Report

	scaffolds
# contigs (>= 1000 bp)	65
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	46
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4563289
Total length (>= 5000 bp)	4529278
Total length (>= 10000 bp)	4505327
Total length (>= 25000 bp)	4414190
Total length (>= 50000 bp)	3949408
# contigs	69
Largest contig	327064
Total length	4566211
Reference length	4641652
GC (‰)	50.74
Reference GC (‰)	50.79
N50	173982
NG50	173982
N75	87064
NG75	87064
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (‰)	98.316
Duplication ratio	1.001
# N's per 100 kbp	3.15
# mismatches per 100 kbp	4.73
# indels per 100 kbp	0.44
Largest alignment	327064
NA50	173982
NGA50	173982
NA75	87064
NGA75	87064
LA50	10
LGA50	10
LA75	20
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

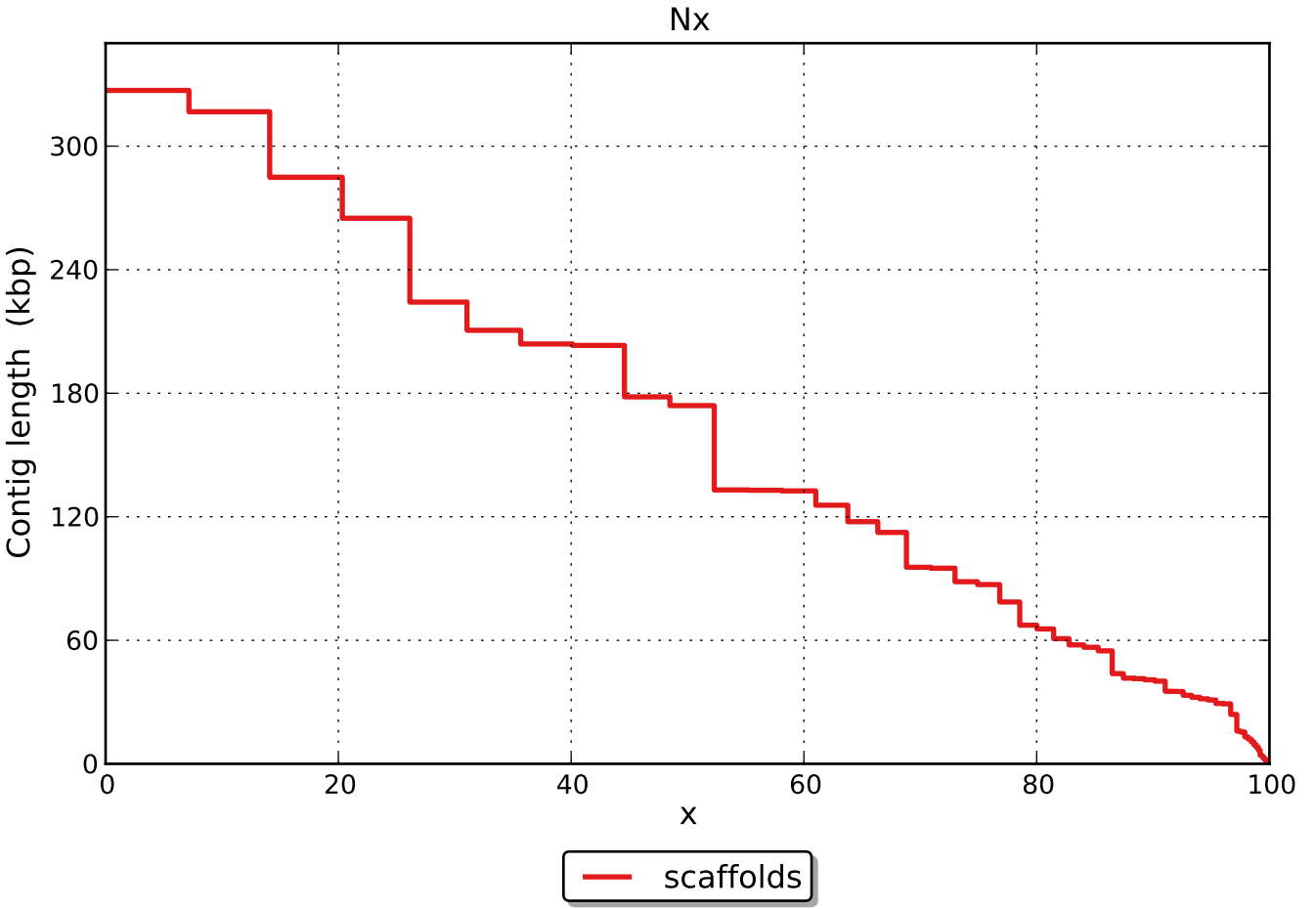
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	216
# indels	20
# short indels	19
# long indels	1
Indels length	49

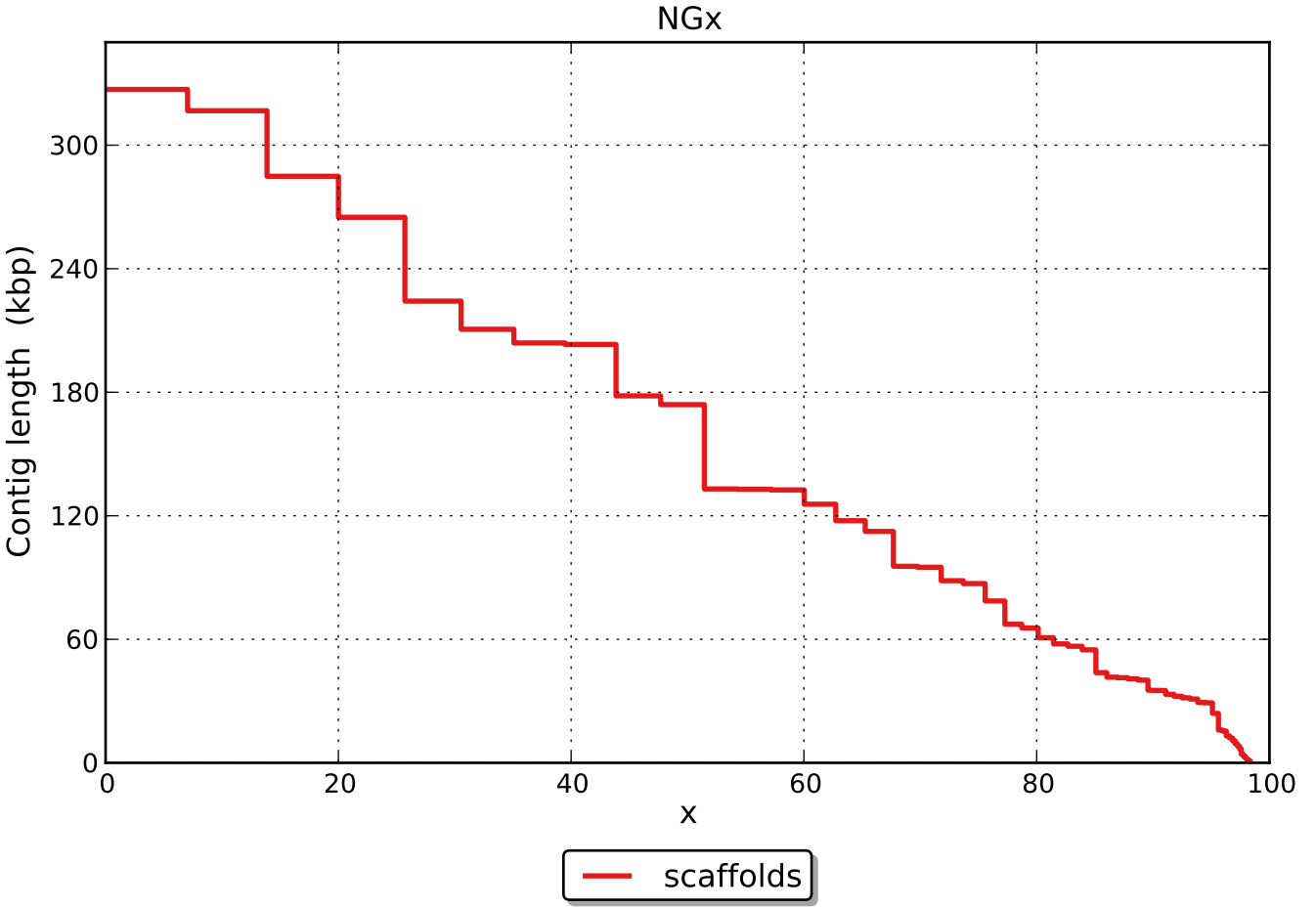
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

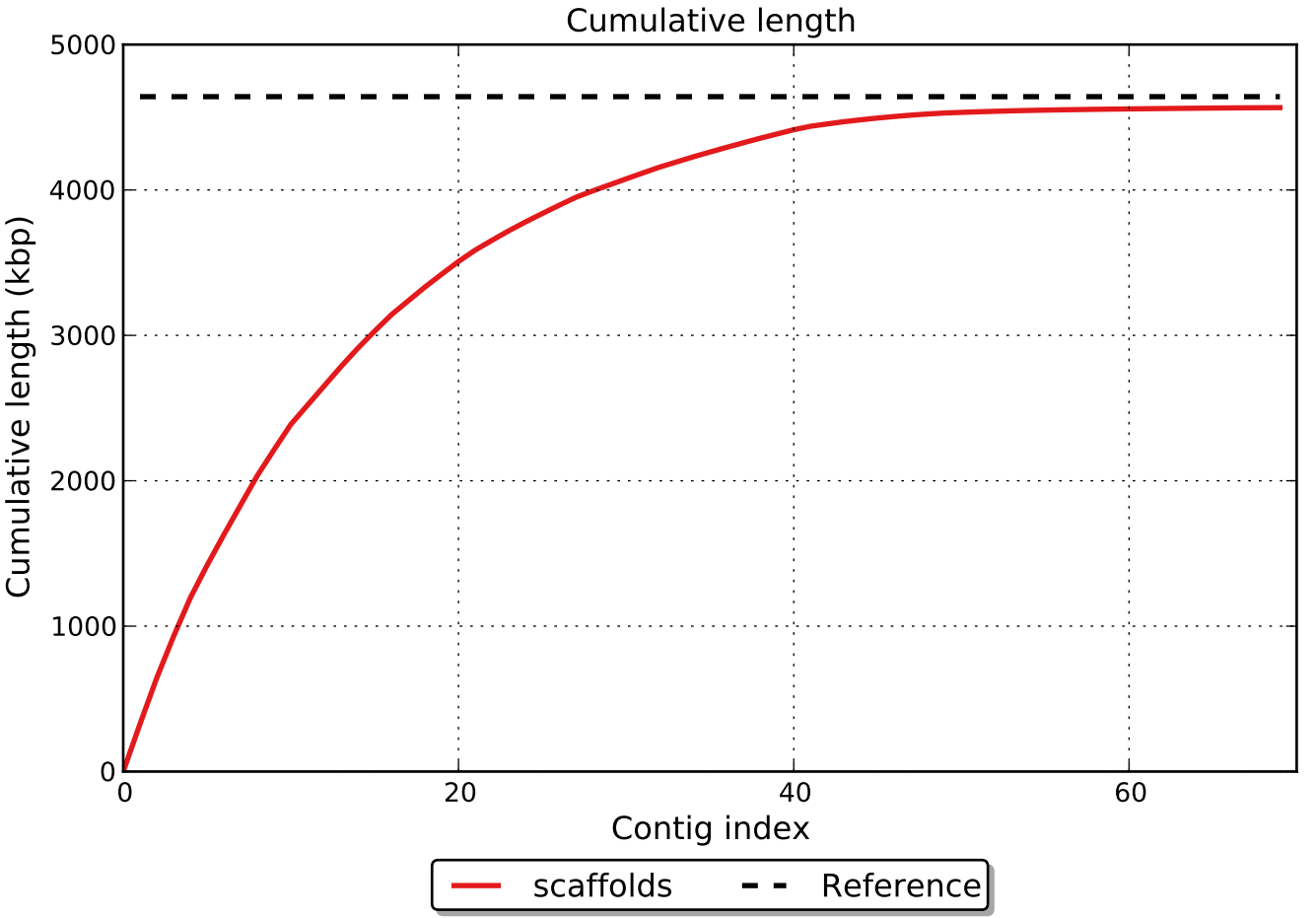
Unaligned report

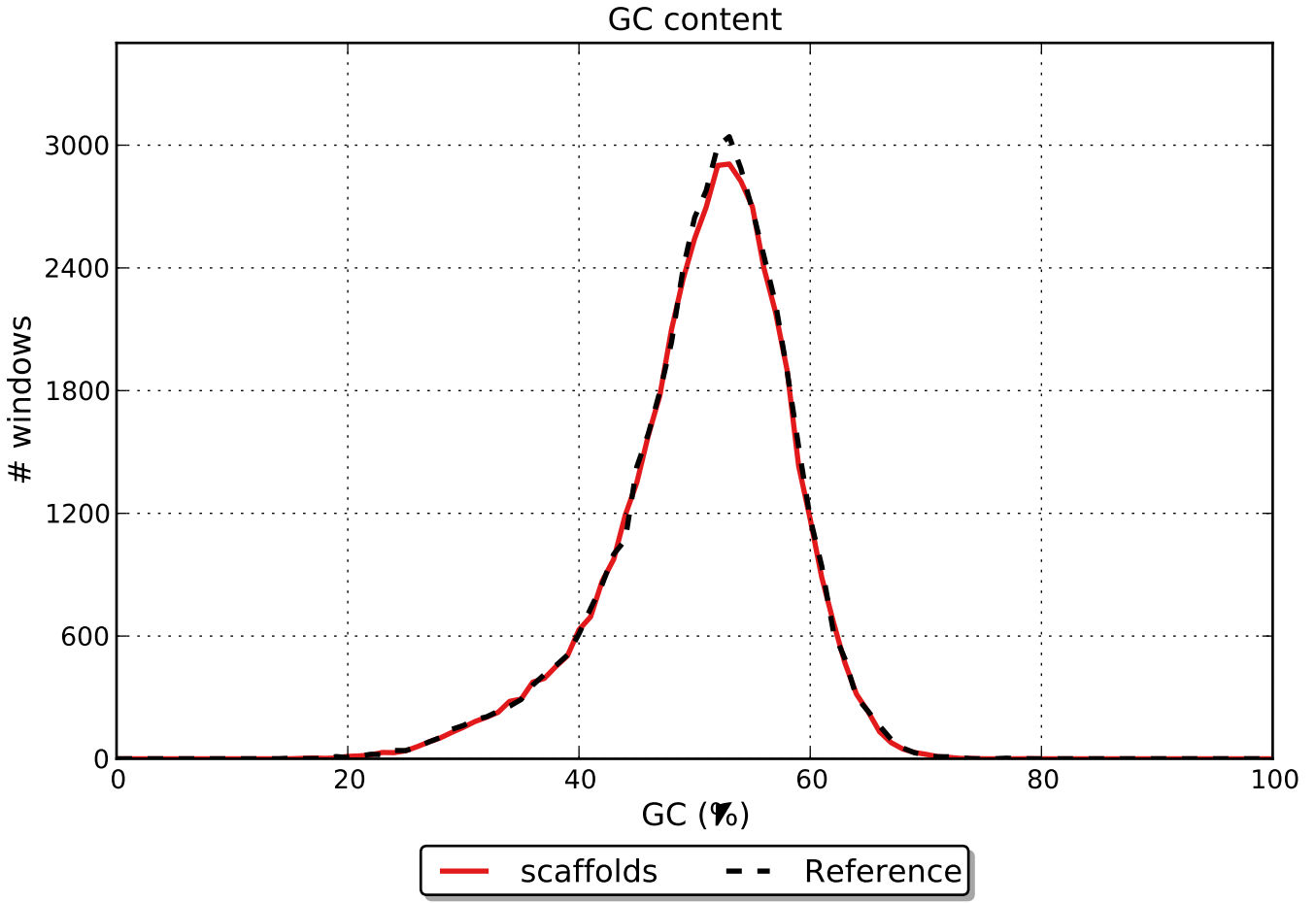
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	144

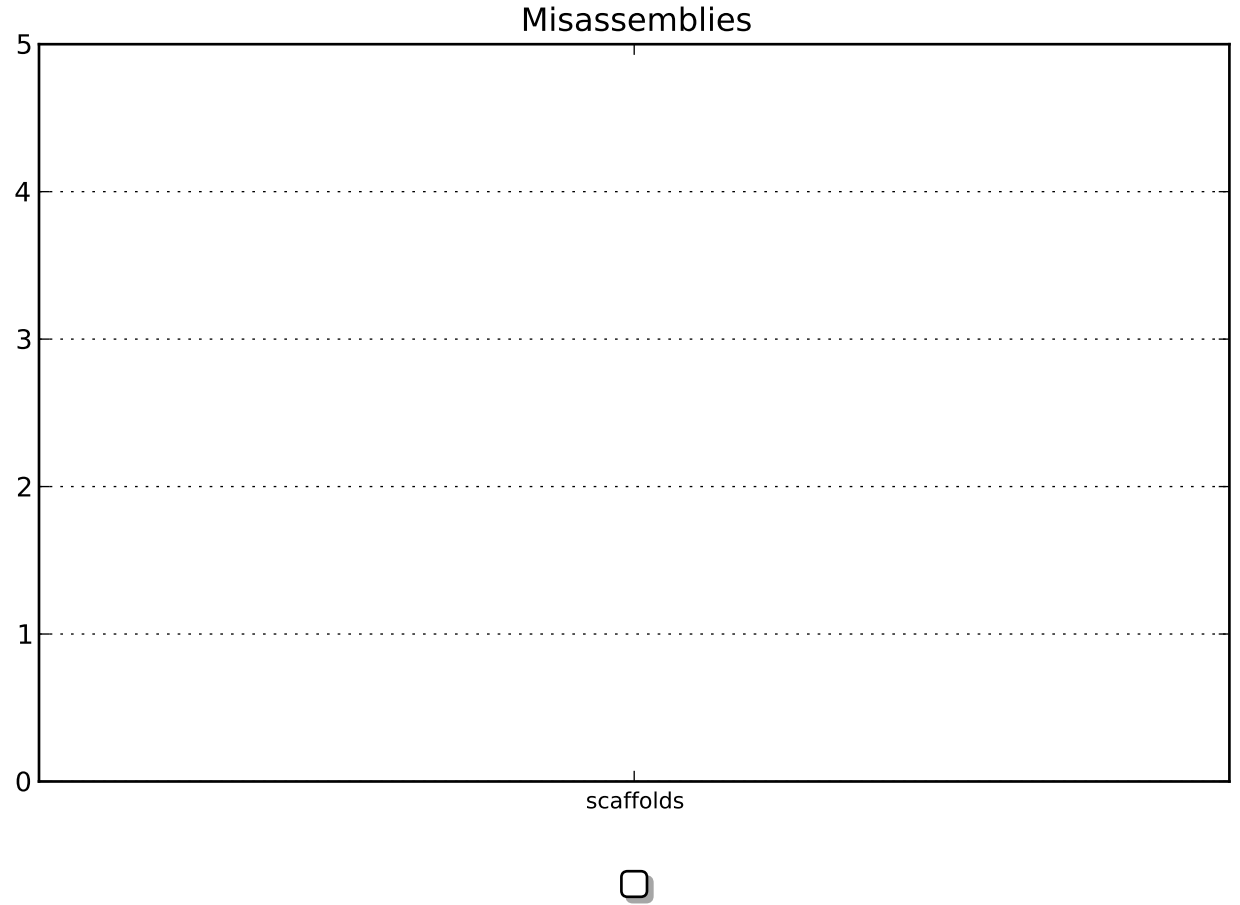
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

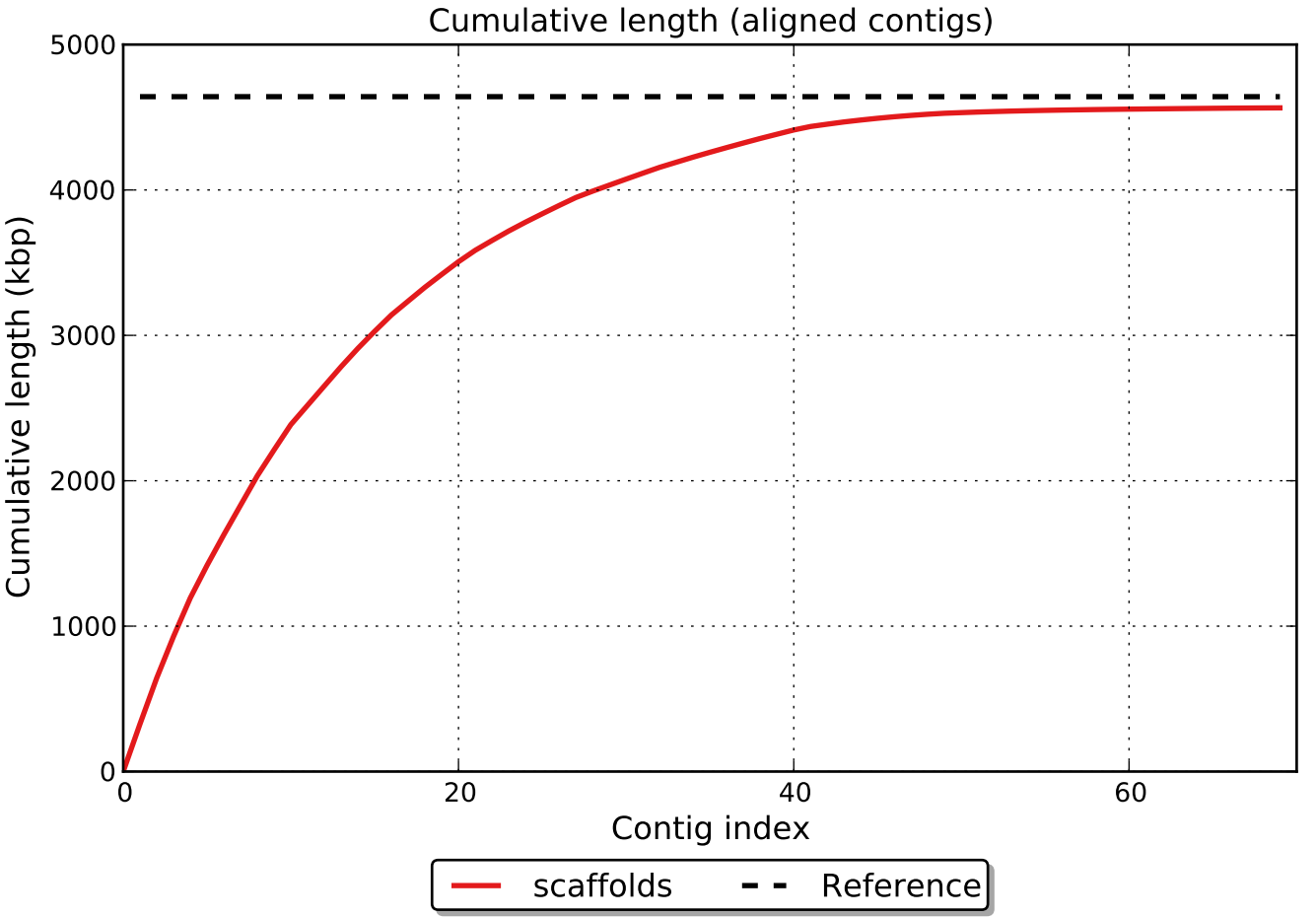

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

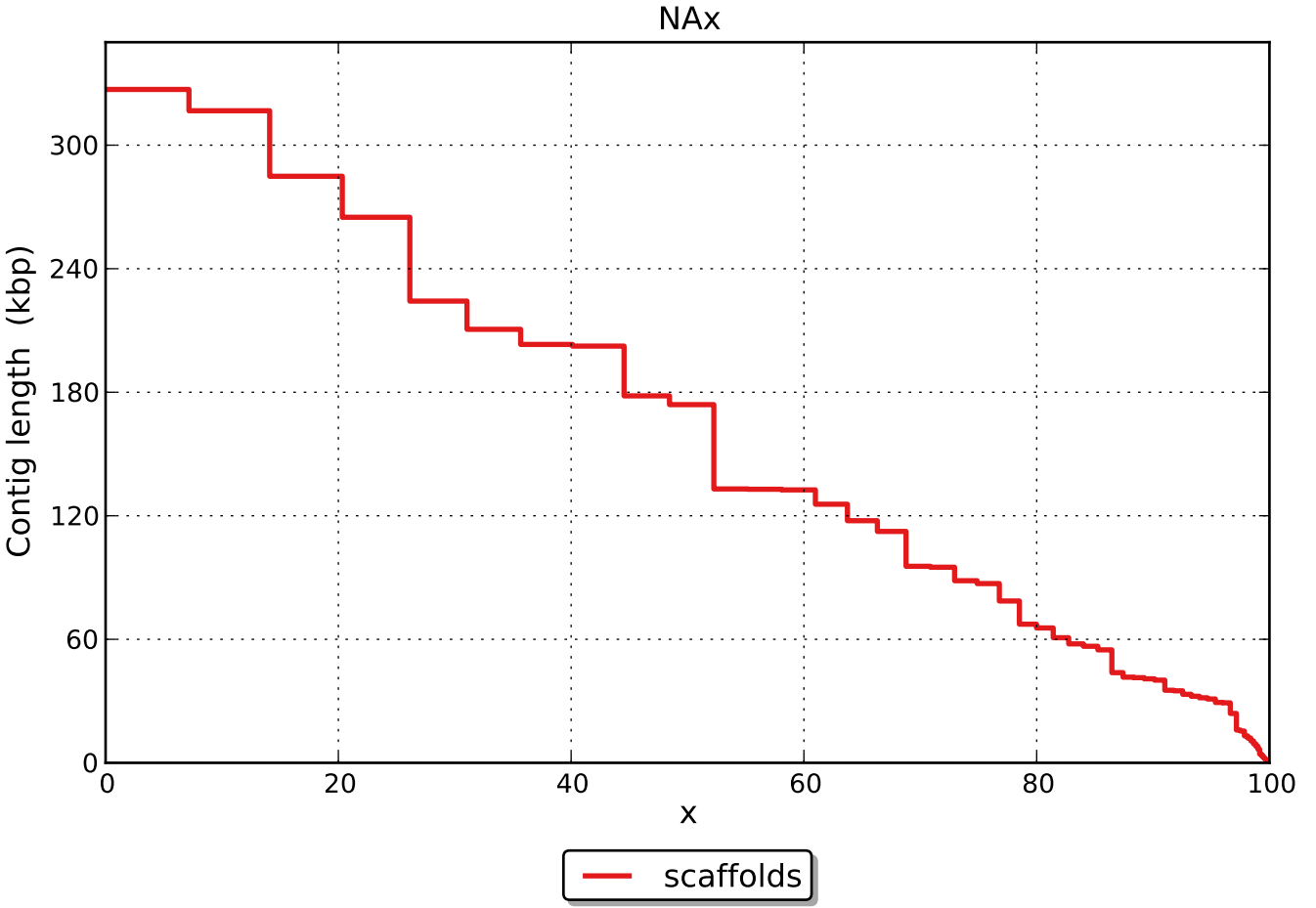

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

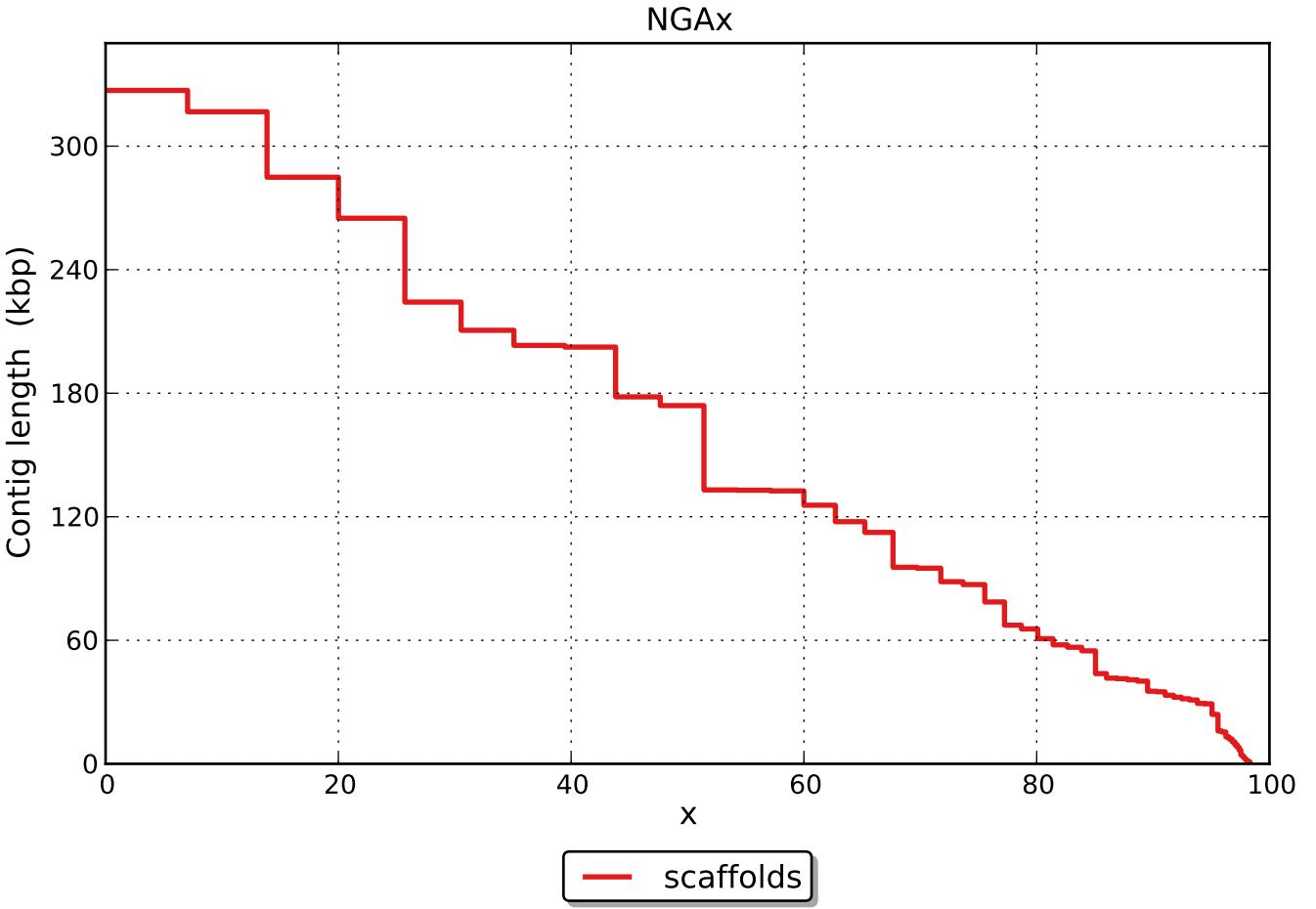

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
Contig index
scaffolds
Reference


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


Misassemblies
5
4
3
2
1
0
scaffolds


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