

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

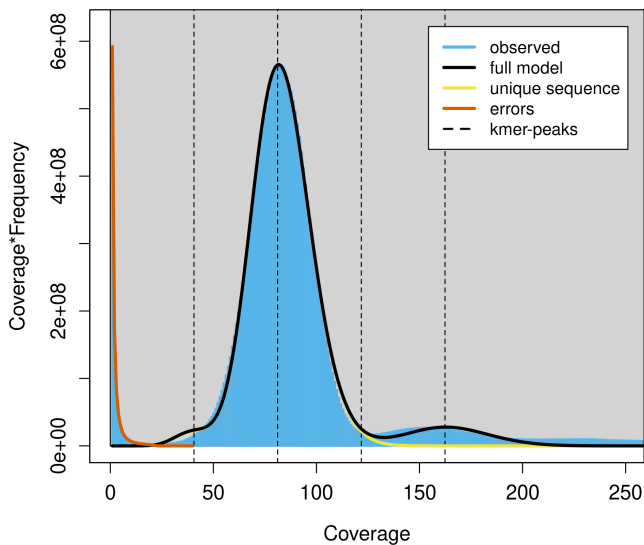
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.18.9-r527
Hifiasm-purge_dups	0.18.9-r527
YaHS	1.2a.1

Genome profiling

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

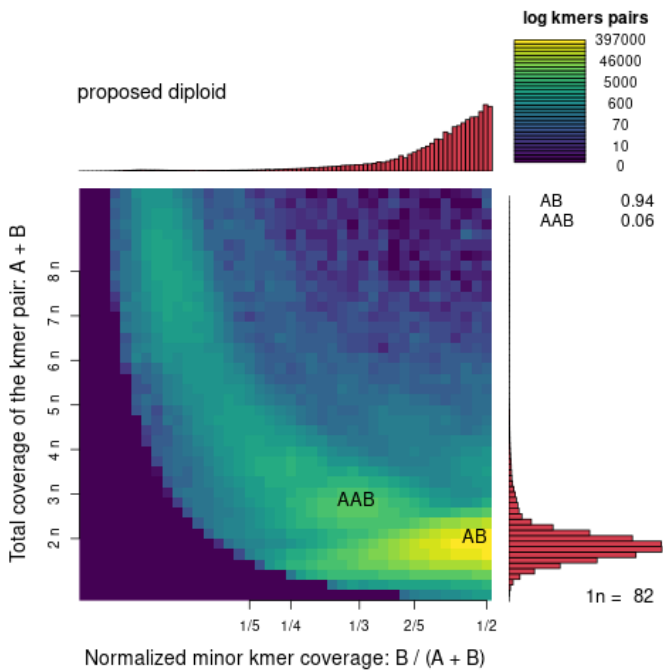
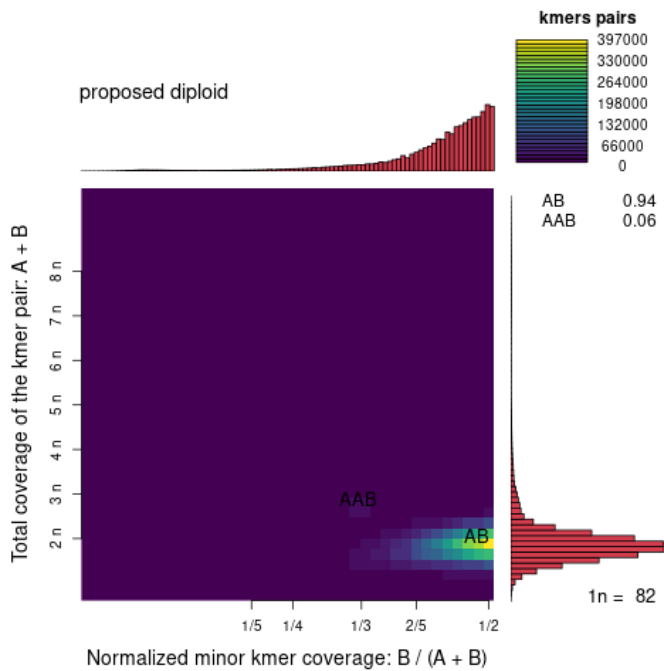
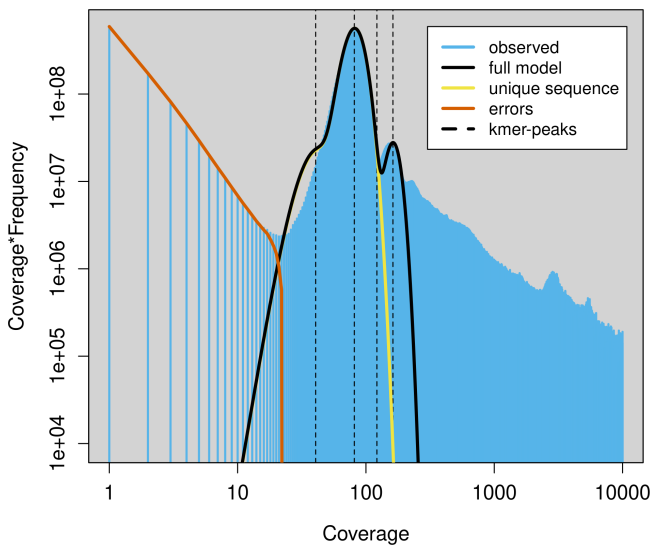
GenomeScope Profile

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



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

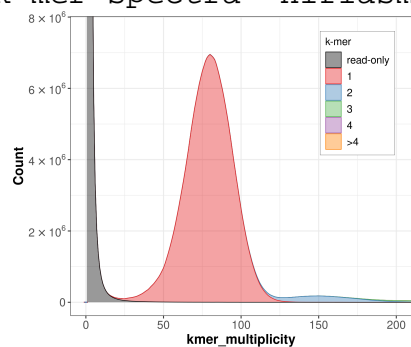


Genome assembly: contigging

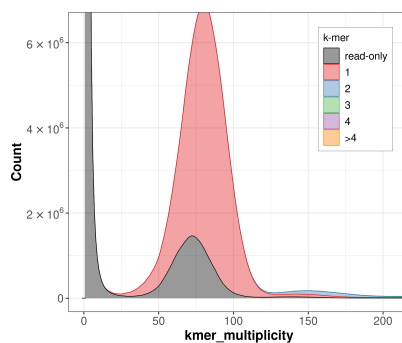
Metrics	Hifiasm hap1	Hifiasm hap2	Hifiasm-purge_dups hap1	Hifiasm-purge_dups hap2
Total bp	366,469,251	277,995,038	366,111,899	356,939,597
GC %	33.69	32.91	33.6	33.64
Gaps	0	0	0	0
Gaps/Gbp	0	0	0	0
Gaps bp	0	0	0	0
Scaffolds	95	104	88	95
Longest Scaf.	36,926,312	33,949,978	36,926,313	36,881,511
Scaffold auN	30,535,640.39	13,410,727.88	30,591,763.84	25,960,149.77
Scaffold N50	30,829,096	11,370,720	30,853,444	29,357,918
Scaffold L50	6	9	6	6
Scaffold L90	11	22	11	14
Contigs	95	104	88	95
Largest Cont.	36,926,312	33,949,978	36,926,313	36,881,511
Contig auN	30,535,640.39	13,410,727.88	30,591,763.84	25,960,149.77
Contig N50	30,829,096	11,370,720	30,853,444	29,357,918
Contig L50	6	9	6	6
Contig L90	11	22	11	14
QV	66.6406	65.7986	67.0945	66.9325
Kmer compl.	99.7435	82.4299	99.7458	97.7577
BUSCO sing.	95.9%	88.3%	95.7%	94.5%
BUSCO dupl.	1.0%	1.2%	1.0%	1.2%
BUSCO frag.	0.5%	0.6%	0.5%	0.6%
BUSCO miss.	2.6%	9.9%	2.8%	3.7%

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

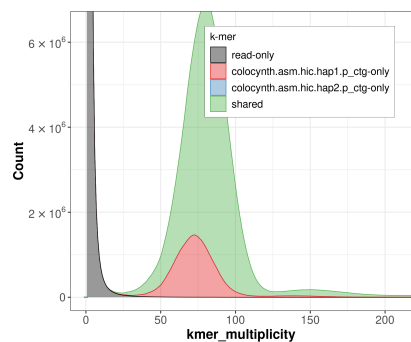
K-mer spectra: Hifiasm



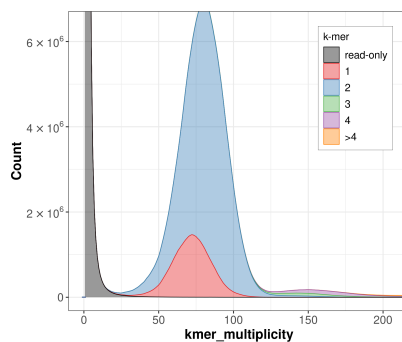
mercury.colocynth.asm.hic.hap1.p_ctg.spectra-cn.st.png



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

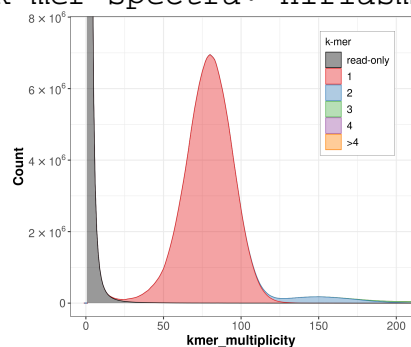


mercury.spectra-asm.st.png

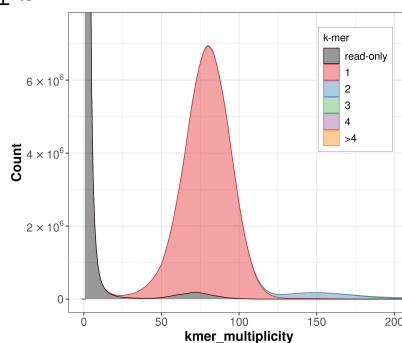


mercury.spectra-cn.st.png

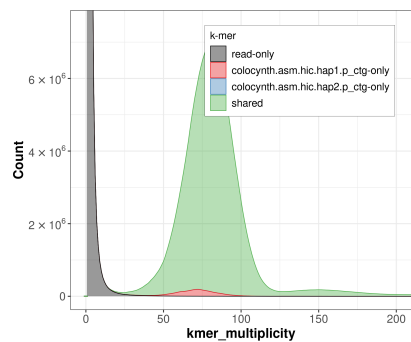
K-mer spectra: Hifiasm-purge_dups



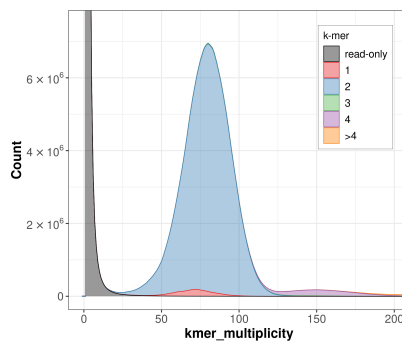
mercury.colocynth.asm.hic.hap1.p_ctg.spectra-cn.st.png



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



mercury.spectra-asm.st.png



mercury.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

Submitter: Anestis Gkanogiannis

Affiliation: International Center for Biosaline Agriculture (ICBA)

Date and time: 2023-09-14 11:52:50 CEST