Report

	scaffolds
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	57
# contigs (>= 10000 bp)	51
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4494857
Total length (>= 5000 bp)	4451416
Total length (>= 10000 bp)	4409585
Total length (>= 25000 bp)	4236257
Total length (>= 50000 bp)	3926012
# contigs	105
Largest contig	431470
Total length	4511408
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.78
N50	105688
NG50	105224
N75	69056
NG75	63924
L50	10
LG50	11
L75	24
LG75	25
# misassemblies	7
# misassembled contigs	2
Misassembled contigs length	196859
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.932
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	954.89
# indels per 100 kbp	1.10
Largest alignment	431470
NA50	105224
NGA50	96103
NA75	63011
NGA75	62885
LA50	10
LGA50	11
LA75	25
LGA75	26

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

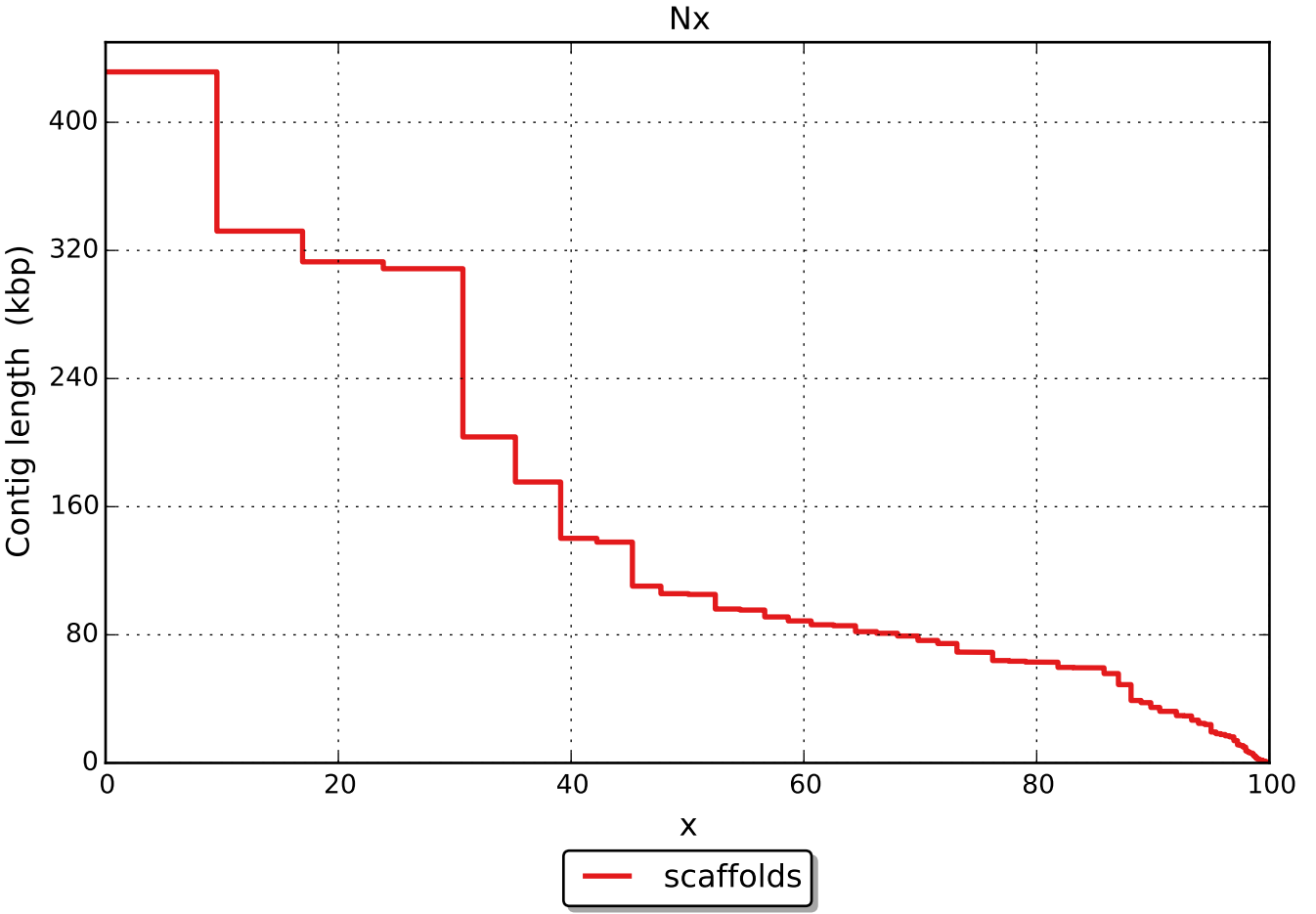
	scaffolds
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	196859
# local misassemblies	4
# mismatches	41633
# indels	48
# short indels	47
# long indels	1
Indels length	57

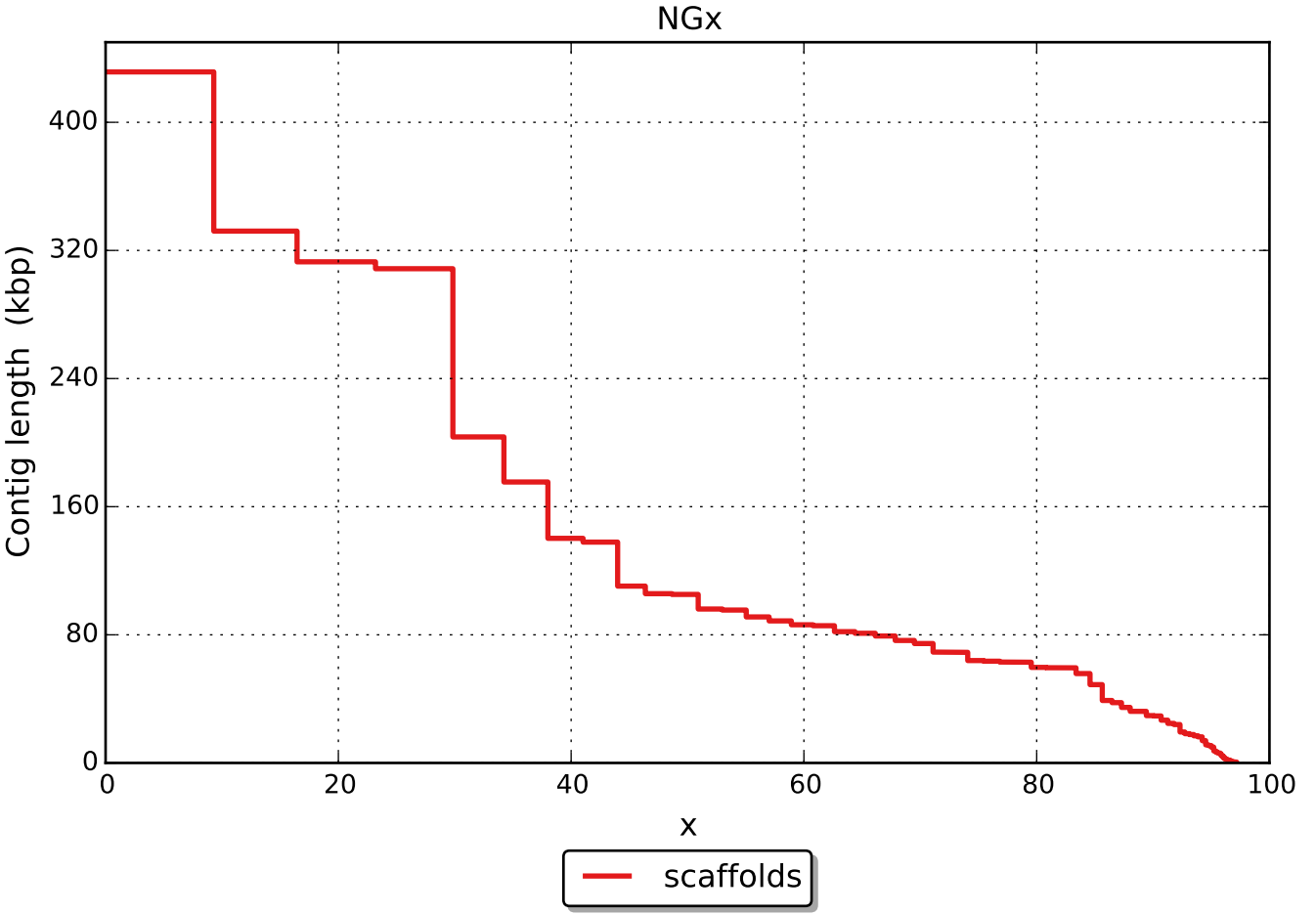
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

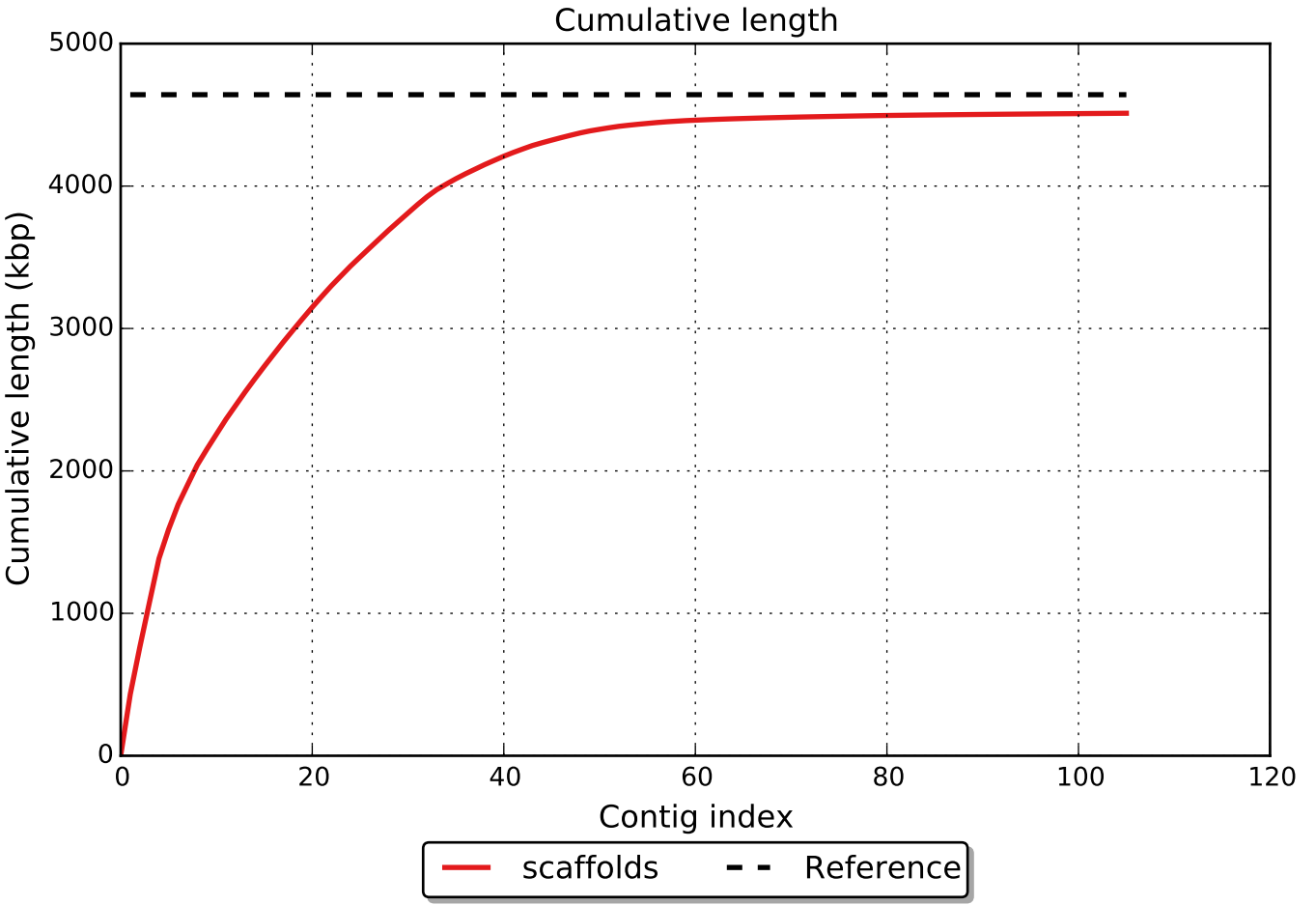
Unaligned report

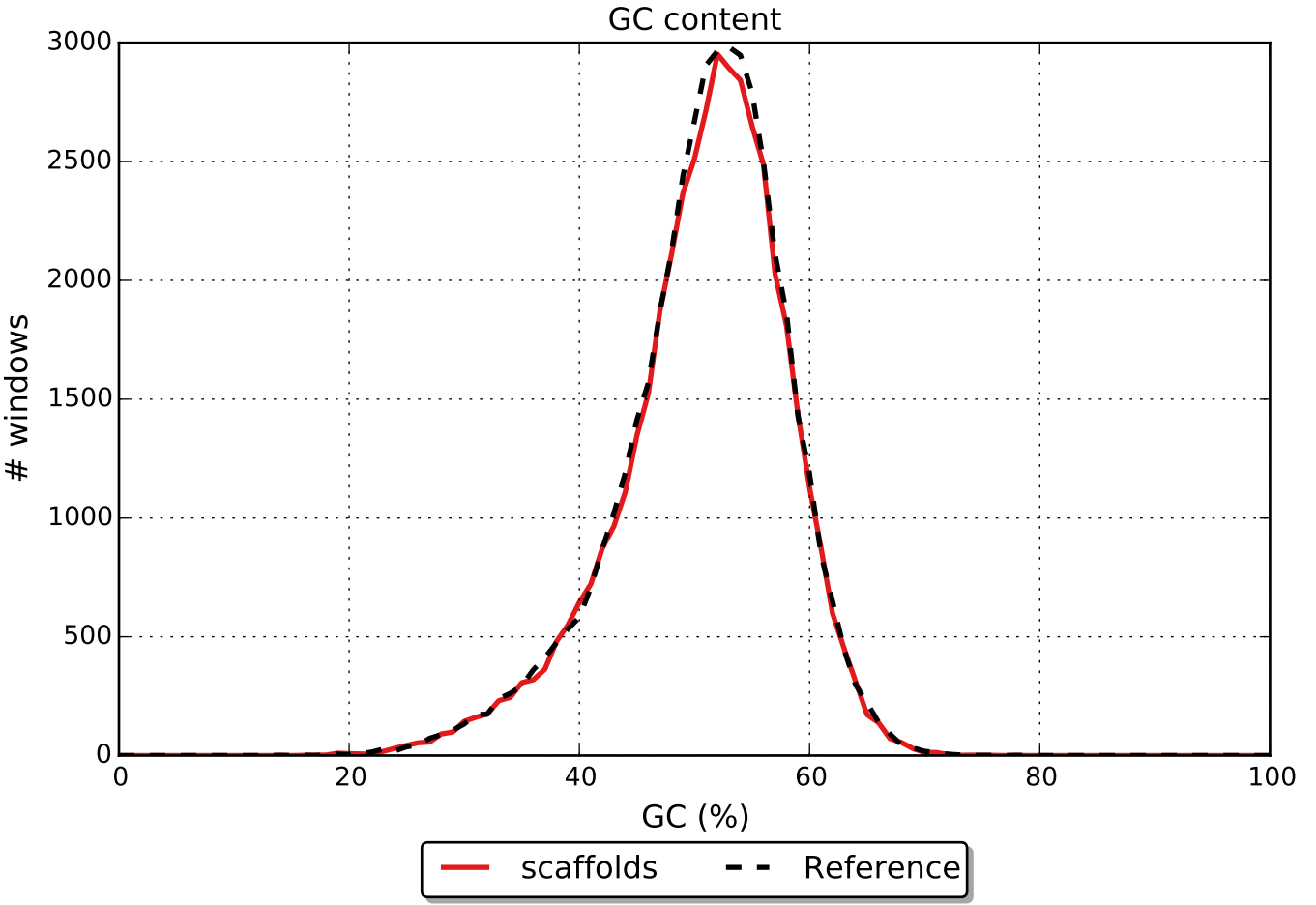
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

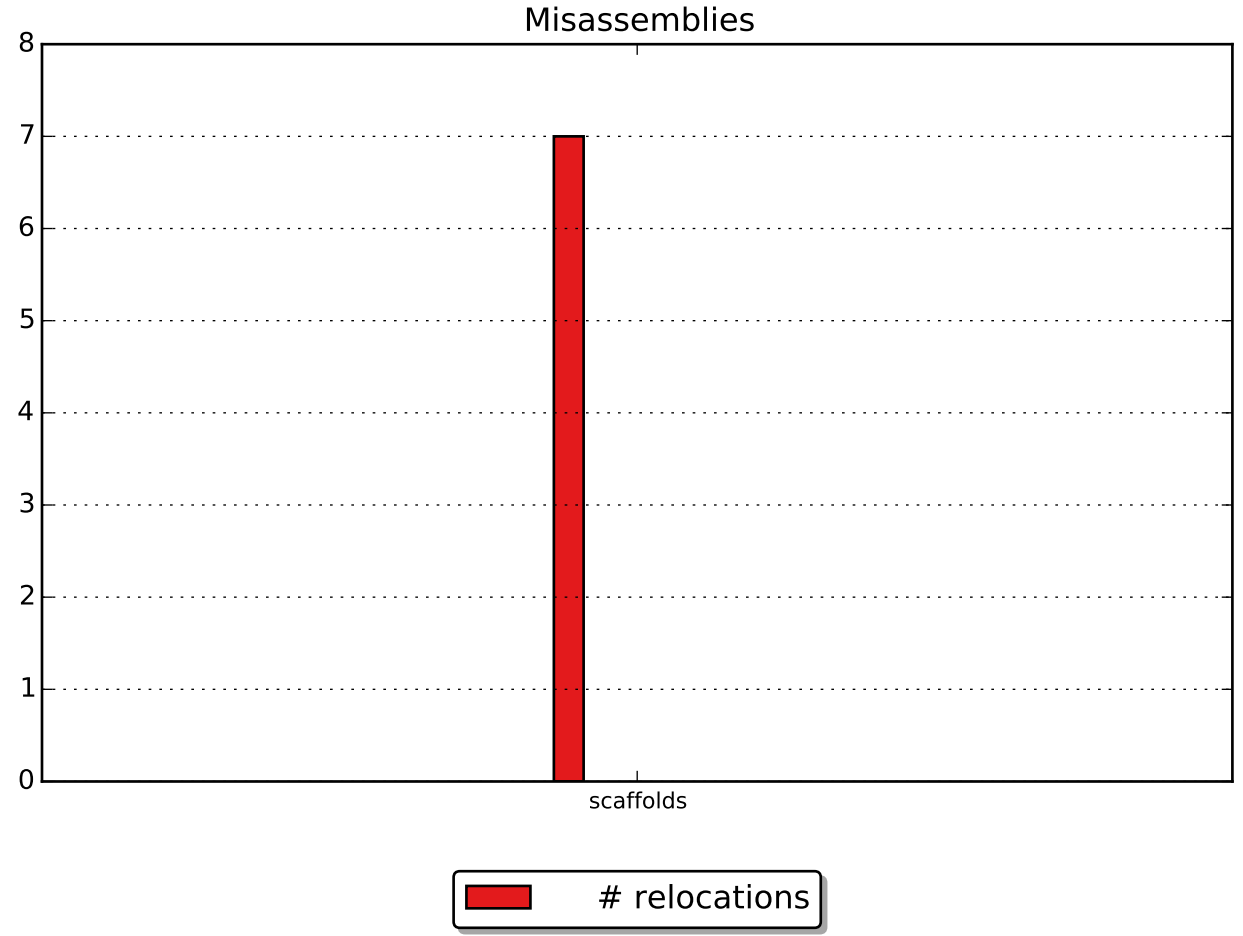
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

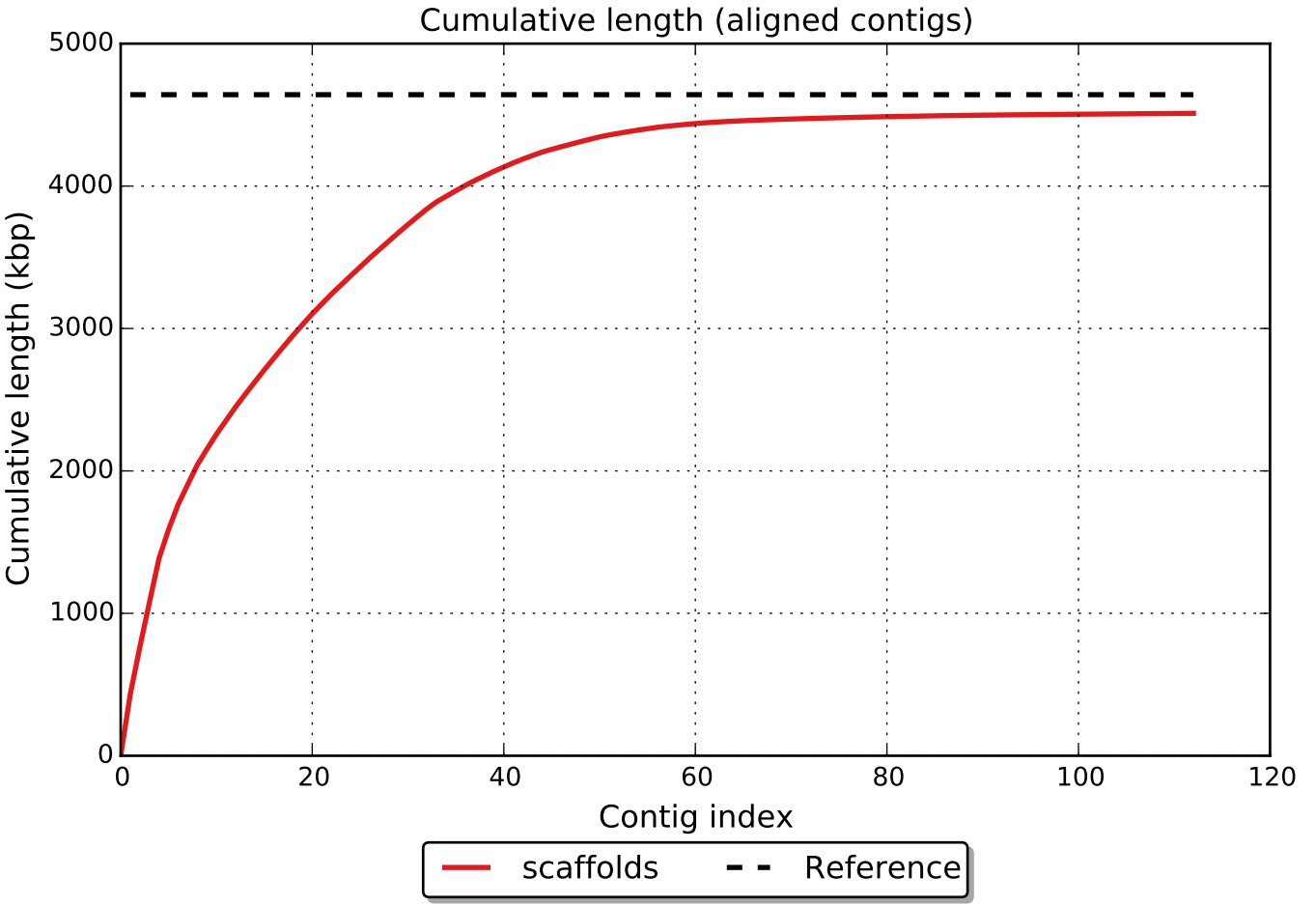

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
scaffolds

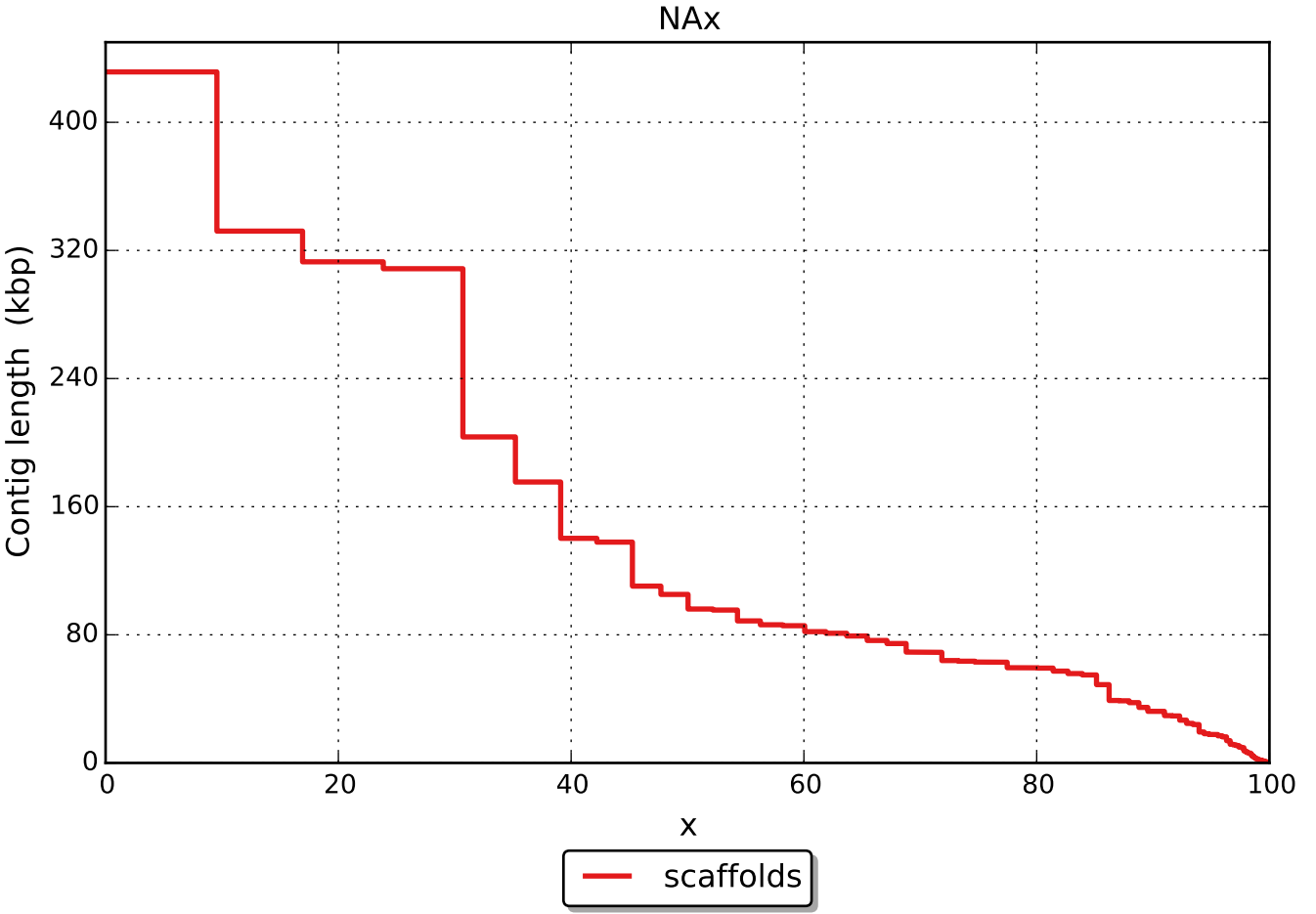

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
scaffolds

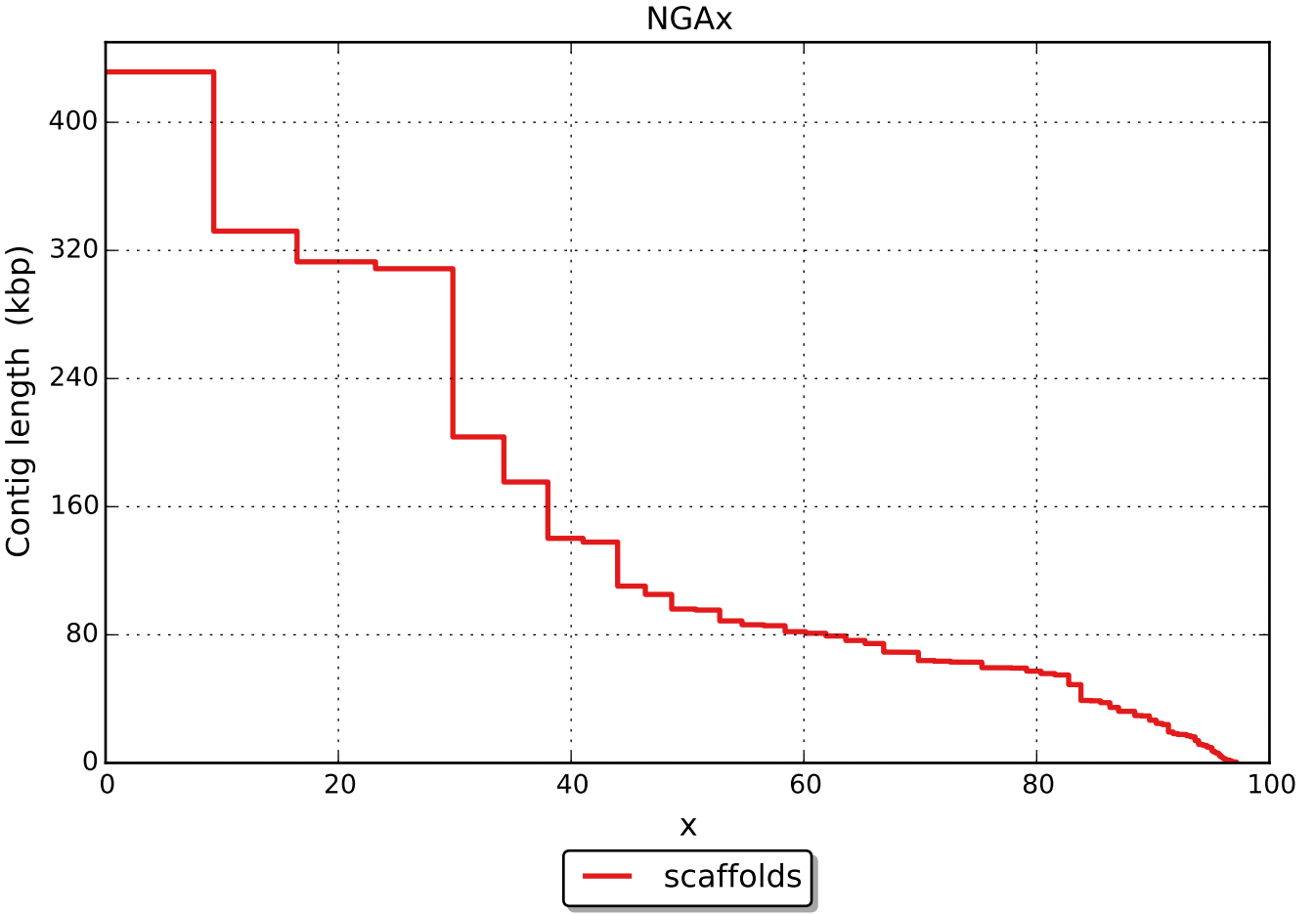

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
scaffolds
Reference


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


Misassemblies
8
7
6
5
4
3
2
1
0
scaffolds
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
scaffolds