

ERGA Assembly Report

v23.09.27_beta

Tags: ERGA-BGE

ToLID	mApoAgr2
Species	Apodemus agrarius
Class	Mammalia
Order	Rodentia
Haploid Number	24 (source: direct)
Ploidy	2
Sex	XY

Data profile

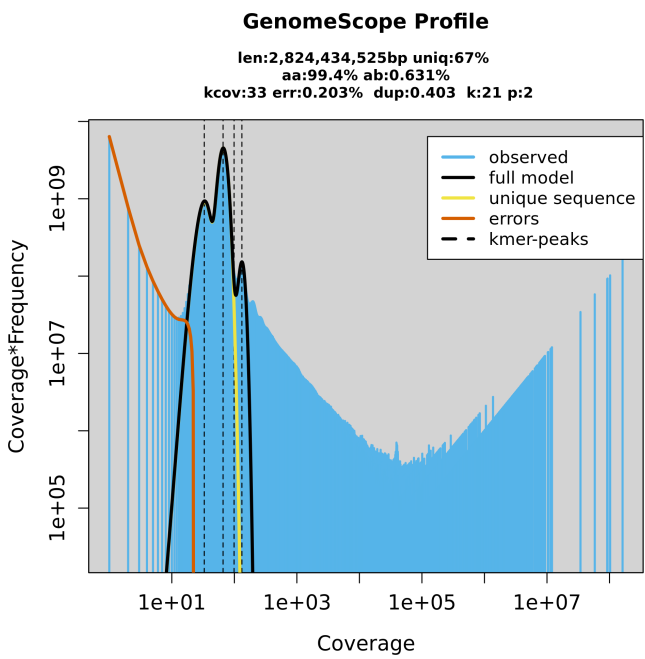
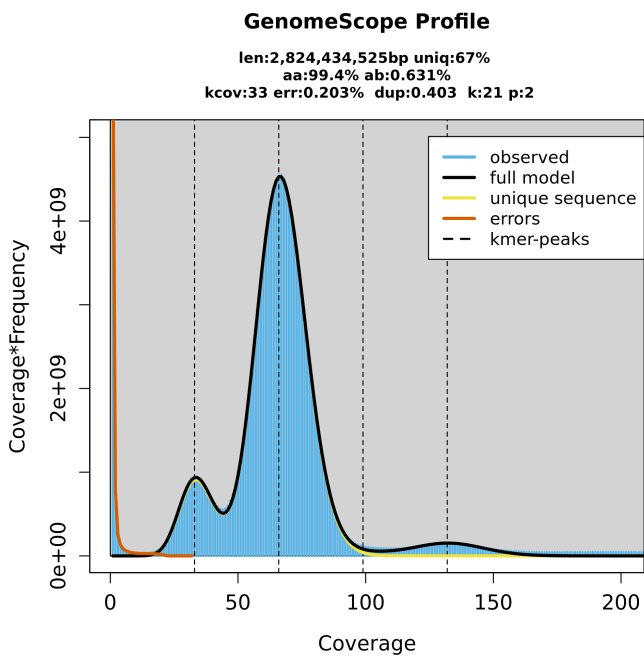
Data	Coverage
ONT	91x
Illumina	87x
OmniC	64x

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	2,822,679,104
Heterozygosity rate	0.62582%
Kmer coverage	32.99
Proposed ploidy	NA



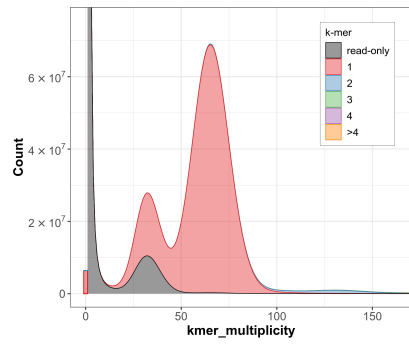
Smudgeplot data not available

Genome assembly: contigging

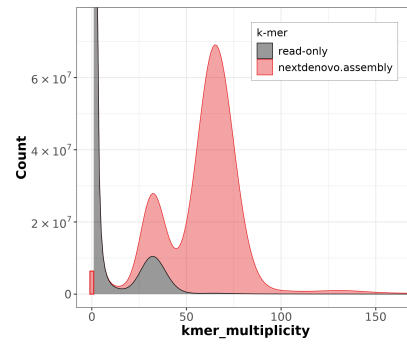
Metrics	nextdenovo collapsed	hypo collapsed	purge_dups collapsed
Total bp	2,739,388,197	2,735,574,192	2,614,502,752
GC %	41.92	41.92	42.15
Gaps	0	0	0
Gaps/Gbp	0	0	0
Gaps bp	0	0	0
Scaffolds	520	520	230
Longest Scaf.	127,681,666	127,492,201	127,492,201
Scaffold auN	42,582,148.1	42,517,659.88	44,447,888.33
Scaffold N50	35,235,519	35,188,814	35,357,088
Scaffold L50	23	23	22
Scaffold L90	101	101	81
Contigs	520	520	230
Largest Cont.	127,681,666	127,492,201	127,492,201
Contig auN	42,582,148.1	42,517,659.88	44,447,888.33
Contig N50	35,235,519	35,188,814	35,357,088
Contig L50	23	23	22
Contig L90	101	101	81
QV	39.5378	46.8002	47.2298
Kmer compl.	91.4232	91.7218	90.9325
BUSCO sing.	96.1%	96.2%	96.3%
BUSCO dupl.	2.1%	2.1%	2.0%
BUSCO frag.	0.6%	0.6%	0.6%
BUSCO miss.	1.2%	1.1%	1.1%

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

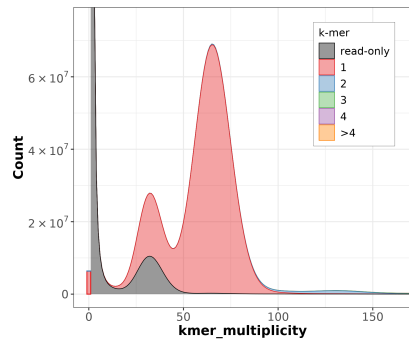
K-mer spectra: nextdenovo



nextdenovo.assembly.spectra-cn.st.png

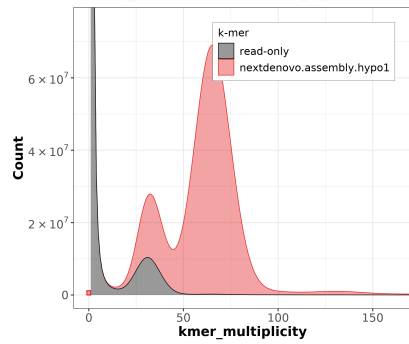


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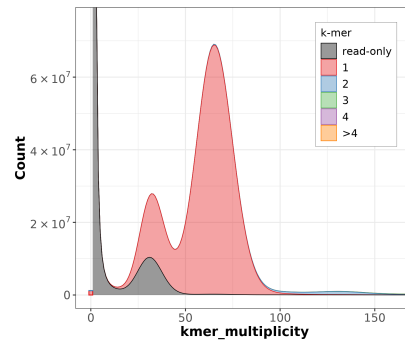


nextdenovo.assembly.nextdenovo.assembly.spectra-cn.st.png

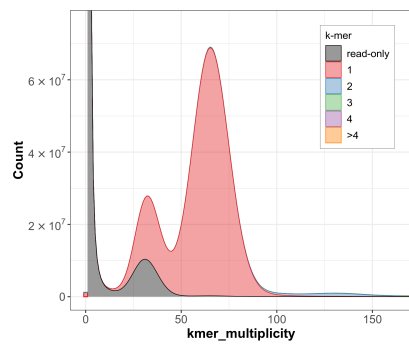
K-mer spectra: hypo



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

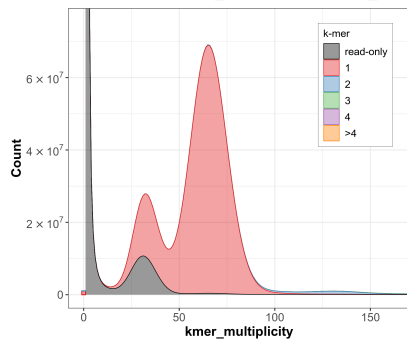


nextdenovo.assembly.hypo1.nextdenovo.assembly.hypo1.spectra-cn.st.png

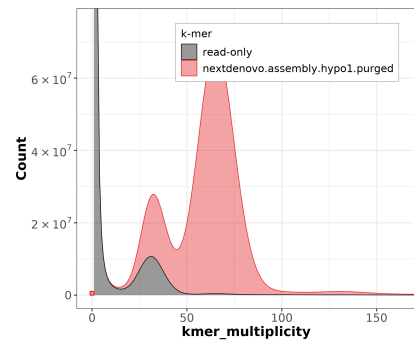


nextdenovo.assembly.hypo1.spectra-cn.st.png

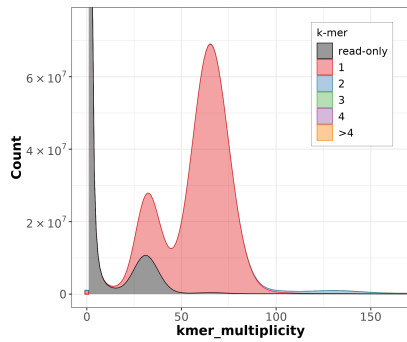
K-mer spectra: purge_dups



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



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



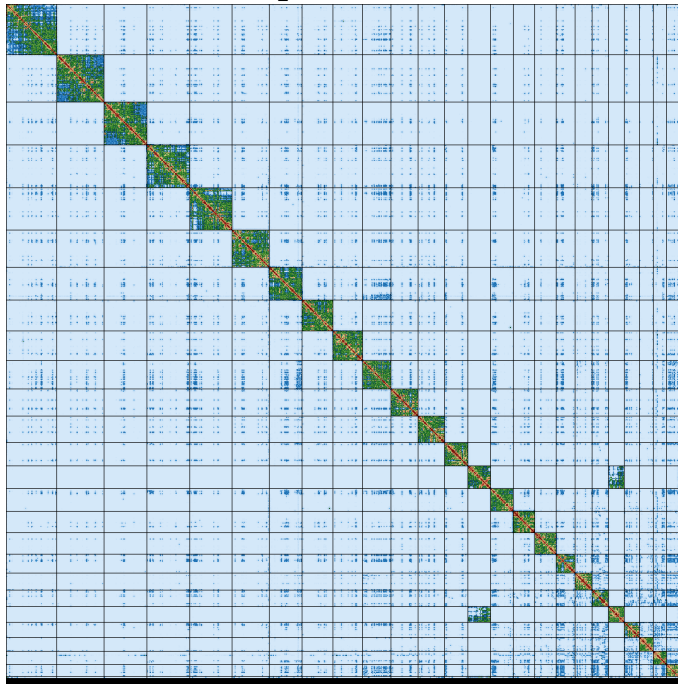
nextdenovo.assembly.hypo1.purged.nextdenovo.assembly.hypo1.purged.spectra-cn.st.png

Genome assembly: scaffolding

Metrics	YaHS collapsed
Total bp	2,614,536,552
GC %	42.15
Gaps	169
Gaps/Gbp	64.64
Gaps bp	33,800
Scaffolds	75
Longest Scaf.	194,999,511
Scaffold auN	119,562,307.49
Scaffold N50	113,335,371
Scaffold L50	9
Scaffold L90	21
Contigs	244
Largest Cont.	127,492,201
Contig auN	43,130,599.87
Contig N50	35,188,814
Contig L50	22
Contig L90	85
QV	47.2298
Kmer compl.	90.9325
BUSCO sing.	96.4%
BUSCO dupl.	1.9%
BUSCO frag.	0.5%
BUSCO miss.	1.2%

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

Pretext Full Map: YaHS



assembly_mq40.mApoAgr_yahs_scaffolds_final_FullMap.png

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Date and time: 2023-10-19 10:32:07 CEST