Report

	spades_scf	mulksg_scf
# contigs (>= 0 bp)	614	623
# contigs (>= 1000 bp)	39	39
# contigs (>= 5000 bp)	25	25
# contigs (>= 10000 bp)	23	23
# contigs (>= 25000 bp)	19	19
# contigs (>= 50000 bp)	12	12
Total length (>= 0 bp)	3019486	3020513
Total length (>= 1000 bp)	2837355	2836792
Total length (>= 5000 bp)	2806166	2806166
Total length (>= 10000 bp)	2794542	2794542
Total length (>= 25000 bp)	2718783	2718783
Total length (>= 50000 bp)	2450070	2450070
# contigs	71	71
Largest contig	381434	381434
Total length	2857660	2856859
Reference length	27041	27041
GC (%)	32.77	32.76
Reference GC (%)	30.52	30.52
N50	242064	242064
NG50	381434	381434
N75	122619	122619
NG75	381434	381434
L50	5	5
LG50	1	1
L75	9	9
LG75	1	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# unaligned contigs	69 + 2 part	69 + 2 part
Unaligned length	2848099	2847298
Genome fraction (%)	31.897	31.897
Duplication ratio	1.109	1.109
# N's per 100 kbp	3.36	3.36
# mismatches per 100 kbp	2469.57	2469.57
# indels per 100 kbp	92.75	92.75
Largest alignment	4181	4181
Total aligned length	9465	9465
NGA50	-	-

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

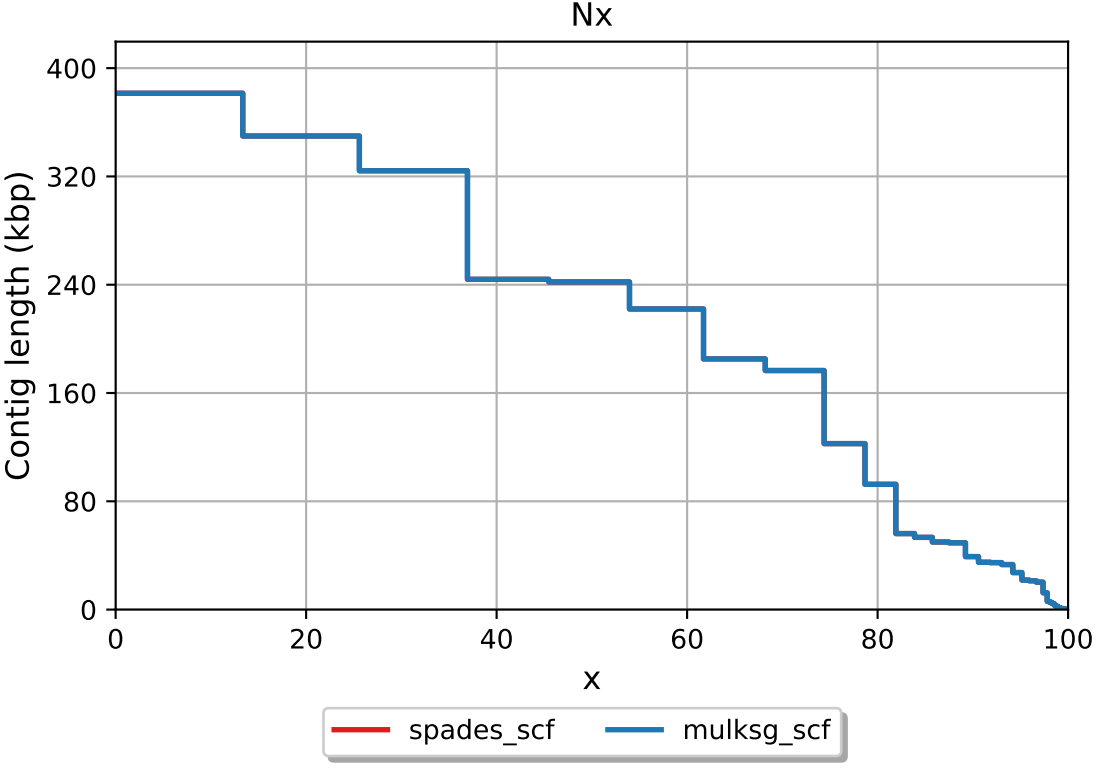
	spades_scf	mulksg_scf
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# mismatches	213	213
# indels	8	8
# indels (<= 5 bp)	6	6
# indels (> 5 bp)	2	2
Indels length	47	47

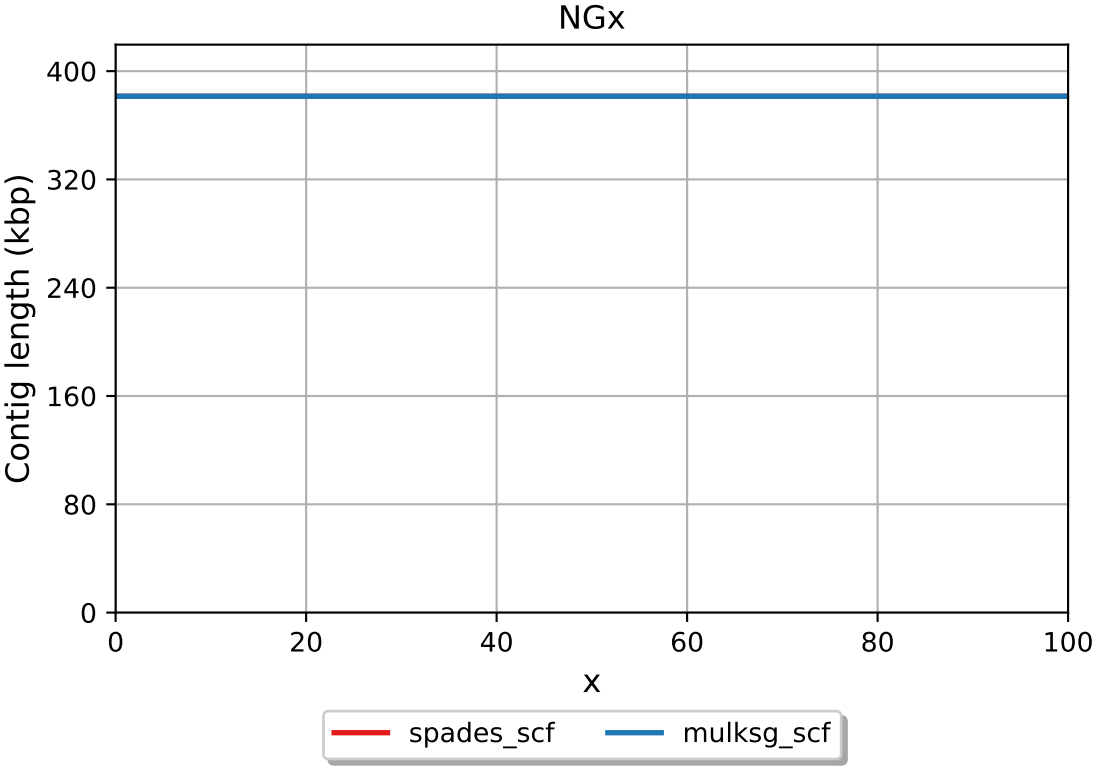
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

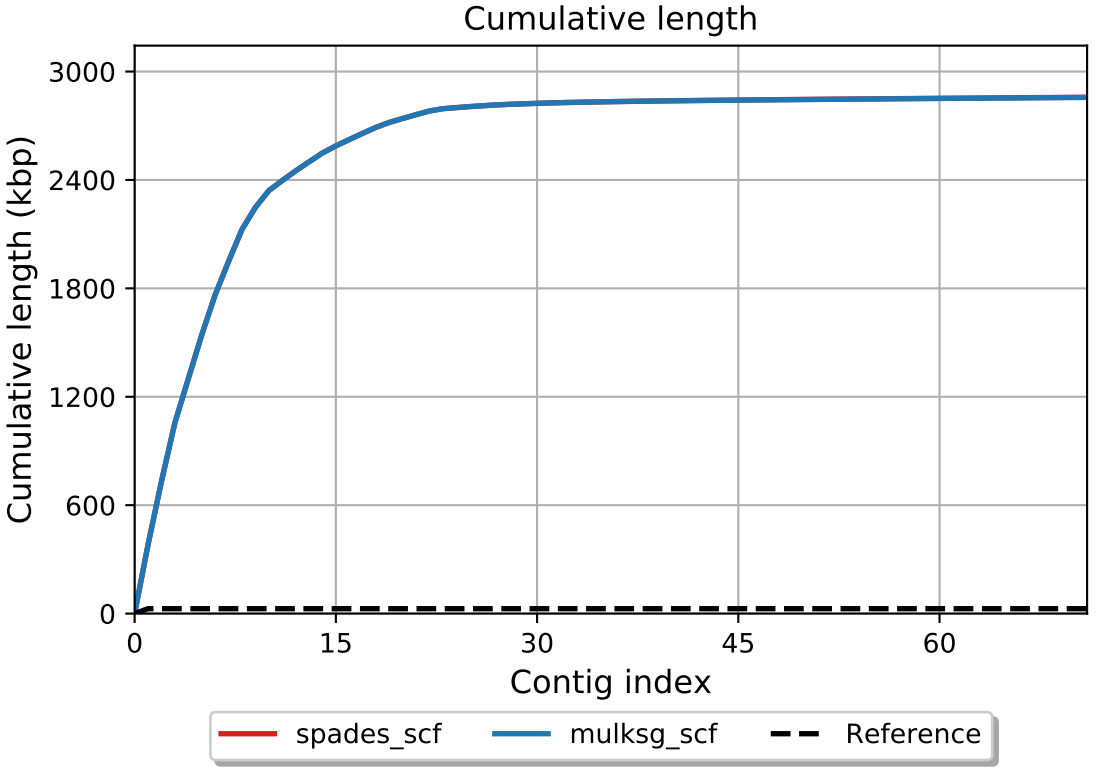
Unaligned report

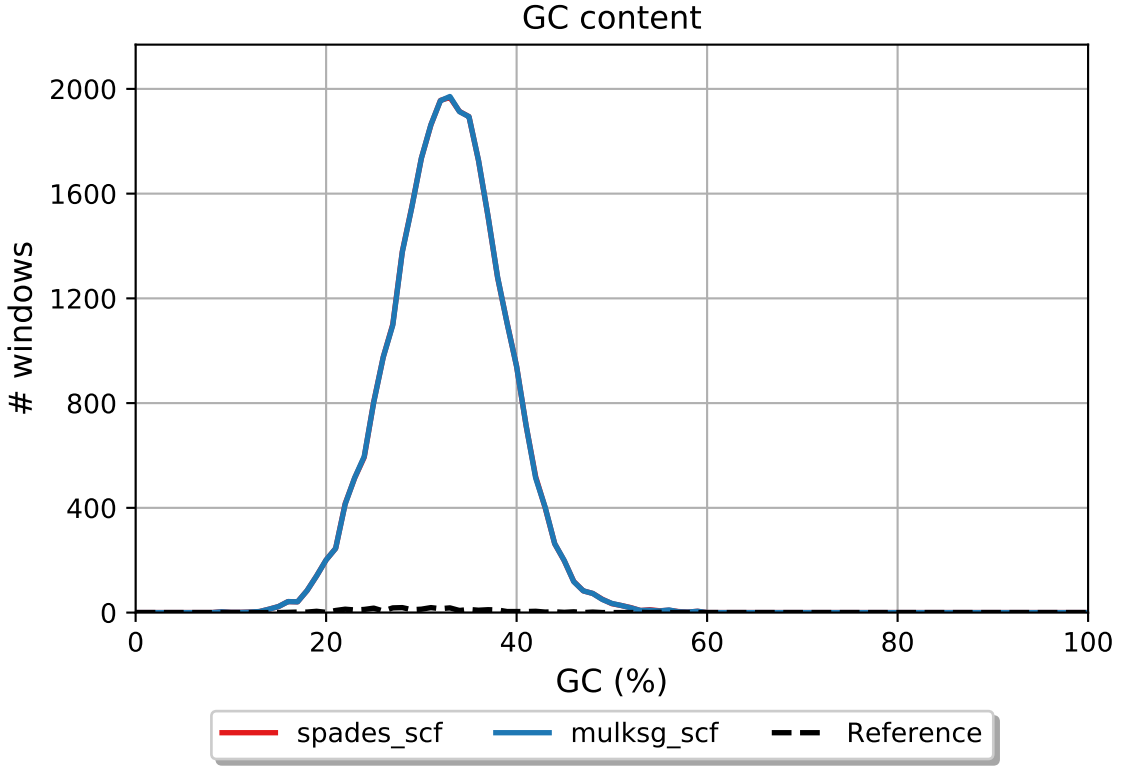
	spades_scf	mulksg_scf
# fully unaligned contigs	69	69
Fully unaligned length	2448784	2447983
# partially unaligned contigs	2	2
Partially unaligned length	399315	399315
# N's	96	96

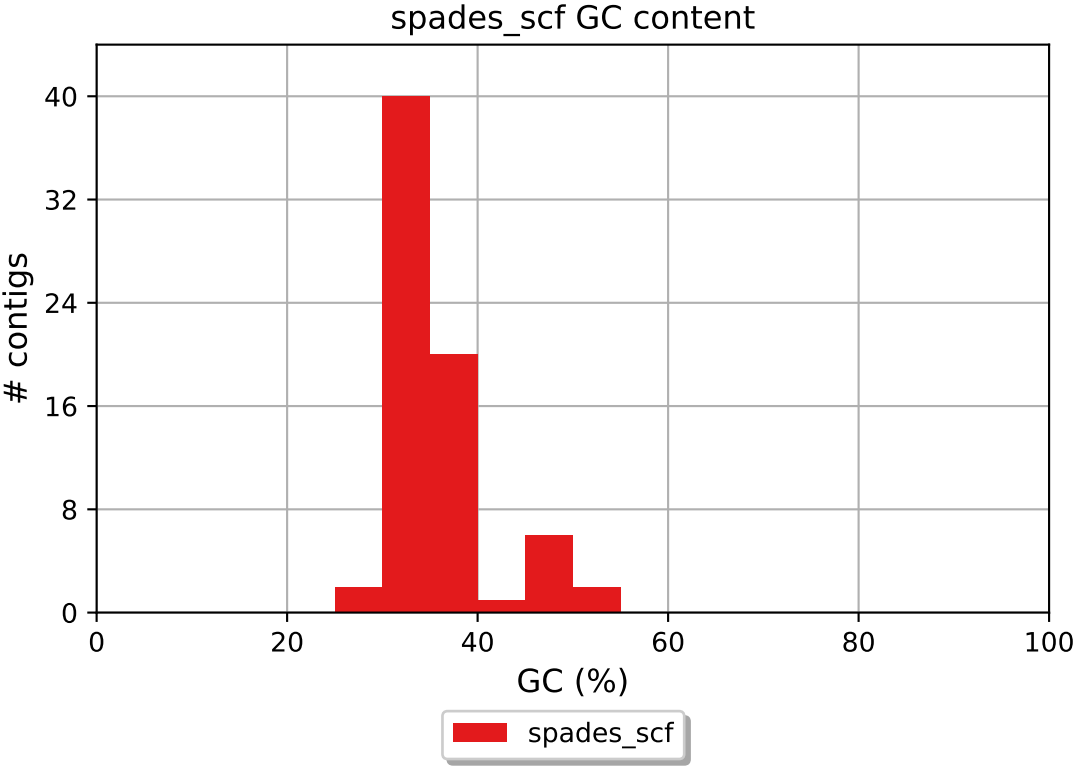
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

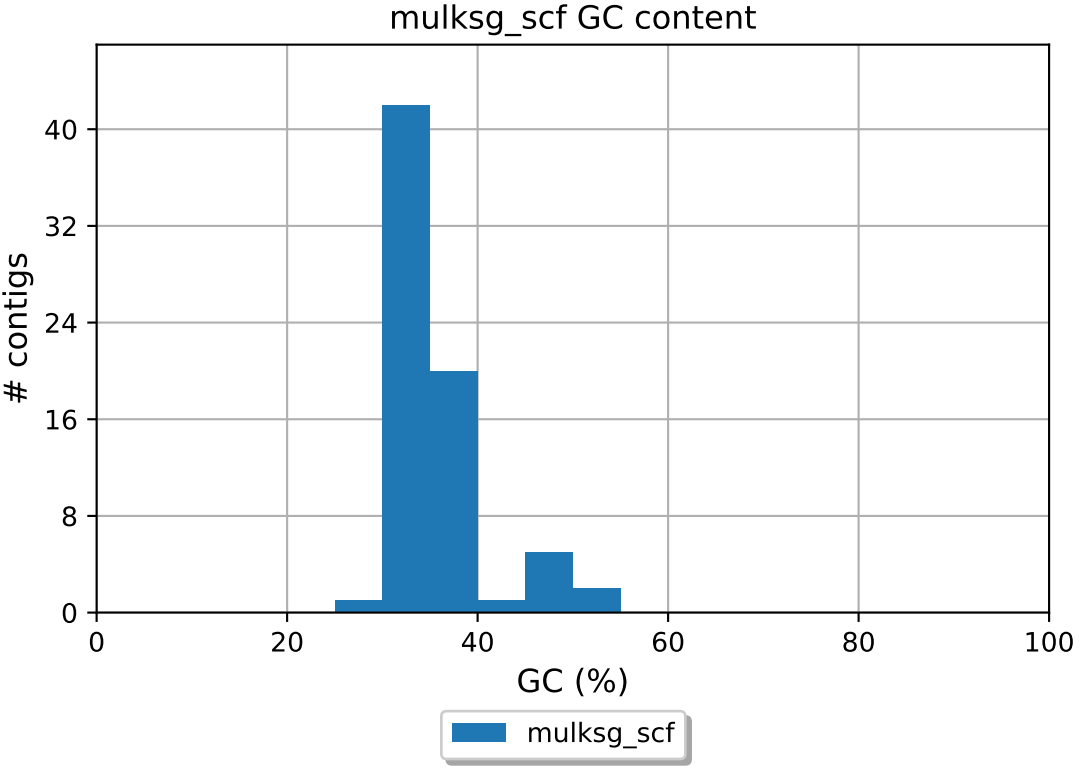

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf

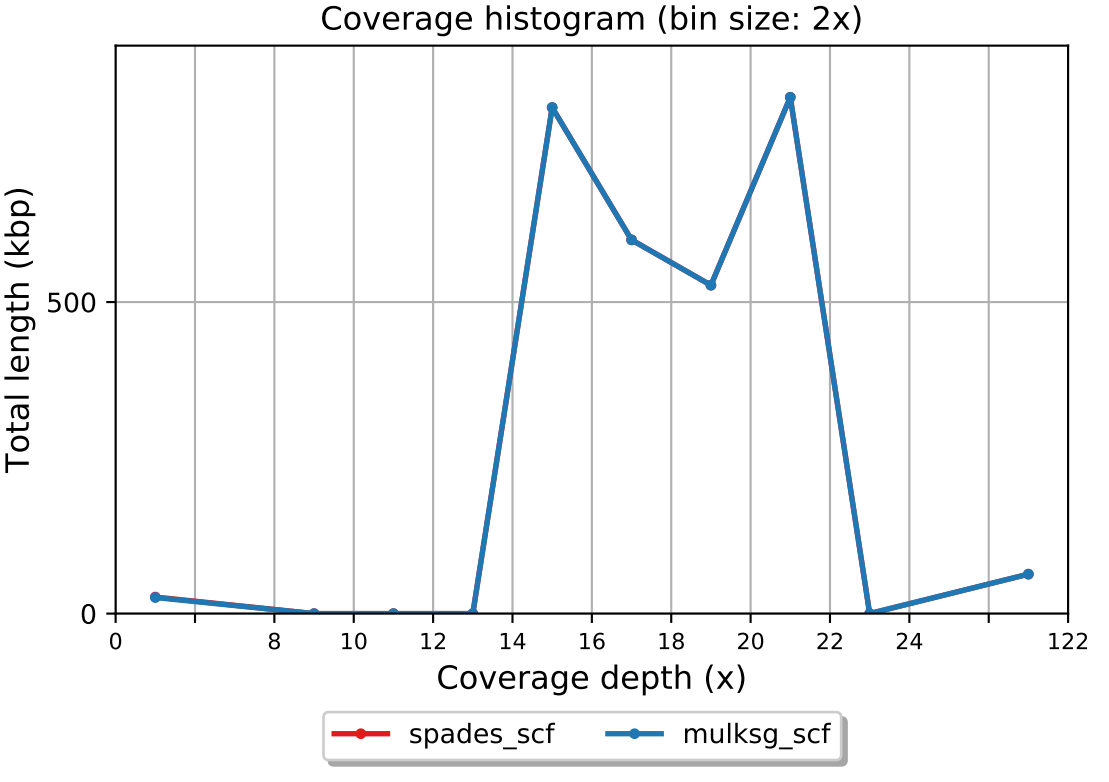

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf

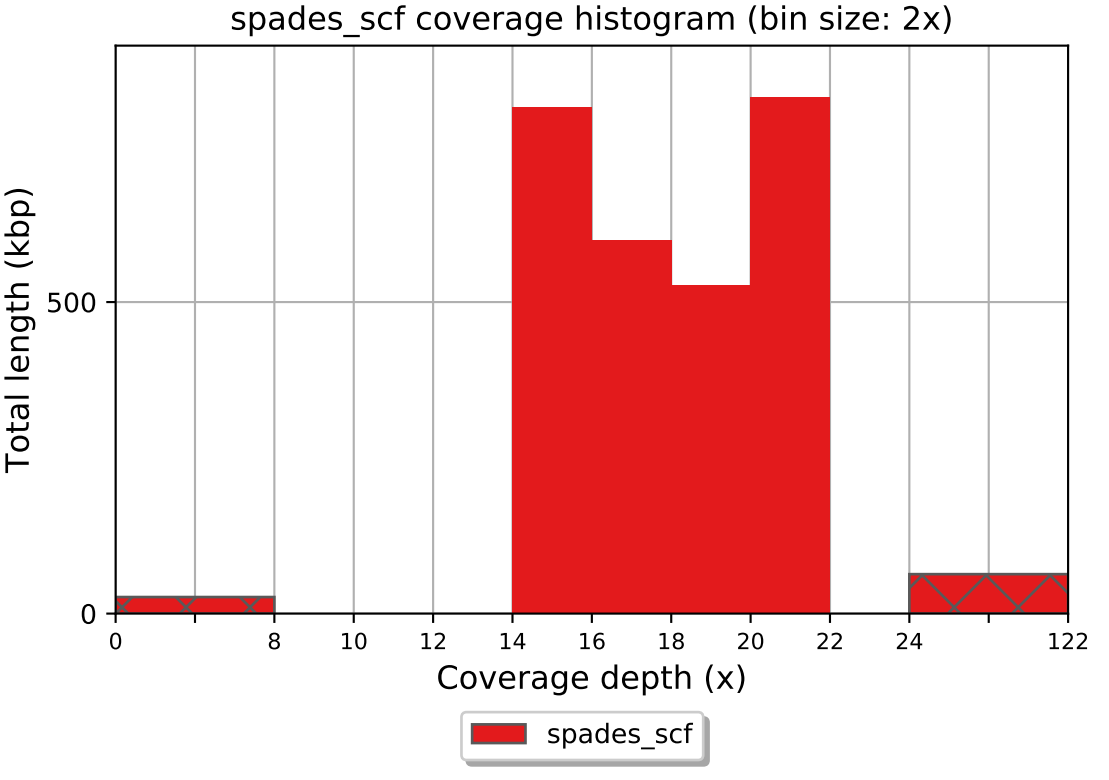

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
15
30
45
60
Contig index
spades_scf
mulksg_scf
Reference

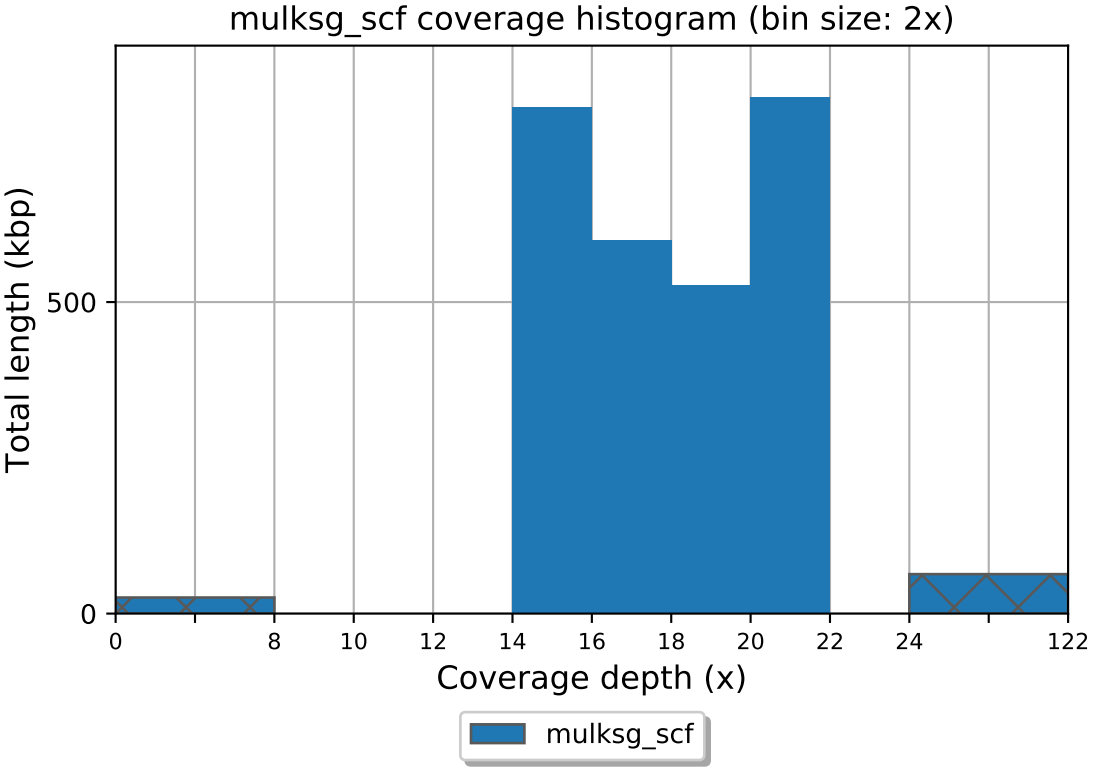

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
spades_scf
mulksg_scf
Reference

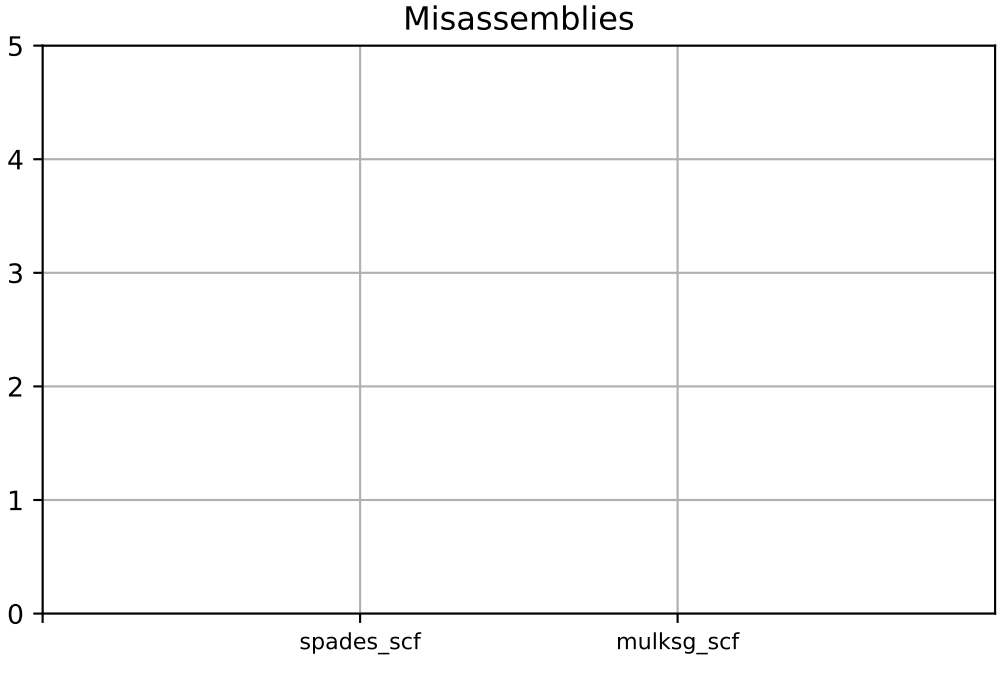

spades_scf GC content
contigs
GC (%)
0
8
16
24
32
40
0
20
40
60
80
100
spades_scf

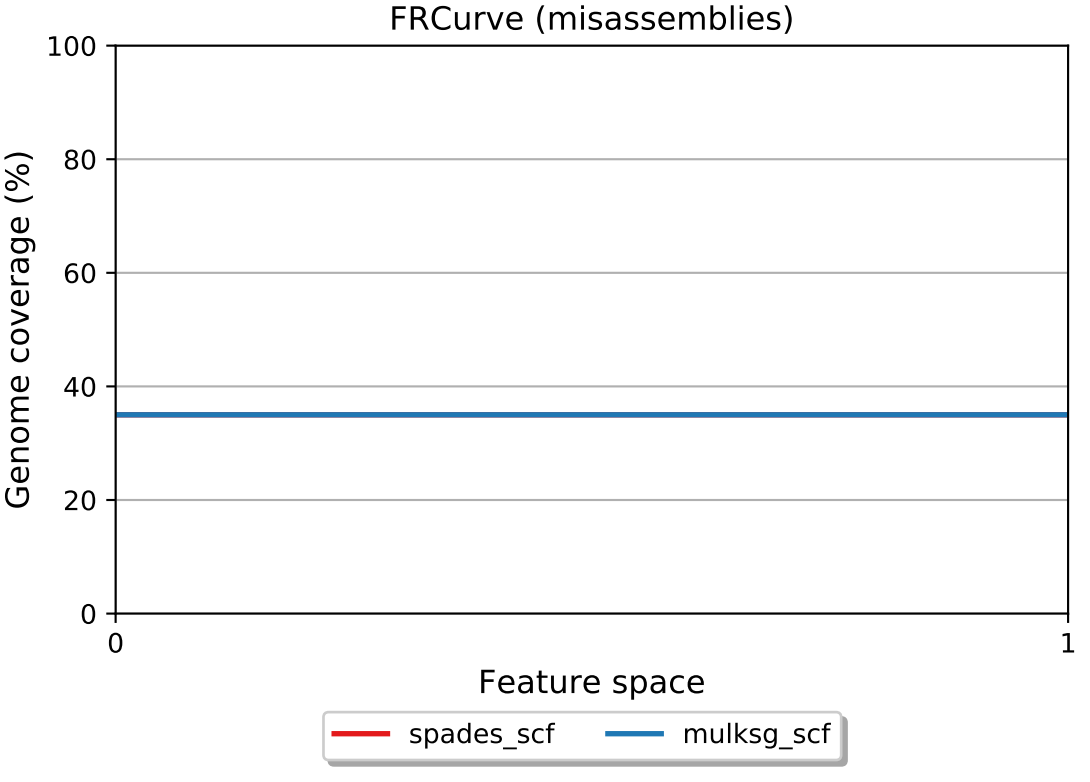

mulksg_scf GC content
contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
mulksg_scf

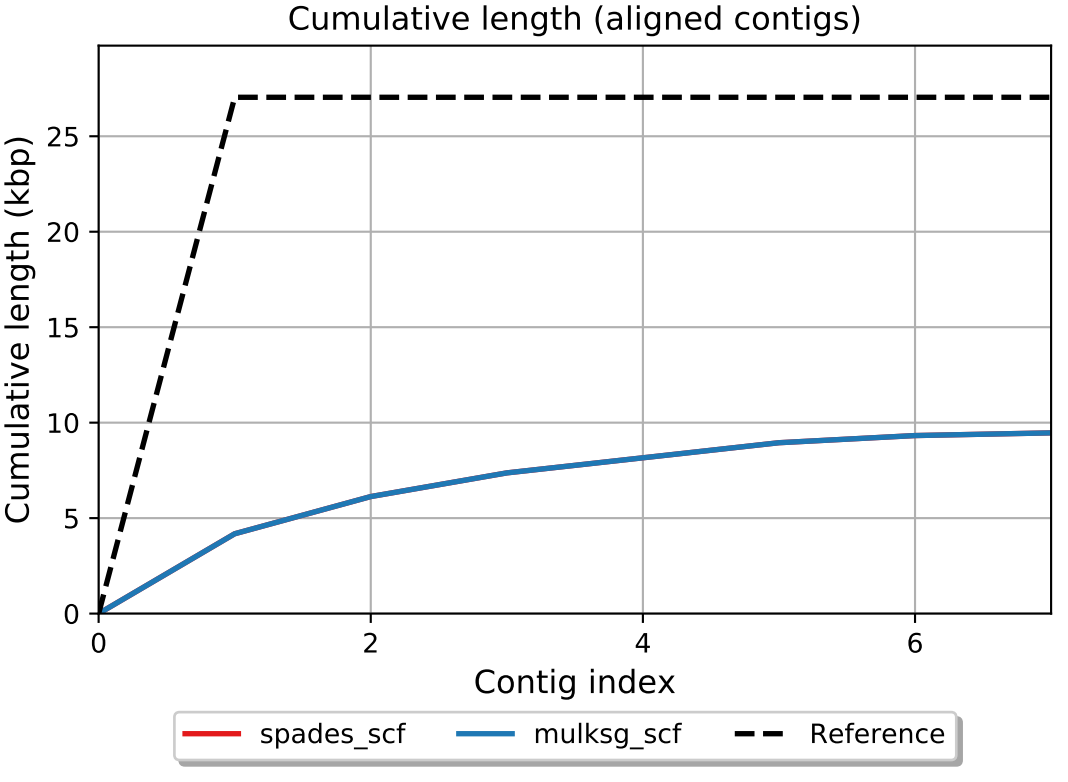

Coverage histogram (bin size: 2x)
Total length (kbp)
500
0
0
8
10
12
14
16
18
20
22
24
122
Coverage depth (x)
spades_scf
mulksg_scf

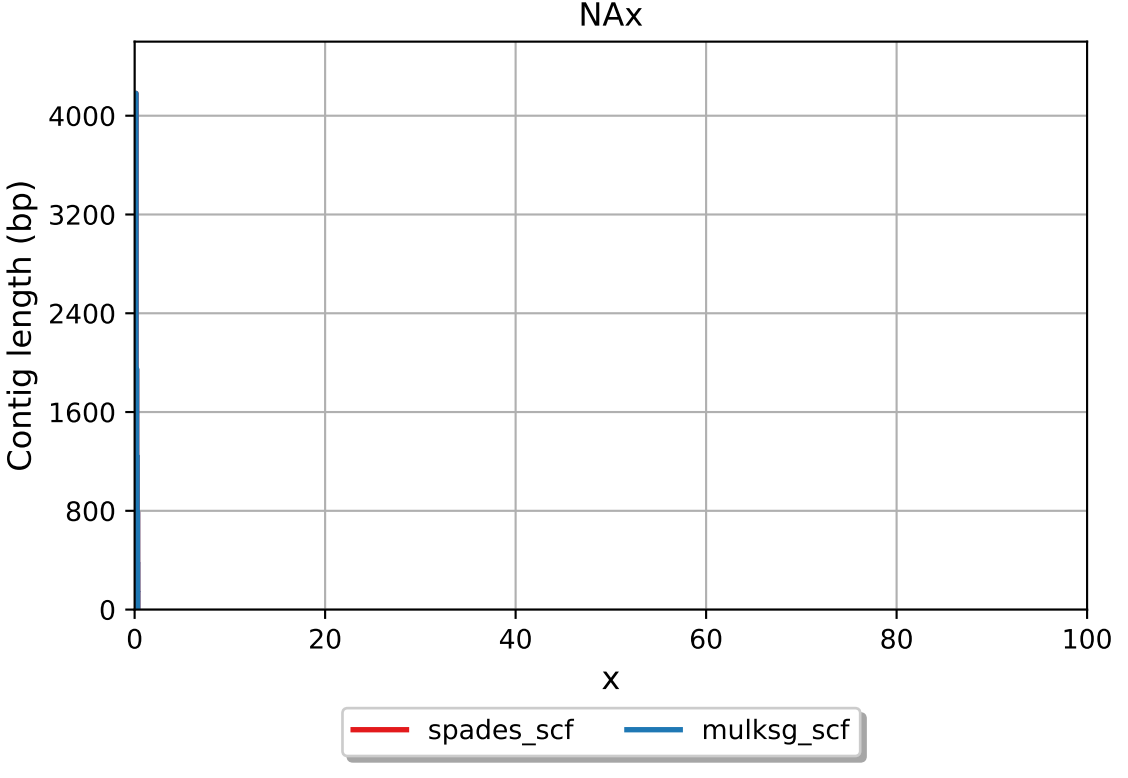

spades_scf coverage histogram (bin size: 2x)
Total length (kbp)
500
0
0
8
10
12
14
16
18
20
22
24
122
Coverage depth (x)
spades_scf

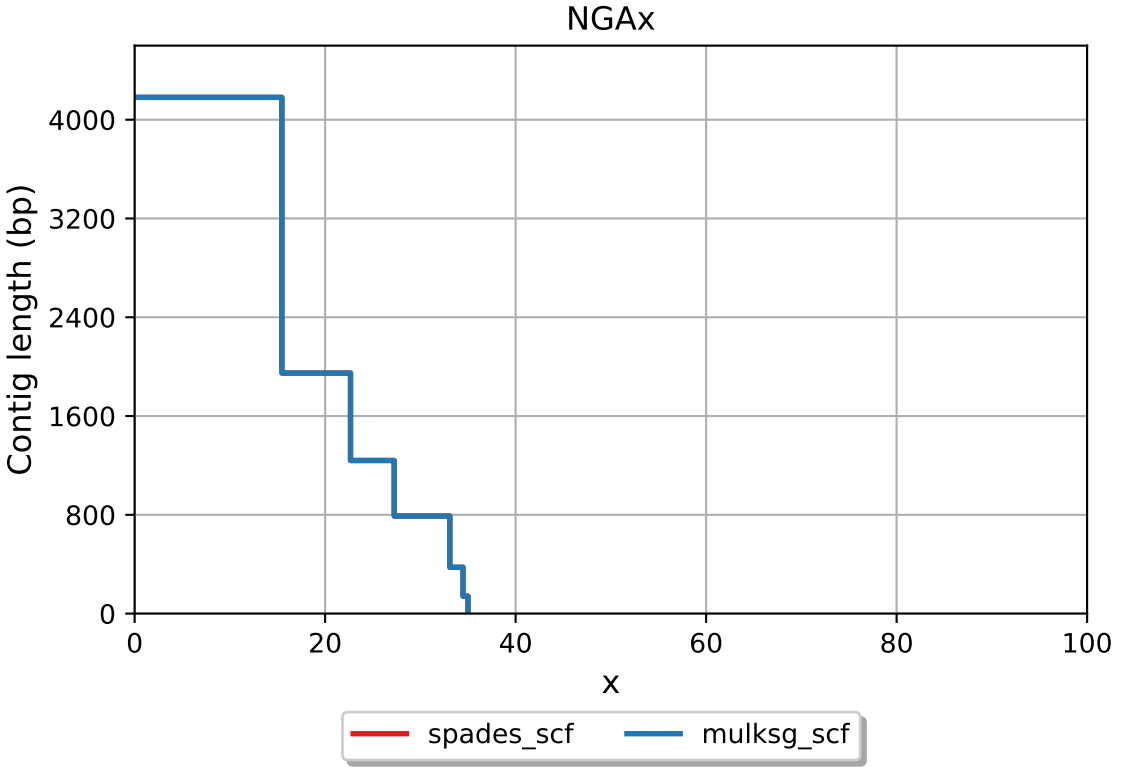

mulksg_scf coverage histogram (bin size: 2x)
Total length (kbp)
500
0
0
8
10
12
14
16
18
20
22
24
122
Coverage depth (x)
mulksg_scf

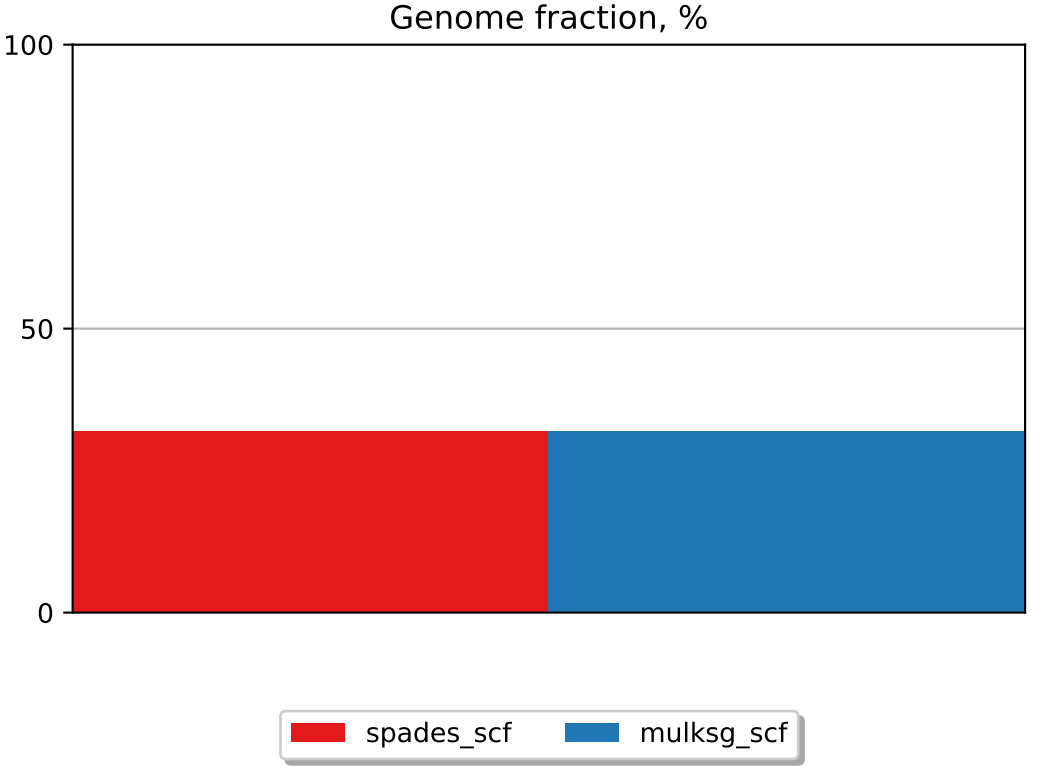

Misassemblies
5
4
3
2
1
0
spades_scf
mulksg_scf


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
spades_scf
mulksg_scf


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
5
10
15
20
25
0
2
4
6
Contig index
spades_scf
mulksg_scf
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf


Genome fraction, %
100
50
0
spades_scf
mulksg_scf