Report

	scaffolds
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	7
Total length (>= 1000 bp)	1321565
Total length (>= 5000 bp)	1320131
Total length (>= 10000 bp)	1320131
Total length (>= 25000 bp)	1304742
Total length (>= 50000 bp)	1304742
# contigs	10
Largest contig	284062
Total length	1322145
Reference length	4641652
GC (%)	50.86
Reference GC (%)	50.78
N50	210555
N75	166049
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 8 part
Unaligned length	1308077
Genome fraction (%)	0.303
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4528.01
# indels per 100 kbp	0.00
Largest alignment	2929
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

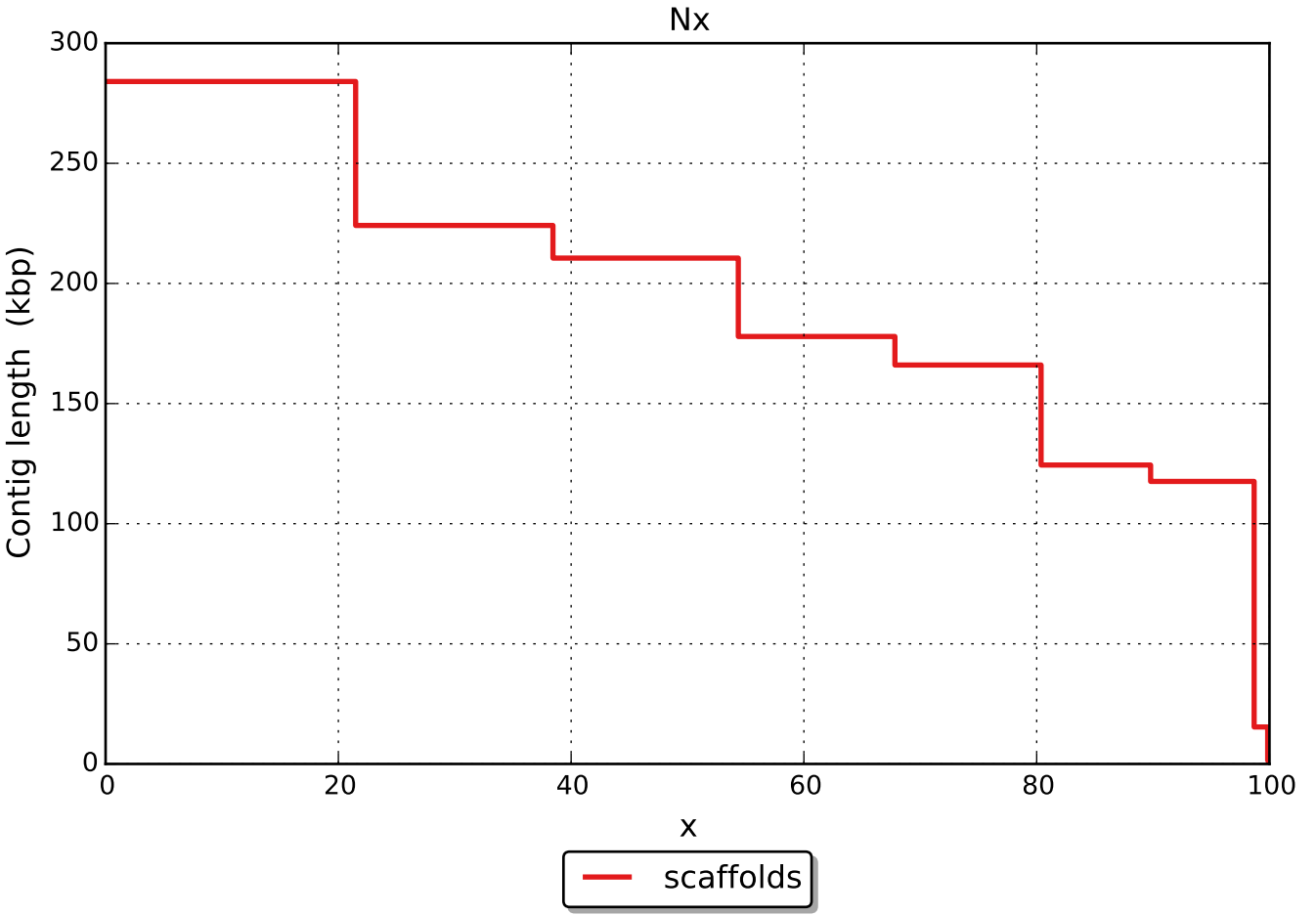
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	6
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	637
# indels	0
# short indels	0
# long indels	0
Indels length	0

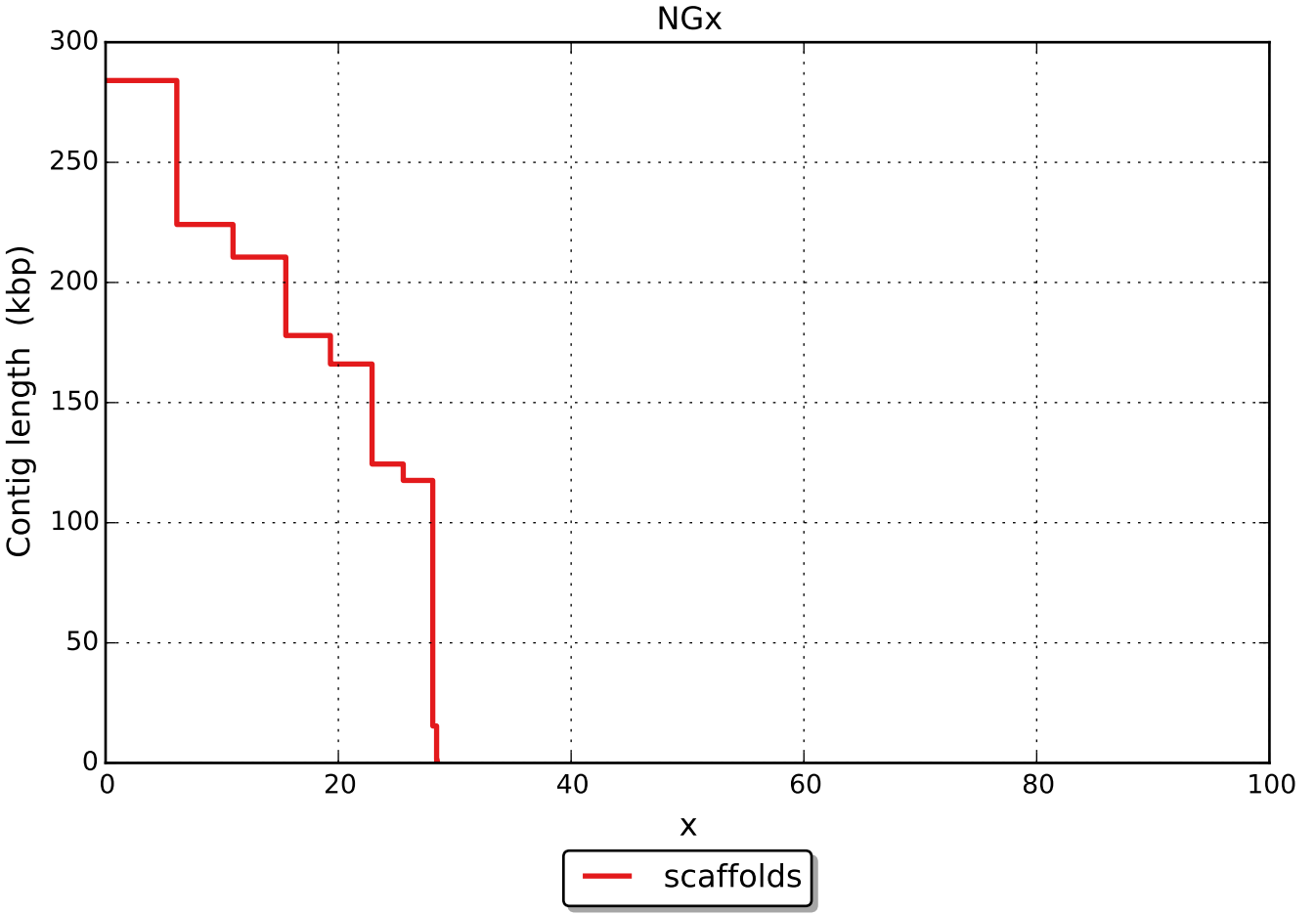
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

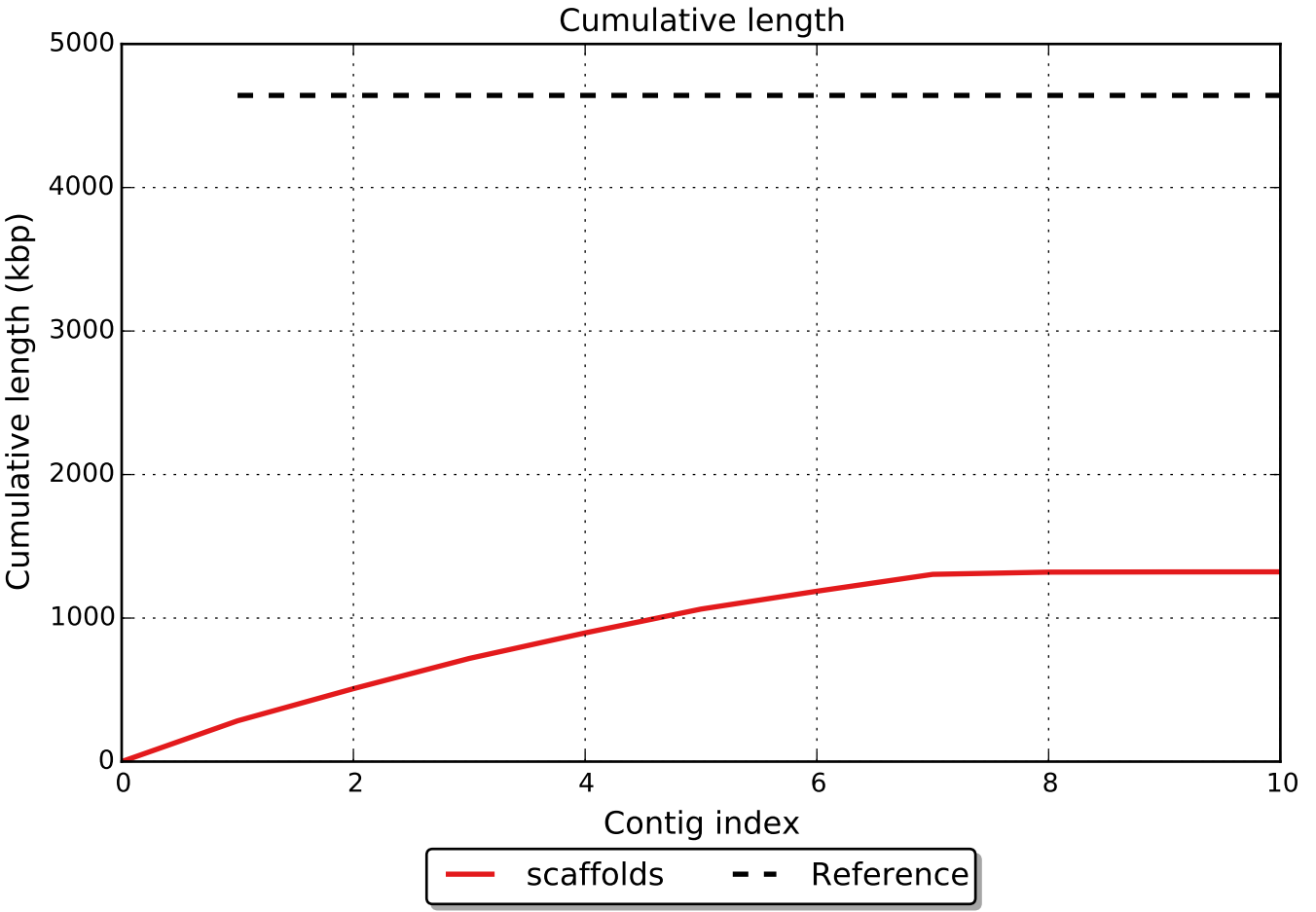
Unaligned report

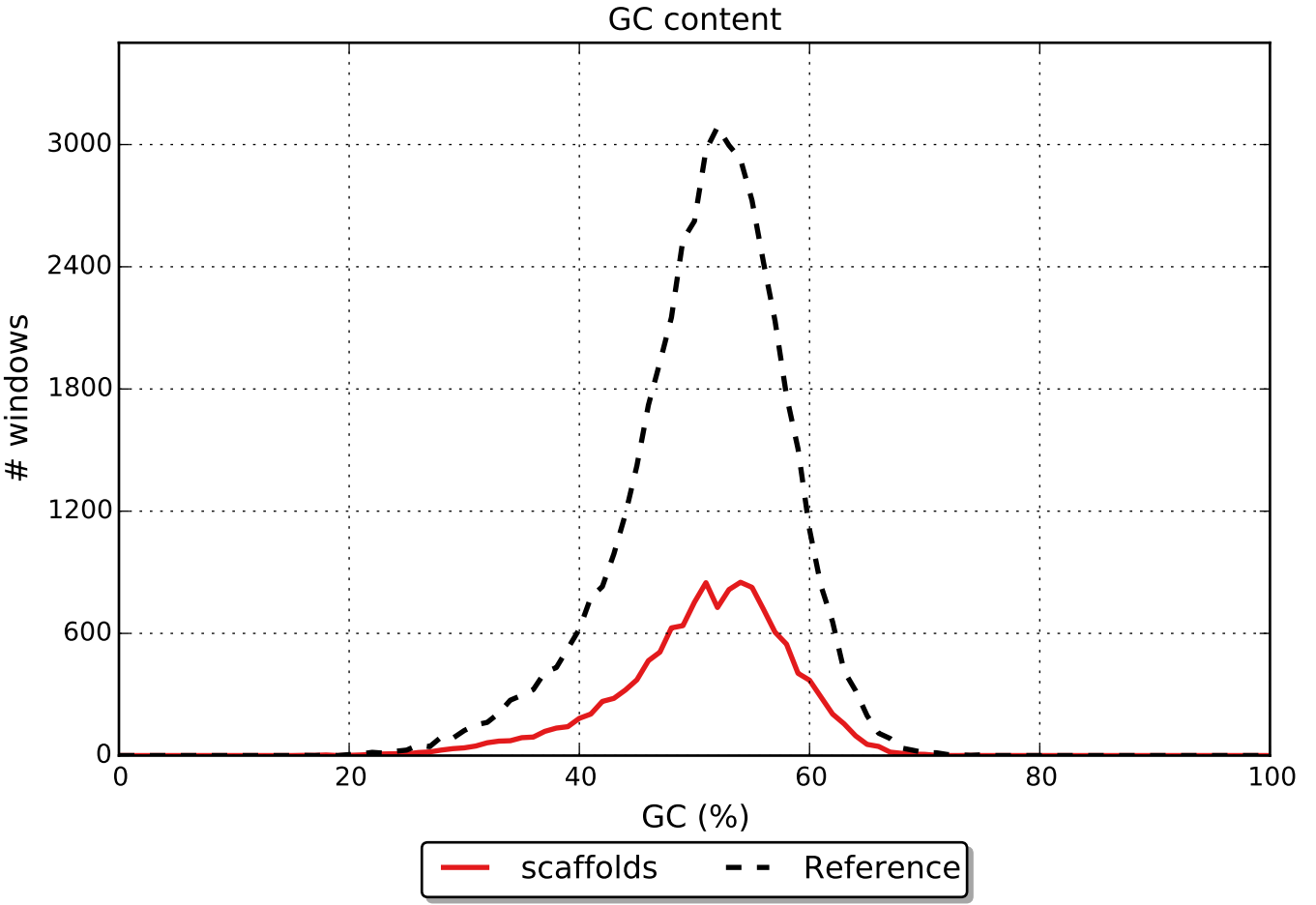
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
# with misassembly	3
# both parts are significant	6
Partially unaligned length	1308077
# N's	0

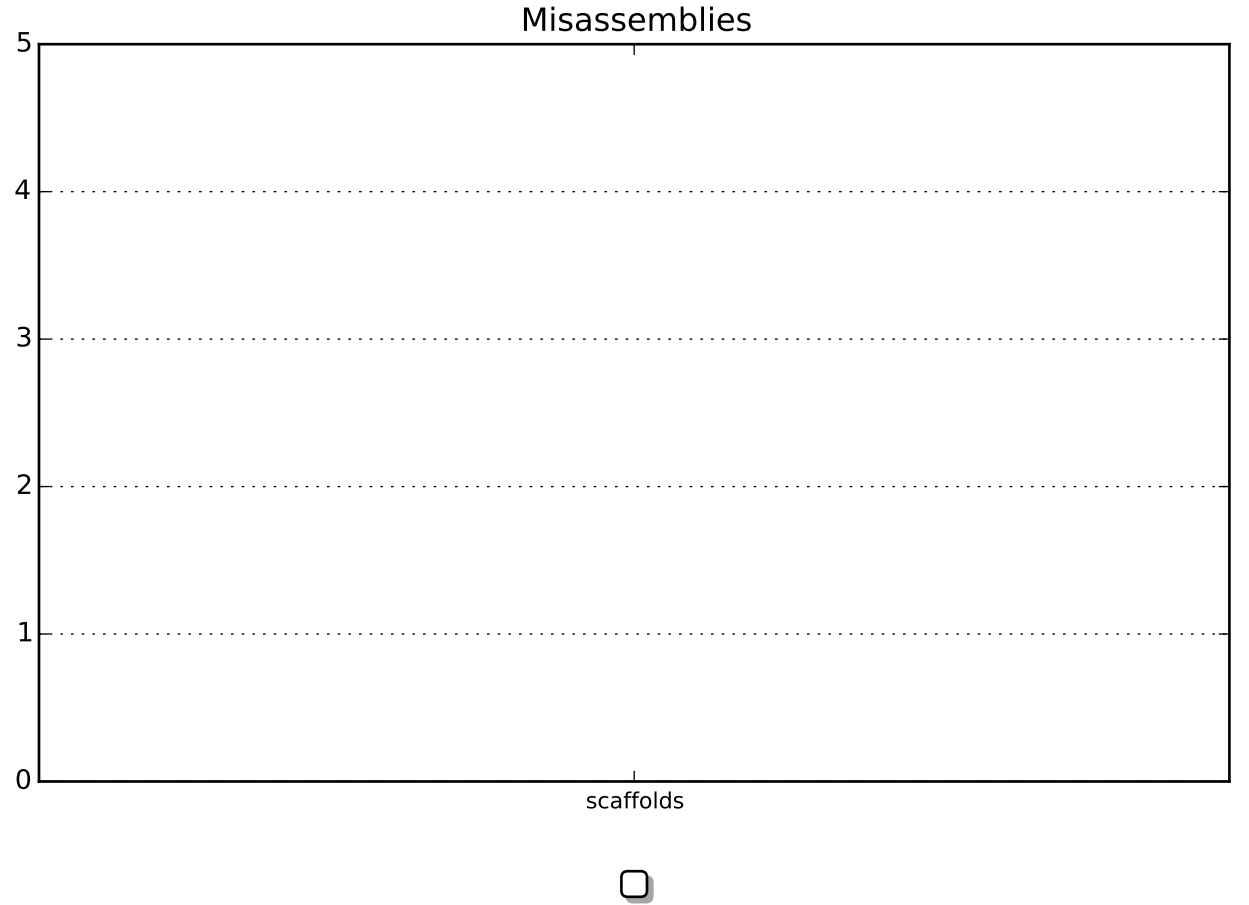
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

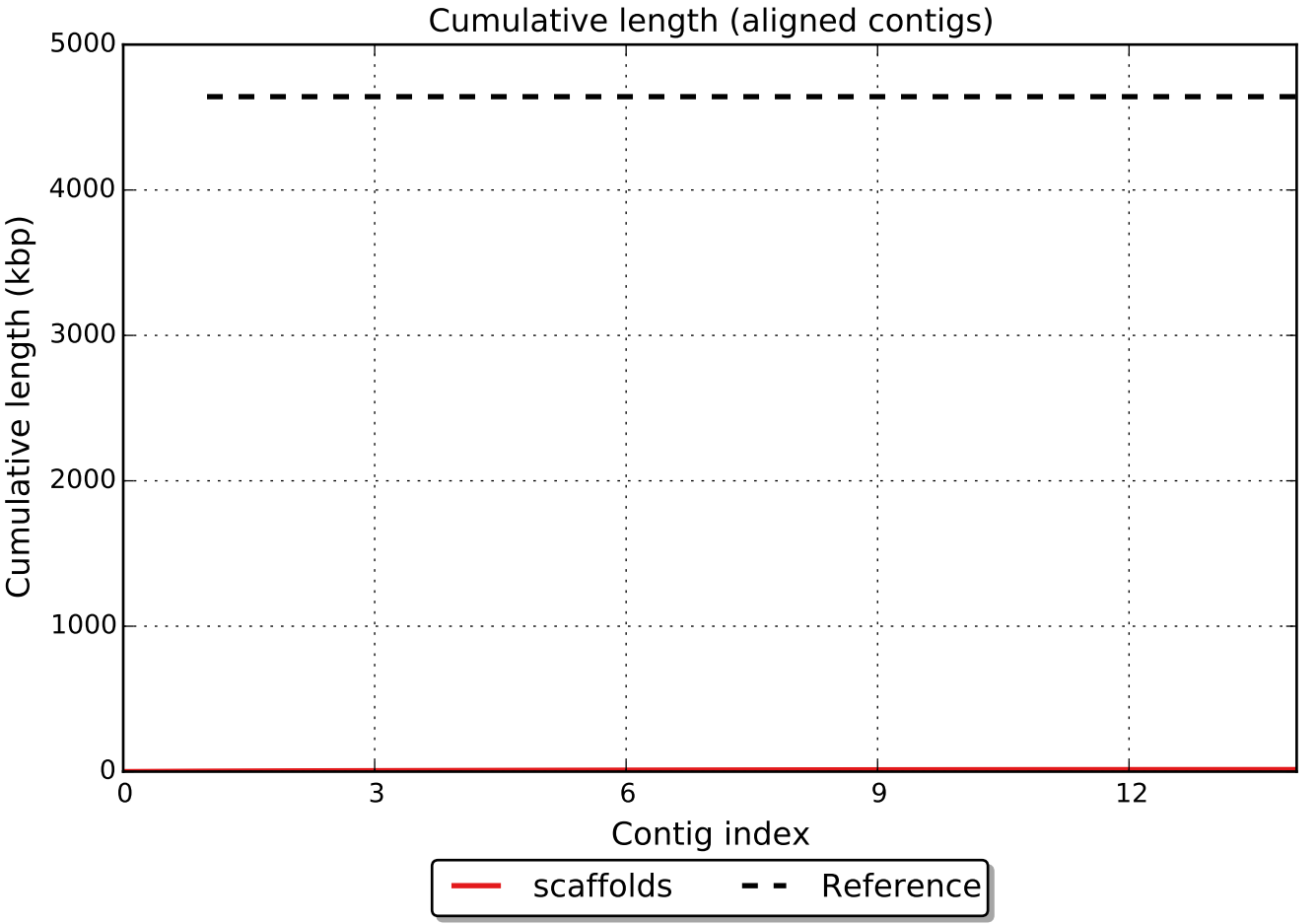

Nx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

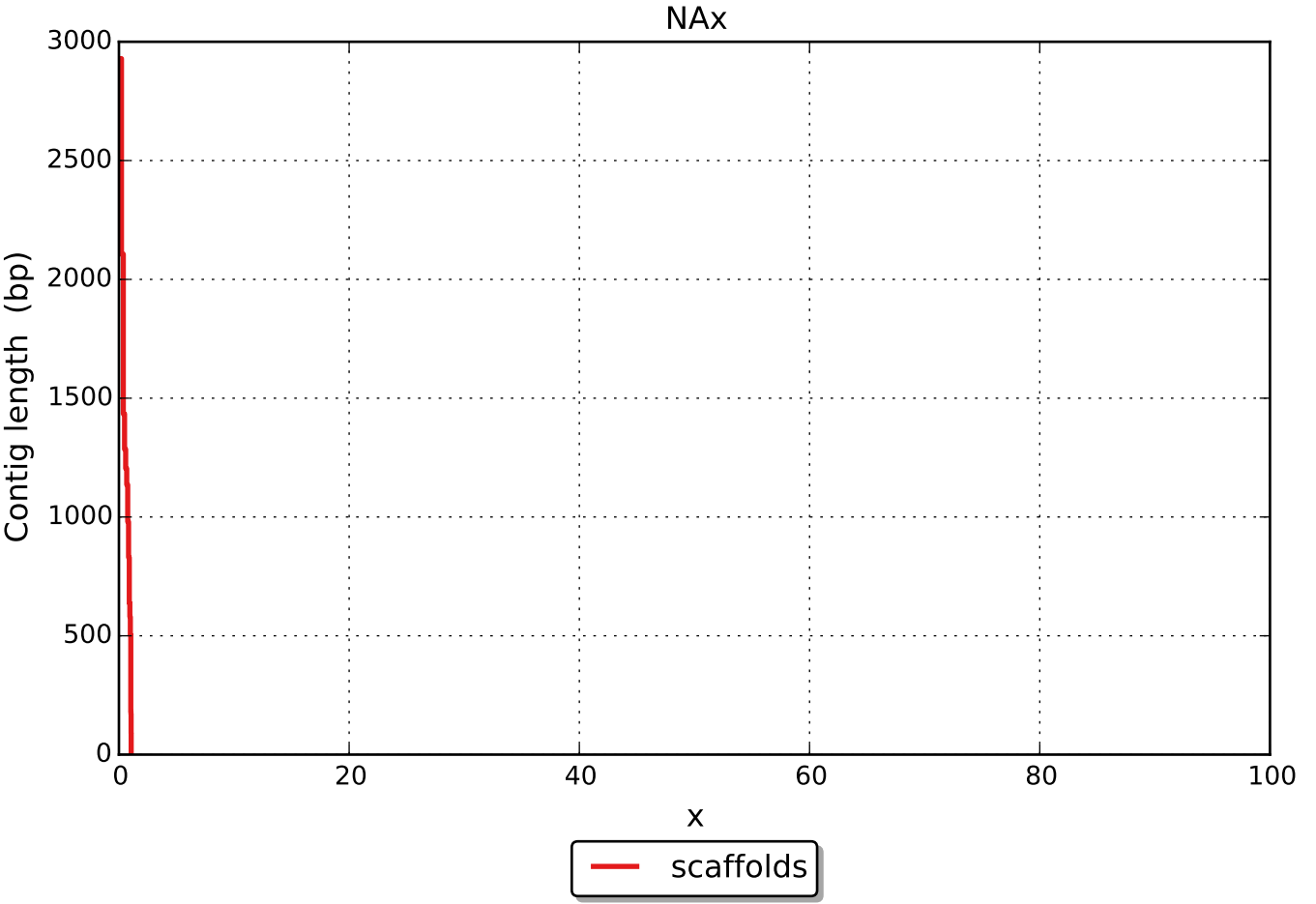

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

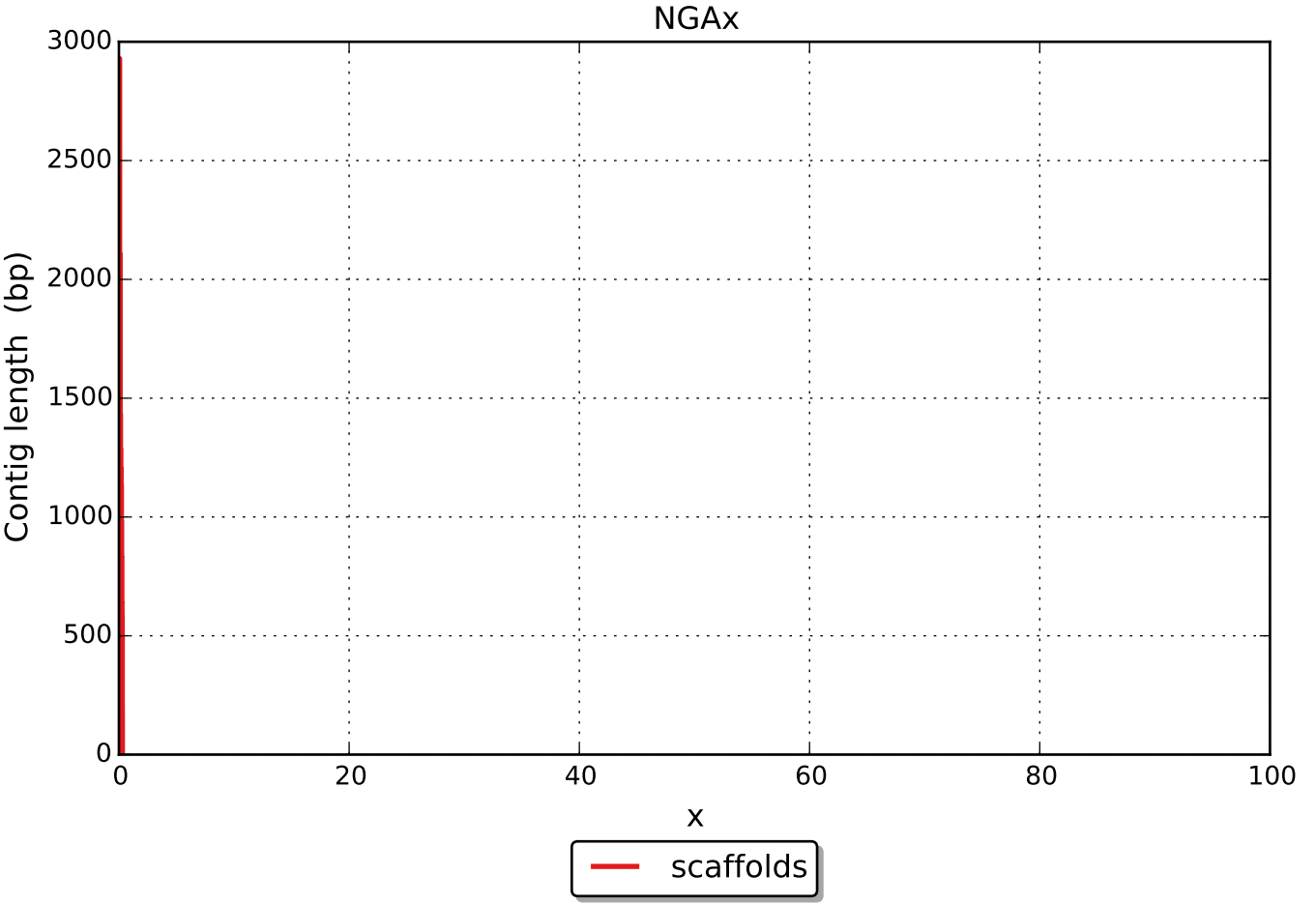

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
2
4
6
8
10
Contig index
scaffolds
Reference


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


Misassemblies
5
4
3
2
1
0
scaffolds


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
Contig index
scaffolds
Reference


NAx
Contig length (bp)
3000
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (bp)
3000
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
scaffolds