

Report

	final.contigs
# contigs (≥ 0 bp)	6912
# contigs (≥ 1000 bp)	3558
# contigs (≥ 5000 bp)	208
# contigs (≥ 10000 bp)	4
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	10364443
Total length (≥ 1000 bp)	8599127
Total length (≥ 5000 bp)	1291397
Total length (≥ 10000 bp)	42431
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5125
Largest contig	11637
Total length	9748246
Reference length	9714864
N50	2515
N75	1483
L50	1249
L75	2503
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	96.576
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.34
# indels per 100 kbp	0.00
Largest alignment	11637
NA50	2515
NA75	1483
LA50	1249
LA75	2503

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

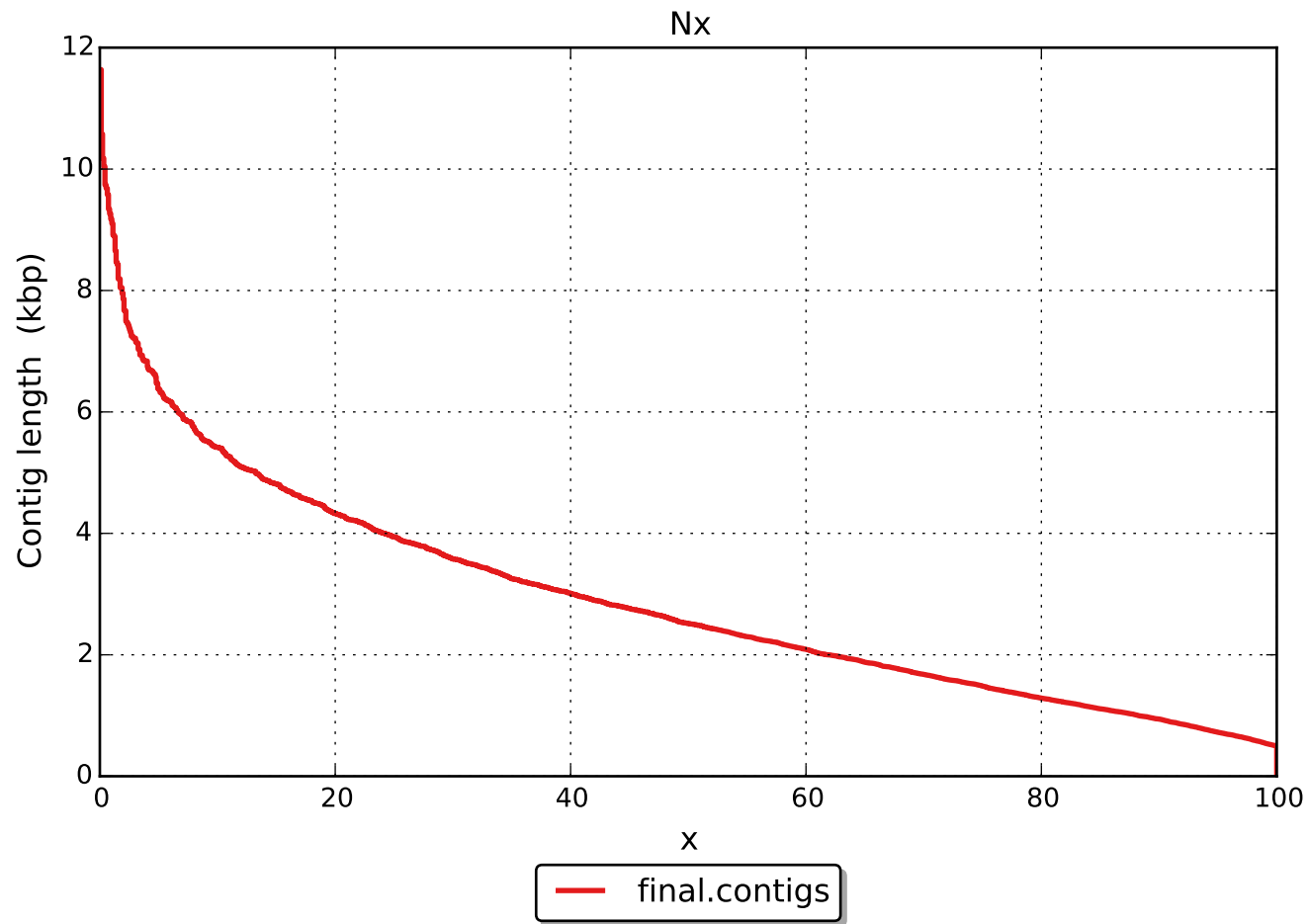
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	4348
# indels	0
# short indels	0
# long indels	0
Indels length	0

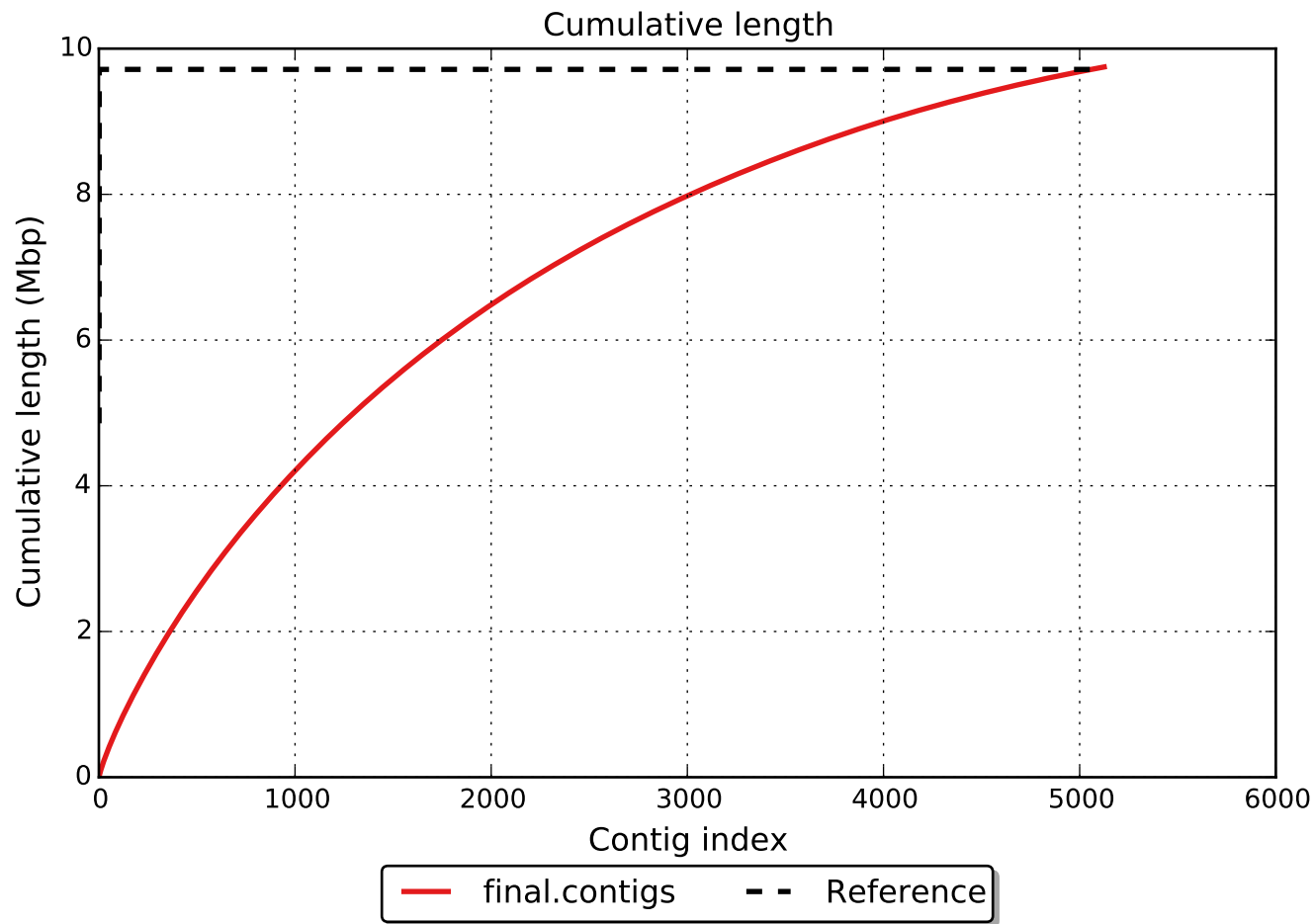
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11
# 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

