Report

	final.contigs
# contigs (>= 1000 bp)	1372
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1967520
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4527
Largest contig	4278
Total length	4192934
Reference length	4857432
GC (%)	52.24
Reference GC (%)	52.22
N50	961
NG50	874
N75	713
NG75	609
L50	1504
LG50	1867
L75	2774
LG75	3530
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	4784
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	79.914
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	270.65
# indels per 100 kbp	0.05
Largest alignment	4278
NA50	961
NGA50	873
NA75	713
NGA75	609
LA50	1505
LGA50	1868
LA75	2775
LGA75	3532

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

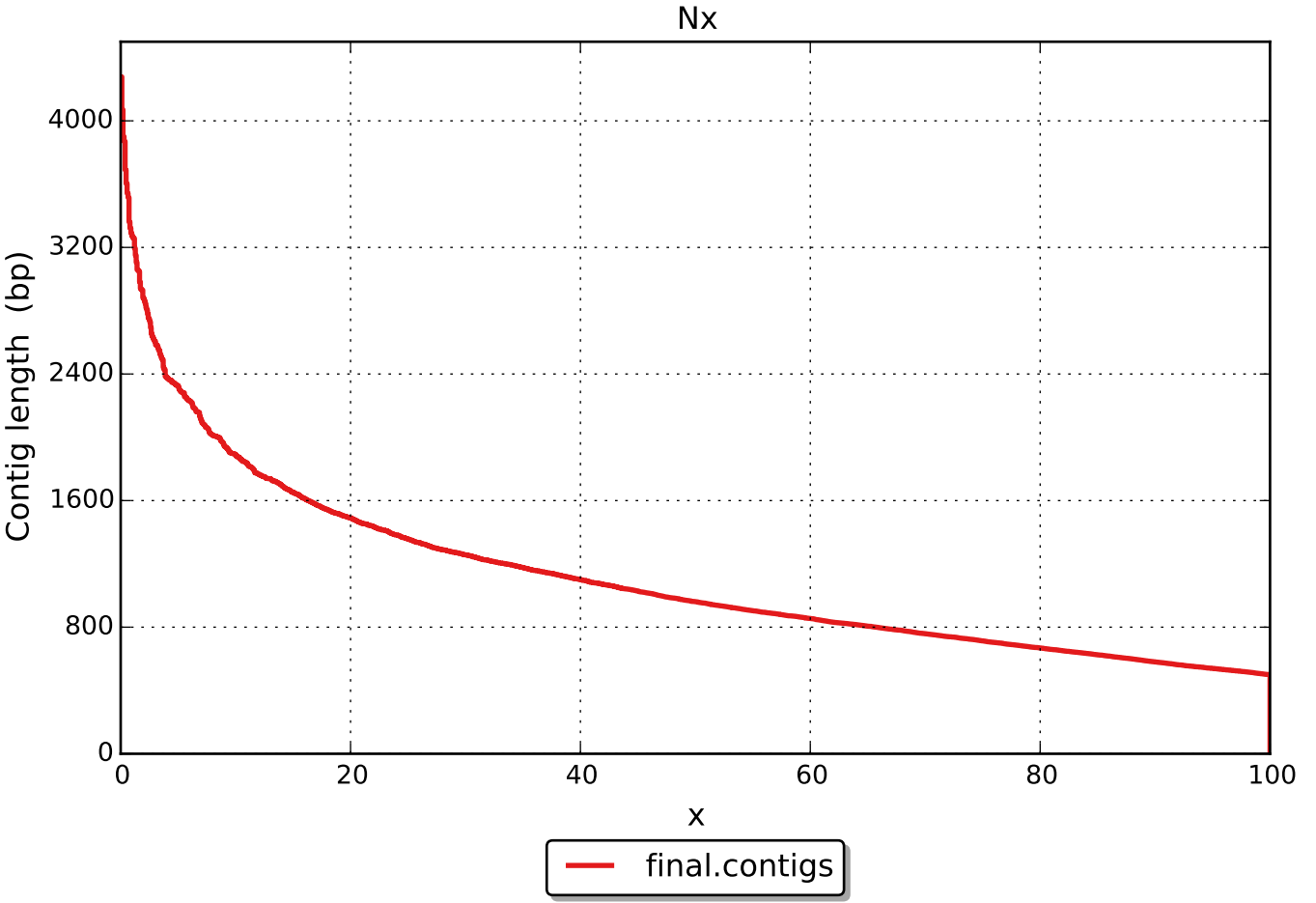
	final.contigs
# misassemblies	4
# relocations	3
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	4784
# local misassemblies	1
# mismatches	10506
# indels	2
# short indels	2
# long indels	0
Indels length	2

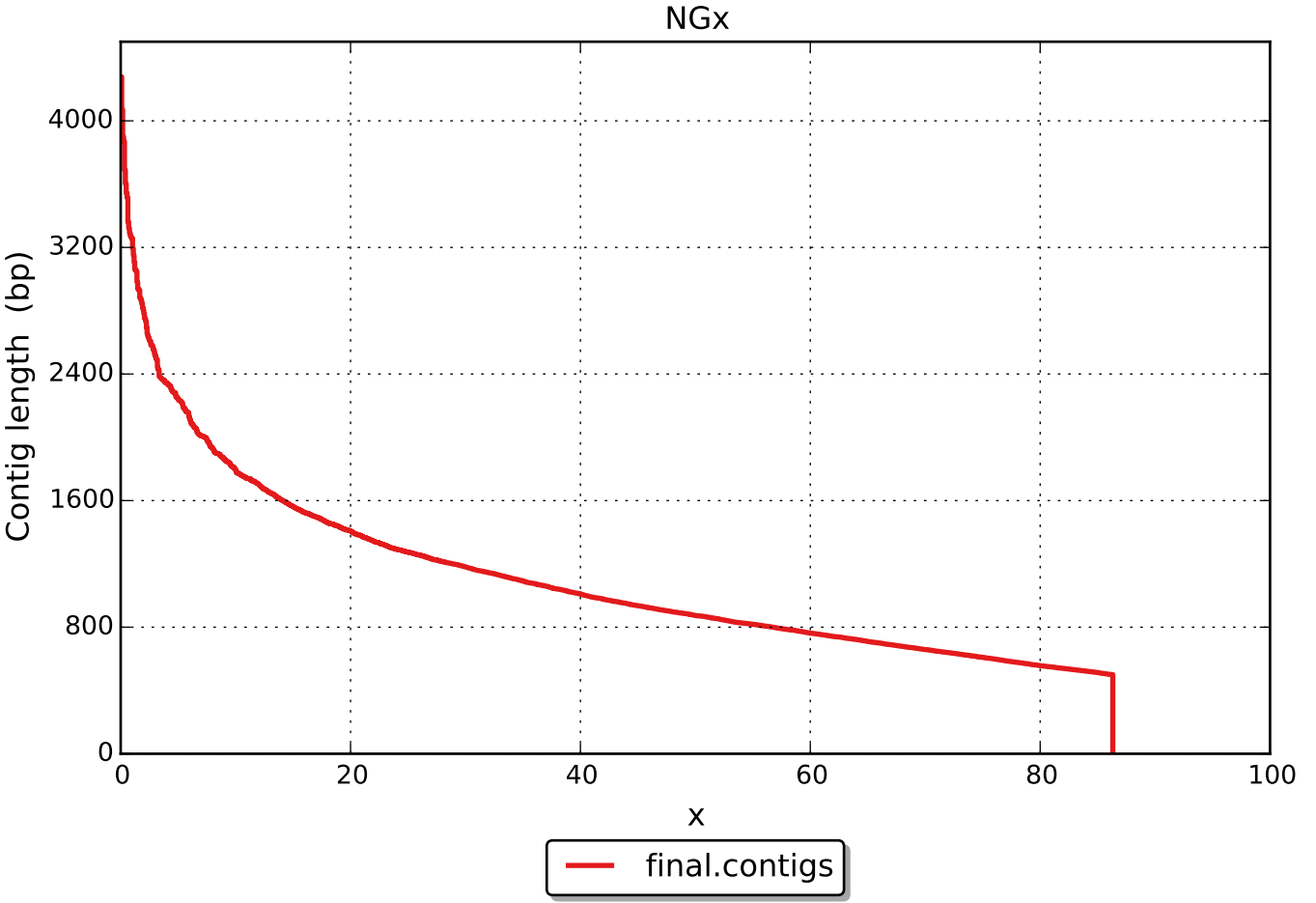
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

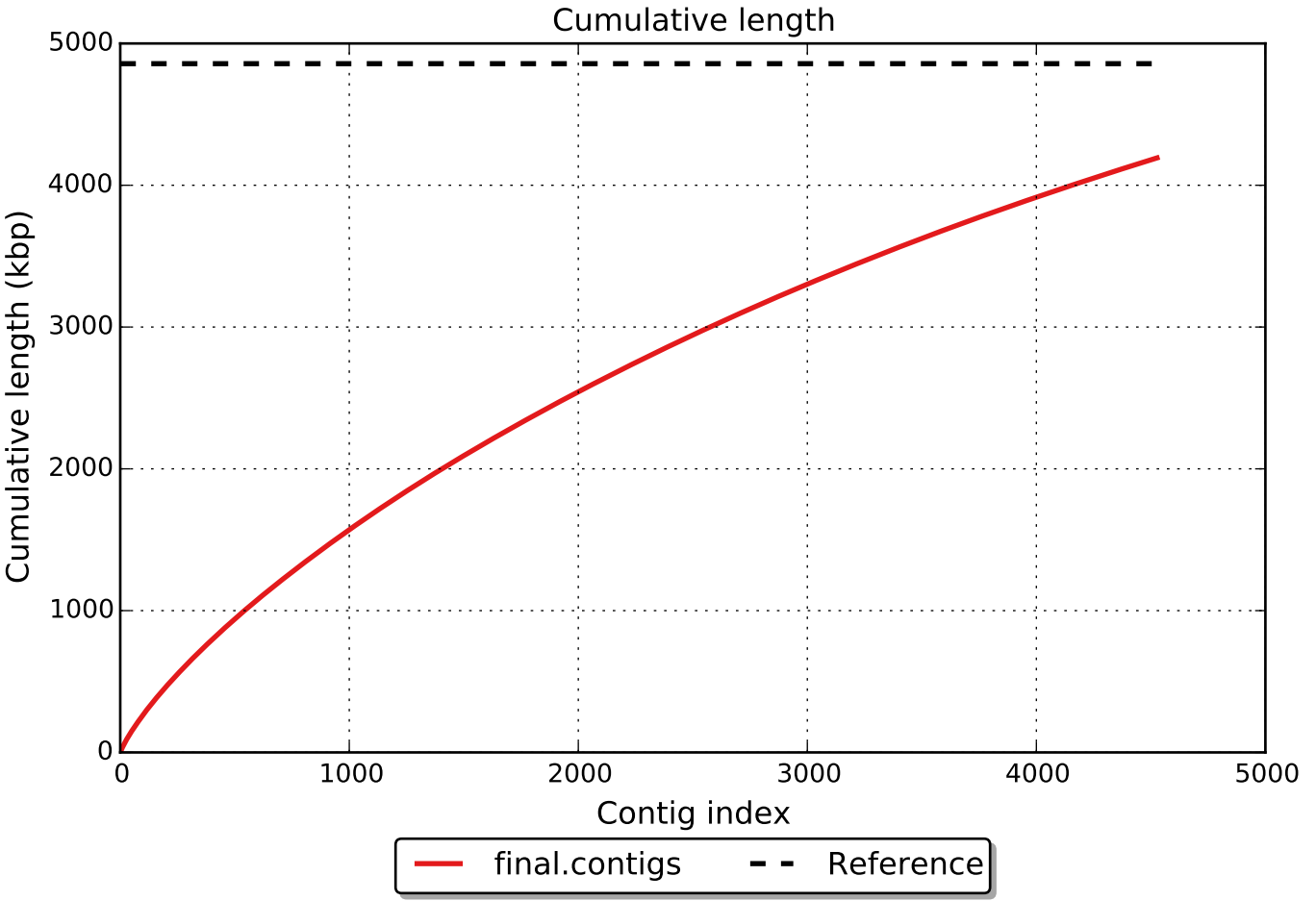
Unaligned report

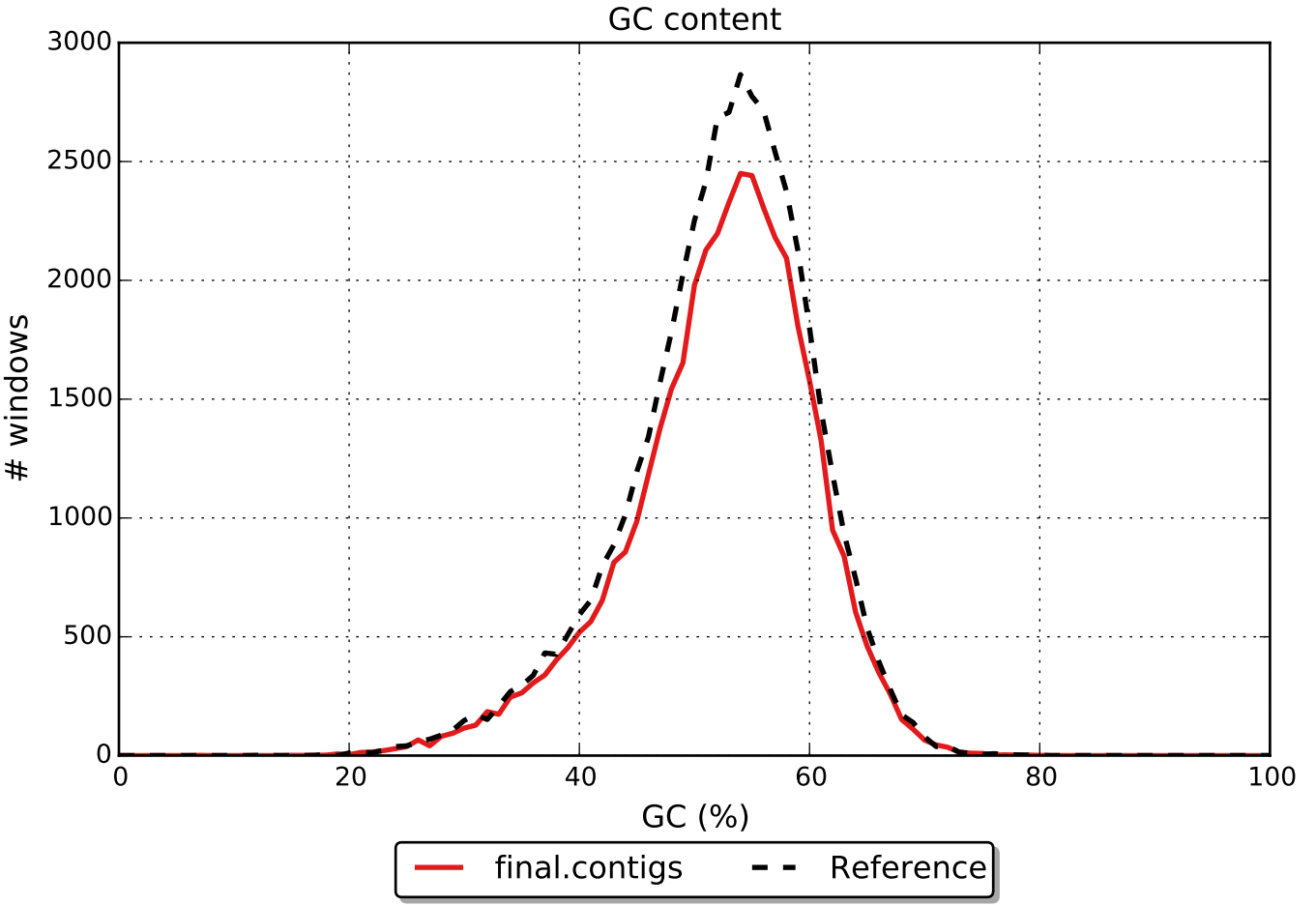
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

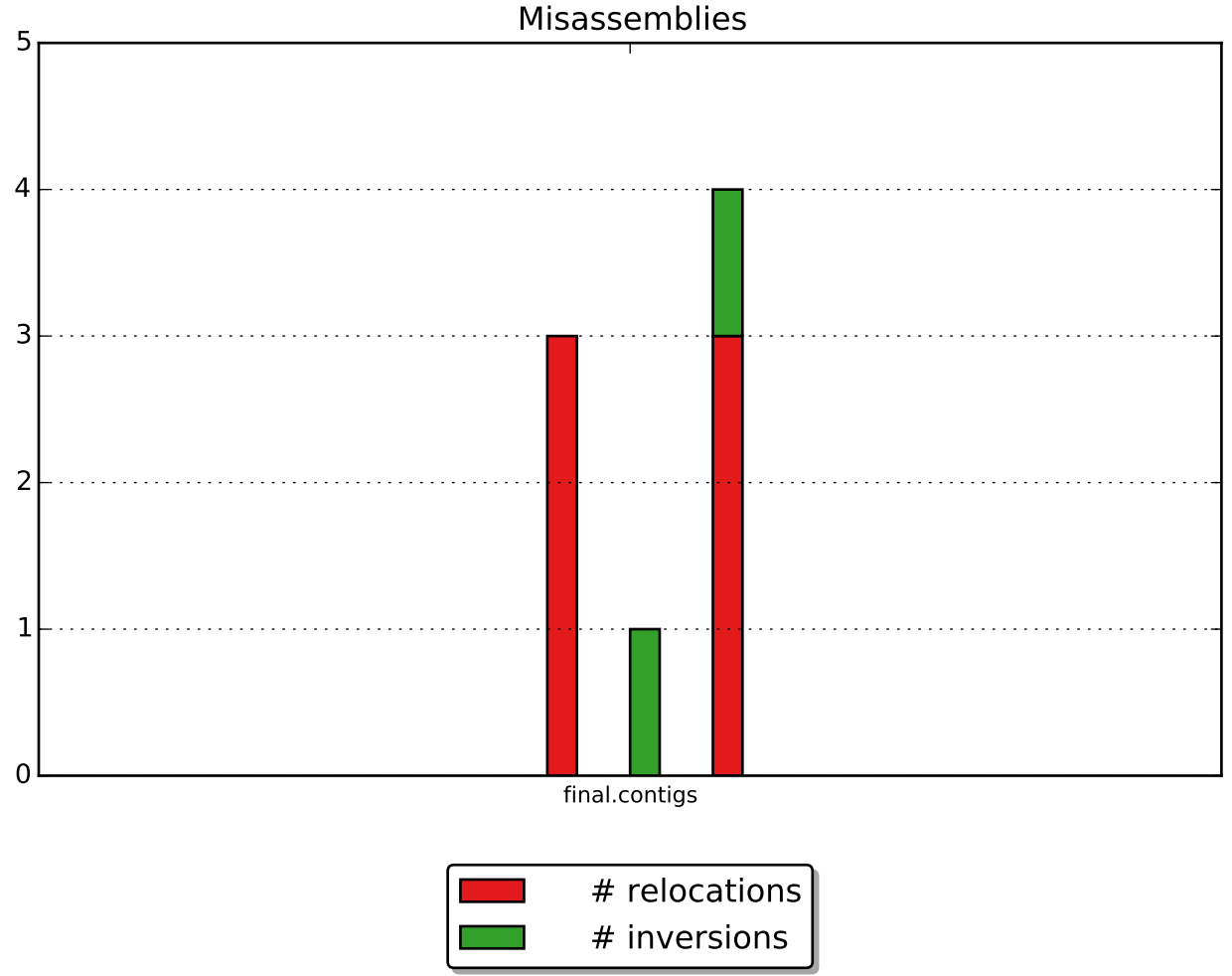
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

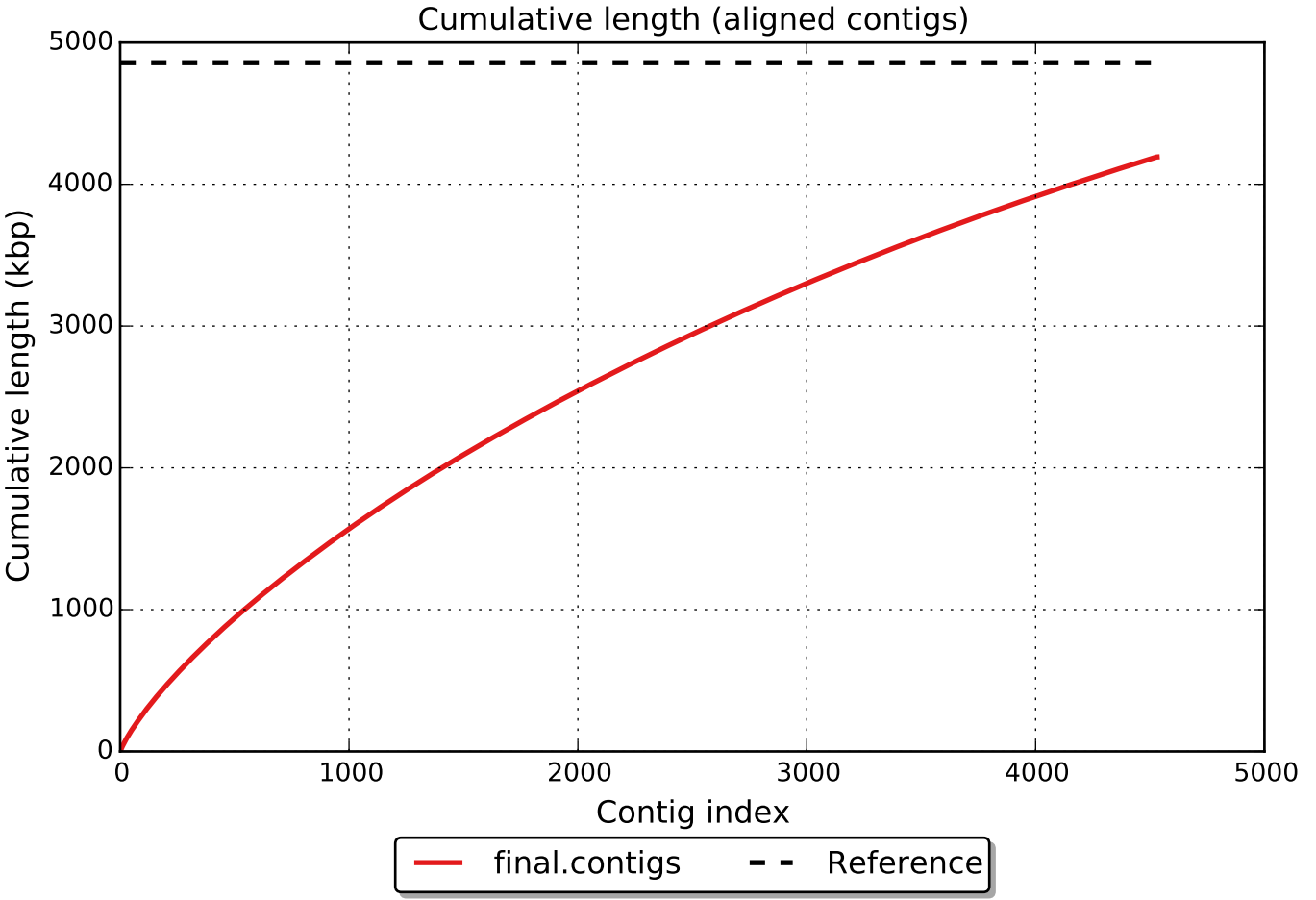

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

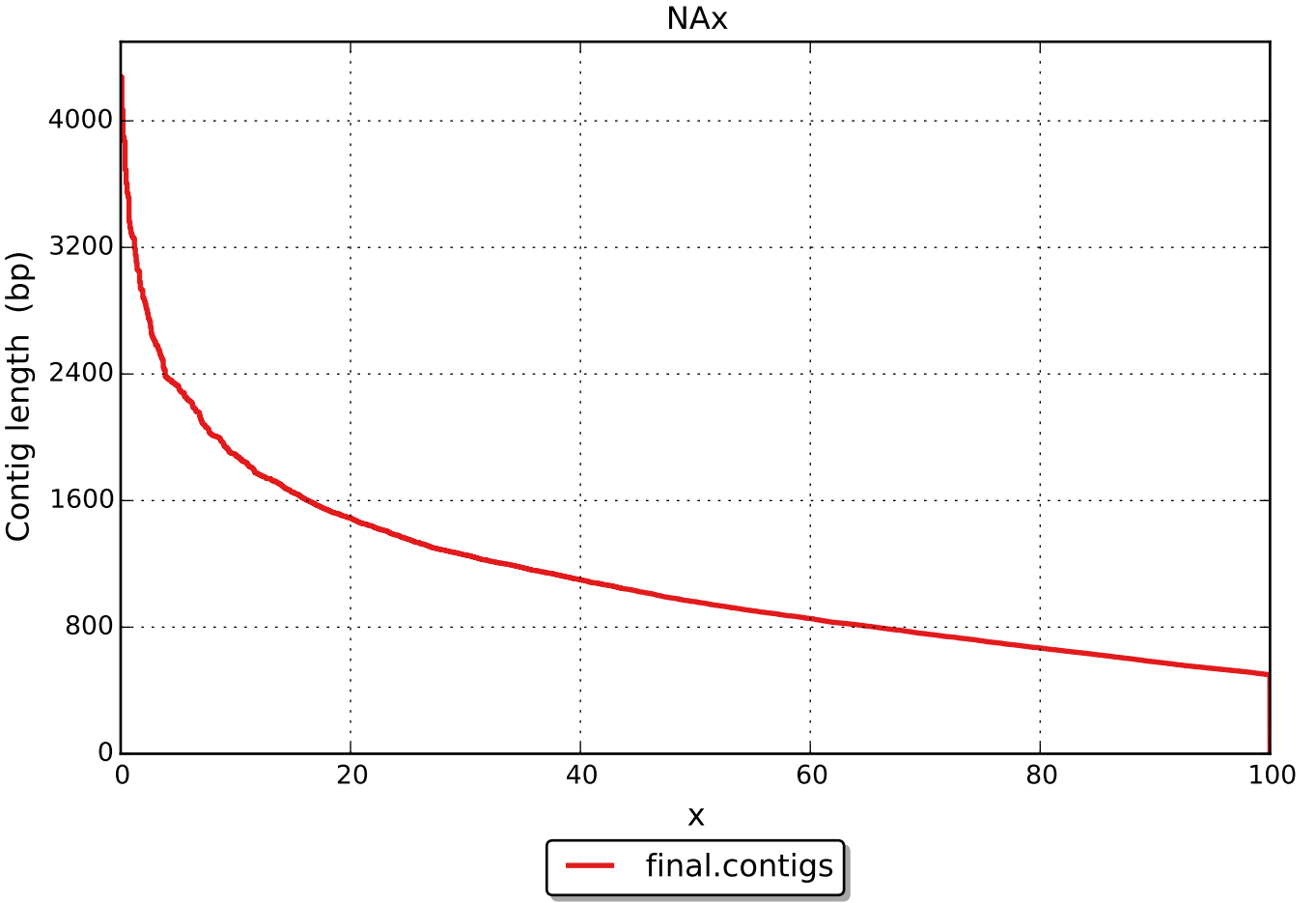

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

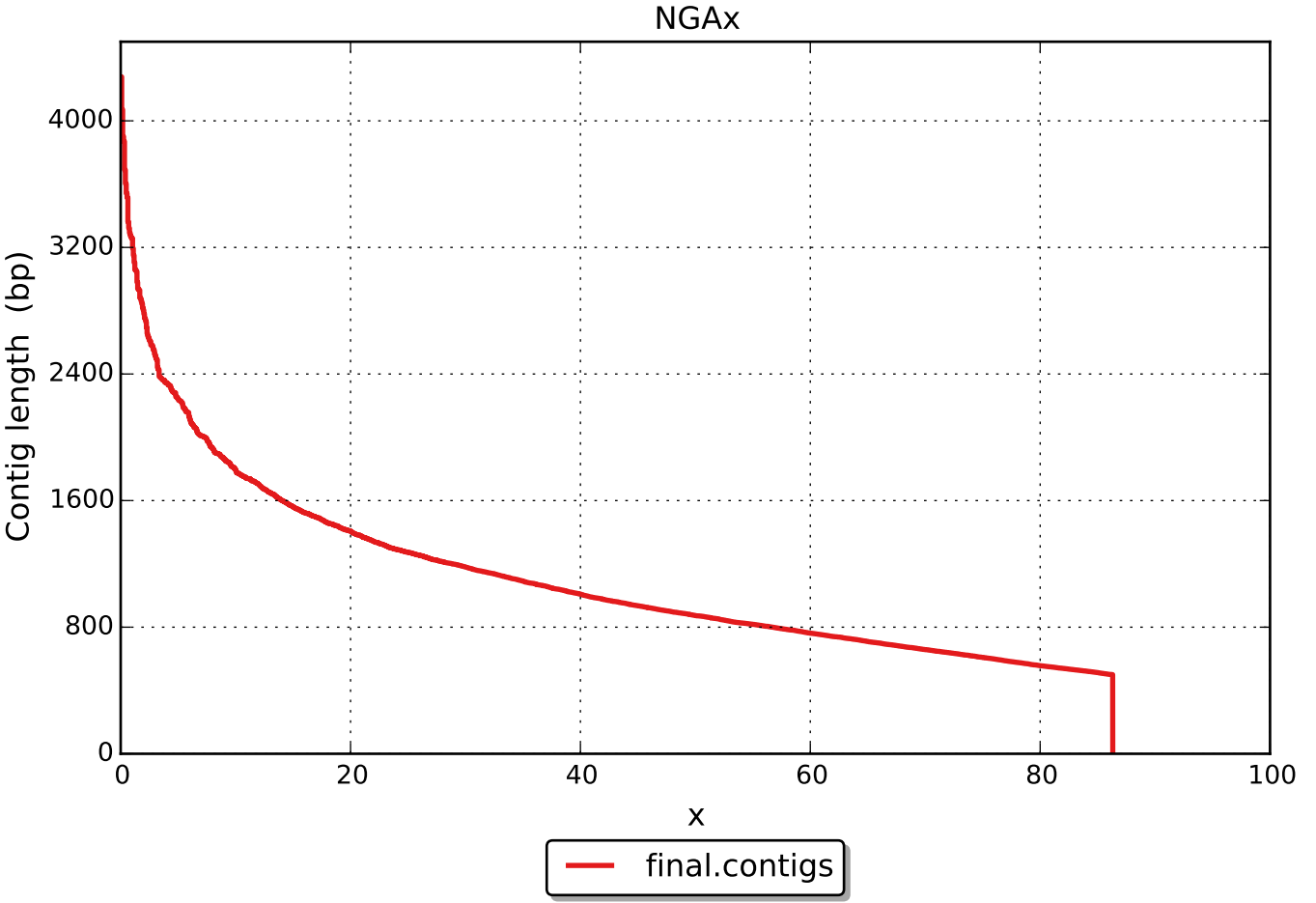

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1000
2000
3000
4000
5000
Contig index
final.contigs
Reference


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
relocations
inversions


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


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs