

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

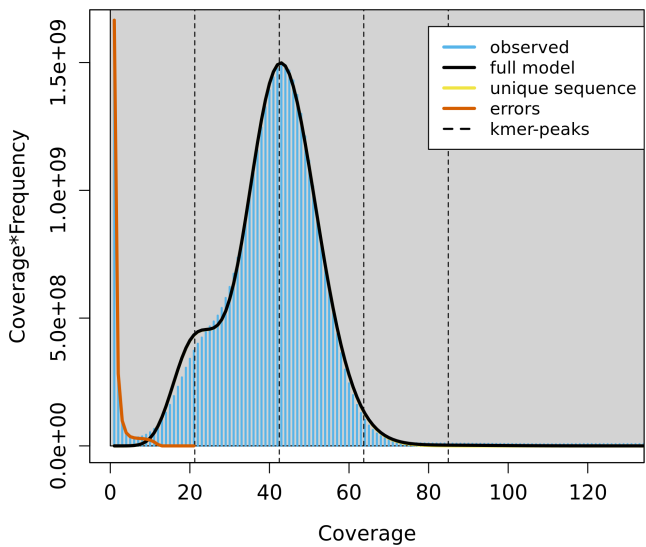
Tool	Version
GenomeScope	2.0
Smudgeplot	0.2.5
Hifiasm	0.18.4-r496
purge_dups	1.2.5
YaHS	1.2a.1

Genome profiling

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

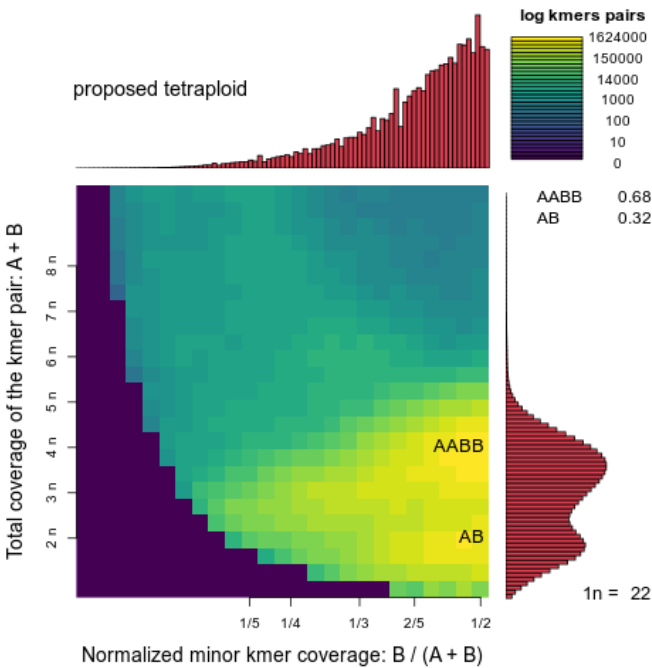
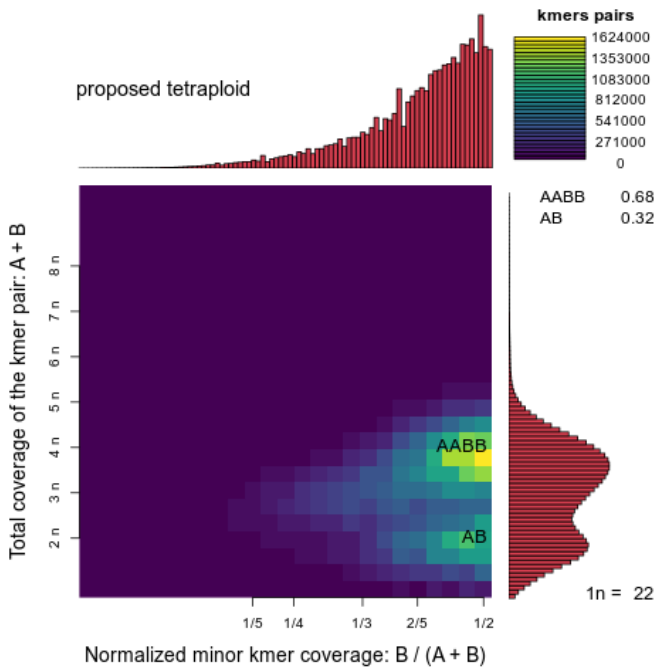
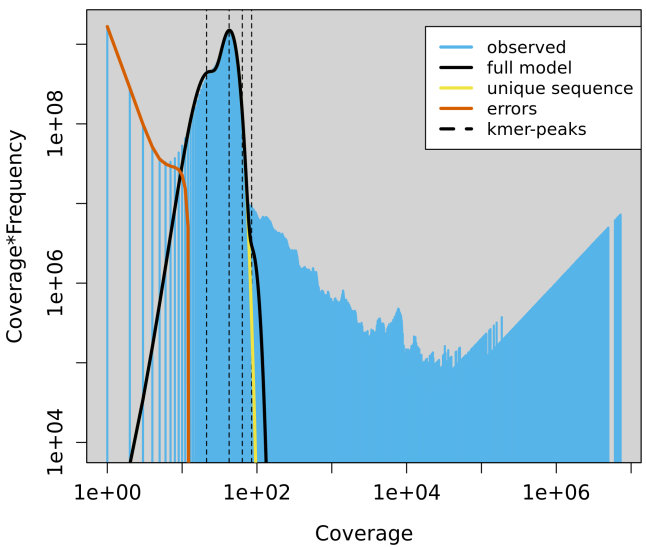
GenomeScope Profile

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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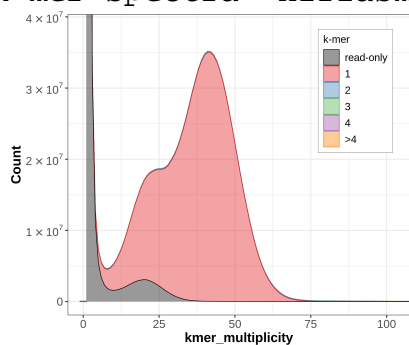


Genome assembly: contigging

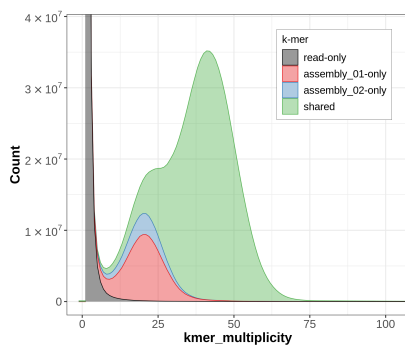
Metrics	Hifiasm hap1	Hifiasm hap2	purge_dups hap1	purge_dups hap2
Total bp	1,358,504,914	1,081,007,549	1,254,260,396	1,014,836,911
GC %	43.8	42.92	43.33	42.55
Gaps	0	0	17	21
Gaps/Gbp	0	0	13.55	20.69
Gaps bp	0	0	391	483
Scaffolds	1,524	1,015	1,092	703
Longest Scaf.	50,893,993	46,782,542	50,893,993	46,782,542
Scaffold auN	13,636,257.35	15,317,115.76	14,722,632.84	16,282,058.18
Scaffold N50	7,440,599	12,112,024	10,025,093	13,360,684
Scaffold L50	34	24	28	21
Scaffold L90	478	240	310	148
Contigs	1,524	1,015	1,109	723
Largest Cont.	50,893,993	46,782,542	50,893,993	46,782,542
Contig auN	13,636,257.35	15,317,115.76	14,715,969.38	16,278,948.41
Contig N50	7,440,599	12,112,024	10,025,093	13,360,684
Contig L50	34	24	28	21
Contig L90	478	240	314	149
QV	59.5672	60.599	59.9306	60.8252
Kmer compl.	95.143	85.5521	94.9429	85.3765
BUSCO sing.	93.8%	86.6%	94.1%	86.6%
BUSCO dupl.	0.6%	0.2%	0.3%	0.2%
BUSCO frag.	1.1%	0.9%	1.1%	0.9%
BUSCO miss.	4.5%	12.3%	4.5%	12.3%

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

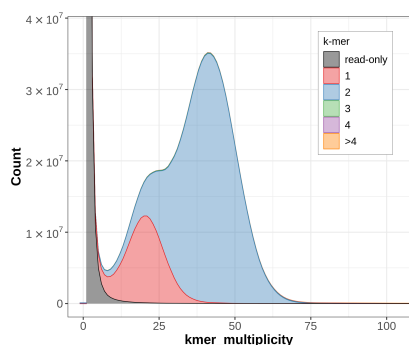
K-mer spectra: Hifiasm



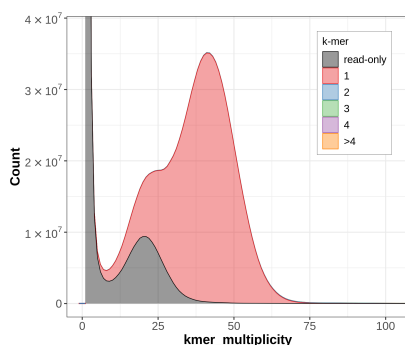
output_mercury.assembly_01.spectra-cn.st.png



output_mercury.spectra-asm.st.png

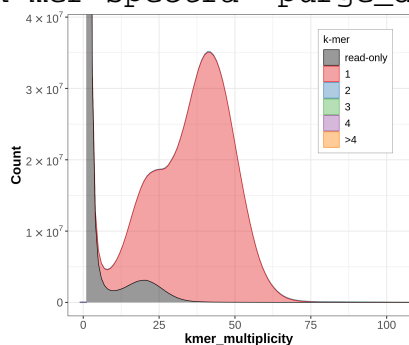


output_mercury.spectra-cn.st.png

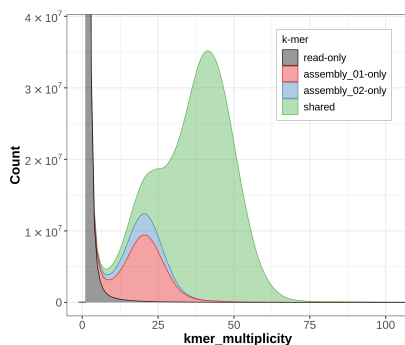


output_mercury.assembly_02.spectra-cn.st.png

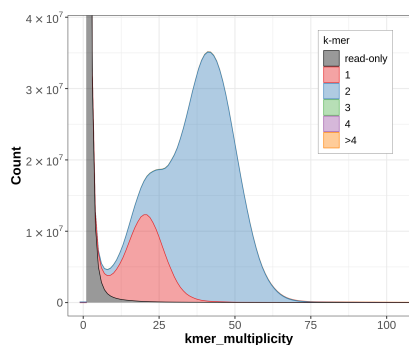
K-mer spectra: purge_dups



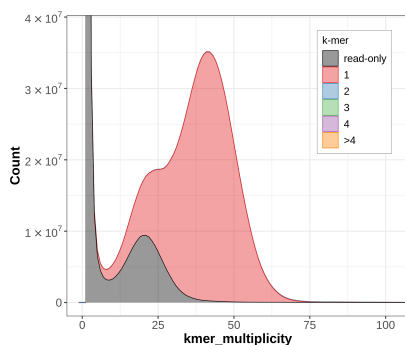
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output_mercury_purged.spectra-asm.st.png



output_mercury_purged.spectra-cn.st.png



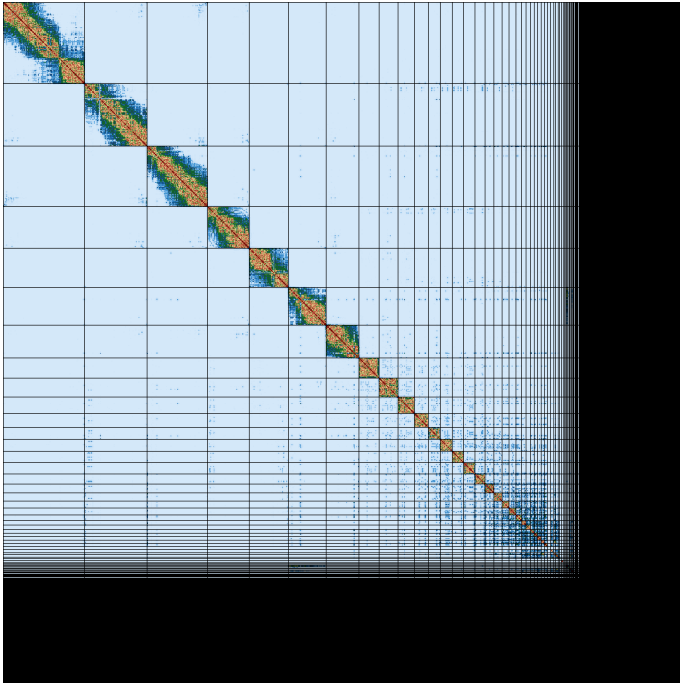
output_mercury_purged.assembly_02.spectra-cn.st.png

Genome assembly: scaffolding

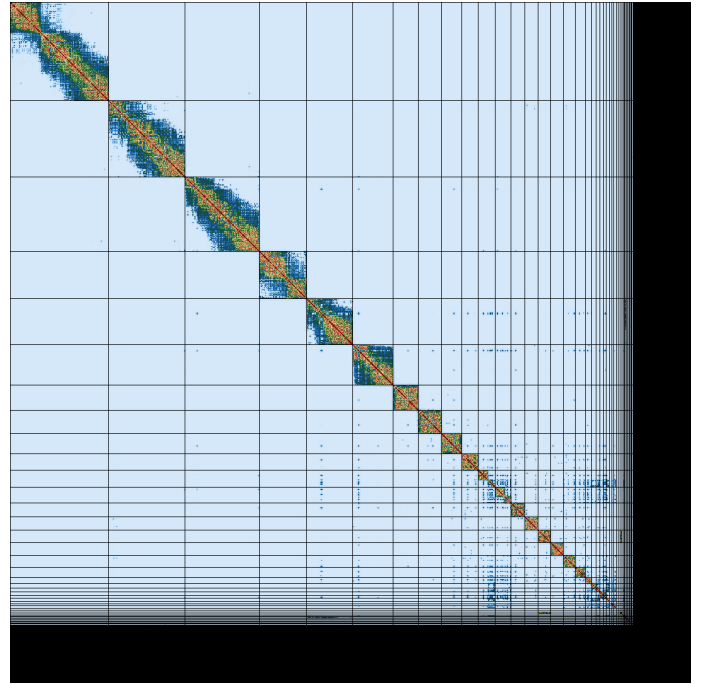
Metrics	YaHS hap1	YaHS hap2
Total bp	1,254,332,796	1,014,886,111
GC %	43.33	42.55
Gaps	379	267
Gaps/Gbp	302.15	263.08
Gaps bp	72,791	49,683
Scaffolds	840	510
Longest Scaf.	150,389,447	147,039,420
Scaffold auN	60,381,493.1	66,906,152.58
Scaffold N50	60,889,355	68,431,036
Scaffold L50	7	5
Scaffold L90	140	31
Contigs	1,219	776
Largest Cont.	50,893,993	46,782,542
Contig auN	14,558,428.38	16,246,624.5
Contig N50	10,025,093	13,360,684
Contig L50	28	21
Contig L90	355	156
QV	59.9306	60.8252
Kmer compl.	94.9428	85.3765
BUSCO sing.	94.3%	86.6%
BUSCO dupl.	0.3%	0.2%
BUSCO frag.	0.9%	0.7%
BUSCO miss.	4.5%	12.5%

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

Pretext Full Map: YaHS



OenLeu_Opt_yash_Hap1_Filter_RG_RD.map.noHR_FullMap.png



OenLeu_Opt_yash_Hap2_Filter_RG_RD.map.noHR_FullMap.png

Submitter: Joao Pedro Marques

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Date and time: 2023-08-07 10:54:52 CEST