Report

	final.contigs
# contigs (>= 0 bp)	1470
# contigs (>= 1000 bp)	912
# contigs (>= 5000 bp)	572
# contigs (>= 10000 bp)	339
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	9441465
Total length (>= 1000 bp)	9231330
Total length (>= 5000 bp)	8251447
Total length (>= 10000 bp)	6534361
Total length (>= 25000 bp)	2272664
Total length (>= 50000 bp)	170210
# contigs	986
Largest contig	66558
Total length	9284698
Reference length	9283304
N50	15462
N75	8869
L50	189
L75	385
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	27
Genome fraction (%)	99.111
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.63
# indels per 100 kbp	0.03
Largest alignment	66558
NA50	15462
NA75	8869
LA50	189
LA75	385

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).
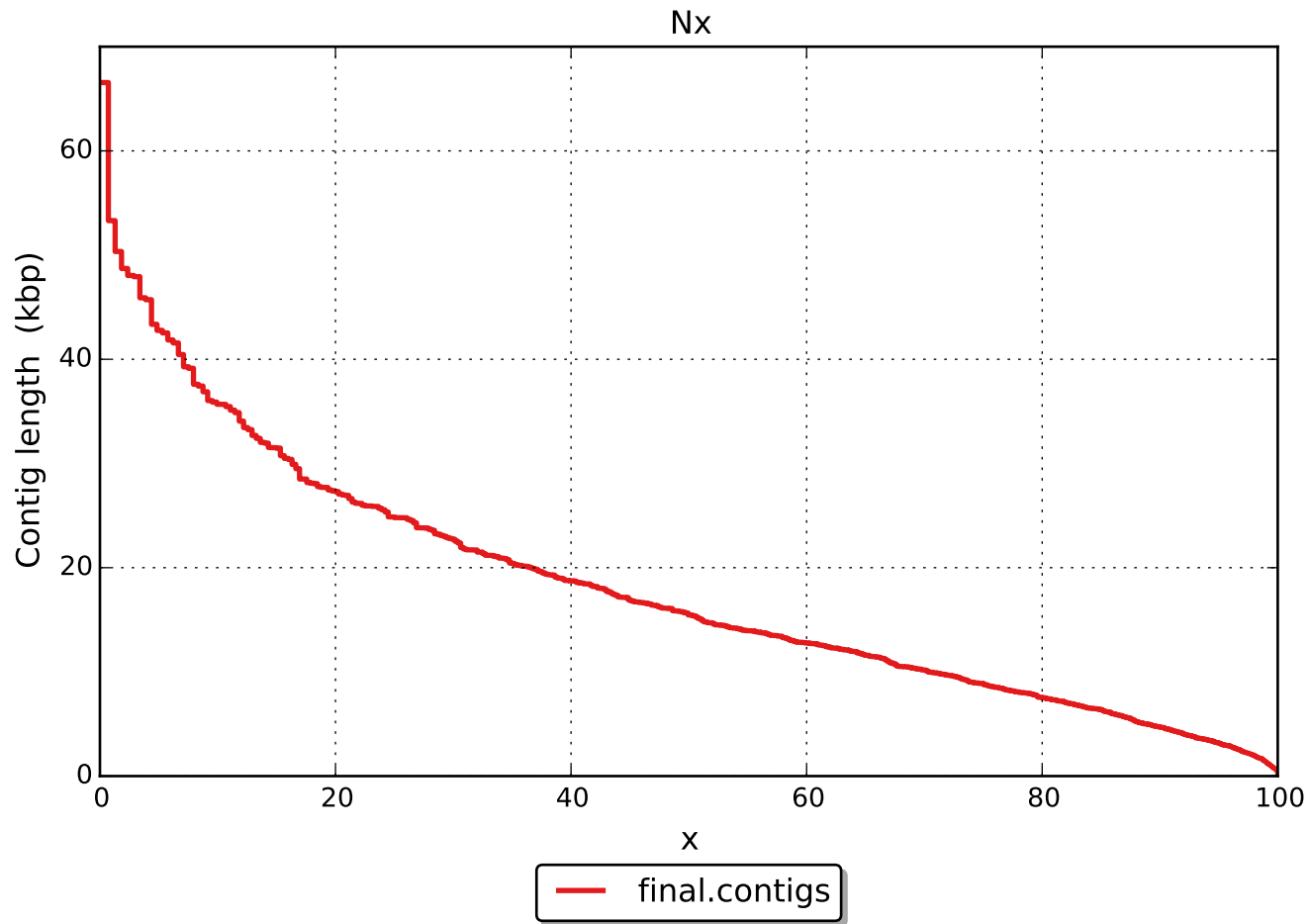
Misassemblies report

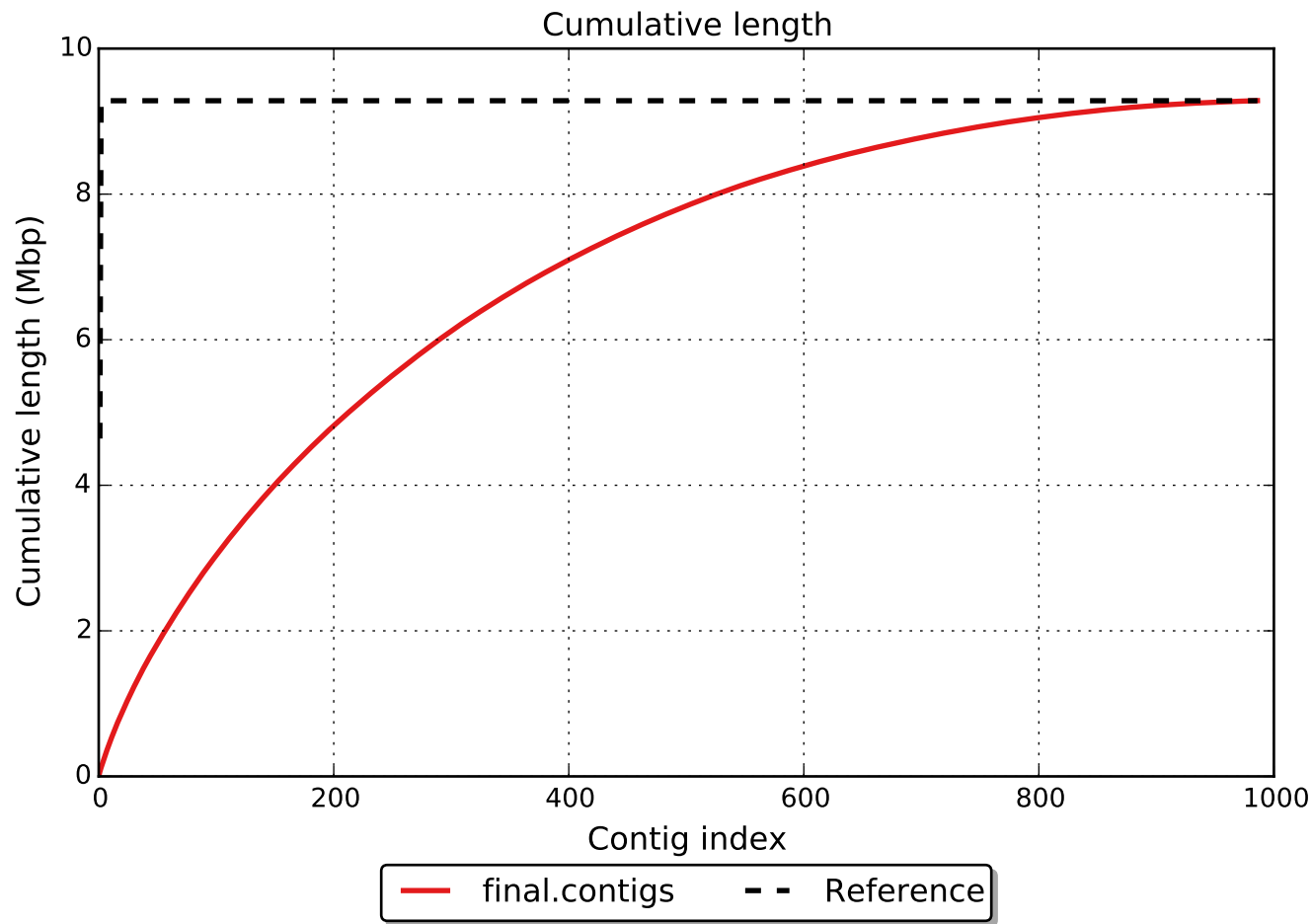|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	1254
# indels	3
# short indels	3
# long indels	0
Indels length	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).
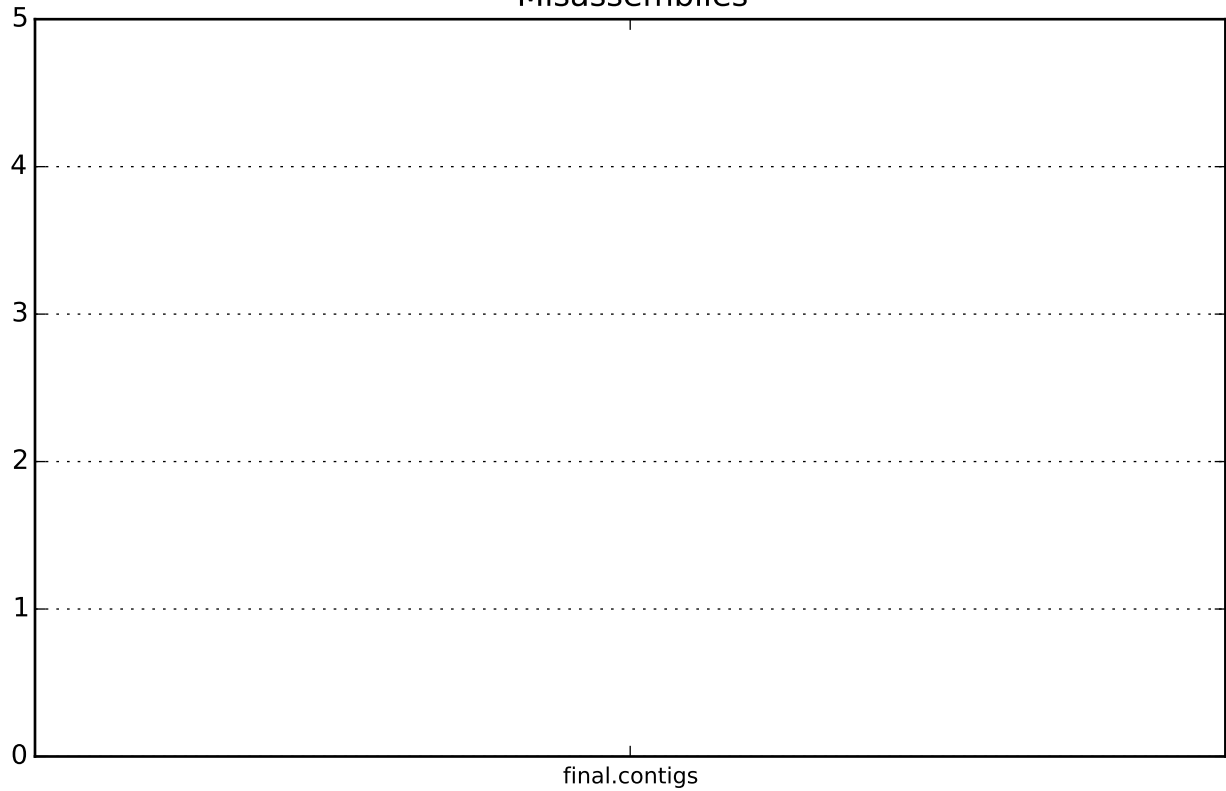
Unaligned report

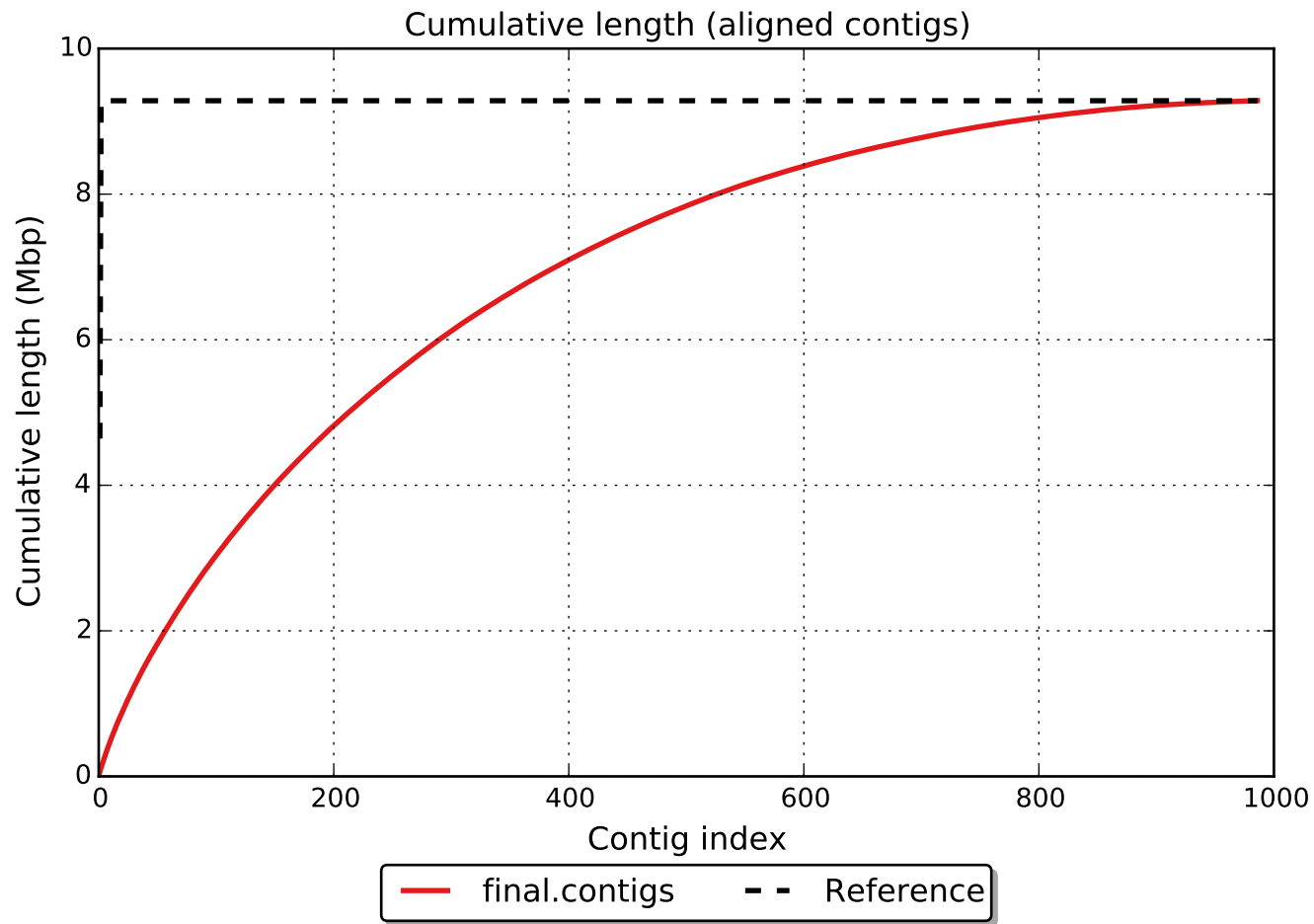|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	27
# N's	0

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

Cumulative length (aligned contigs)