Report

	scaffolds
# contigs (>= 1000 bp)	872
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1393156
Total length (>= 5000 bp)	21011
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2155
Largest contig	8898
Total length	2302637
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	1191
N75	801
L50	650
L75	1244
# misassemblies	18
# misassembled contigs	17
Misassembled contigs length	37784
# local misassemblies	3
# unaligned contigs	0 + 22 part
Unaligned length	14496
Genome fraction (%)	49.096
Duplication ratio	1.004
# N's per 100 kbp	838.60
# mismatches per 100 kbp	225.90
# indels per 100 kbp	48.18
Largest alignment	6590
NA50	1155
NGA50	-
NA75	783
LA50	668
LA75	1276

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

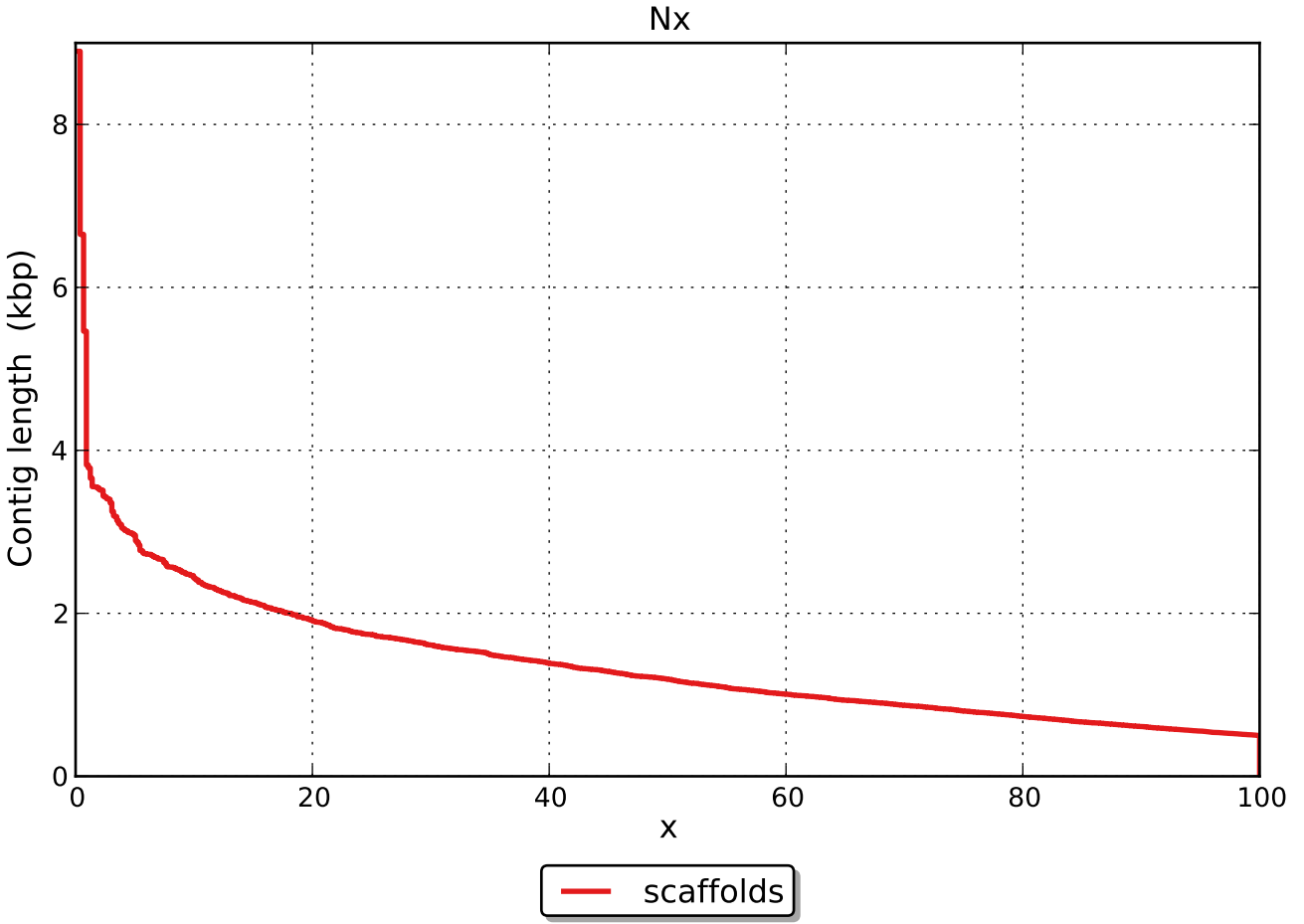
	scaffolds
# misassemblies	18
# relocations	18
# translocations	0
# inversions	0
# possibly misassembled contigs	8
# misassembled contigs	17
Misassembled contigs length	37784
# local misassemblies	3
# mismatches	5148
# indels	1098
# short indels	531
# long indels	567
Indels length	9465

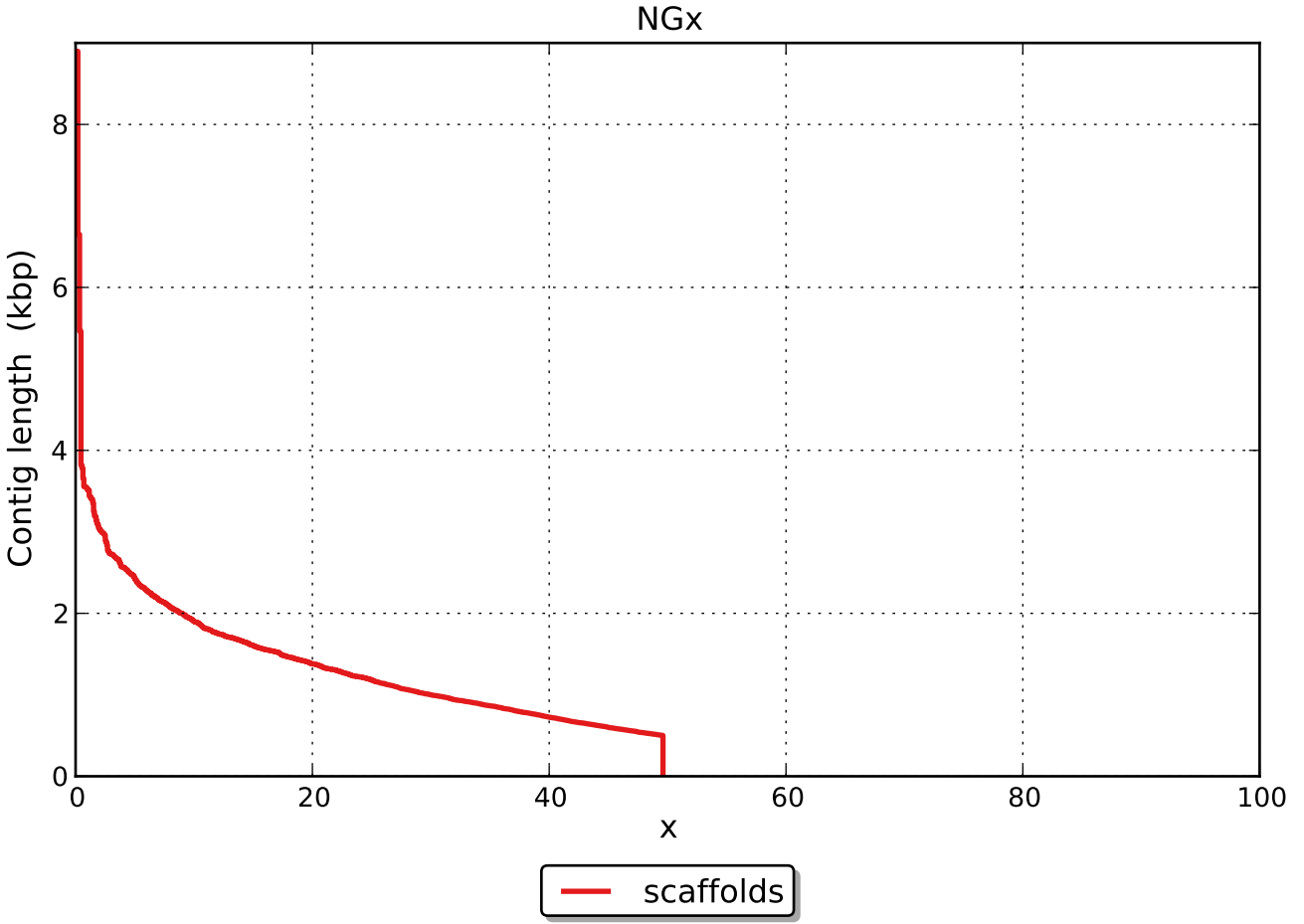
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

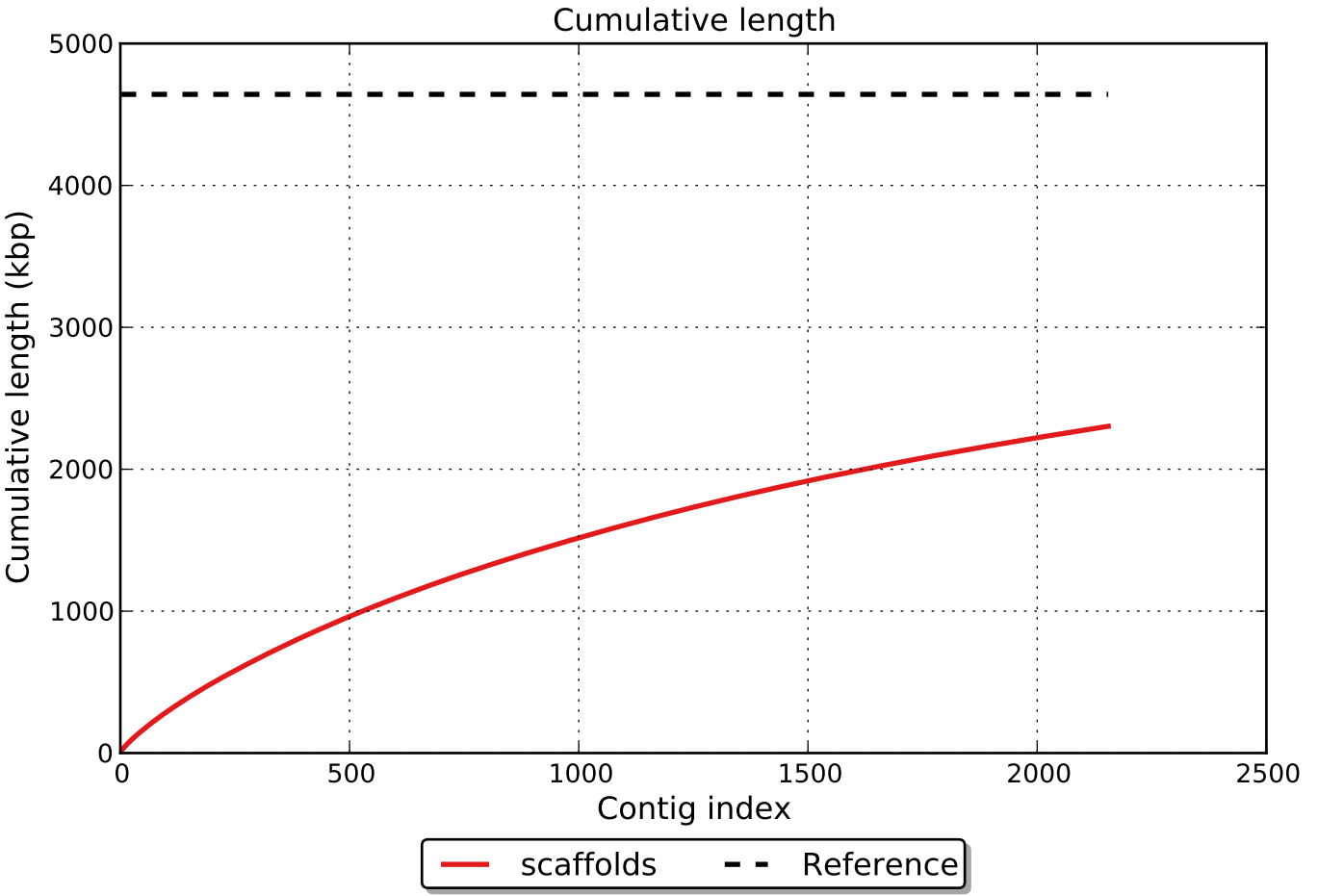
Unaligned report

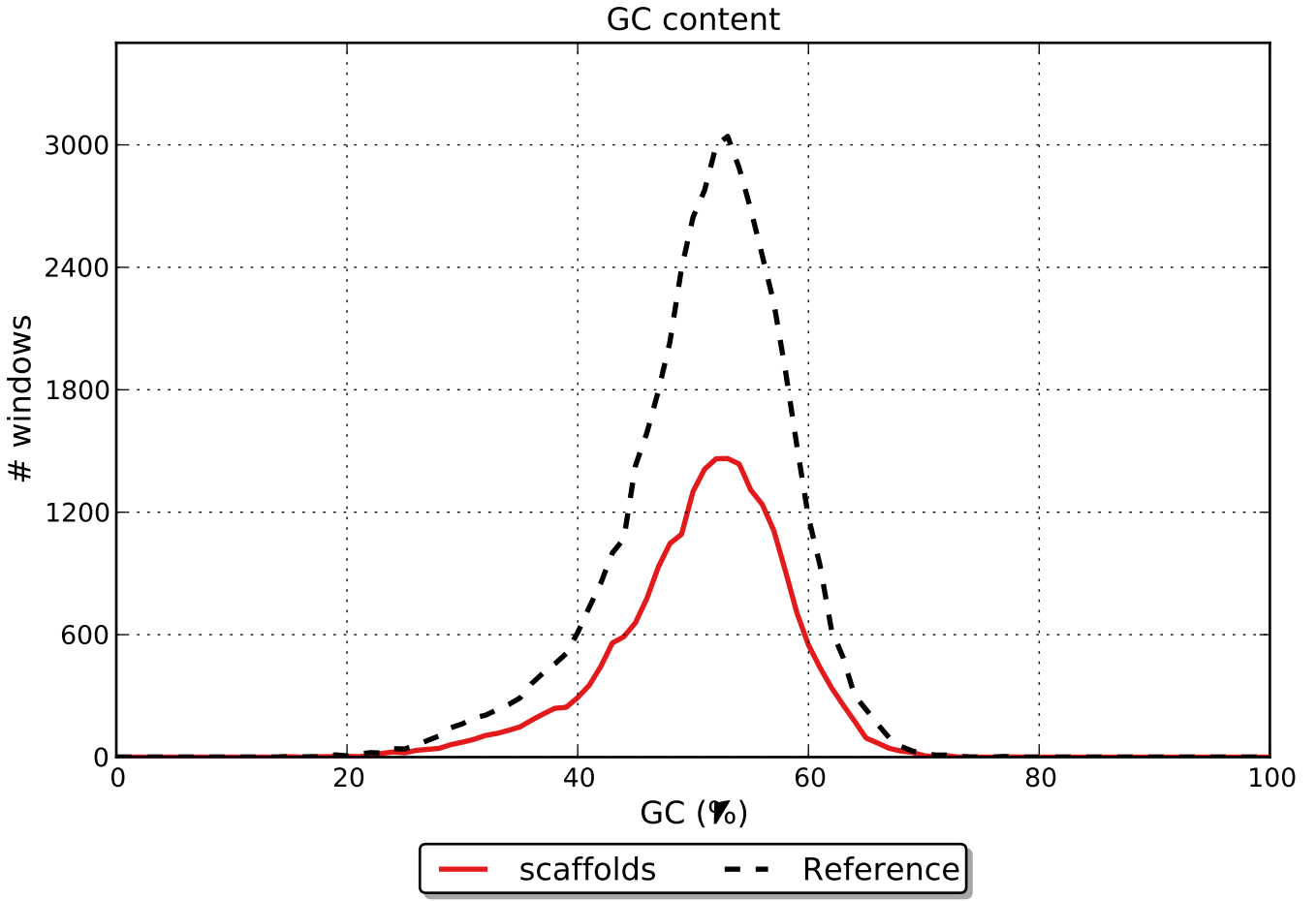
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	22
# with misassembly	0
# both parts are significant	6
Partially unaligned length	14496
# N's	19310

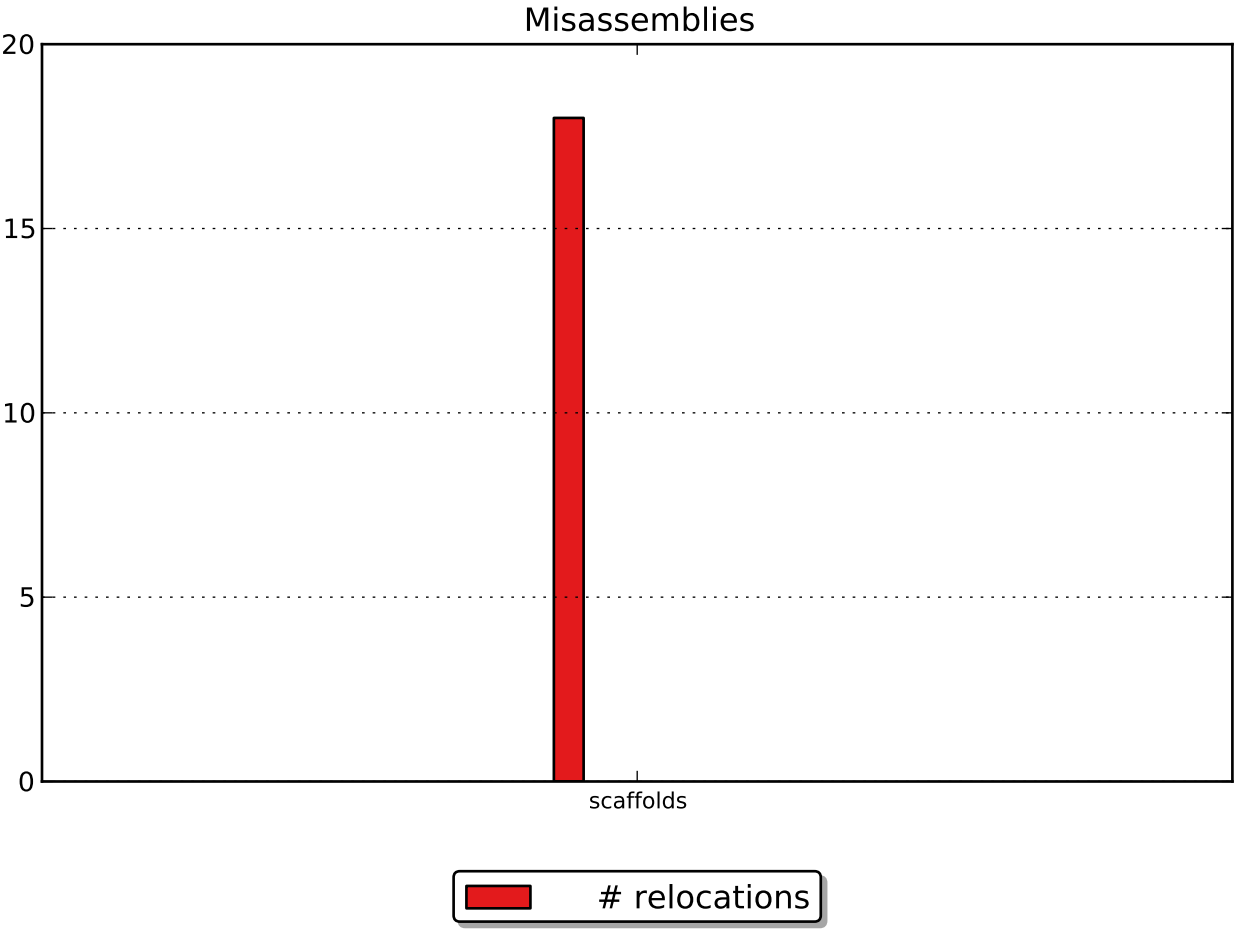
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

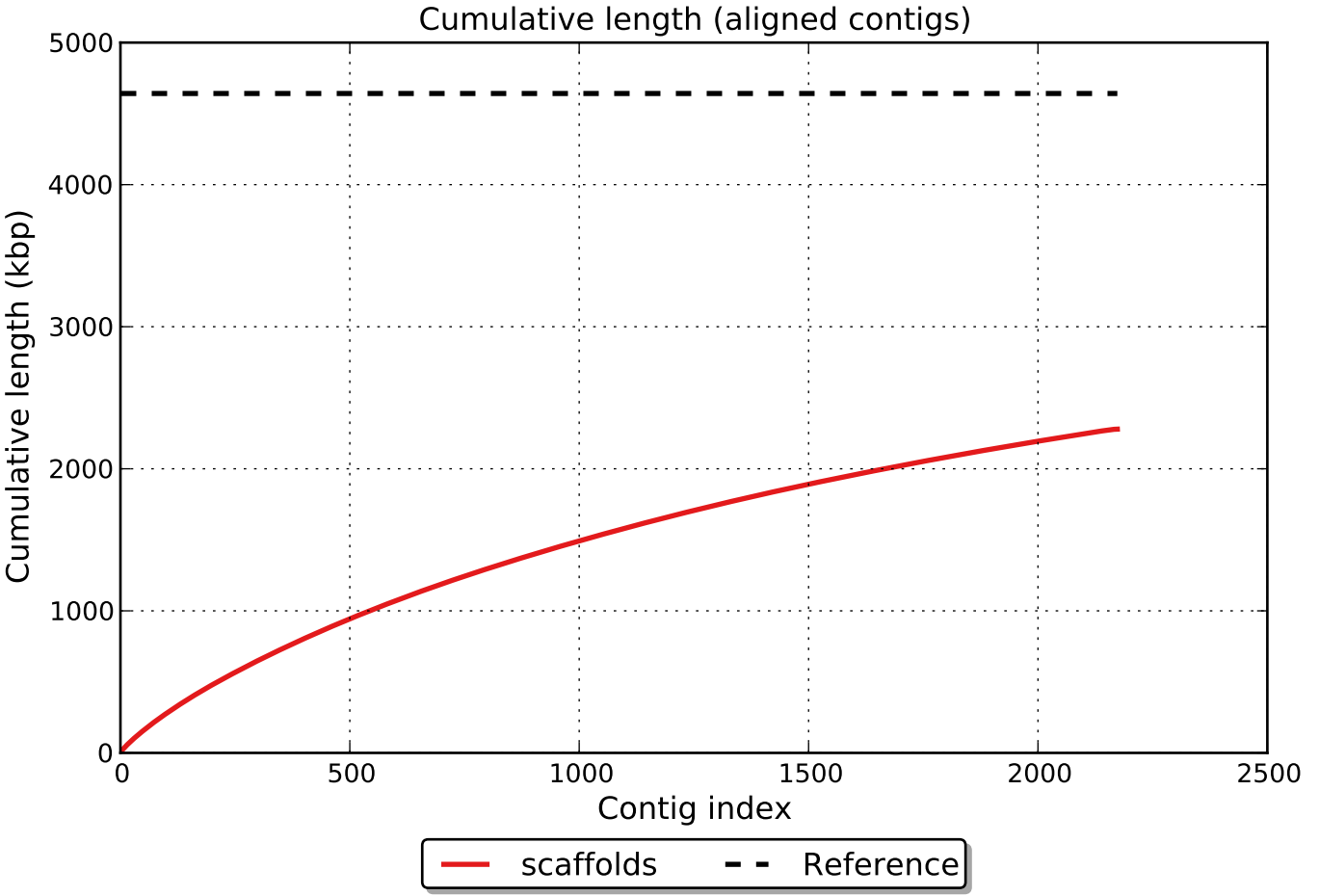

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
scaffolds

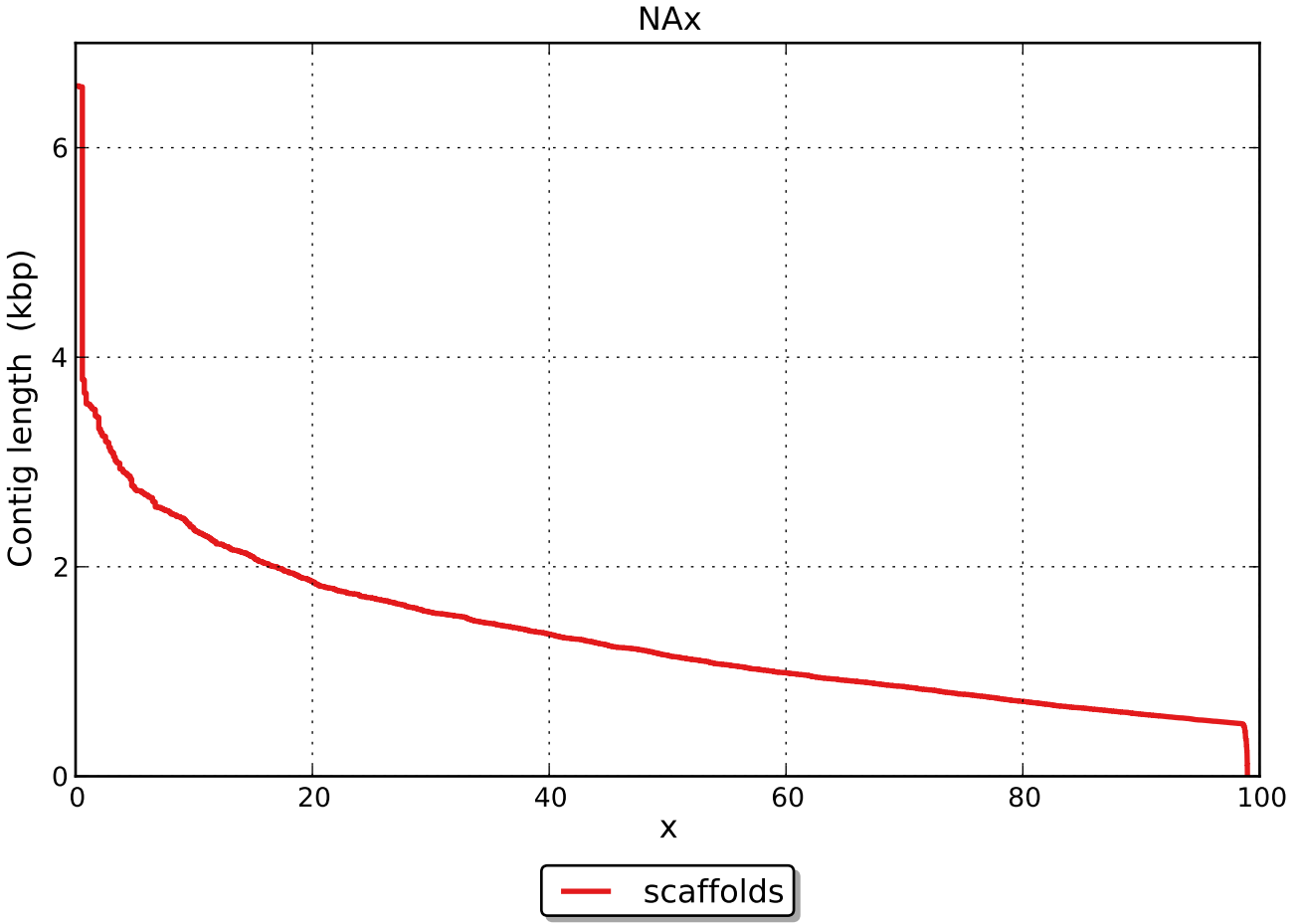

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
scaffolds

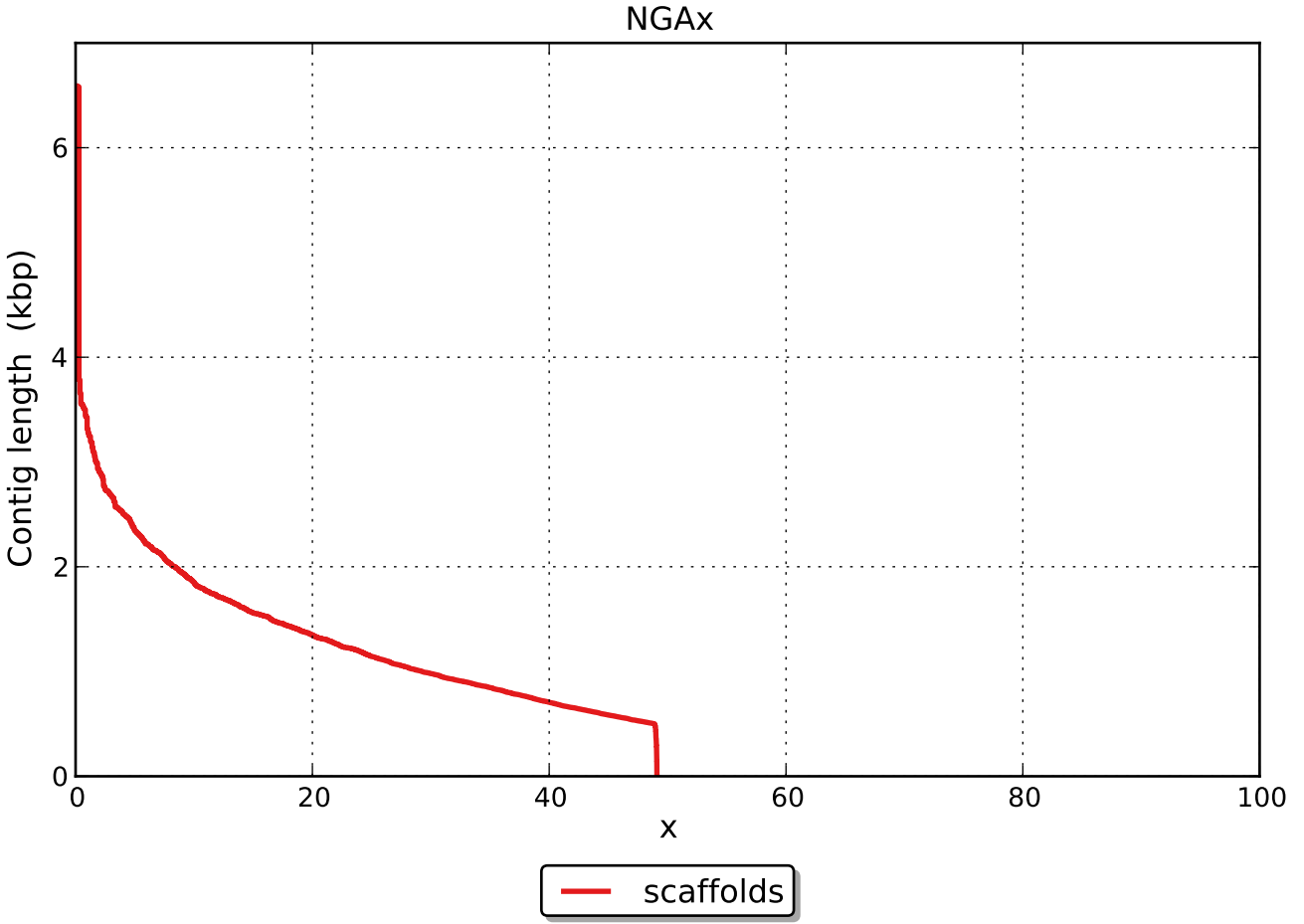

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
scaffolds
Reference


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


Misassemblies
20
15
10
5
0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
scaffolds