Report

	final.contigs
# contigs (>= 1000 bp)	341
# contigs (>= 5000 bp)	174
# contigs (>= 10000 bp)	74
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2357750
Total length (>= 5000 bp)	1882513
Total length (>= 10000 bp)	1166646
Total length (>= 25000 bp)	173599
Total length (>= 50000 bp)	0
# contigs	465
Largest contig	35550
Total length	2436589
Reference length	4641652
GC (%)	50.85
Reference GC (%)	50.78
N50	9738
NG50	1614
N75	5427
L50	80
LG50	313
L75	164
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	52.134
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	428.79
# indels per 100 kbp	0.00
Largest alignment	35550
NA50	9738
NGA50	1614
NA75	5385
LA50	80
LGA50	313
LA75	164

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

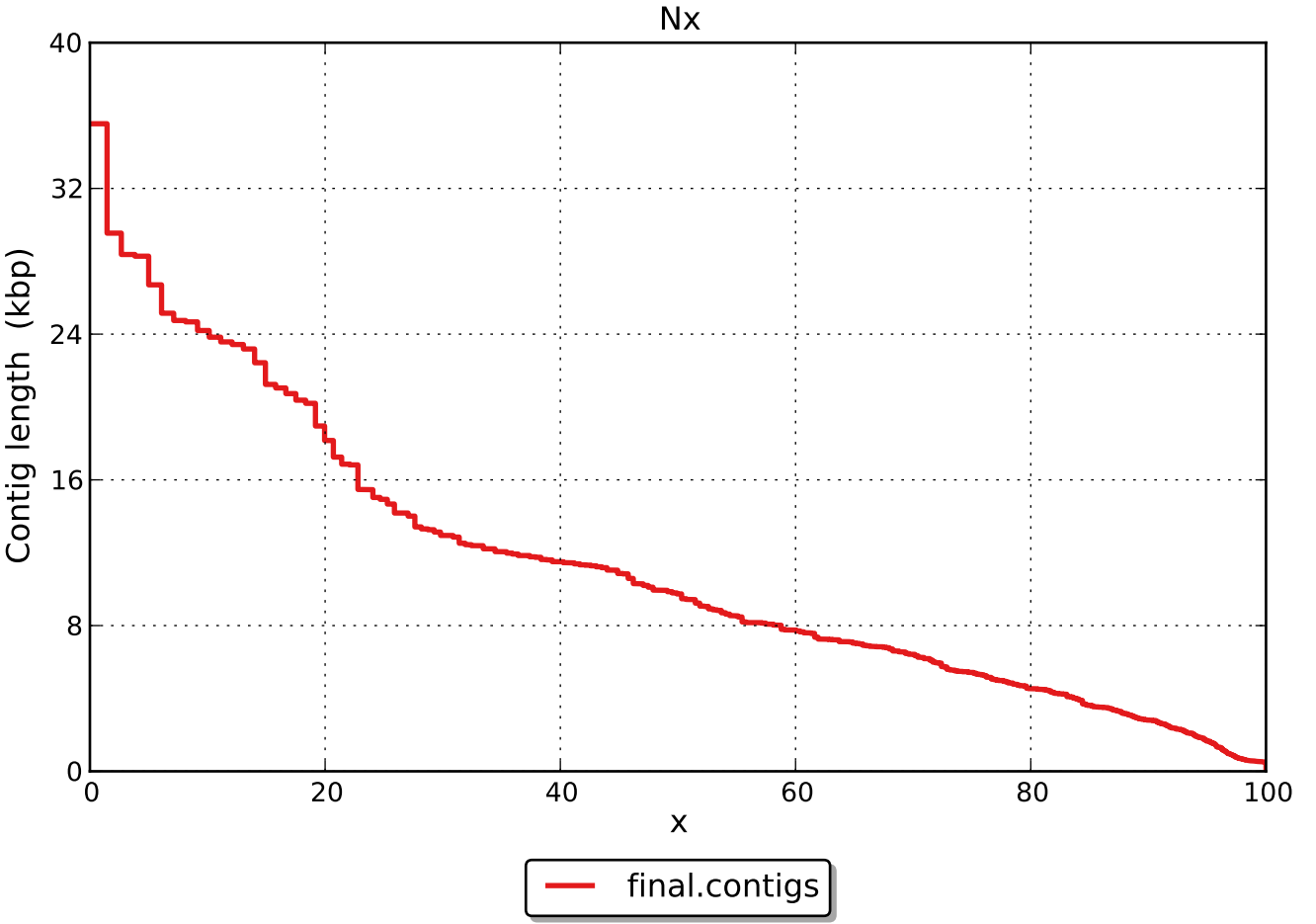
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	10376
# indels	0
# short indels	0
# long indels	0
Indels length	0

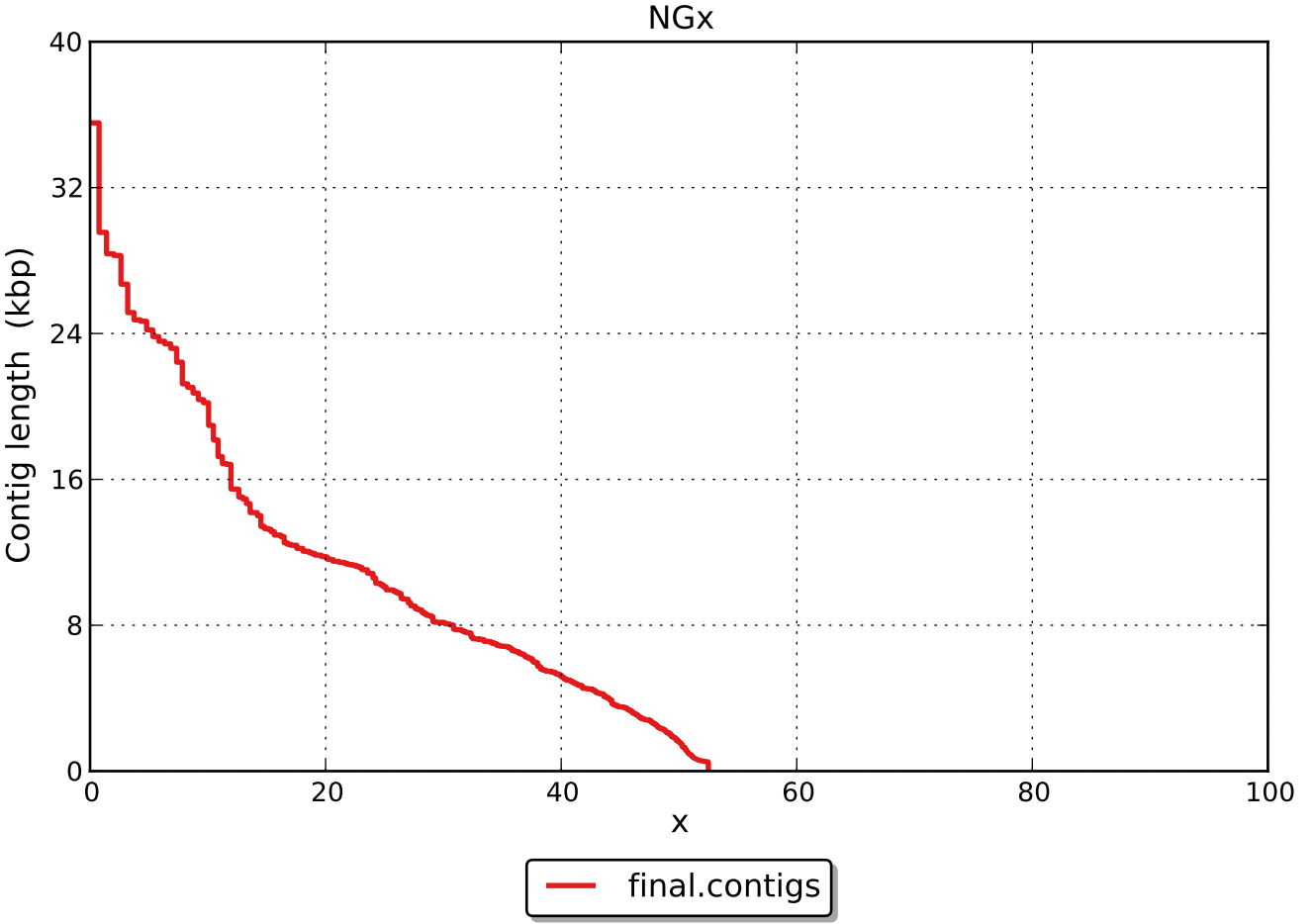
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

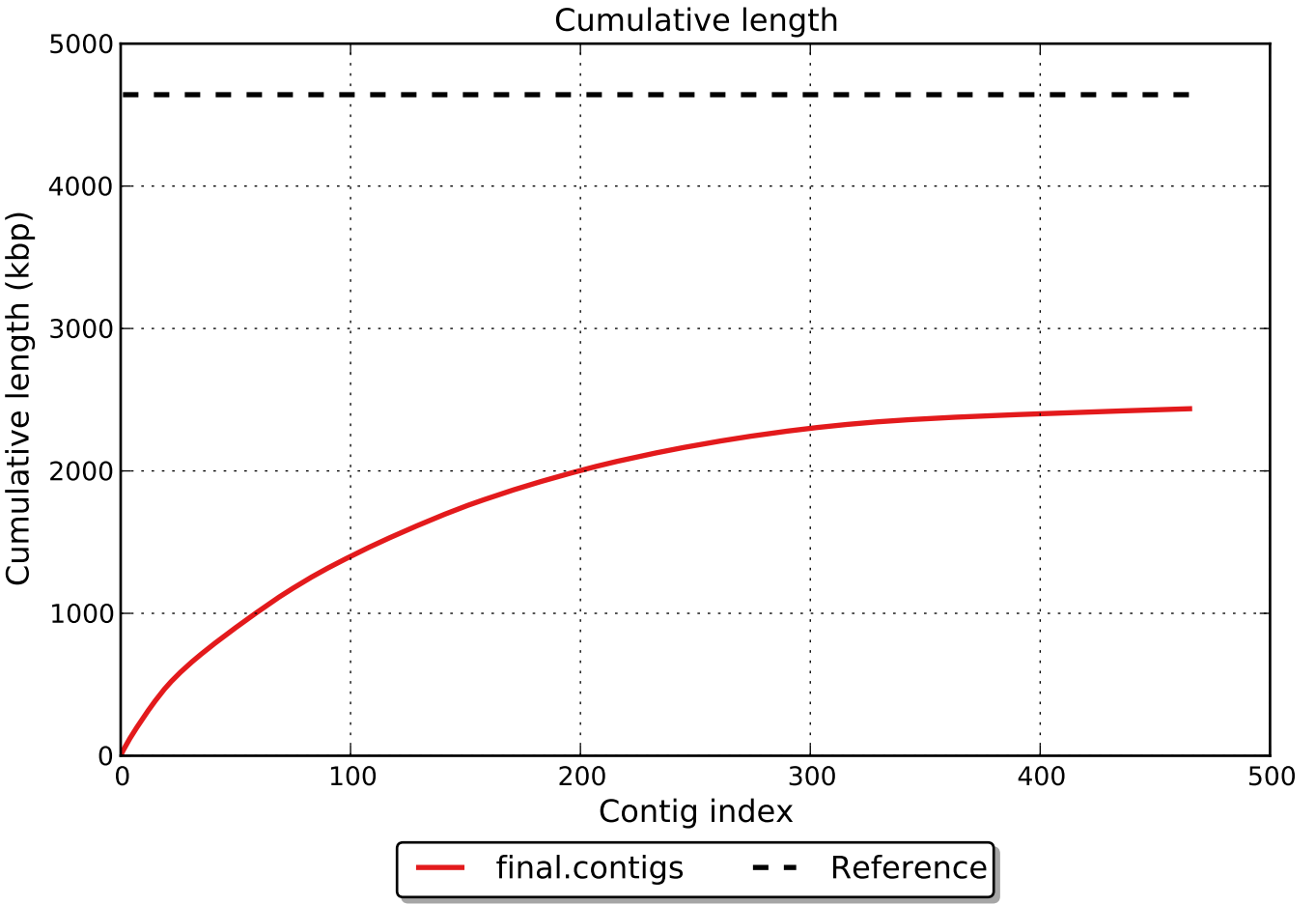
Unaligned report

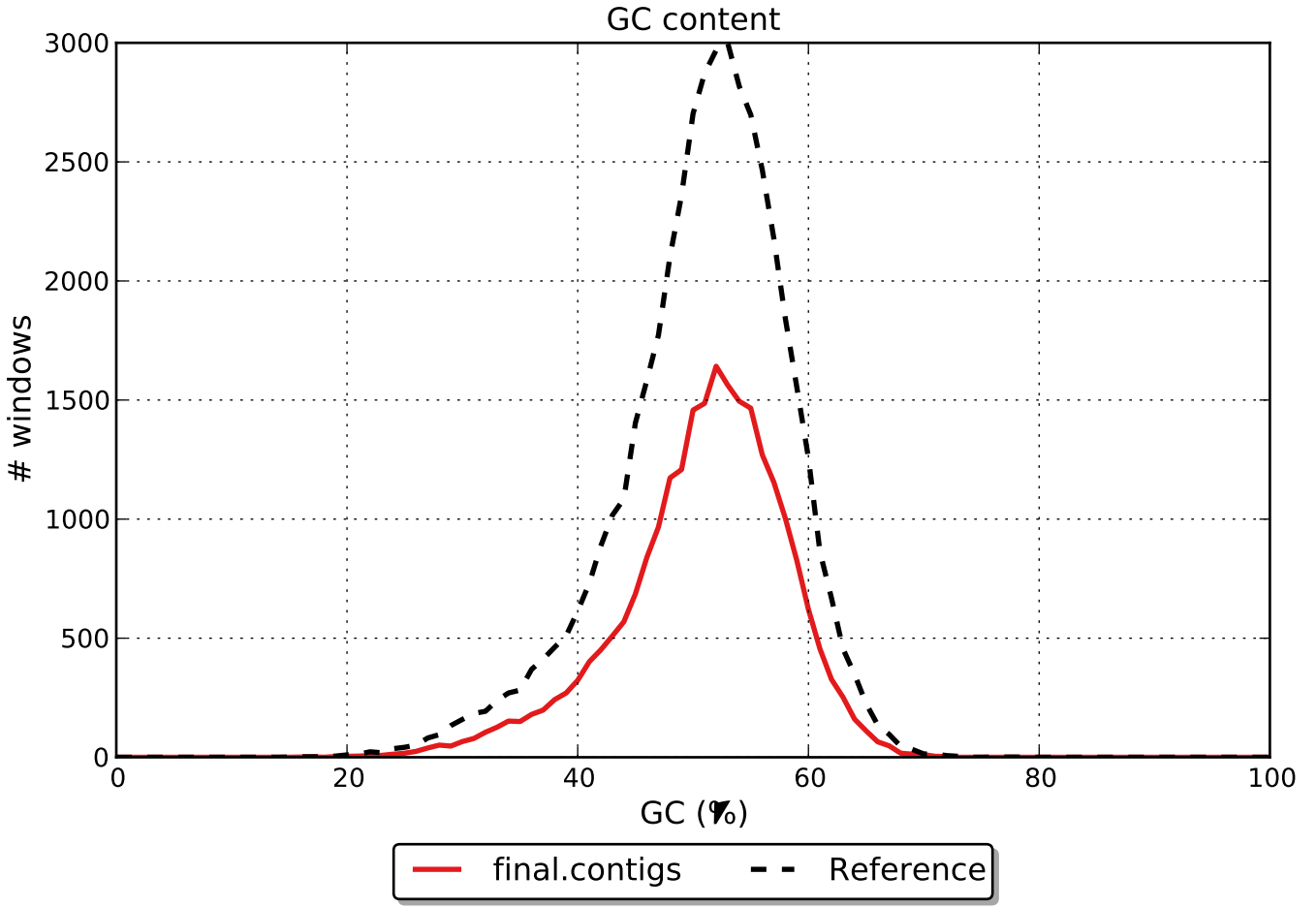
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

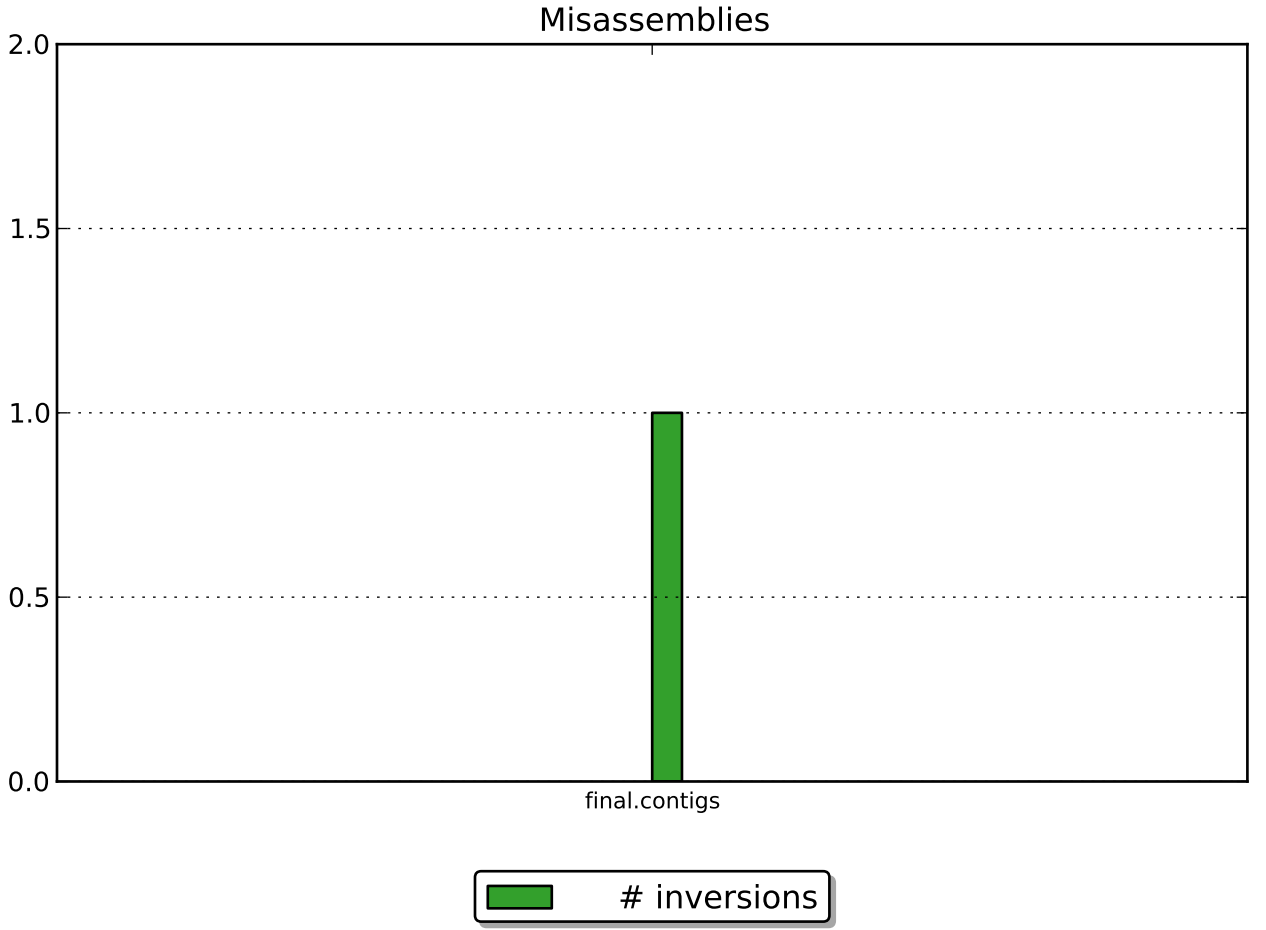
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

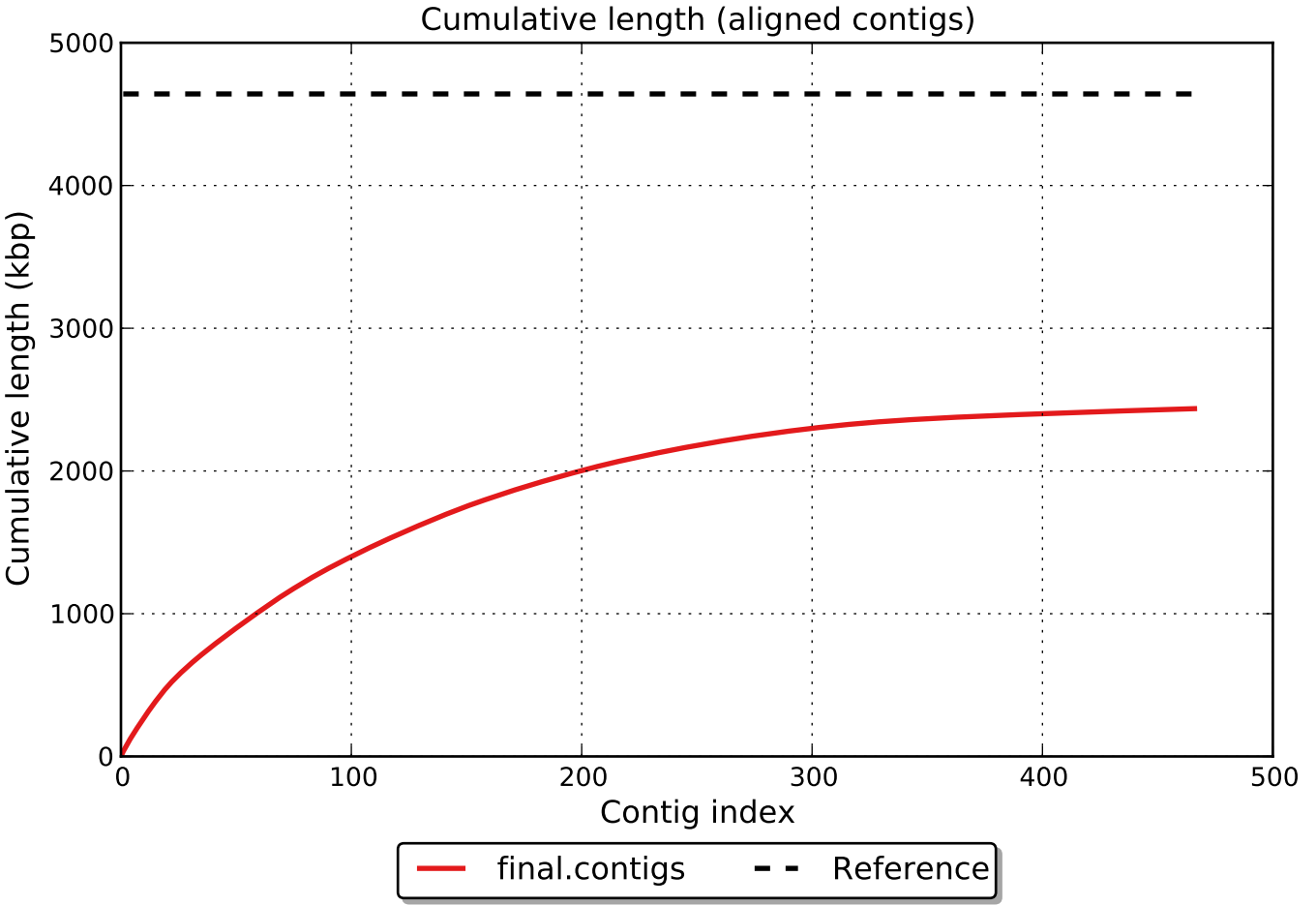

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

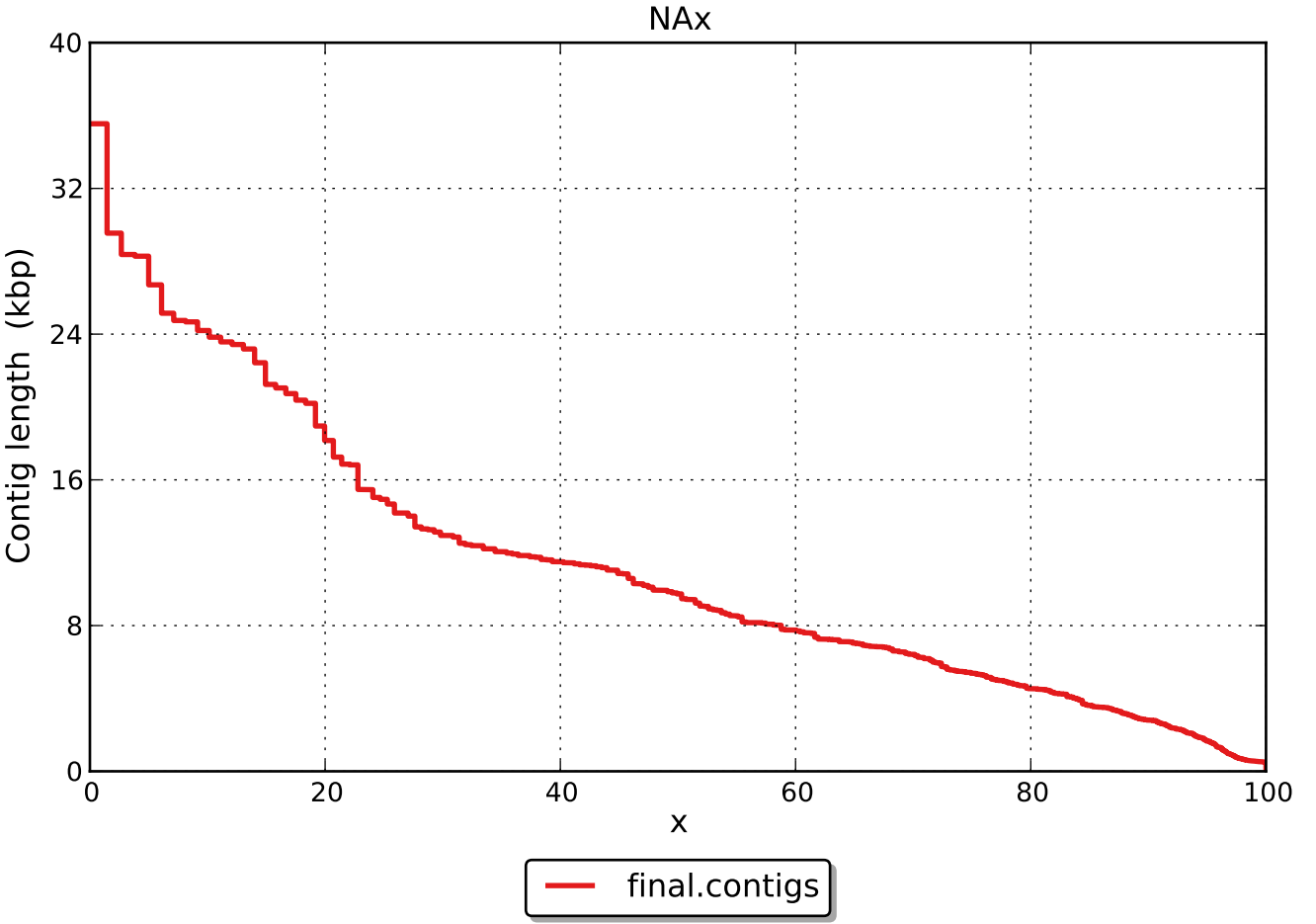

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

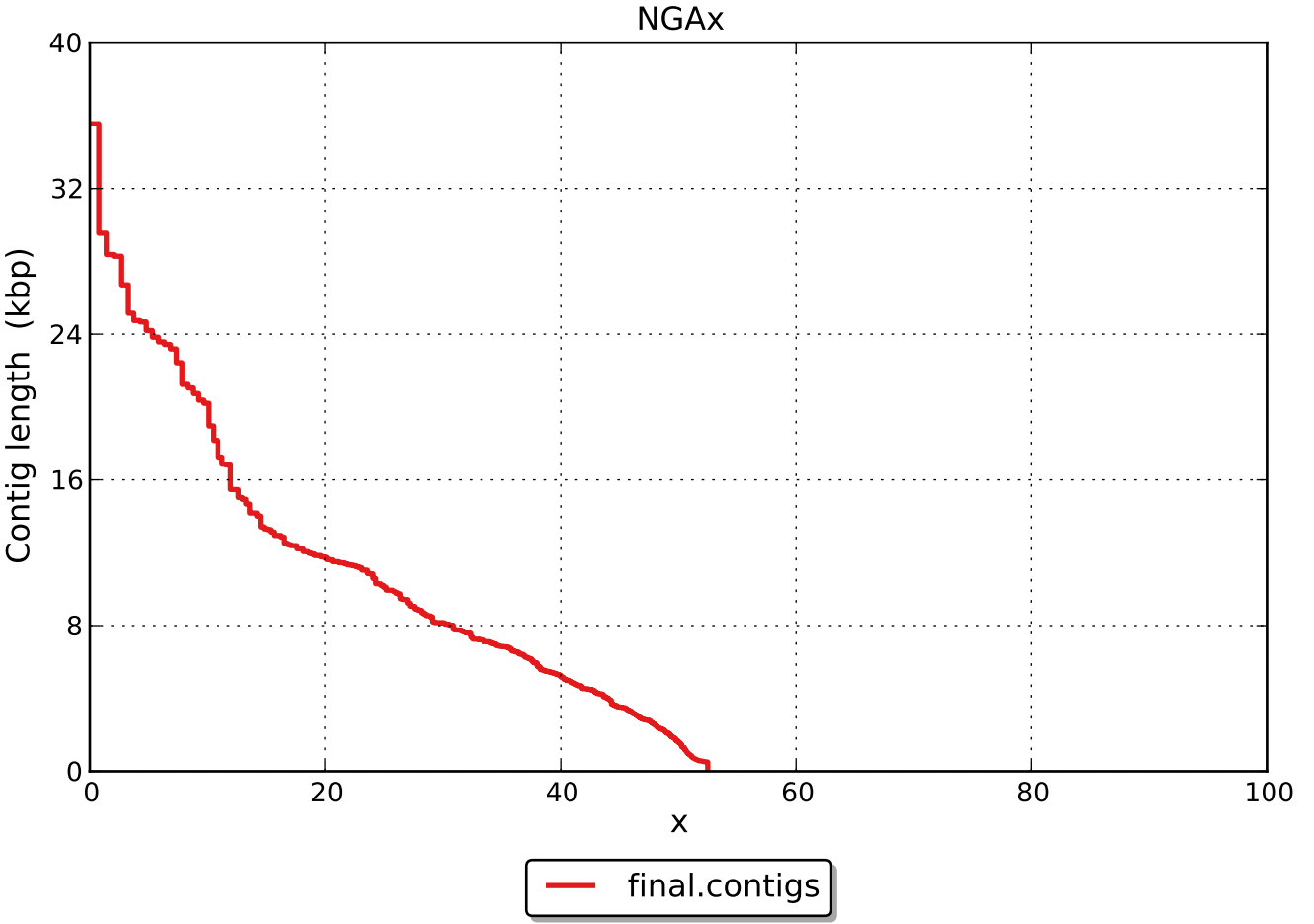

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs