Report

	scaffolds
# contigs (>= 1000 bp)	238
# contigs (>= 5000 bp)	182
# contigs (>= 10000 bp)	148
# contigs (>= 25000 bp)	71
# contigs (>= 50000 bp)	15
Total length (>= 1000 bp)	4681396
Total length (>= 5000 bp)	4554718
Total length (>= 10000 bp)	4296558
Total length (>= 25000 bp)	3033633
Total length (>= 50000 bp)	1100704
# contigs	262
Largest contig	132022
Total length	4696790
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	31972
NG50	32027
N75	19156
NG75	19781
L50	48
LG50	47
L75	94
LG75	92
# misassemblies	25
# misassembled contigs	19
Misassembled contigs length	706576
# local misassemblies	4
# unaligned contigs	0 + 9 part
Unaligned length	1634
Genome fraction (%)	98.109
Duplication ratio	1.031
# N's per 100 kbp	25.91
# mismatches per 100 kbp	921.09
# indels per 100 kbp	0.68
Largest alignment	125463
NA50	29578
NGA50	30018
NA75	17458
NGA75	17754
LA50	53
LGA50	52
LA75	103
LGA75	101

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

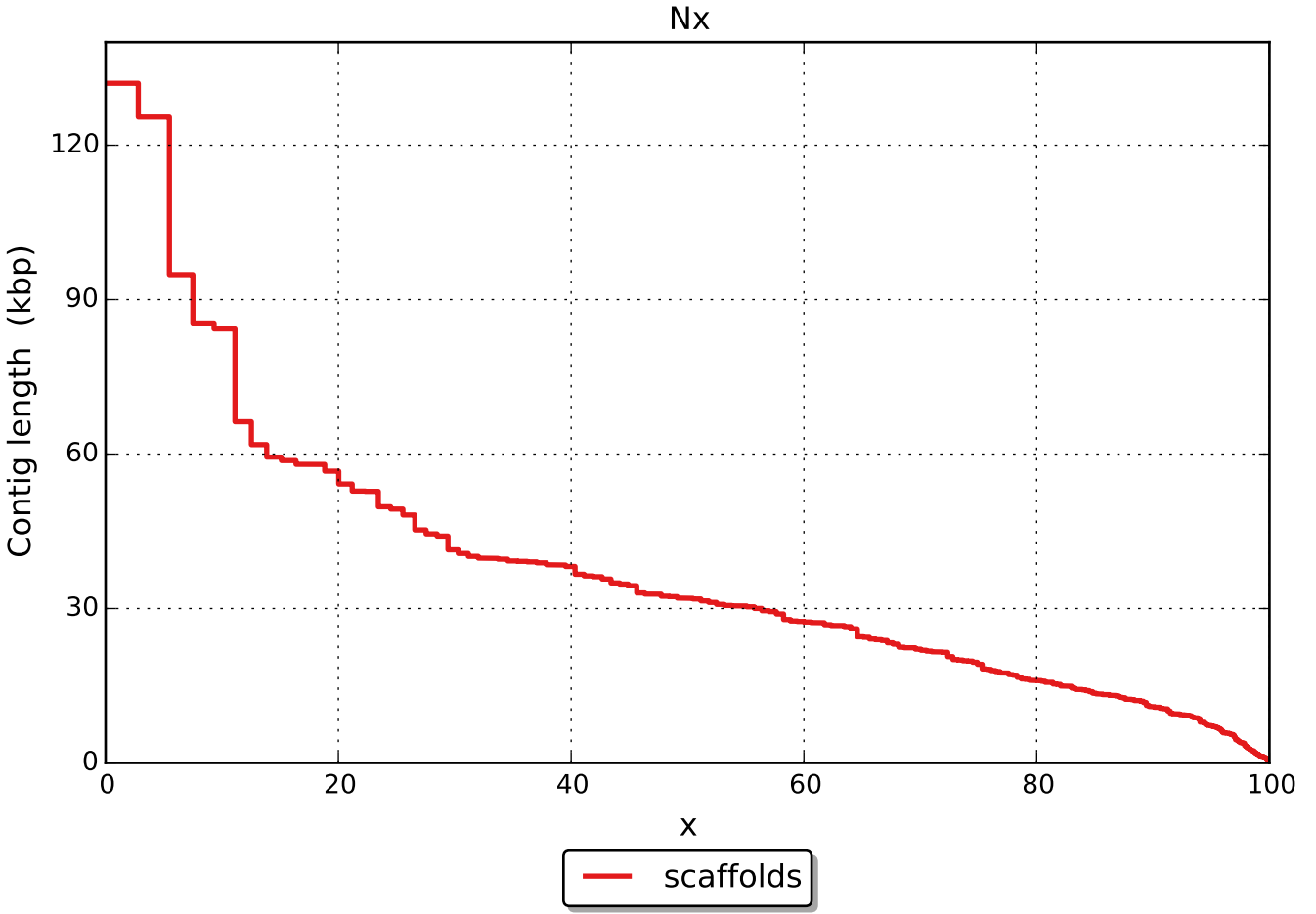
	scaffolds
# misassemblies	25
# relocations	18
# translocations	0
# inversions	7
# possibly misassembled contigs	1
# misassembled contigs	19
Misassembled contigs length	706576
# local misassemblies	4
# mismatches	41945
# indels	31
# short indels	27
# long indels	4
Indels length	254

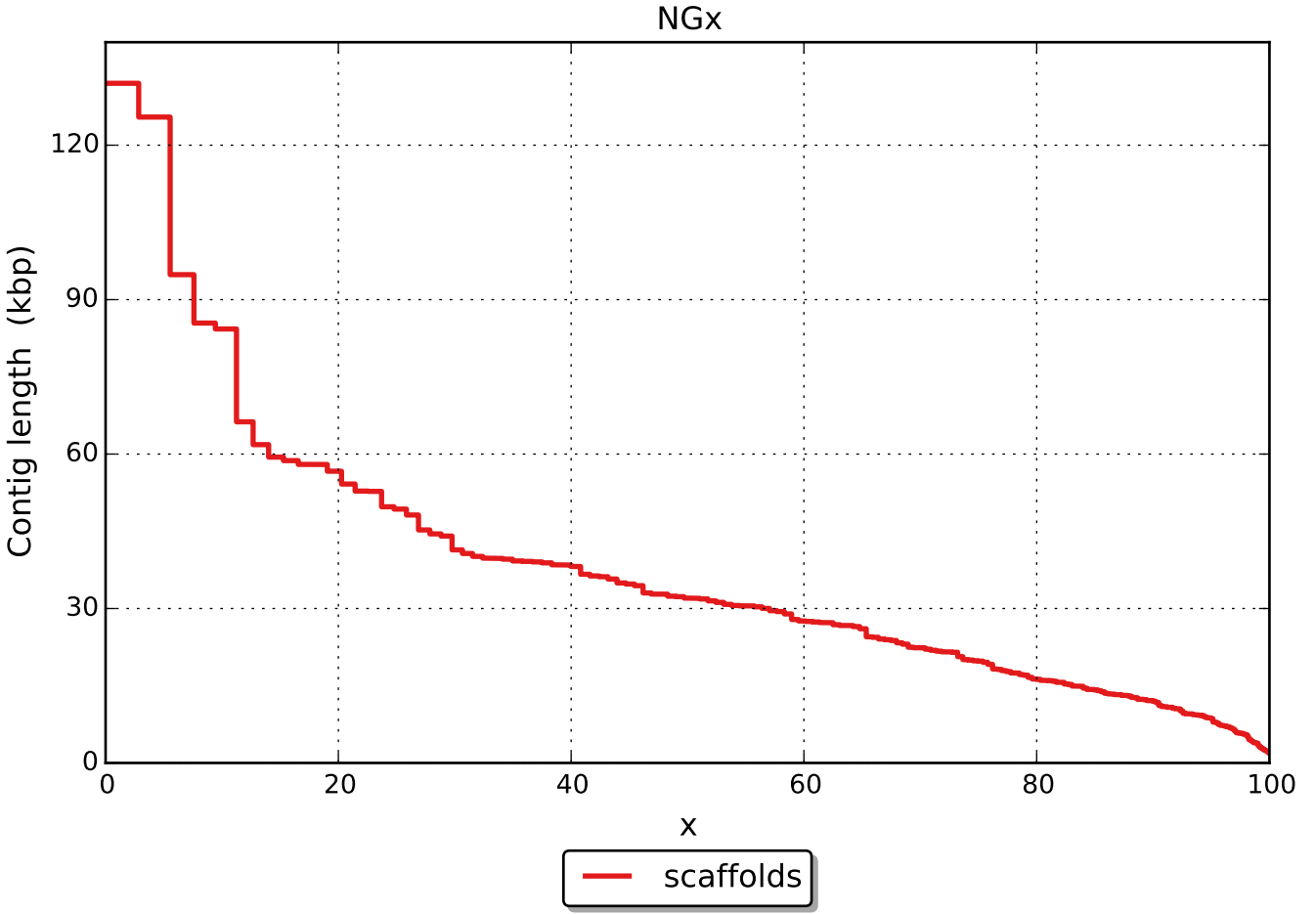
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

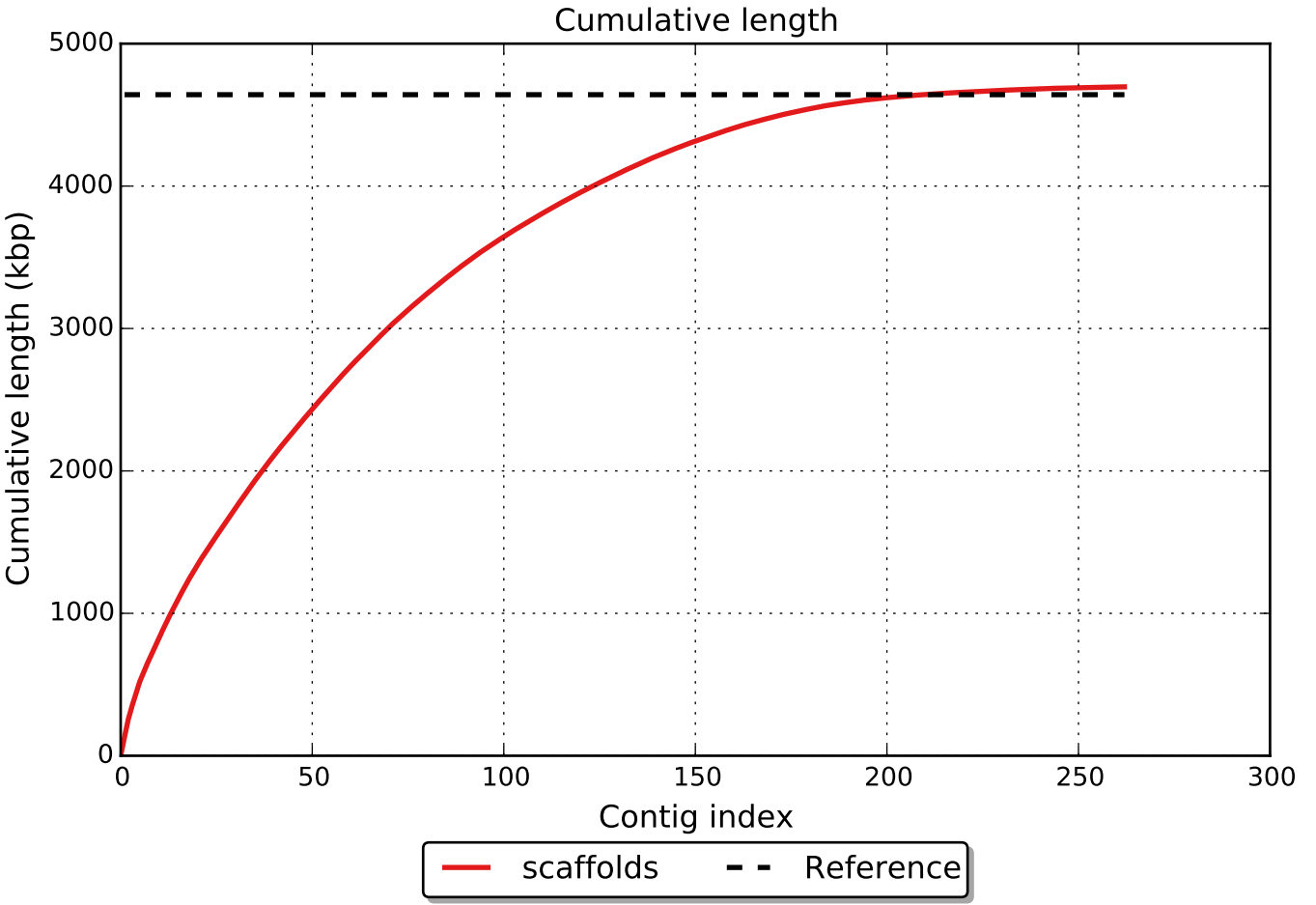
Unaligned report

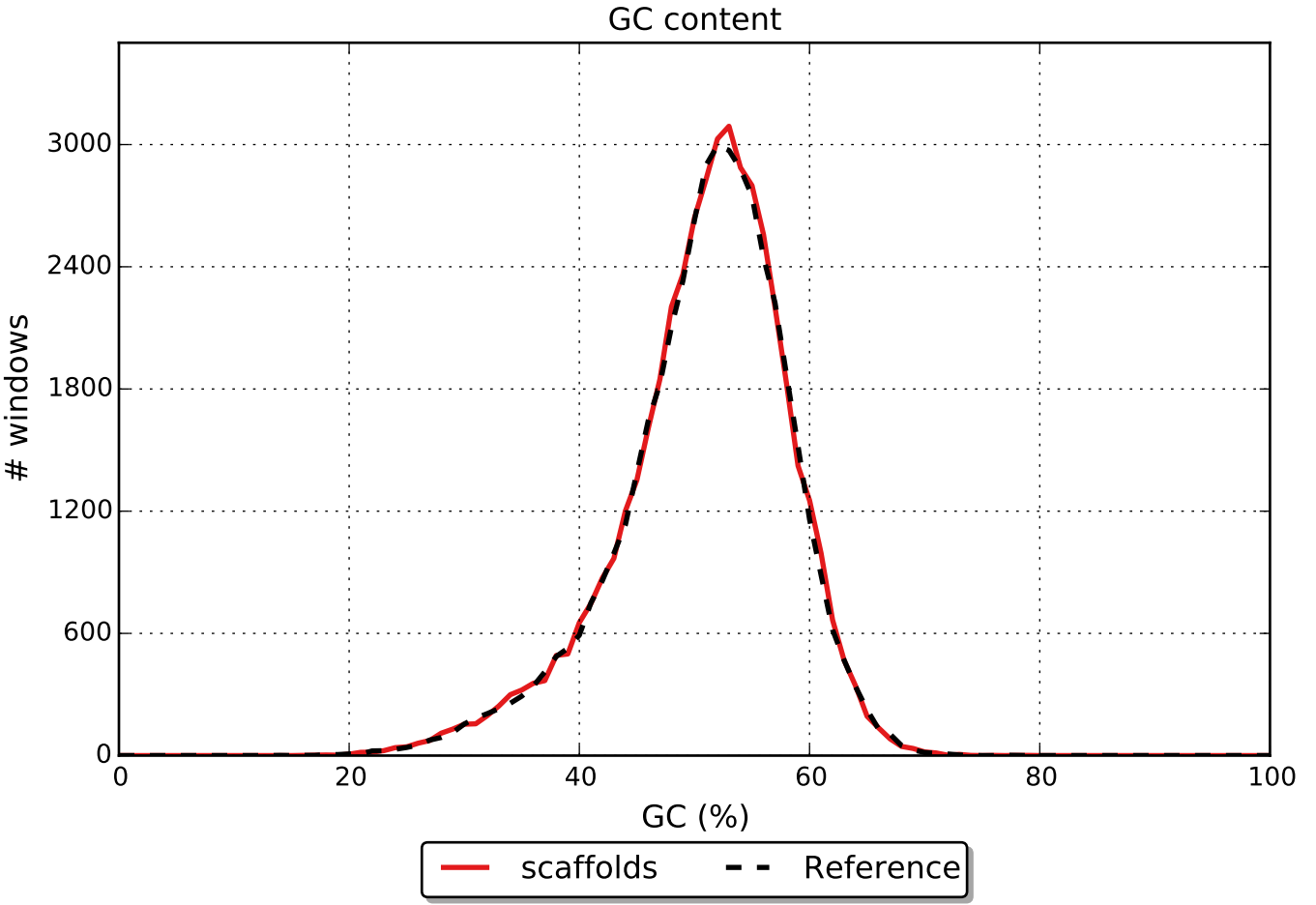
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1634
# N's	1217

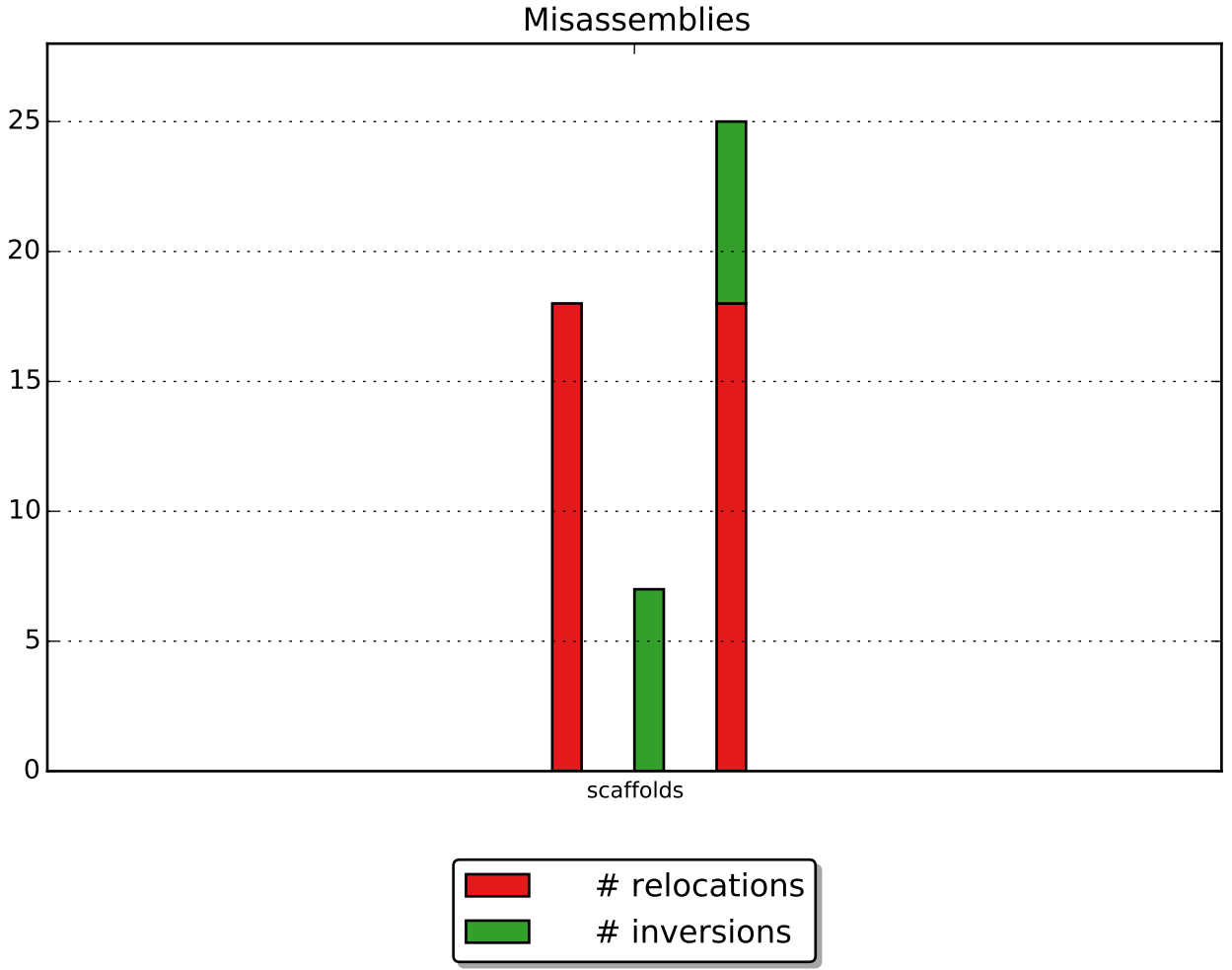
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

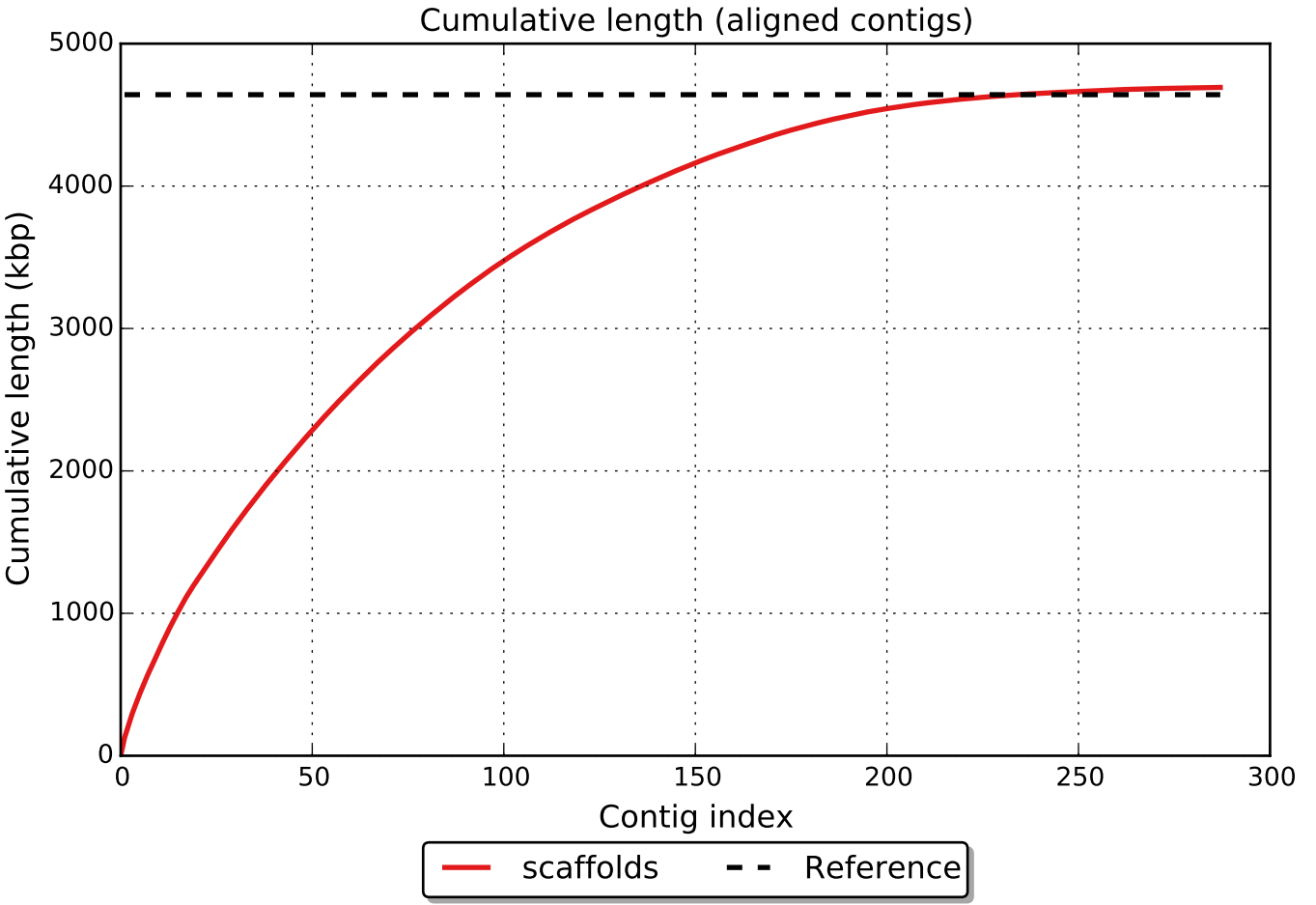

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

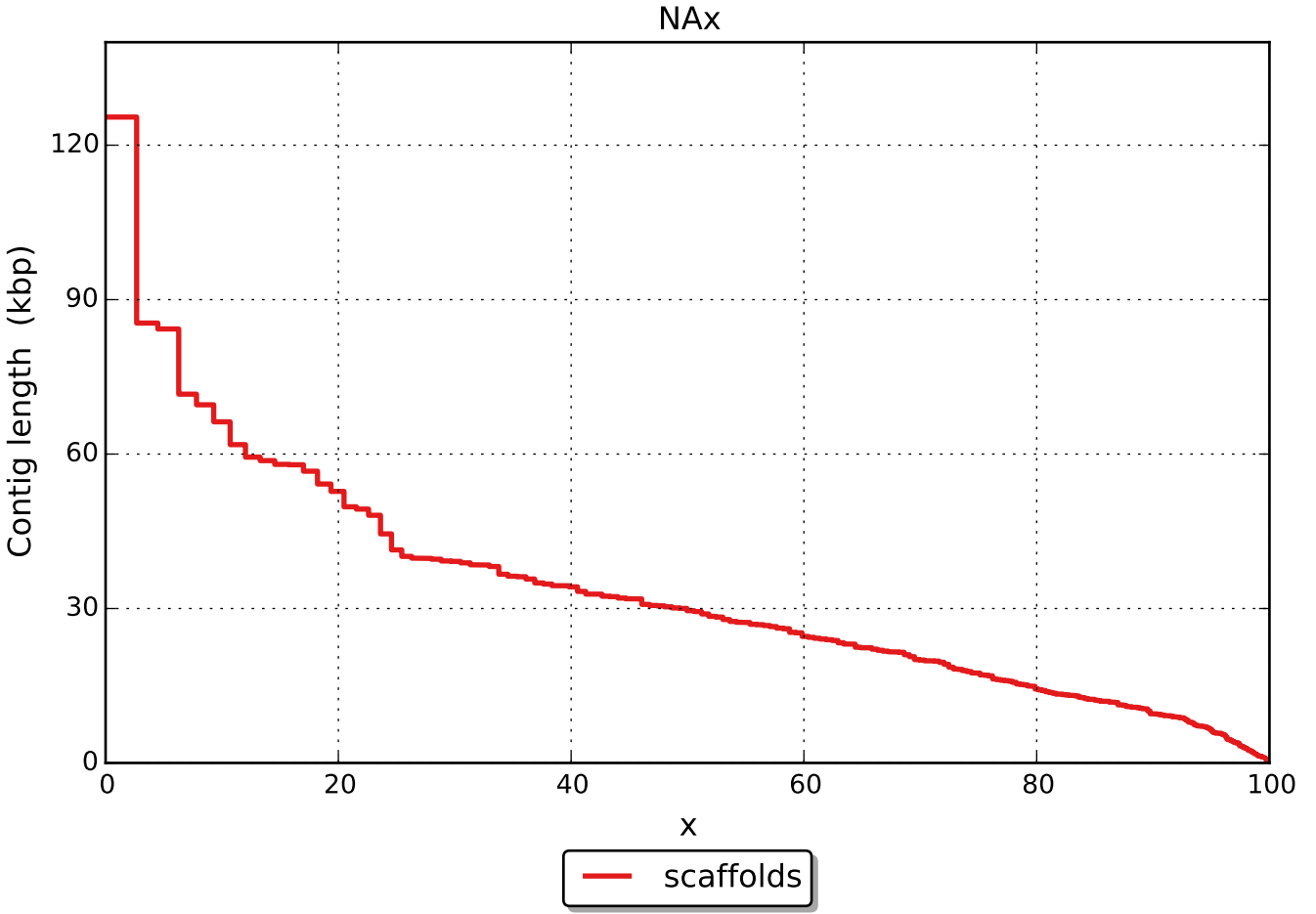

NGx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

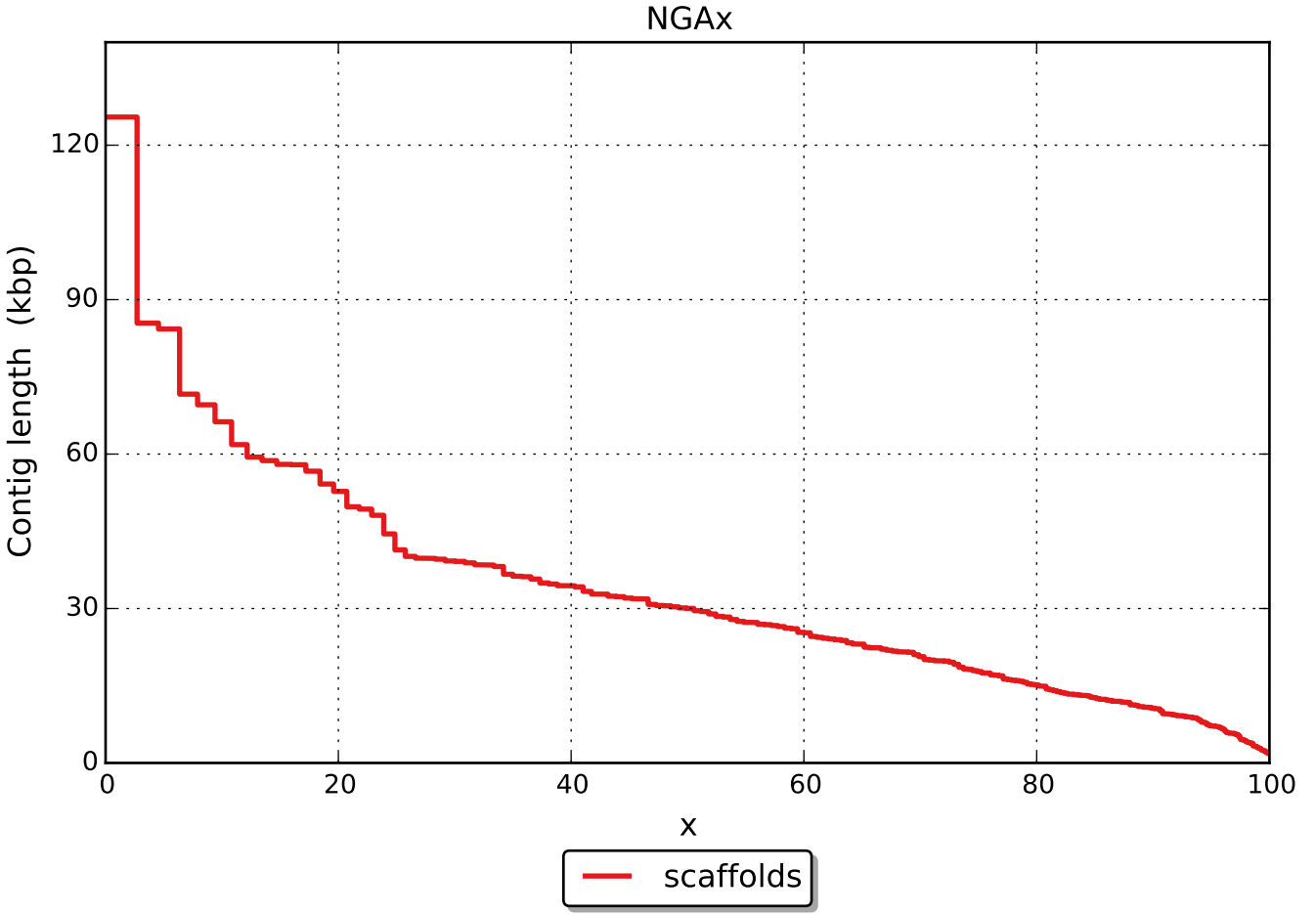

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
scaffolds
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
scaffolds
Reference


Misassemblies
25
20
15
10
5
0
scaffolds
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds