Report

	scaffolds
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	17
Total length (>= 1000 bp)	4783047
Total length (>= 5000 bp)	4781640
Total length (>= 10000 bp)	4781640
Total length (>= 25000 bp)	4765238
Total length (>= 50000 bp)	4736548
# contigs	21
Largest contig	768359
Total length	4783640
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	404504
NG50	404504
N75	302312
NG75	302312
L50	5
LG50	5
L75	8
LG75	8
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.468
Duplication ratio	1.036
# N's per 100 kbp	2.01
# mismatches per 100 kbp	298.77
# indels per 100 kbp	1.04
Largest alignment	607862
NA50	404504
NGA50	404504
NA75	248289
NGA75	302312
LA50	5
LGA50	5
LA75	9
LGA75	8

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

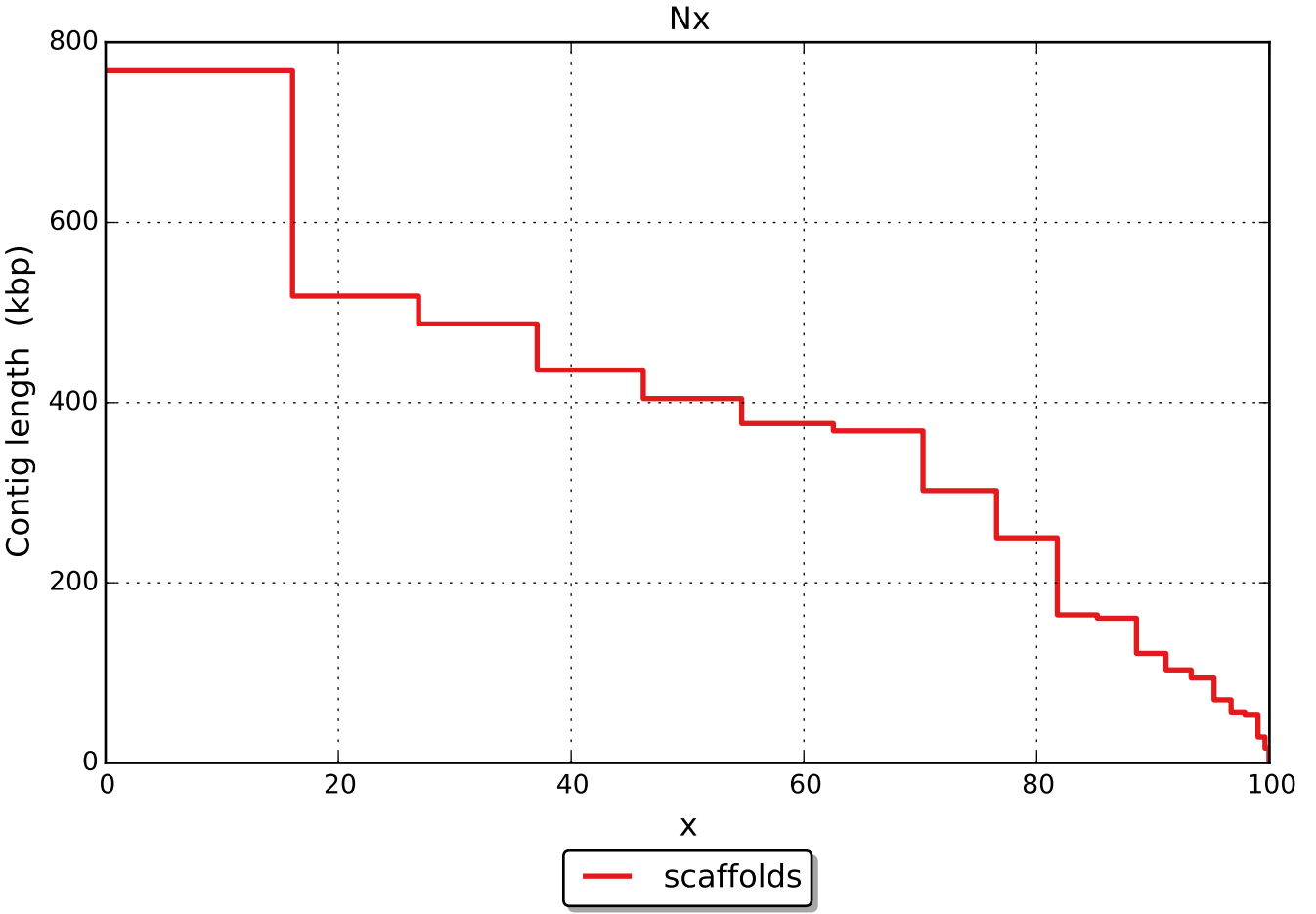
	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# mismatches	13794
# indels	48
# short indels	48
# long indels	0
Indels length	55

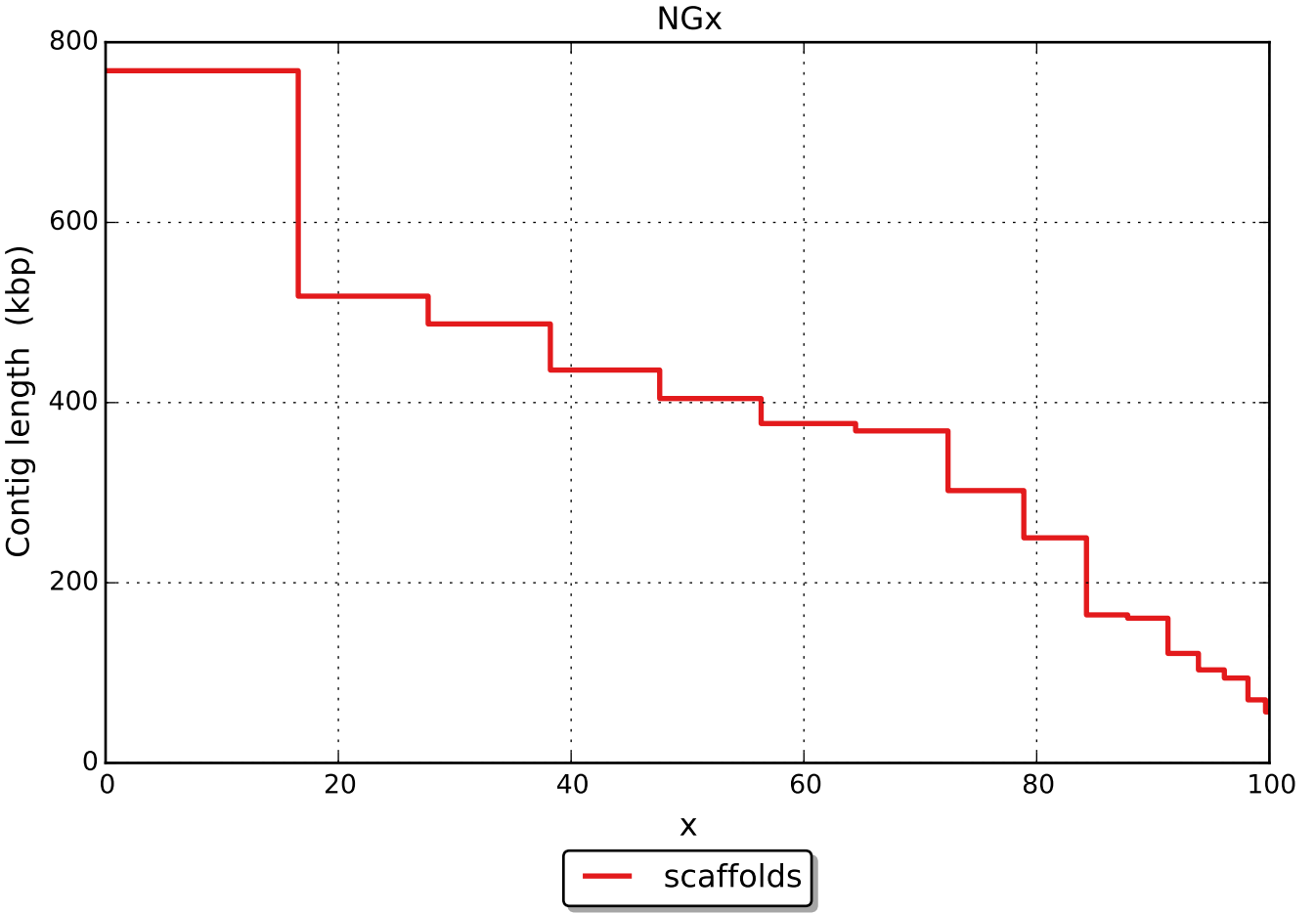
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

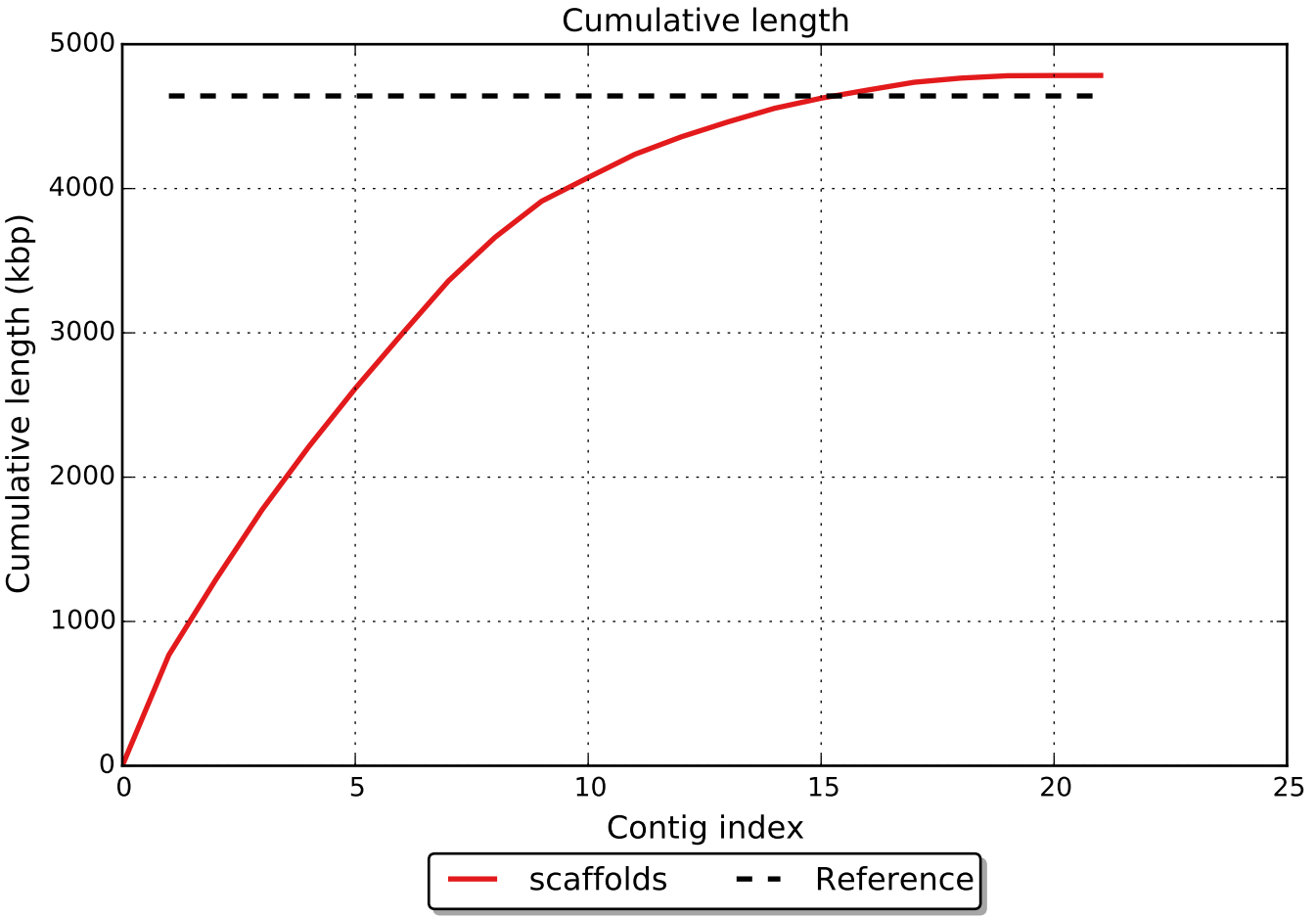
Unaligned report

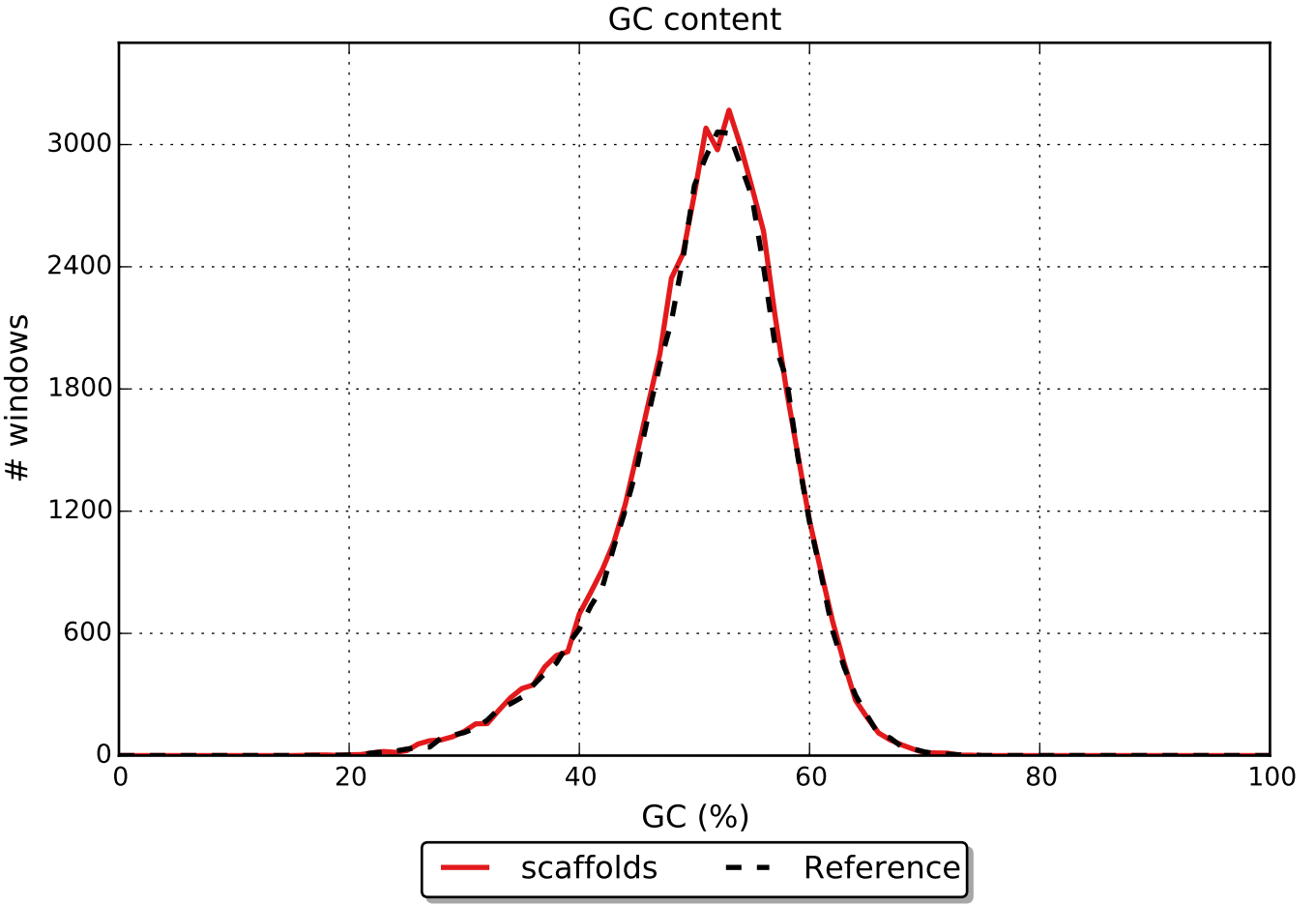
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	96

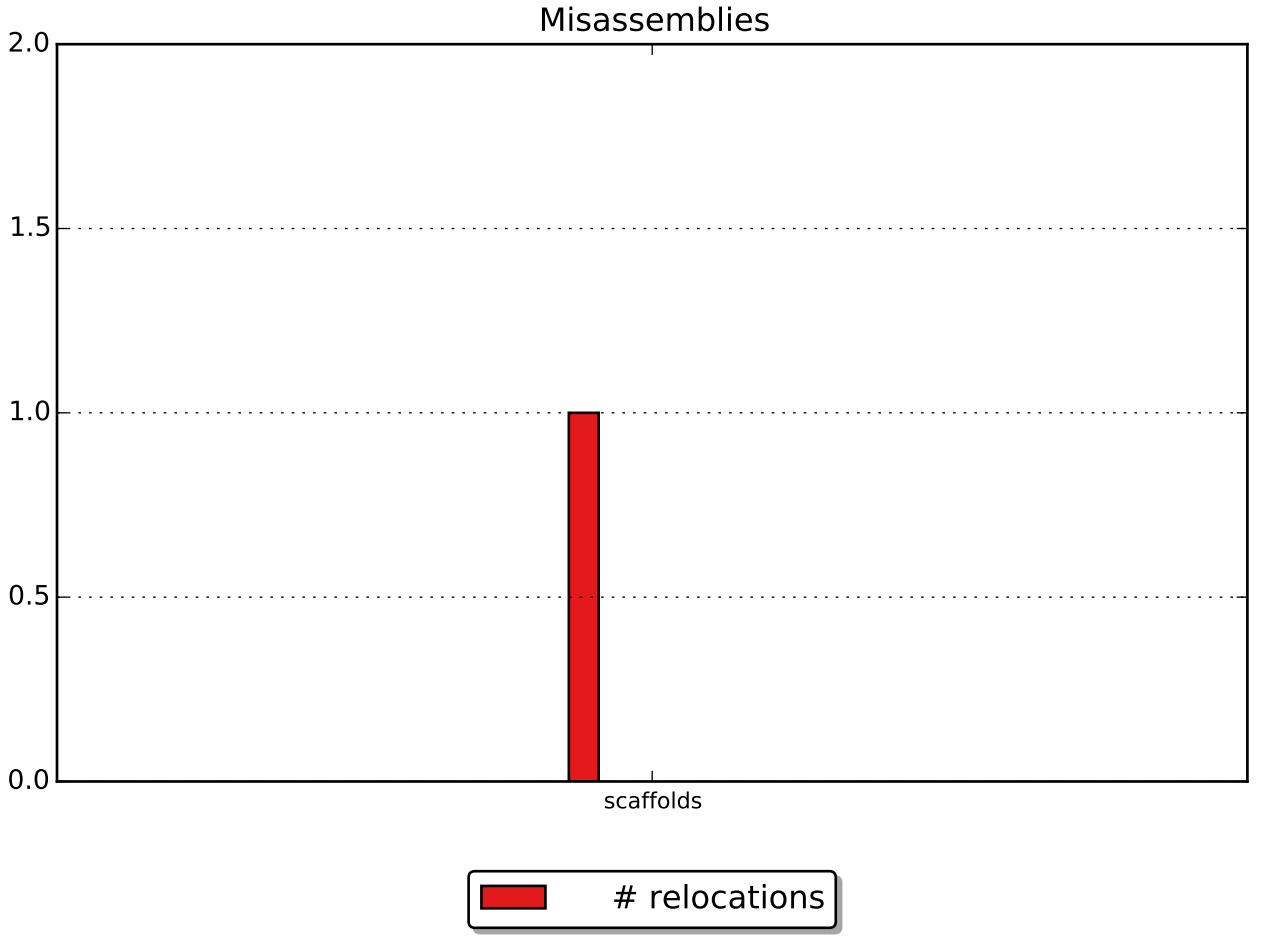
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

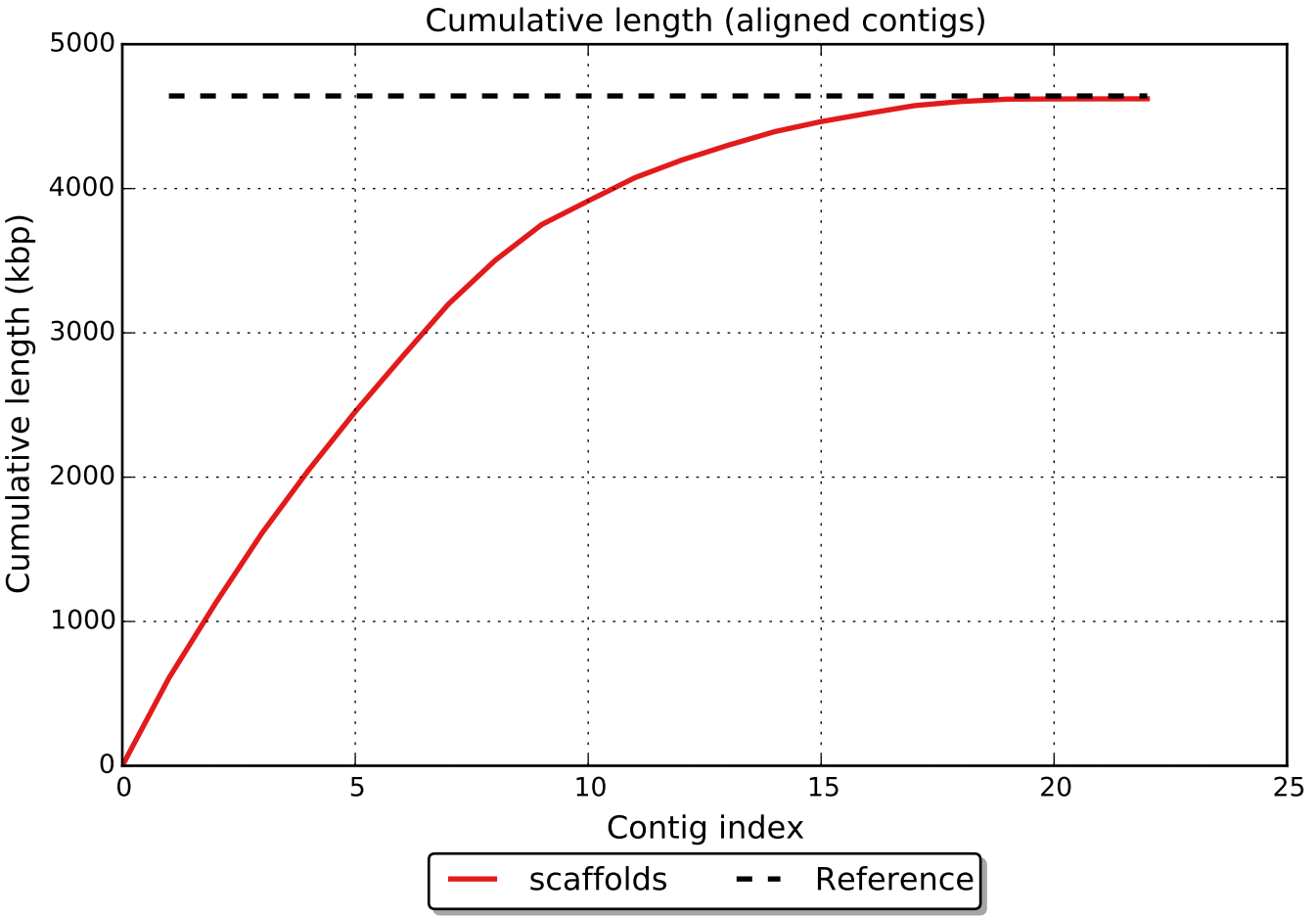

Nx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

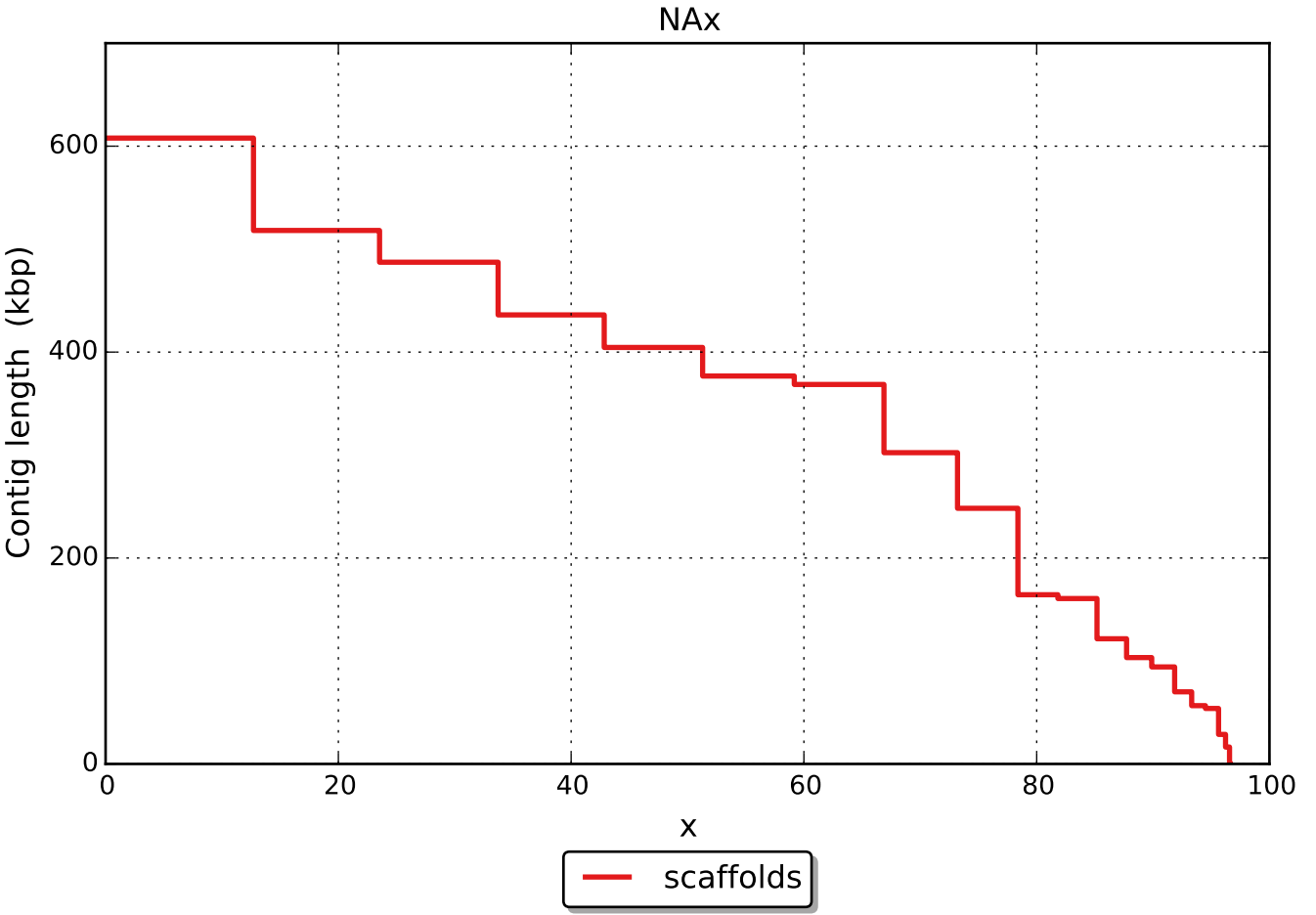

NGx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

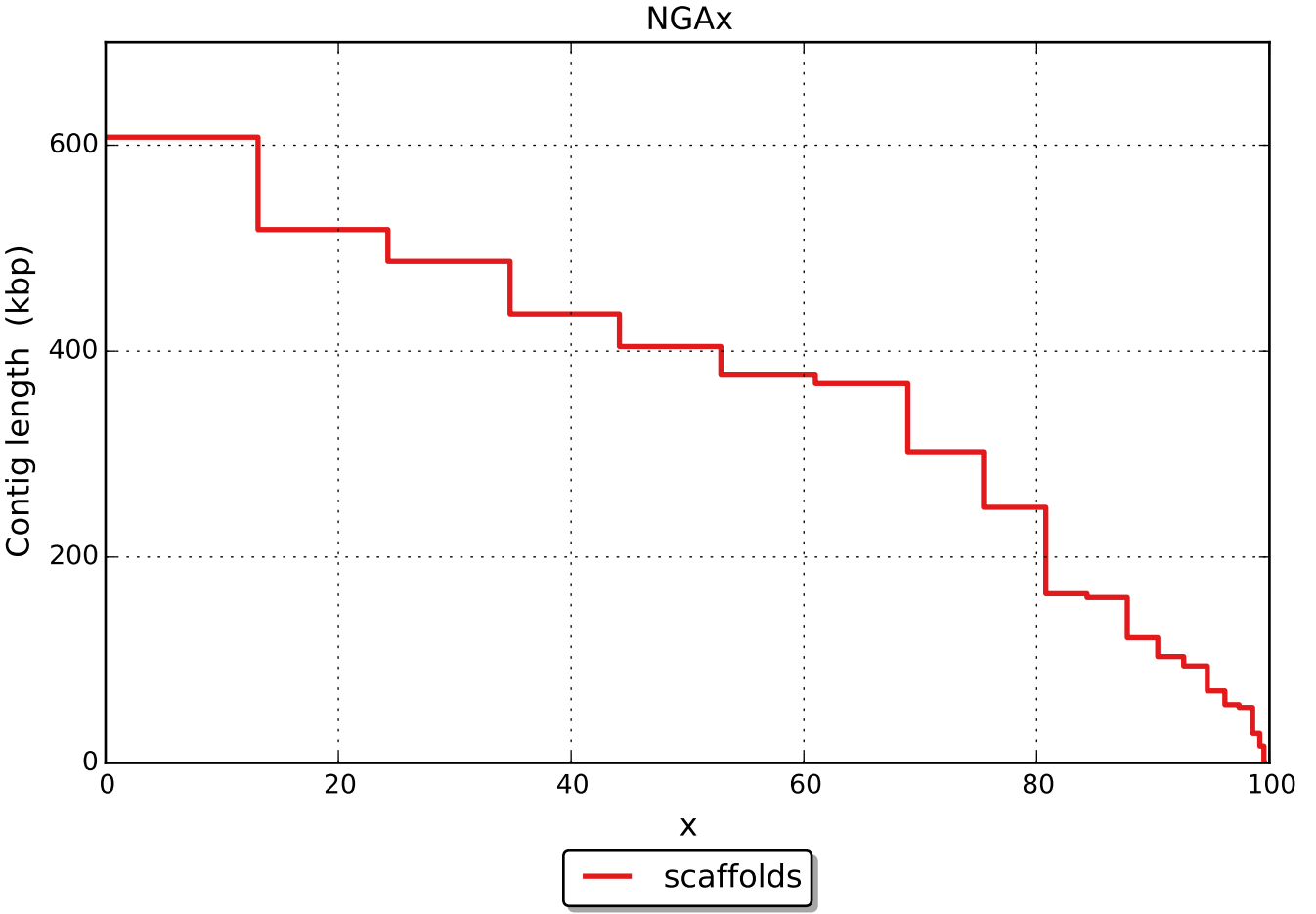

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
scaffolds
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
scaffolds
relocations


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


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


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