Report

	final.contigs
# contigs (>= 0 bp)	6680
# contigs (>= 1000 bp)	1466
Total length (>= 0 bp)	6750421
Total length (>= 1000 bp)	4538844
# contigs	2864
Largest contig	18963
Total length	5460626
Reference length	10957366
GC (%)	50.28
Reference GC (%)	50.49
N50	3267
N75	1475
L50	487
L75	1100
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	88.383
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	612.54
# indels per 100 kbp	0.08
Largest alignment	18963
NA50	3267
NA75	1475
LA50	487
LA75	1100

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).
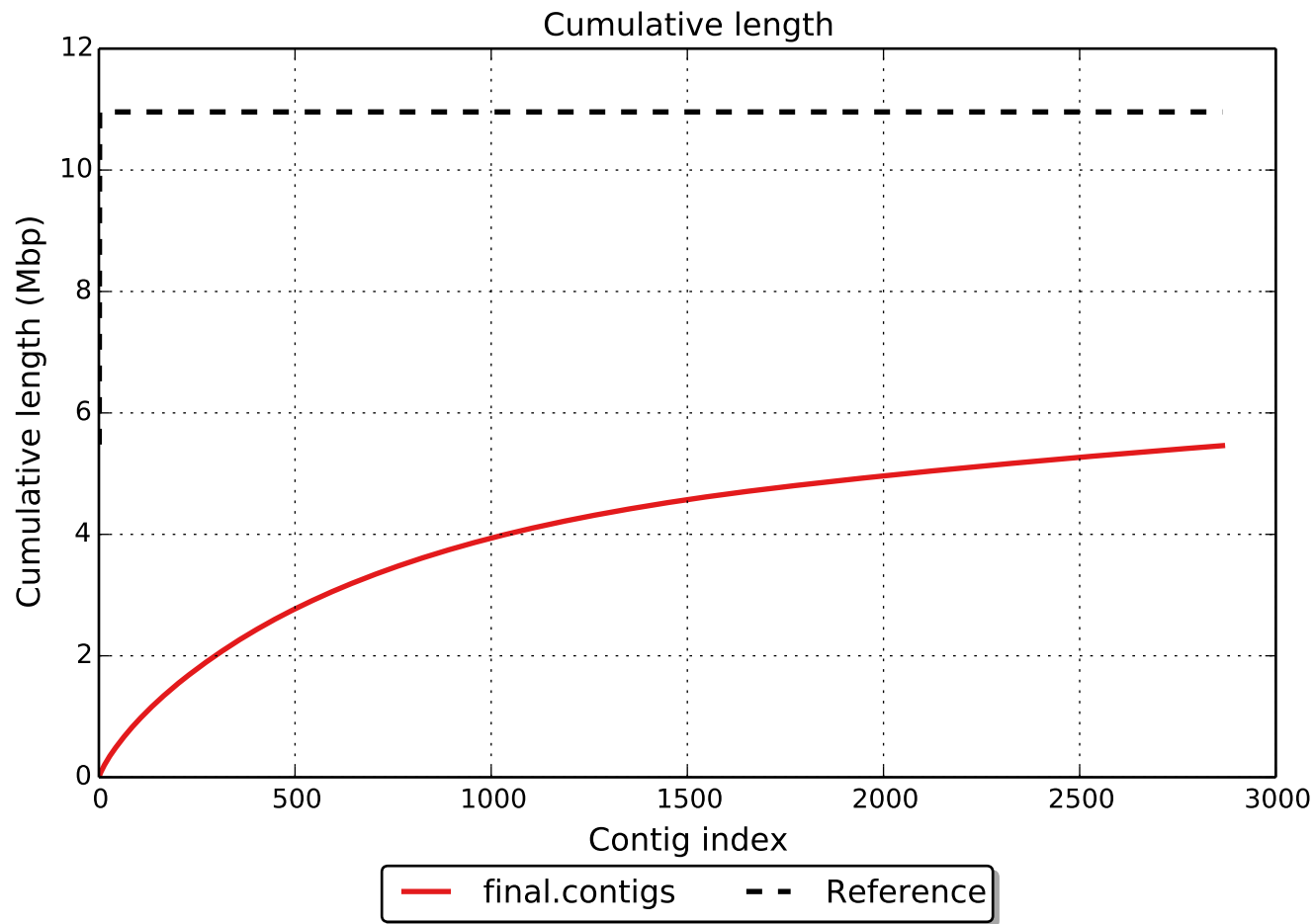
Misassemblies report

	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	1
# mismatches	59321
# indels	8
# short indels	4
# long indels	4
Indels length	52

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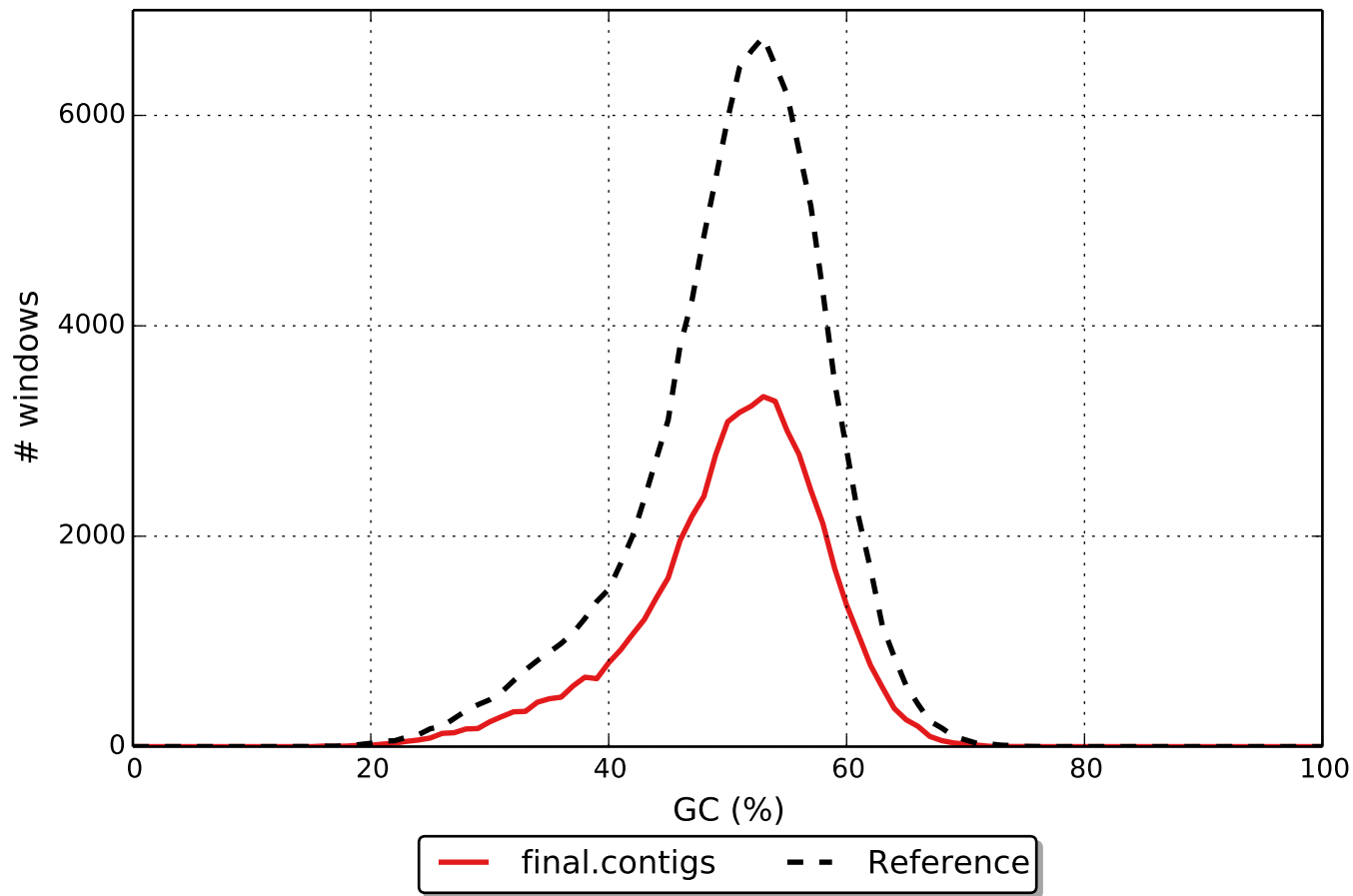(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

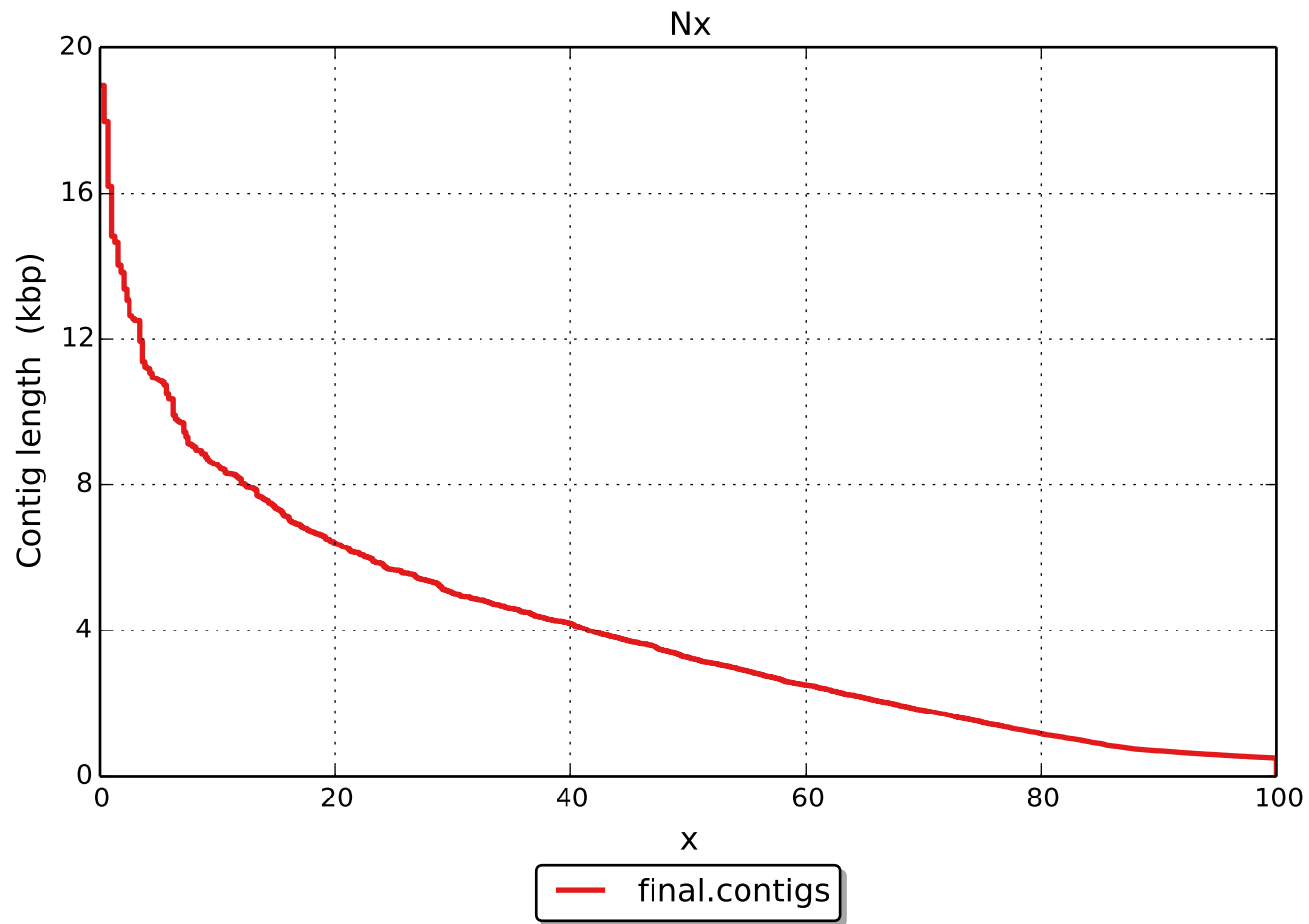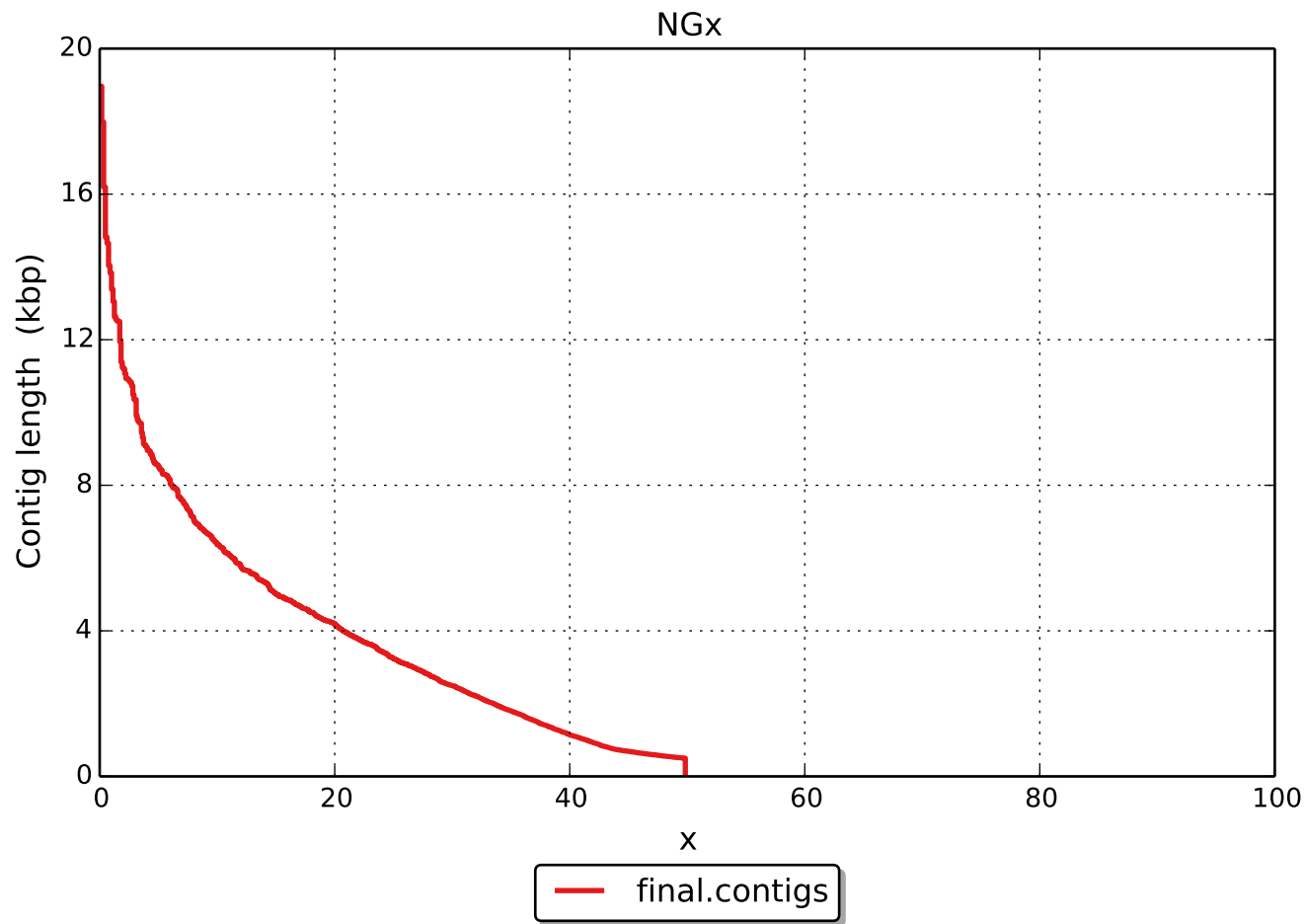|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

Misassemblies

final.contigs

Cumulative length (aligned contigs)

Cumulative length (Mbp) vs Contig index

- final.contigs
- Reference