Report

	scaffolds
# contigs (>= 1000 bp)	82
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	69
# contigs (>= 25000 bp)	62
# contigs (>= 50000 bp)	45
Total length (>= 1000 bp)	8700582
Total length (>= 5000 bp)	8685534
Total length (>= 10000 bp)	8655322
Total length (>= 25000 bp)	8551163
Total length (>= 50000 bp)	7928822
# contigs	98
Largest contig	472565
Total length	8711893
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.78
N50	214400
NG50	308025
N75	117603
NG75	283870
L50	14
LG50	7
L75	27
LG75	11
# misassemblies	90
# misassembled contigs	20
Misassembled contigs length	2198687
# local misassemblies	6
# unaligned contigs	0 + 26 part
Unaligned length	1271079
Genome fraction (%)	99.055
Duplication ratio	1.618
# N's per 100 kbp	0.11
# mismatches per 100 kbp	580.63
# indels per 100 kbp	1.20
Largest alignment	472565
NA50	60605
NGA50	304586
NA75	7193
NGA75	183277
LA50	21
LGA50	7
LA75	129
LGA75	12

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

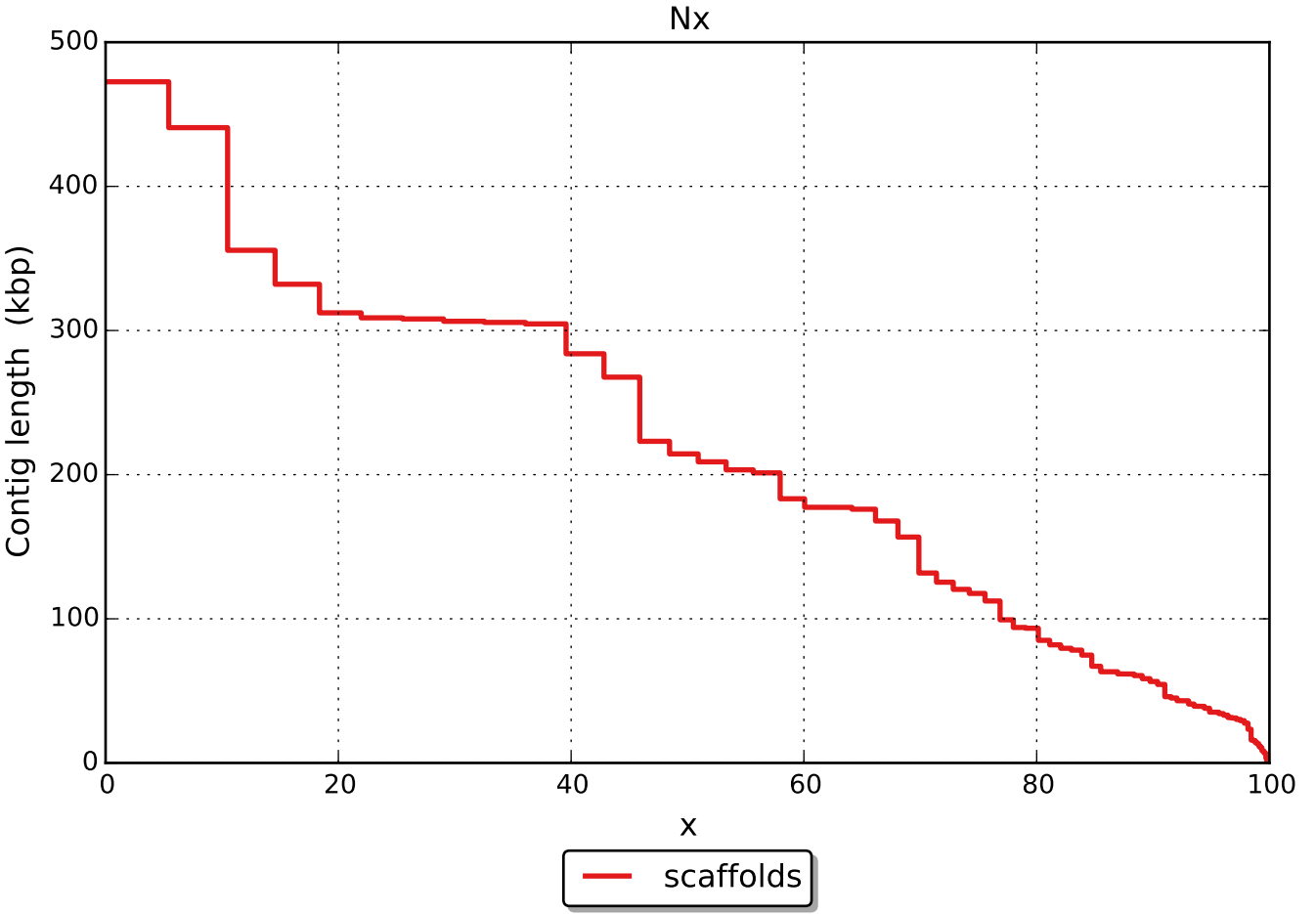
	scaffolds
# misassemblies	90
# relocations	86
# translocations	0
# inversions	4
# possibly misassembled contigs	38
# misassembled contigs	20
Misassembled contigs length	2198687
# local misassemblies	6
# mismatches	26696
# indels	55
# short indels	55
# long indels	0
Indels length	57

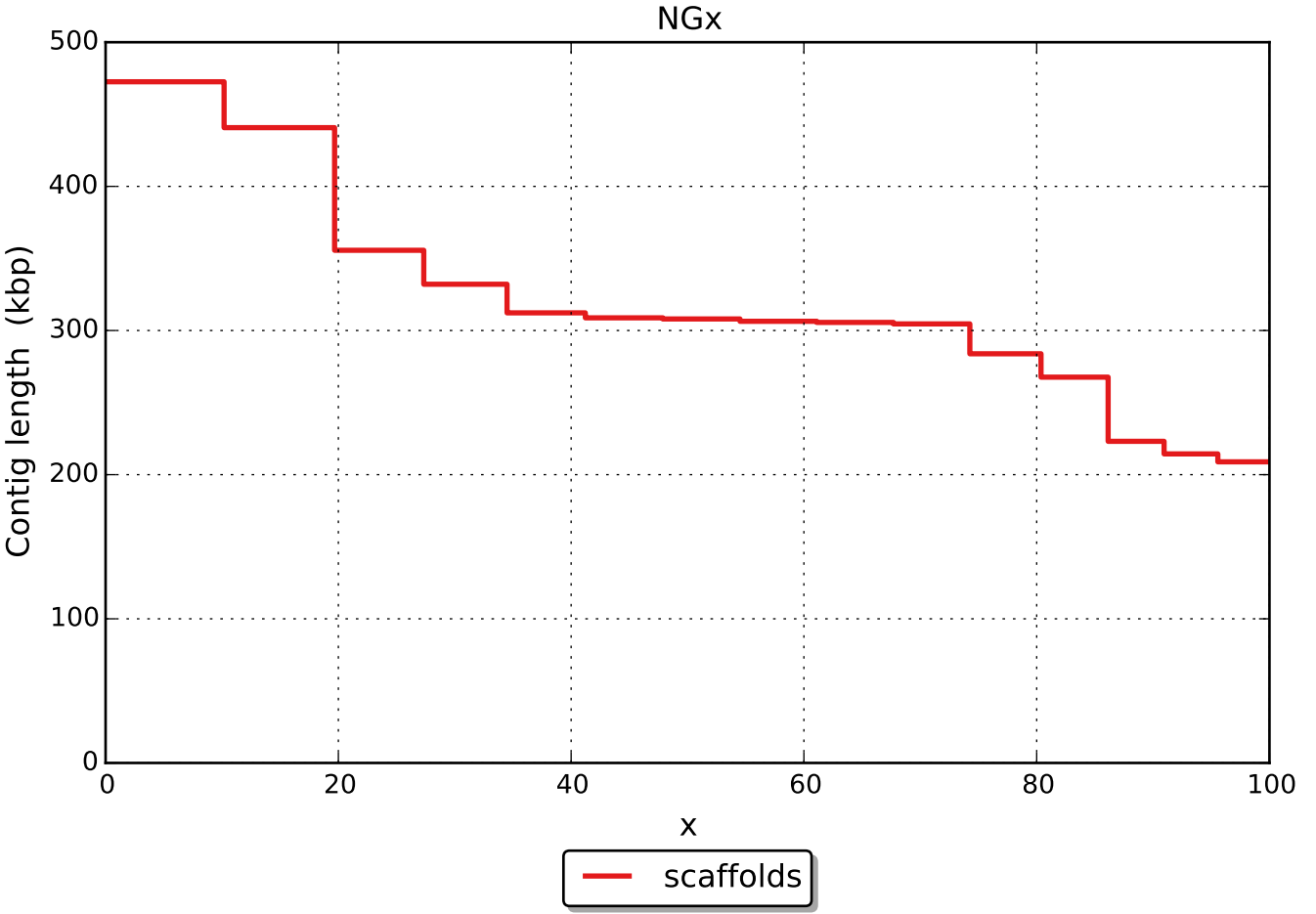
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

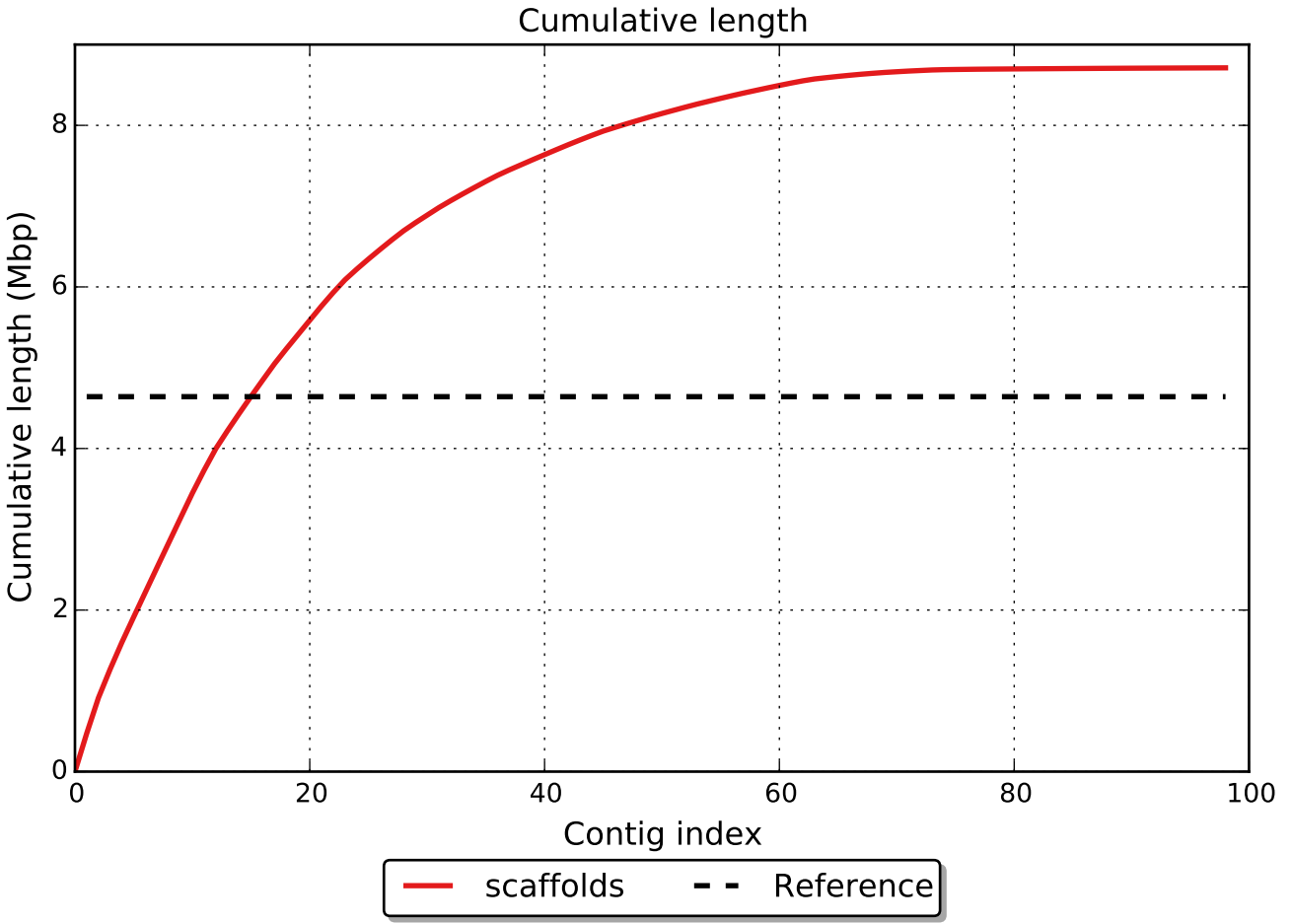
Unaligned report

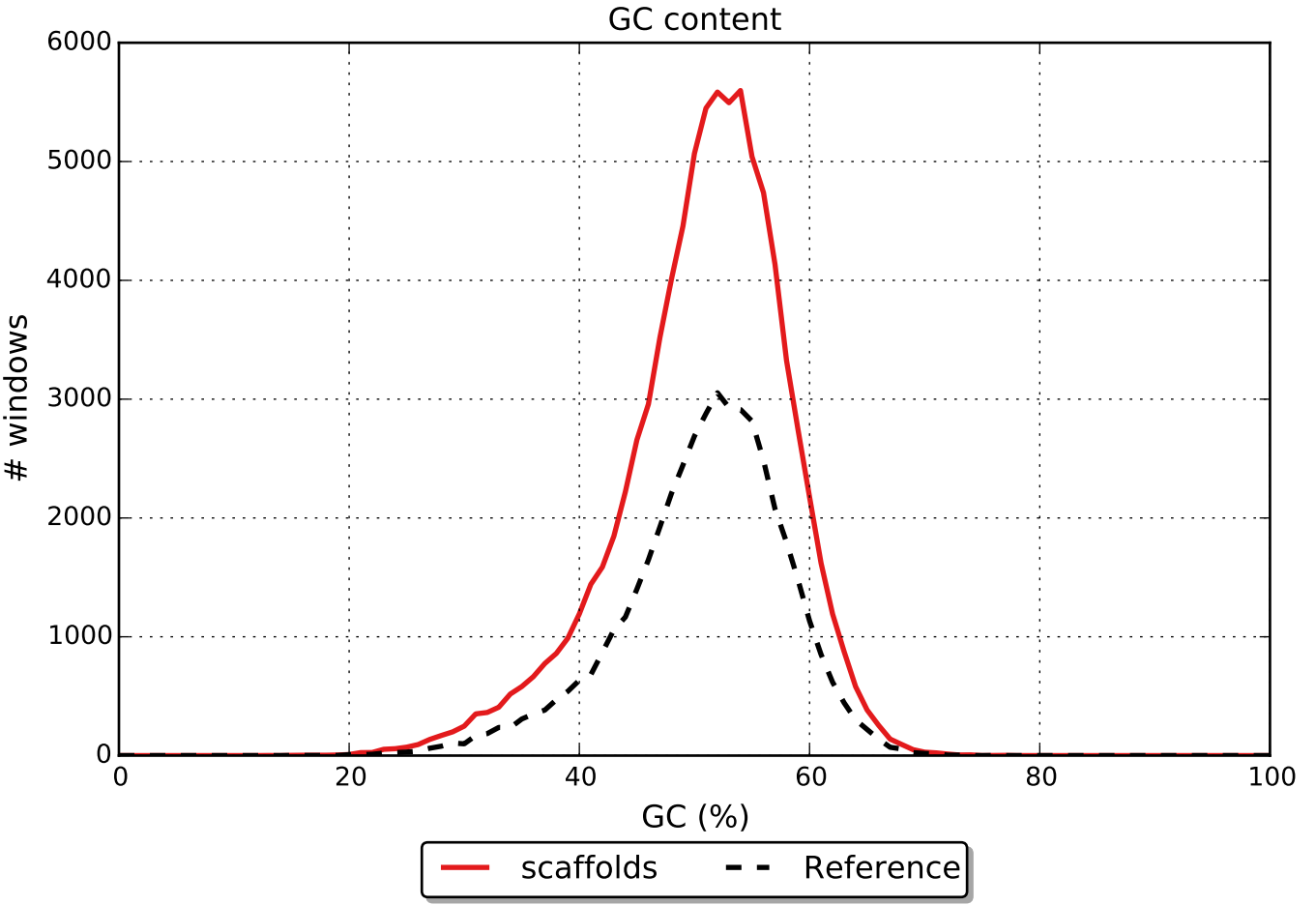
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	26
# with misassembly	12
# both parts are significant	21
Partially unaligned length	1271079
# N's	10

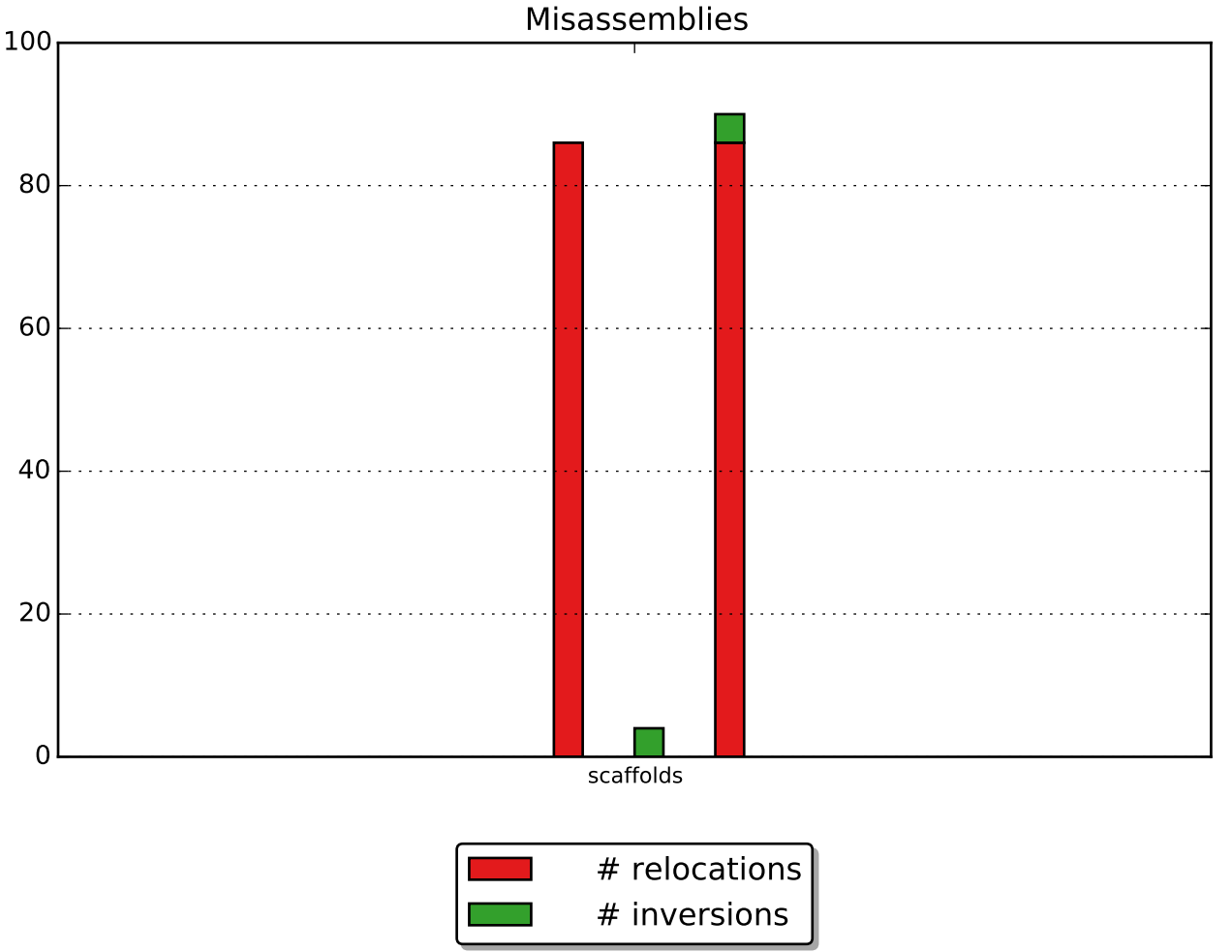
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

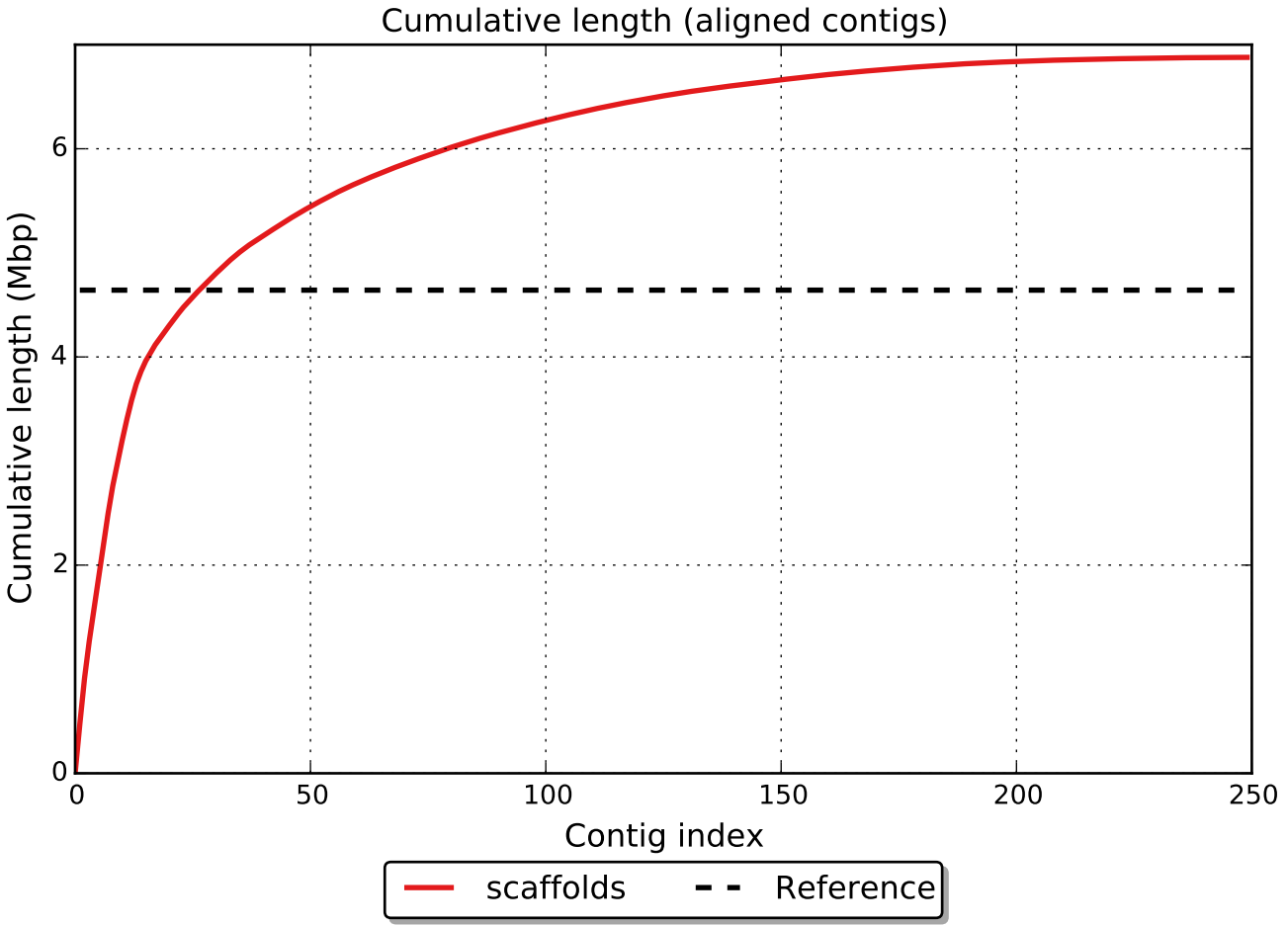

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds

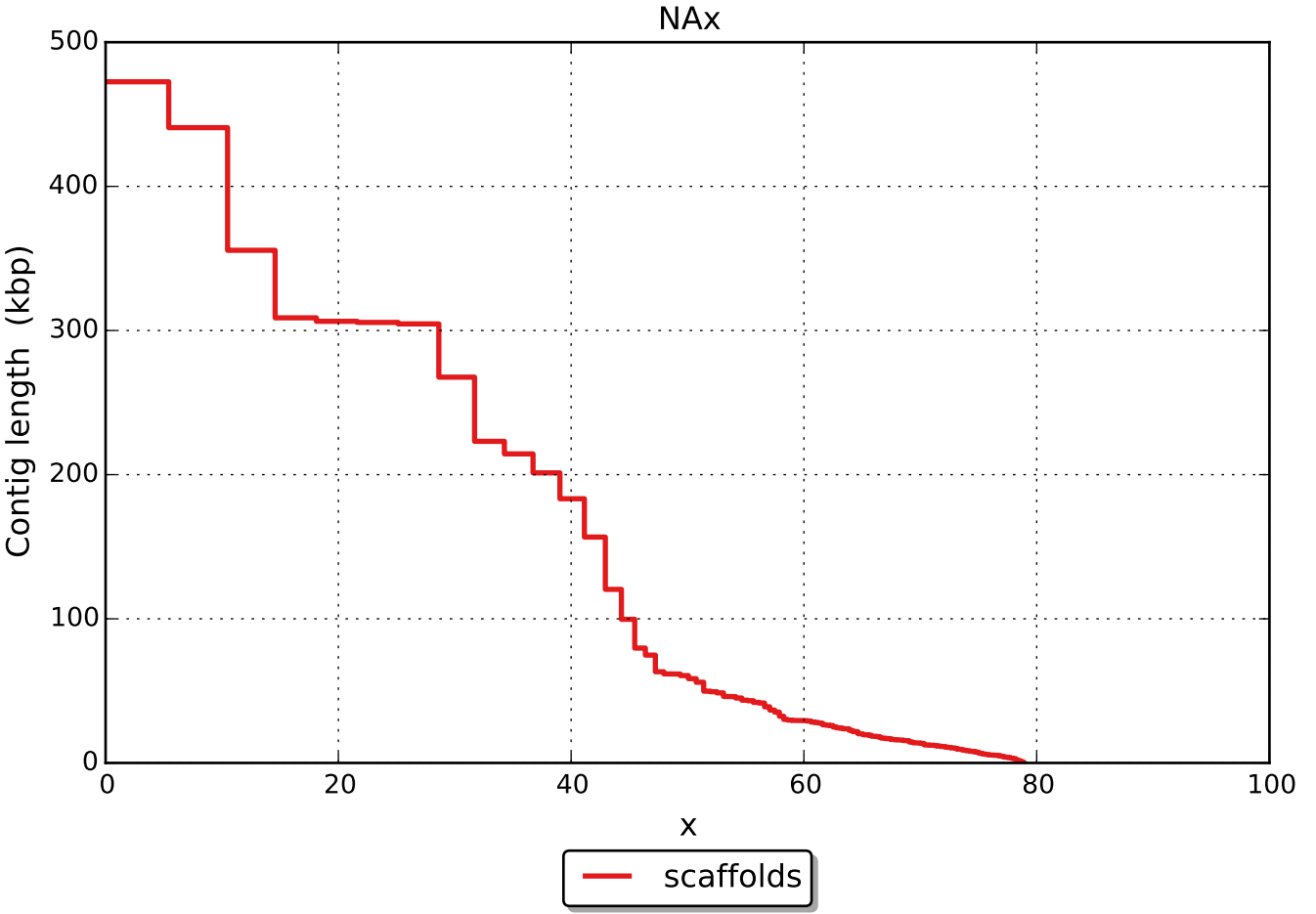

NGx
500
400
300
200
100
0
Contig length (kbp)
0
20
40
60
80
100
x
scaffolds

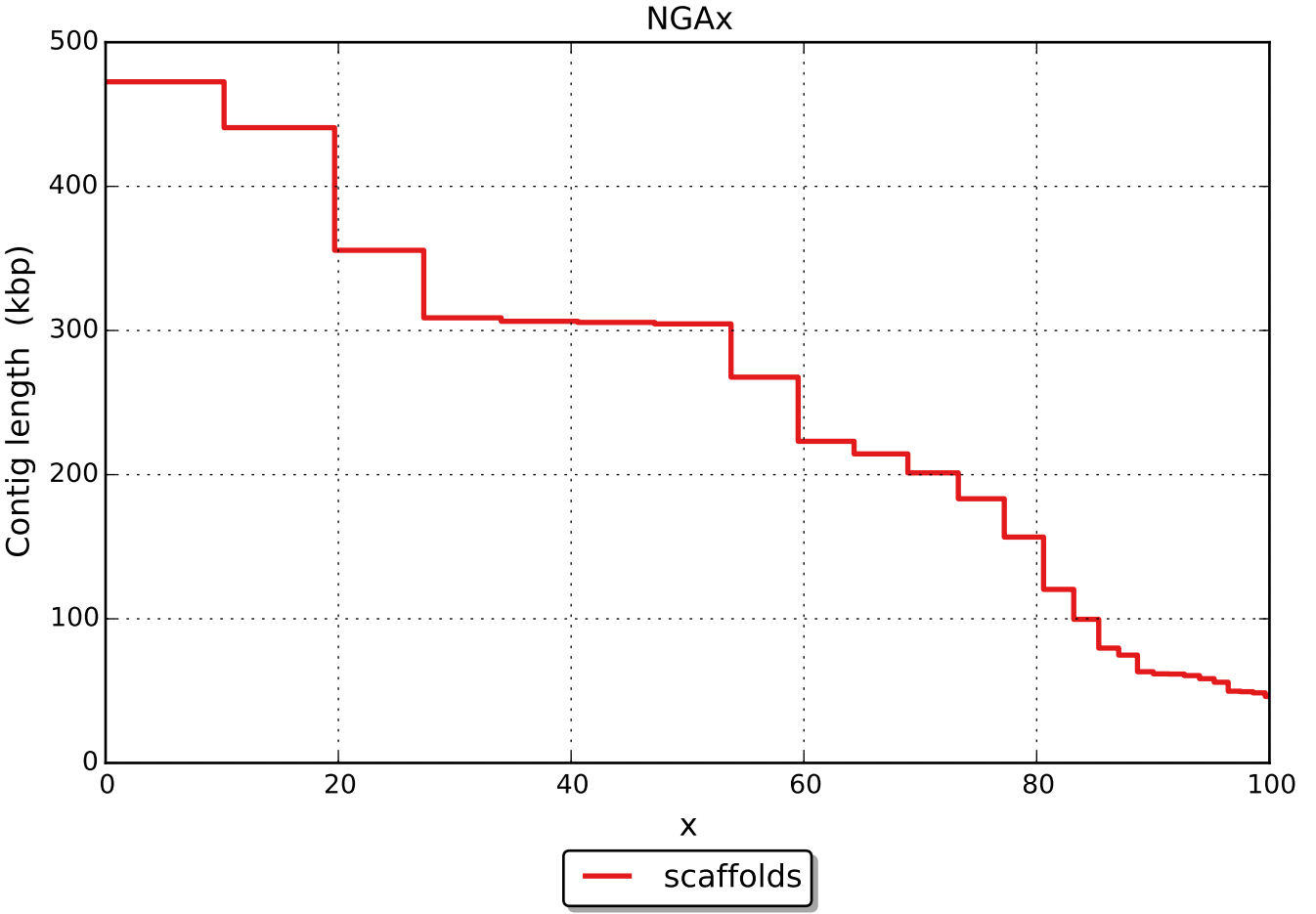

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
0
20
40
60
80
100
Contig index
scaffolds
Reference


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


Misassemblies
100
80
60
40
20
0
scaffolds
relocations
inversions


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


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


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