Report

	scaffolds
# contigs (>= 1000 bp)	80
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	55
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4550585
Total length (>= 5000 bp)	4507705
Total length (>= 10000 bp)	4463142
Total length (>= 25000 bp)	4275525
Total length (>= 50000 bp)	3733992
# contigs	87
Largest contig	326979
Total length	4555927
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	132611
NG50	132611
N75	60768
NG75	59038
L50	11
LG50	11
L75	23
LG75	24
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	78666
# local misassemblies	14
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.114
Duplication ratio	1.000
# N's per 100 kbp	6.21
# mismatches per 100 kbp	62.82
# indels per 100 kbp	8.08
Largest alignment	326979
NA50	132611
NGA50	132611
NA75	60768
NGA75	59037
LA50	11
LGA50	11
LA75	23
LGA75	24

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

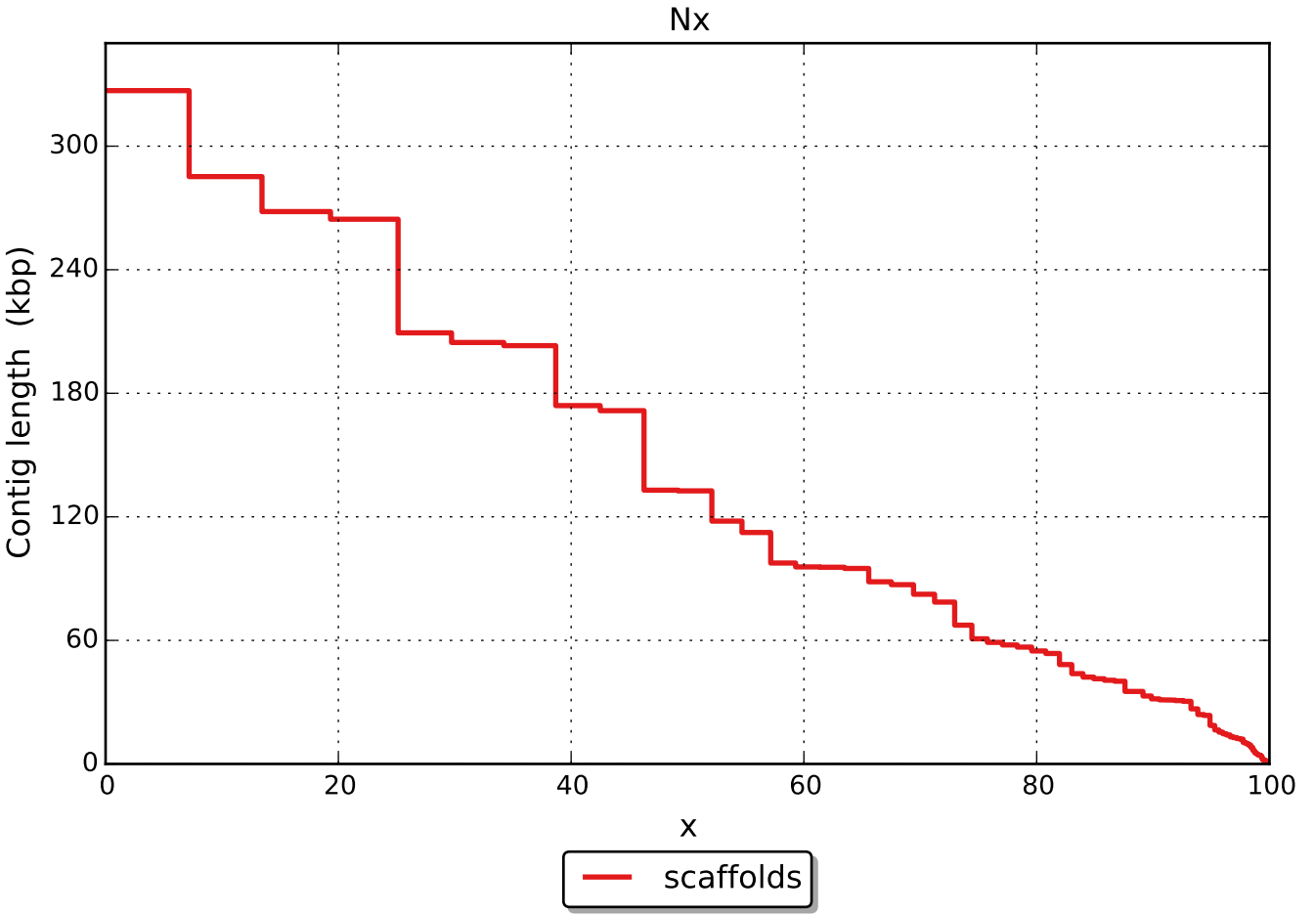
	scaffolds
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	78666
# local misassemblies	14
# mismatches	2861
# indels	368
# short indels	364
# long indels	4
Indels length	686

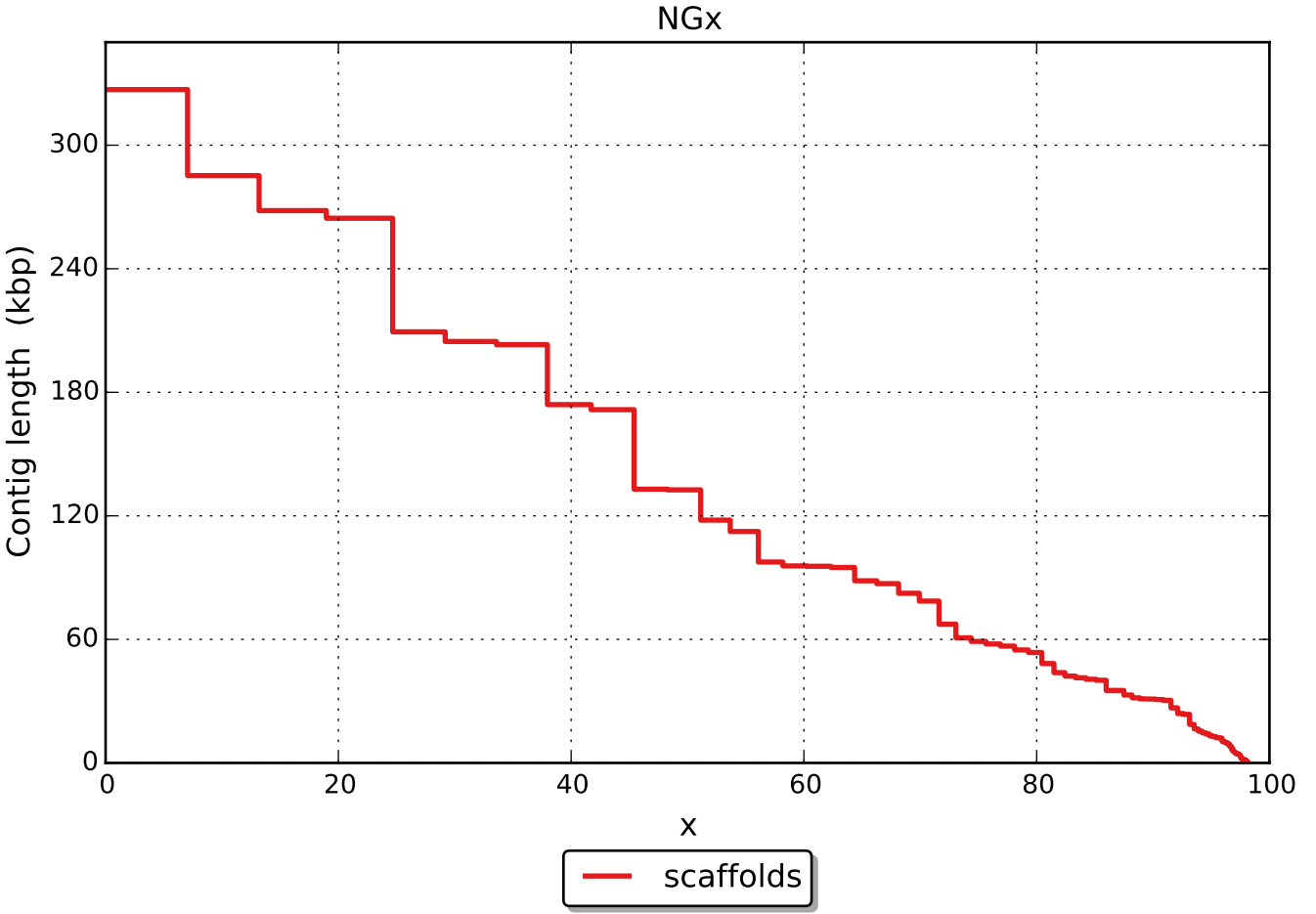
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

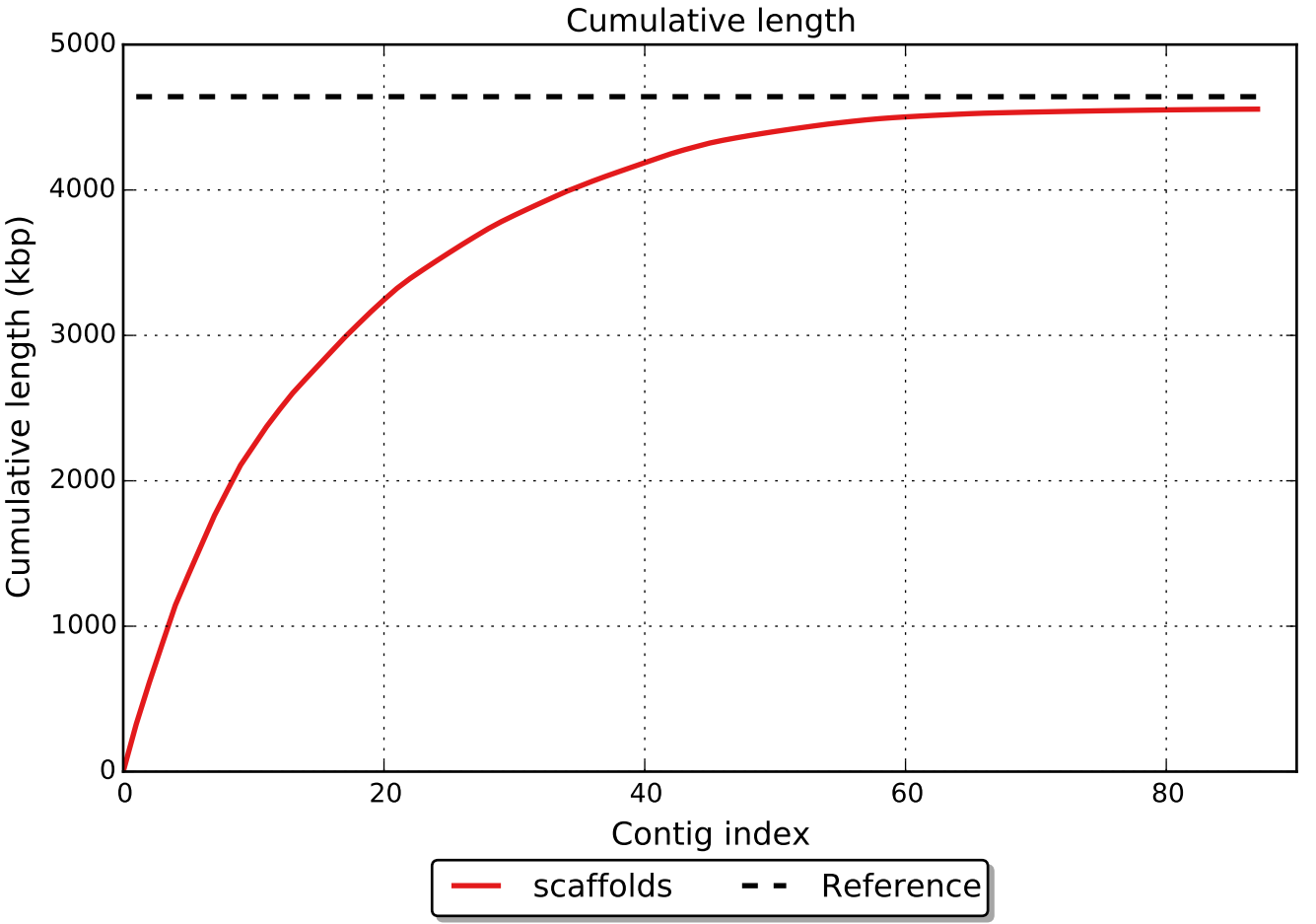
Unaligned report

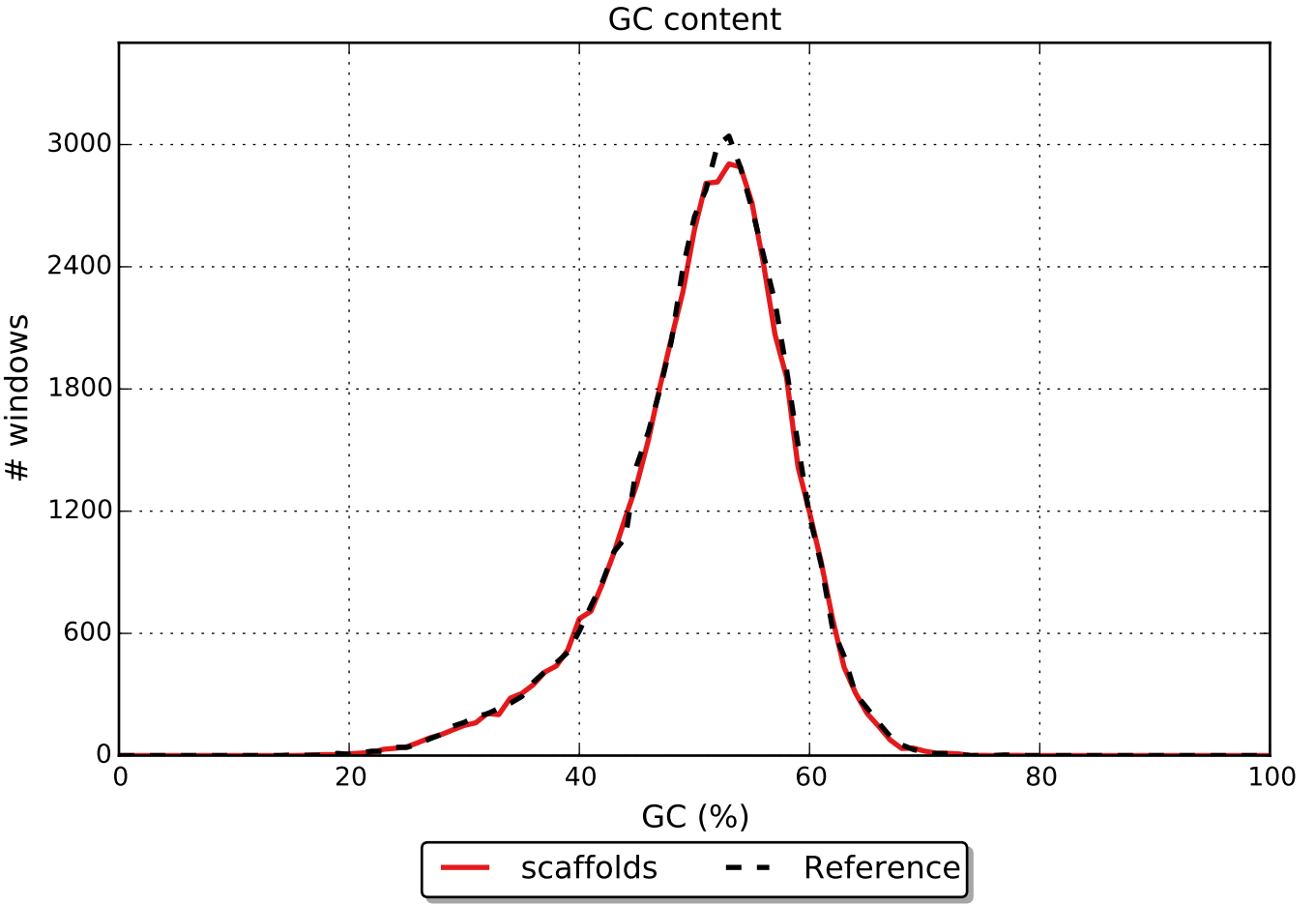
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	283

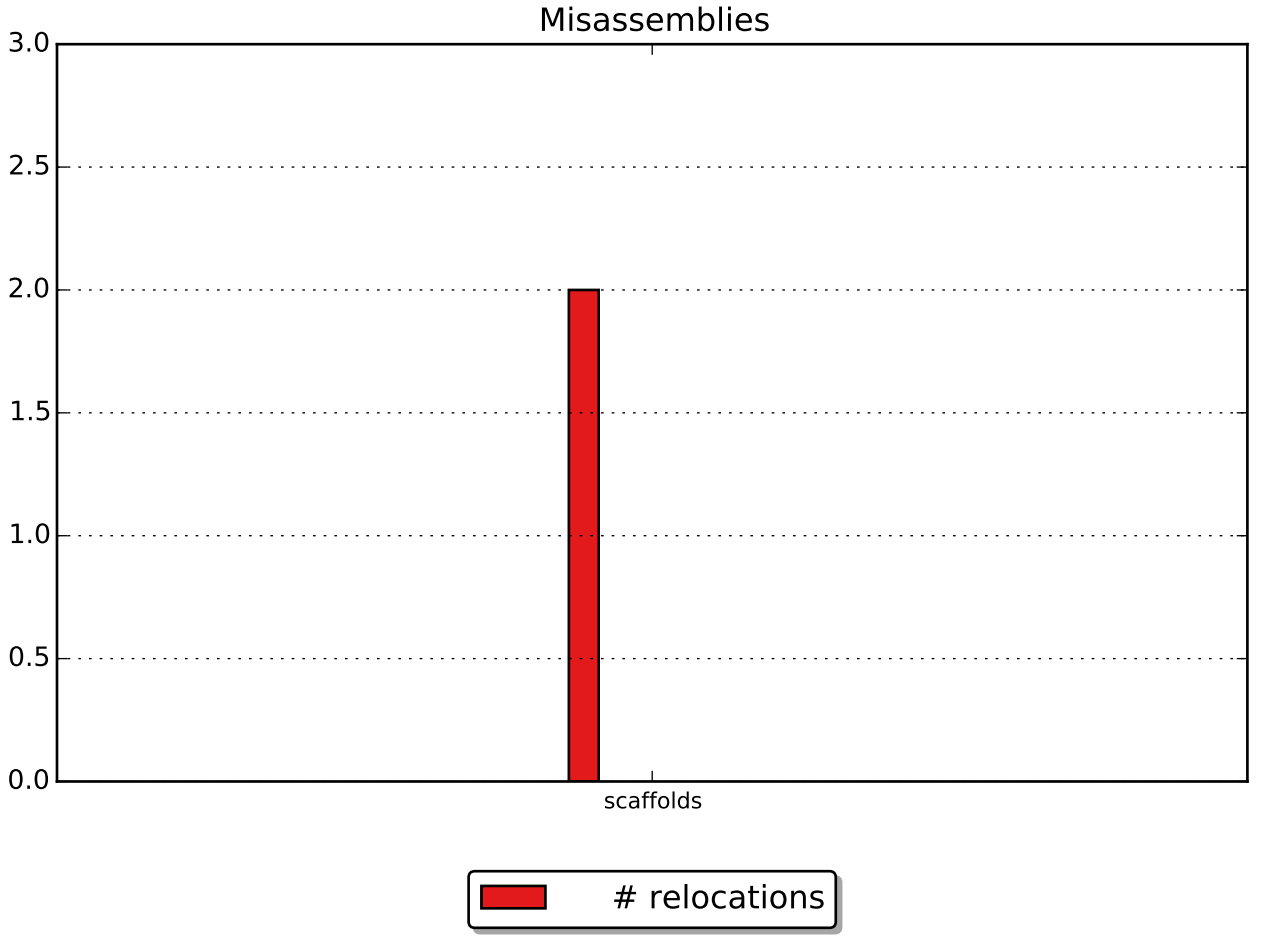
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

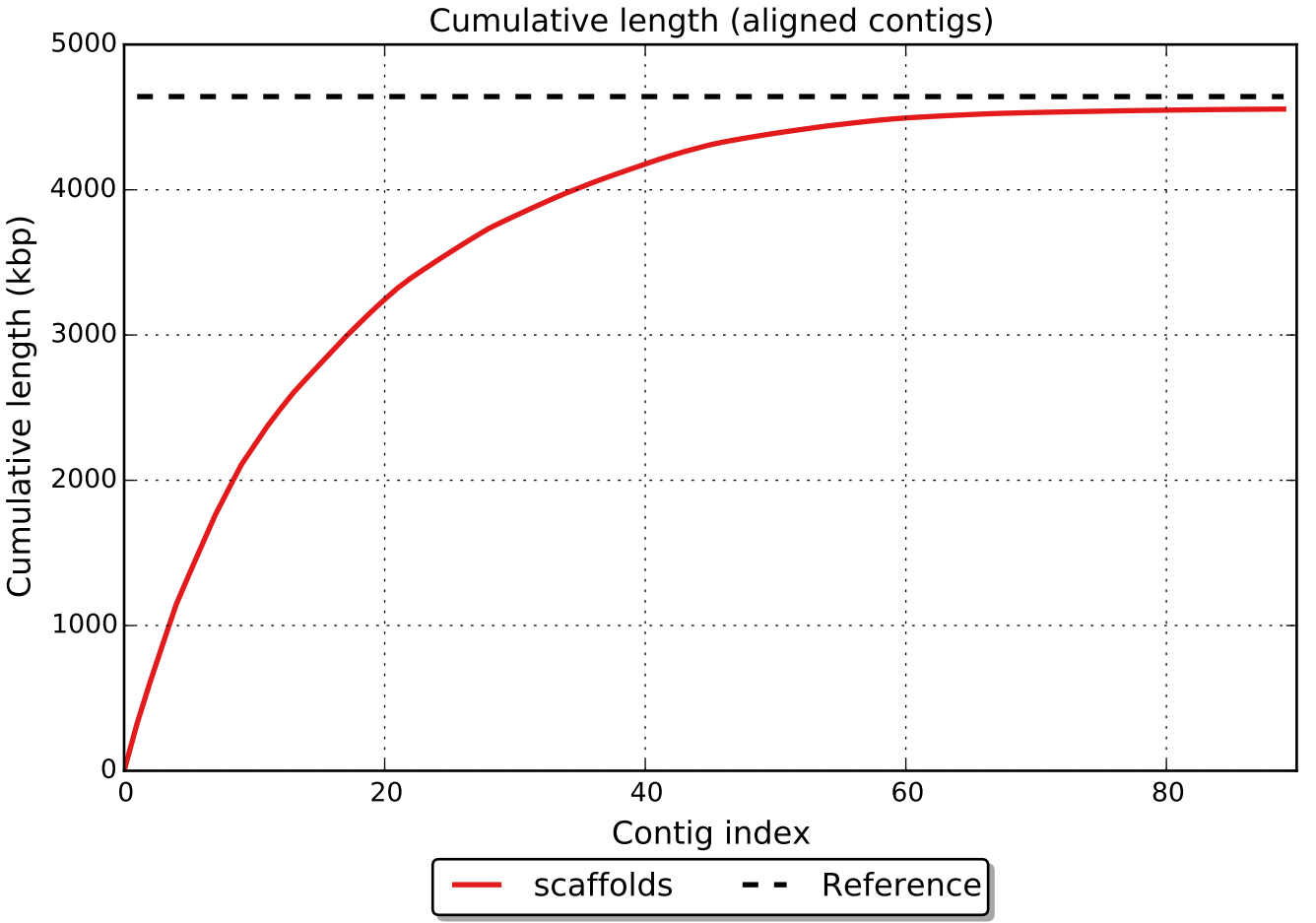

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

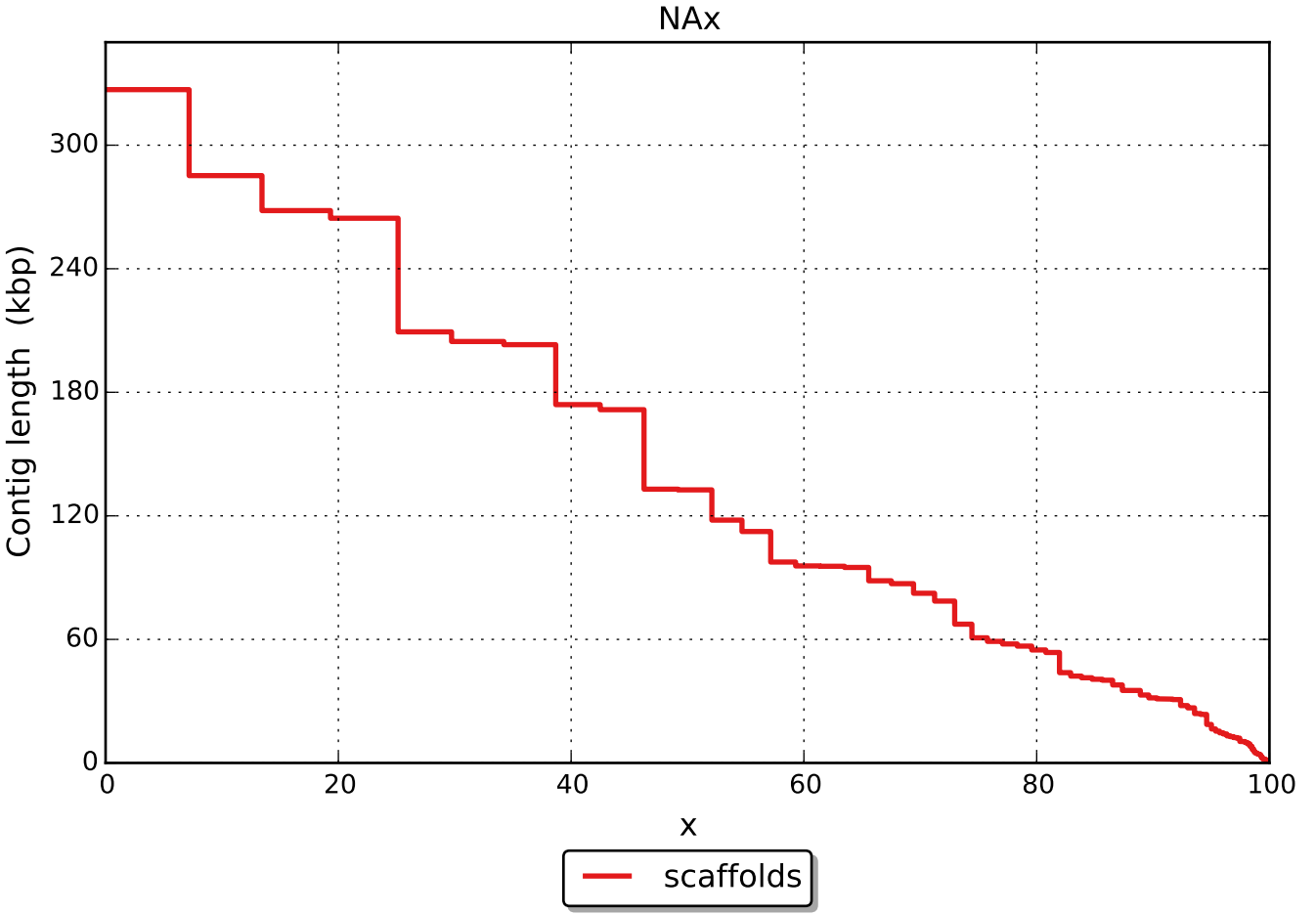

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

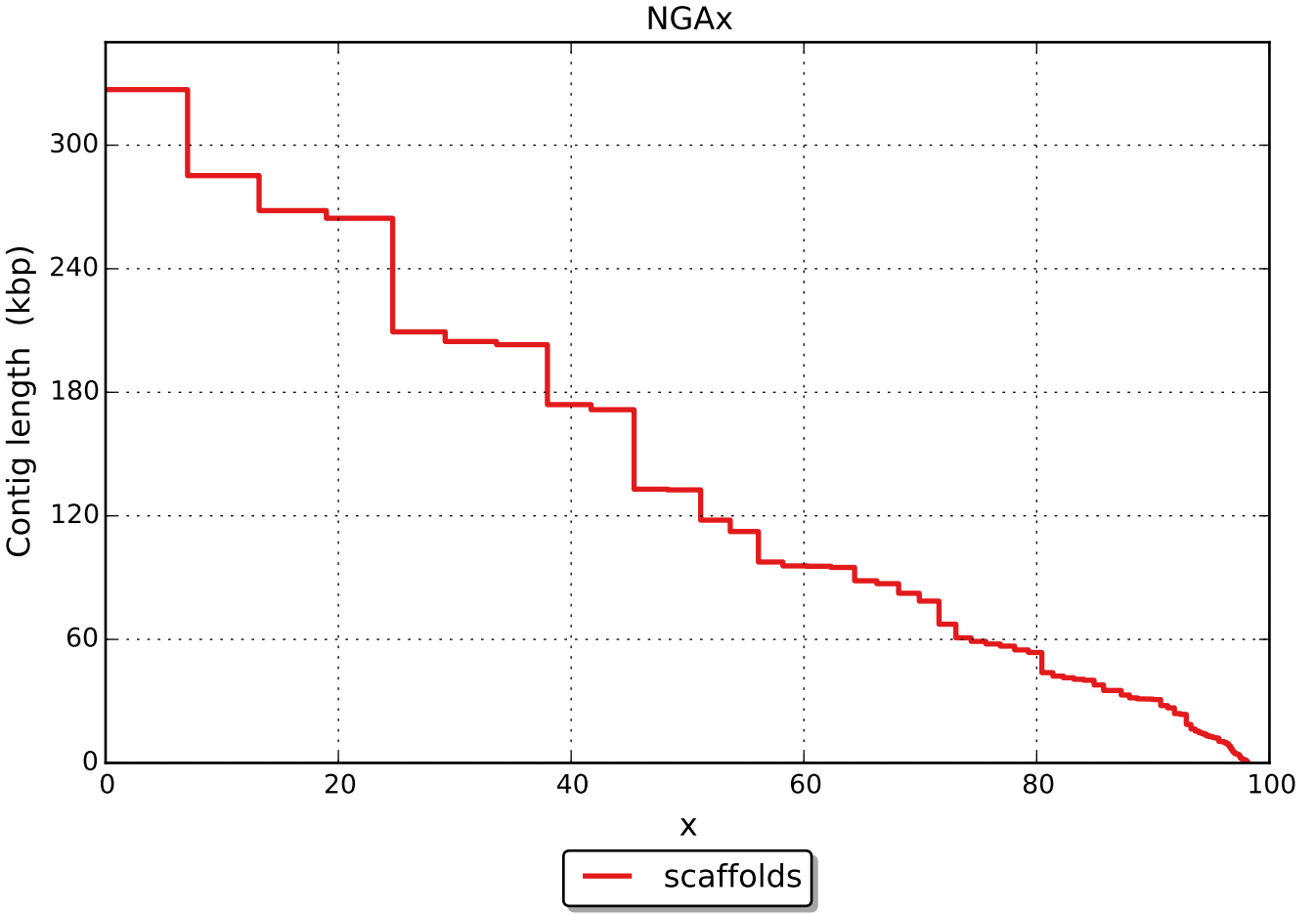

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


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


Misassemblies
3.0
2.5
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
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