Report

	scaffolds	scaffolds_broken
# contigs (>= 0 bp)	548	-
# contigs (>= 1000 bp)	81	90
# contigs (>= 5000 bp)	55	60
# contigs (>= 10000 bp)	48	53
# contigs (>= 25000 bp)	35	38
# contigs (>= 50000 bp)	26	27
Total length (>= 0 bp)	4649099	-
Total length (>= 1000 bp)	4544542	4543670
Total length (>= 5000 bp)	4483437	4475102
Total length (>= 10000 bp)	4432606	4420078
Total length (>= 25000 bp)	4198794	4154588
Total length (>= 50000 bp)	3895309	3790930
# contigs	97	106
Largest contig	472970	472970
Total length	4555720	4554848
Reference length	4602977	4602977
GC (%)	68.83	68.83
Reference GC (%)	68.79	68.79
N50	135342	127930
NG50	135342	127930
N75	100705	73315
NG75	100705	73315
L50	10	11
LG50	10	11
L75	20	22
LG75	20	22
# misassemblies	3	3
# misassembled contigs	3	3
Misassembled contigs length	190750	108828
# local misassemblies	11	6
# scaffold gap size misassemblies	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 0 part	2 + 0 part
Unaligned length	1166	1166
Genome fraction (%)	98.689	98.689
Duplication ratio	1.003	1.002
# N's per 100 kbp	19.14	0.00
# mismatches per 100 kbp	16.51	16.53
# indels per 100 kbp	1.28	1.19
# predicted genes (unique)	4329	4329
# predicted genes (>= 0 bp)	4329	4329
# predicted genes (>= 300 bp)	3838	3838
# predicted genes (>= 1500 bp)	531	531
# predicted genes (>= 3000 bp)	45	45
Largest alignment	472912	472912
Total aligned length	4550762	4550820
NA50	135264	127906
NGA50	135264	127906
NA75	100390	73315
NGA75	100390	73315
LA50	10	11
LGA50	10	11
LA75	20	22
LGA75	20	22

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

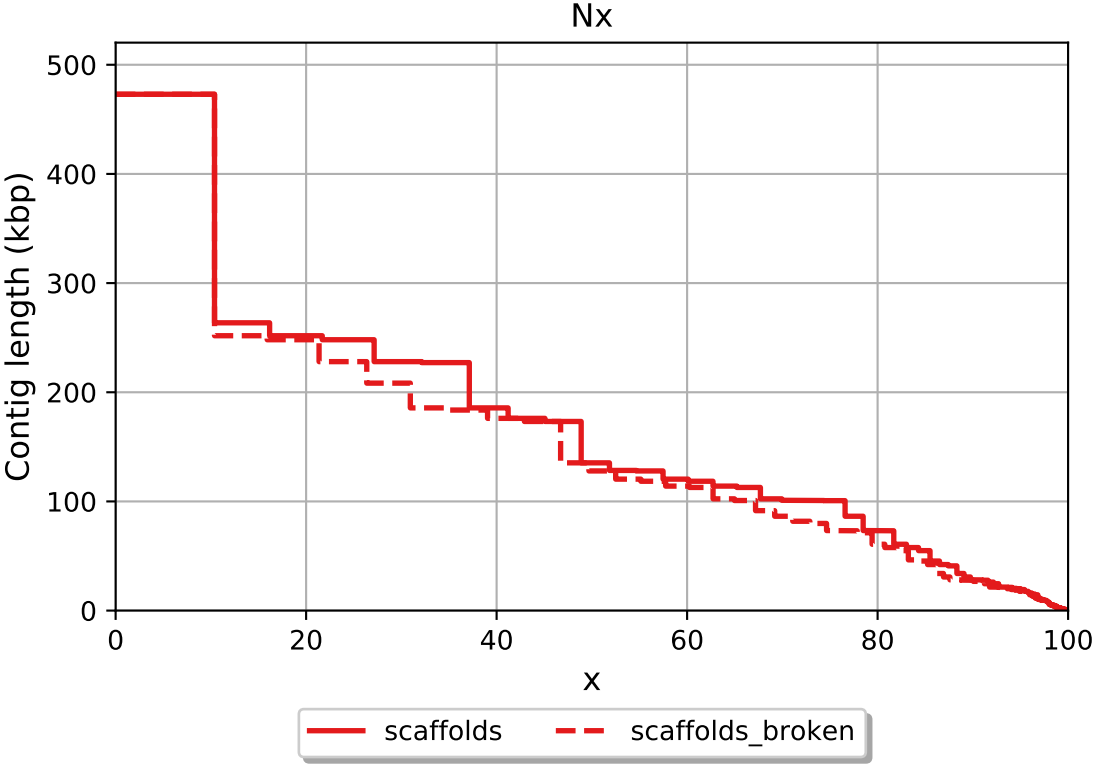
	scaffolds	scaffolds_broken
# misassemblies	3	3
# relocations	0	0
# translocations	3	3
# inversions	0	0
# misassembled contigs	3	3
Misassembled contigs length	190750	108828
# local misassemblies	11	6
# scaffold gap size misassemblies	0	-
# unaligned mis. contigs	0	0
# mismatches	750	751
# indels	58	54
# indels (<= 5 bp)	45	45
# indels (> 5 bp)	13	9
Indels length	541	309

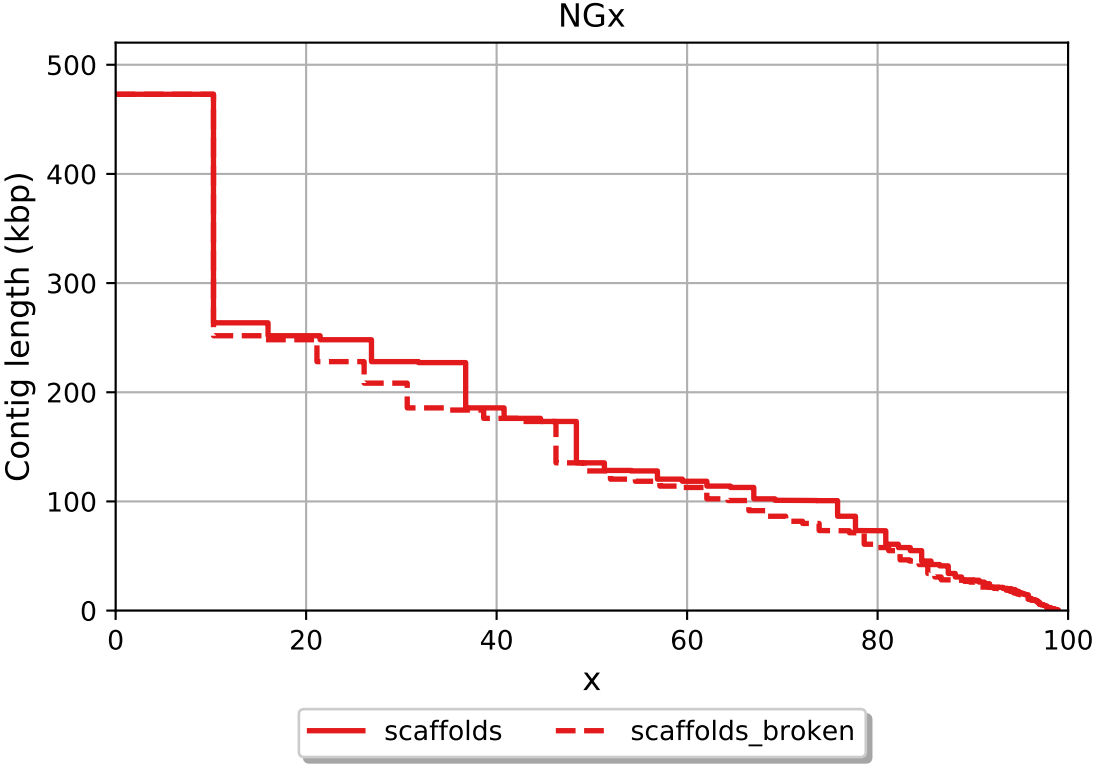
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

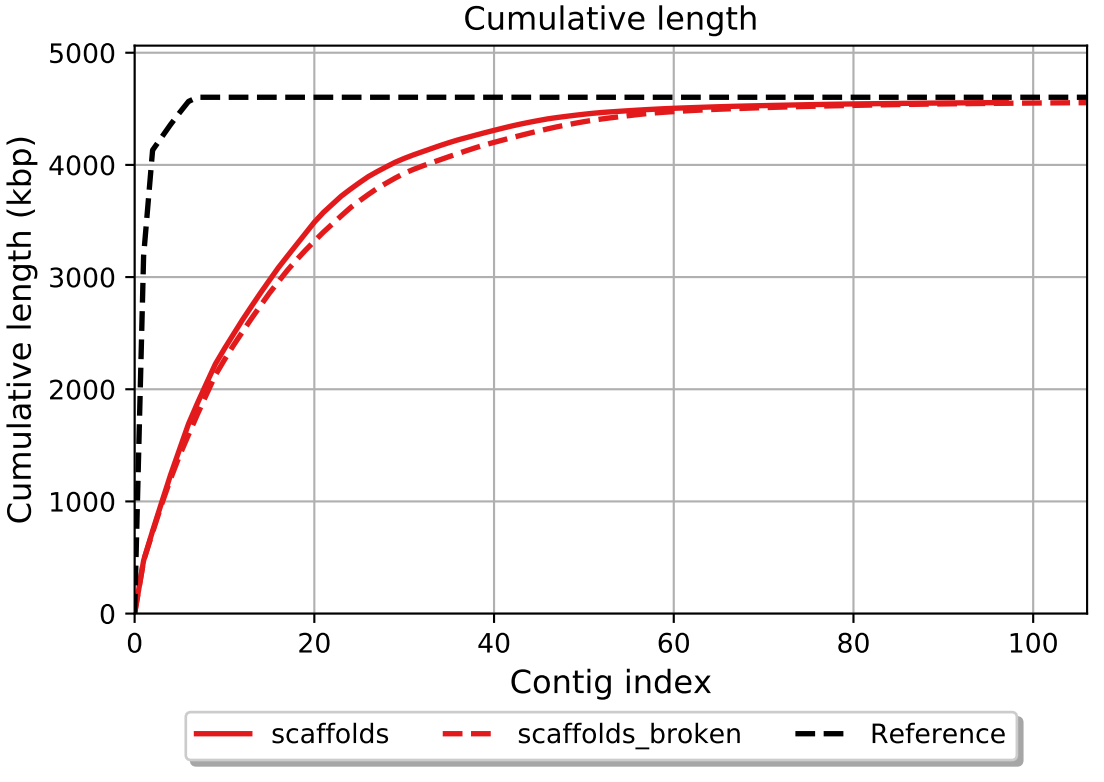
Unaligned report

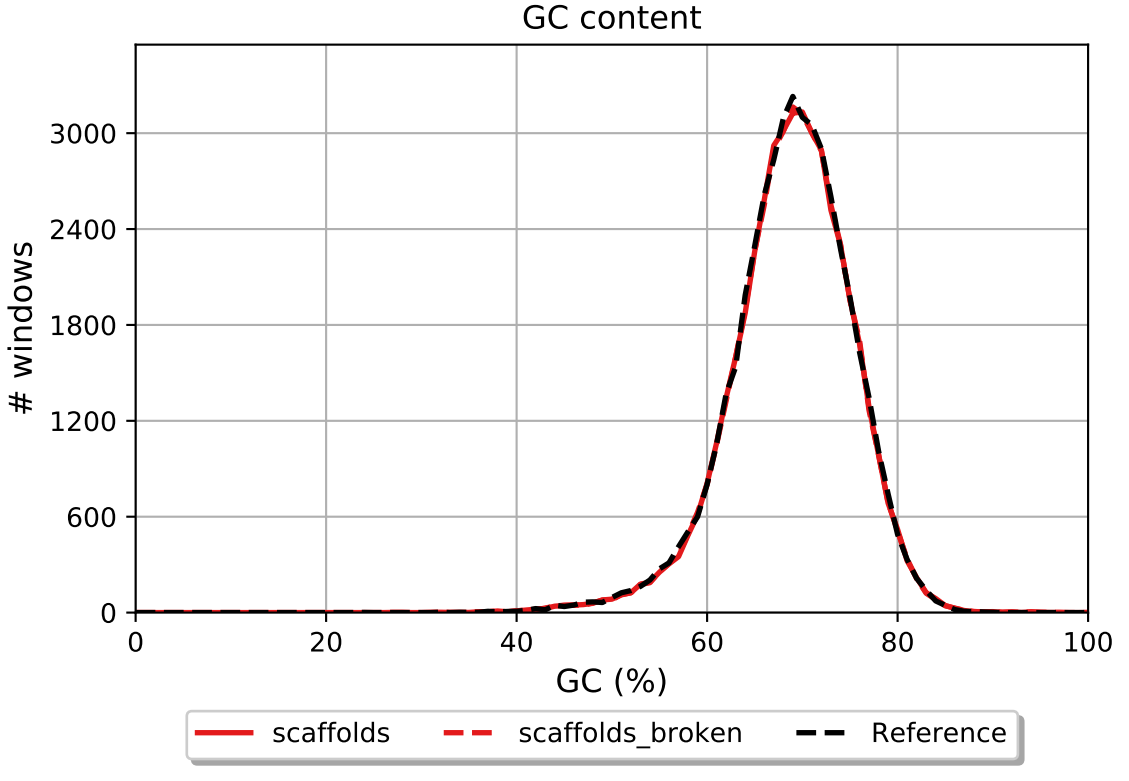
	scaffolds	scaffolds_broken
# fully unaligned contigs	2	2
Fully unaligned length	1166	1166
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	872	0

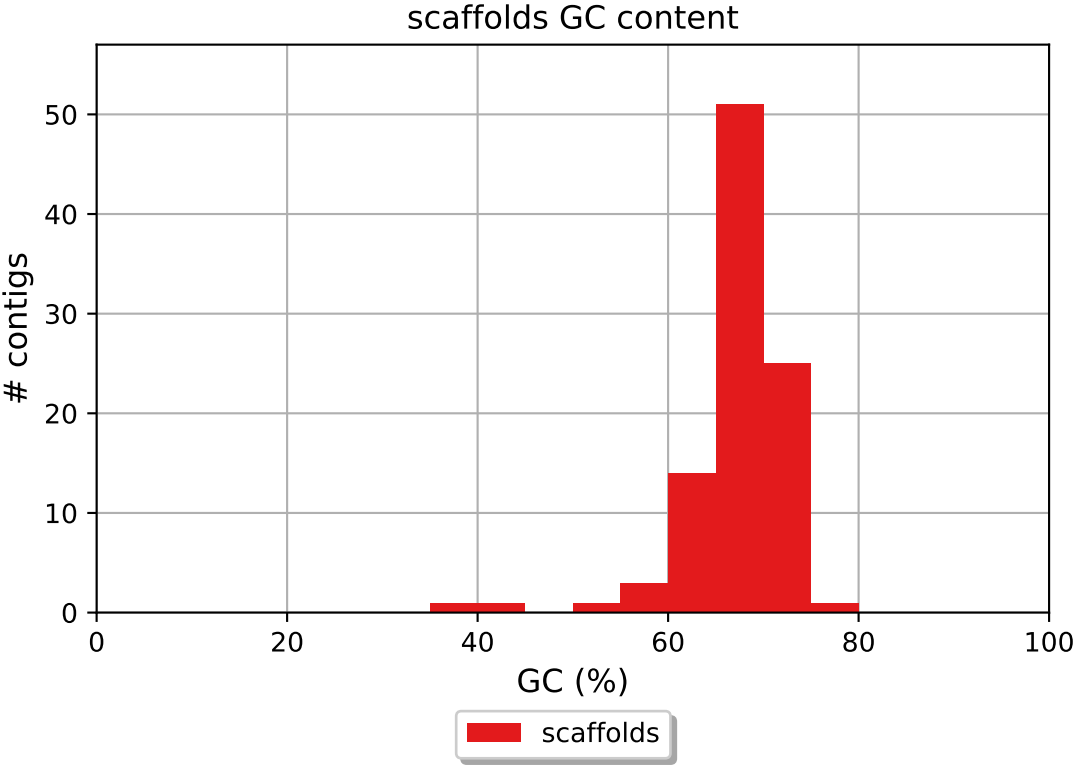
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

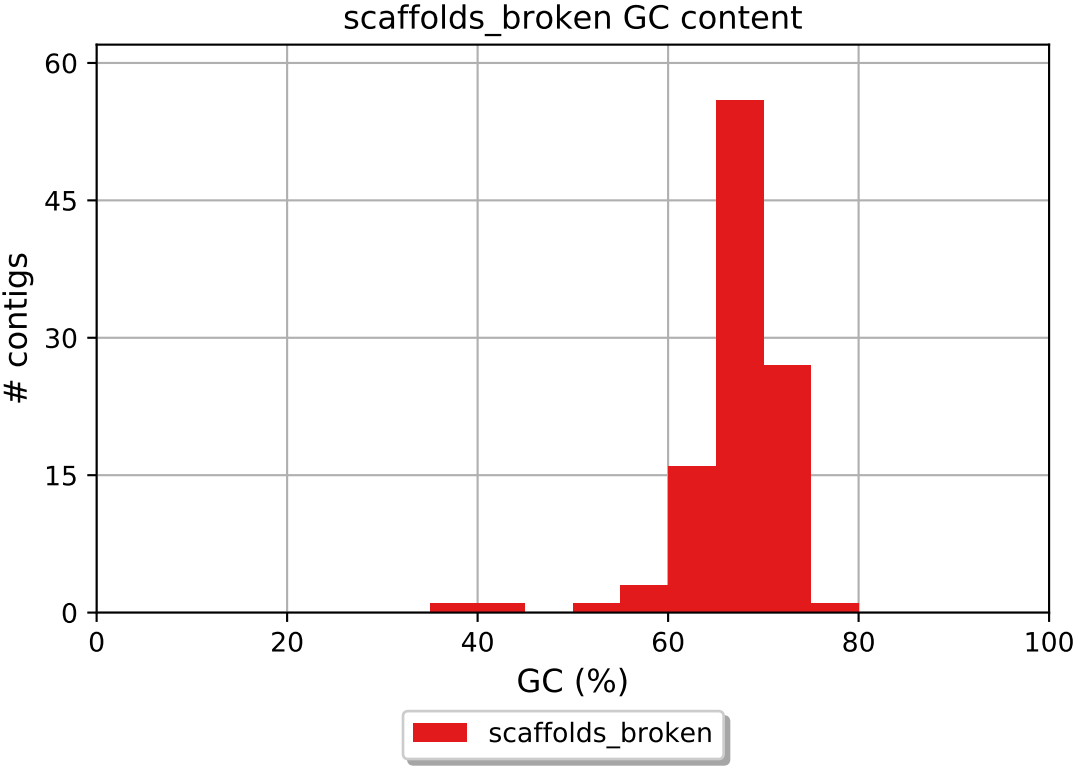

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
scaffolds
scaffolds_broken

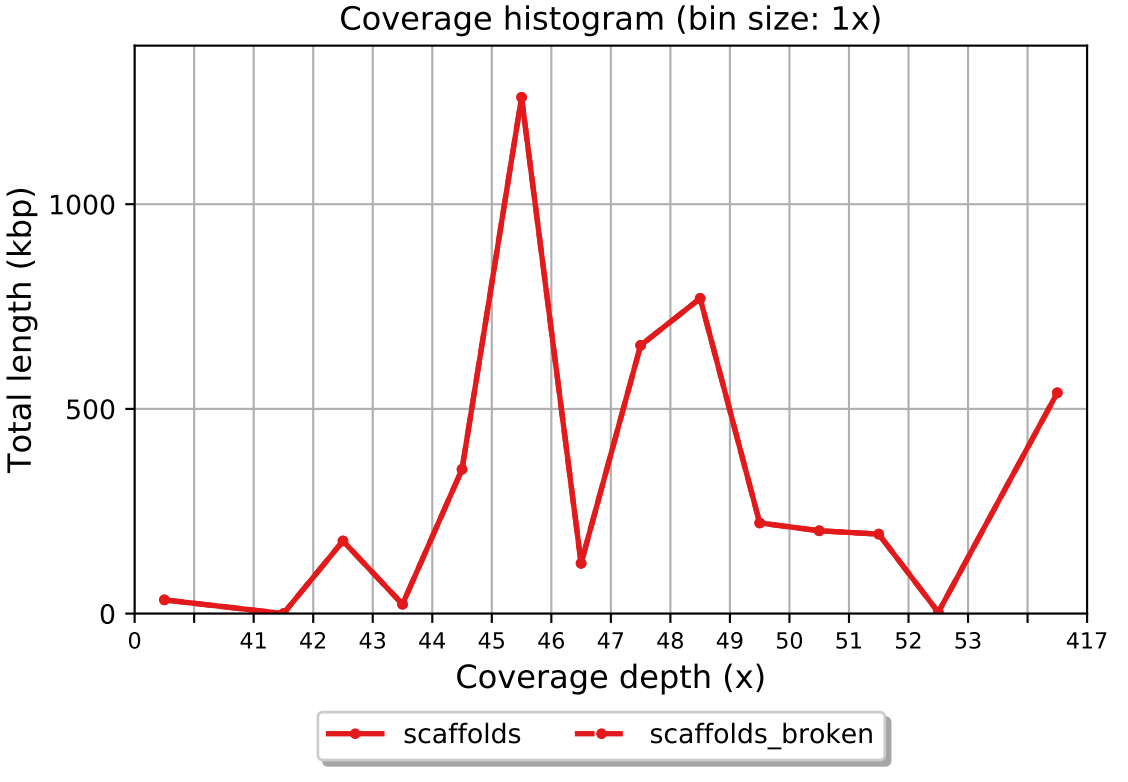

NGx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
scaffolds
scaffolds_broken

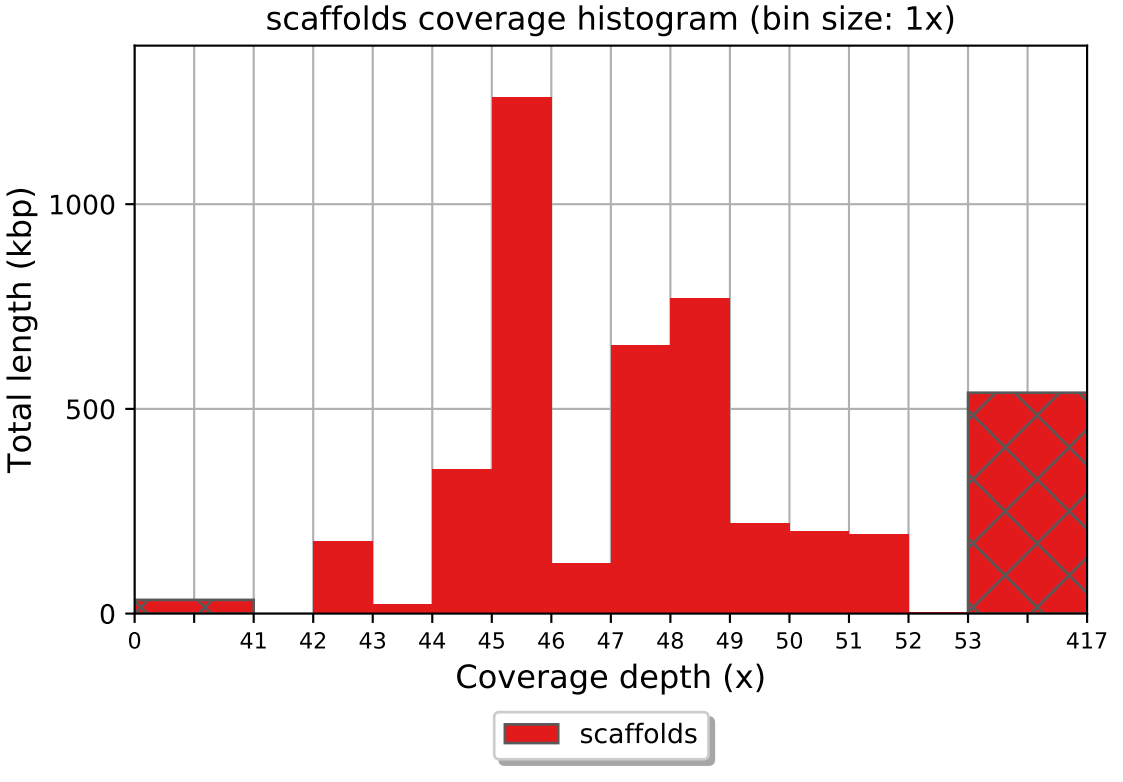

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
scaffolds
scaffolds_broken
Reference

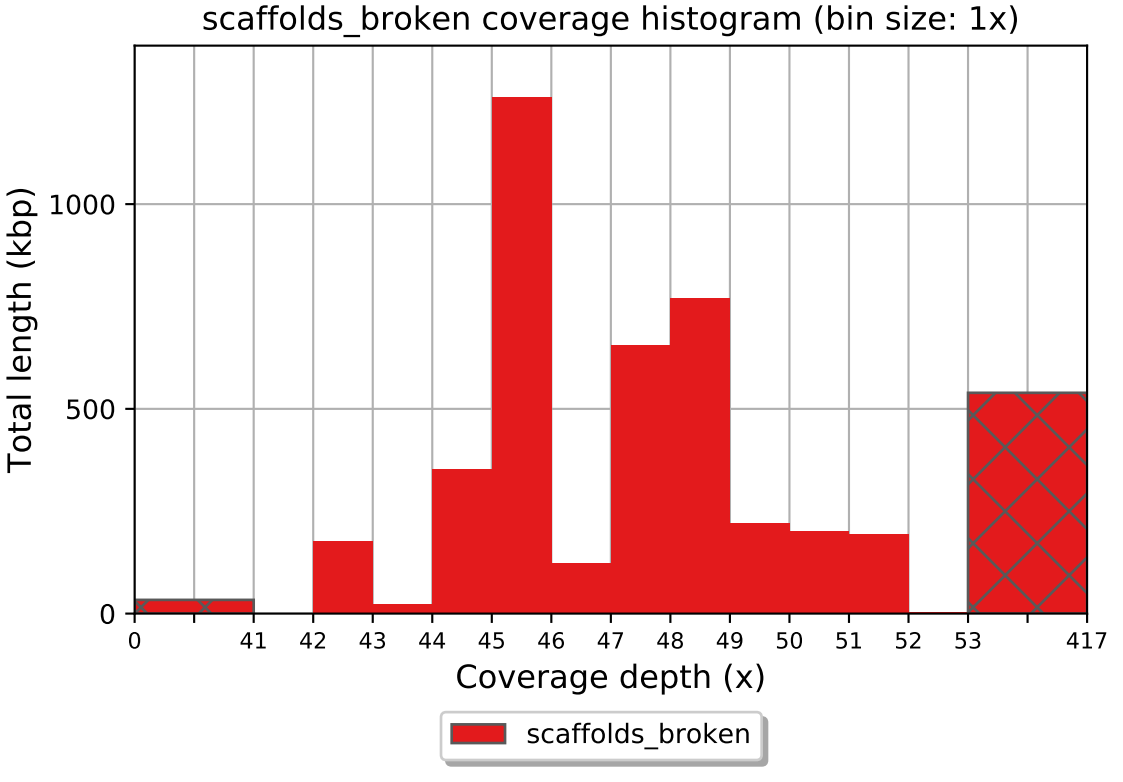

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
scaffolds
scaffolds_broken
Reference


scaffolds GC content
contigs
0
10
20
30
40
50
0
20
40
60
80
100
GC (%)
scaffolds

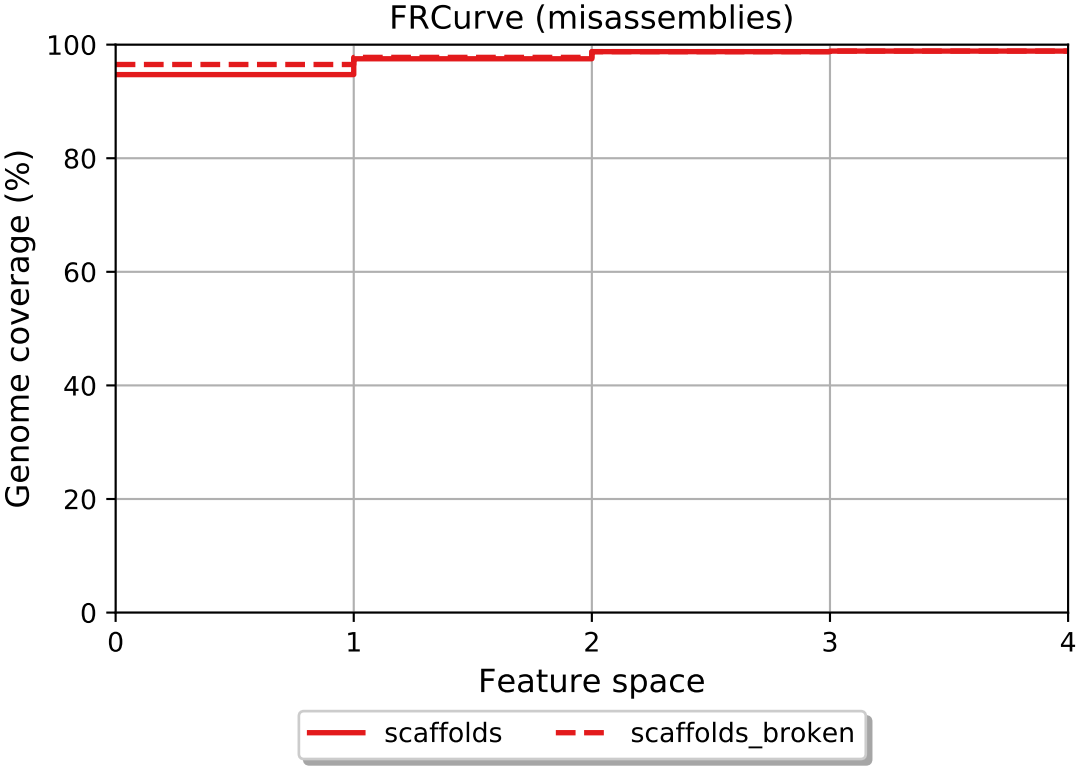

scaffolds_broken GC content
contigs
GC (%)
0
15
30
45
60
0
20
40
60
80
100
scaffolds_broken

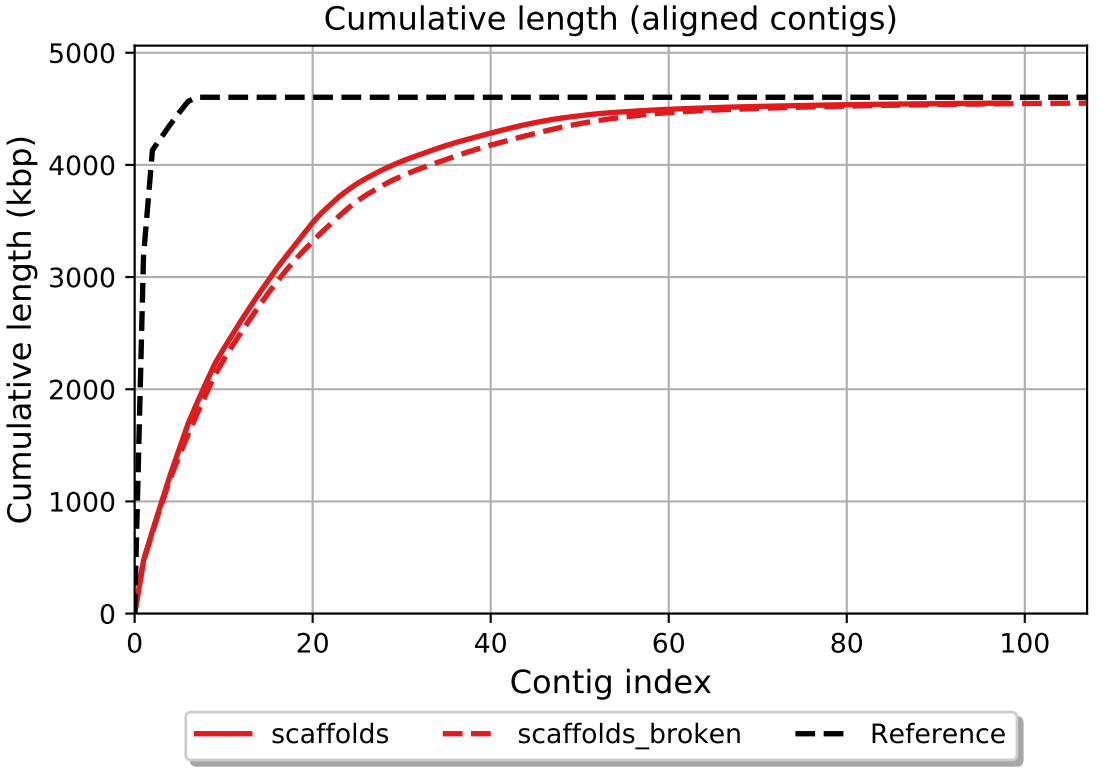

Coverage histogram (bin size: 1x)
Total length (kbp)
1000
500
0
0
41
42
43
44
45
46
47
48
49
50
51
52
53
417
Coverage depth (x)
scaffolds
scaffolds_broken

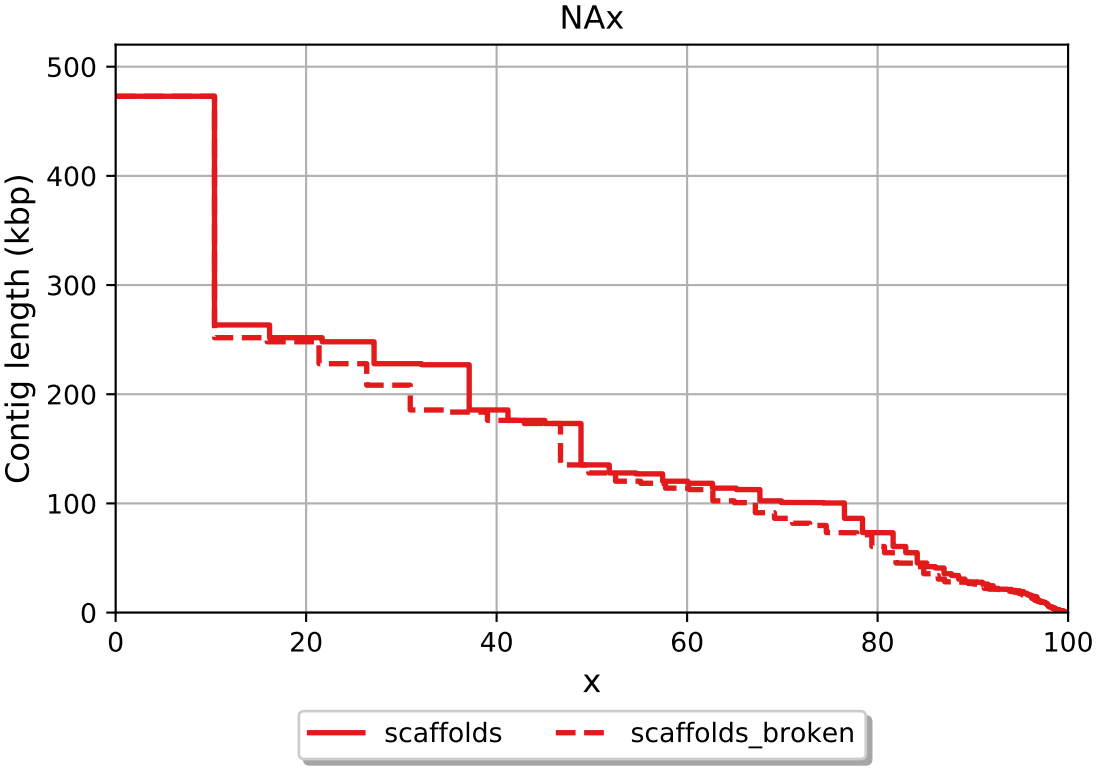

scaffolds coverage histogram (bin size: 1x)
Total length (kbp)
1000
500
0
0
41
42
43
44
45
46
47
48
49
50
51
52
53
417
Coverage depth (x)
scaffolds

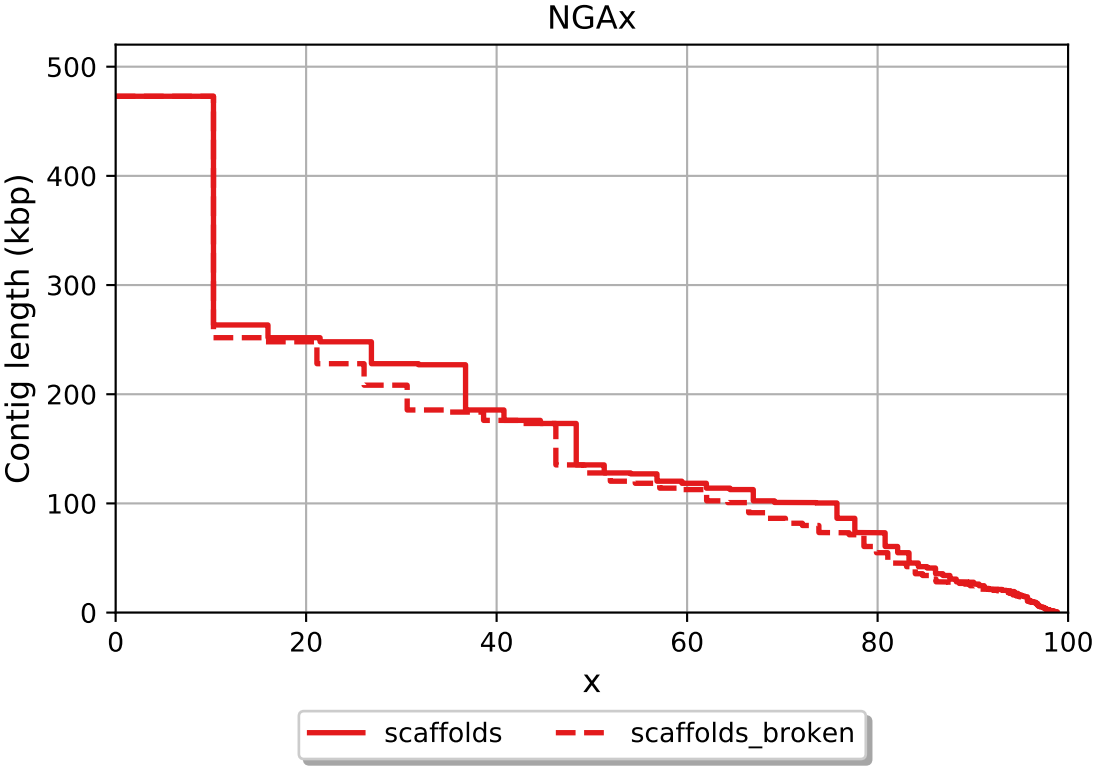

scaffolds_broken coverage histogram (bin size: 1x)
Total length (kbp)
1000
500
0
0
41
42
43
44
45
46
47
48
49
50
51
52
53
417
Coverage depth (x)
scaffolds_broken

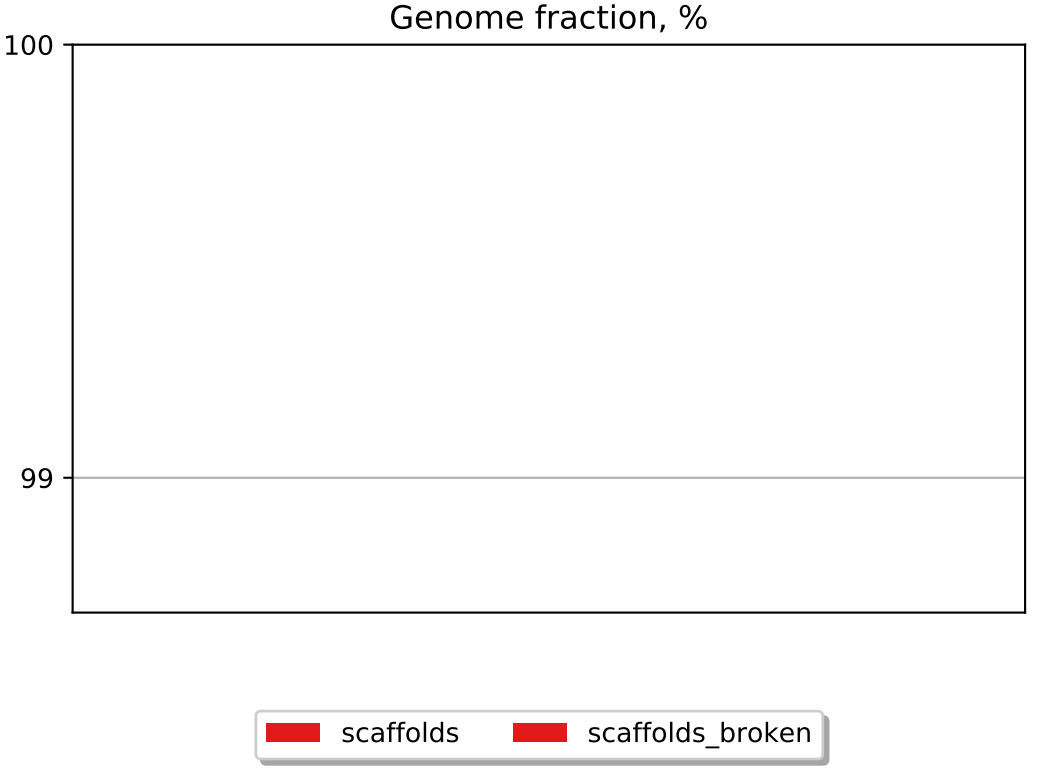
Misassemblies
5
4
3
2
1
0
scaffolds
scaffolds_broken
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
Feature space
scaffolds
scaffolds_broken


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
scaffolds
scaffolds_broken
Reference


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


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


Genome fraction, %
100
99
scaffolds
scaffolds_broken