Report

	Scafolds
# contigs (>= 0 bp)	173
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	2877995
Total length (>= 1000 bp)	2856004
Total length (>= 5000 bp)	2835484
Total length (>= 10000 bp)	2814064
Total length (>= 25000 bp)	2793476
Total length (>= 50000 bp)	2793476
# contigs	26
Largest contig	989718
Total length	2860883
Reference length	2903081
GC (%)	32.57
Reference GC (%)	32.73
N50	762333
NG50	762333
N75	528332
NG75	528332
L50	2
LG50	2
L75	3
LG75	3
# misassemblies	25
# misassembled contigs	4
Misassembled contigs length	2518079
# local misassemblies	9
# scaffold gap ext. mis.	1
# scaffold gap loc. mis.	56
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	3451
Genome fraction (%)	97.825
Duplication ratio	1.006
# N's per 100 kbp	618.27
# mismatches per 100 kbp	10.77
# indels per 100 kbp	3.03
Largest alignment	435529
Total aligned length	2839055
NA50	157373
NGA50	157373
NA75	72824
NGA75	72824
LA50	6
LGA50	6
LA75	12
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

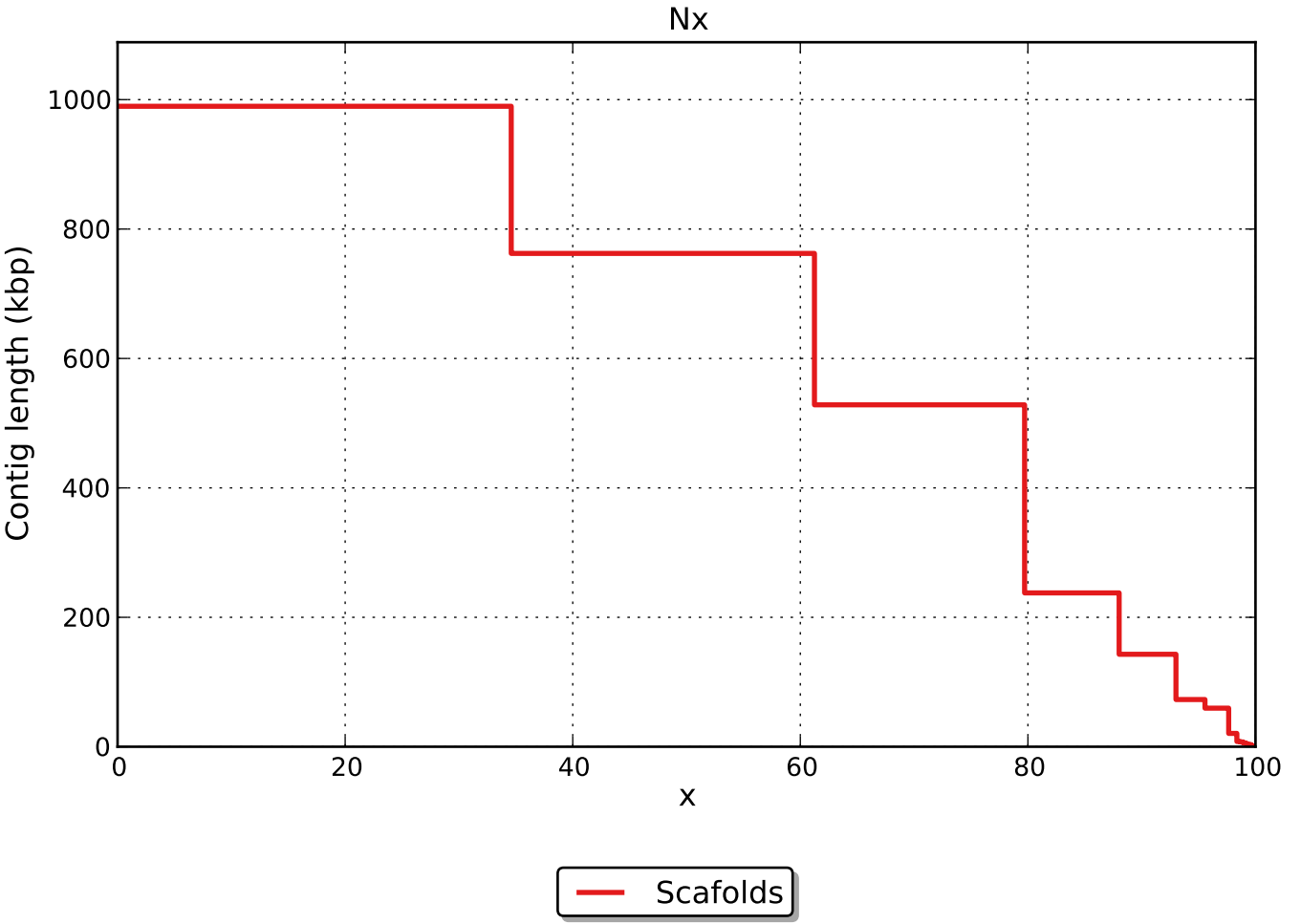
	Scafolds
# misassemblies	25
# contig misassemblies	8
# c. relocations	8
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	17
# s. relocations	17
# s. translocations	0
# s. inversions	0
# misassembled contigs	4
Misassembled contigs length	2518079
# local misassemblies	9
# scaffold gap ext. mis.	1
# scaffold gap loc. mis.	56
# unaligned mis. contigs	0
# mismatches	306
# indels	86
# indels (<= 5 bp)	33
# indels (> 5 bp)	53
Indels length	2562

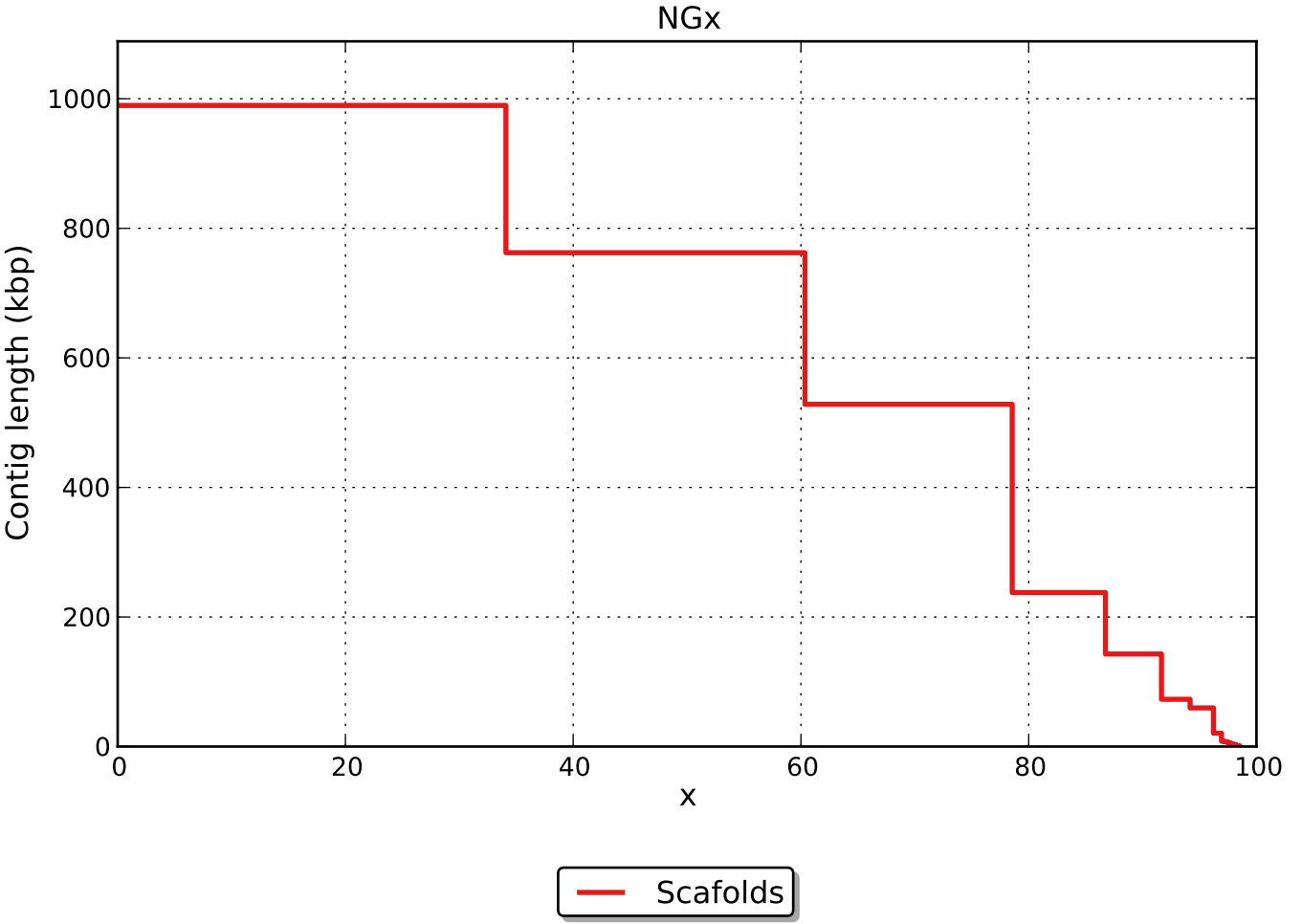
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

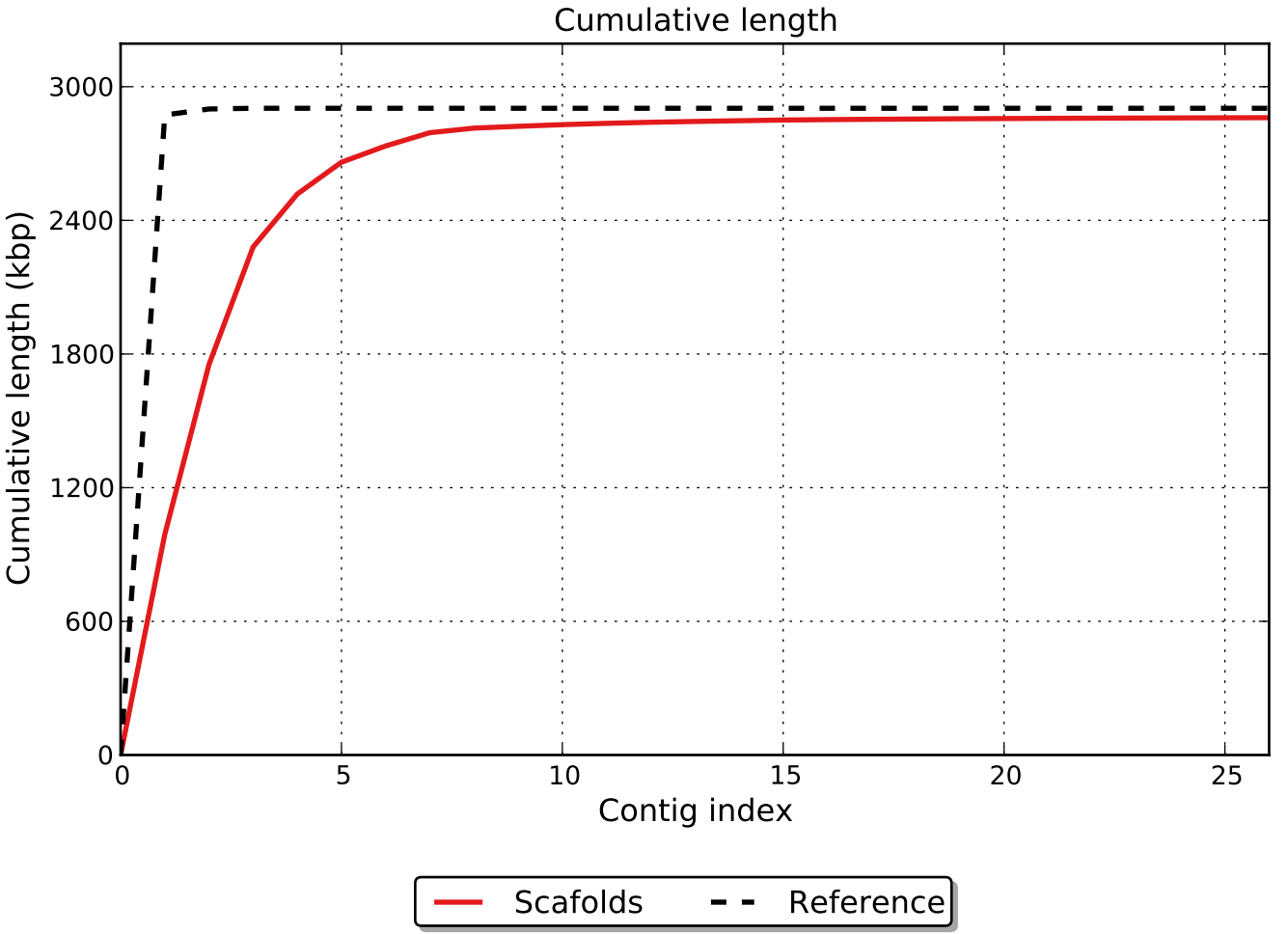
Unaligned report

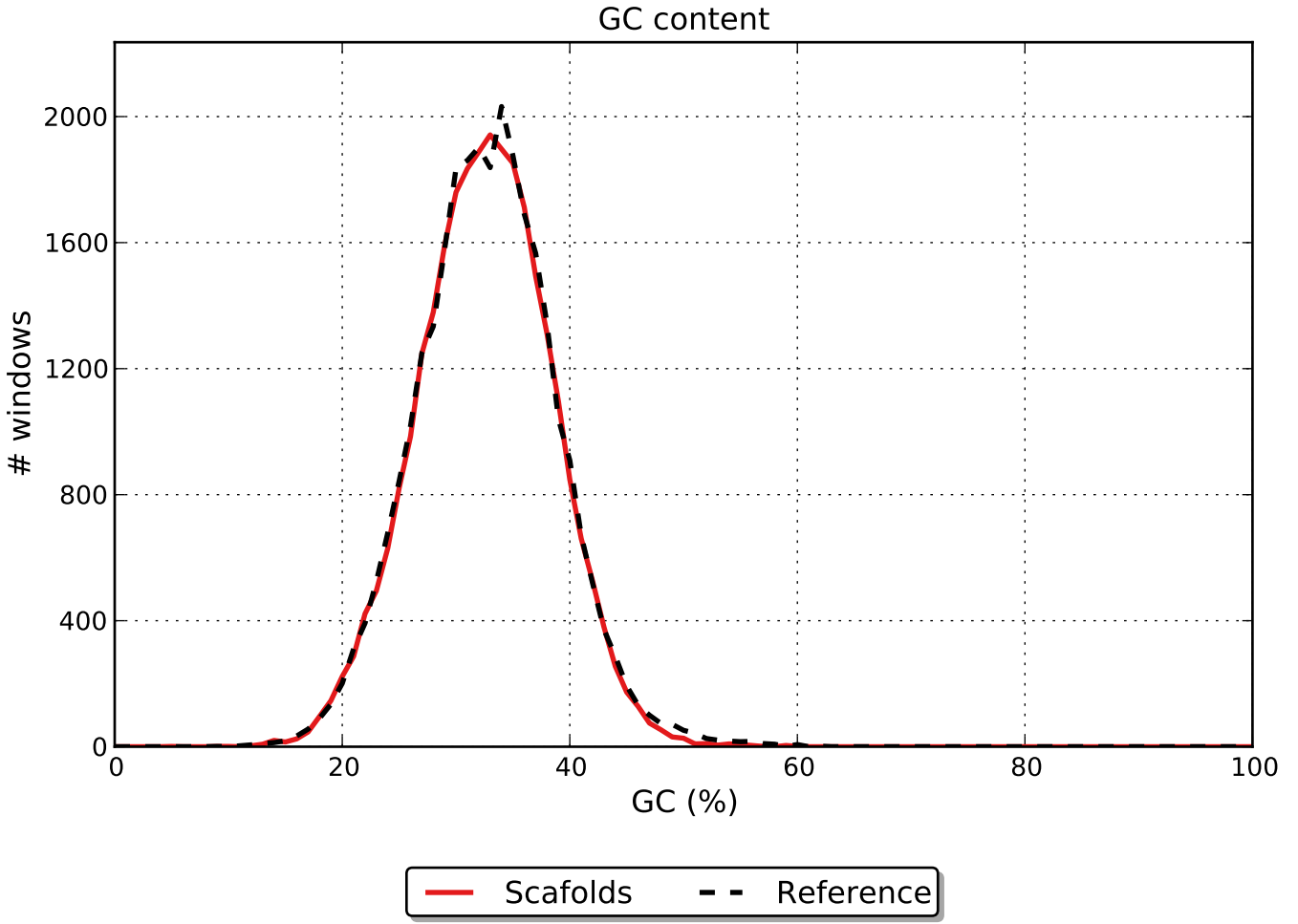
	Scafolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	3451
# N's	17688

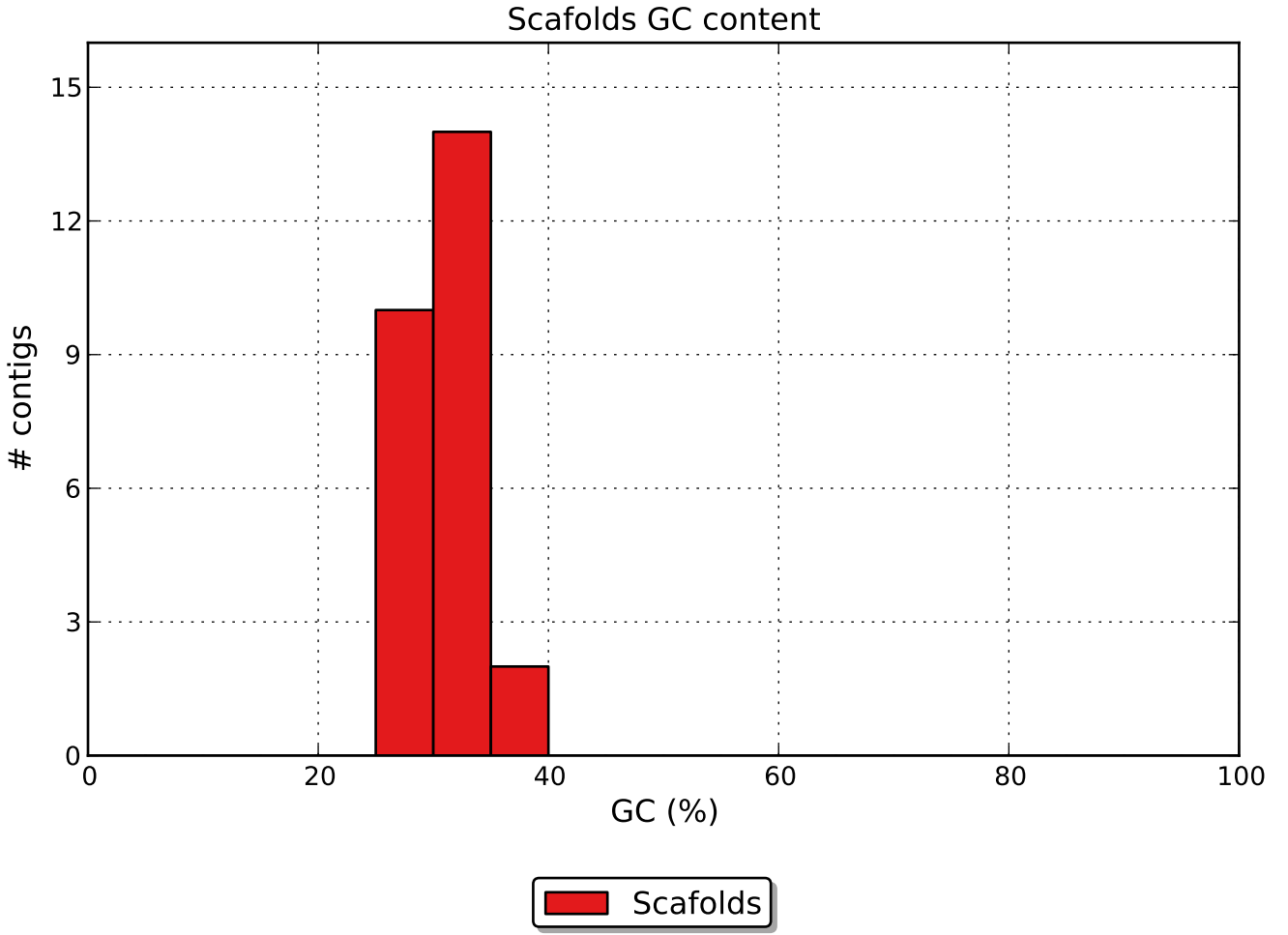
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
Scafolds

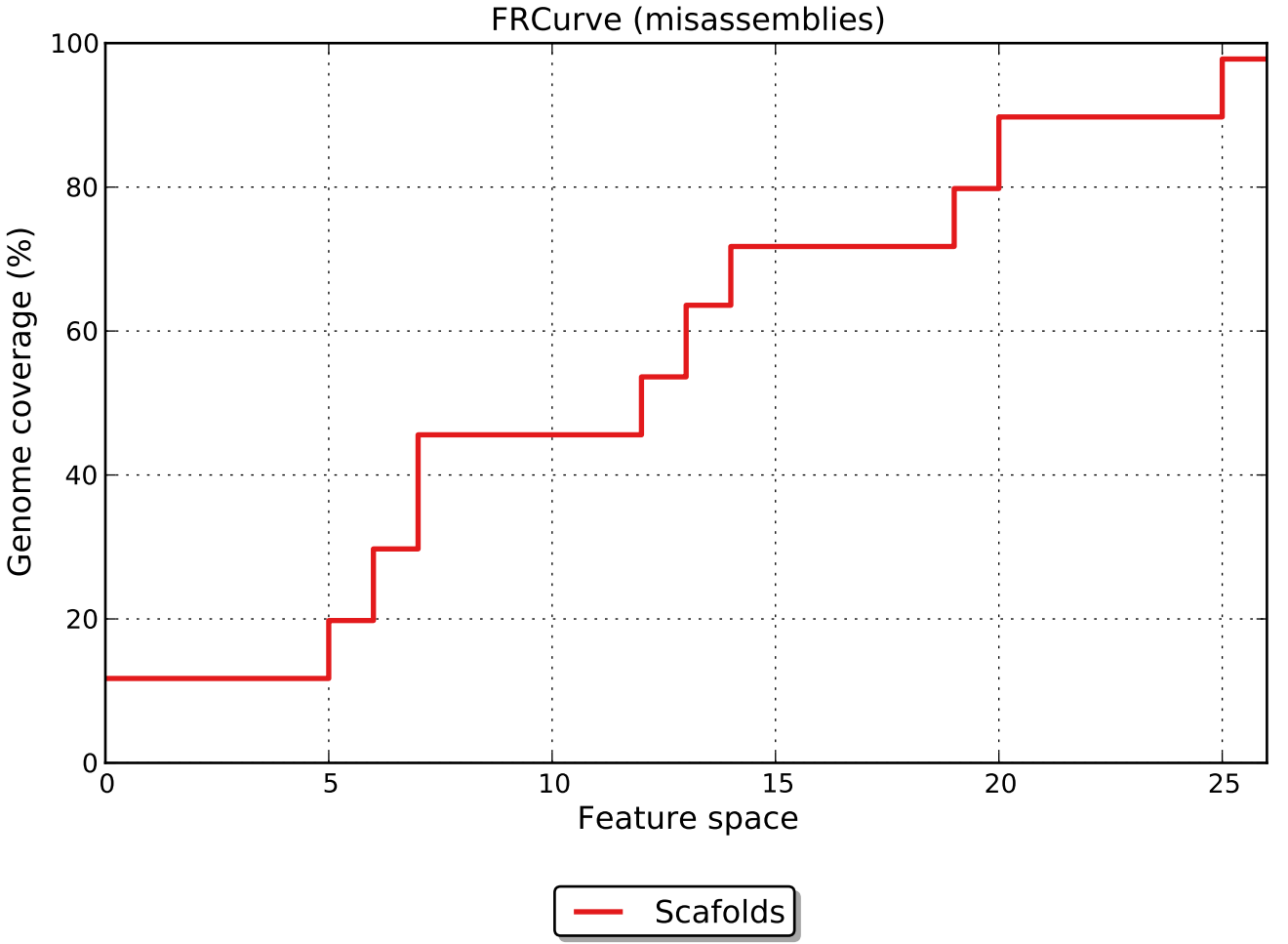

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
Scafolds

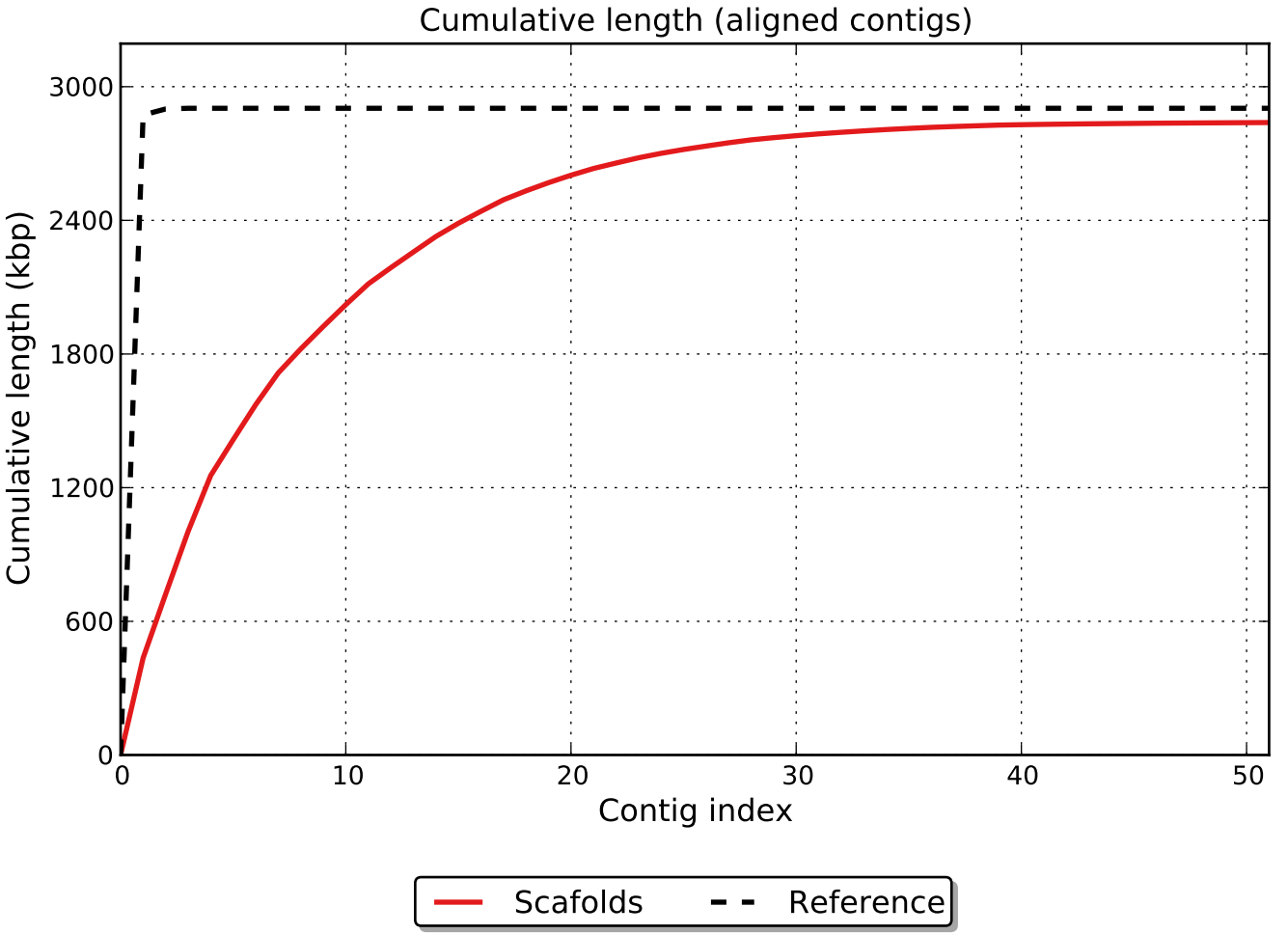

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
5
10
15
20
25
Contig index
Scafolds
Reference

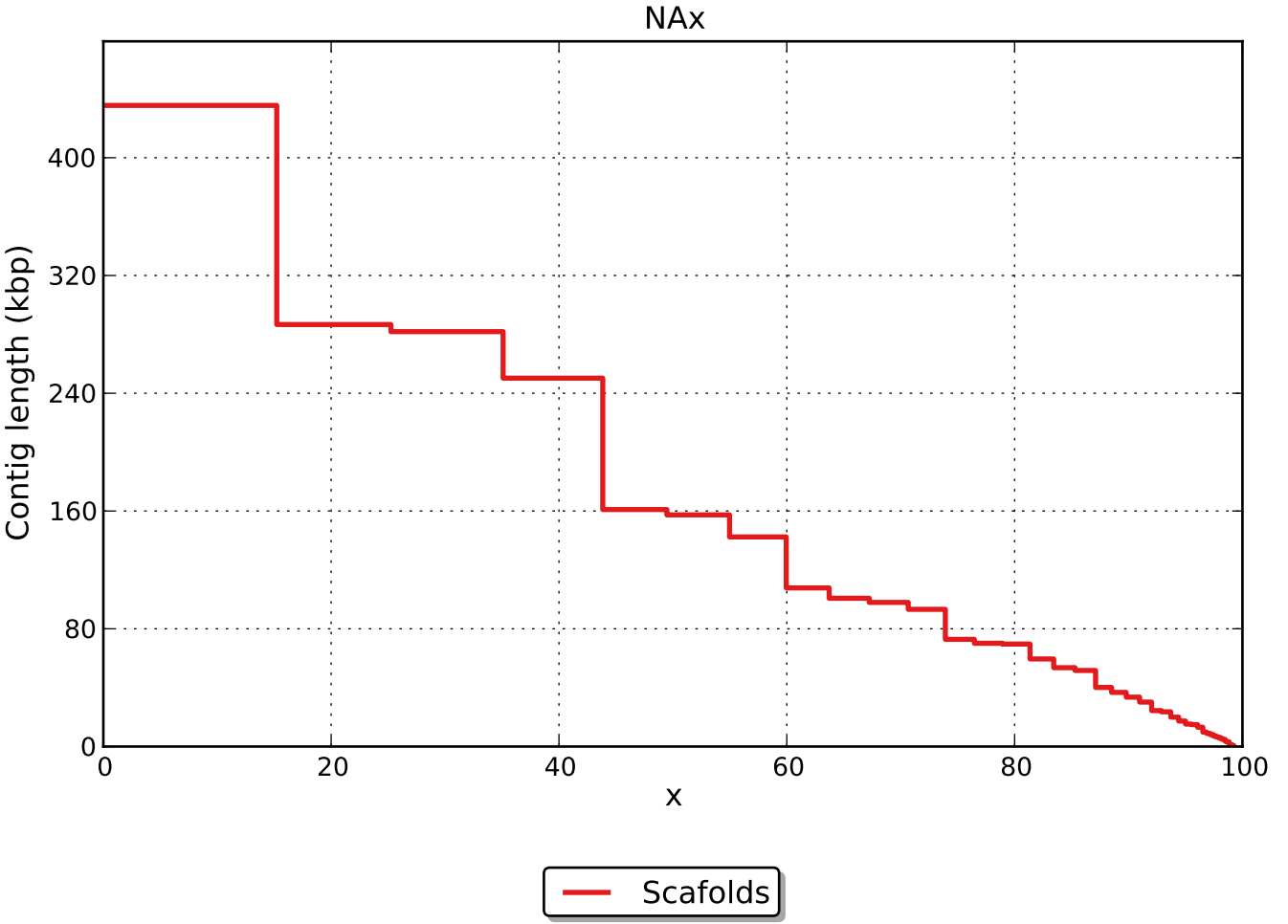

GC content
windows
GC (%)
0
400
800
1200
1600
2000
0
20
40
60
80
100
Scafolds
Reference

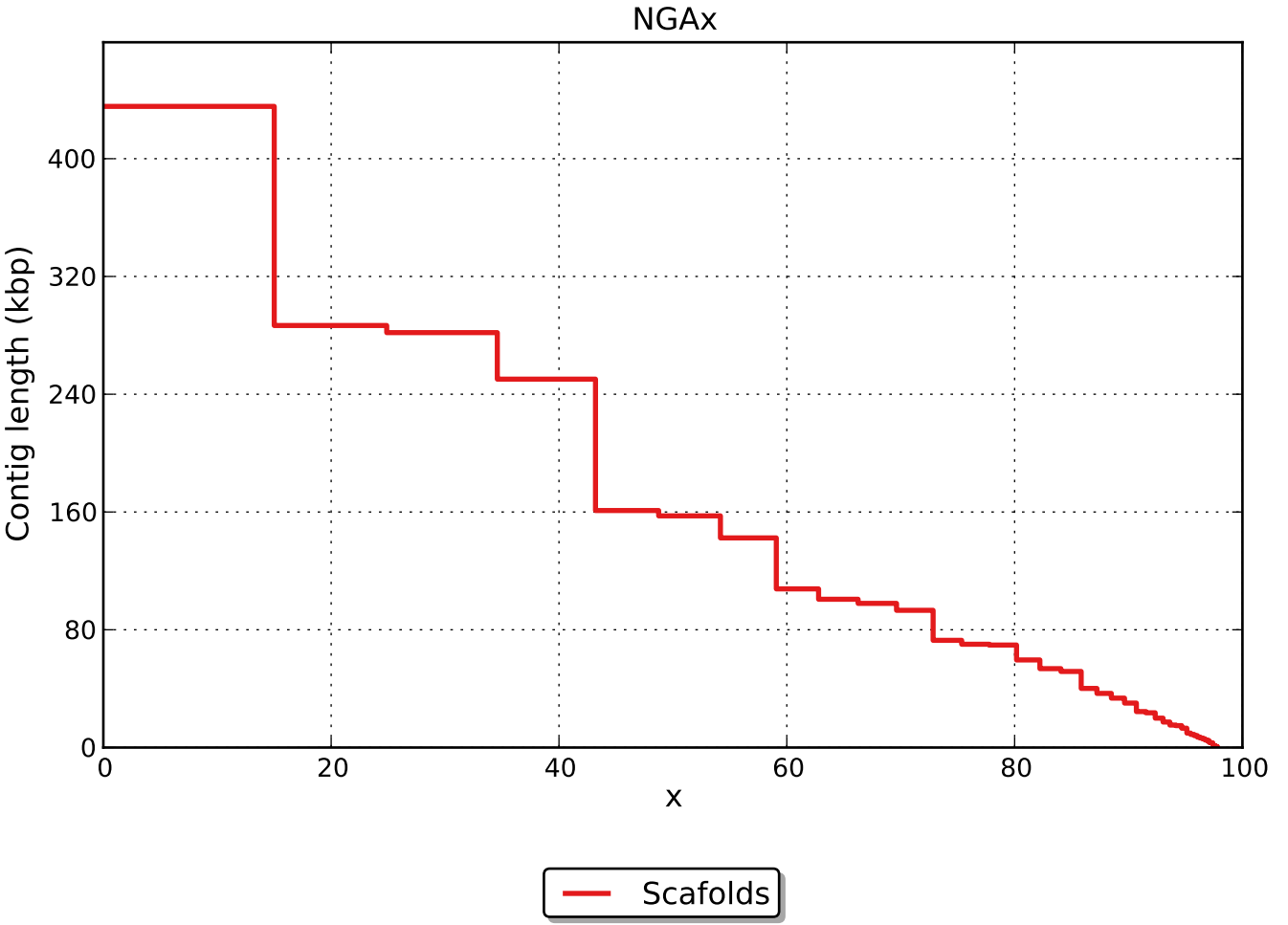

Scafolds GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
Scafolds

Misassemblies
25
20
15
10
5
0
Scafolds
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
5
10
15
20
25
Feature space
Scafolds


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
10
20
30
40
50
Contig index
Scafolds
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
Scafolds


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
Scafolds