Report

	scaffolds
# contigs (>= 1000 bp)	92
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4315187
Total length (>= 5000 bp)	4243195
Total length (>= 10000 bp)	4202941
Total length (>= 25000 bp)	4025078
Total length (>= 50000 bp)	3420432
# contigs	129
Largest contig	317313
Total length	4339480
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	96440
NG50	94928
N75	59591
NG75	48192
L50	12
LG50	14
L75	26
LG75	30
# misassemblies	18
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.559
Duplication ratio	1.068
# N's per 100 kbp	1.20
# mismatches per 100 kbp	1010.92
# indels per 100 kbp	0.89
Largest alignment	317313
NA50	86515
NGA50	83030
NA75	48192
NGA75	36005
LA50	13
LGA50	15
LA75	29
LGA75	35

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

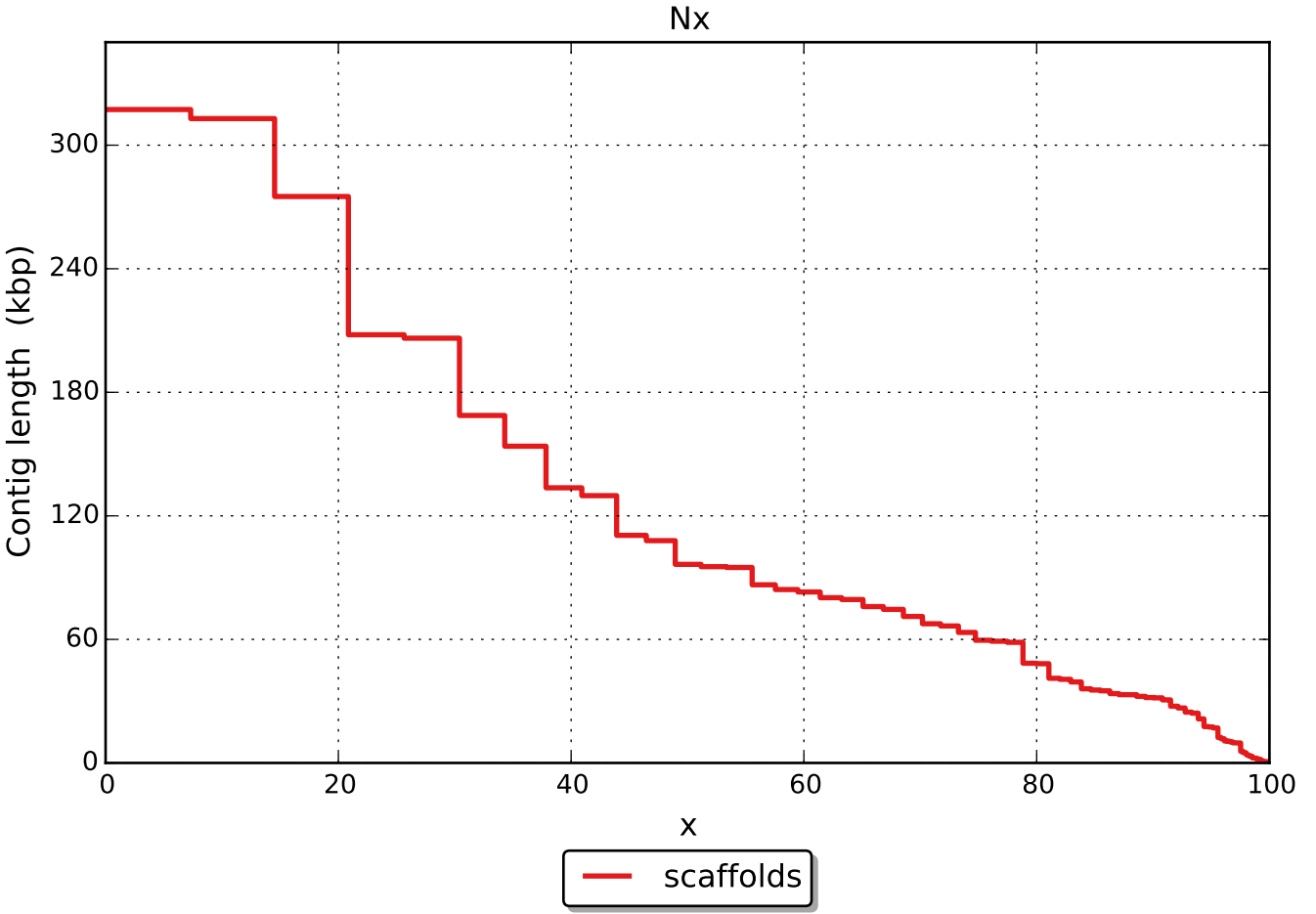
	scaffolds
# misassemblies	18
# relocations	15
# translocations	0
# inversions	3
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	302873
# local misassemblies	4
# mismatches	41086
# indels	36
# short indels	36
# long indels	0
Indels length	43

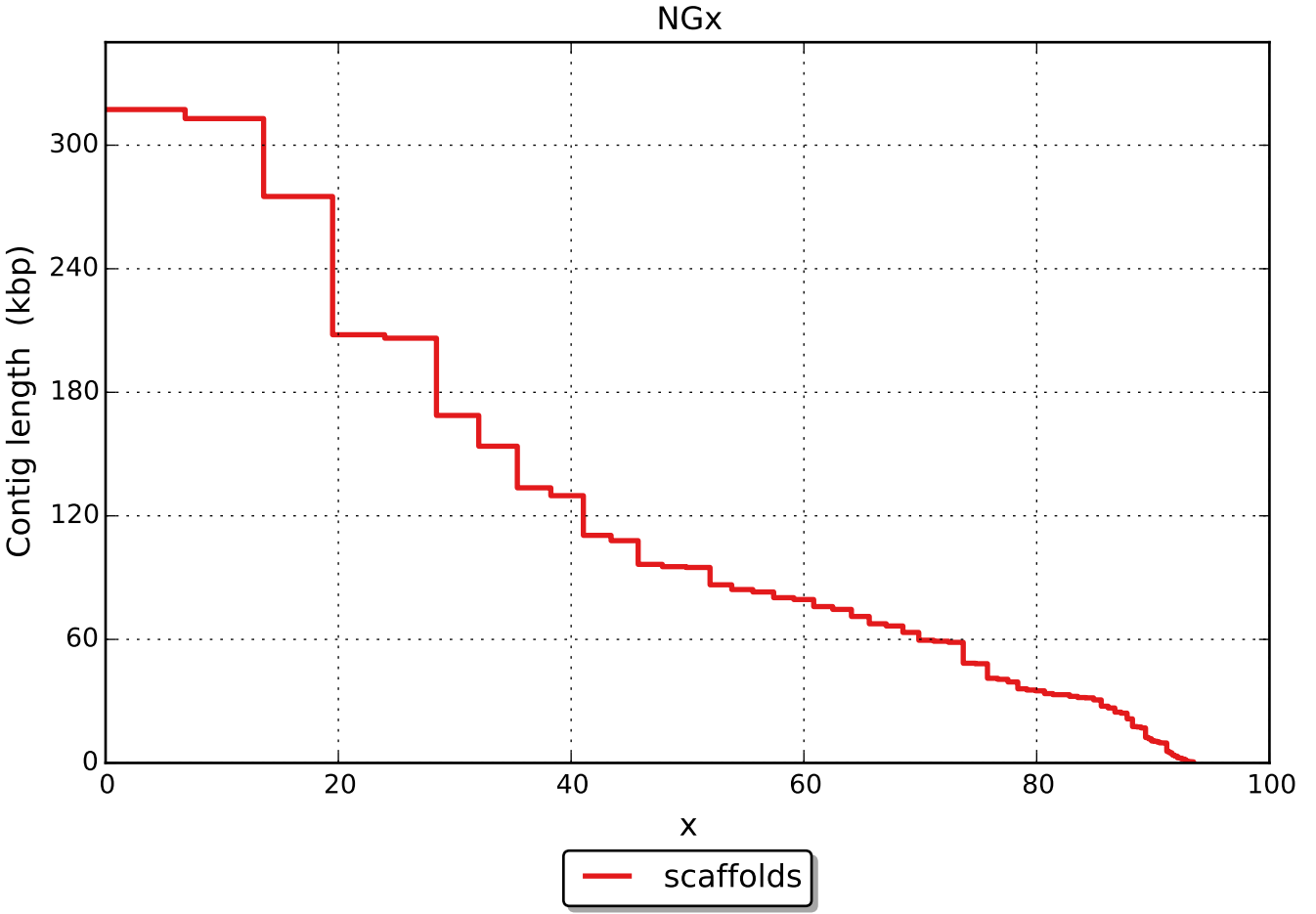
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

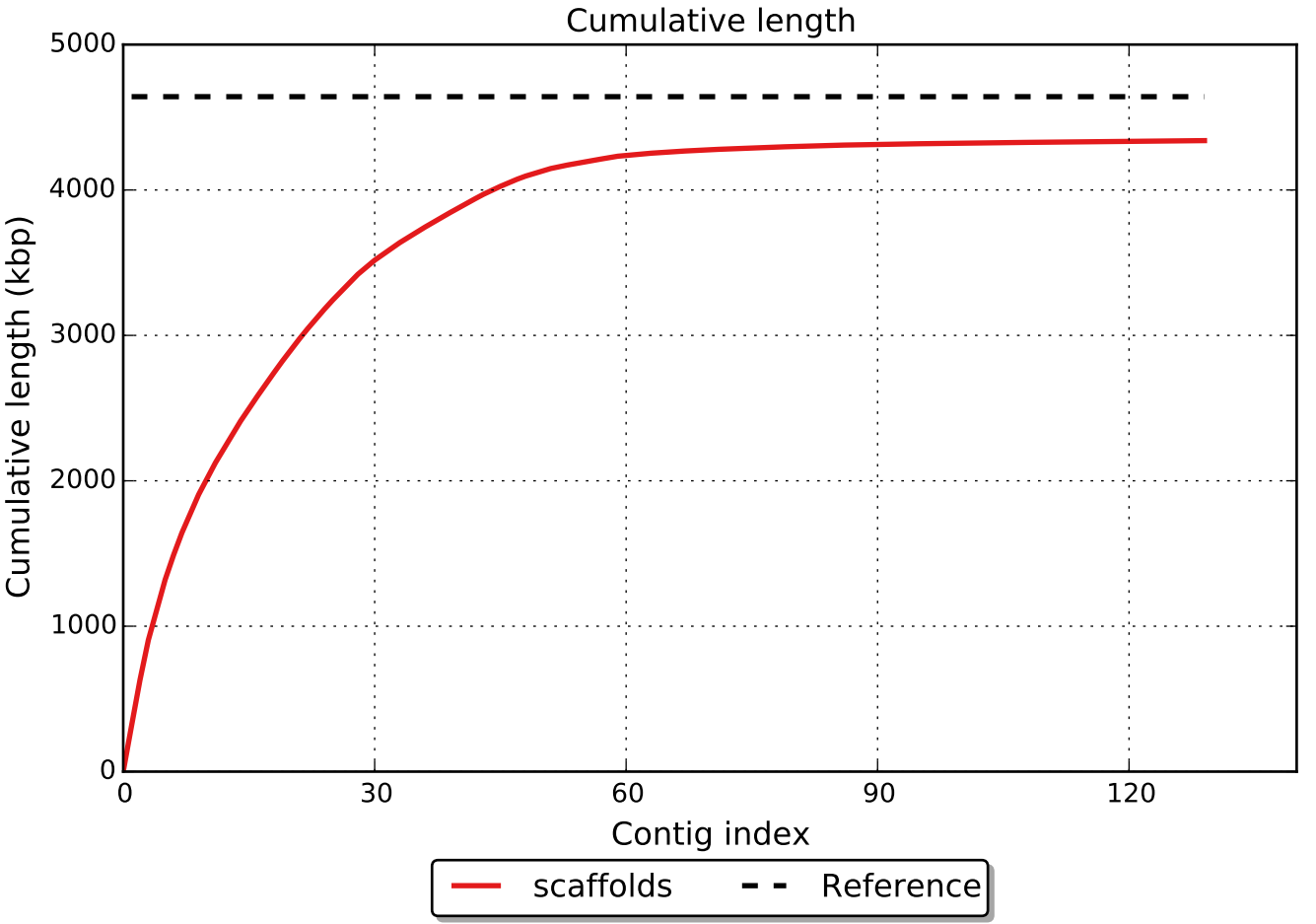
Unaligned report

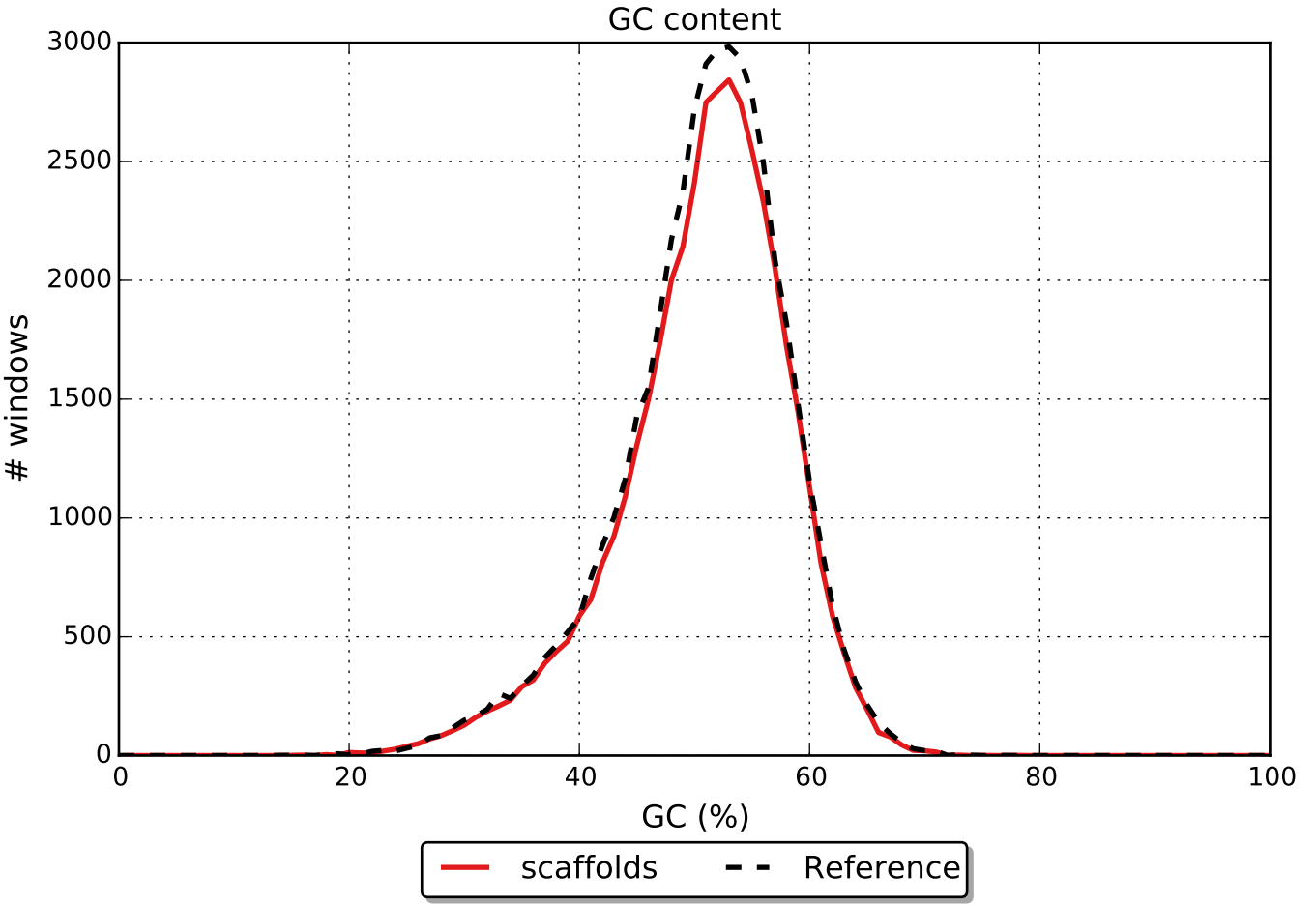
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	52

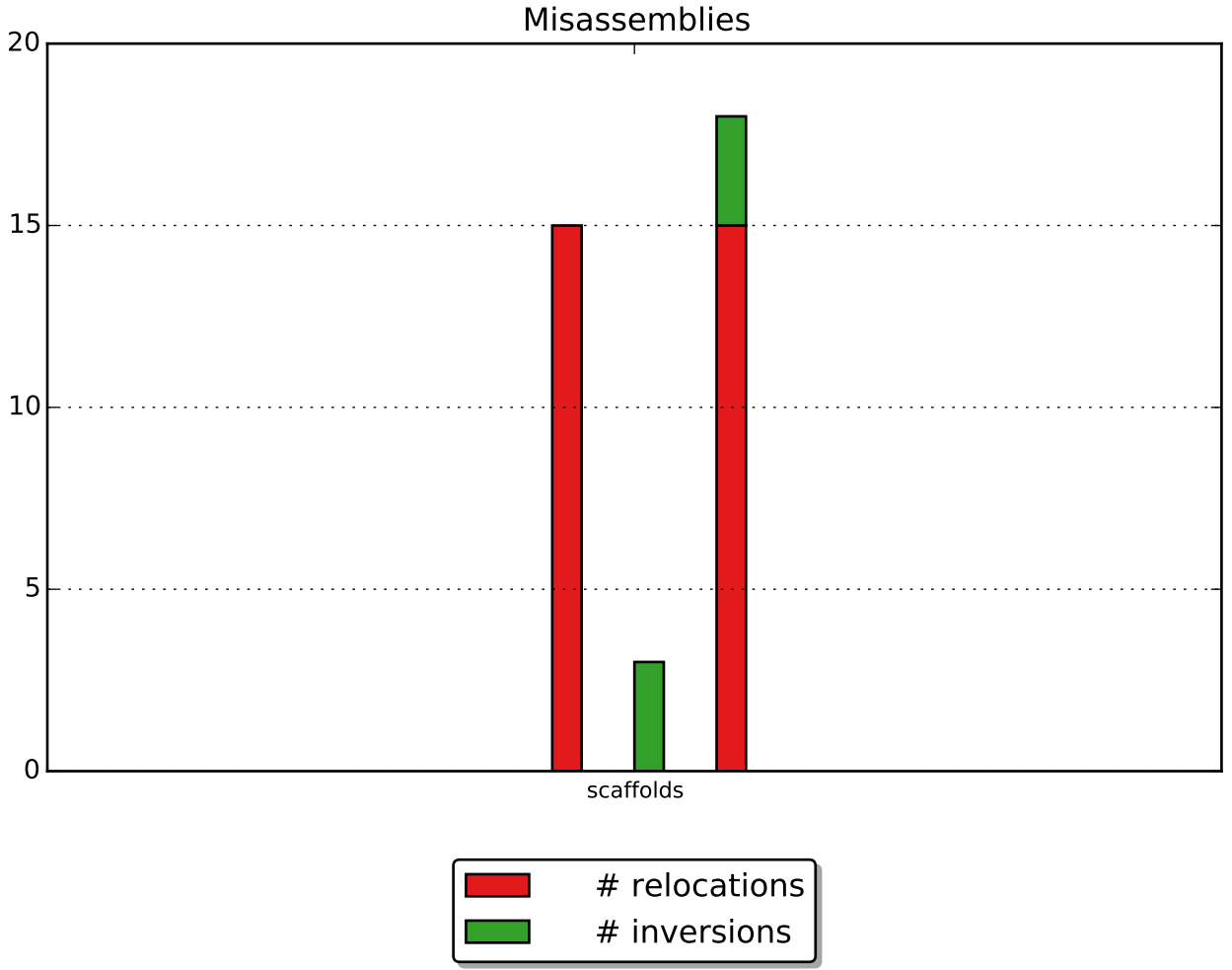
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

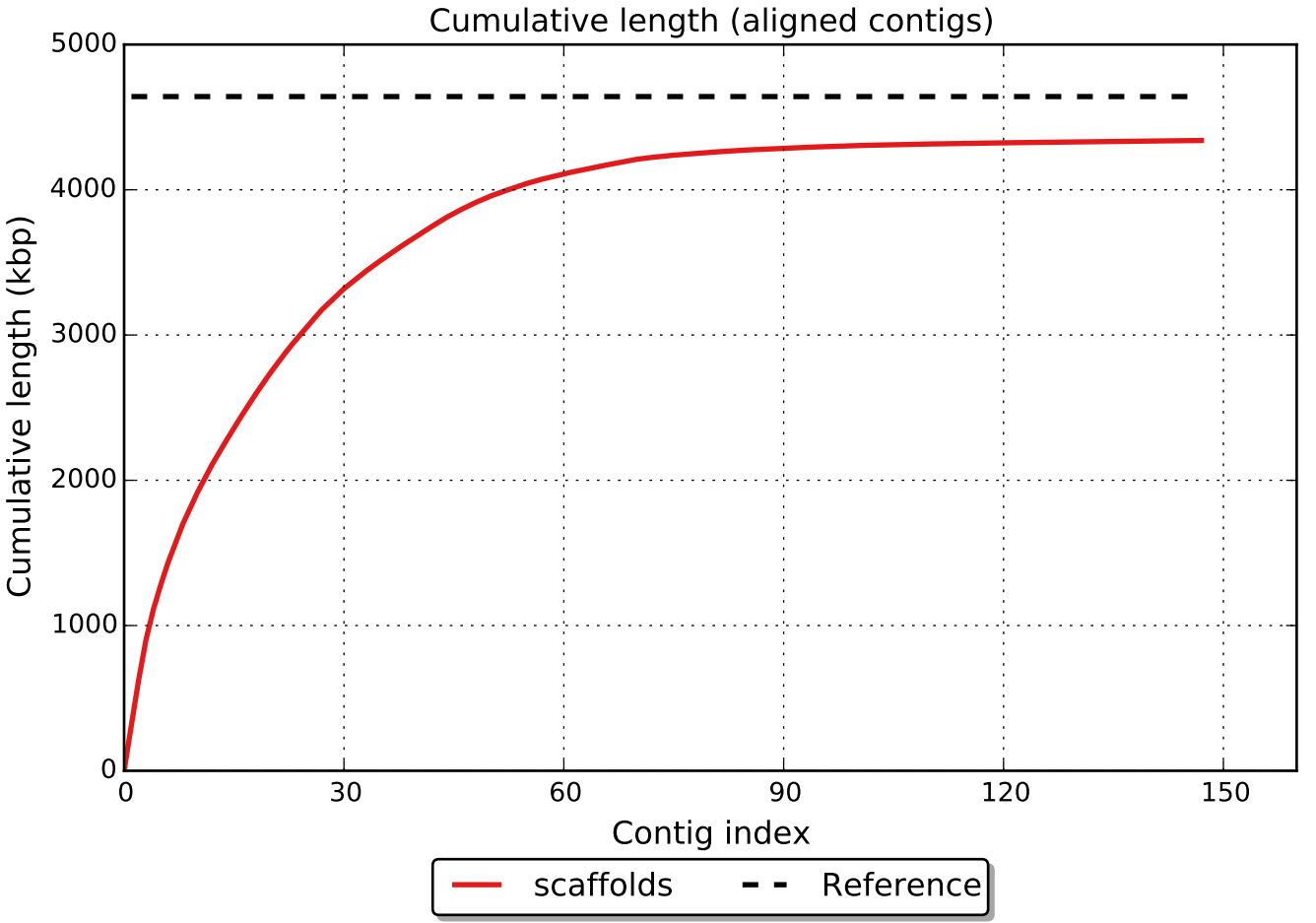

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

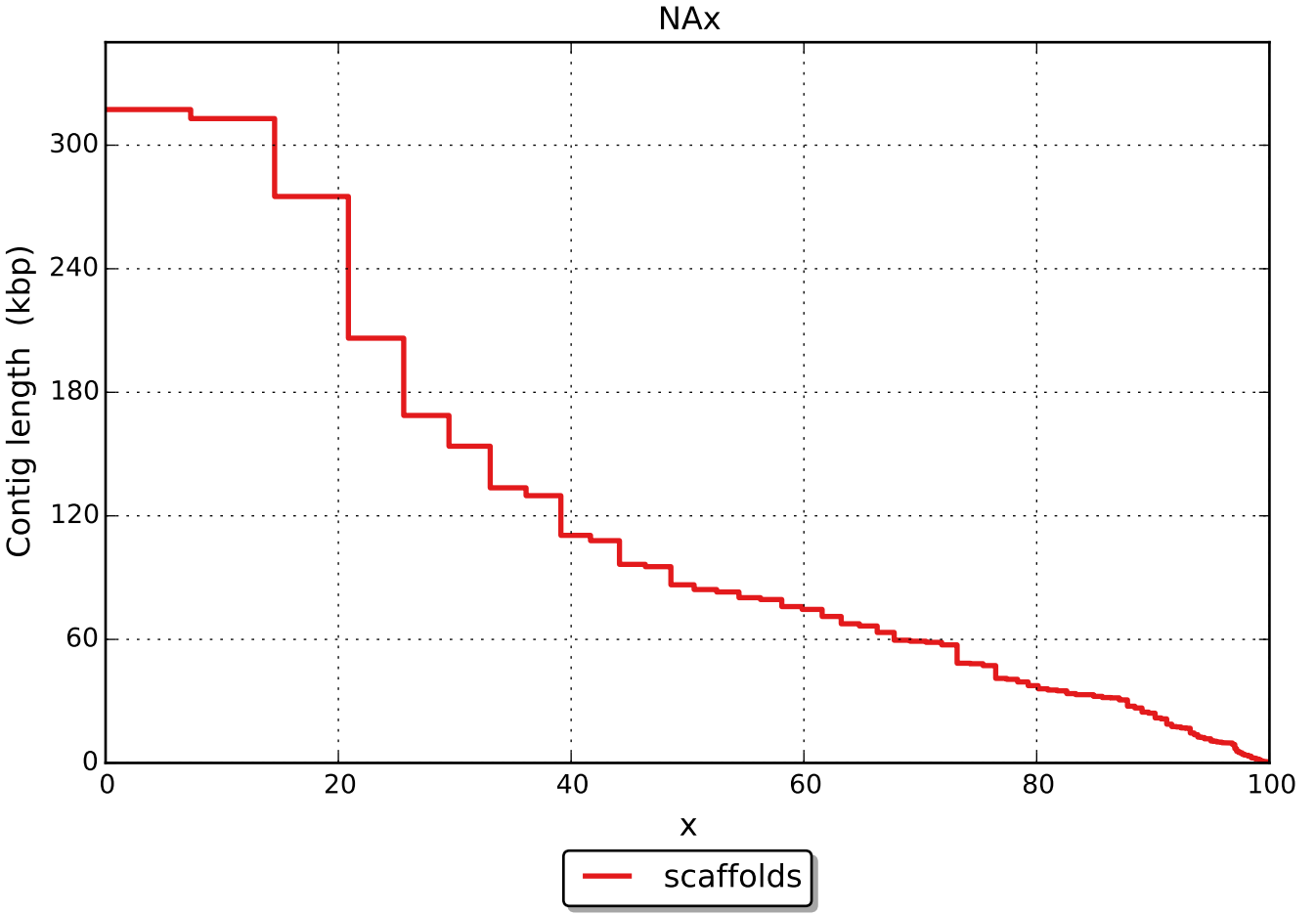

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

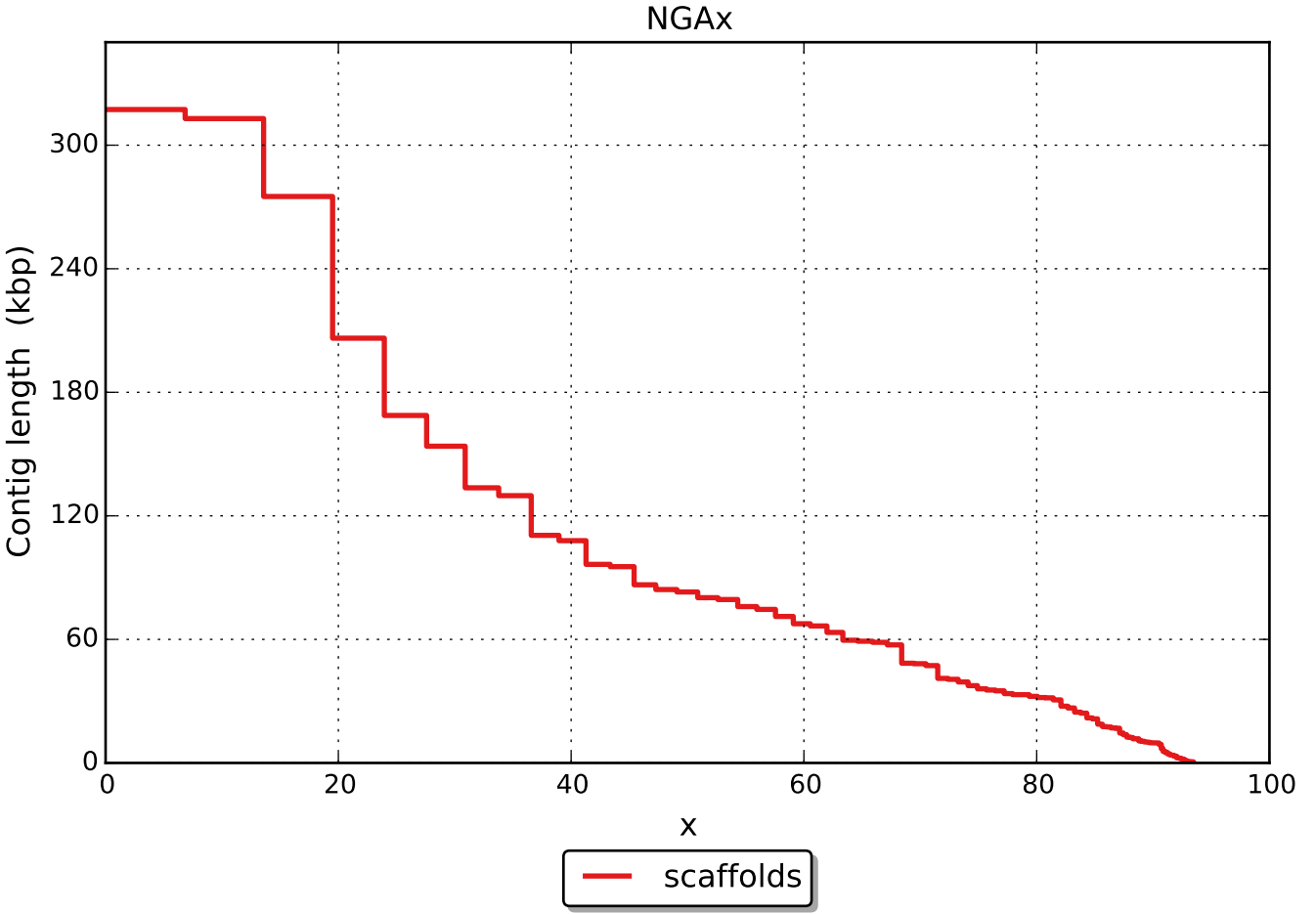

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
30
60
90
120
Contig index
scaffolds
Reference


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