

Report

	final.contigs
# contigs (>= 1000 bp)	1702
# contigs (>= 5000 bp)	119
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4203627
Total length (>= 5000 bp)	748508
Total length (>= 10000 bp)	41982
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2390
Largest contig	10907
Total length	4712992
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	2569
NG50	2603
N75	1558
NG75	1604
L50	591
LG50	577
L75	1171
LG75	1138
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	297
Genome fraction (%)	97.465
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.10
# indels per 100 kbp	0.02
Largest alignment	10907
NA50	2569
NGA50	2603
NA75	1549
NGA75	1604
LA50	591
LGA50	577
LA75	1172
LGA75	1138

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

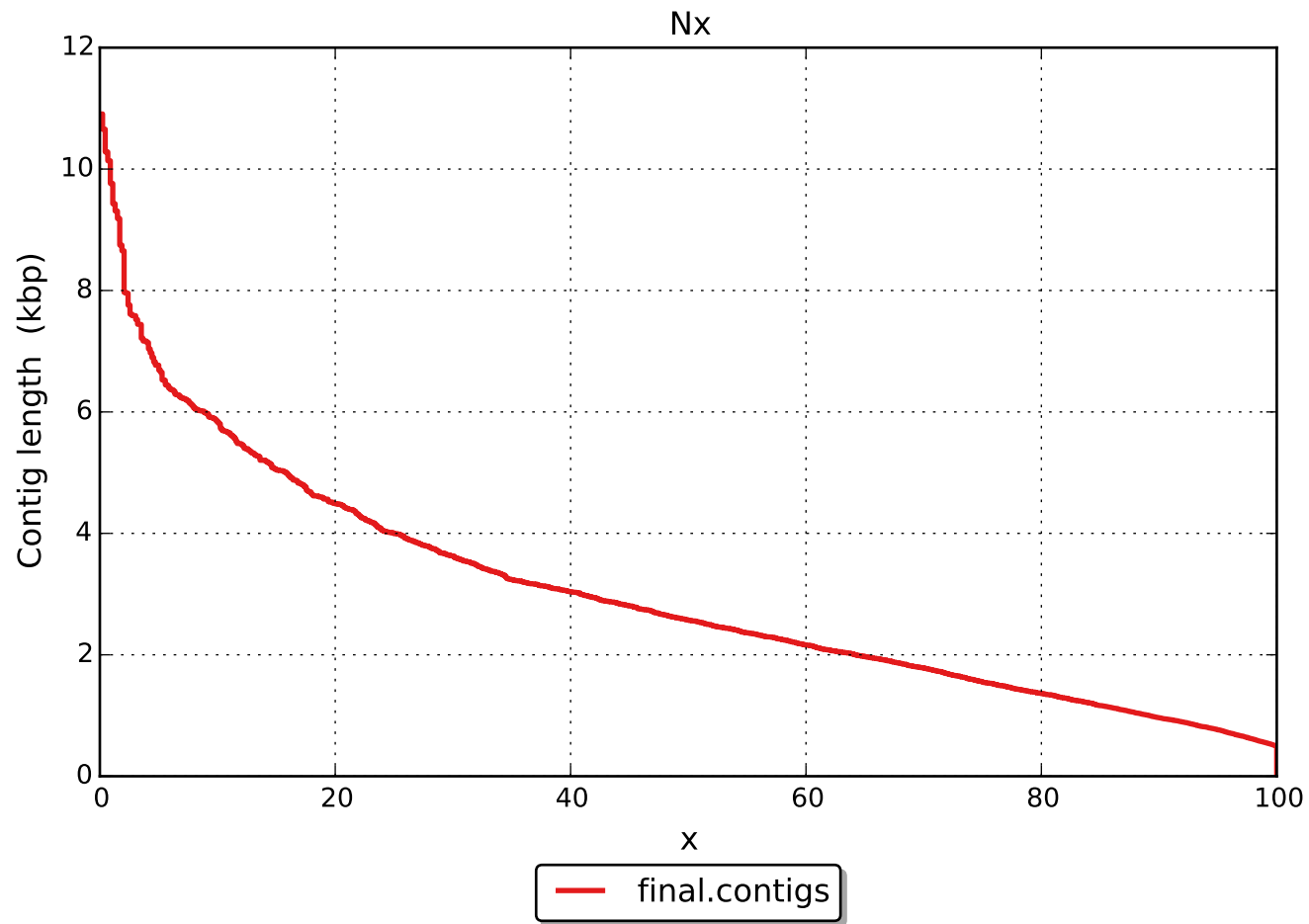
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	0
# mismatches	2357
# indels	1
# short indels	1
# long indels	0
Indels length	1

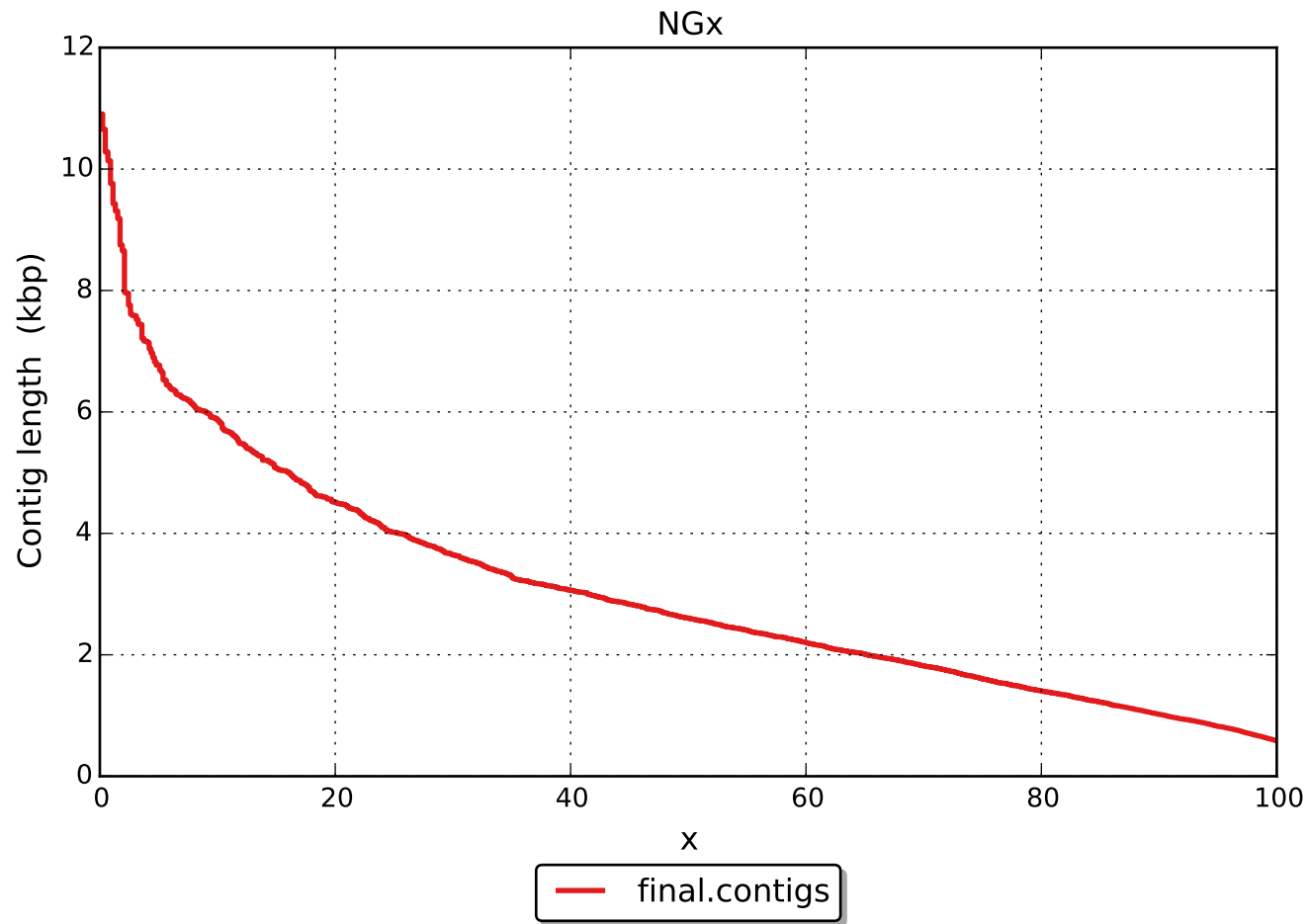
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

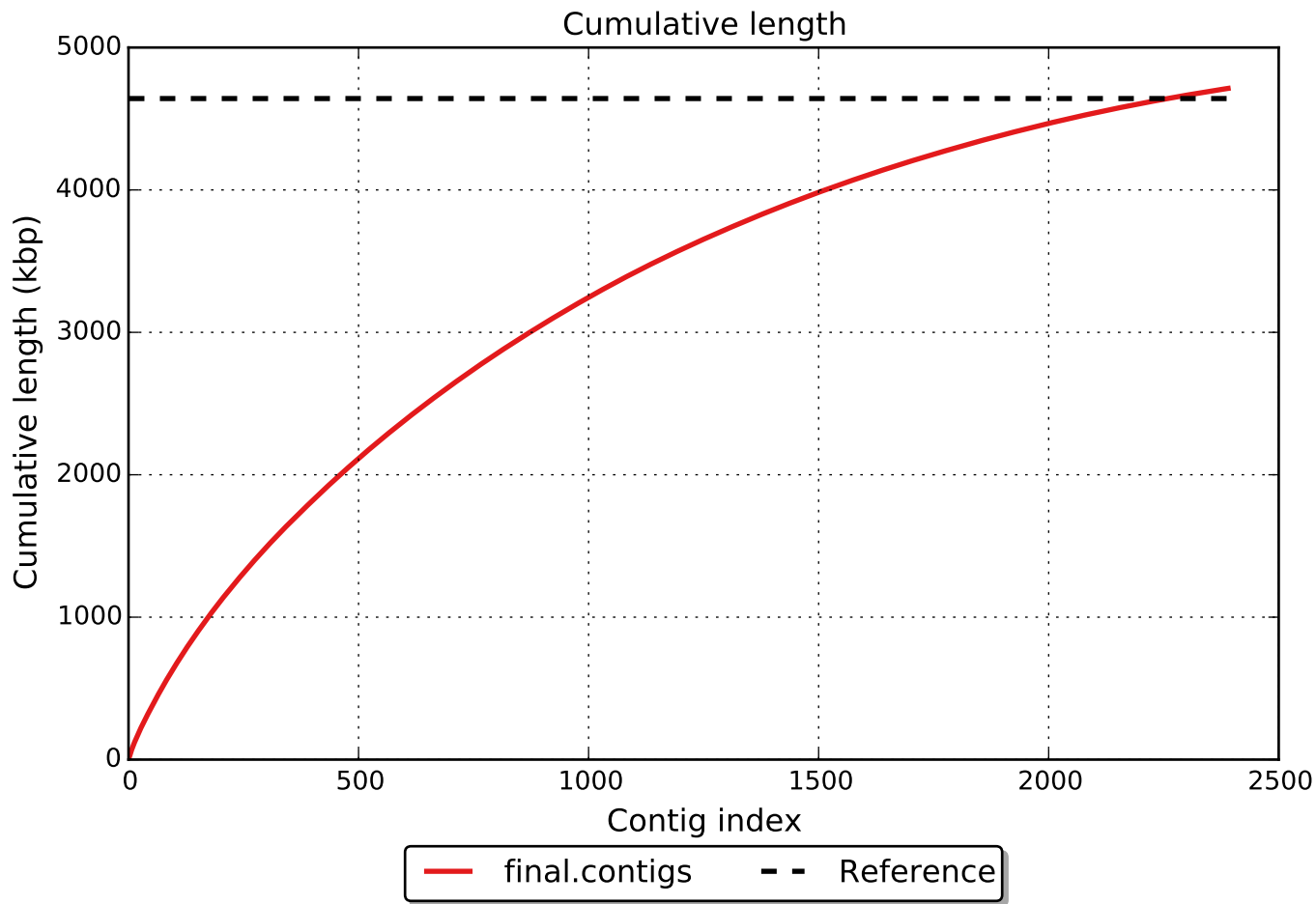
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	297
# N's	0

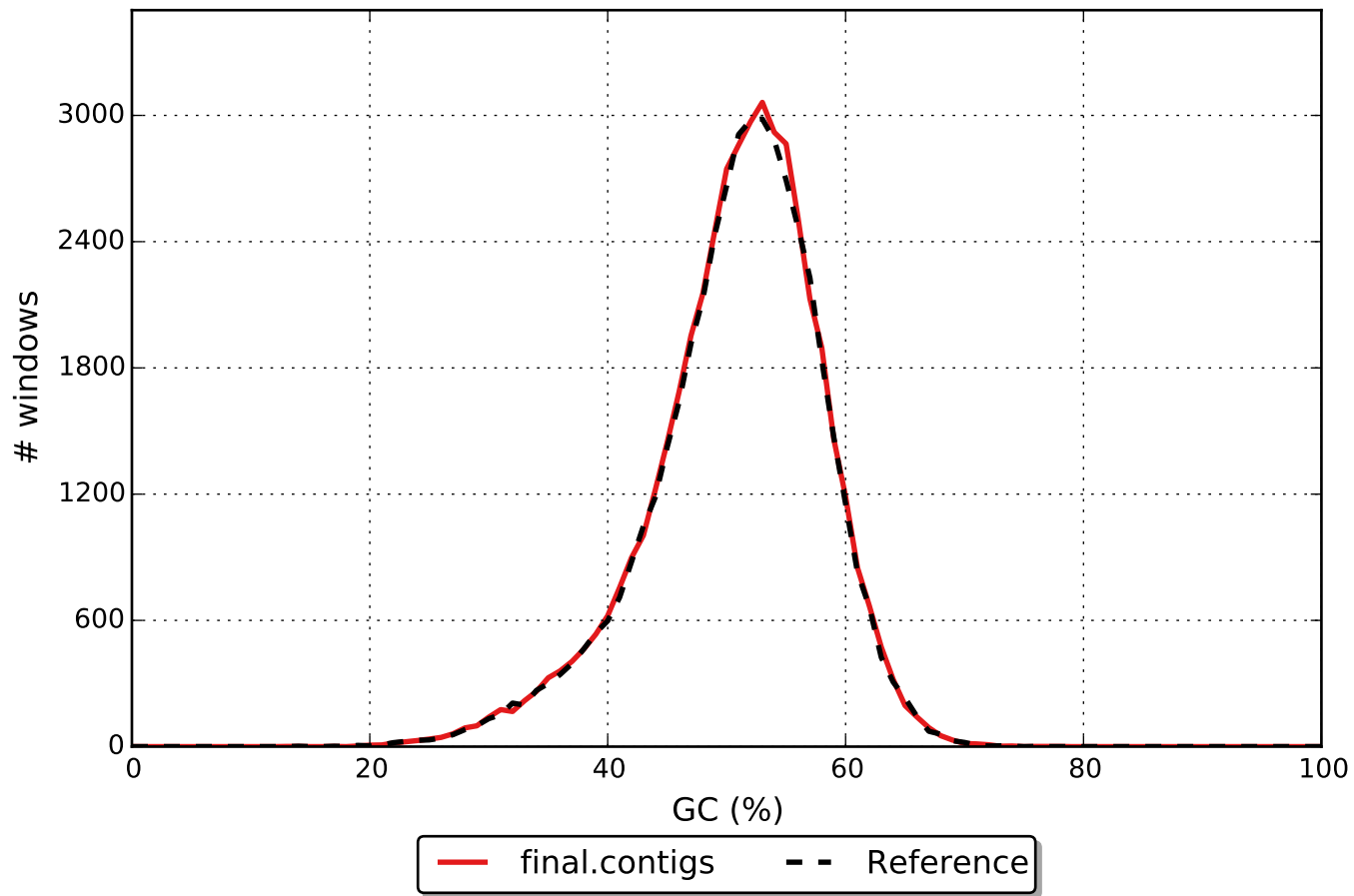
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







GC content





Cumulative length (aligned contigs)

