Report

	final.contigs
# contigs (>= 1000 bp)	290
# contigs (>= 5000 bp)	228
# contigs (>= 10000 bp)	167
# contigs (>= 25000 bp)	70
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	4892564
Total length (>= 5000 bp)	4713929
Total length (>= 10000 bp)	4289378
Total length (>= 25000 bp)	2746301
Total length (>= 50000 bp)	775975
# contigs	305
Largest contig	78170
Total length	4902978
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	26858
NG50	26965
N75	15433
NG75	15721
L50	59
LG50	58
L75	118
LG75	116
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.965
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.88
# indels per 100 kbp	0.08
Largest alignment	78170
NA50	26858
NGA50	26965
NA75	15433
NGA75	15721
LA50	59
LGA50	58
LA75	118
LGA75	116

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

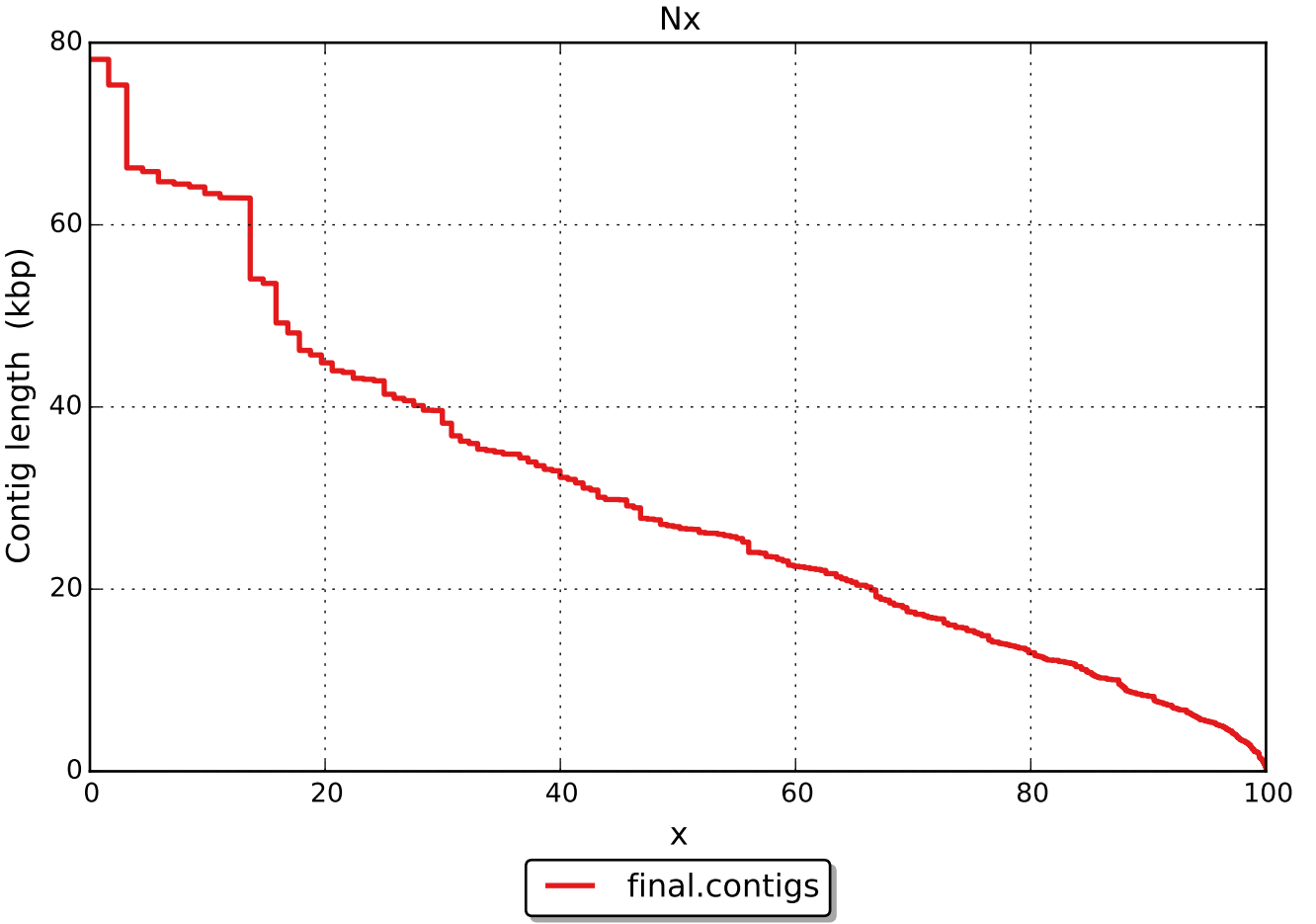
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1548
# indels	4
# short indels	4
# long indels	0
Indels length	4

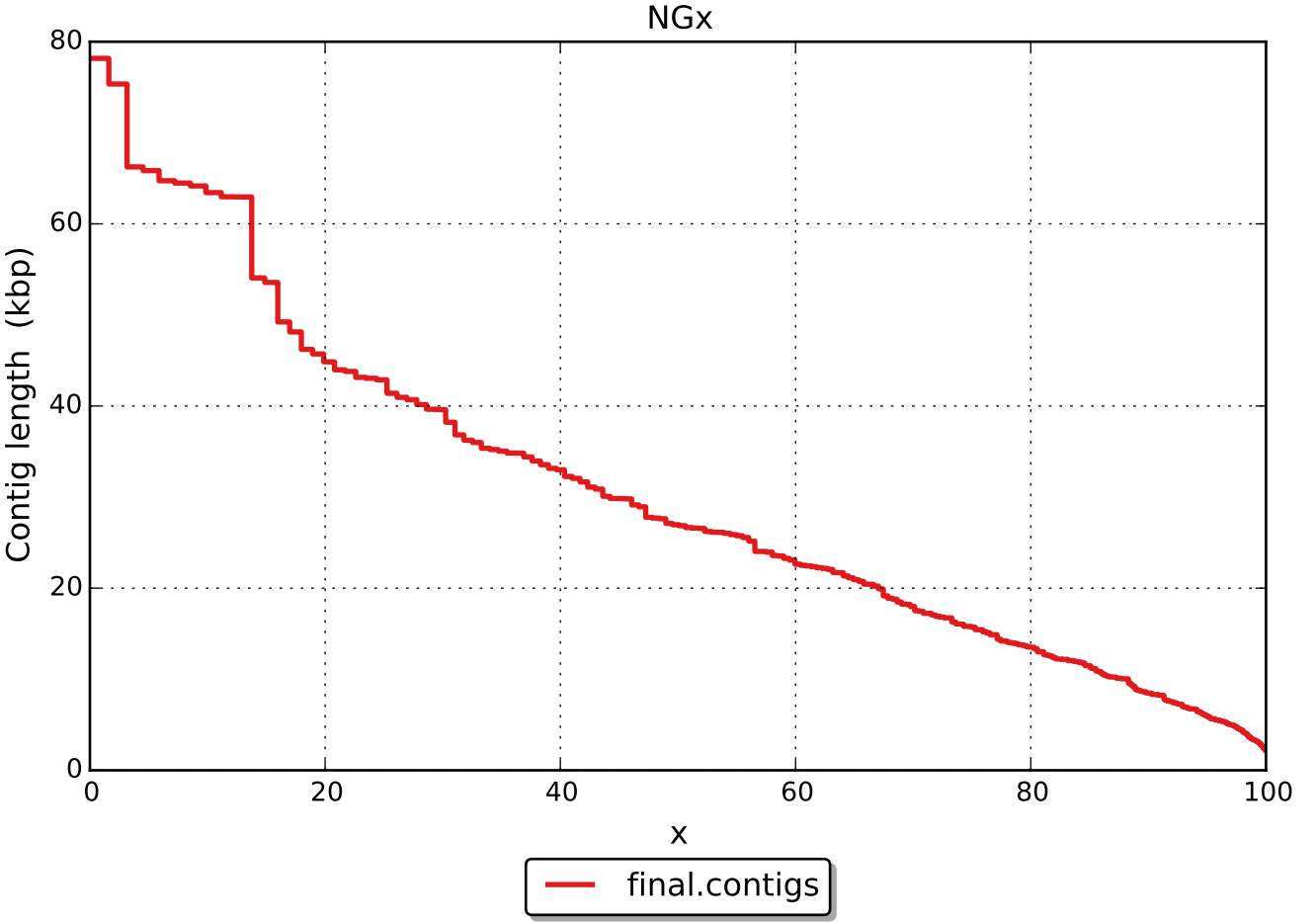
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

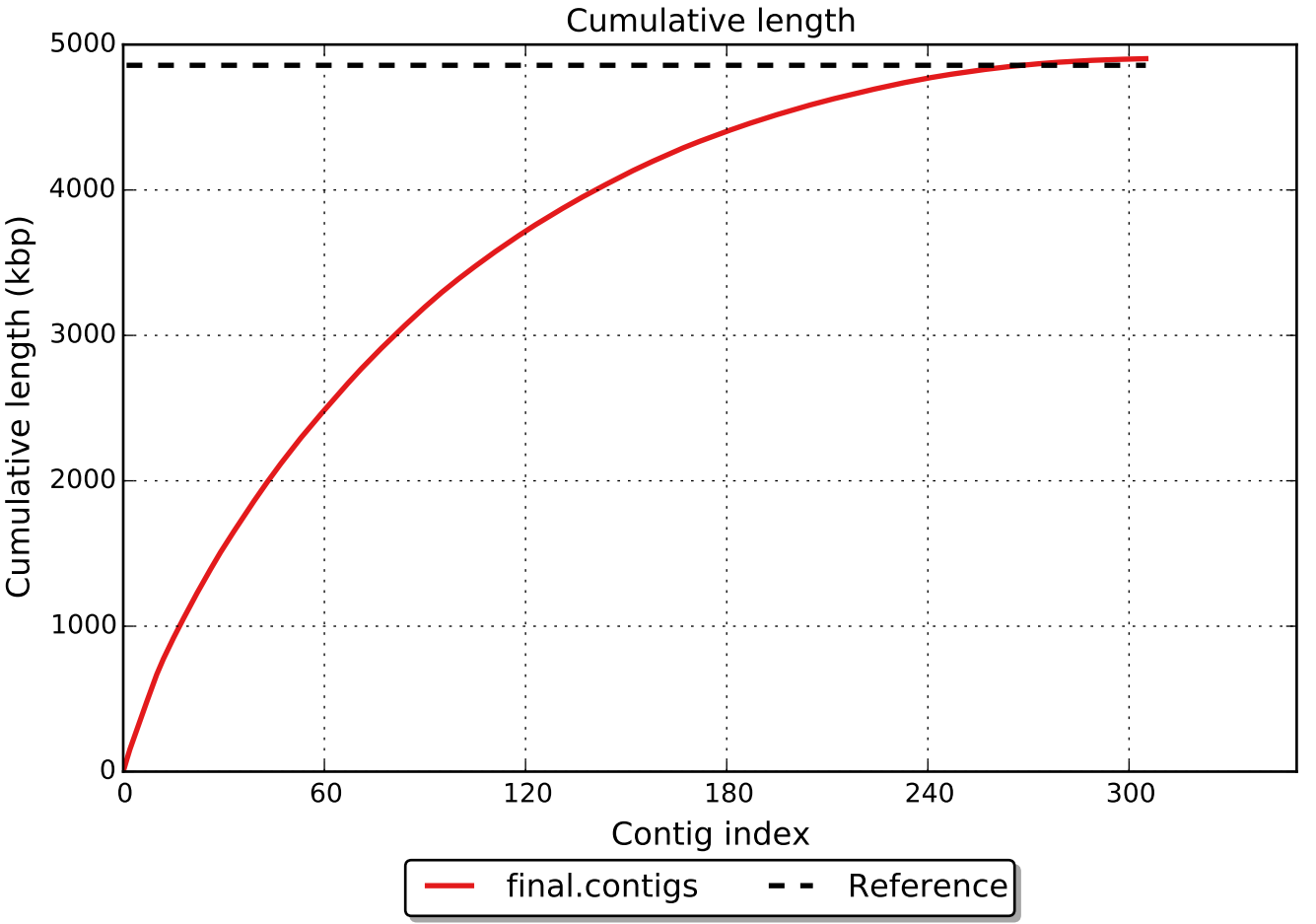
Unaligned report

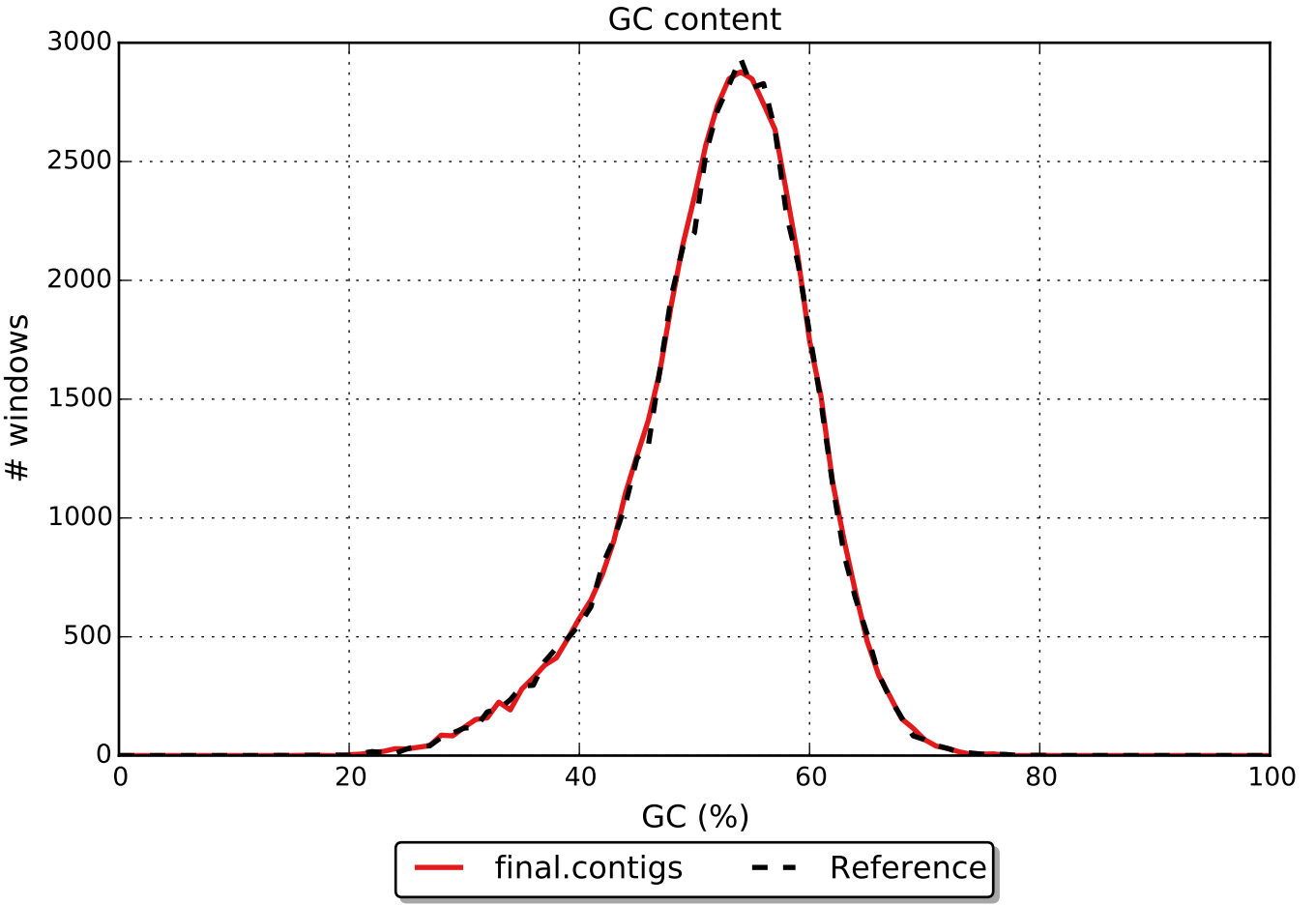
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

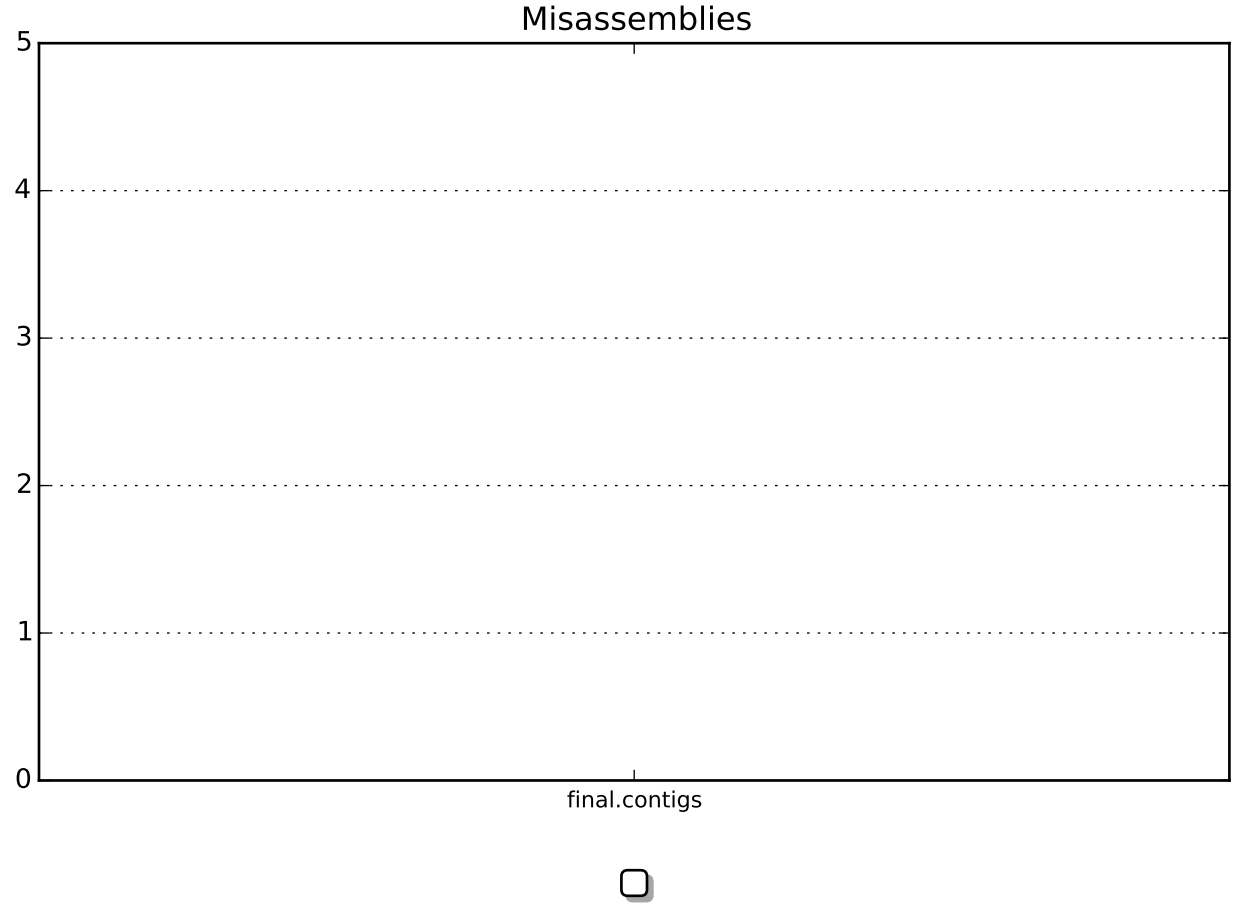
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

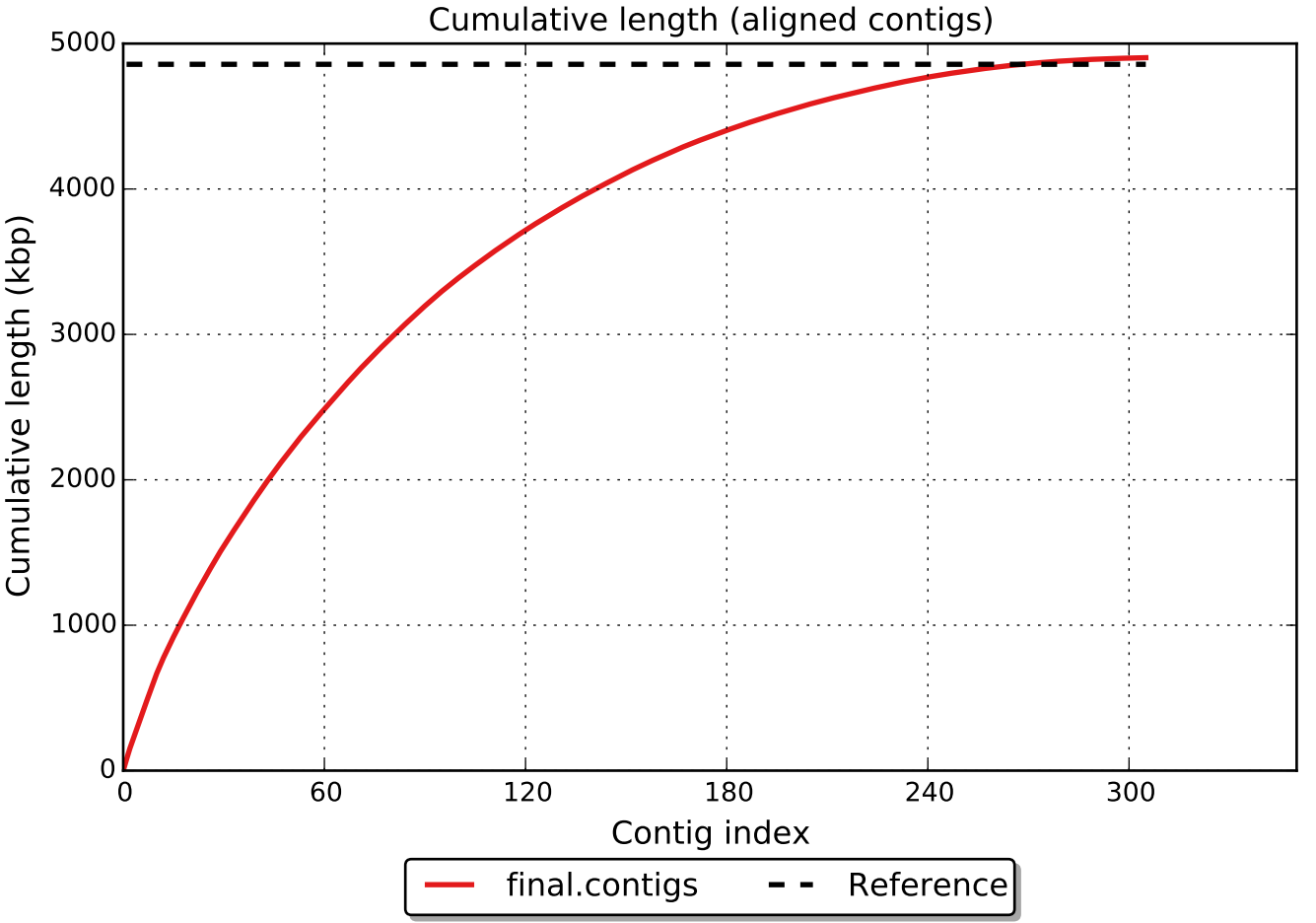

Nx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

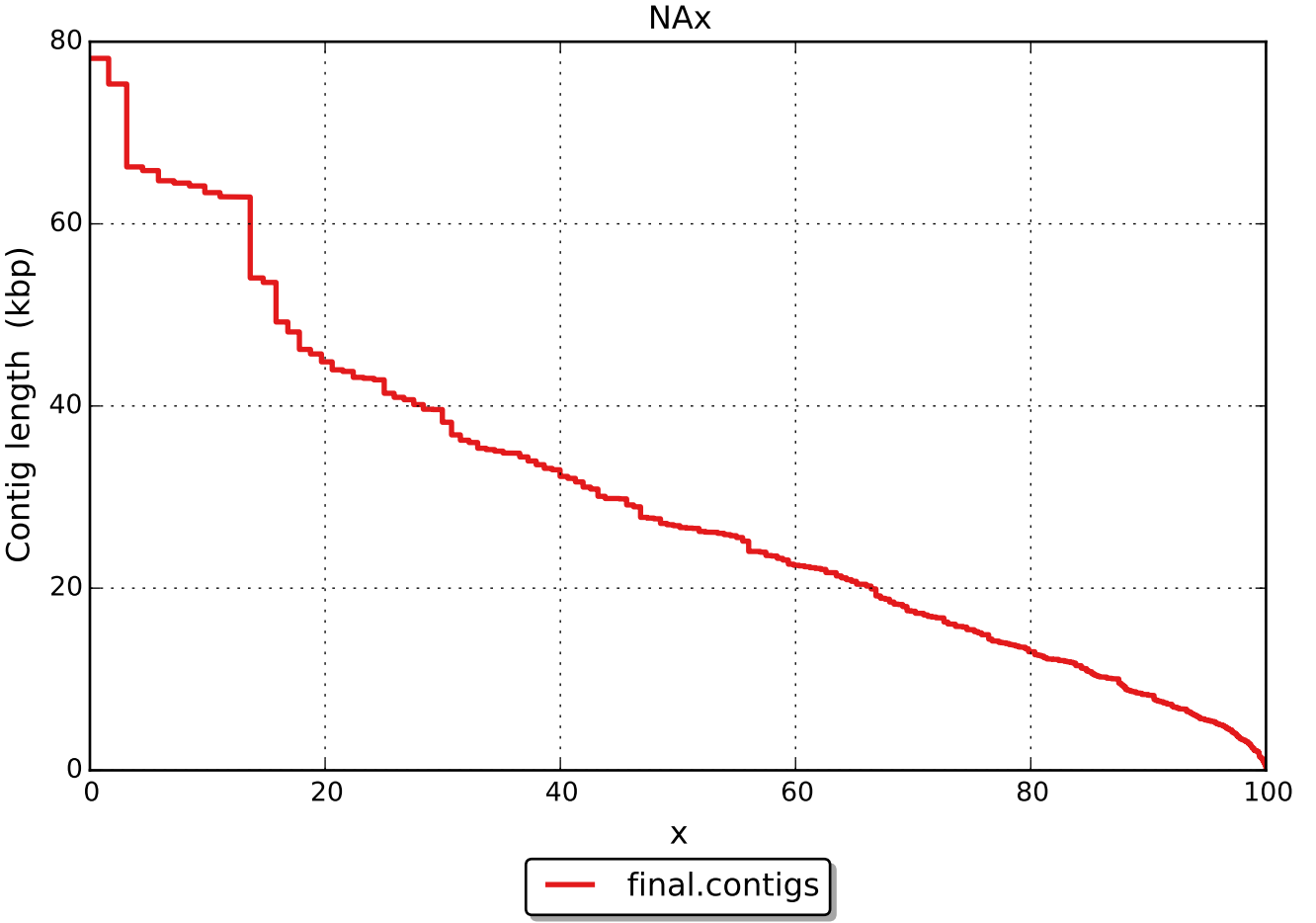

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

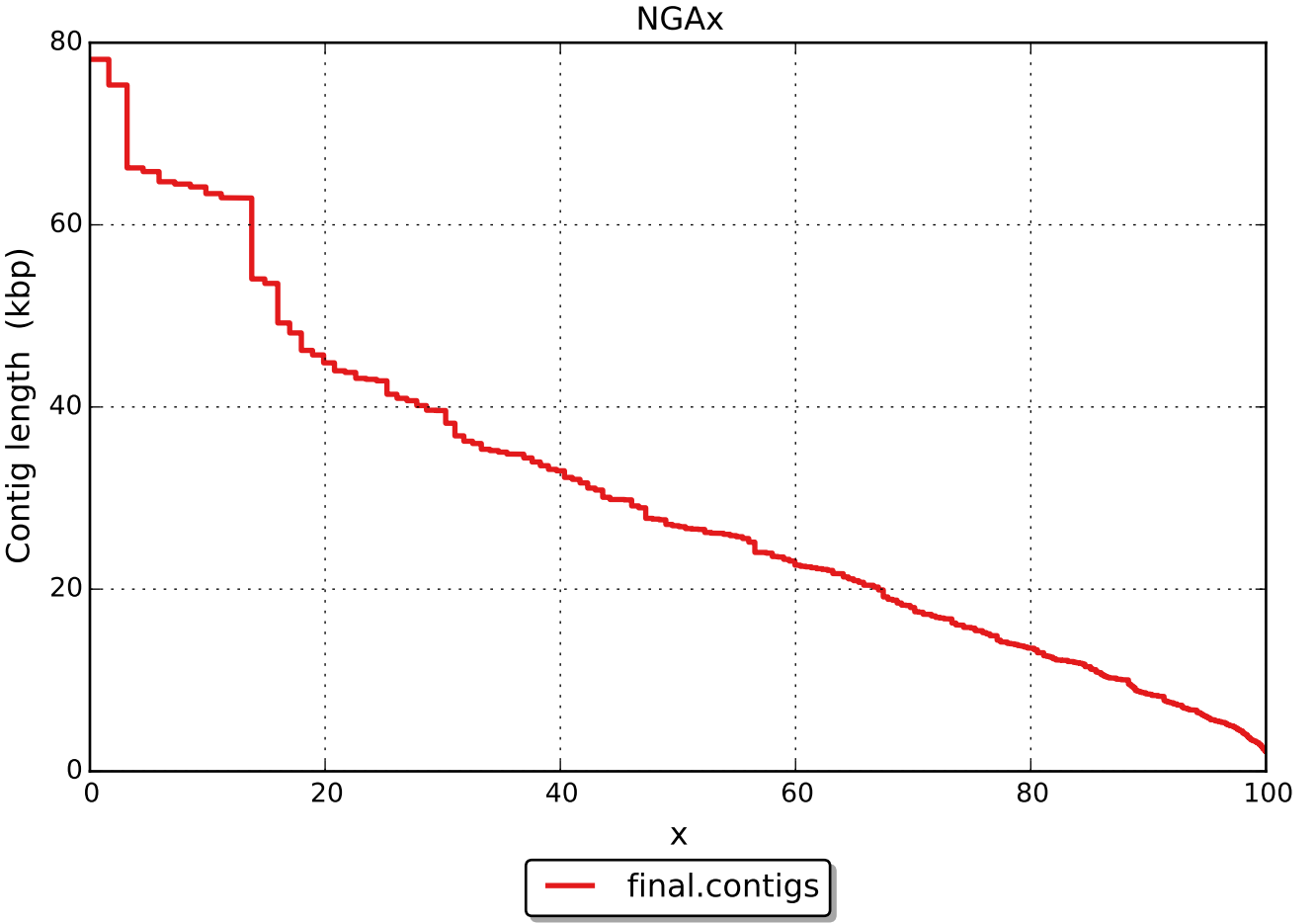

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs