

# ERGA Assembly Report

v21.07.23\_beta

Tags: ERGA-Pilot

ToLID	<b>ddCorAlbu1</b>
Species	Corema album
Class	Magnoliopsida
Order	Ericales
Haploid Number	13 (source: direct)
Ploidy	2

## Data profile

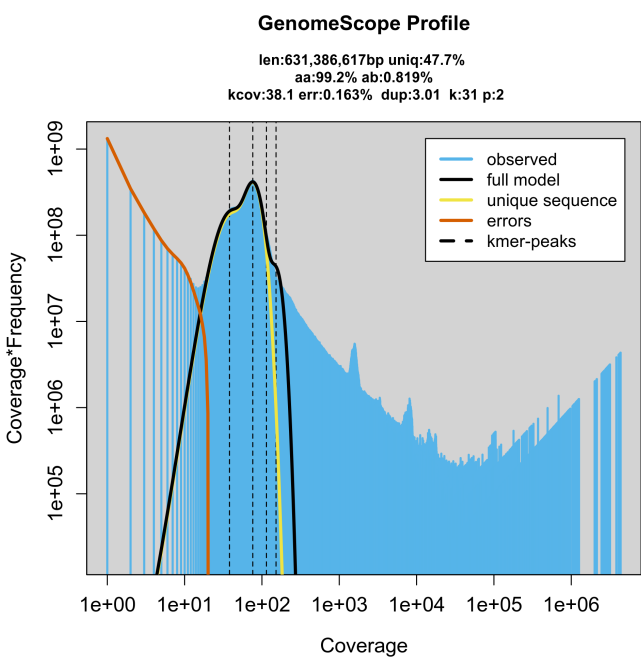
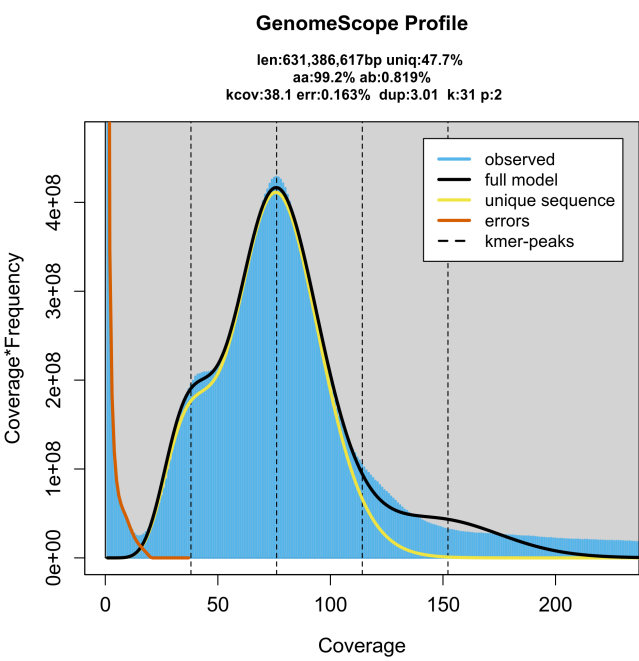
Data	Coverage
HiFi	54
Omni-C	NA

## Pipeline summary

Tool	Version
GenomeScope	2.0
Hifiasm	0.19.5-r587
purge_dups	1.2.5
YaHS	1.2a.1

# Genome profiling

Estimated Haploid Length	628,535,441
Heterozygosity rate	0.805151%
Kmer coverage	38.05
Proposed ploidy	NA



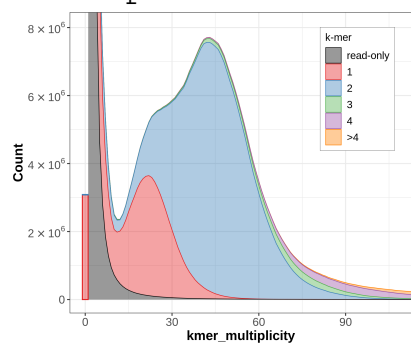
Smudgeplot data not available

# Genome assembly: contigging

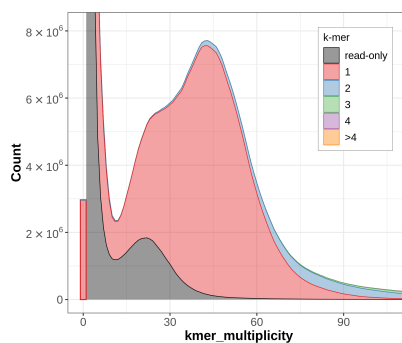
Metrics	Hifiasm hap1	Hifiasm hap2	purge_dups hap1	purge_dups hap2
Total bp	693,899,620	585,939,858	582,237,577	544,601,350
GC %	40.29	39.11	39.78	38.8
Gaps	0	0	0	0
Gaps/Gbp	0	0	0	0
Gaps bp	0	0	0	0
Scaffolds	2,341	700	1,374	379
Longest Scaf.	27,668,060	34,903,143	27,668,060	34,903,143
Scaffold auN	9,731,875.15	11,822,527.96	10,631,576.68	13,096,651.92
Scaffold N50	8,195,862	9,874,059	9,076,745	12,491,130
Scaffold L50	25	18	19	15
Scaffold L90	301	69	108	49
Contigs	2,341	700	1,374	379
Largest Cont.	27,668,060	34,903,143	27,668,060	34,903,143
Contig auN	9,731,875.15	11,822,527.96	10,631,576.68	13,096,651.92
Contig N50	8,195,862	9,874,059	9,076,745	12,491,130
Contig L50	25	18	19	15
Contig L90	301	69	108	49
QV	36.893	50.251	56.5491	62.8245
Kmer compl.	89.7209	88.8426	83.0462	83.7507
BUSCO sing.	95.1%	95.4%	95.4%	95.7%
BUSCO dupl.	3.0%	2.5%	2.2%	2.2%
BUSCO frag.	0.4%	0.5%	0.5%	0.6%
BUSCO miss.	1.5%	1.6%	1.9%	1.5%

Lineage: embryophyta\_odb10 (genomes:50, BUSCOs:1614)

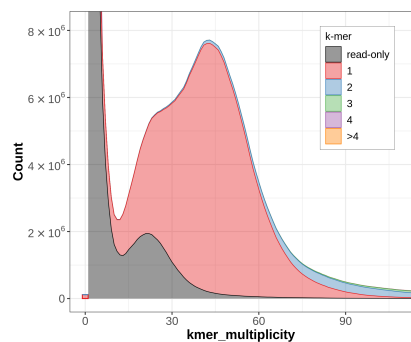
## K-mer spectra: Hifiiasm



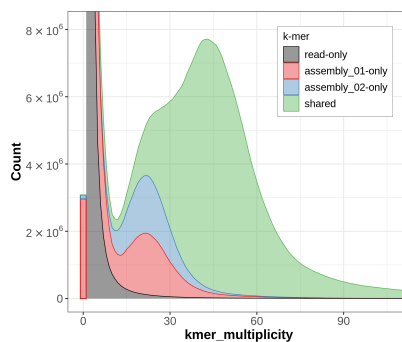
output\_mercury\_assemblyHiC.spectra-cn.st.png



output\_mercury\_assemblyHiC.assembly\_01.spectra-cn.st.png

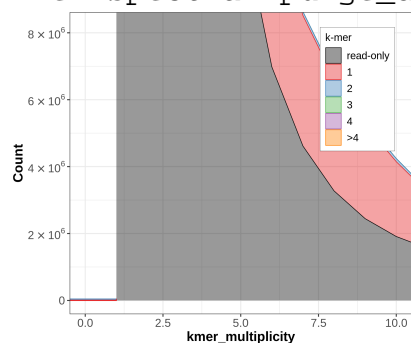


output\_mercury\_assemblyHiC.assembly\_02.spectra-cn.st.png

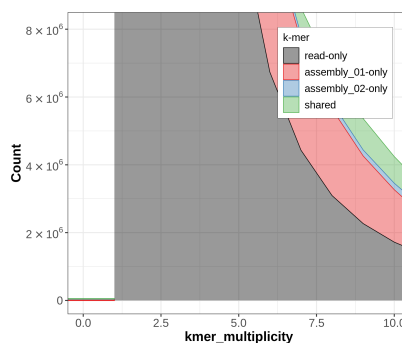


output\_mercury\_assemblyHiC.spectra-asm.st.png

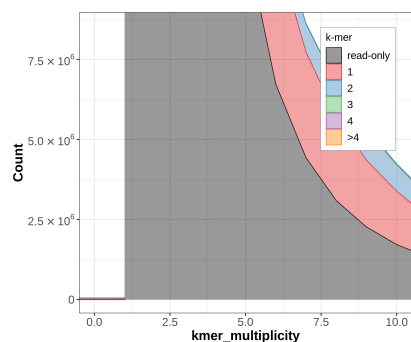
## K-mer spectra: purge\_dups



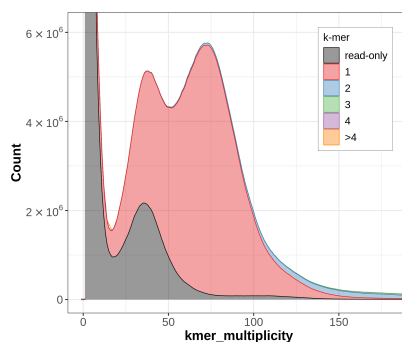
output\_mercury\_purged.assembly\_01.spectra-cn.st.png



output\_mercury\_purged.spectra-asm.st.png



output\_mercury\_purged.spectra-cn.st.png



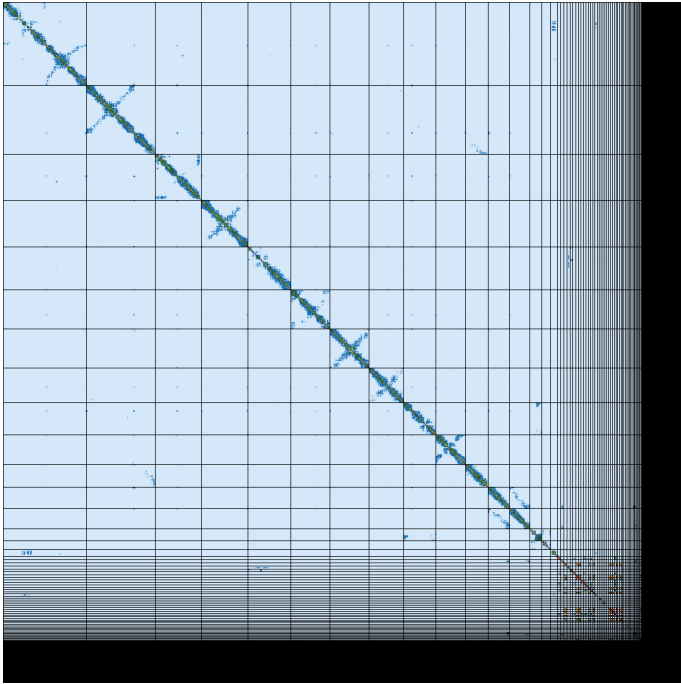
output\_mercury\_purged.assembly\_02.spectra-cn.st.png

# Genome assembly: scaffolding

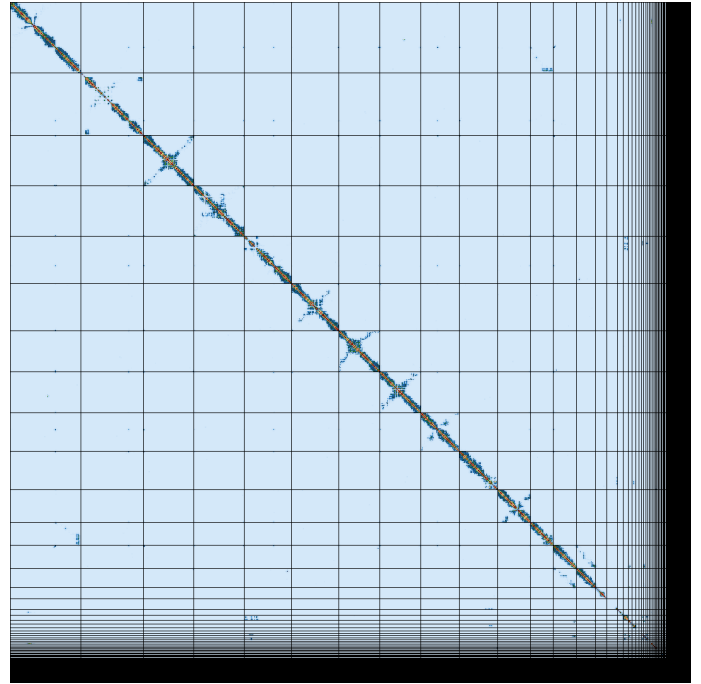
Metrics	YaHS hap1	YaHS hap2
Total bp	582,378,577	544,629,750
GC %	39.78	38.8
Gaps	705	142
Gaps/Gbp	1,210.55	260.73
Gaps bp	141,000	28,400
Scaffolds	746	301
Longest Scaf.	71,296,163	56,980,160
Scaffold auN	32,443,115.19	32,529,727.91
Scaffold N50	33,272,160	32,972,539
Scaffold L50	7	7
Scaffold L90	41	17
Contigs	1,451	443
Largest Cont.	18,934,263	34,903,143
Contig auN	7,938,806.74	11,043,486.39
Contig N50	7,577,508	8,986,633
Contig L50	25	18
Contig L90	161	67
QV	56.5491	62.8245
Kmer compl.	83.0462	83.7507
BUSCO sing.	95.4%	95.7%
BUSCO dupl.	2.3%	2.2%
BUSCO frag.	0.5%	0.4%
BUSCO miss.	1.8%	1.7%

Lineage: embryophyta\_odb10 (genomes:50, BUSCOs:1614)

Pretext Full Map: YaHS



CorAlb\_withHiC\_yash\_sort\_Hapl\_Filter.map\_FullMap.png



CorAlb\_withHiC\_yash\_sort\_Hap2\_Filter.map\_FullMap.png

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Affiliation: BIOPOLIS-CIBIO

Date and time: 2023-08-29 14:44:57 CEST