Report

	scaffolds
# contigs (>= 1000 bp)	70
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	90309
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1215
Largest contig	3978
Total length	825536
Reference length	4641652
GC (%)	50.69
Reference GC (%)	50.79
N50	655
N75	567
L50	487
L75	828
# misassemblies	22
# misassembled contigs	22
Misassembled contigs length	24093
# local misassemblies	0
# unaligned contigs	0 + 21 part
Unaligned length	1956
Genome fraction (%)	17.670
Duplication ratio	1.004
# N's per 100 kbp	26.77
# mismatches per 100 kbp	1819.59
# indels per 100 kbp	14.27
Largest alignment	3704
NA50	648
NGA50	-
NA75	561
LA50	495
LA75	838

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

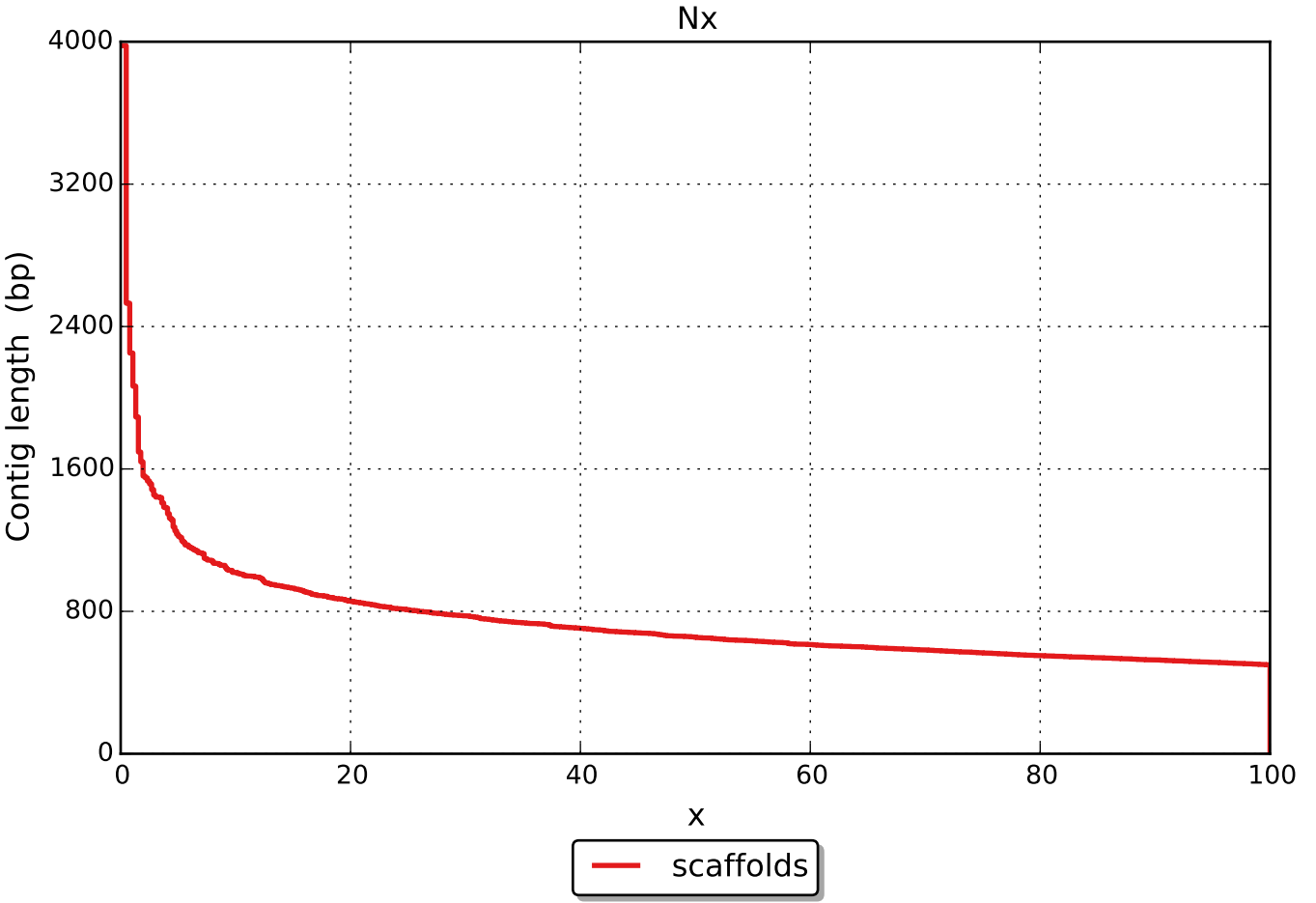
	scaffolds
# misassemblies	22
# relocations	22
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	22
Misassembled contigs length	24093
# local misassemblies	0
# mismatches	14924
# indels	117
# short indels	108
# long indels	9
Indels length	247

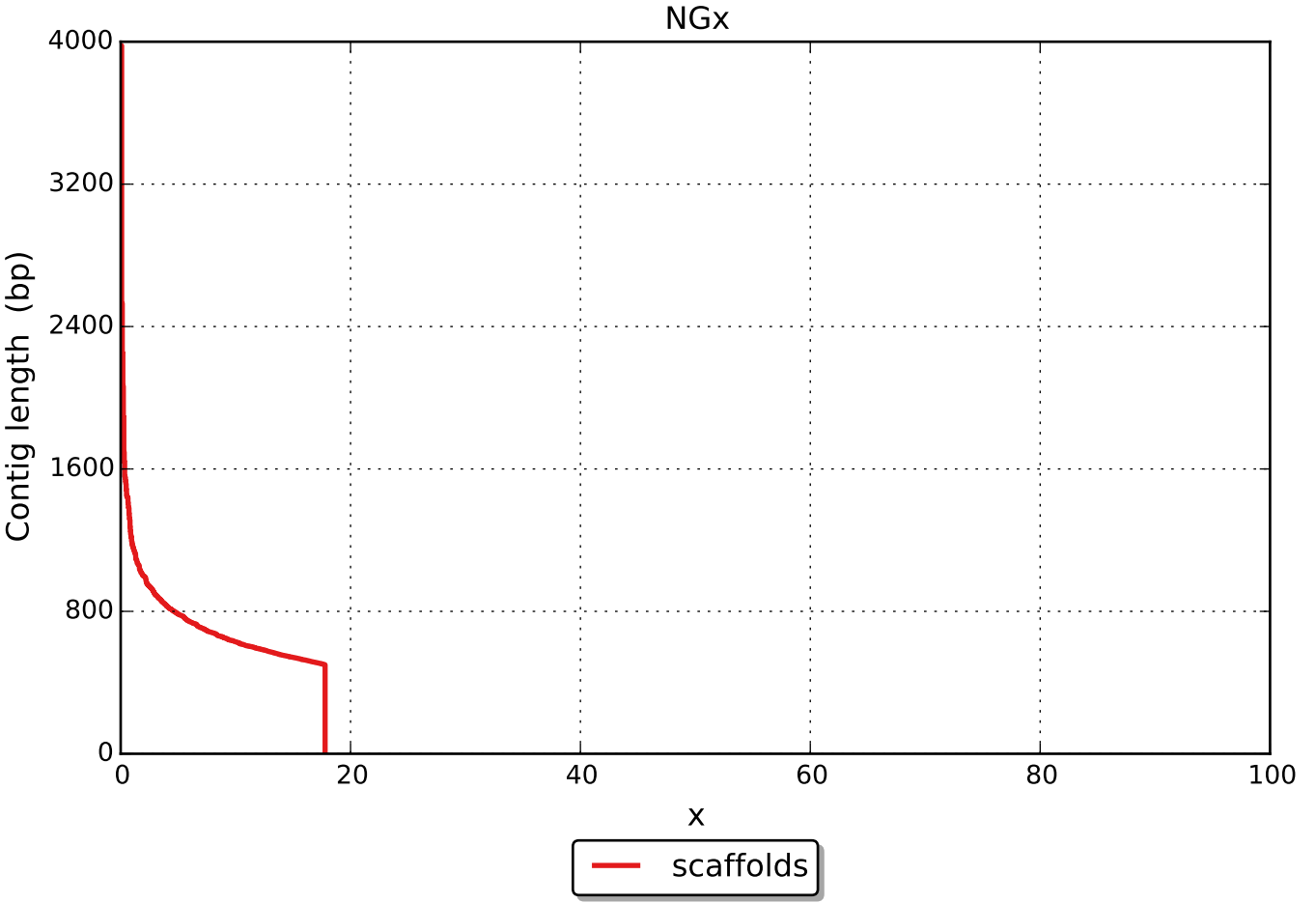
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

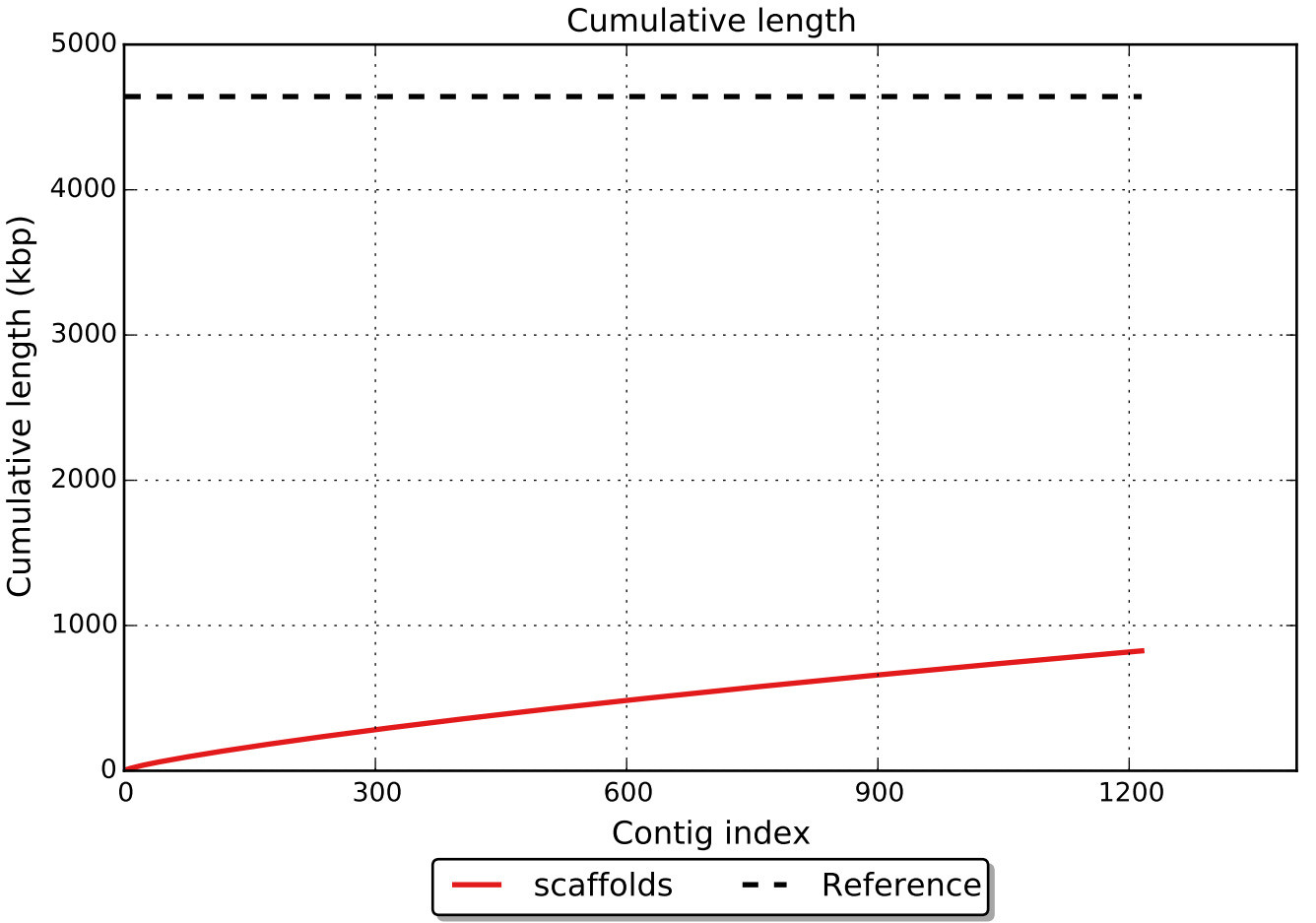
Unaligned report

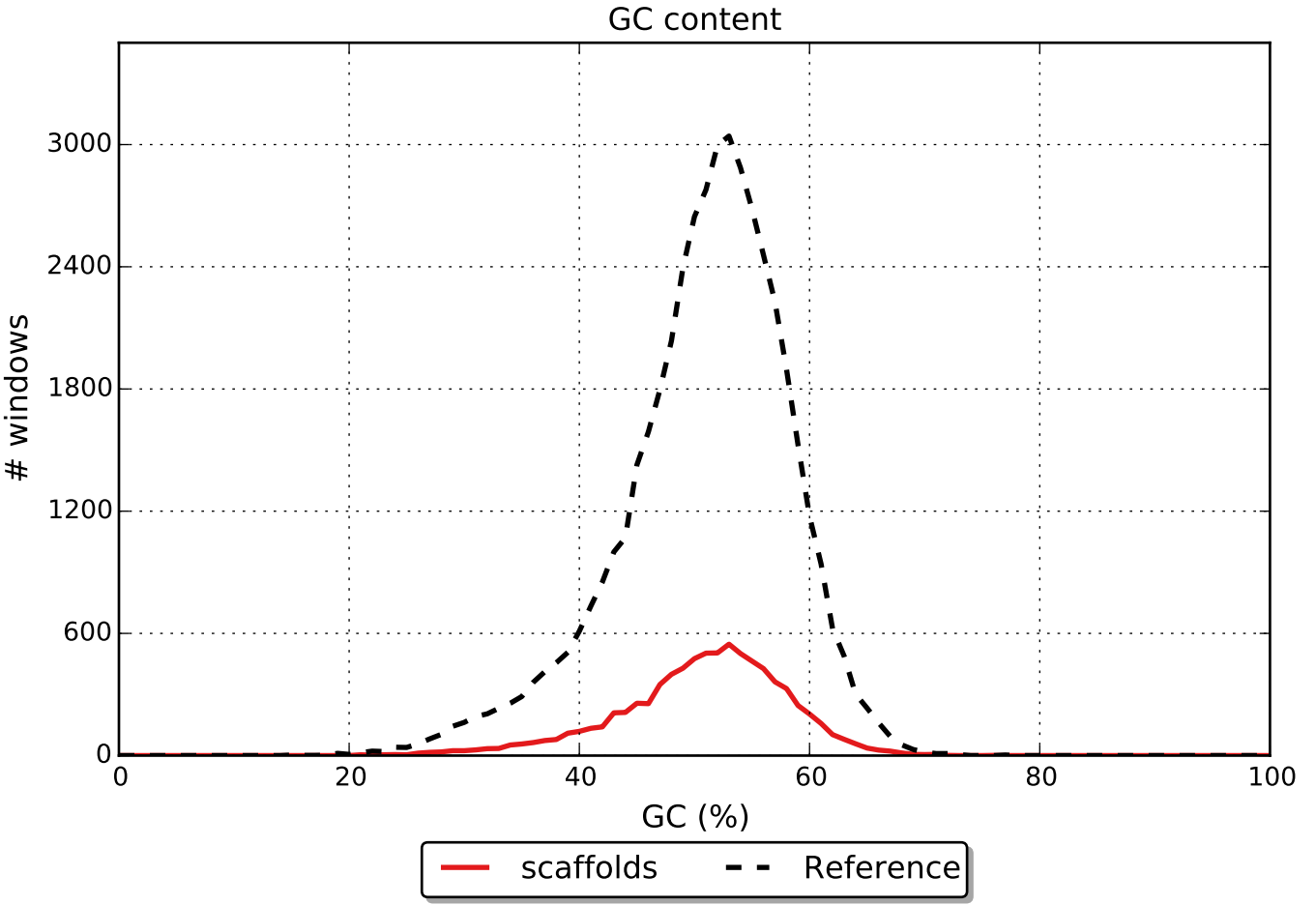
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	21
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1956
# N's	221

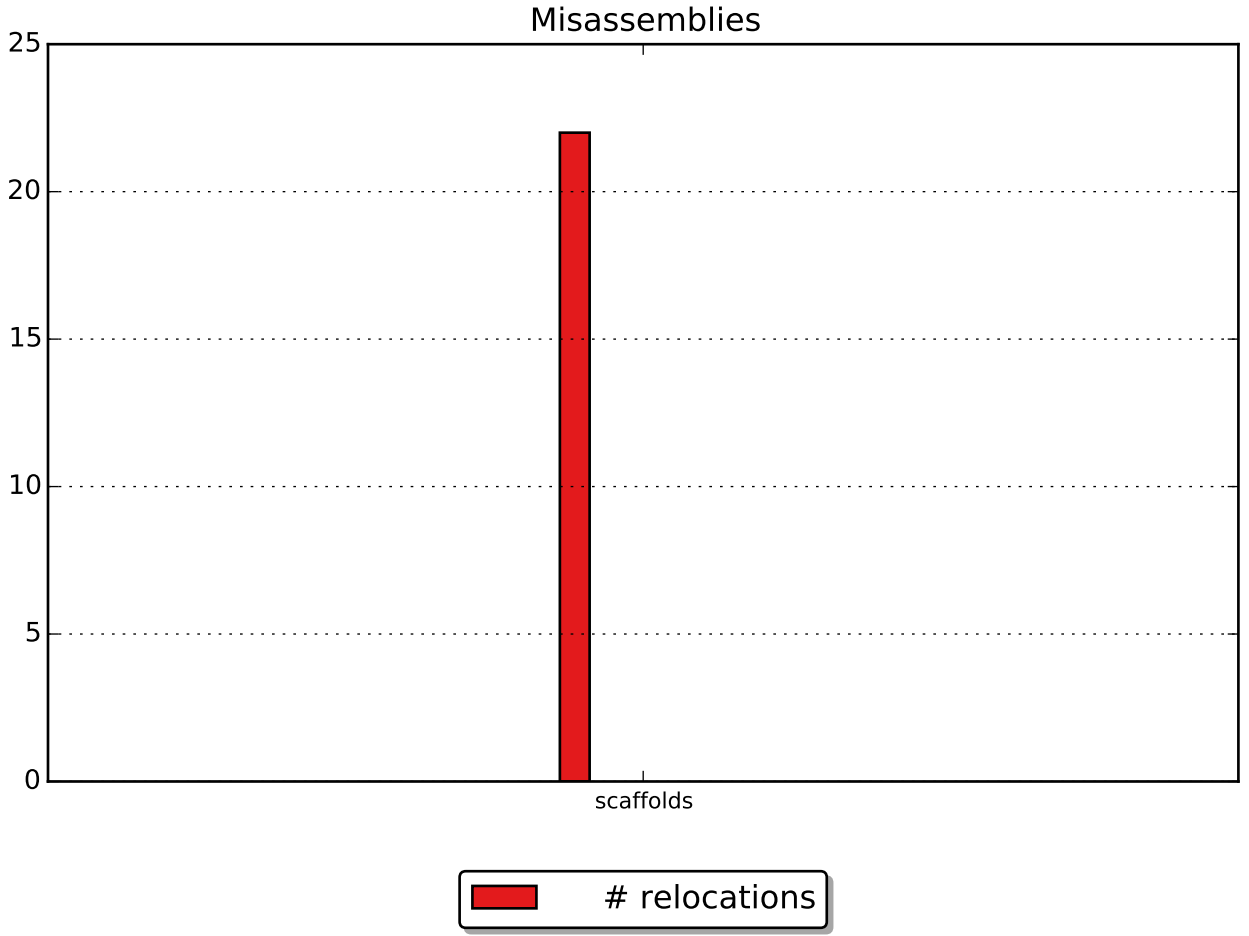
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

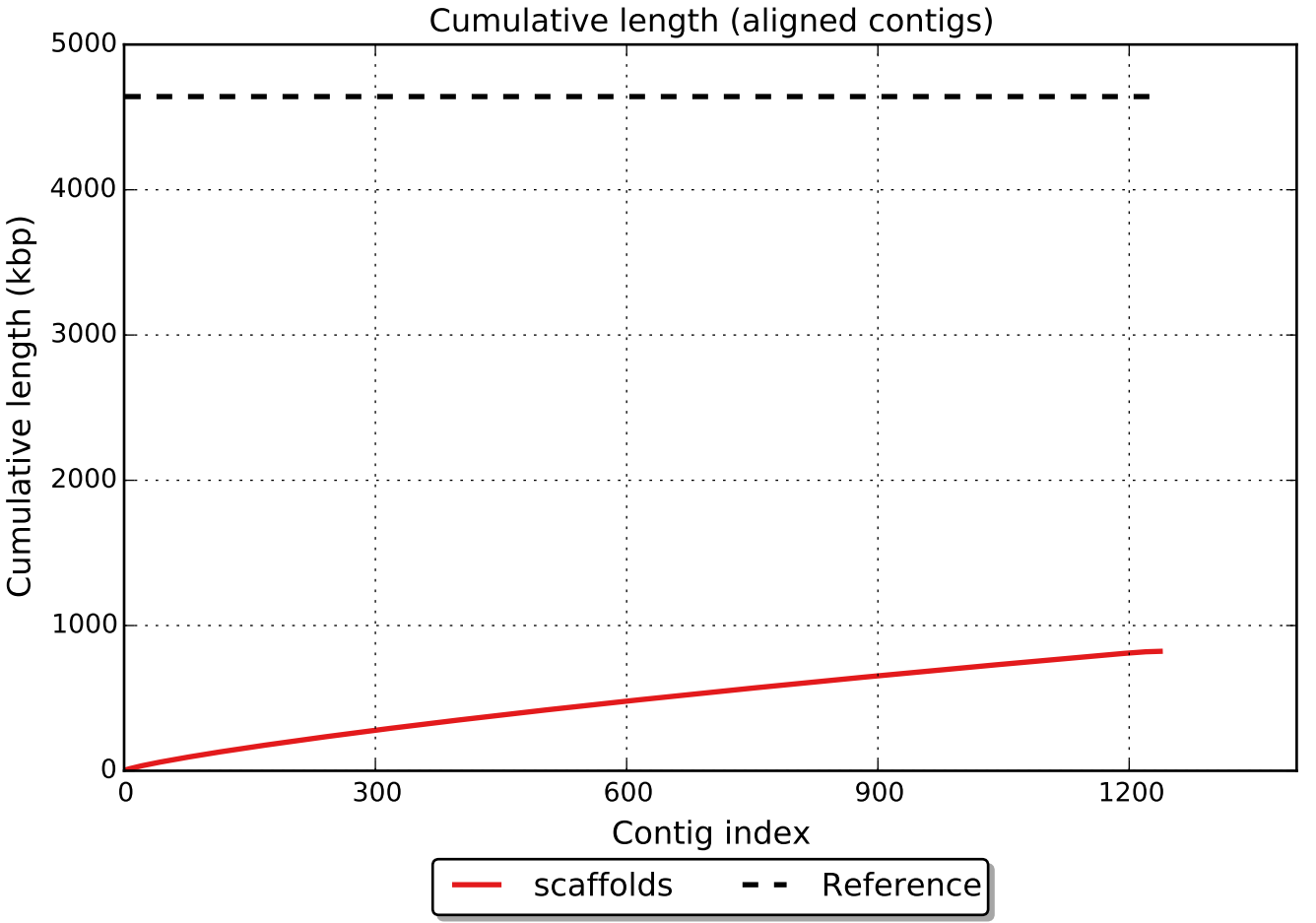

Nx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
scaffolds

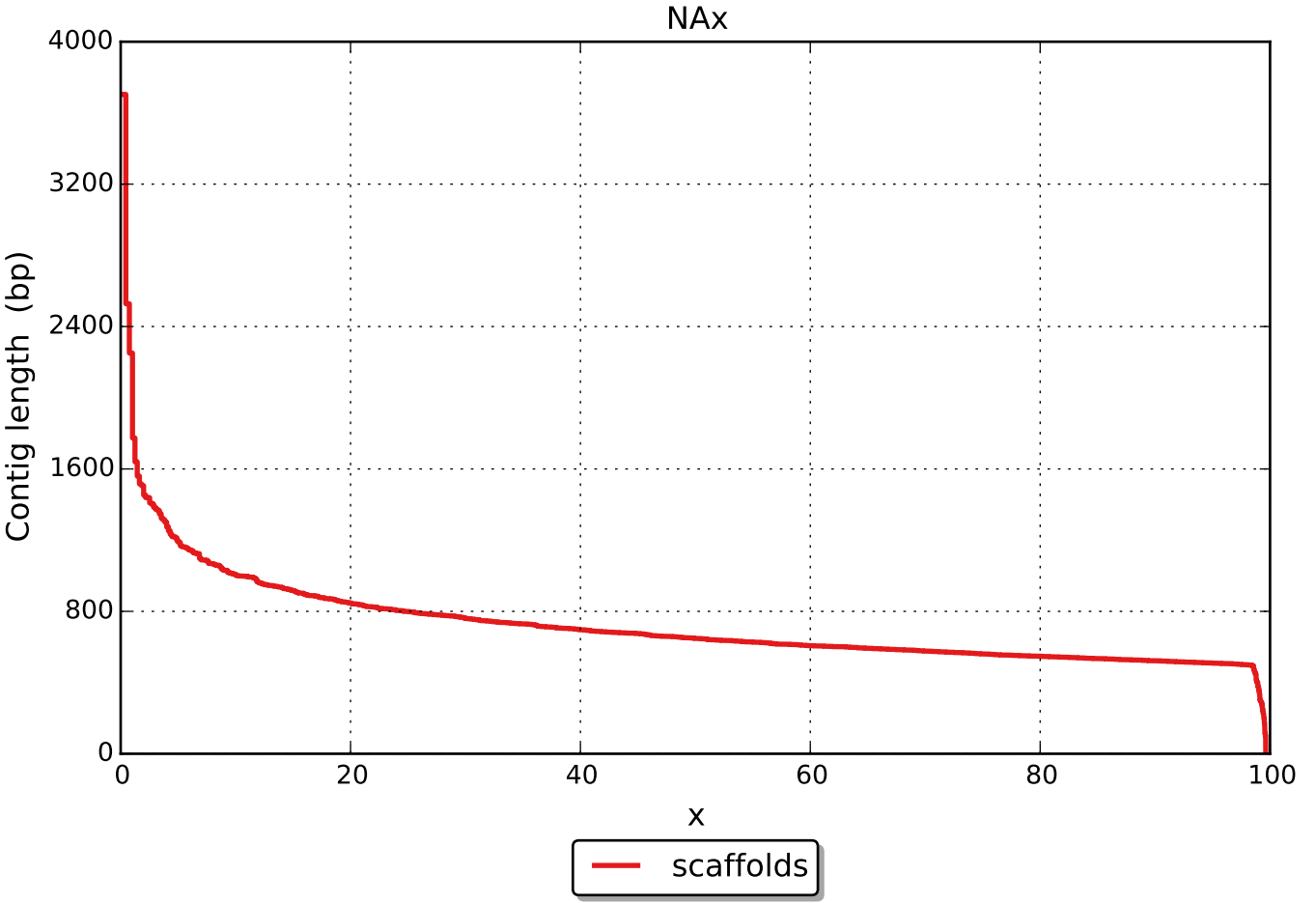

NGx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
scaffolds

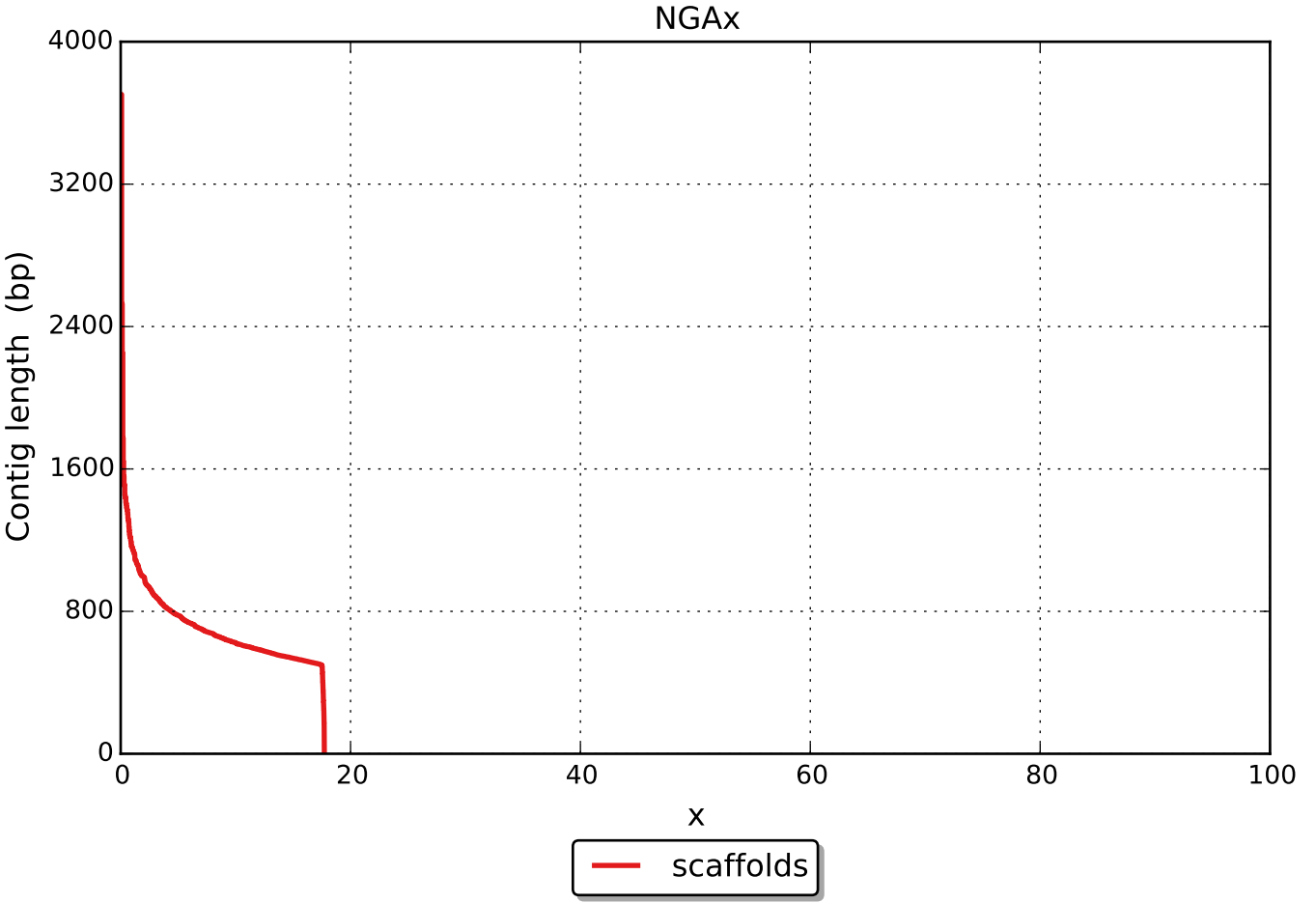

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
scaffolds
Reference


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
scaffolds
Reference


NAx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
scaffolds


NGAx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
scaffolds