

Report

	final.contigs
# contigs (>= 1000 bp)	709
# contigs (>= 5000 bp)	110
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2174113
Total length (>= 5000 bp)	734597
Total length (>= 10000 bp)	51798
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1019
Largest contig	18957
Total length	2389808
Reference length	4641652
GC (%)	50.64
Reference GC (%)	50.78
N50	3520
NG50	612
N75	2015
L50	221
LG50	894
L75	446
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	507
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	50.593
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	384.10
# indels per 100 kbp	0.09
Largest alignment	18957
NA50	3520
NGA50	612
NA75	2015
LA50	221
LGA50	894
LA75	446

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

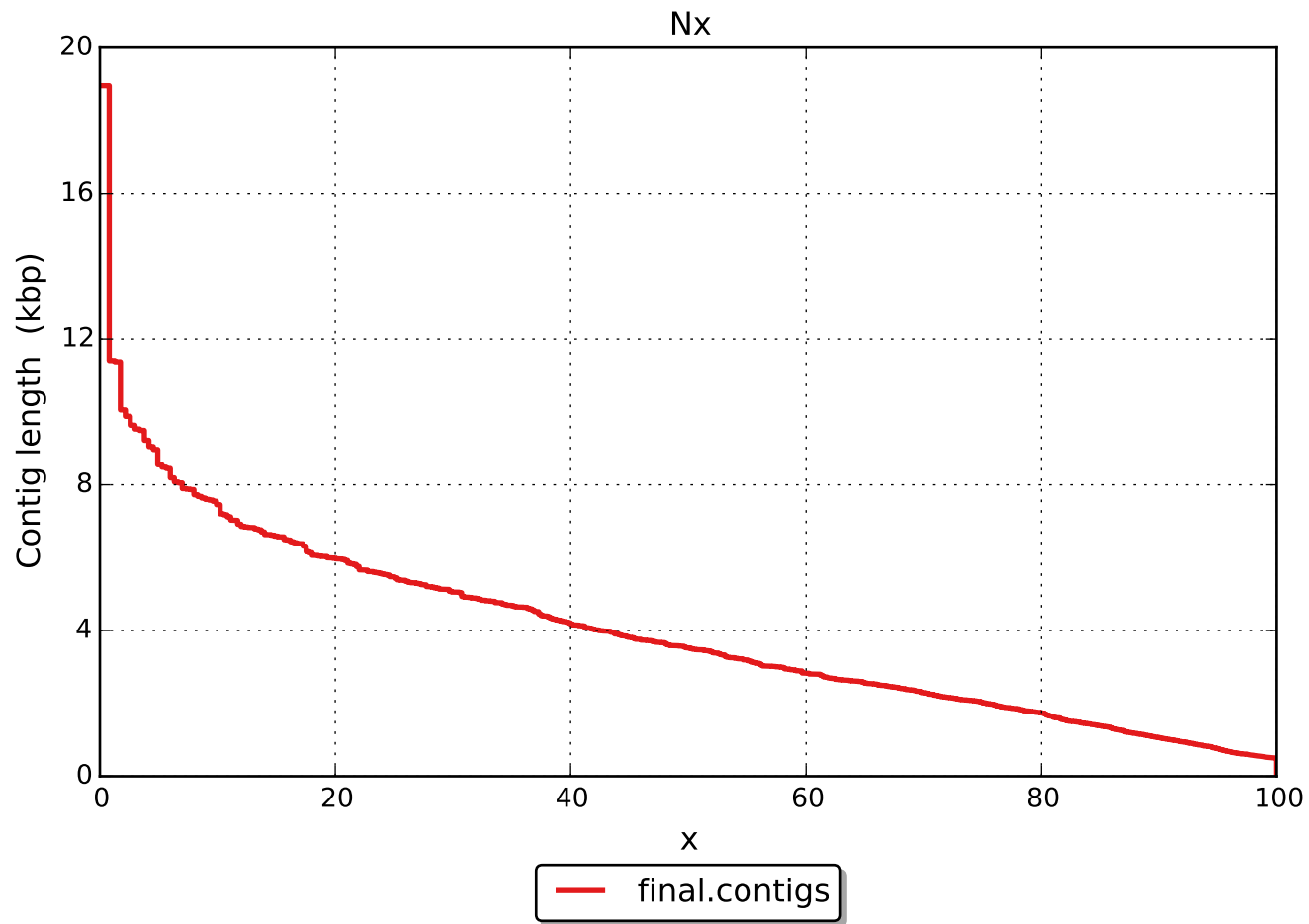
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	507
# local misassemblies	1
# mismatches	9020
# indels	2
# short indels	2
# long indels	0
Indels length	2

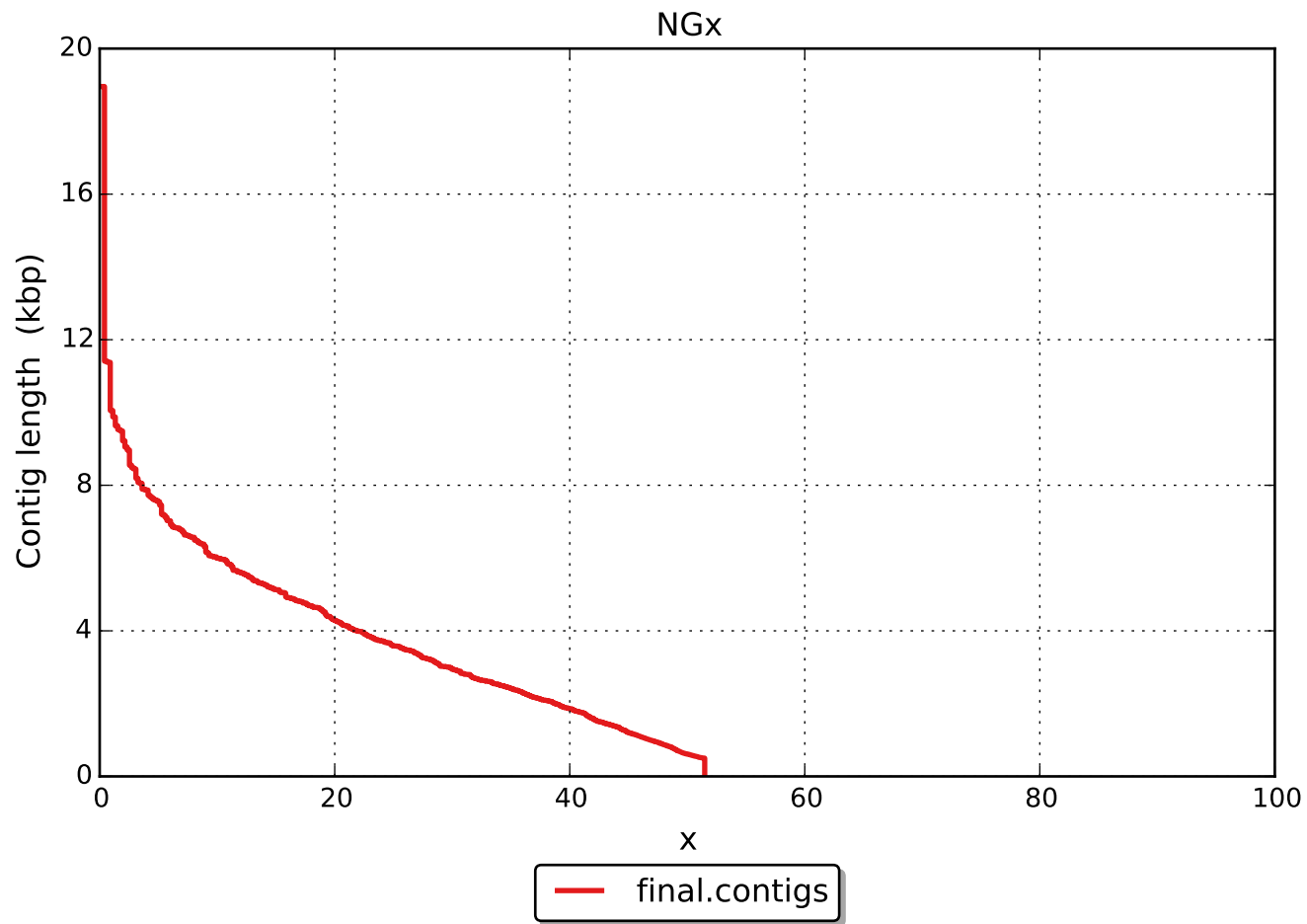
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

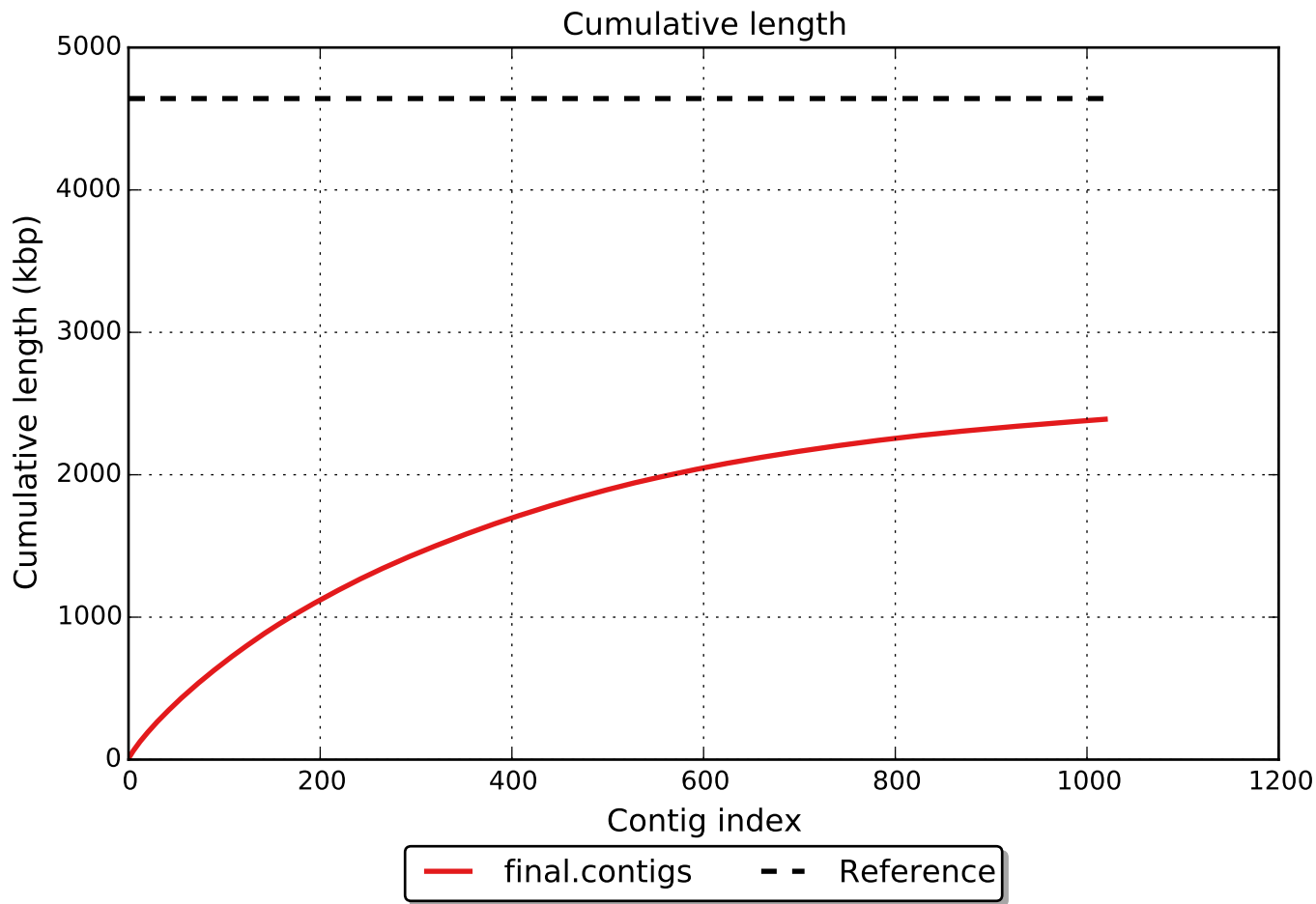
Unaligned report

	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

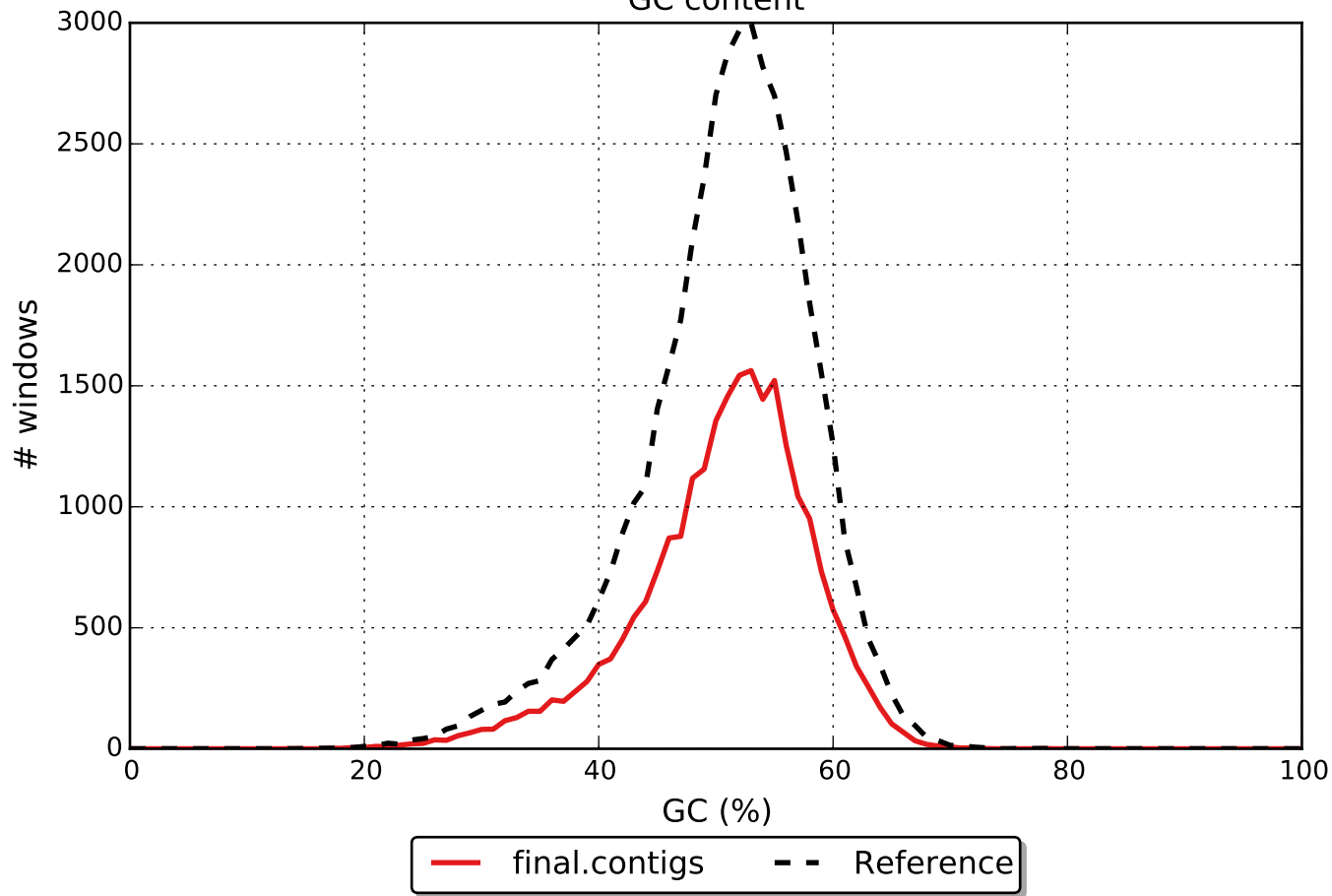
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



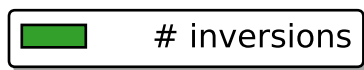
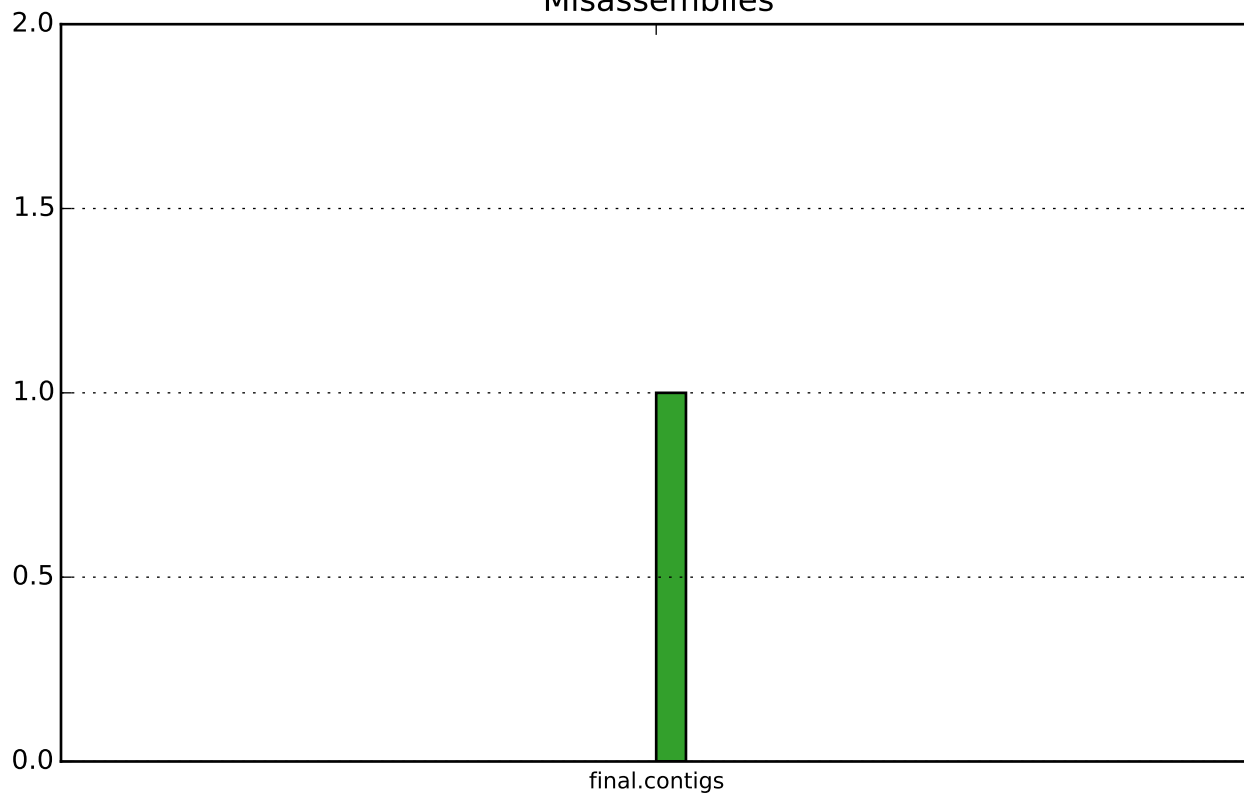




GC content



Misassemblies



Cumulative length (aligned contigs)

