

# ERGA Assembly Report

v23.09.27\_beta

Tags: ERGA-Satellite

ToLID	<b>ddCitColo1</b>
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

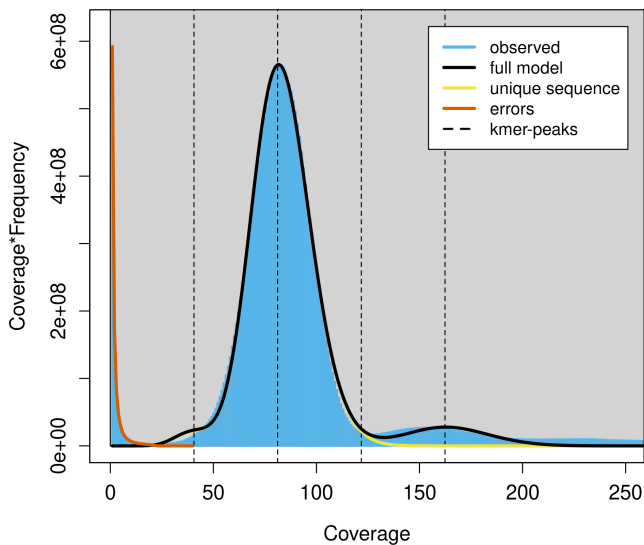
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.18.9-r527
YaHS	1.2a.1

# Genome profiling

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

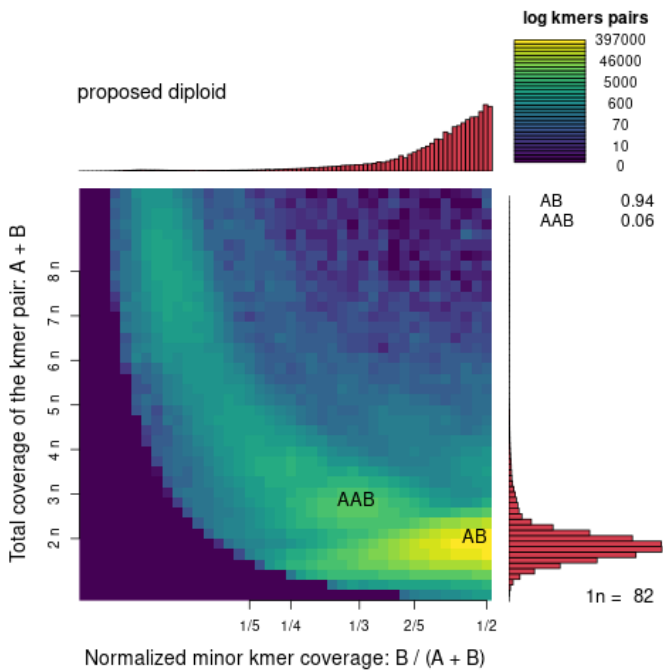
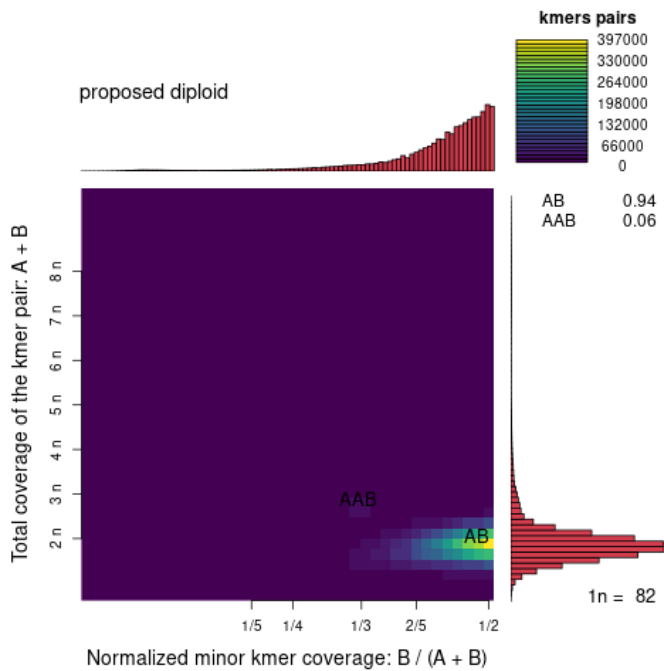
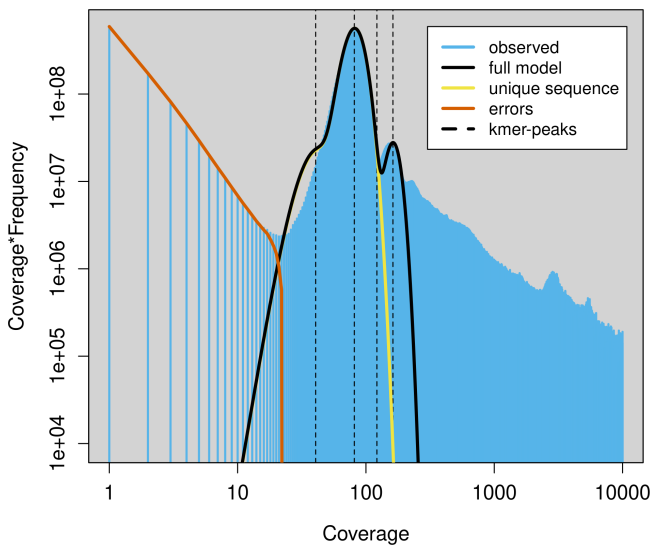
GenomeScope Profile

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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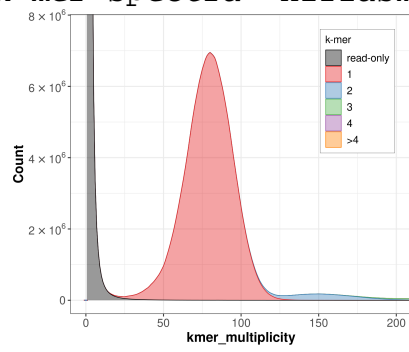


# Genome assembly: contigging

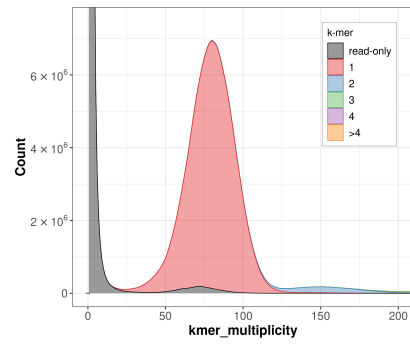
Metrics	Hifiasm hap1	Hifiasm hap2
Total bp	366,111,899	356,939,597
GC %	33.6	33.64
Gaps	0	0
Gaps/Gbp	0	0
Gaps bp	0	0
Scaffolds	88	95
Longest Scaf.	36,926,313	36,881,511
Scaffold auN	30,591,763.84	25,960,149.77
Scaffold N50	30,853,444	29,357,918
Scaffold L50	6	6
Scaffold L90	11	14
Contigs	88	95
Largest 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)

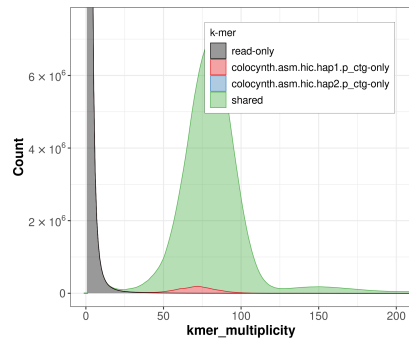
## K-mer spectra: Hifiasm



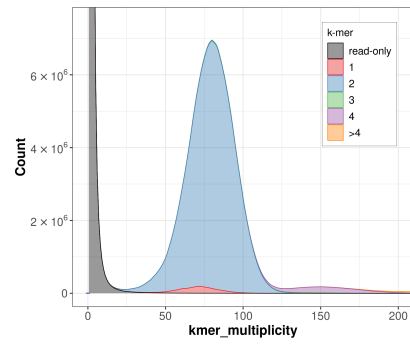
merqury.colocynth.asm.hic.hap1.p\_ctg.spectra-cn.st.png



merqury.colocynth.asm.hic.hap2.p\_ctg.spectra-cn.st.png



merqury.spectra-asm.st.png



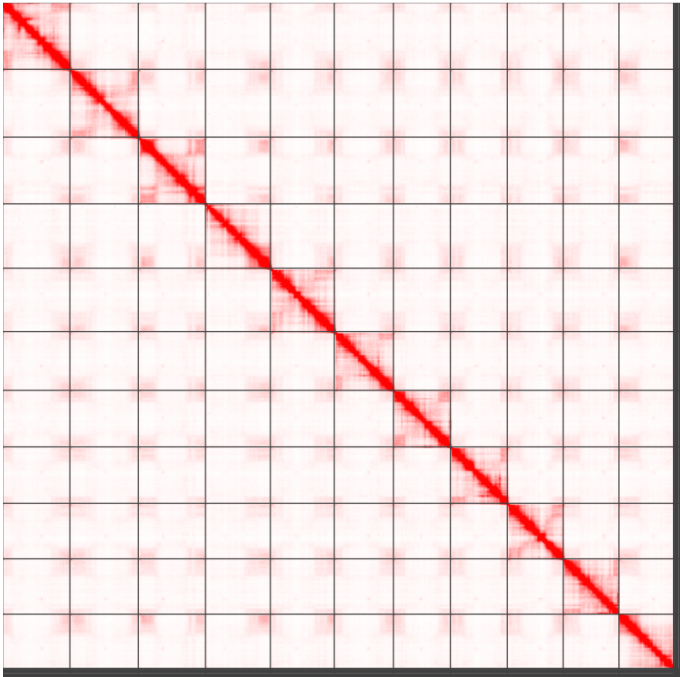
merqury.spectra-cn.st.png

# Genome assembly: scaffolding

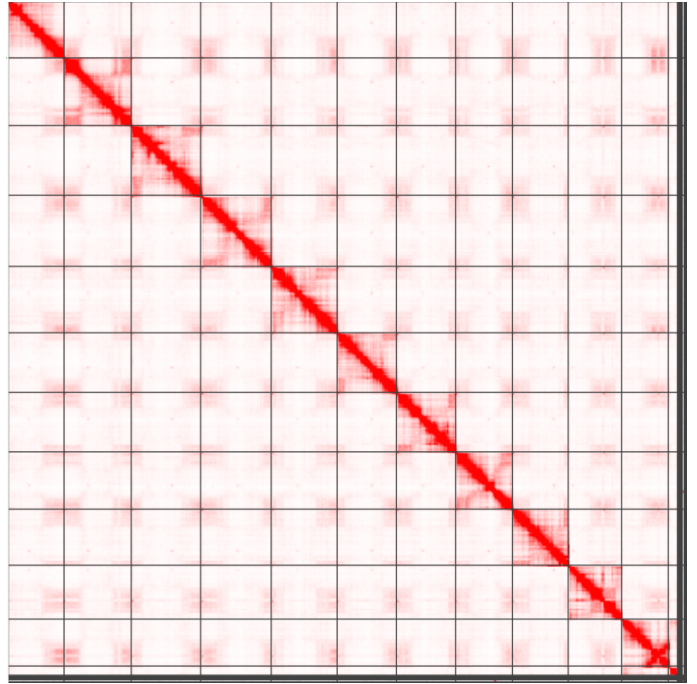
Metrics	YaHS hap1	YaHS hap2
Total bp	366,112,299	356,935,950
GC %	33.6	33.64
Gaps	2	9
Gaps/Gbp	5.46	25.21
Gaps bp	400	1,800
Scaffolds	86	88
Longest Scaf.	36,926,313	36,881,511
Scaffold auN	32,639,924.03	31,161,560.63
Scaffold N50	31,341,397	30,674,282
Scaffold L50	6	6
Scaffold L90	10	10
Contigs	88	97
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)

Pretext Full Map: YaHS



chromosomes.hap1.png



chromosomes.hap2.png

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Date and time: 2023-09-28 14:43:41 CEST