Report

	scaffolds
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	1462865
Total length (>= 5000 bp)	1461795
Total length (>= 10000 bp)	1461795
Total length (>= 25000 bp)	1461795
Total length (>= 50000 bp)	1461795
# contigs	8
Largest contig	768359
Total length	1464394
Reference length	4641652
GC (%)	50.04
Reference GC (%)	50.78
N50	768359
N75	176518
L50	1
L75	3
# misassemblies	14
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	0
# unaligned contigs	0 + 4 part
Unaligned length	686848
Genome fraction (%)	13.248
Duplication ratio	1.264
# N's per 100 kbp	1.16
# mismatches per 100 kbp	1410.89
# indels per 100 kbp	1.46
Largest alignment	111117
NGA50	-

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

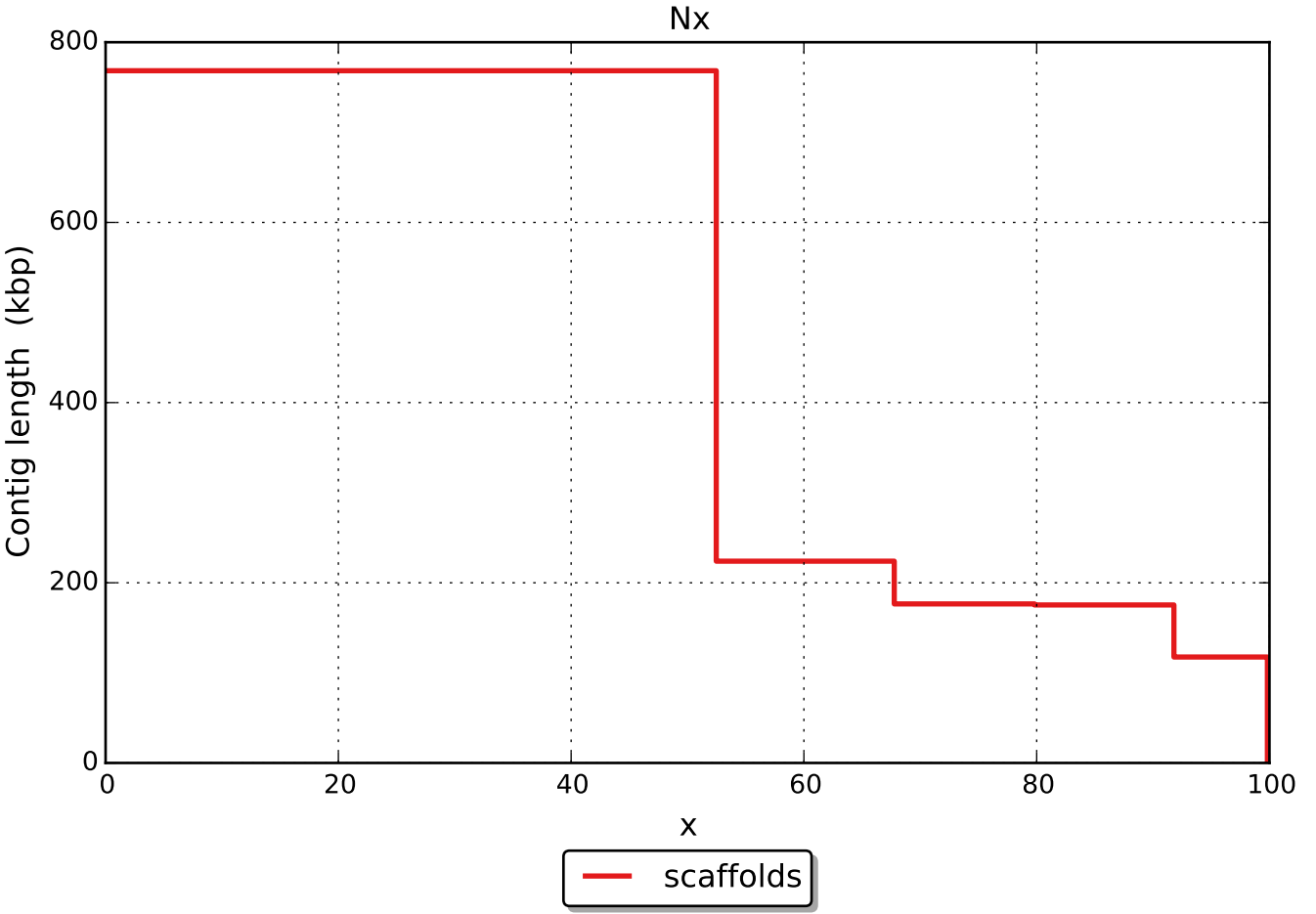
	scaffolds
# misassemblies	14
# relocations	10
# translocations	0
# inversions	4
# possibly misassembled contigs	3
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	0
# mismatches	8676
# indels	9
# short indels	9
# long indels	0
Indels length	12

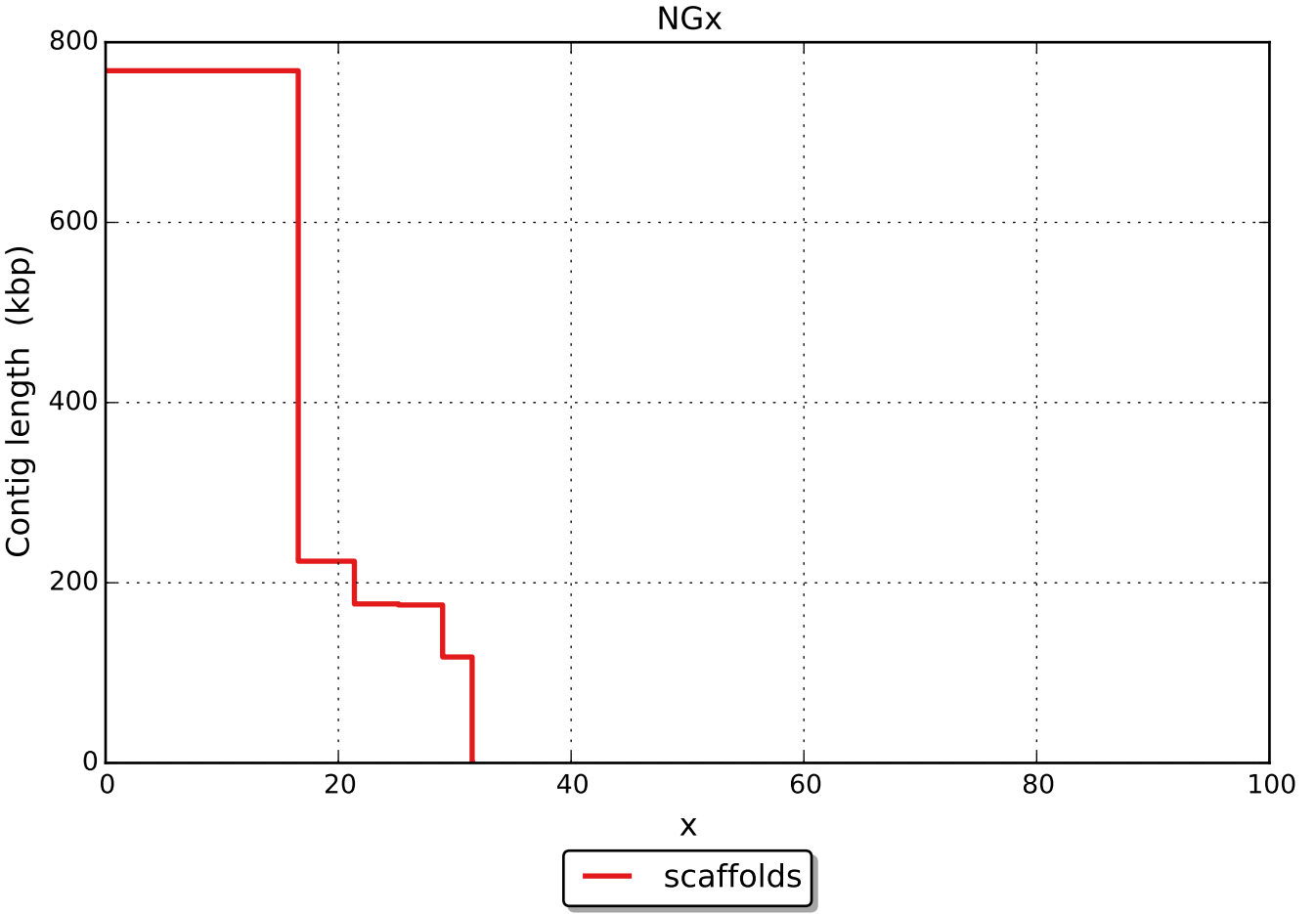
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

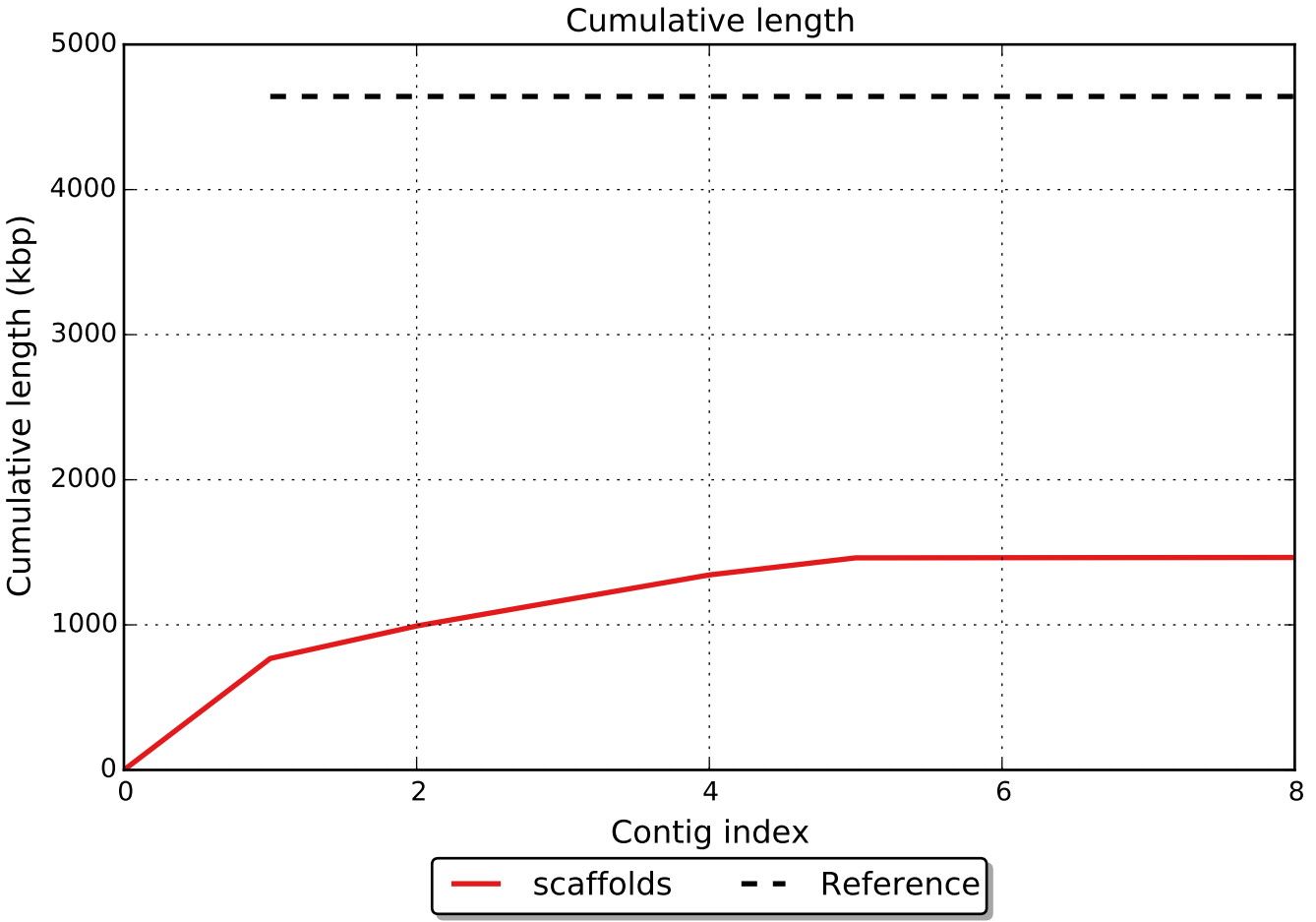
Unaligned report

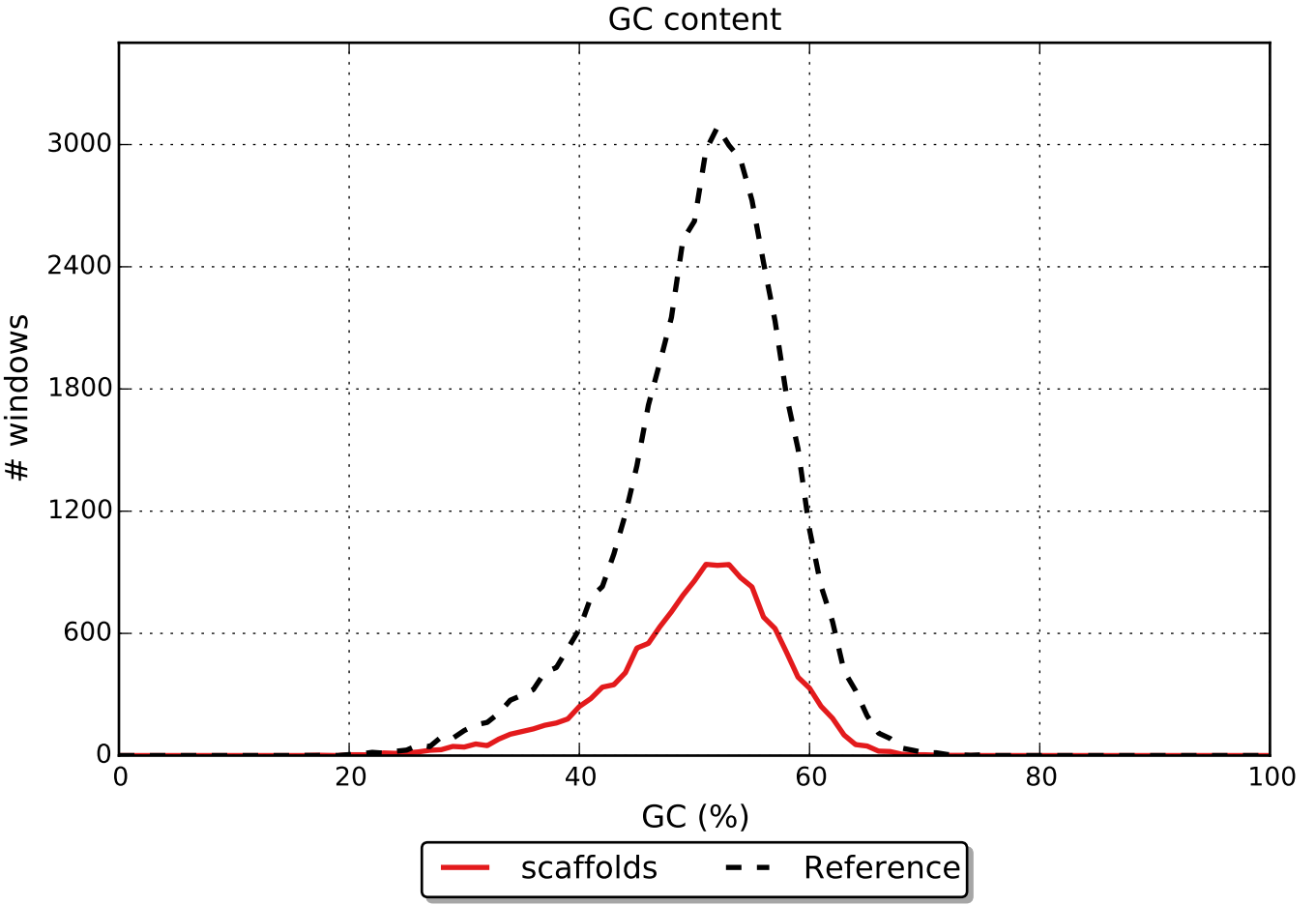
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	1
# both parts are significant	2
Partially unaligned length	686848
# N's	17

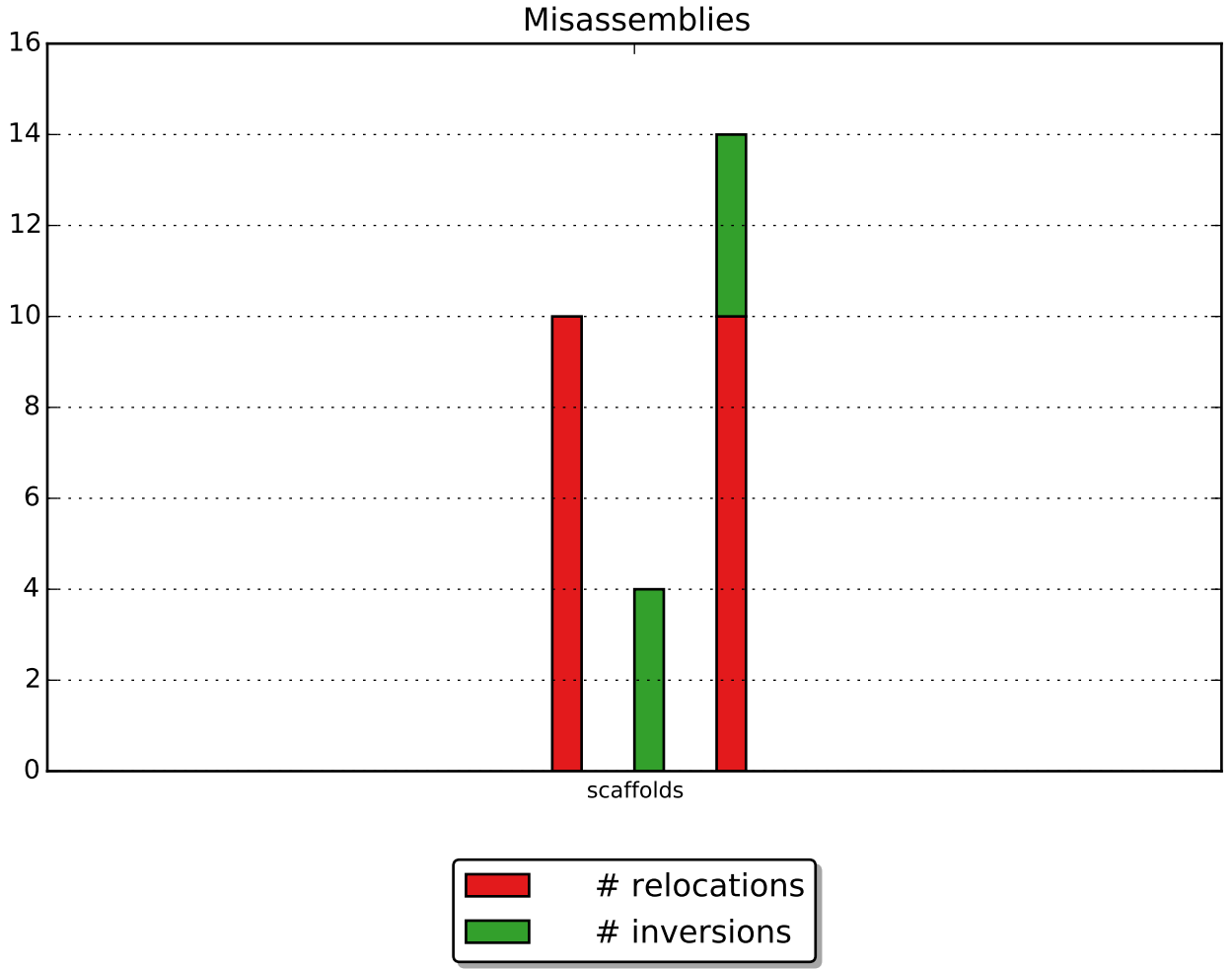
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

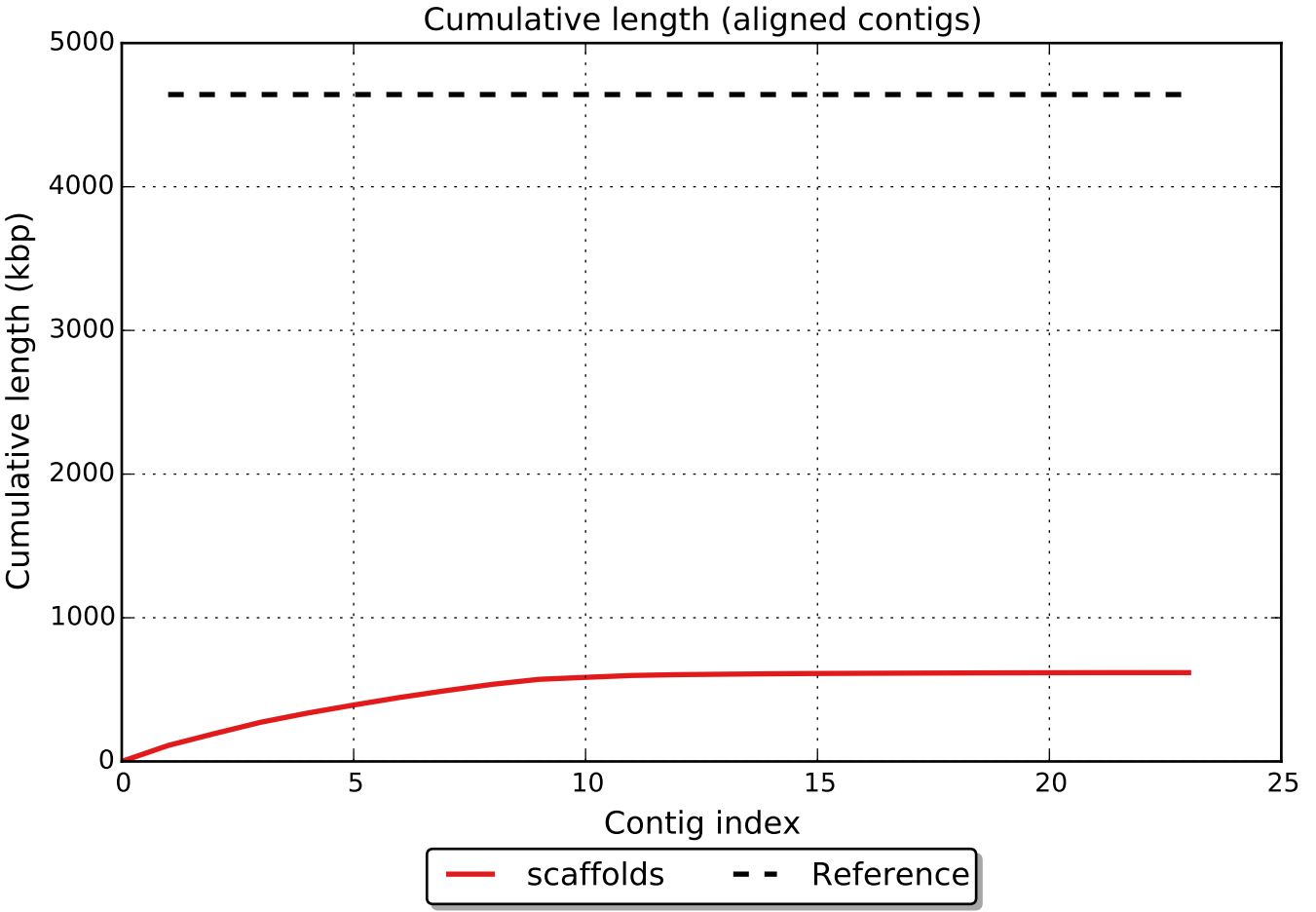

Nx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

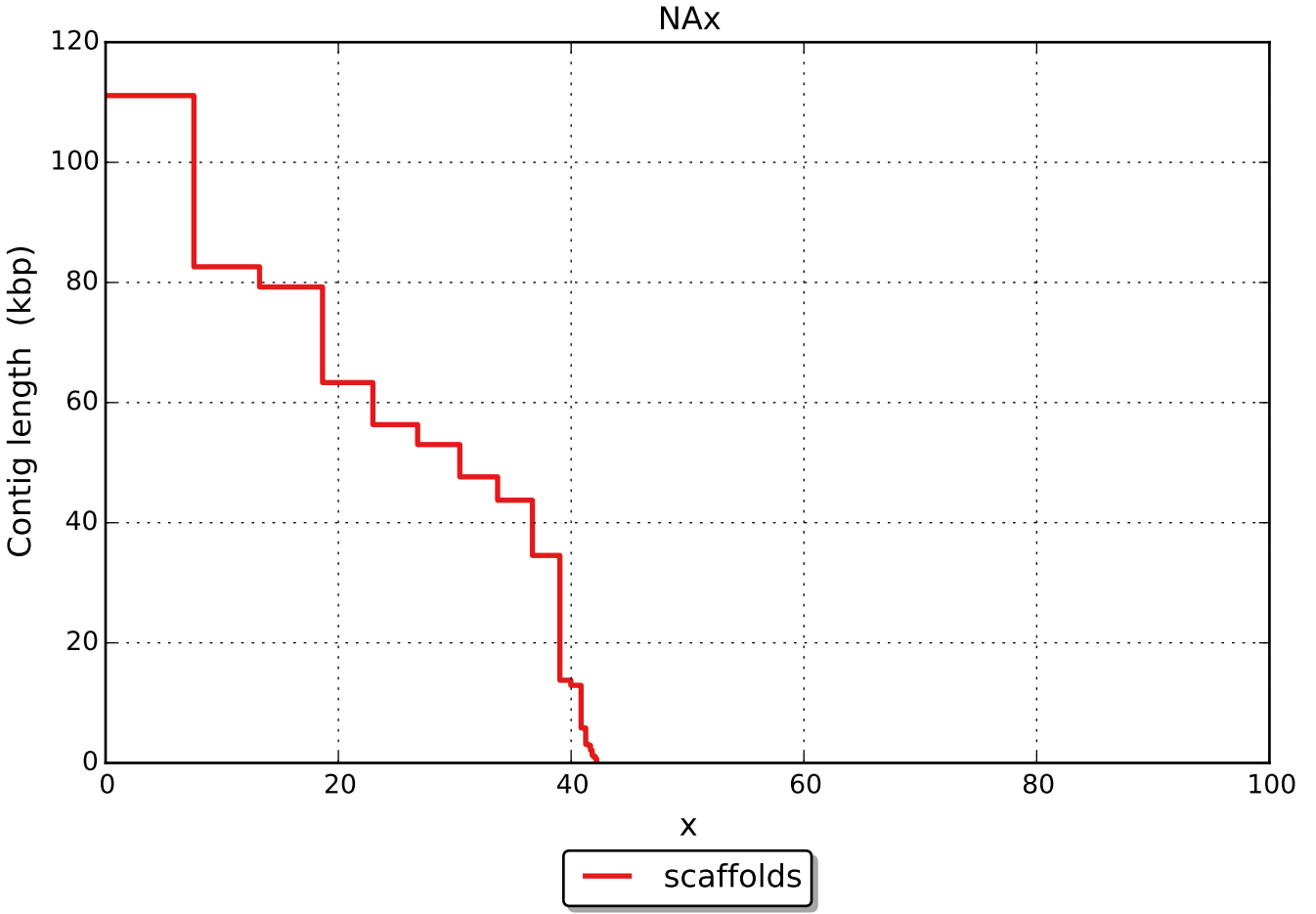

NGx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

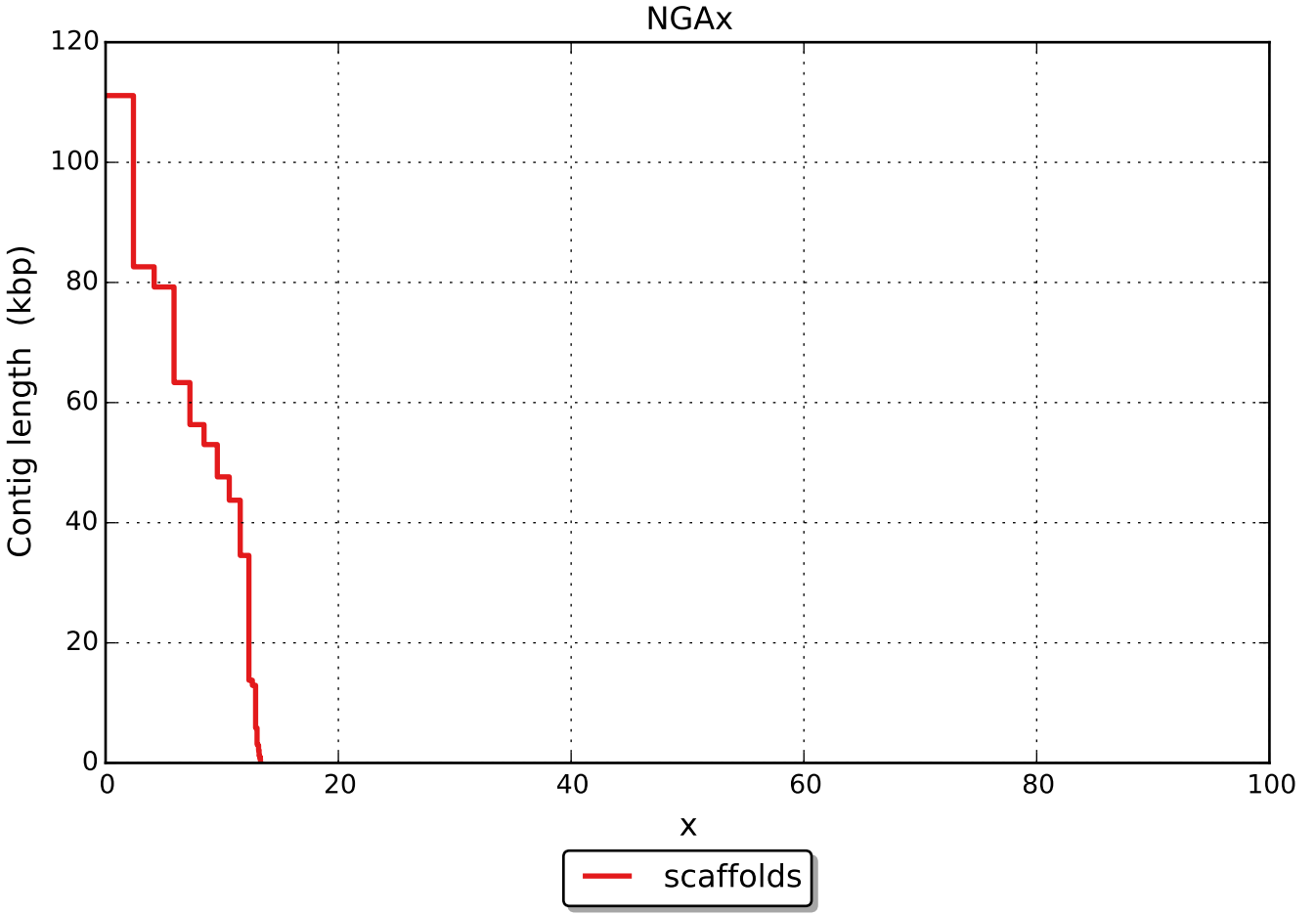

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
2
4
6
8
Contig index
scaffolds
Reference


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


Misassemblies
16
14
12
10
8
6
4
2
0
scaffolds
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
scaffolds
Reference


NAx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
120
100
80
60
40
20
0
0
20
40
60
80
100
x
scaffolds