Report

	scaffolds
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	18193
Total length (>= 5000 bp)	5473
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	205
Largest contig	5473
Total length	140187
Reference length	4641652
GC (‰)	50.99
Reference GC (‰)	50.79
N50	637
N75	550
L50	79
L75	139
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	8125
# local misassemblies	0
# unaligned contigs	0 + 5 part
Unaligned length	884
Genome fraction (‰)	2.995
Duplication ratio	1.002
# N's per 100 kbp	585.65
# mismatches per 100 kbp	353.14
# indels per 100 kbp	51.06
Largest alignment	5390
NA50	627
NGA50	-
NA75	544
LA50	80
LA75	141

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

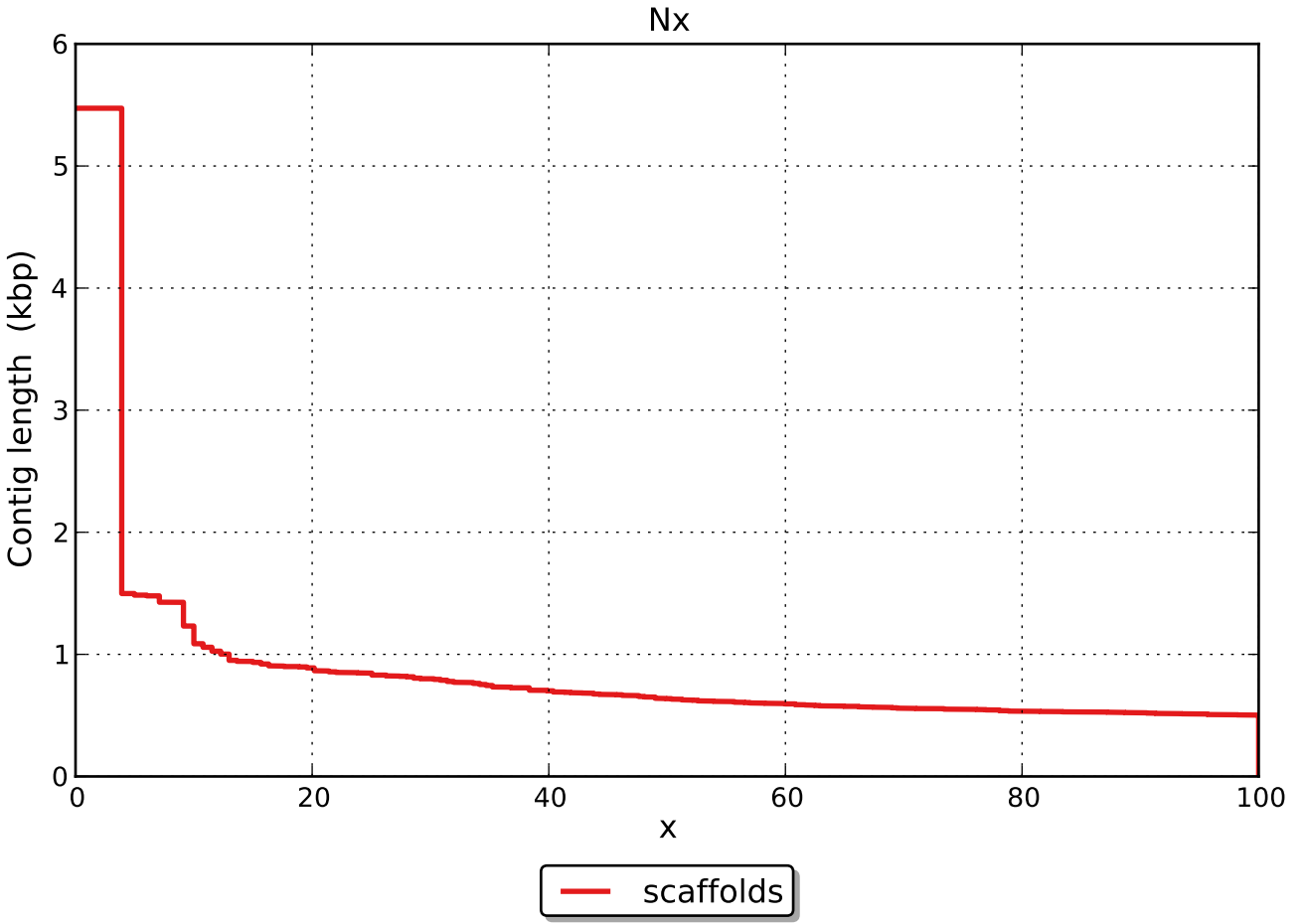
	scaffolds
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	8125
# local misassemblies	0
# mismatches	491
# indels	71
# short indels	42
# long indels	29
Indels length	537

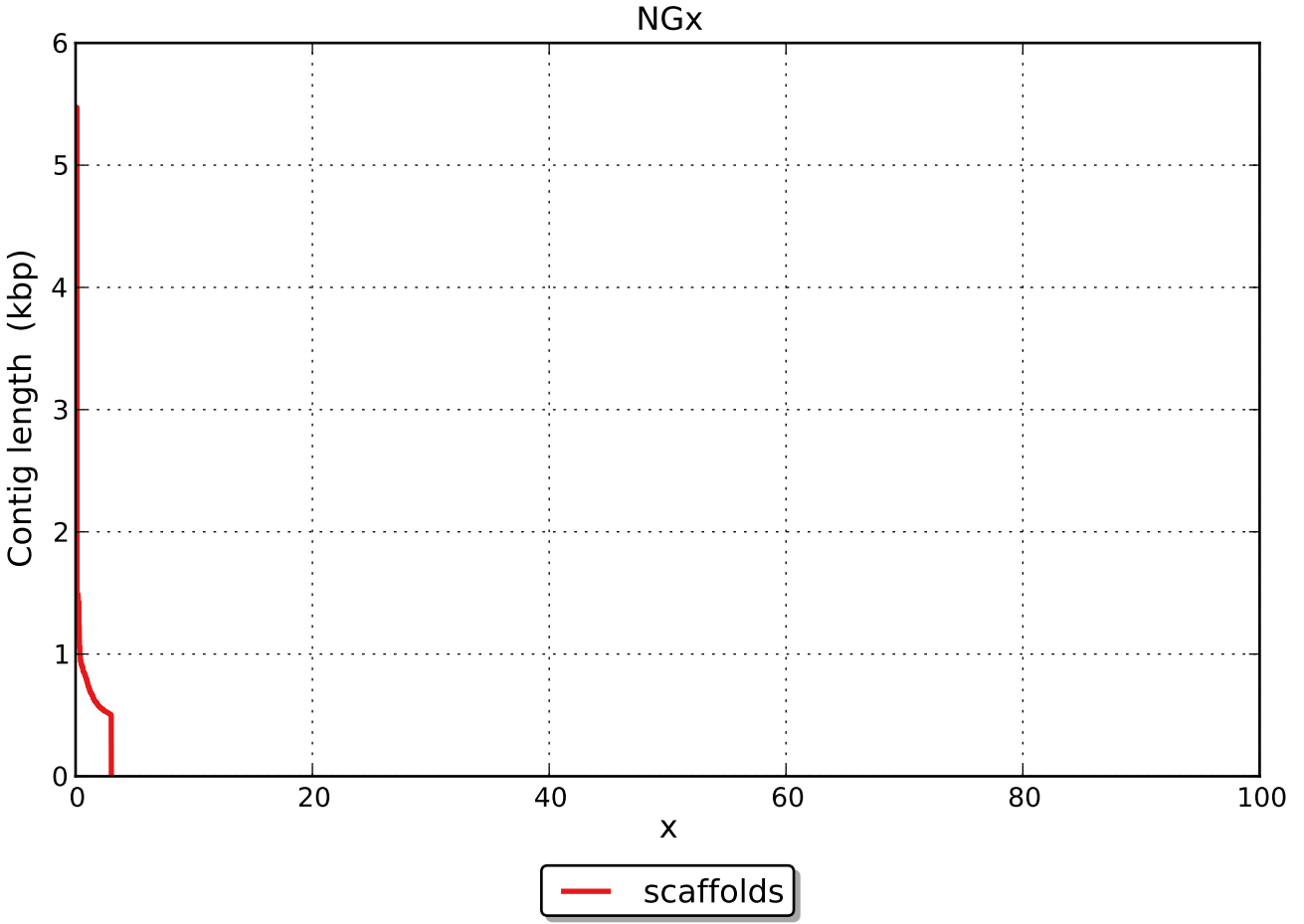
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

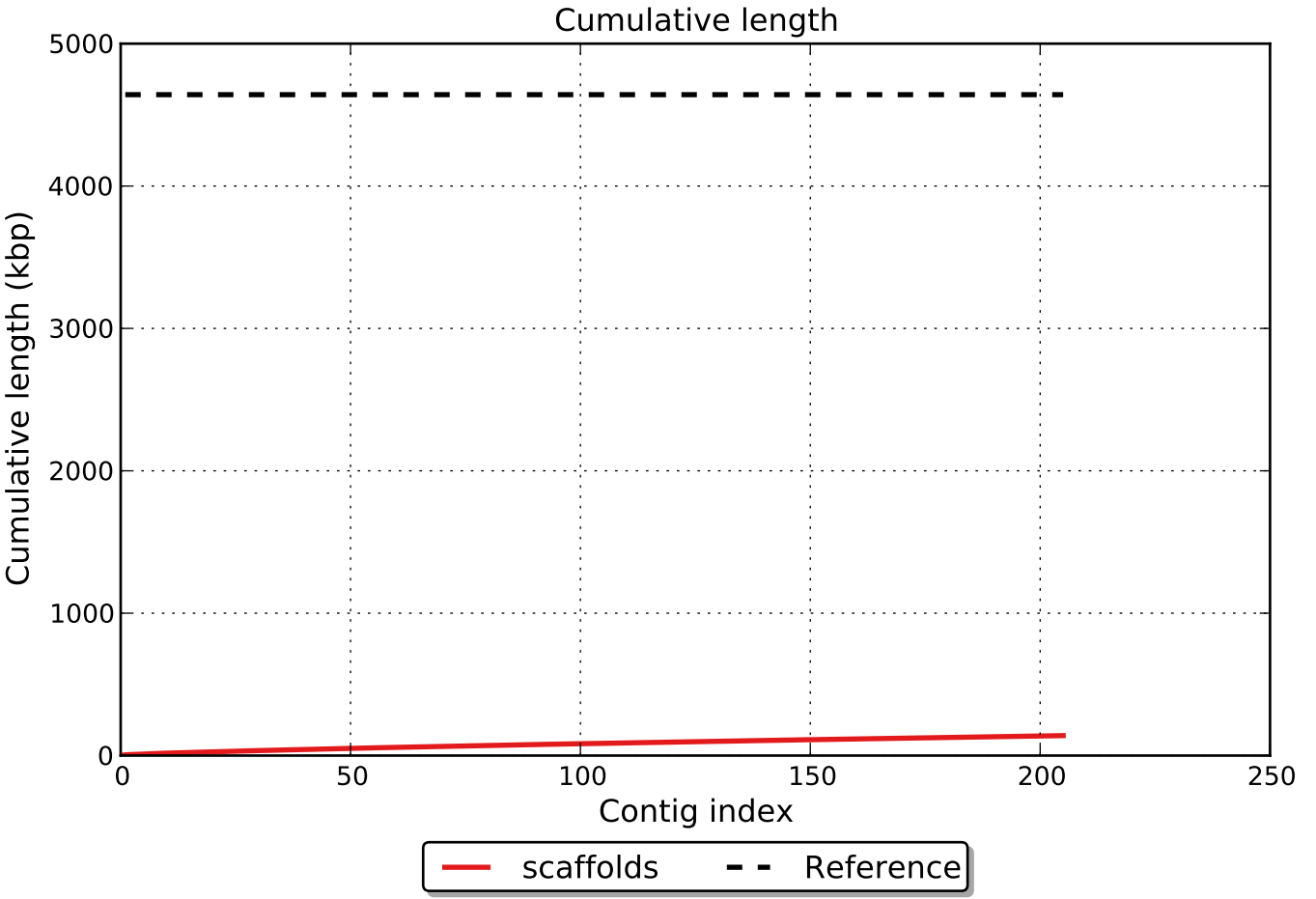
Unaligned report

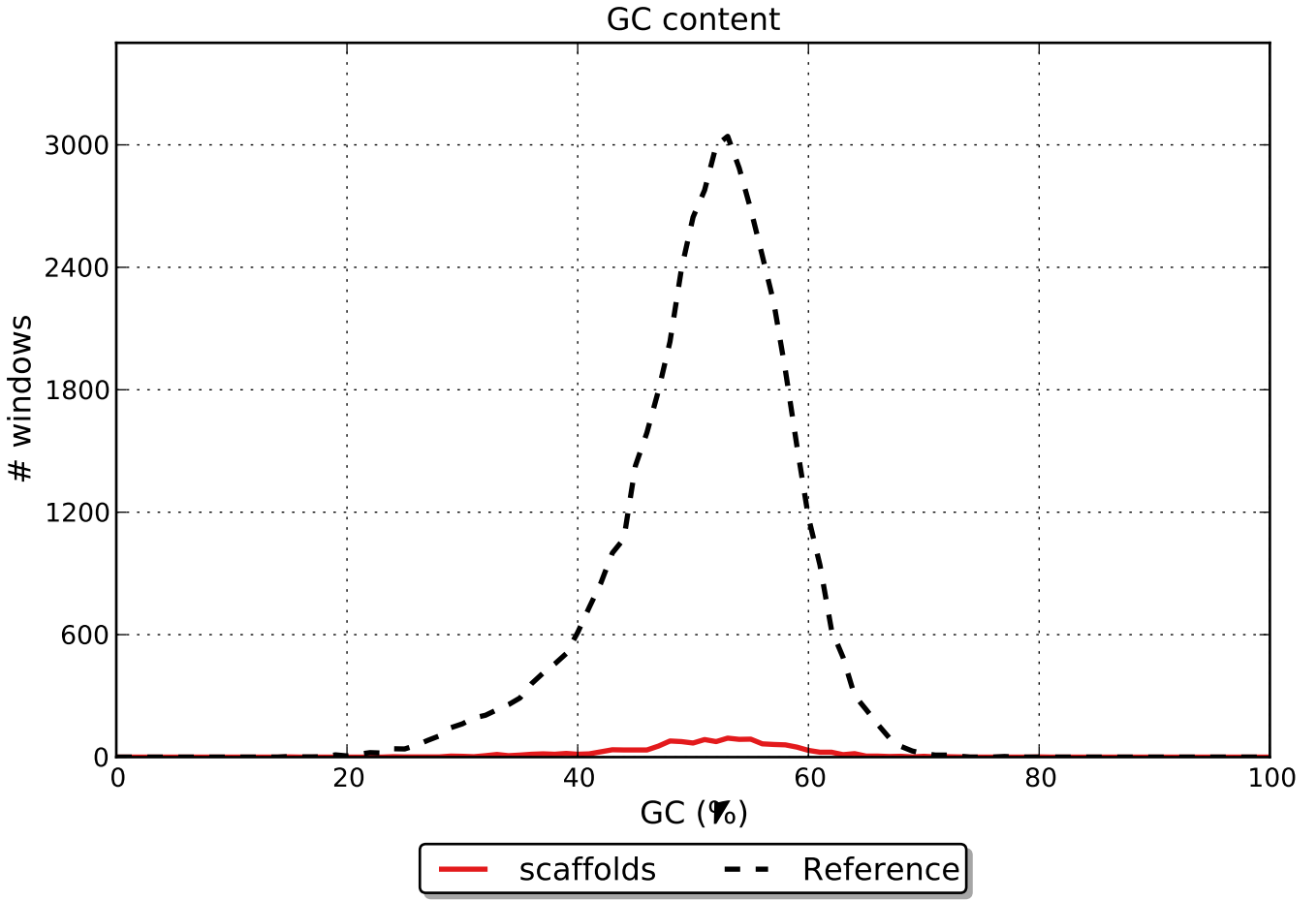
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	884
# N's	821

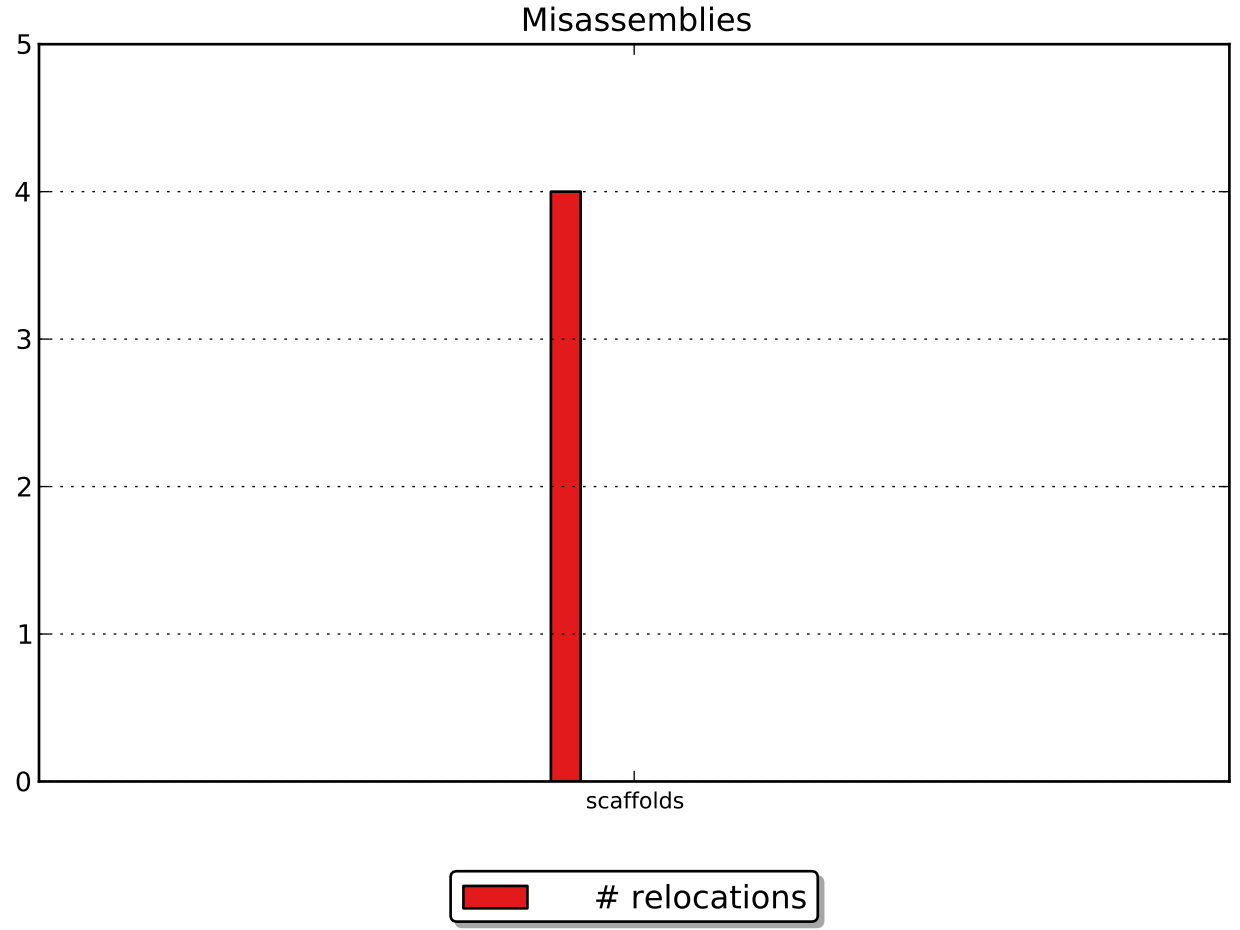
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

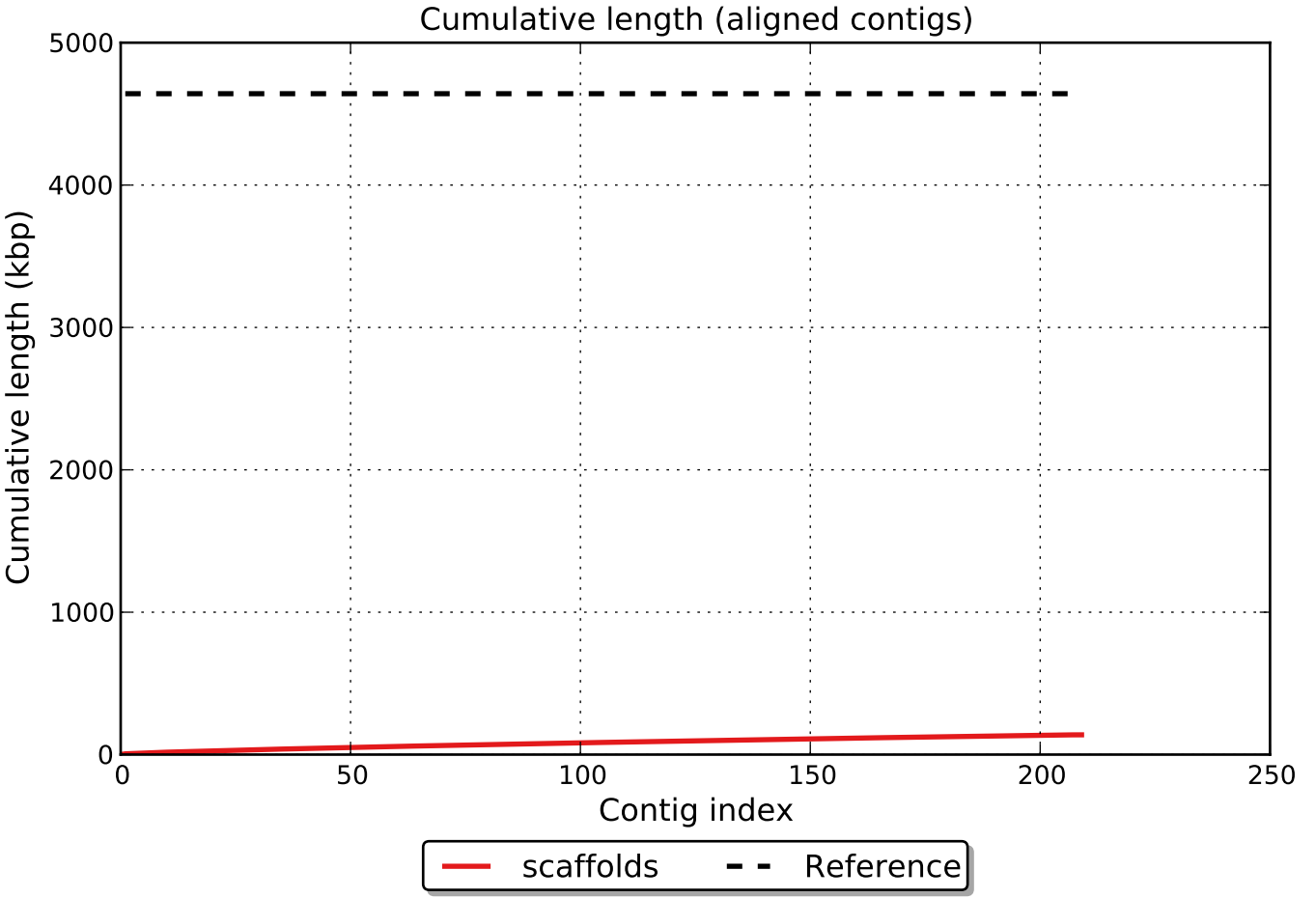

Nx
Contig length (kbp)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
scaffolds

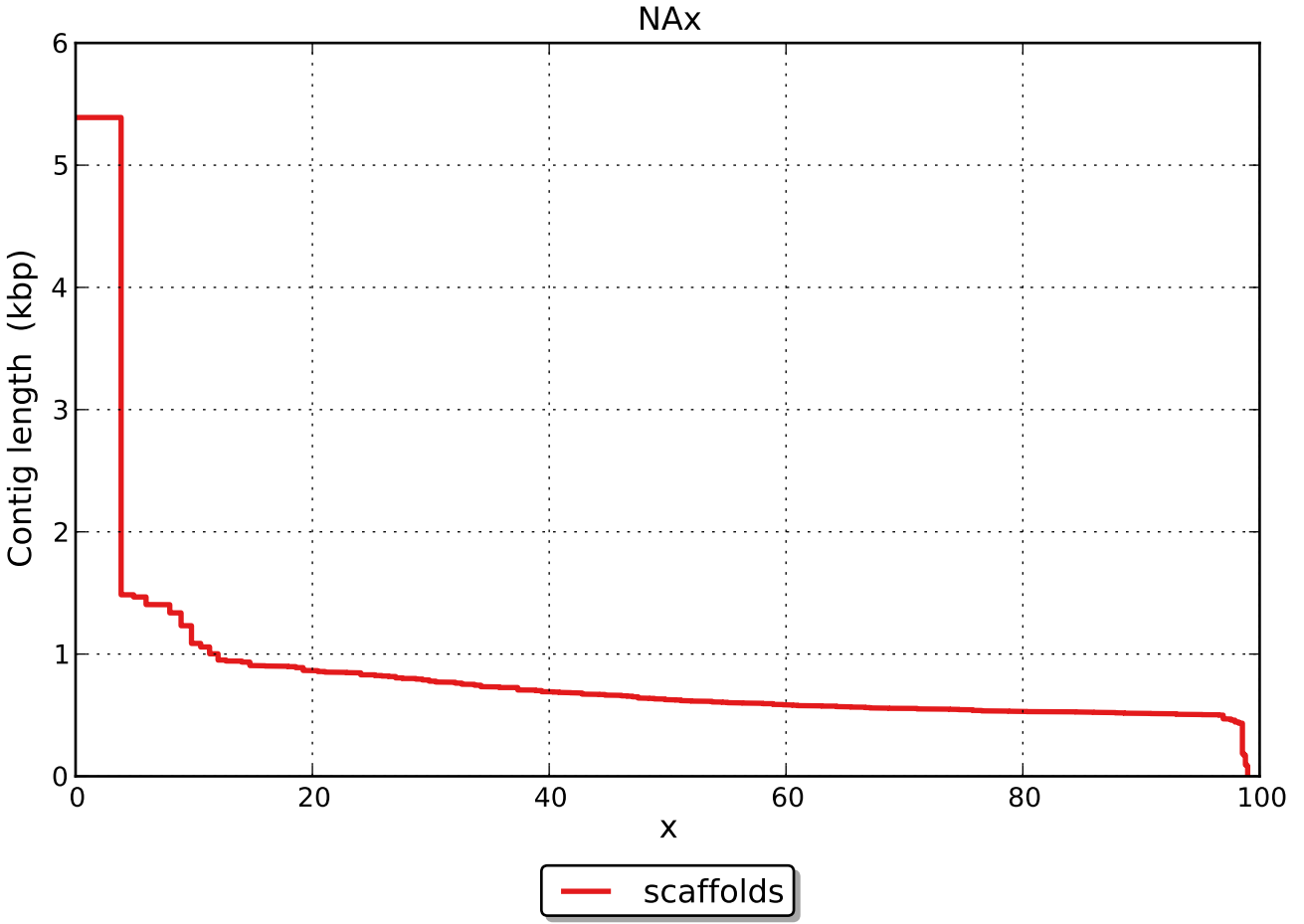

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds

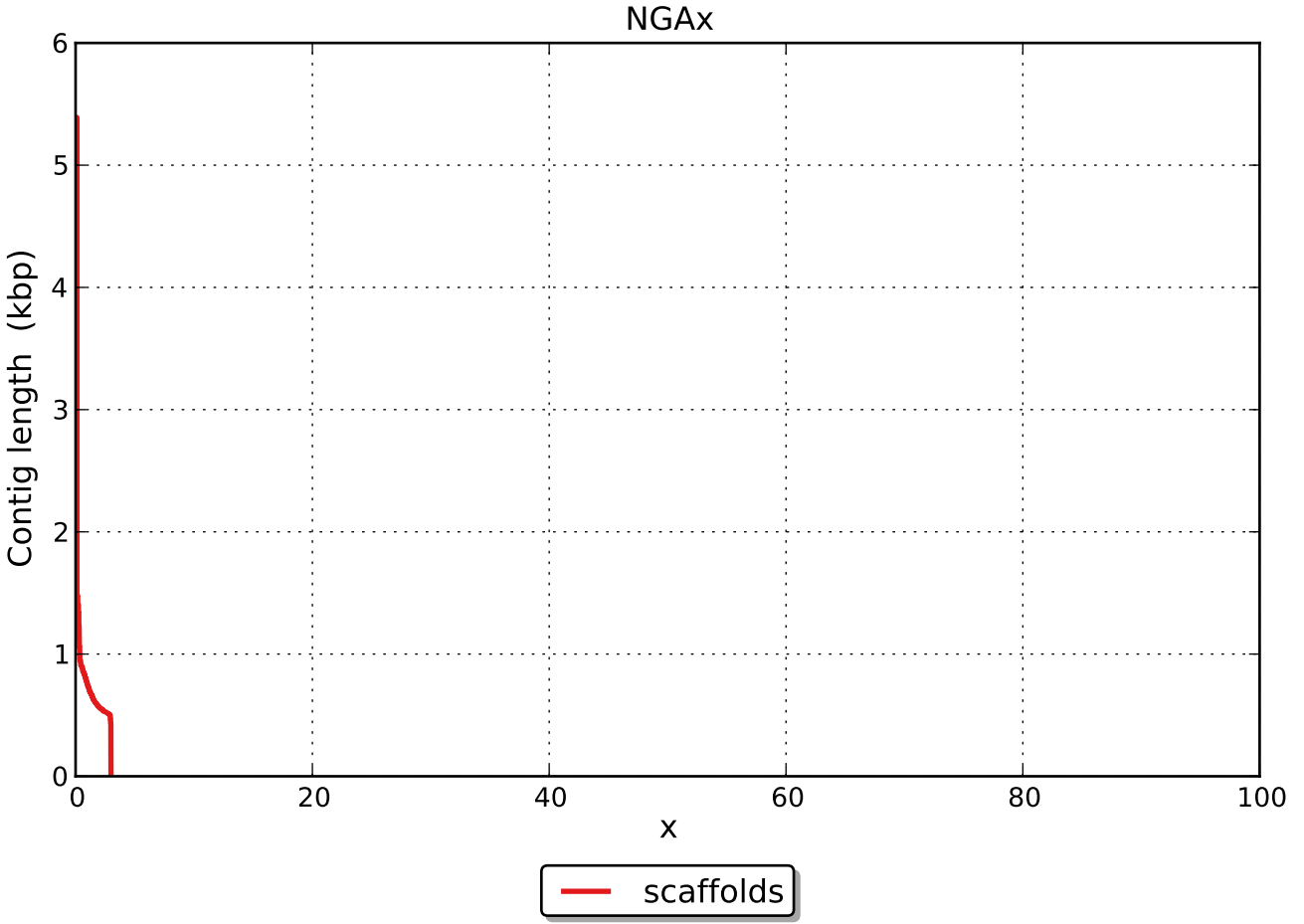

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
scaffolds
Reference


GC content
windows
3000
2400
1800
1200
600
0
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
50
100
150
200
250
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
scaffolds