Report

	scaffolds
# contigs (>= 1000 bp)	65
# contigs (>= 5000 bp)	47
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4472769
Total length (>= 5000 bp)	4437064
Total length (>= 10000 bp)	4405031
Total length (>= 25000 bp)	4328971
Total length (>= 50000 bp)	3963118
# contigs	87
Largest contig	332068
Total length	4487534
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	164195
NG50	164195
N75	86542
NG75	86186
L50	11
LG50	11
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.629
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	733.64
# indels per 100 kbp	0.62
Largest alignment	332068
NA50	164195
NGA50	164195
NA75	86542
NGA75	86186
LA50	11
LGA50	11
LA75	20
LGA75	21

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

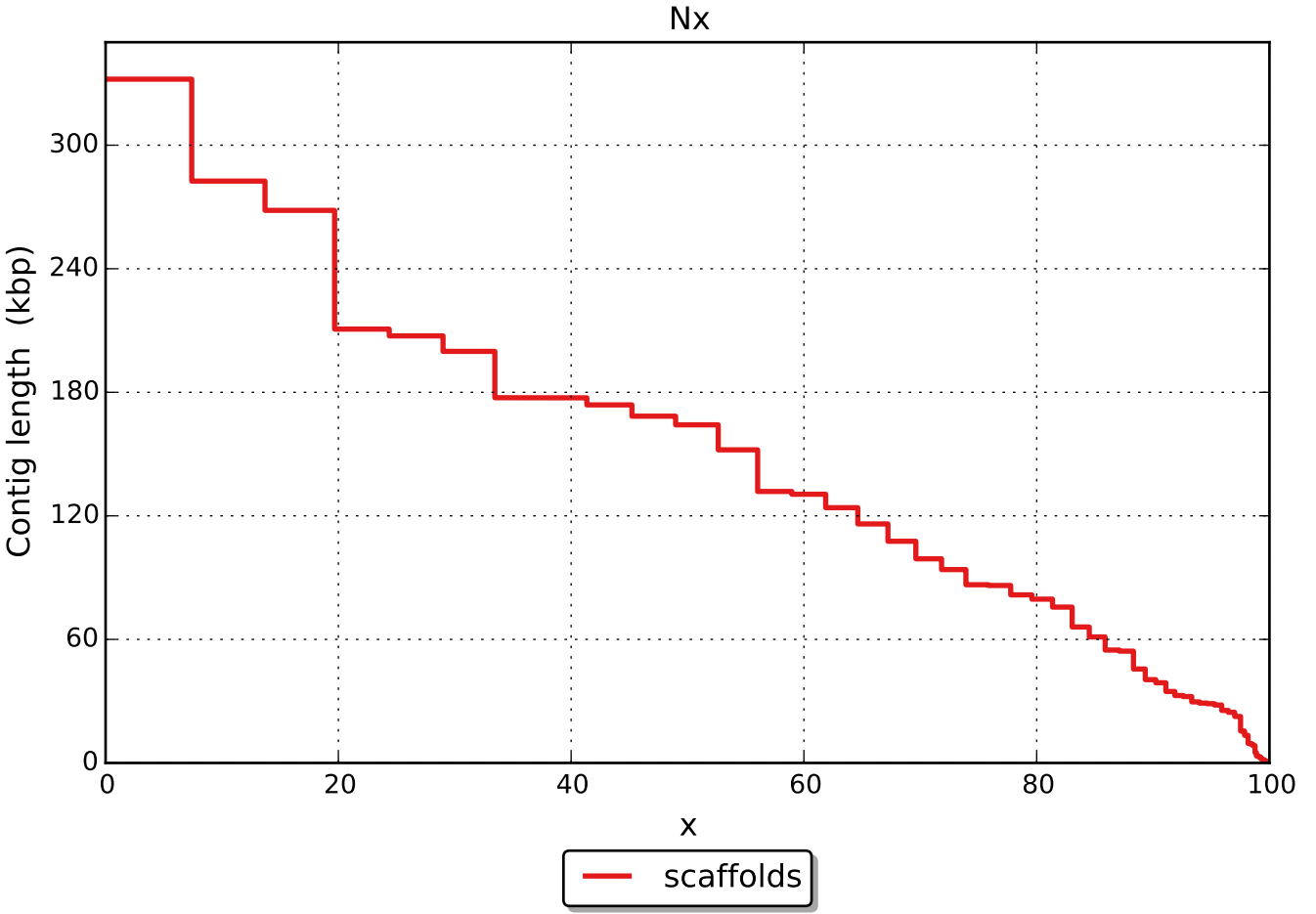
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	32905
# indels	28
# short indels	28
# long indels	0
Indels length	34

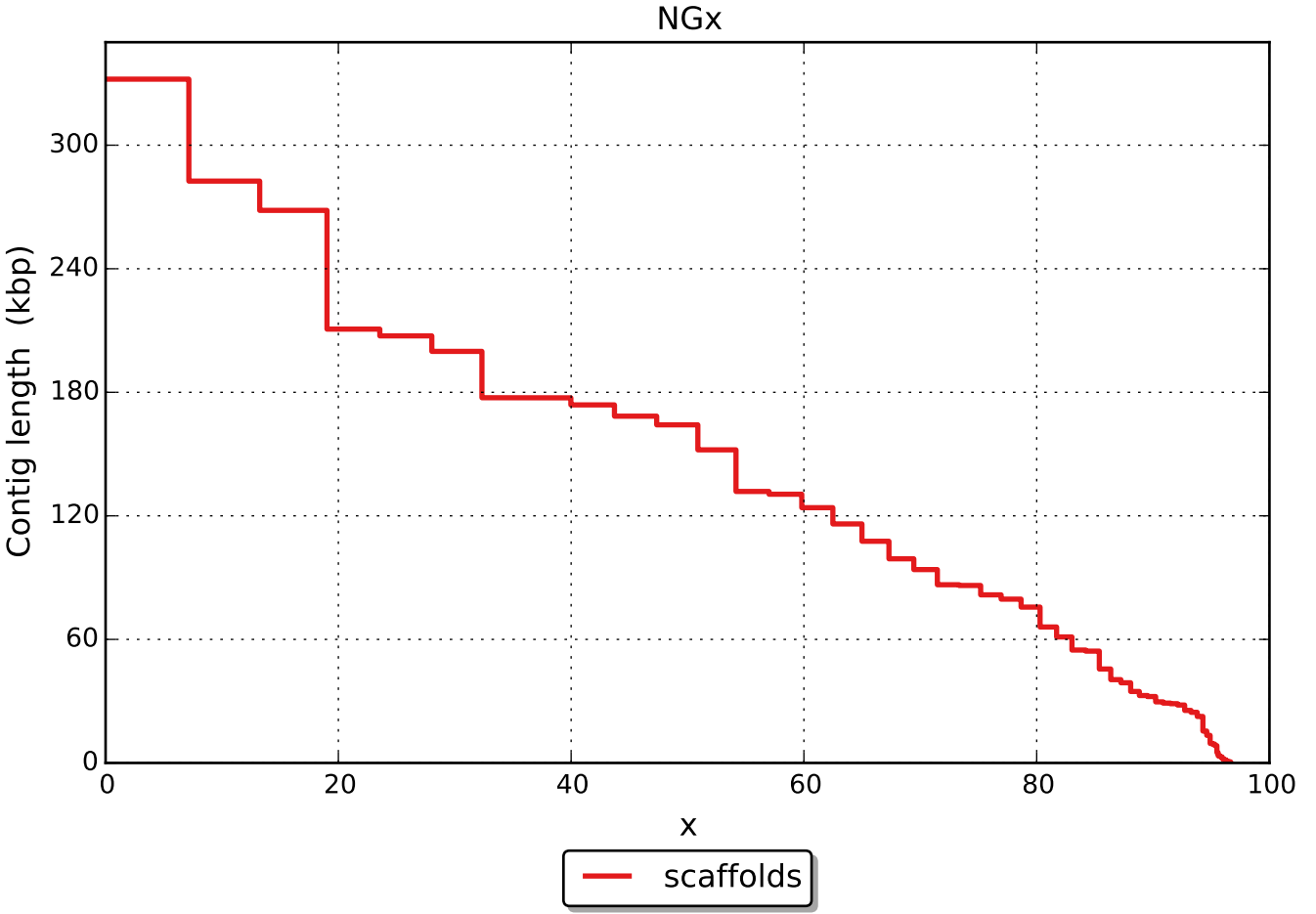
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

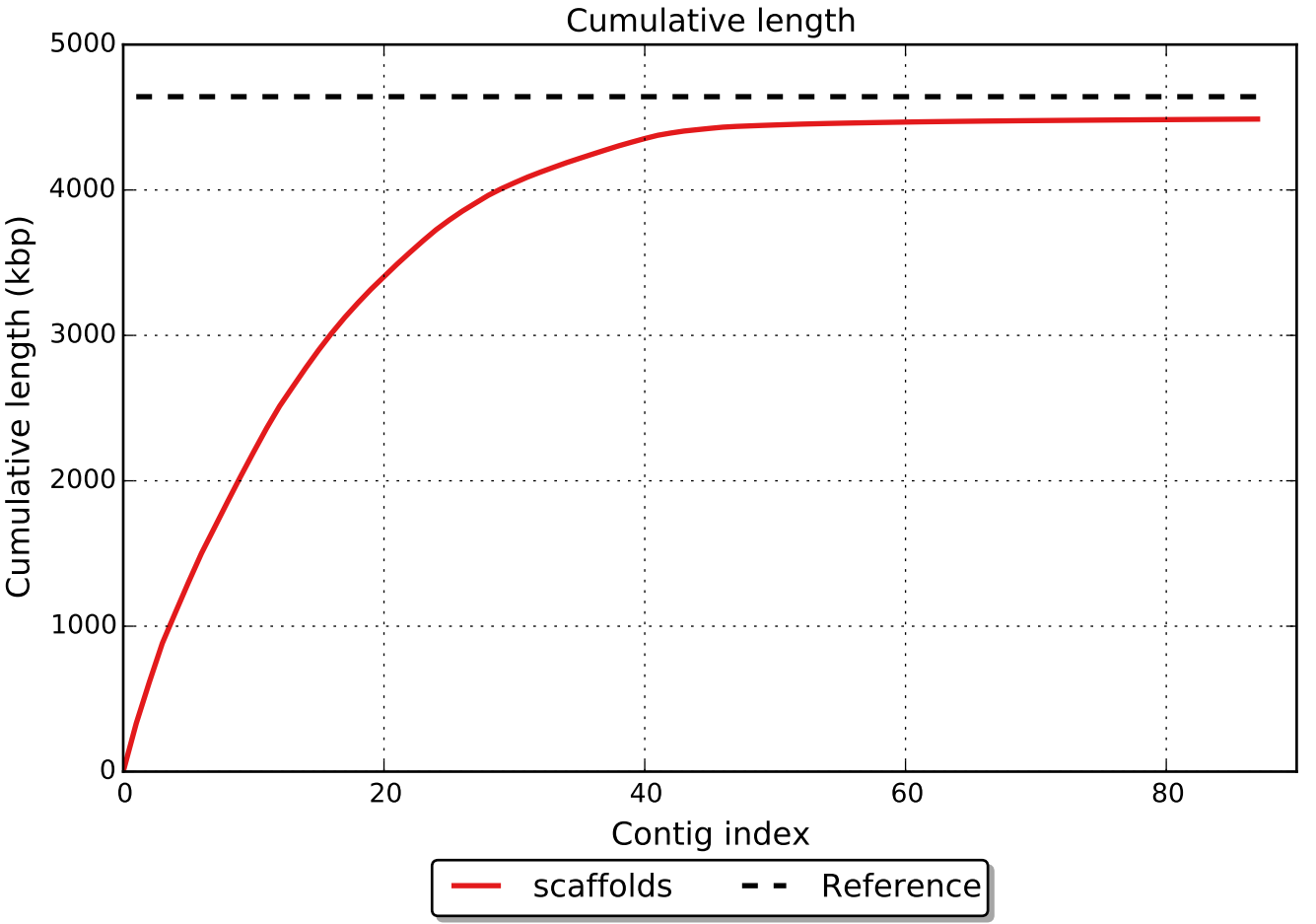
Unaligned report

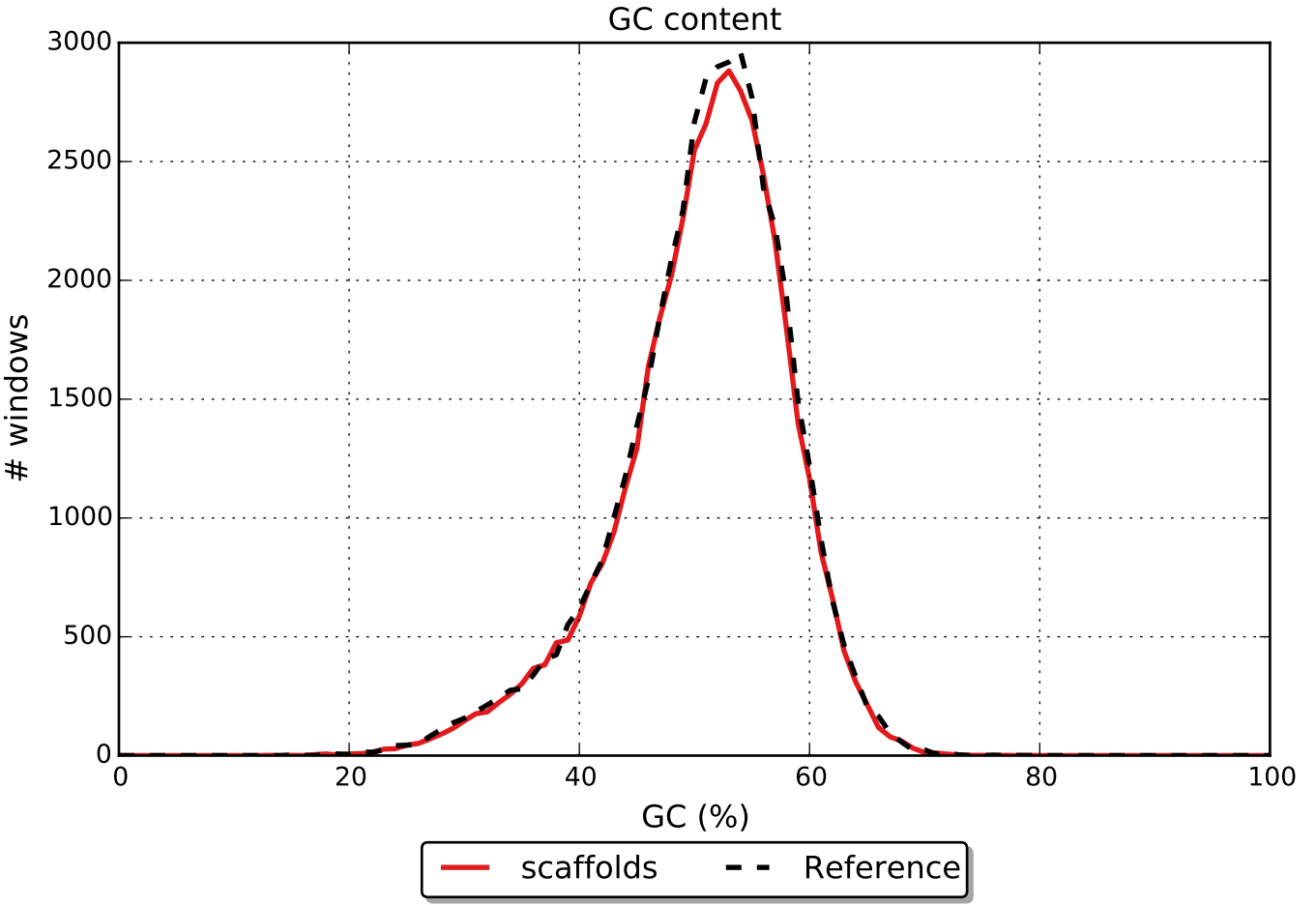
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

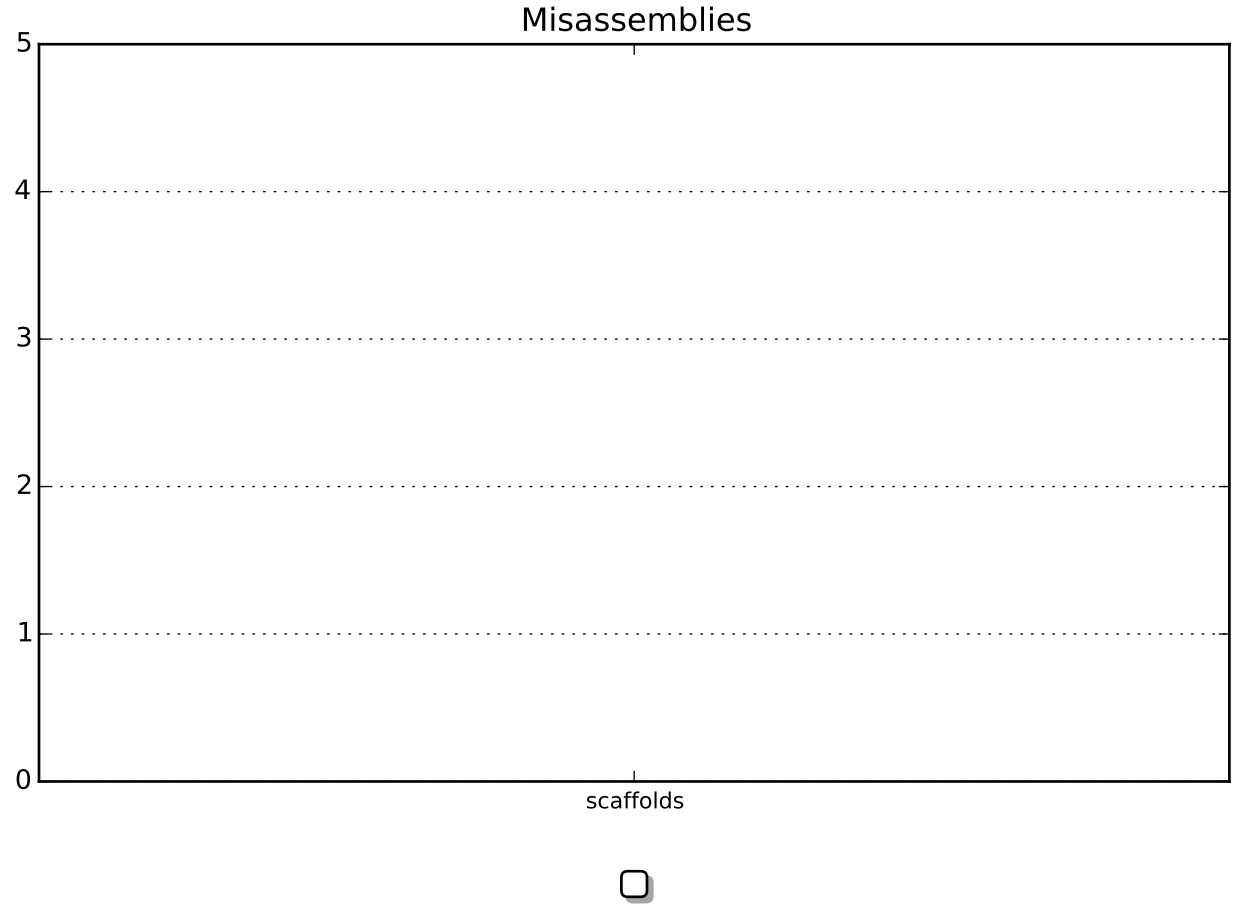
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

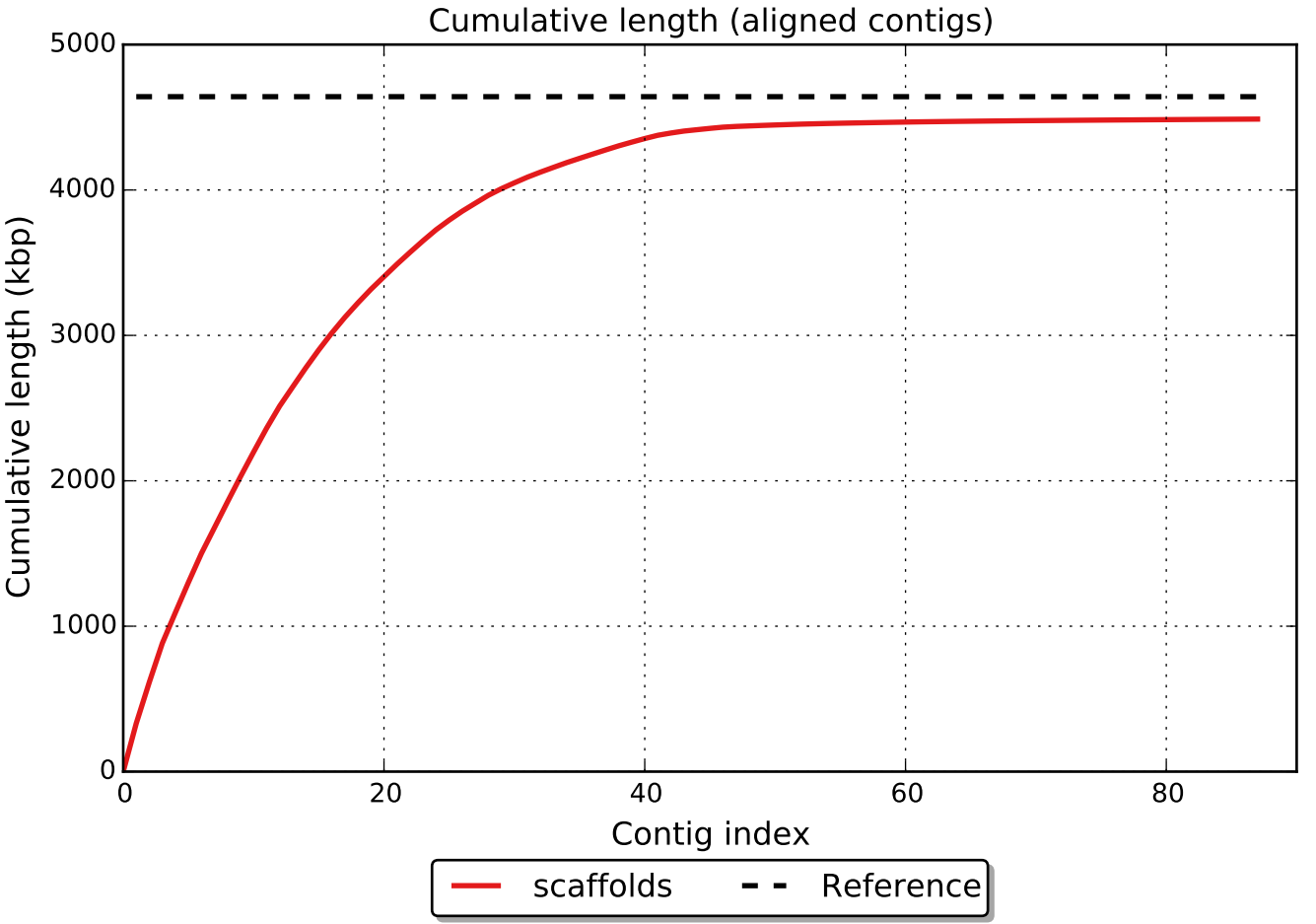

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

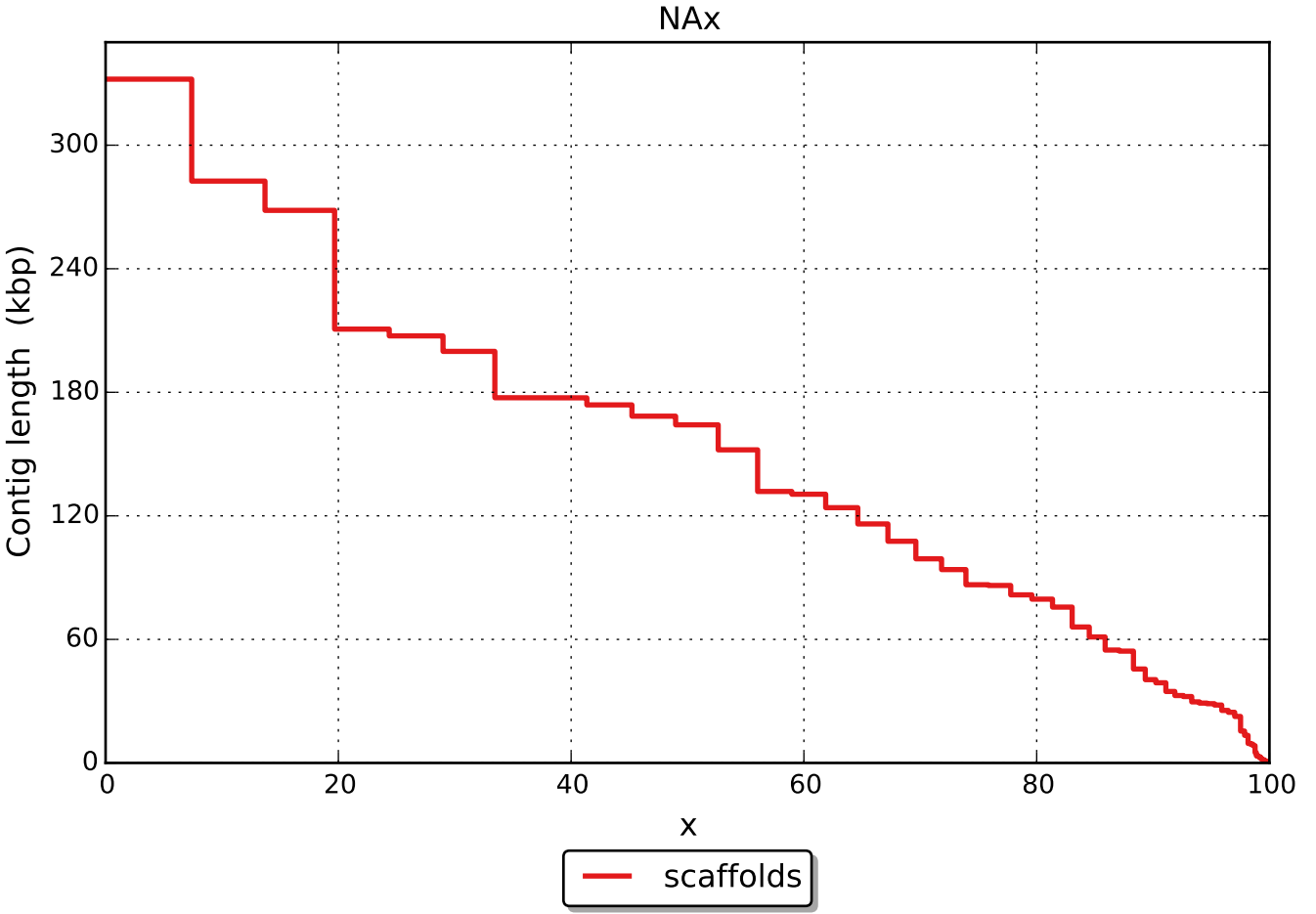

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

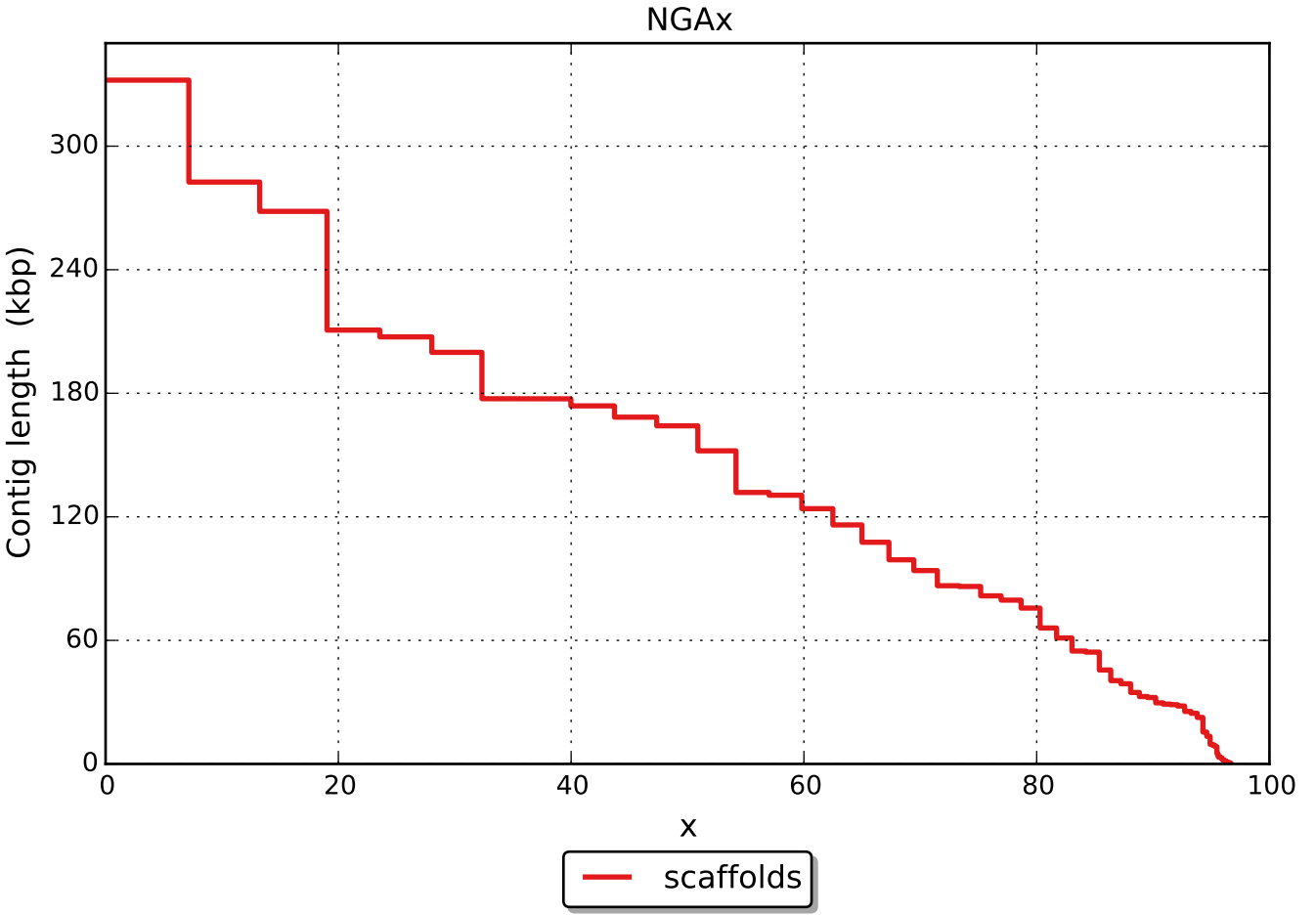

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
scaffolds
Reference


Misassemblies
5
4
3
2
1
0
scaffolds


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds