Report

	final.contigs
# contigs (>= 1000 bp)	150
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	180665
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2312
Largest contig	1993
Total length	1592427
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.79
N50	673
N75	577
L50	928
L75	1568
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	9513
# local misassemblies	0
# unaligned contigs	0 + 12 part
Unaligned length	747
Genome fraction (%)	33.596
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1539.92
# indels per 100 kbp	9.94
Largest alignment	1885
NA50	671
NGA50	-
NA75	575
LA50	931
LA75	1573

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

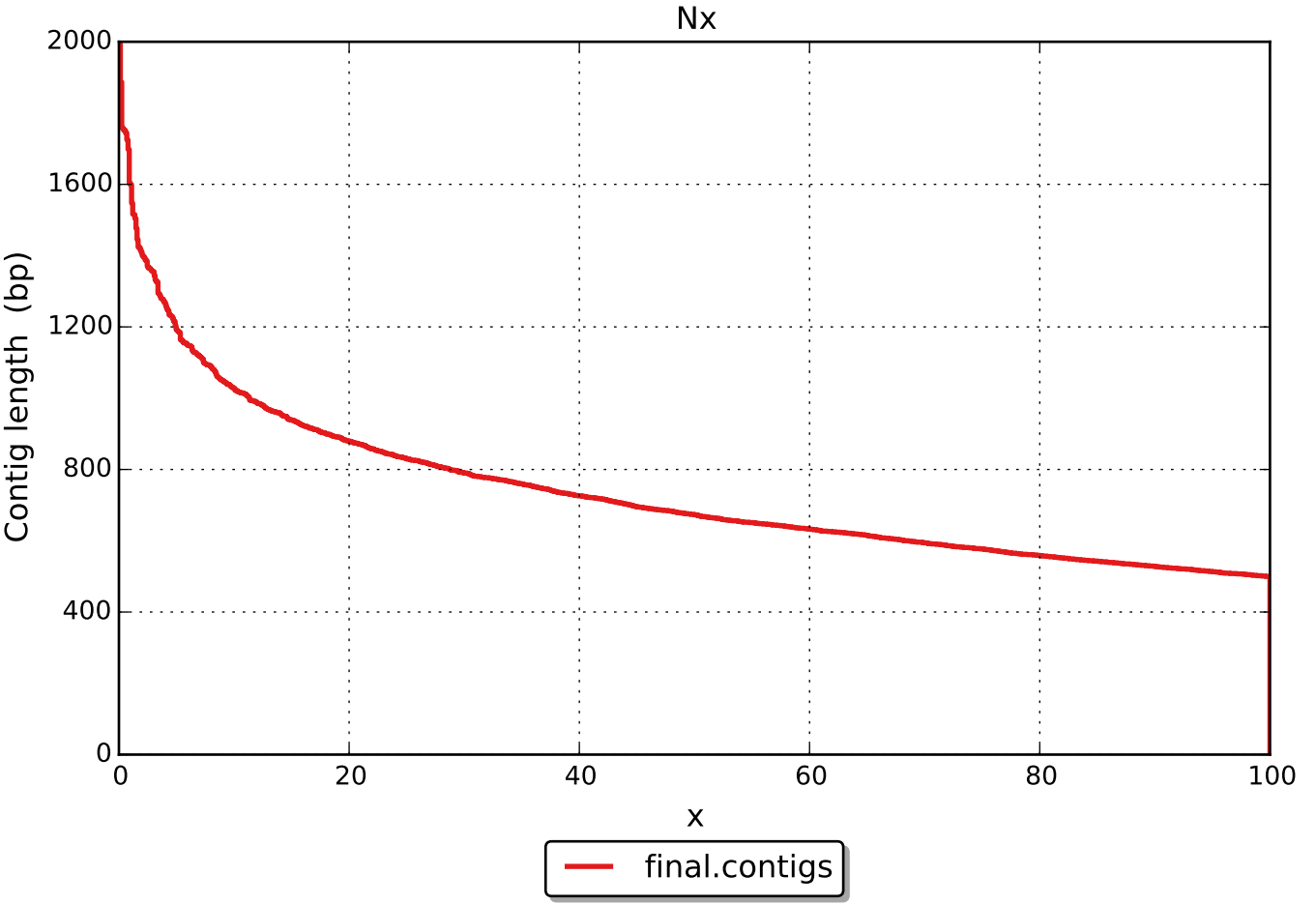
	final.contigs
# misassemblies	10
# relocations	9
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	9513
# local misassemblies	0
# mismatches	24014
# indels	155
# short indels	155
# long indels	0
Indels length	210

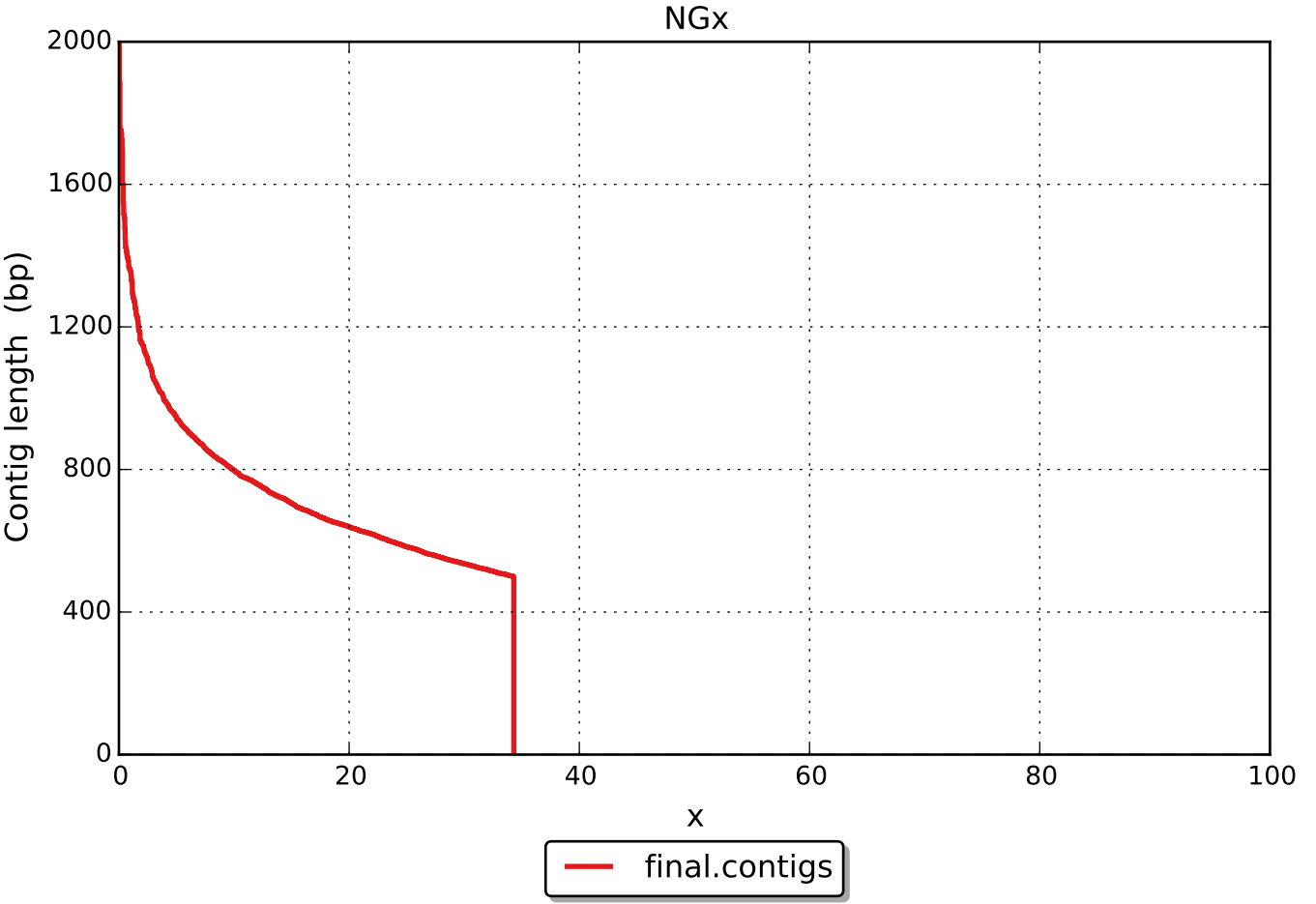
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

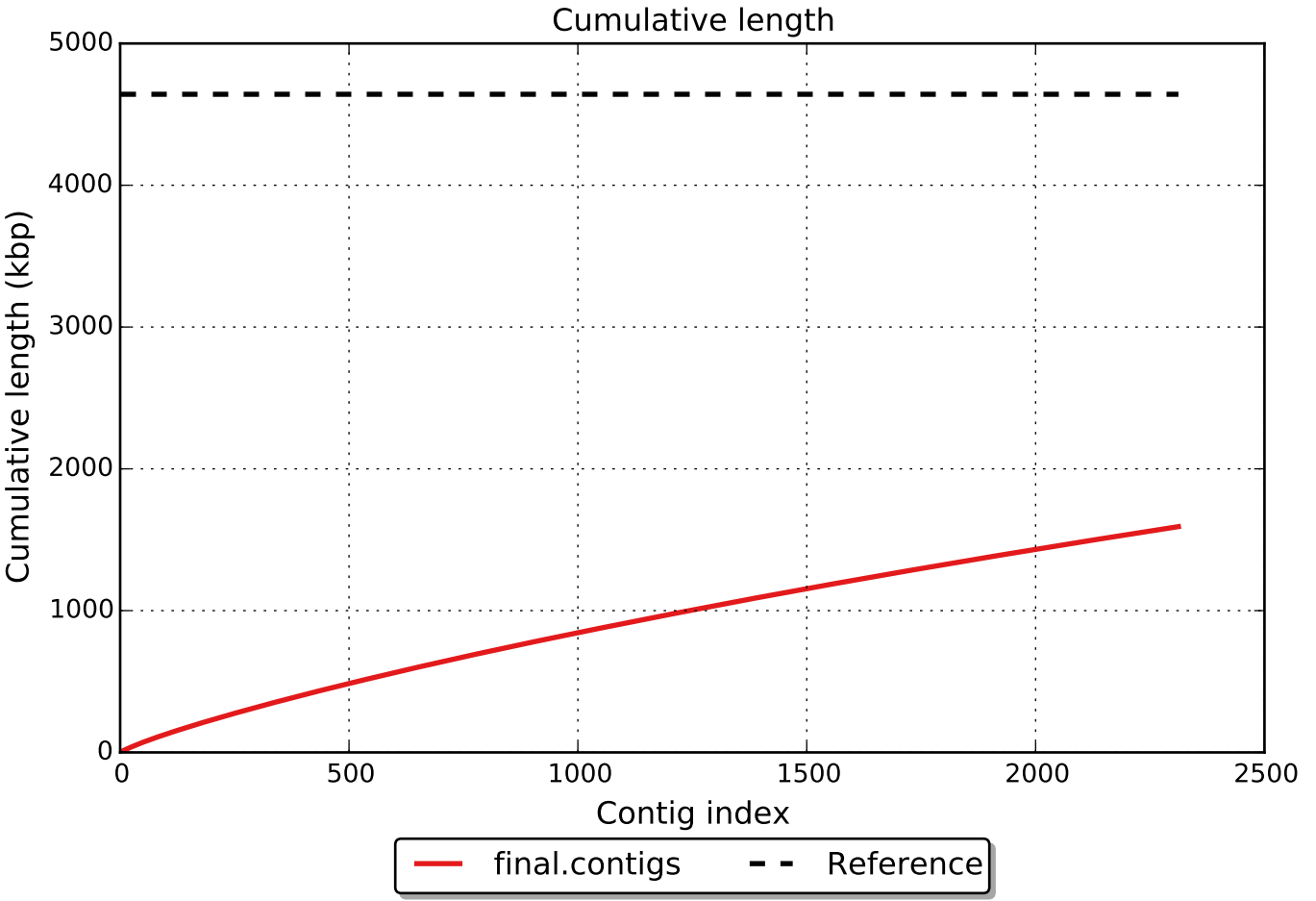
Unaligned report

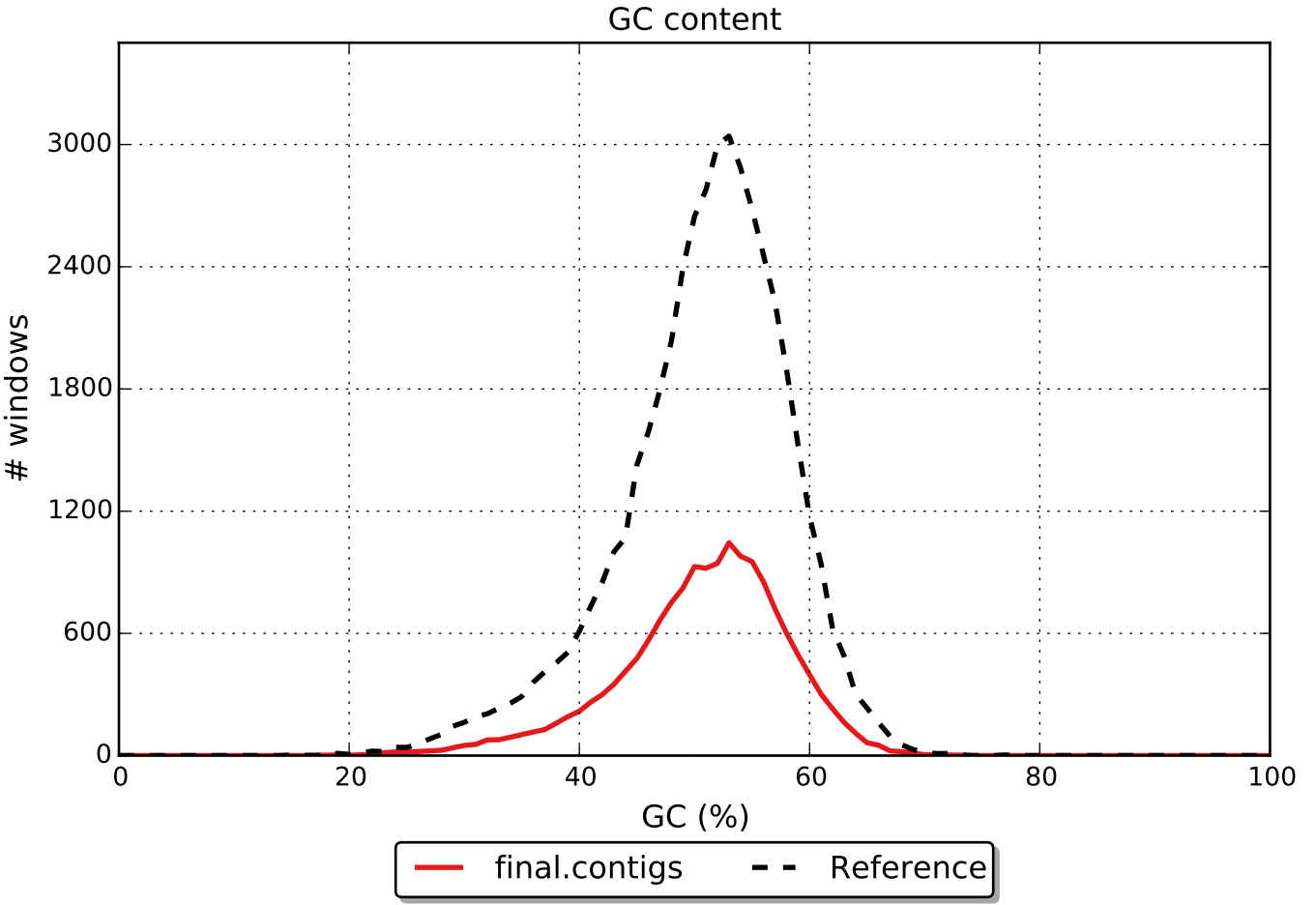
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
# with misassembly	0
# both parts are significant	0
Partially unaligned length	747
# N's	0

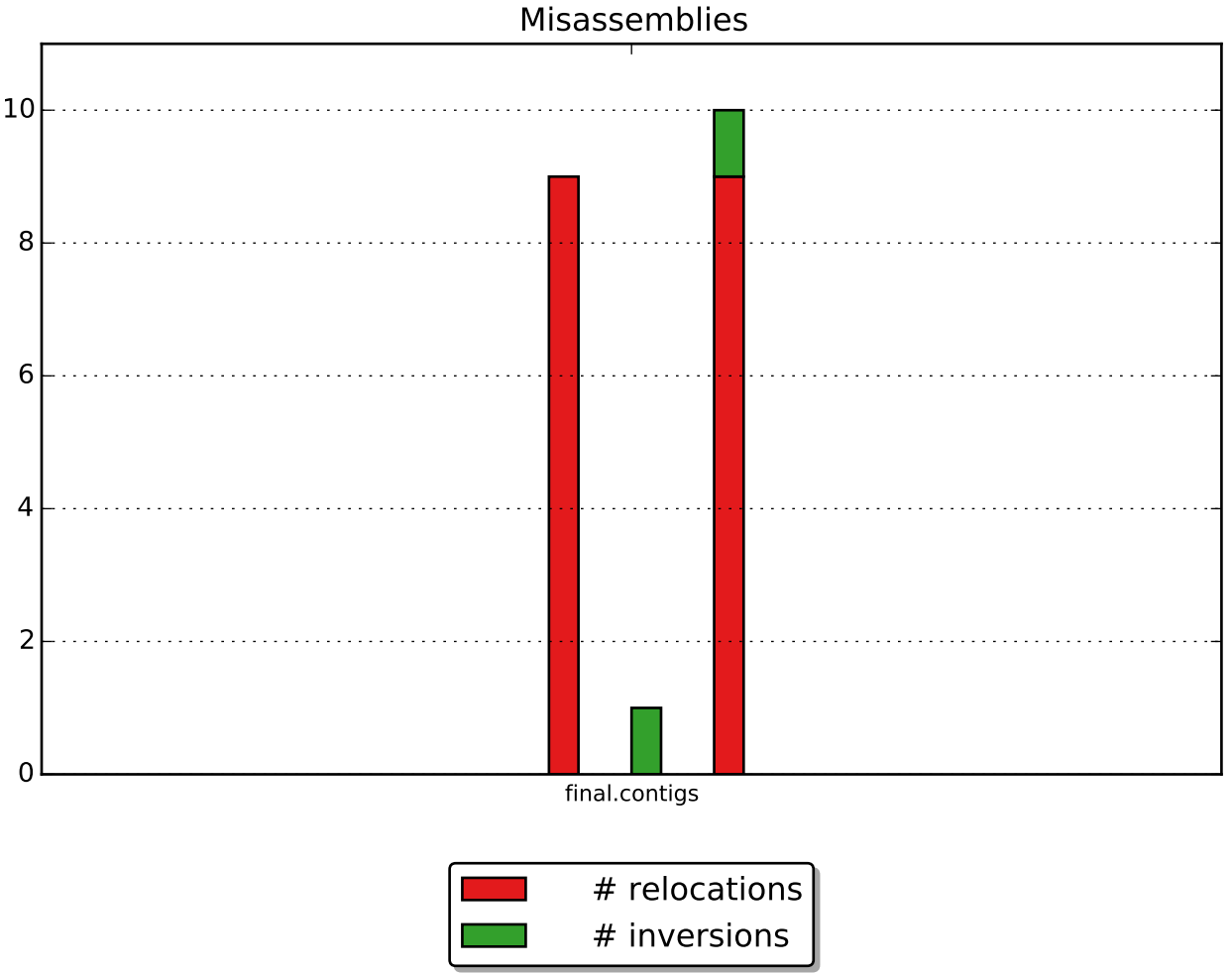
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

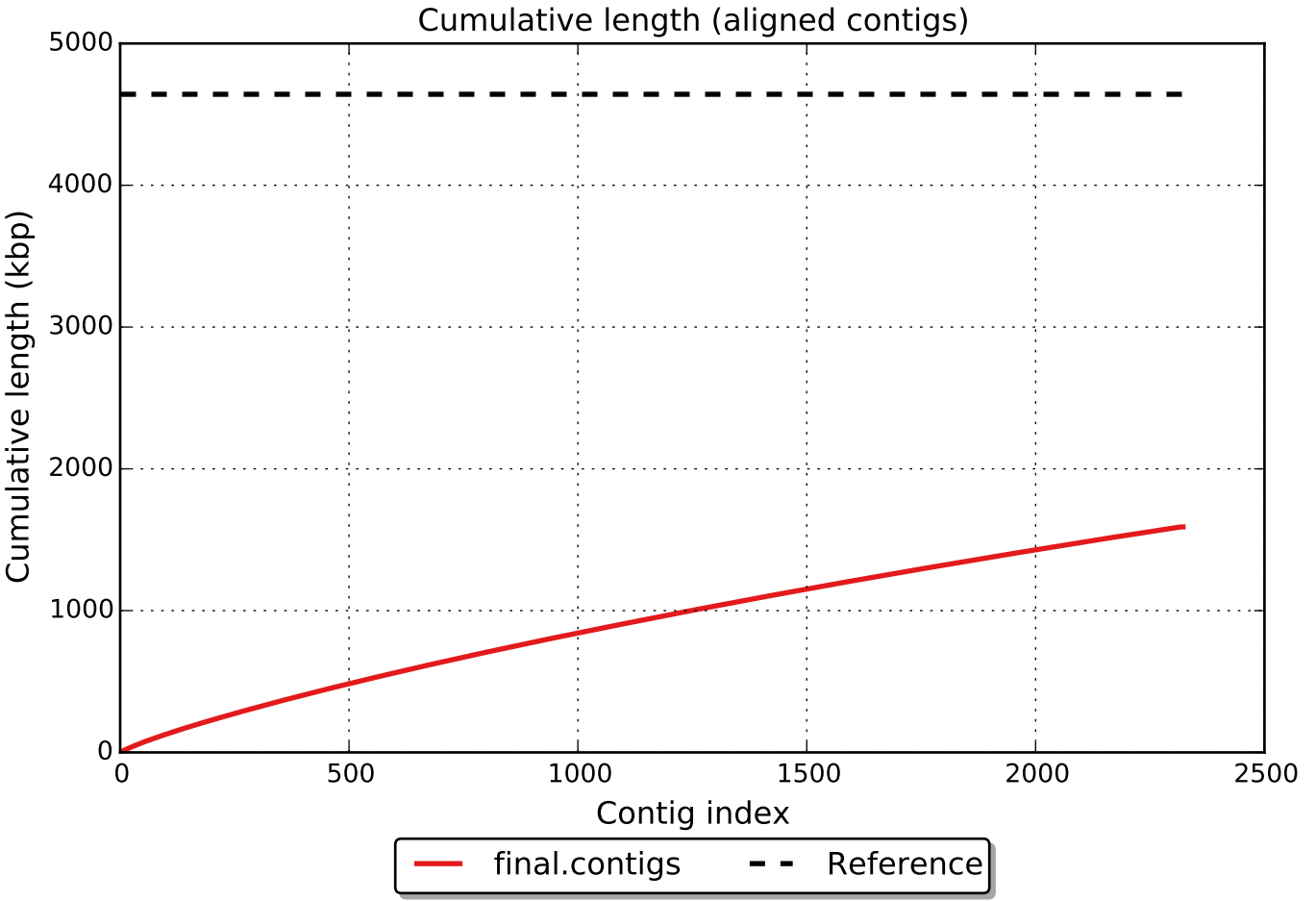

Nx
2000
1600
1200
800
400
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

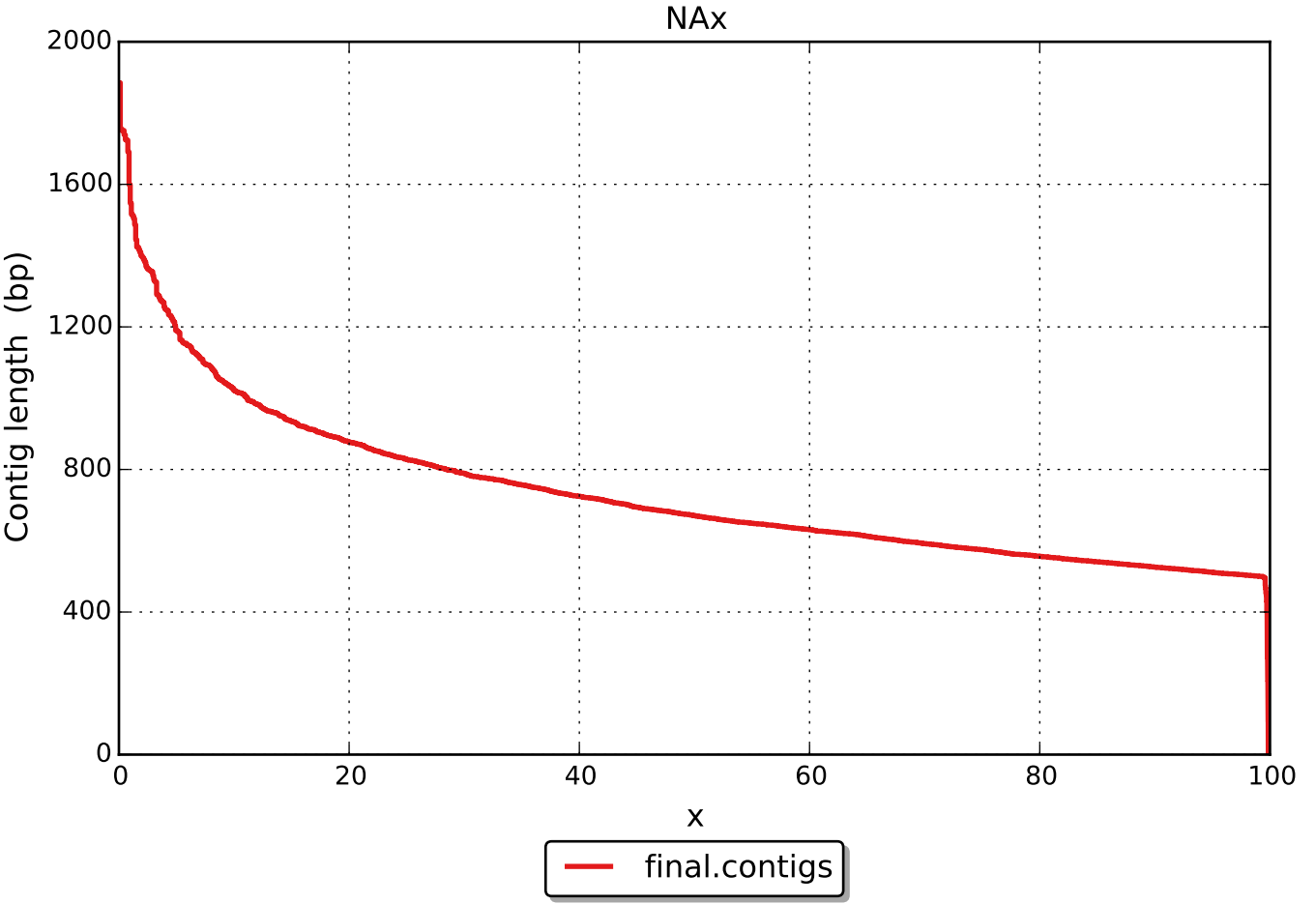

NGx
Contig length (bp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
final.contigs

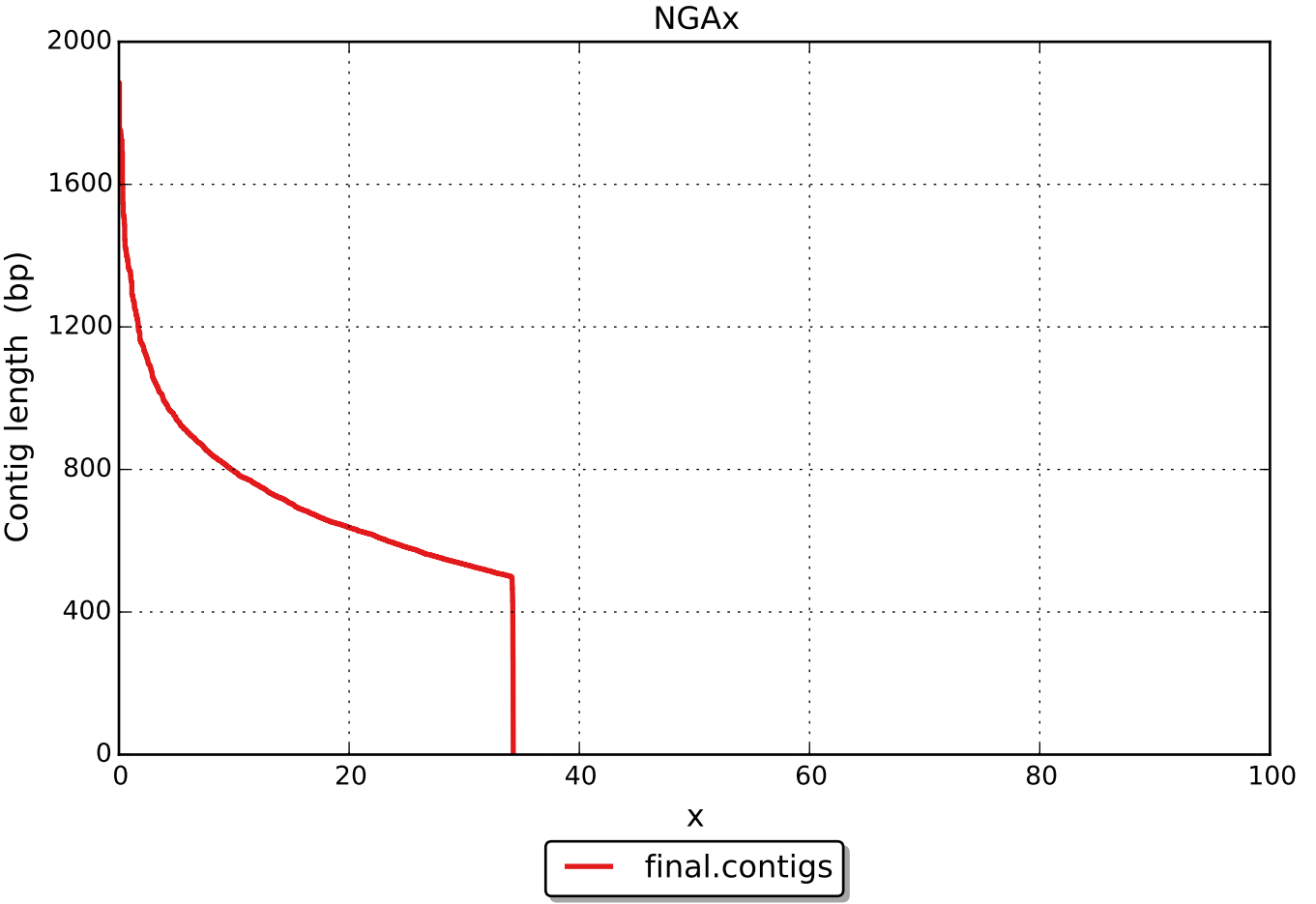

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
10
8
6
4
2
0
final.contigs
relocations
inversions


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
2000
1600
1200
800
400
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
2000
1600
1200
800
400
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs