Report

	scaffolds
# contigs (>= 1000 bp)	56
# contigs (>= 5000 bp)	47
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	29
Total length (>= 1000 bp)	4824082
Total length (>= 5000 bp)	4806169
Total length (>= 10000 bp)	4783142
Total length (>= 25000 bp)	4744192
Total length (>= 50000 bp)	4335349
# contigs	61
Largest contig	401996
Total length	4827693
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	174787
NG50	174787
N75	94470
NG75	109022
L50	10
LG50	10
L75	19
LG75	18
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	69931
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	290386
Genome fraction (%)	97.580
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	307.64
# indels per 100 kbp	0.71
Largest alignment	315025
NA50	154629
NGA50	165140
NA75	79549
NGA75	82473
LA50	12
LGA50	11
LA75	23
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

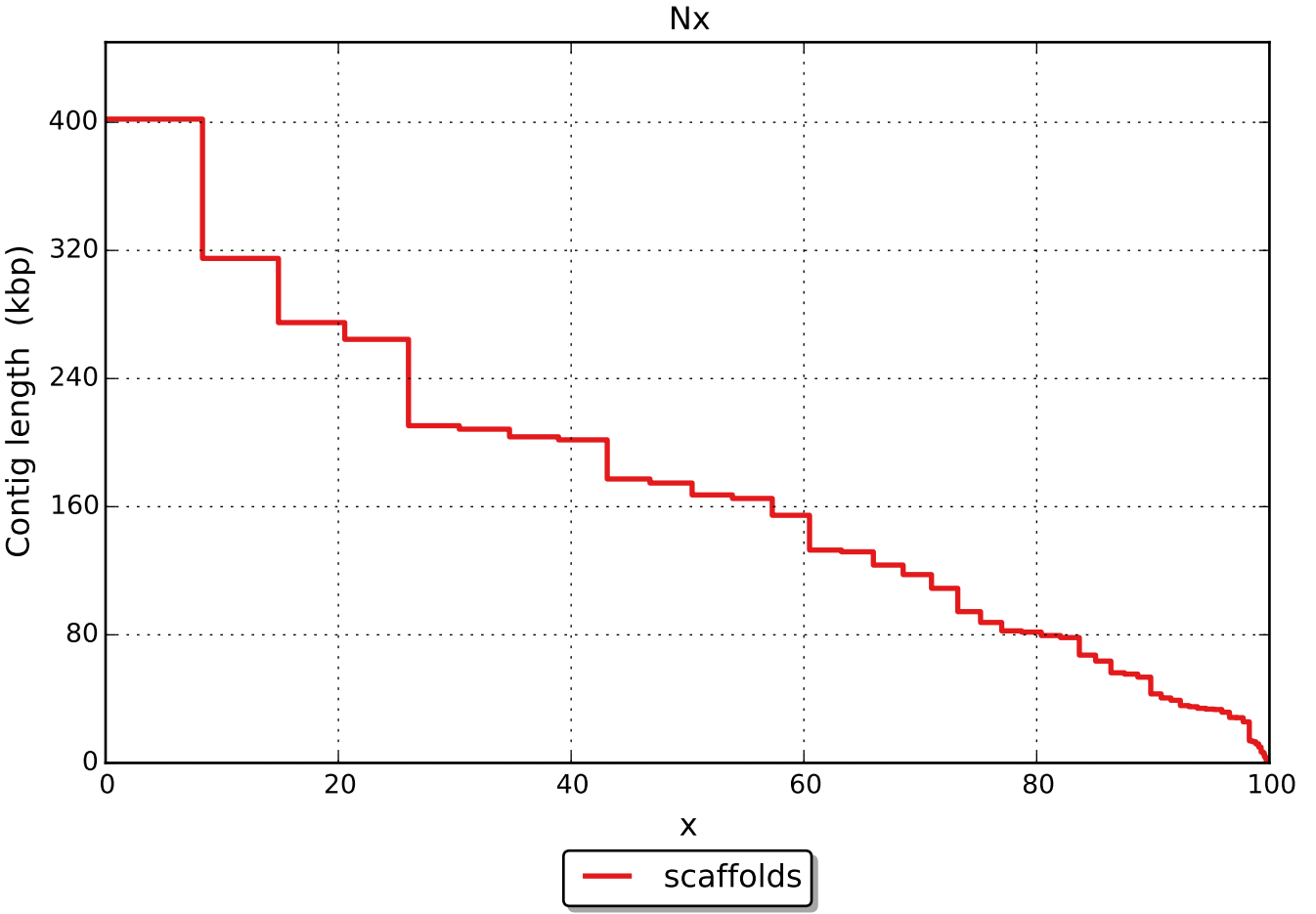
	scaffolds
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	2
Misassembled contigs length	69931
# local misassemblies	2
# mismatches	13934
# indels	32
# short indels	32
# long indels	0
Indels length	38

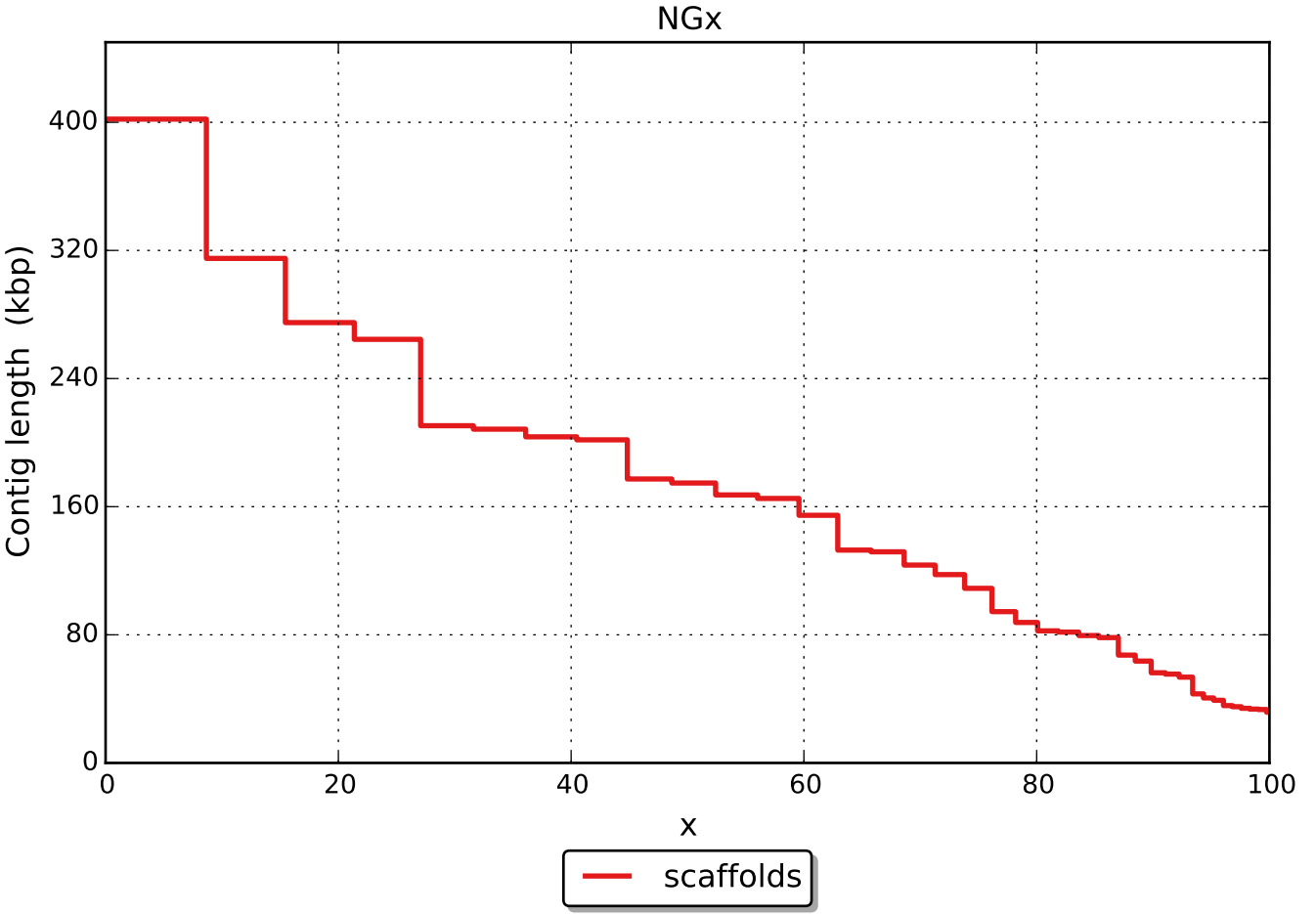
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

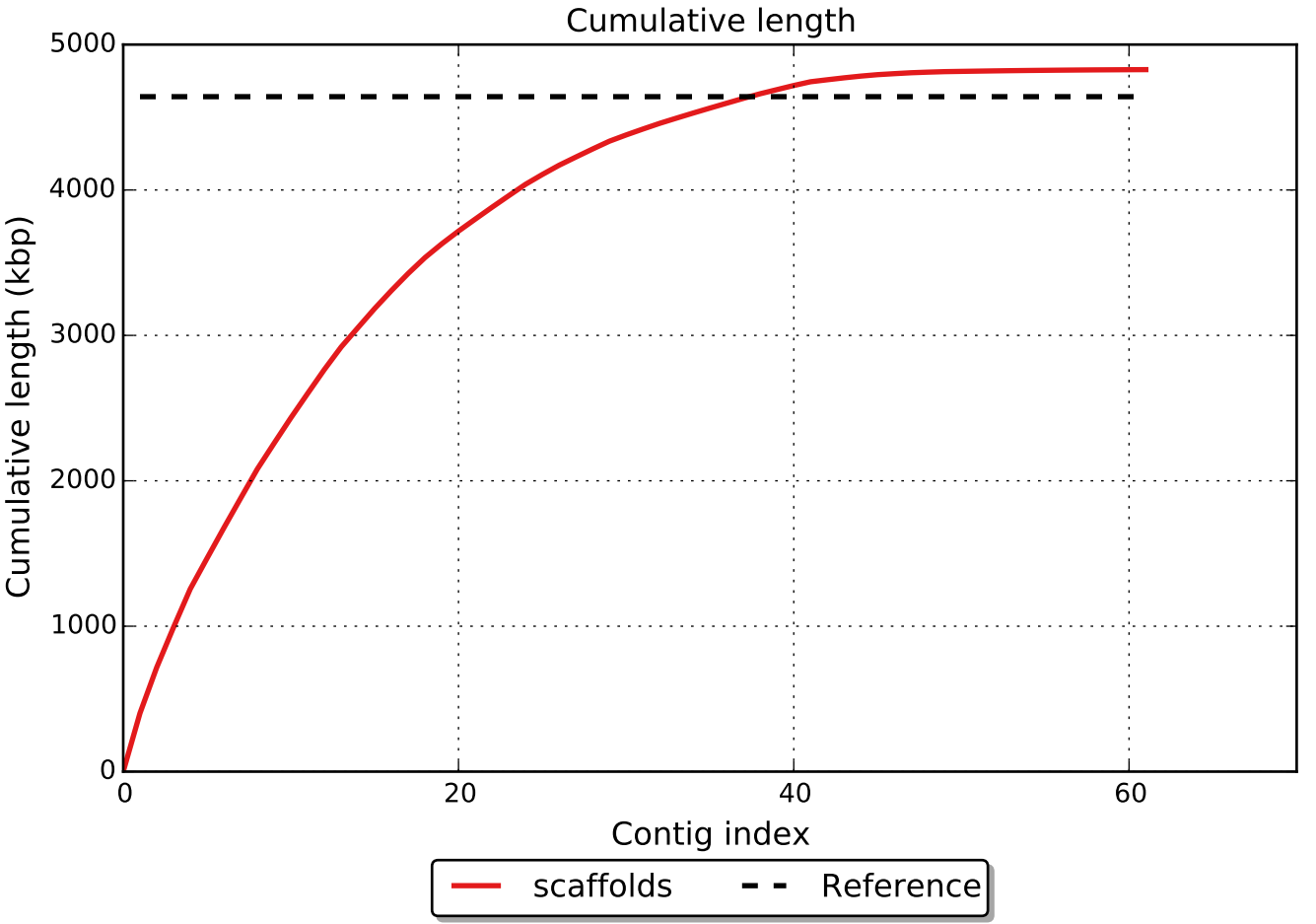
Unaligned report

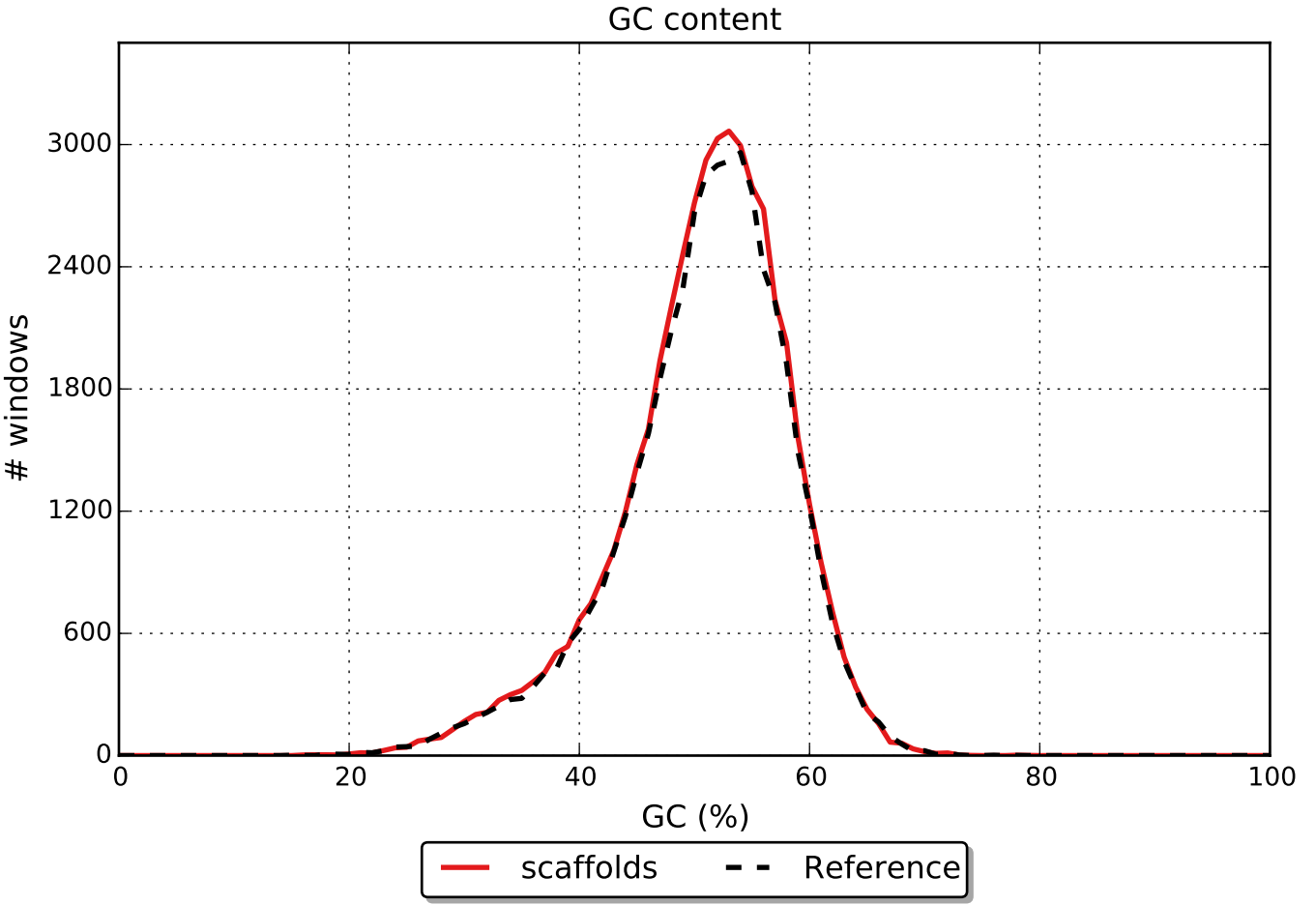
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	1
# both parts are significant	1
Partially unaligned length	290386
# N's	0

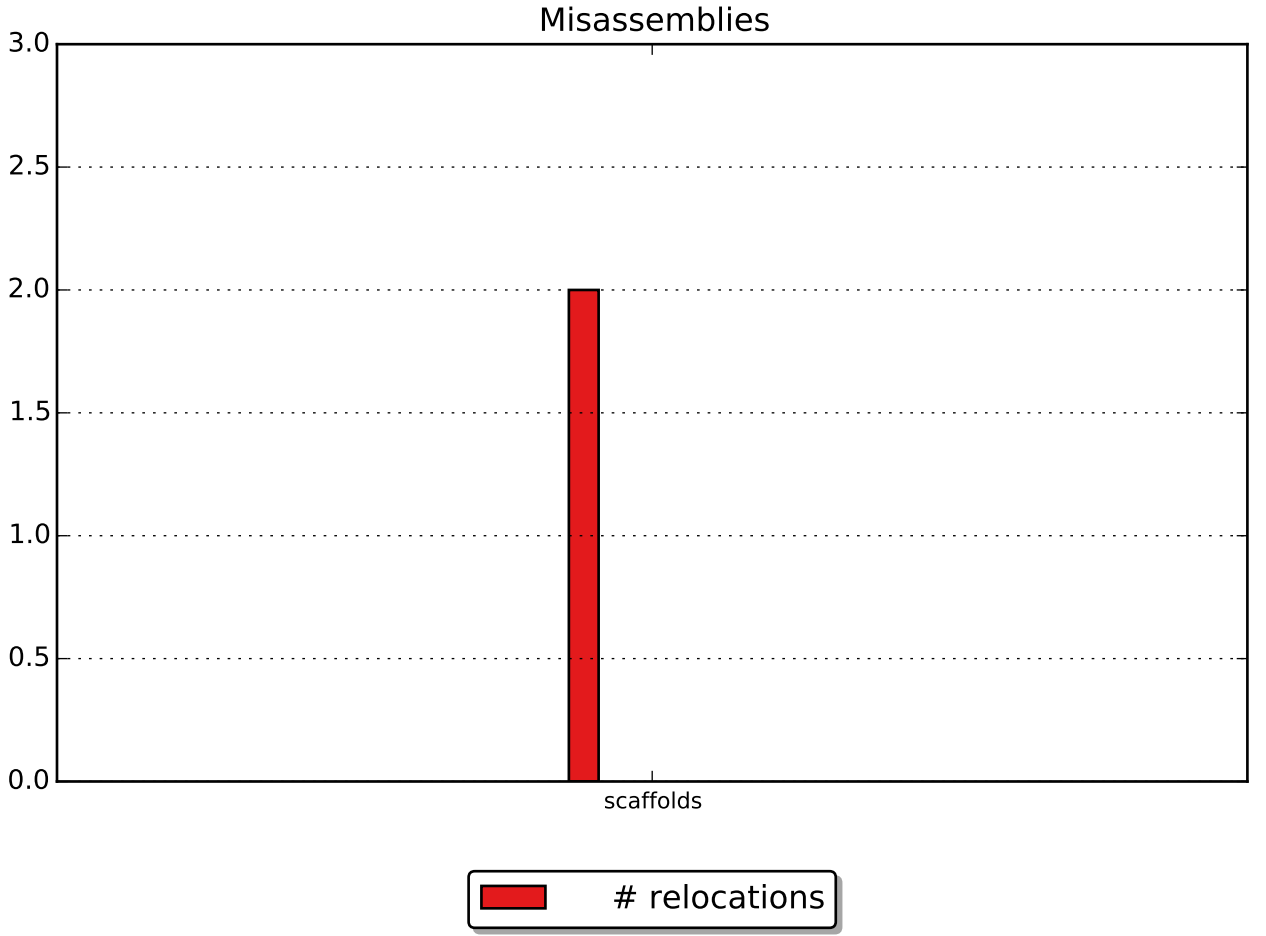
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

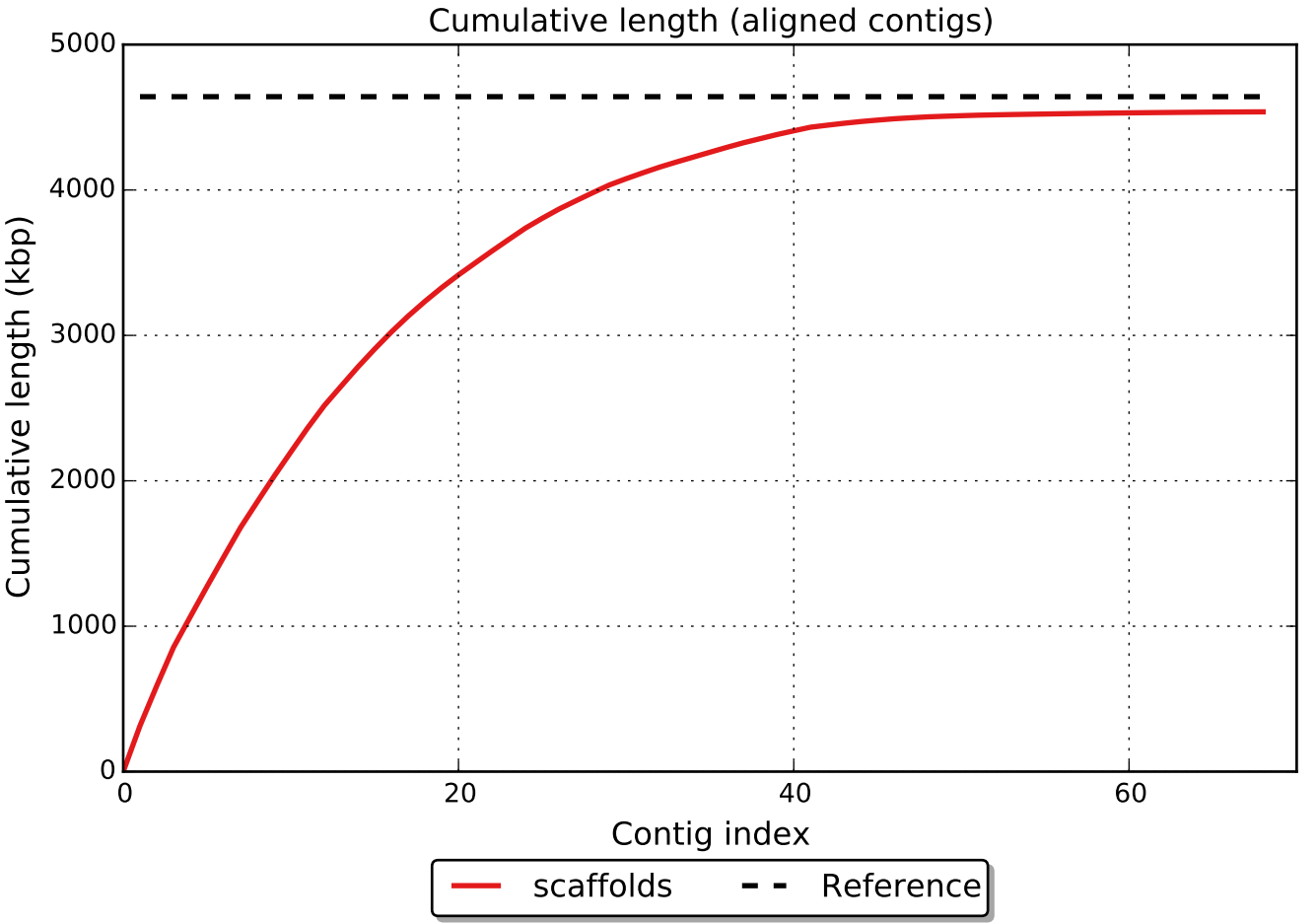

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
scaffolds

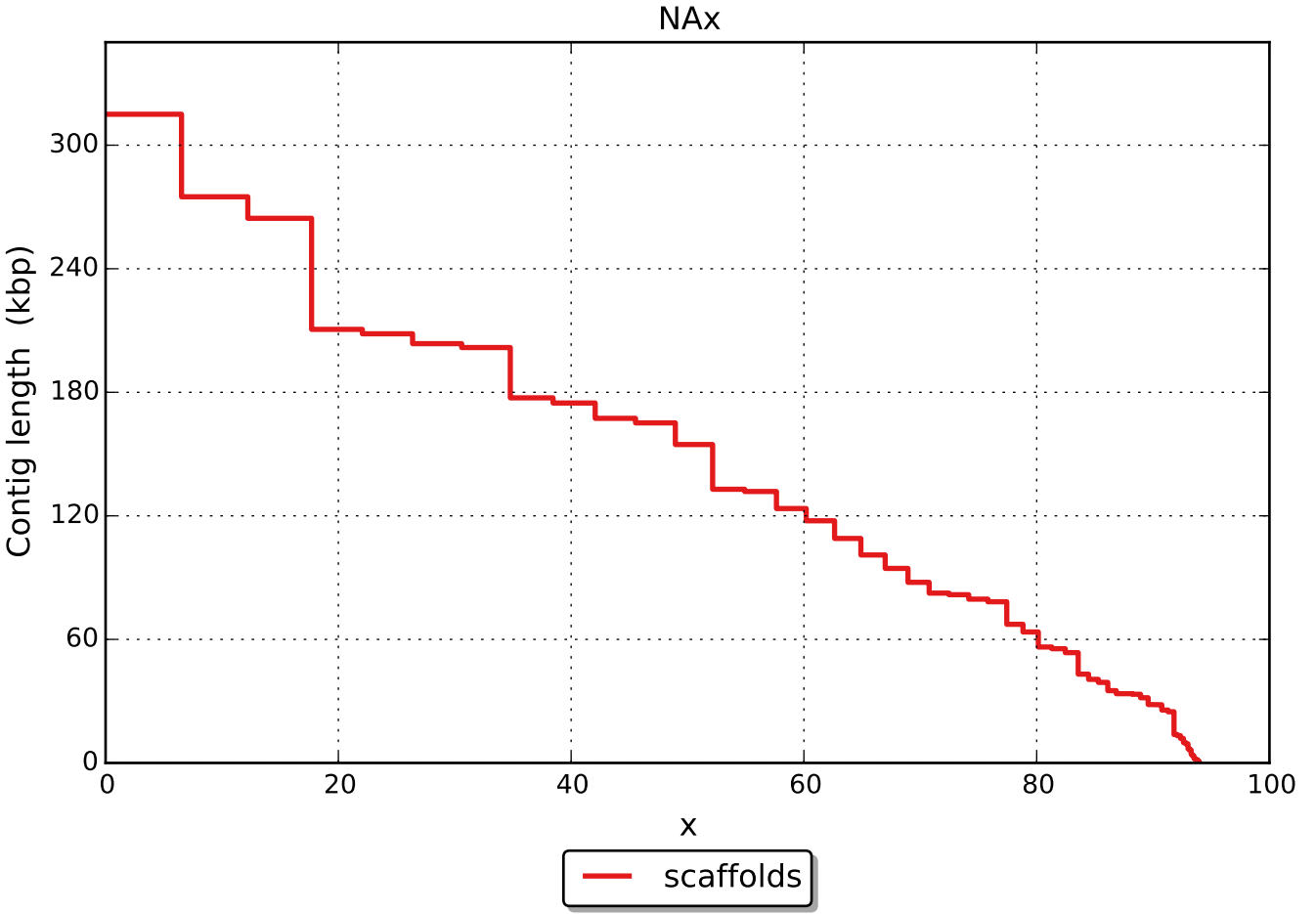

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
scaffolds

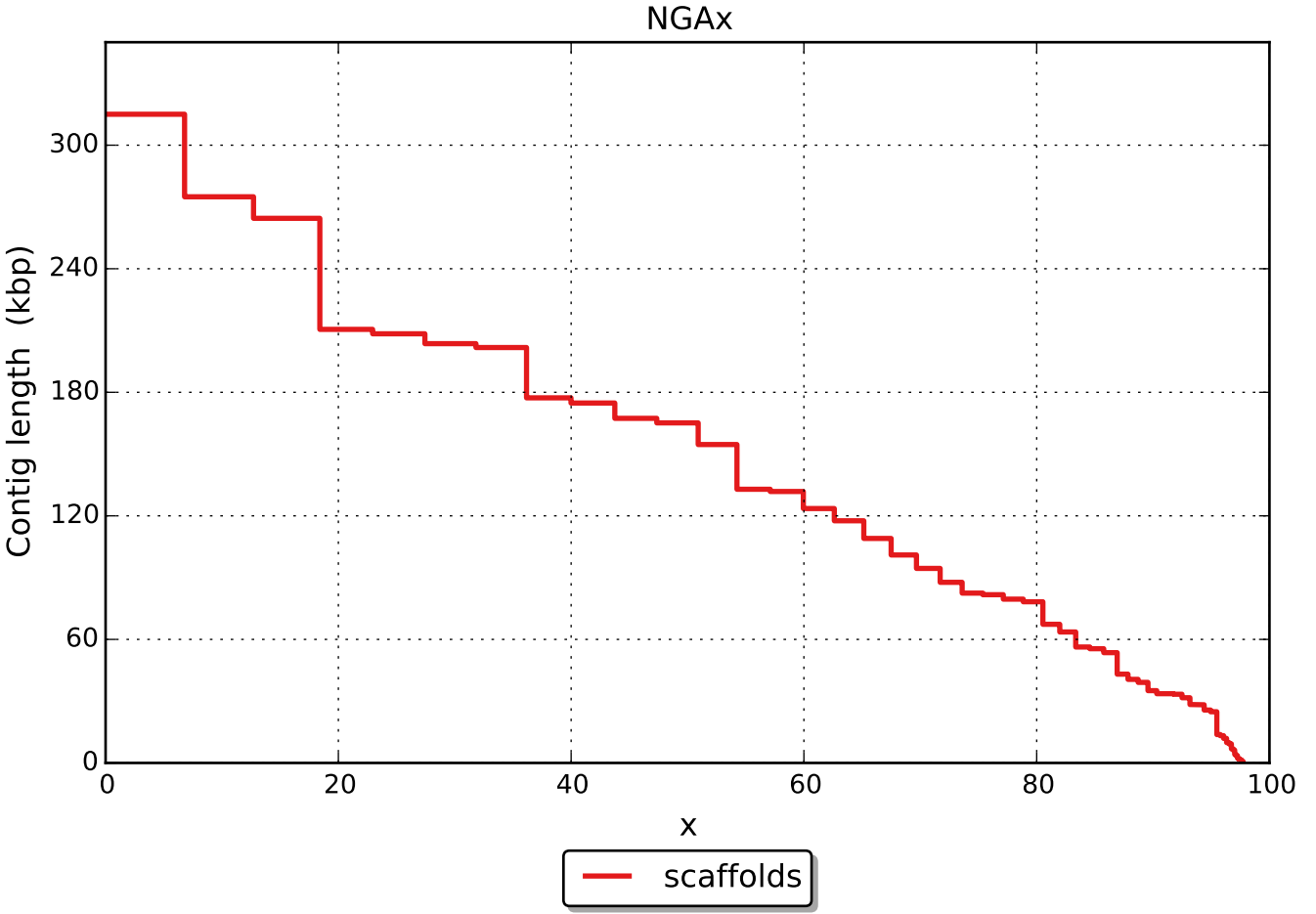

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
Contig index
scaffolds
Reference


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


Misassemblies
3.0
2.5
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