

Report

	final.contigs
# contigs (≥ 0 bp)	1367
# contigs (≥ 1000 bp)	420
# contigs (≥ 5000 bp)	270
# contigs (≥ 10000 bp)	163
# contigs (≥ 25000 bp)	36
# contigs (≥ 50000 bp)	6
Total length (≥ 0 bp)	4826548
Total length (≥ 1000 bp)	4519724
Total length (≥ 5000 bp)	4071858
Total length (≥ 10000 bp)	3282081
Total length (≥ 25000 bp)	1354521
Total length (≥ 50000 bp)	365330
# contigs	457
Largest contig	84650
Total length	4543625
Reference length	4641652
N50	15943
N75	9590
L50	84
L75	176
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	1 + 0 part
Unaligned length	511
Genome fraction (▼)	97.778
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.75
# indels per 100 kbp	0.07
Largest alignment	84650
NA50	15943
NA75	9590
LA50	84
LA75	176

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

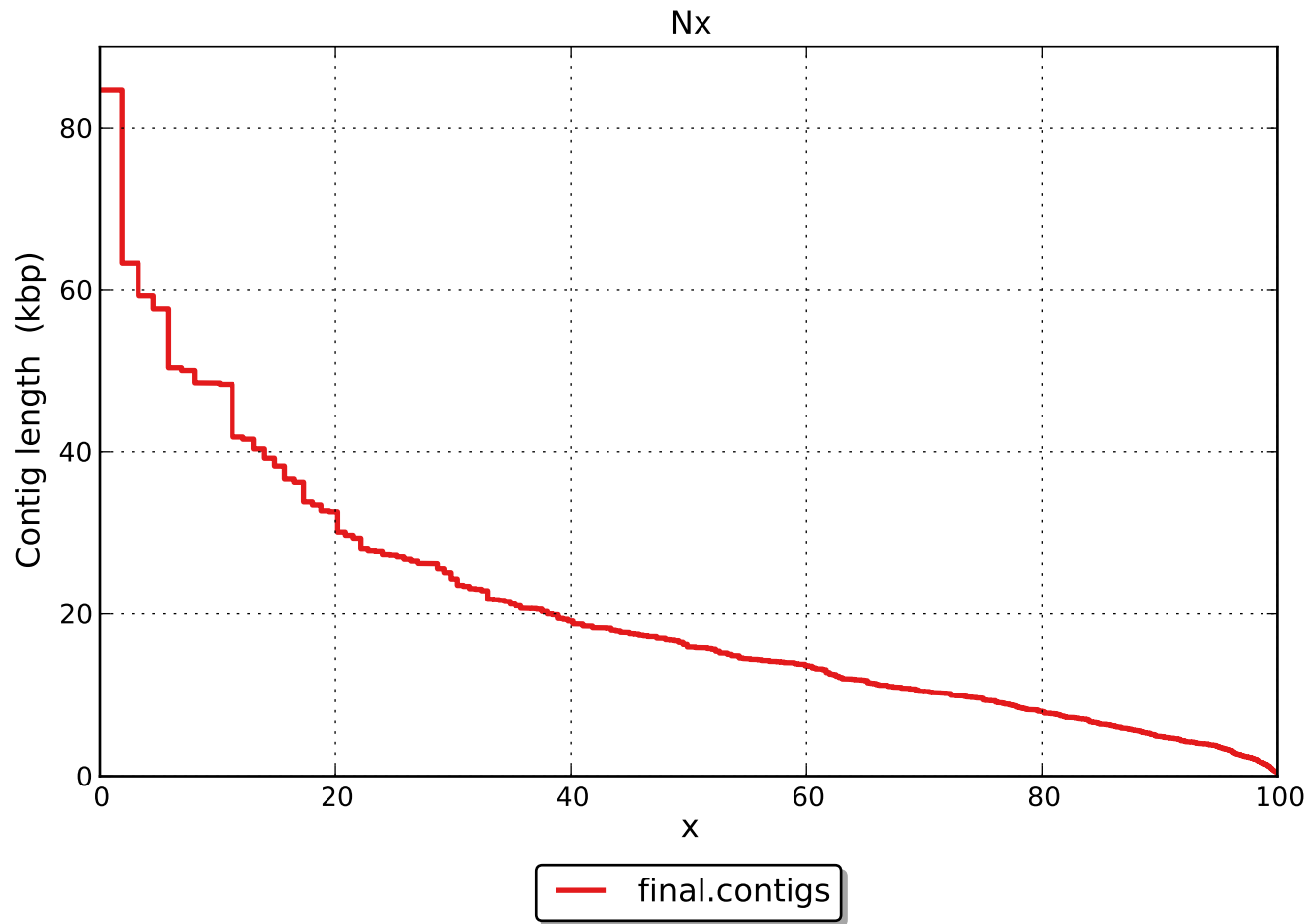
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	261
# indels	3
# short indels	3
# long indels	0
Indels length	3

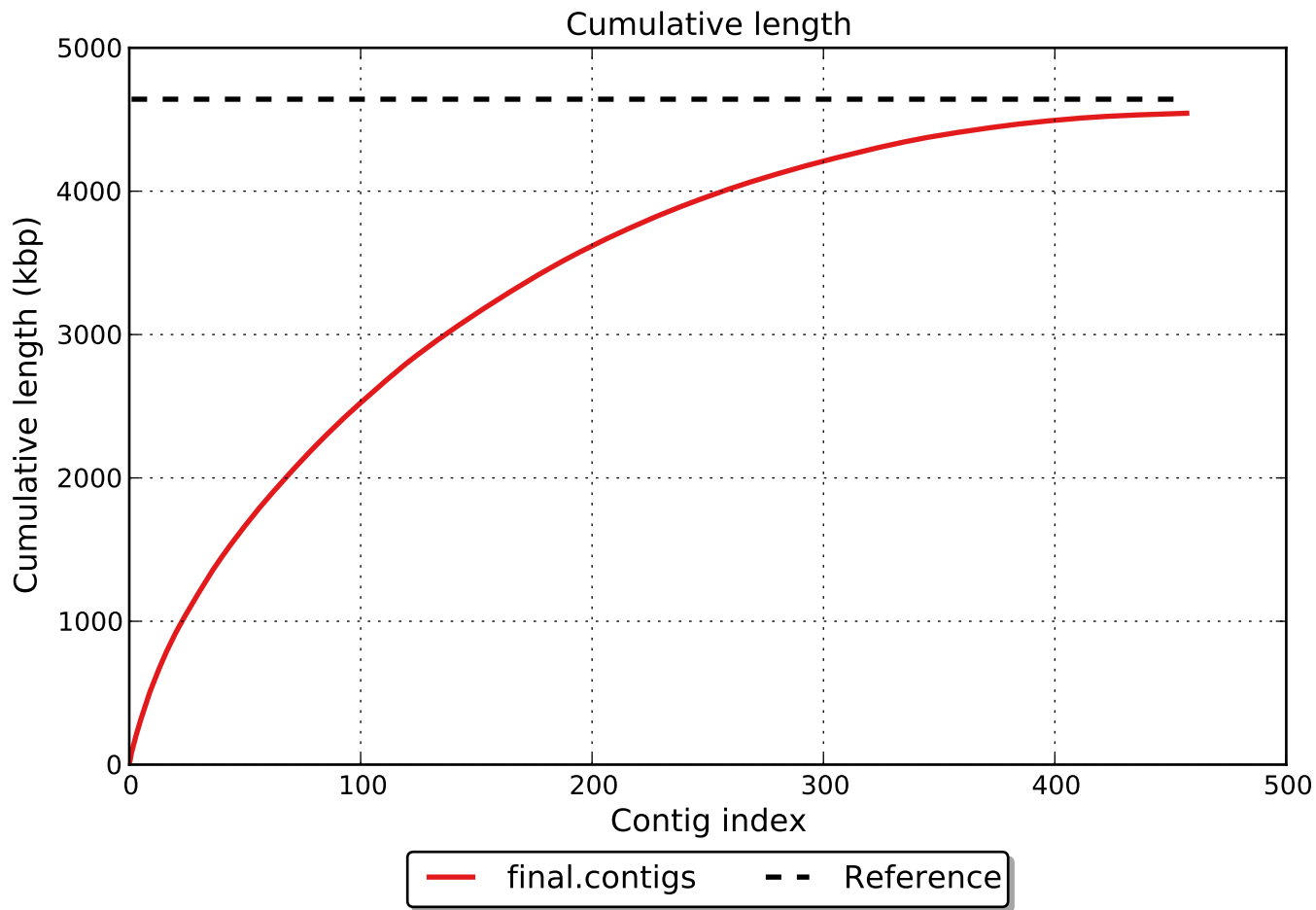
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

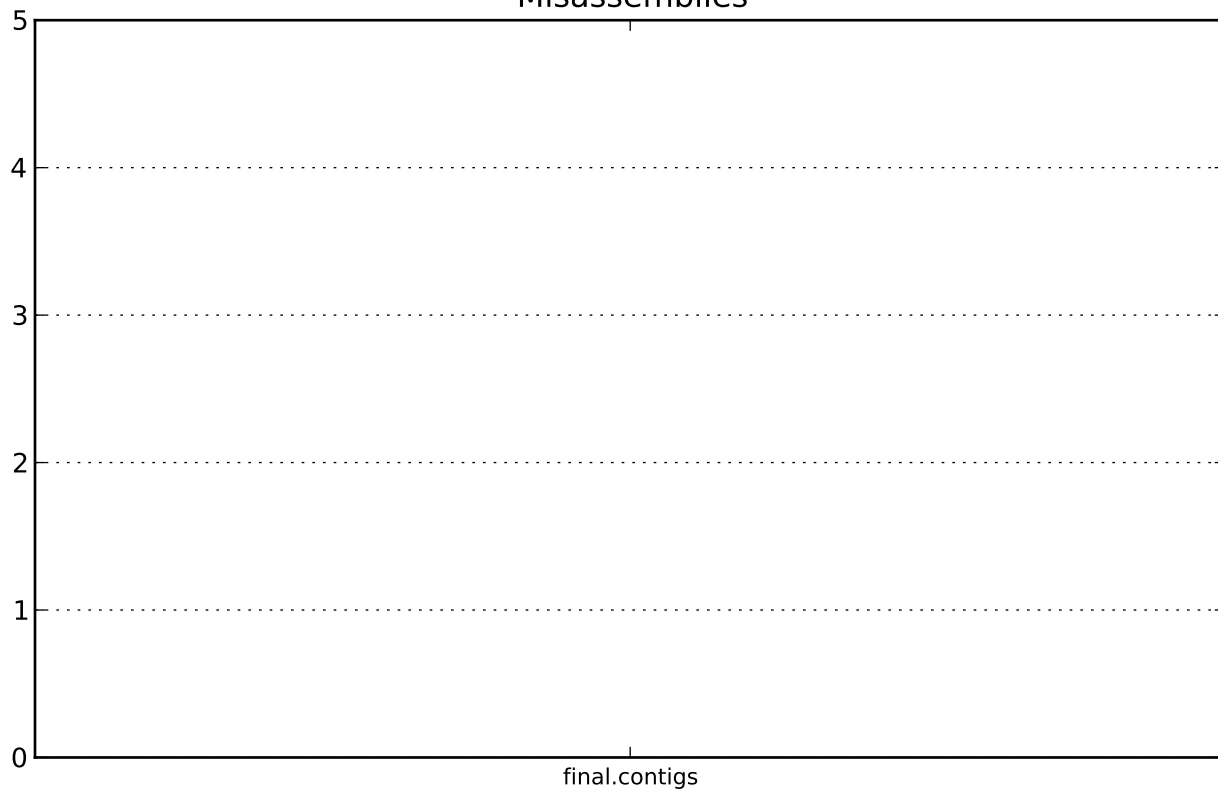
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	511
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

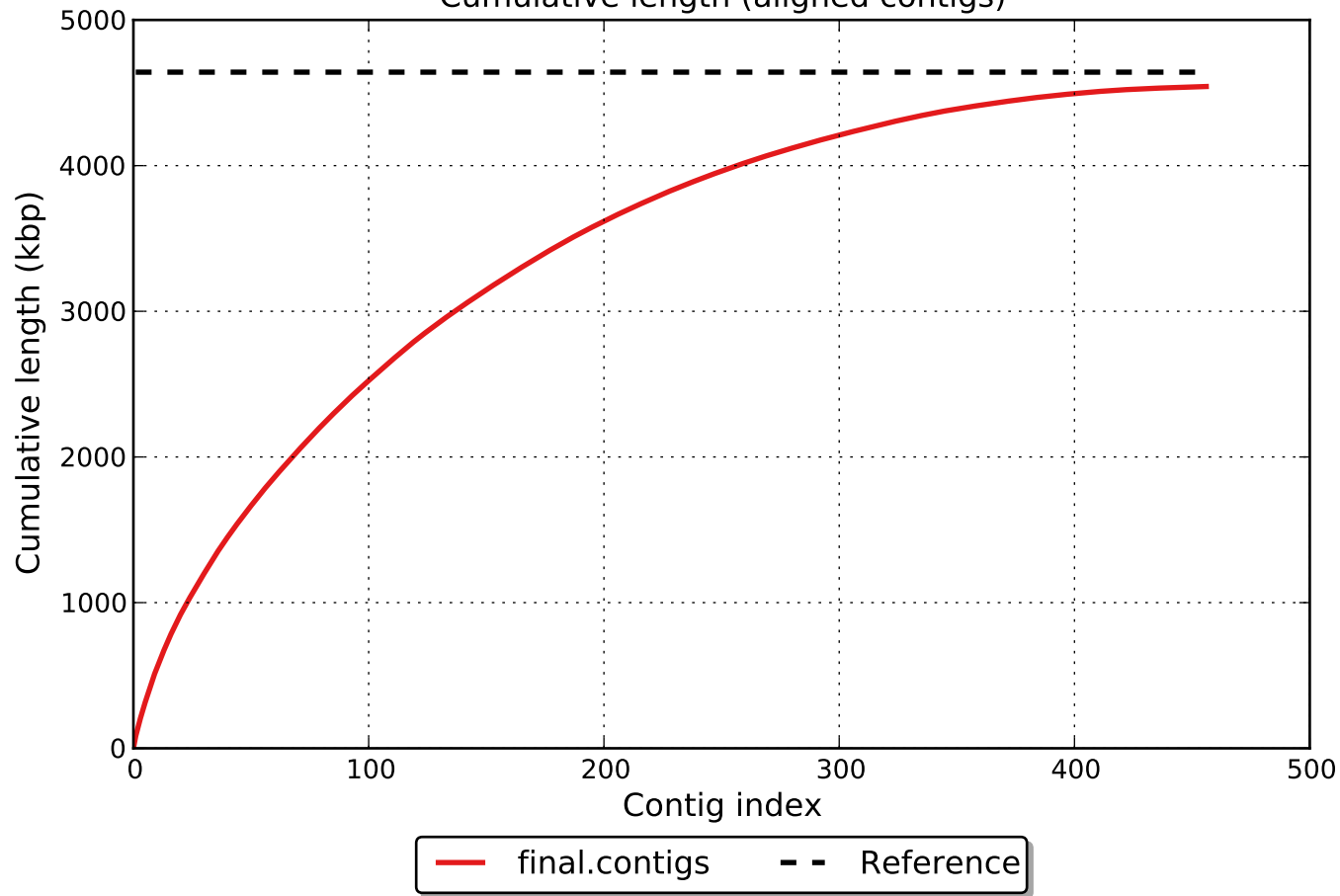




Misassemblies



Cumulative length (aligned contigs)



NAx

