Report

	scaffolds
# contigs (>= 1000 bp)	107
# contigs (>= 5000 bp)	81
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	3379532
Total length (>= 5000 bp)	3312262
Total length (>= 10000 bp)	3190915
Total length (>= 25000 bp)	2851649
Total length (>= 50000 bp)	2311394
# contigs	113
Largest contig	264572
Total length	3384103
Reference length	4641652
GC (%)	50.83
Reference GC (%)	50.79
N50	73015
NG50	43987
N75	33667
L50	16
LG50	27
L75	32
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	307071
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	72.791
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	559.06
# indels per 100 kbp	0.53
Largest alignment	264572
NA50	71281
NGA50	43808
NA75	33414
LA50	17
LGA50	28
LA75	34

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

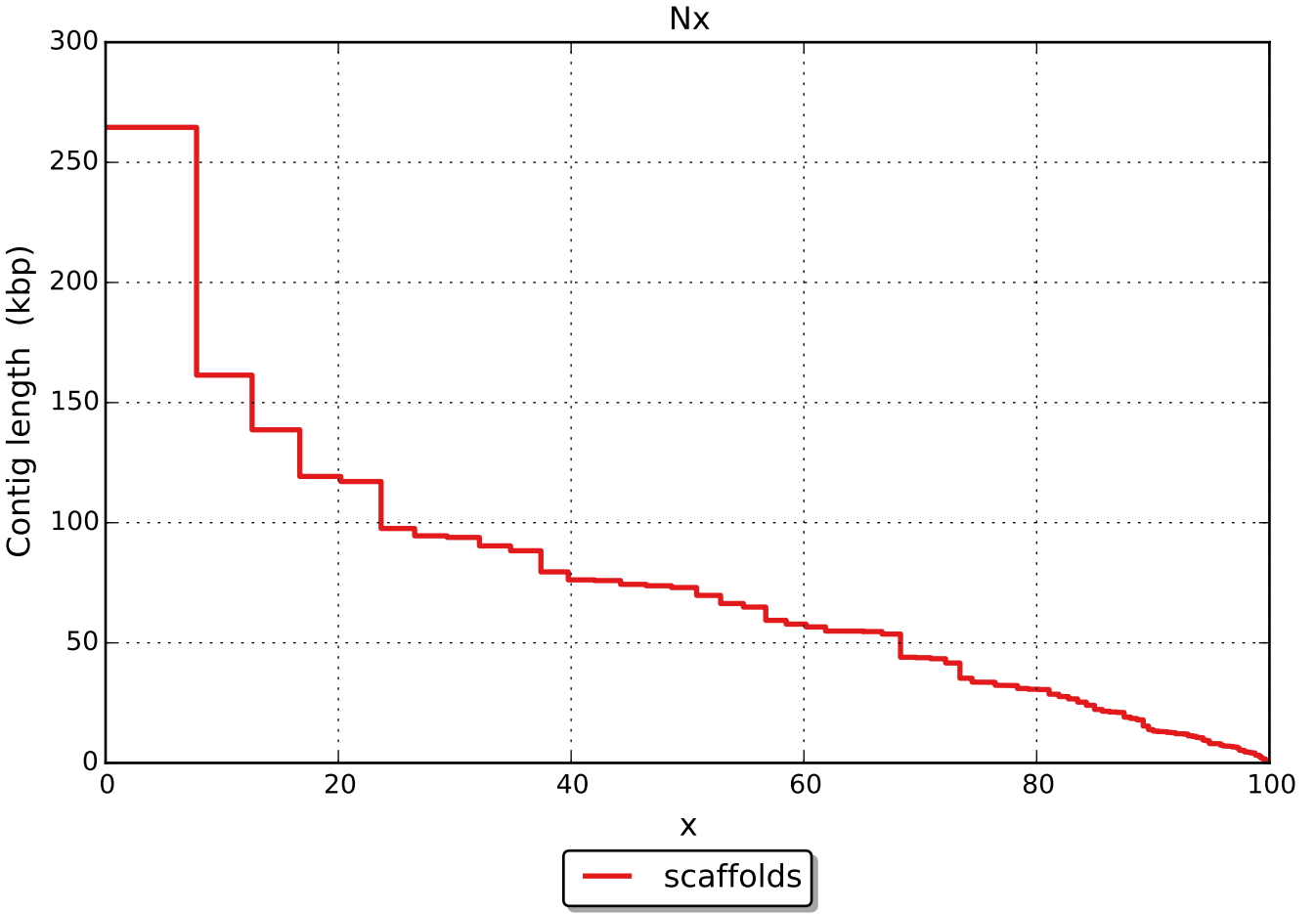
	scaffolds
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	307071
# local misassemblies	1
# mismatches	18889
# indels	18
# short indels	18
# long indels	0
Indels length	24

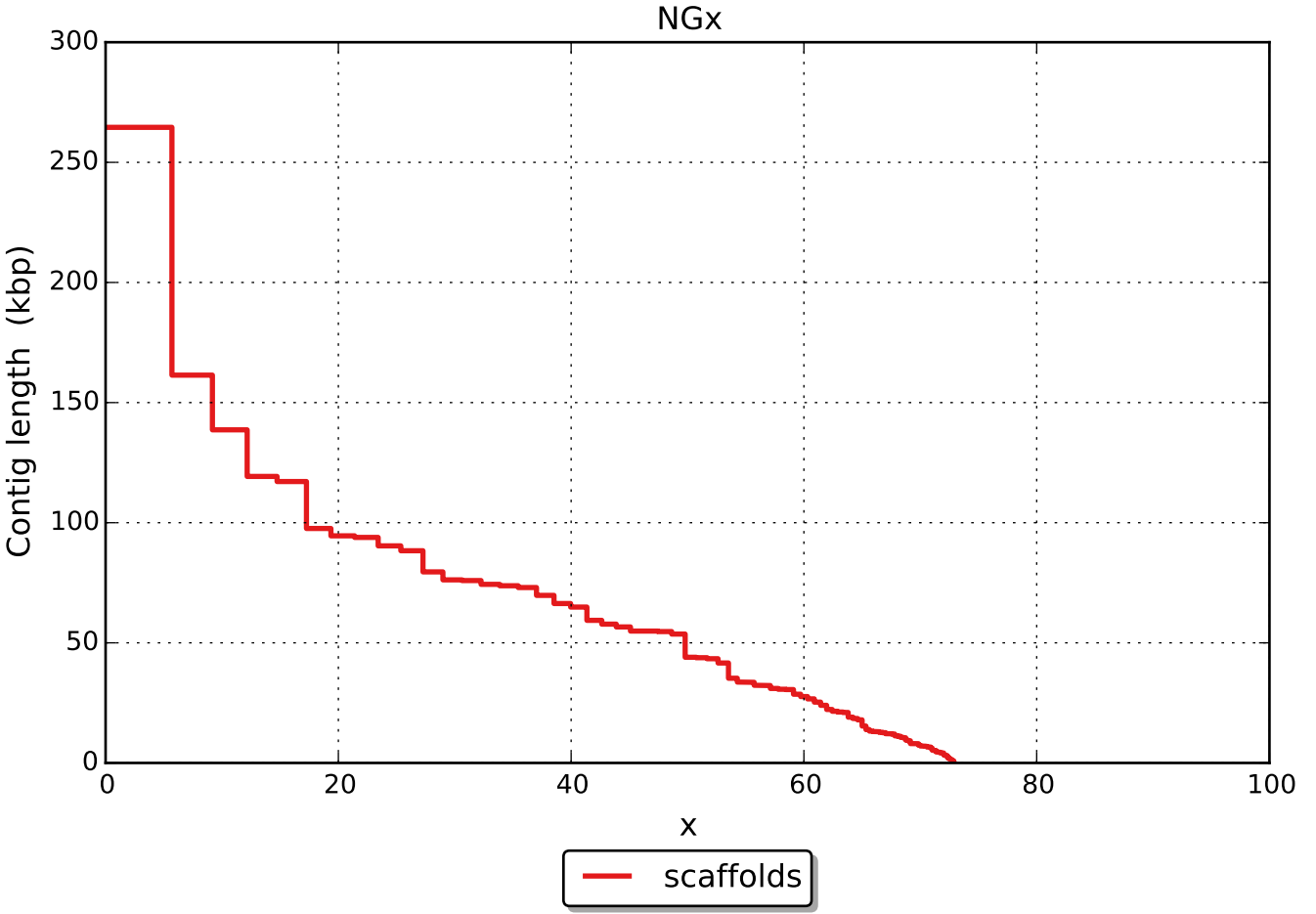
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

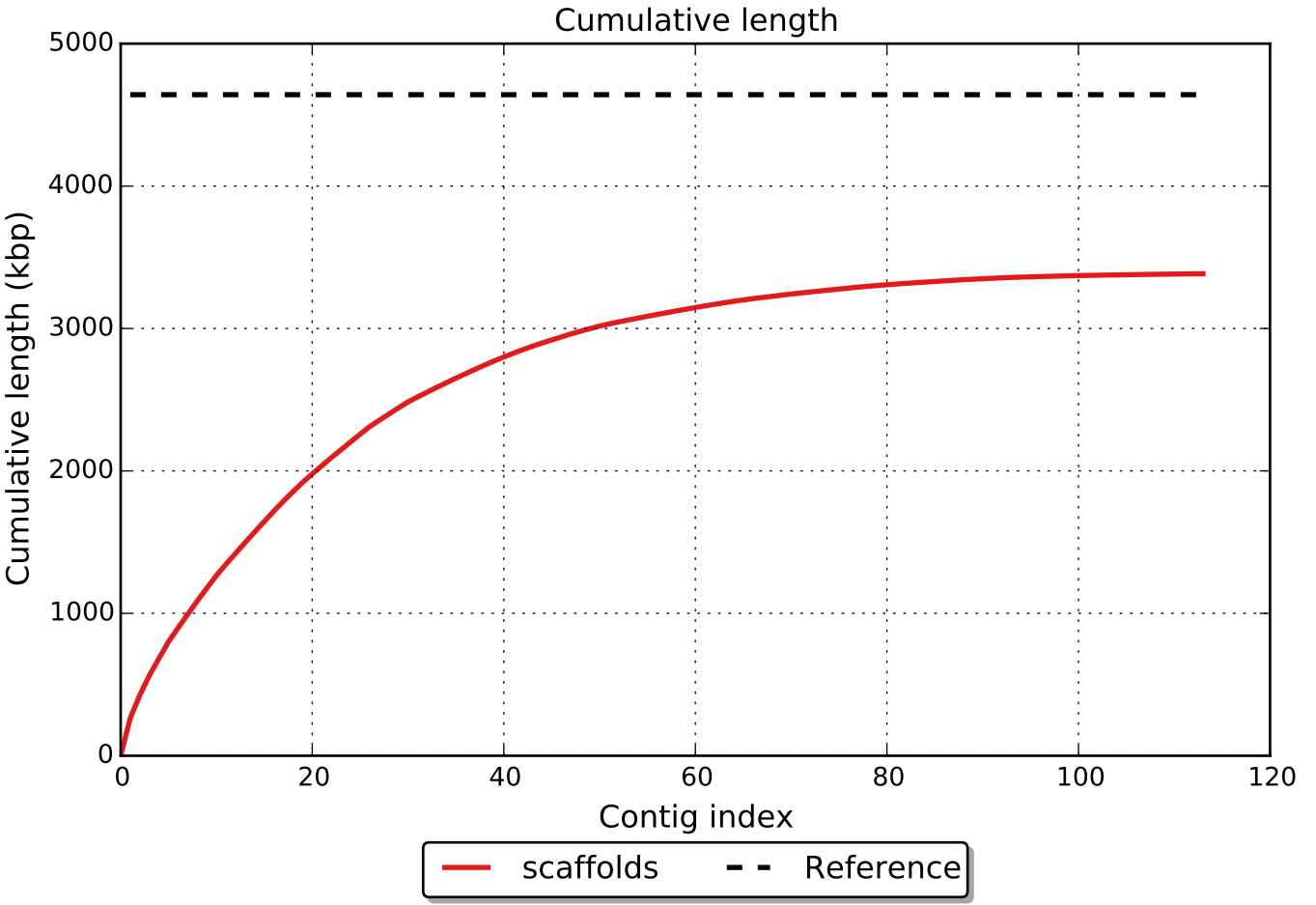
Unaligned report

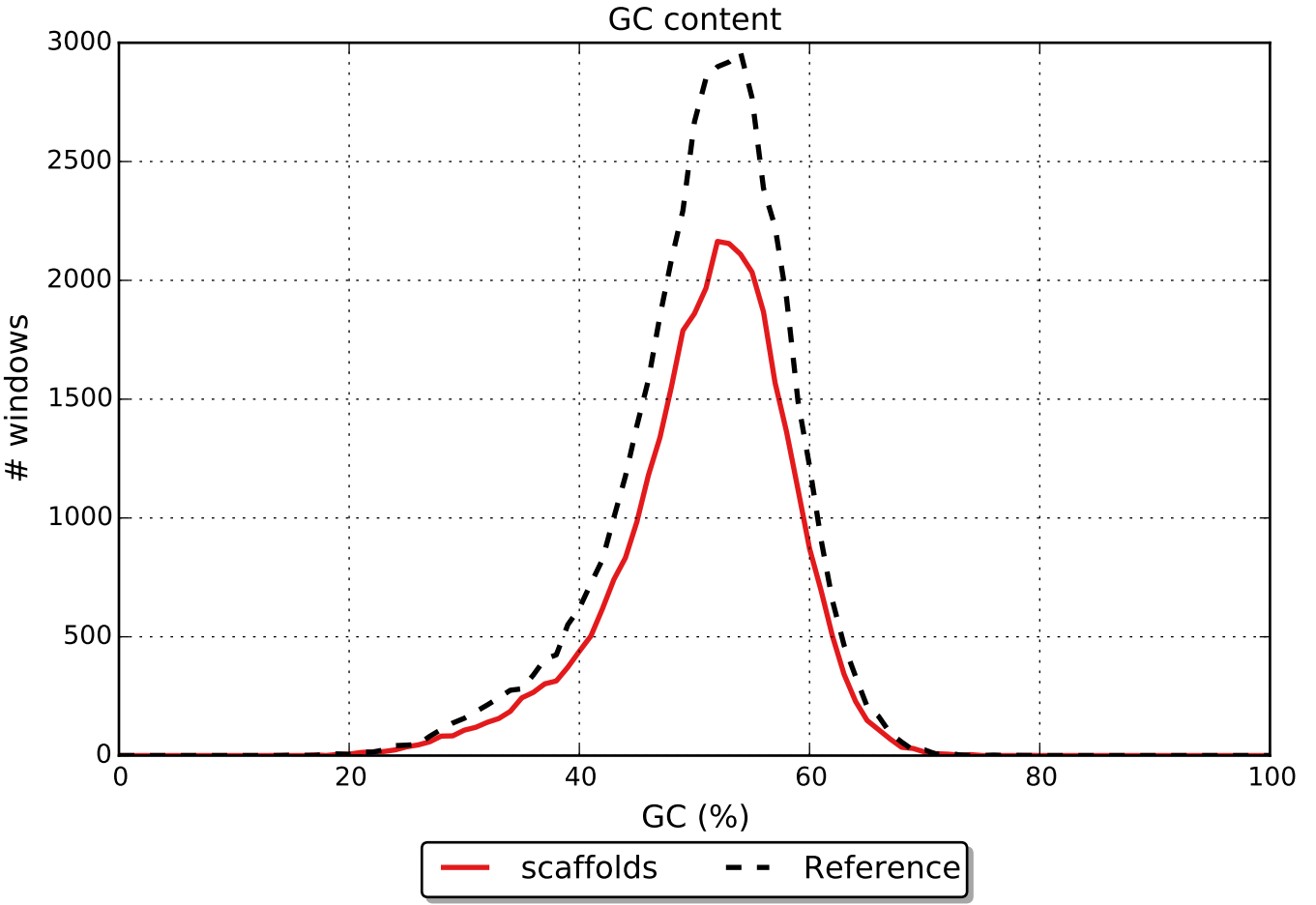
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

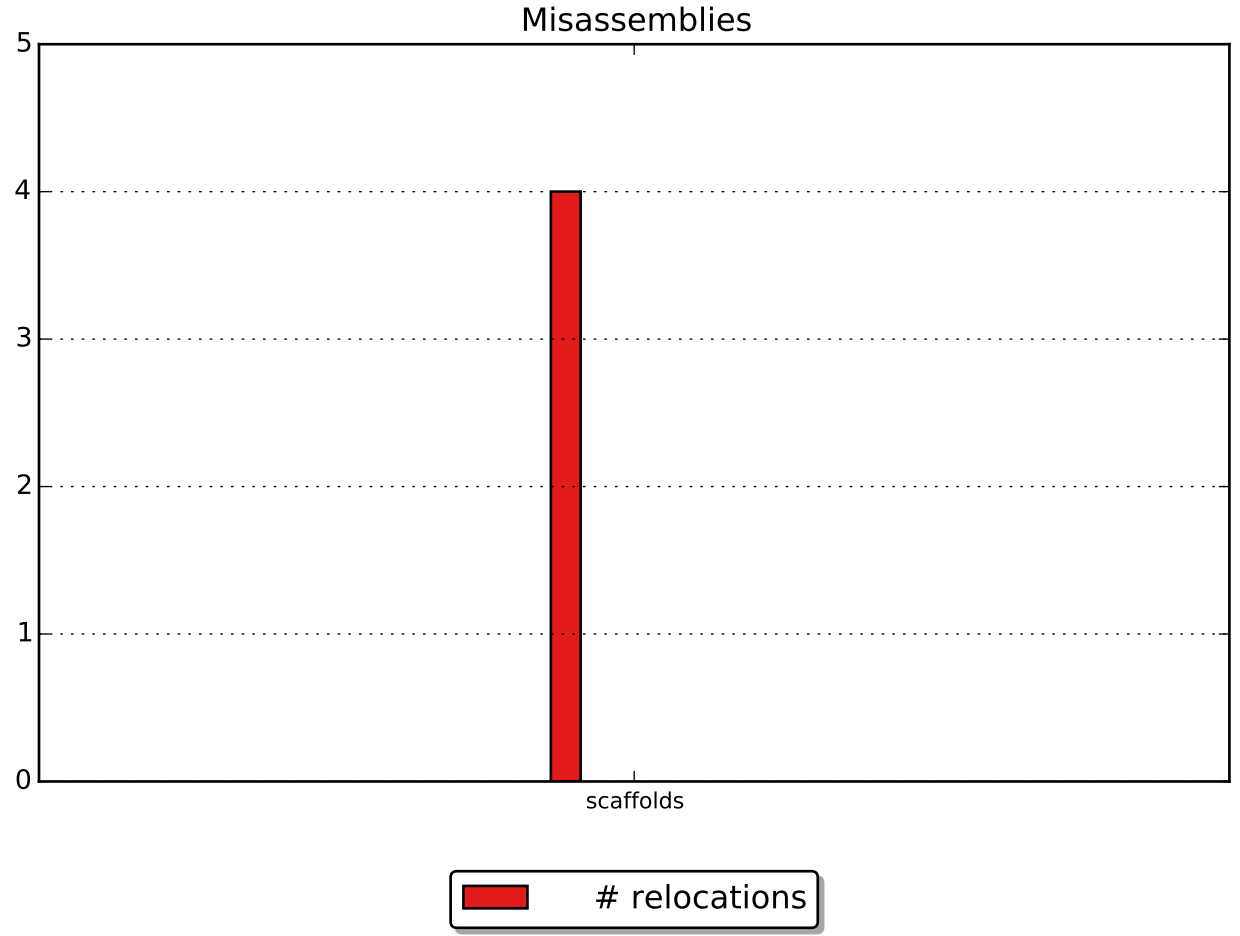
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

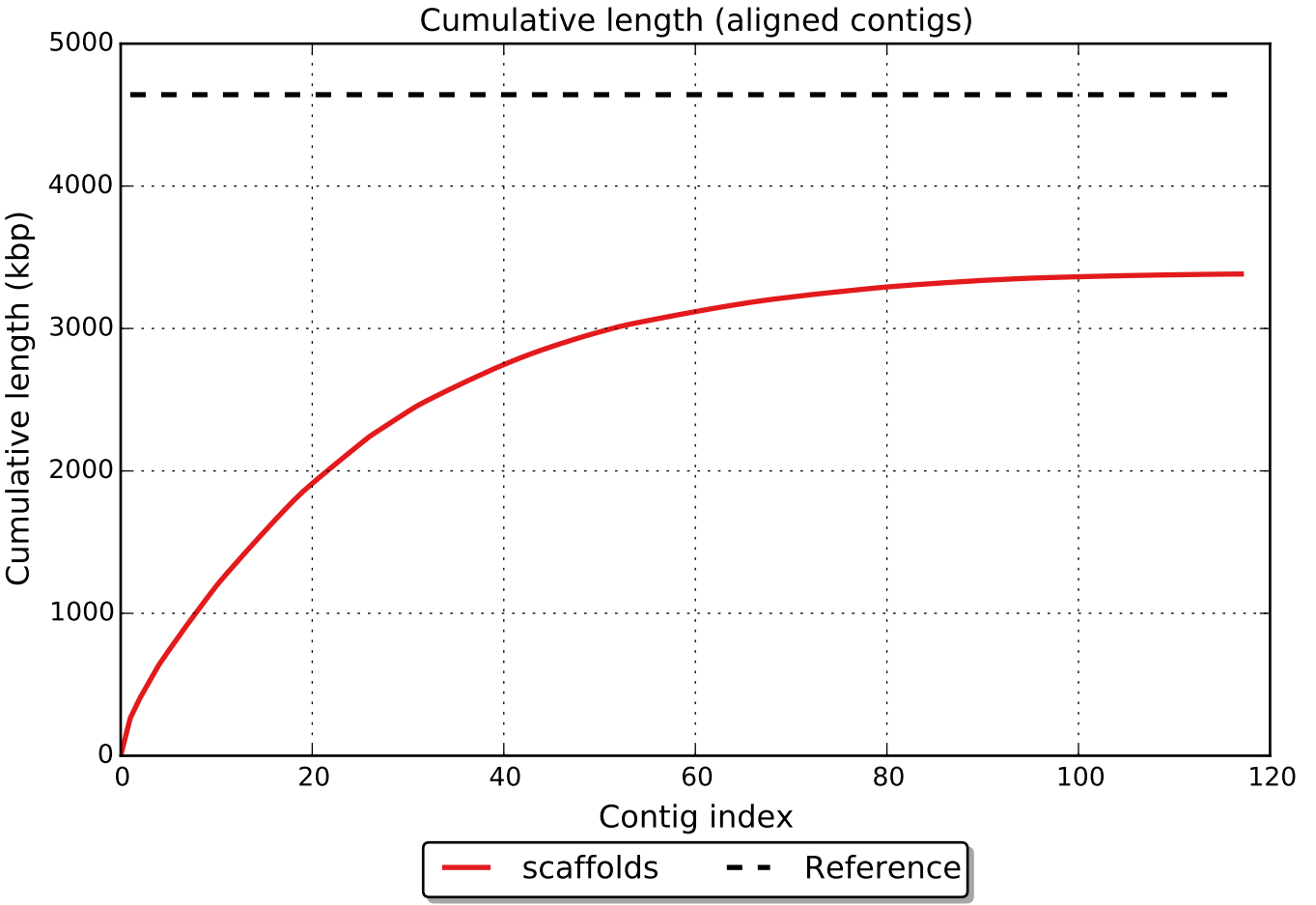

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds

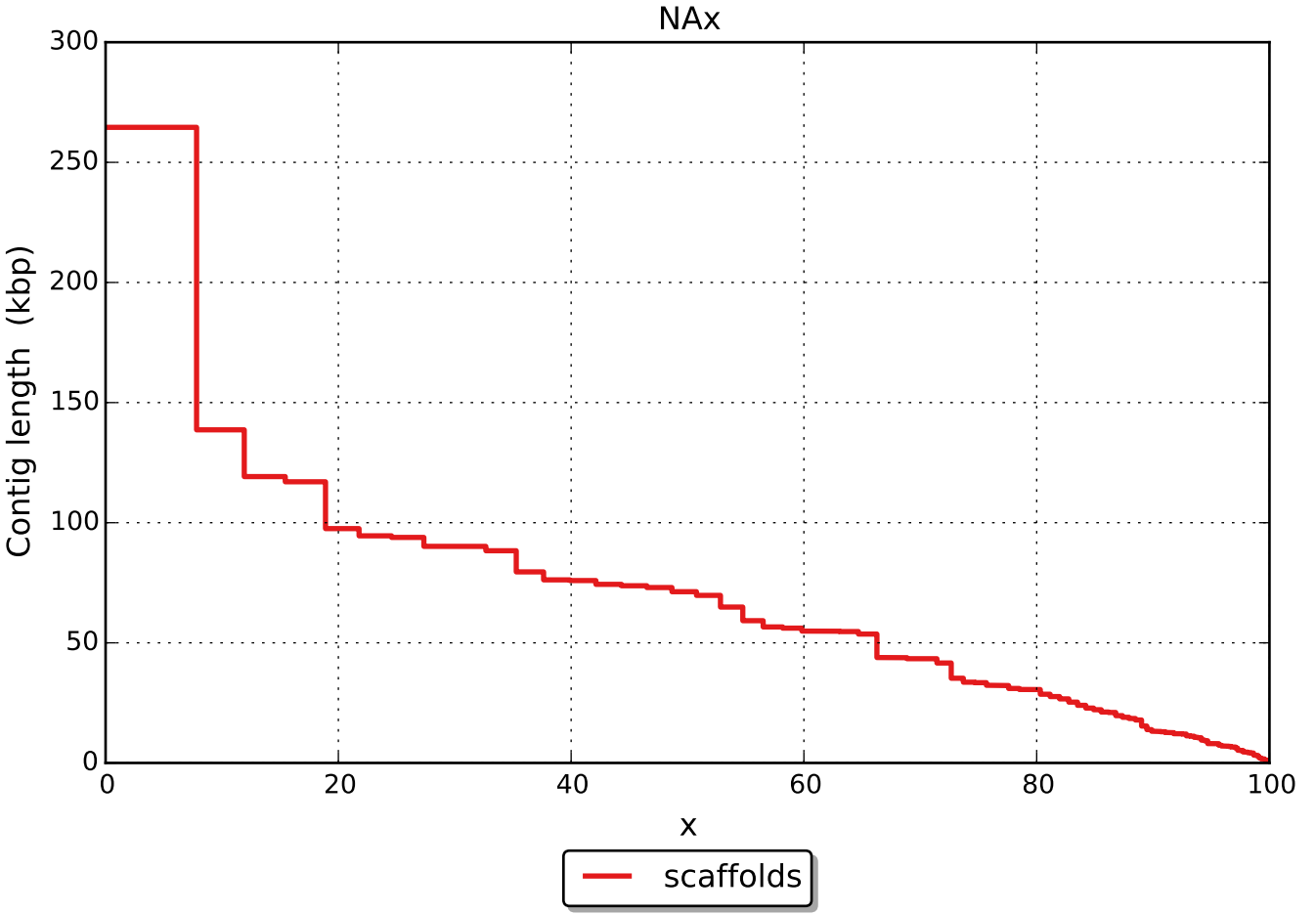

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

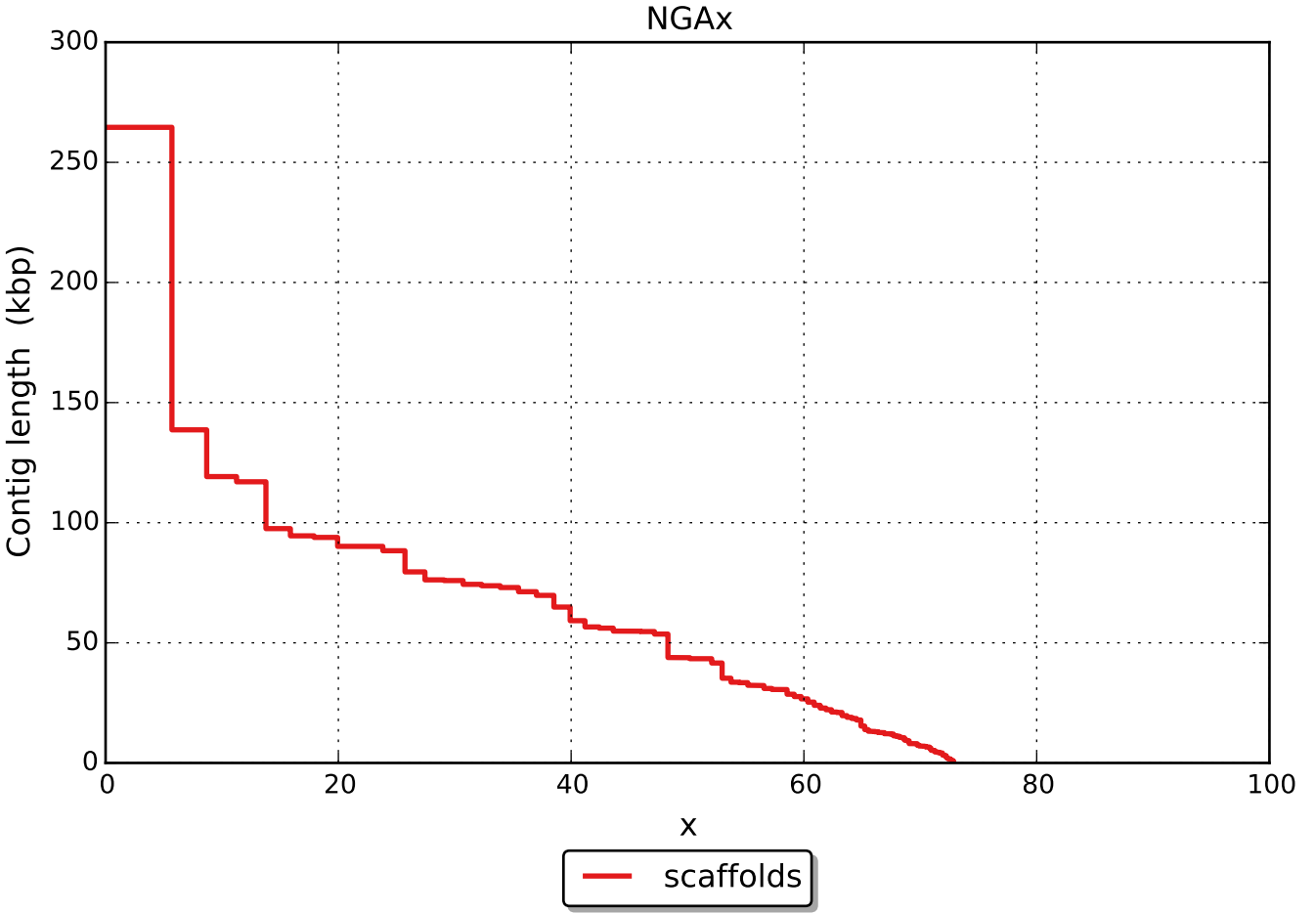

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
scaffolds
Reference


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


Misassemblies
5
4
3
2
1
0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
scaffolds
Reference


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


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