Report

	scaffolds
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	616744
Total length (>= 5000 bp)	616744
Total length (>= 10000 bp)	616744
Total length (>= 25000 bp)	616744
Total length (>= 50000 bp)	591579
# contigs	5
Largest contig	283870
Total length	616744
Reference length	4641652
GC (%)	51.00
Reference GC (%)	50.78
N50	132188
N75	108452
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 5 part
Unaligned length	596151
Genome fraction (%)	0.444
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4696.00
# indels per 100 kbp	19.43
Largest alignment	5186
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

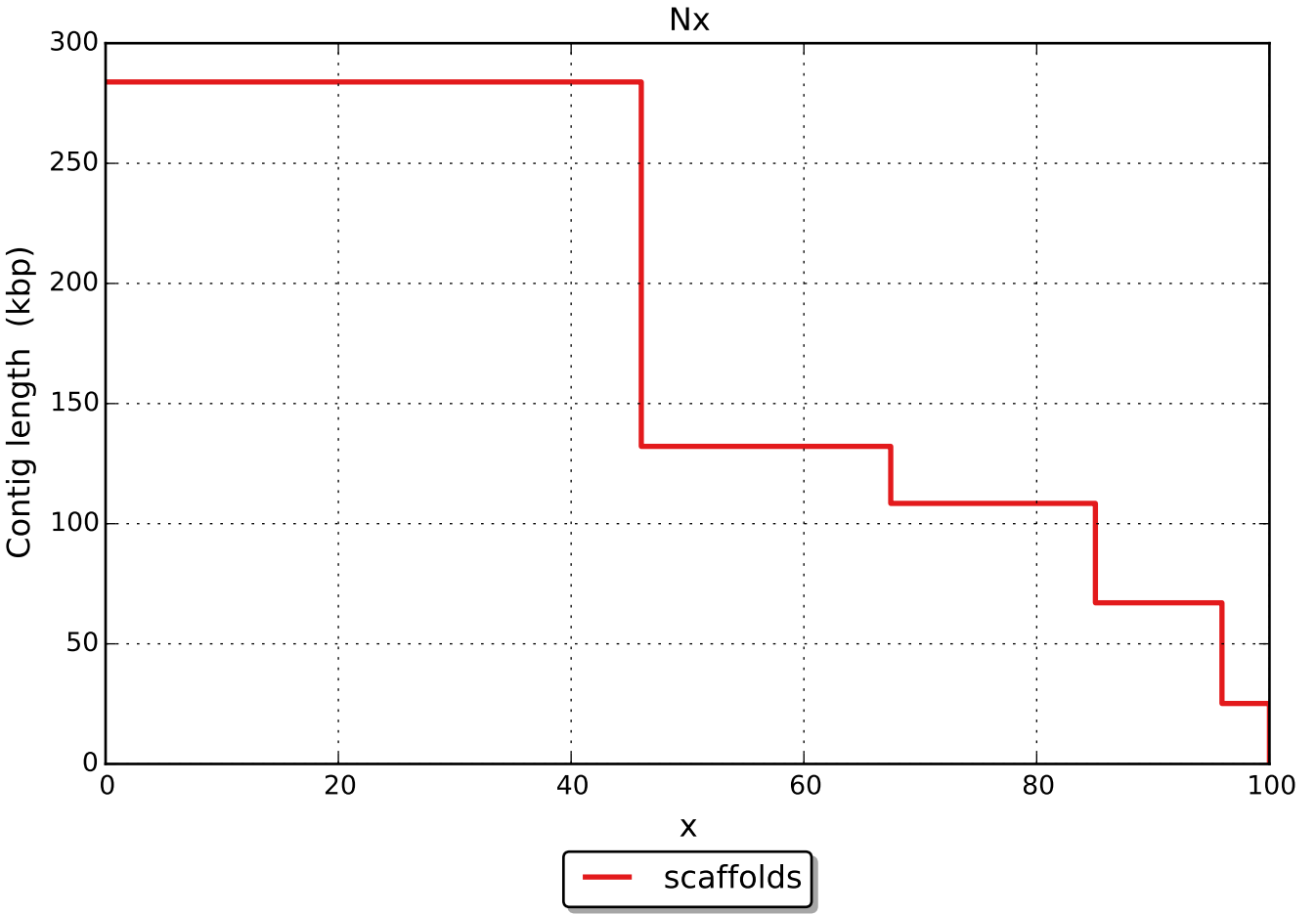
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	967
# indels	4
# short indels	4
# long indels	0
Indels length	4

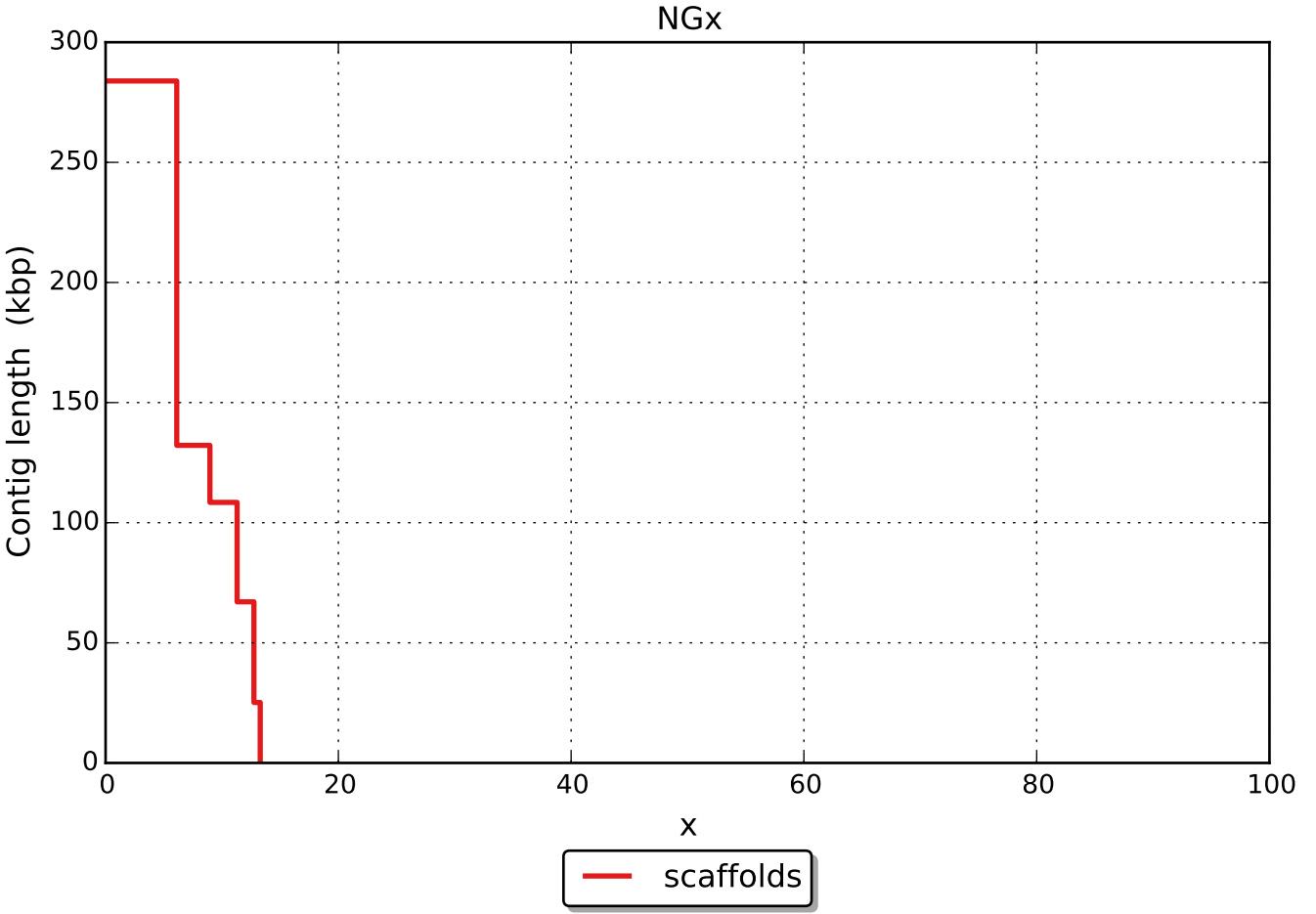
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

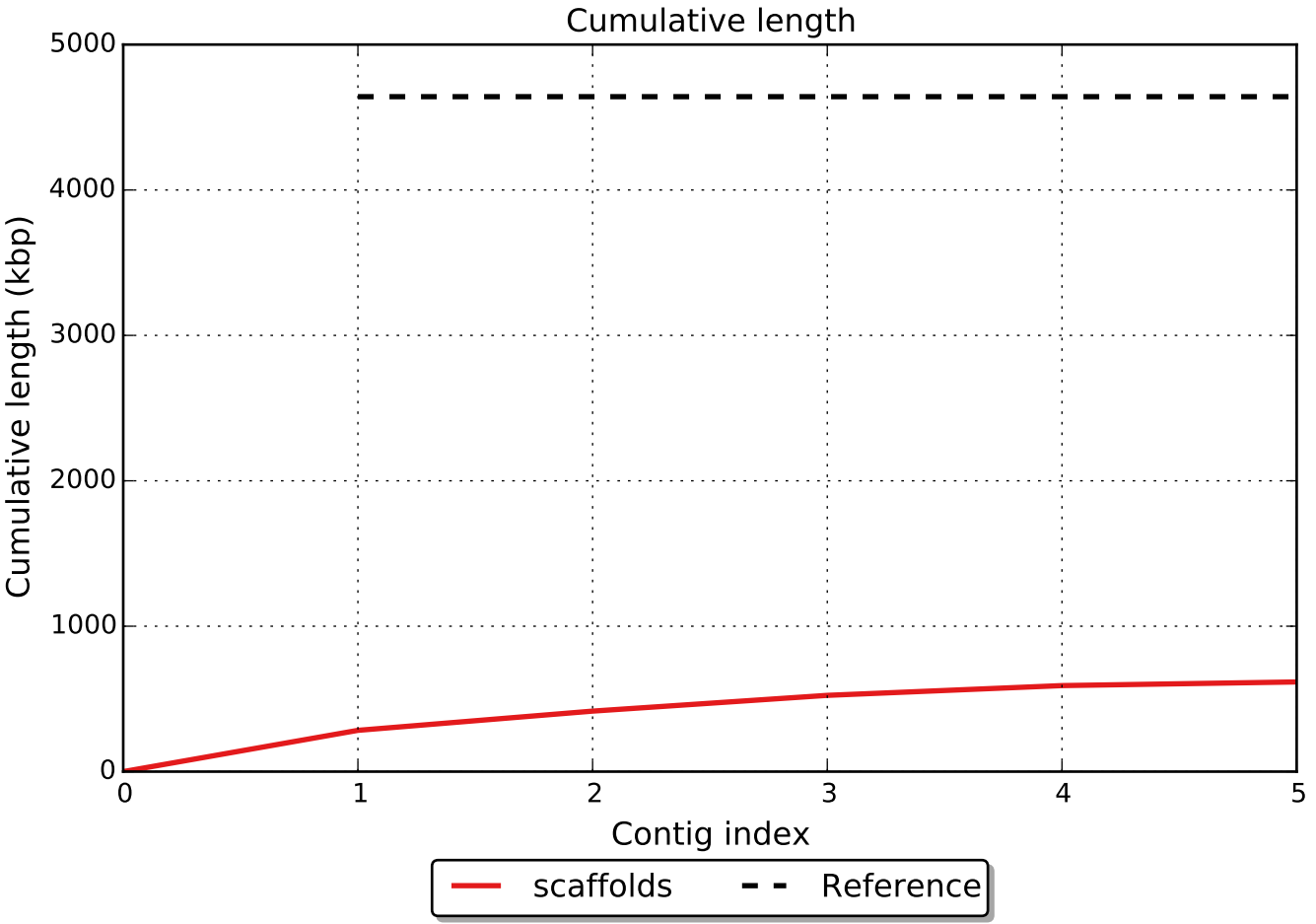
Unaligned report

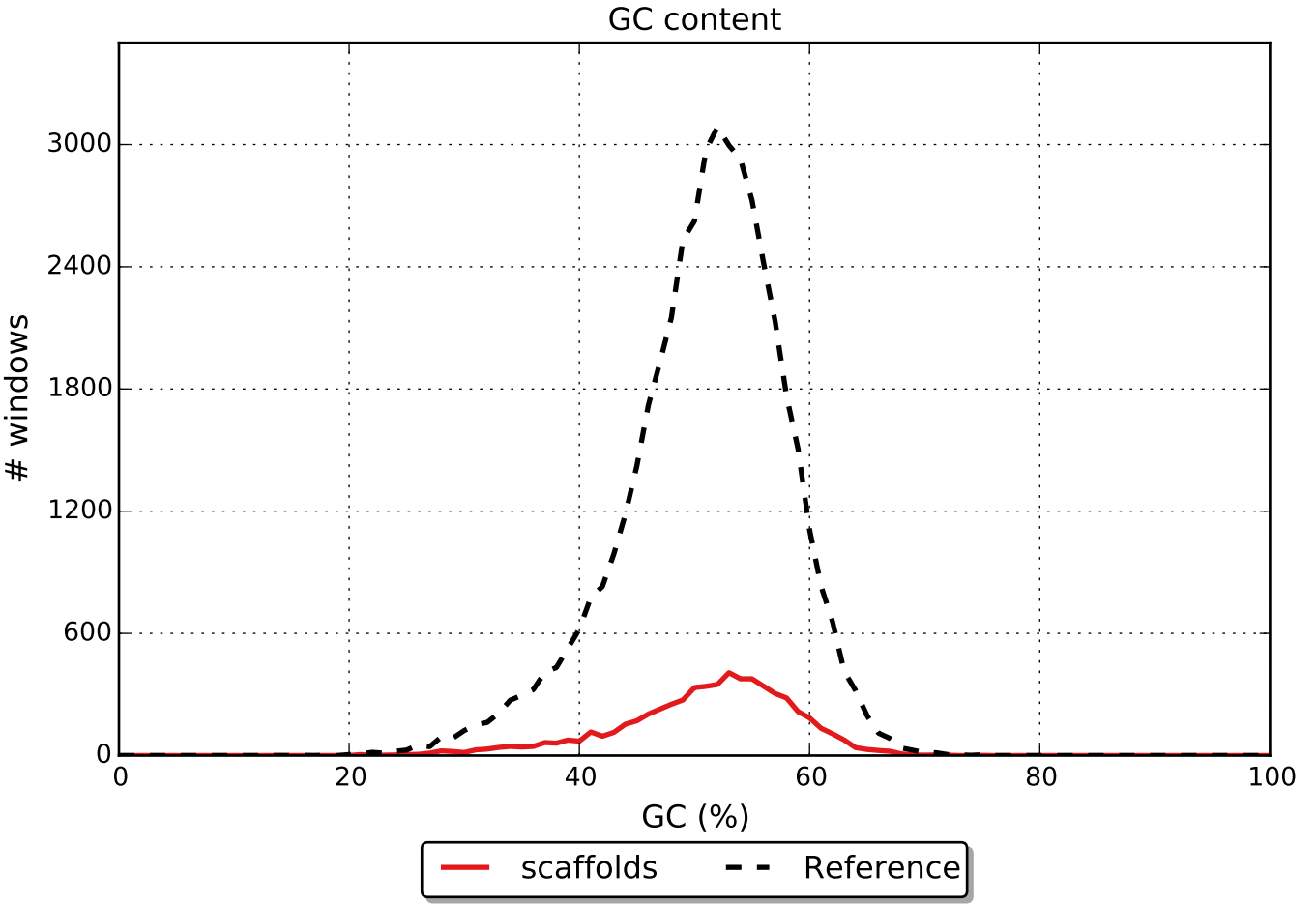
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	3
# both parts are significant	4
Partially unaligned length	596151
# N's	0

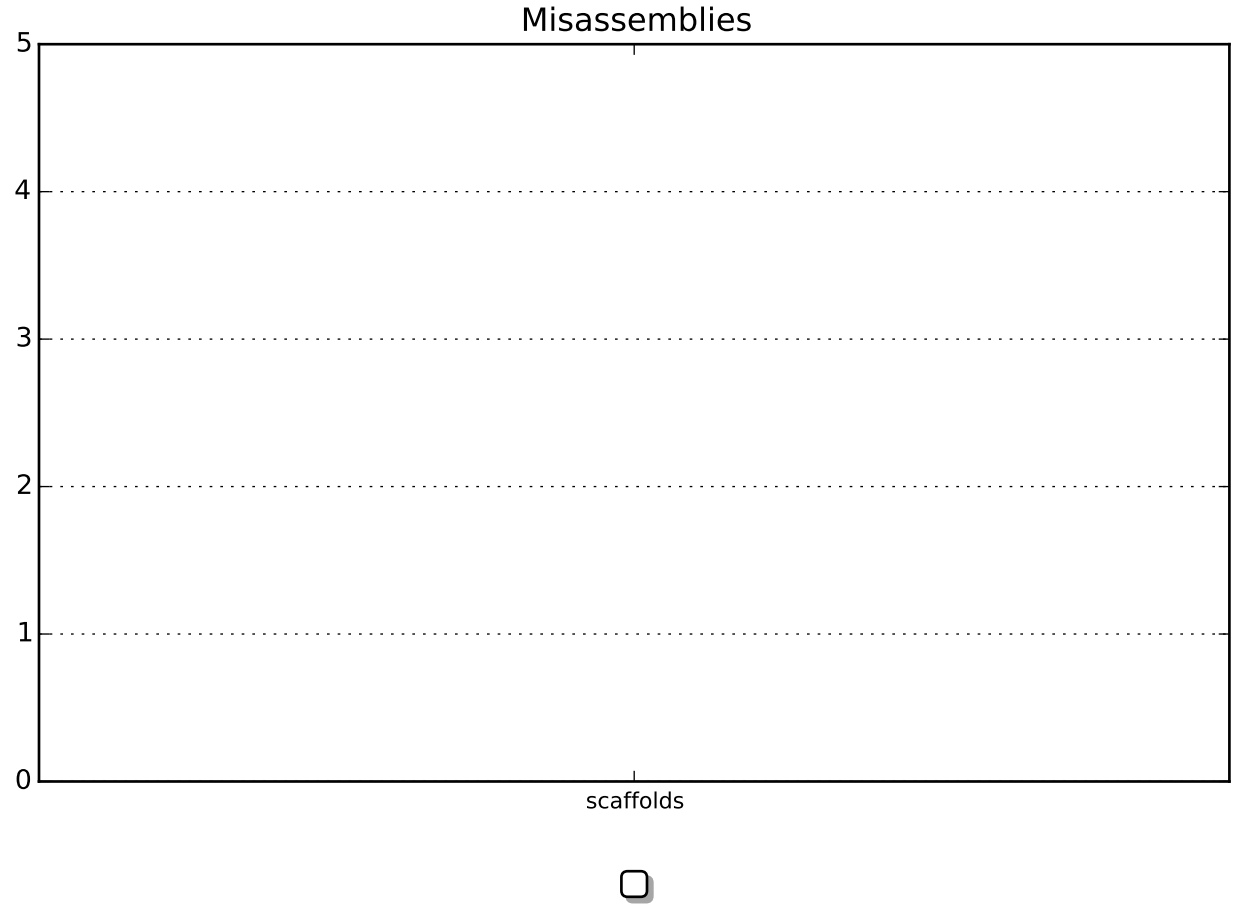
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

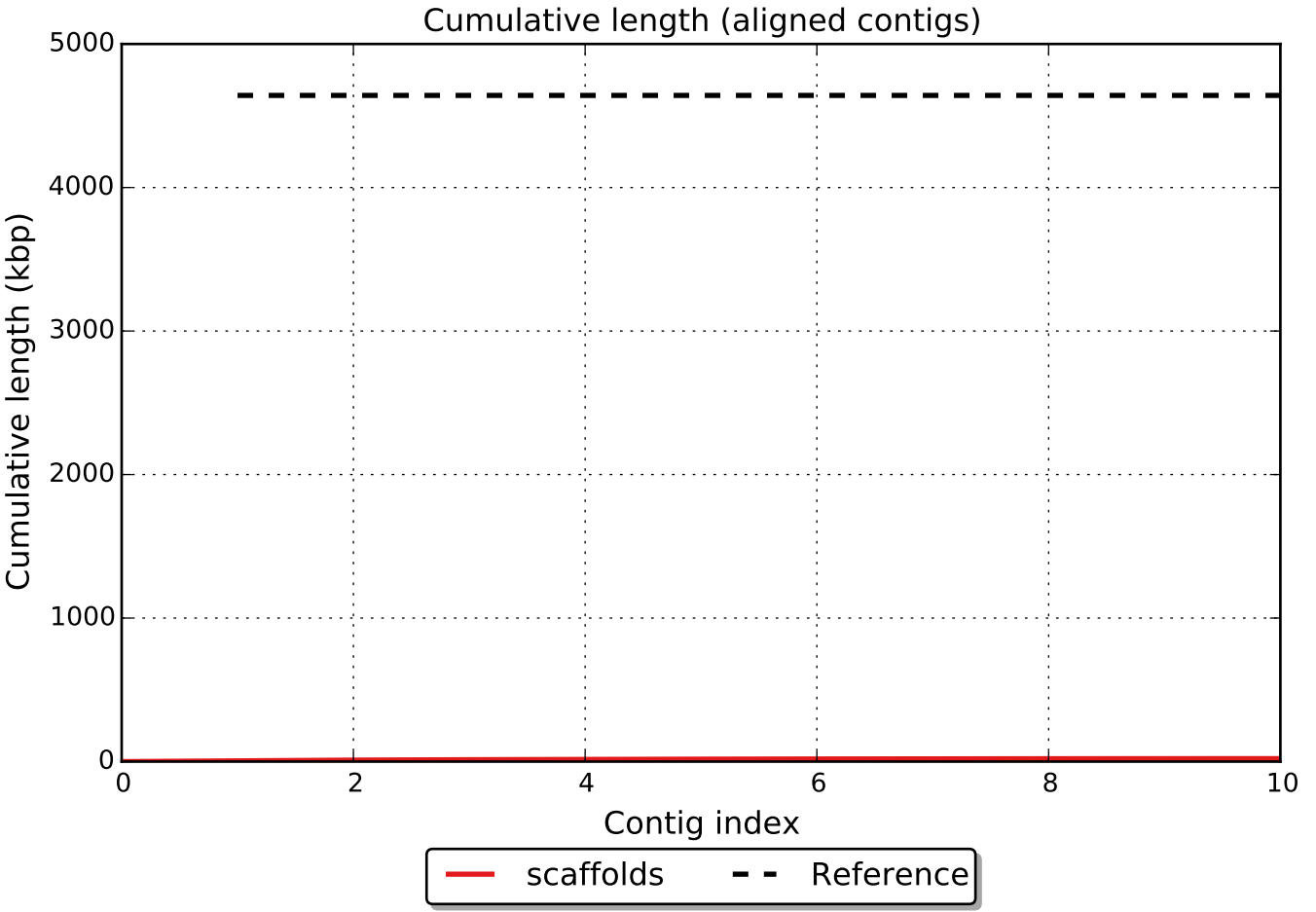

Nx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

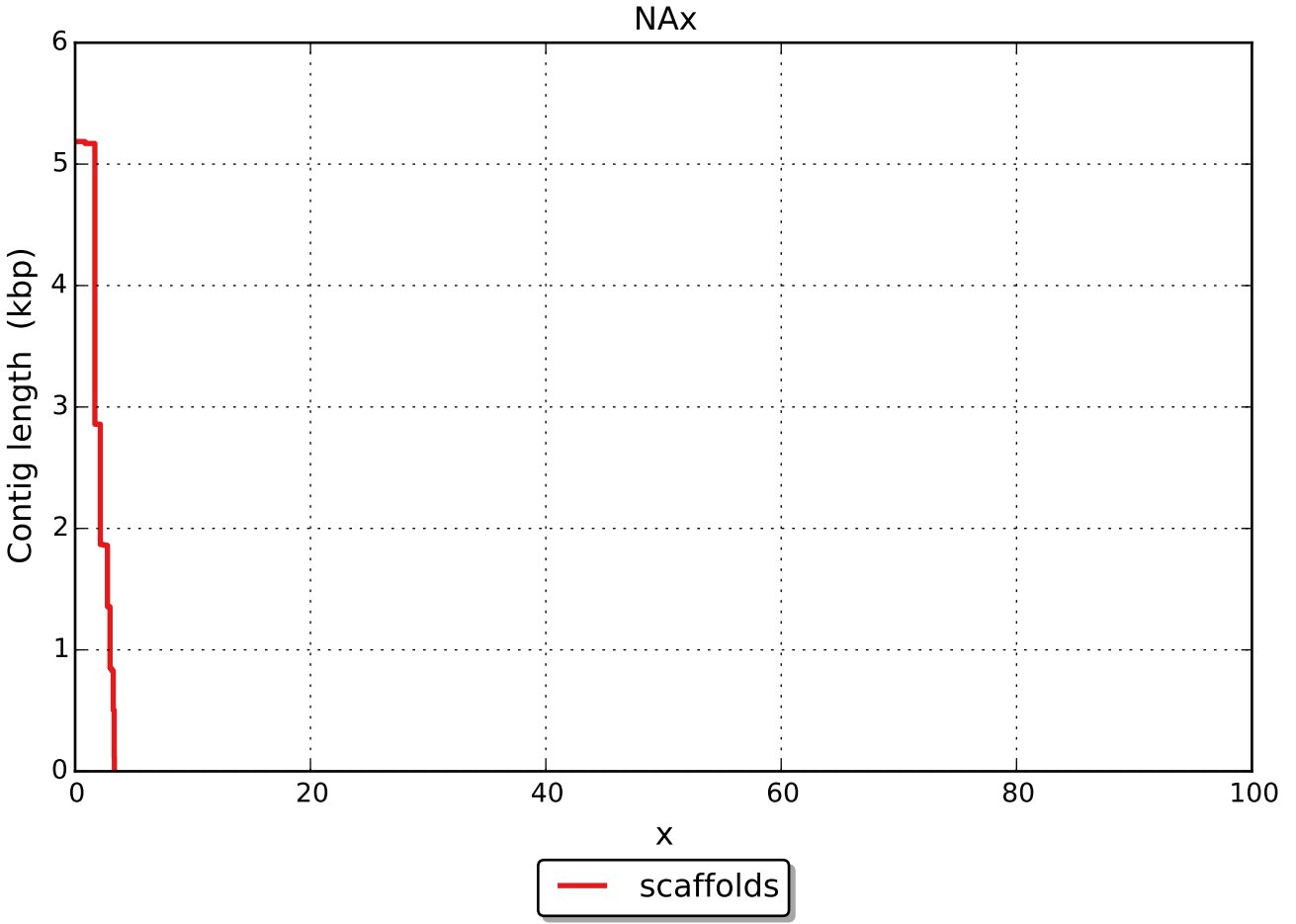

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

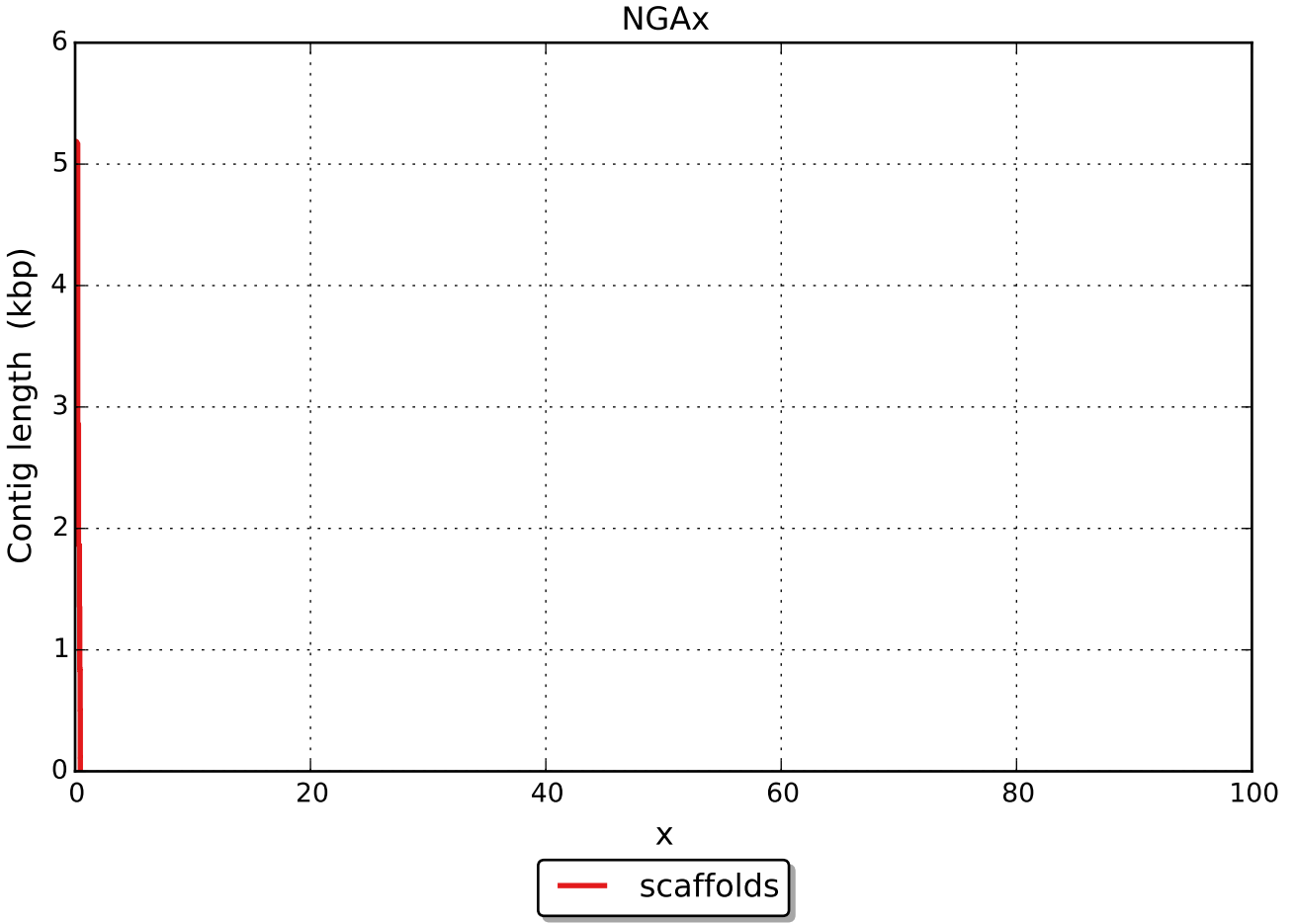

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
4
5
Contig index
scaffolds
Reference


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
8
10
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds