Report

	final.contigs
# contigs (>= 0 bp)	3864
# contigs (>= 1000 bp)	842
Total length (>= 0 bp)	5973678
Total length (>= 1000 bp)	4880343
# contigs	1286
Largest contig	39846
Total length	5169320
Reference length	11094646
GC (%)	50.27
Reference GC (%)	50.48
N50	8472
N75	4218
L50	183
L75	397
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.592
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	528.05
# indels per 100 kbp	0.12
Largest alignment	39846
NA50	8472
NA75	4218
LA50	183
LA75	397

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).
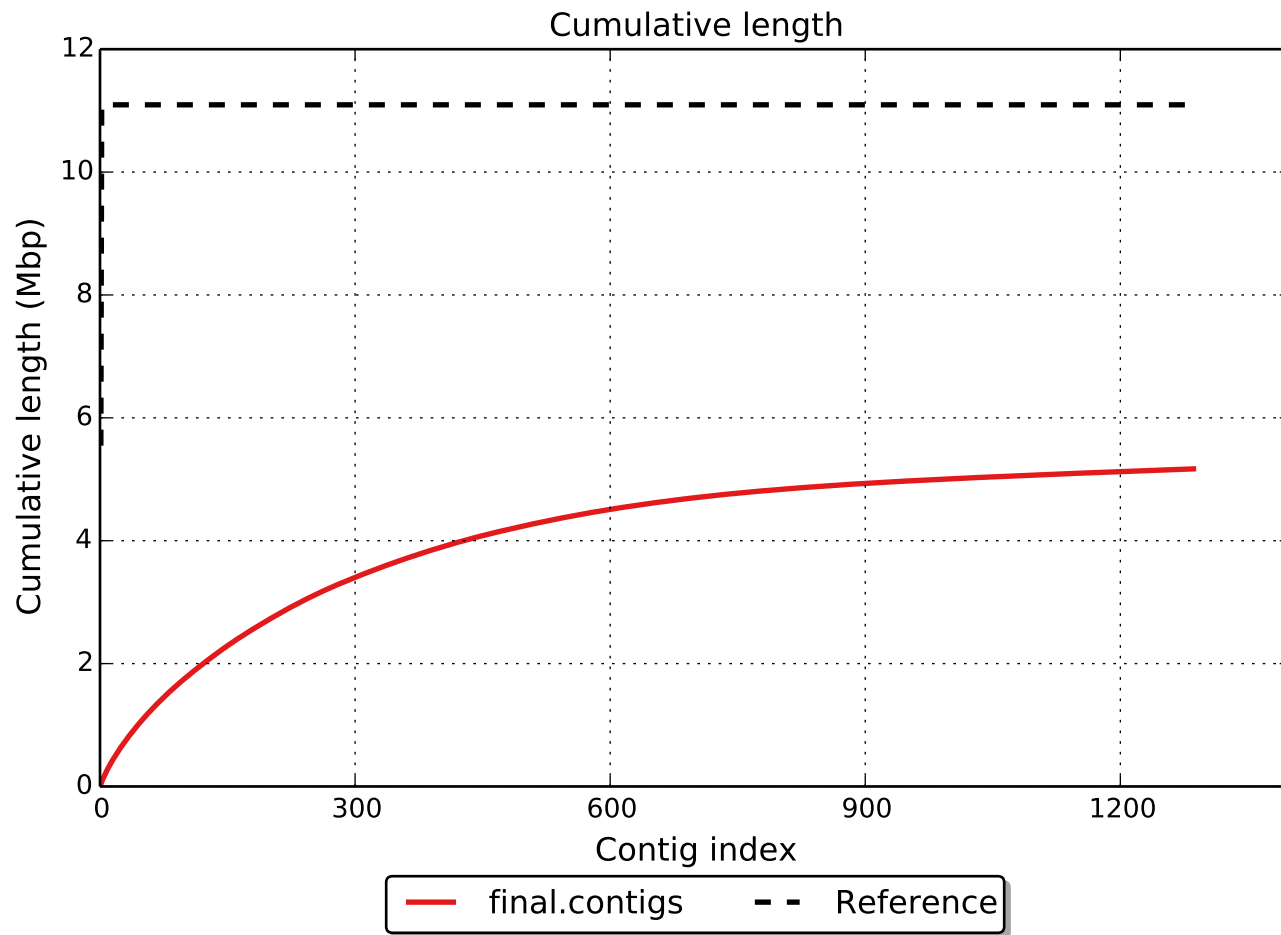
Misassemblies report

	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	53659
# indels	12
# short indels	12
# long indels	0
Indels length	16

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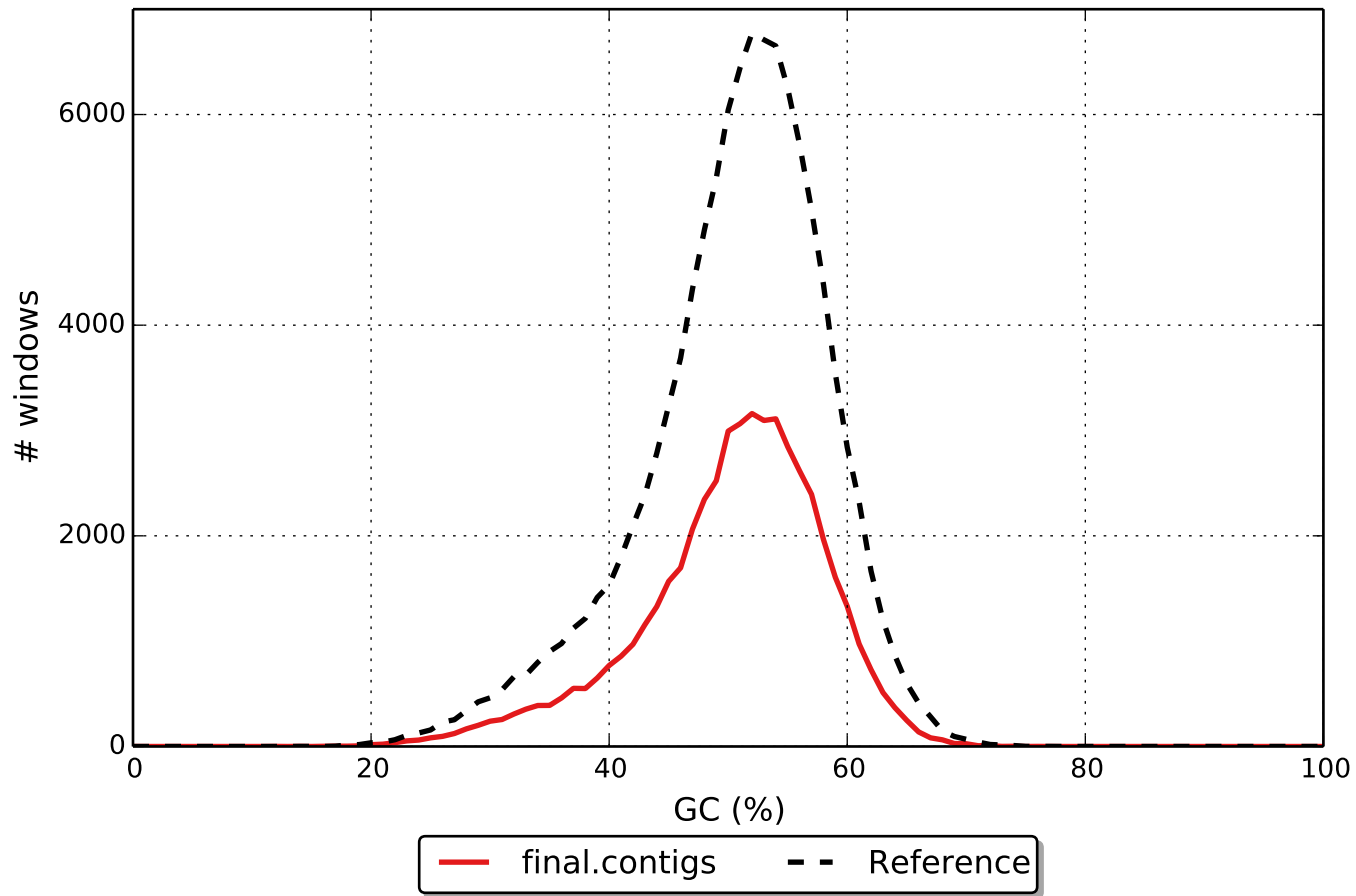(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
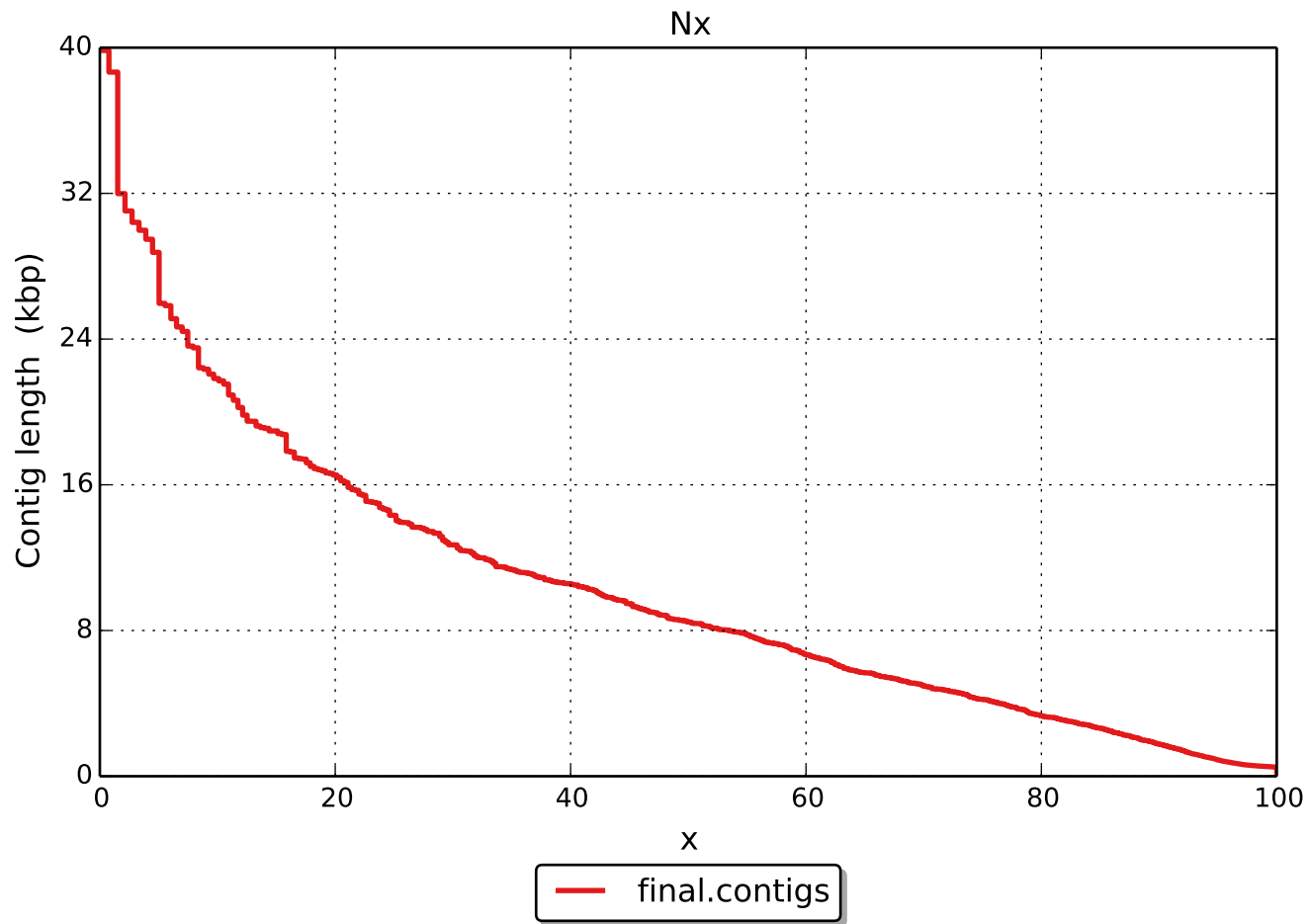
Unaligned report

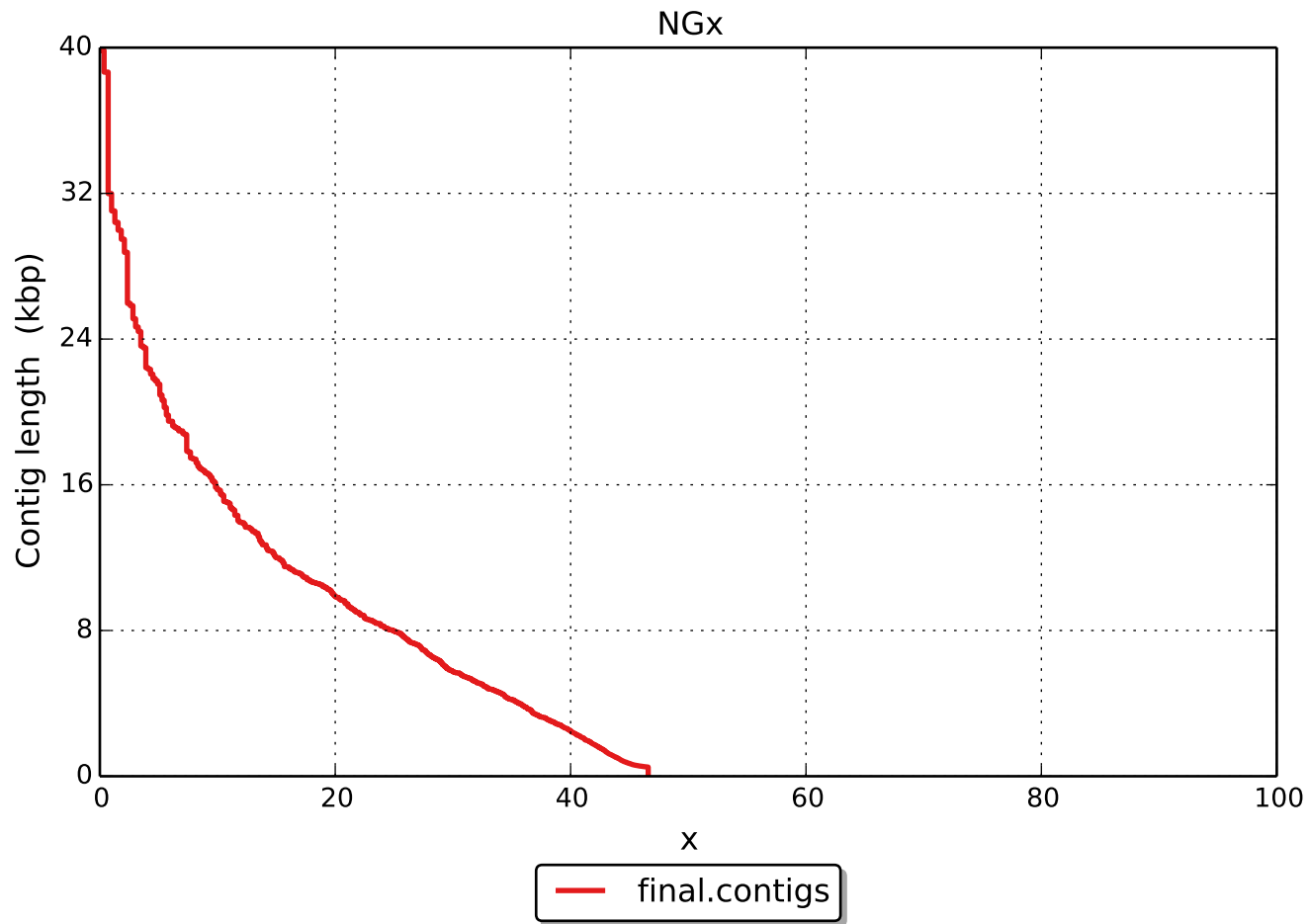|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

GC content

windows

GC (%)

— final.contigs - - - Reference

Nx

Misassemblies

final.contigs

Cumulative length (aligned contigs)