

Report

	final.contigs
# contigs (>= 1000 bp)	556
# contigs (>= 5000 bp)	356
# contigs (>= 10000 bp)	164
# contigs (>= 25000 bp)	21
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	4886841
Total length (>= 5000 bp)	4323492
Total length (>= 10000 bp)	2946494
Total length (>= 25000 bp)	761041
Total length (>= 50000 bp)	214079
# contigs	588
Largest contig	54266
Total length	4910610
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	12479
NG50	12558
N75	7141
NG75	7278
L50	120
LG50	118
L75	252
LG75	247
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.905
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.56
# indels per 100 kbp	0.00
Largest alignment	54266
NA50	12479
NGA50	12558
NA75	7141
NGA75	7278
LA50	120
LGA50	118
LA75	252
LGA75	247

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

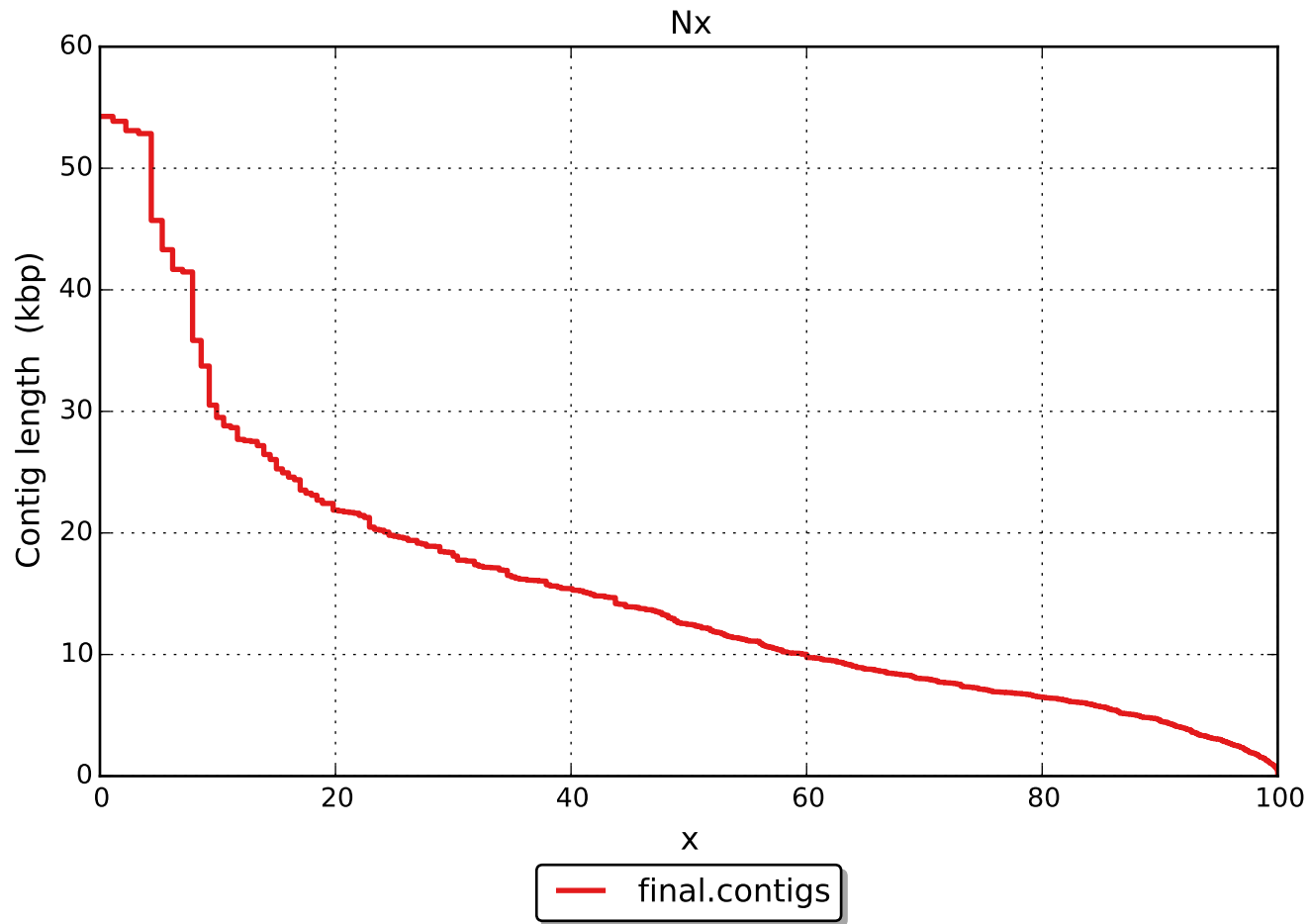
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	658
# indels	0
# short indels	0
# long indels	0
Indels length	0

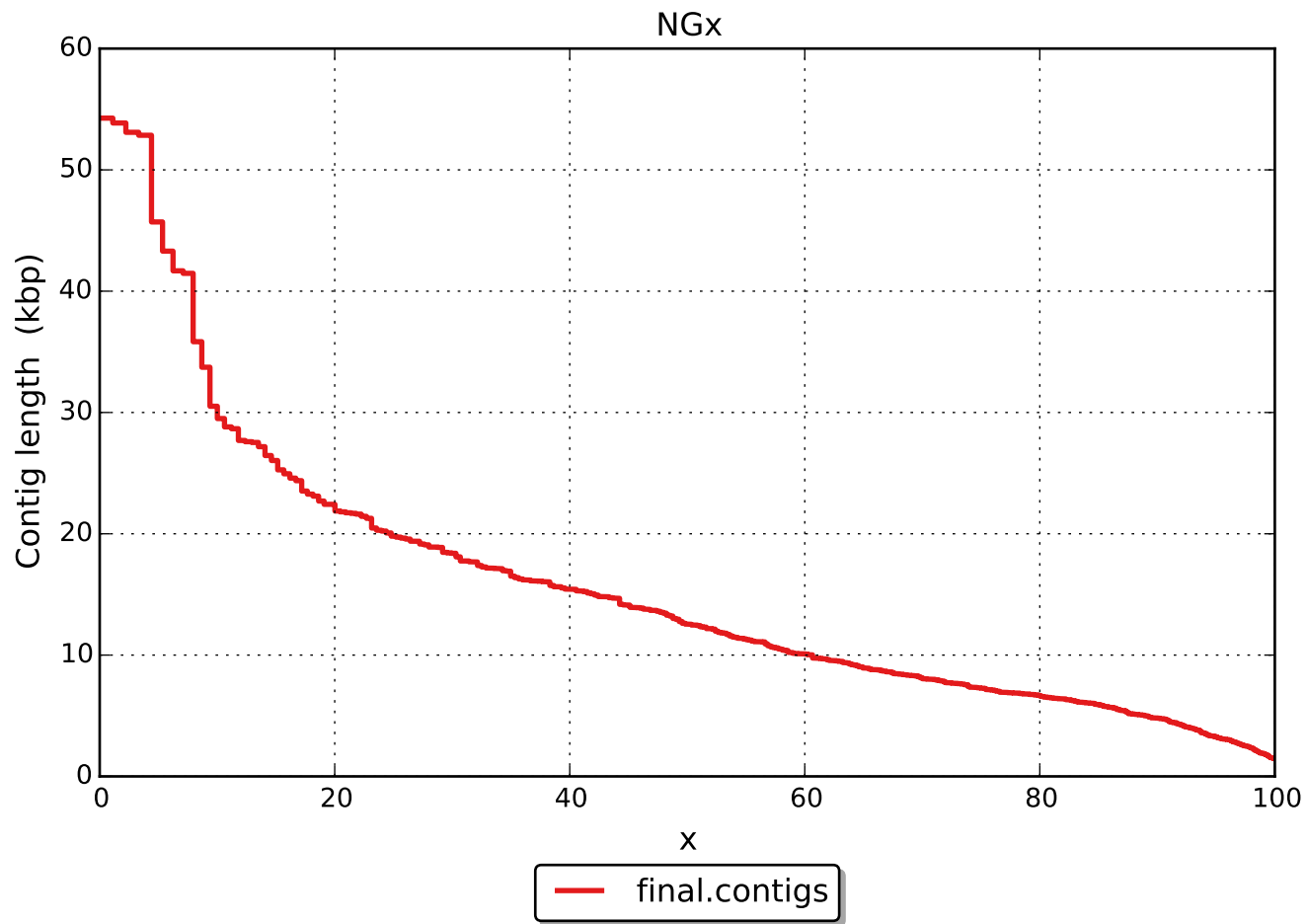
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

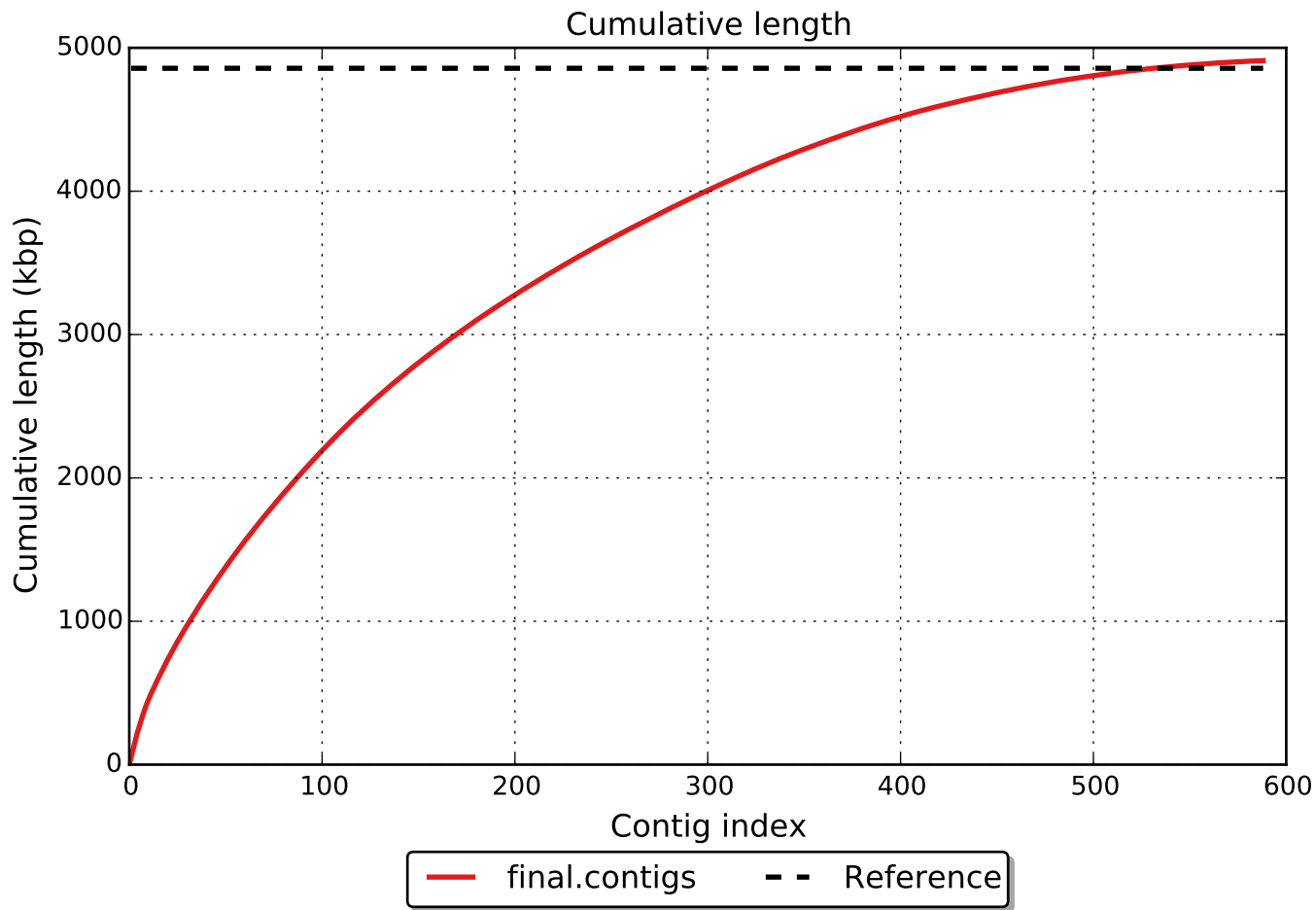
Unaligned report

	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

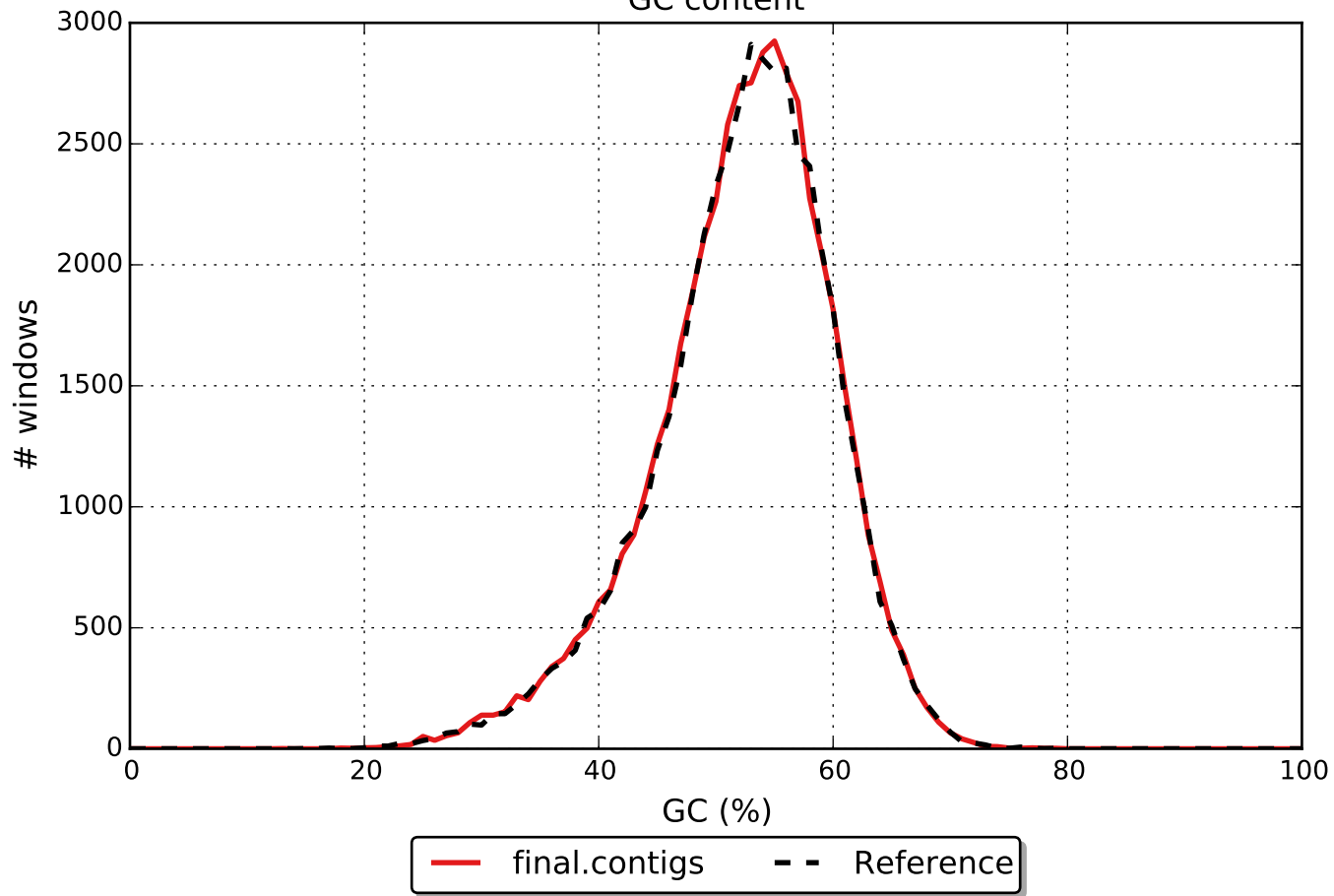
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







GC content



Misassemblies



Cumulative length (aligned contigs)

