

ERGA Assembly Report

v13.09.23_beta

Tags: ERGA-Satellite

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

Data profile

Data	Coverage
PacBio-HiFi	85x
HiC	120x

Pipeline summary

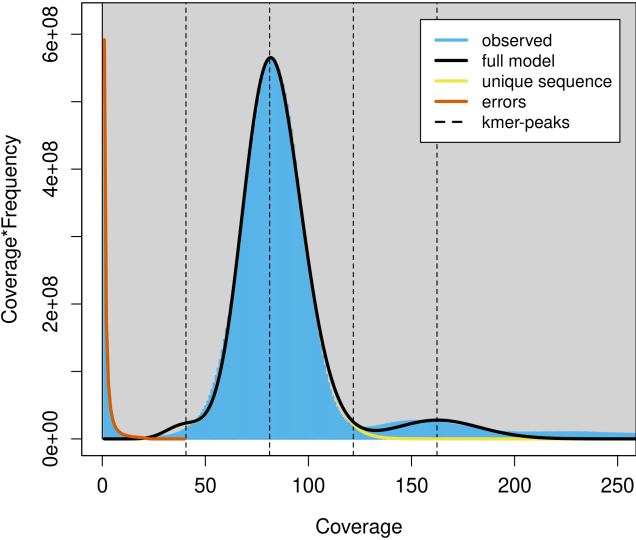
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.18.9-r527
YaHS	1.2a.1

Genome profiling

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

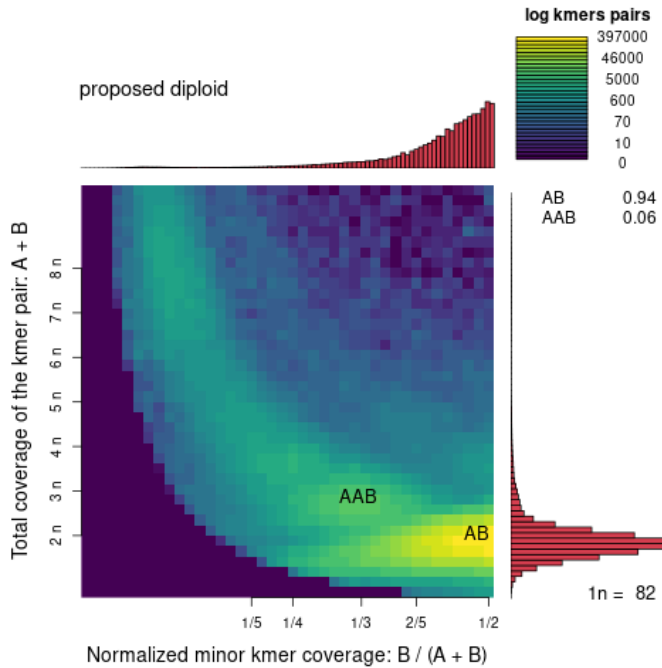
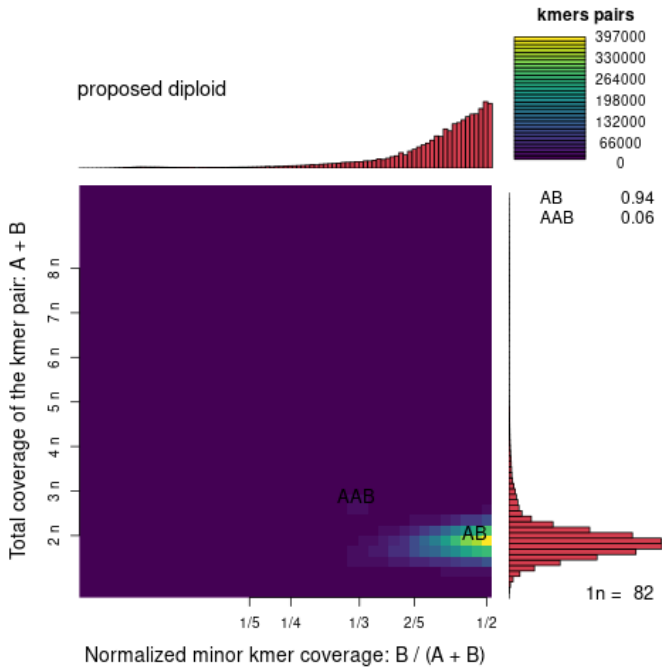
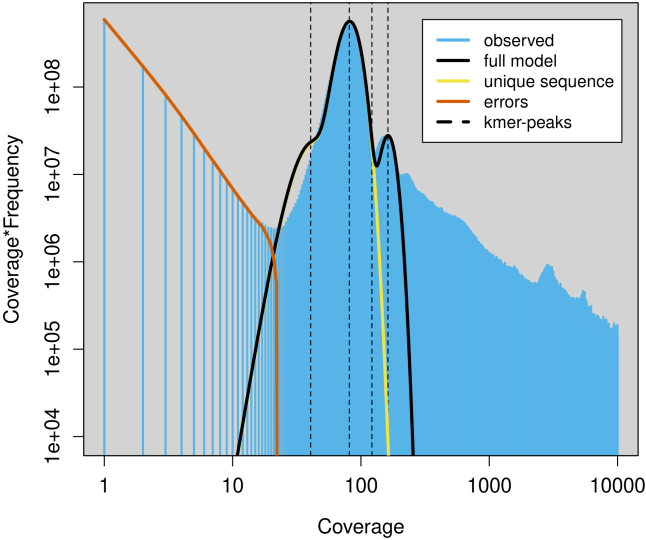
GenomeScope Profile

len:337,571,770bp uniq:74.6%
aa:99.9% ab:0.125%
kcov:40.6 err:0.173% dup:1.42 k:21 p:2



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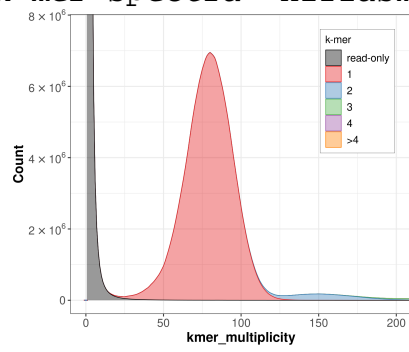


Genome assembly: contigging

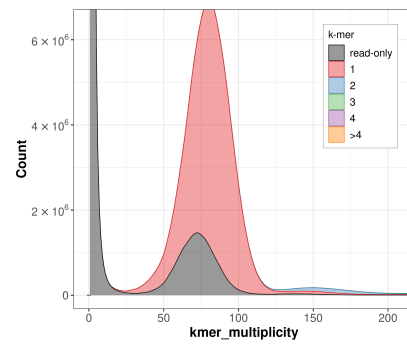
Metrics	Hifiasm hap1	Hifiasm hap2
Total bp	366,469,251	277,995,038
GC %	33.69	32.91
Gaps	0	0
Gaps/Gbp	0	0
Gaps bp	0	0
Scaffolds	95	104
Longest Scaf.	36,926,312	33,949,978
Scaffold auN	30,535,640.39	13,410,727.88
Scaffold N50	30,829,096	11,370,720
Scaffold L50	6	9
Scaffold L90	11	22
Contigs	95	104
Largest Cont.	36,926,312	33,949,978
Contig auN	30,535,640.39	13,410,727.88
Contig N50	30,829,096	11,370,720
Contig L50	6	9
Contig L90	11	22
QV	66.6406	
Kmer compl.	99.7435	
BUSCO sing.	95.9%	88.3%
BUSCO dupl.	1.0%	1.2%
BUSCO frag.	0.5%	0.6%
BUSCO miss.	2.6%	9.9%

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

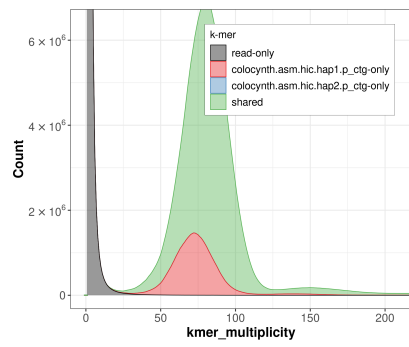
K-mer spectra: Hifiiasm



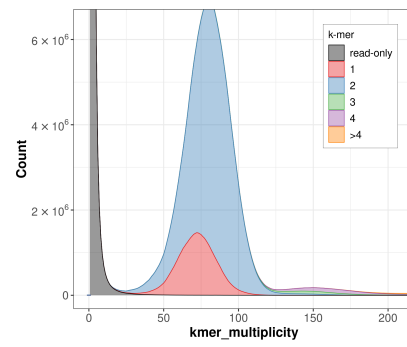
merqury.colocynth.asm.hic.hap1.p_ctg.spectra-cn.st.png



merqury.colocynth.asm.hic.hap2.p_ctg.spectra-cn.st.png



merqury.spectra-asm.st.png



merqury.spectra-cn.st.png

Genome assembly: scaffolding

Metrics	YaHS hap1	YaHS hap2
Total bp	366,470,251	277,998,838
GC %	33.69	32.91
Gaps	5	19
Gaps/Gbp	13.64	68.35
Gaps bp	1,000	3,800
Scaffolds	93	87
Longest Scaf.	36,926,312	33,949,978
Scaffold auN	32,549,100.53	23,796,417
Scaffold N50	31,331,276	25,970,831
Scaffold L50	6	5
Scaffold L90	10	11
Contigs	98	106
Largest Cont.	36,926,312	33,949,978
Contig auN	30,453,043.08	13,194,836.73
Contig N50	30,829,096	11,042,140
Contig L50	6	9
Contig L90	11	23
QV	66.6406	65.7986
Kmer compl.	99.7435	82.4299
BUSCO sing.	95.9%	88.3%
BUSCO dupl.	1.0%	1.1%
BUSCO frag.	0.6%	0.6%
BUSCO miss.	2.5%	10.0%

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

Pretext Full Map: YaHS



Screenshot.png

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