

# ERGA Assembly Report

v21.07.23\_beta

Tags: ERGA-Satellite

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

## Data profile

Data	Coverage
DNBSEQ-G400-WGS	260x
PacBio-HiFi	85x
HiC	120x

## Pipeline summary

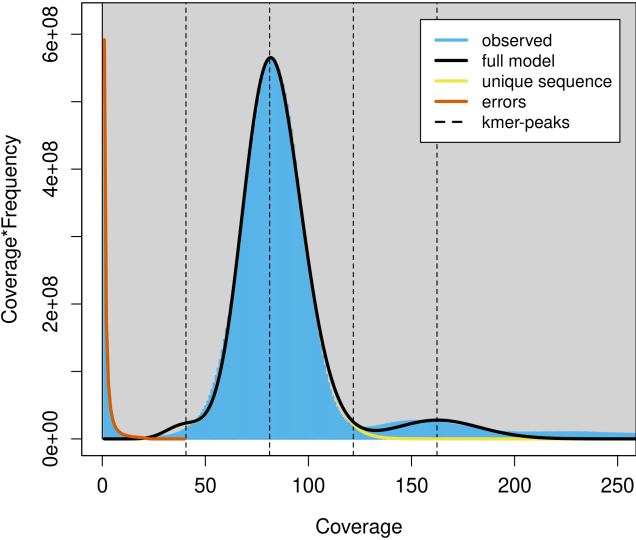
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.18.9-r527
YaHS	1.2a.1

# Genome profiling

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

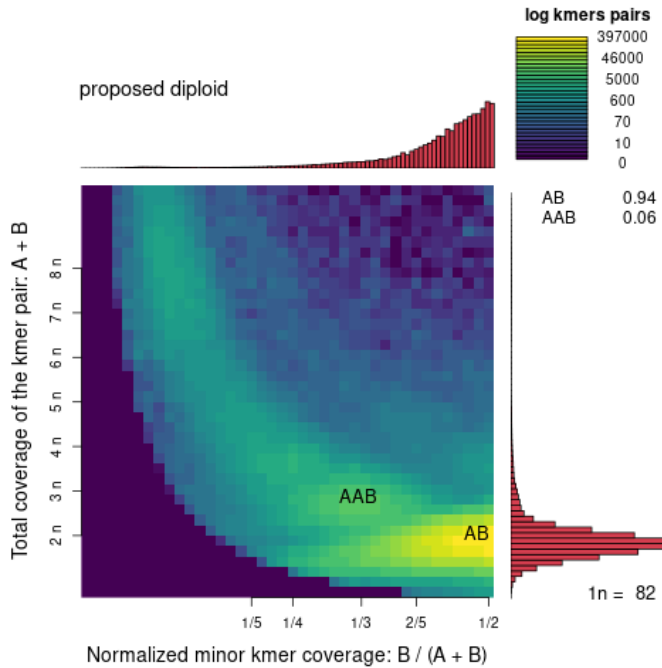
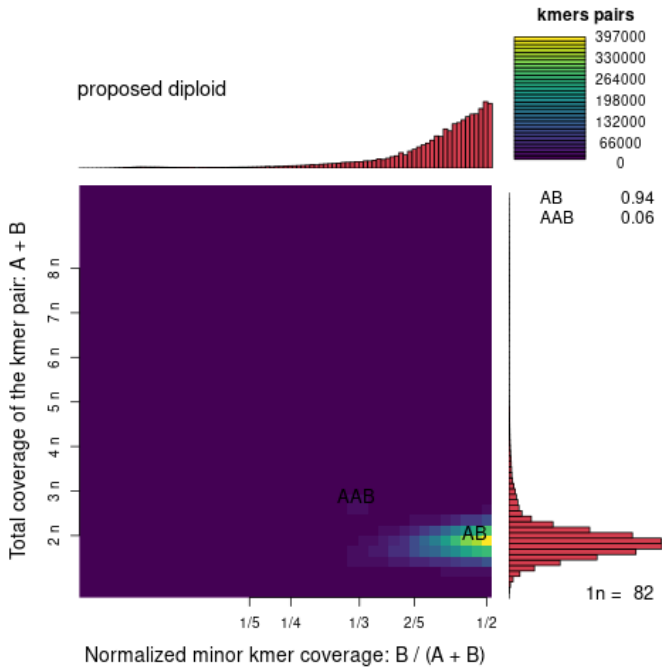
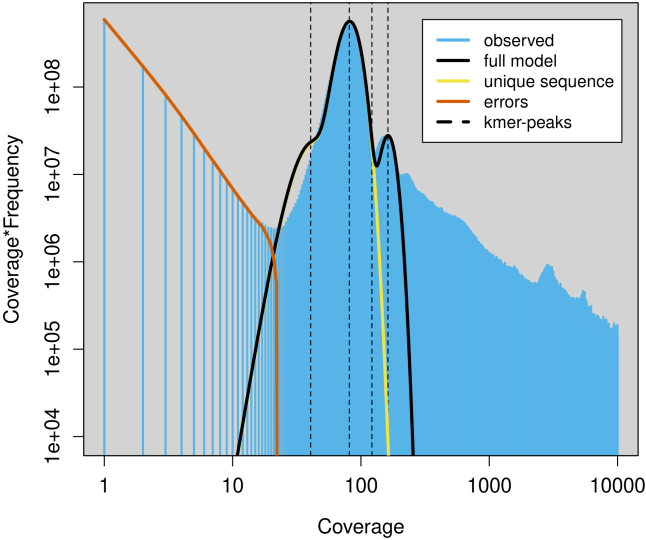
GenomeScope Profile

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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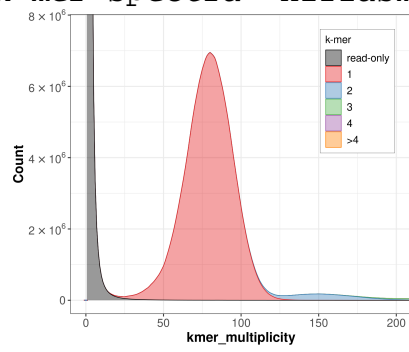


# Genome assembly: contigging

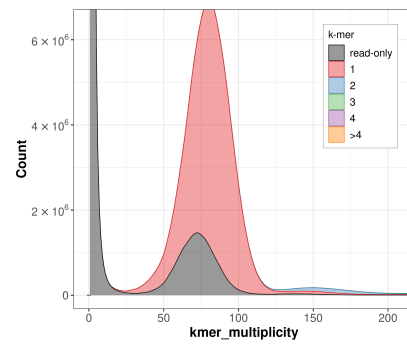
Metrics	Hifiasm hap1
Total bp	366,469,251
GC %	33.69
Gaps	0
Gaps/Gbp	0
Gaps bp	0
Scaffolds	95
Longest Scaf.	36,926,312
Scaffold auN	30,535,640.39
Scaffold N50	30,829,096
Scaffold L50	6
Scaffold L90	11
Contigs	95
Largest Cont.	36,926,312
Contig auN	30,535,640.39
Contig N50	30,829,096
Contig L50	6
Contig L90	11
QV	66.6406
Kmer compl.	99.7435
BUSCO sing.	95.9%
BUSCO dupl.	1.0%
BUSCO frag.	0.5%
BUSCO miss.	2.6%

Lineage: eudicotyledons\_odb10 (genomes:31, BUSCOs:2326)

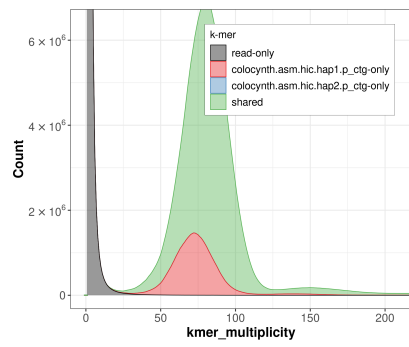
## K-mer spectra: Hifiiasm



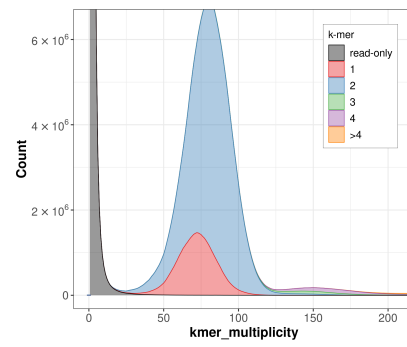
merqury.colocynth.asm.hic.hap1.p\_ctg.spectra-cn.st.png



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
Total bp	366,470,251
GC %	33.69
Gaps	5
Gaps/Gbp	13.64
Gaps bp	1,000
Scaffolds	93
Longest Scaf.	36,926,312
Scaffold auN	32,549,100.53
Scaffold N50	31,331,276
Scaffold L50	6
Scaffold L90	10
Contigs	98
Largest Cont.	36,926,312
Contig auN	30,453,043.08
Contig N50	30,829,096
Contig L50	6
Contig L90	11
QV	
Kmer compl.	99.7435
BUSCO sing.	95.9%
BUSCO dupl.	1.0%
BUSCO frag.	0.6%
BUSCO miss.	2.5%

Lineage: eudicotyledons\_odb10 (genomes:31, BUSCOs:2326)

# Pretext Full Map: YaHS



Screenshot.png

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