Report

	scaffolds
# contigs (>= 1000 bp)	70
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	33
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	2947870
Total length (>= 5000 bp)	2917073
Total length (>= 10000 bp)	2836518
Total length (>= 25000 bp)	2571976
Total length (>= 50000 bp)	2331243
# contigs	74
Largest contig	161420
Total length	2950538
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.78
N50	88331
NG50	53647
N75	56618
L50	13
LG50	26
L75	24
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	63.477
Duplication ratio	1.001
# N's per 100 kbp	20.81
# mismatches per 100 kbp	542.50
# indels per 100 kbp	0.31
Largest alignment	142244
NA50	88331
NGA50	34830
NA75	43878
LA50	13
LGA50	28
LA75	25

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

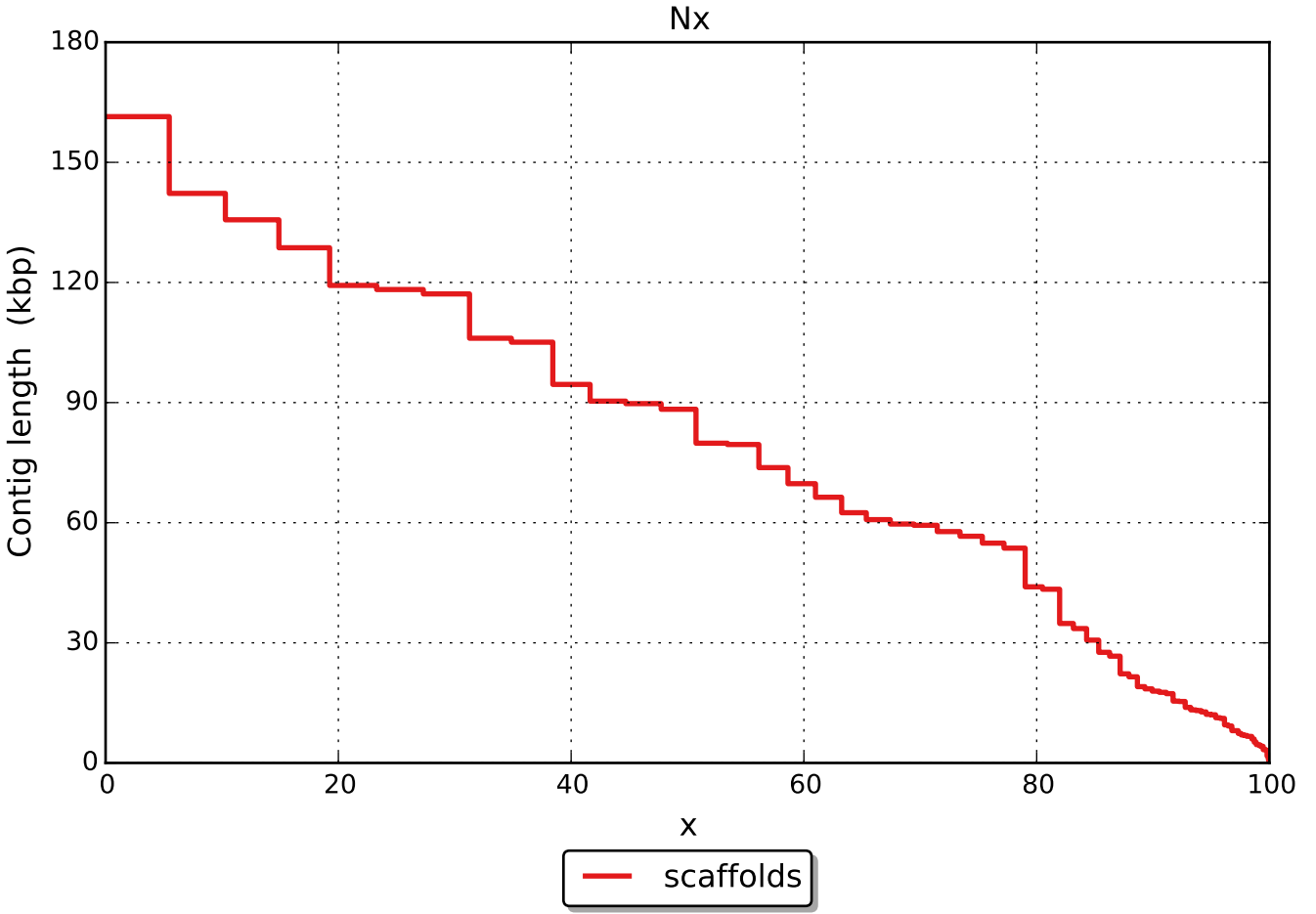
	scaffolds
# misassemblies	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# mismatches	15984
# indels	9
# short indels	7
# long indels	2
Indels length	118

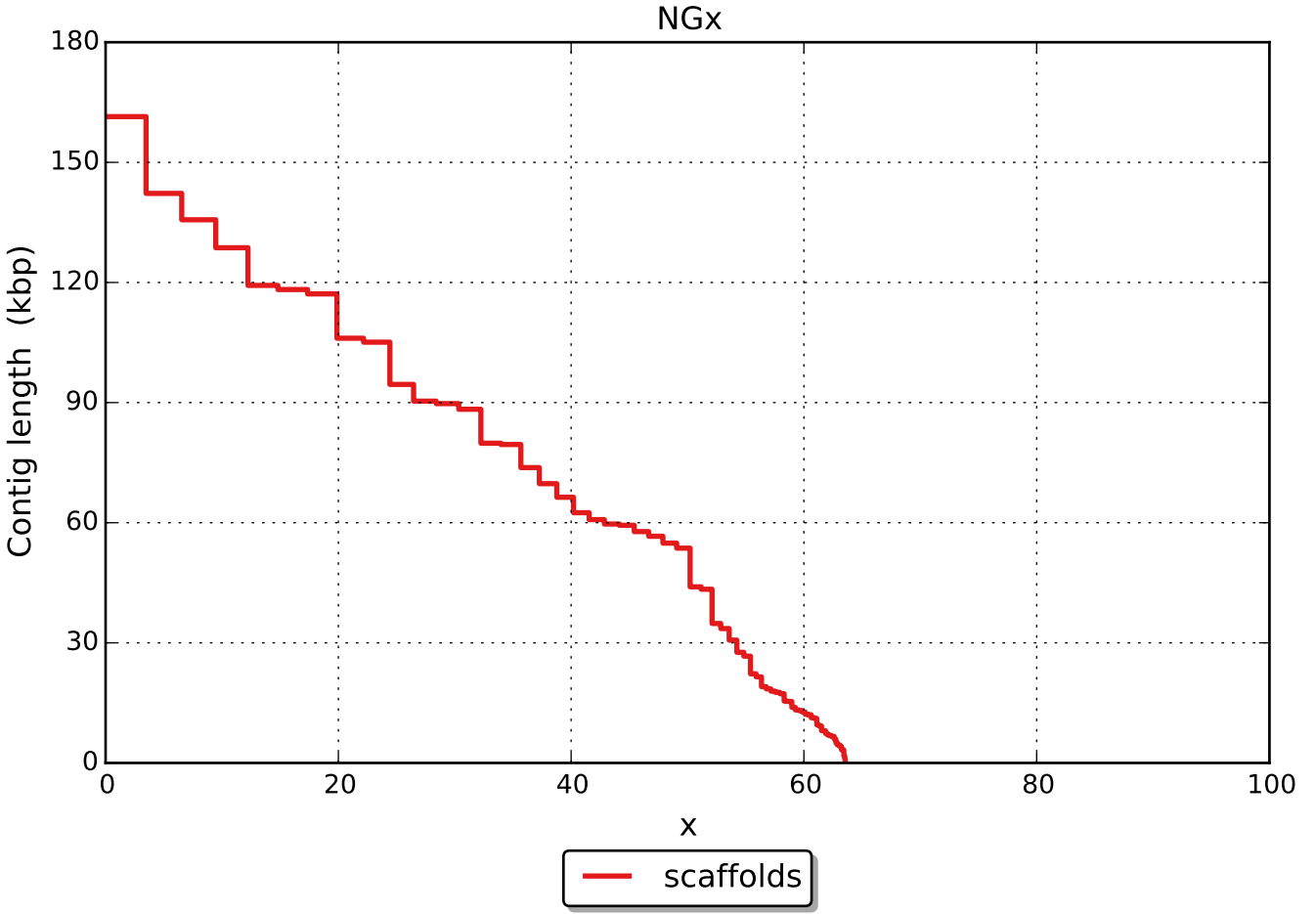
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

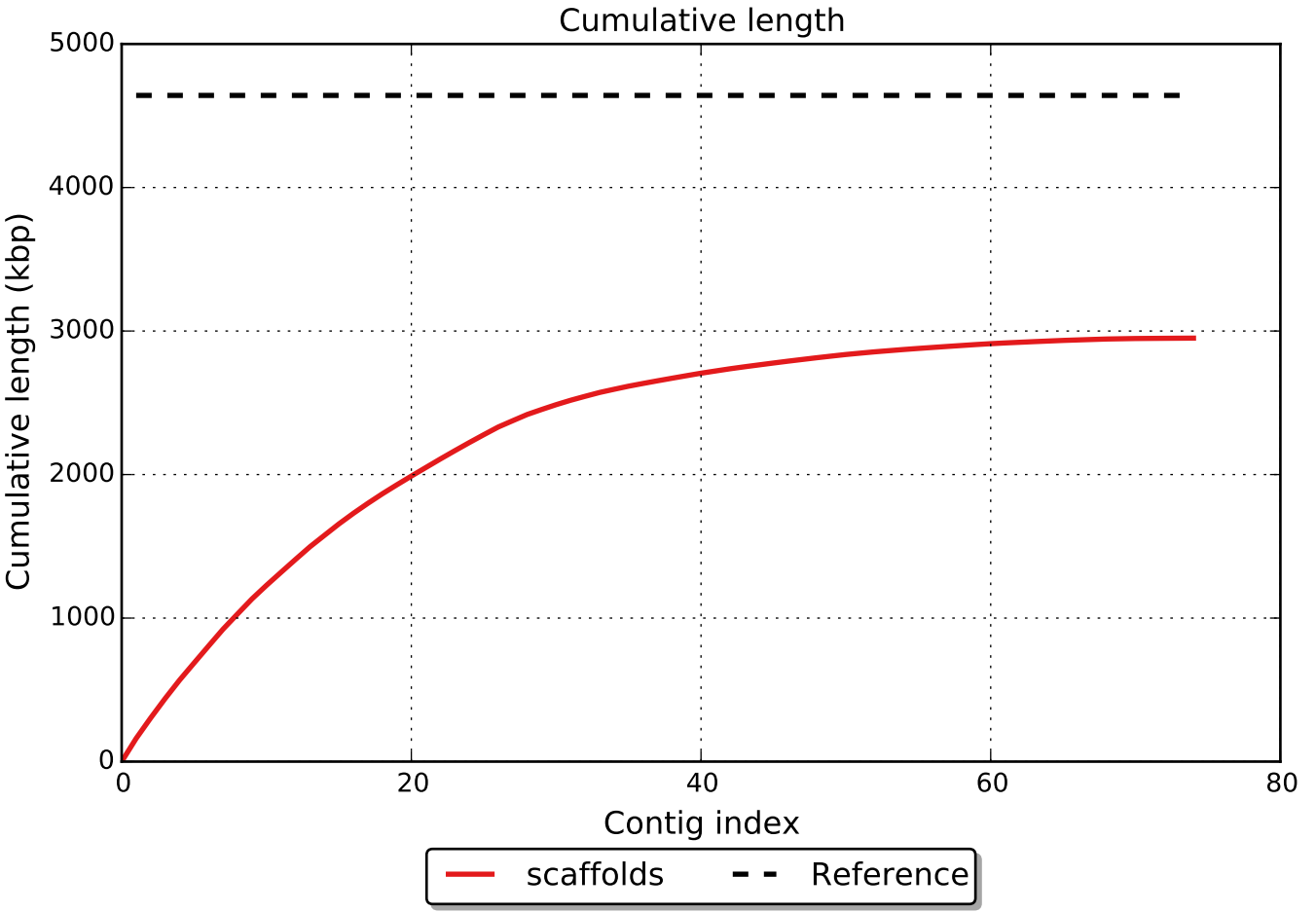
Unaligned report

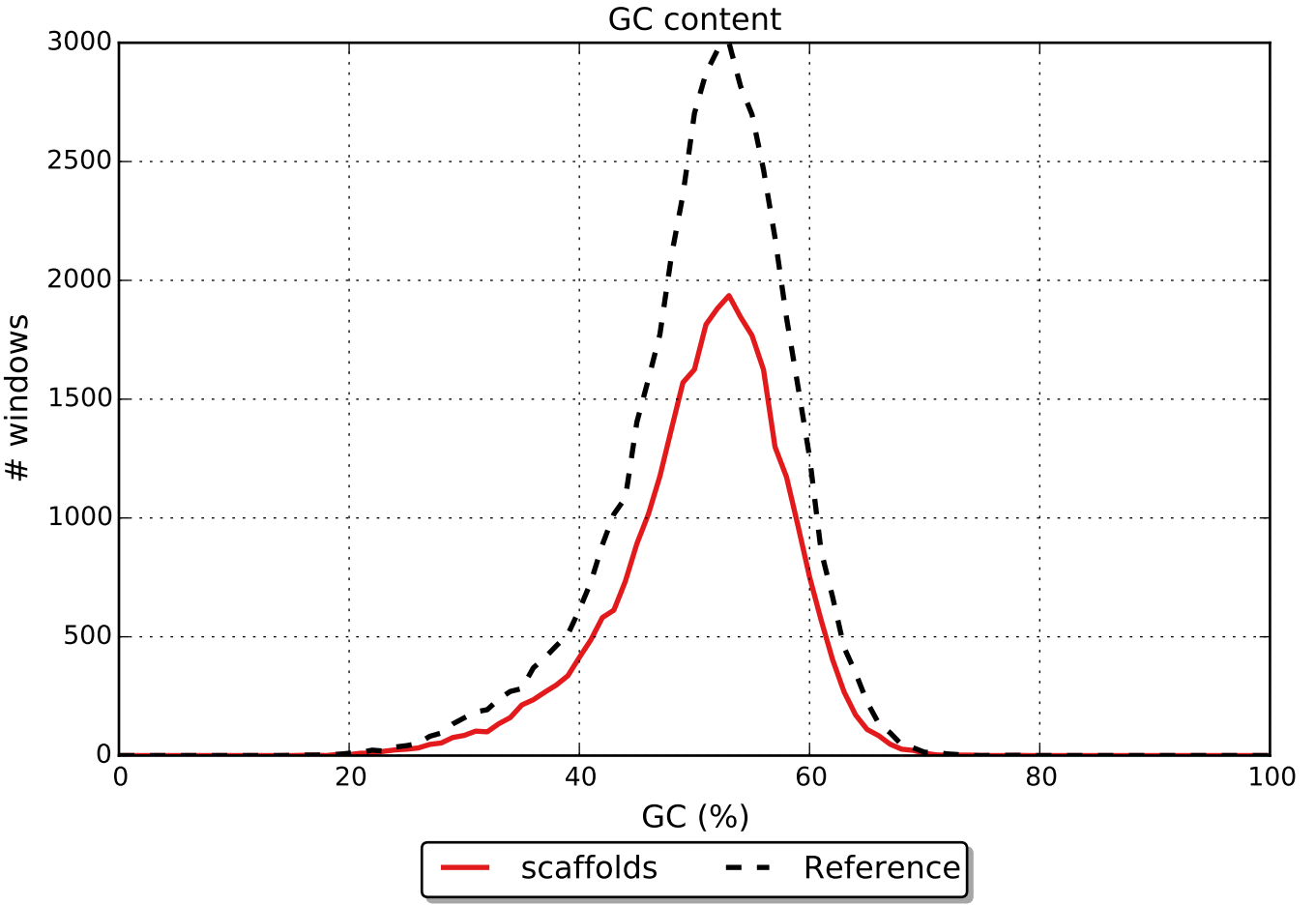
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	614

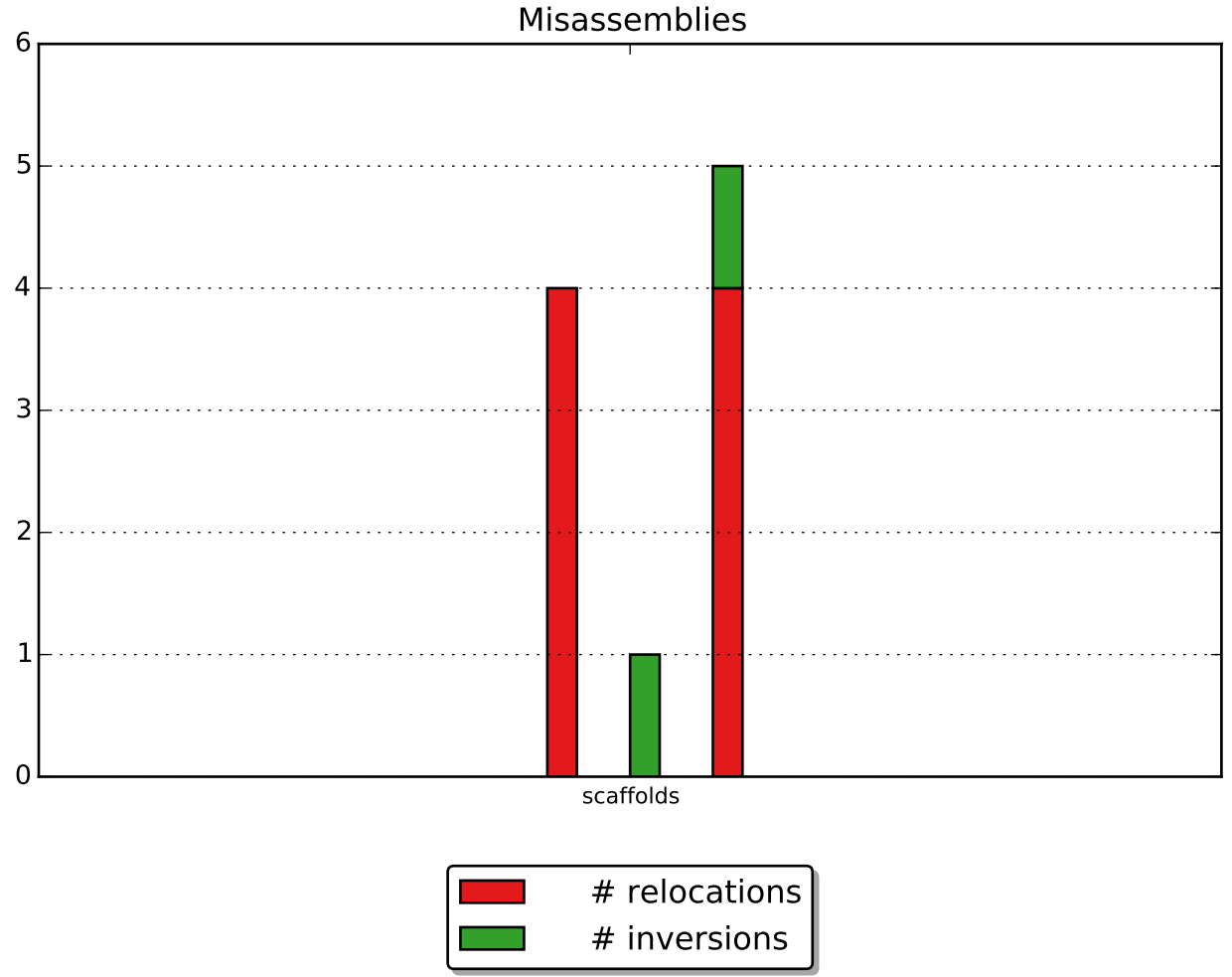
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

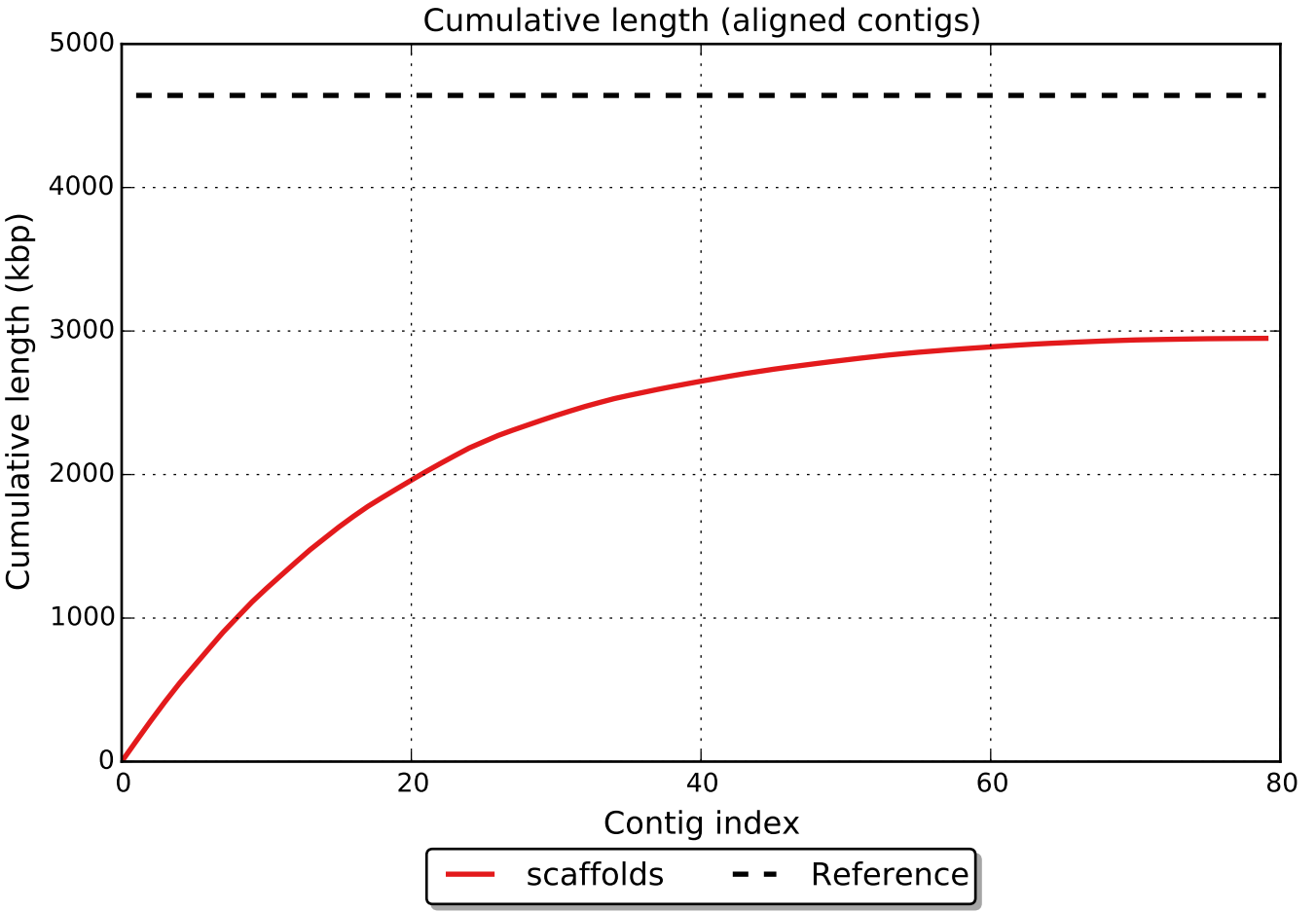

Nx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

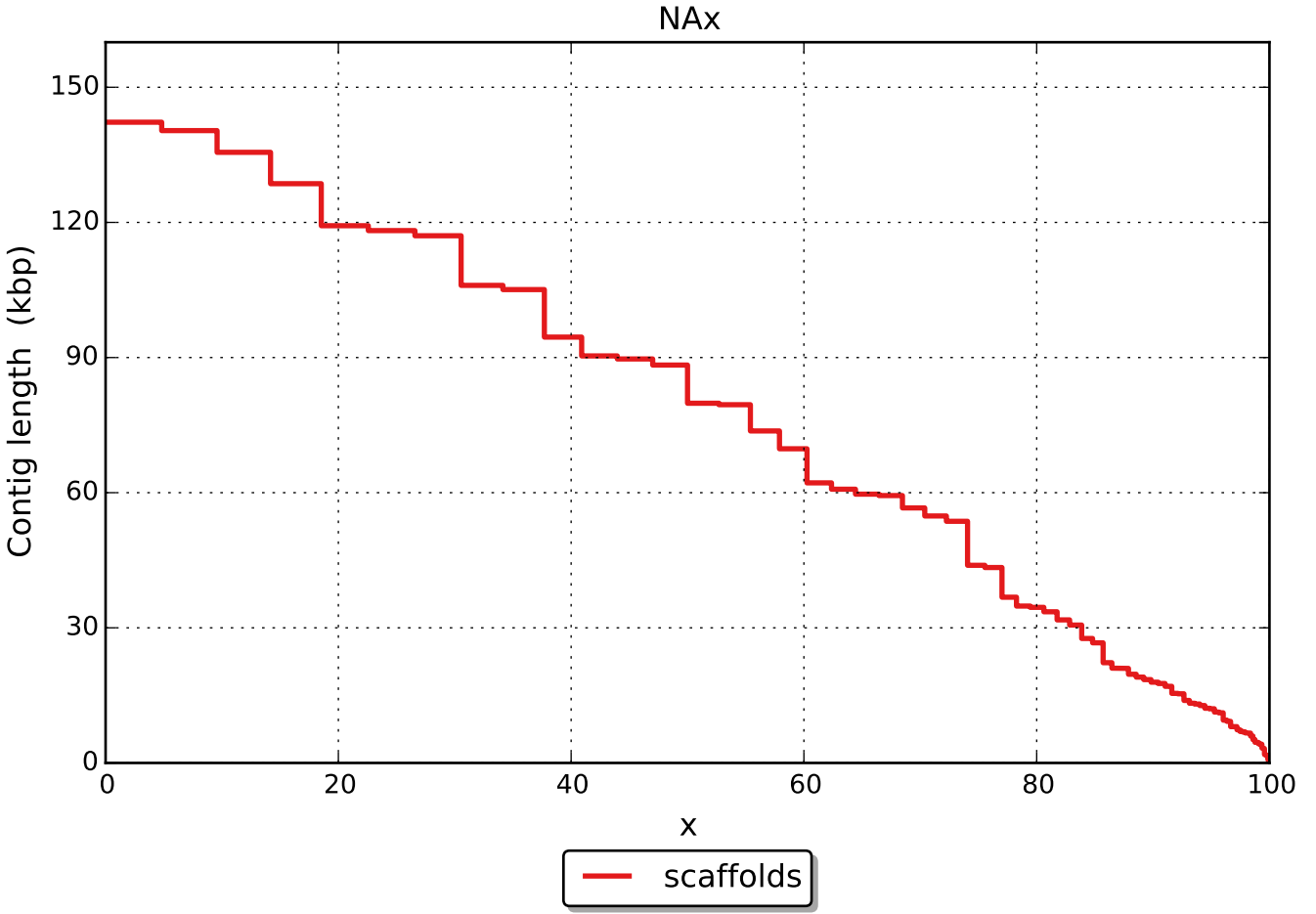

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds

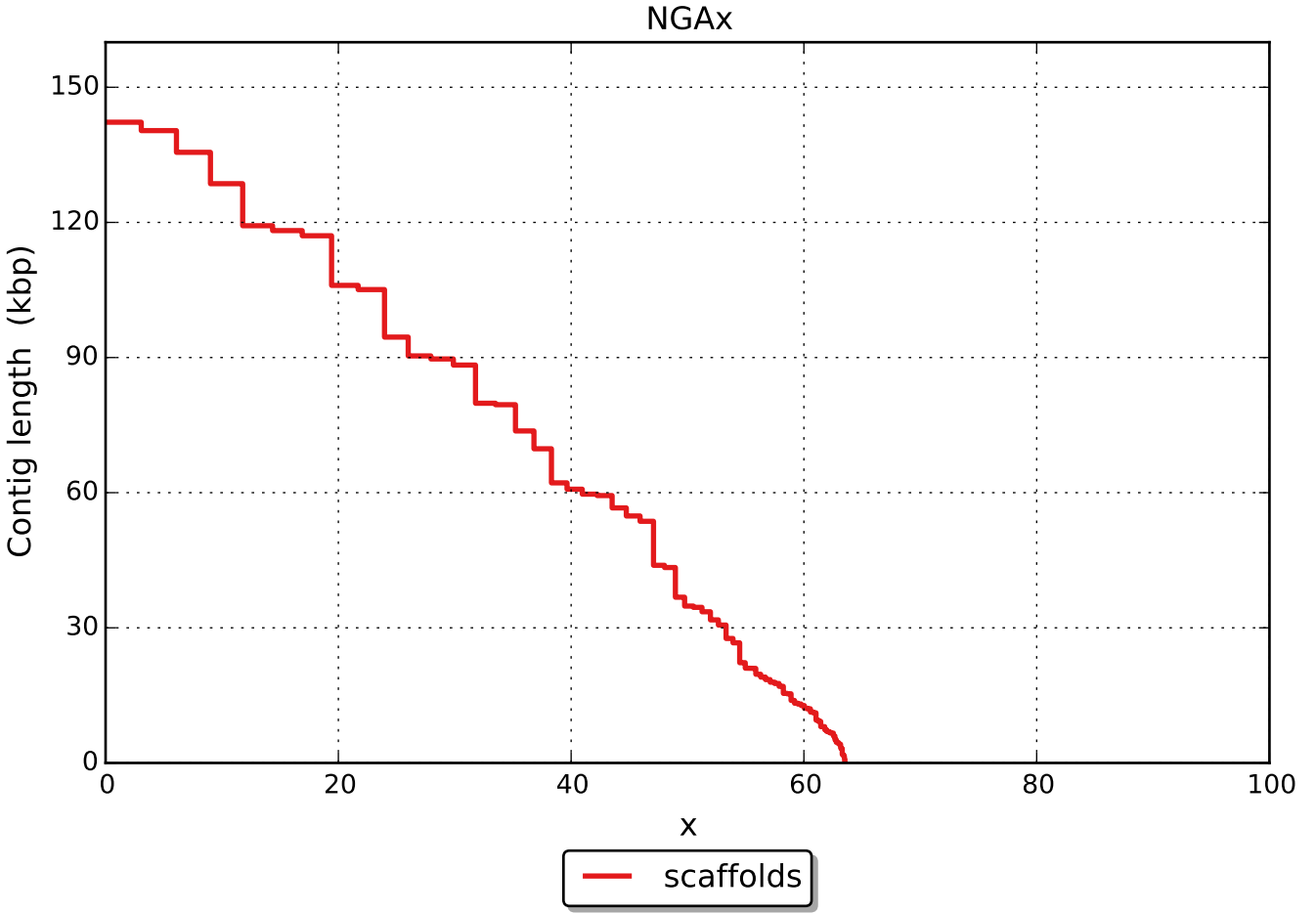

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
Contig index
scaffolds
Reference


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


Misassemblies
6
5
4
3
2
1
0
scaffolds
relocations
inversions


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


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds