Report

	scaffolds
# contigs (>= 1000 bp)	106
# contigs (>= 5000 bp)	67
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4493024
Total length (>= 5000 bp)	4396833
Total length (>= 10000 bp)	4344583
Total length (>= 25000 bp)	4117236
Total length (>= 50000 bp)	3512590
# contigs	143
Largest contig	317313
Total length	4517317
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	95318
NG50	94928
N75	59591
NG75	58576
L50	13
LG50	14
L75	27
LG75	29
# misassemblies	18
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.572
Duplication ratio	1.087
# N's per 100 kbp	1.15
# mismatches per 100 kbp	1047.45
# indels per 100 kbp	0.91
Largest alignment	317313
NA50	86515
NGA50	84208
NA75	47277
NGA75	40613
LA50	14
LGA50	15
LA75	31
LGA75	33

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

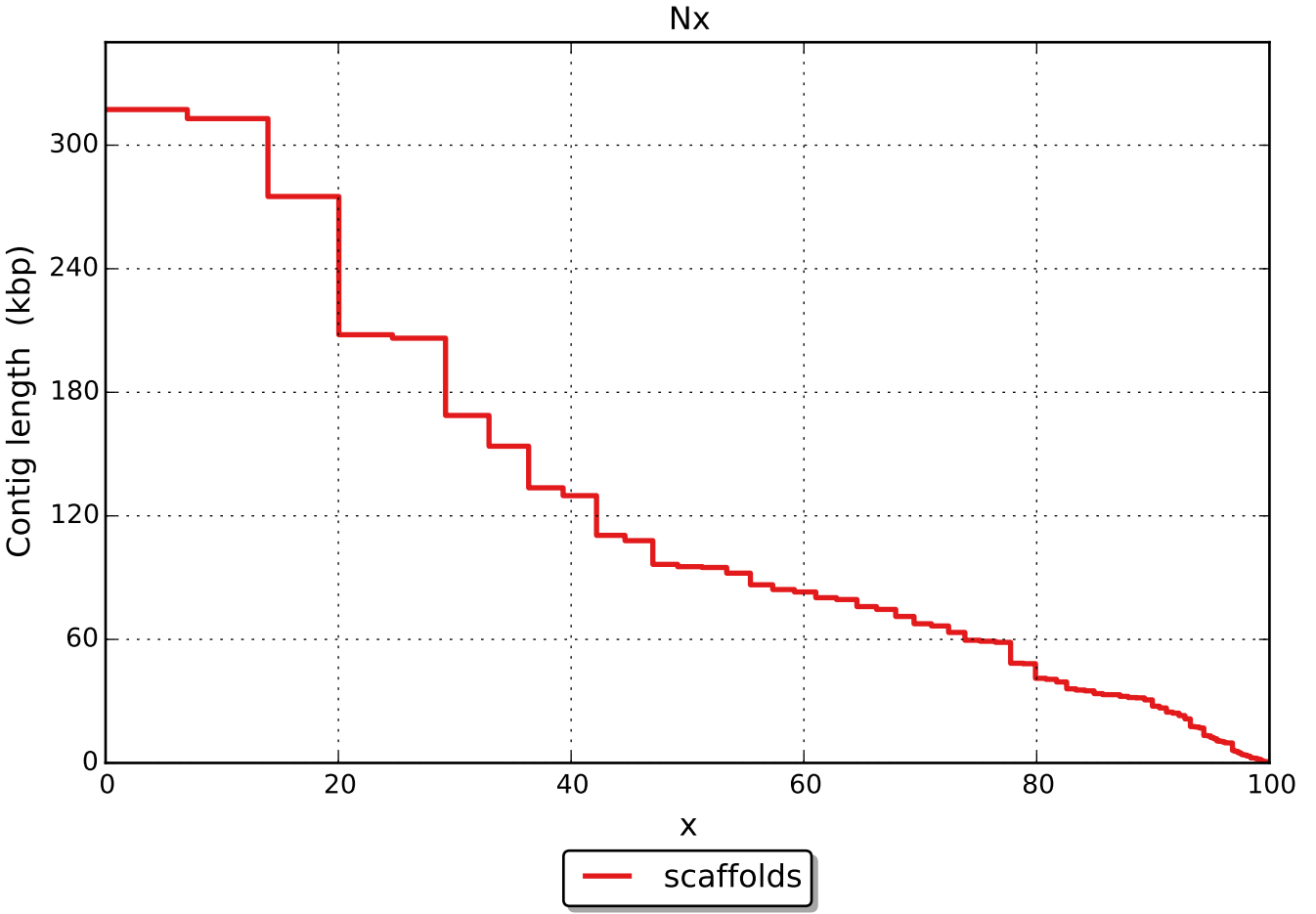
	scaffolds
# misassemblies	18
# relocations	15
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	4
# mismatches	43549
# indels	38
# short indels	38
# long indels	0
Indels length	45

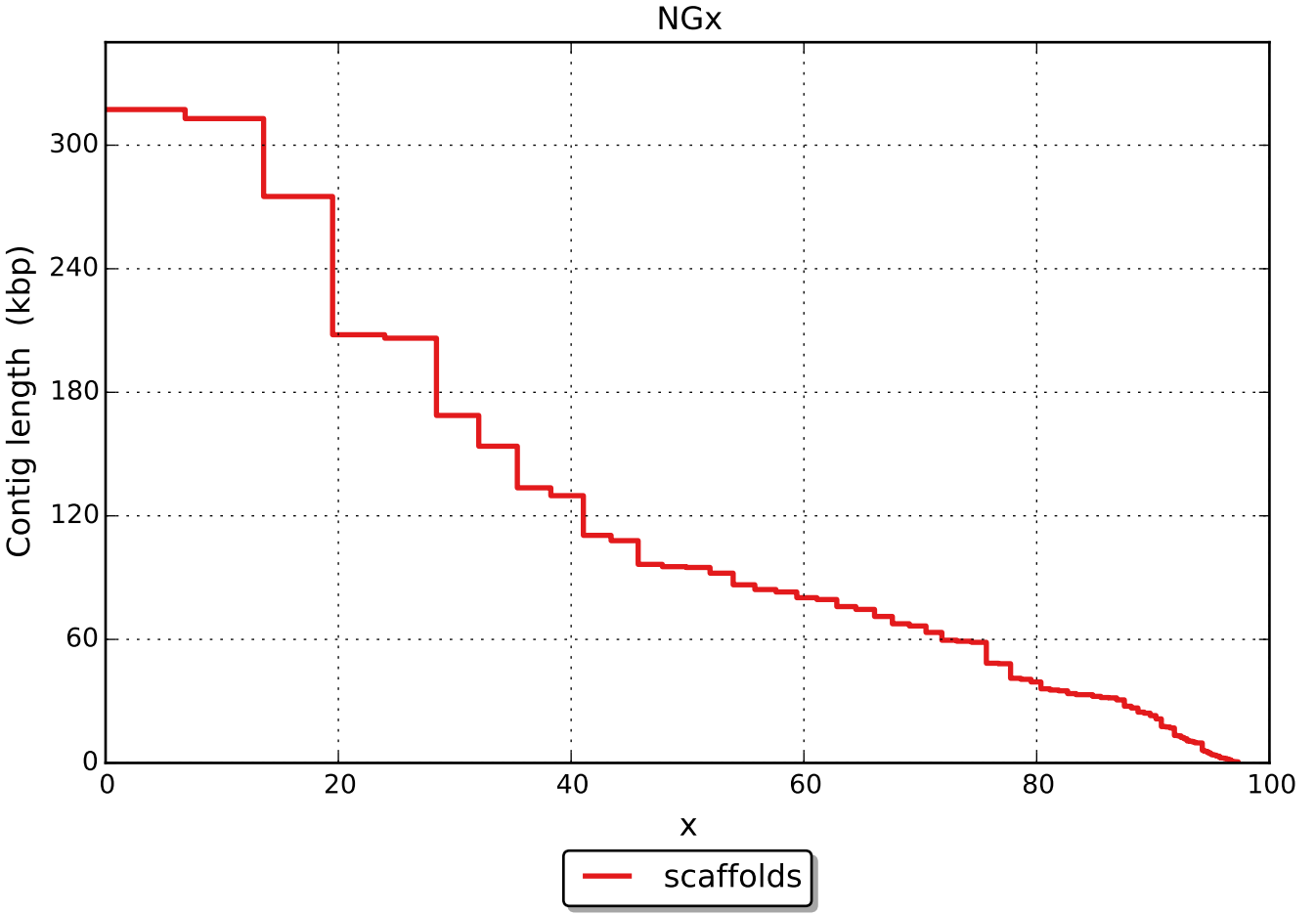
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

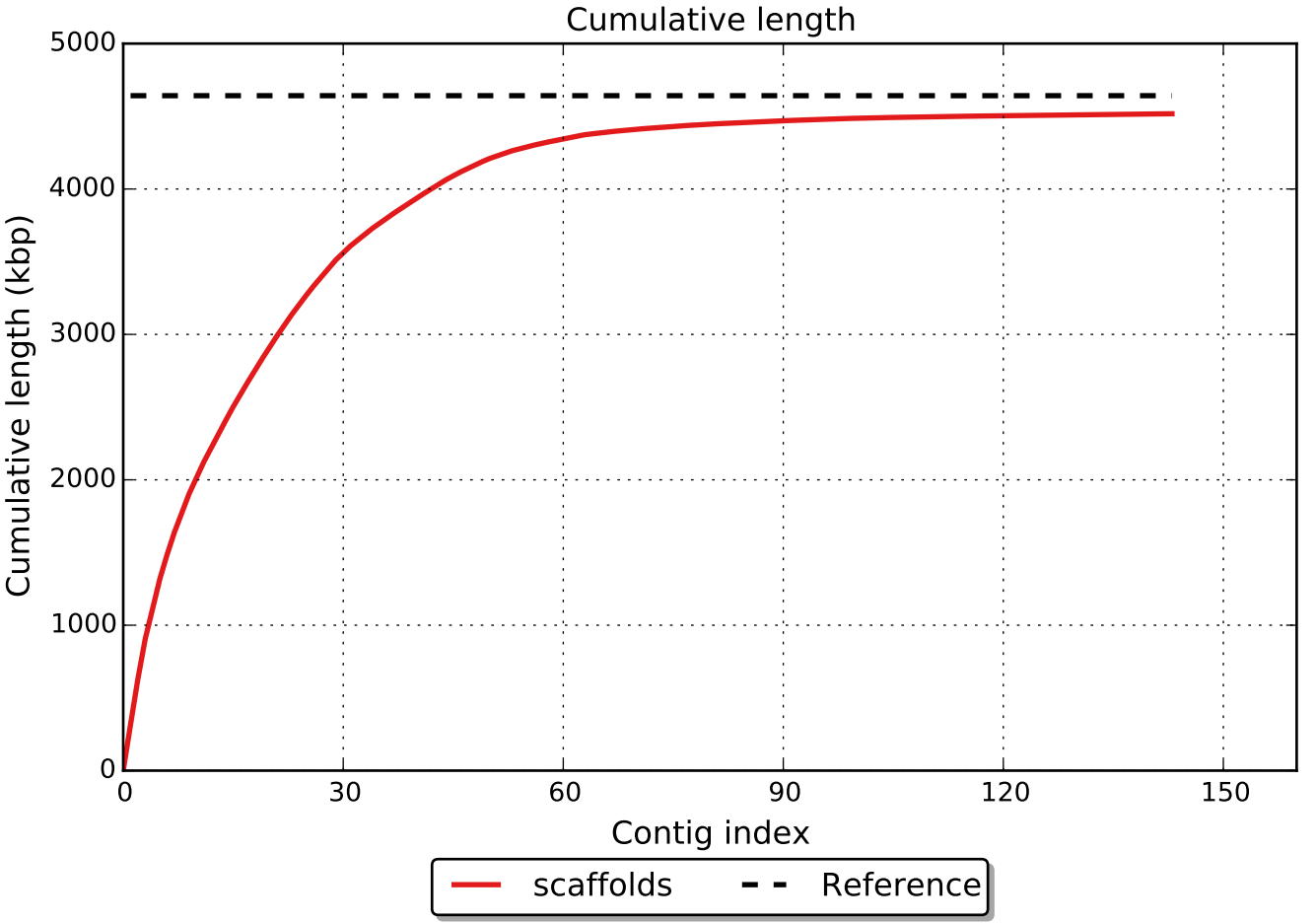
Unaligned report

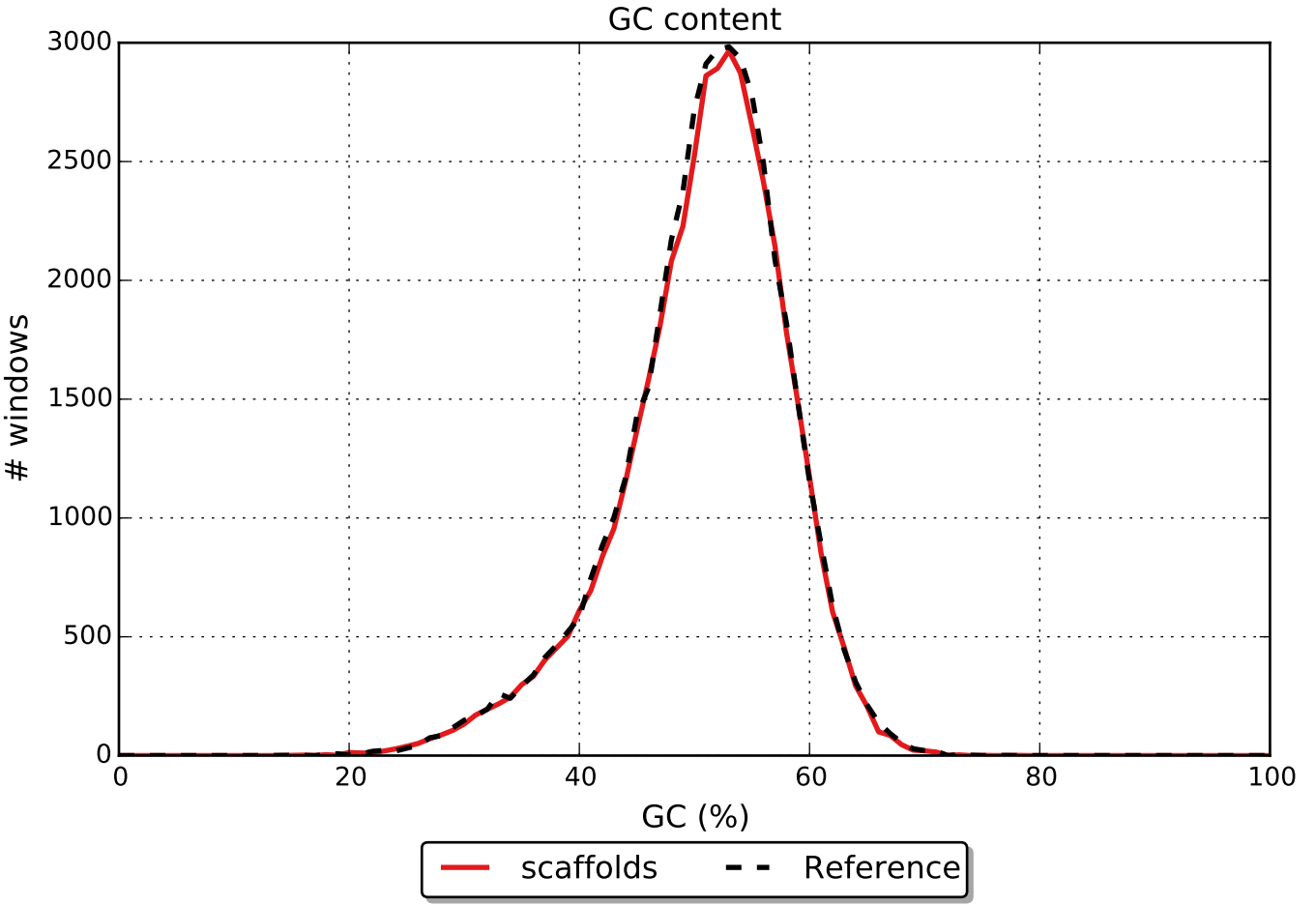
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	52

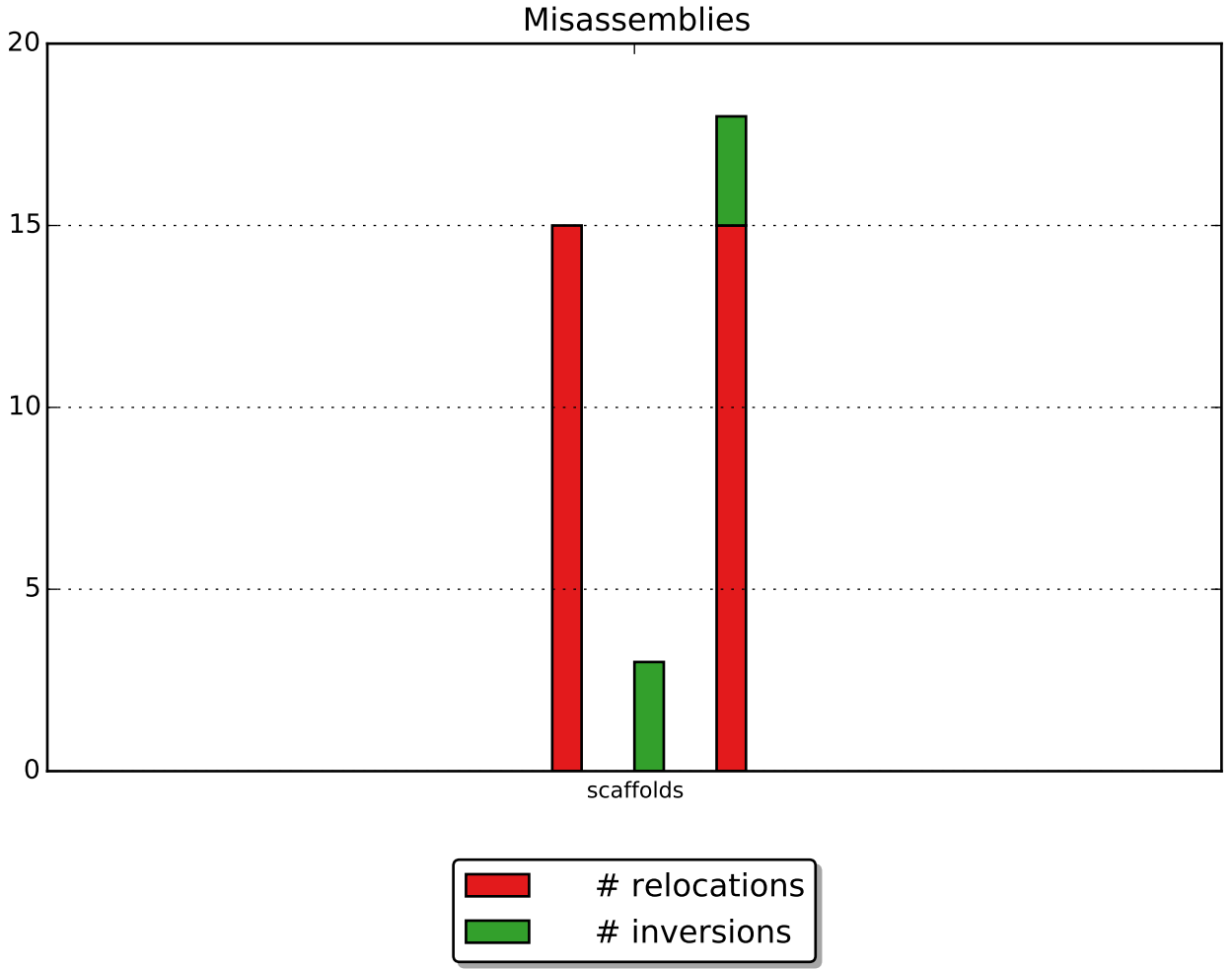
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

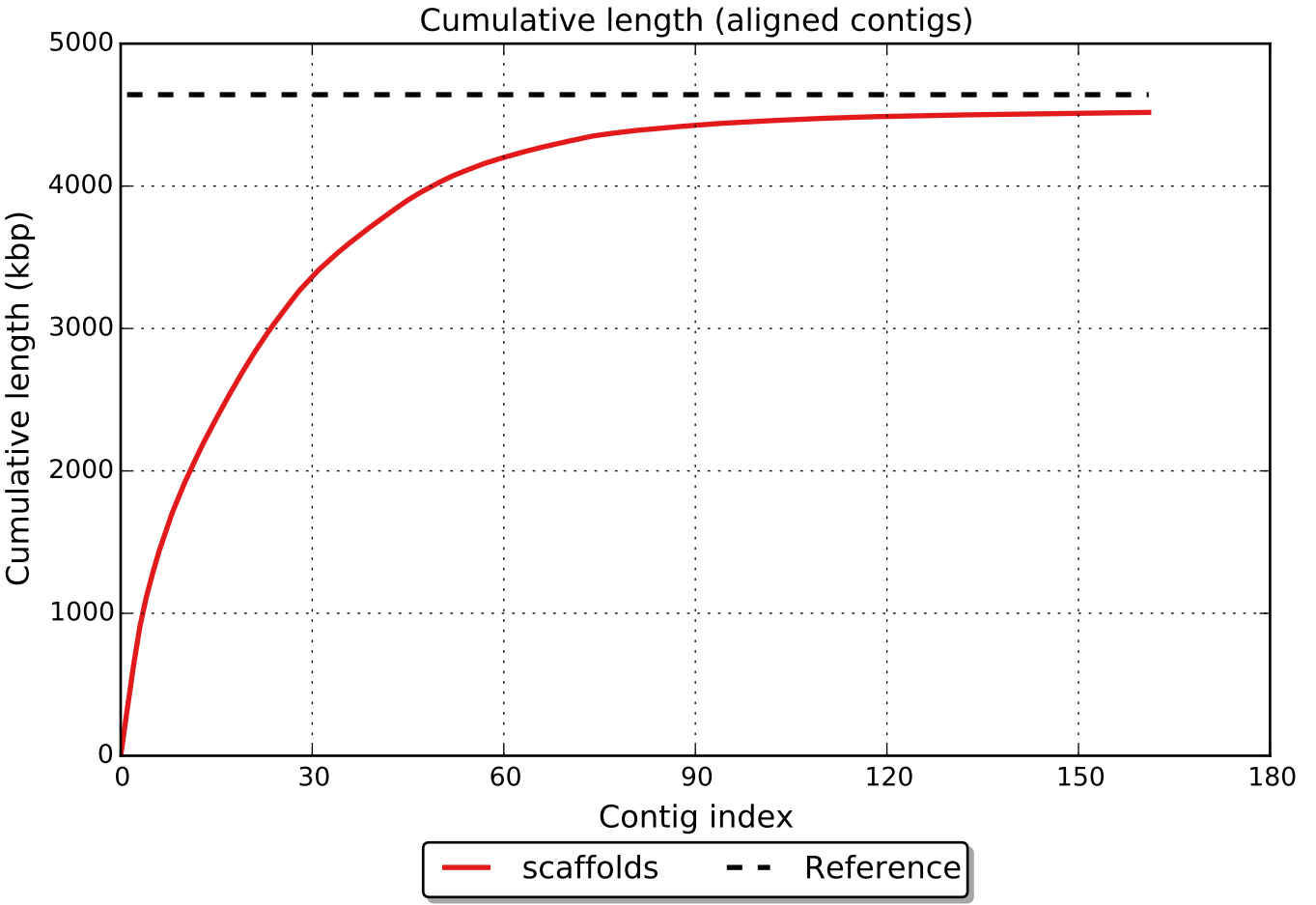

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

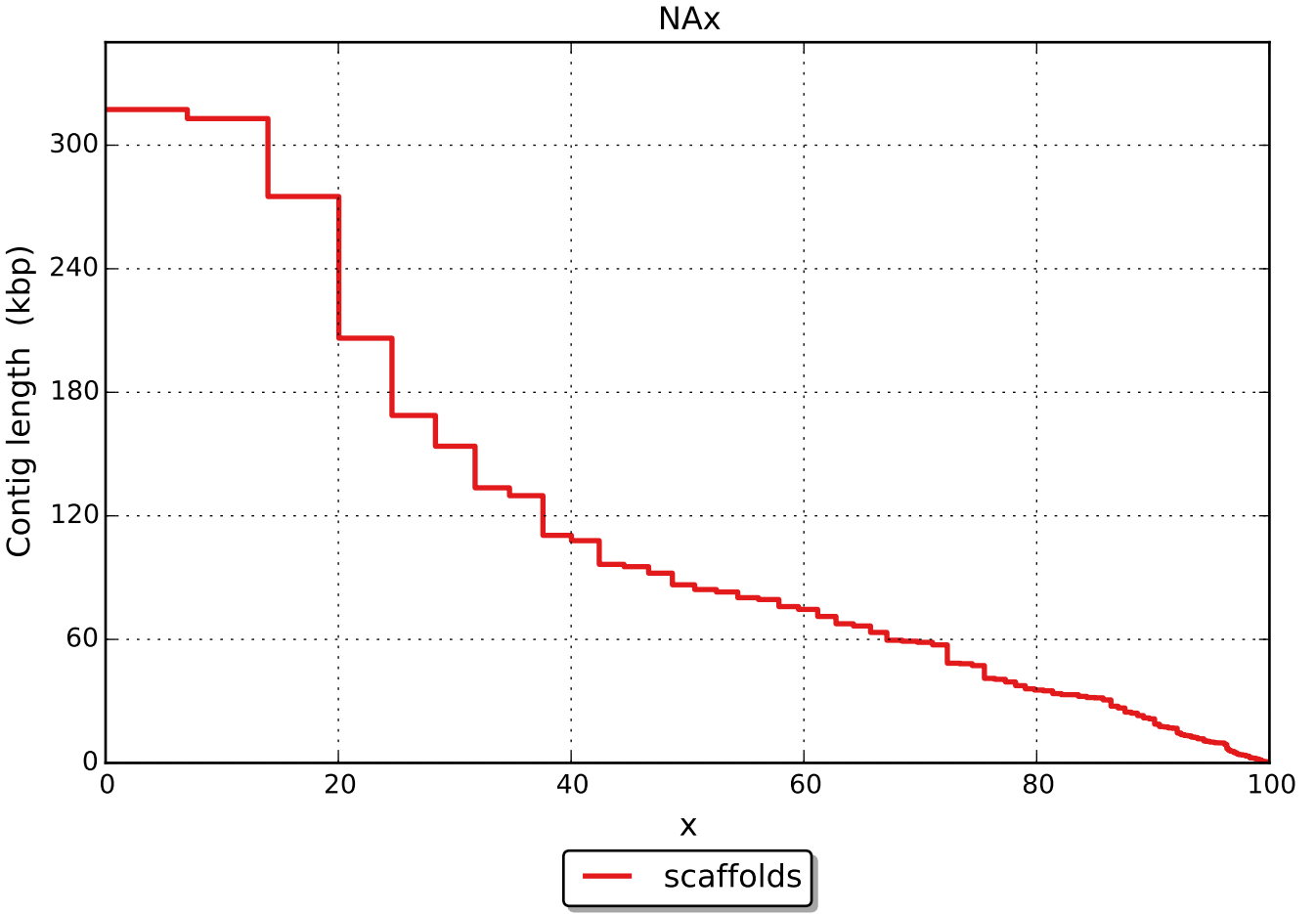

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

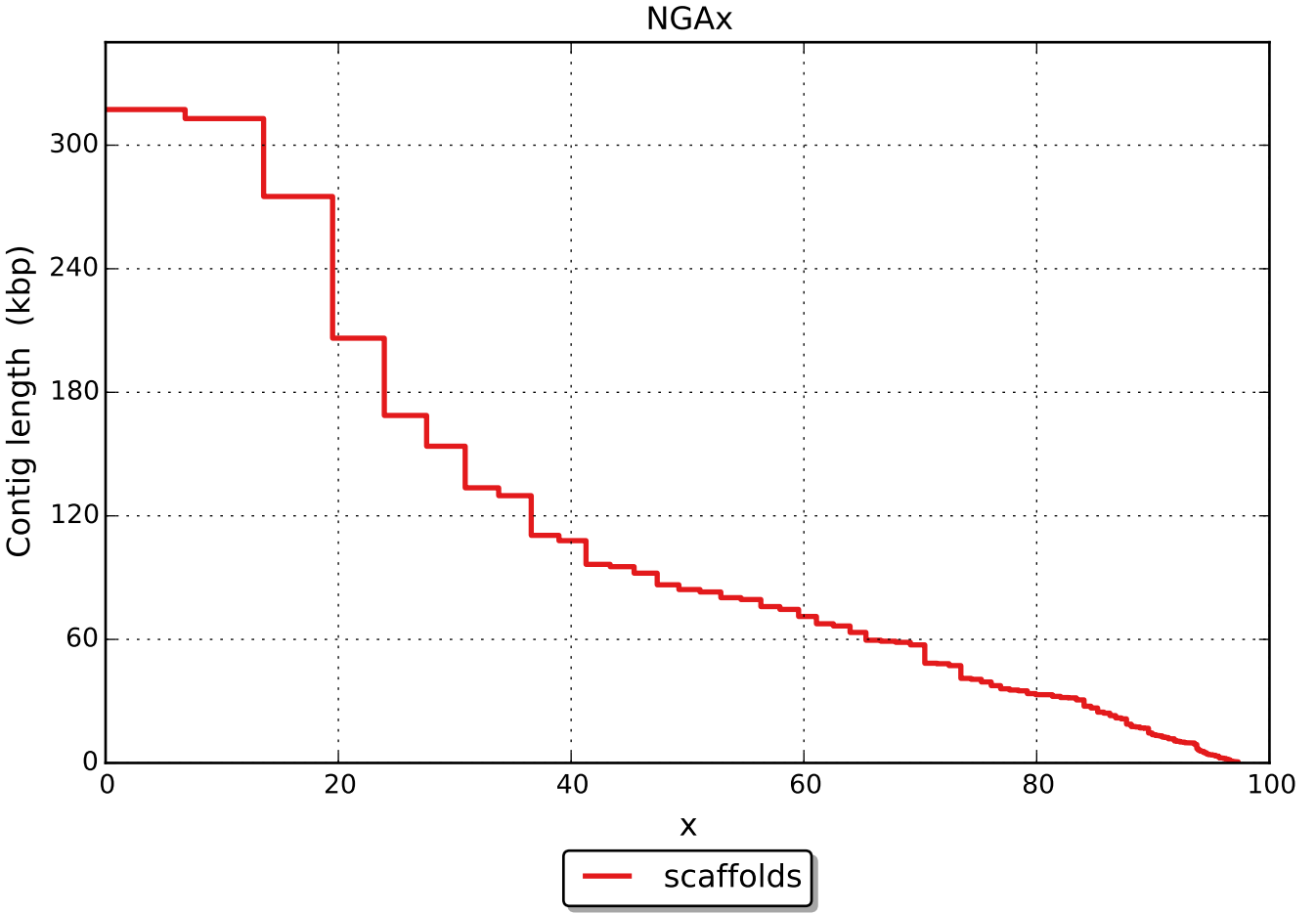

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
scaffolds
Reference


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


Misassemblies
20
15
10
5
0
scaffolds
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
180
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