

Report

	final.contigs
# contigs (≥ 0 bp)	506
# contigs (≥ 1000 bp)	371
# contigs (≥ 5000 bp)	312
# contigs (≥ 10000 bp)	252
# contigs (≥ 25000 bp)	133
# contigs (≥ 50000 bp)	45
Total length (≥ 0 bp)	9257110
Total length (≥ 1000 bp)	9208467
Total length (≥ 5000 bp)	9039652
Total length (≥ 10000 bp)	8588599
Total length (≥ 25000 bp)	6463224
Total length (≥ 50000 bp)	3403962
# contigs	394
Largest contig	177974
Total length	9225256
Reference length	9283304
N50	37676
N75	22685
L50	73
L75	152
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36763
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.162
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.01
# indels per 100 kbp	0.00
Largest alignment	177974
NA50	37676
NA75	22582
LA50	73
LA75	153

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

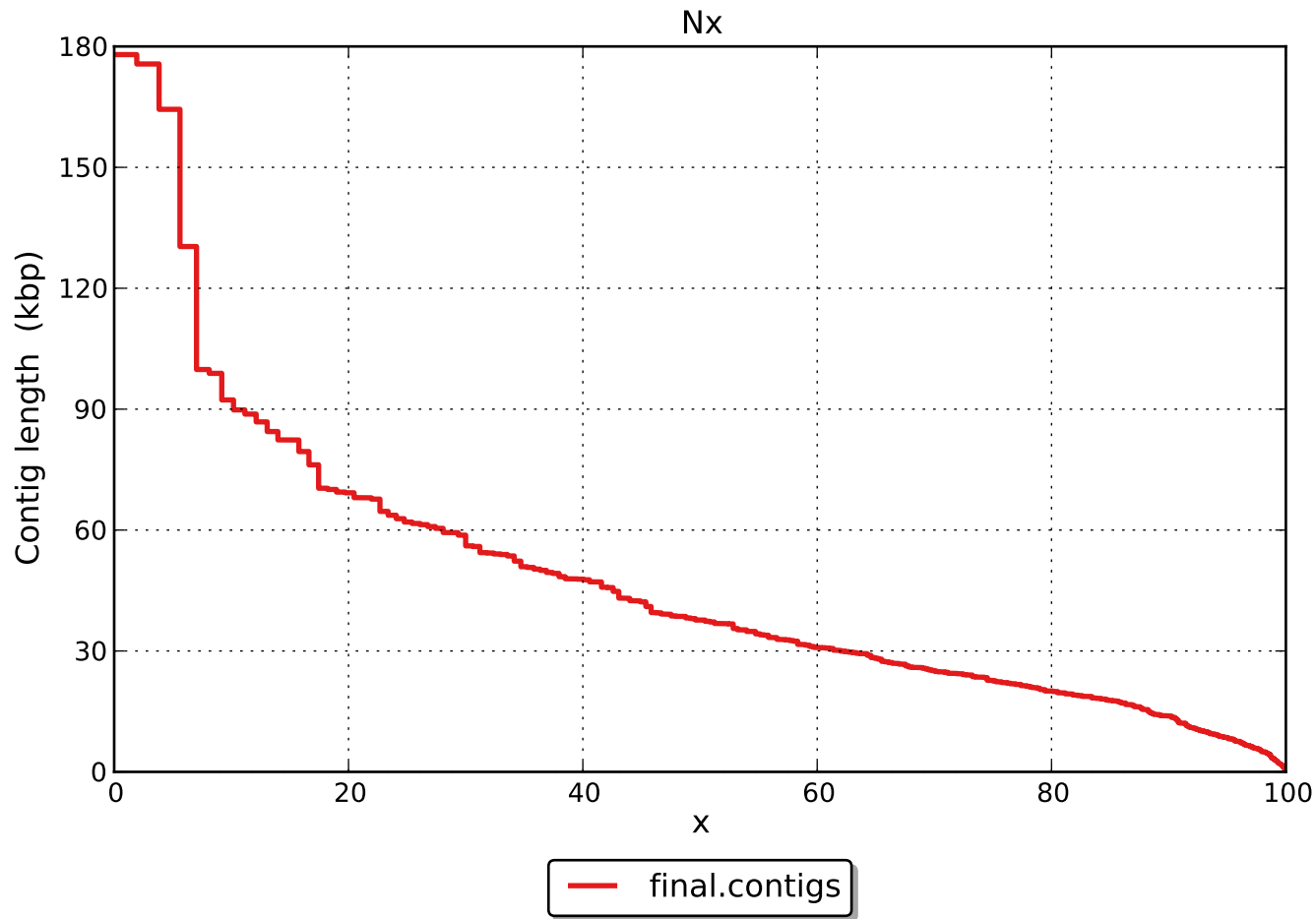
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36763
# local misassemblies	0
# mismatches	93
# indels	0
# short indels	0
# long indels	0
Indels length	0

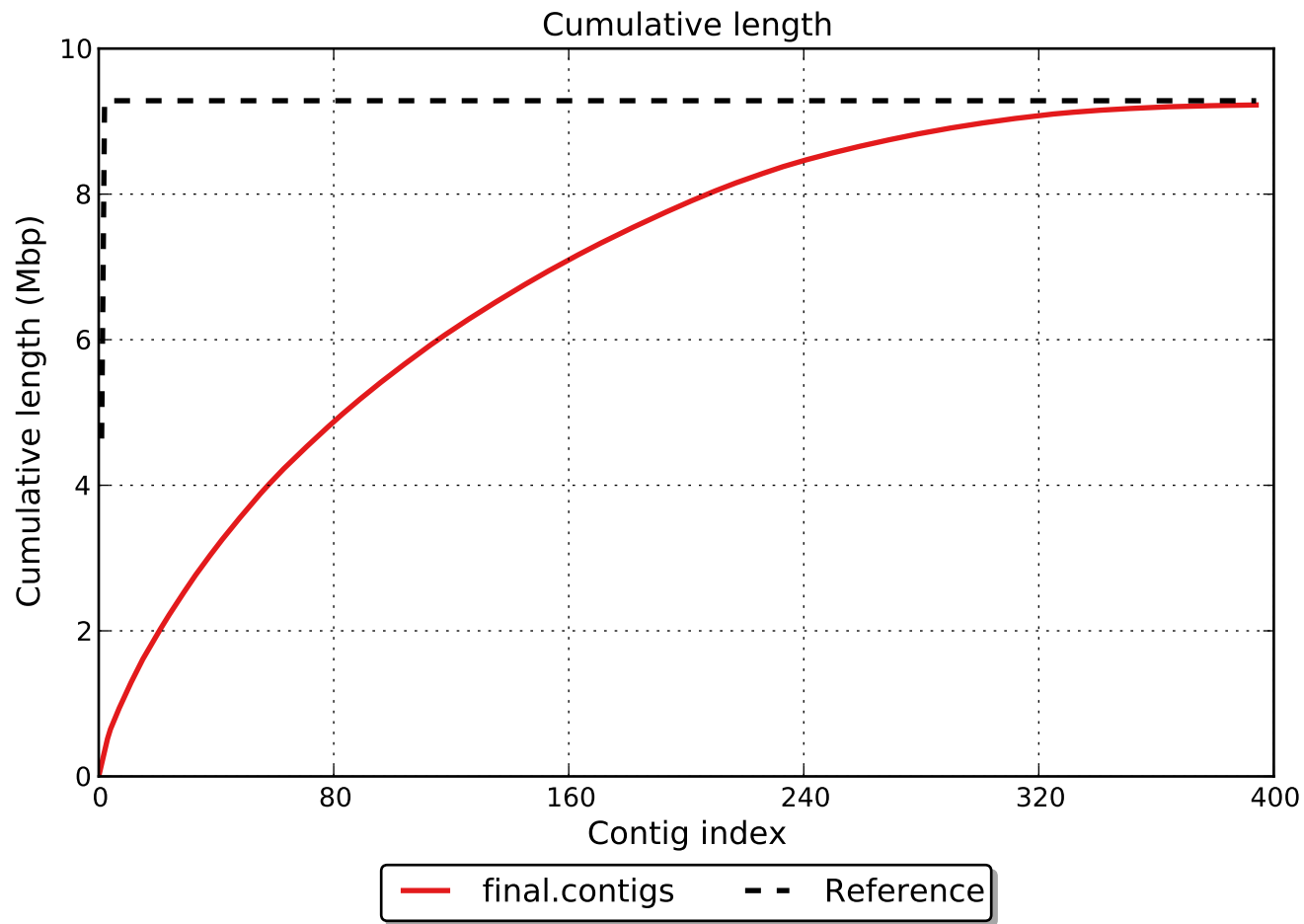
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

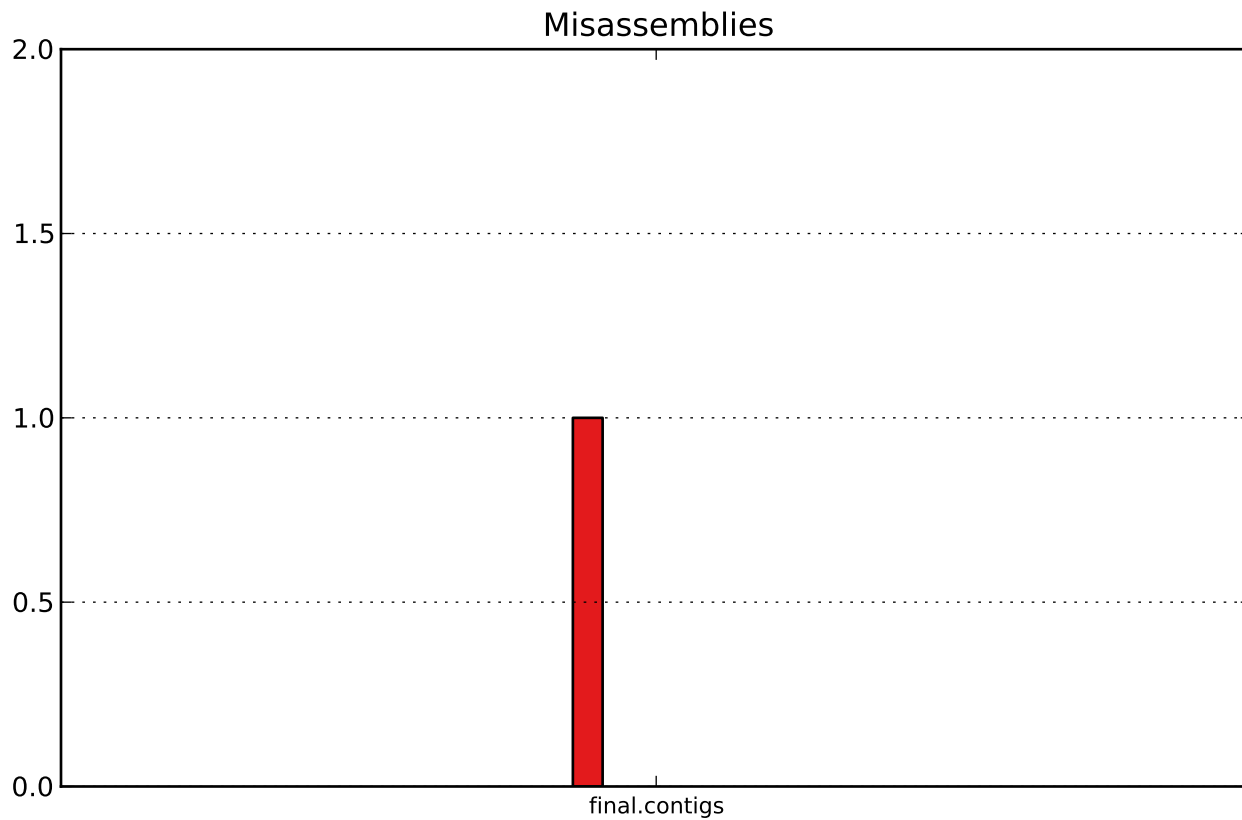
Unaligned report

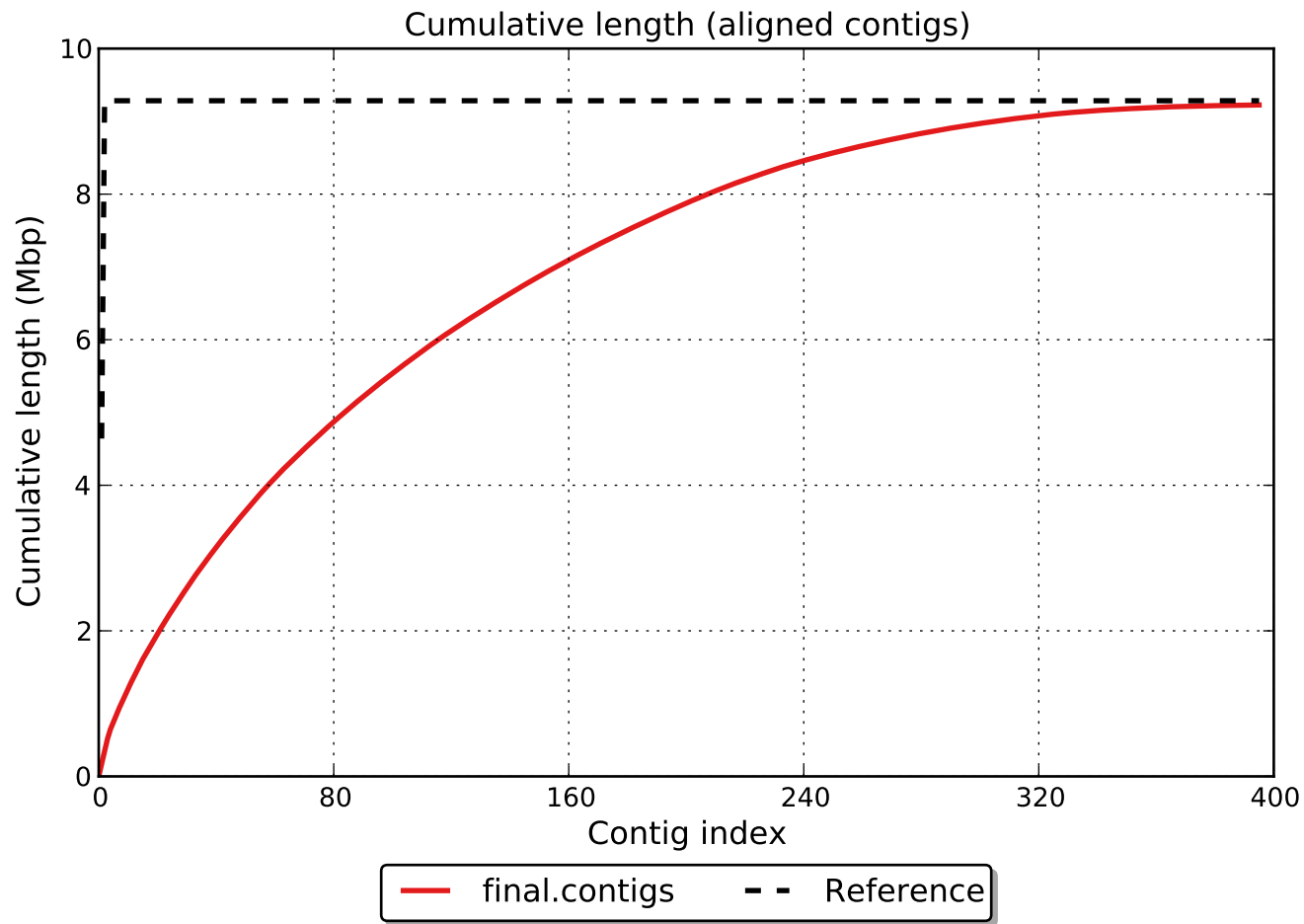
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).









NAx

