Report

	final.contigs
# contigs (>= 0 bp)	2065
# contigs (>= 1000 bp)	480
Total length (>= 0 bp)	2262474
Total length (>= 1000 bp)	1594380
# contigs	894
Largest contig	21352
Total length	1872469
Reference length	3785550
GC (%)	32.29
Reference GC (%)	32.26
N50	3660
N75	1790
L50	155
L75	338
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.749
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	599.24
# indels per 100 kbp	0.18
Largest alignment	21352
NA50	3660
NA75	1790
LA50	155
LA75	338

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).
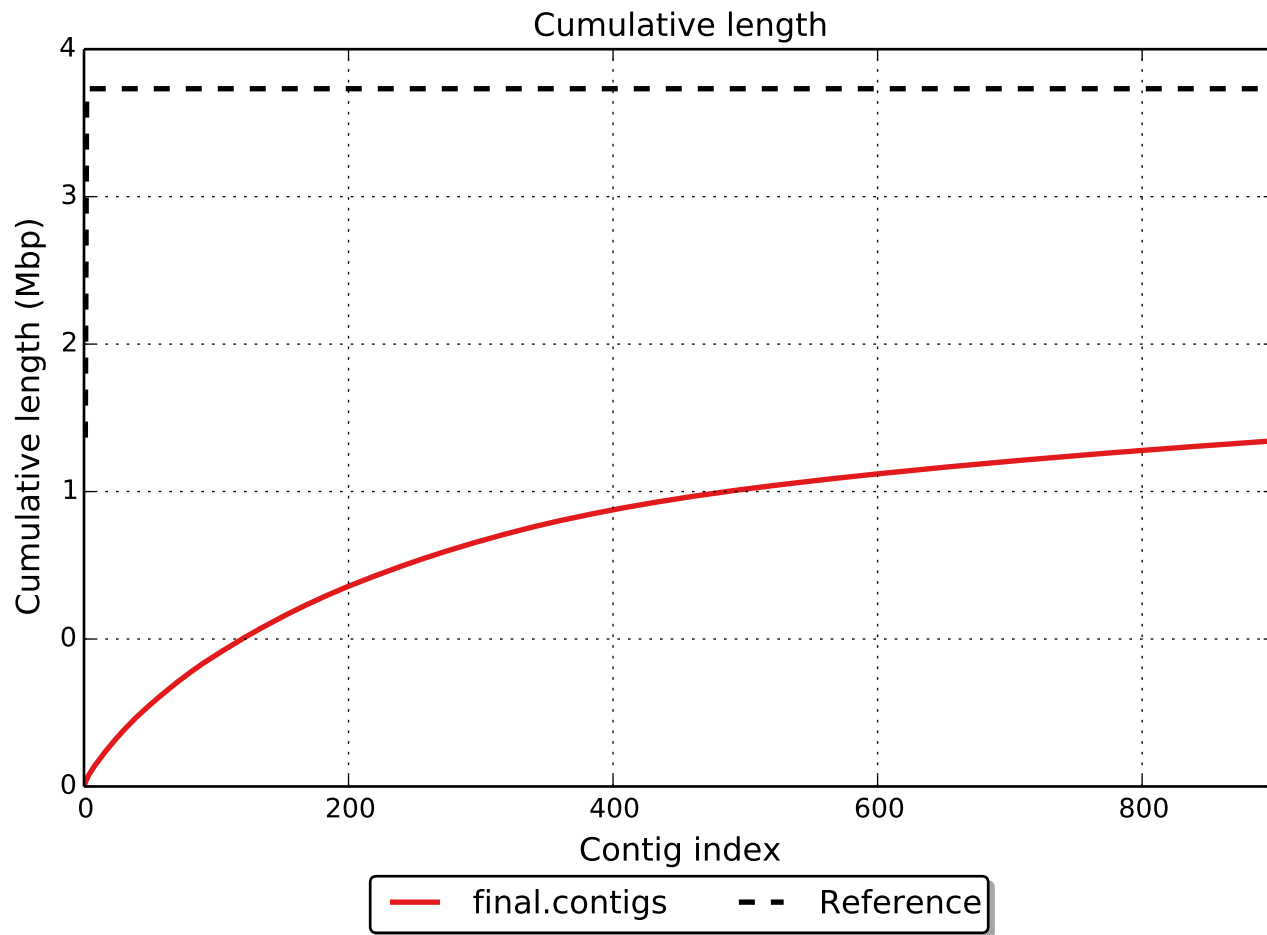
Misassemblies report

	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	20359
# indels	6
# short indels	4
# long indels	2
Indels length	40

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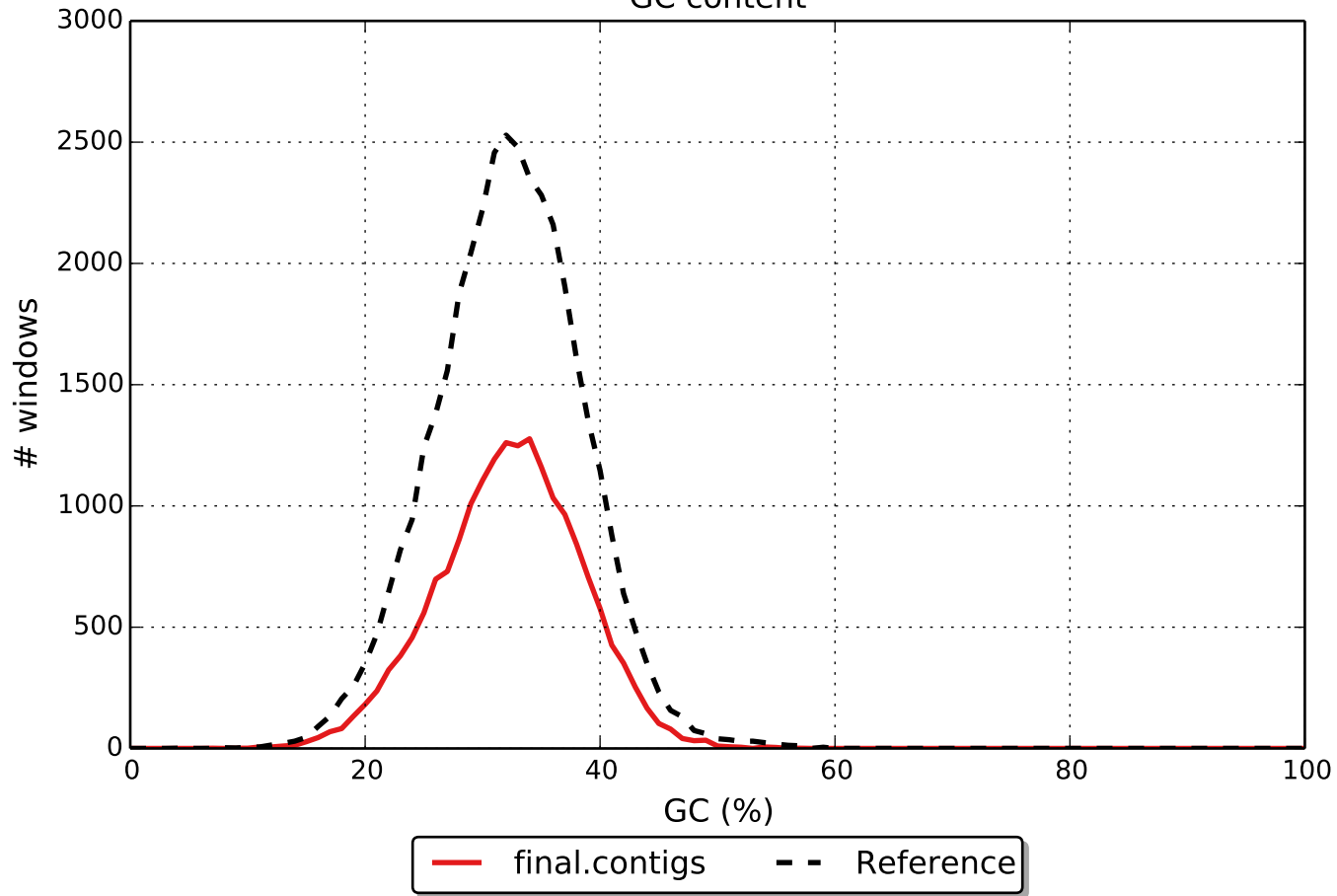(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
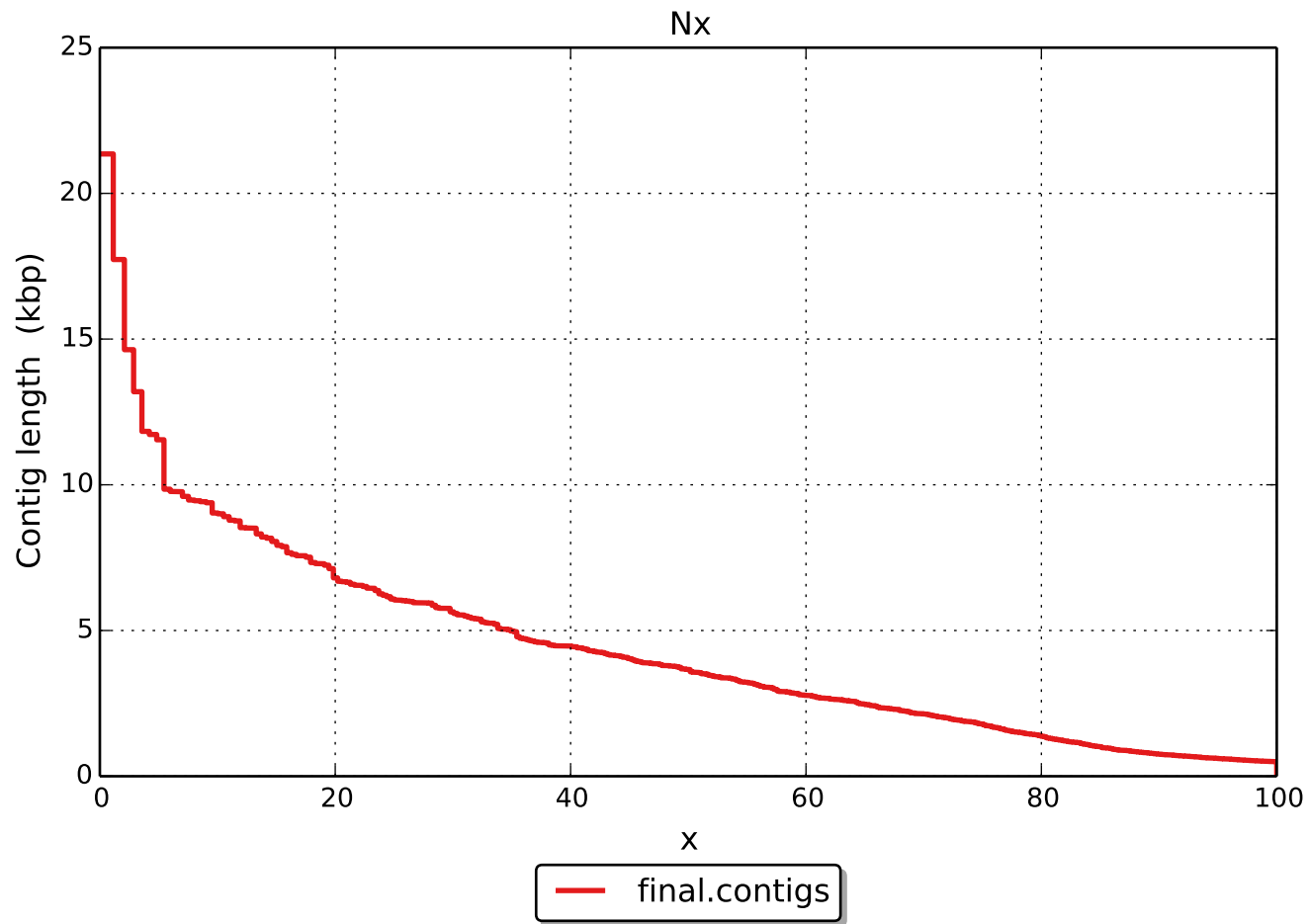
Unaligned report

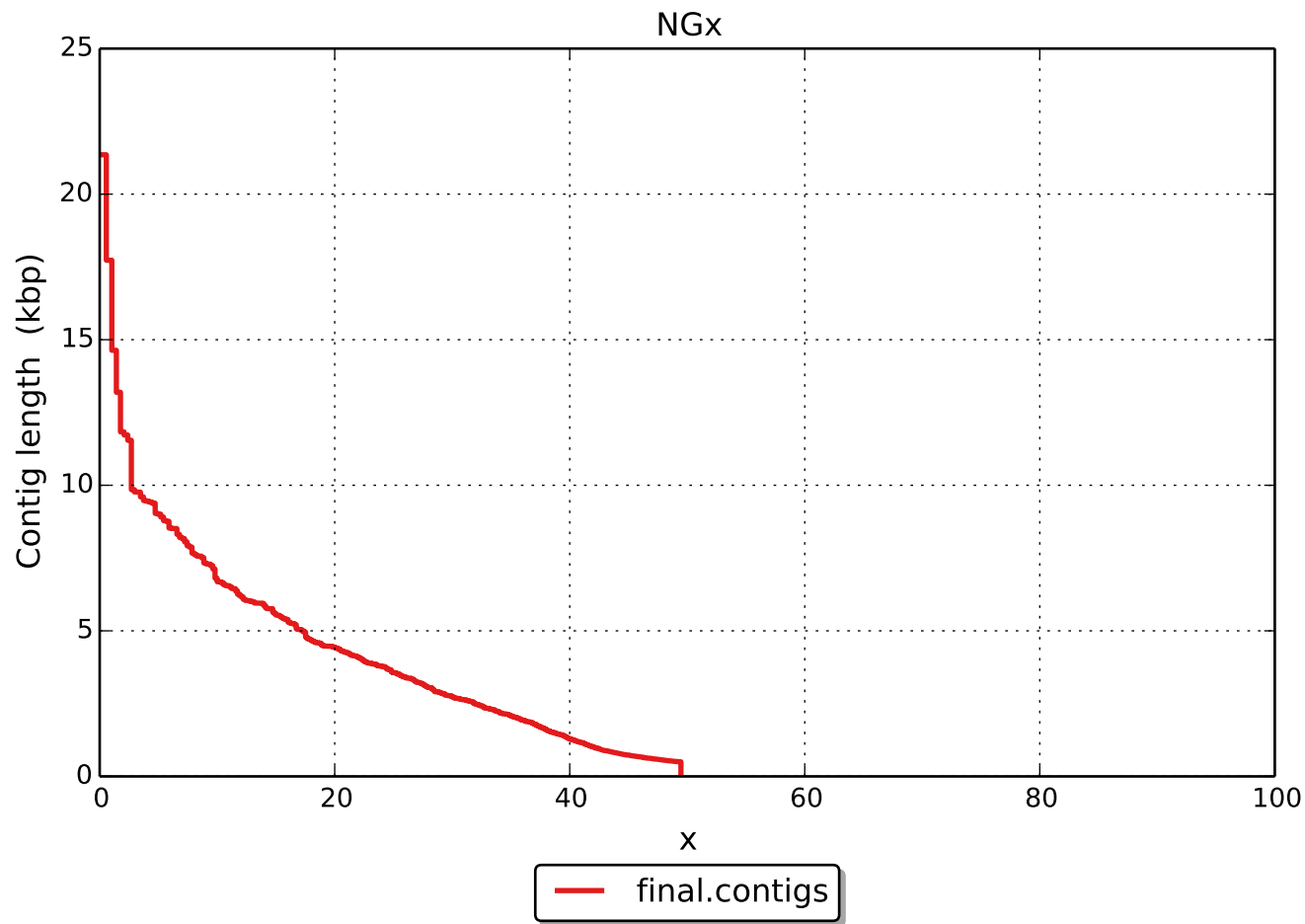|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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 vs GC (%)

Misassemblies

final.contigs

Cumulative length (aligned contigs)