Report

	scaffolds
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	550584
Total length (>= 5000 bp)	550584
Total length (>= 10000 bp)	550584
Total length (>= 25000 bp)	550584
Total length (>= 50000 bp)	480601
# contigs	5
Largest contig	275891
Total length	550584
Reference length	4641652
GC (%)	51.64
Reference GC (%)	50.78
N50	275891
N75	83030
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 3 part
Unaligned length	412372
Genome fraction (%)	2.975
Duplication ratio	1.001
# N's per 100 kbp	9.44
# mismatches per 100 kbp	4759.35
# indels per 100 kbp	3.62
Largest alignment	83028
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

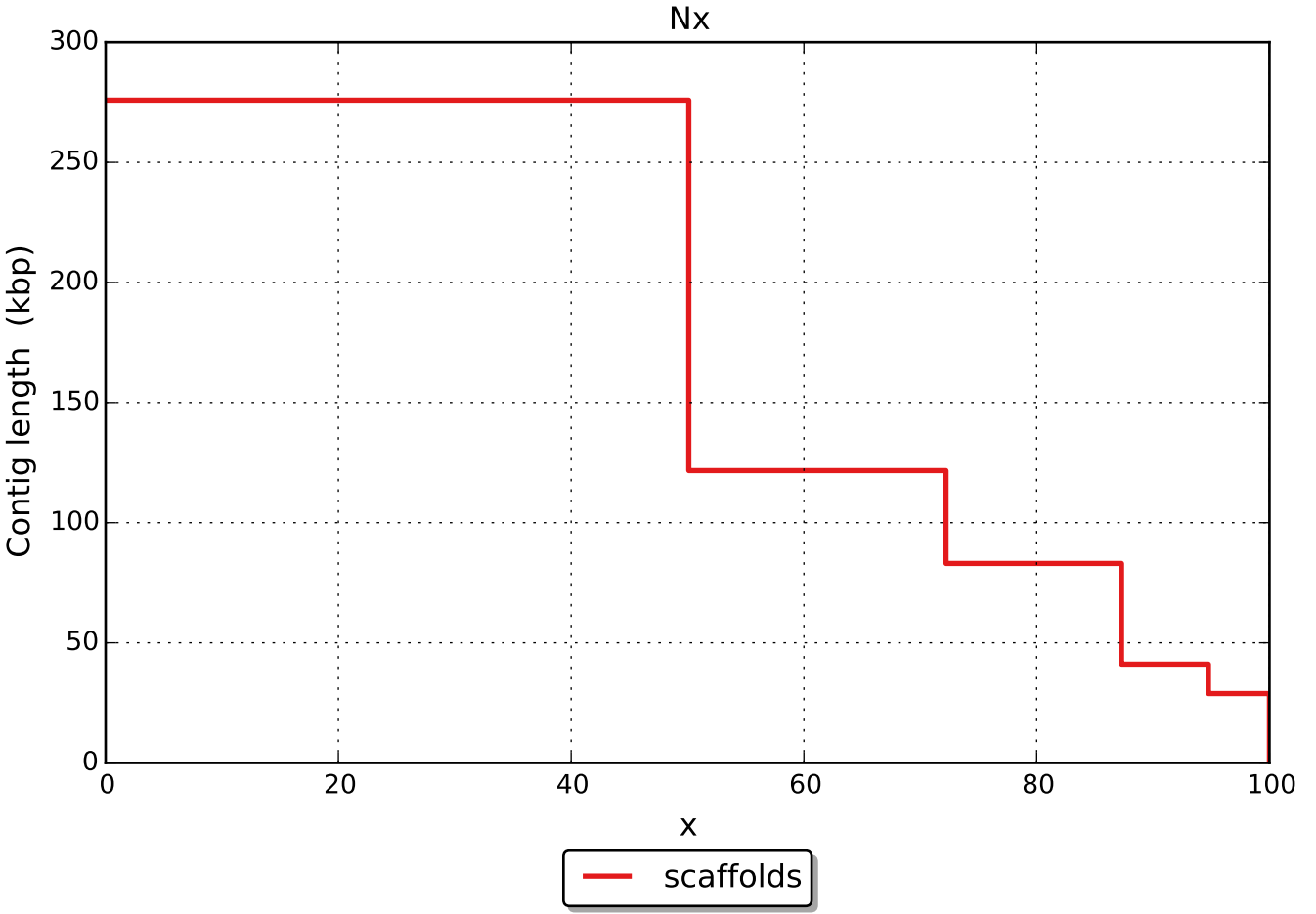
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	6573
# indels	5
# short indels	5
# long indels	0
Indels length	5

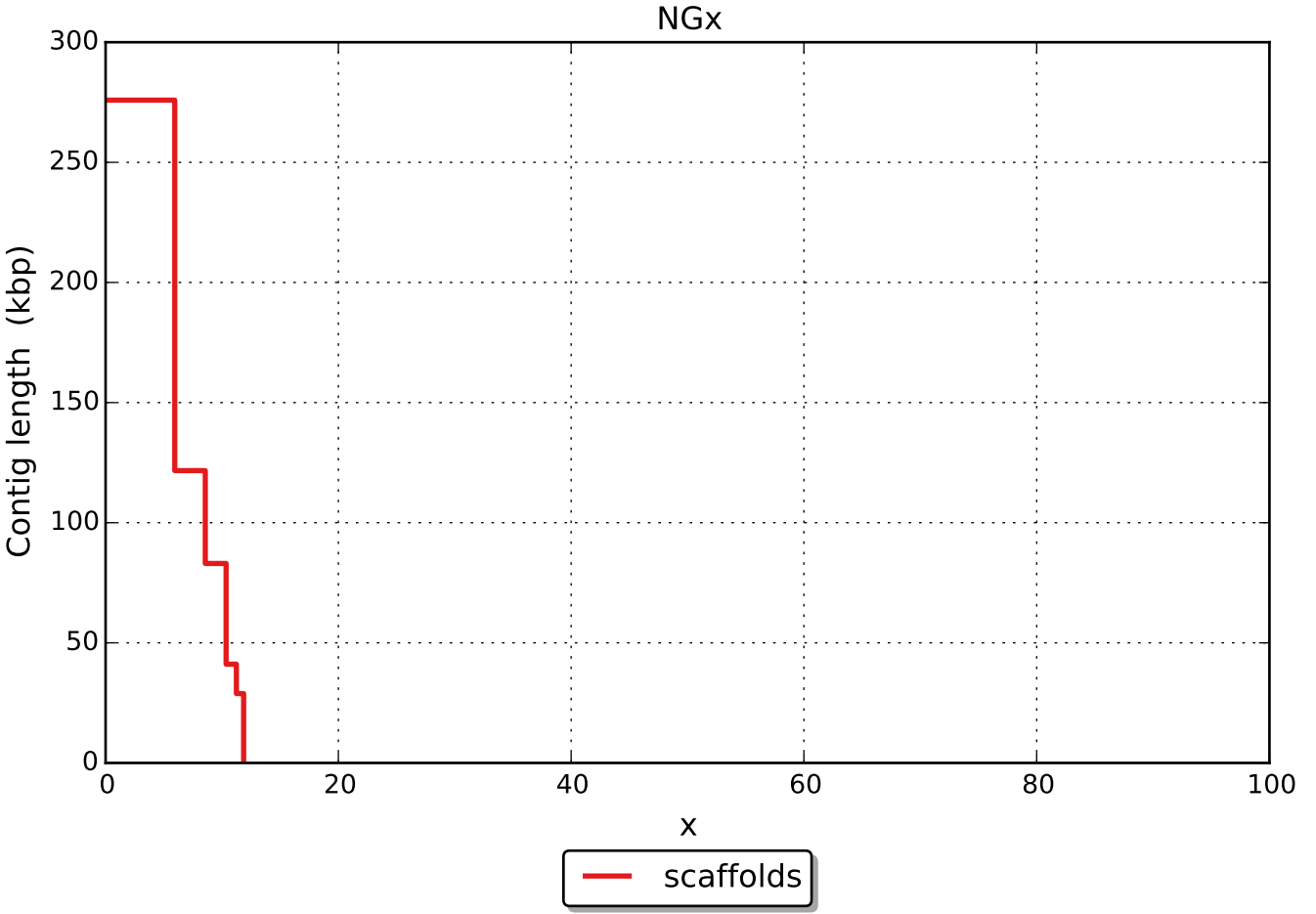
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

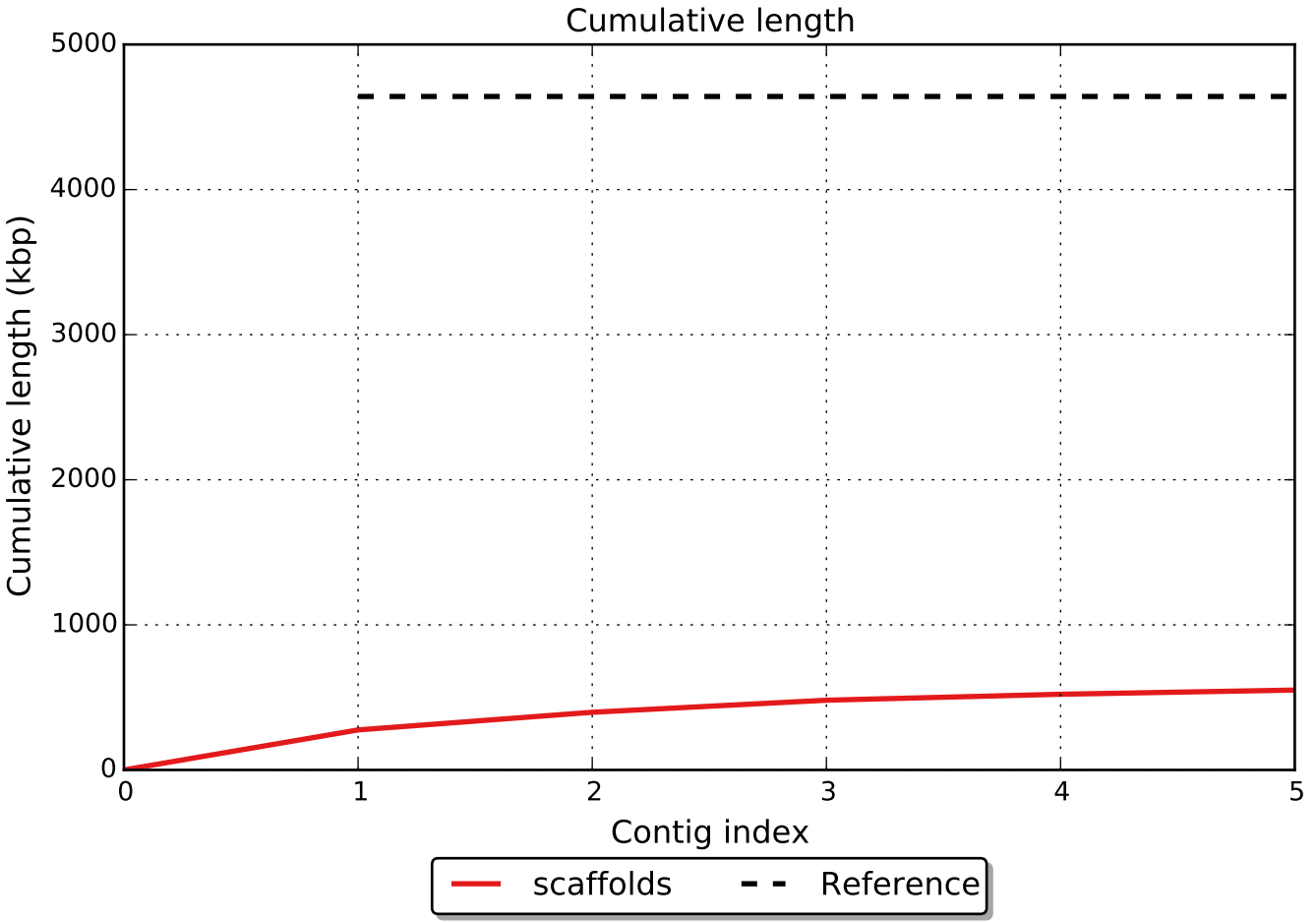
Unaligned report

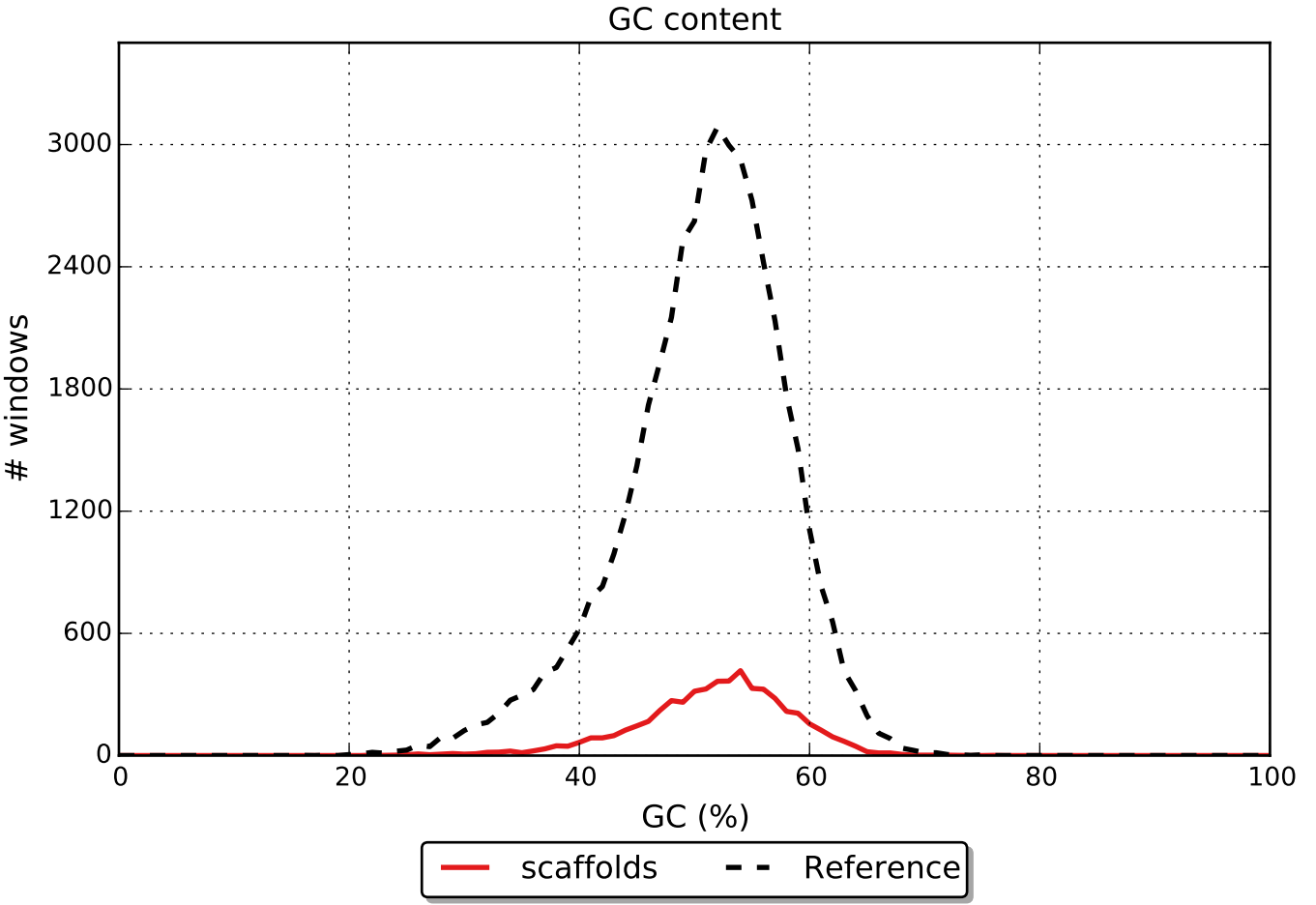
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	1
# both parts are significant	3
Partially unaligned length	412372
# N's	52

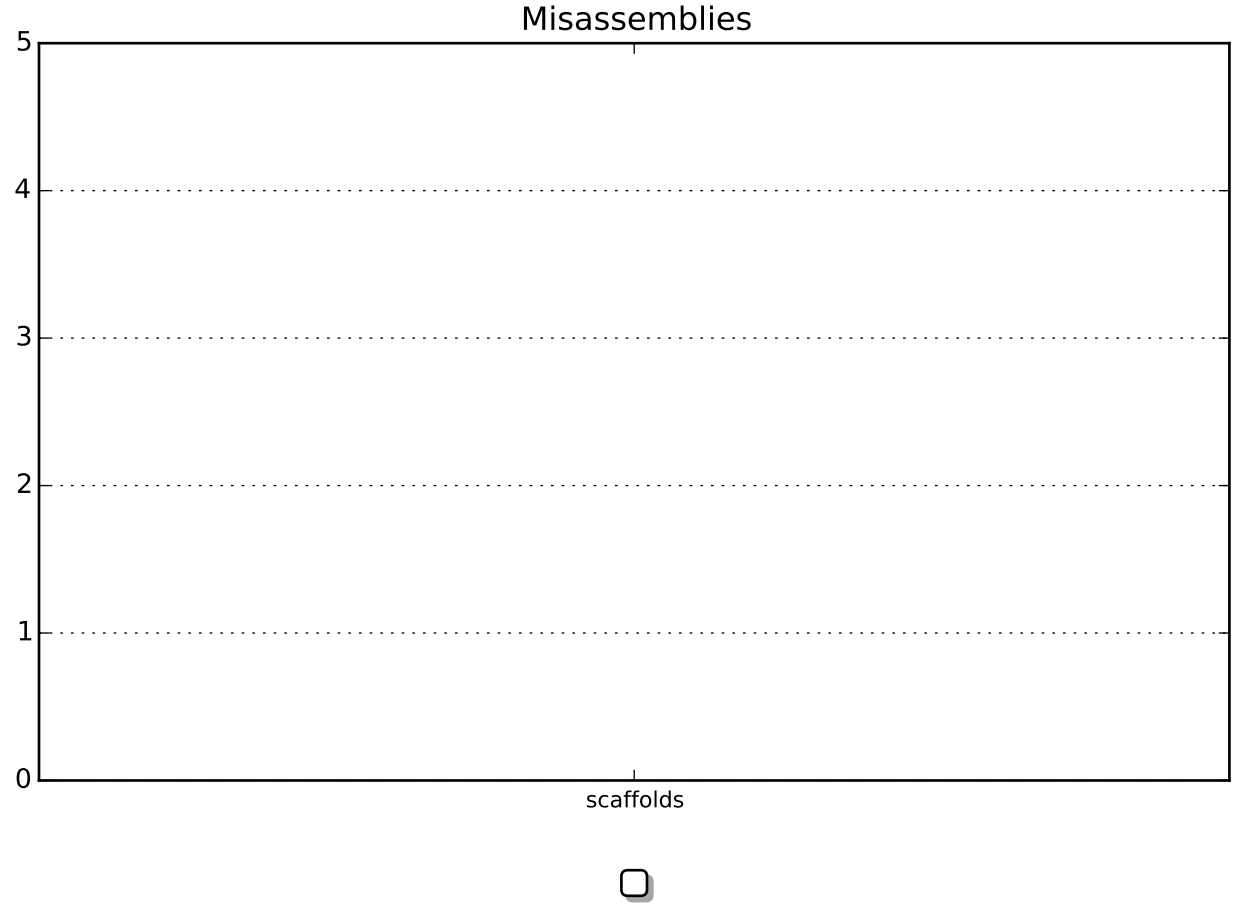
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

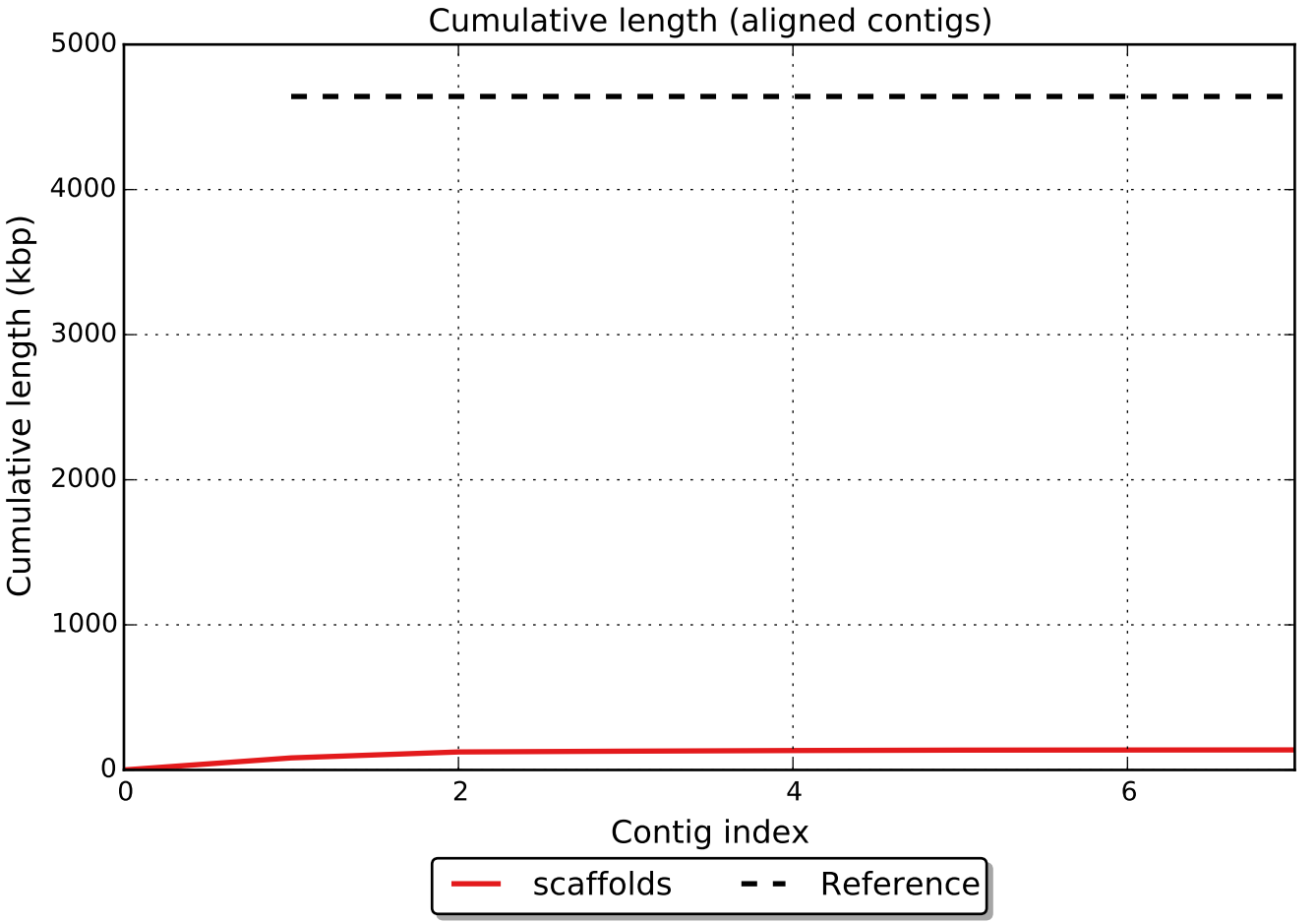

Nx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

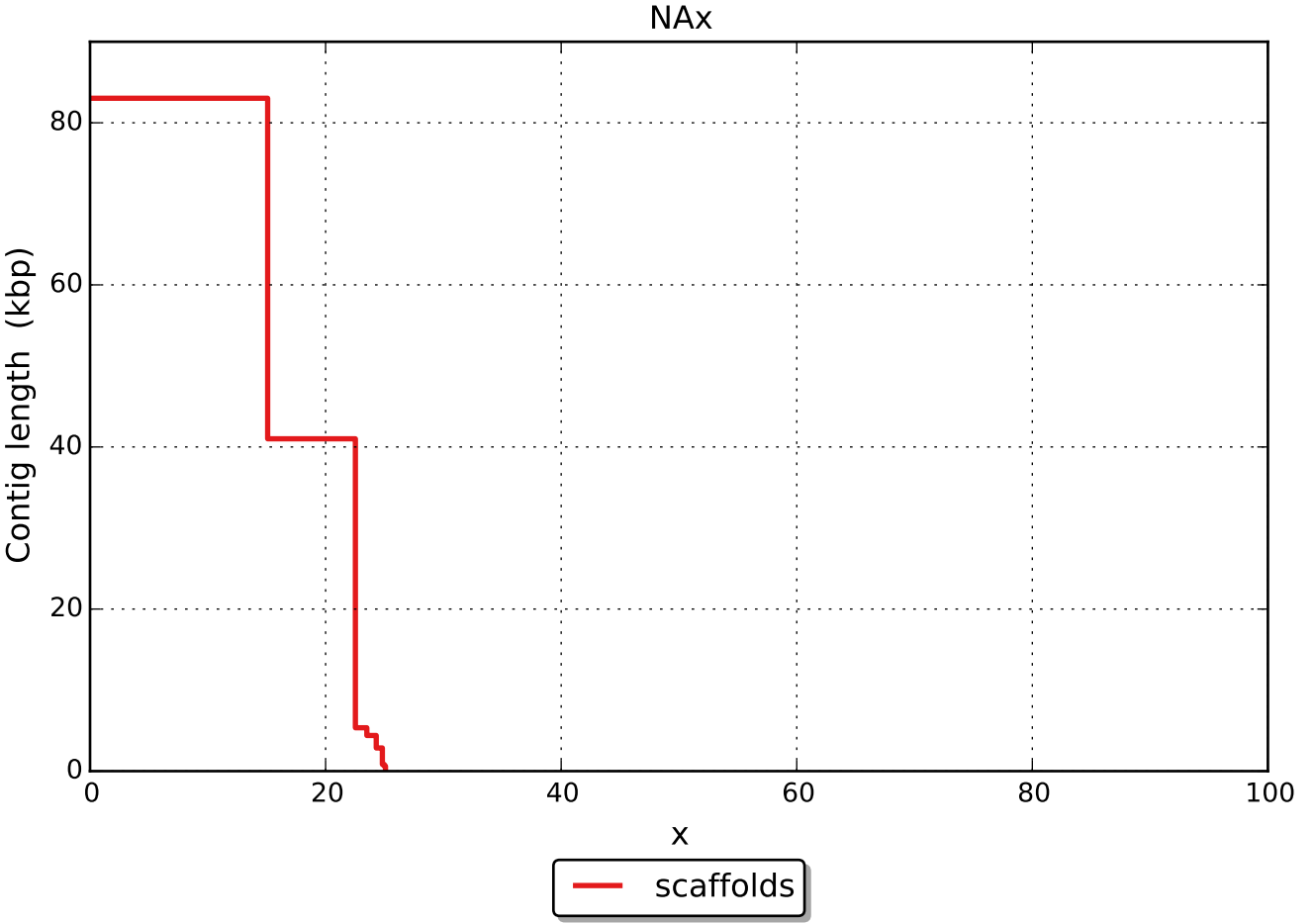

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

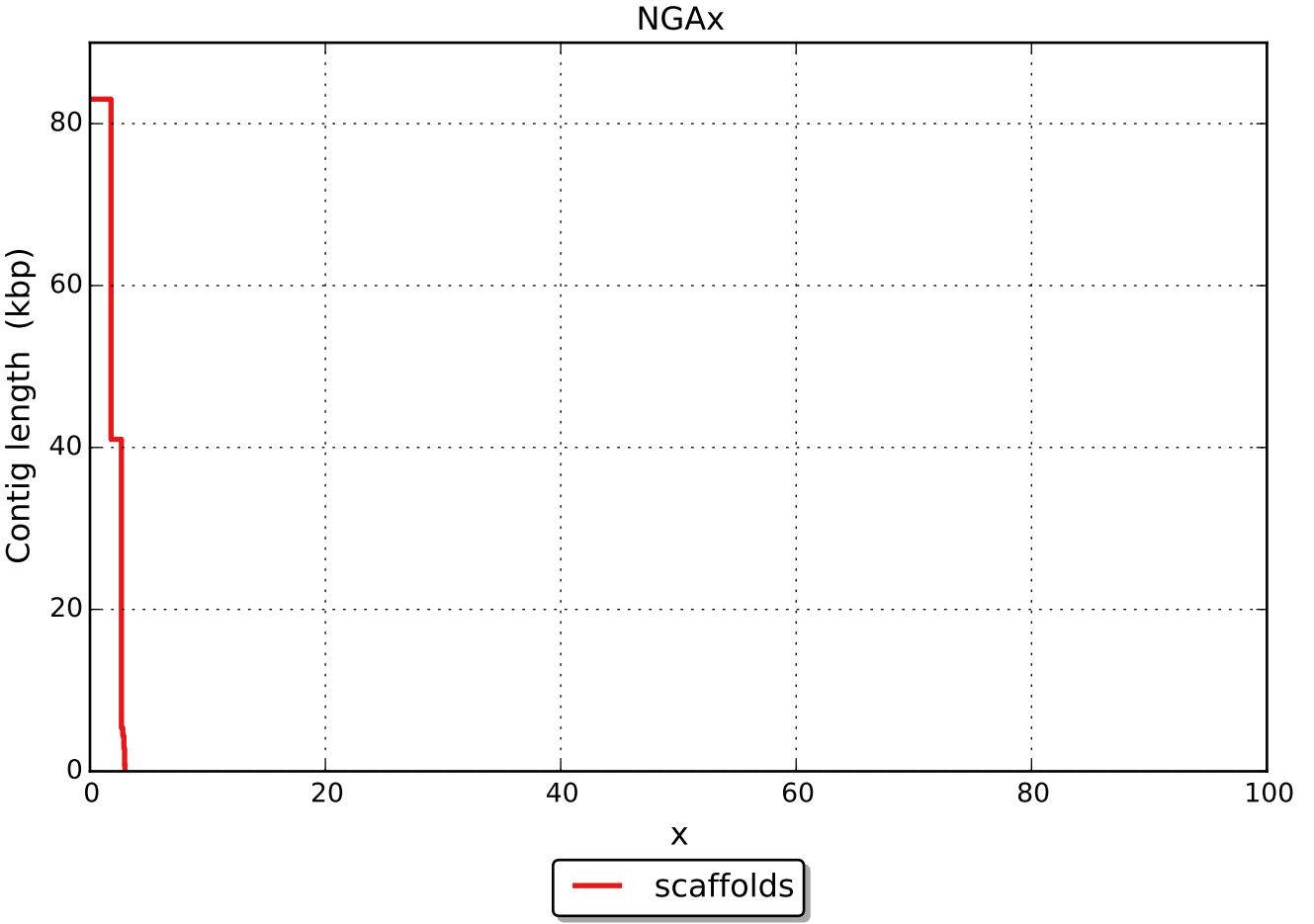

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
4
5
Contig index
scaffolds
Reference


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
2
4
6
Contig index
scaffolds
Reference


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


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