Report

	scaffolds
# contigs (>= 1000 bp)	58
# contigs (>= 5000 bp)	40
# contigs (>= 10000 bp)	33
# contigs (>= 25000 bp)	24
# contigs (>= 50000 bp)	14
Total length (>= 1000 bp)	1921718
Total length (>= 5000 bp)	1881948
Total length (>= 10000 bp)	1835177
Total length (>= 25000 bp)	1688556
Total length (>= 50000 bp)	1354204
# contigs	62
Largest contig	264572
Total length	1924924
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	74344
N75	35258
L50	8
L75	17
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	307071
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	41.398
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	545.55
# indels per 100 kbp	0.88
Largest alignment	264572
NA50	73015
NGA50	-
NA75	35258
LA50	9
LA75	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).

Misassemblies report

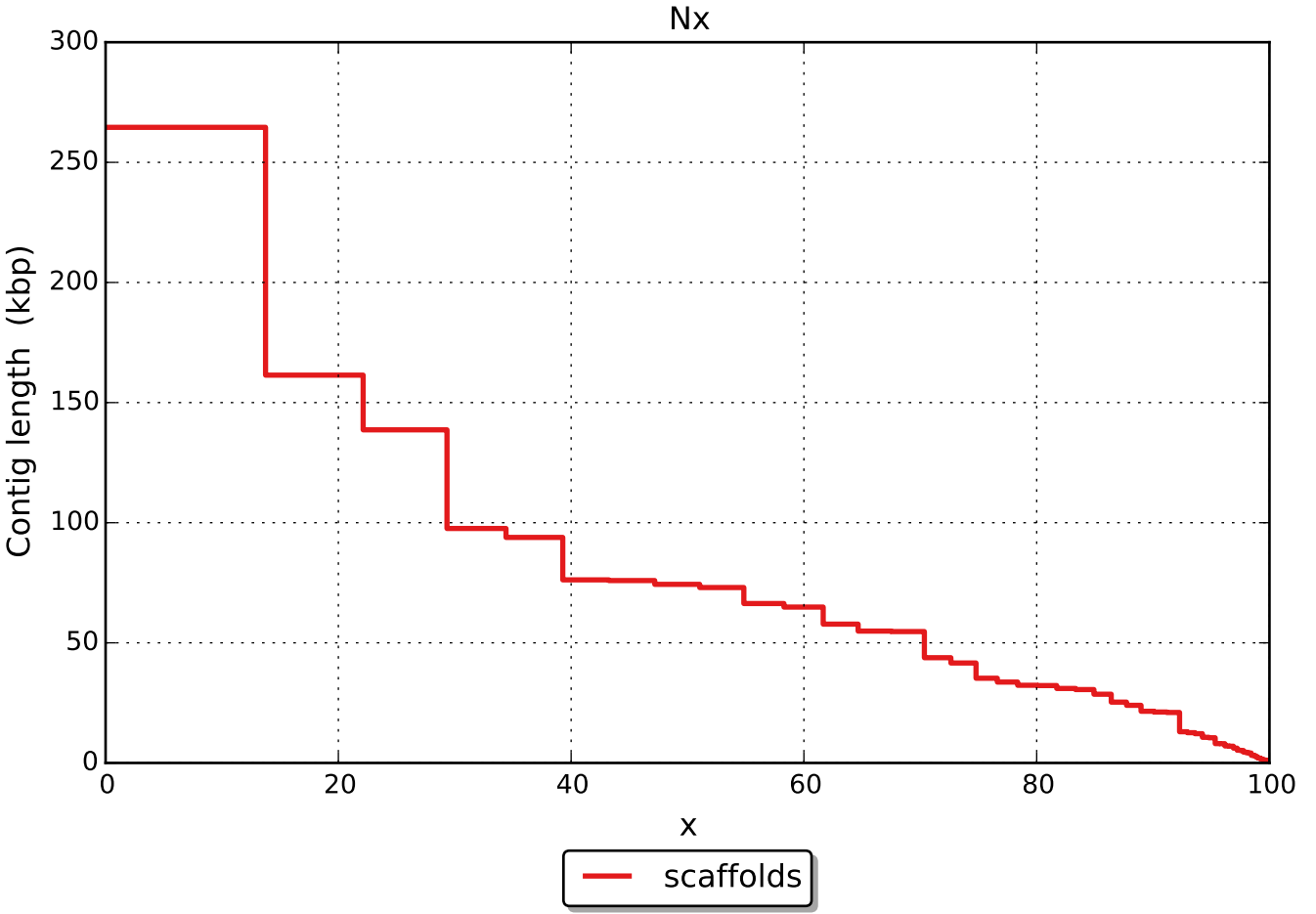
	scaffolds
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	307071
# local misassemblies	1
# mismatches	10483
# indels	17
# short indels	17
# long indels	0
Indels length	23

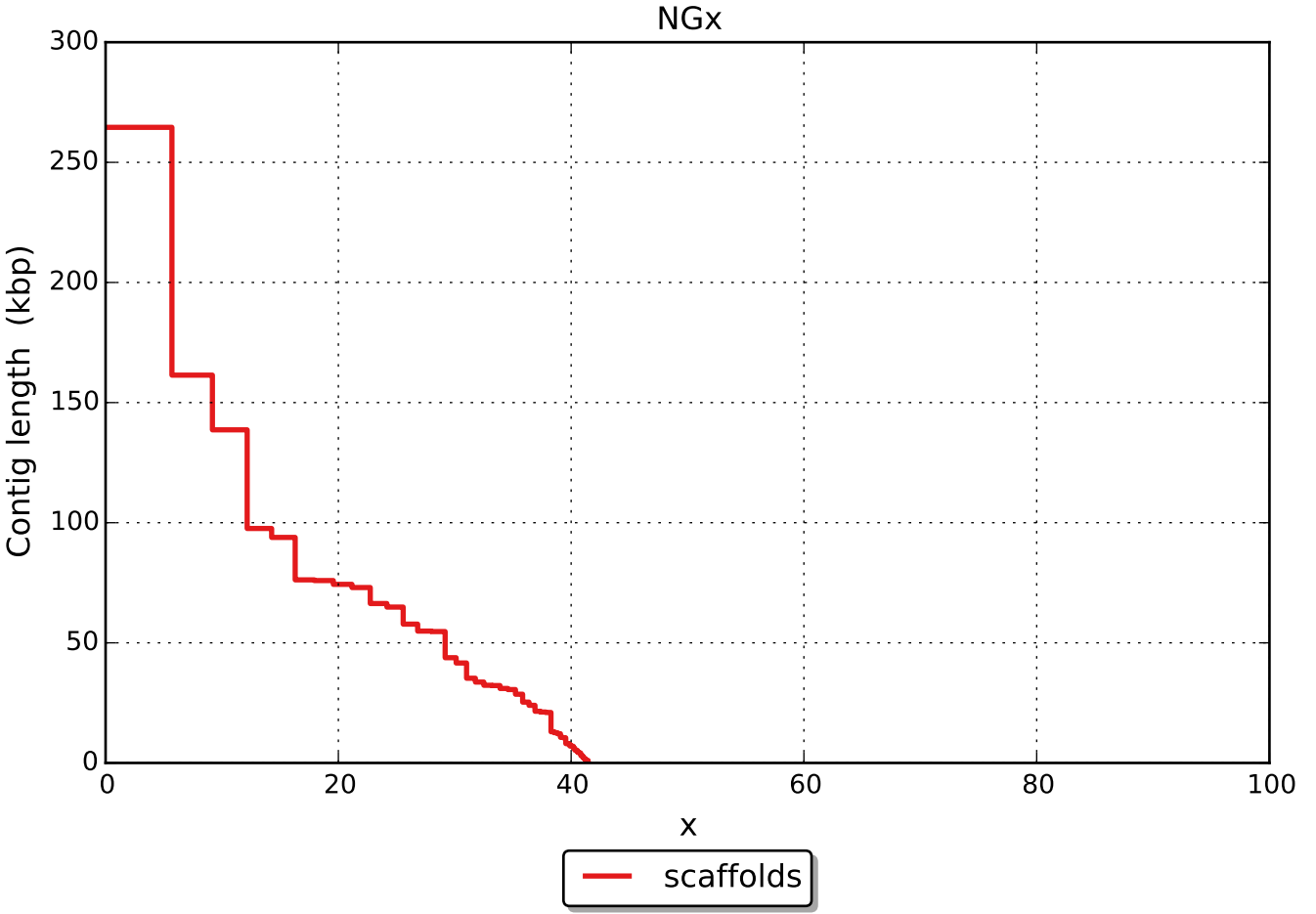
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

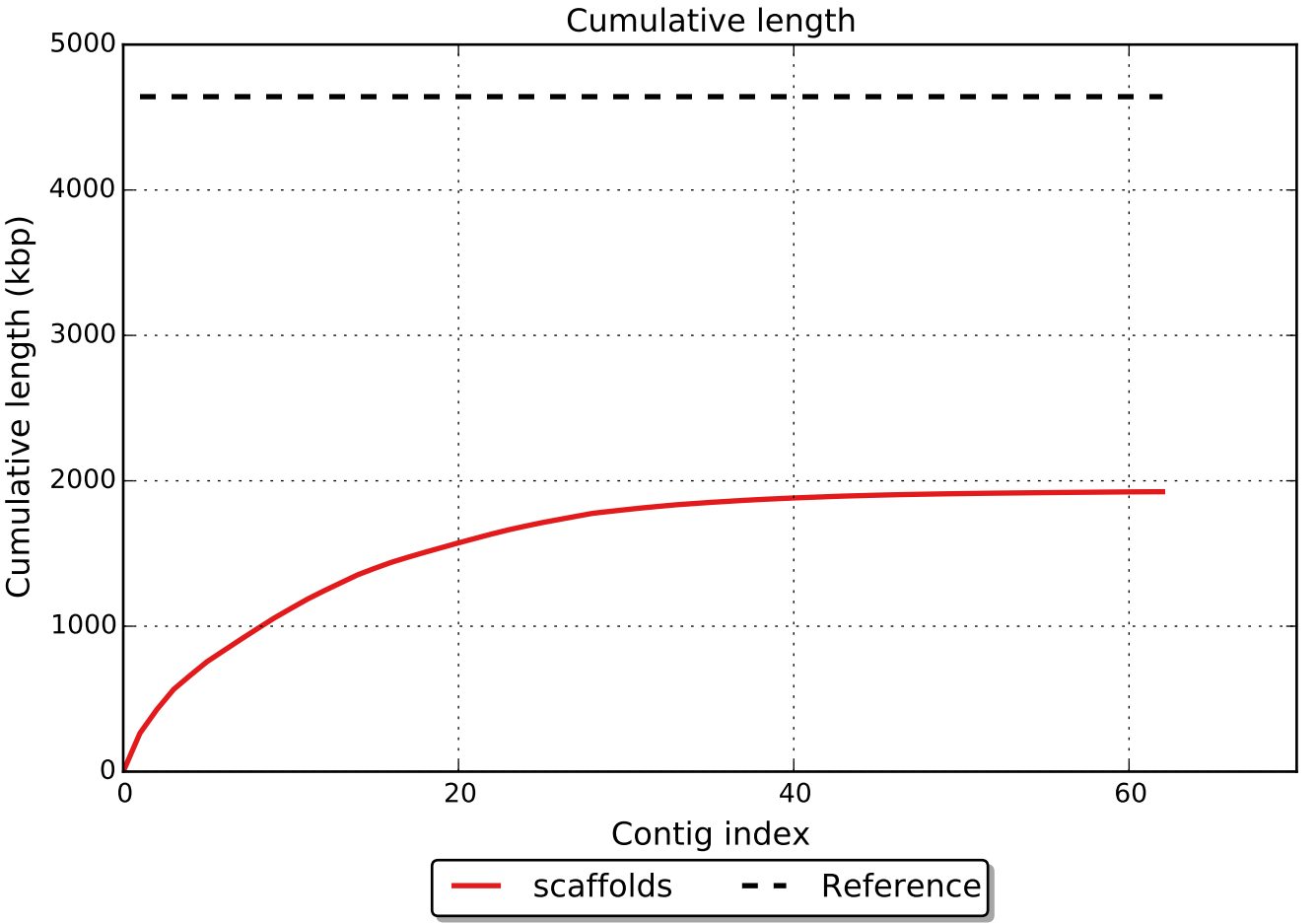
Unaligned report

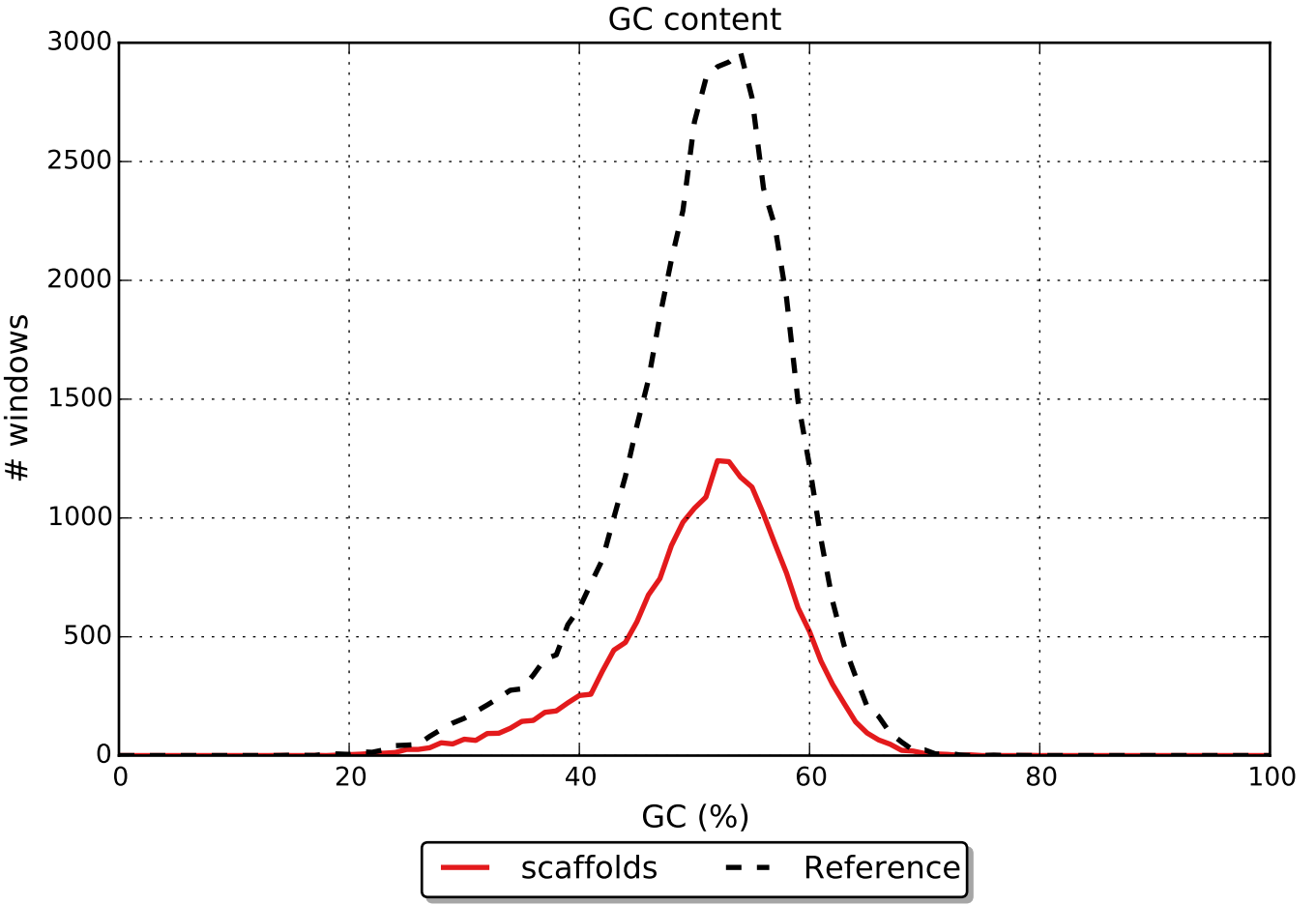
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

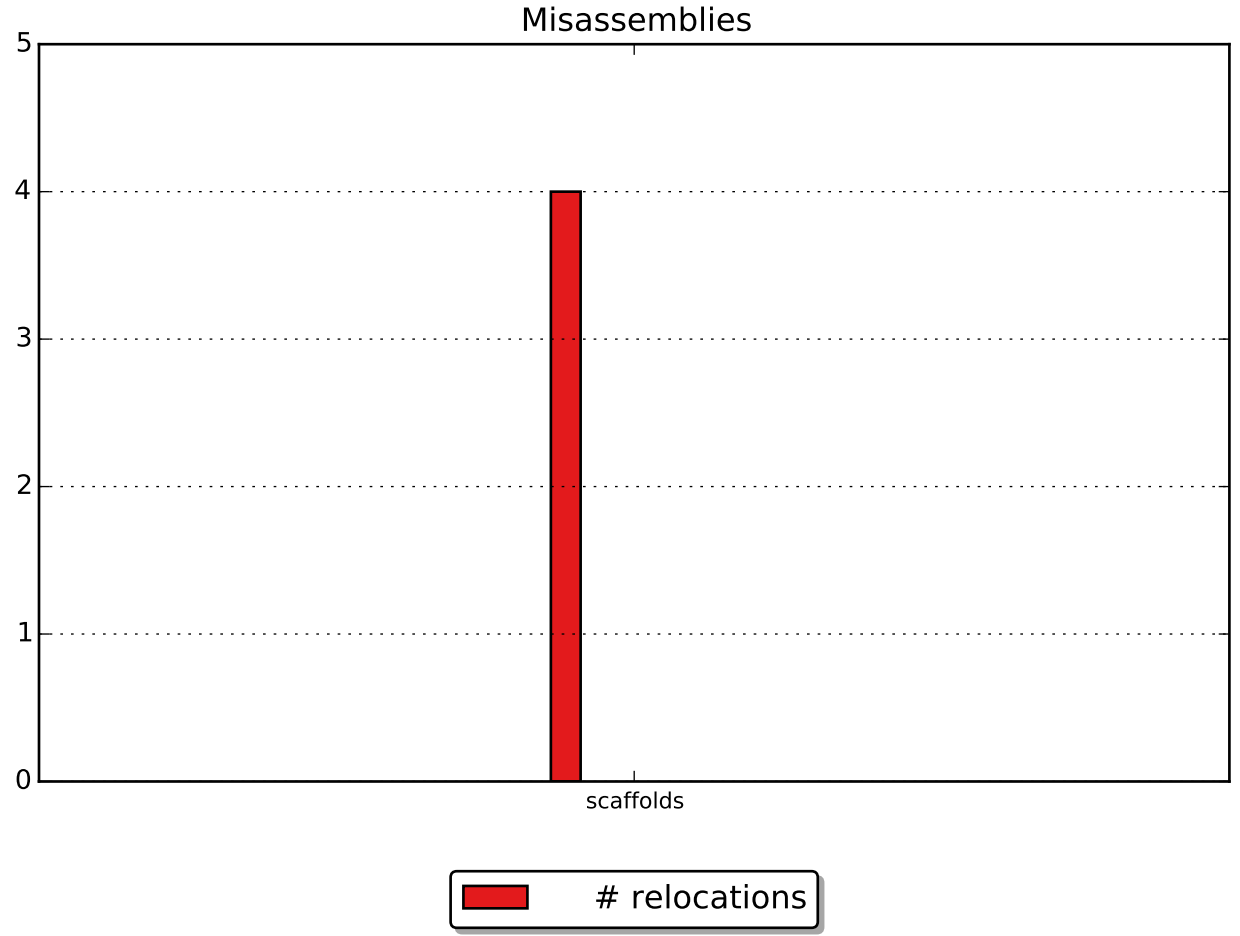
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

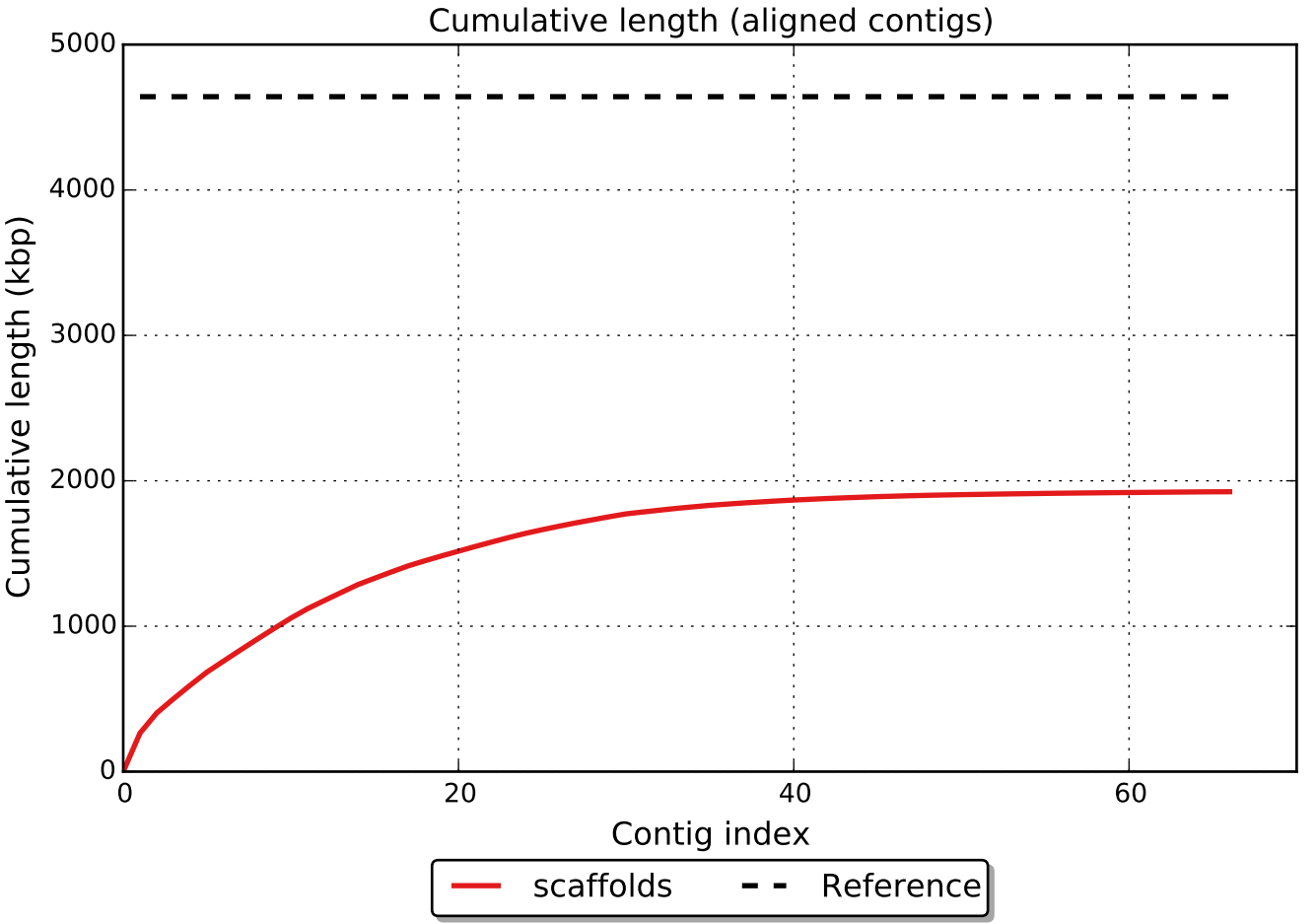

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
scaffolds

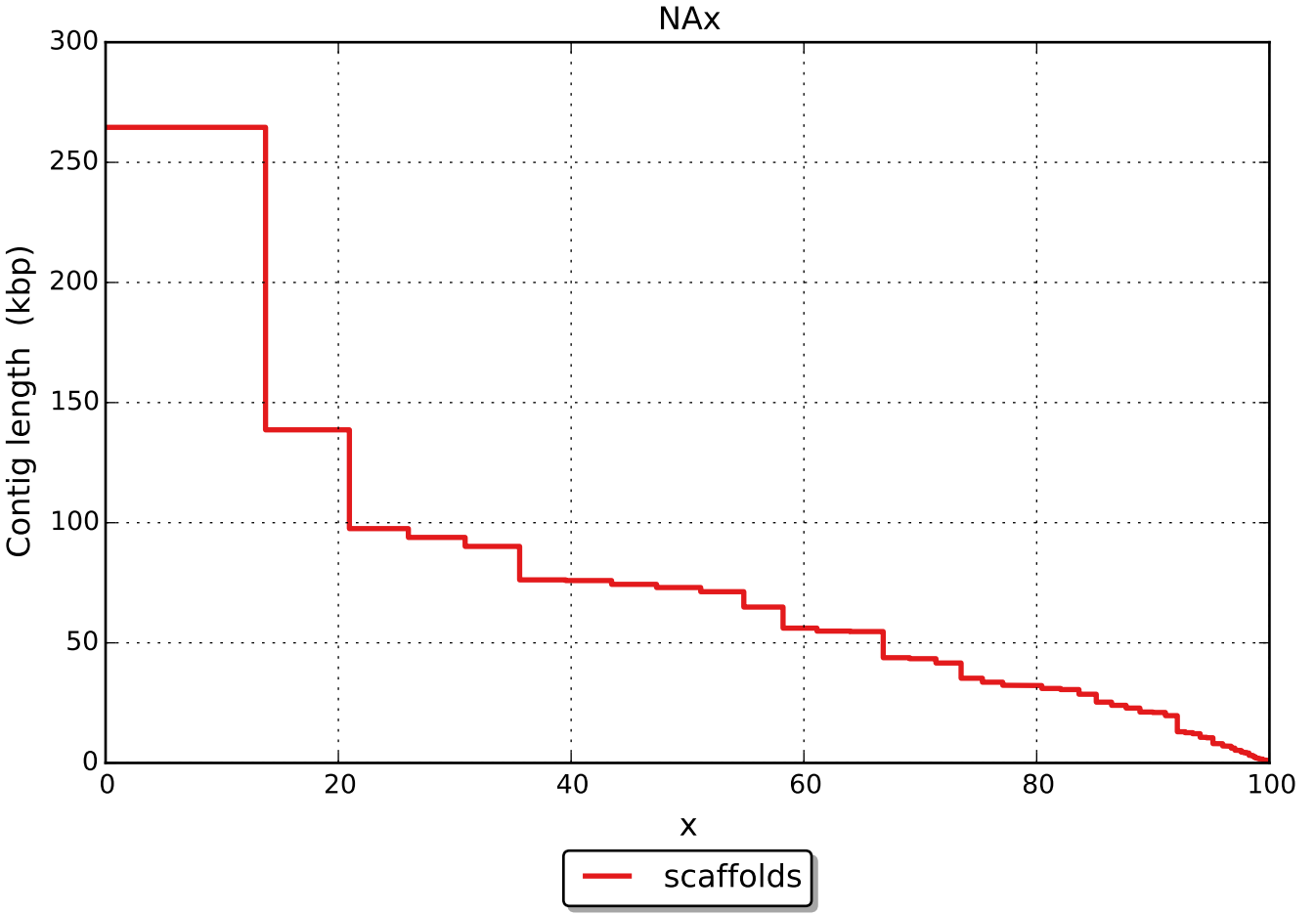

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

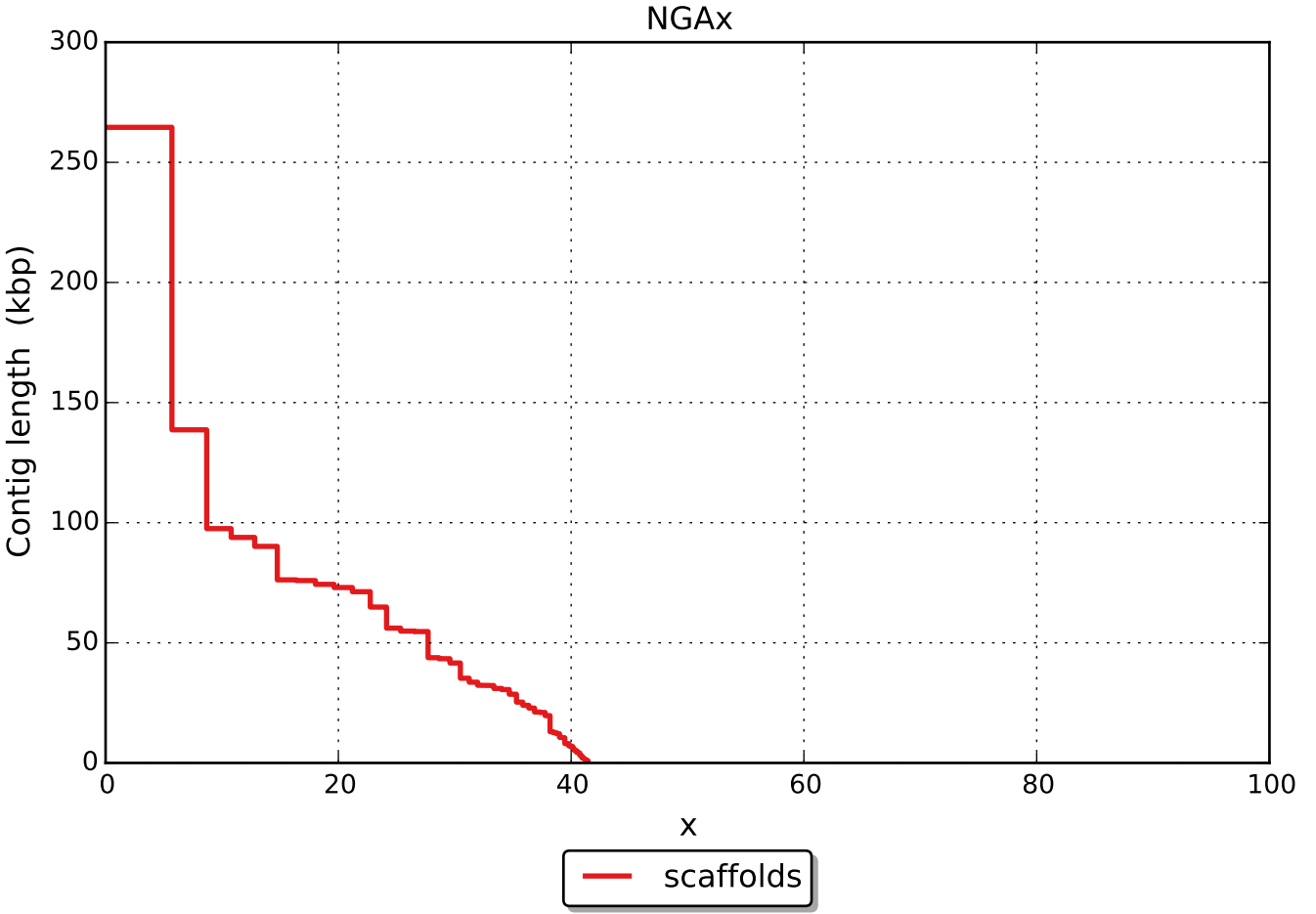

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
Contig index
scaffolds
Reference


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


Misassemblies
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
Contig index
scaffolds
Reference


NAx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds


NGAx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds