Report

	final.contigs
# contigs (>= 1000 bp)	1261
# contigs (>= 5000 bp)	229
# contigs (>= 10000 bp)	25
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4130463
Total length (>= 5000 bp)	1622290
Total length (>= 10000 bp)	301231
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2034
Largest contig	16739
Total length	4649709
Reference length	4857432
GC (%)	52.18
Reference GC (%)	52.22
N50	3655
NG50	3534
N75	1992
NG75	1778
L50	394
LG50	423
L75	819
LG75	901
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	8147
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.822
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	608.02
# indels per 100 kbp	0.13
Largest alignment	16739
NA50	3655
NGA50	3534
NA75	1992
NGA75	1778
LA50	394
LGA50	423
LA75	819
LGA75	901

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

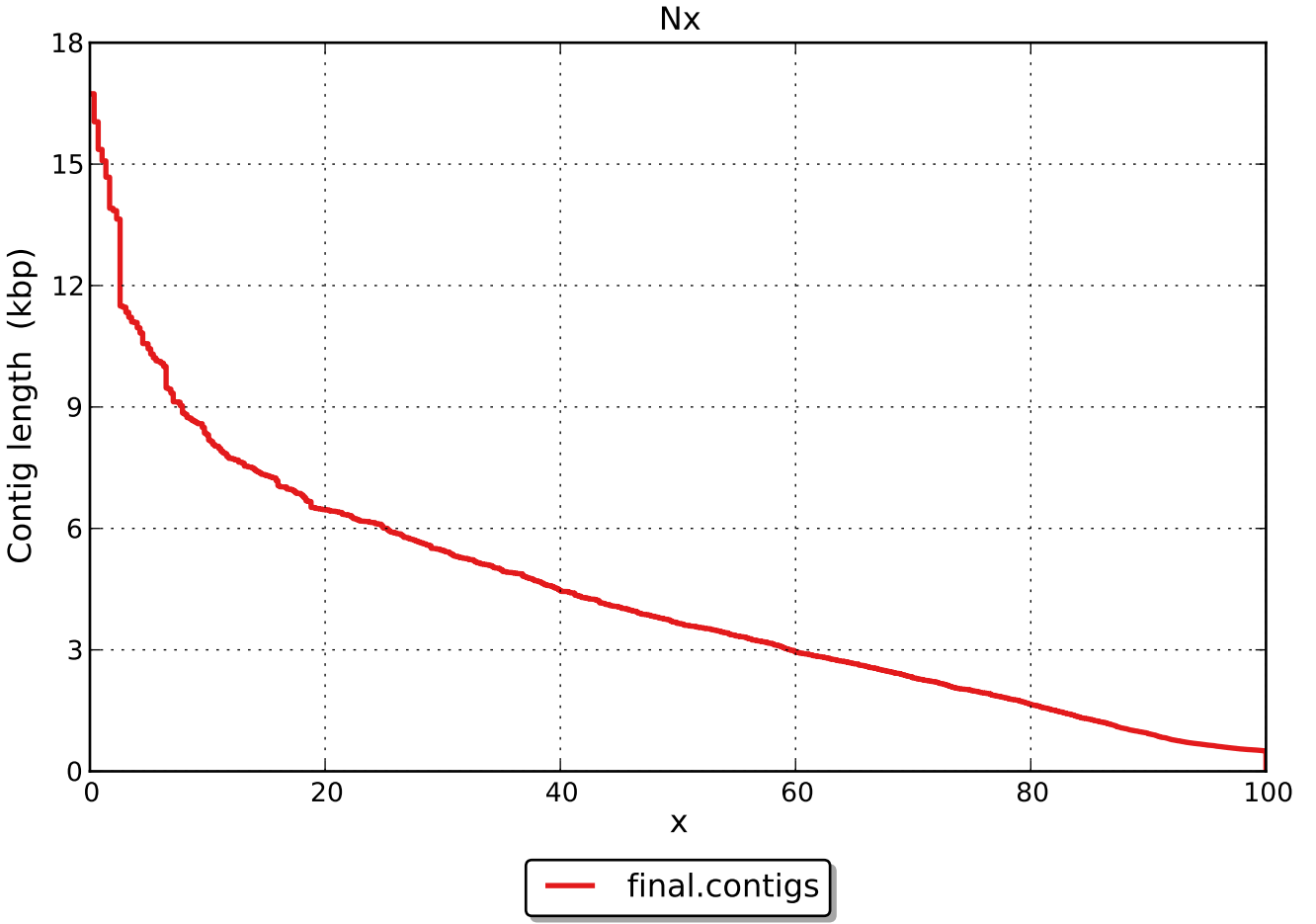
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	8147
# local misassemblies	0
# mismatches	27119
# indels	6
# short indels	6
# long indels	0
Indels length	6

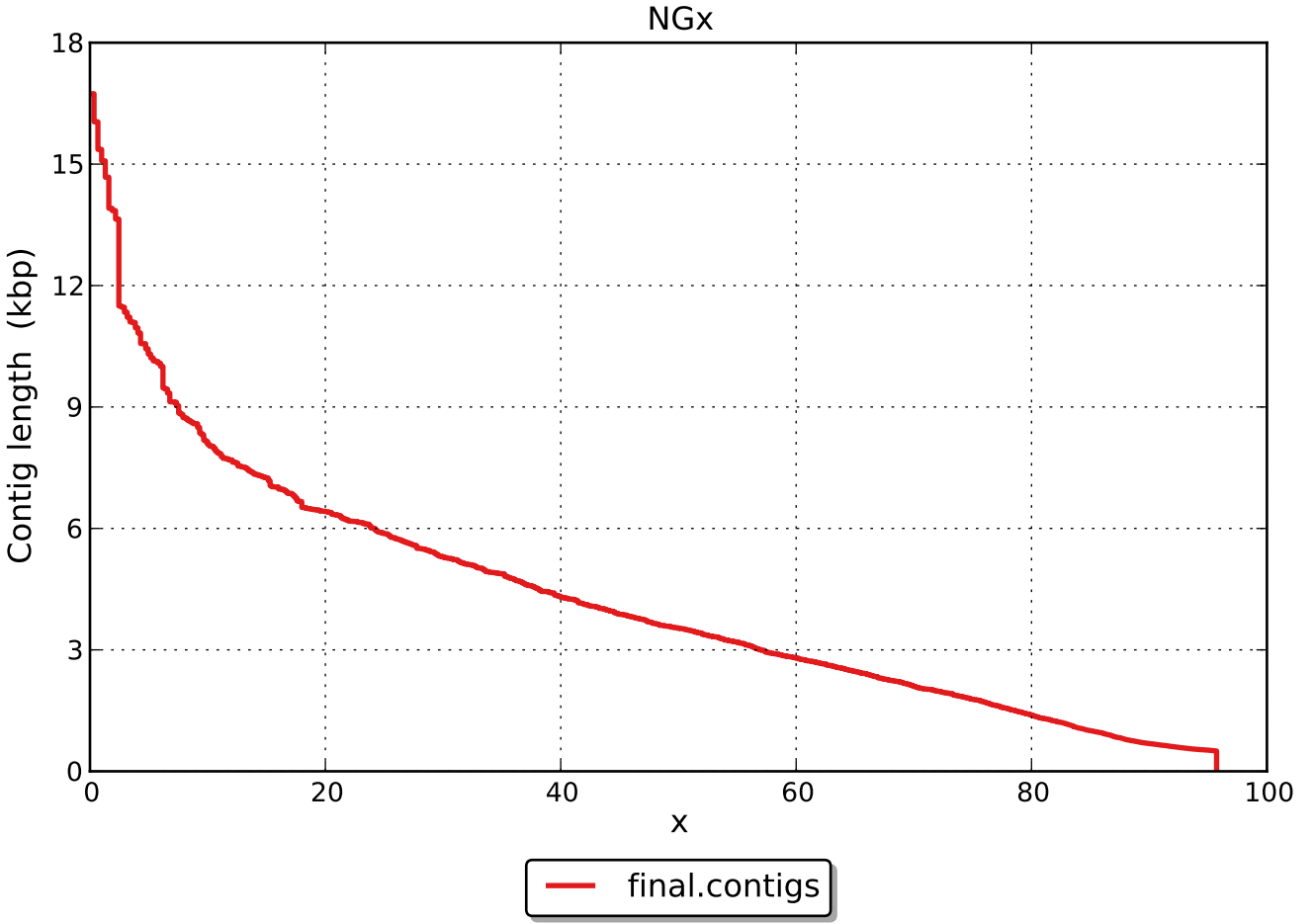
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

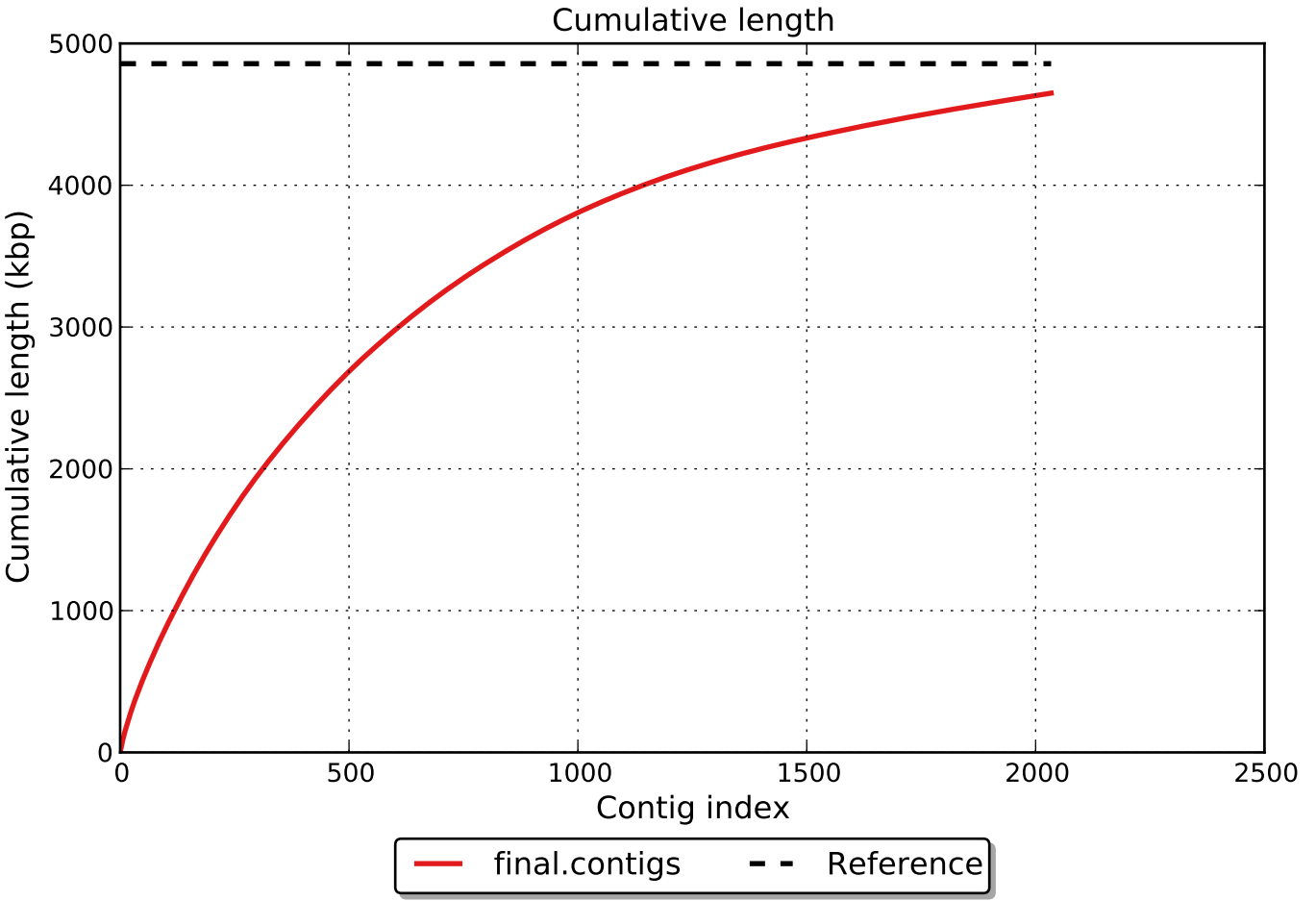
Unaligned report

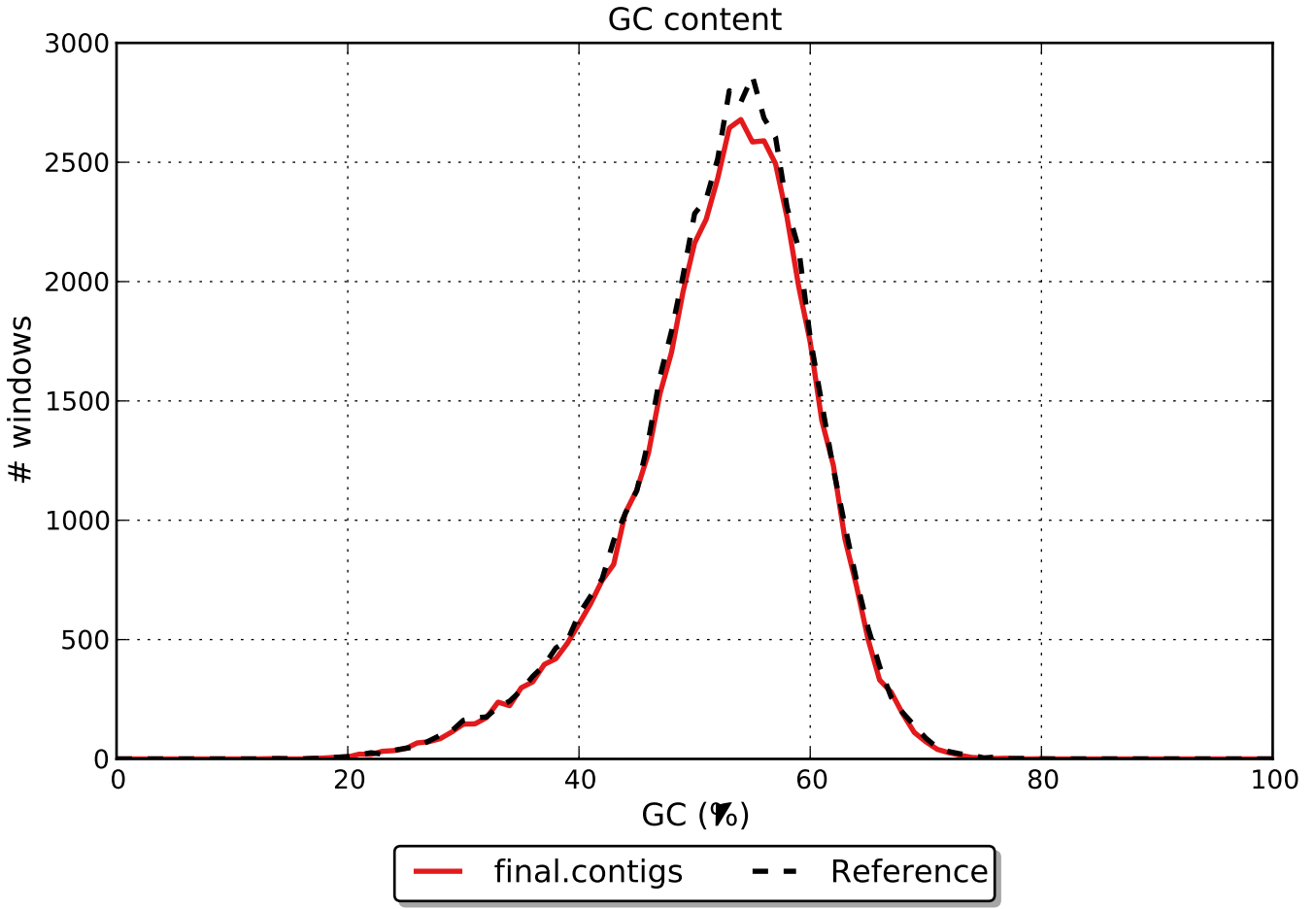
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

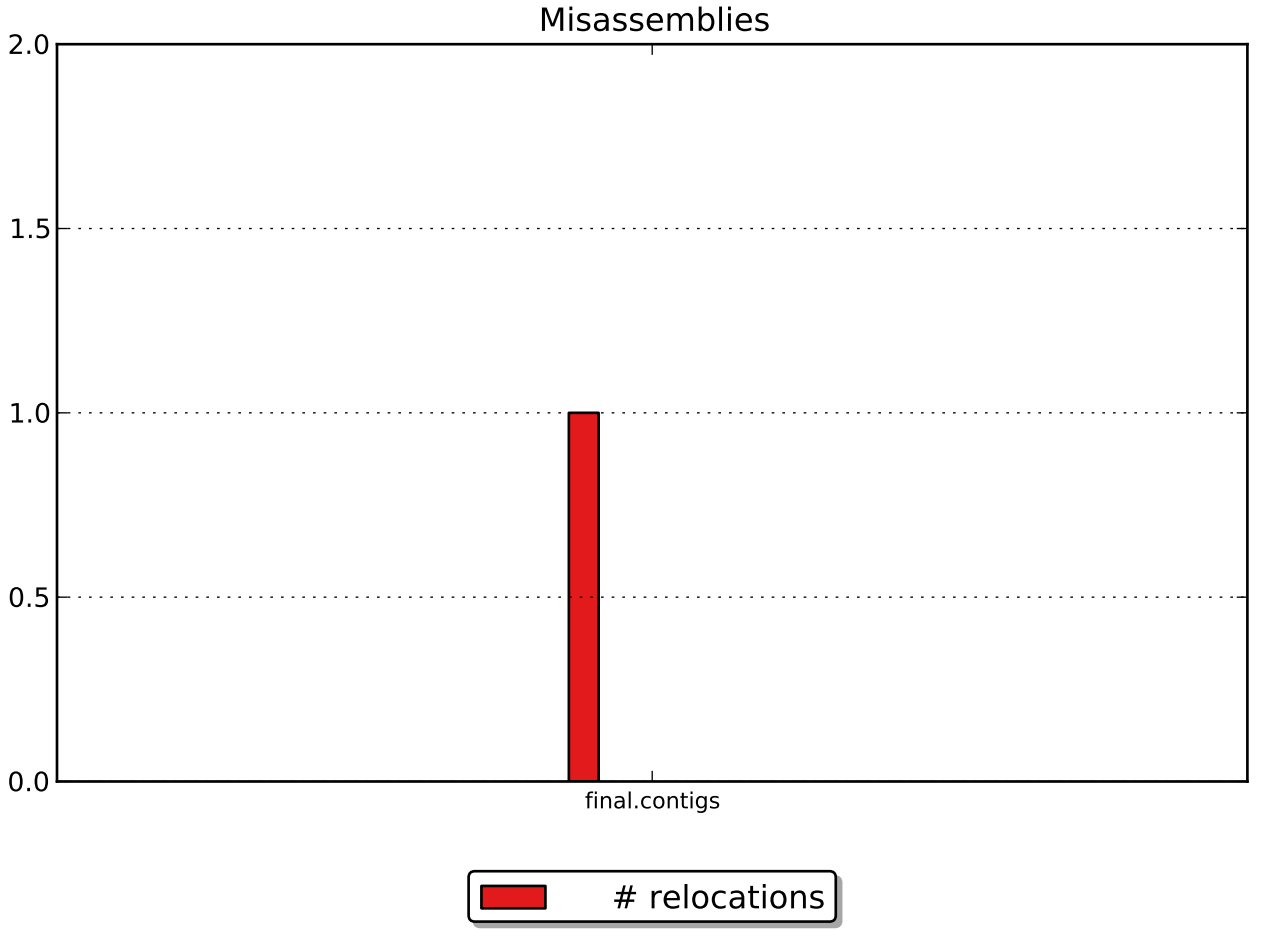
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

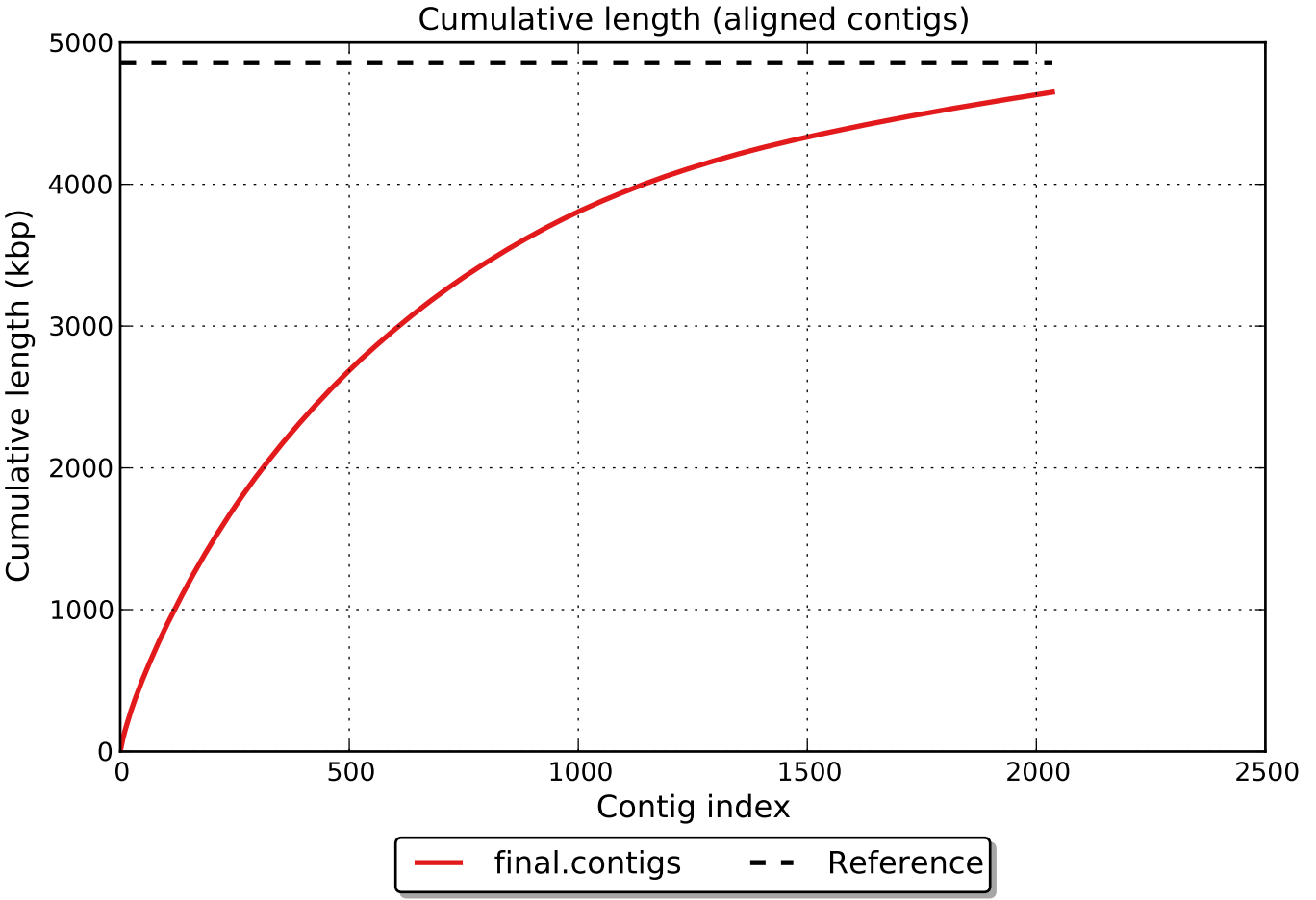

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

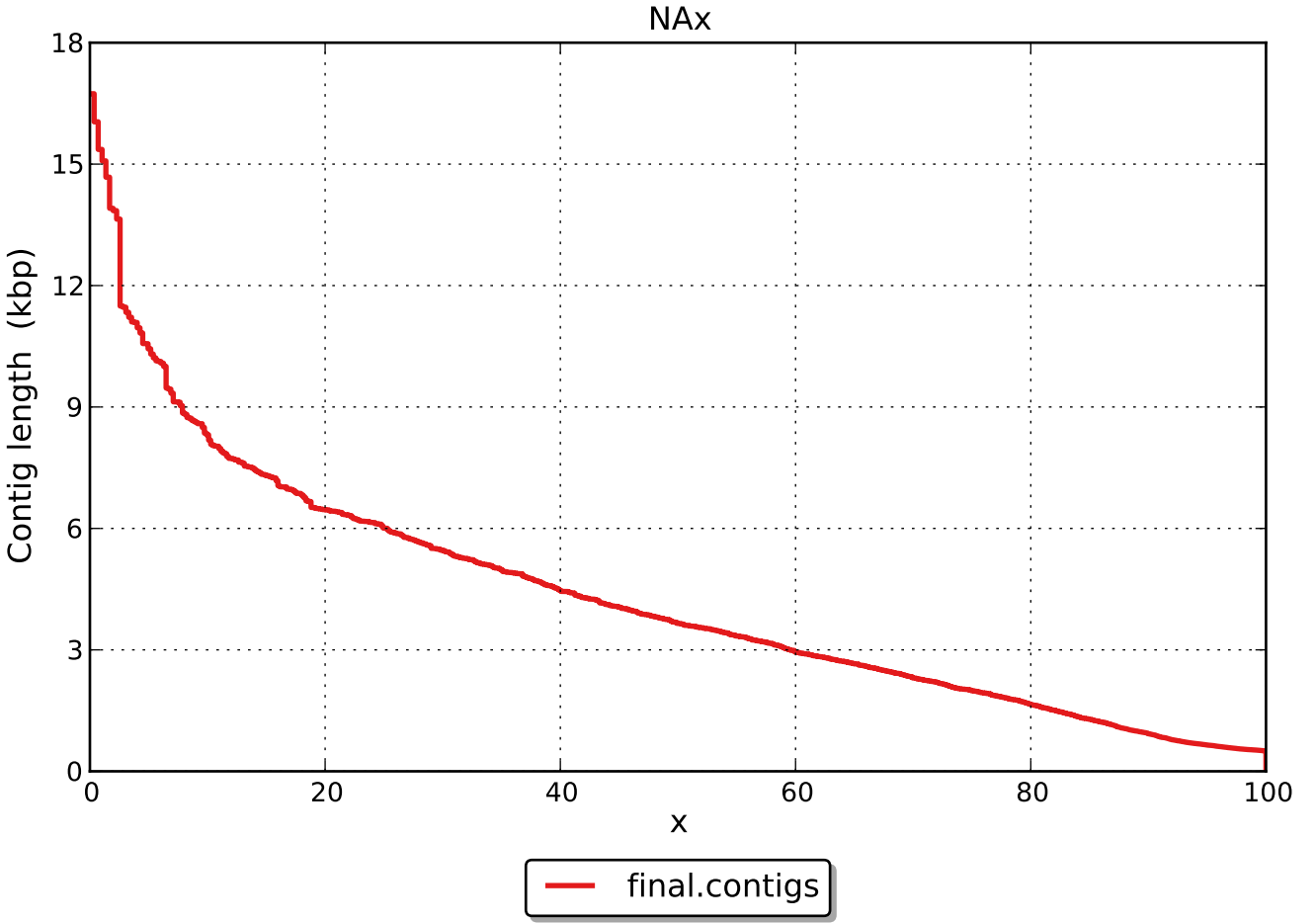

NGx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

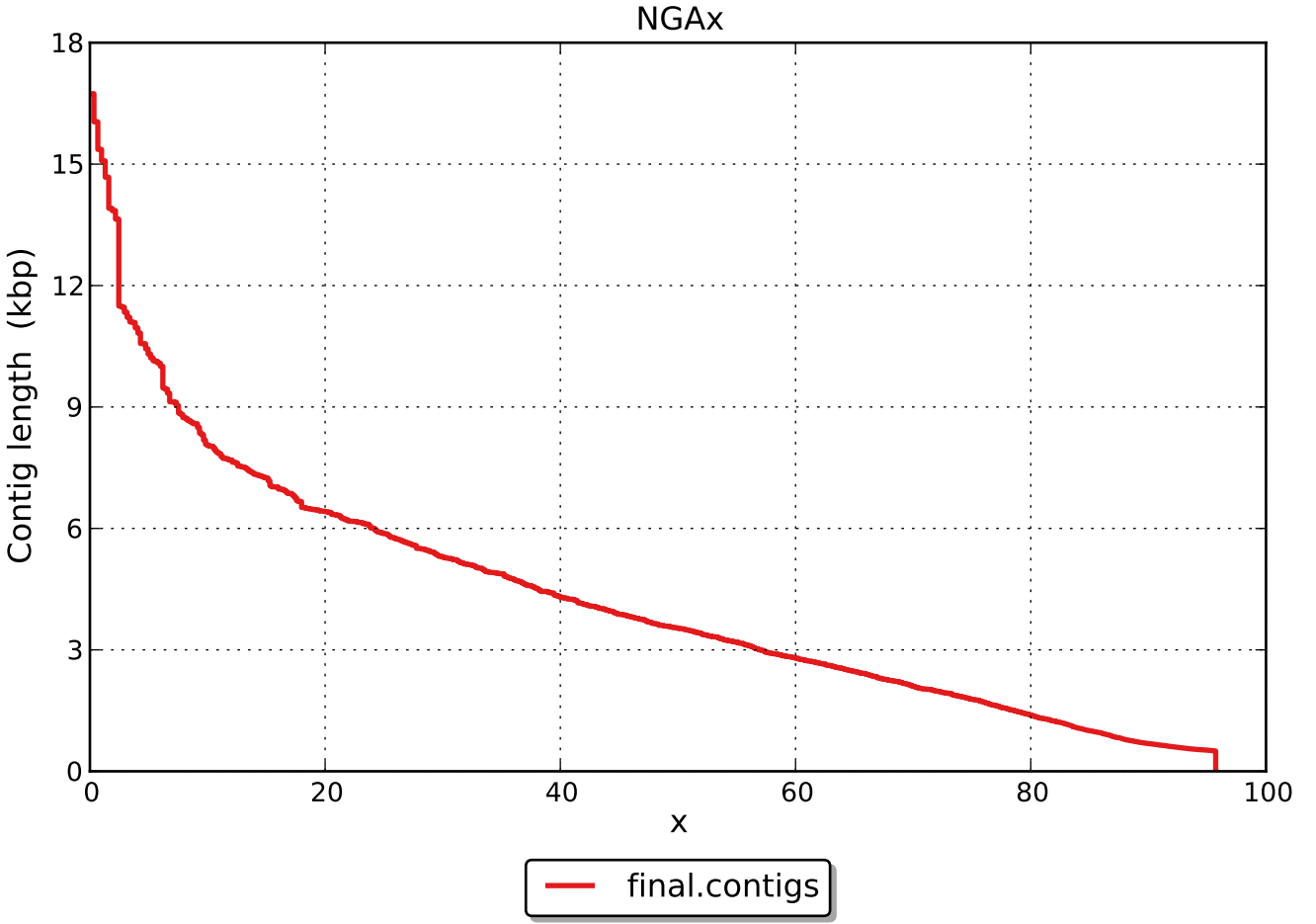

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


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
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs