

Report

	final.contigs
# contigs (≥ 0 bp)	318
# contigs (≥ 1000 bp)	262
Total length (≥ 0 bp)	1298209
Total length (≥ 1000 bp)	1256062
# contigs	318
Largest contig	23356
Total length	1298209
Reference length	641799
GC (%)	26.30
Reference GC (%)	26.30
N50	6054
NG50	10788
N75	3538
NG75	7803
L50	65
LG50	22
L75	136
LG75	40
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	13730
# local misassemblies	0
# unaligned contigs	81 + 18 part
Unaligned length	527845
Genome fraction (%)	99.525
Duplication ratio	1.206
# N's per 100 kbp	0.00
# mismatches per 100 kbp	426.46
# indels per 100 kbp	1.10
Largest alignment	23356
NA50	2089
NGA50	6098
NGA75	3723
LA50	126
LGA50	30
LGA75	65

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Misassemblies report

	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	13
# misassembled contigs	4
Misassembled contigs length	13730
# local misassemblies	0
# mismatches	2724
# indels	7
# short indels	7
# long indels	0
Indels length	7

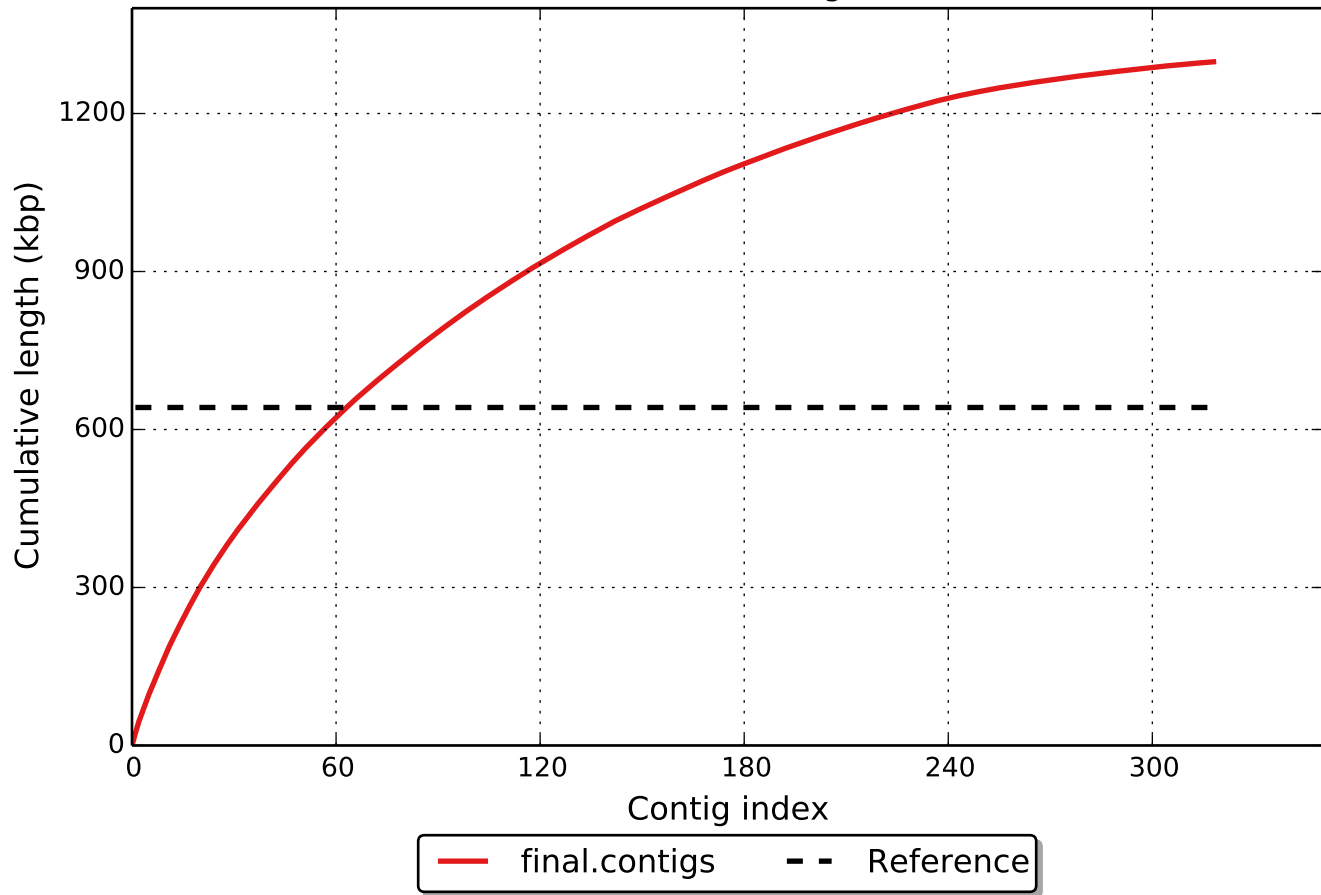
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	81
Fully unaligned length	421408
# partially unaligned contigs	18
# with misassembly	1
# both parts are significant	13
Partially unaligned length	106437
# N's	0

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Cumulative length



GC content

