Report

	scaffolds	output.scafSeq
# contigs (>= 0 bp)	1164864	261294
# contigs (>= 1000 bp)	600	13064
# contigs (>= 5000 bp)	178	1269
# contigs (>= 10000 bp)	99	142
# contigs (>= 25000 bp)	25	2
# contigs (>= 50000 bp)	7	0
Total length (>= 0 bp)	114900536	86862967
Total length (>= 1000 bp)	3428660	29133144
Total length (>= 5000 bp)	2701093	9502075
Total length (>= 10000 bp)	2163148	1712941
Total length (>= 25000 bp)	1015757	54918
Total length (>= 50000 bp)	404782	0
# contigs	12069	33585
Largest contig	66390	27938
Total length	10455664	43973845
Reference length	3380749	3380749
GC (%)	40.90	40.41
Reference GC (%)	45.32	45.32
N50	682	1378
NG50	14612	10035
N75	570	853
NG75	6436	9479
L50	2911	6934
LG50	61	140
L75	7165	17250
LG75	149	227
# misassemblies	10	2
# misassembled contigs	9	2
Misassembled contigs length	159655	11980
# local misassemblies	163	14
# unaligned mis. contigs	0	0
# unaligned contigs	11657 + 5 part	32216 + 1 part
Unaligned length	7295819	41055009
Genome fraction (%)	92.722	85.931
Duplication ratio	1.008	1.005
# N's per 100 kbp	417.12	54699.83
# mismatches per 100 kbp	43.03	24.47
# indels per 100 kbp	10.14	1.34
Largest alignment	66151	16563
Total aligned length	3140364	2912567
NGA50	14287	2587
NGA75	6198	1097
LGA50	63	372
LGA75	155	870

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

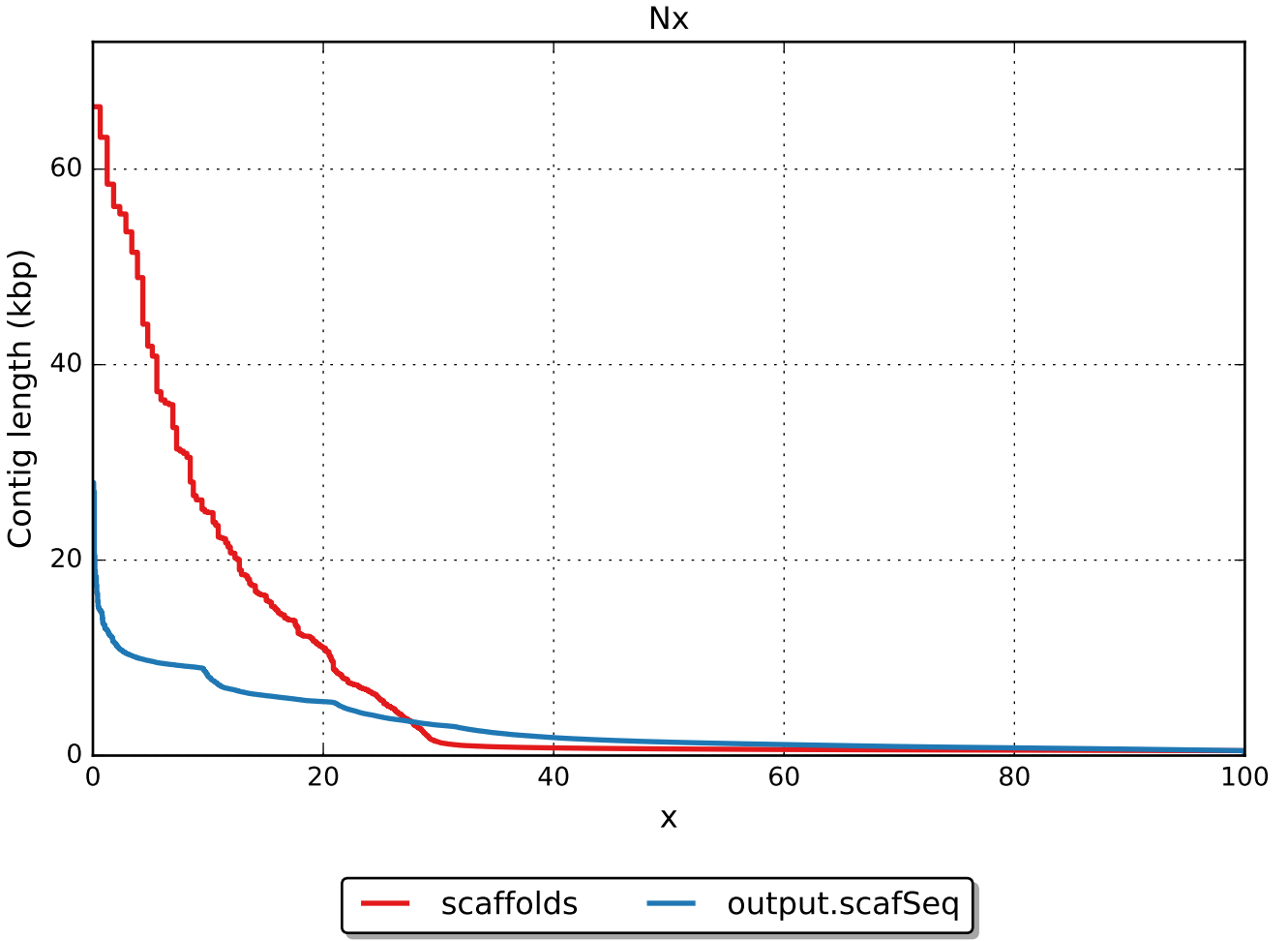
	scaffolds	output.scafSeq
# misassemblies	10	2
# relocations	10	2
# translocations	0	0
# inversions	0	0
# misassembled contigs	9	2
Misassembled contigs length	159655	11980
# local misassemblies	163	14
# unaligned mis. contigs	0	0
# mismatches	1349	711
# indels	318	39
# indels (<= 5 bp)	211	27
# indels (> 5 bp)	107	12
Indels length	5014	659

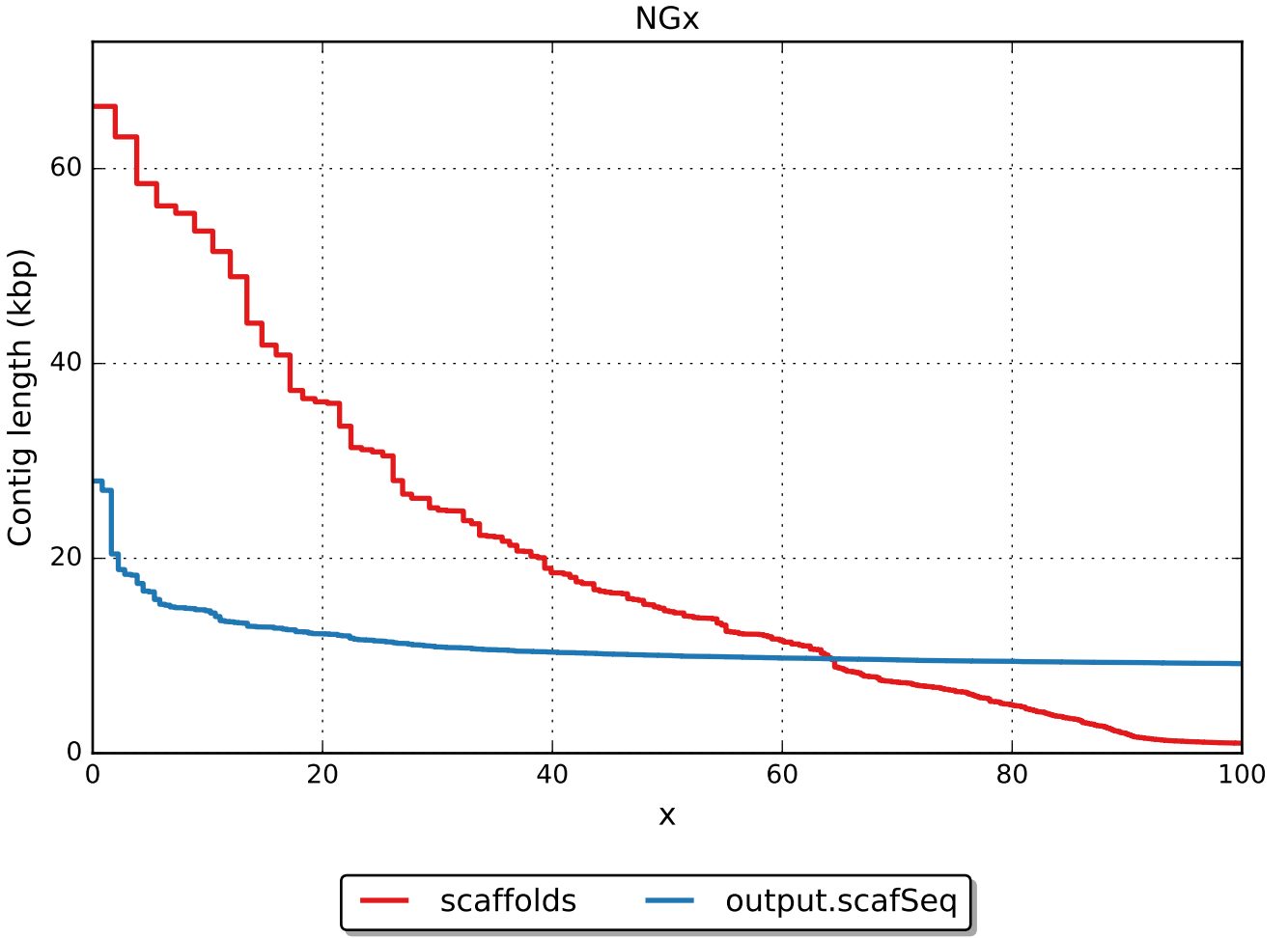
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

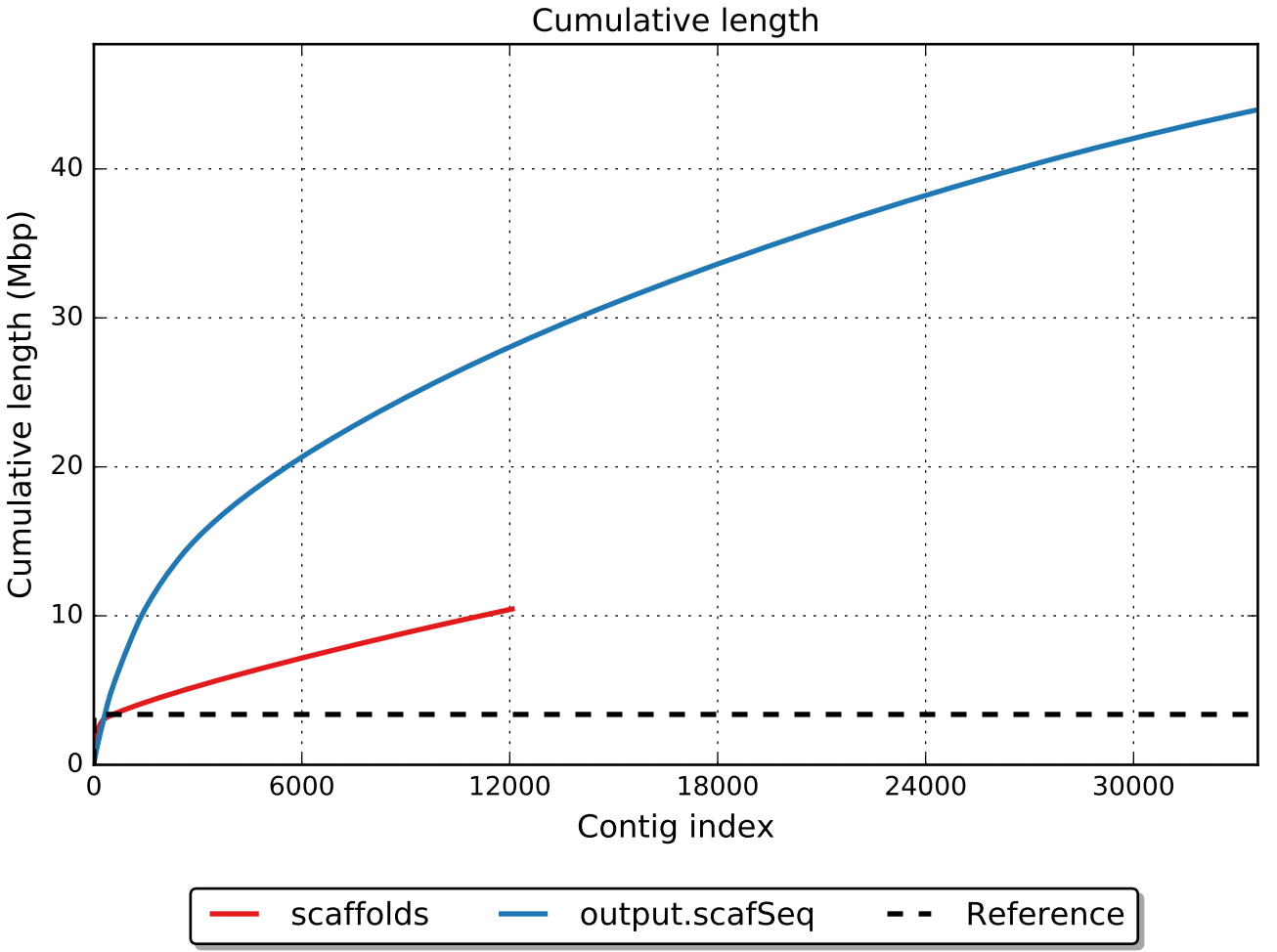
Unaligned report

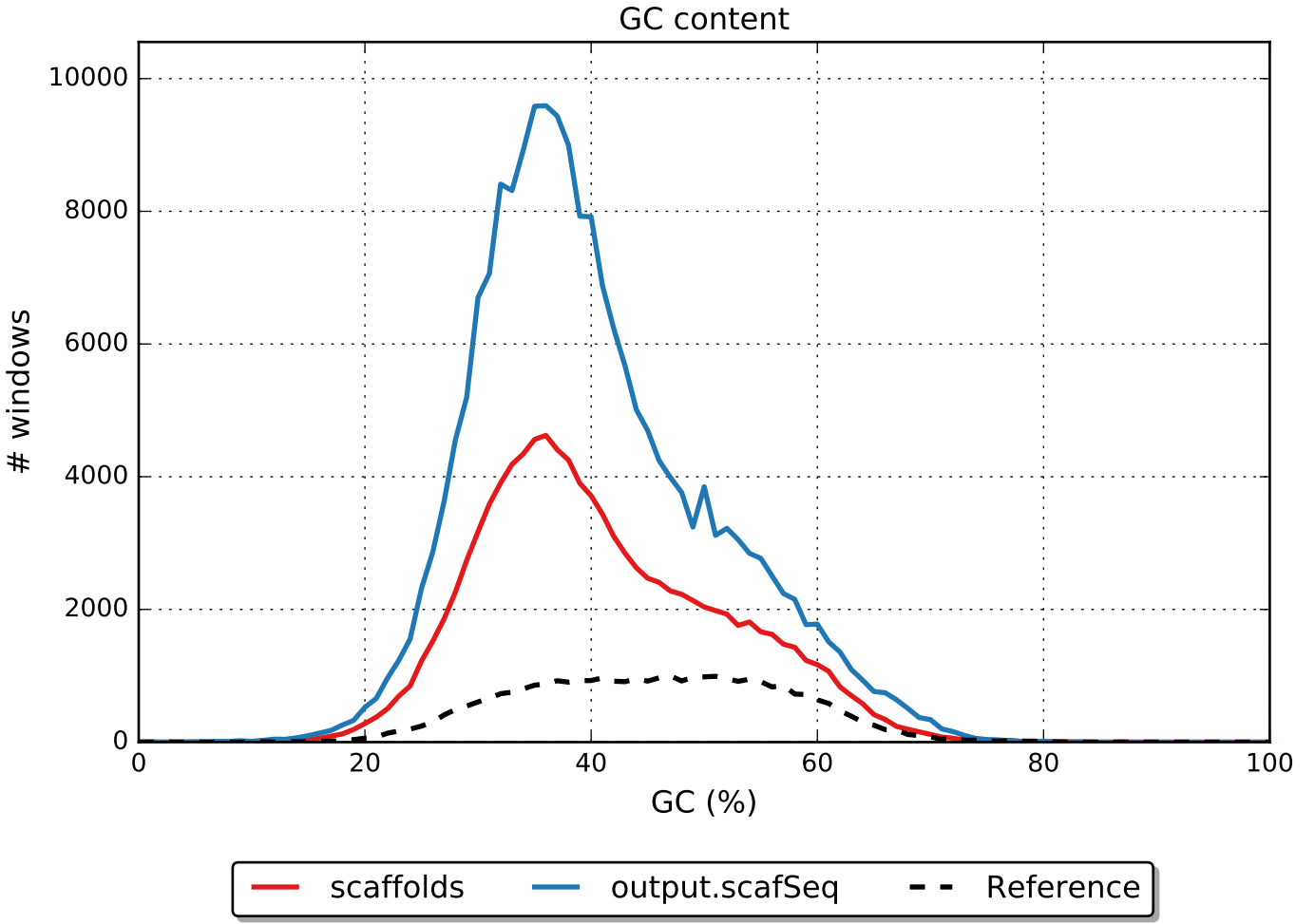
	scaffolds	output.scafSeq
# fully unaligned contigs	11657	32216
Fully unaligned length	7291182	41052036
# partially unaligned contigs	5	1
Partially unaligned length	4637	2973
# N's	43613	24053618

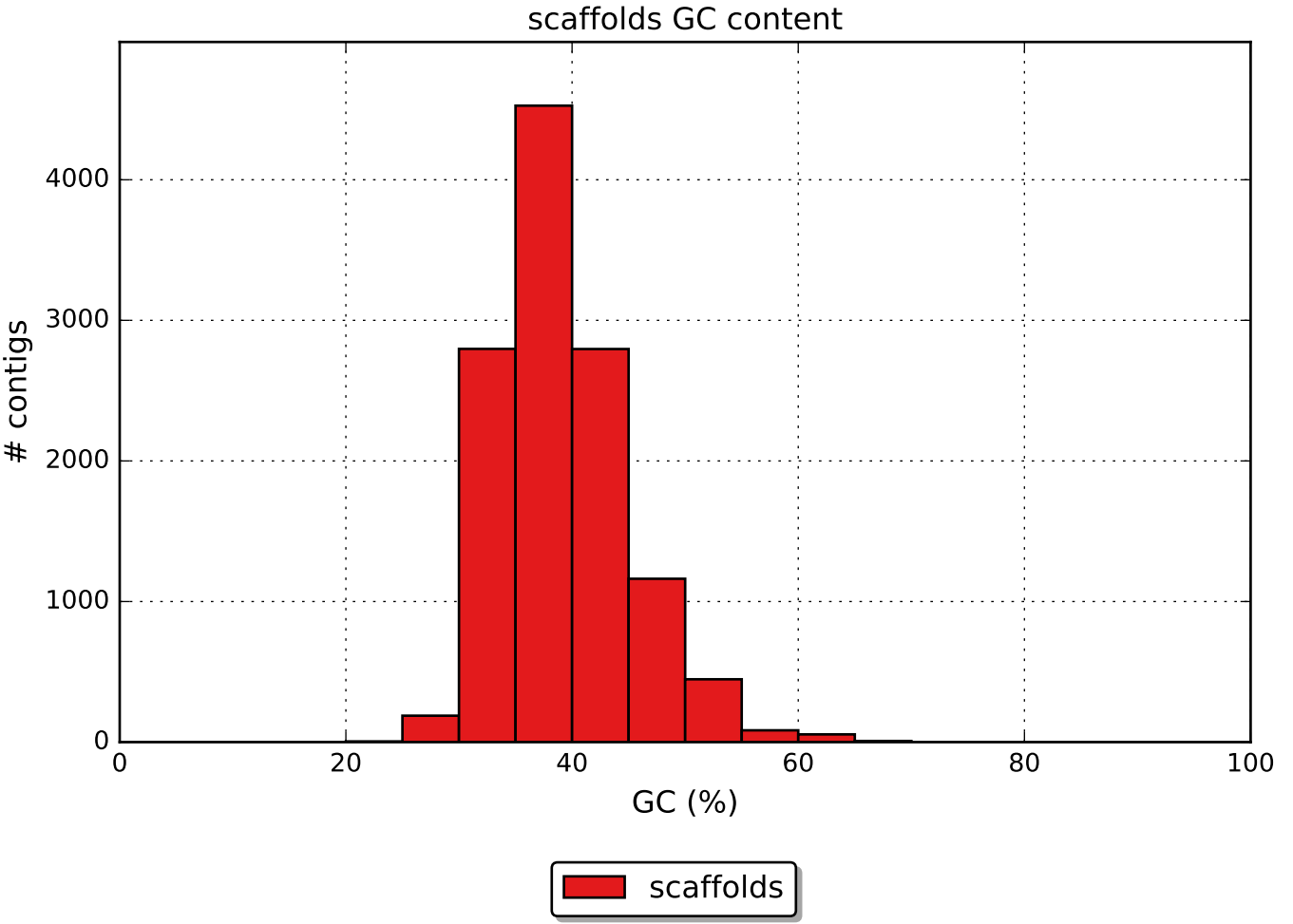
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

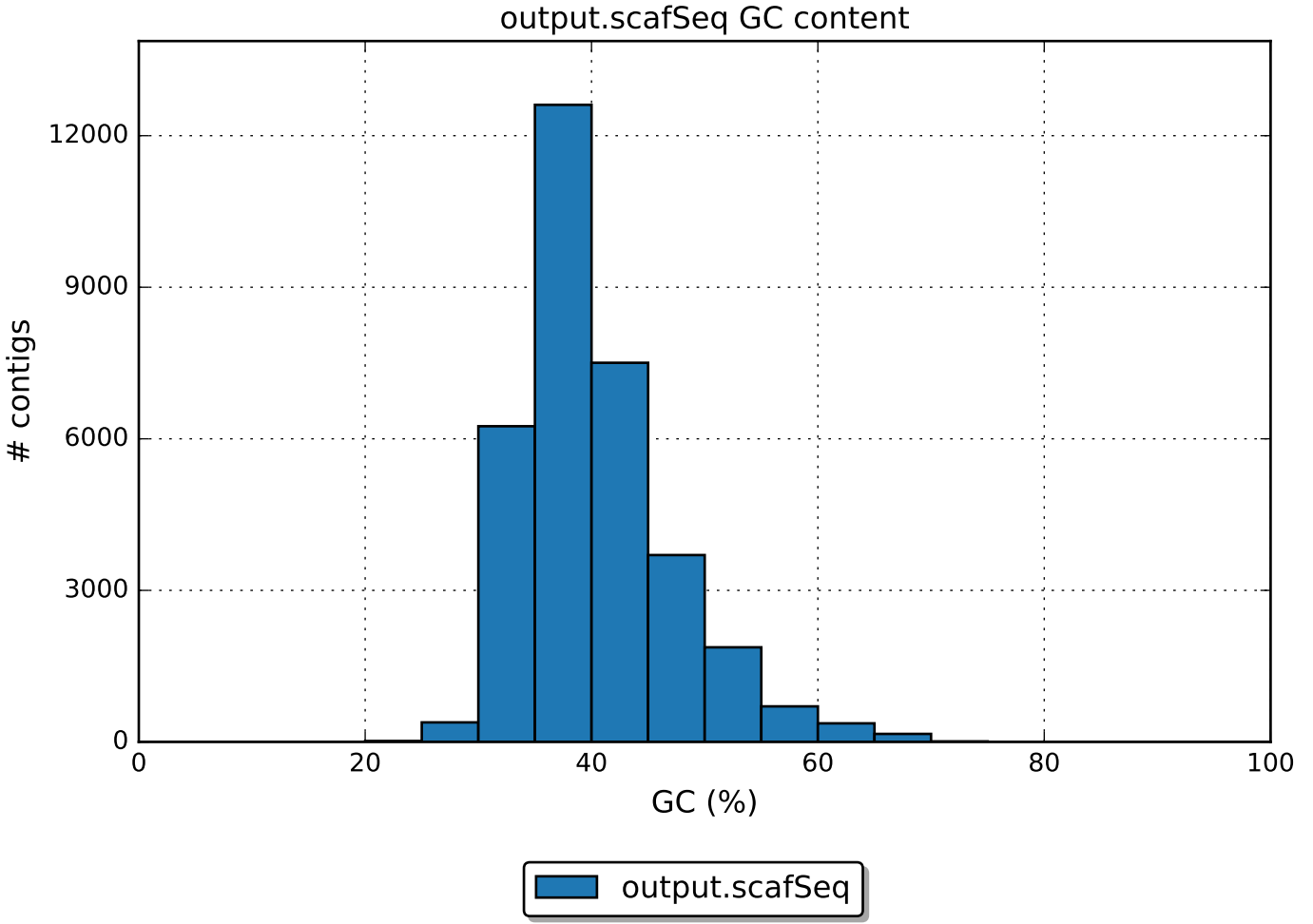

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds
output.scafSeq

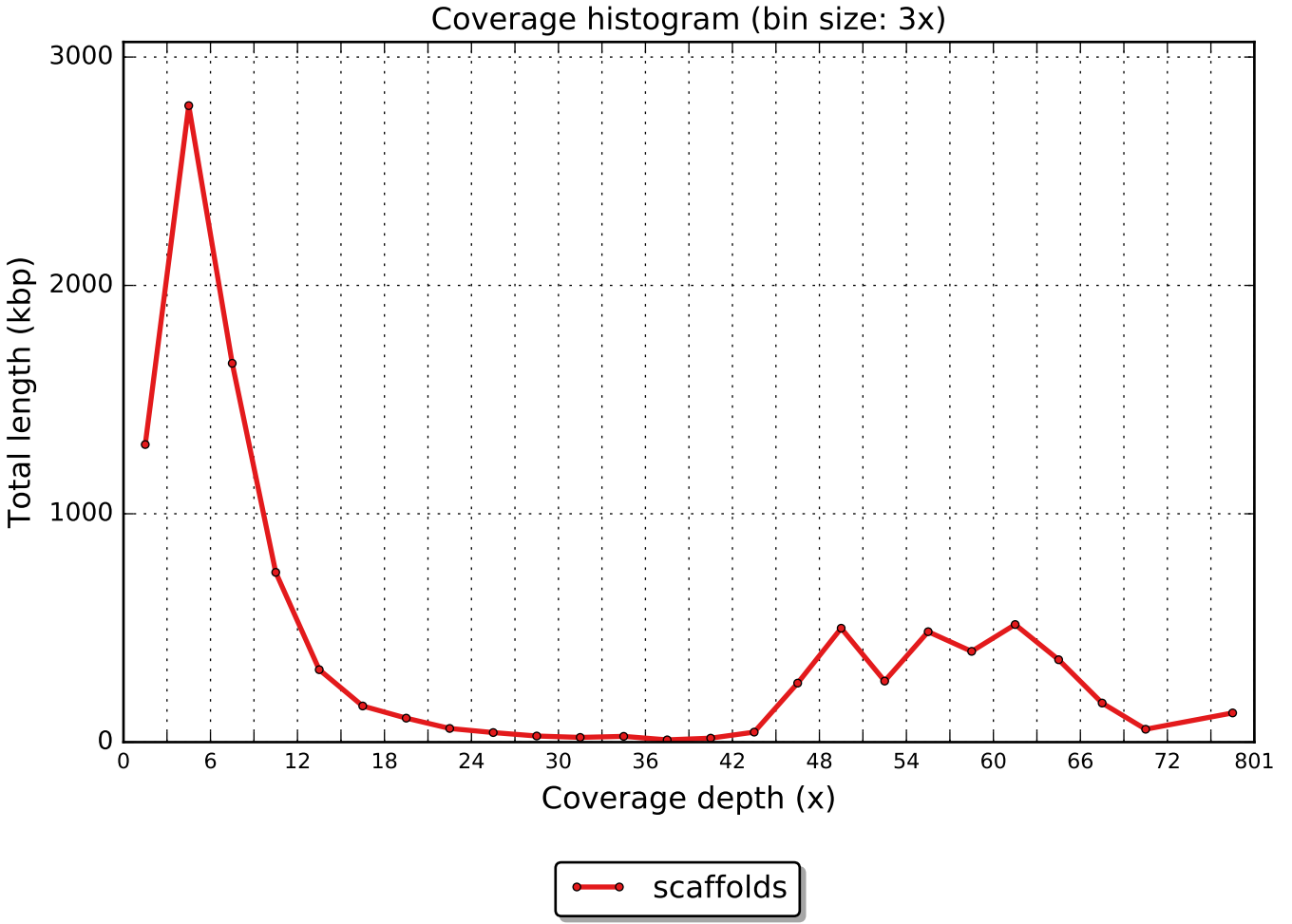

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds
output.scafSeq

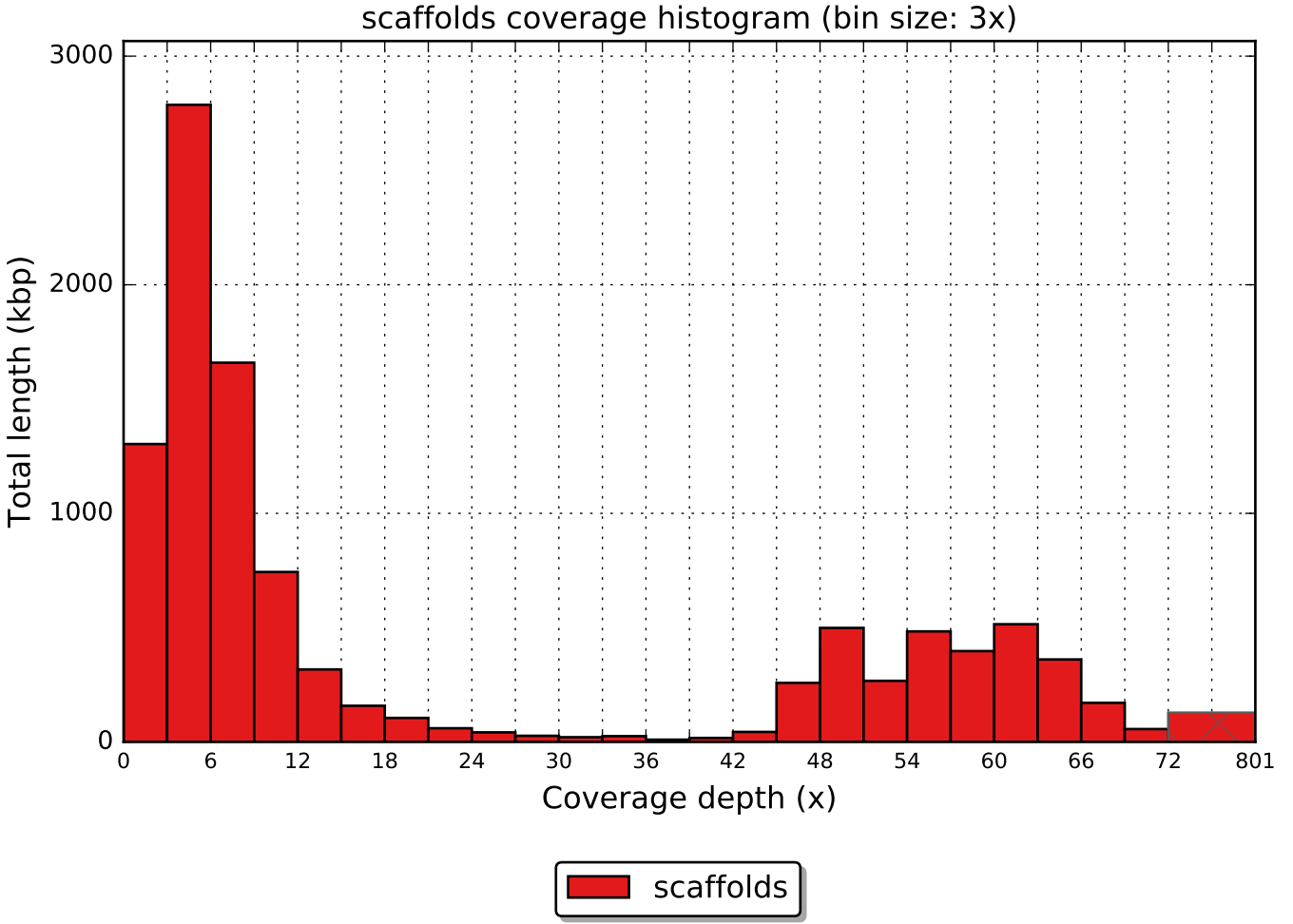

Cumulative length
Cumulative length (Mbp)
0
10
20
30
40
0
6000
12000
18000
24000
30000
Contig index
scaffolds
output.scafSeq
Reference

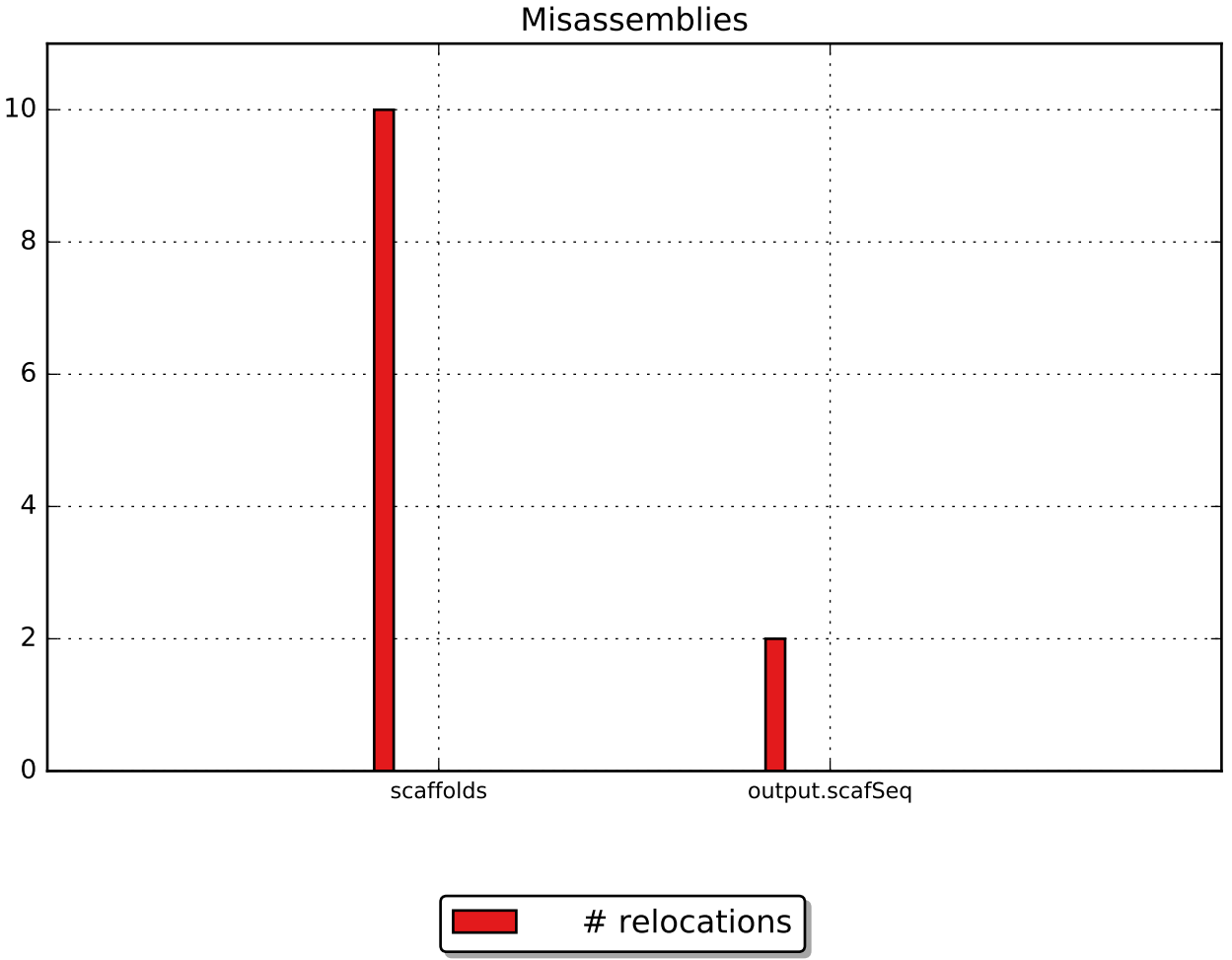

GC content
windows
GC (%)
0
2000
4000
6000
8000
10000
0
20
40
60
80
100
scaffolds
output.scafSeq
Reference

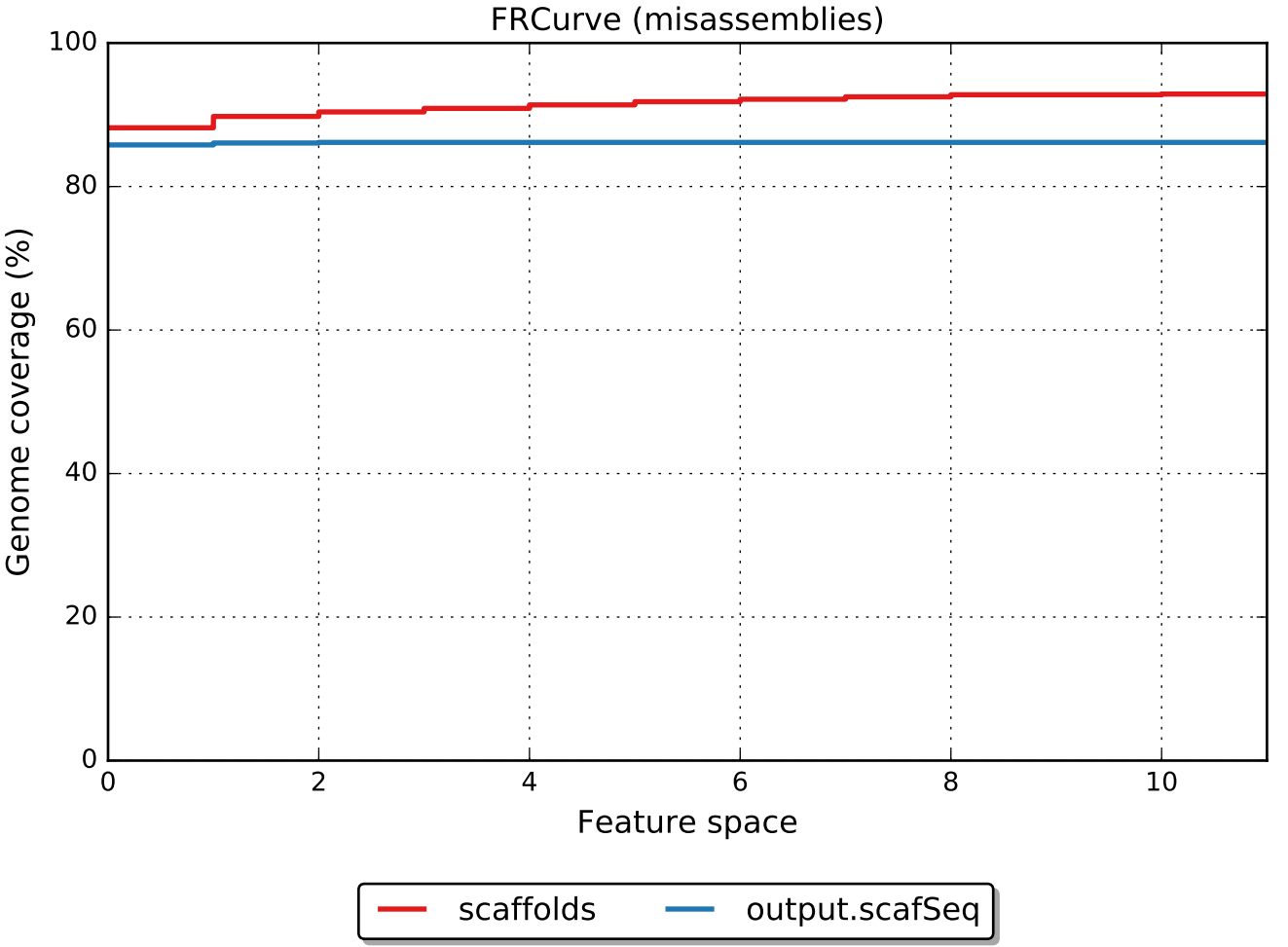

scaffolds GC content
contigs
GC (%)
0
1000
2000
3000
4000
0
20
40
60
80
100
scaffolds

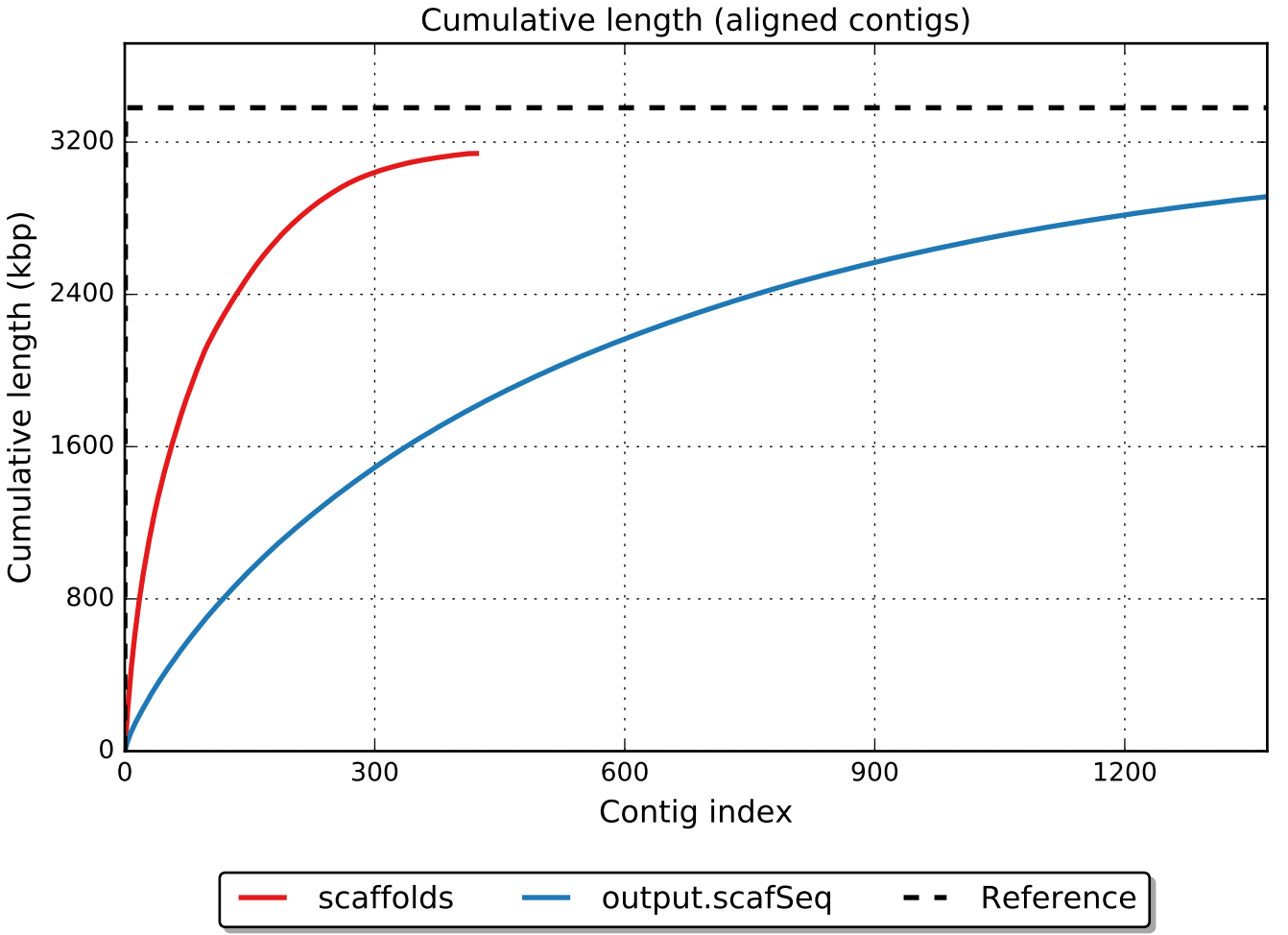

output.scafSeq GC content
12000
9000
6000
3000
0
contigs
0
20
40
60
80
100
GC (%)
output.scafSeq

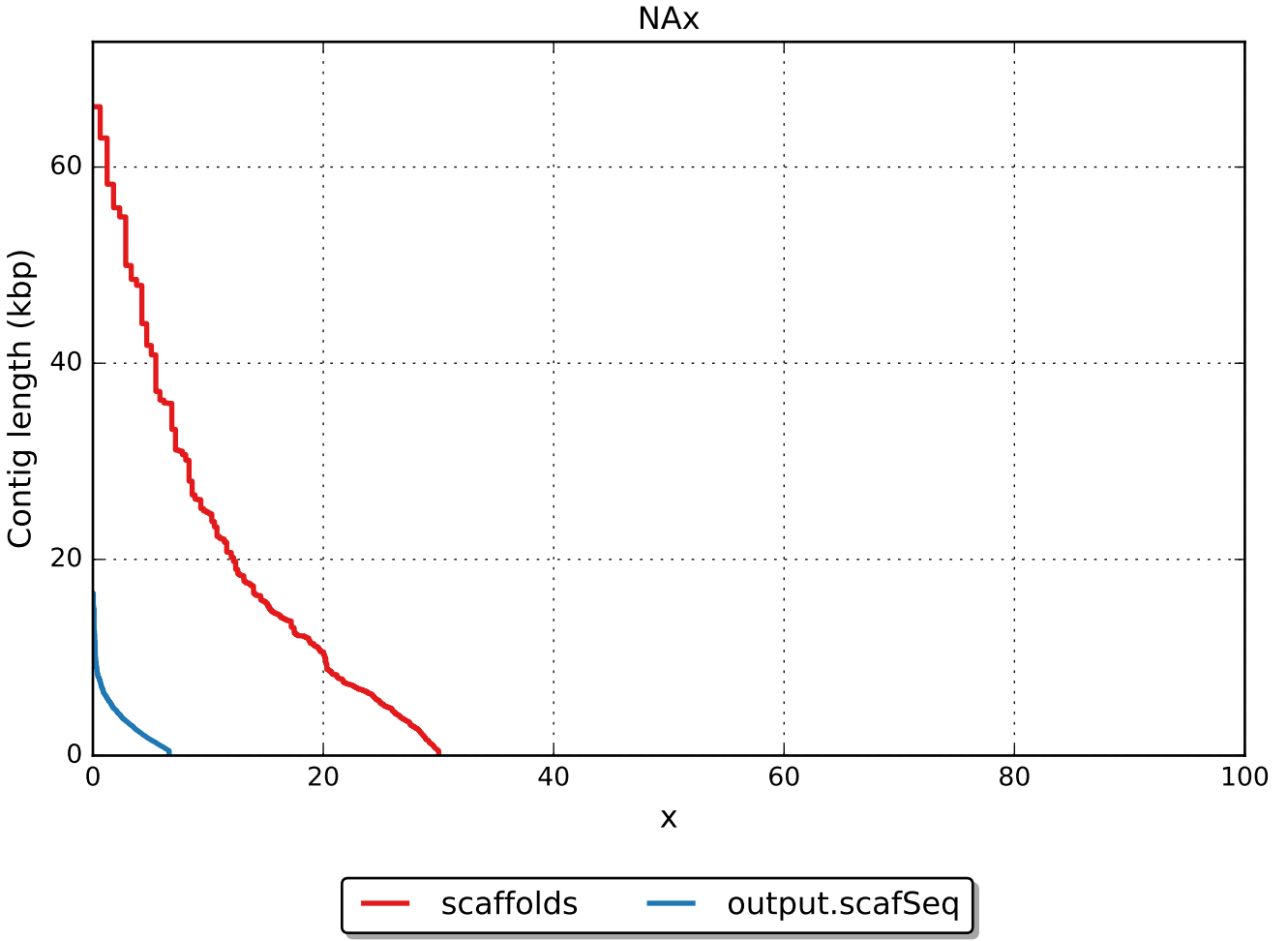

Coverage histogram (bin size: 3x)
Total length (kbp)
3000
2000
1000
0
0
6
12
18
24
30
36
42
48
54
60
66
72
801
Coverage depth (x)
scaffolds

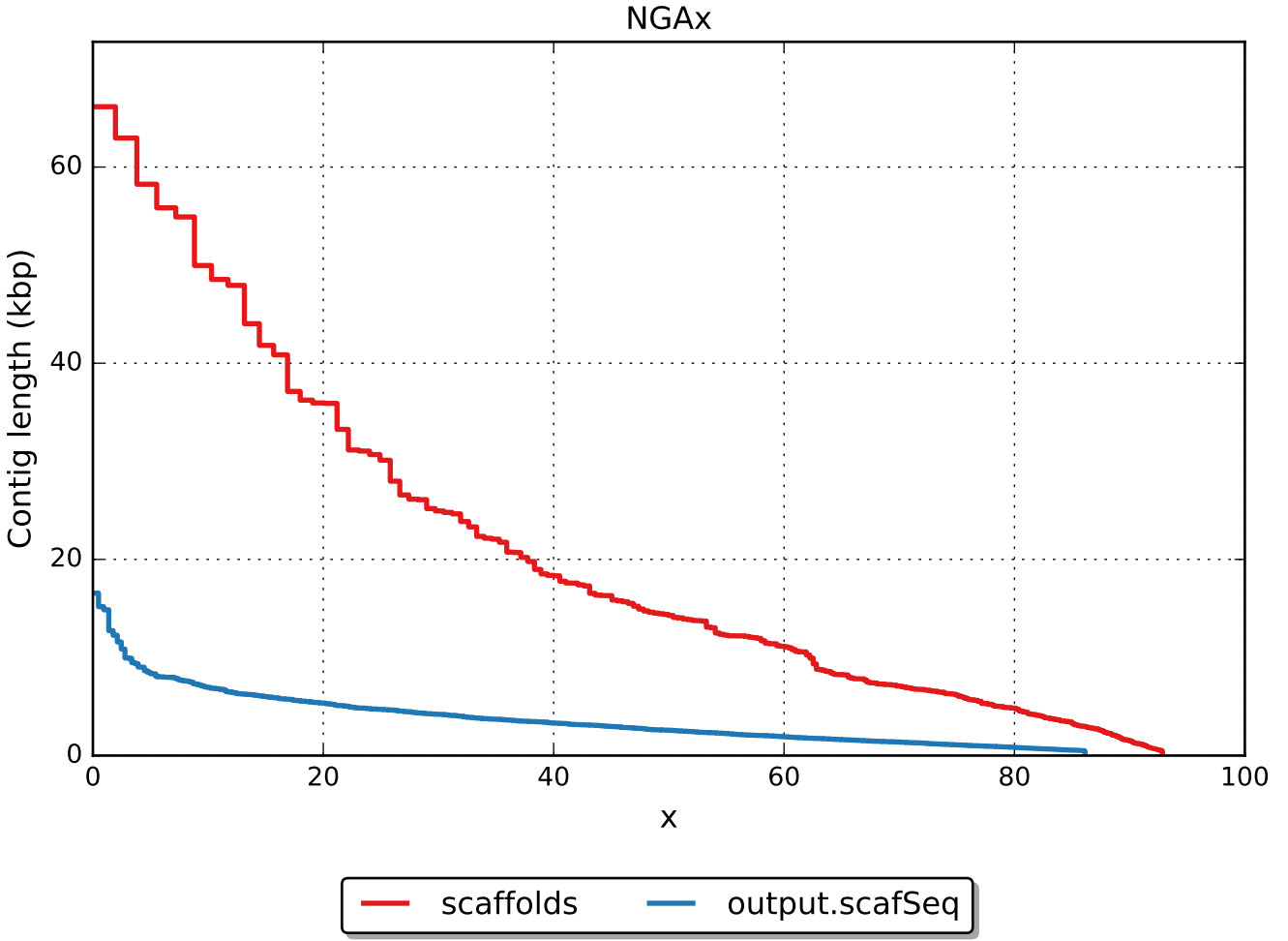

scaffolds coverage histogram (bin size: 3x)
Total length (kbp)
3000
2000
1000
0
0
6
12
18
24
30
36
42
48
54
60
66
72
801
Coverage depth (x)
scaffolds

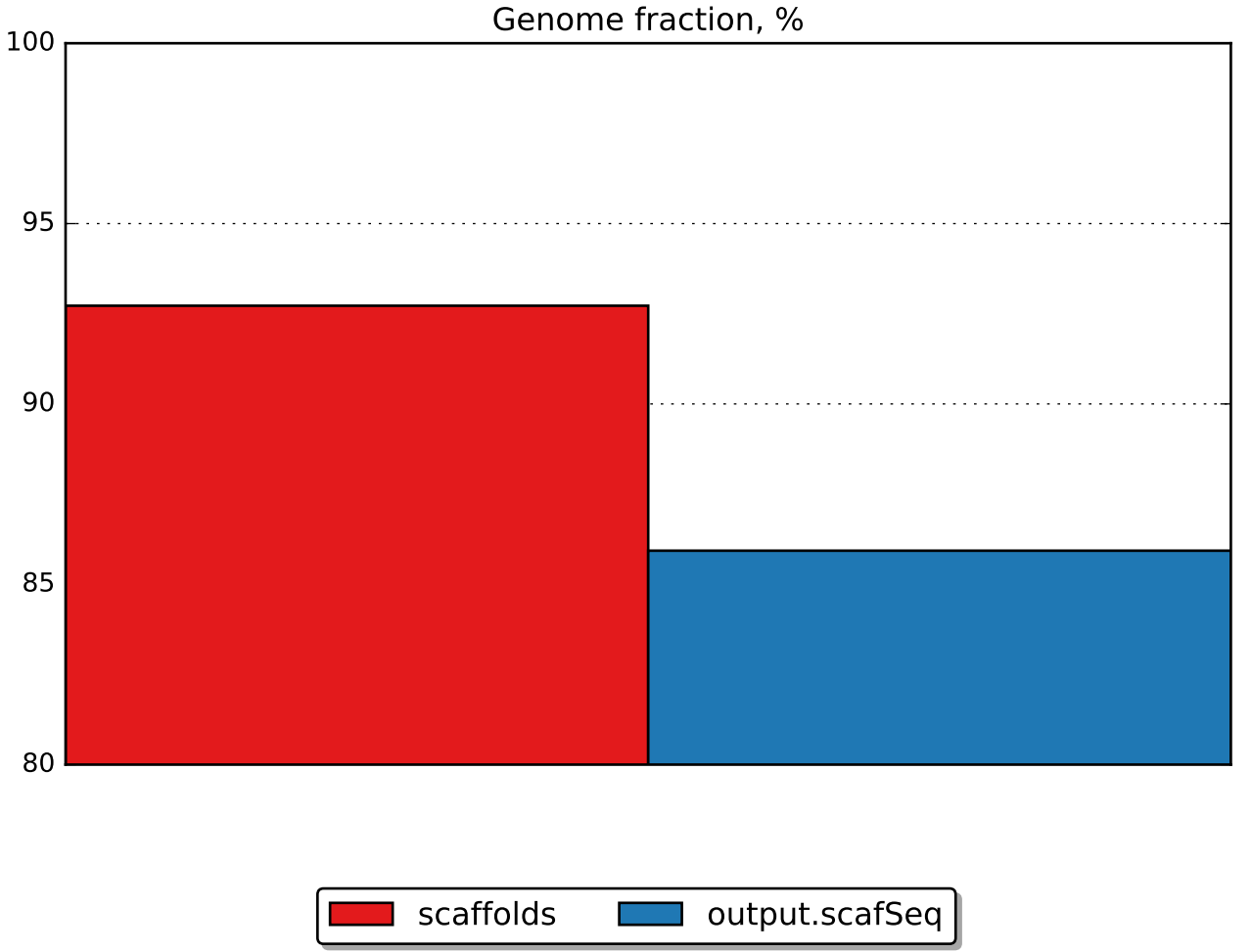

Misassemblies
10
8
6
4
2
0
scaffolds
output.scafSeq
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
scaffolds
output.scafSeq


Cumulative length (aligned contigs)
Cumulative length (kbp)
3200
2400
1600
800
0
0
300
600
900
1200
Contig index
scaffolds
output.scafSeq
Reference


NAx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds
output.scafSeq


NGAx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
scaffolds
output.scafSeq


Genome fraction, %
100
95
90
85
80
scaffolds
output.scafSeq