Report

	final.contigs
# contigs (>= 0 bp)	10481
# contigs (>= 1000 bp)	3838
# contigs (>= 5000 bp)	33
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10533556
Total length (>= 1000 bp)	6964886
Total length (>= 5000 bp)	184734
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	7132
Largest contig	6648
Total length	9351290
Reference length	9714864
N50	1521
N75	987
L50	1989
L75	3887
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1359
# local misassemblies	0
# unaligned contigs	1 + 1 part
Unaligned length	615
Genome fraction (%)	91.737
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	73.50
# indels per 100 kbp	0.07
Largest alignment	6648
NA50	1520
NA75	987
LA50	1989
LA75	3888

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).
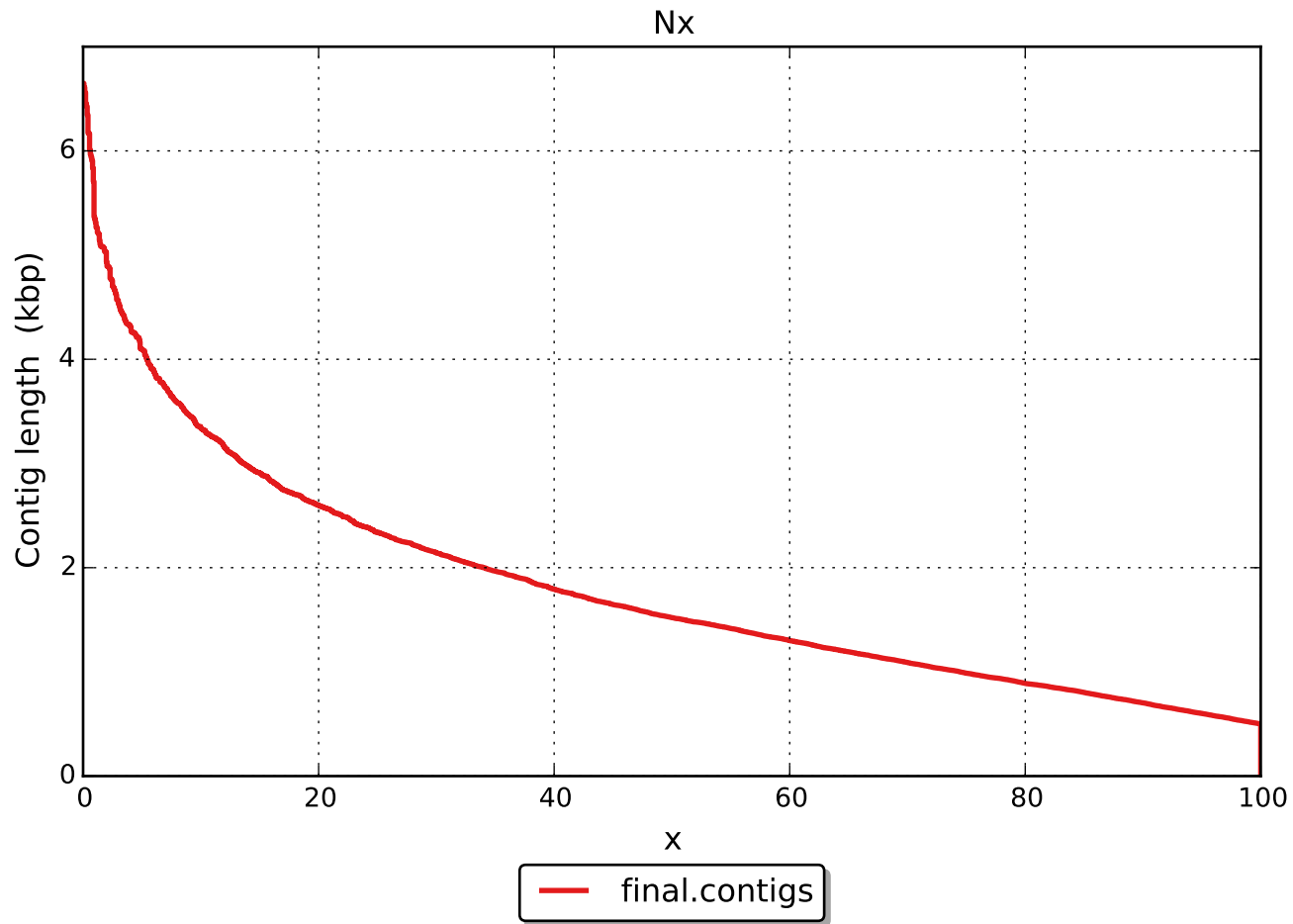
Misassemblies report

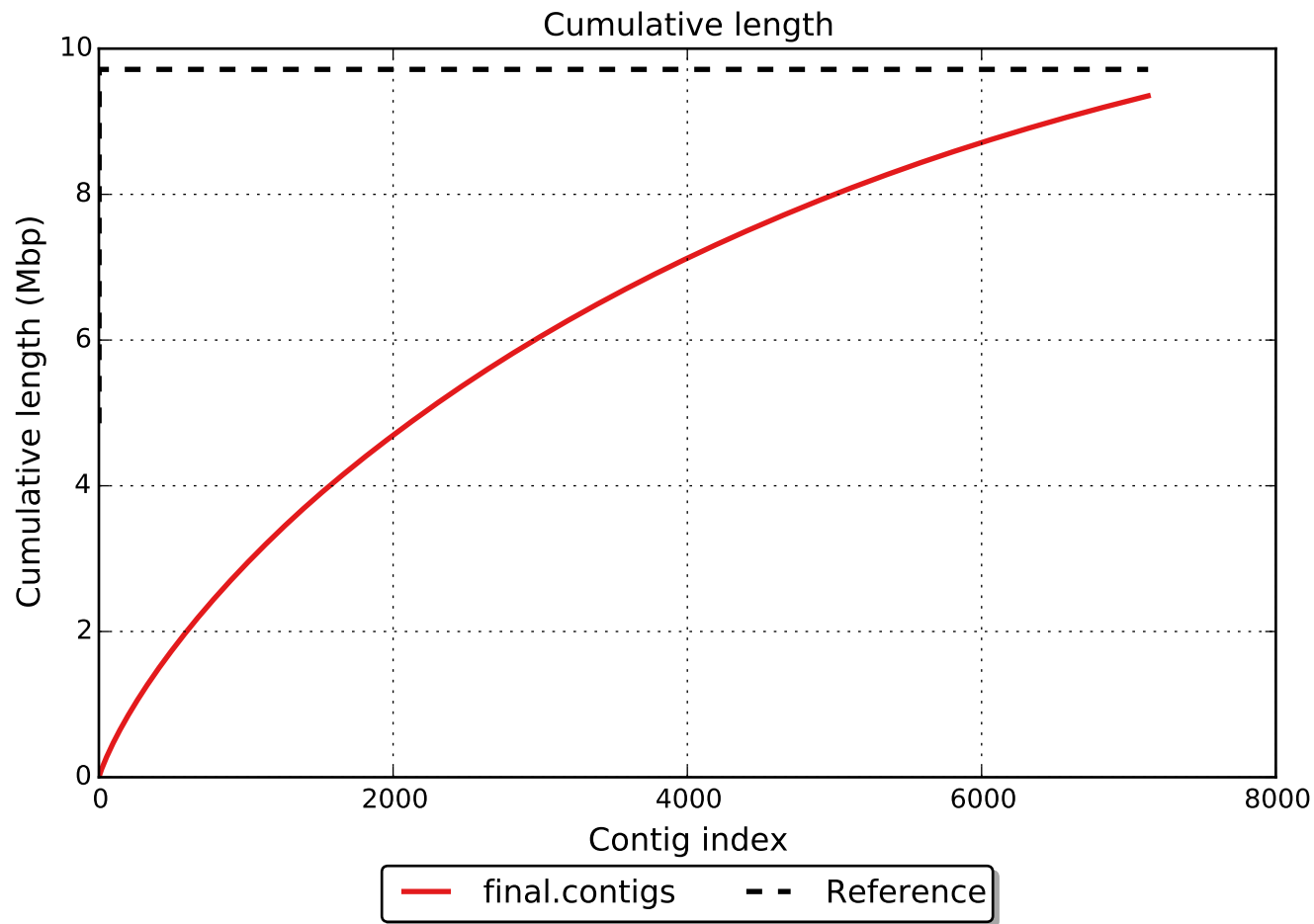|	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1359
# local misassemblies	0
# mismatches	6550
# indels	6
# short indels	6
# long indels	0
Indels length	13

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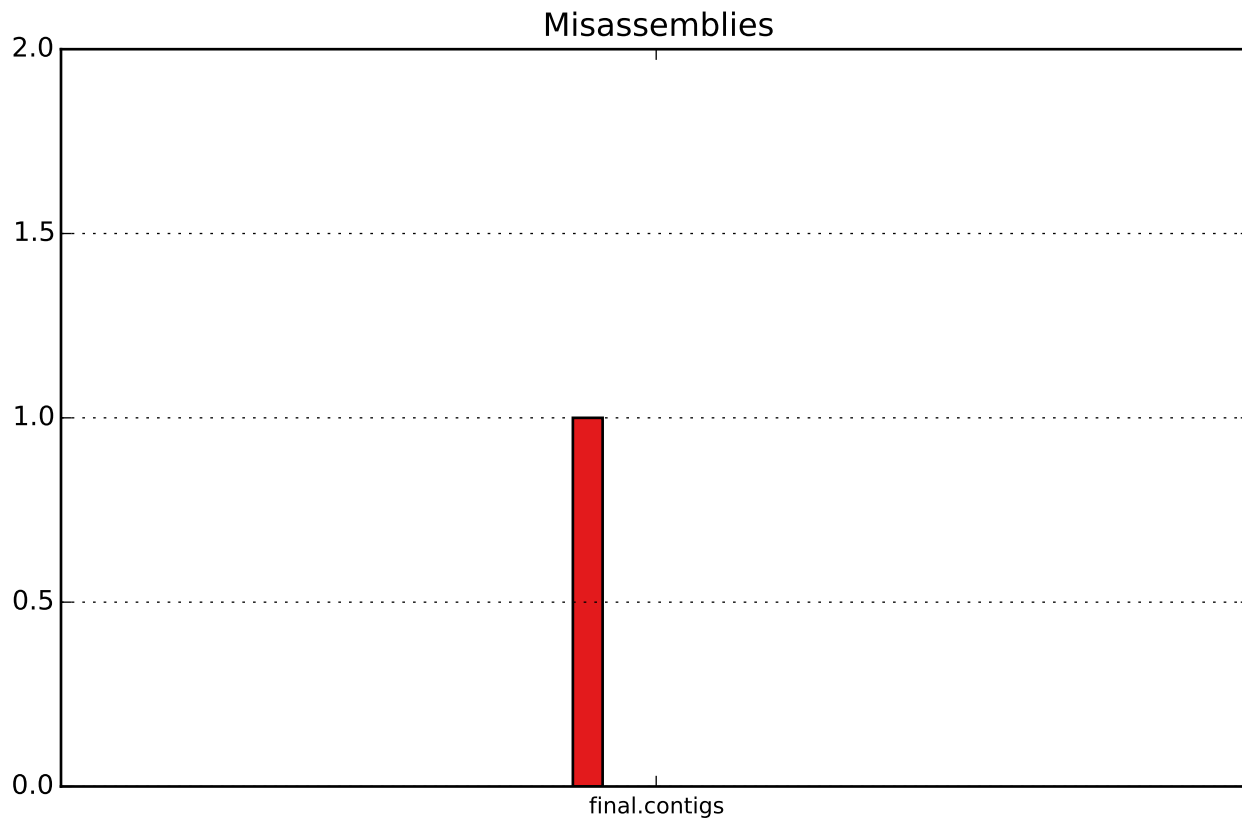(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
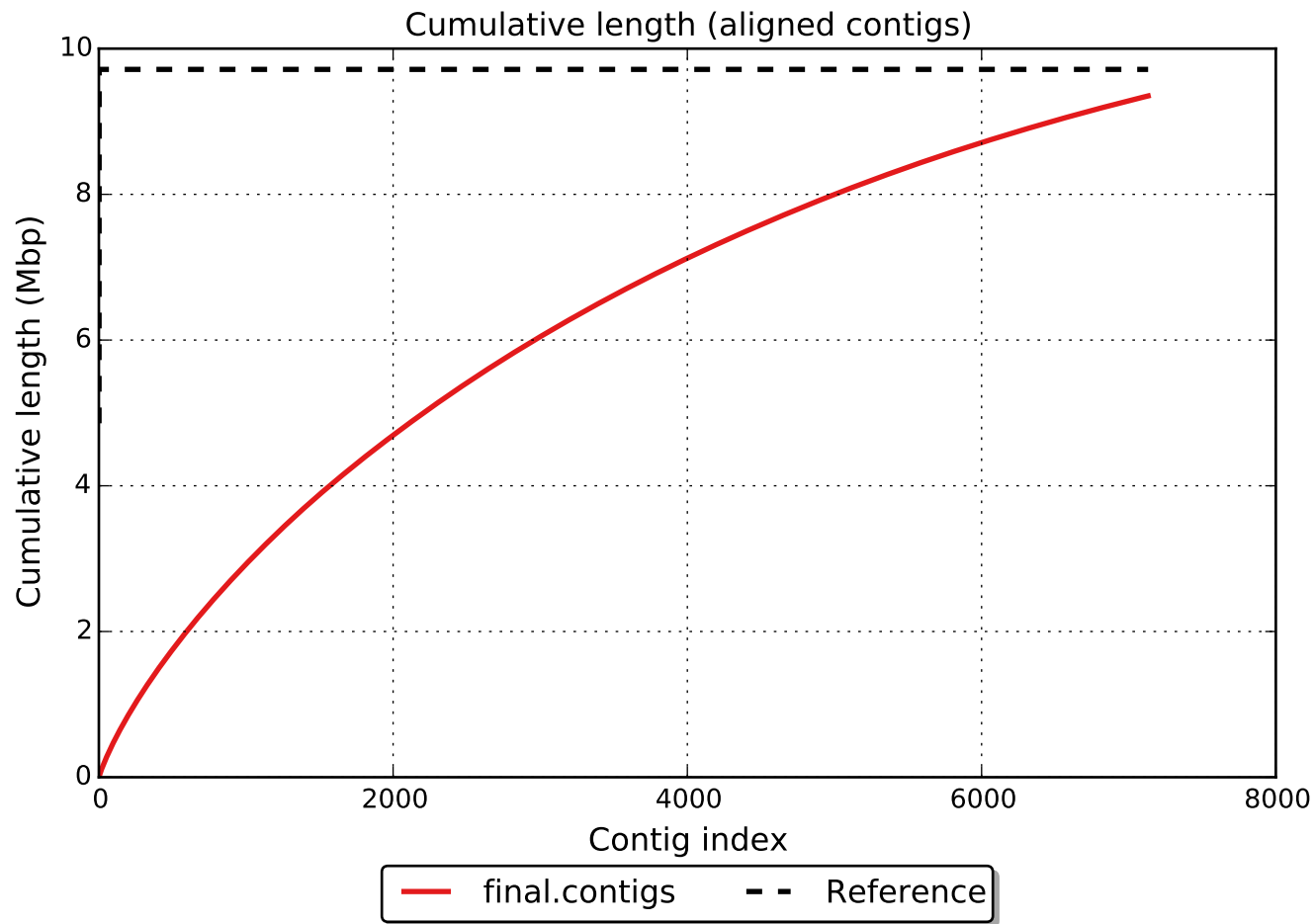
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	556
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	59
# 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)