

Report

	final.contigs
# contigs (≥ 0 bp)	1035
# contigs (≥ 1000 bp)	835
# contigs (≥ 5000 bp)	551
# contigs (≥ 10000 bp)	337
# contigs (≥ 25000 bp)	77
# contigs (≥ 50000 bp)	6
Total length (≥ 0 bp)	9299677
Total length (≥ 1000 bp)	9207785
Total length (≥ 5000 bp)	8408737
Total length (≥ 10000 bp)	6804599
Total length (≥ 25000 bp)	2593174
Total length (≥ 50000 bp)	330573
# contigs	903
Largest contig	62774
Total length	9260863
Reference length	9283304
N50	17067
N75	9627
L50	174
L75	352
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	99.032
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.18
# indels per 100 kbp	0.00
Largest alignment	62774
NA50	17067
NA75	9627
LA50	174
LA75	352

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

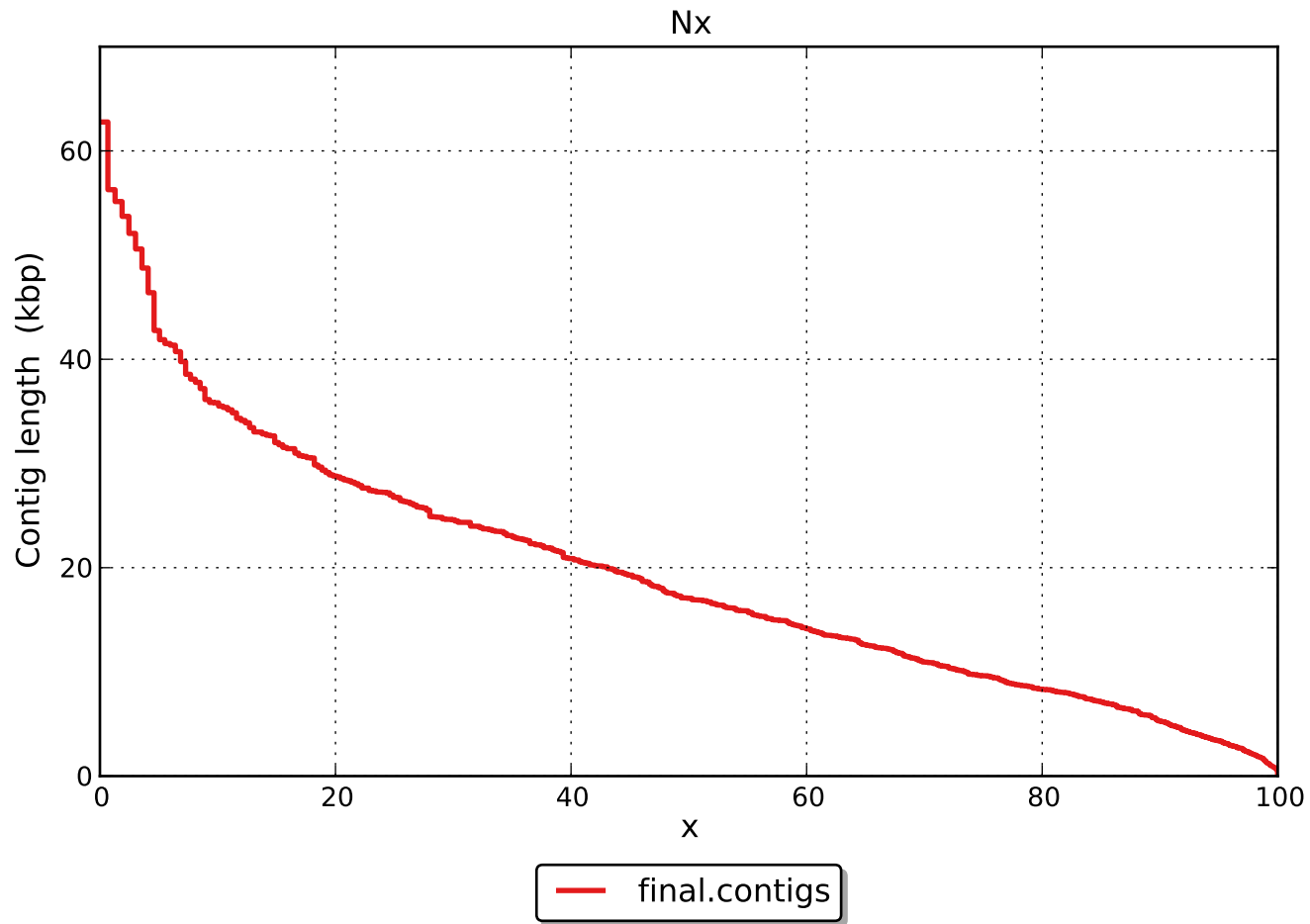
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# mismatches	17
# indels	0
# short indels	0
# long indels	0
Indels length	0

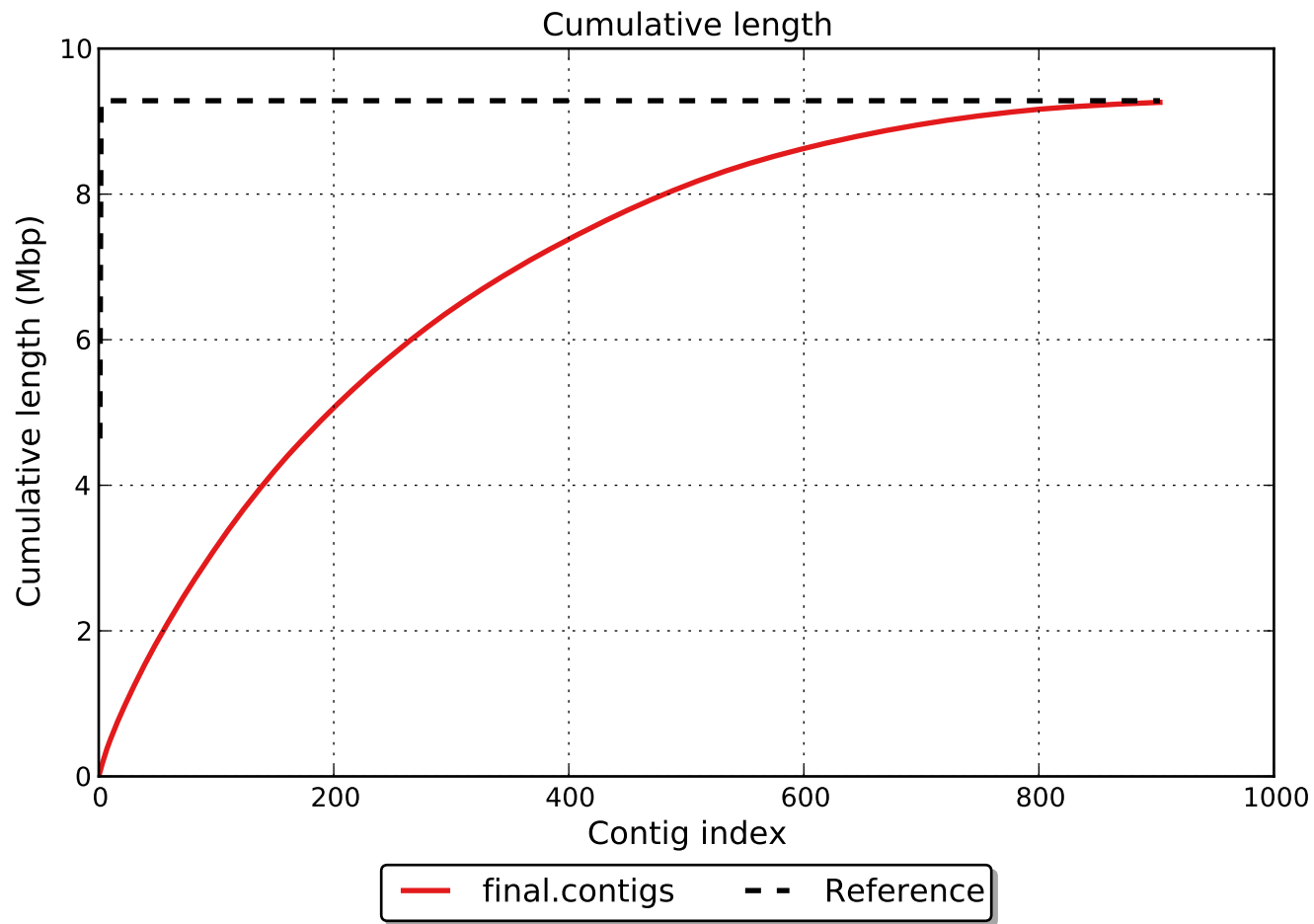
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

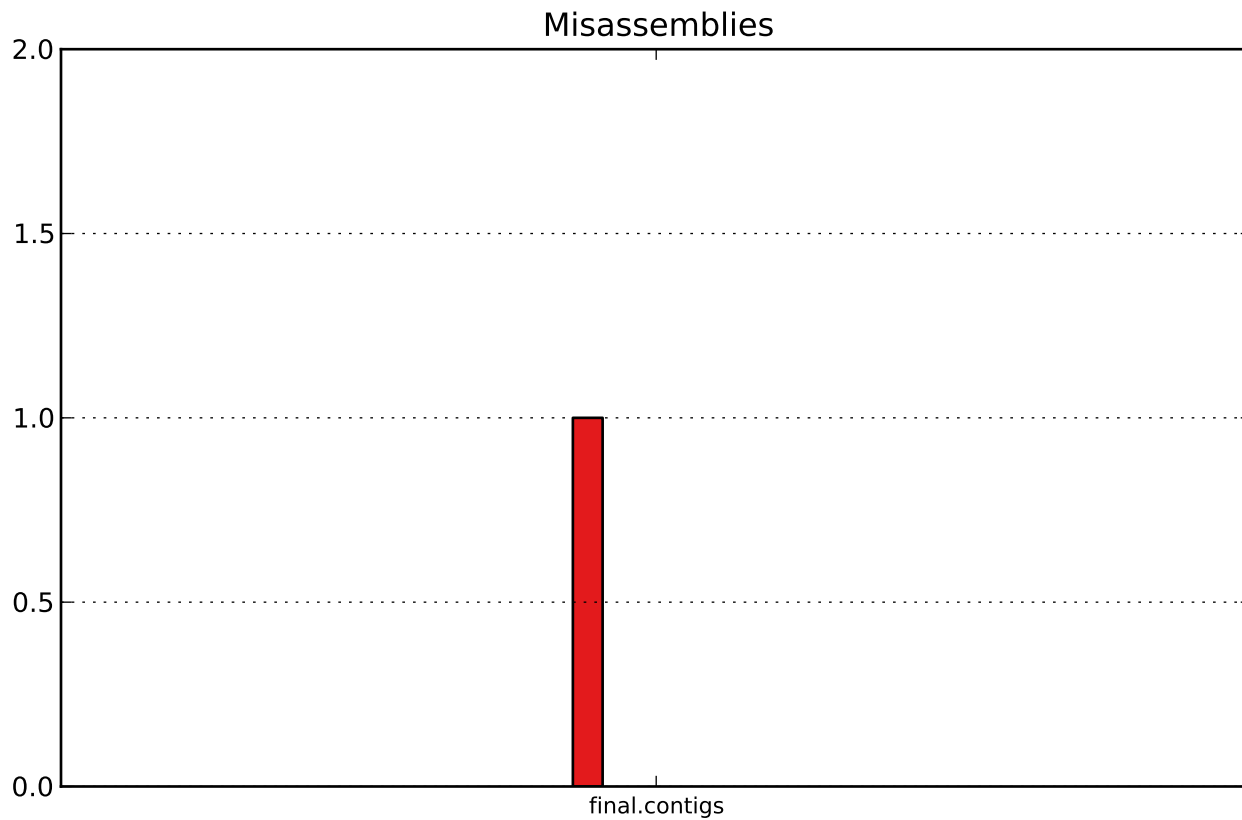
Unaligned report

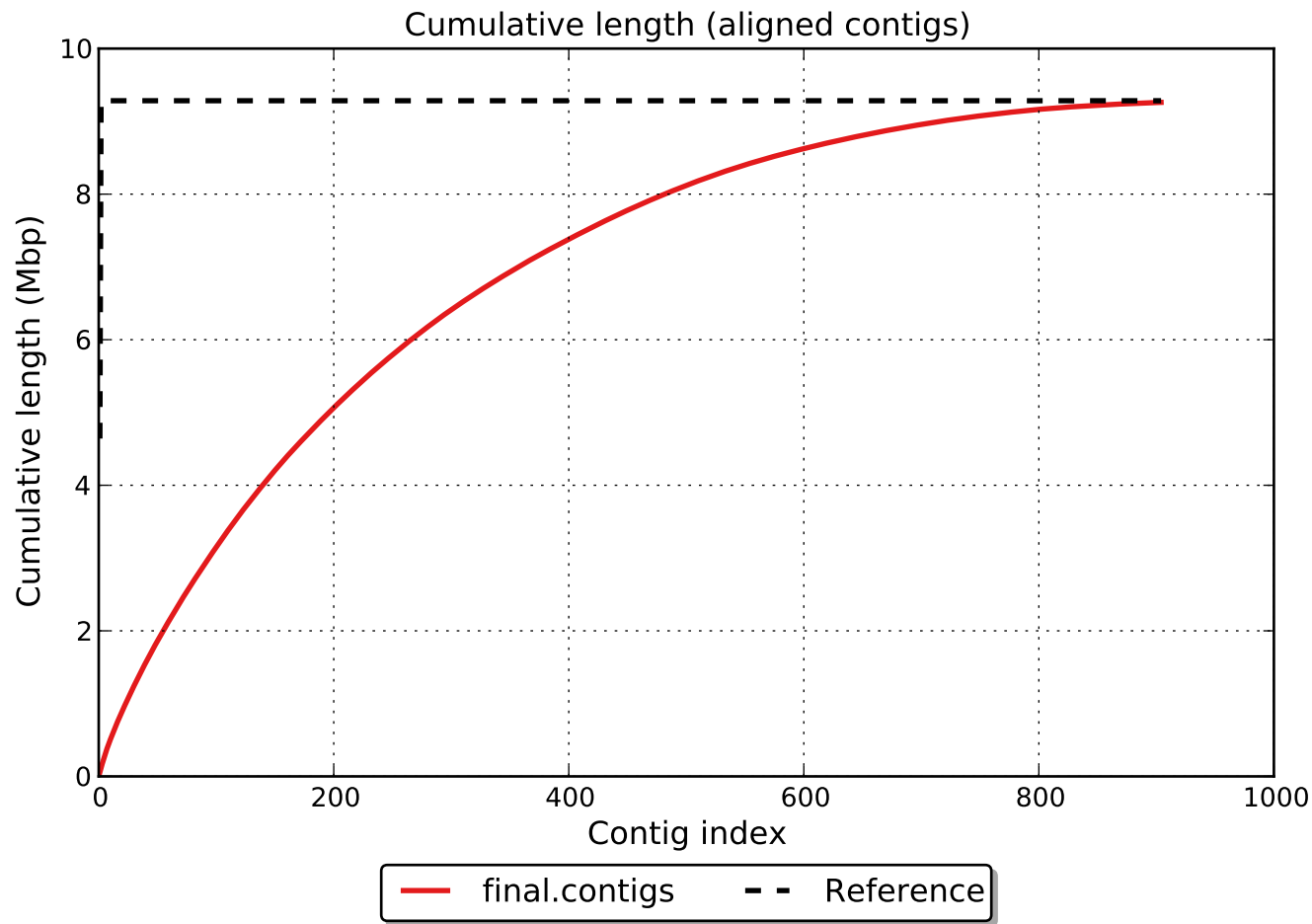
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

