Report

	scaffolds
# contigs (>= 1000 bp)	113
# contigs (>= 5000 bp)	76
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	25
Total length (>= 1000 bp)	3944198
Total length (>= 5000 bp)	3853498
Total length (>= 10000 bp)	3773929
Total length (>= 25000 bp)	3398832
Total length (>= 50000 bp)	2780703
# contigs	149
Largest contig	276573
Total length	3967452
Reference length	4641652
GC (%)	50.94
Reference GC (%)	50.79
N50	90939
NG50	67605
N75	40060
NG75	22038
L50	13
LG50	17
L75	30
LG75	47
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.365
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1010.56
# indels per 100 kbp	0.61
Largest alignment	276573
NA50	90939
NGA50	61149
NA75	38351
NGA75	22023
LA50	13
LGA50	18
LA75	31
LGA75	49

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

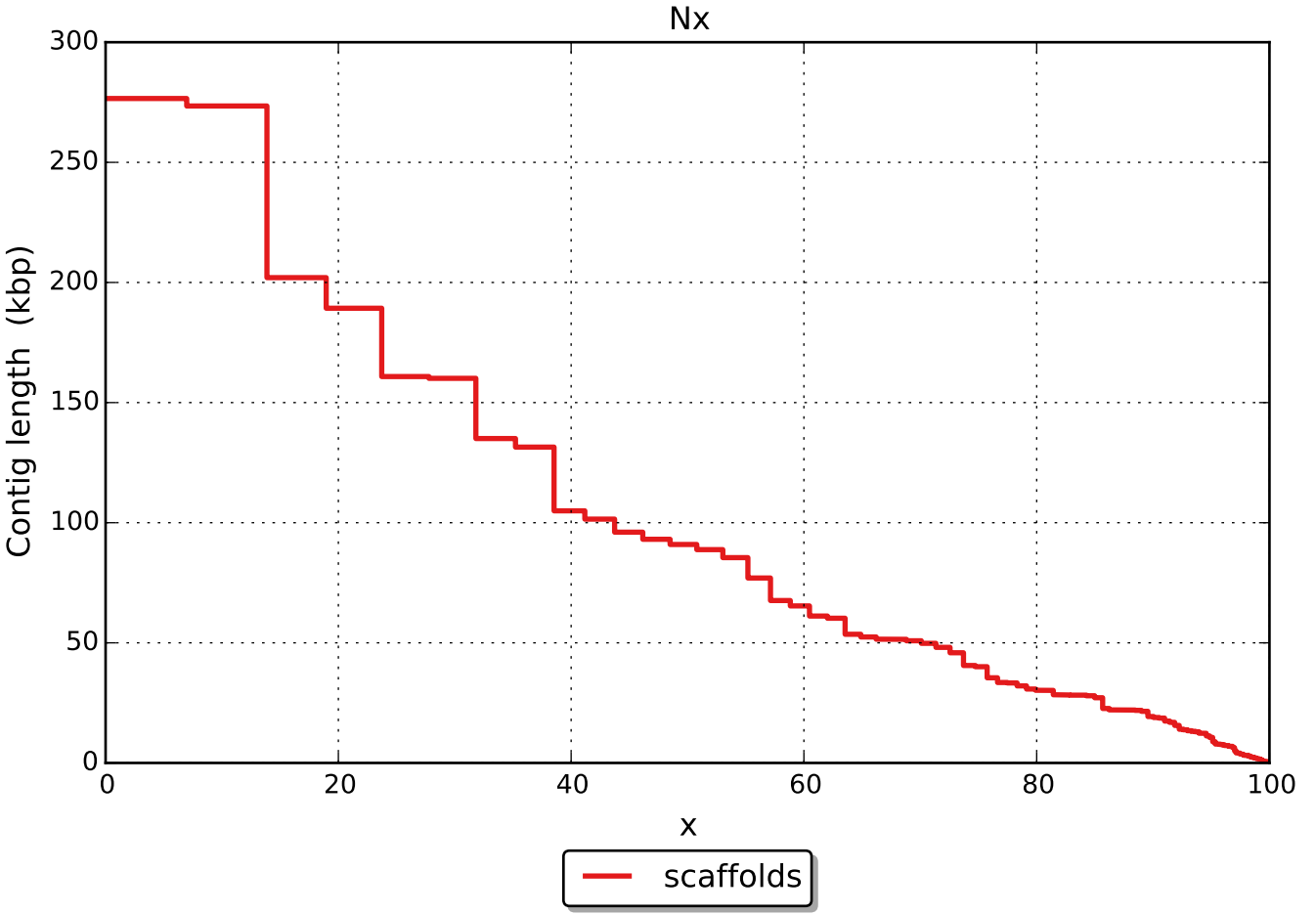
	scaffolds
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	156398
# local misassemblies	3
# mismatches	39573
# indels	24
# short indels	24
# long indels	0
Indels length	32

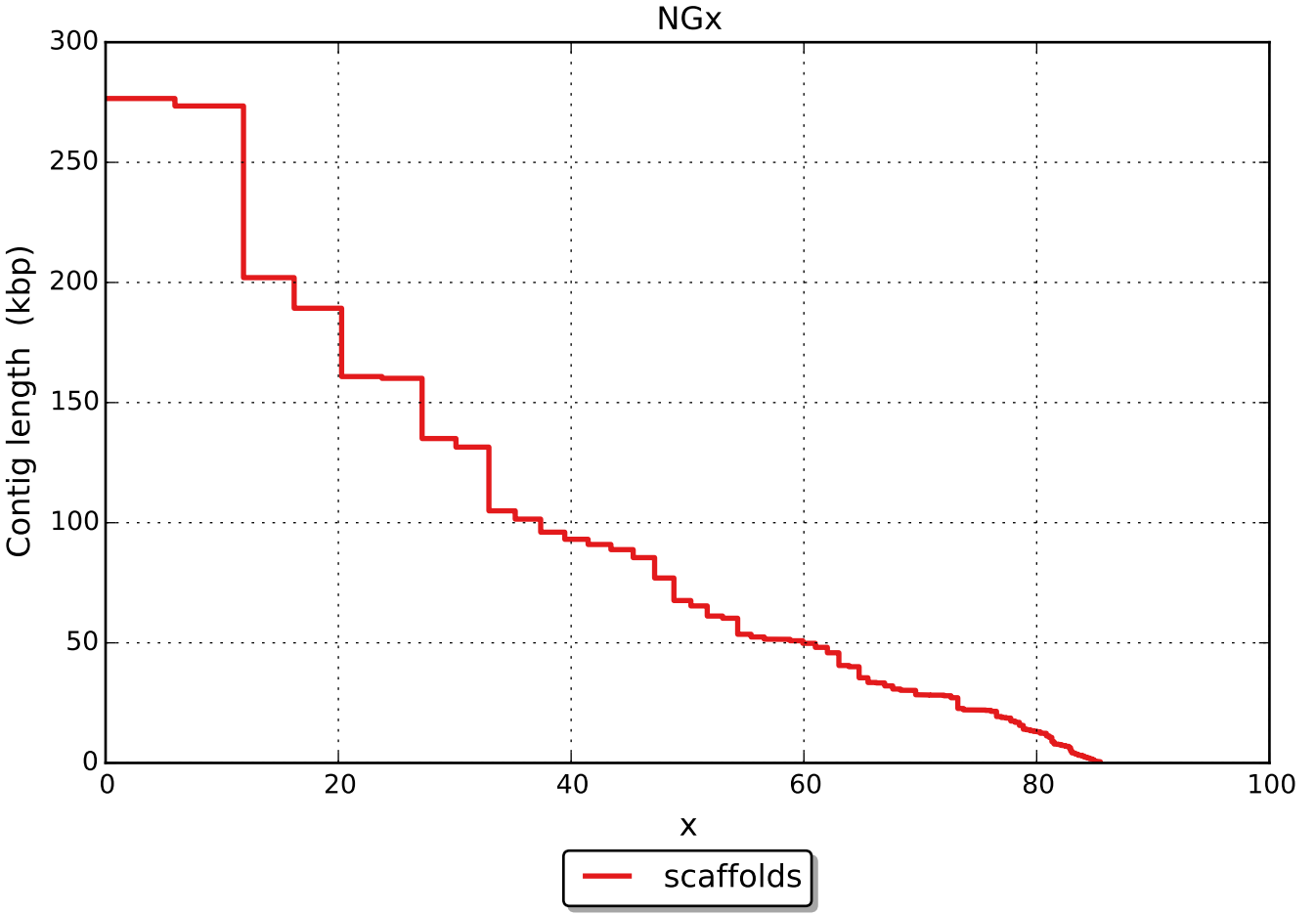
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

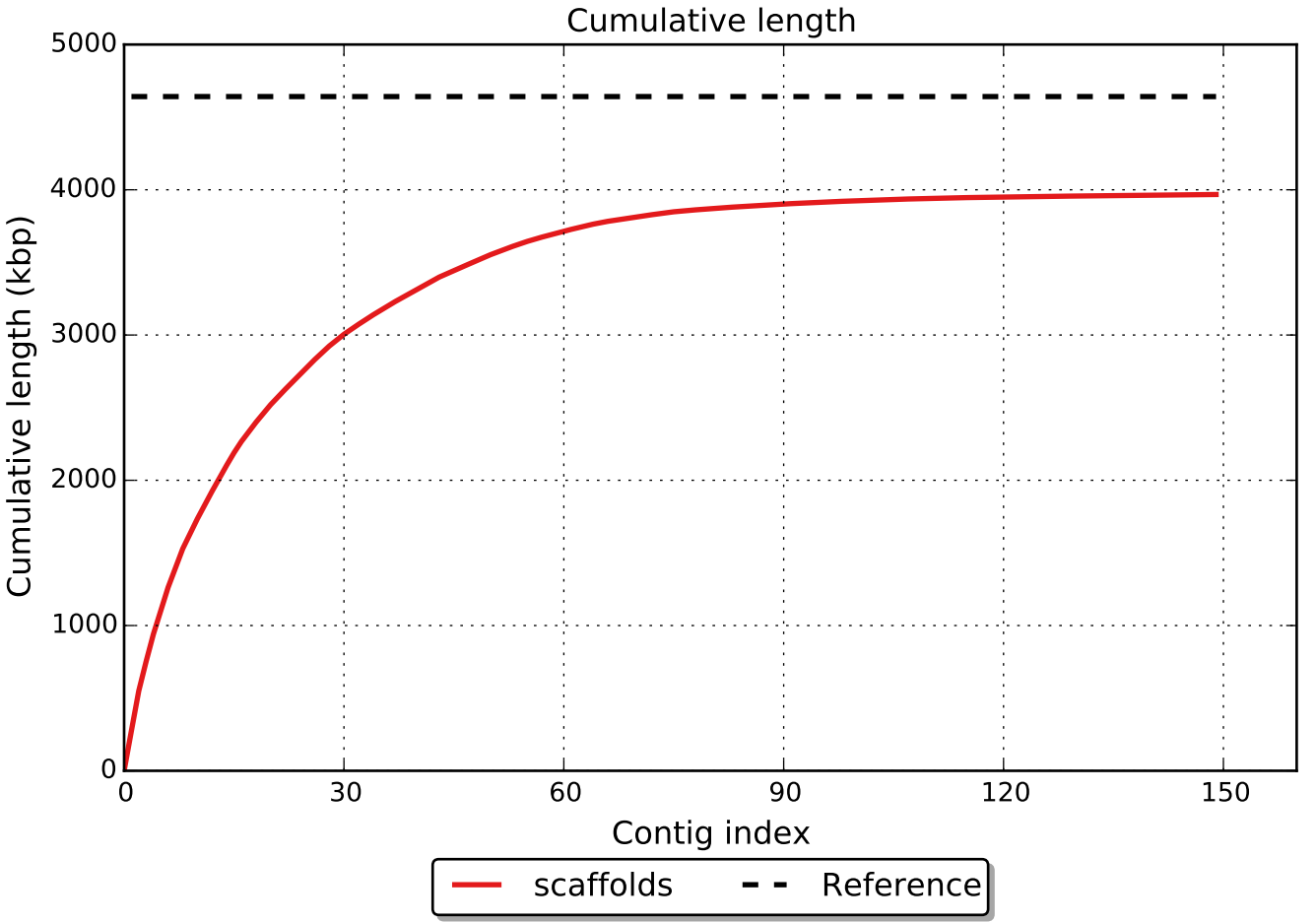
Unaligned report

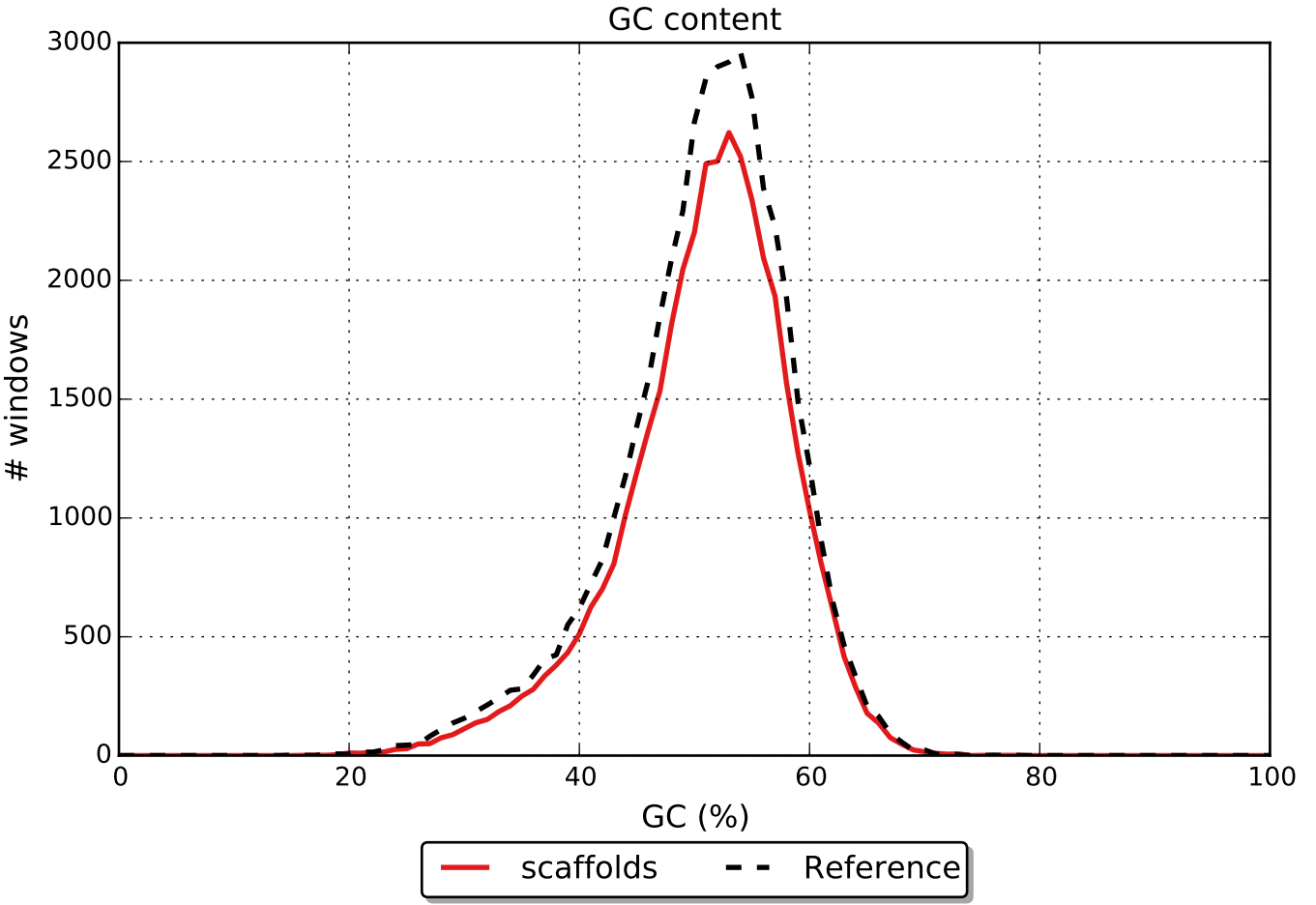
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

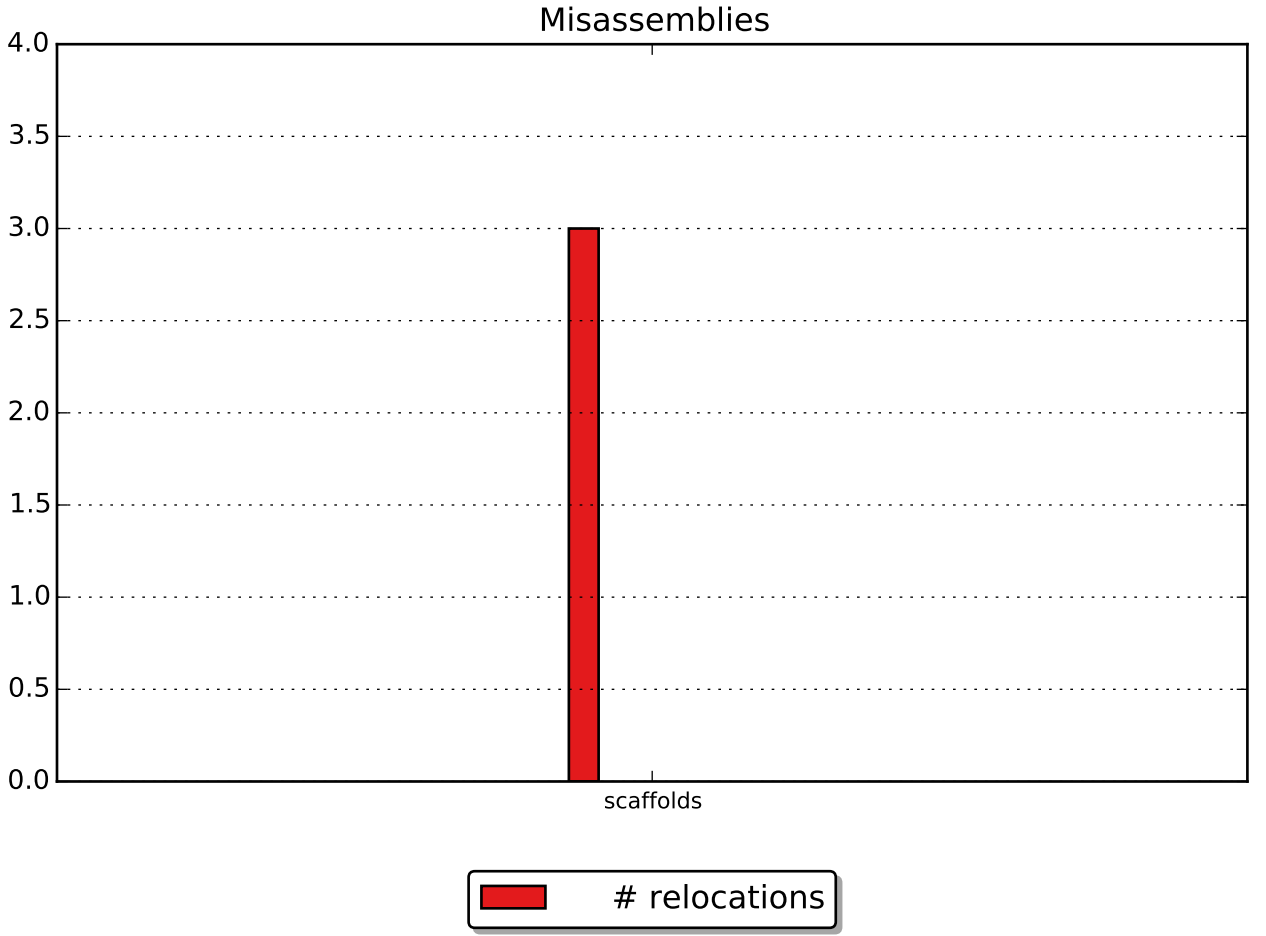
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

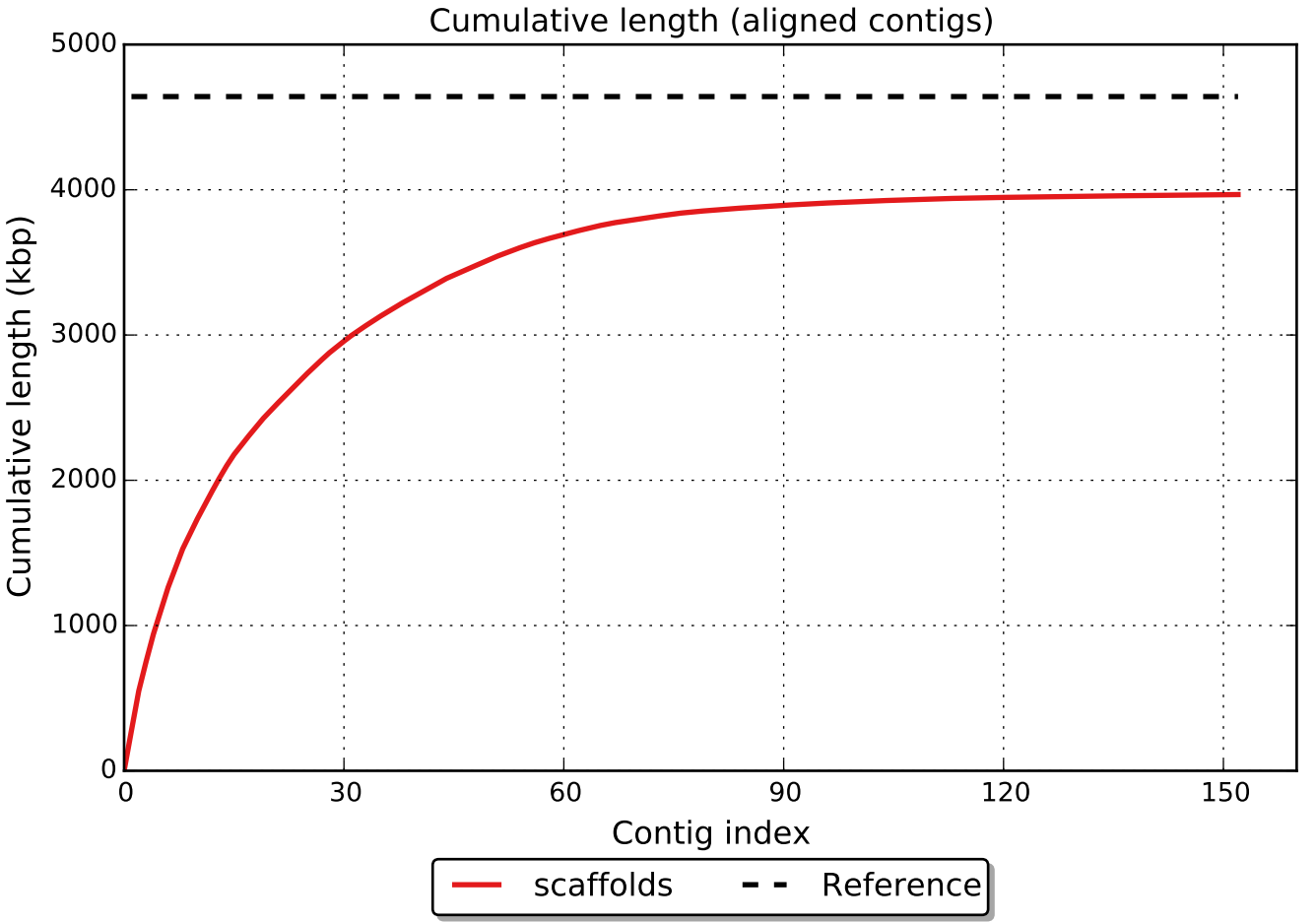

Nx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

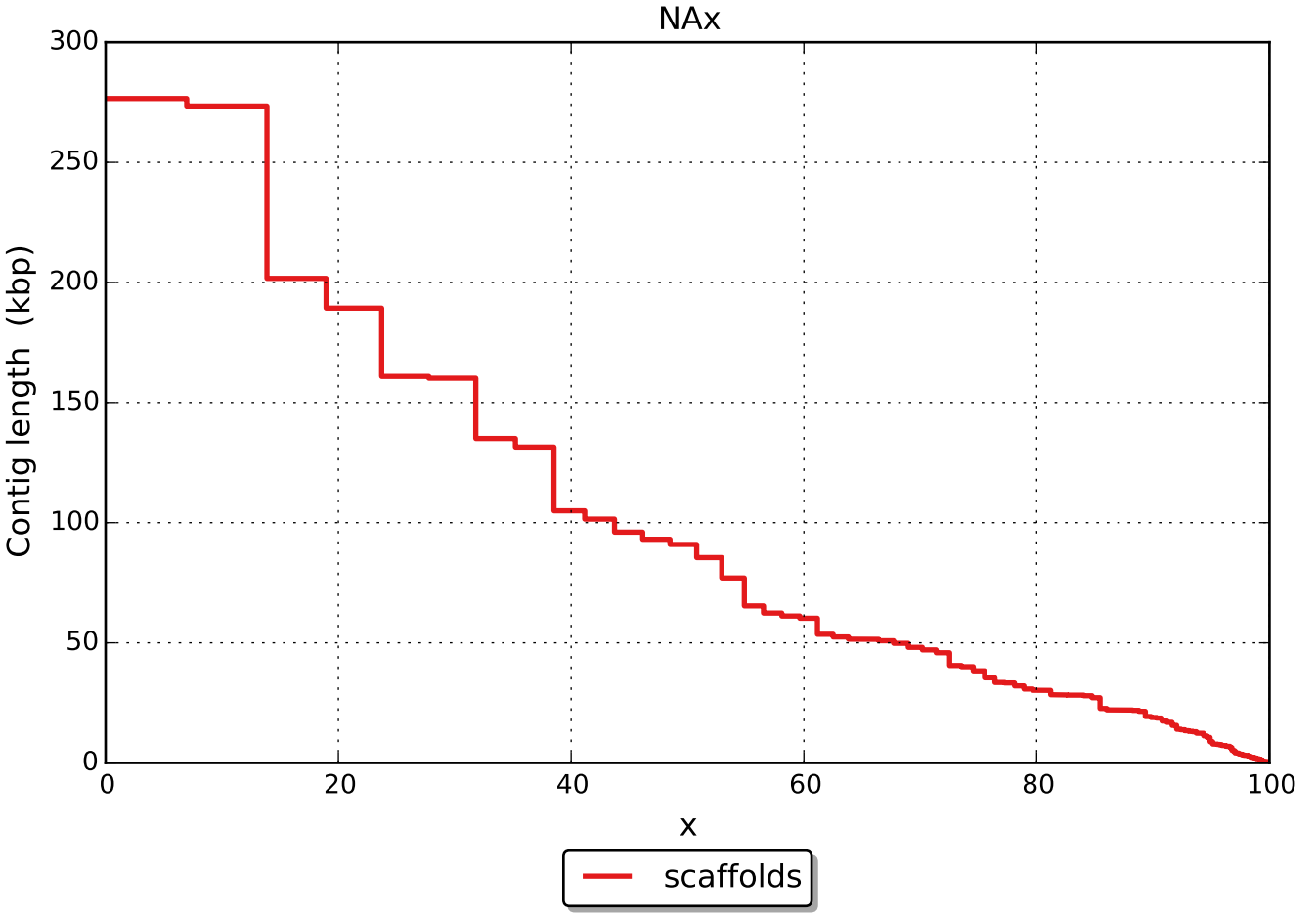

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

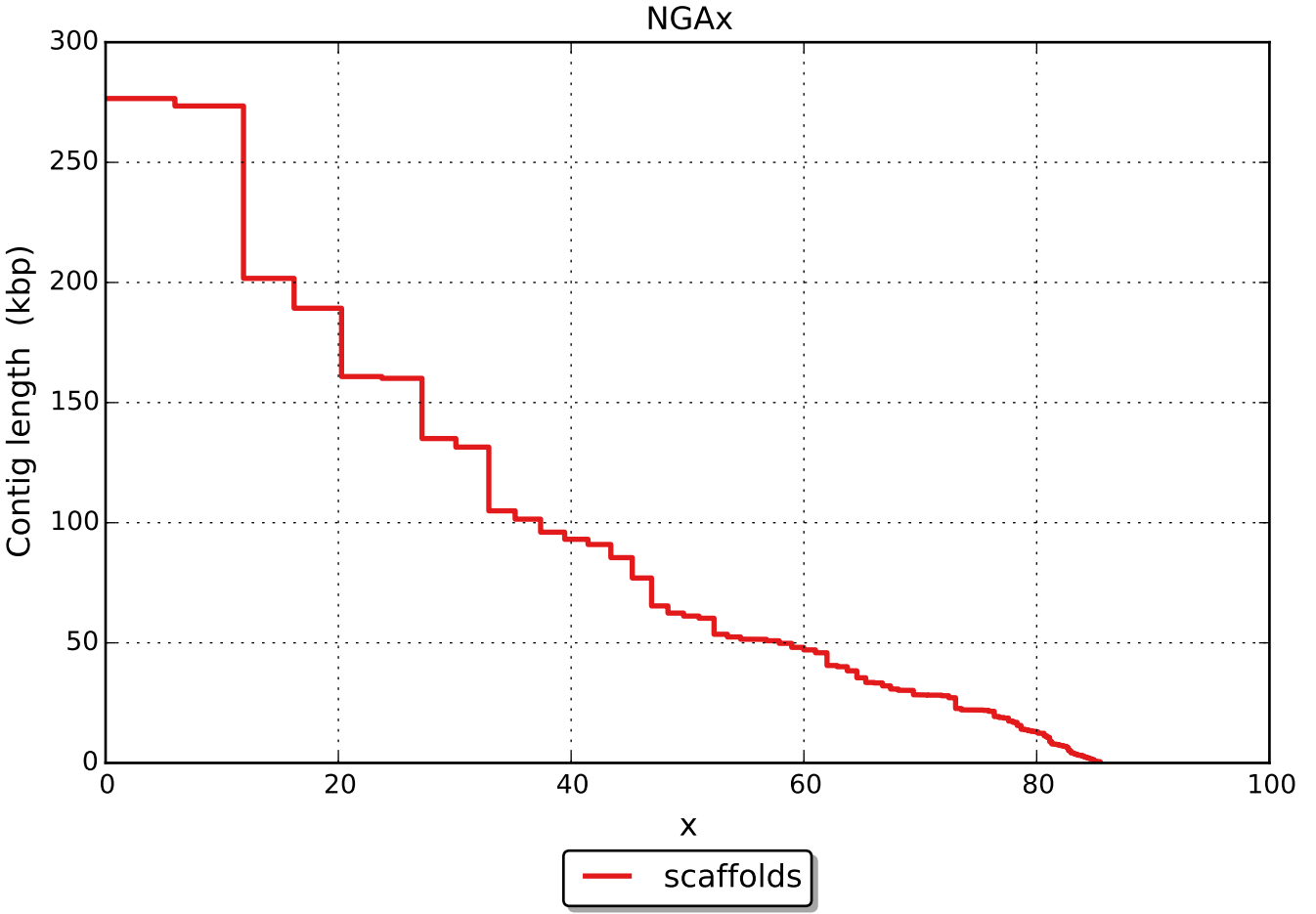

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
scaffolds
Reference


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


Misassemblies
4.0
3.5
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
30
60
90
120
150
Contig index
scaffolds
Reference


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


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