

ERGA Assembly Report

v21.07.23_beta

Tags: ERGA-Pilot

ToLID	bOenLec1
Species	Oenanthe leucura
Class	Aves
Order	Passeriformes
Haploid Number	41 (source: ['ancestor'])
Ploidy	2

Data profile

Data	Coverage
HiFi	40
Omni-C	62

Pipeline summary

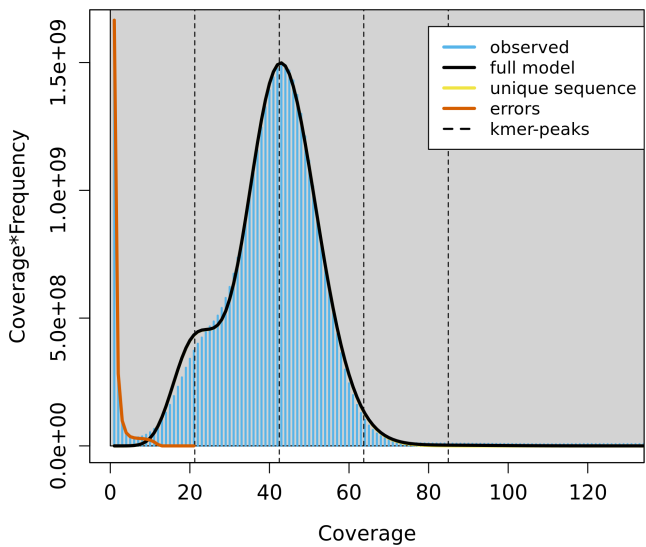
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.19.5-r587
purge_dups	1.2.5
YaHS	1.2a.1

Genome profiling

Estimated Haploid Length	1,074,610,835
Heterozygosity rate	0.560172%
Kmer coverage	21.24
Proposed ploidy	4

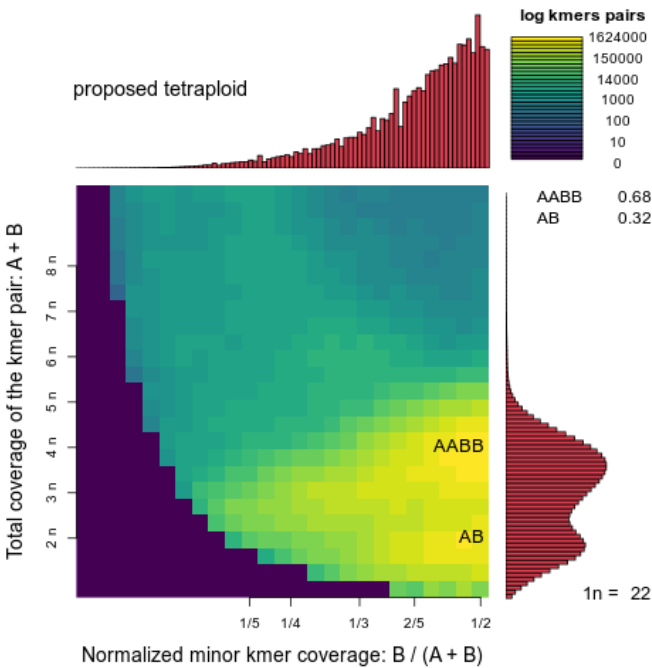
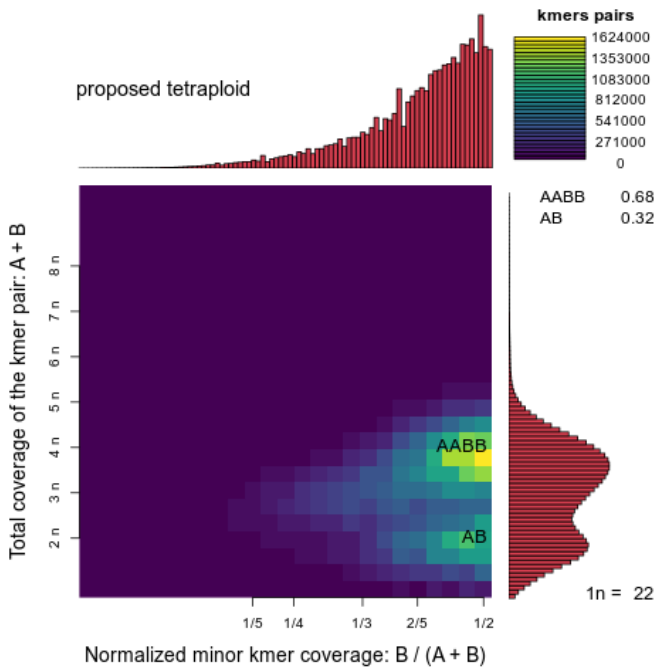
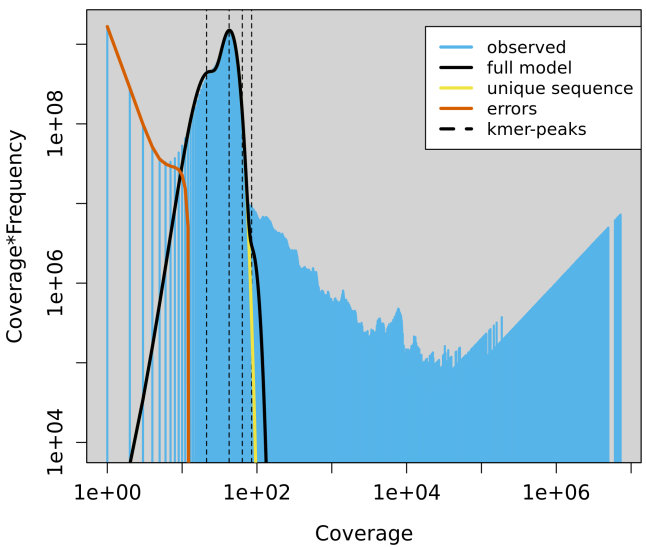
GenomeScope Profile

len:1,075,728,846bp uniq:83.9%
aa:99.4% ab:0.565%
kcov:21.2 err:0.153% dup:0.716 k:32 p:2



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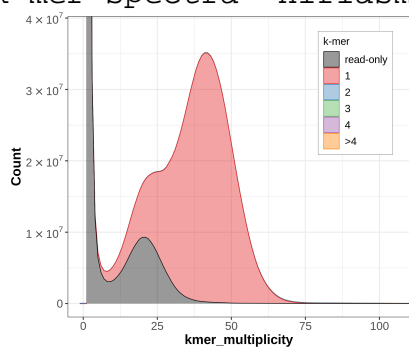


Genome assembly: contigging

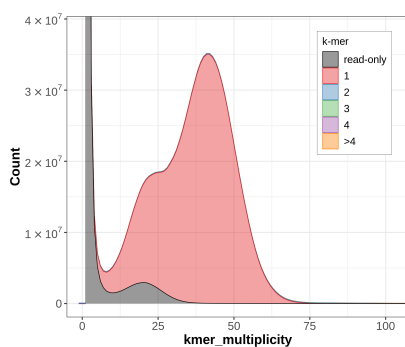
Metrics	Hifiasm hap1	Hifiasm hap2	purge_dups hap1	purge_dups hap2
Total bp	1,419,116,716	1,082,018,623	1,287,024,143	1,014,594,015
GC %	44.03	42.93	43.49	42.57
Gaps	0	0	0	0
Gaps/Gbp	0	0	0	0
Gaps bp	0	0	0	0
Scaffolds	1,840	968	1,248	701
Longest Scaf.	50,893,815	46,781,288	50,893,815	46,781,288
Scaffold auN	13,115,678.05	15,260,962.33	14,411,178.17	16,239,281.34
Scaffold N50	6,335,672	12,112,024	9,593,778	13,360,684
Scaffold L50	38	24	30	21
Scaffold L90	628	245	364	154
Contigs	1,840	968	1,248	701
Largest Cont.	50,893,815	46,781,288	50,893,815	46,781,288
Contig auN	13,115,678.05	15,260,962.33	14,411,178.17	16,239,281.34
Contig N50	6,335,672	12,112,024	9,593,778	13,360,684
Contig L50	38	24	30	21
Contig L90	628	245	364	154
QV	59.5944	60.7433	60.0307	60.8987
Kmer compl.	95.3311	85.6436	95.1185	85.4956
BUSCO sing.	96.0%	88.0%	96.0%	88.1%
BUSCO dupl.	0.4%	0.3%	0.4%	0.2%
BUSCO frag.	0.6%	0.6%	0.6%	0.6%
BUSCO miss.	3.0%	11.1%	3.0%	11.1%

Lineage: passeriformes_odb10 (genomes:15, BUSCOs:10844)

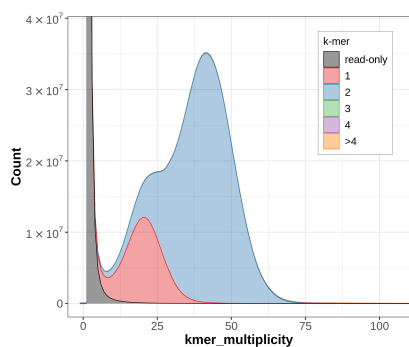
K-mer spectra: Hifiasm



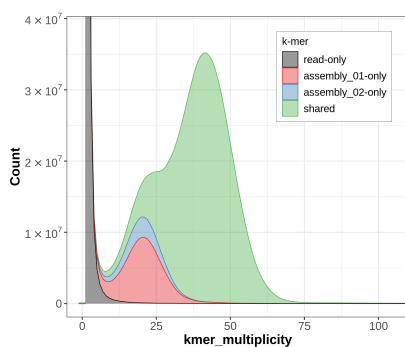
output_mercury_hifiasm.assembly_02.spectra-cn.st.png



output_mercury_hifiasm.assembly_01.spectra-cn.st.png

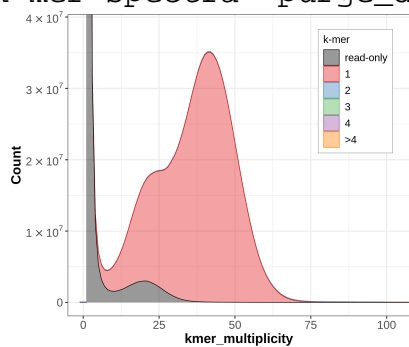


output_mercury_hifiasm.spectra-cn.st.png

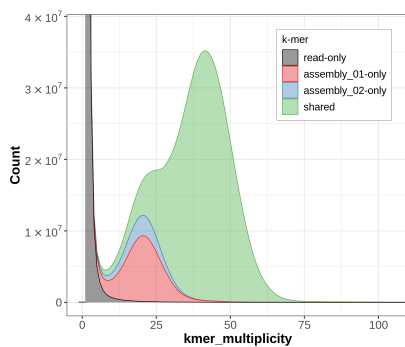


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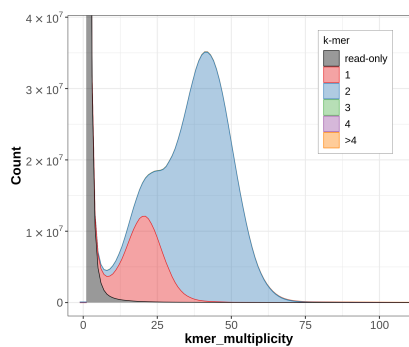
K-mer spectra: purge_dups



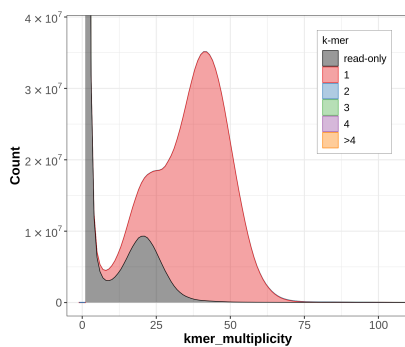
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output_mercury_purged.spectra-asm.st.png



output_mercury_purged.spectra-cn.st.png



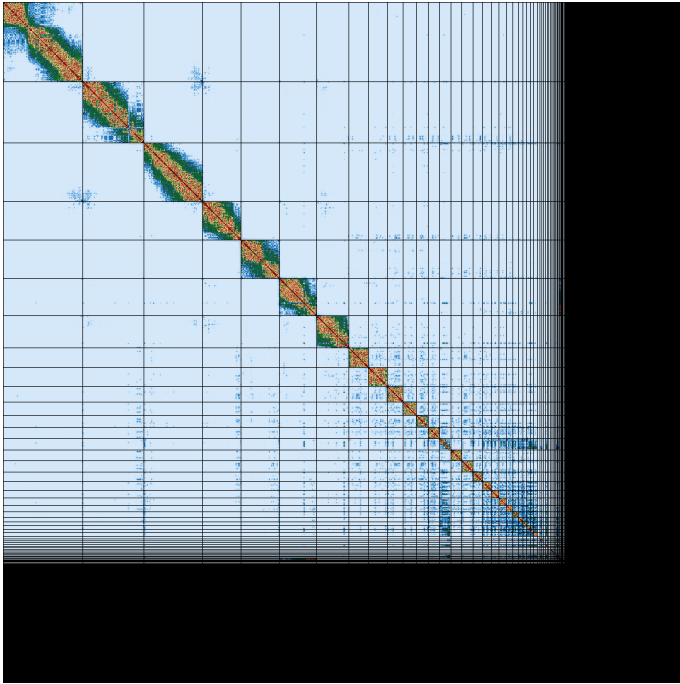
output_mercury_purged.assembly_02.spectra-cn.st.png

Genome assembly: scaffolding

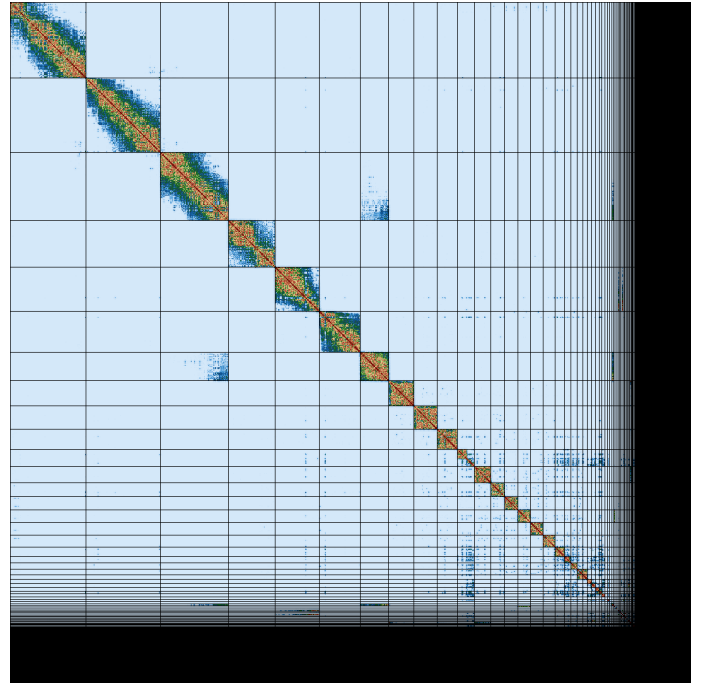
Metrics	YaHS hap1	YaHS hap2
Total bp	1,287,096,543	1,014,641,815
GC %	43.49	42.57
Gaps	362	239
Gaps/Gbp	281.25	235.55
Gaps bp	72,400	47,800
Scaffolds	996	520
Longest Scaf.	150,531,765	113,289,874
Scaffold auN	58,902,299.86	56,587,863.86
Scaffold N50	60,879,671	60,438,311
Scaffold L50	7	6
Scaffold L90	193	38
Contigs	1,358	759
Largest Cont.	50,893,815	46,781,288
Contig auN	14,241,011.25	16,214,975.83
Contig N50	9,254,000	13,360,684
Contig L50	30	21
Contig L90	413	159
QV	60.0307	60.8987
Kmer compl.	95.1185	85.4956
BUSCO sing.	96.1%	88.2%
BUSCO dupl.	0.4%	0.2%
BUSCO frag.	0.6%	0.6%
BUSCO miss.	2.9%	11.0%

Lineage: passeriformes_odb10 (genomes:15, BUSCOs:10844)

Pretext Full Map: YaHS



OenLeu_withHiC_yash_sort_Hap1_Filter.map_FullMap.png



OenLeu_withHiC_yash_sort_Hap2_Filter.map_FullMap.png

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Affiliation: BIOPOLIS-CIBIO

Date and time: 2023-08-28 18:28:53 CEST