

Report

	final.contigs
# contigs (≥ 0 bp)	5276
# contigs (≥ 1000 bp)	3026
# contigs (≥ 5000 bp)	358
# contigs (≥ 10000 bp)	35
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9795447
Total length (≥ 1000 bp)	8656184
Total length (≥ 5000 bp)	2463019
Total length (≥ 10000 bp)	427464
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	3962
Largest contig	18483
Total length	9348620
Reference length	9283304
N50	3195
N75	1904
L50	918
L75	1864
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 3 part
Unaligned length	198
Genome fraction (%)	97.324
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.67
# indels per 100 kbp	0.18
Largest alignment	18483
NA50	3195
NA75	1904
LA50	918
LA75	1864

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

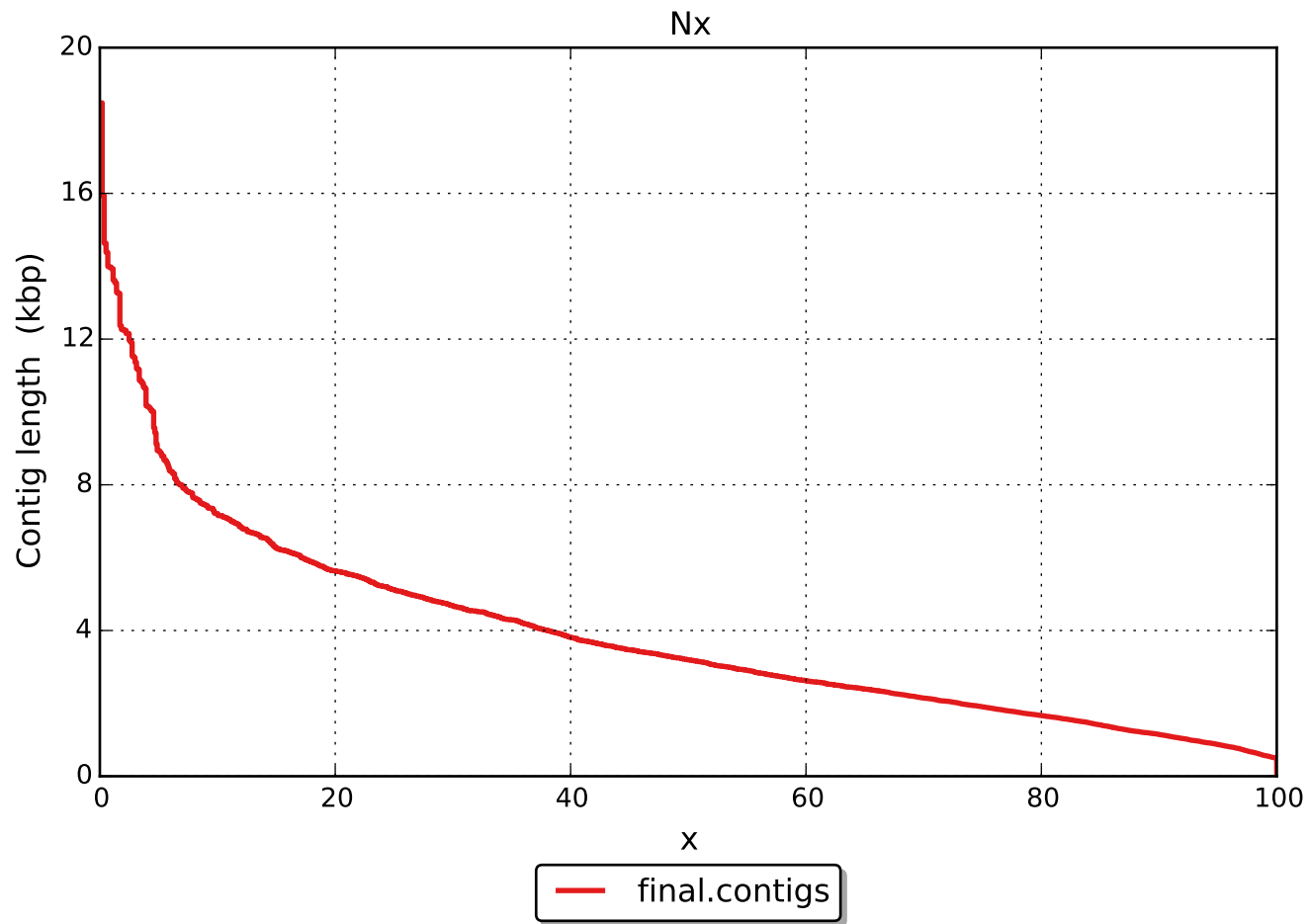
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	4759
# indels	16
# short indels	16
# long indels	0
Indels length	16

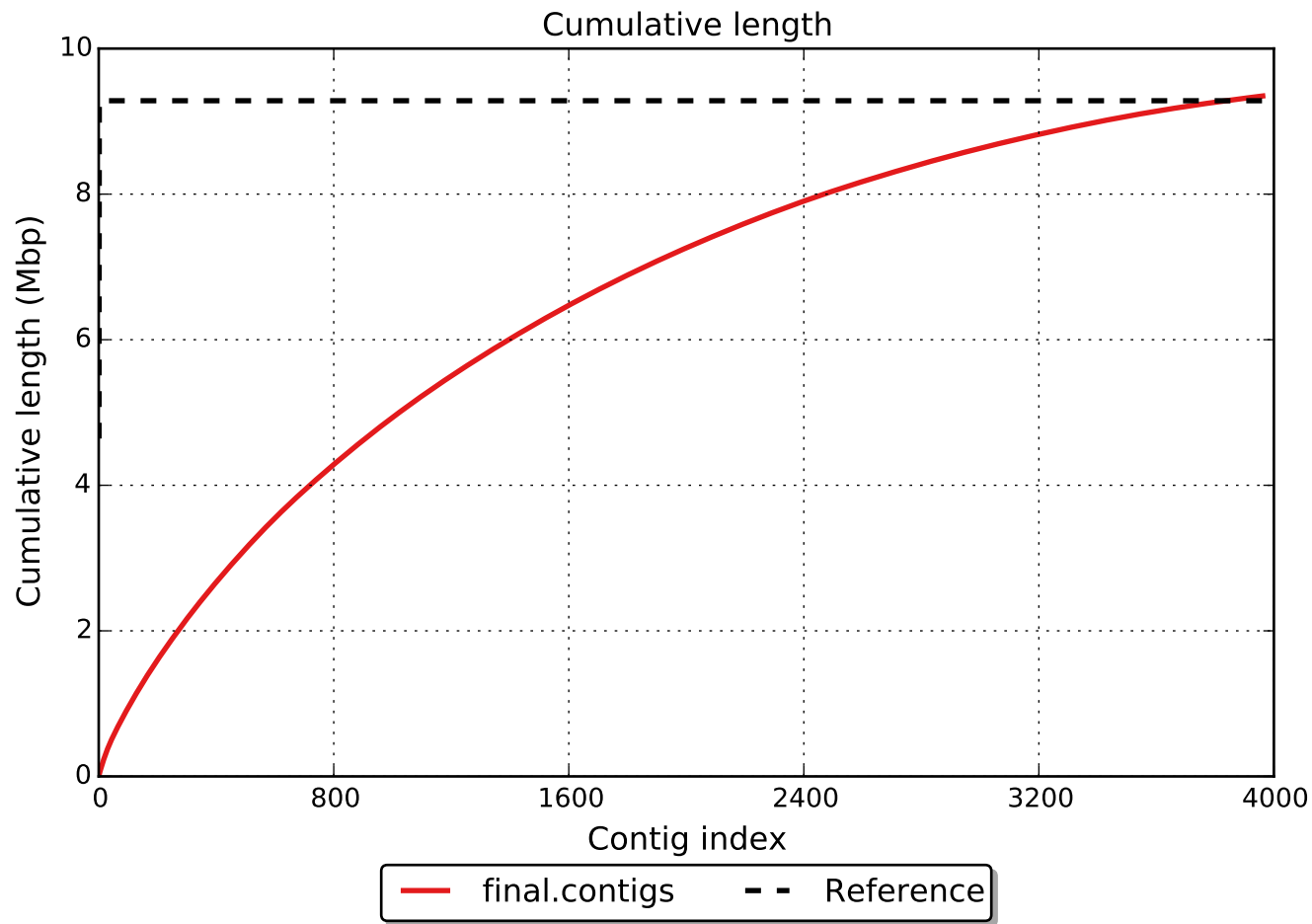
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Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	198
# N's	0

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

