

Report

	final.contigs
# contigs (≥ 0 bp)	4946
# contigs (≥ 1000 bp)	1357
# contigs (≥ 5000 bp)	212
# contigs (≥ 10000 bp)	14
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	5639850
Total length (≥ 1000 bp)	4220988
Total length (≥ 5000 bp)	1466786
Total length (≥ 10000 bp)	183388
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1992
Largest contig	18957
Total length	4658494
Reference length	9283304
N50	3481
N75	1992
L50	422
L75	864
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	5828
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	49.306
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	382.06
# indels per 100 kbp	0.07
Largest alignment	18957
NA50	3473
NA75	1992
LA50	423
LA75	865

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

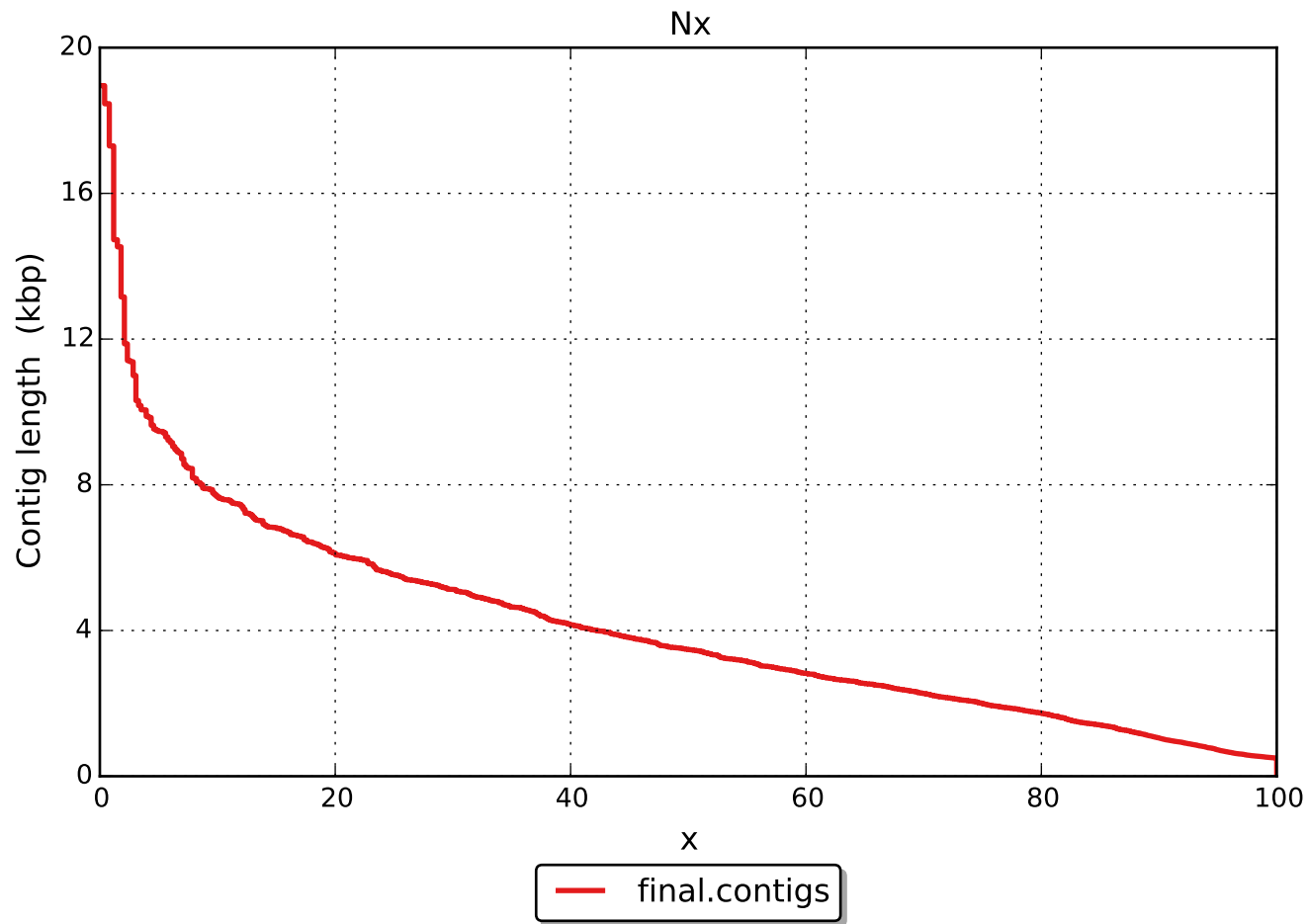
	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	1
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	5828
# local misassemblies	0
# mismatches	17488
# indels	3
# short indels	3
# long indels	0
Indels length	3

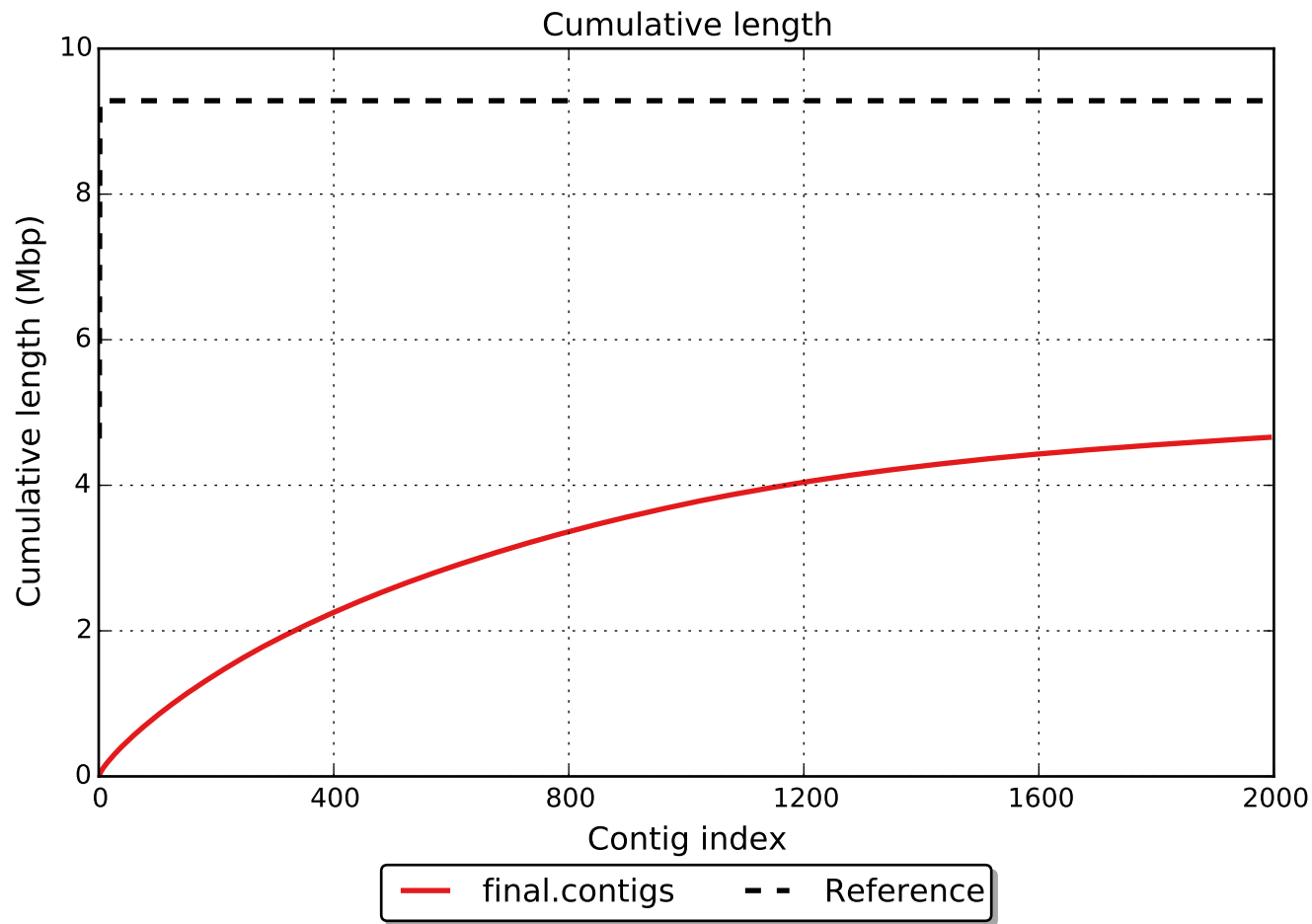
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Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# 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

