Report

	final.contigs
# contigs (>= 1000 bp)	877
# contigs (>= 5000 bp)	28
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1896667
Total length (>= 5000 bp)	171476
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1843
Largest contig	8340
Total length	2545449
Reference length	4857432
GC (%)	52.14
Reference GC (%)	52.22
N50	1831
NG50	548
N75	992
L50	418
LG50	1621
L75	890
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	50.846
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	393.51
# indels per 100 kbp	0.04
Largest alignment	8340
NA50	1831
NGA50	548
NA75	992
LA50	418
LGA50	1621
LA75	890

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

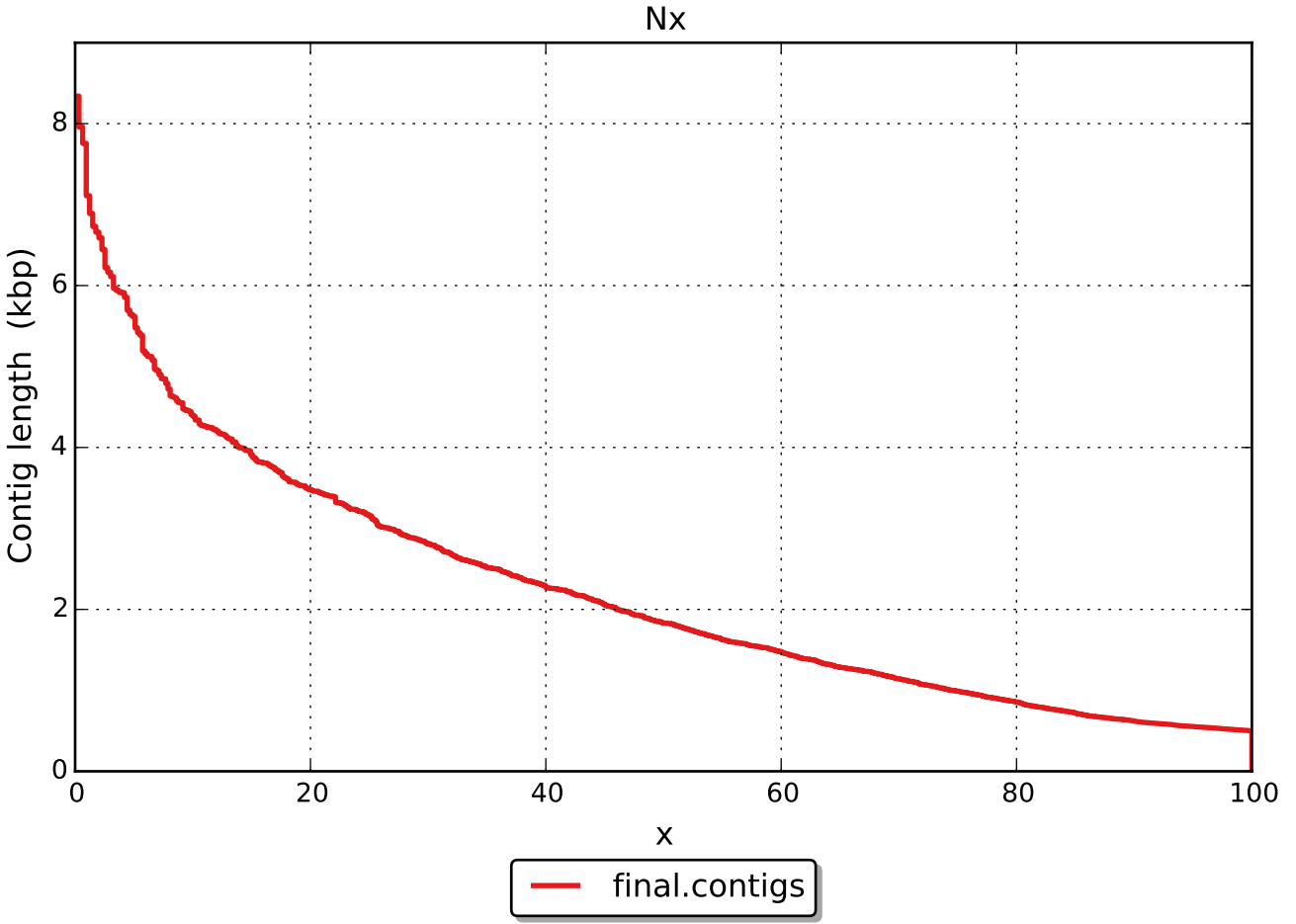
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1540
# local misassemblies	1
# mismatches	9719
# indels	1
# short indels	1
# long indels	0
Indels length	1

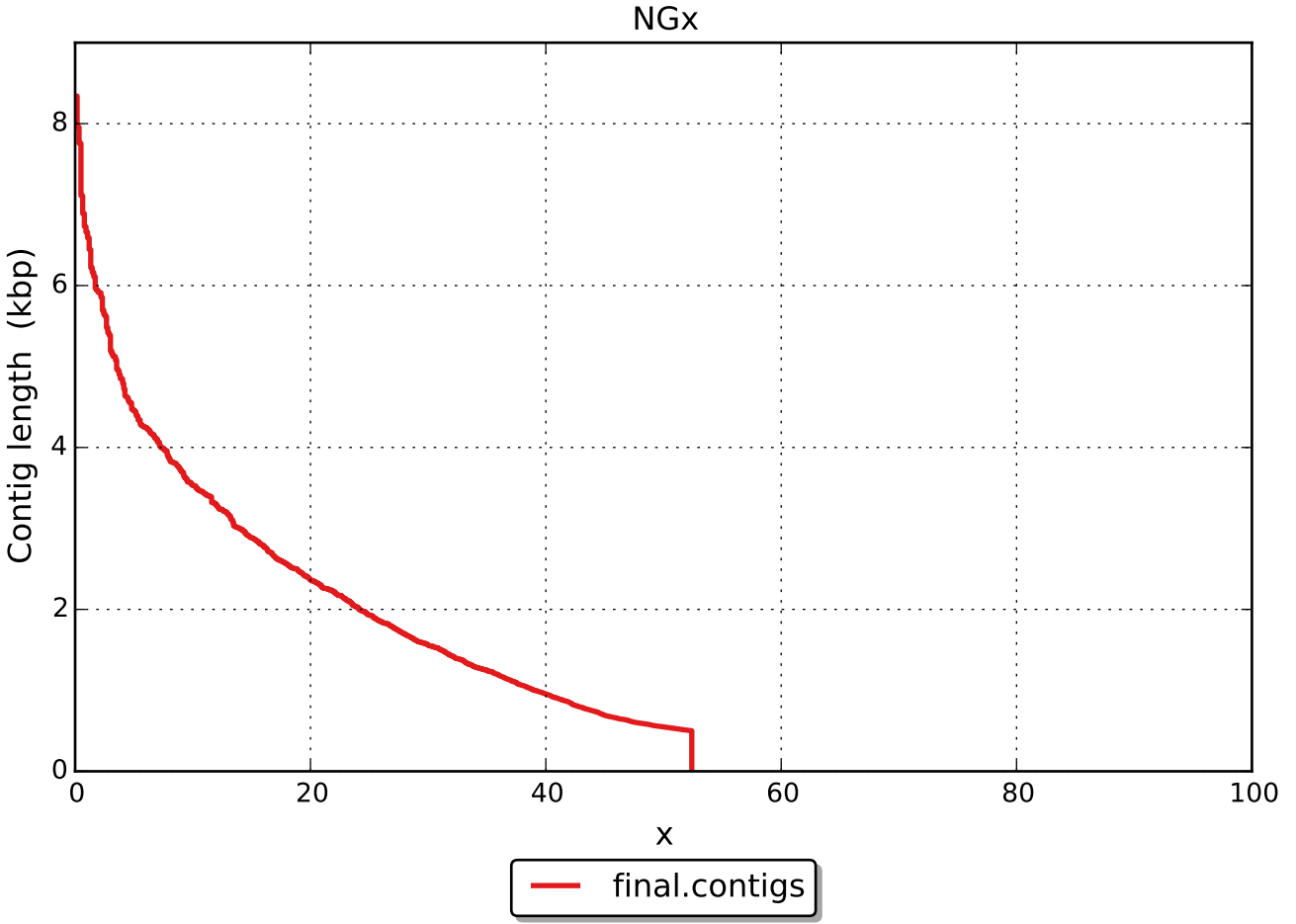
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

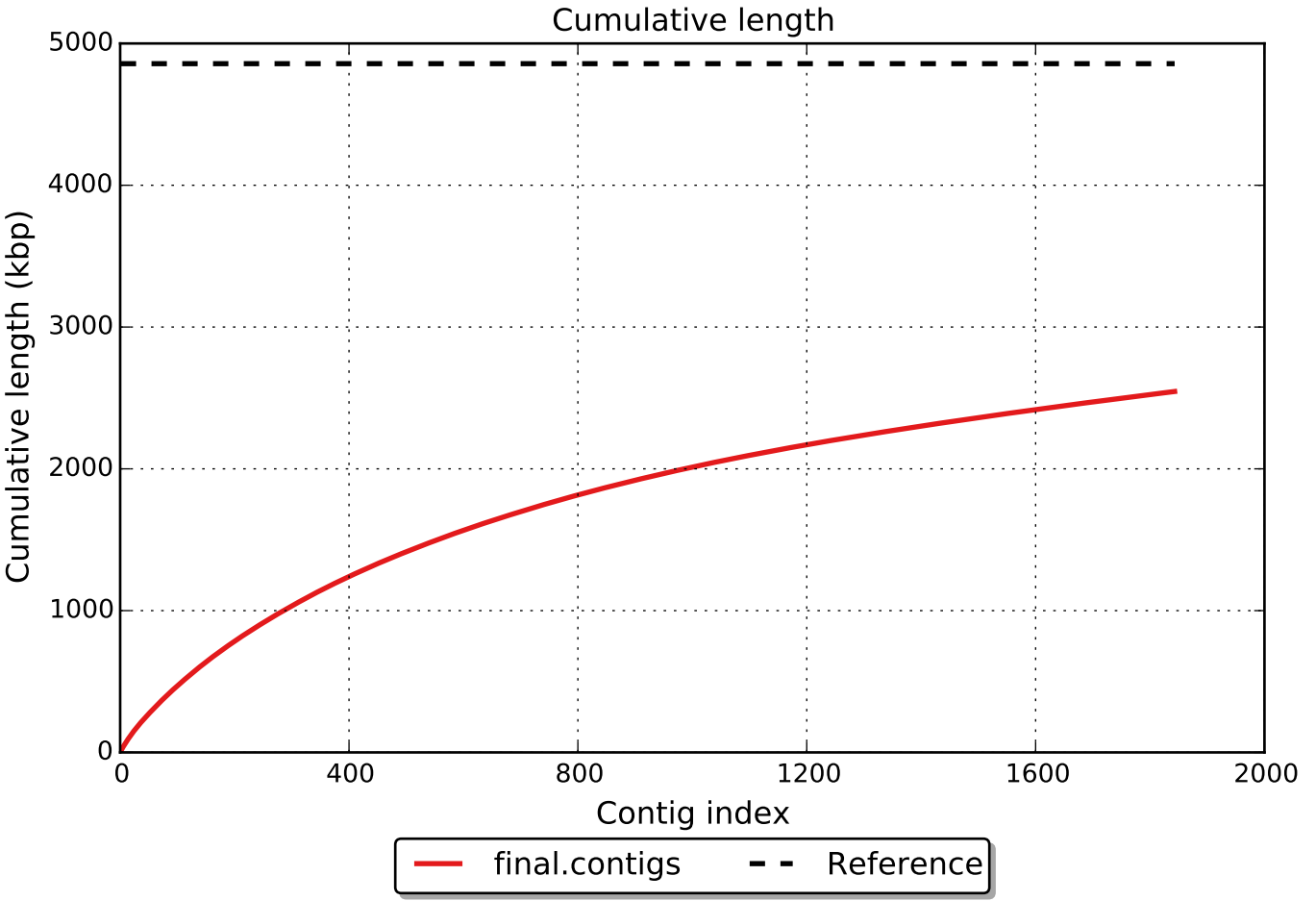
Unaligned report

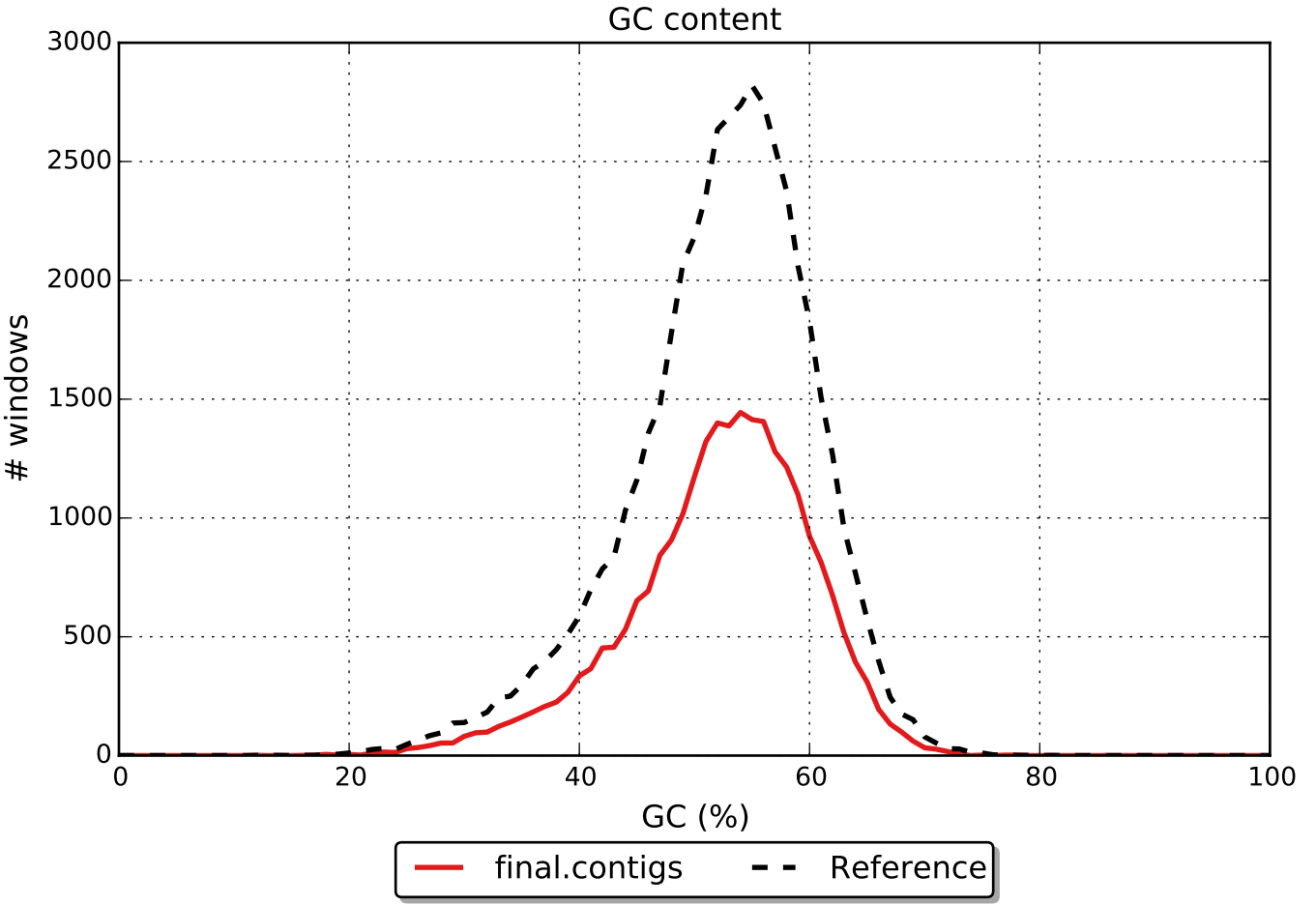
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

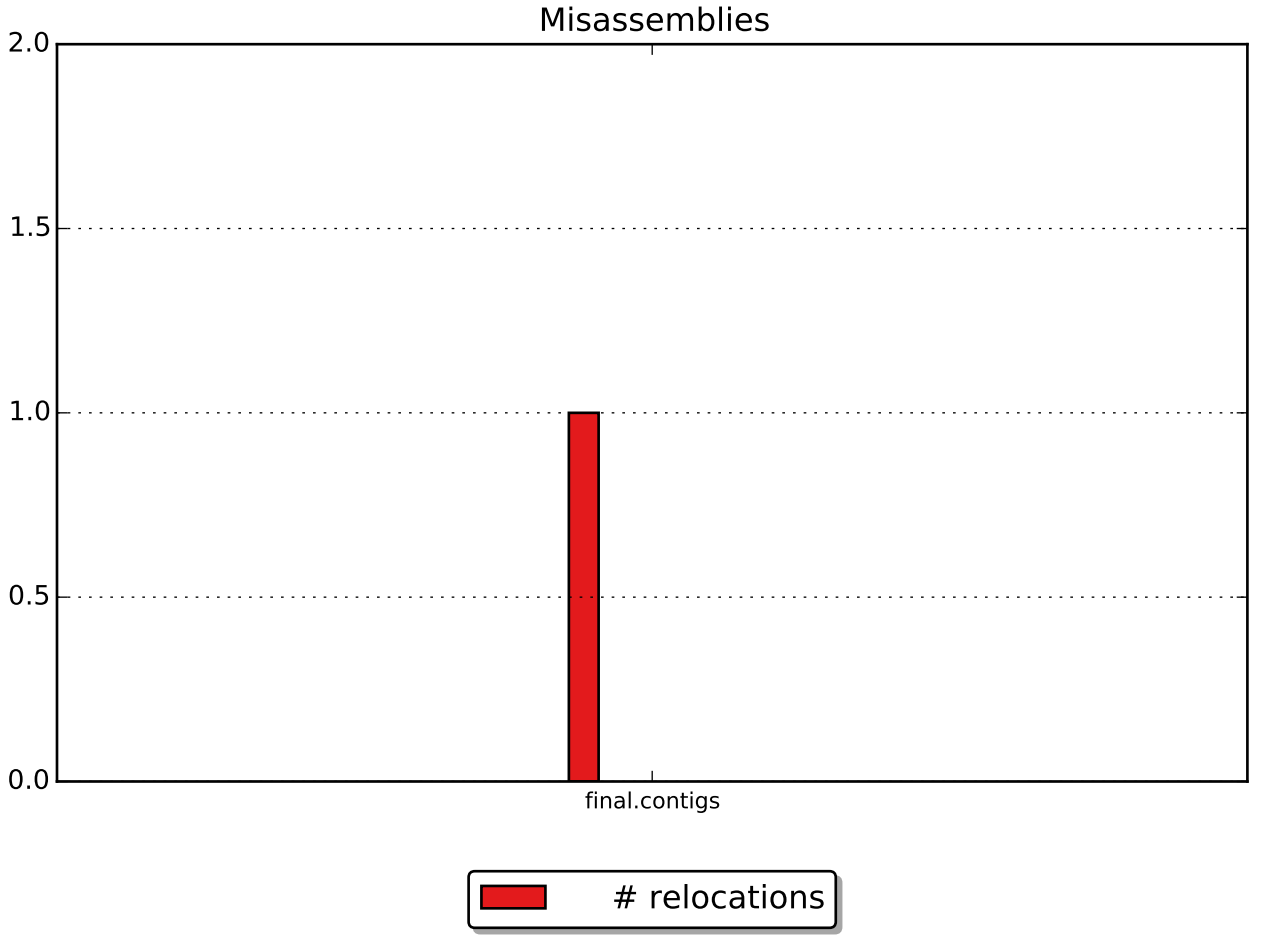
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

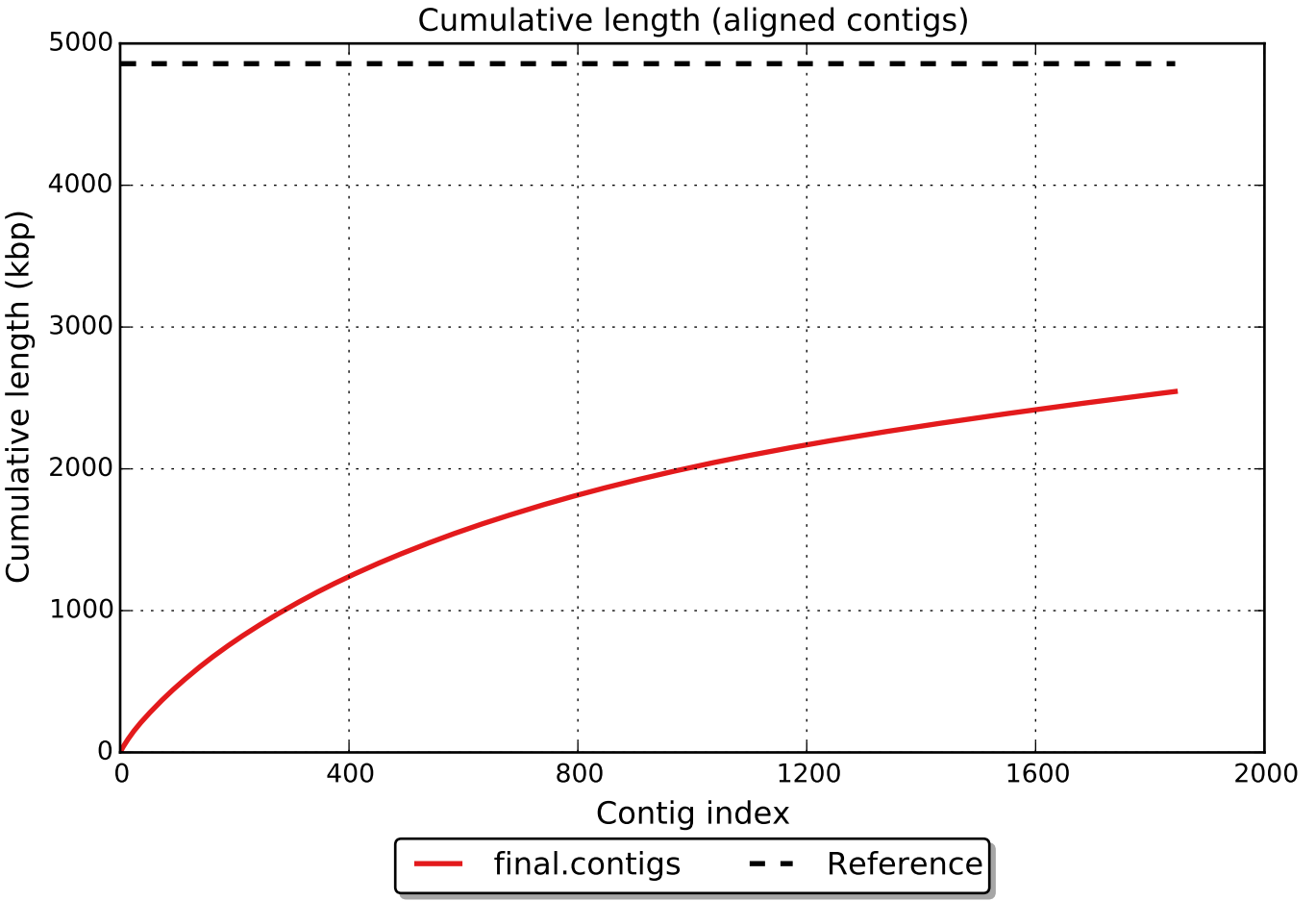

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

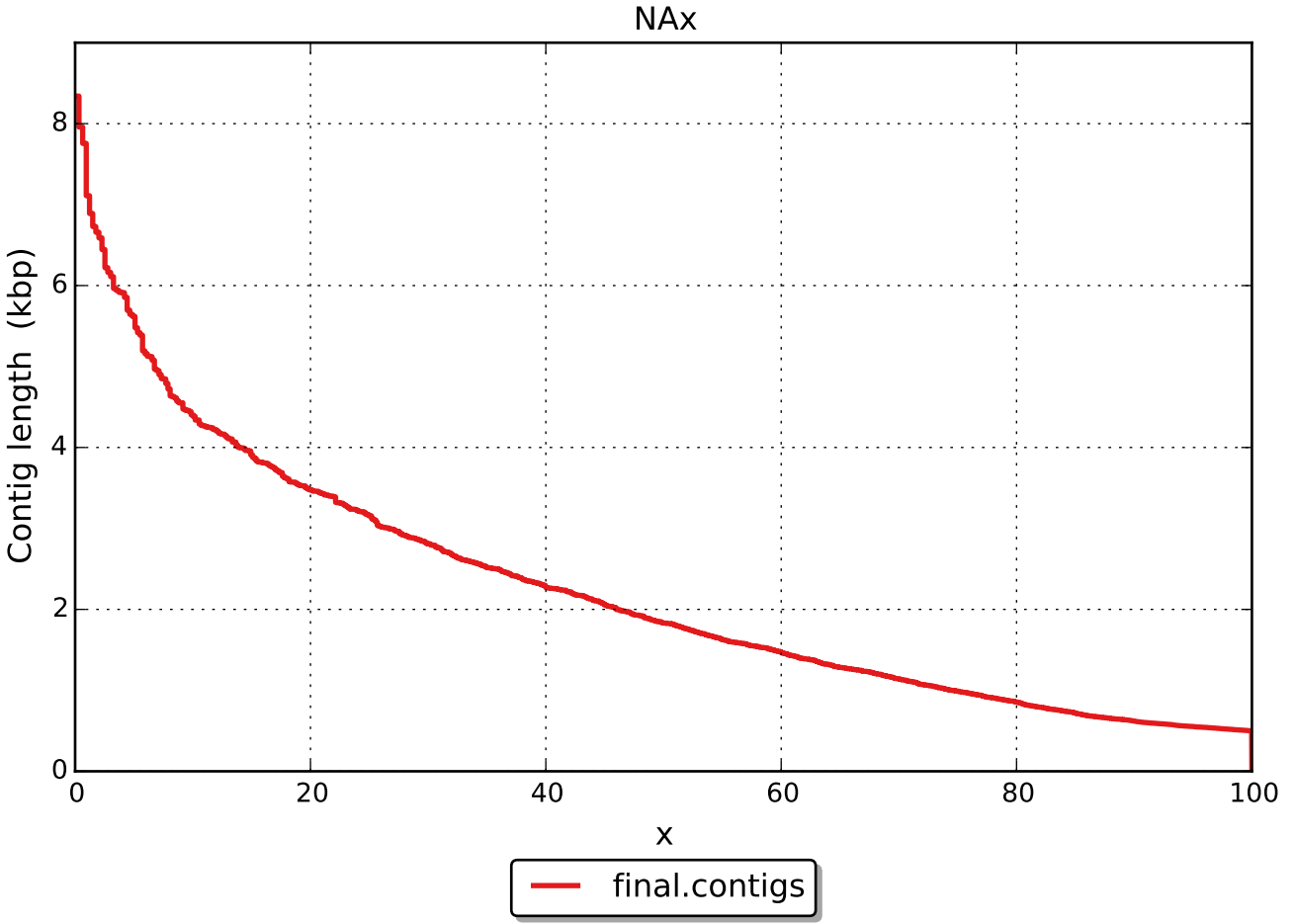

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

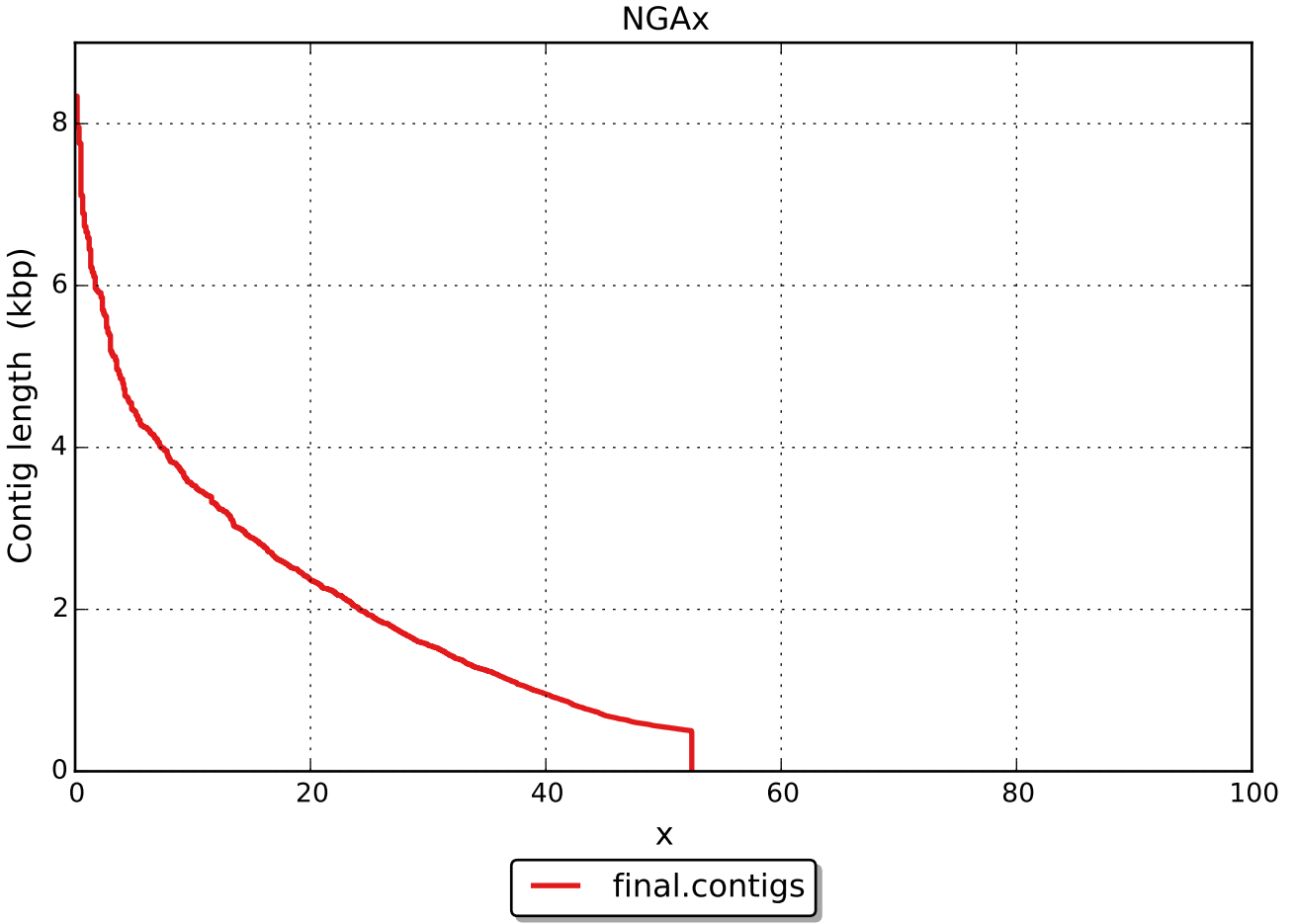

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
400
800
1200
1600
2000
Contig index
final.contigs
Reference


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
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
400
800
1200
1600
2000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs