Report

	scaffolds
# contigs (>= 1000 bp)	178
# contigs (>= 5000 bp)	122
# contigs (>= 10000 bp)	109
# contigs (>= 25000 bp)	81
# contigs (>= 50000 bp)	51
Total length (>= 1000 bp)	8057406
Total length (>= 5000 bp)	7922221
Total length (>= 10000 bp)	7825936
Total length (>= 25000 bp)	7352421
Total length (>= 50000 bp)	6316616
# contigs	221
Largest contig	333495
Total length	8085605
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	97773
NG50	188986
N75	63382
NG75	125151
L50	22
LG50	9
L75	47
LG75	17
# misassemblies	178
# misassembled contigs	38
Misassembled contigs length	3564233
# local misassemblies	6
# unaligned contigs	0 + 2 part
Unaligned length	1233
Genome fraction (%)	97.857
Duplication ratio	1.780
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1322.01
# indels per 100 kbp	1.19
Largest alignment	317313
NA50	54877
NGA50	92158
NA75	24175
NGA75	63382
LA50	39
LGA50	14
LA75	99
LGA75	30

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

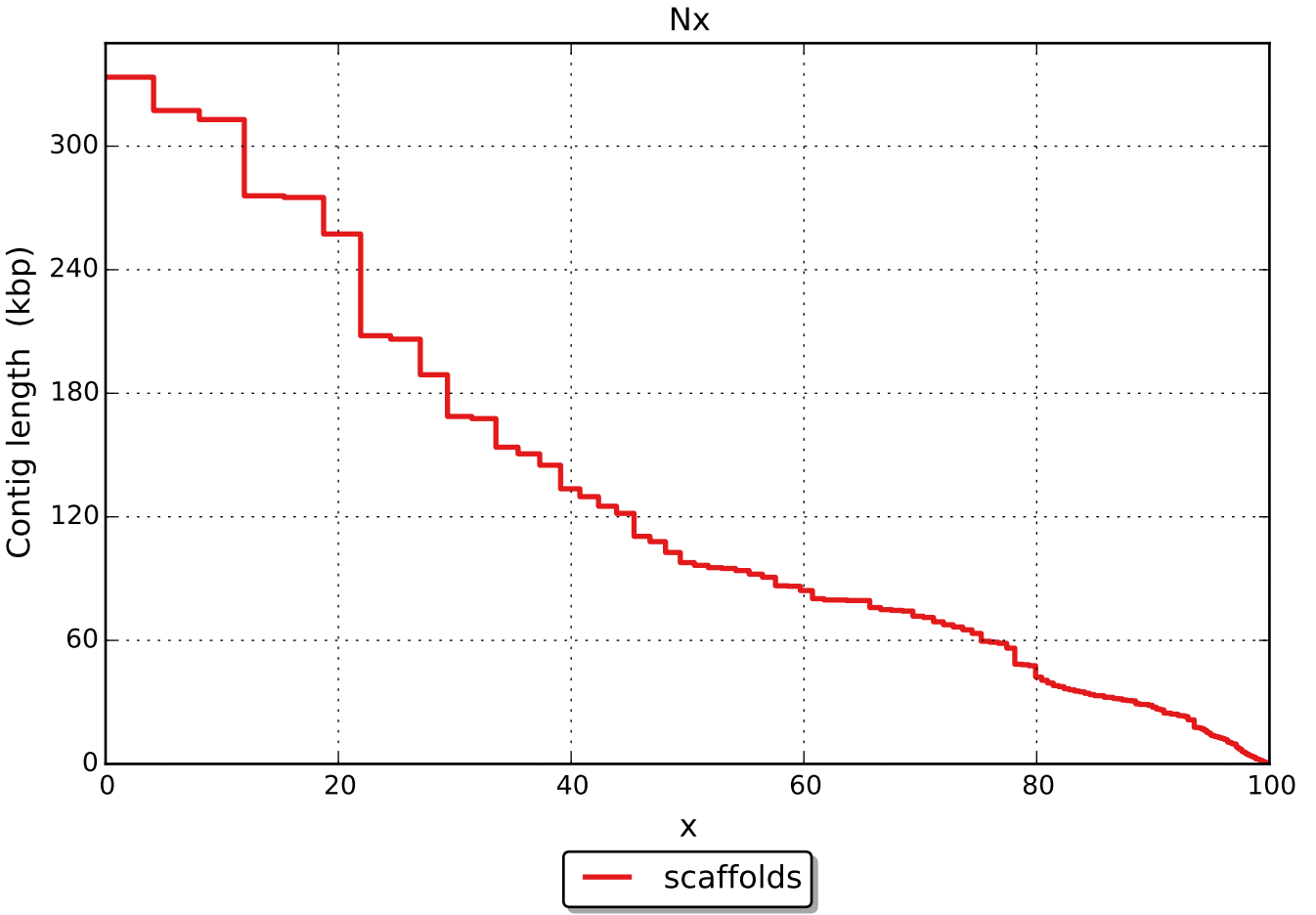
	scaffolds
# misassemblies	178
# relocations	151
# translocations	0
# inversions	27
# possibly misassembled contigs	3
# misassembled contigs	38
Misassembled contigs length	3564233
# local misassemblies	6
# mismatches	60048
# indels	54
# short indels	54
# long indels	0
Indels length	62

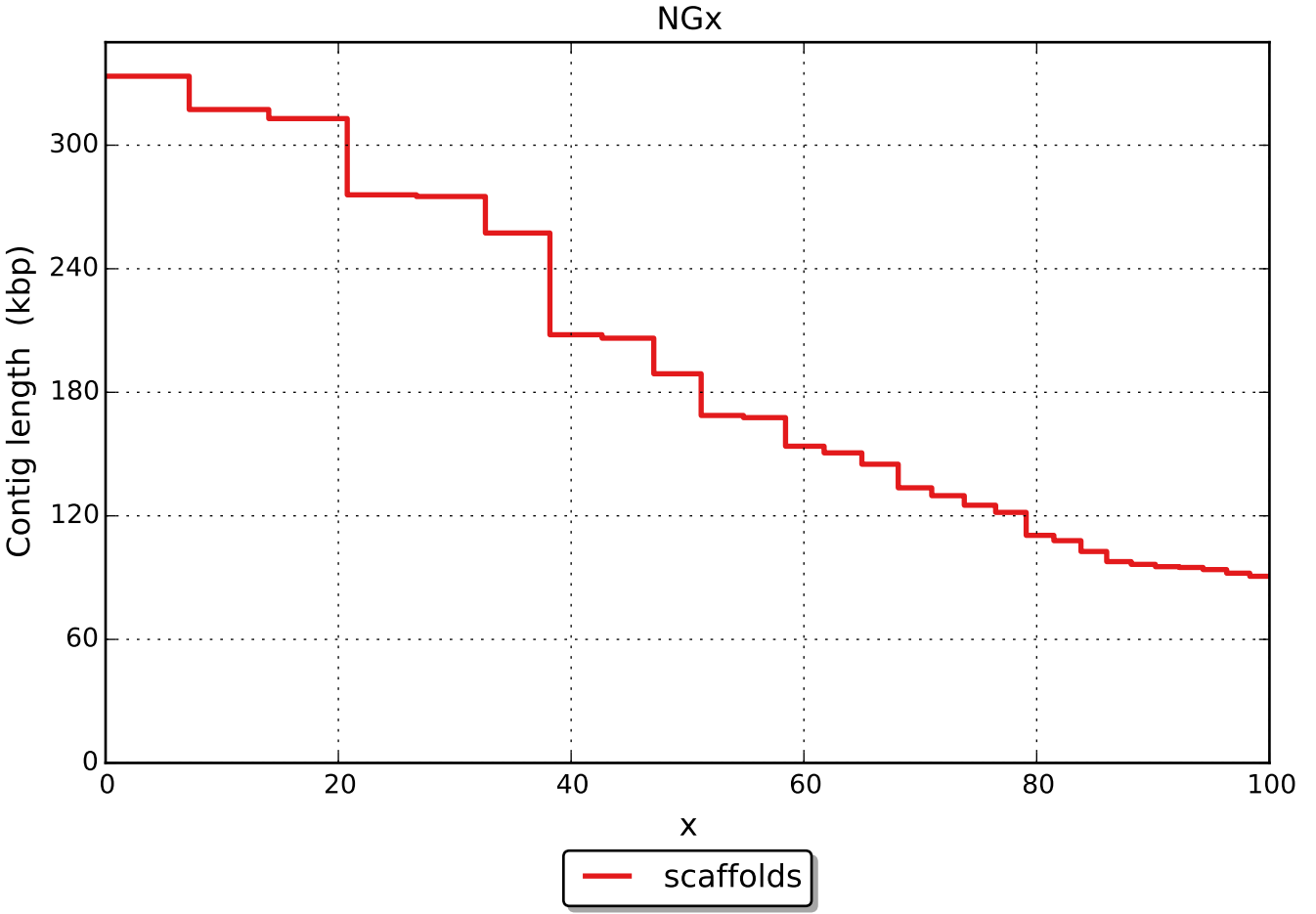
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

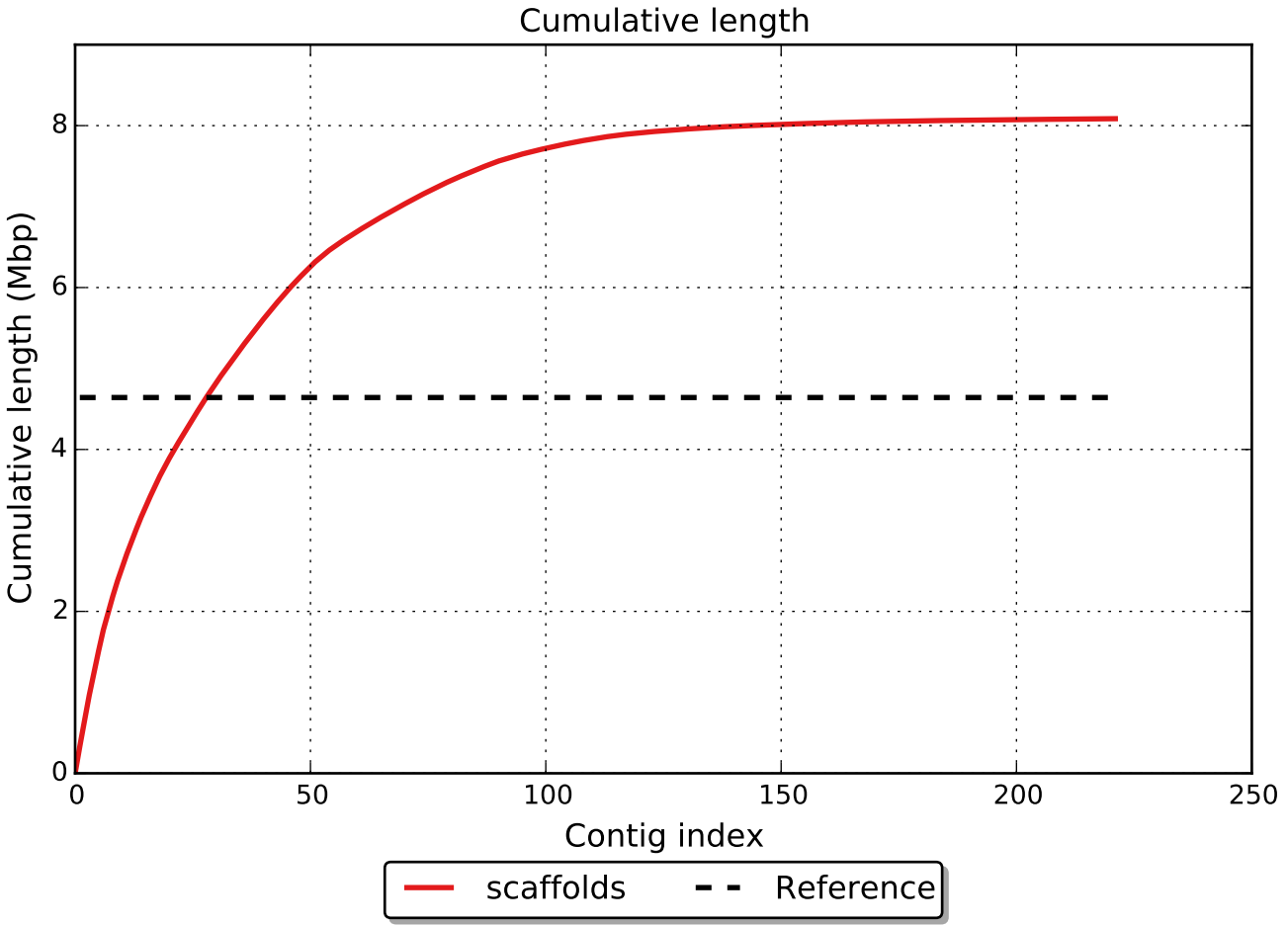
Unaligned report

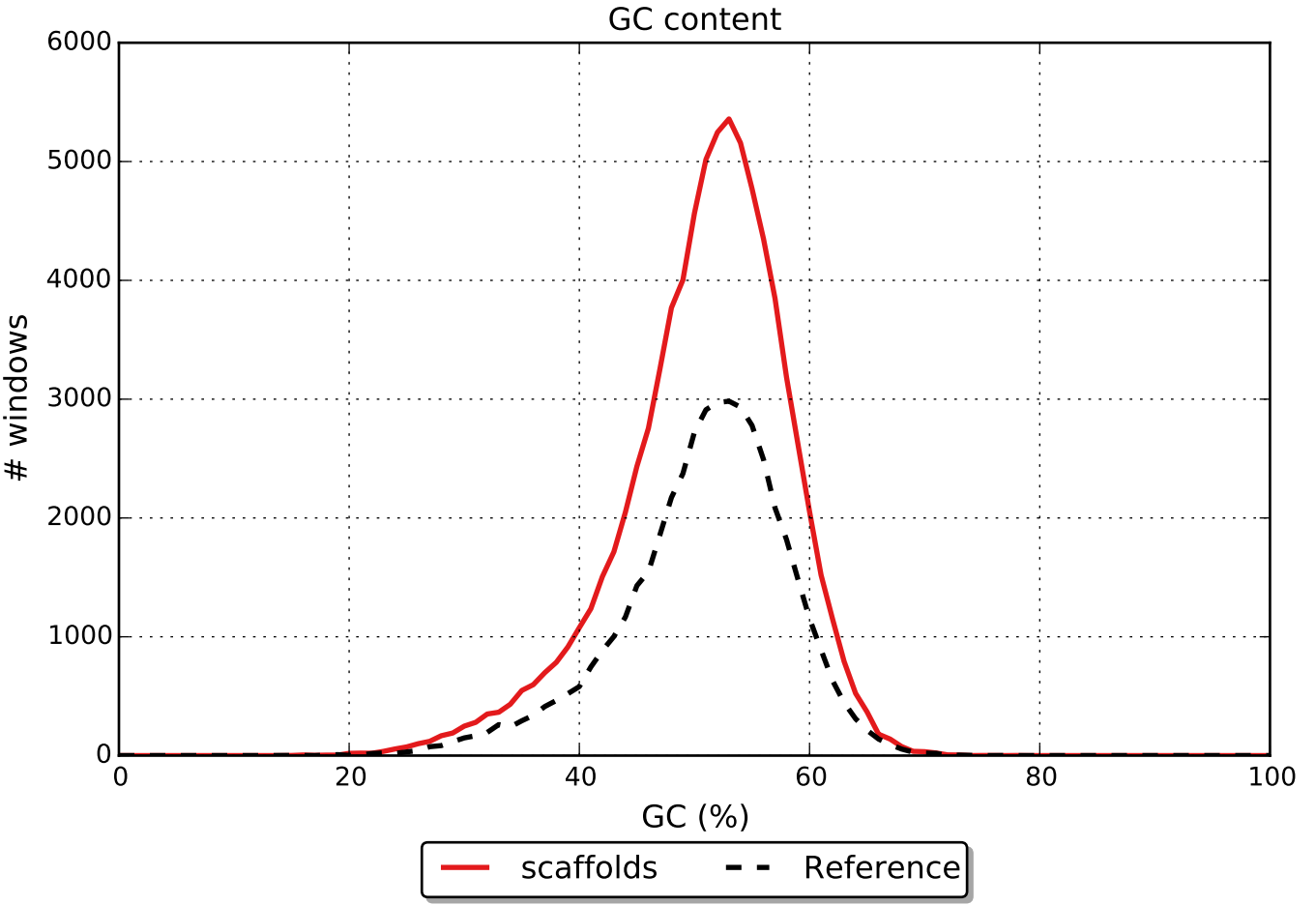
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	1233
# N's	0

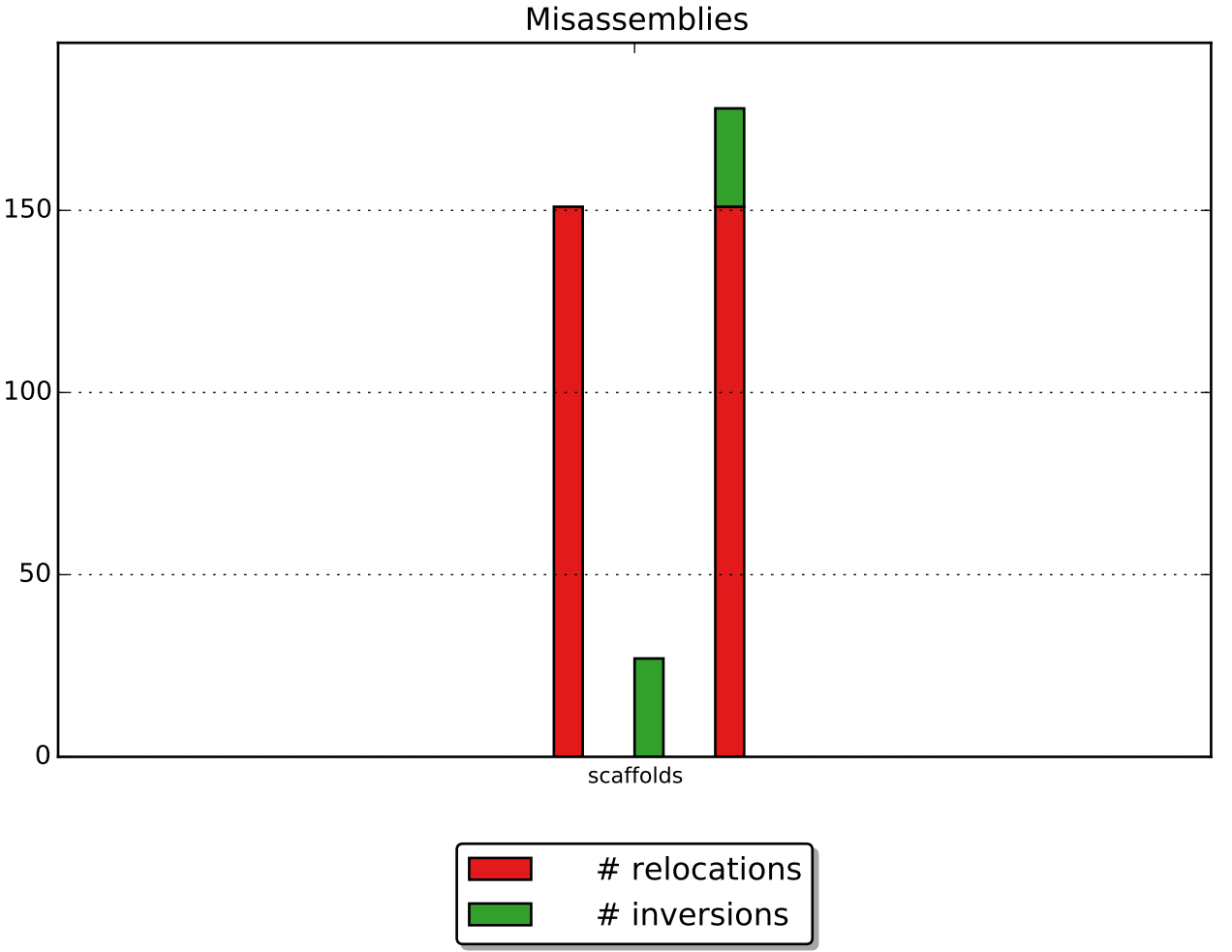
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

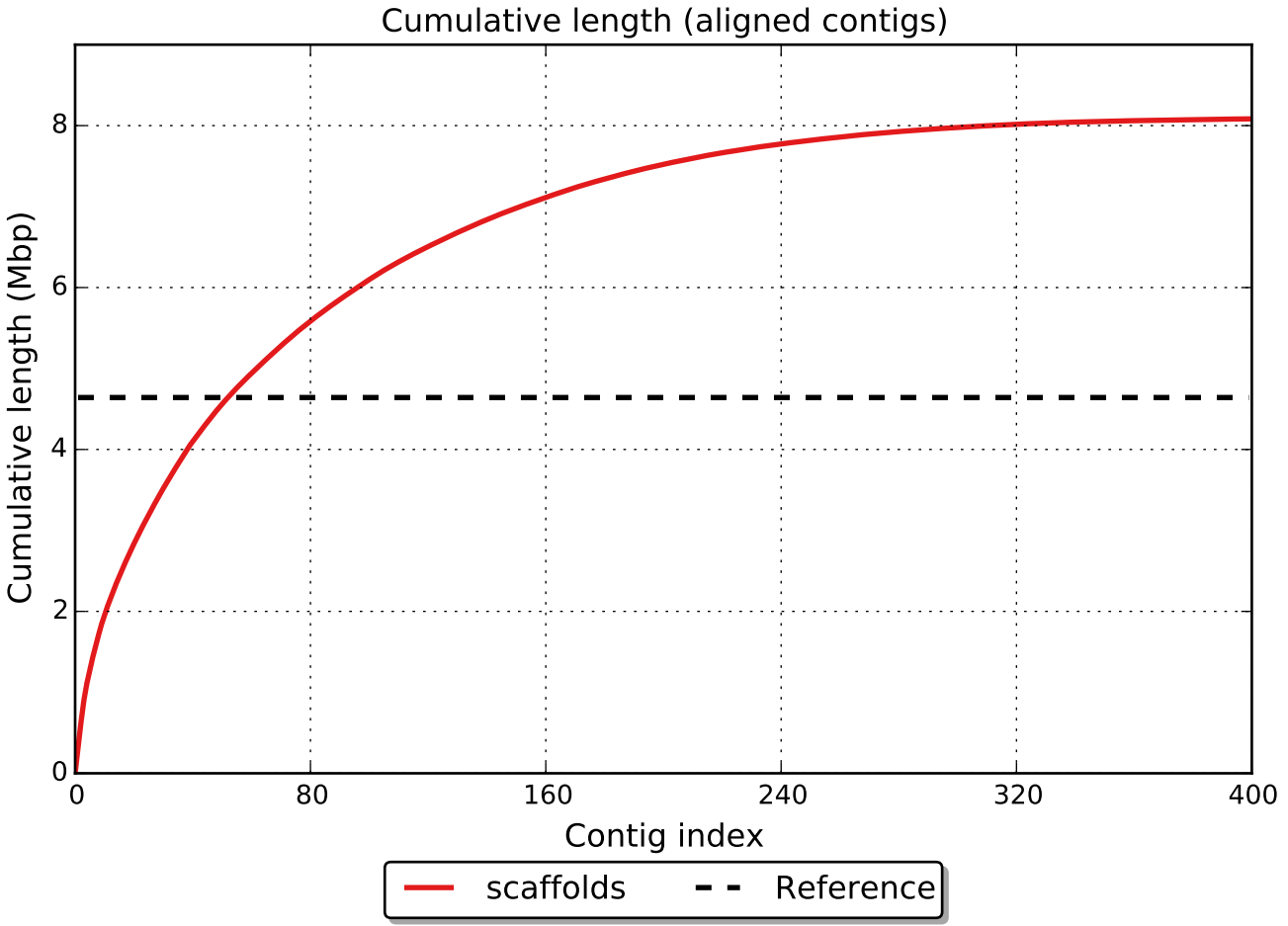

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

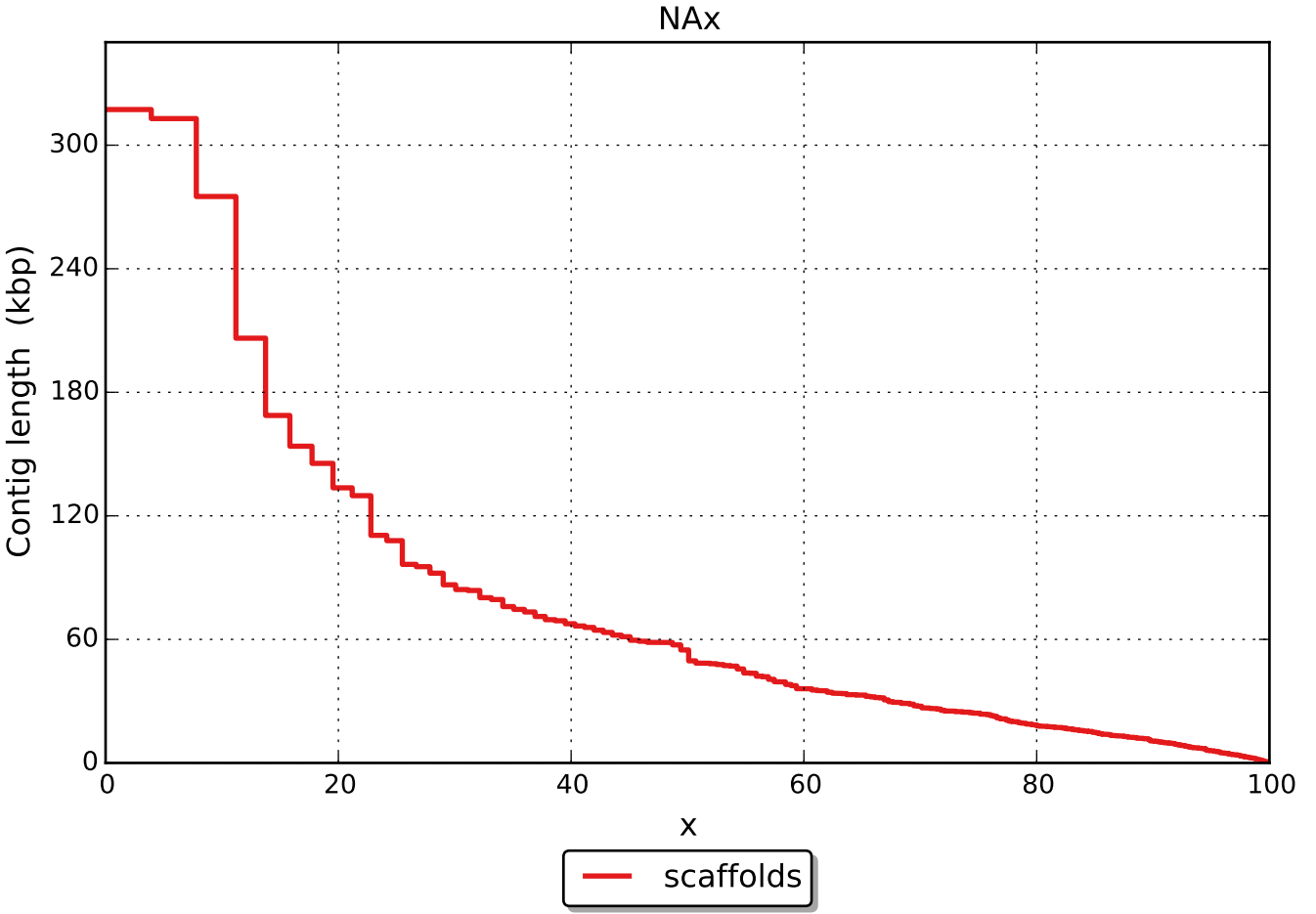

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
scaffolds

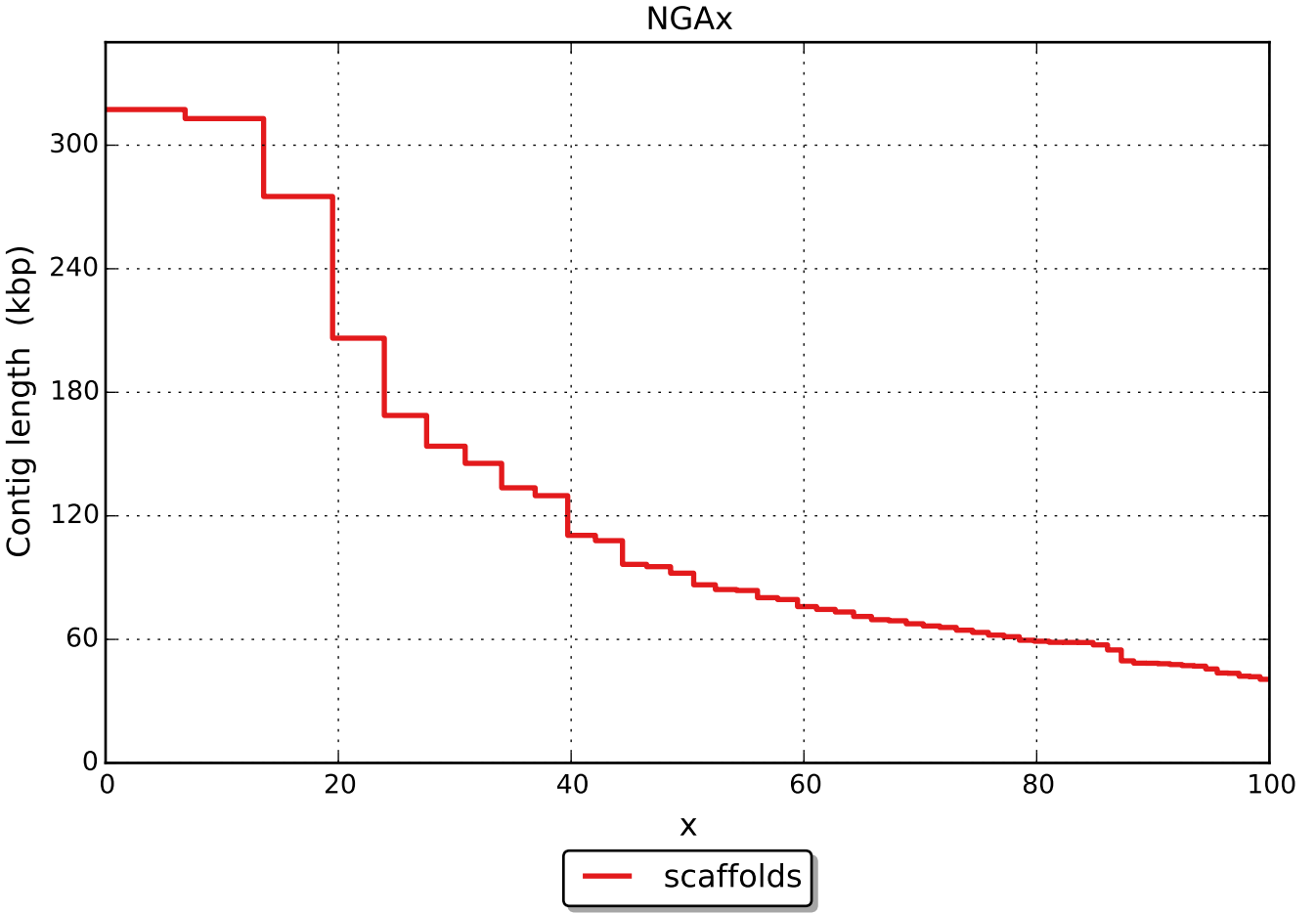

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
0
50
100
150
200
250
Contig index
scaffolds
Reference


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


Misassemblies
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
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