

ERGA Assembly Report

v21.07.23_beta

Tags: ERGA-Pilot

ToLID	mLepGra1
Species	Lepus granatensis
Class	Mammalia
Order	Lagomorpha
Haploid Number	24 (source: ['ancestor'])
Ploidy	2

Data profile

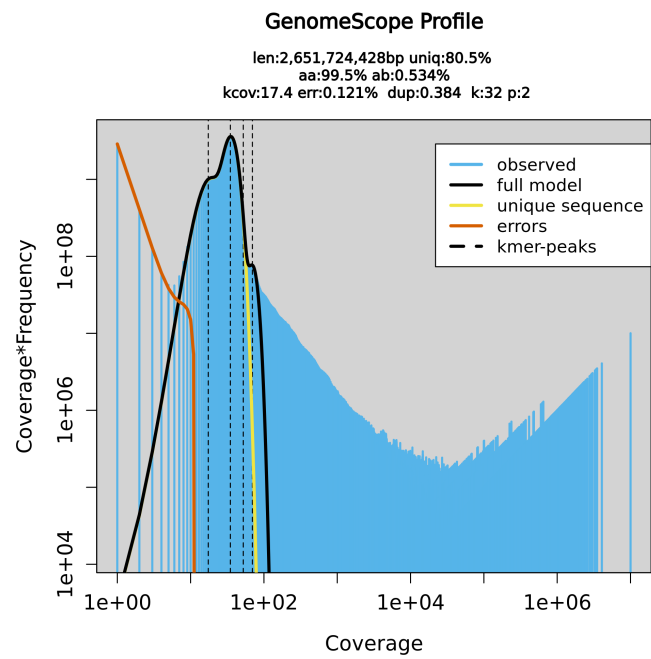
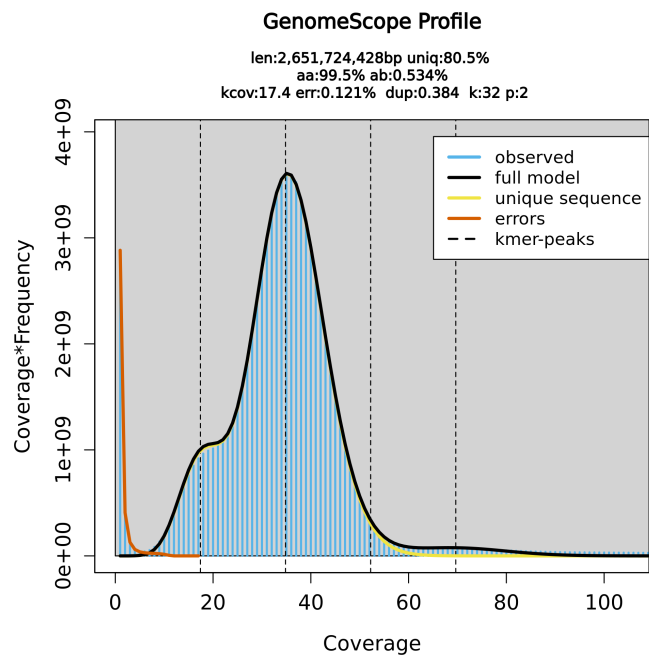
Data	Coverage
HiFi	30
Omni-C	41

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	2,649,839,768
Heterozygosity rate	0.528403%
Kmer coverage	17.41
Proposed ploidy	NA



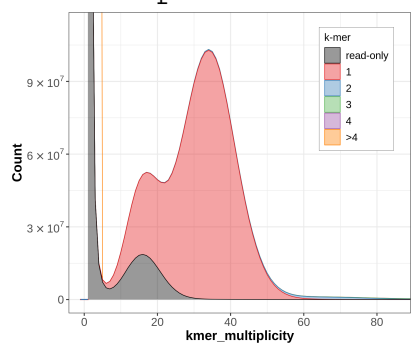
Smudgeplot data not available

Genome assembly: contigging

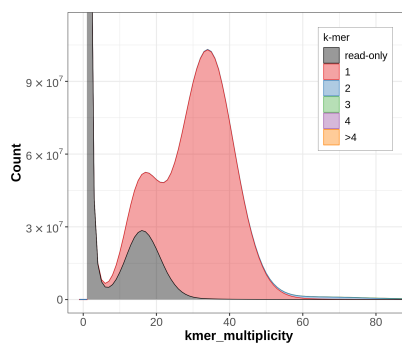
Metrics	Hifiasm hap1	Hifiasm hap2	purge_dups hap1	purge_dups hap2
Total bp	2,854,707,454	2,648,734,717	2,767,824,691	2,611,805,755
GC %	44.14	44.23	44	44.2
Gaps	0	0	0	0
Gaps/Gbp	0	0	0	0
Gaps bp	0	0	0	0
Scaffolds	668	518	387	378
Longest Scaf.	118,284,076	96,004,977	118,284,076	96,004,977
Scaffold auN	49,428,277.25	39,280,000.49	50,888,338.02	39,857,519.85
Scaffold N50	39,923,227	33,181,983	41,926,770	33,181,983
Scaffold L50	21	24	20	24
Scaffold L90	96	102	80	93
Contigs	668	518	387	378
Largest Cont.	118,284,076	96,004,977	118,284,076	96,004,977
Contig auN	49,428,277.25	39,280,000.49	50,888,338.02	39,857,519.85
Contig N50	39,923,227	33,181,983	41,926,770	33,181,983
Contig L50	21	24	20	24
Contig L90	96	102	80	93
QV	63.0814	63.2415	63.5575	63.485
Kmer compl.	90.9177	86.2998	90.6465	86.2182
BUSCO sing.	92.5%	90.0%	92.7%	90.1%
BUSCO dupl.	2.7%	2.5%	2.6%	2.5%
BUSCO frag.	0.9%	0.9%	0.9%	0.9%
BUSCO miss.	3.9%	6.6%	3.8%	6.5%

Lineage: euarchontoglires_odb10 (genomes:51, BUSCOs:12692)

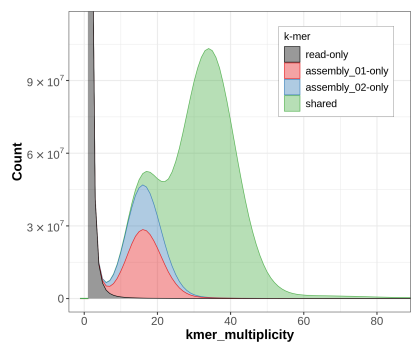
K-mer spectra: Hifiiasm



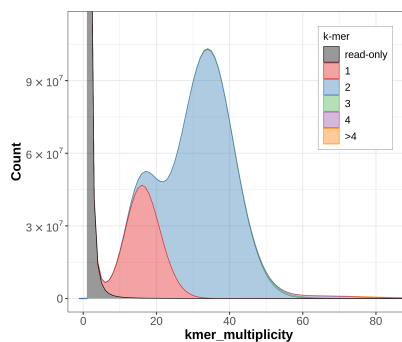
output_mercury_assembly_withHiC.assembly_01.spectra-cn.st.png



output_mercury_assembly_withHiC.assembly_02.spectra-cn.st.png

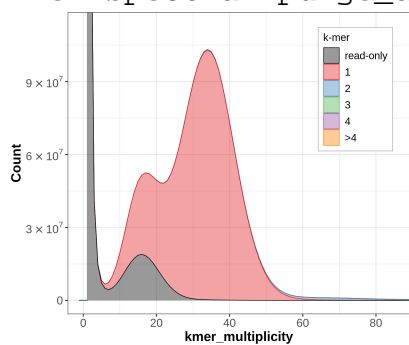


output_mercury_assembly_withHiC.spectra-asm.st.png

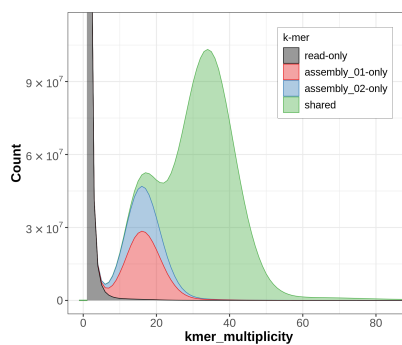


output_mercury_assembly_withHiC.spectra-cn.st.png

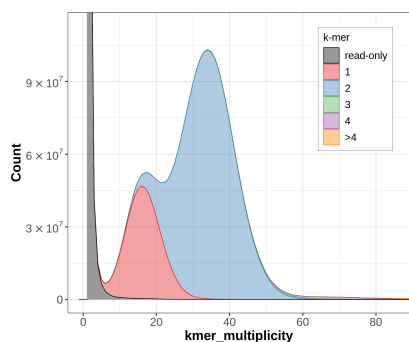
K-mer spectra: purge_dups



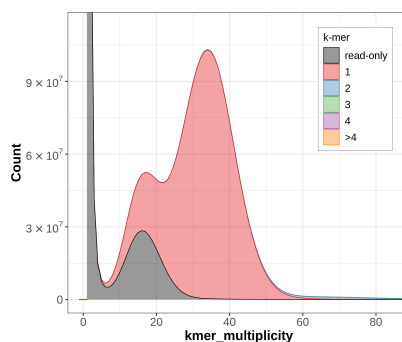
output_mercury_purged.assembly_01.spectra-cn.st.png



output_mercury_purged.spectra-asm.st.png



output_mercury_purged.spectra-cn.st.png



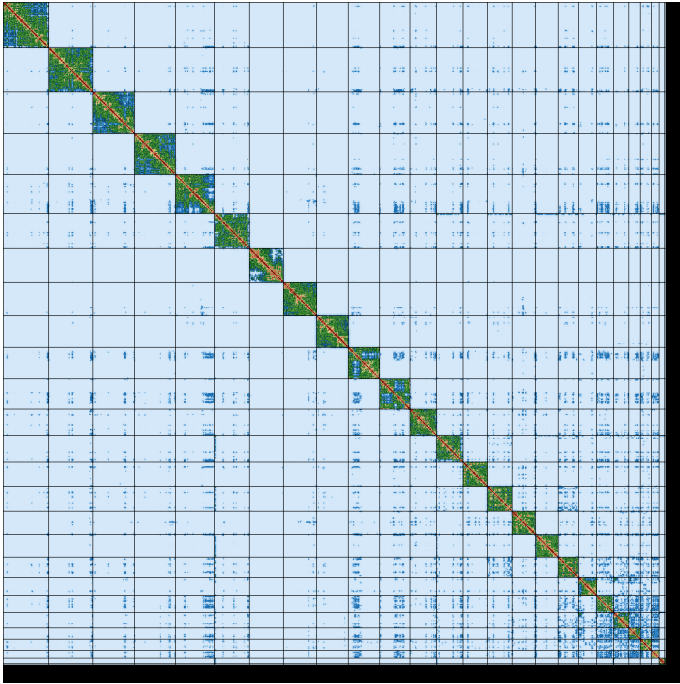
output_mercury_purged.assembly_02.spectra-cn.st.png

Genome assembly: scaffolding

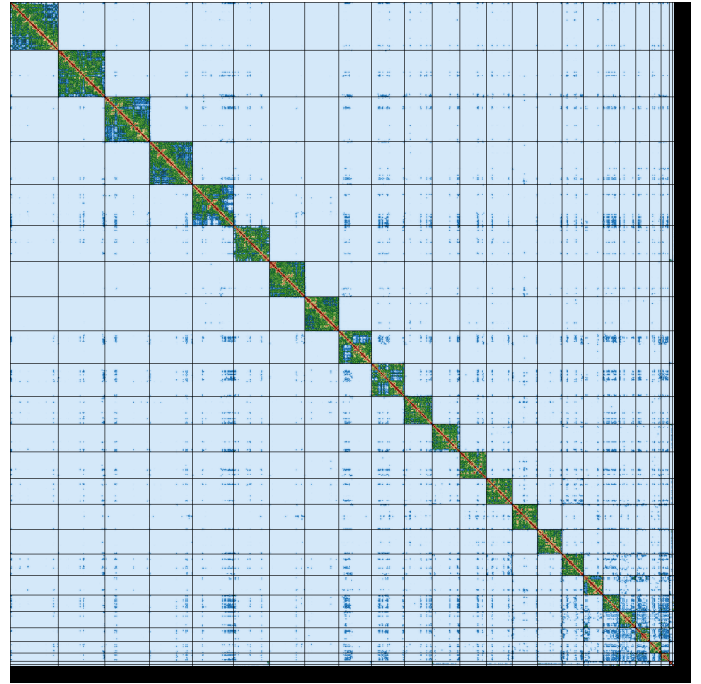
Metrics	YaHS hap1	YaHS hap2
Total bp	2,767,865,091	2,611,846,755
GC %	44	44.2
Gaps	202	205
Gaps/Gbp	72.98	78.49
Gaps bp	40,400	41,000
Scaffolds	226	207
Longest Scaf.	186,713,132	185,802,554
Scaffold auN	123,262,719.36	122,843,397.86
Scaffold N50	129,958,636	125,776,363
Scaffold L50	9	9
Scaffold L90	21	20
Contigs	428	412
Largest Cont.	118,284,076	96,004,977
Contig auN	47,381,042.56	39,720,531.91
Contig N50	41,926,770	33,181,983
Contig L50	21	24
Contig L90	83	95
QV	63.5575	63.485
Kmer compl.	90.6465	86.2182
BUSCO sing.	92.8%	90.2%
BUSCO dupl.	2.6%	2.4%
BUSCO frag.	0.9%	0.8%
BUSCO miss.	3.7%	6.6%

Lineage: euarchontoglires_odb10 (genomes:51, BUSCOs:12692)

Pretext Full Map: YaHS



LepGra_withHiC_yash_sort_Hap1_Filter.map_FullMap.png



LepGra_withHiC_yash_sort_Hap2_Filter.map_FullMap.png

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Date and time: 2023-09-02 09:44:51 CEST