Report

	final.contigs
# contigs (>= 0 bp)	650
# contigs (>= 1000 bp)	509
# contigs (>= 5000 bp)	394
# contigs (>= 10000 bp)	290
# contigs (>= 25000 bp)	122
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	9267983
Total length (>= 1000 bp)	9209946
Total length (>= 5000 bp)	8877400
Total length (>= 10000 bp)	8106846
Total length (>= 25000 bp)	5276110
Total length (>= 50000 bp)	2052085
# contigs	543
Largest contig	116977
Total length	9236754
Reference length	9283304
N50	28921
N75	17087
L50	98
L75	202
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	20093
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.161
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.21
# indels per 100 kbp	0.00
Largest alignment	116977
NA50	28921
NA75	17087
LA50	98
LA75	202

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).
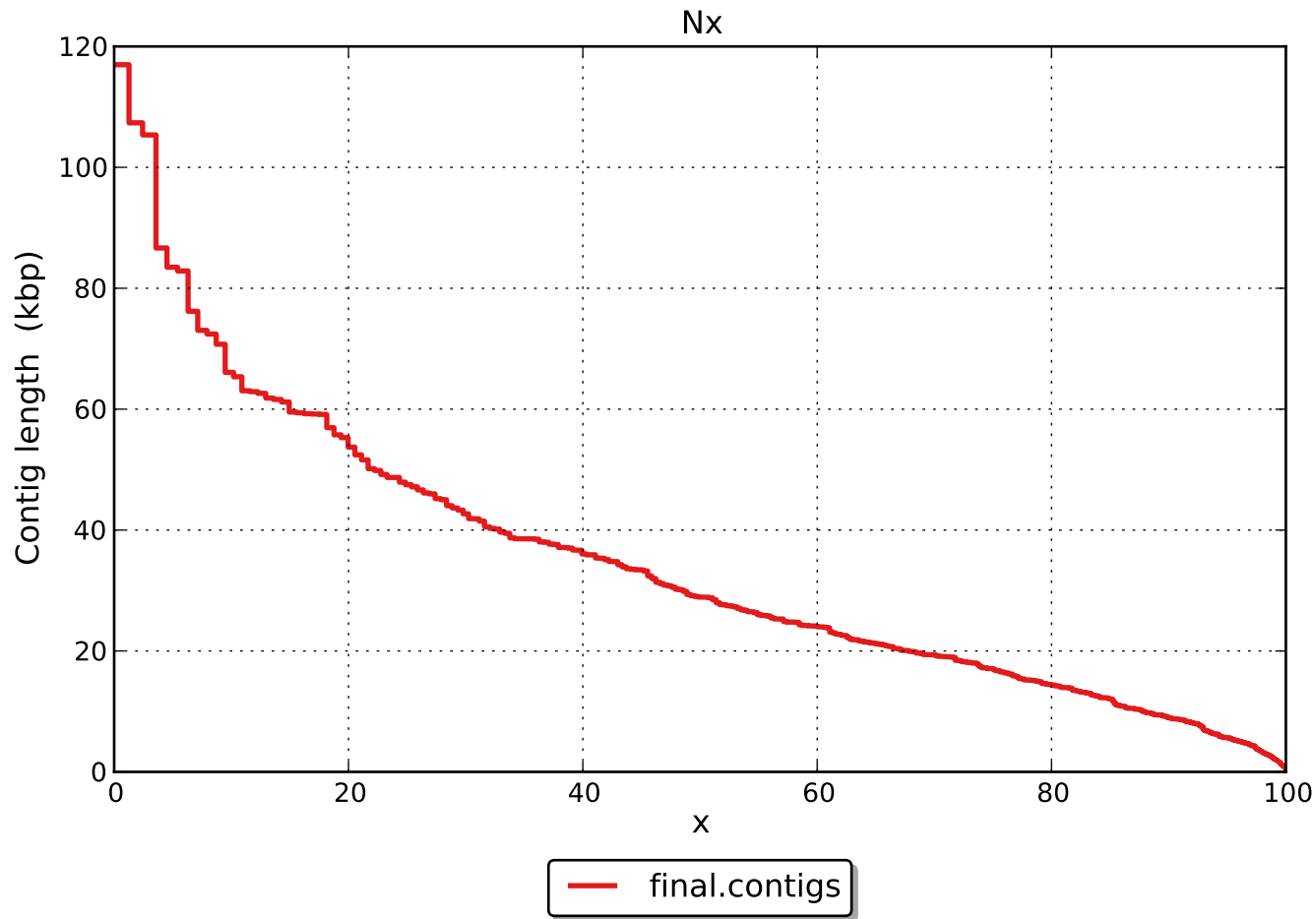
Misassemblies report

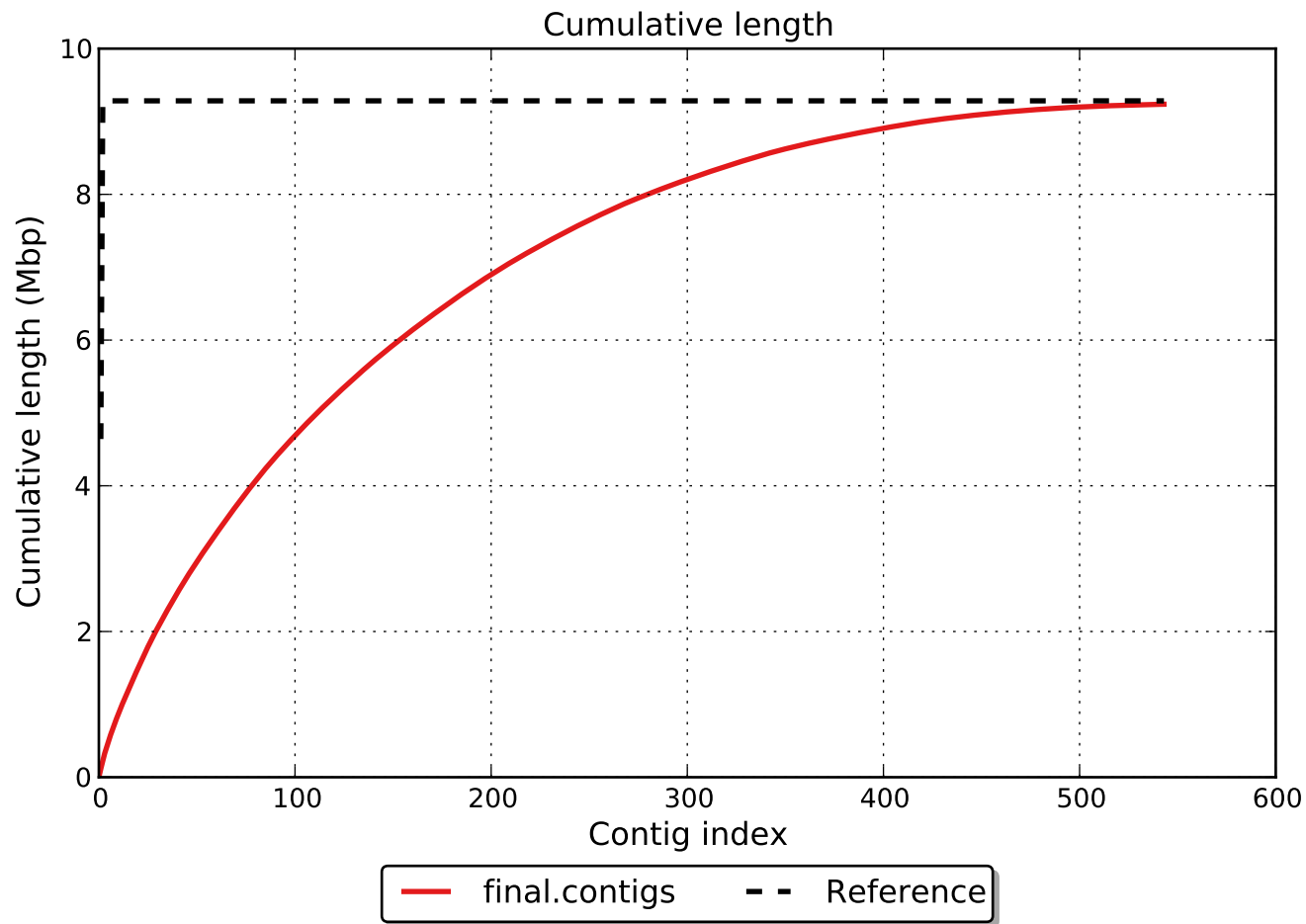|	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	20093
# local misassemblies	0
# mismatches	111
# indels	0
# short indels	0
# long indels	0
Indels length	0

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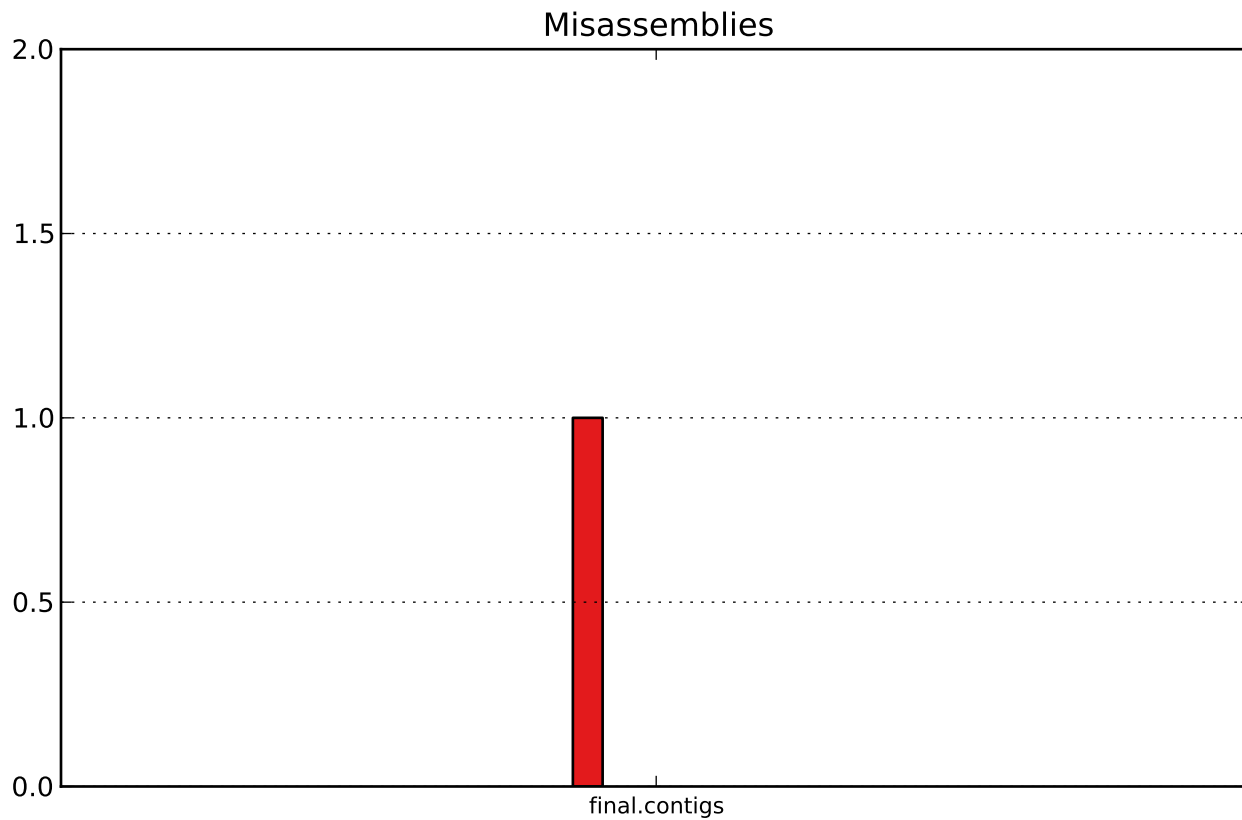(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

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
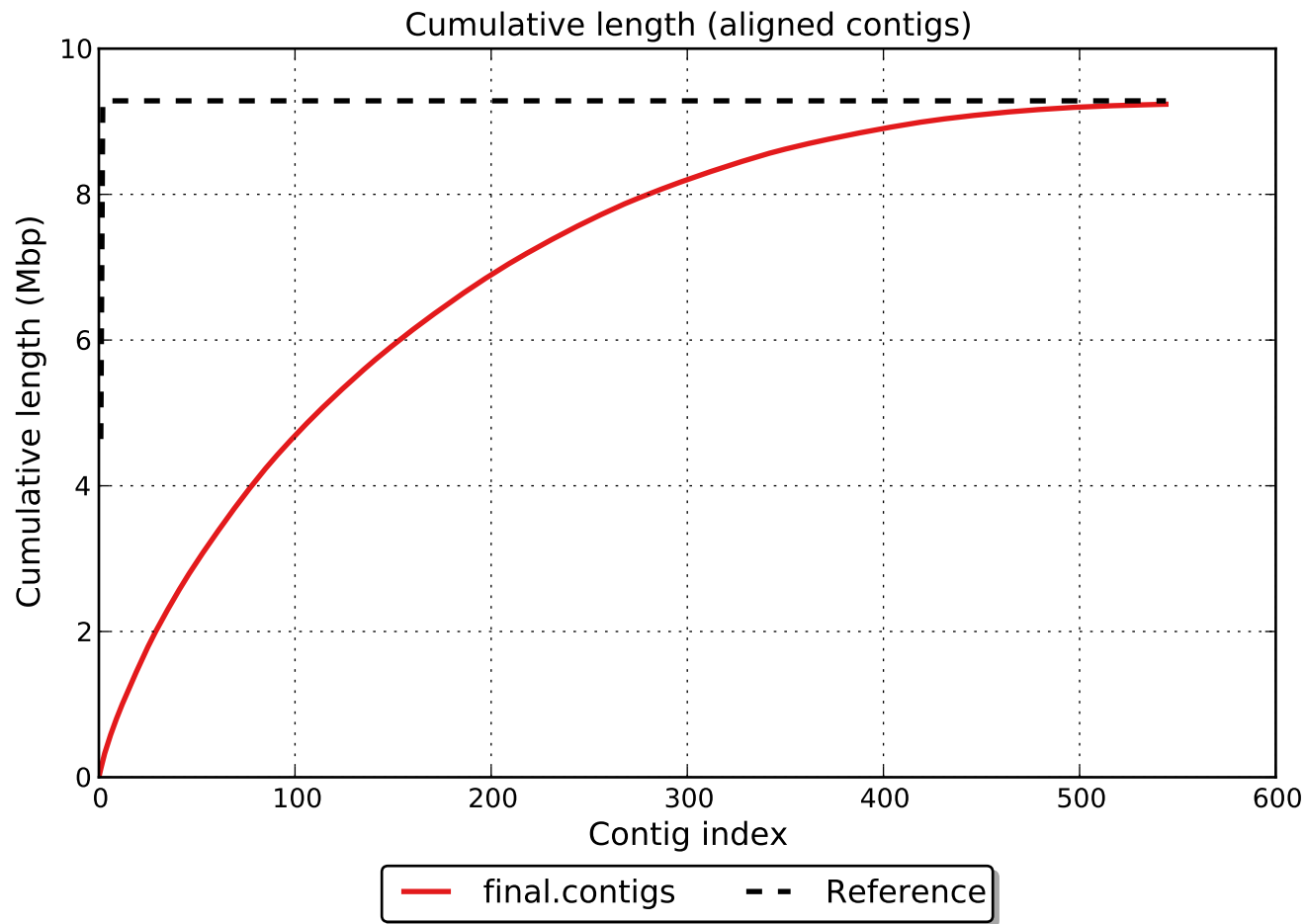(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

Misassemblies

final.contigs

relocations

Cumulative length (aligned contigs)