Report

	scaffolds
# contigs (>= 0 bp)	34
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	3148669
Total length (>= 1000 bp)	3143672
Total length (>= 5000 bp)	3137112
Total length (>= 10000 bp)	3127739
Total length (>= 25000 bp)	3115356
Total length (>= 50000 bp)	3041642
# contigs	10
Largest contig	2057303
Total length	3143672
Reference length	2919198
GC (%)	37.69
Reference GC (%)	37.88
N50	2057303
NG50	2057303
N75	697966
NG75	697966
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	188
# misassembled contigs	2
Misassembled contigs length	2755269
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	5
# unaligned contigs	3 + 7 part
Unaligned length	564838
Genome fraction (%)	84.736
Duplication ratio	1.043
# N's per 100 kbp	6.36
# mismatches per 100 kbp	392.87
# indels per 100 kbp	14.80
Largest alignment	137660
Total aligned length	2577392
NA50	24553
NGA50	28708
NA75	4229
NGA75	9933
LA50	31
LGA50	27
LA75	89
LGA75	67

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

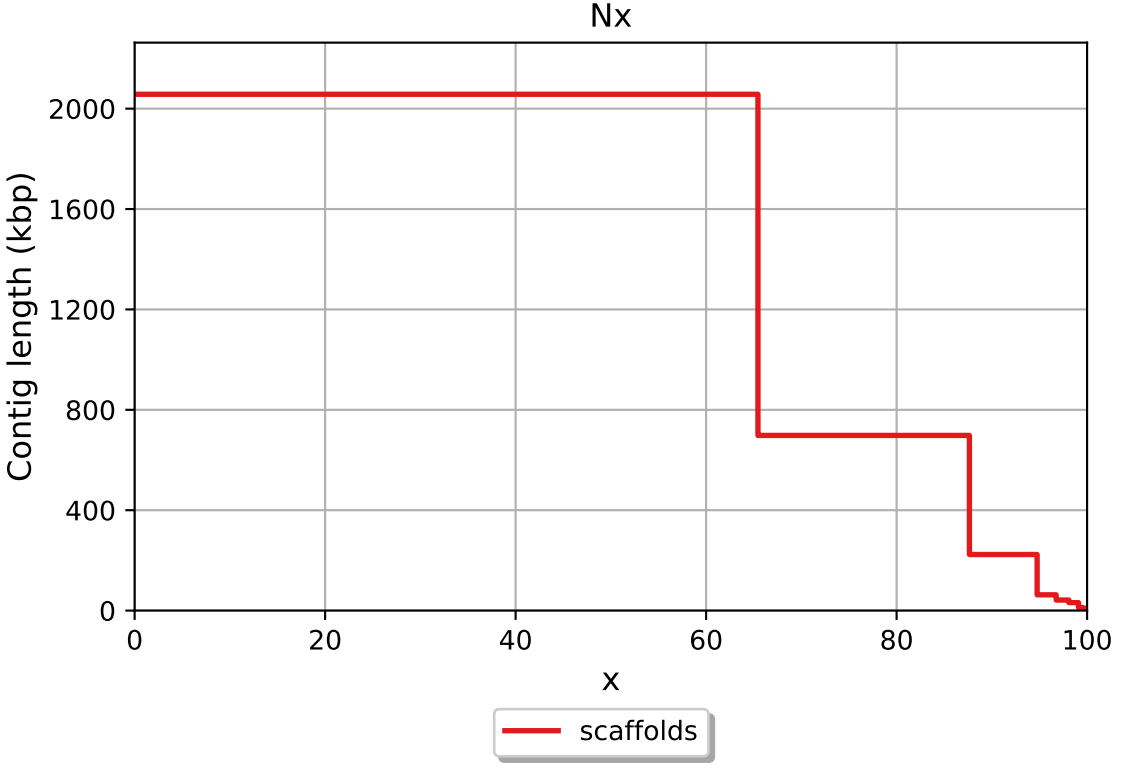
	scaffolds
# misassemblies	188
# contig misassemblies	188
# c. relocations	173
# c. translocations	12
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	2755269
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	1
# unaligned mis. contigs	5
# mismatches	9718
# indels	366
# indels (<= 5 bp)	329
# indels (> 5 bp)	37
Indels length	1453

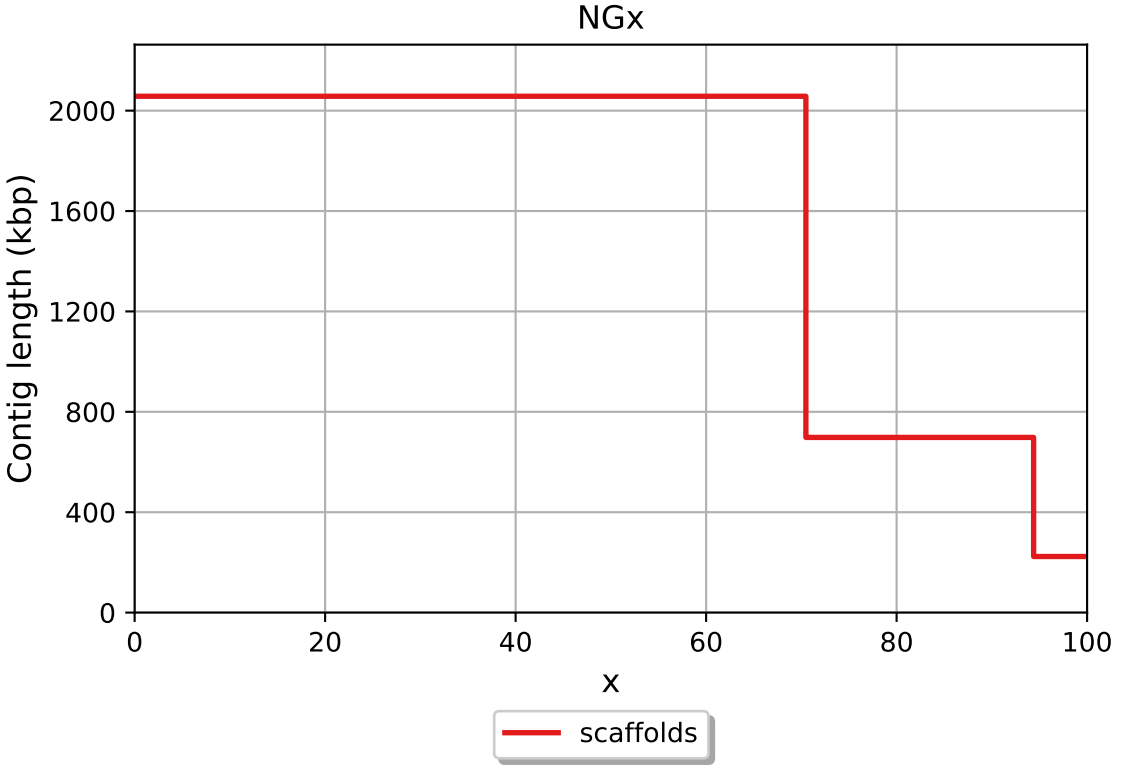
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

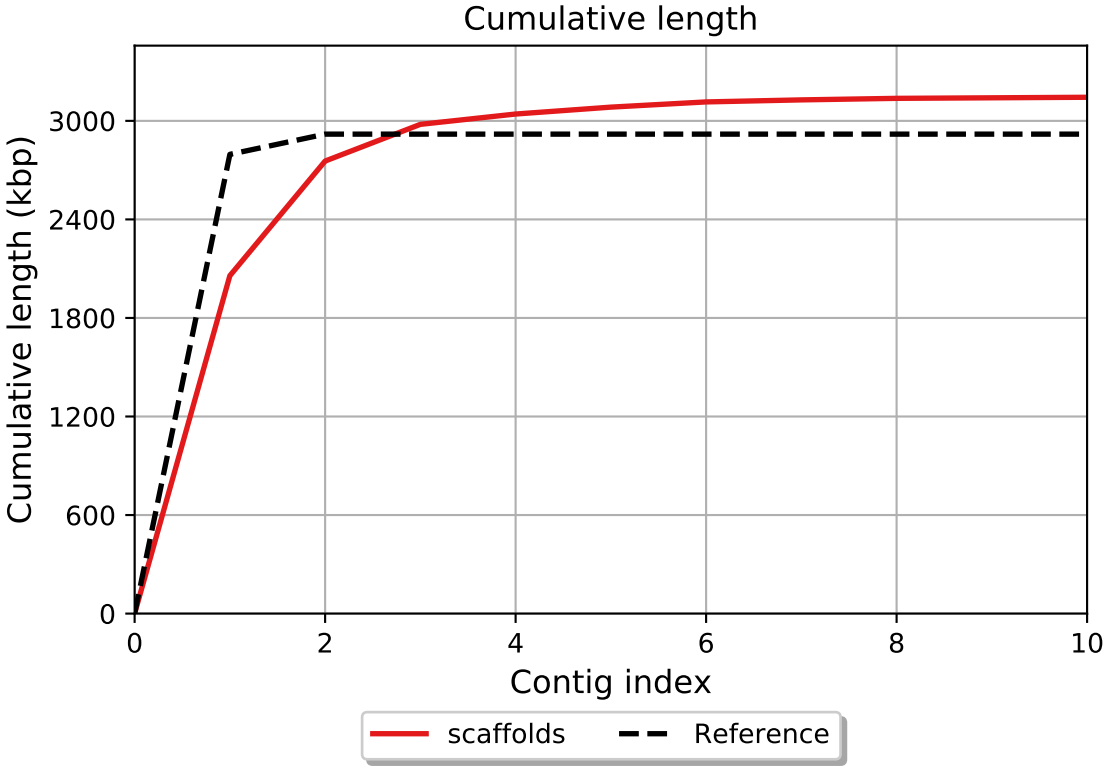
Unaligned report

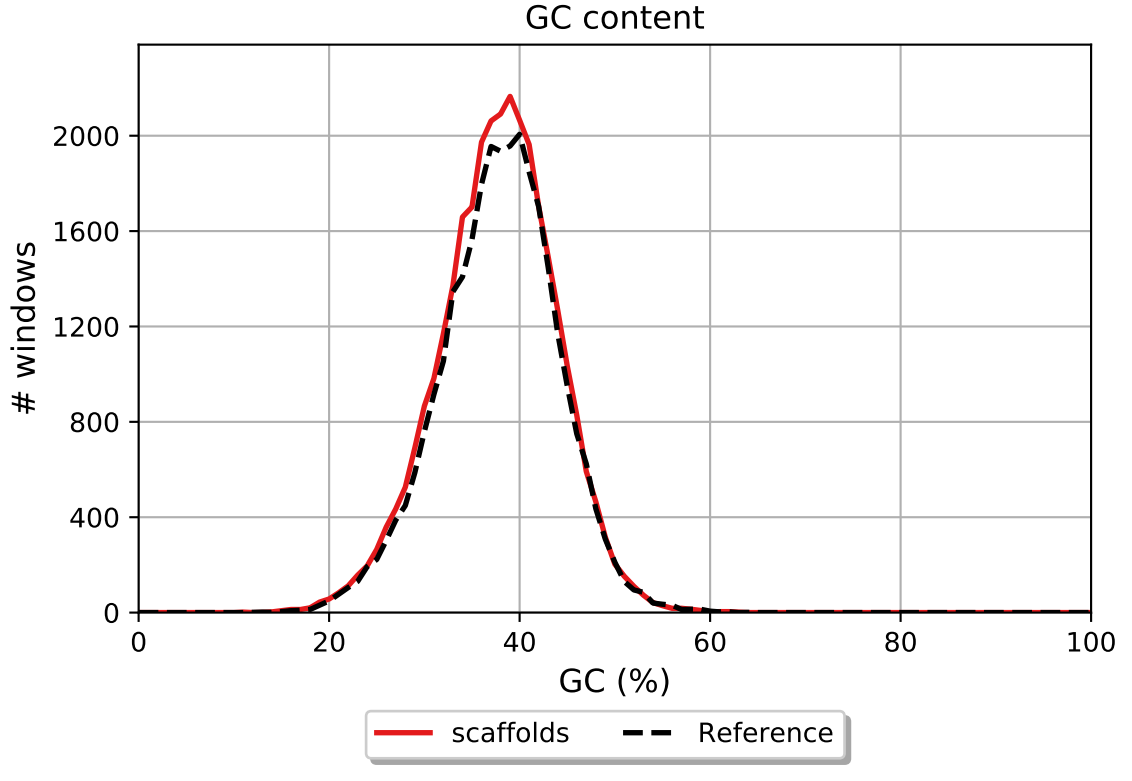
	scaffolds
# fully unaligned contigs	3
Fully unaligned length	15933
# partially unaligned contigs	7
Partially unaligned length	548905
# N's	200

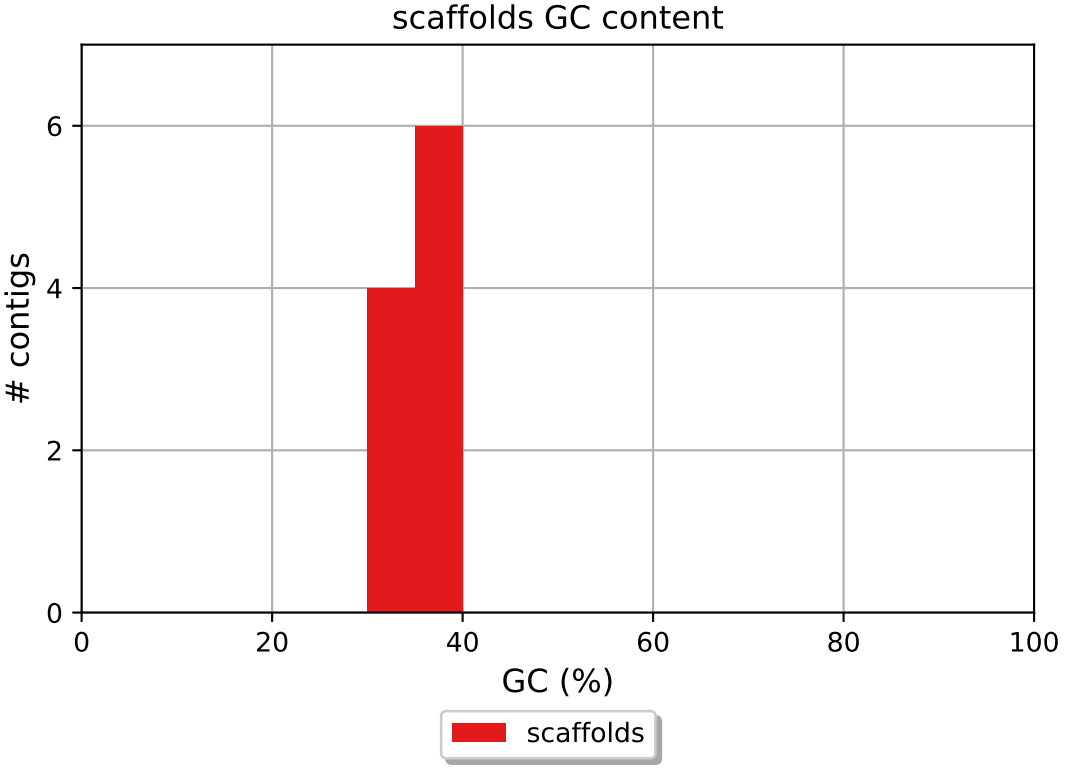
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

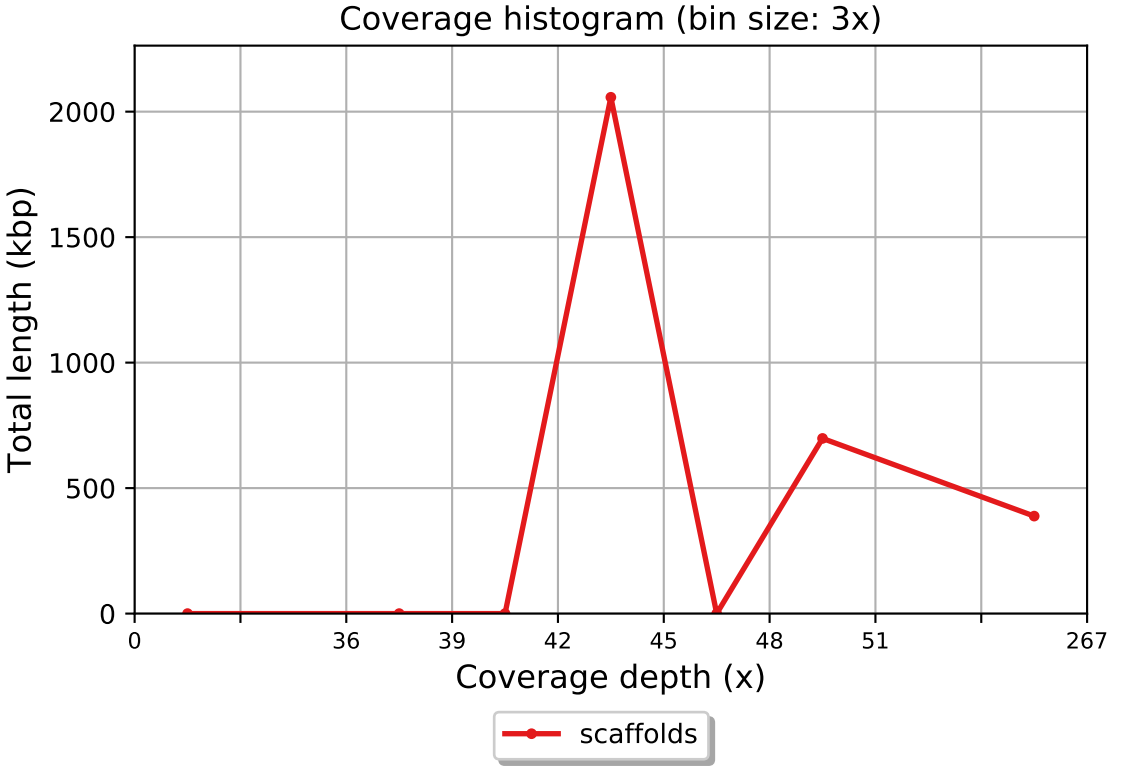

Nx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
scaffolds

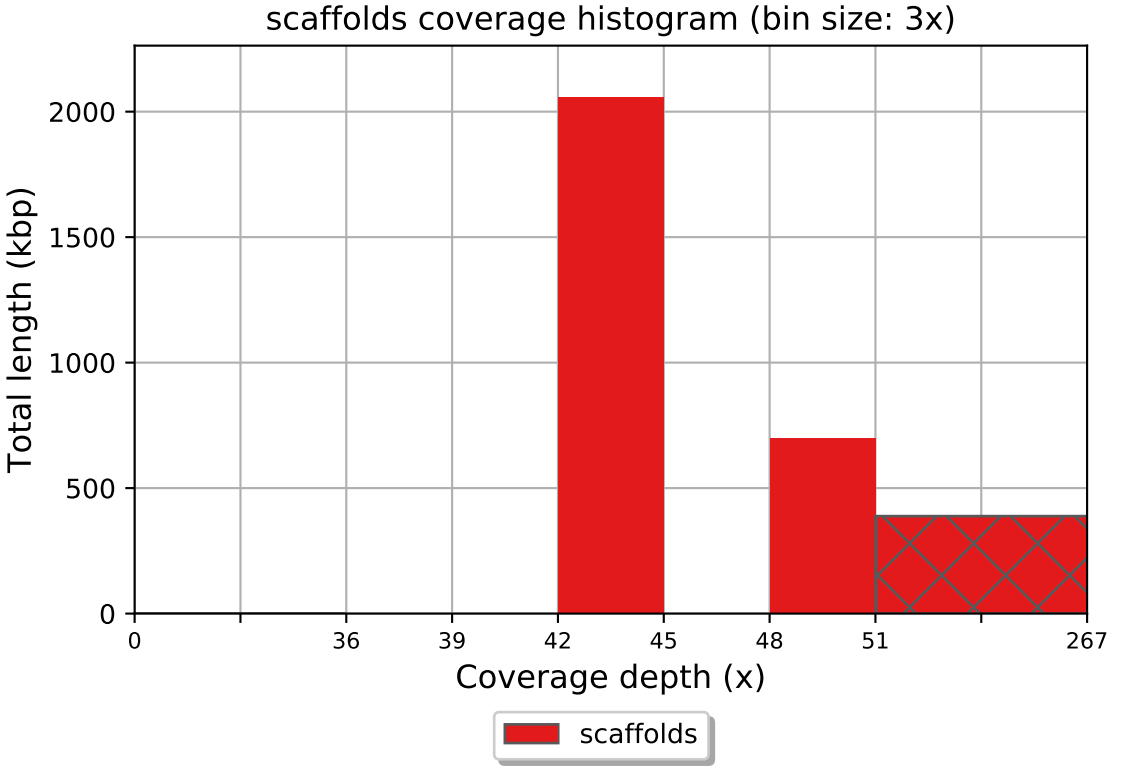

NGx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
scaffolds

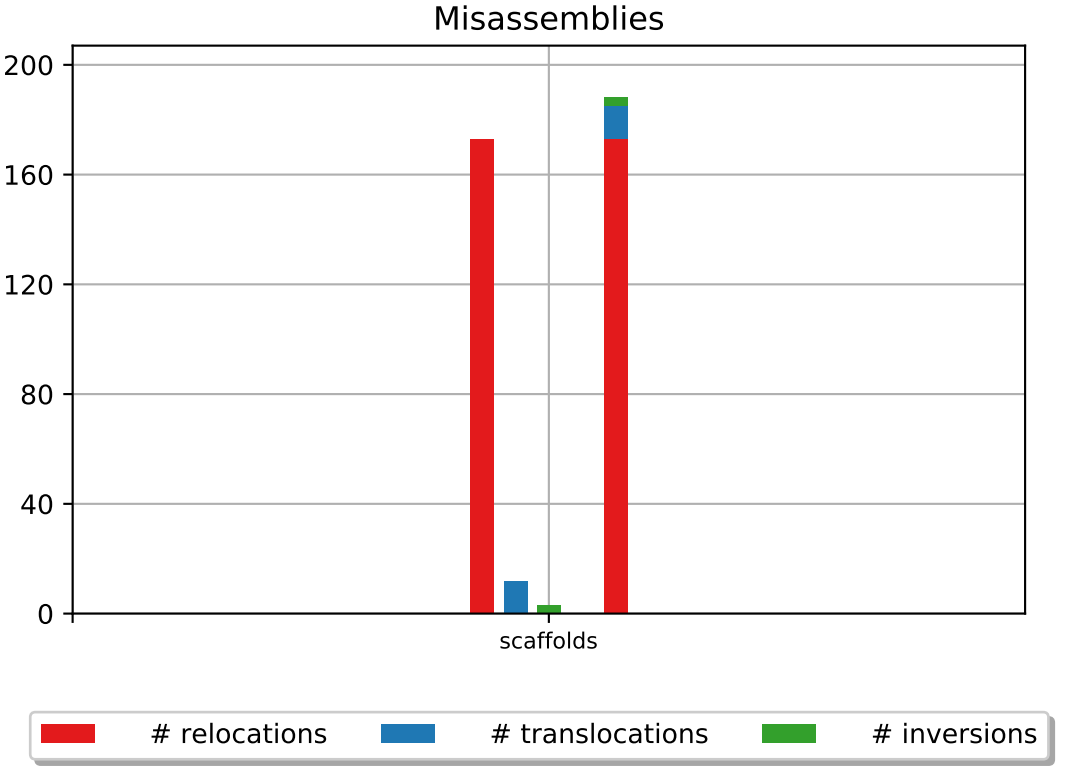

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
10
Contig index
scaffolds
Reference

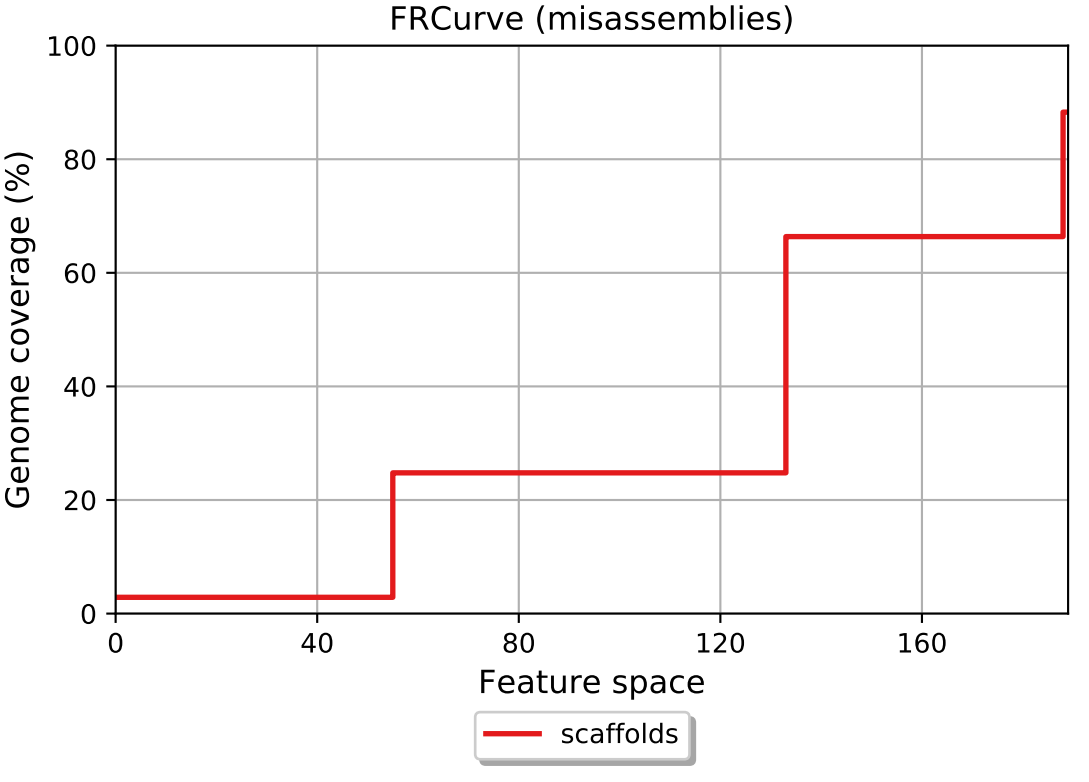

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
scaffolds
Reference

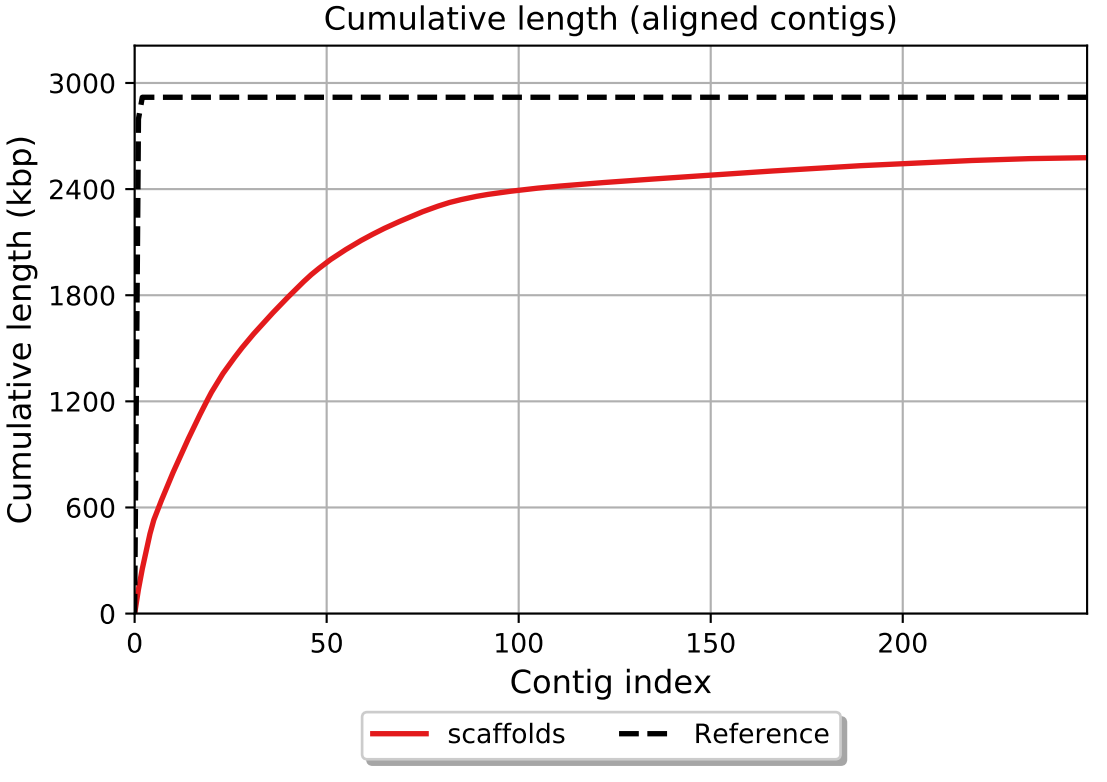

scaffolds GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
scaffolds

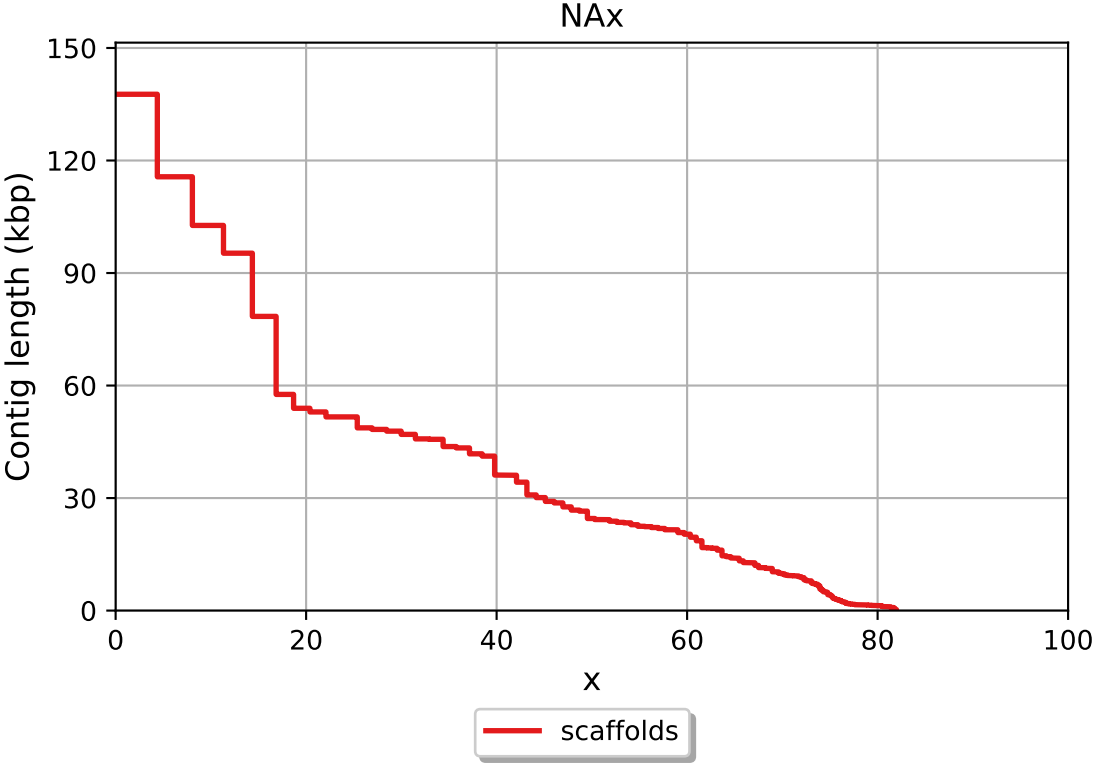

Coverage histogram (bin size: 3x)
Total length (kbp)
2000
1500
1000
500
0
0
36
39
42
45
48
51
267
Coverage depth (x)
scaffolds

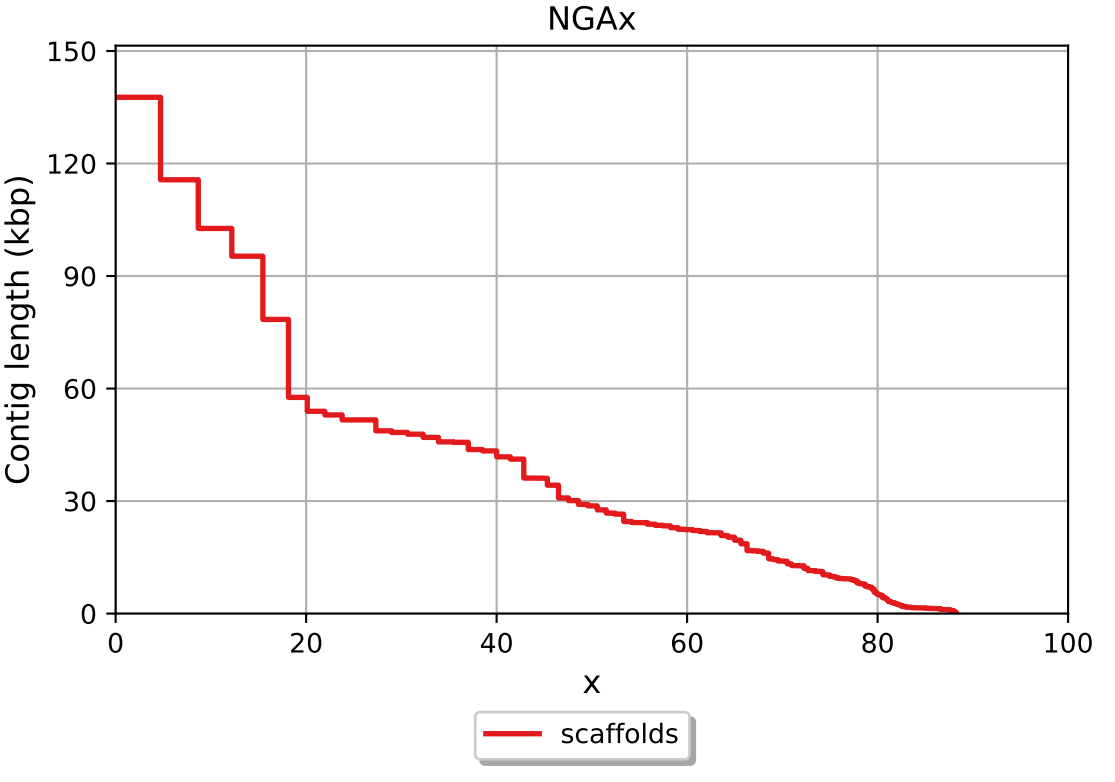

scaffolds coverage histogram (bin size: 3x)
Total length (kbp)
2000
1500
1000
500
0
0
36
39
42
45
48
51
267
Coverage depth (x)
scaffolds


Misassemblies
200
160
120
80
40
0
scaffolds
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
40
80
120
160
Feature space
scaffolds


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
50
100
150
200
Contig index
scaffolds
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
scaffolds