

Report

	final.contigs
# contigs (≥ 0 bp)	3425
# contigs (≥ 1000 bp)	2240
# contigs (≥ 5000 bp)	687
# contigs (≥ 10000 bp)	142
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	10091779
Total length (≥ 1000 bp)	9537985
Total length (≥ 5000 bp)	5546545
Total length (≥ 10000 bp)	1856805
Total length (≥ 25000 bp)	26127
Total length (≥ 50000 bp)	0
# contigs	2610
Largest contig	26127
Total length	9816782
Reference length	9714864
N50	5535
N75	3213
L50	566
L75	1136
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 3 part
Unaligned length	491
Genome fraction (%)	98.876
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.75
# indels per 100 kbp	0.02
Largest alignment	26127
NA50	5535
NA75	3209
LA50	566
LA75	1137

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

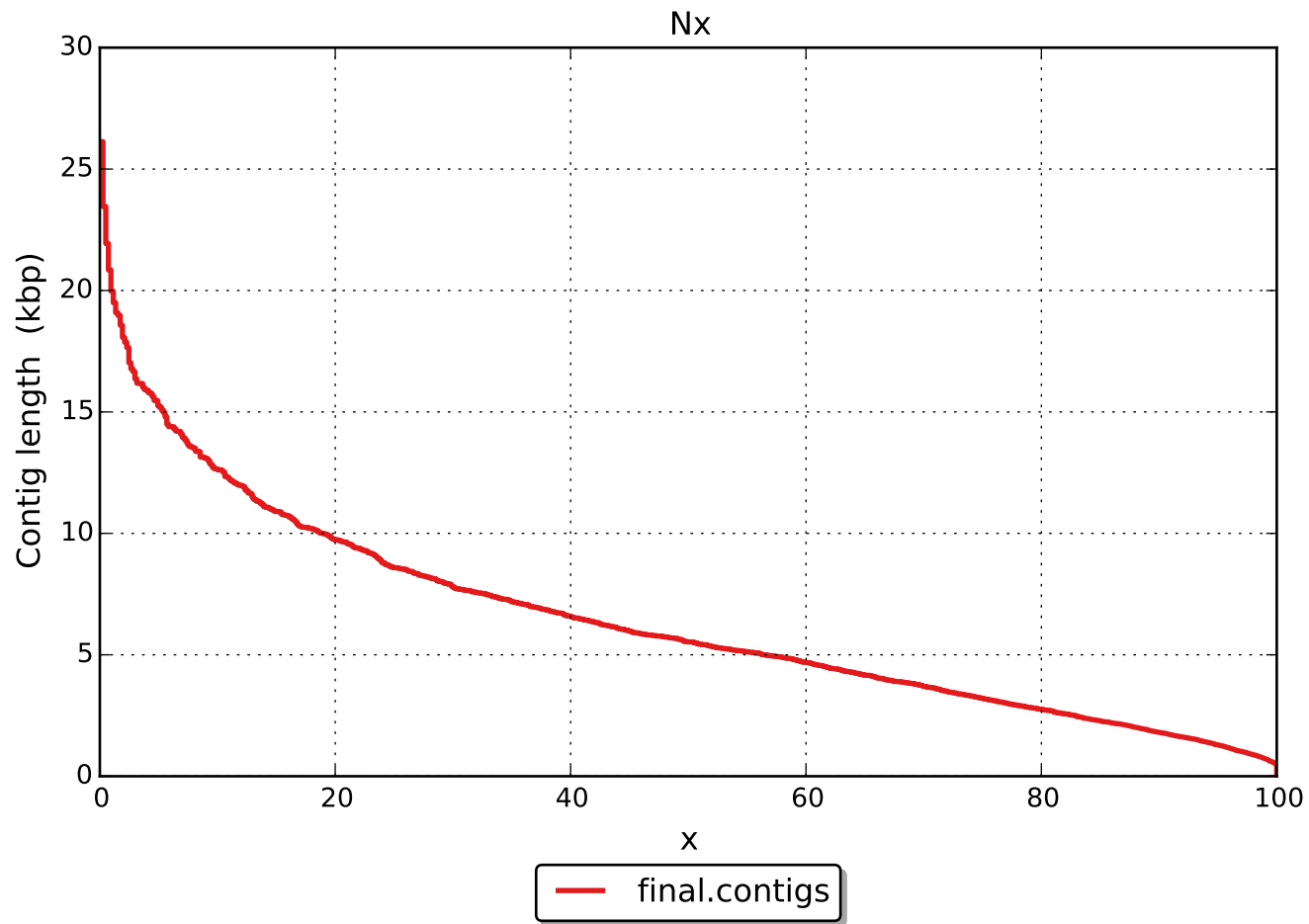
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2858
# indels	2
# short indels	2
# long indels	0
Indels length	2

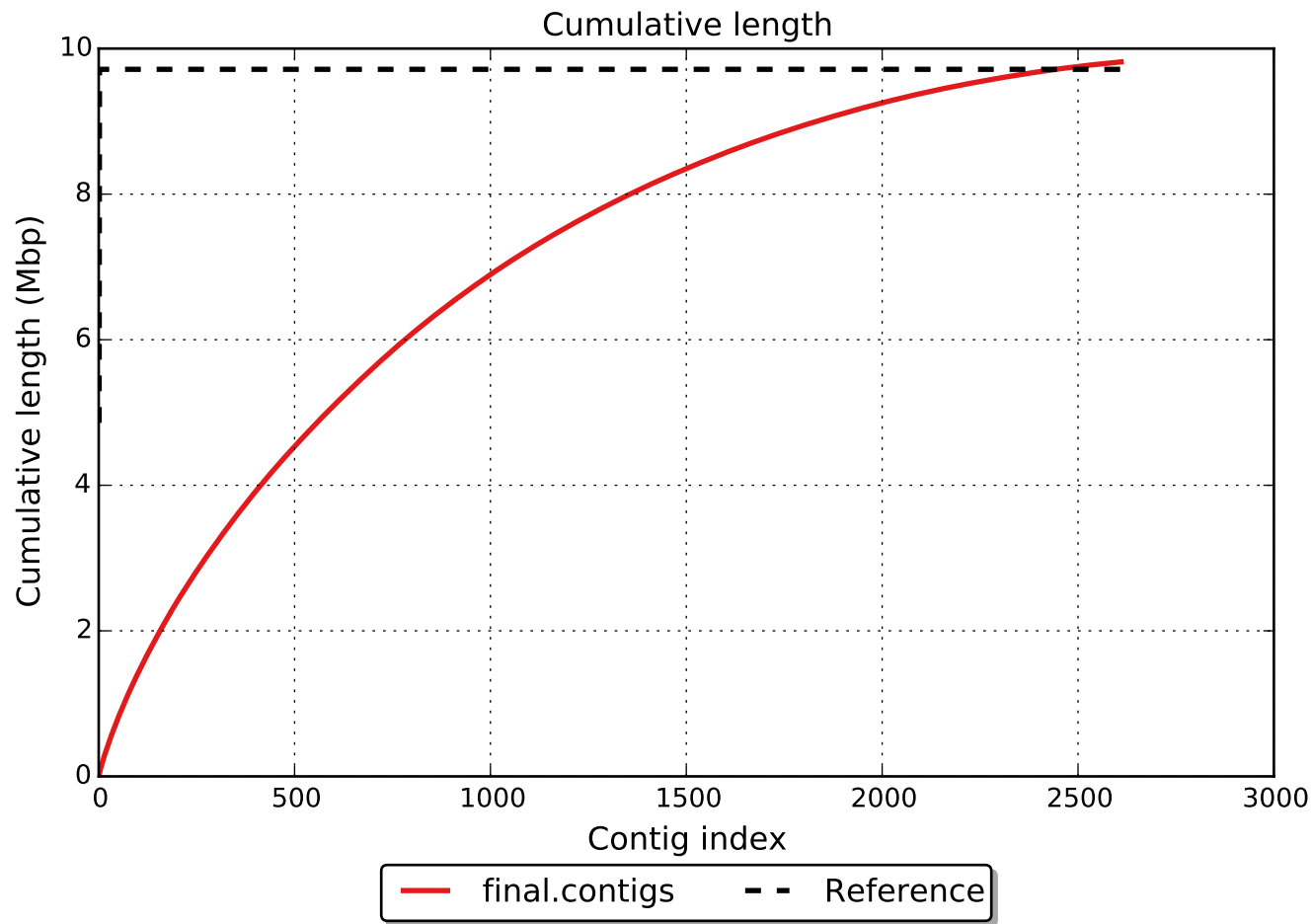
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	491
# 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

