Report

	scaffolds
# contigs (>= 1000 bp)	335
# contigs (>= 5000 bp)	212
# contigs (>= 10000 bp)	124
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	3487830
Total length (>= 5000 bp)	3201252
Total length (>= 10000 bp)	2541176
Total length (>= 25000 bp)	1109545
Total length (>= 50000 bp)	61819
# contigs	471
Largest contig	61819
Total length	3579837
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.79
N50	16762
NG50	11953
N75	9150
NG75	1033
L50	67
LG50	104
L75	140
LG75	329
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	73.647
Duplication ratio	1.047
# N's per 100 kbp	4056.41
# mismatches per 100 kbp	982.64
# indels per 100 kbp	11.99
Largest alignment	59611
NA50	15076
NGA50	10550
NA75	7995
LA50	72
LGA50	114
LA75	154

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

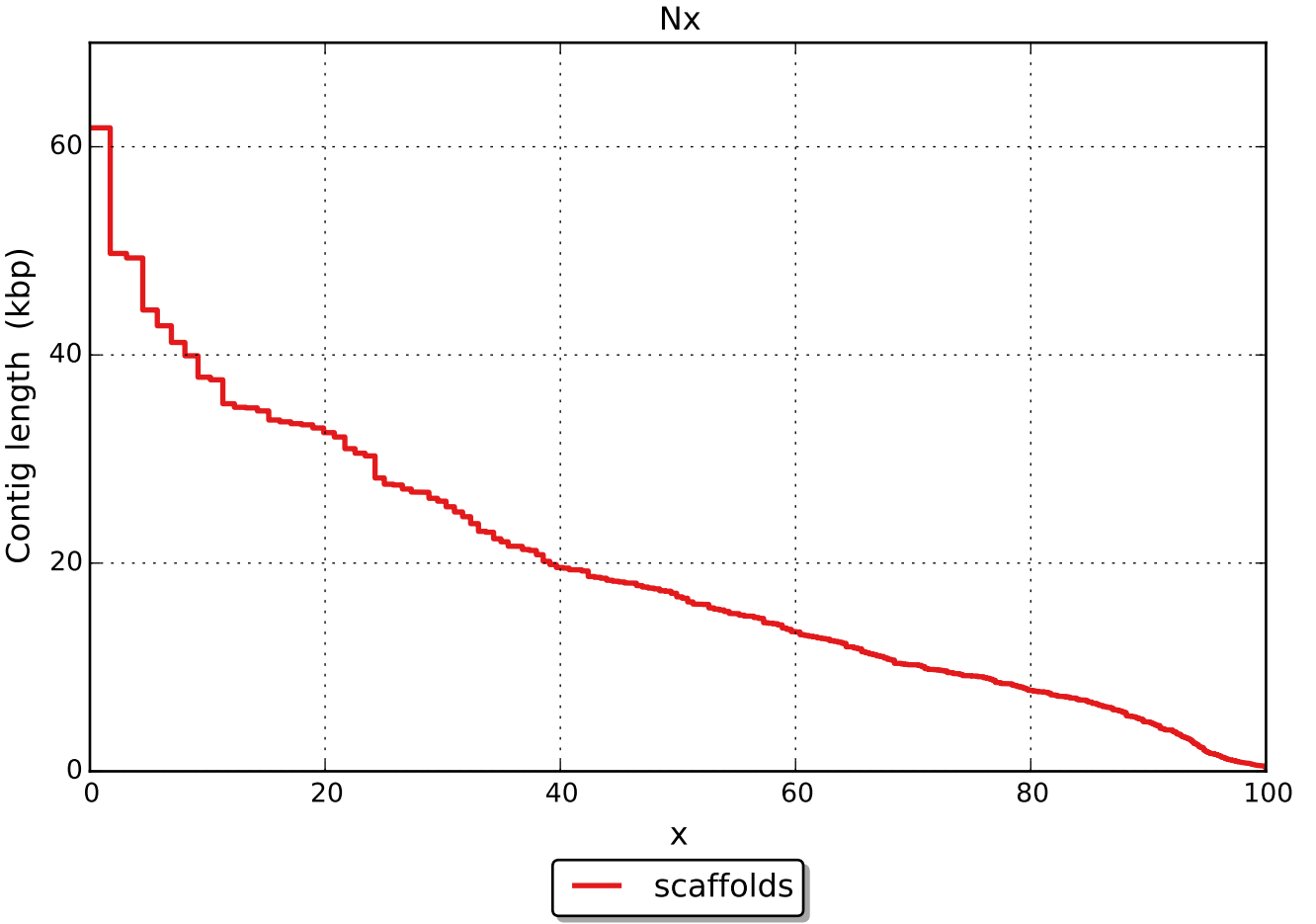
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	99
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	33591
# indels	410
# short indels	27
# long indels	383
Indels length	21085

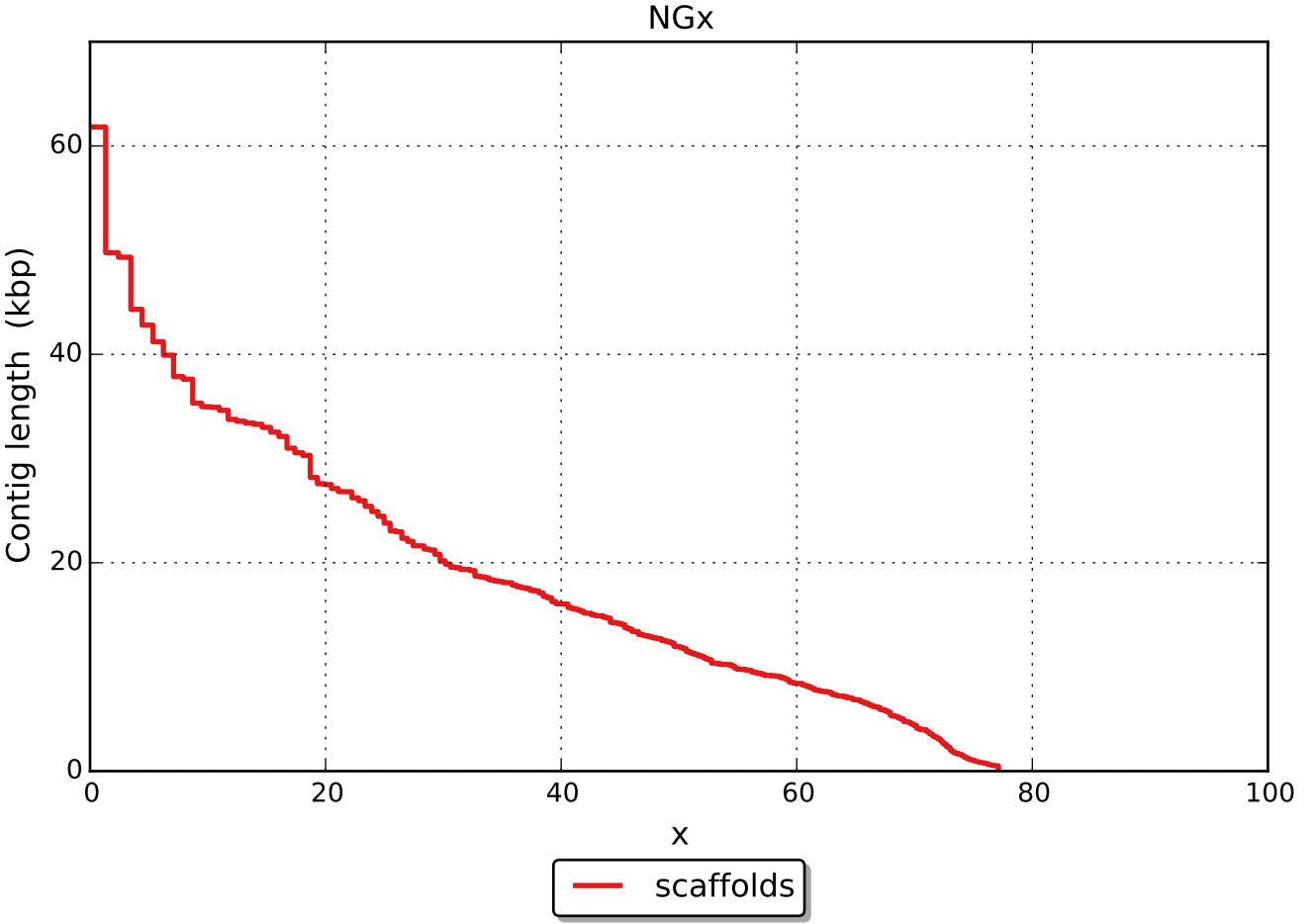
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

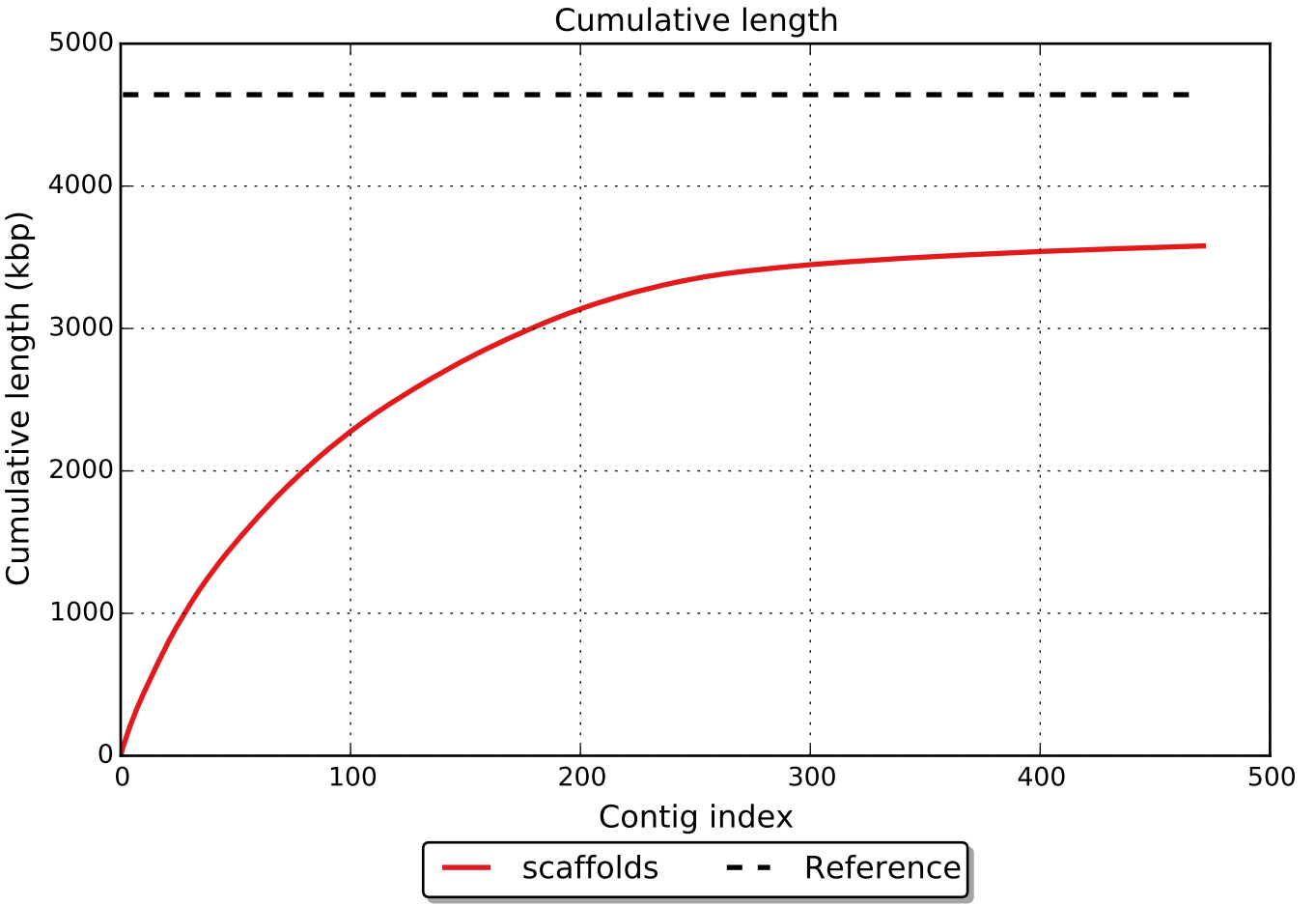
Unaligned report

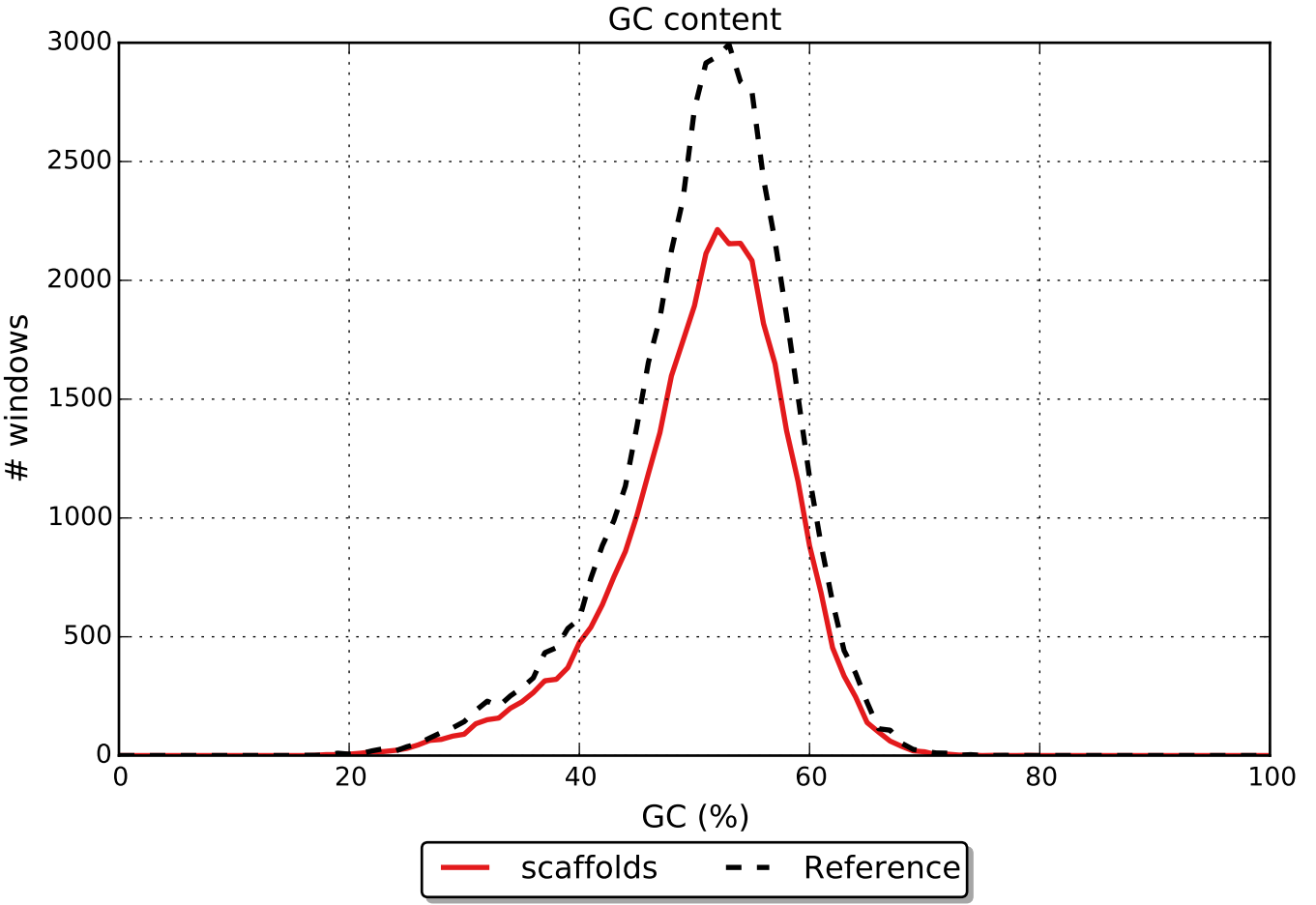
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	145213

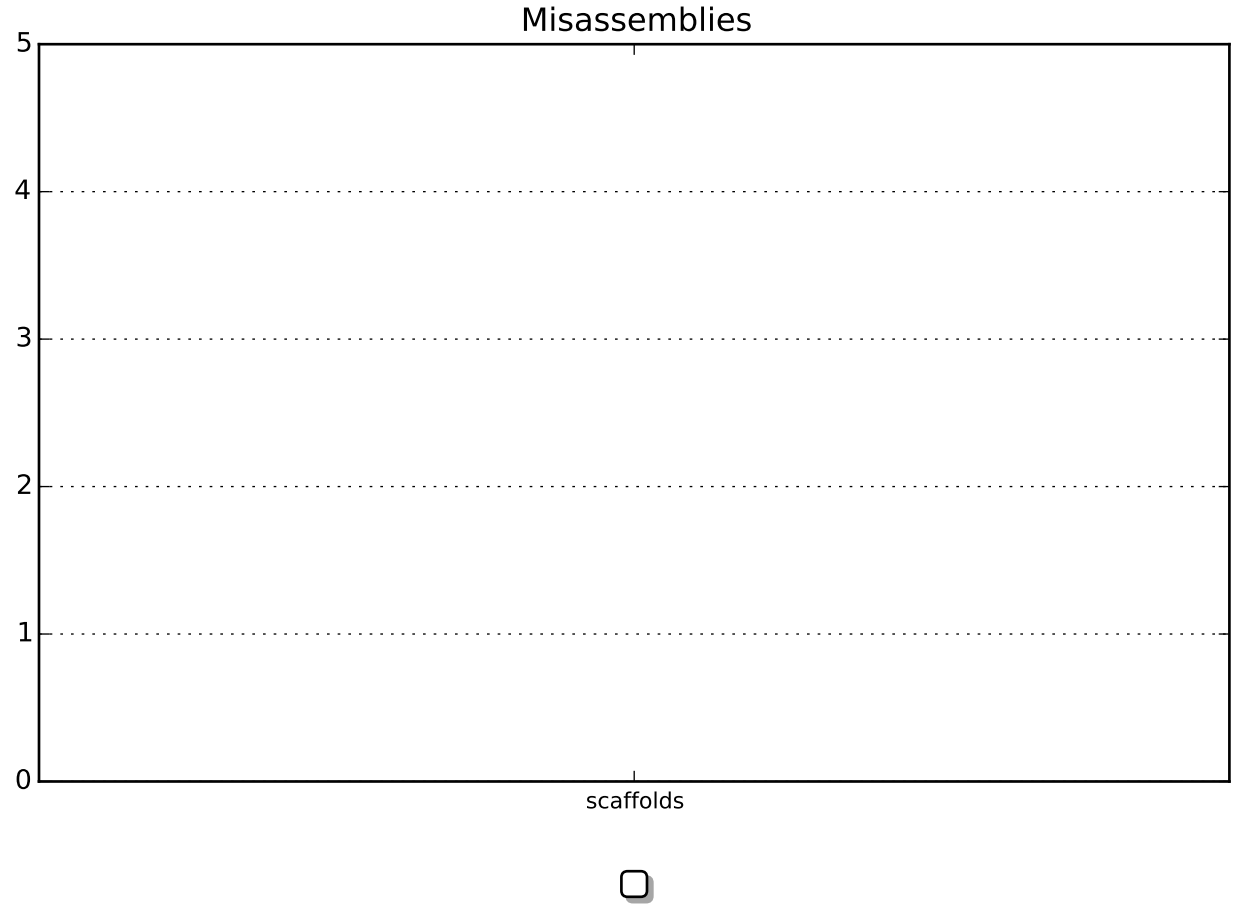
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

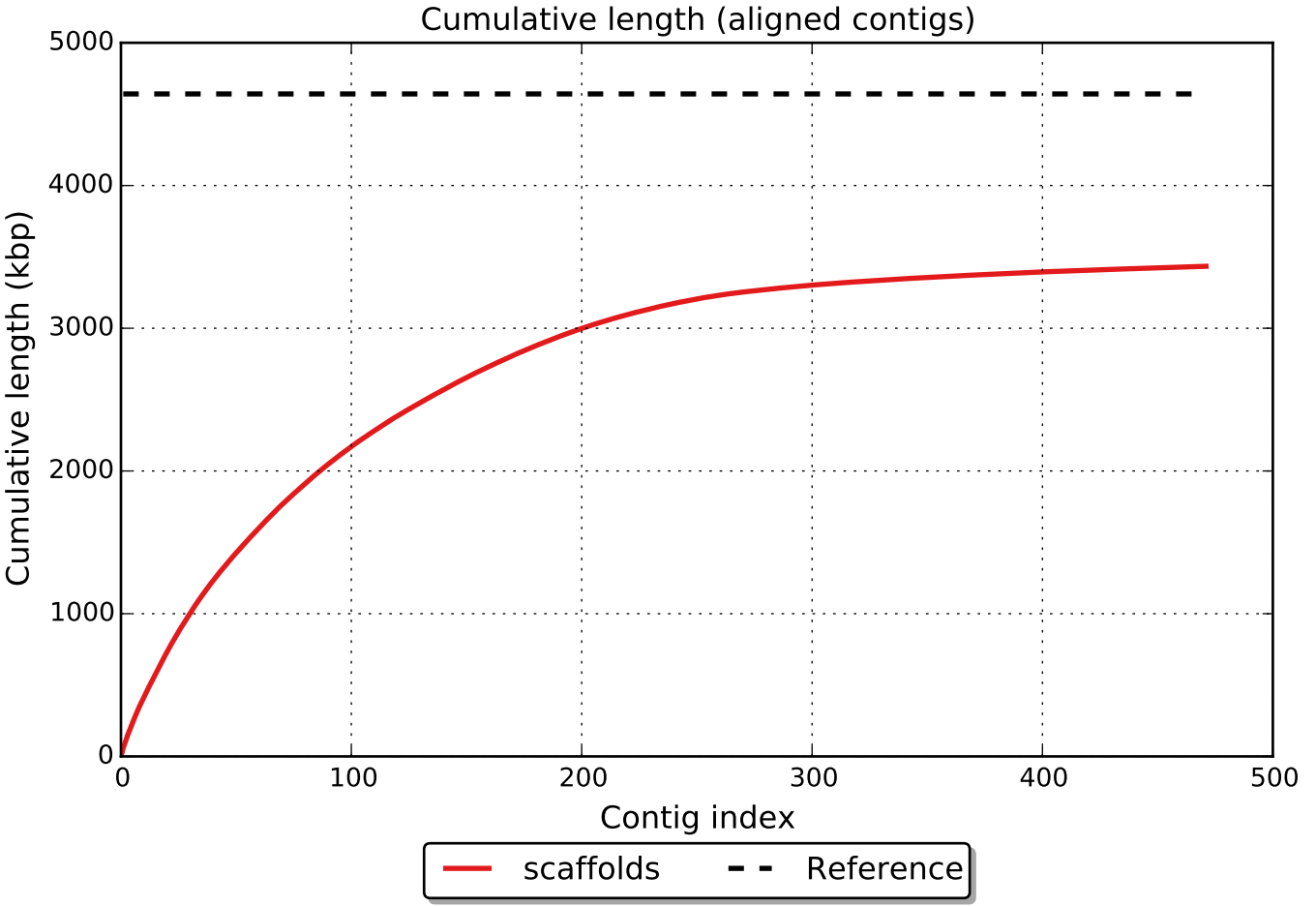

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds

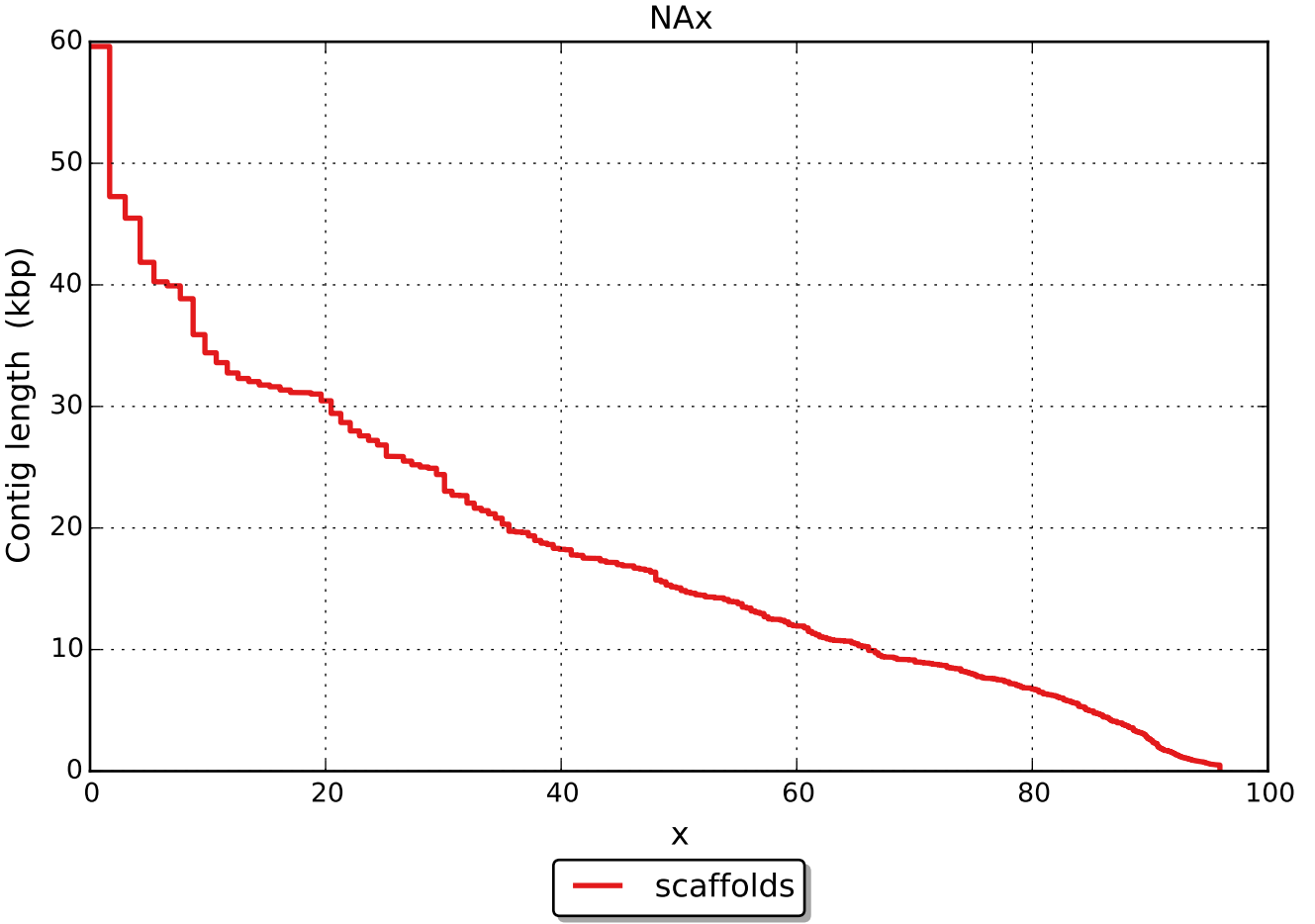

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds

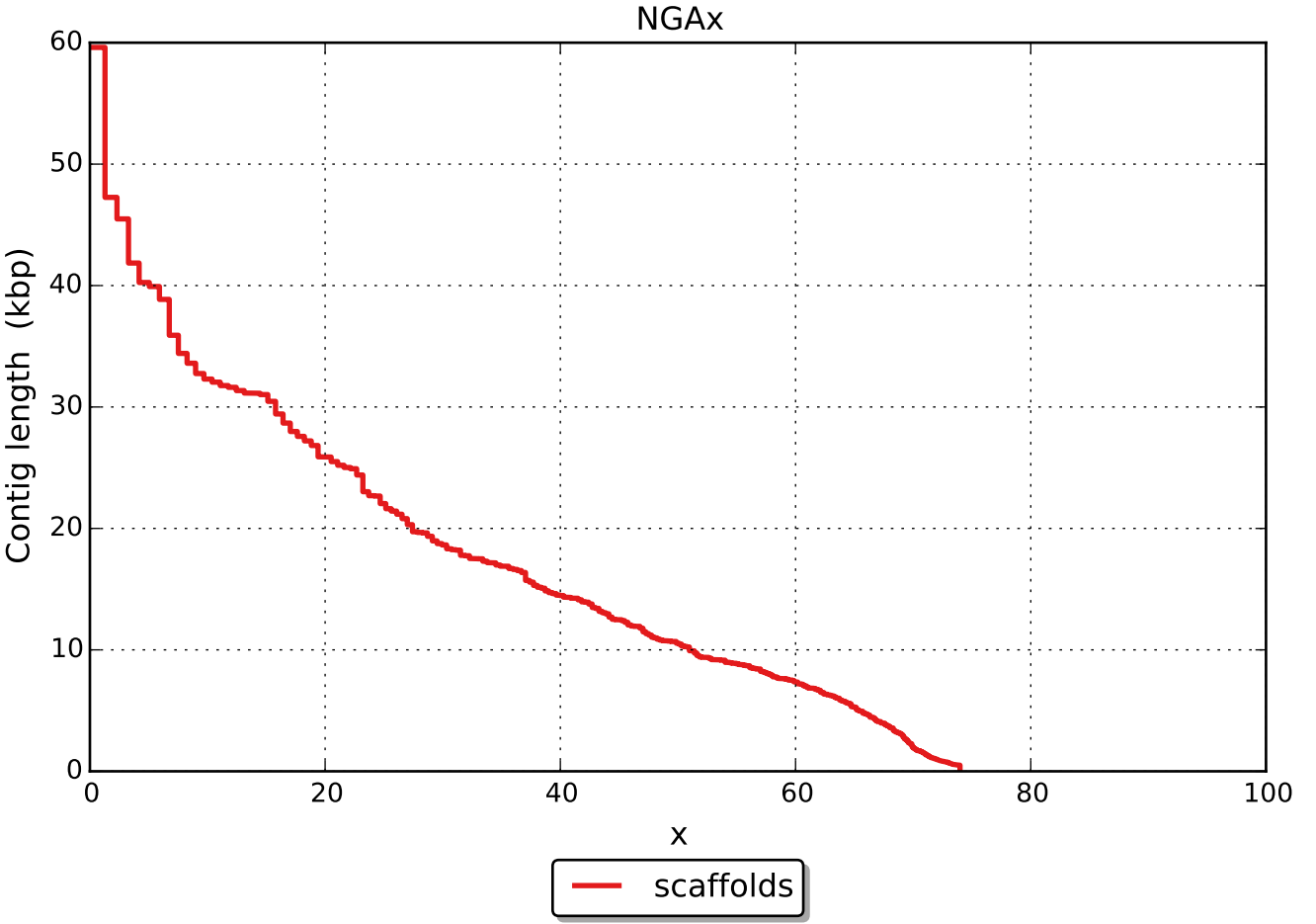

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
scaffolds
Reference


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
0
10
20
30
40
50
60
0
20
40
60
80
100
x
scaffolds