Report

	scaffolds
# contigs (>= 1000 bp)	59
# contigs (>= 5000 bp)	46
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4528851
Total length (>= 5000 bp)	4500135
Total length (>= 10000 bp)	4476440
Total length (>= 25000 bp)	4389531
Total length (>= 50000 bp)	3981473
# contigs	69
Largest contig	333130
Total length	4535694
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	166049
NG50	166049
N75	94985
NG75	87829
L50	10
LG50	10
L75	19
LG75	20
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36005
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.689
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	112.23
# indels per 100 kbp	0.40
Largest alignment	333130
NA50	166049
NGA50	166049
NA75	94985
NGA75	87829
LA50	10
LGA50	10
LA75	19
LGA75	20

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

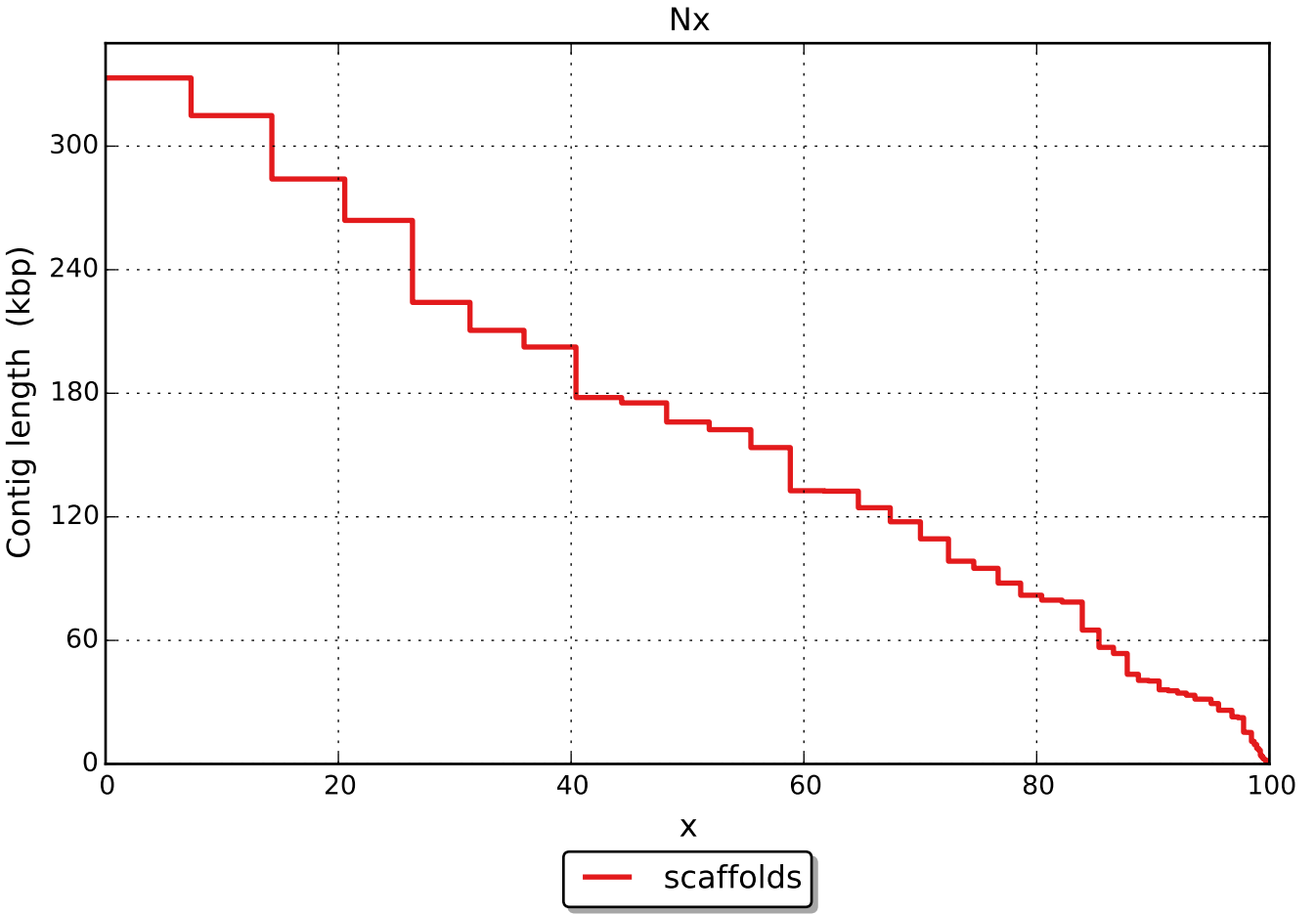
	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36005
# local misassemblies	2
# mismatches	5089
# indels	18
# short indels	18
# long indels	0
Indels length	18

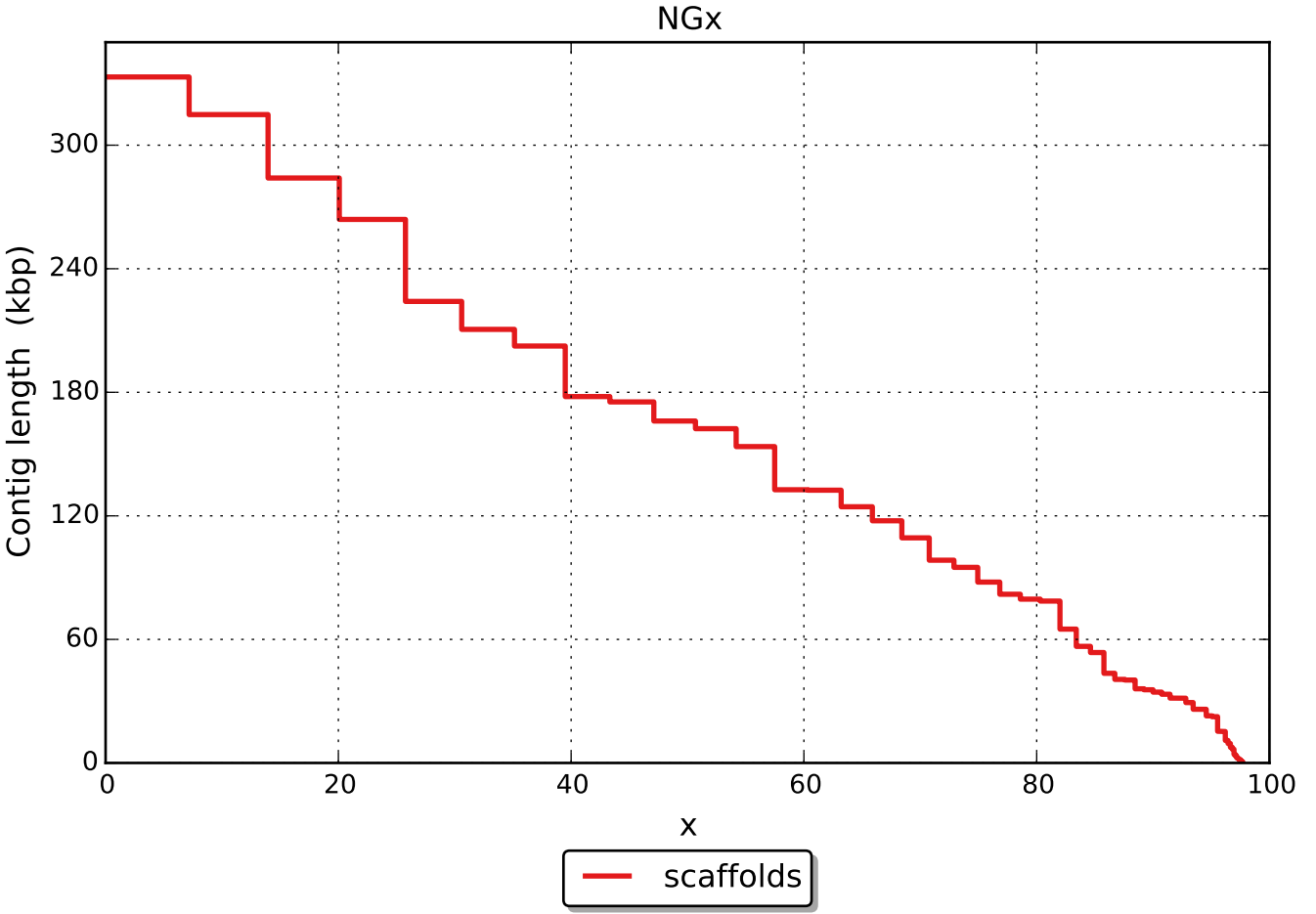
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

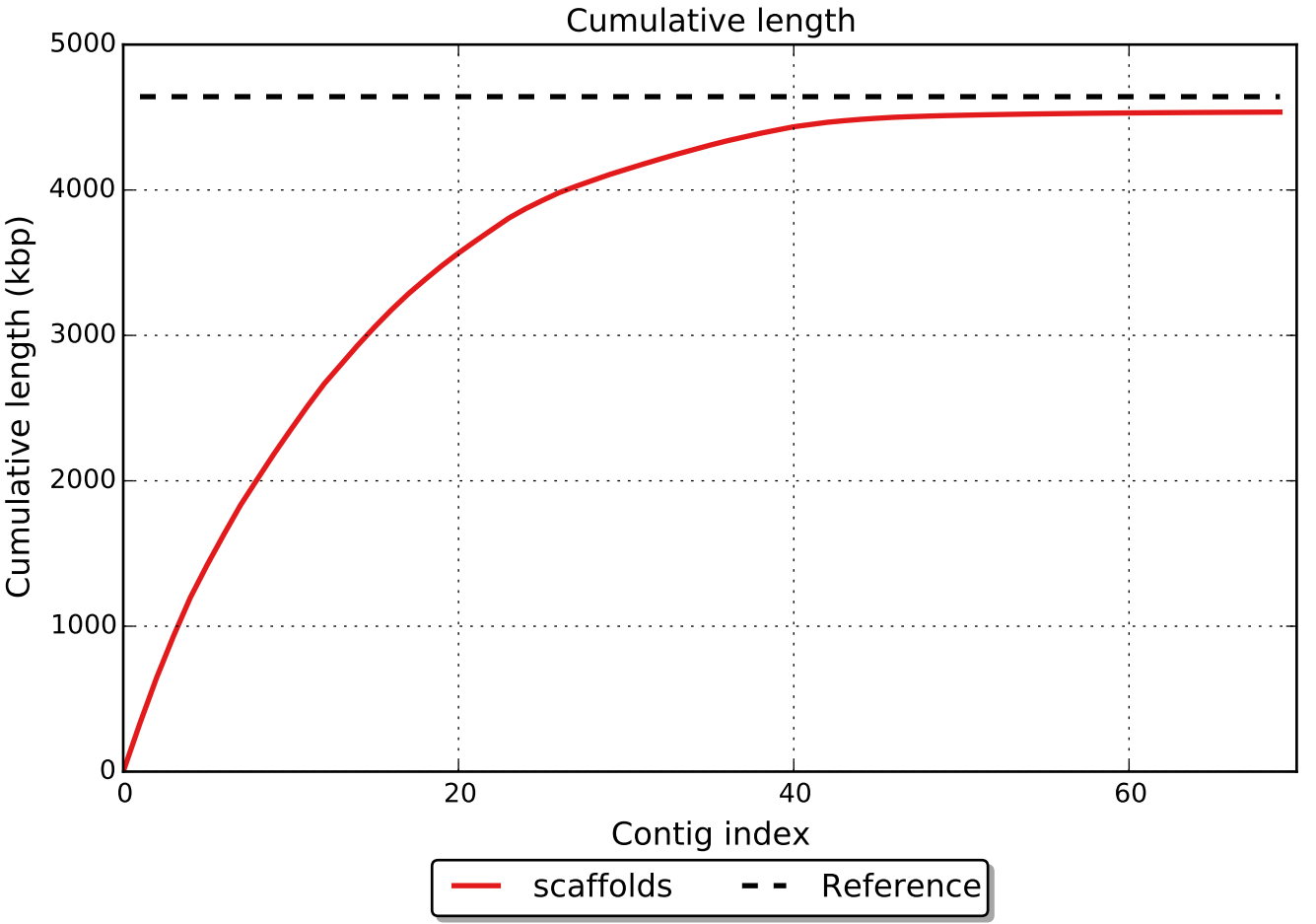
Unaligned report

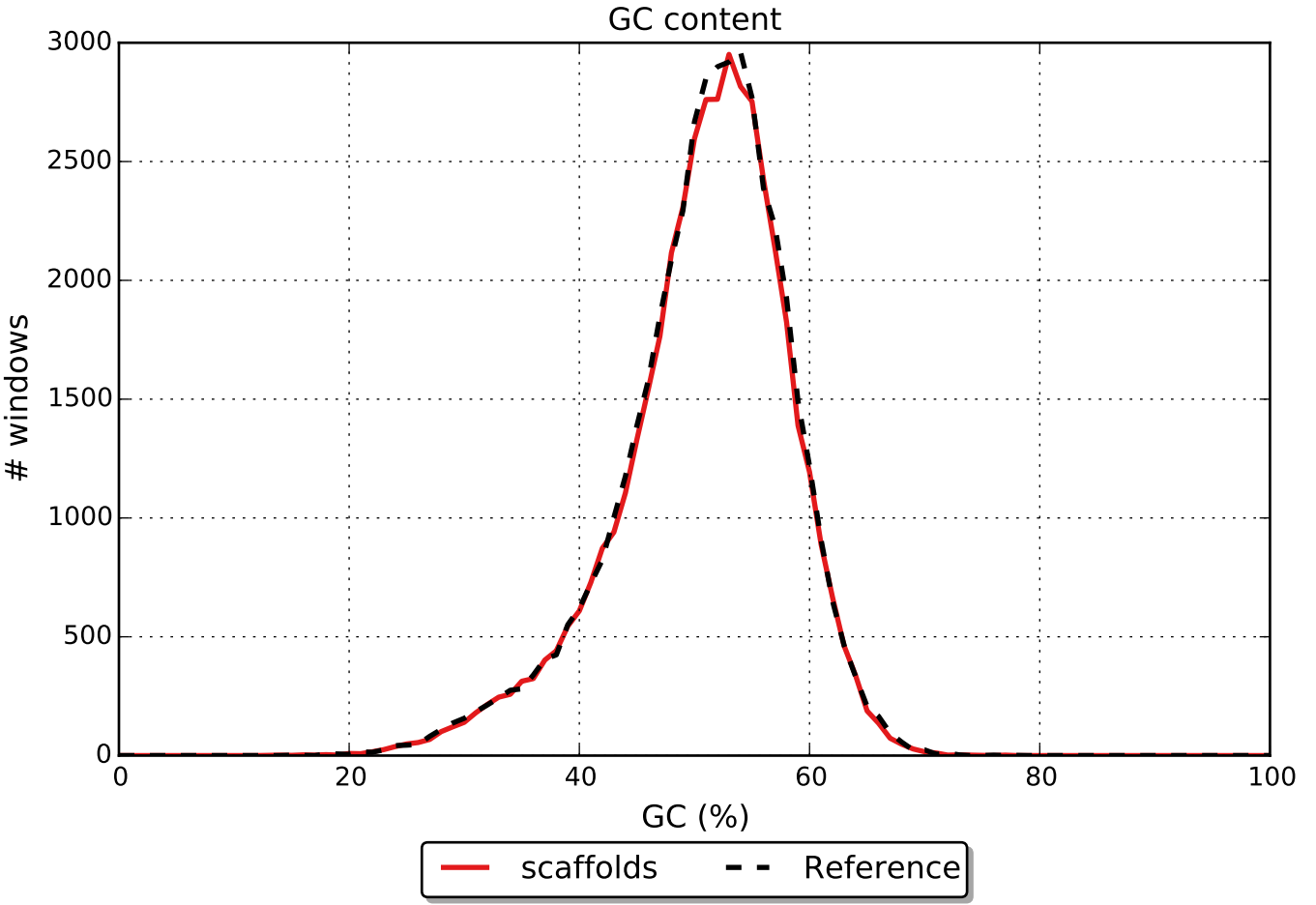
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

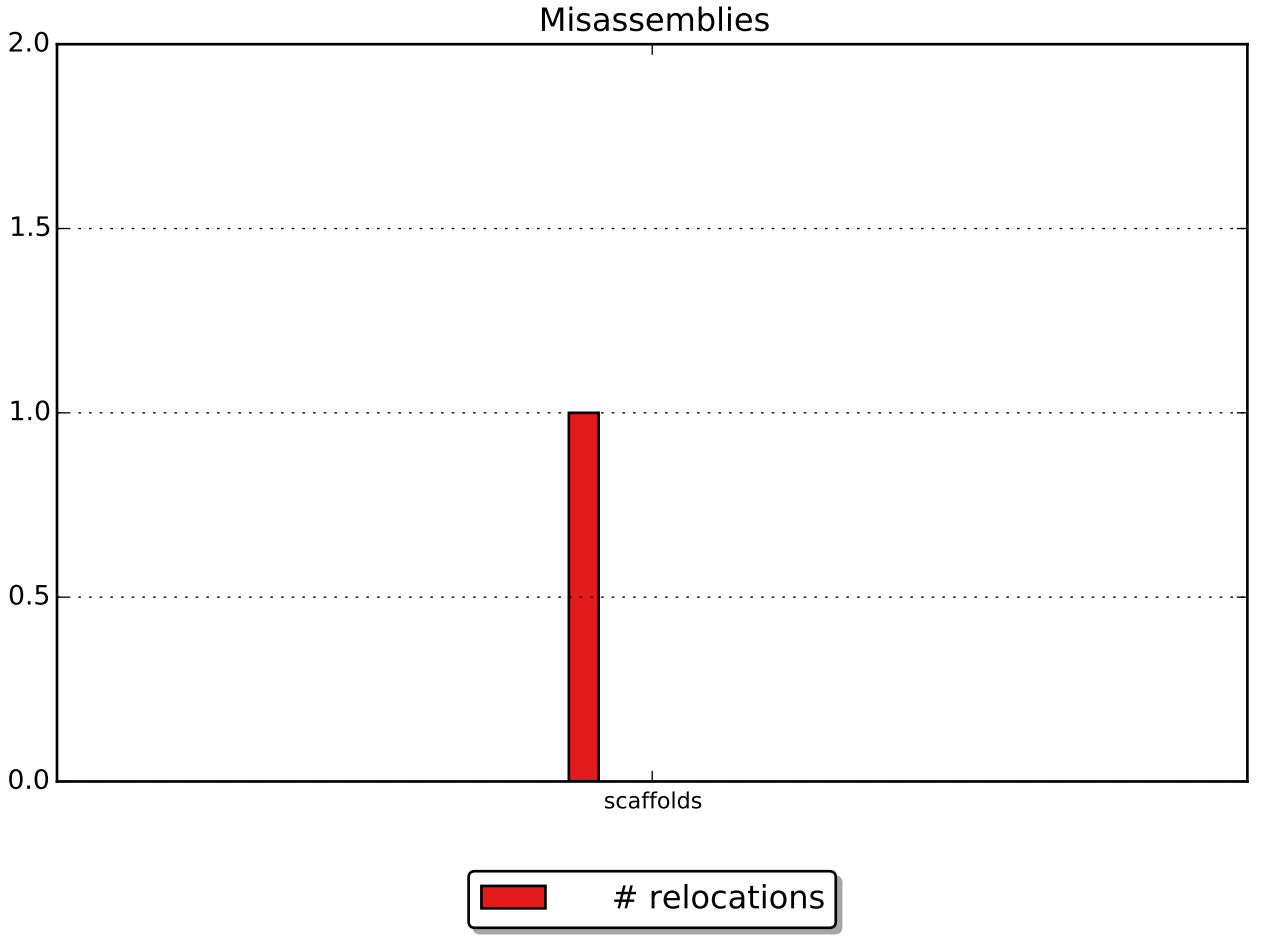
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

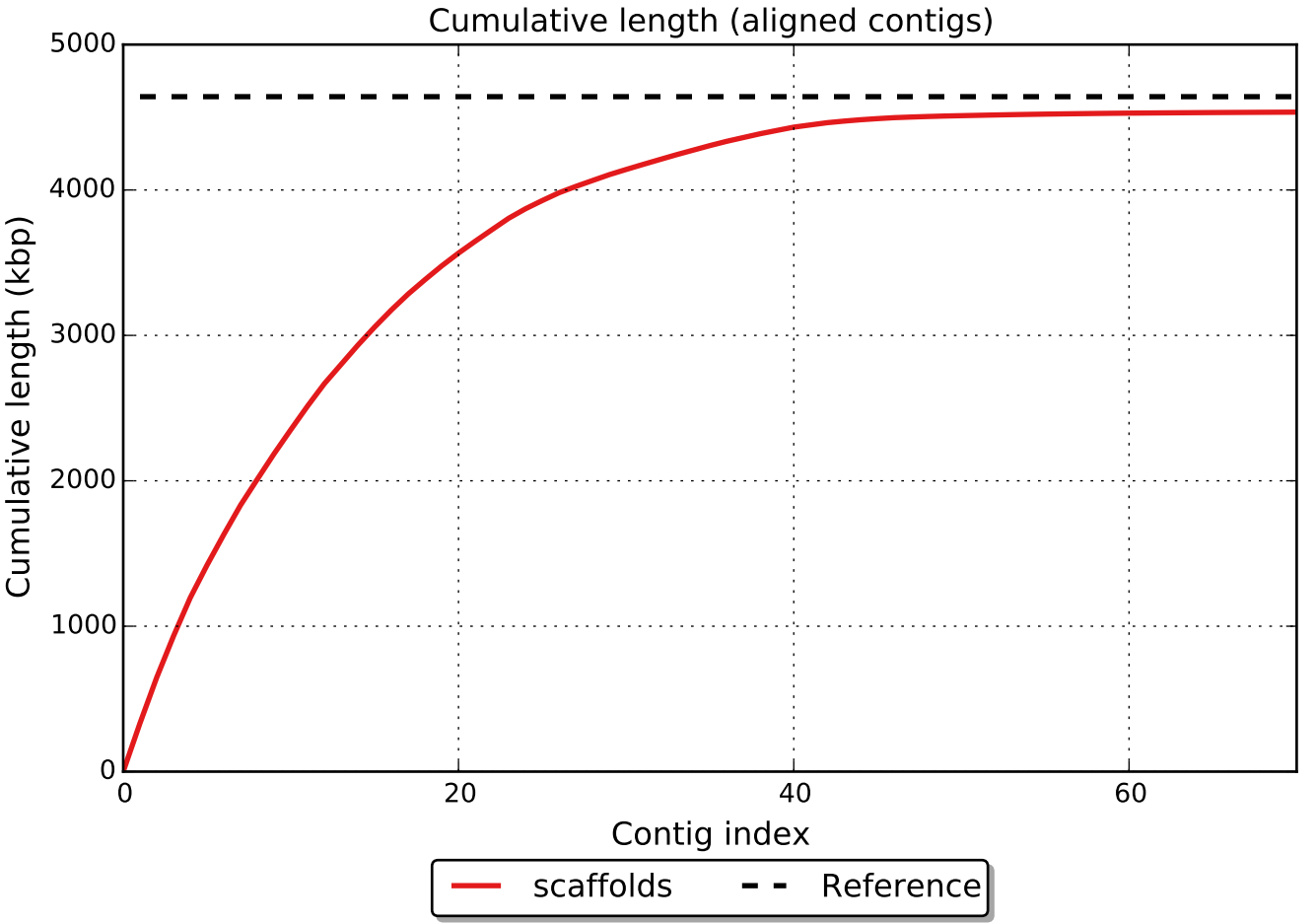

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

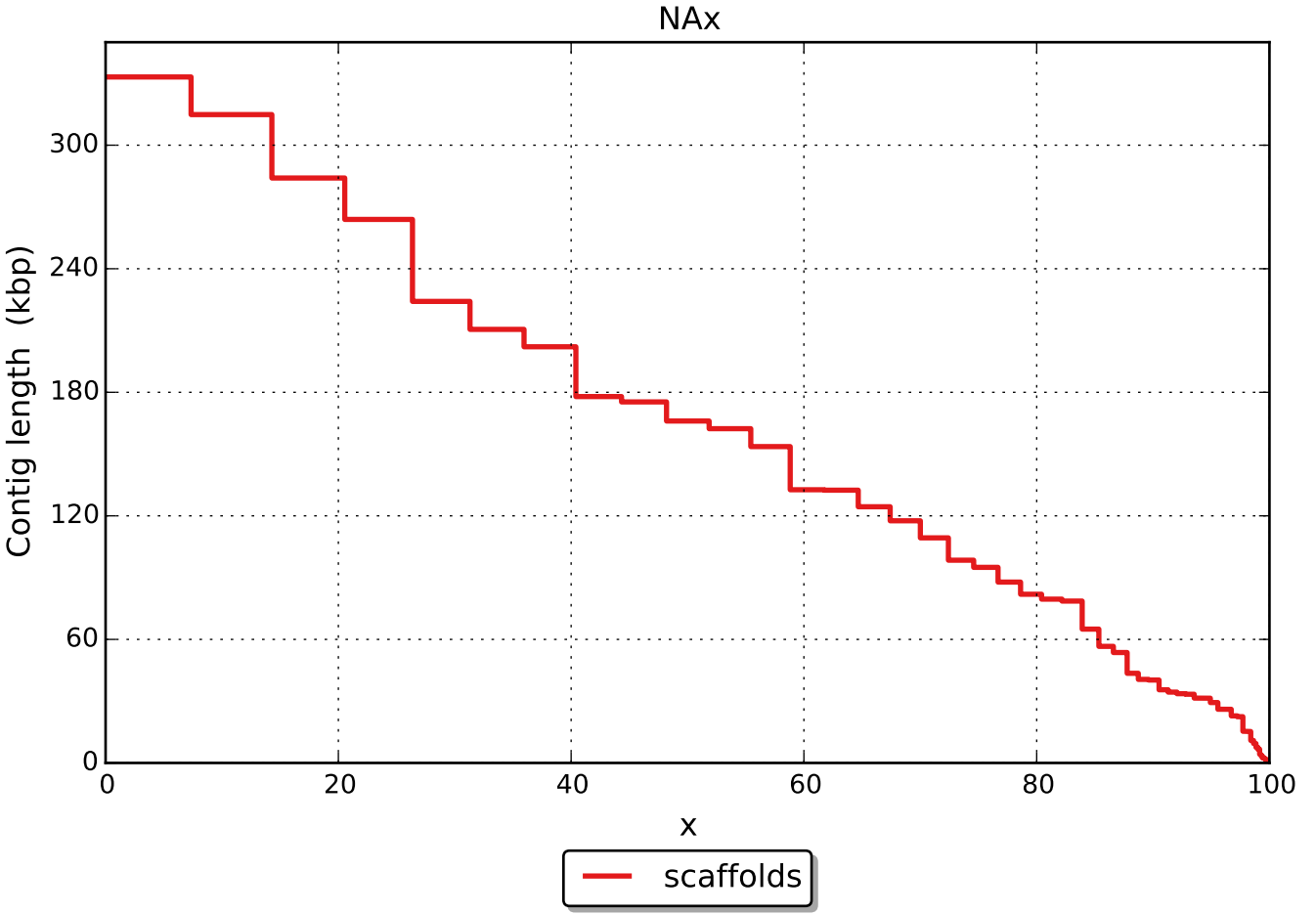

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

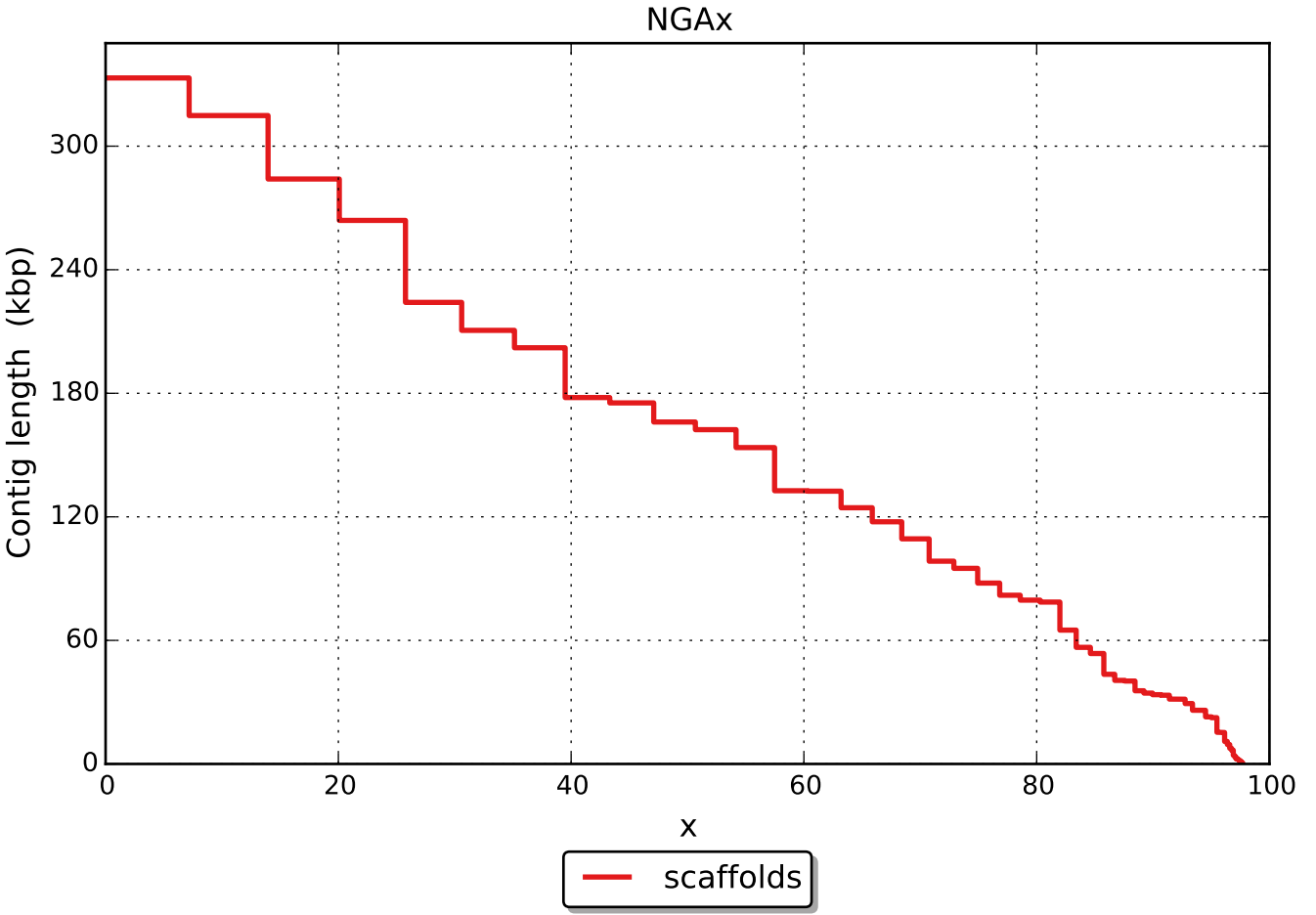

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
Contig index
scaffolds
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
scaffolds
relocations


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


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds