Report

	scaffolds
# contigs (>= 1000 bp)	124
# contigs (>= 5000 bp)	97
# contigs (>= 10000 bp)	79
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	37
Total length (>= 1000 bp)	4562517
Total length (>= 5000 bp)	4491950
Total length (>= 10000 bp)	4364624
Total length (>= 25000 bp)	3974973
Total length (>= 50000 bp)	3399888
# contigs	132
Largest contig	264572
Total length	4568391
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.78
N50	76208
NG50	76208
N75	43987
NG75	43808
L50	20
LG50	20
L75	38
LG75	39
# misassemblies	14
# misassembled contigs	11
Misassembled contigs length	1018010
# local misassemblies	3
# unaligned contigs	0 + 2 part
Unaligned length	126
Genome fraction (%)	98.266
Duplication ratio	1.002
# N's per 100 kbp	13.44
# mismatches per 100 kbp	553.85
# indels per 100 kbp	0.42
Largest alignment	183386
NA50	73703
NGA50	73703
NA75	34543
NGA75	33513
LA50	22
LGA50	22
LA75	43
LGA75	45

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

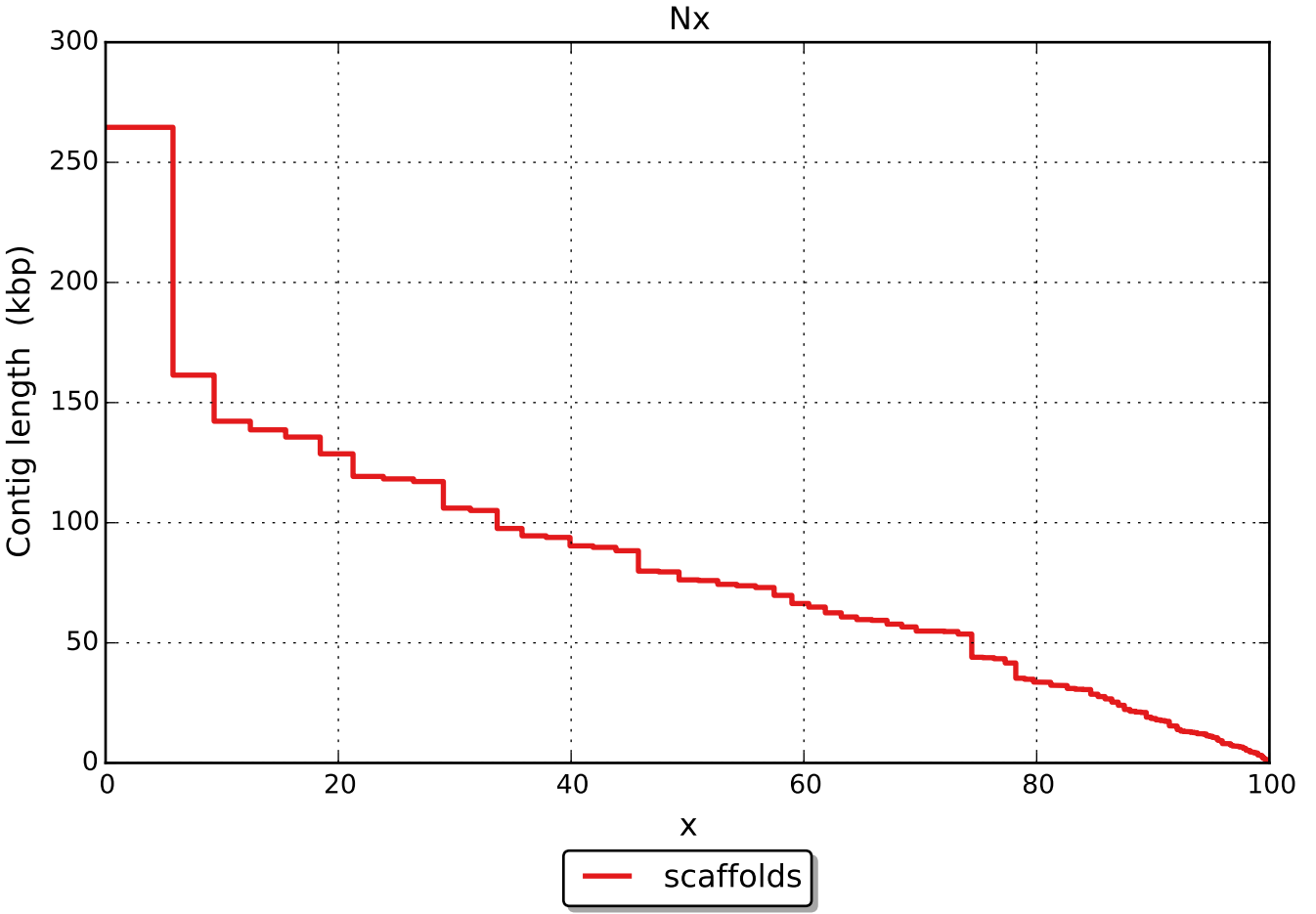
	scaffolds
# misassemblies	14
# relocations	11
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	11
Misassembled contigs length	1018010
# local misassemblies	3
# mismatches	25262
# indels	19
# short indels	17
# long indels	2
Indels length	133

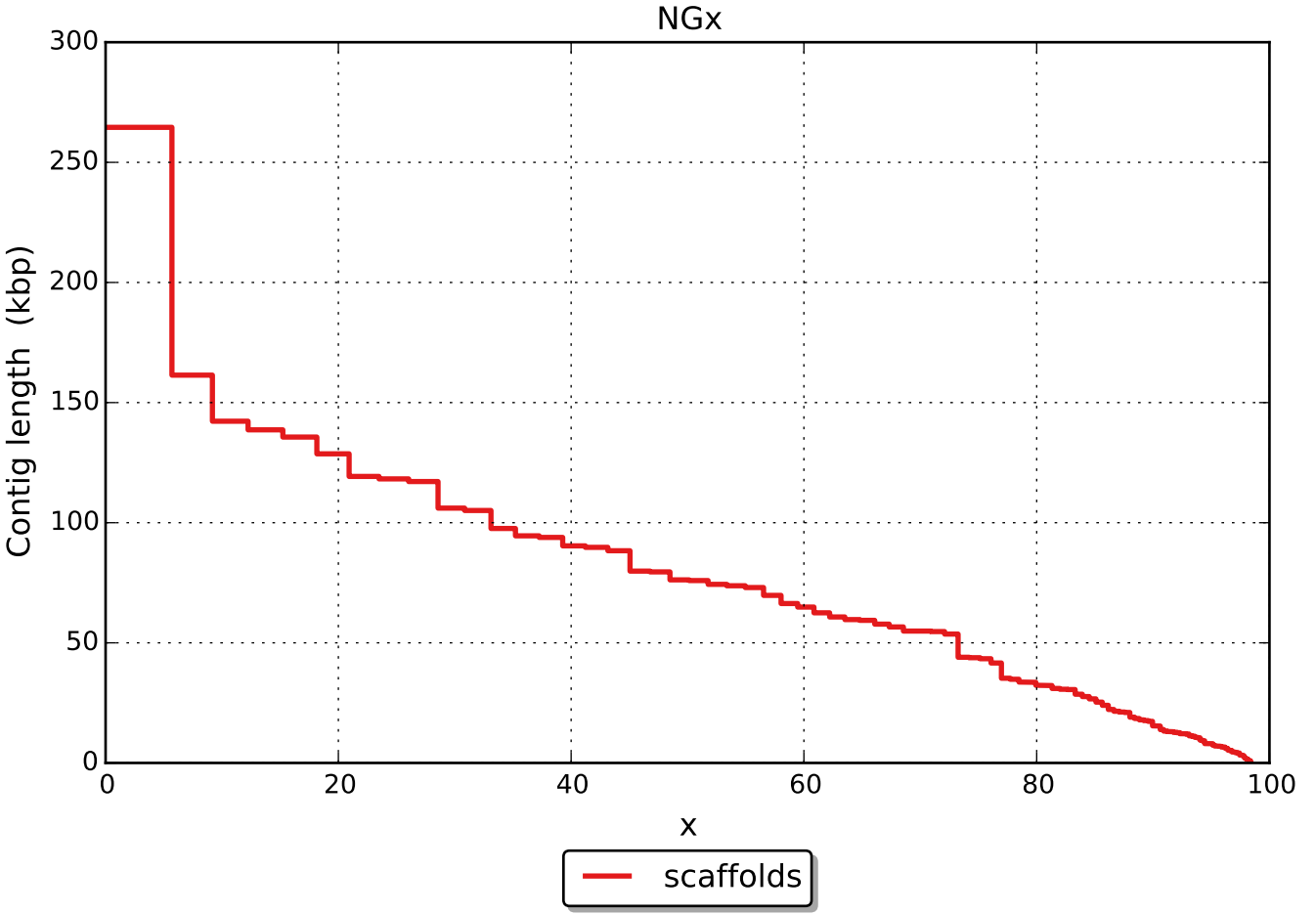
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

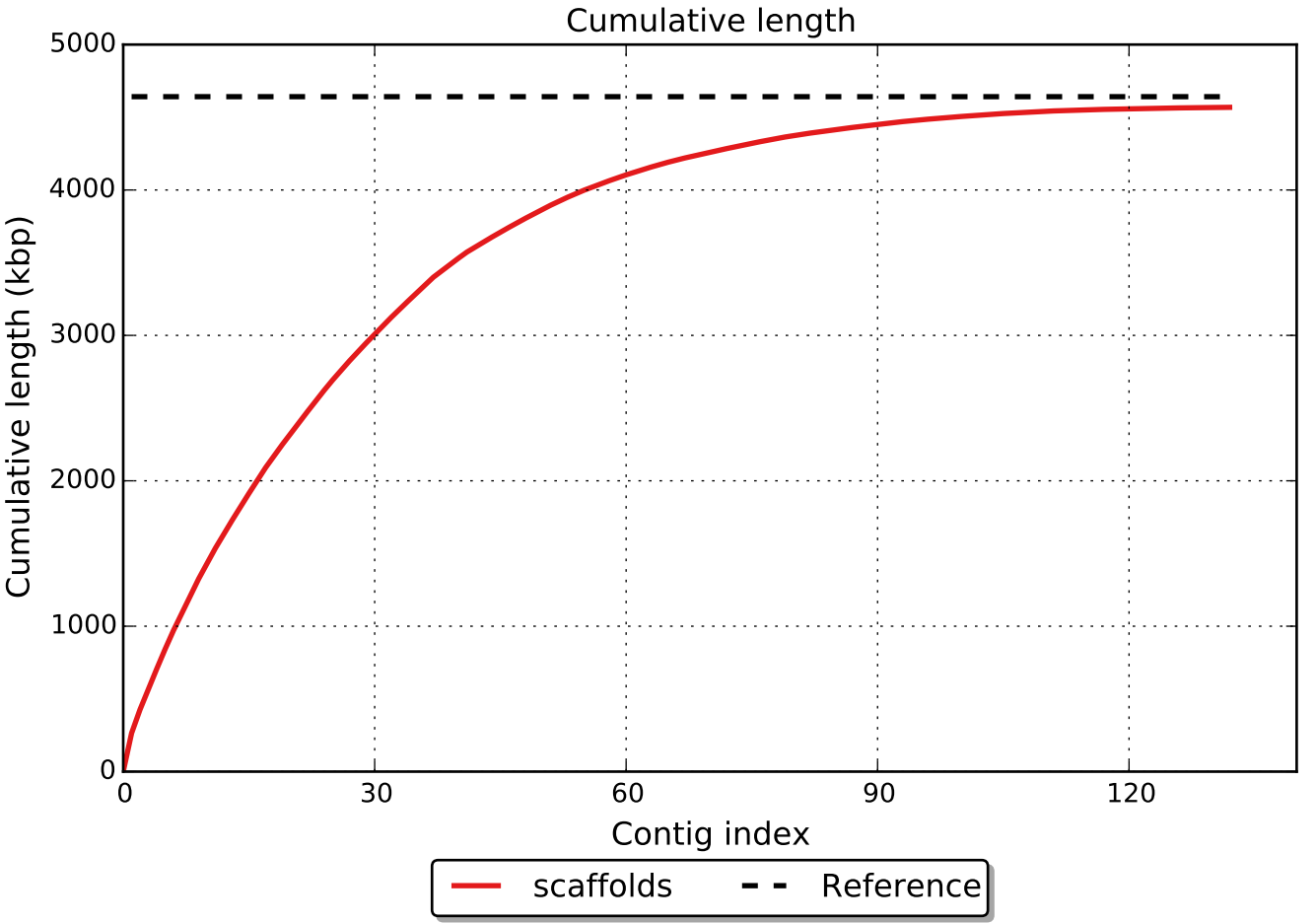
Unaligned report

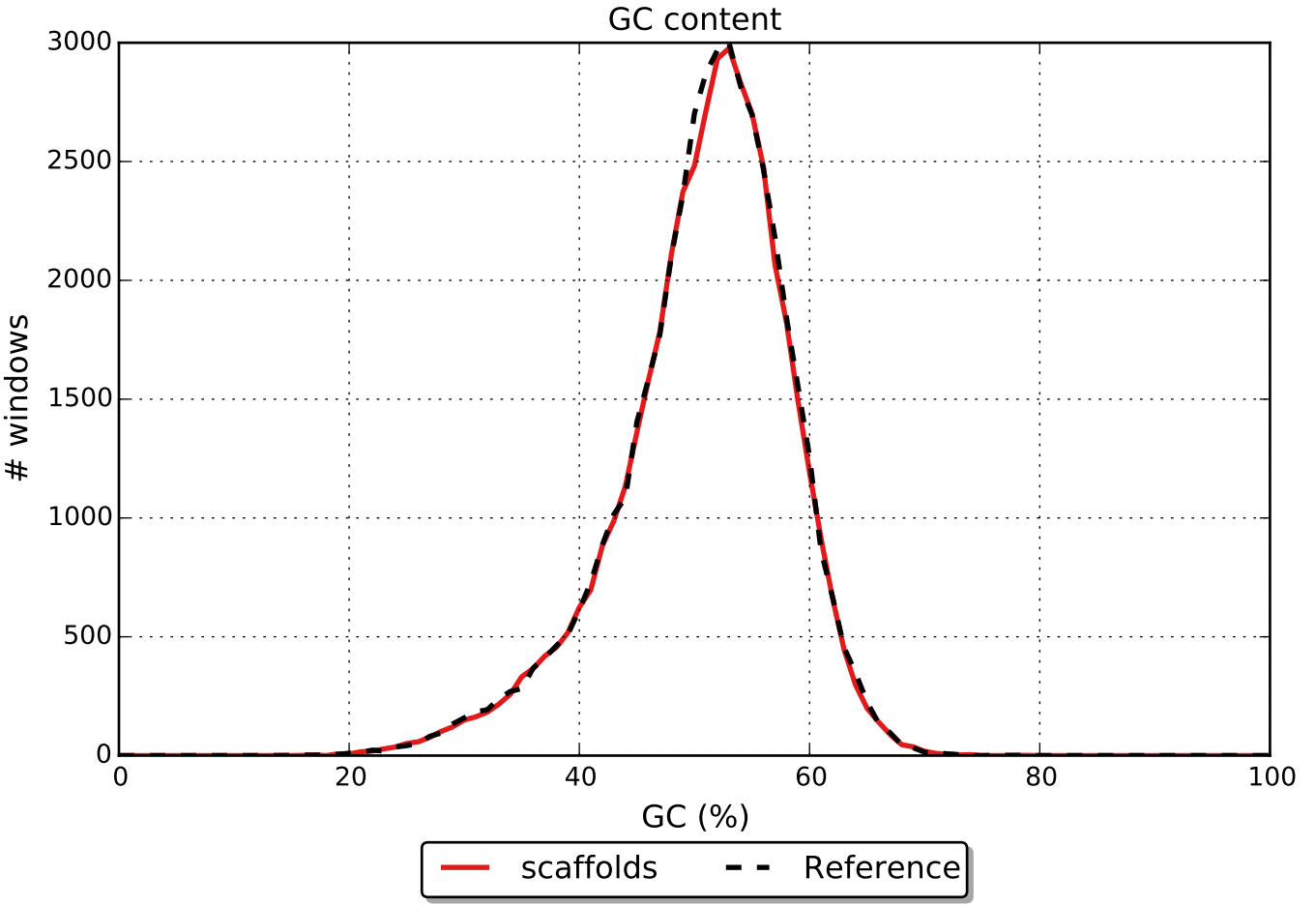
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	126
# N's	614

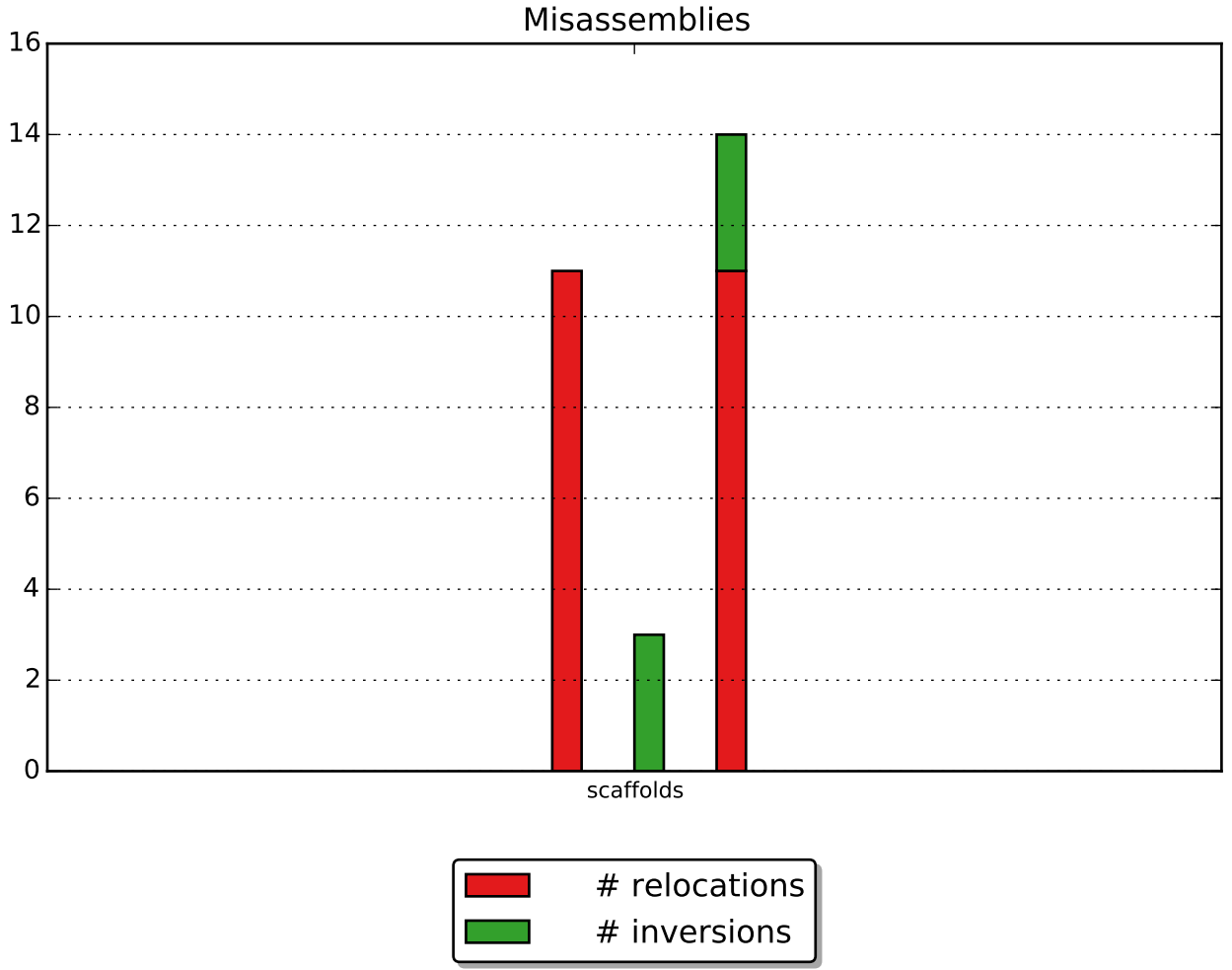
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

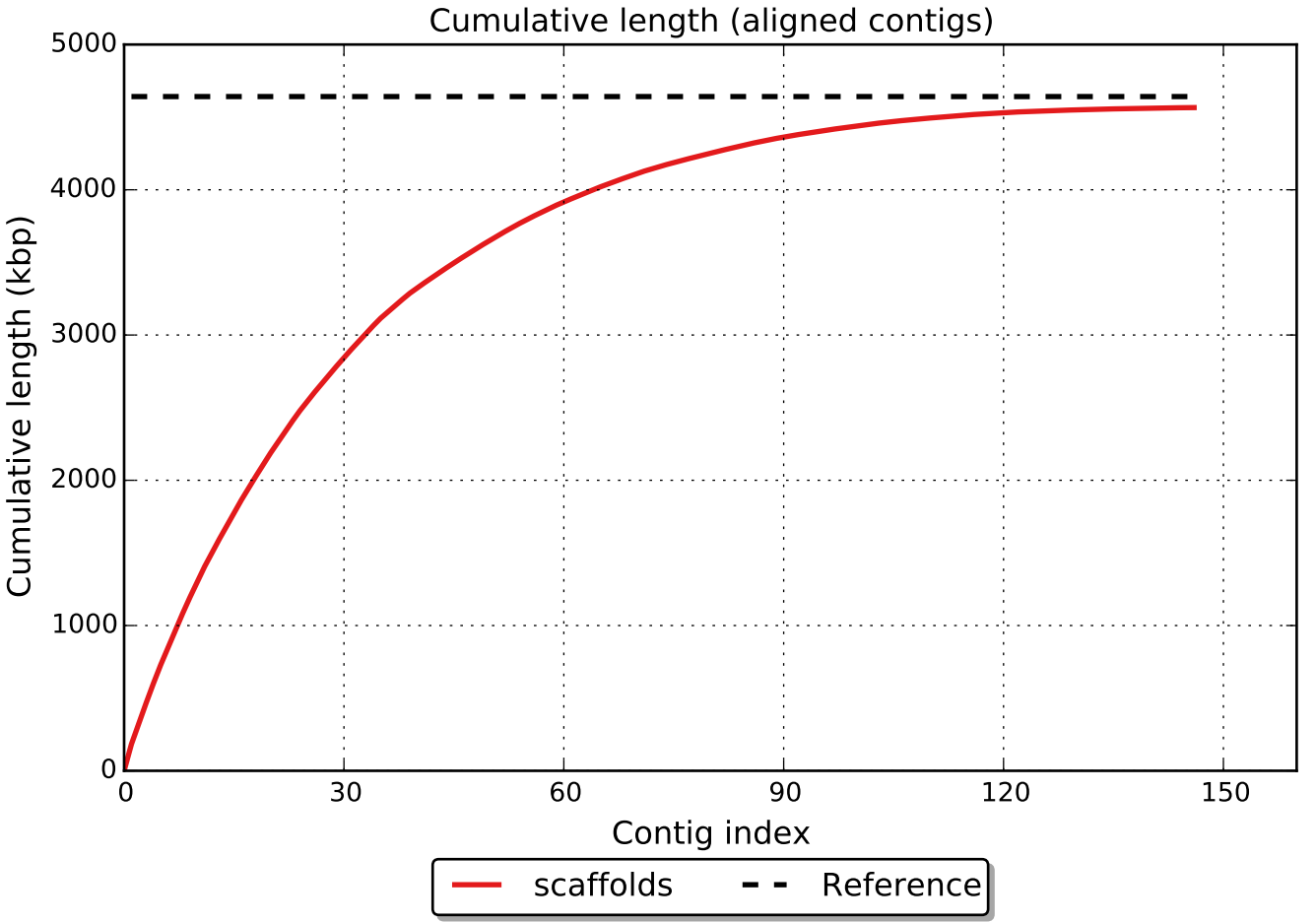

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds

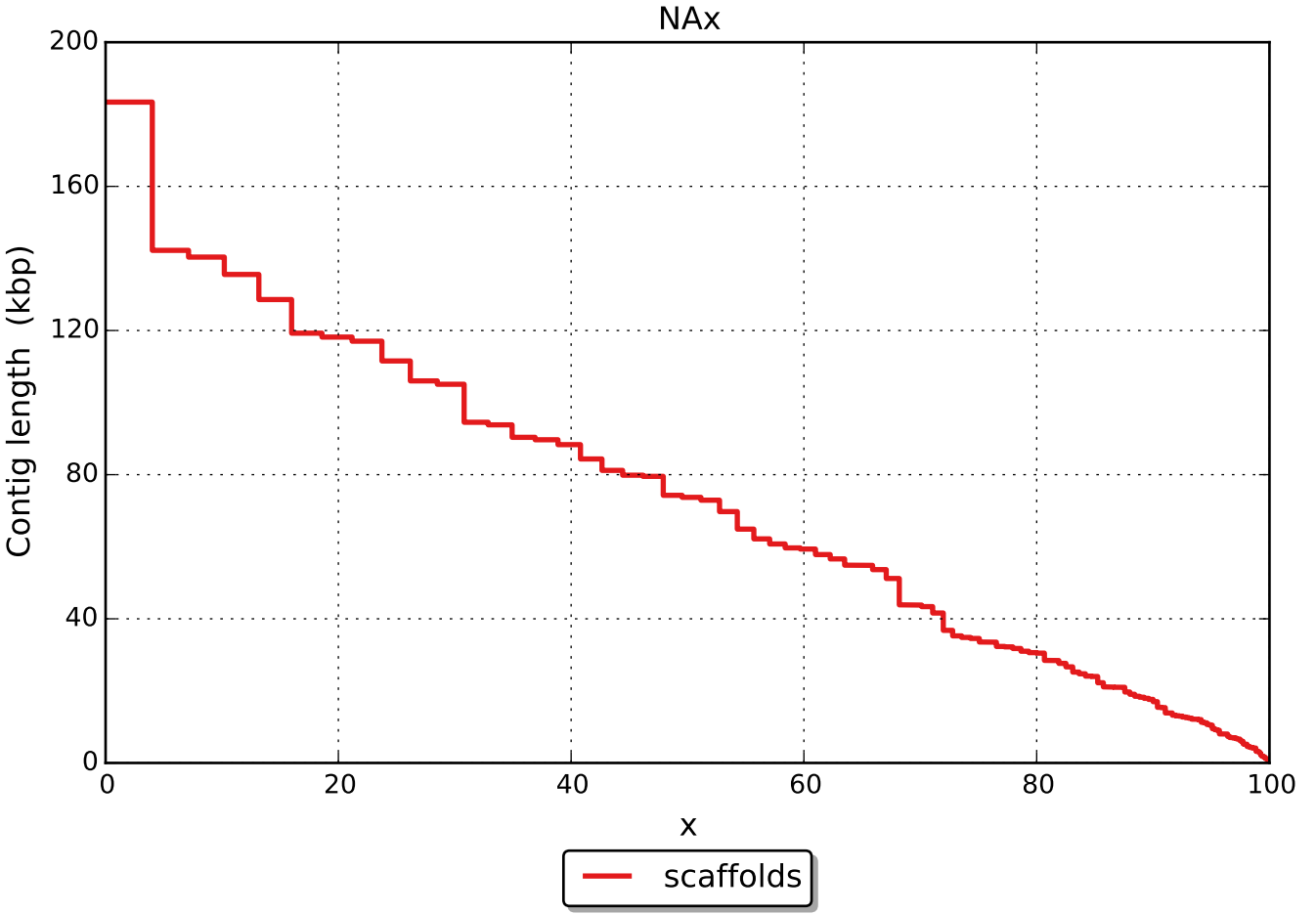

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

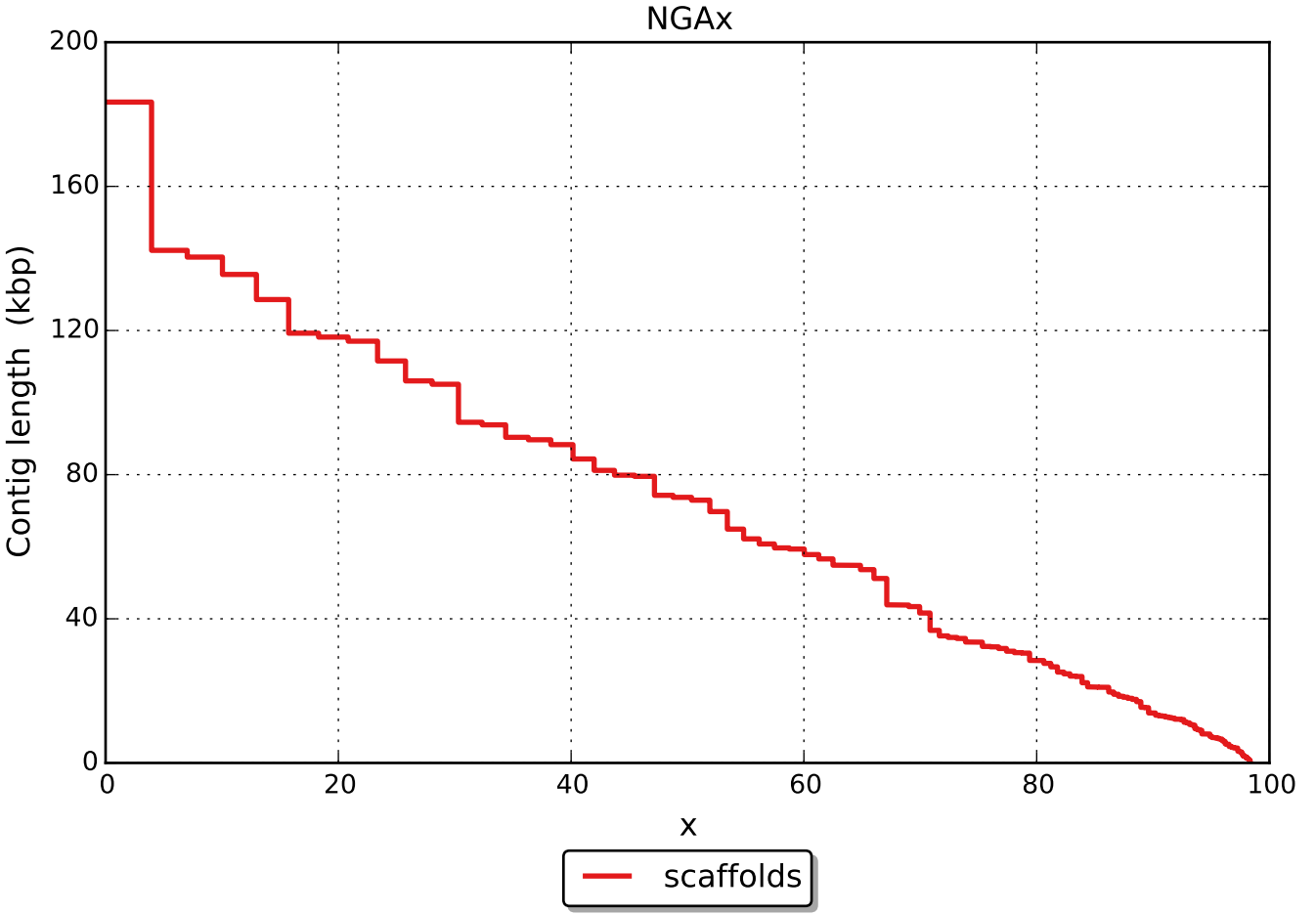

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
30
60
90
120
Contig index
scaffolds
Reference


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


Misassemblies
16
14
12
10
8
6
4
2
0
scaffolds
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
scaffolds