Report

	scaffolds
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	879
Total length	879
Reference length	4641652
GC (%)	50.17
Reference GC (%)	50.78
N50	879
N75	879
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	0.019
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3526.73
# indels per 100 kbp	0.00
Largest alignment	879
NA50	879
NGA50	-
NA75	879
LA50	1
LA75	1

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

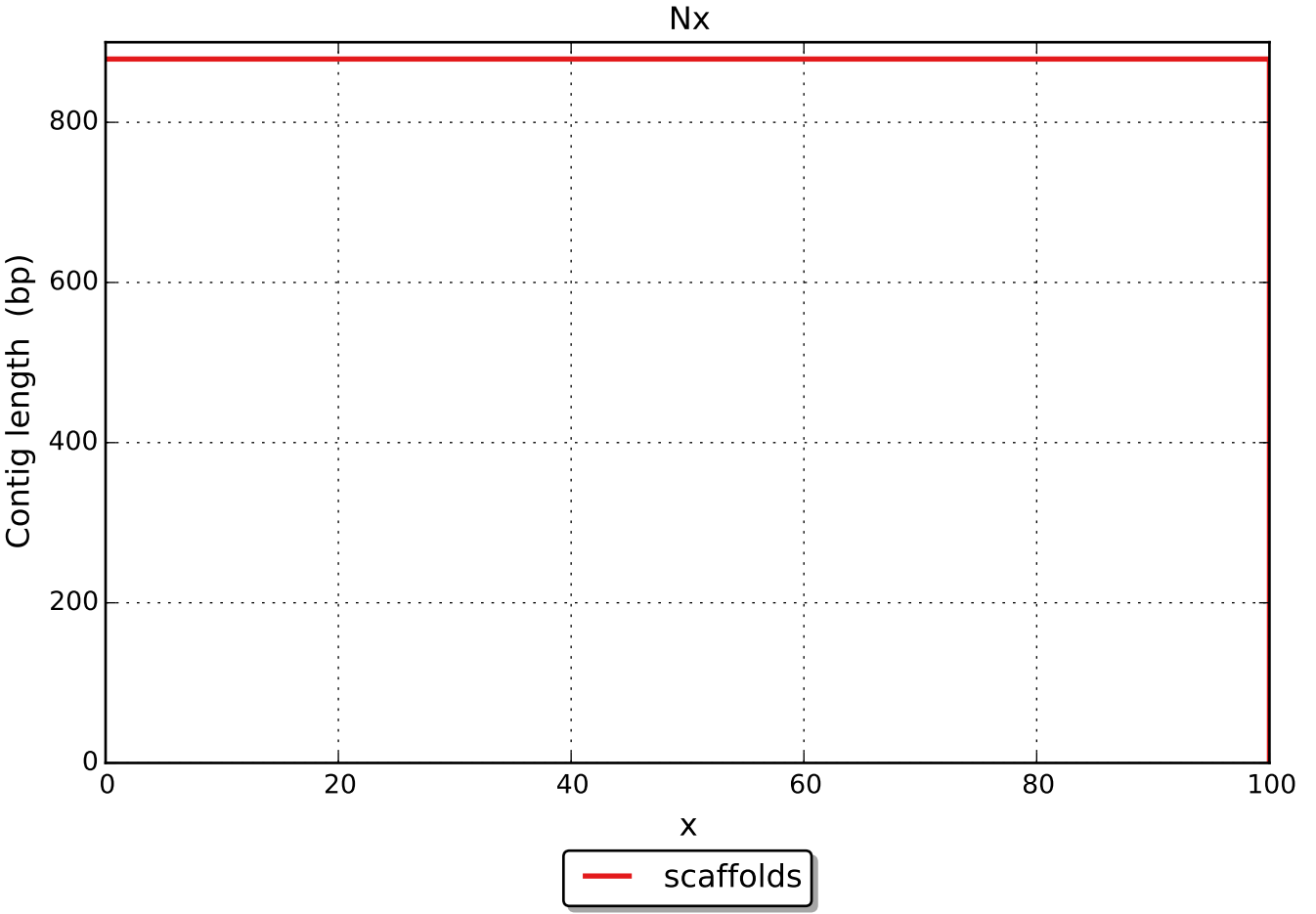
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	31
# indels	0
# short indels	0
# long indels	0
Indels length	0

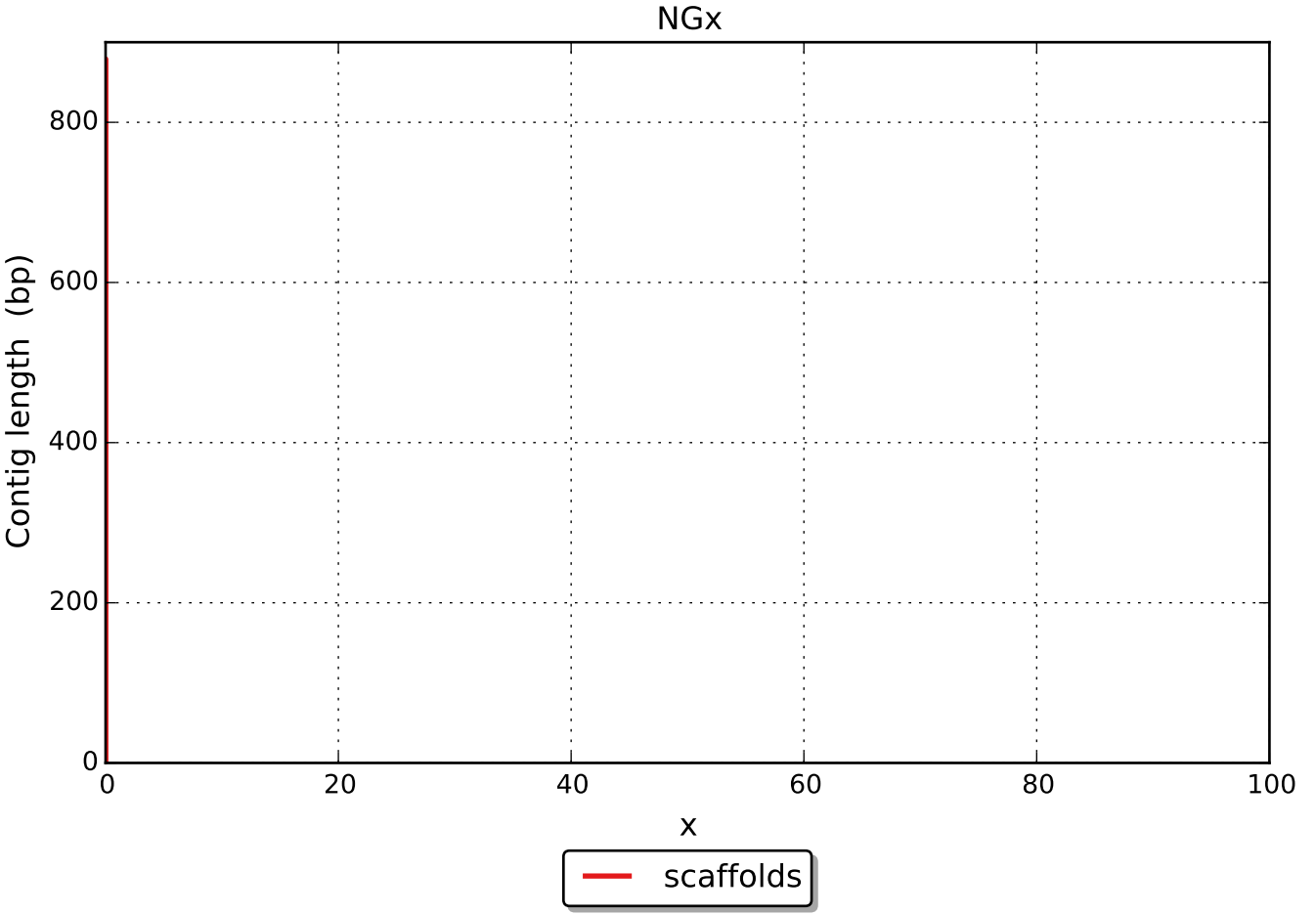
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

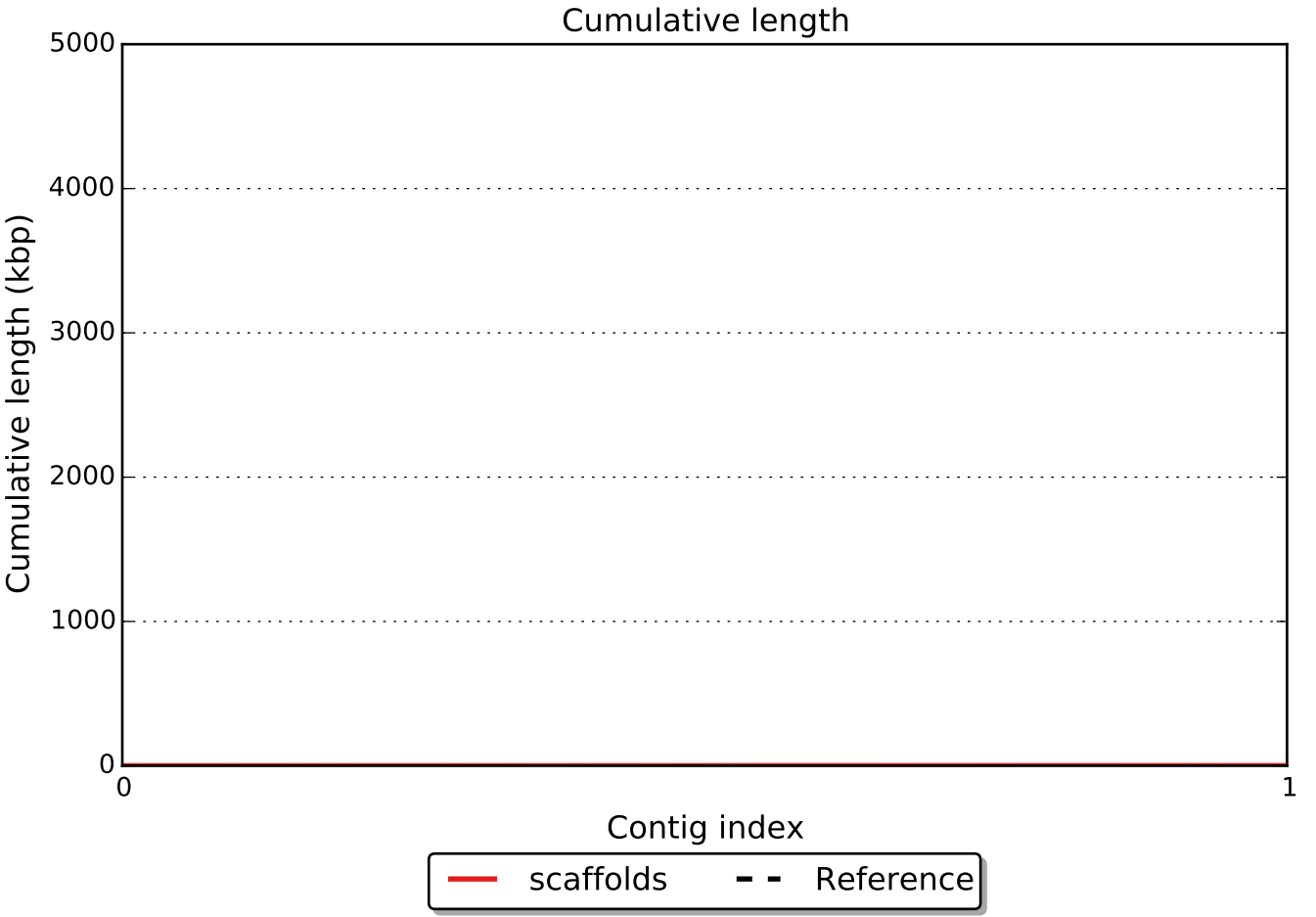
Unaligned report

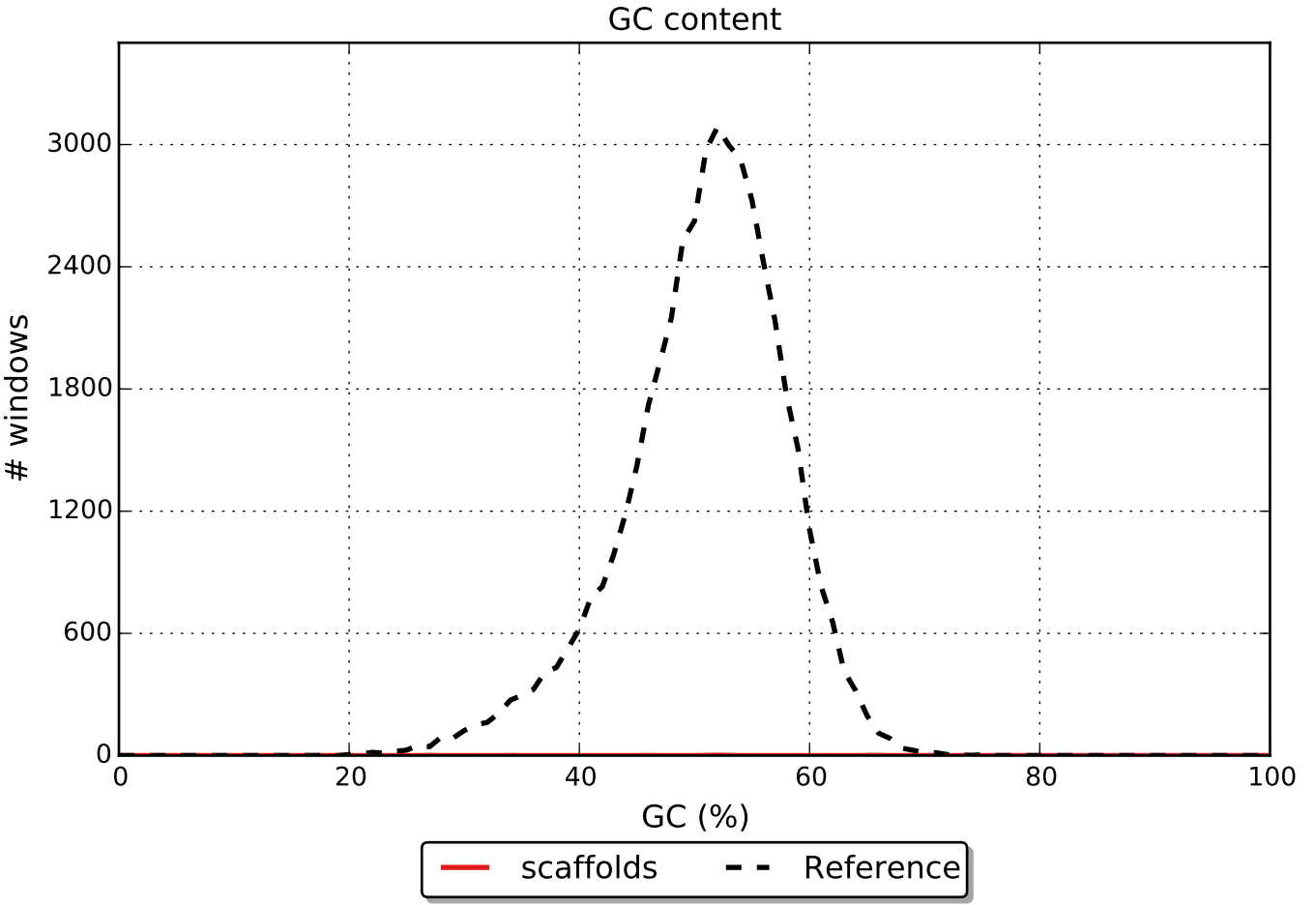
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

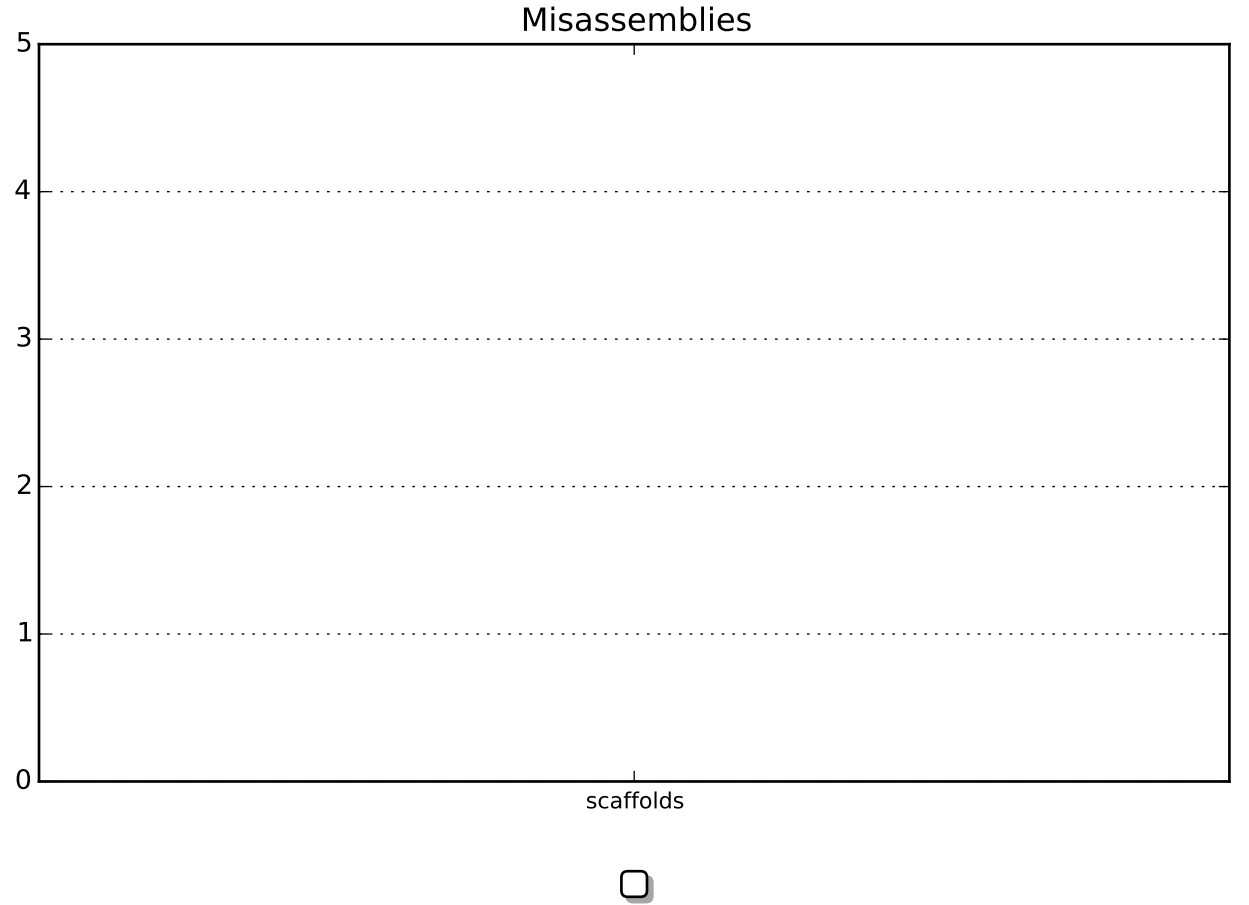
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

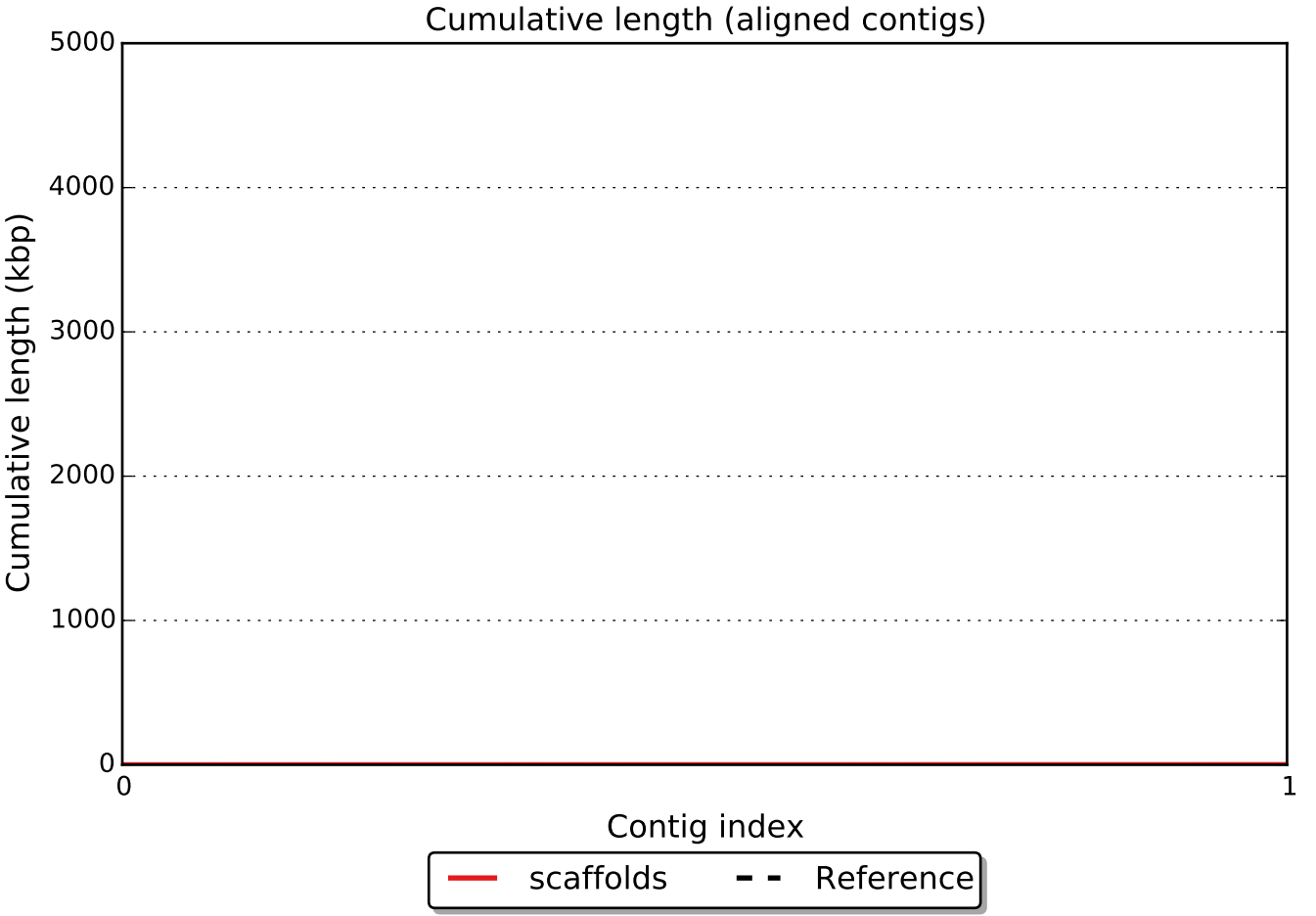

Nx
Contig length (bp)
800
600
400
200
0
0
20
40
60
80
100
x
scaffolds

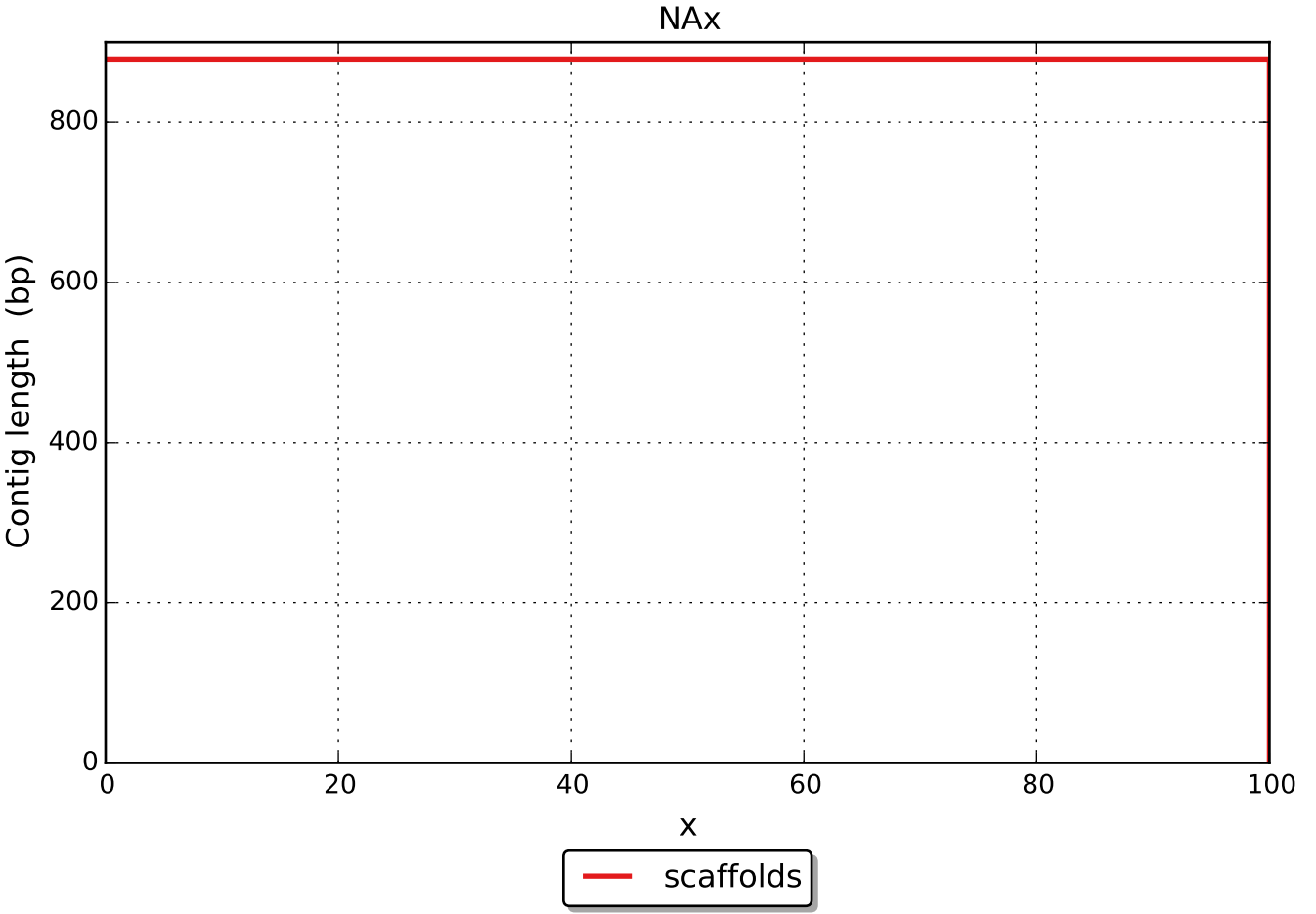

NGx
Contig length (bp)
0
200
400
600
800
0
20
40
60
80
100
x
scaffolds

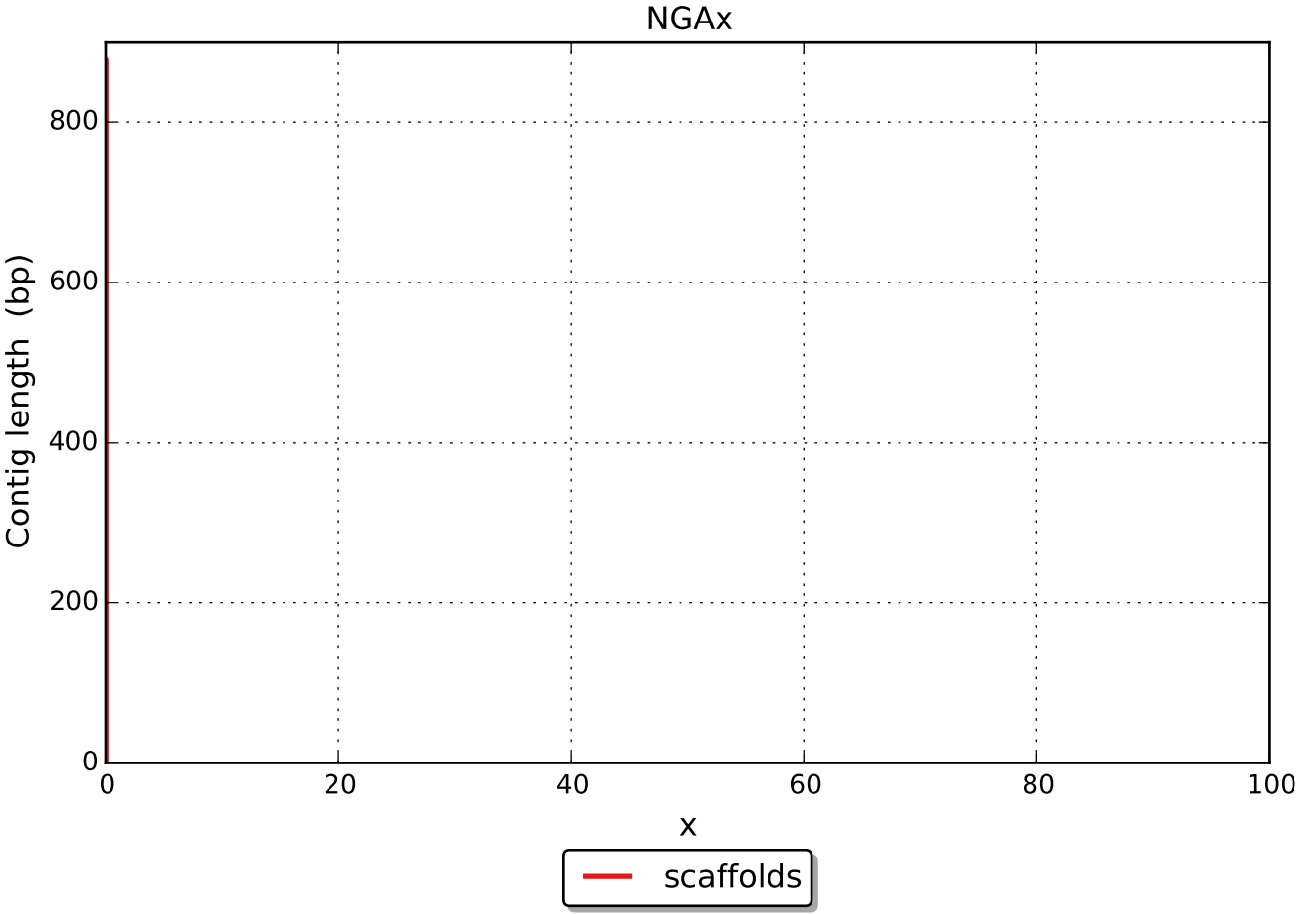

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
1
Contig index
scaffolds
Reference


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


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


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