Report

	scaffolds
# contigs (>= 1000 bp)	29
# contigs (>= 5000 bp)	23
# contigs (>= 10000 bp)	23
# contigs (>= 25000 bp)	23
# contigs (>= 50000 bp)	21
Total length (>= 1000 bp)	4600654
Total length (>= 5000 bp)	4594036
Total length (>= 10000 bp)	4594036
Total length (>= 25000 bp)	4594036
Total length (>= 50000 bp)	4540240
# contigs	34
Largest contig	529642
Total length	4604057
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	291704
NG50	291704
N75	242035
NG75	242035
L50	6
LG50	6
L75	10
LG75	10
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.145
Duplication ratio	1.000
# N's per 100 kbp	0.65
# mismatches per 100 kbp	447.22
# indels per 100 kbp	0.98
Largest alignment	529642
NA50	291704
NGA50	291704
NA75	240233
NGA75	240233
LA50	6
LGA50	6
LA75	10
LGA75	10

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

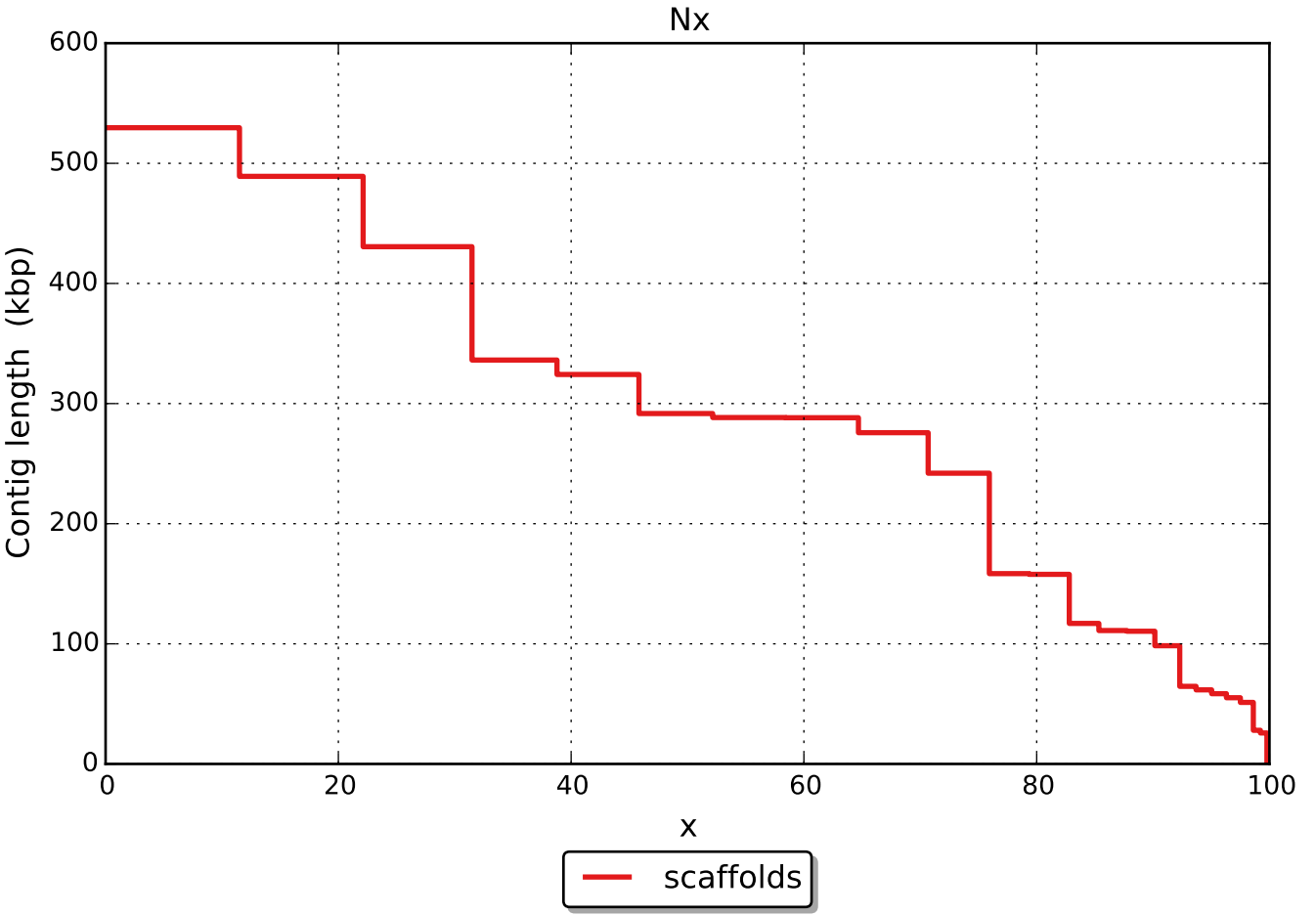
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	20581
# indels	45
# short indels	45
# long indels	0
Indels length	48

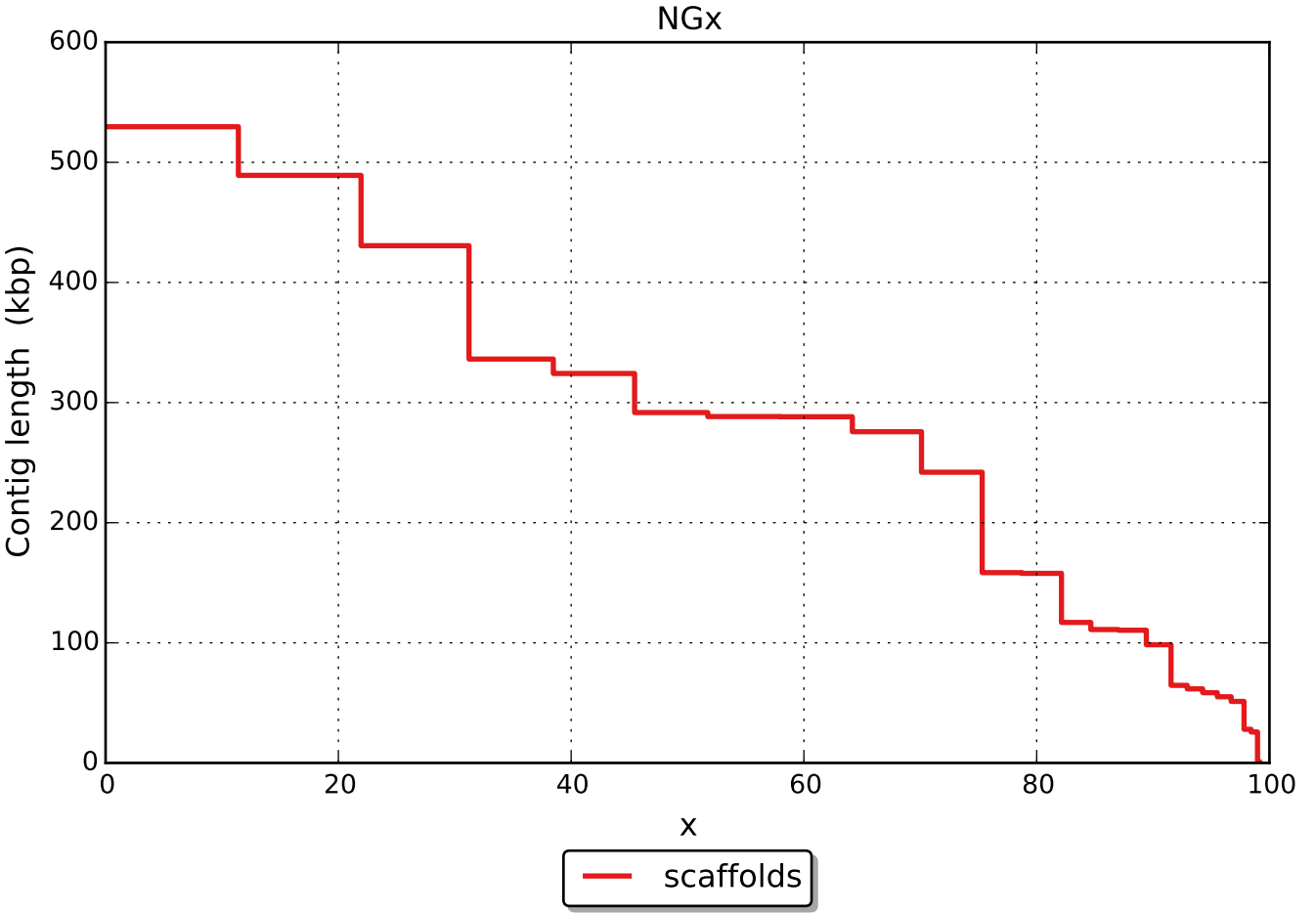
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

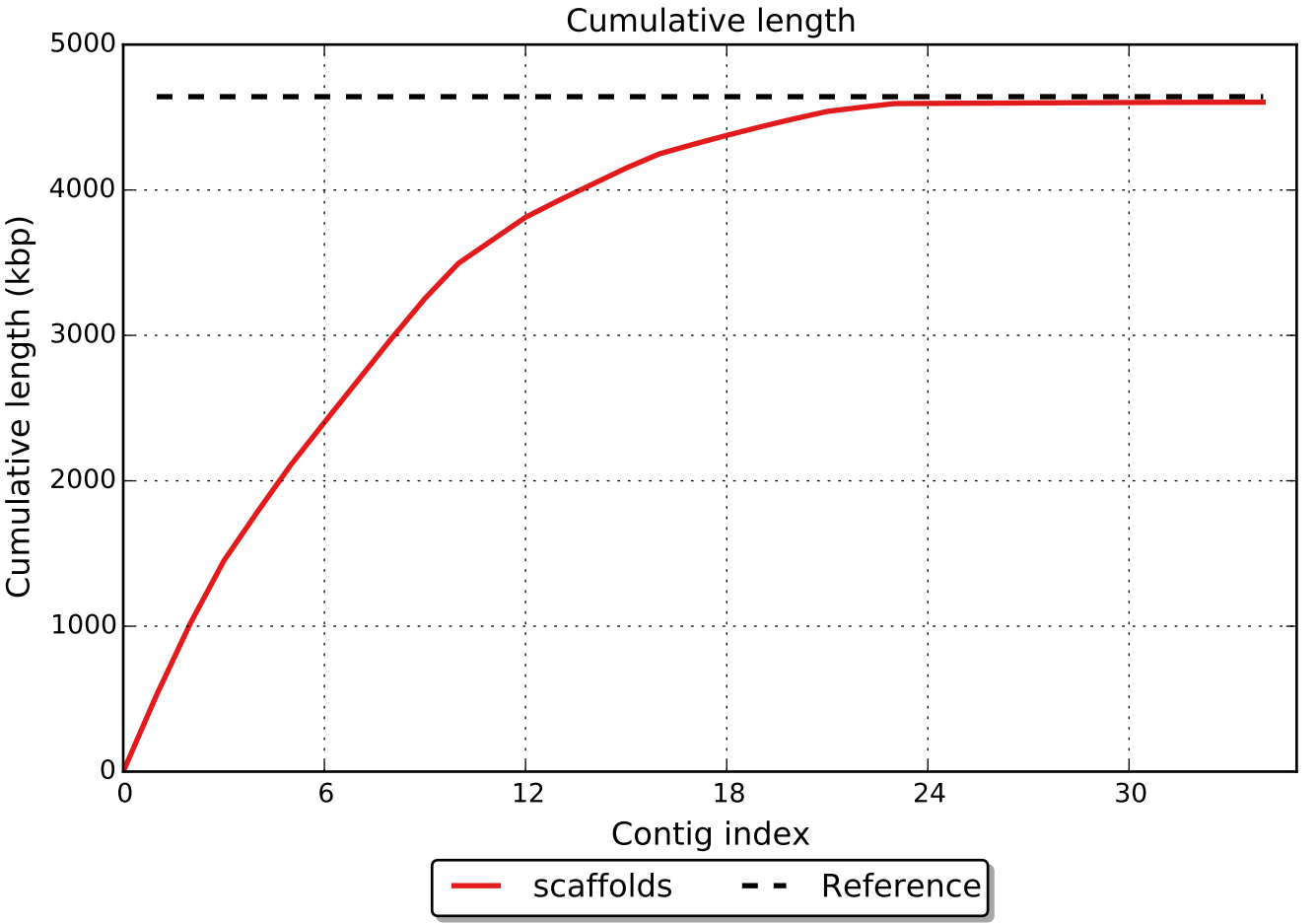
Unaligned report

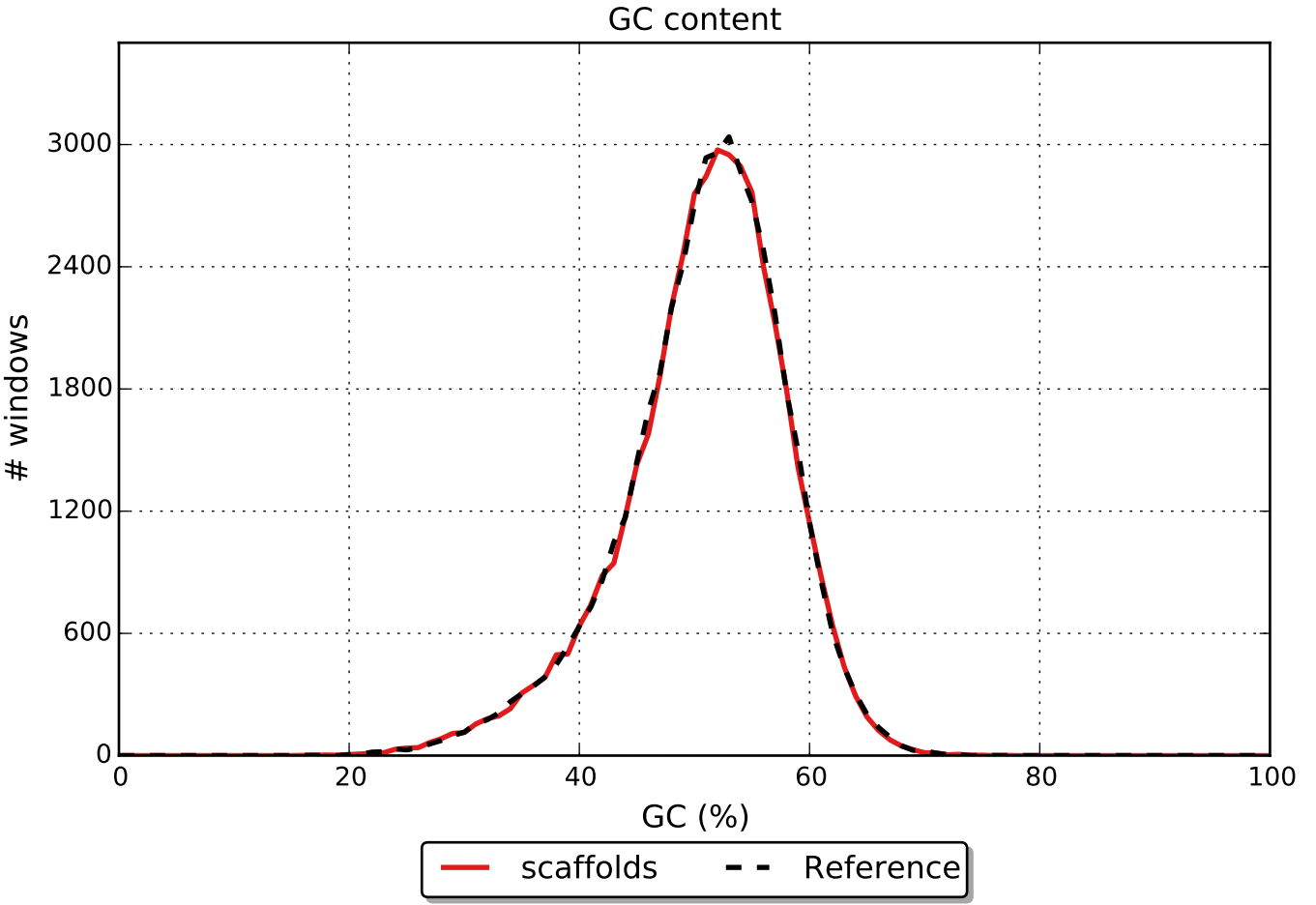
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	30

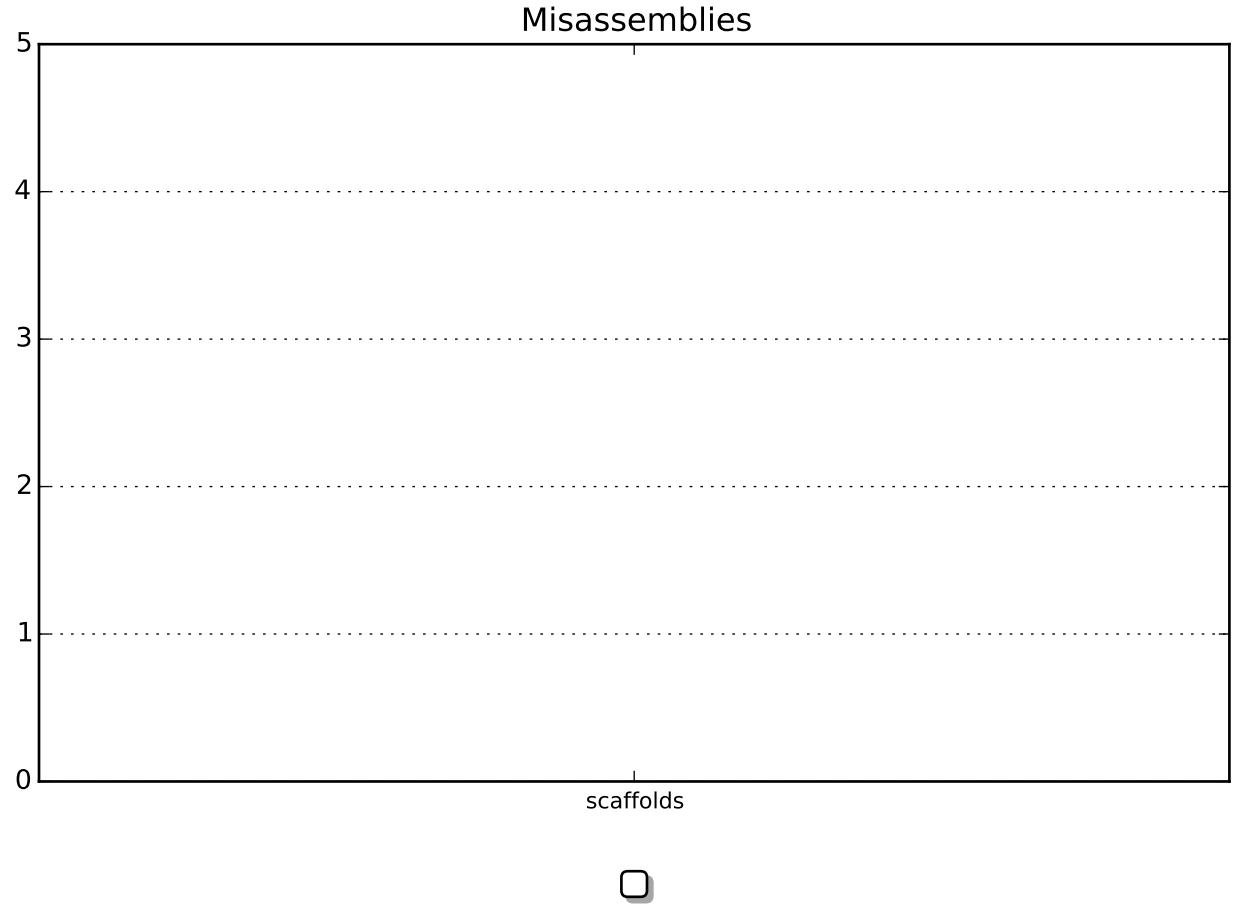
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

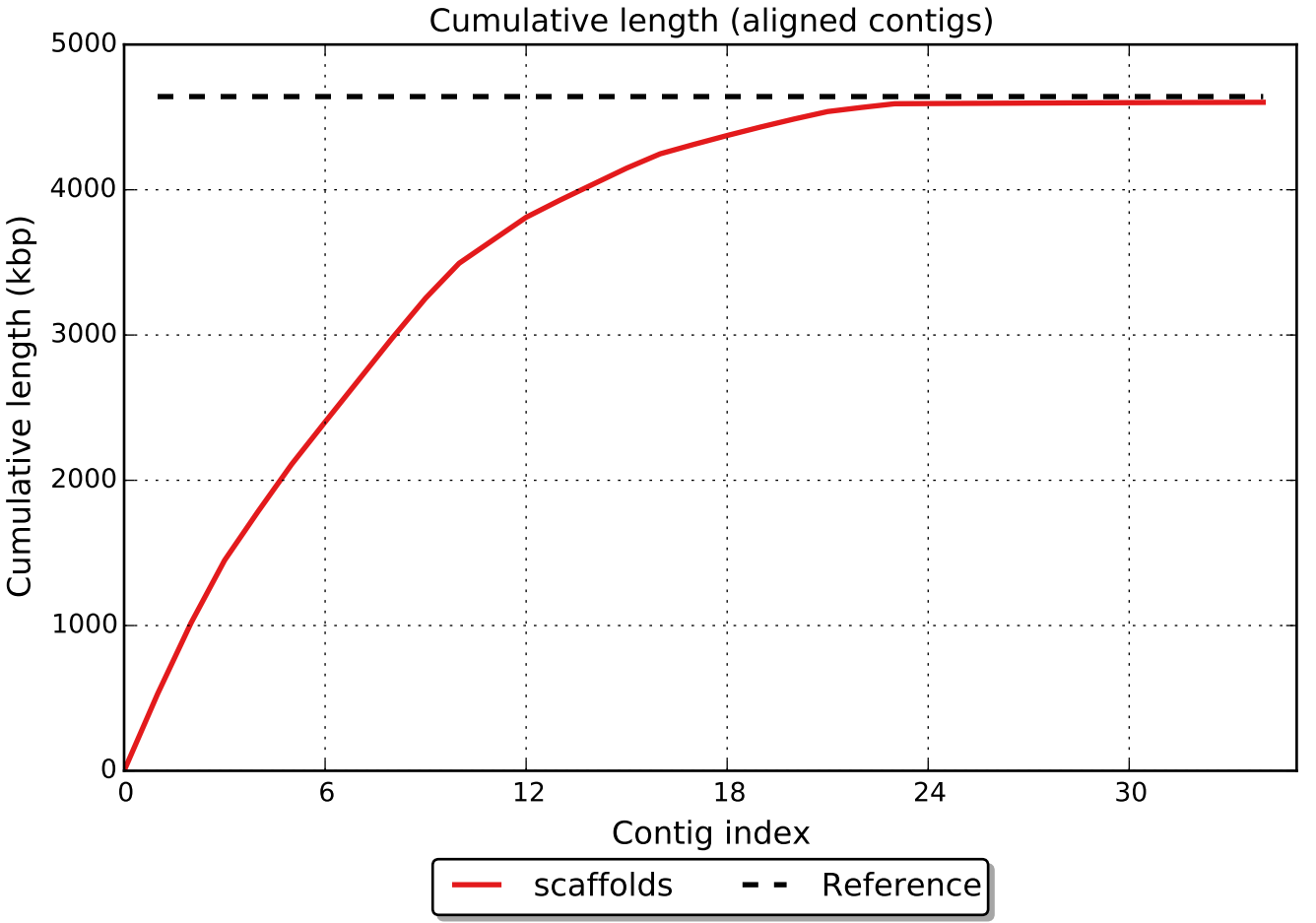

Nx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

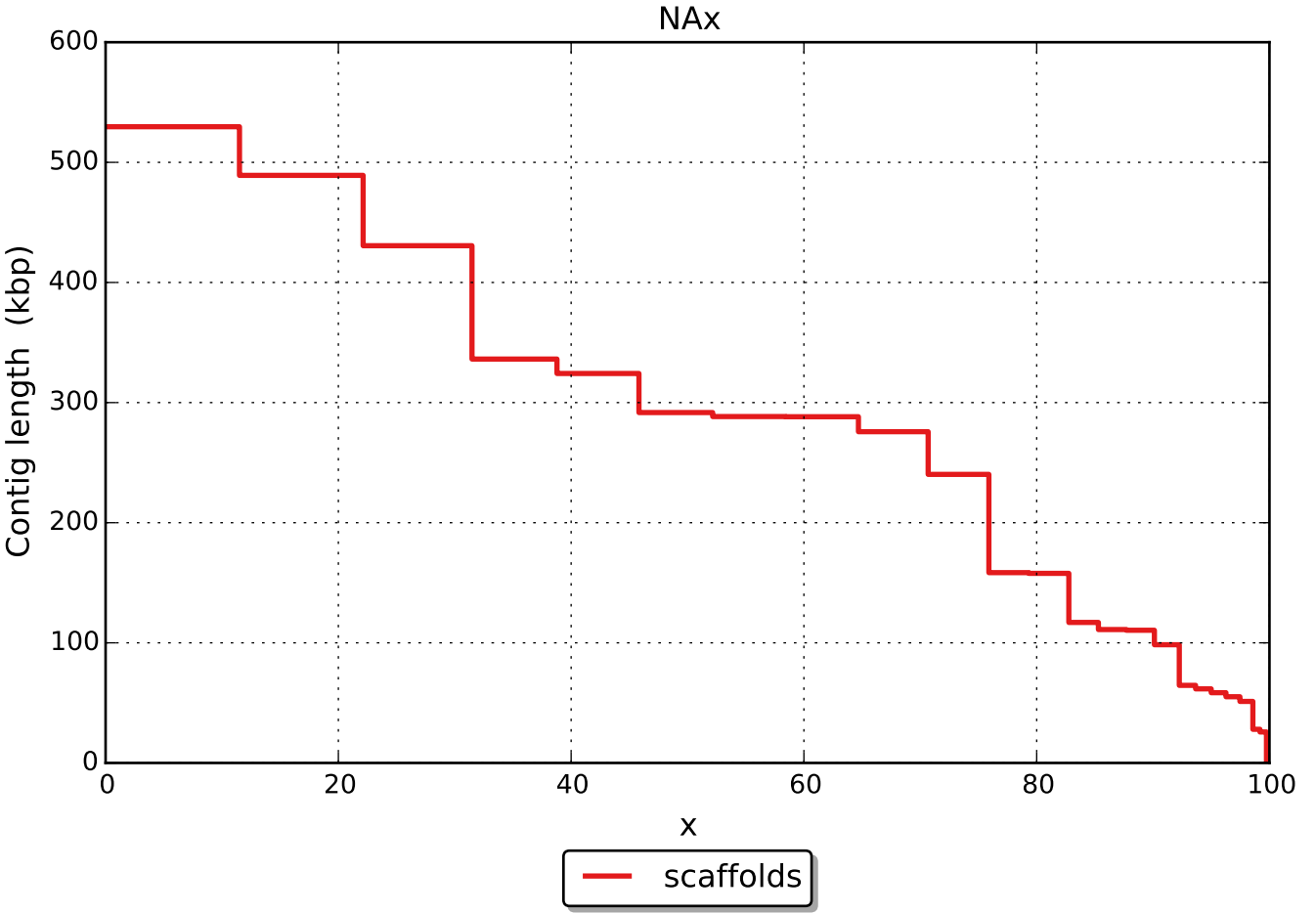

NGx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

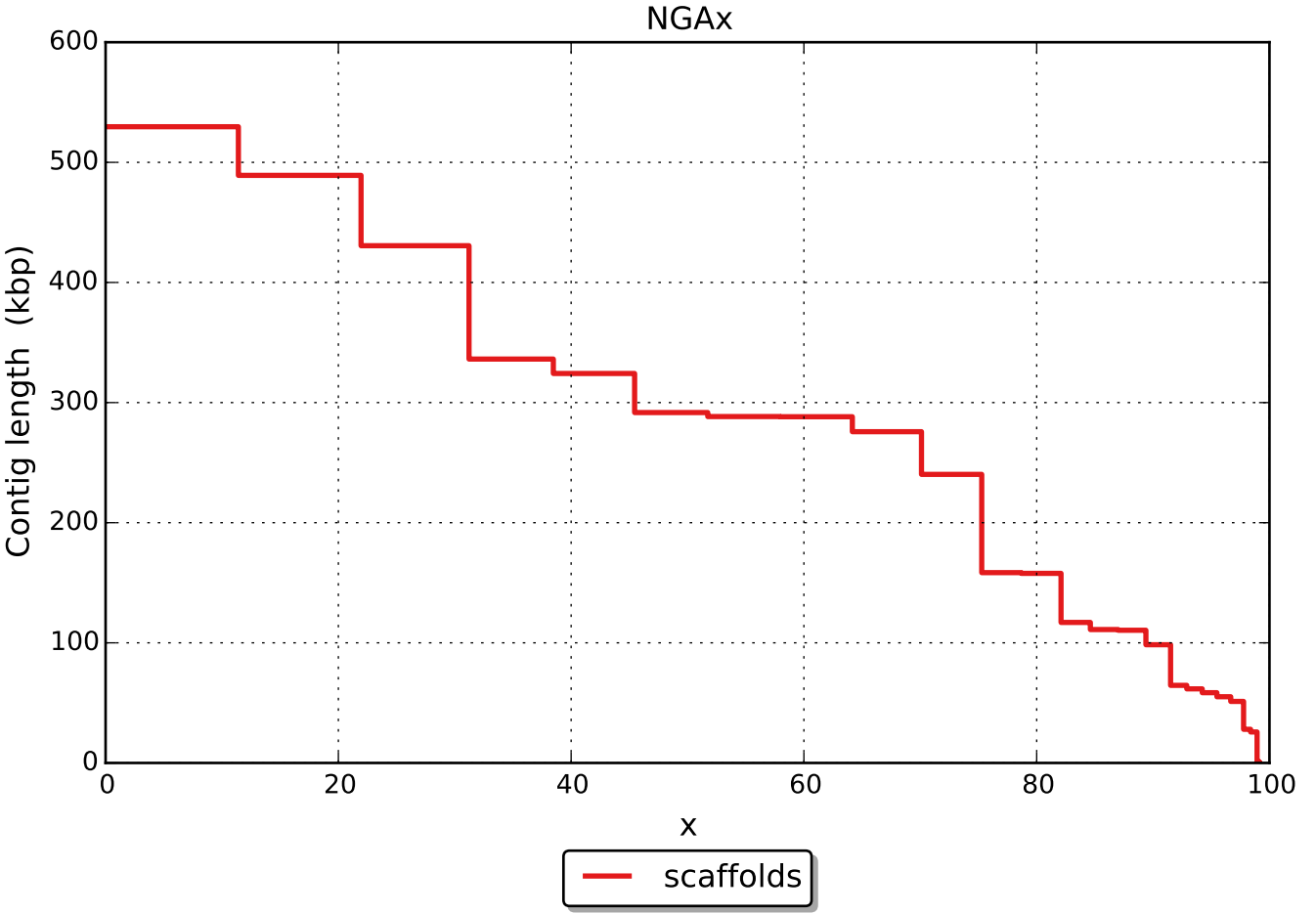

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
6
12
18
24
30
Contig index
scaffolds
Reference


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
6
12
18
24
30
Contig index
scaffolds
Reference


NAx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds


NGAx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds