Report

	final.contigs
# contigs (>= 0 bp)	1419
# contigs (>= 1000 bp)	691
Total length (>= 0 bp)	2519234
Total length (>= 1000 bp)	2040196
# contigs	1419
Largest contig	18963
Total length	2519234
Reference length	5478683
GC (%)	50.38
Reference GC (%)	50.49
N50	2985
N75	1301
L50	250
L75	560
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	44.966
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	416.27
# indels per 100 kbp	0.04
Largest alignment	18963
NA50	2985
NA75	1301
LA50	250
LA75	560

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).
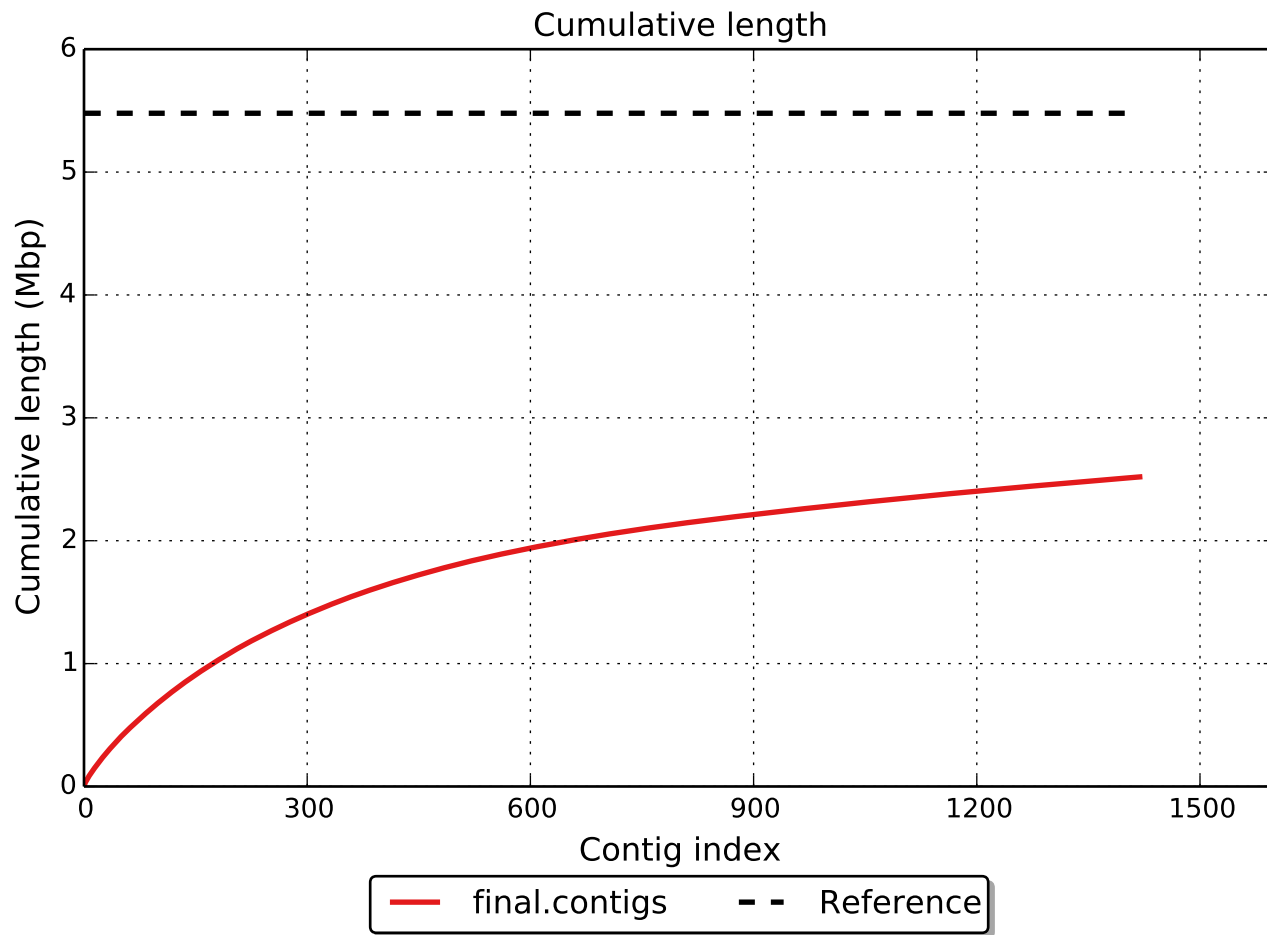
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	10255
# indels	1
# short indels	0
# long indels	1
Indels length	18

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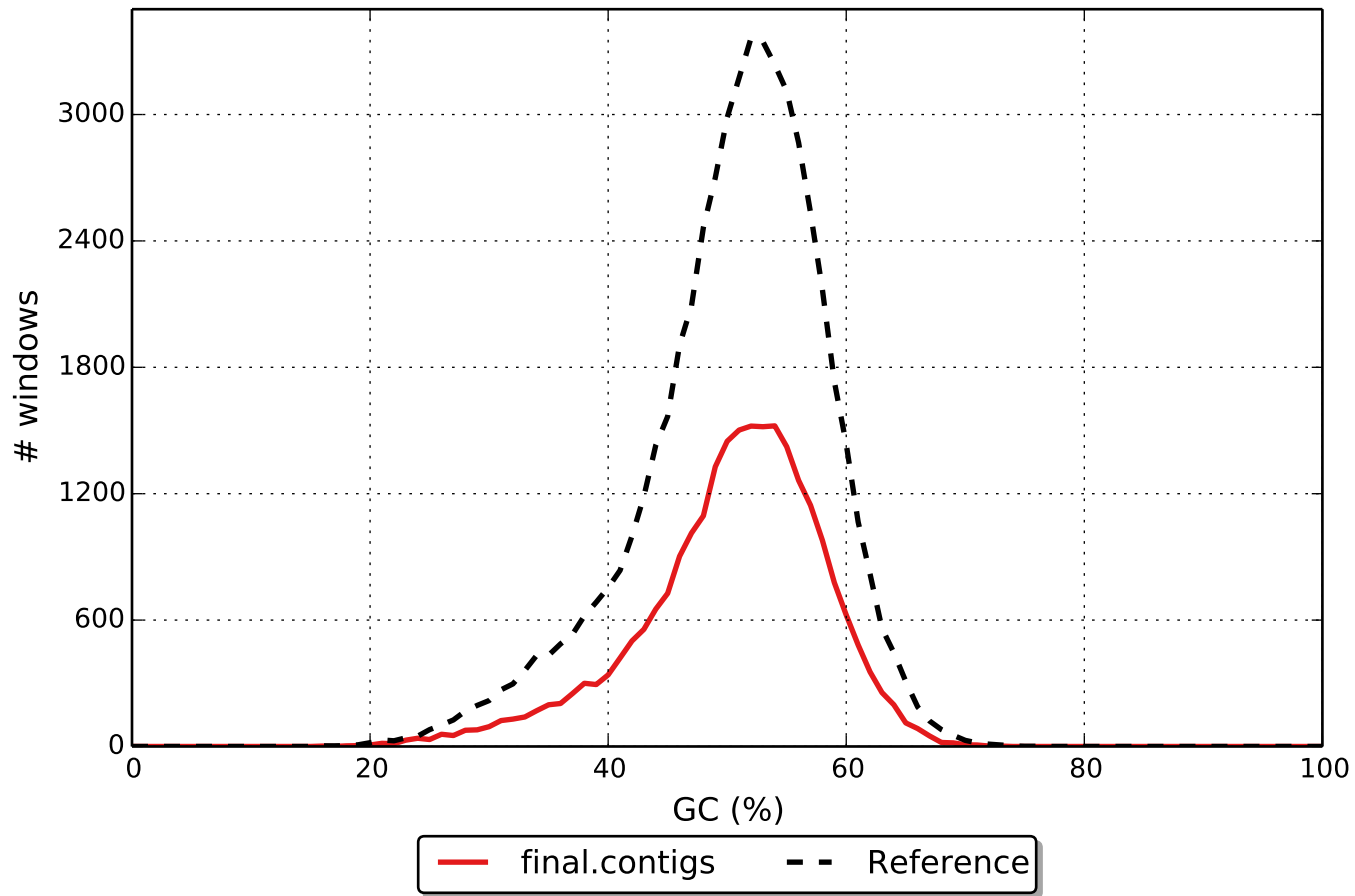(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
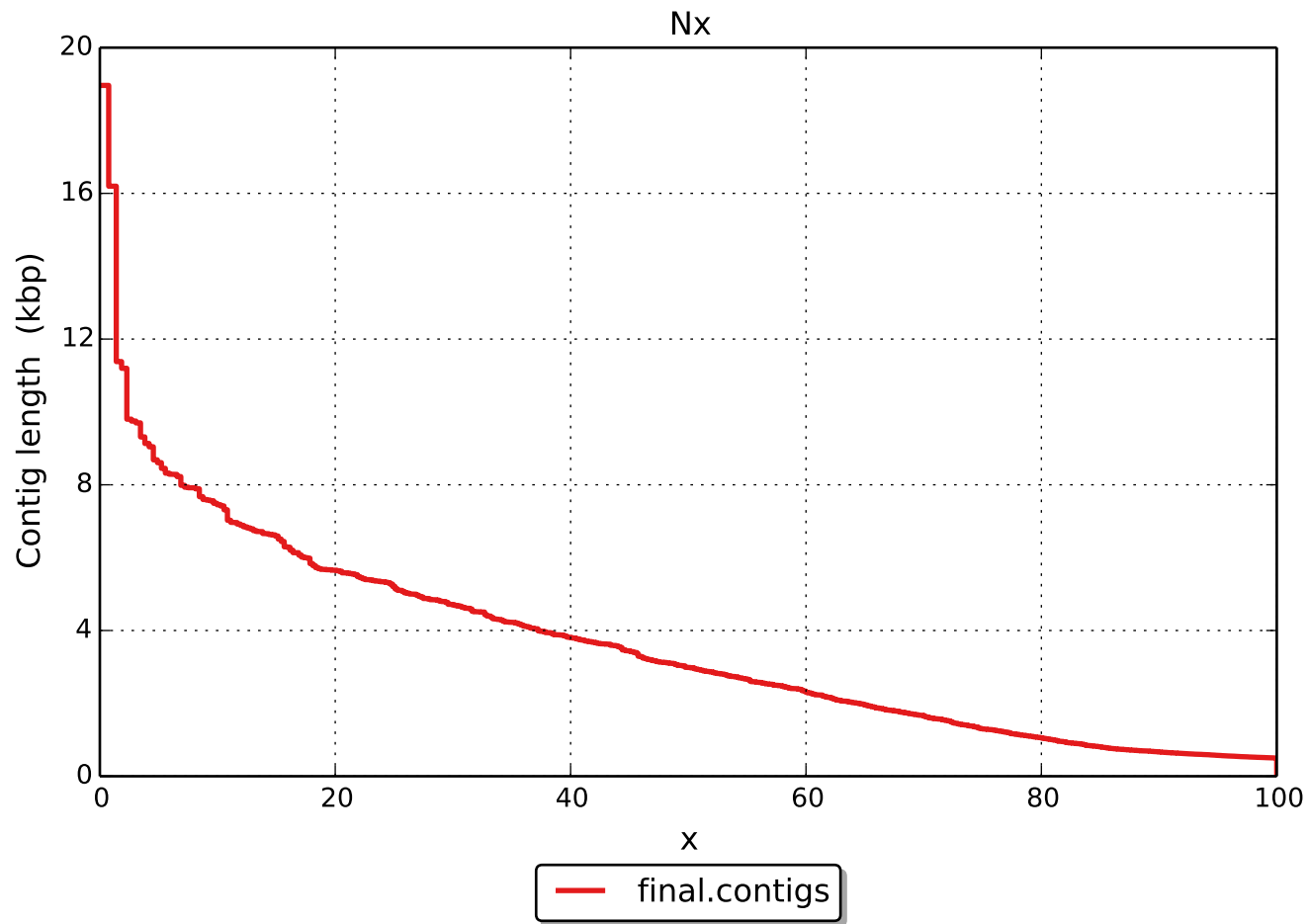
Unaligned report

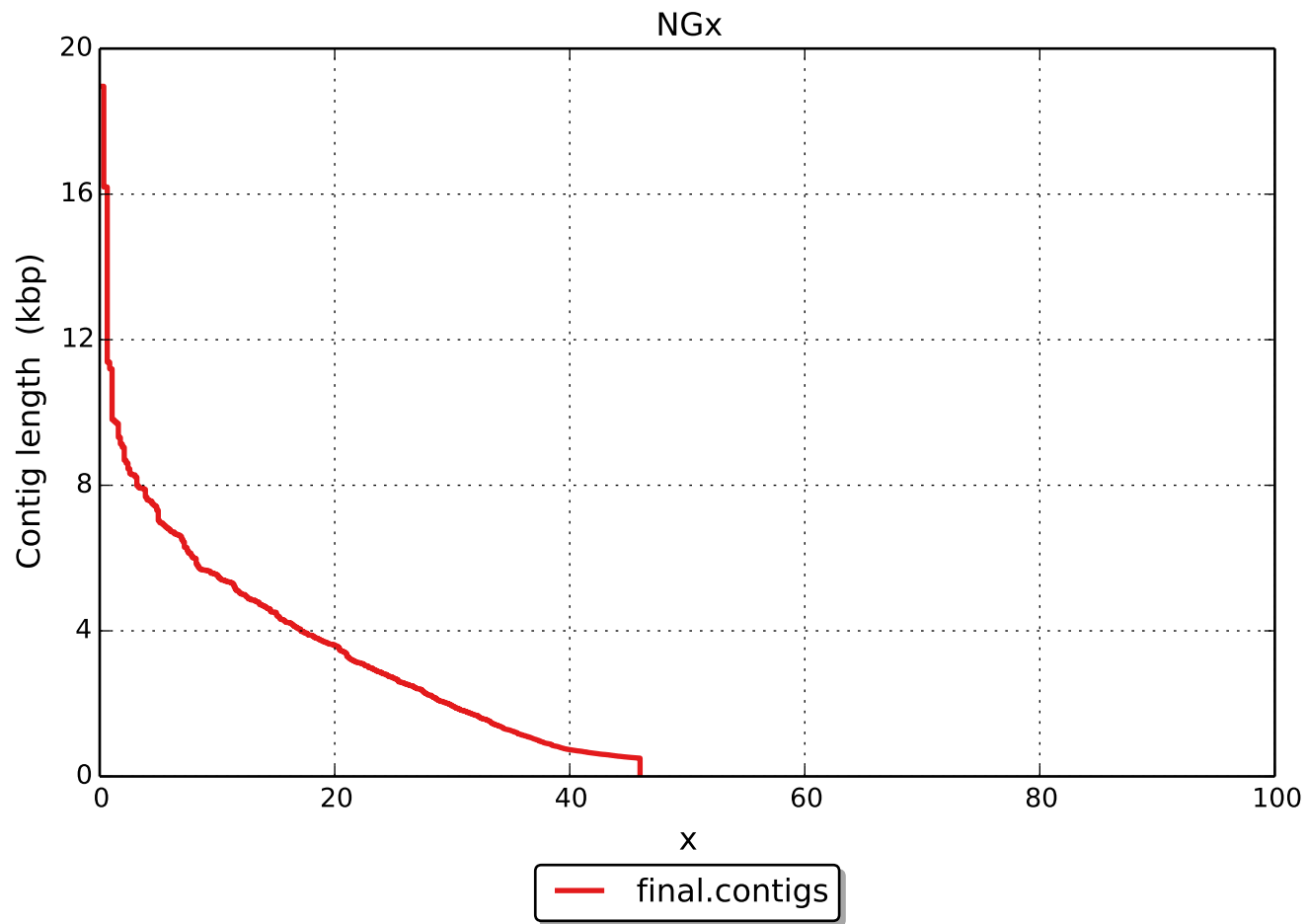|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

Cumulative length (Mbp) vs Contig index

— final.contigs - - Reference

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs