

ERGA Assembly Report

v21.07.23_beta

Tags: ERGA-test

ToLID	rCarCar2
Species	Caretta caretta
Class	NA
Order	Testudines
Haploid Number	27 (source: direct)
Ploidy	2

Data profile

Data	Coverage
HiFi	40x
Bionano	NA
OmniC	90x

Pipeline summary

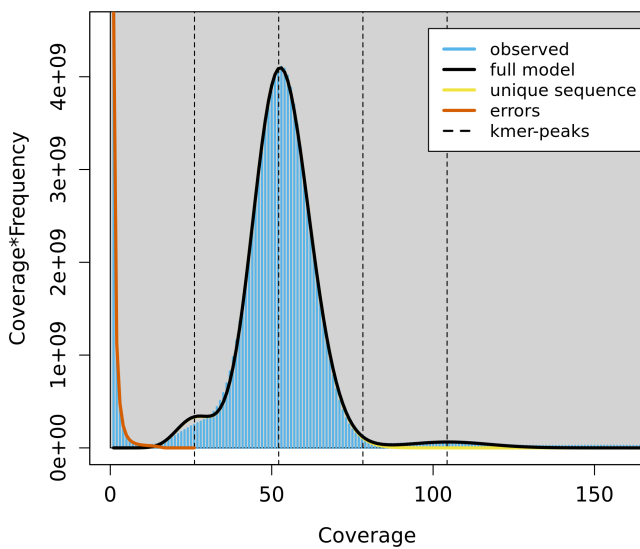
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.19.4
purge_dups	1.2.6
Bionano	Galaxy_3.7.0
YaHS	1.1

Genome profiling

Estimated Haploid Length	2,188,220,914
Heterozygosity rate	0.171093%
Kmer coverage	26.08
Proposed ploidy	2

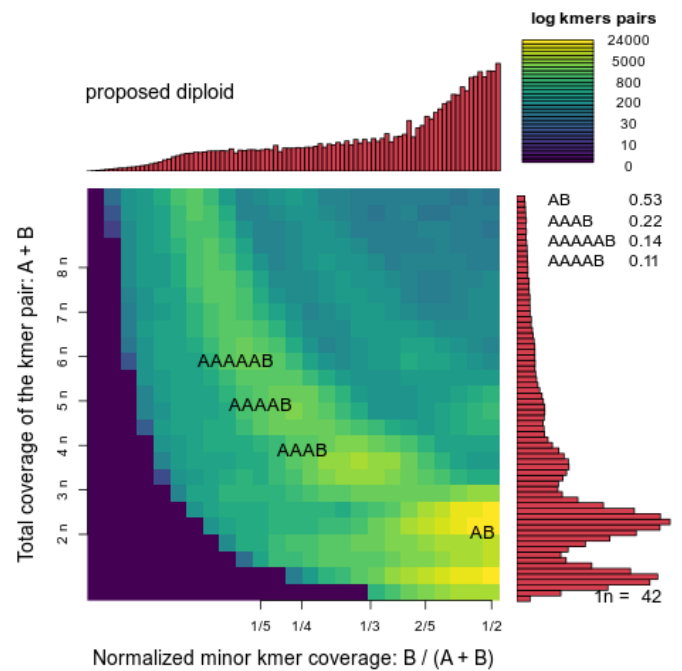
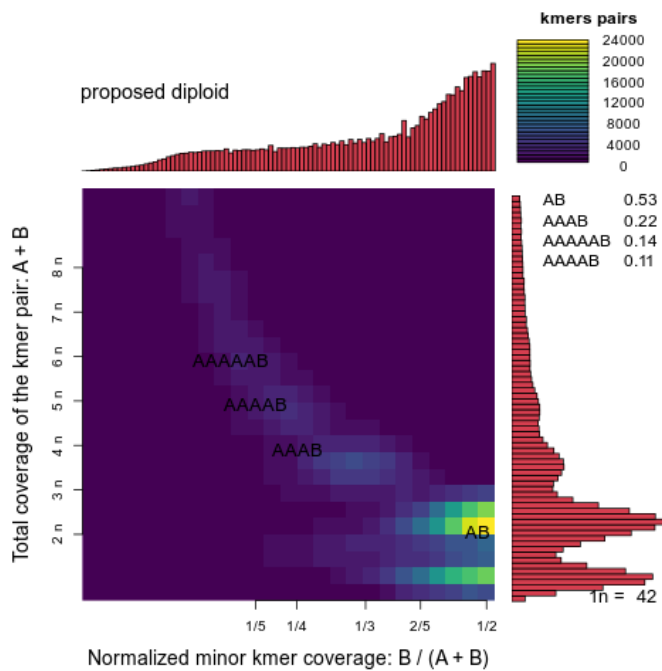
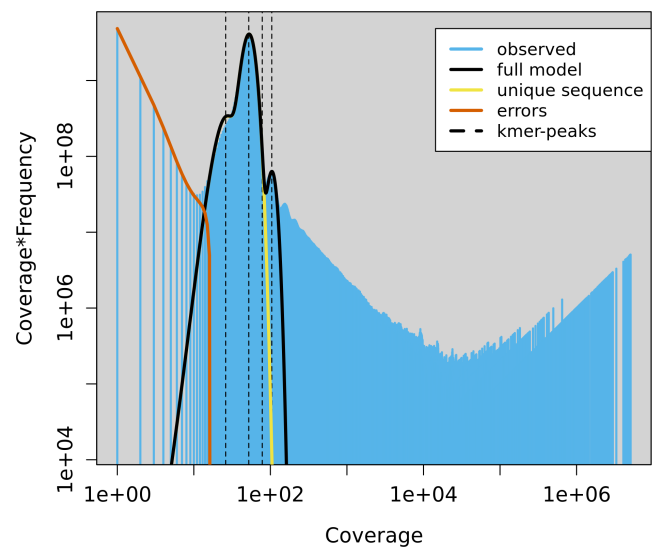
GenomeScope Profile

len:2,189,749,816bp uniq:82.2%
aa:99.8% ab:0.176%
kcov:26.1 err:0.196% dup:0.435 k:31 p:2



GenomeScope Profile

len:2,189,749,816bp uniq:82.2%
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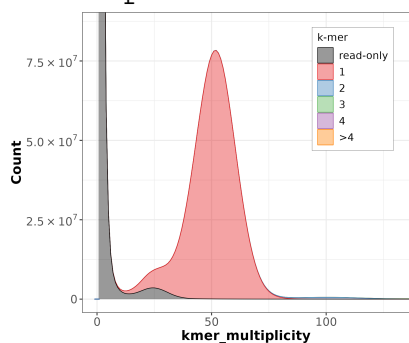


Genome assembly: contigging

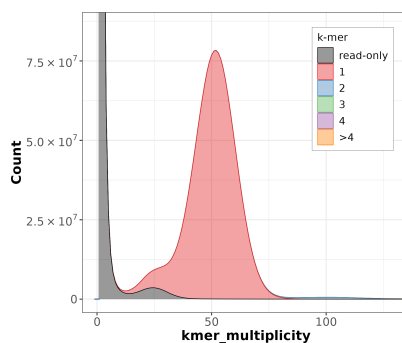
Metrics	Hifiasm hap1	Hifiasm hap2	purge_dups hap1	purge_dups hap2
Total bp	2,257,253,306	2,239,458,145	2,216,692,574	2,205,561,400
GC %	44.27	44.23	44.12	44.11
Gaps	0	0	0	0
Gaps/Gbp	0	0	0	0
Gaps bp	0	0	0	0
Scaffolds	172	144	95	84
Longest Scaf.	354,291,630	210,263,708	354,291,630	210,263,708
Scaffold auN	138,591,508.98	107,233,503	141,094,921.93	108,830,894.98
Scaffold N50	124,322,749	119,638,208	124,322,749	119,638,208
Scaffold L50	7	8	7	8
Scaffold L90	26	27	24	25
Contigs	172	144	95	84
Largest Cont.	354,291,630	210,263,708	354,291,630	210,263,708
Contig auN	138,591,508.98	107,233,503	141,094,921.93	108,830,894.98
Contig N50	124,322,749	119,638,208	124,322,749	119,638,208
Contig L50	7	8	7	8
Contig L90	26	27	24	25
QV	68.4529	67.9108	68.7149	67.9889
Kmer compl.	96.7687	96.8198	96.6829	96.6394
BUSCO sing.	96.4%	96.4%	96.4%	96.4%
BUSCO dupl.	0.9%	0.9%	0.9%	0.9%
BUSCO frag.	0.3%	0.3%	0.3%	0.3%
BUSCO miss.	2.4%	2.4%	2.4%	2.4%

Lineage: sauropsida_odb10 (genomes:76, BUSCOs:7480)

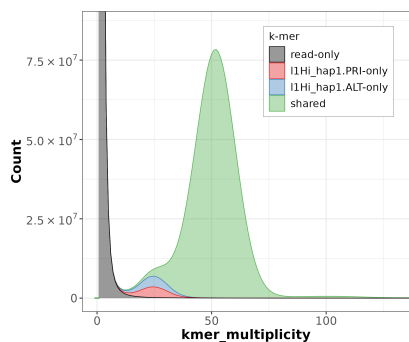
K-mer spectra: Hifiasm



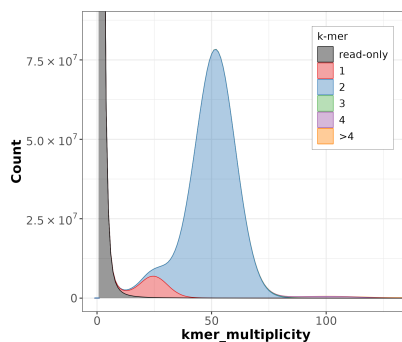
11Hi_hap1_merqOutput.11Hi_hap1.ALT.spectra-cn.st.png



11Hi_hap1_merqOutput.11Hi_hap1.PRI.spectra-cn.st.png

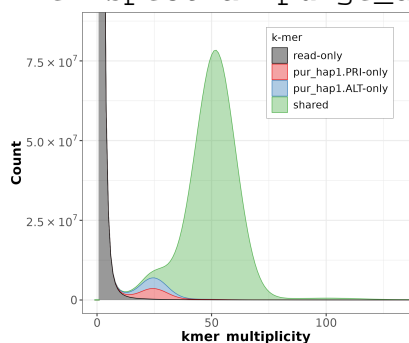


11Hi_hap1_merqOutput.spectra-asm.st.png

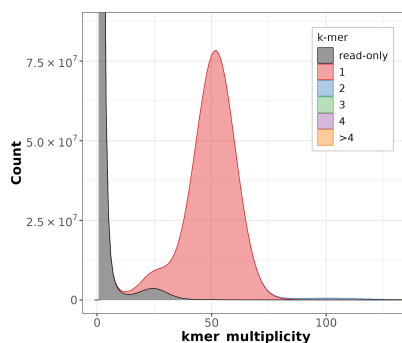


11Hi_hap1_merqOutput.spectra-cn.st.png

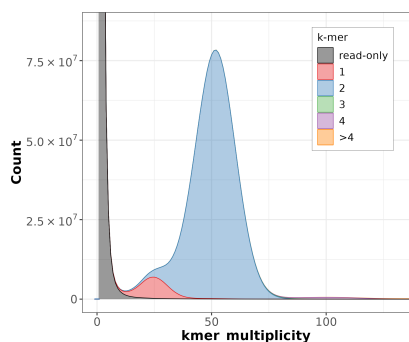
K-mer spectra: purge_dups



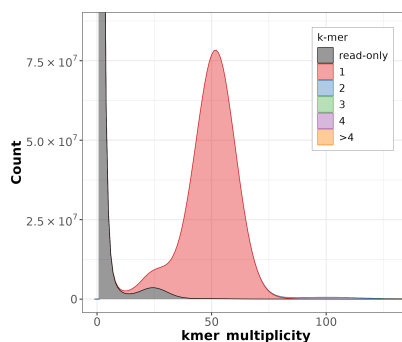
pur_hap1_merqOutput.spectra-asm.st.png



pur_hap1_merqOutput.pur_hap1.PRI.spectra-cn.st.png



pur_hap1_merqOutput.spectra-cn.st.png



pur_hap1_merqOutput.pur_hap1.ALT.spectra-cn.st.png

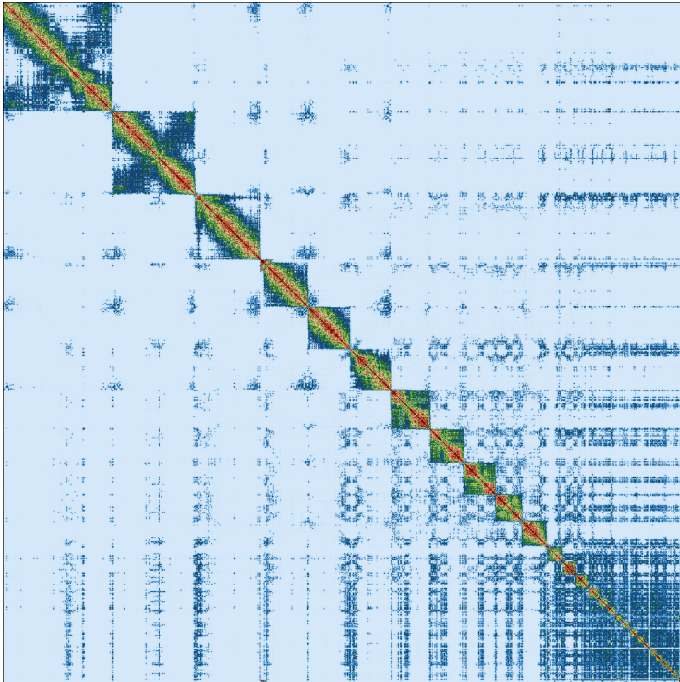
Genome assembly: scaffolding

Metrics	Bionano hap1	Bionano hap2	YaHS hap1	YaHS hap2
Total bp	2,220,191,759	2,207,617,369	2,220,195,358	2,207,621,769
GC %	44.12	44.11	44.12	44.11
Gaps	38	27	55	49
Gaps/Gbp	17.12	12.23	24.77	22.2
Gaps bp	3,499,185	2,055,969	3,502,772	2,060,369
Scaffolds	57	57	41	35
Longest Scaf.	355,489,124	210,263,708	355,489,123	356,830,969
Scaffold auN	144,780,868.66	114,892,365.06	167,596,863.48	167,403,878.03
Scaffold N50	127,105,400	126,644,623	137,541,926	137,610,697
Scaffold L50	7	8	5	5
Scaffold L90	21	22	18	18
Contigs	95	84	96	84
Largest Cont.	354,291,630	210,263,708	355,007,410	210,263,708
Contig auN	141,094,921.93	108,830,894.98	141,322,292.78	108,830,894.98
Contig N50	124,322,749	119,638,208	124,322,749	119,638,208
Contig L50	7	8	7	8
Contig L90	24	25	24	25
QV	68.7149	67.9889	68.7149	67.9889
Kmer compl.	96.6829	96.6394	96.6829	96.6394
BUSCO sing.	96.4%	96.4%	96.4%	96.4%
BUSCO dupl.	0.9%	0.9%	0.9%	0.8%
BUSCO frag.	0.4%	0.4%	0.4%	0.4%
BUSCO miss.	2.3%	2.3%	2.3%	2.4%

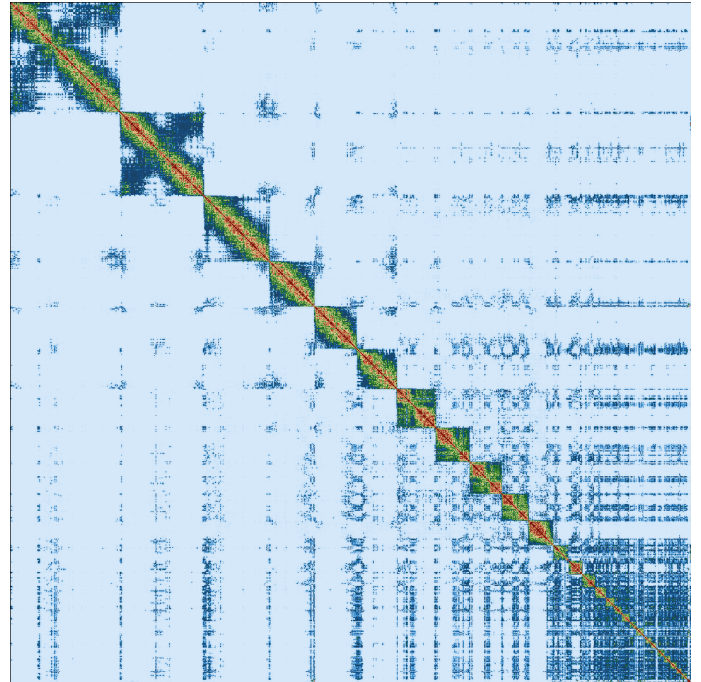
Lineage: sauropsida_odb10 (genomes:76, BUSCOs:7480)

Pretext Full Map: Bionano
Data not available

Pretext Full Map: YaHS



yahs_hap1FullMap.png



yahs_hap2FullMap.png

Submitter: Diego De Panis

Affiliation: BeGenDiv

Date and time: 2023-07-21 14:10:13 CEST