

Report

	final.contigs
# contigs (≥ 0 bp)	2726
# contigs (≥ 1000 bp)	1769
# contigs (≥ 5000 bp)	682
# contigs (≥ 10000 bp)	187
# contigs (≥ 25000 bp)	8
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	9576173
Total length (≥ 1000 bp)	9146454
Total length (≥ 5000 bp)	6210374
Total length (≥ 10000 bp)	2735013
Total length (≥ 25000 bp)	234899
Total length (≥ 50000 bp)	0
# contigs	2043
Largest contig	39629
Total length	9350524
Reference length	9283304
N50	6852
N75	4016
L50	423
L75	862
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.755
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.28
# indels per 100 kbp	0.02
Largest alignment	39629
NA50	6852
NA75	4016
LA50	423
LA75	862

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

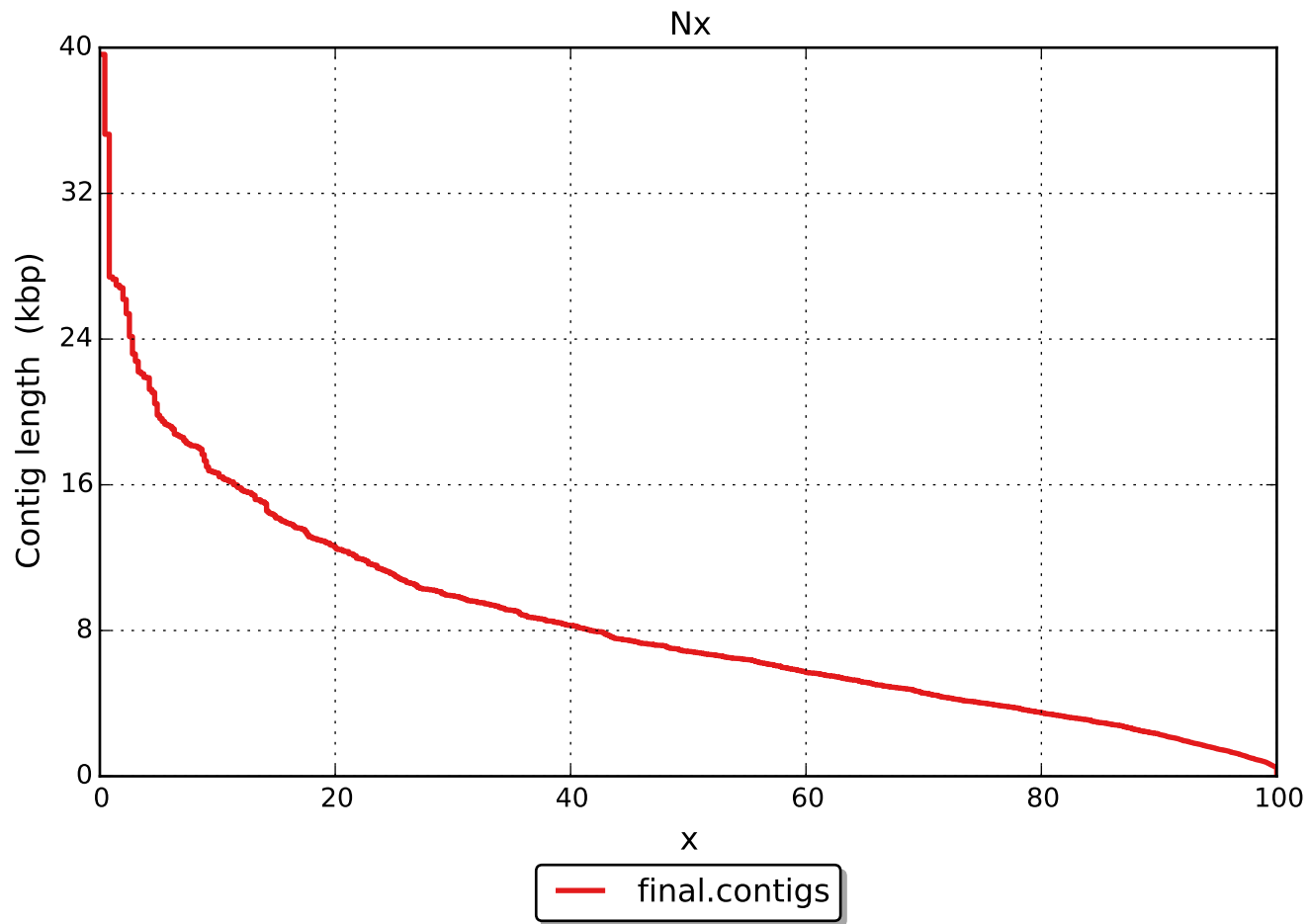
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	1951
# indels	2
# short indels	2
# long indels	0
Indels length	2

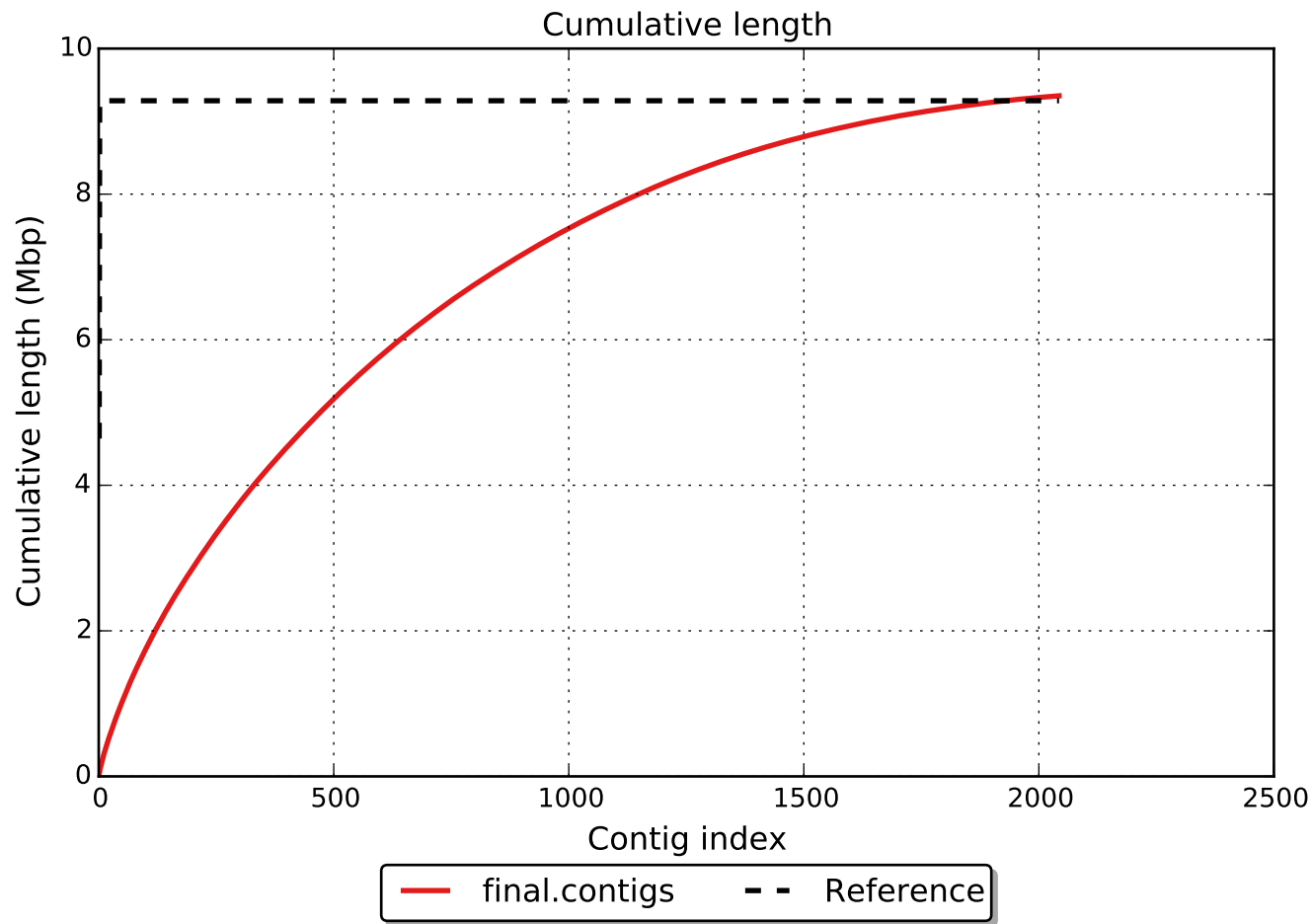
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	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

