Report

	scaffolds
# contigs (>= 1000 bp)	61
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	45
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4521804
Total length (>= 5000 bp)	4498456
Total length (>= 10000 bp)	4464986
Total length (>= 25000 bp)	4365334
Total length (>= 50000 bp)	3956668
# contigs	69
Largest contig	333130
Total length	4527443
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	161095
NG50	161095
N75	86002
NG75	81925
L50	11
LG50	11
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.530
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	148.73
# indels per 100 kbp	0.33
Largest alignment	333130
NA50	161095
NGA50	161095
NA75	86002
NGA75	81925
LA50	11
LGA50	11
LA75	20
LGA75	21

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

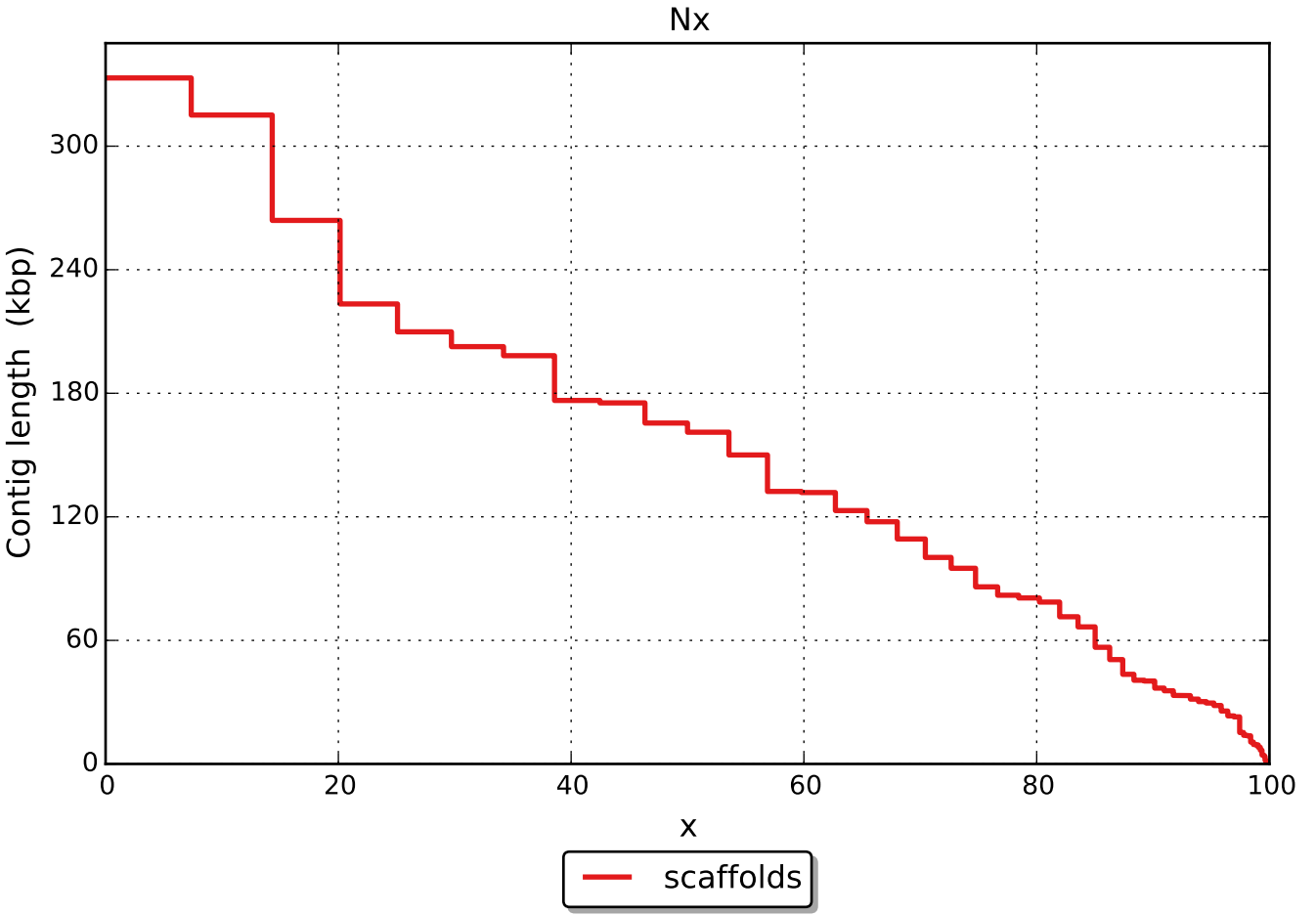
	scaffolds
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	36823
# local misassemblies	1
# mismatches	6733
# indels	15
# short indels	15
# long indels	0
Indels length	16

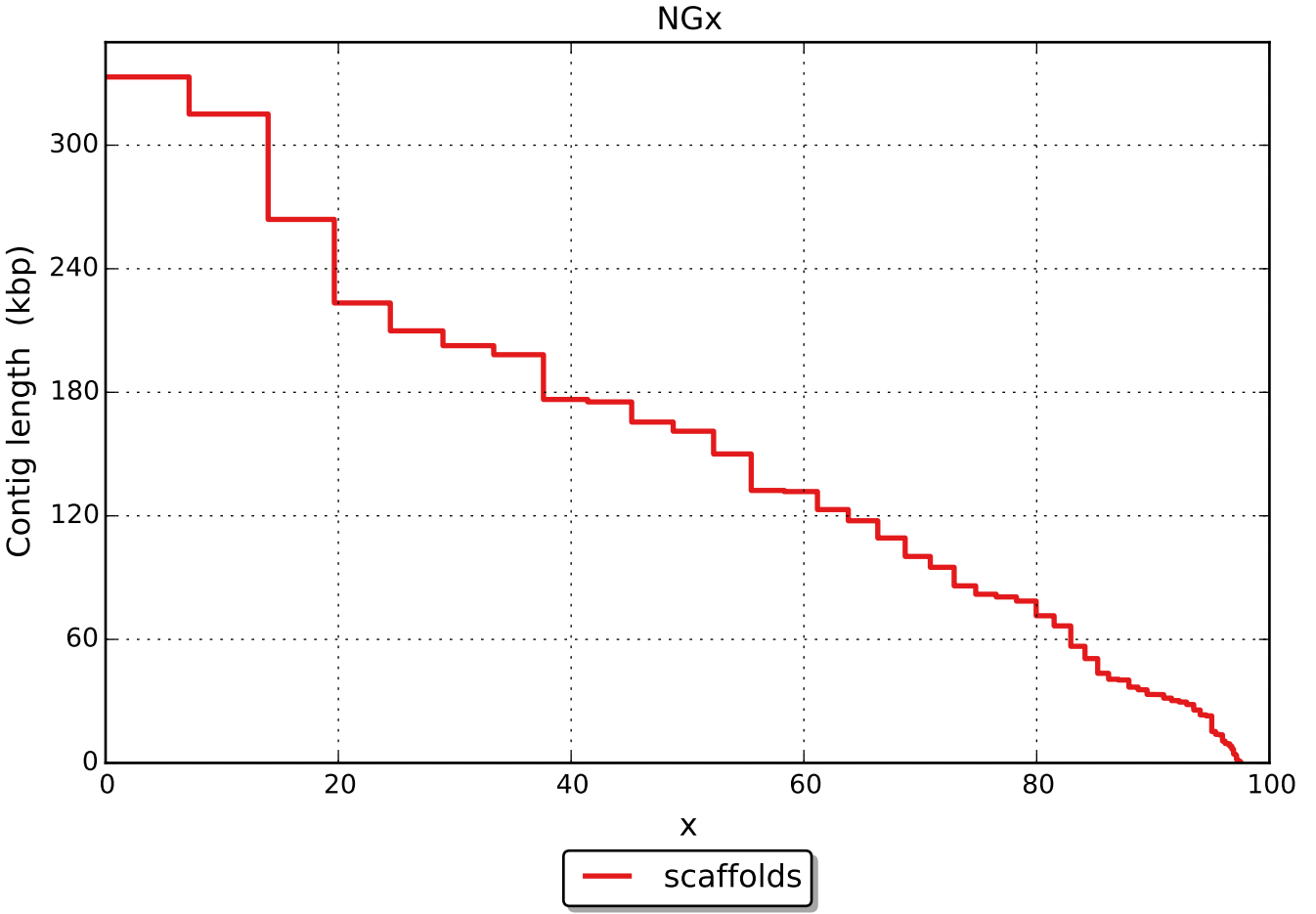
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

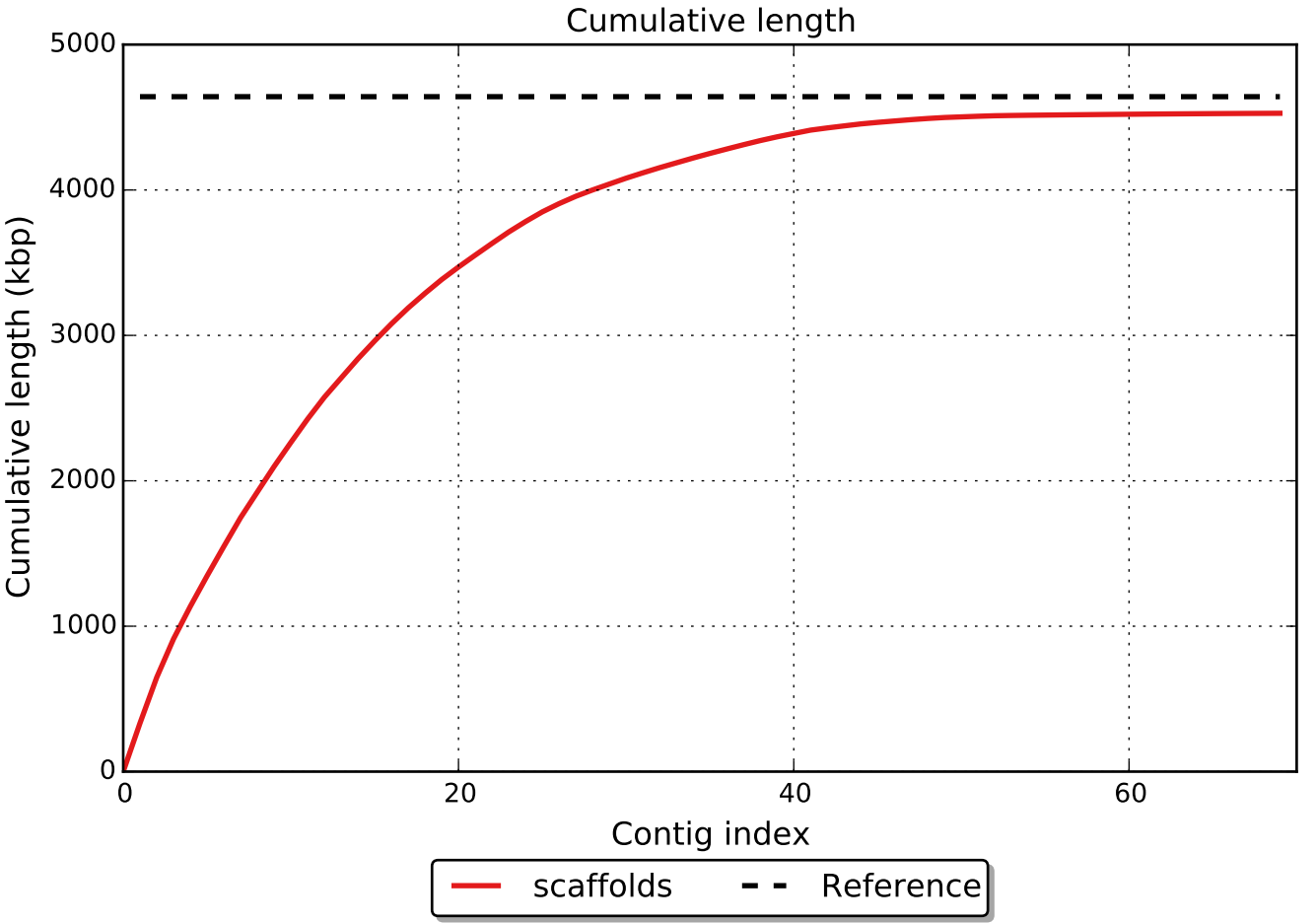
Unaligned report

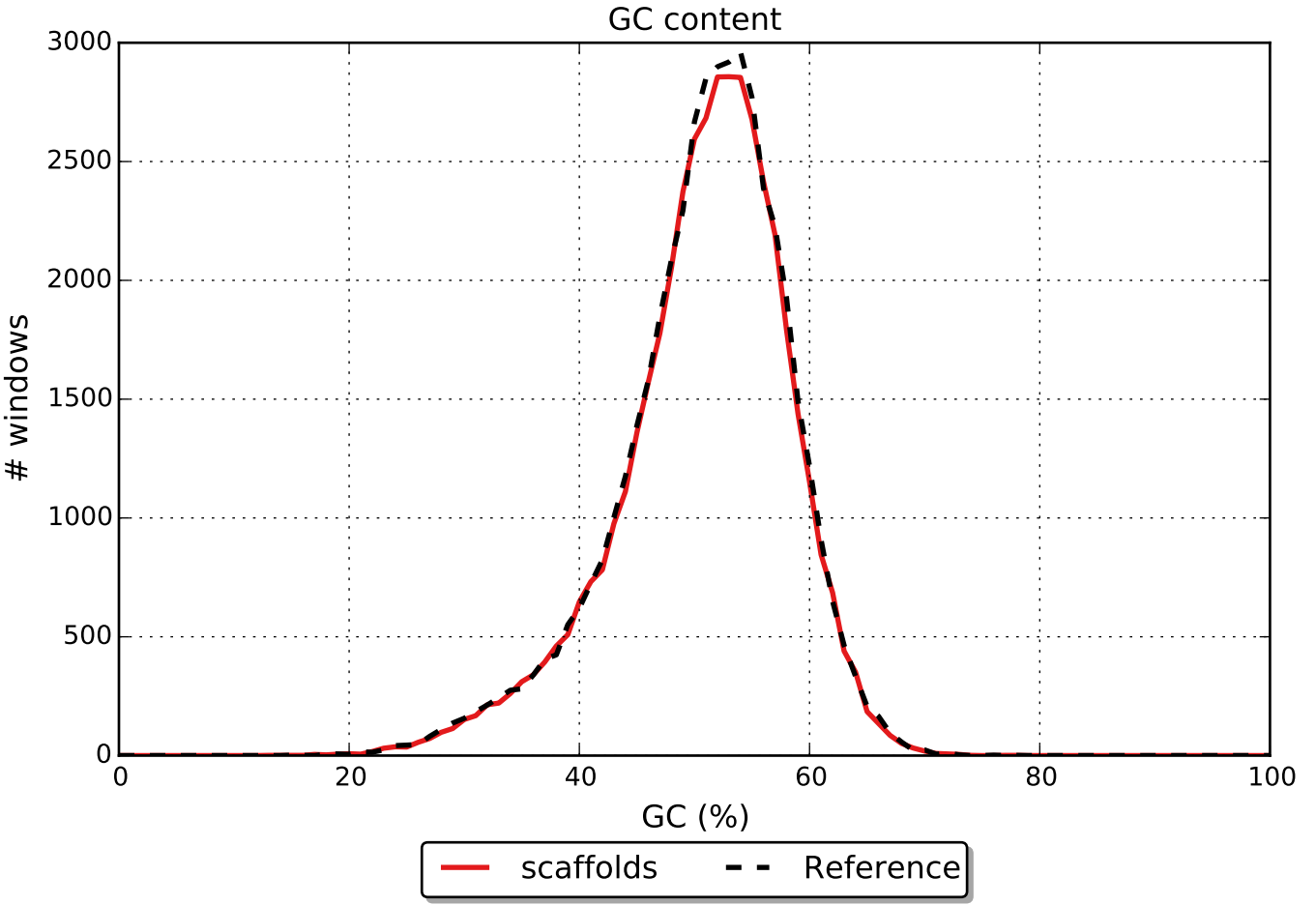
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

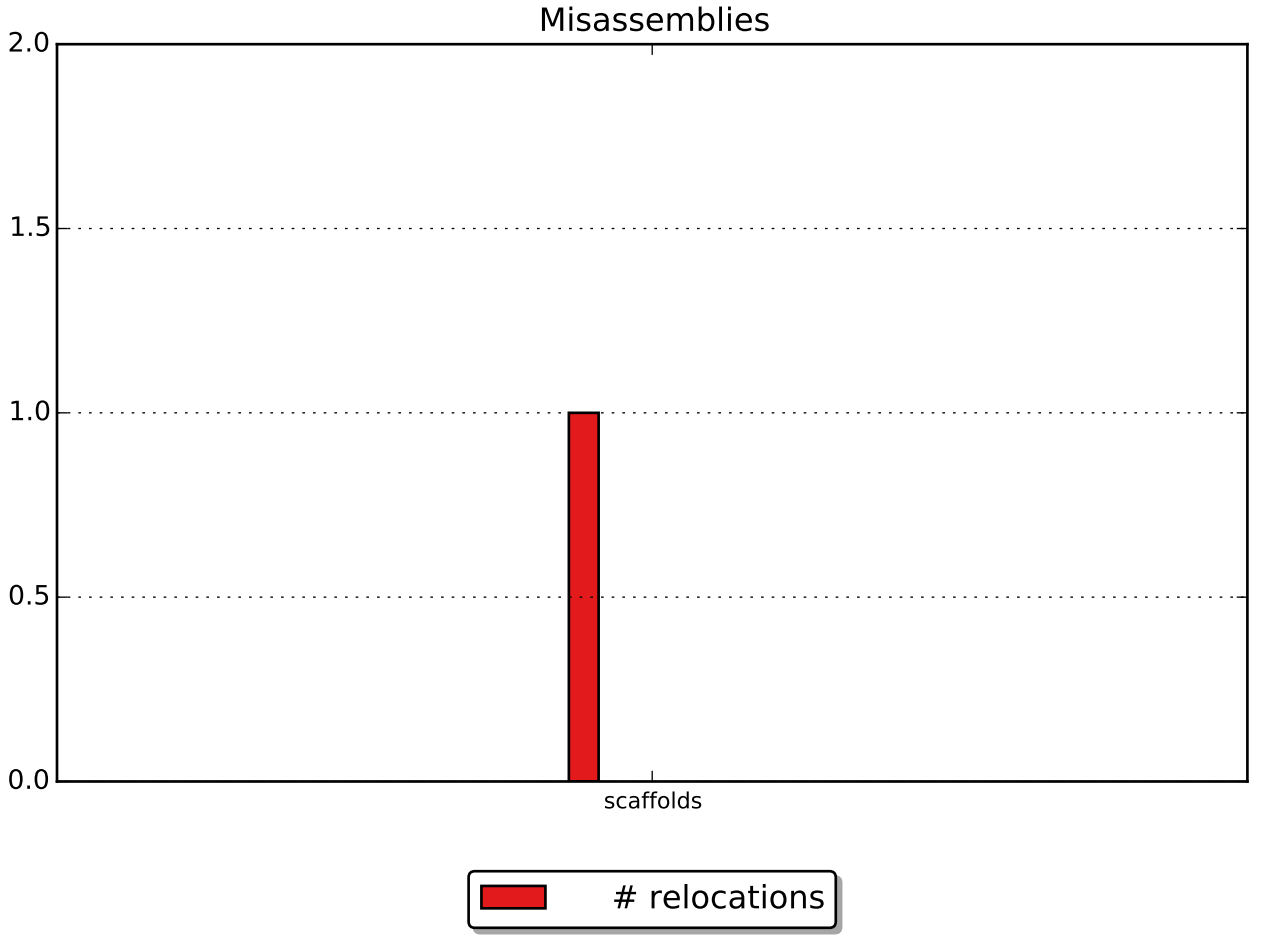
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

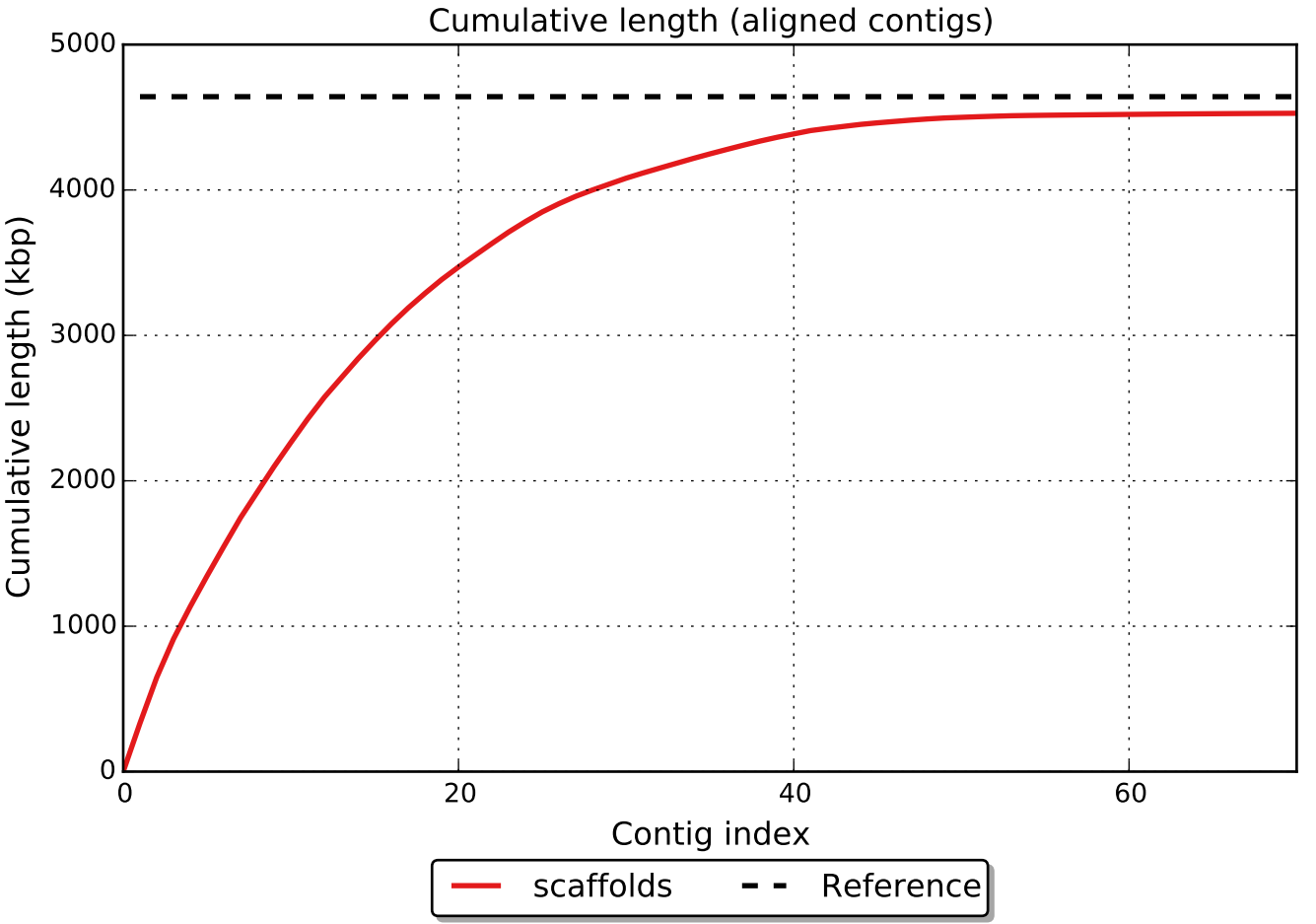

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

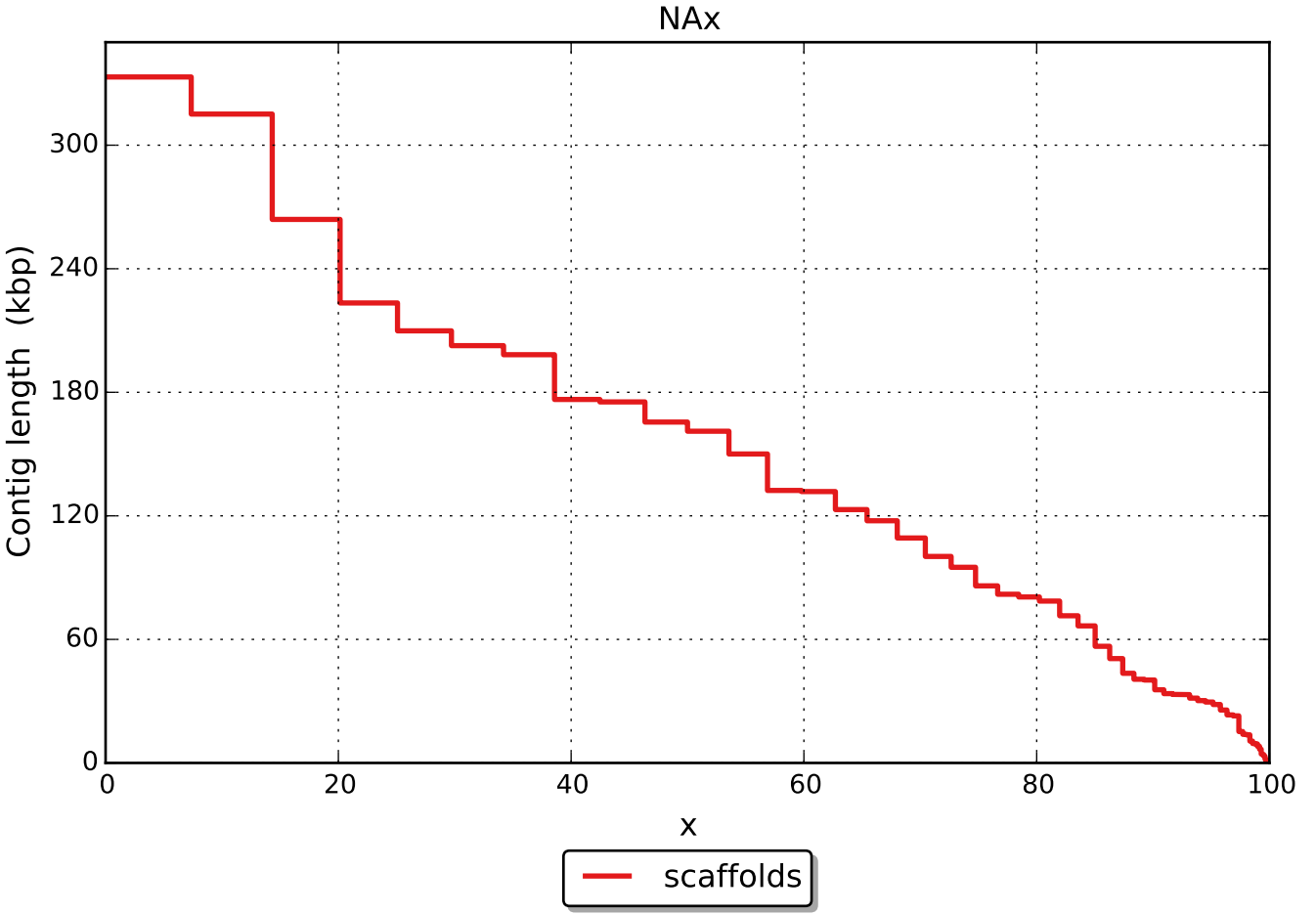

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

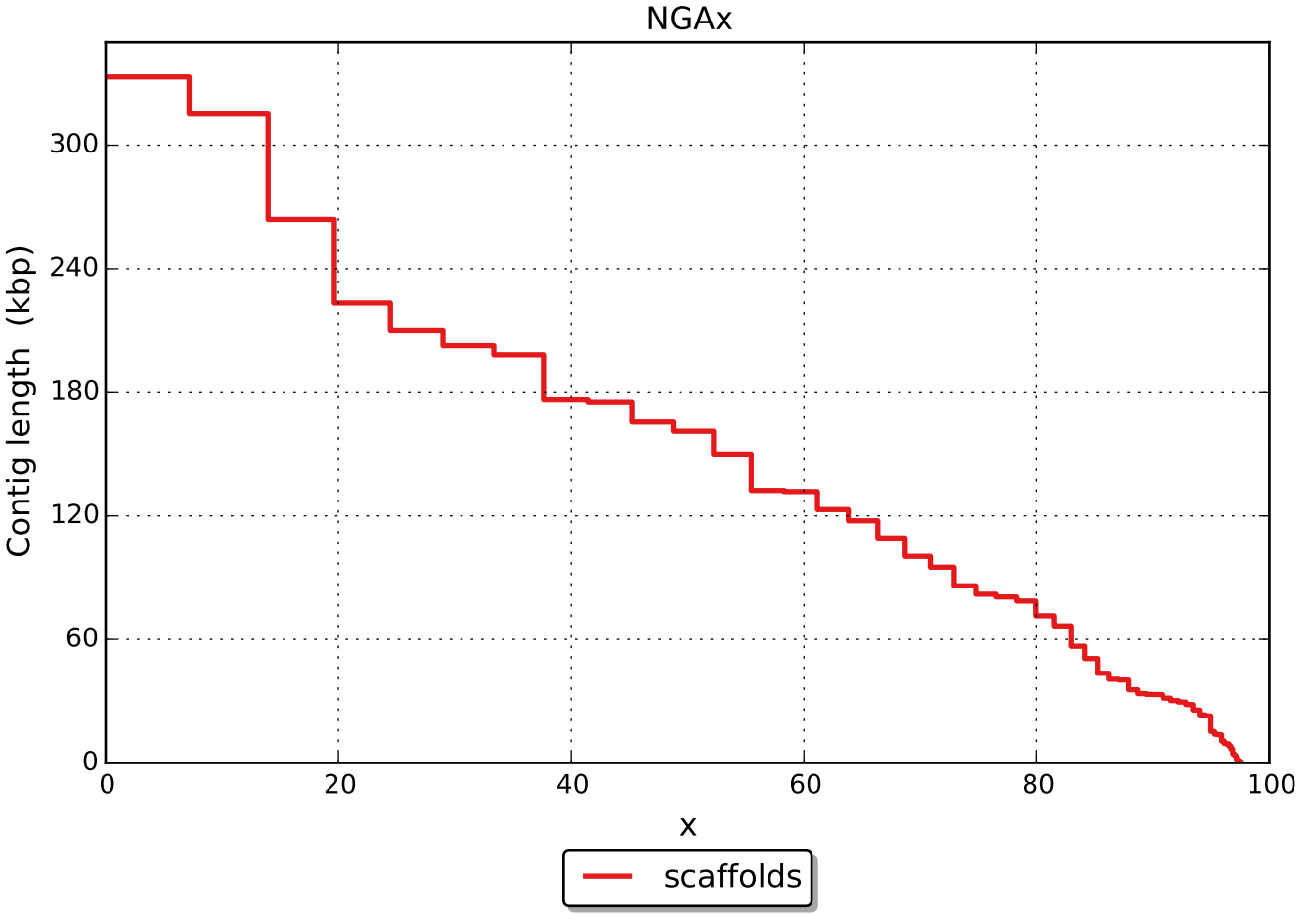

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
Contig index
scaffolds
Reference


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