

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

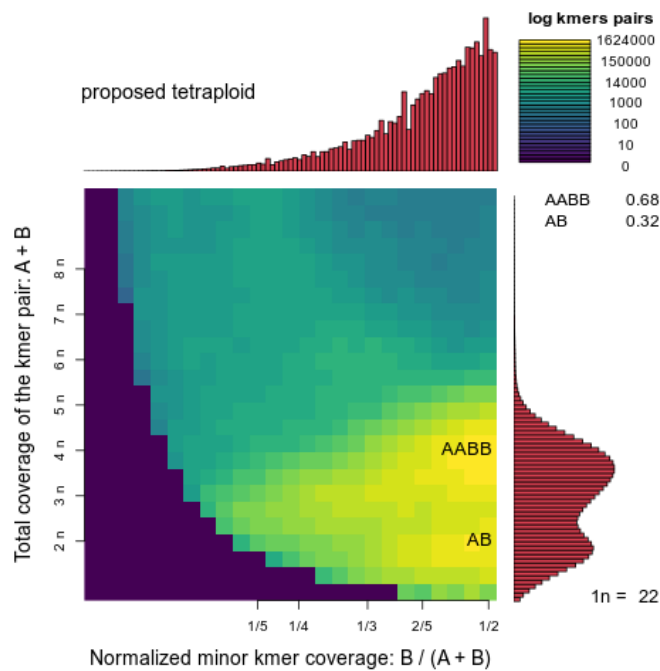
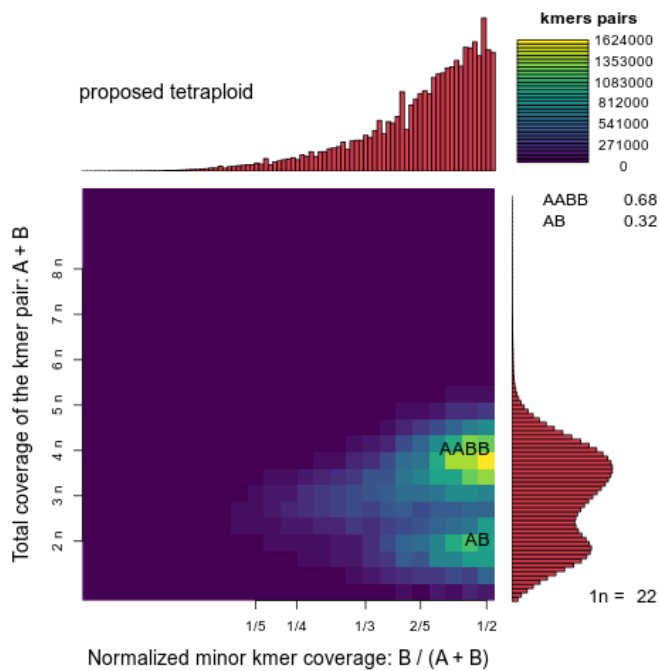
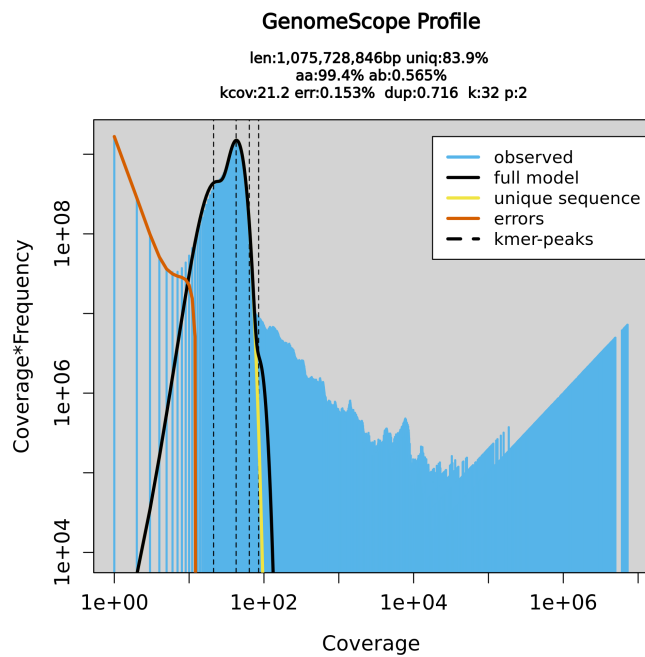
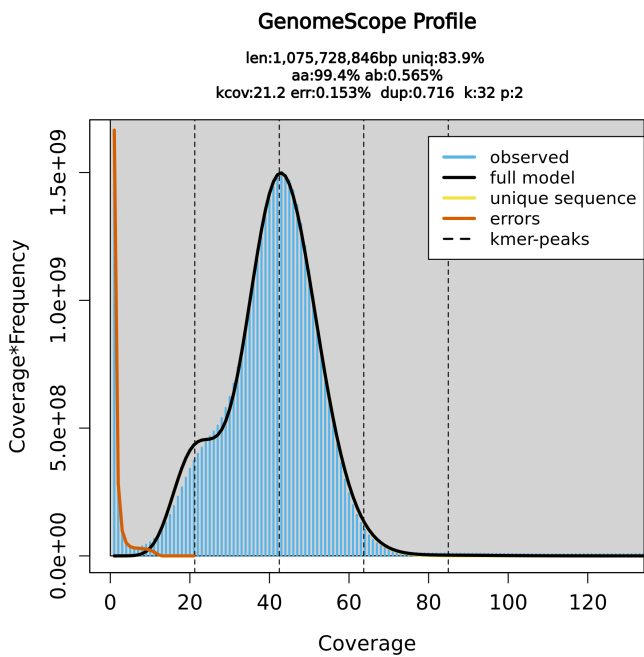
Data	Coverage
HiFi	40
Omni-C	62

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

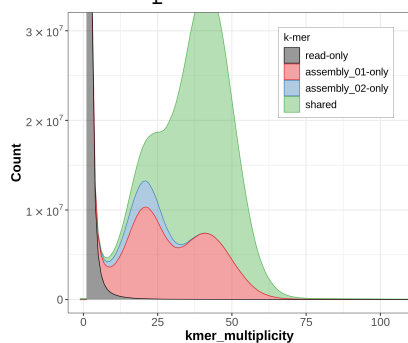


Genome assembly: contigging

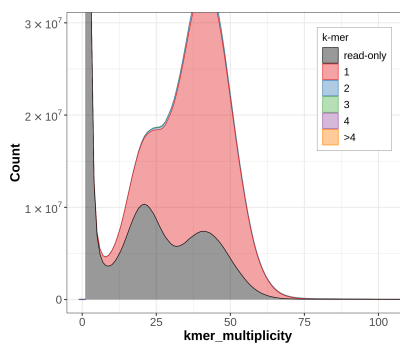
Metrics	Hifiasm pri	Hifiasm alt	purge_dups pri	purge_dups alt
Total bp	1,439,947,800	961,987,949	1,287,398,044	867,152,945
GC %	44.08	43.38	43.51	42.83
Gaps	0	0	0	0
Gaps/Gbp	0	0	0	0
Gaps bp	0	0	0	0
Scaffolds	1,771	7,495	1,082	4,106
Longest Scaf.	52,532,269	2,594,042	52,532,269	3,133,655
Scaffold auN	16,710,502.73	523,850.29	18,569,467.89	617,742.32
Scaffold N50	9,121,822	386,472	13,613,749	481,464
Scaffold L50	29	667	23	520
Scaffold L90	505	3,604	282	2,006
Contigs	1,771	7,495	1,082	4,106
Largest Cont.	52,532,269	2,594,042	52,532,269	3,133,655
Contig auN	16,710,502.73	523,850.29	18,569,467.89	617,742.32
Contig N50	9,121,822	386,472	13,613,749	481,464
Contig L50	29	667	23	520
Contig L90	505	3,604	282	2,006
QV	59.2146	60.2918	60.0324	60.3211
Kmer compl.	95.3192	69.5031	95.1355	71.1488
BUSCO sing.	94.5%	69.2%	96.1%	71.0%
BUSCO dupl.	2.0%	0.8%	0.4%	0.4%
BUSCO frag.	0.6%	1.3%	0.6%	1.5%
BUSCO miss.	2.9%	28.7%	2.9%	27.1%

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

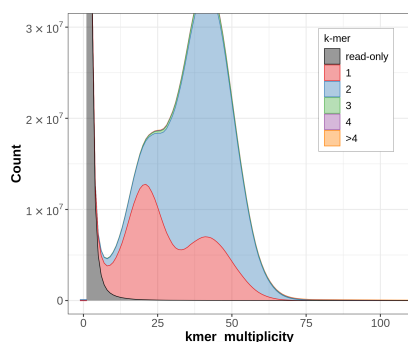
K-mer spectra: Hifiasm



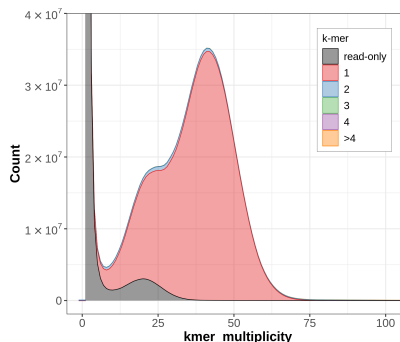
output_mercury_hifiasm_noHiC_pri_alt.spectra-asm.st.png



output_mercury_hifiasm_noHiC_pri_alt.assembly_02.spectra-cn.st.png

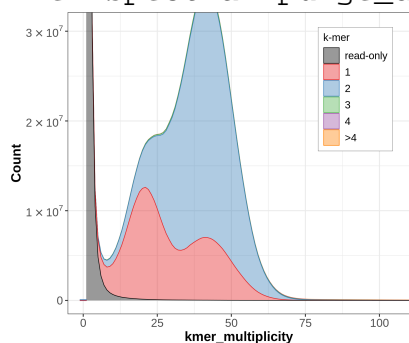


output_mercury_hifiasm_noHiC_pri_alt.spectra-cn.st.png

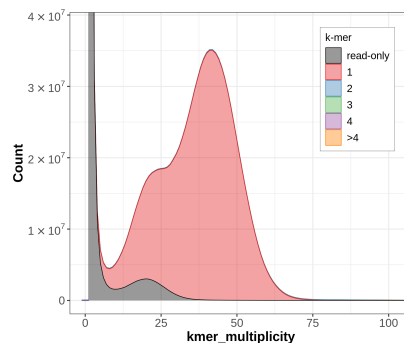


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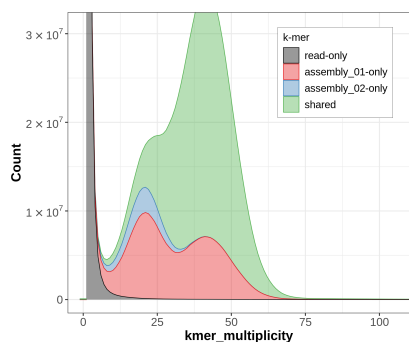
K-mer spectra: purge_dups



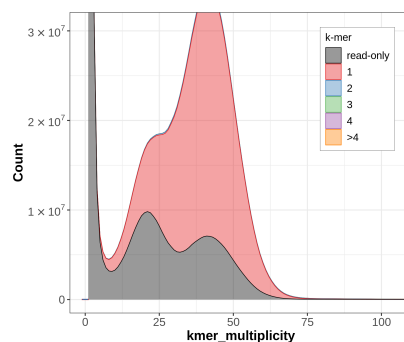
output_mercury_purged_noHiC.spectra-cn.st.png



output_mercury_purged_noHiC.assembly_01.spectra-cn.st.png



output_mercury_purged_noHiC.spectra-asm.st.png



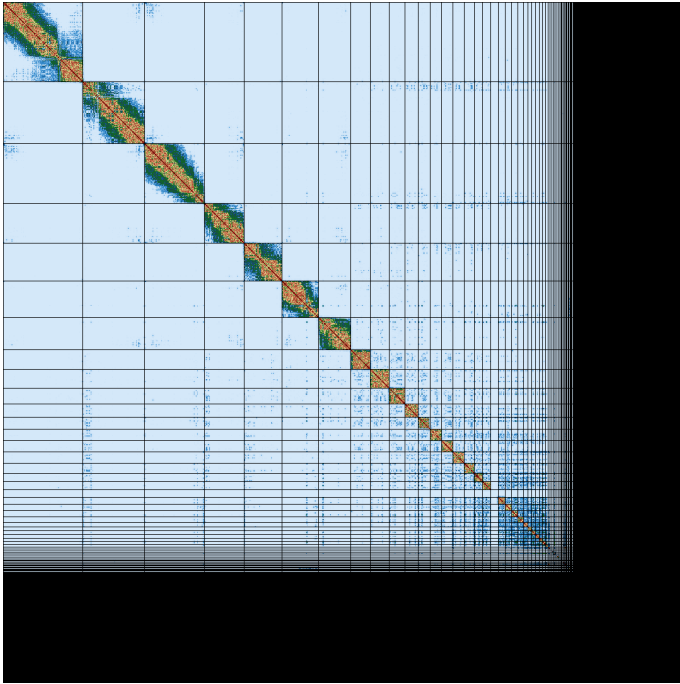
output_mercury_purged_noHiC.assembly_02.spectra-cn.st.png

Genome assembly: scaffolding

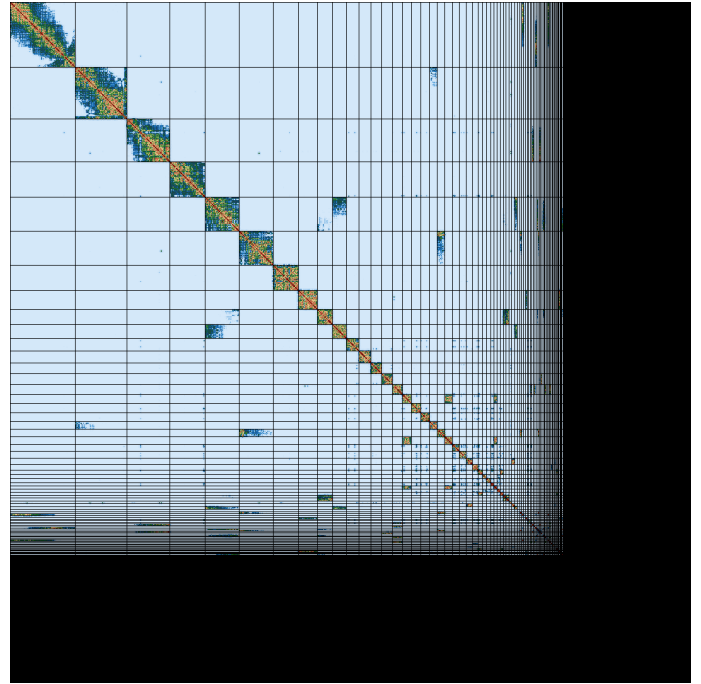
Metrics	YaHS pri	YaHS alt
Total bp	1,287,457,044	867,557,145
GC %	43.51	42.83
Gaps	295	2,021
Gaps/Gbp	229.13	2,329.53
Gaps bp	59,000	404,200
Scaffolds	870	2,127
Longest Scaf.	151,357,496	83,286,743
Scaffold auN	59,532,087.41	28,401,071.64
Scaffold N50	60,927,470	15,355,889
Scaffold L50	7	11
Scaffold L90	157	277
Contigs	1,165	4,148
Largest Cont.	52,532,269	3,133,655
Contig auN	18,437,257.38	609,699.19
Contig N50	13,563,000	474,302
Contig L50	23	526
Contig L90	314	2,042
QV	60.0324	60.3211
Kmer compl.	95.1354	71.1488
BUSCO sing.	96.1%	71.6%
BUSCO dupl.	0.4%	0.4%
BUSCO frag.	0.6%	0.0%
BUSCO miss.	2.9%	28.0%

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

Pretext Full Map: YaHS



OenLeu_noHiC_yash_PRI_Filter.map_FullMap.png



OenLeu_noHiC_yash_ALT_Filter.map_FullMap.png

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