

ERGA Assembly Report

v23.09.27_beta

Tags: ERGA-BGE

ToLID	mRupRup1
Species	Rupicapra rupicapra
Class	Mammalia
Order	Artiodactyla
Haploid Number	29 (source: direct)
Ploidy	2
Sex	XY

Data profile

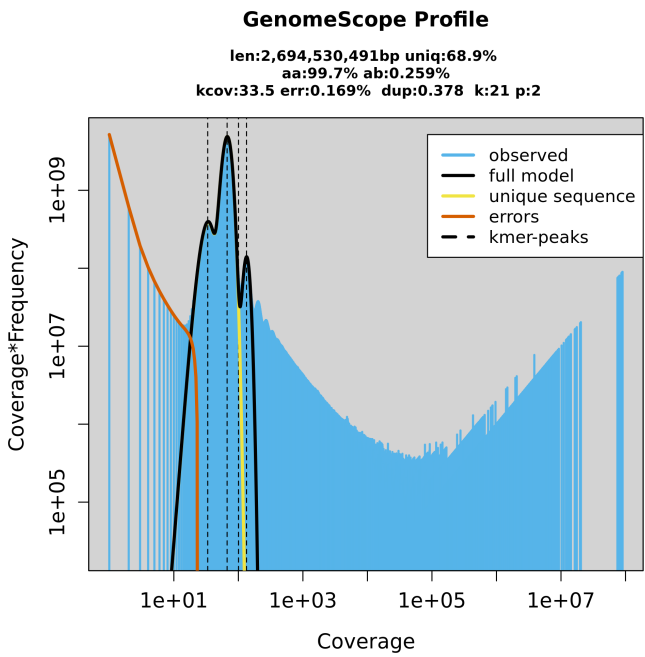
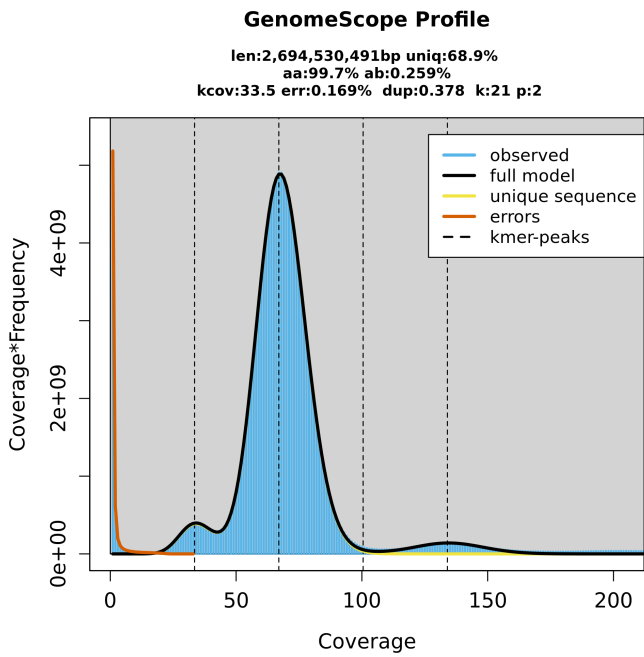
Data	Coverage
ONT	125x
Illumina	84x
OmniC	90x

Pipeline summary

Tool	Version
GenomeScope	2.0
nextdenovo	2.5.0
hypo	1.0.3
purge_dups	1.2.6
YaHS	1.2a

Genome profiling

Estimated Haploid Length	2,693,478,497
Heterozygosity rate	0.255429%
Kmer coverage	33.49
Proposed ploidy	NA



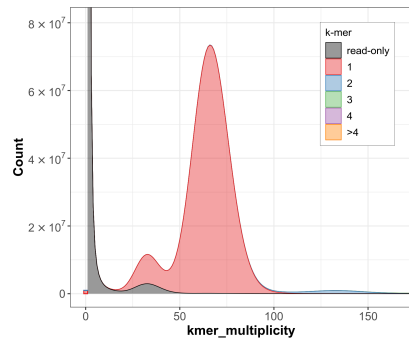
Smudgeplot data not available

Genome assembly: contigging

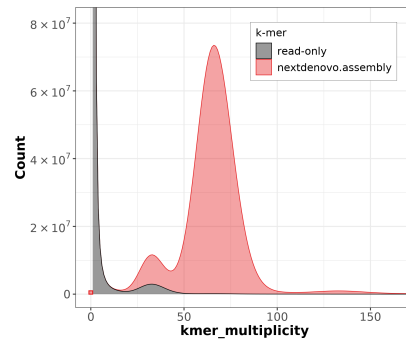
Metrics	nextdenovo collapsed	hypo collapsed	purge_dups collapsed
Total bp	2,635,138,187	2,634,216,371	2,623,456,591
GC %	42.03	42.04	41.99
Gaps	0	0	0
Gaps/Gbp	0	0	0
Gaps bp	0	0	0
Scaffolds	161	161	110
Longest Scaf.	231,319,989	231,237,611	231,237,611
Scaffold auN	84,338,779.48	84,308,539.14	84,650,578.7
Scaffold N50	77,685,936	77,662,214	77,662,214
Scaffold L50	12	12	12
Scaffold L90	36	36	35
Contigs	161	161	110
Largest Cont.	231,319,989	231,237,611	231,237,611
Contig auN	84,338,779.48	84,308,539.14	84,650,578.7
Contig N50	77,685,936	77,662,214	77,662,214
Contig L50	12	12	12
Contig L90	36	36	35
QV	47.455	54.8133	55.4348
Kmer compl.	97.0513	97.1149	97.0448
BUSCO sing.	93.4%	93.4%	93.5%
BUSCO dupl.	4.1%	4.2%	4.1%
BUSCO frag.	1.2%	1.1%	1.1%
BUSCO miss.	1.3%	1.3%	1.3%

Lineage: vertebrata_odb10 (genomes:67, BUSCOs:3354)

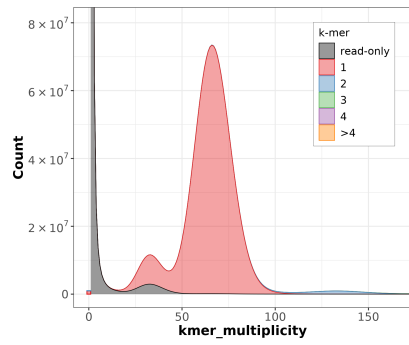
K-mer spectra: nextdenovo



nextdenovo.assembly.spectra-cn.st.png

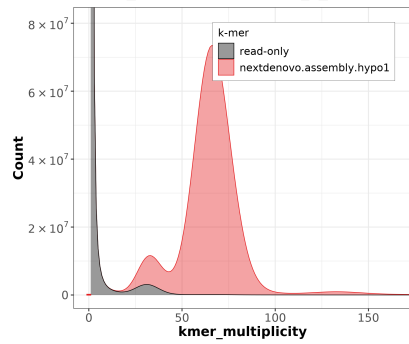


nextdenovo.assembly.spectra-asm.st.png

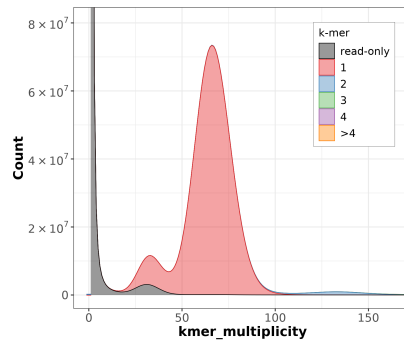


nextdenovo.assembly.nextdenovo.assembly.spectra-cn.st.png

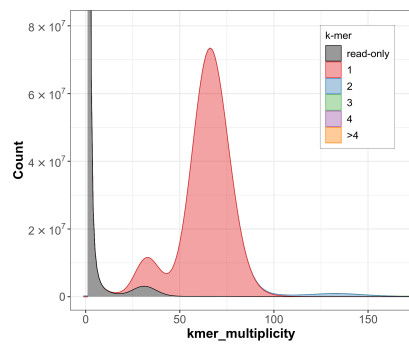
K-mer spectra: hypo



nextdenovo.assembly.hypo1.spectra-asm.st.png

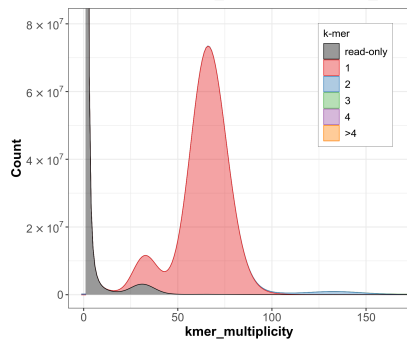


nextdenovo.assembly.hypo1.nextdenovo.assembly.hypo1.spectra-cn.st.png

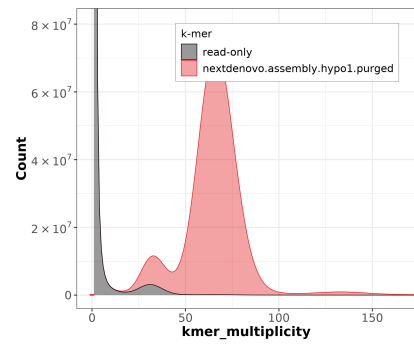


nextdenovo.assembly.hypo1.spectra-cn.st.png

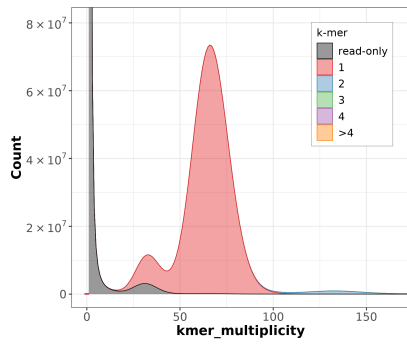
K-mer spectra: purge_dups



nextdenovo.assembly.hypo1.purged.spectra-cn.st.png



nextdenovo.assembly.hypo1.purged.spectra-asm.st.png



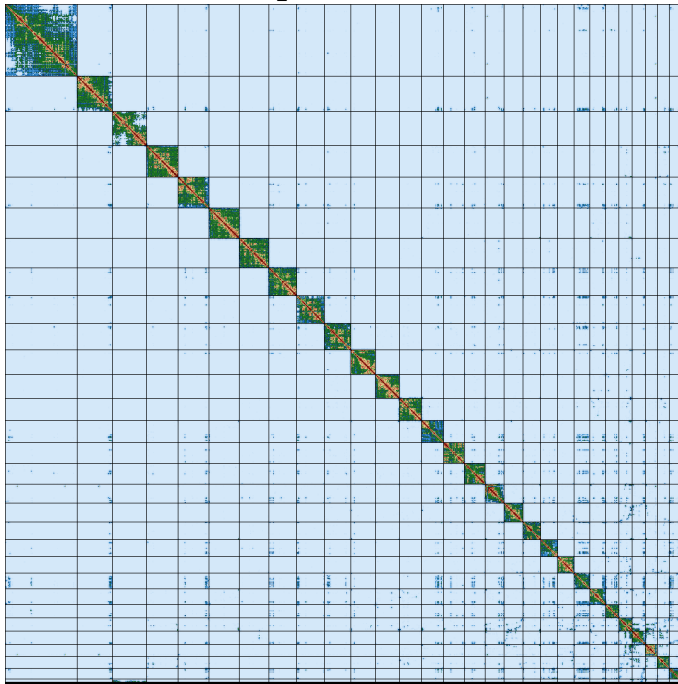
nextdenovo.assembly.hypo1.purged.nextdenovo.assembly.hypo1.purged.spectra-cn.st.png

Genome assembly: scaffolding

Metrics	YaHS collapsed
Total bp	2,623,465,591
GC %	41.99
Gaps	45
Gaps/Gbp	17.15
Gaps bp	9,000
Scaffolds	80
Longest Scaf.	277,742,375
Scaffold auN	111,088,511.92
Scaffold N50	100,920,001
Scaffold L50	10
Scaffold L90	24
Contigs	125
Largest Cont.	151,282,611
Contig auN	75,427,999
Contig N50	77,662,214
Contig L50	13
Contig L90	36
QV	55.4348
Kmer compl.	97.0448
BUSCO sing.	93.6%
BUSCO dupl.	4.1%
BUSCO frag.	1.1%
BUSCO miss.	1.2%

Lineage: vertebrata_odb10 (genomes:67, BUSCOs:3354)

Pretext Full Map: YaHS



assembly_mq40.mRupRup_yahs_scaffolds_final_FullMap.png

Submitter: Francisco Camara Ferreira
Affiliation: CNAG Barcelona

Date and time: 2023-10-19 17:04:33 CEST