Report

	scaffolds
# contigs (>= 1000 bp)	118
# contigs (>= 5000 bp)	92
# contigs (>= 10000 bp)	87
# contigs (>= 25000 bp)	75
# contigs (>= 50000 bp)	58
Total length (>= 1000 bp)	9007220
Total length (>= 5000 bp)	8960493
Total length (>= 10000 bp)	8921146
Total length (>= 25000 bp)	8704633
Total length (>= 50000 bp)	8130674
# contigs	137
Largest contig	527156
Total length	9019919
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	132337
NG50	263375
N75	86976
NG75	200796
L50	19
LG50	7
L75	39
LG75	13
# misassemblies	268
# misassembled contigs	42
Misassembled contigs length	4251762
# local misassemblies	4
# unaligned contigs	0 + 2 part
Unaligned length	7180
Genome fraction (%)	98.671
Duplication ratio	1.968
# N's per 100 kbp	0.00
# mismatches per 100 kbp	853.00
# indels per 100 kbp	1.24
Largest alignment	527156
NA50	61543
NGA50	197358
NA75	20909
NGA75	89865
LA50	33
LGA50	8
LA75	98
LGA75	19

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

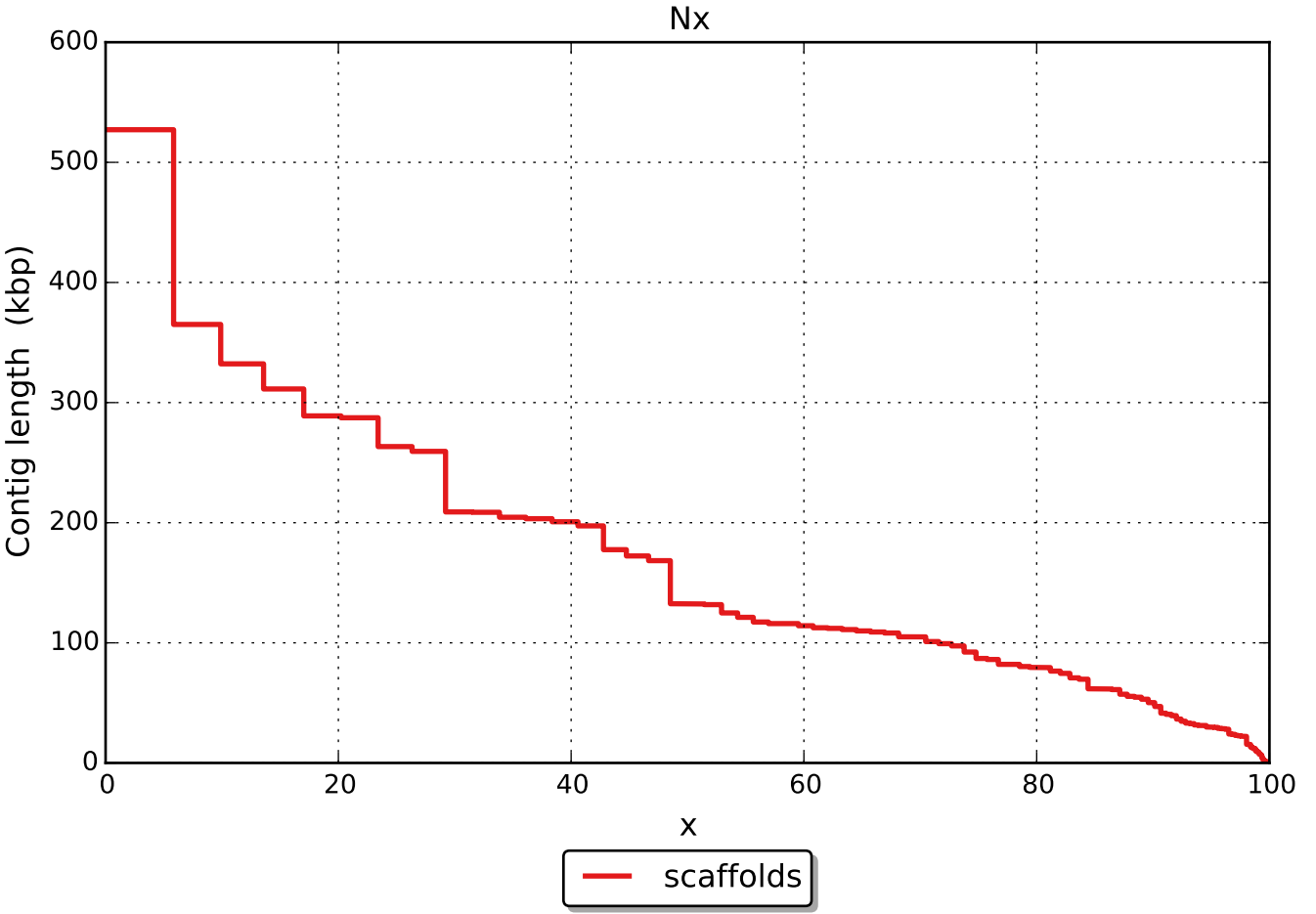
	scaffolds
# misassemblies	268
# relocations	222
# translocations	0
# inversions	46
# possibly misassembled contigs	13
# misassembled contigs	42
Misassembled contigs length	4251762
# local misassemblies	4
# mismatches	39067
# indels	57
# short indels	57
# long indels	0
Indels length	58

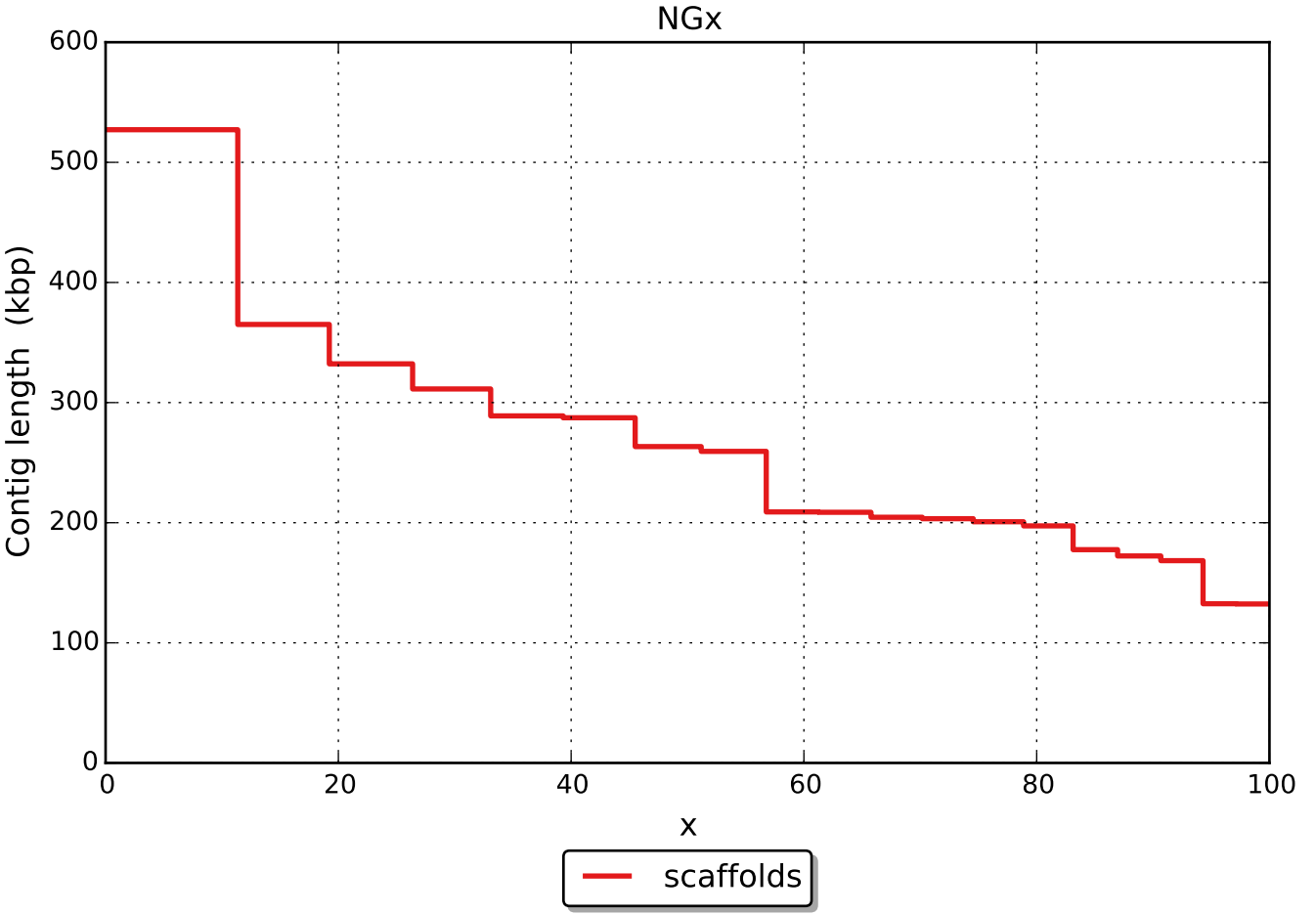
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

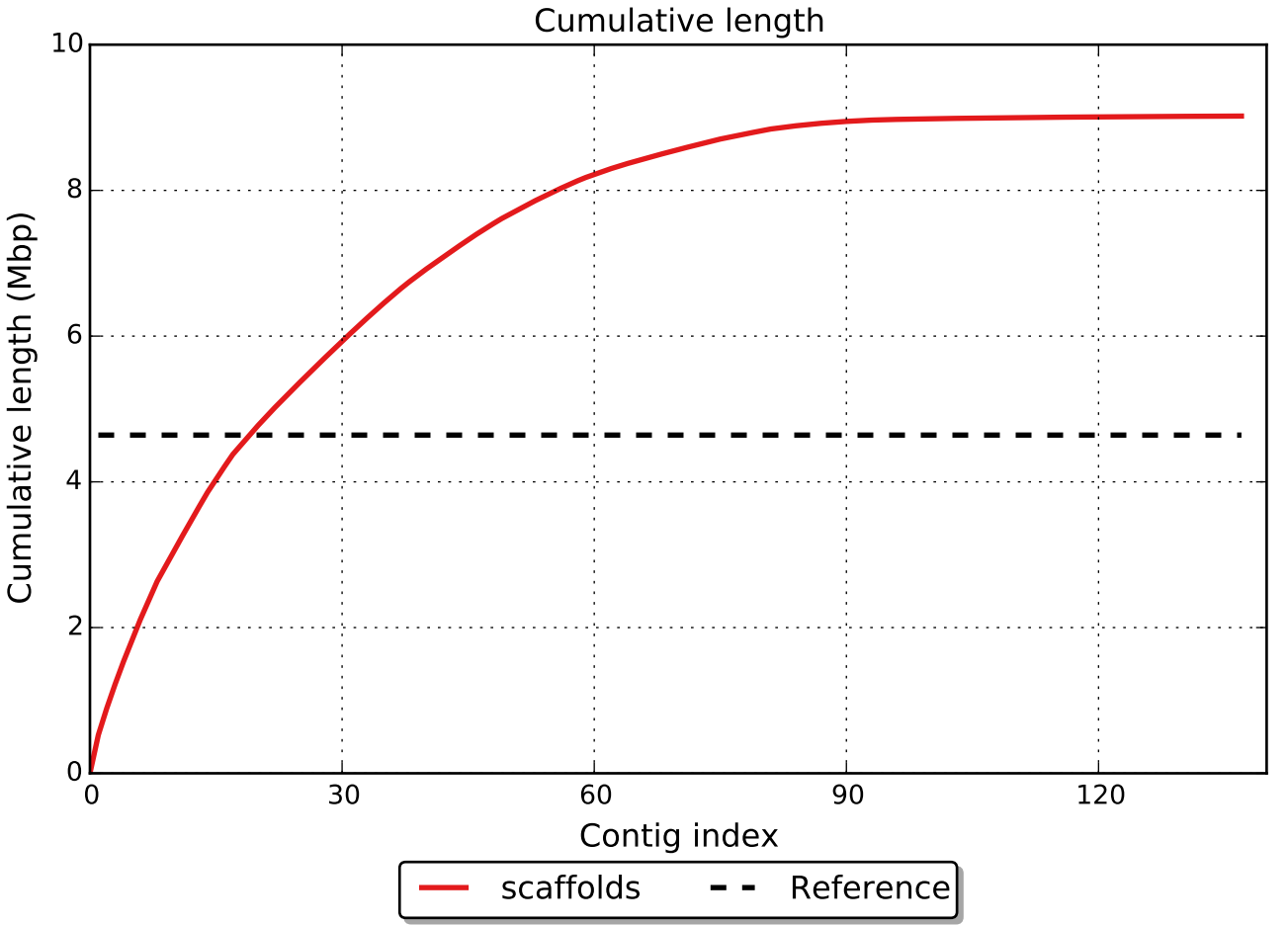
Unaligned report

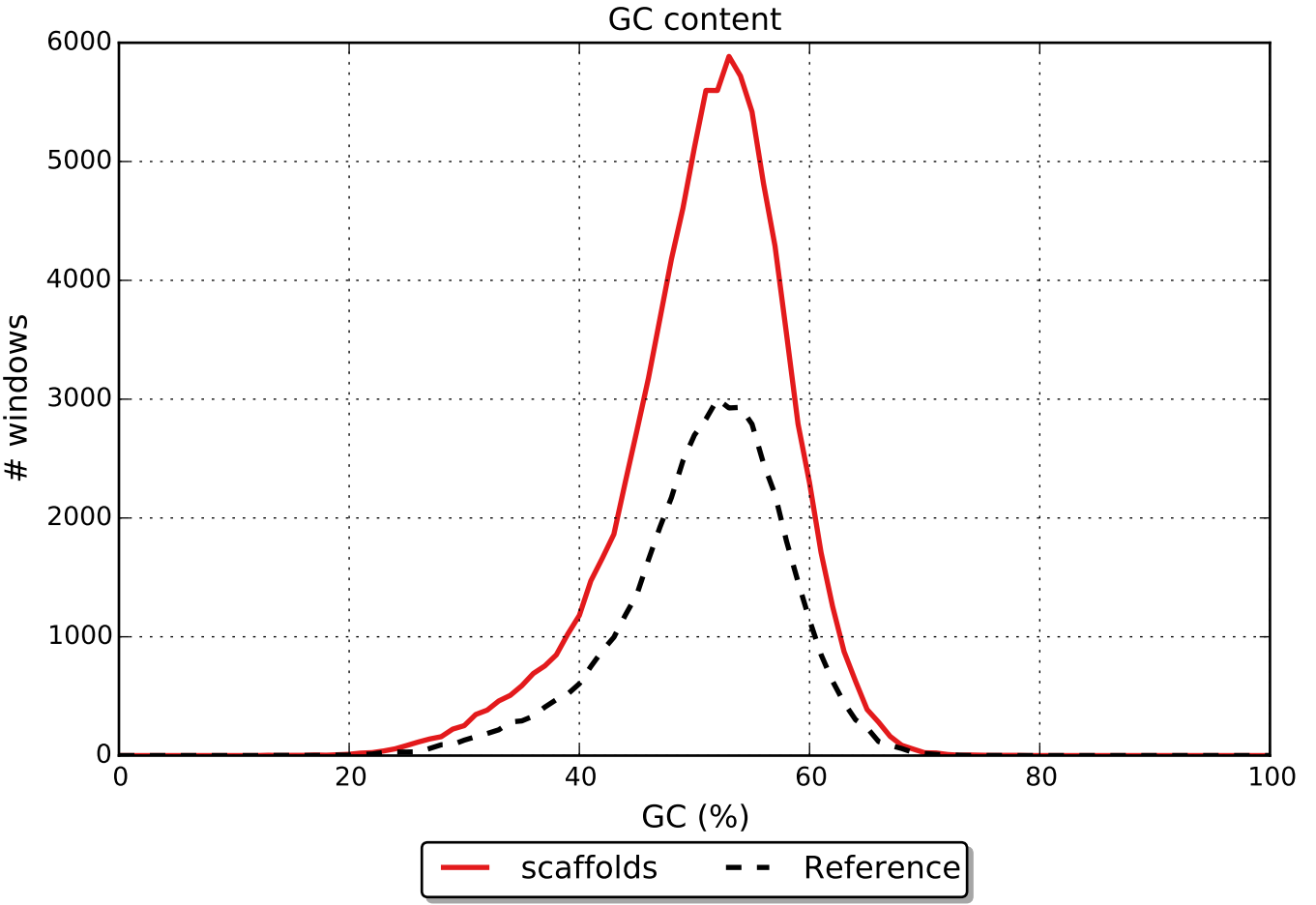
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	7180
# N's	0

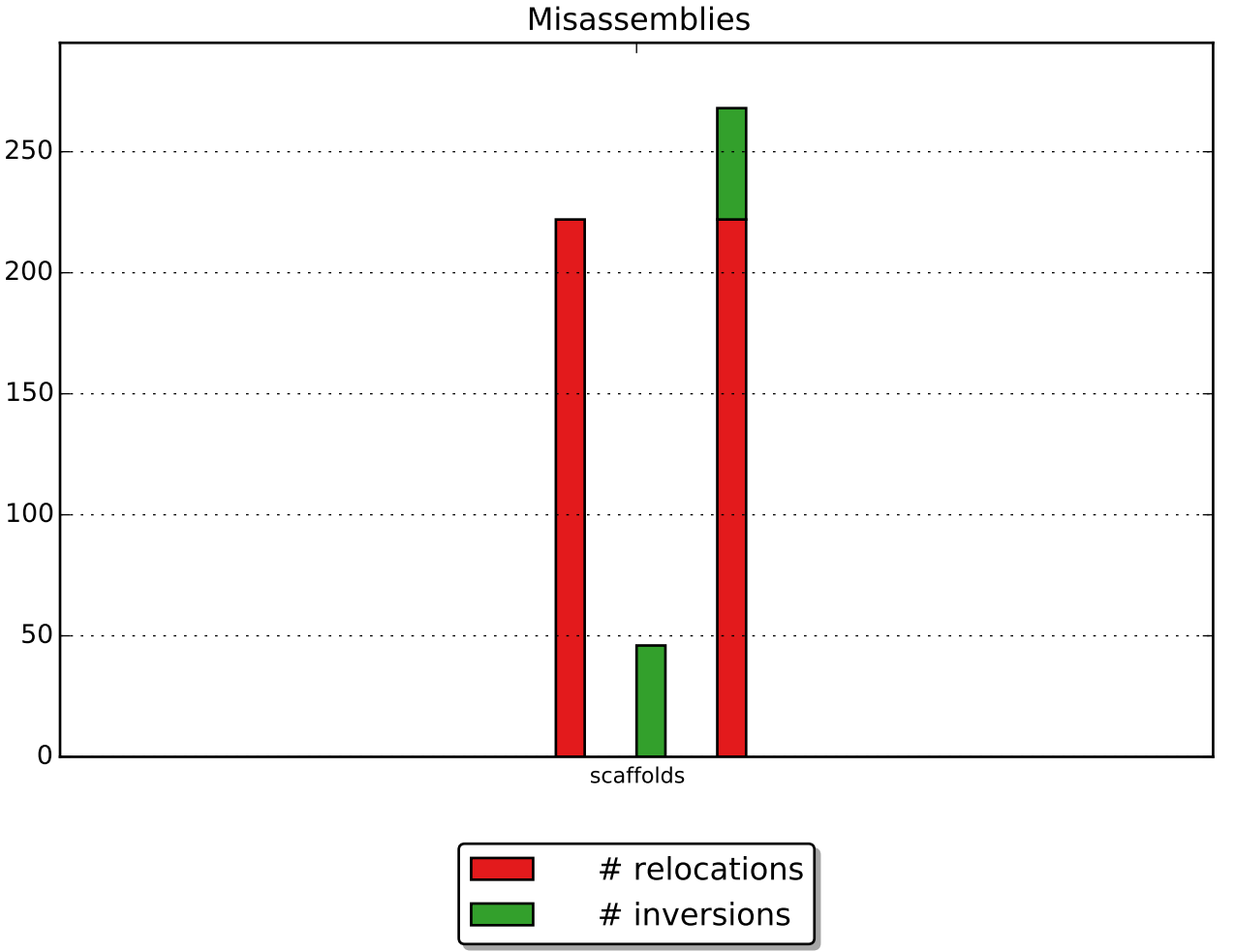
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

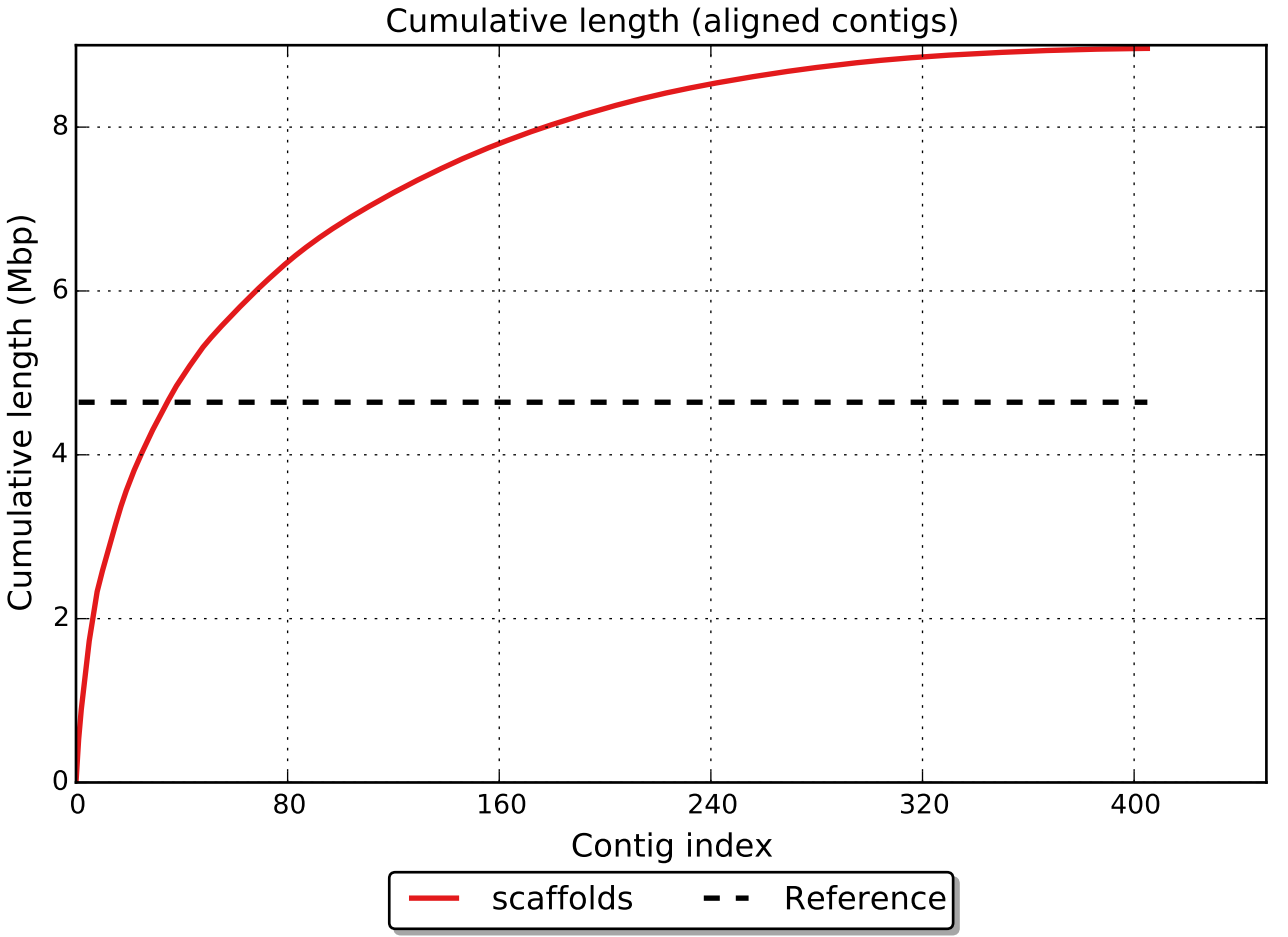

Nx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

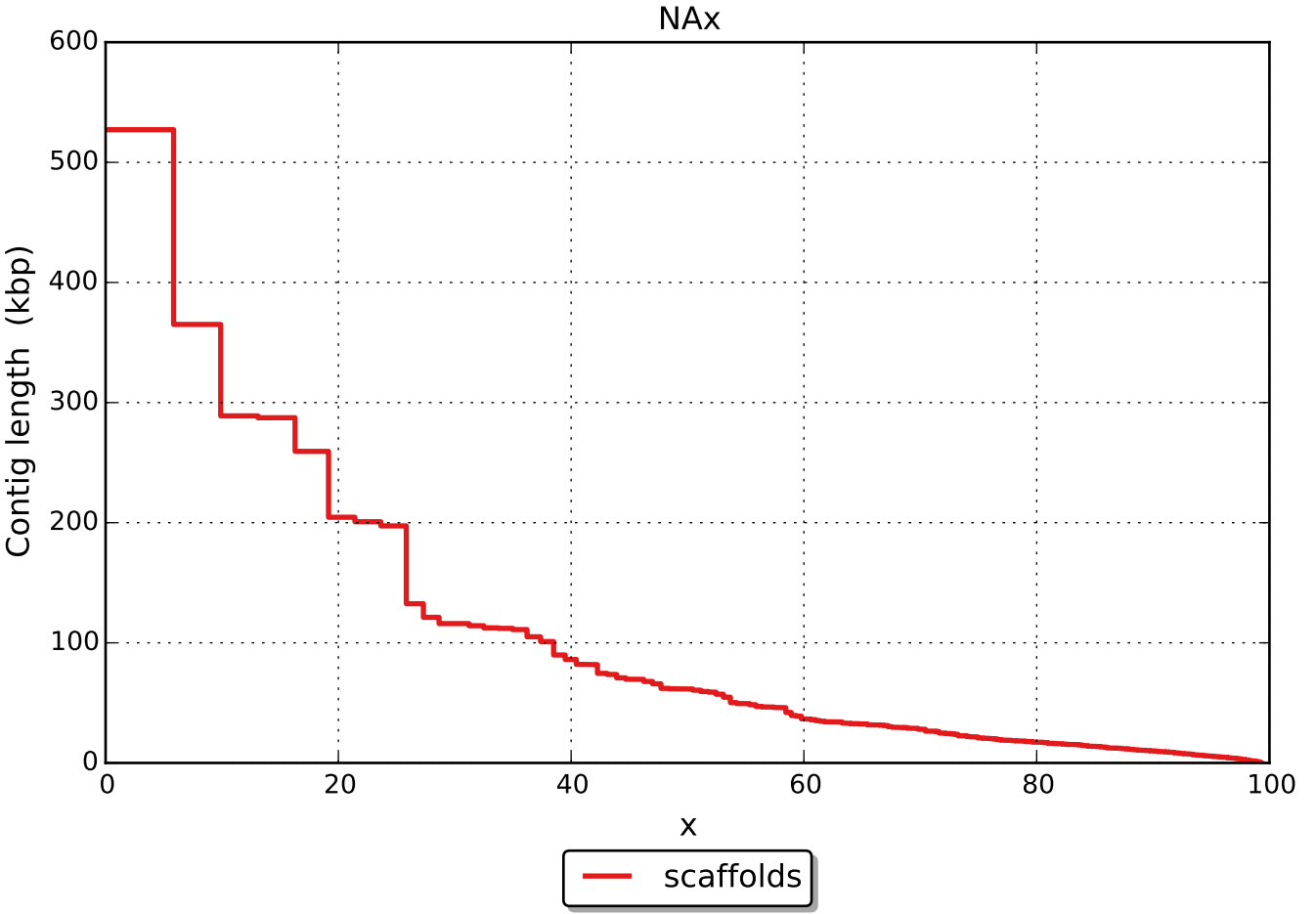

NGx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

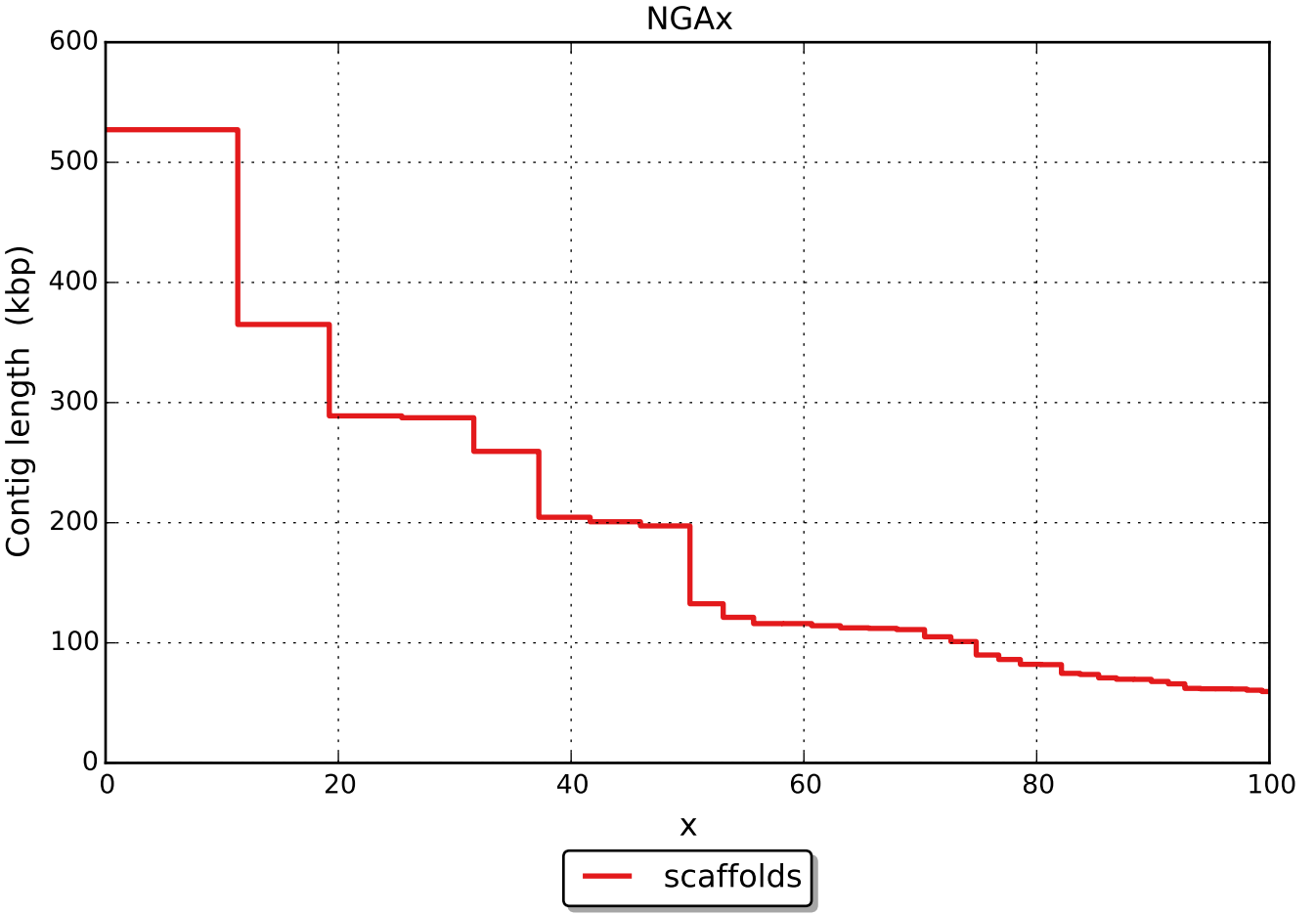

Cumulative length
Cumulative length (Mbp)
10
8
6
4
2
0
0
30
60
90
120
Contig index
scaffolds
Reference


GC content
windows
GC (%)
0
1000
2000
3000
4000
5000
6000
0
20
40
60
80
100
scaffolds
Reference


Misassemblies
250
200
150
100
50
0
scaffolds
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
0
80
160
240
320
400
Contig index
scaffolds
Reference


NAx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds


NGAx
600
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds