Report

	final.contigs
# contigs (>= 0 bp)	5507
# contigs (>= 1000 bp)	3154
# contigs (>= 5000 bp)	390
# contigs (>= 10000 bp)	29
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10268622
Total length (>= 1000 bp)	9072671
Total length (>= 5000 bp)	2697186
Total length (>= 10000 bp)	361432
Total length (>= 25000 bp)	31374
Total length (>= 50000 bp)	0
# contigs	4152
Largest contig	31374
Total length	9803107
Reference length	9714864
N50	3230
N75	1918
L50	953
L75	1933
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2589
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	56
Genome fraction (%)	97.642
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	45.33
# indels per 100 kbp	0.03
Largest alignment	31374
NA50	3230
NA75	1916
LA50	953
LA75	1933

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).
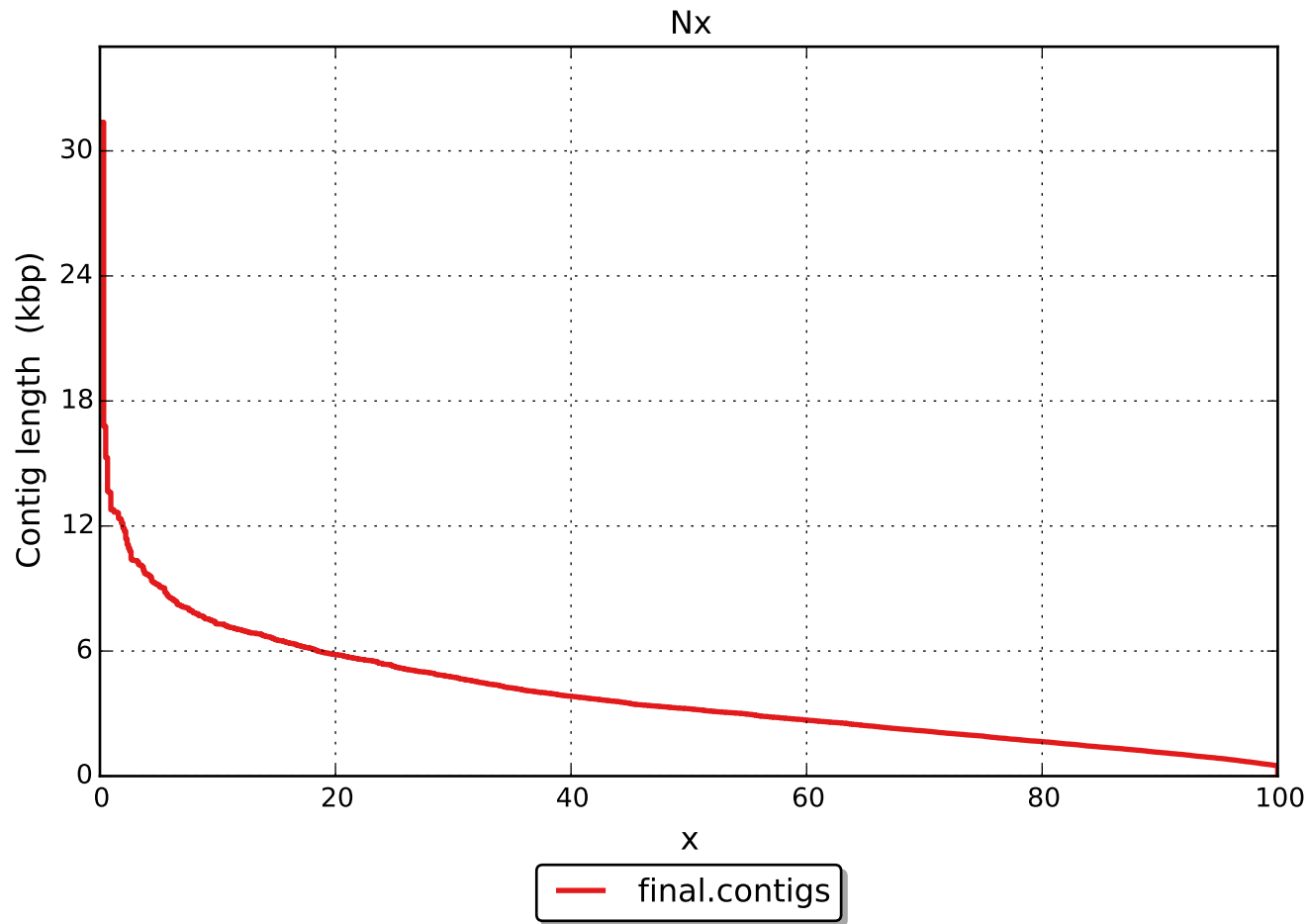
Misassemblies report

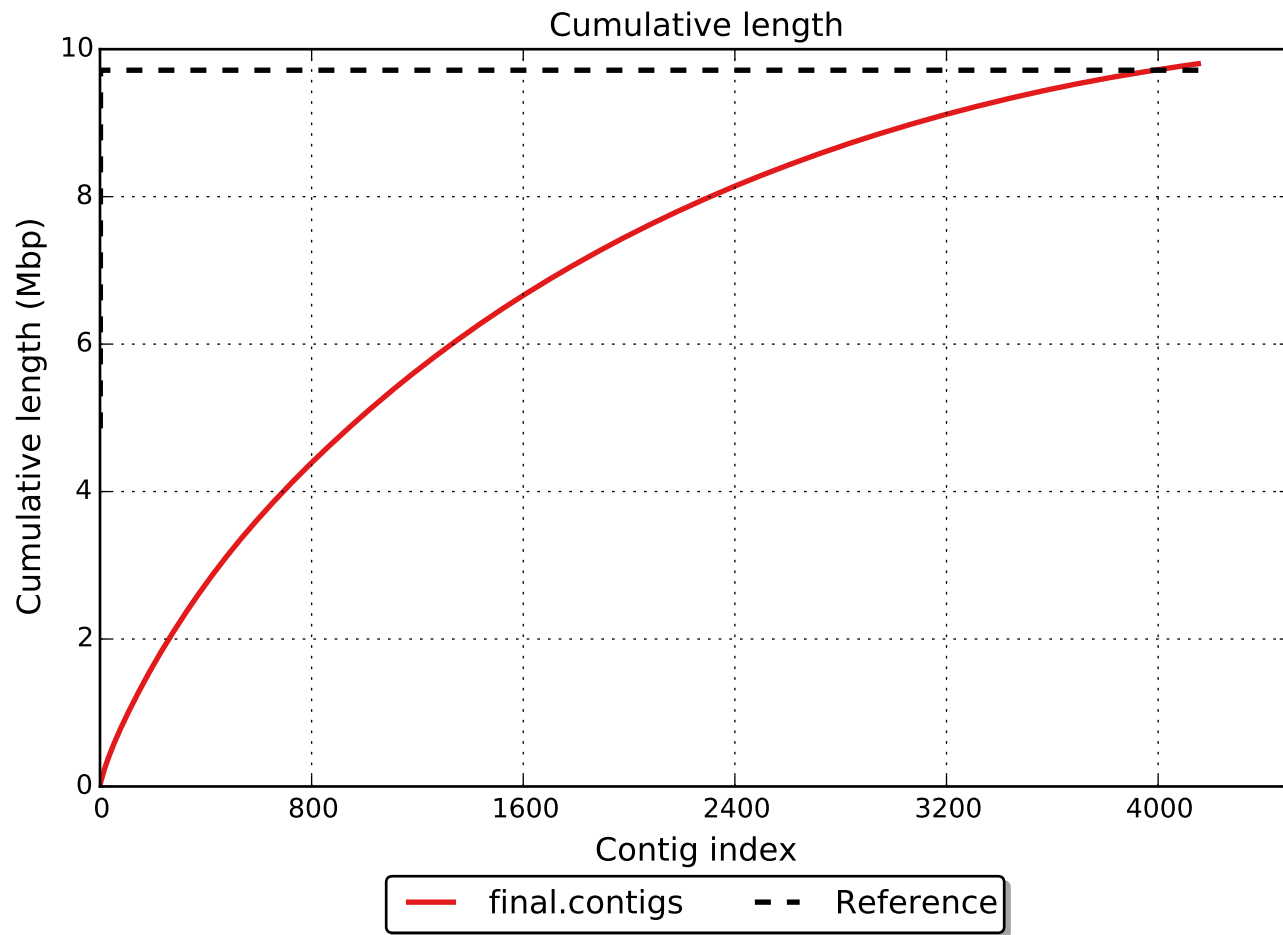|	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2589
# local misassemblies	0
# mismatches	4300
# indels	3
# short indels	3
# long indels	0
Indels length	3

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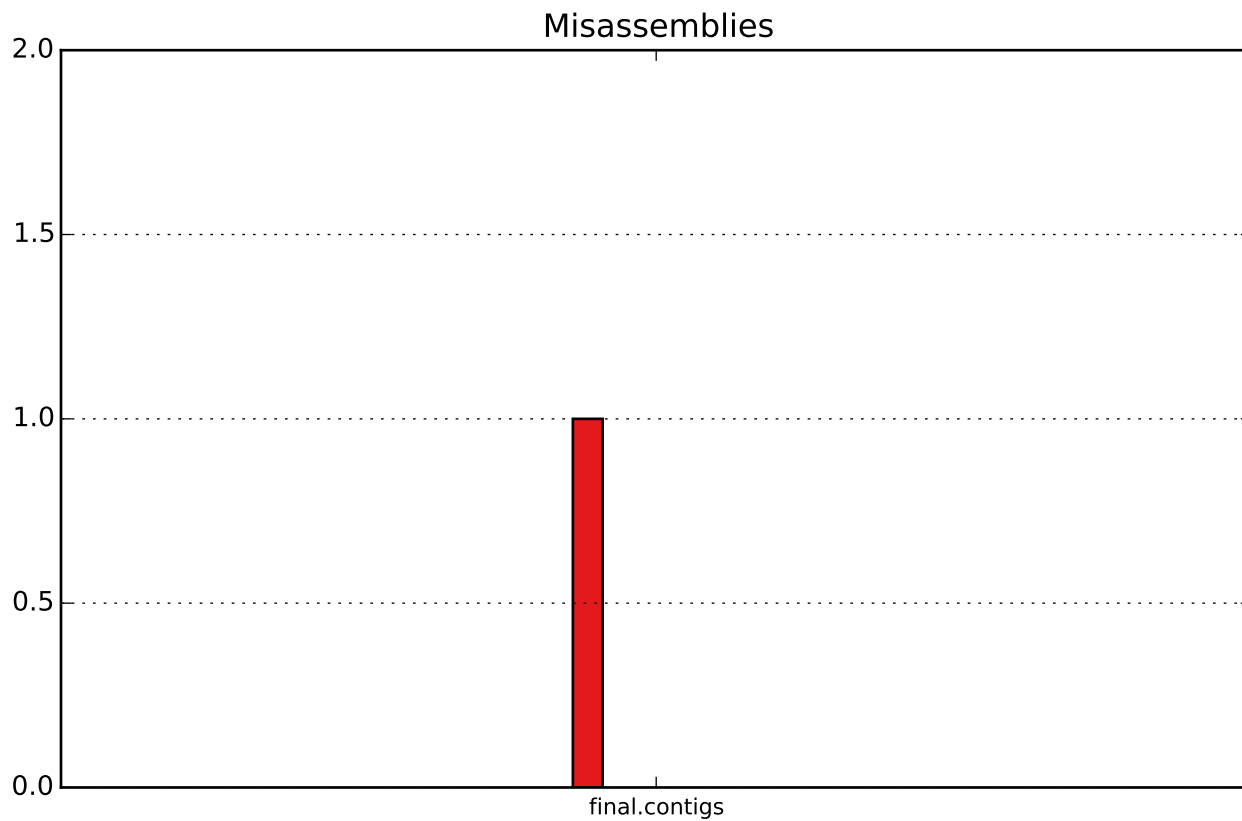(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
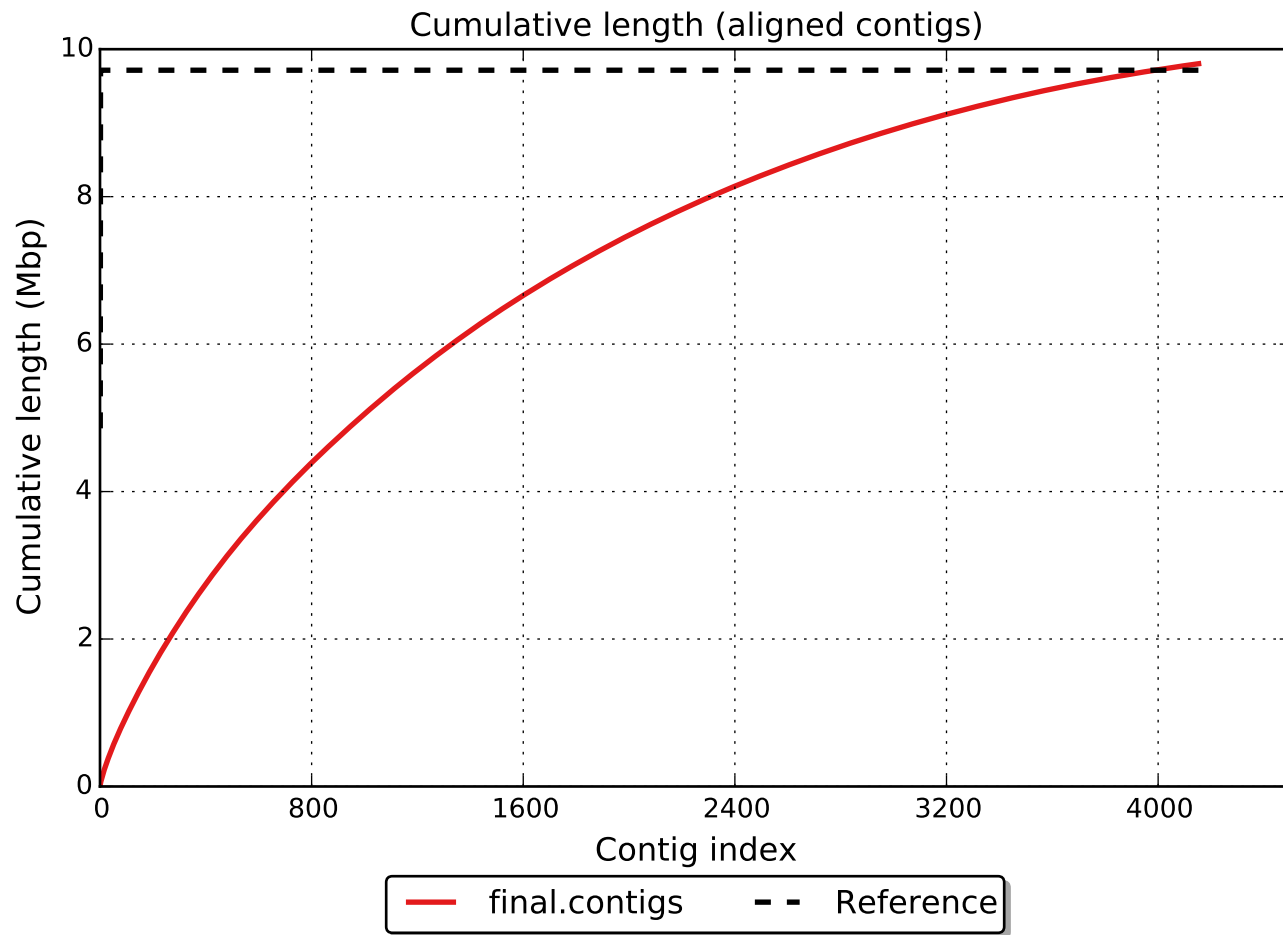
Unaligned report

	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	56
# 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

Cumulative length (aligned contigs)

NAx