Report

	final.contigs
# contigs (>= 0 bp)	10681
# contigs (>= 1000 bp)	1918
Total length (>= 0 bp)	8011239
Total length (>= 1000 bp)	3760775
# contigs	5504
Largest contig	9465
Total length	6209297
Reference length	10957366
GC (%)	50.34
Reference GC (%)	50.49
N50	1300
NG50	608
N75	751
L50	1338
LG50	4181
L75	2964
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	360
Genome fraction (%)	54.554
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	323.33
# indels per 100 kbp	0.03
Largest alignment	9465
NA50	1300
NGA50	607
NA75	751
LA50	1338
LGA50	4182
LA75	2964

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).
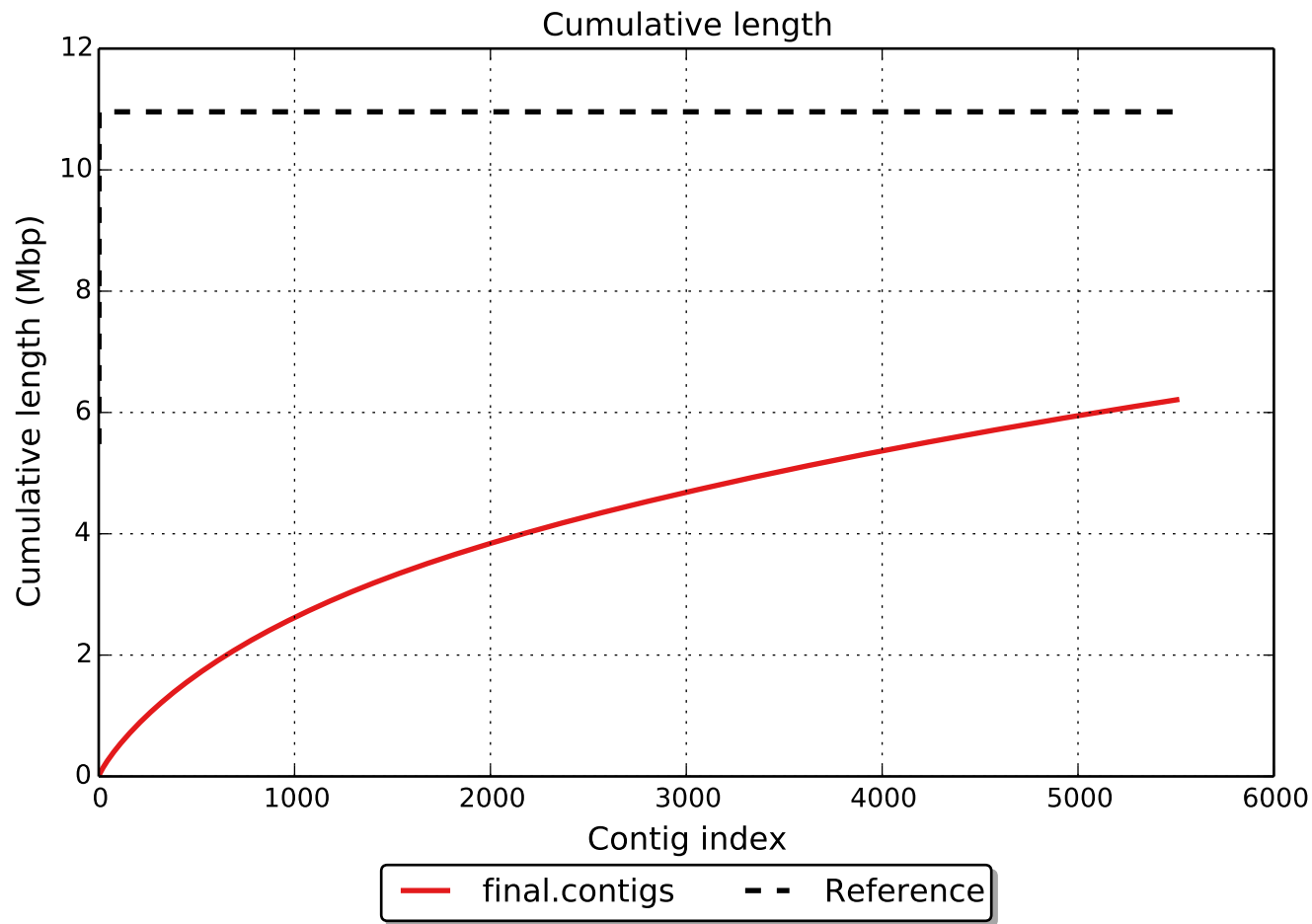
Misassemblies report

	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	0
# mismatches	19328
# indels	2
# short indels	0
# long indels	2
Indels length	24

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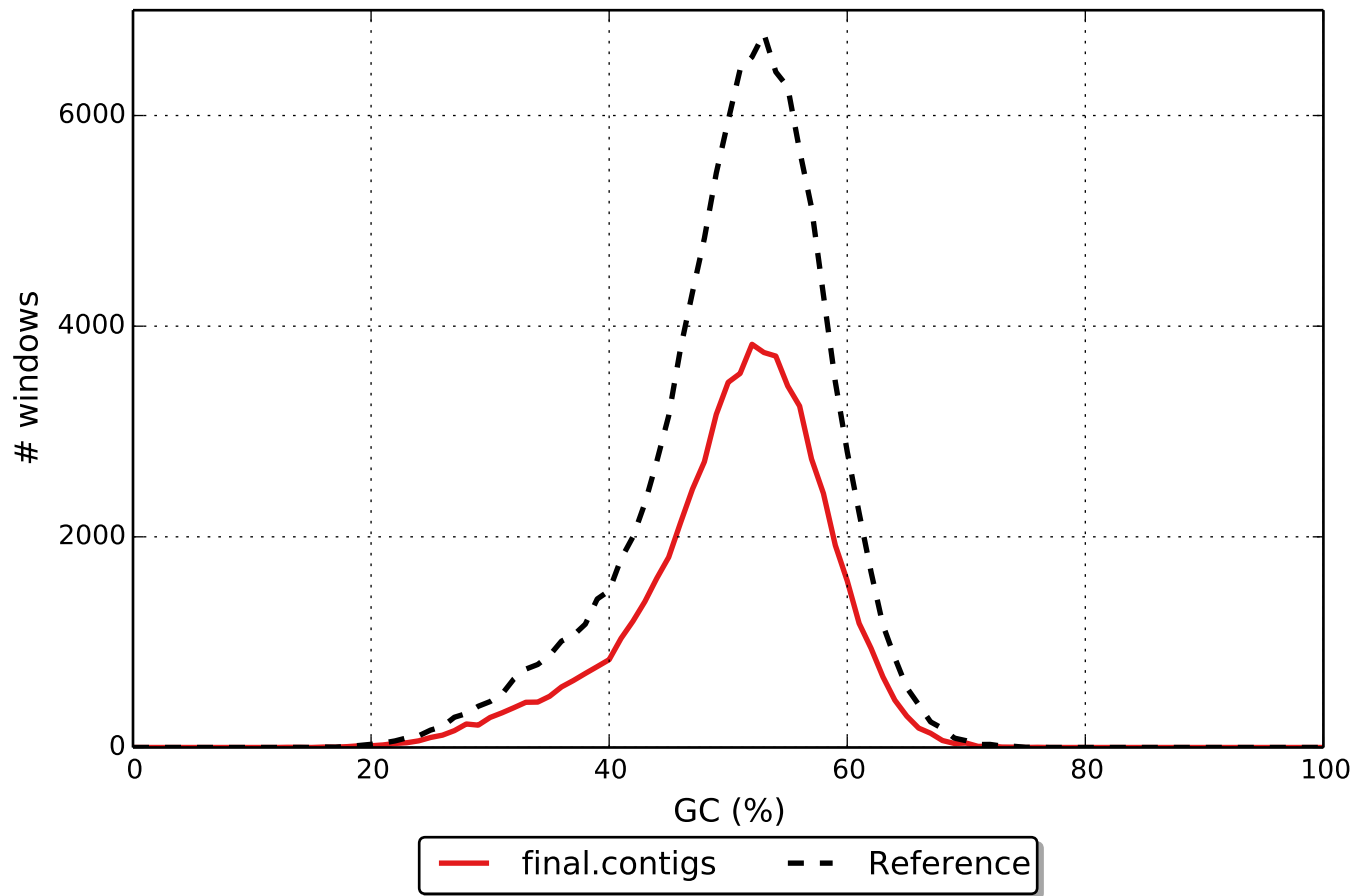(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
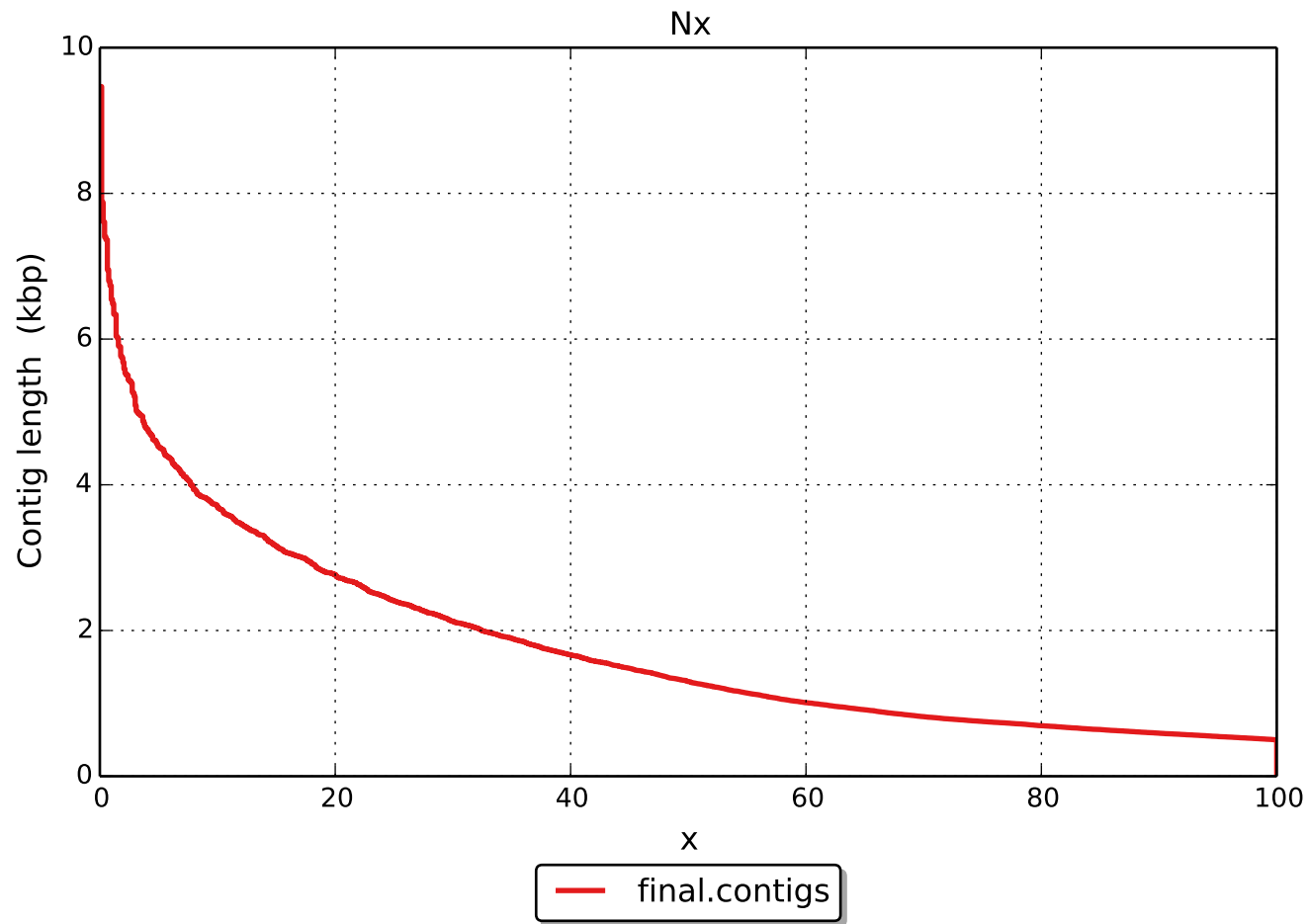
Unaligned report

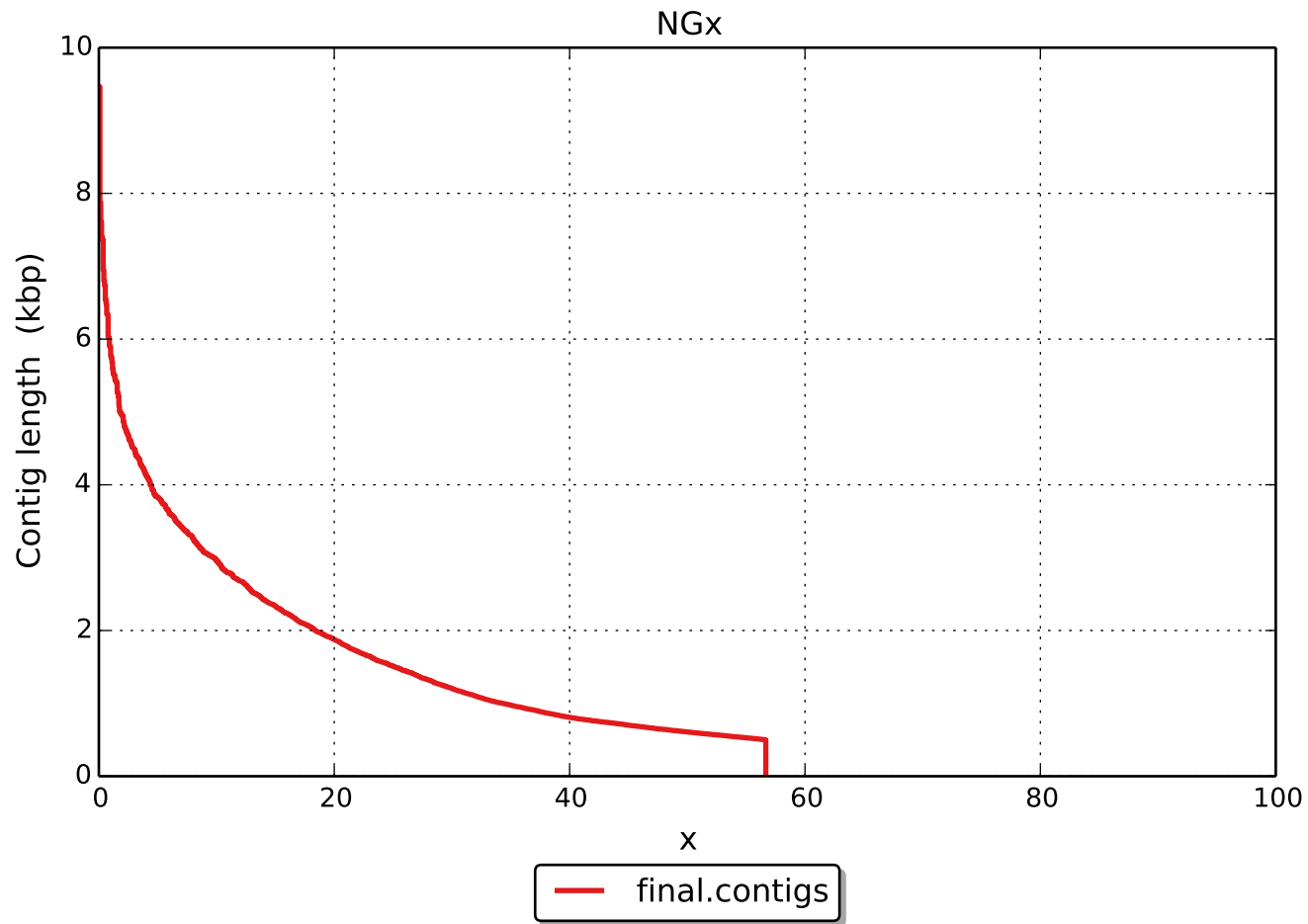|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	360
# N's	0

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

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)