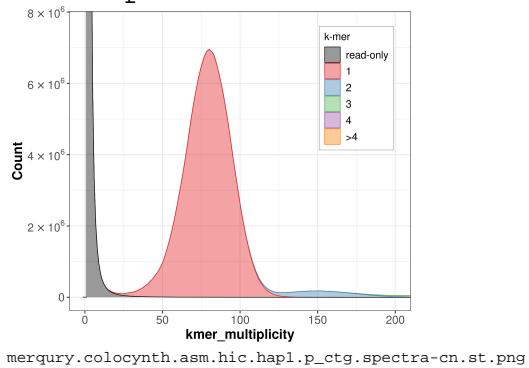


Genome assembly: contigging

Metrics	Hifiasm hap1	Hifiasm hap2
Total bp	366,111,899	356,939,597
GC %	33.6	33.64
Gaps	0	0
Gaps /Gbp	0	0
Gaps bp	0	0
Scaffolds	88	95
Longest Scaf.	36,926,313	36,881,511
Scaffold auN	30,591,763.84	25,960,149.77
Scaffold N50	30,853,444	29,357,918
Scaffold L50	6	6
Scaffold L90	11	14
Contigs	88	95
Largest Cont.	36,926,313	36,881,511
Contig auN	30,591,763.84	25,960,149.77
Contig N50	30,853,444	29,357,918
Contig L50	6	6
Contig L90	11	14
QV	67.0945	66.9325
Kmer compl.	99.7458	97.7577
BUSCO sing.	95.7%	94.5%
BUSCO dupl.	1.0%	1.2%
BUSCO frag.	0.5%	0.6%
BUSCO miss.	2.8%	3.7%

Lineage: eudicotyledons_odb10 (genomes:31, BUSCOs:2326)

K-mer spectra: Hifiiasm

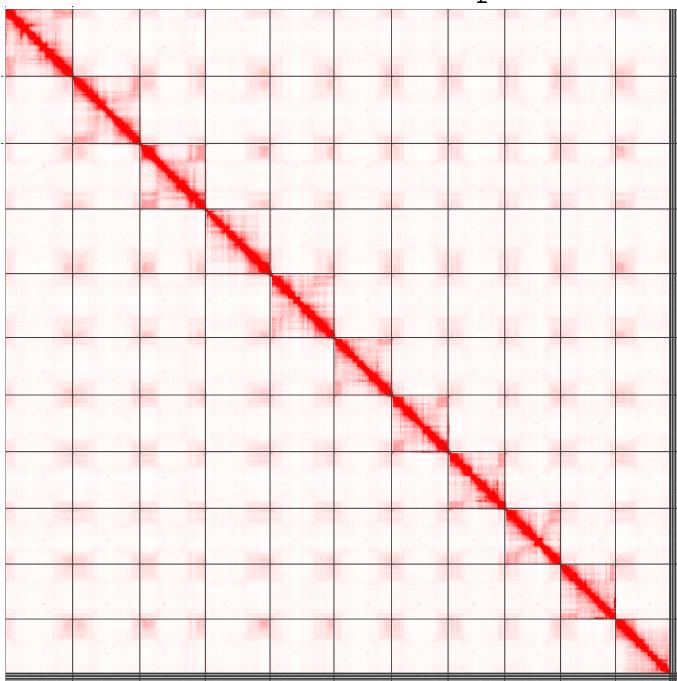


Genome assembly: scaffolding

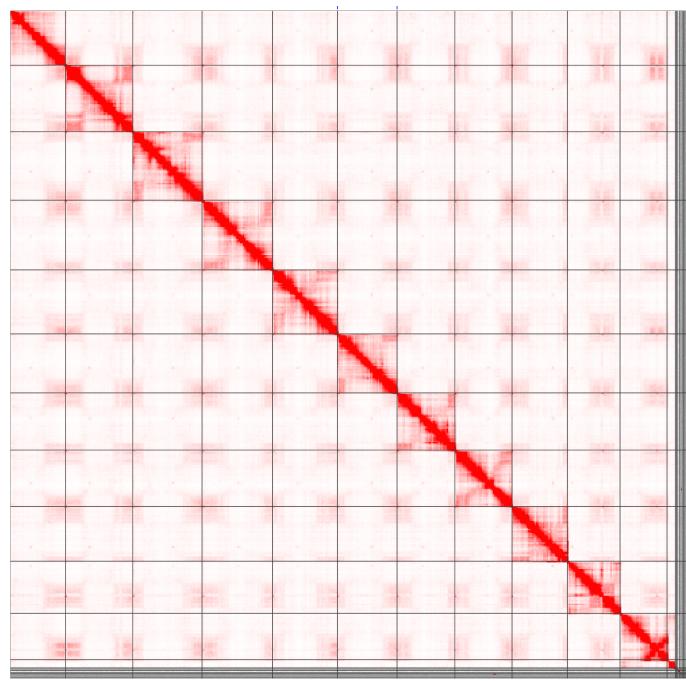
Metrics	YaHS hap1	YaHS hap2
Total bp	366,112,299	356,935,950
GC %	33.6	33.64
Gaps	2	9
Gaps/Gbp	5.46	25.21
Gaps bp	400	1,800
Scaffolds	86	88
Longest Scaf.	36,926,313	36,881,511
Scaffold auN	32,639,924.03	31,161,560.63
Scaffold N50	31,341,397	30,674,282
Scaffold L50	6	6
Scaffold L90	10	10
Contigs	88	97
Largest Cont.	36,926,313	36,881,511
Contig auN	30,591,763.84	25,935,568.74
Contig N50	30,853,444	29,345,706
Contig L50	6	6
Contig L90	11	14
QV	67.0945	66.9325
Kmer compl.	99.7458	97.7577
BUSCO sing.	95.7%	94.5%
BUSCO dupl.	1.0%	1.2%
BUSCO frag.	0.6%	0.6%
BUSCO miss.	2.7%	3.7%

Lineage: eudicotyledons_odb10 (genomes:31, BUSCOs:2326)

HiC Full-contact Map: YaHS



chromosomes.hapl.png



chromosomes.hap2.png

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