Report

	spades_scf	mulksg_scf
# contigs (>= 0 bp)	1743	1861
# contigs (>= 1000 bp)	126	124
# contigs (>= 5000 bp)	84	85
# contigs (>= 10000 bp)	69	68
# contigs (>= 25000 bp)	49	49
# contigs (>= 50000 bp)	31	31
Total length (>= 0 bp)	6172679	6202016
Total length (>= 1000 bp)	5660692	5646672
Total length (>= 5000 bp)	5571474	5562319
Total length (>= 10000 bp)	5463049	5441628
Total length (>= 25000 bp)	5116089	5118423
Total length (>= 50000 bp)	4447881	4450443
# contigs	212	225
Largest contig	638900	639472
Total length	5717747	5714078
Reference length	5224283	5224283
GC (%)	35.24	35.24
Reference GC (%)	35.58	35.58
N50	112026	112026
NG50	136462	136462
N75	56899	58330
NG75	69136	69136
L50	11	11
LG50	9	9
L75	29	28
LG75	23	23
# misassemblies	3	3
# misassembled contigs	3	3
Misassembled contigs length	4422	4403
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	39	39
# unaligned contigs	140 + 67 part	153 + 67 part
Unaligned length	5448870	5444727
Genome fraction (%)	5.065	5.062
Duplication ratio	1.016	1.019
# N's per 100 kbp	13.50	13.51
# mismatches per 100 kbp	3807.01	3813.20
# indels per 100 kbp	21.92	22.31
Largest alignment	30865	30865
Total aligned length	267783	268257
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

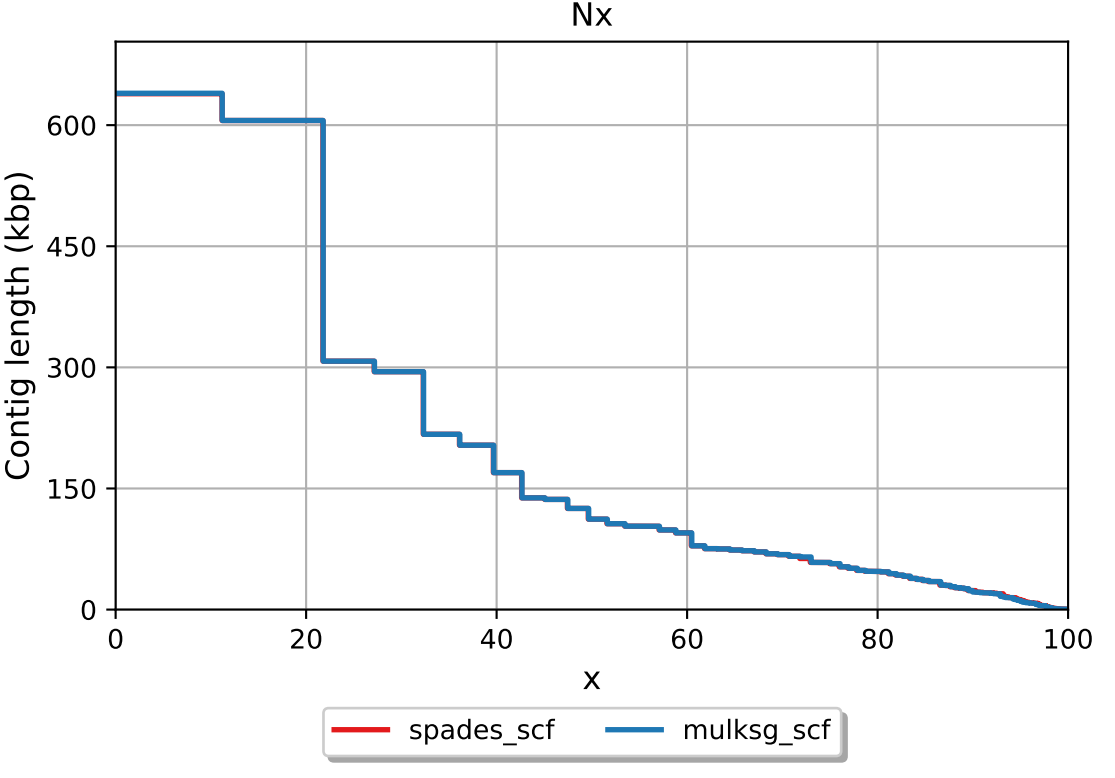
	spades_scf	mulksg_scf
# misassemblies	3	3
# contig misassemblies	3	3
# c. relocations	3	3
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	3	3
Misassembled contigs length	4422	4403
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	39	39
# mismatches	10073	10084
# indels	58	59
# indels (<= 5 bp)	55	56
# indels (> 5 bp)	3	3
Indels length	130	133

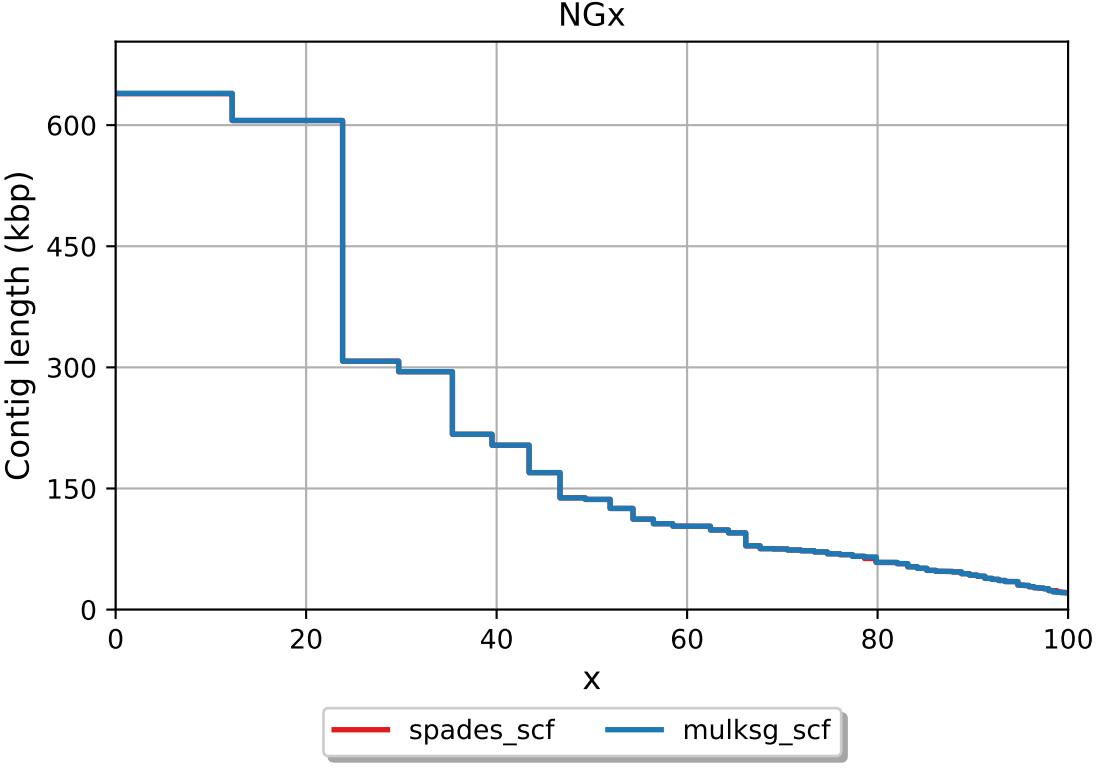
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

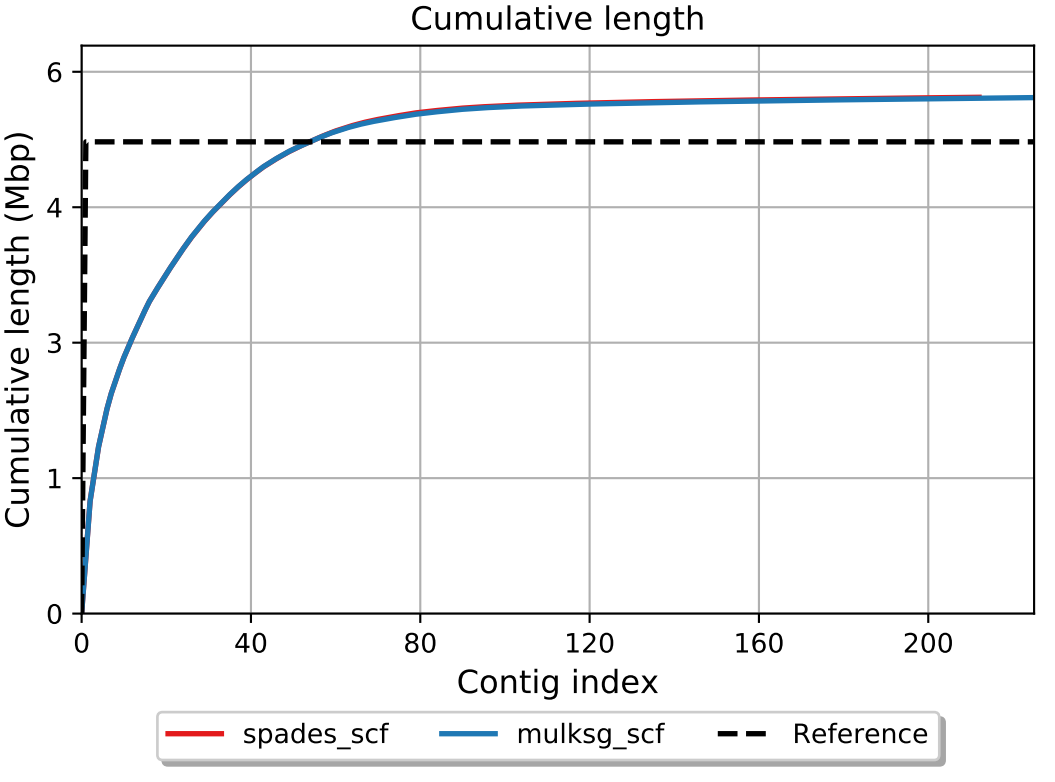
Unaligned report

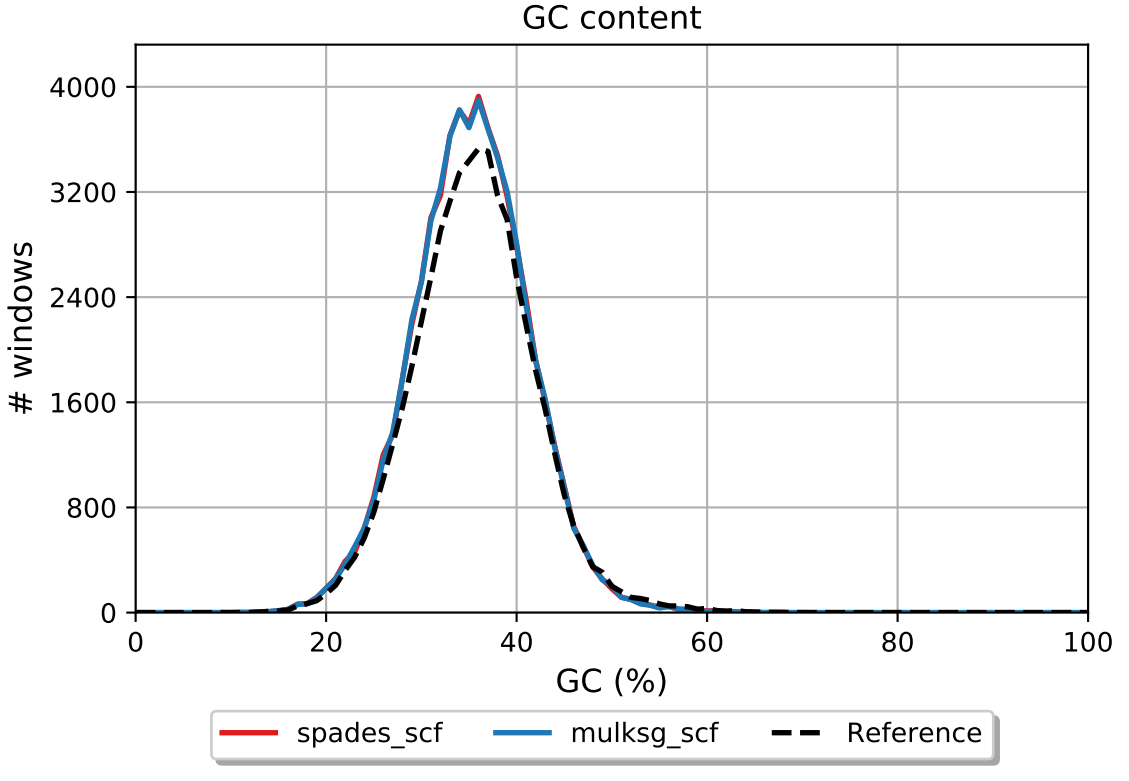
	spades_scf	mulksg_scf
# fully unaligned contigs	140	153
Fully unaligned length	635358	631405
# partially unaligned contigs	67	67
Partially unaligned length	4813512	4813322
# N's	772	772

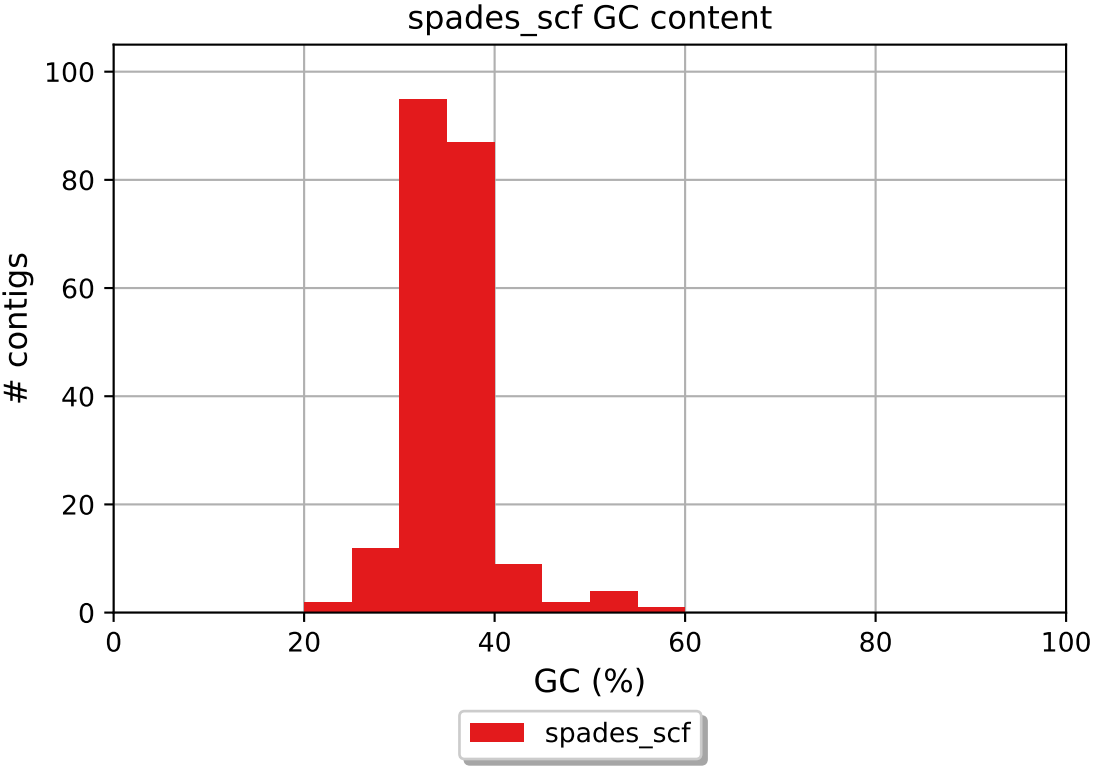
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

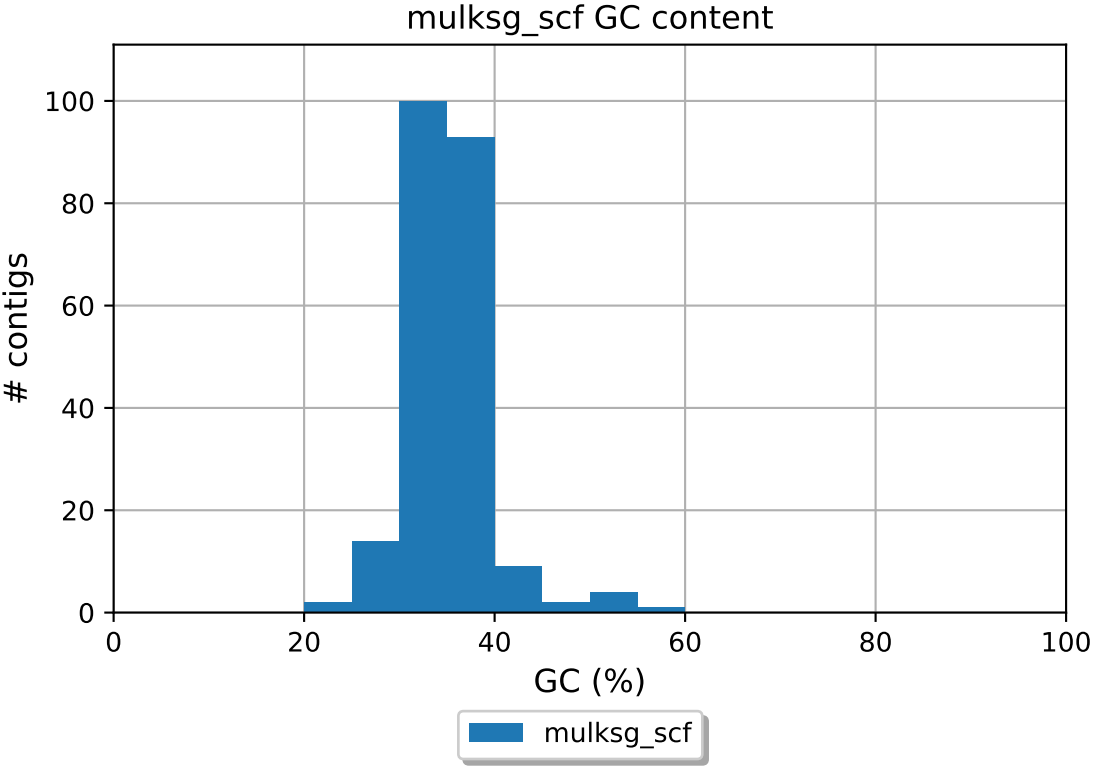

Nx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf

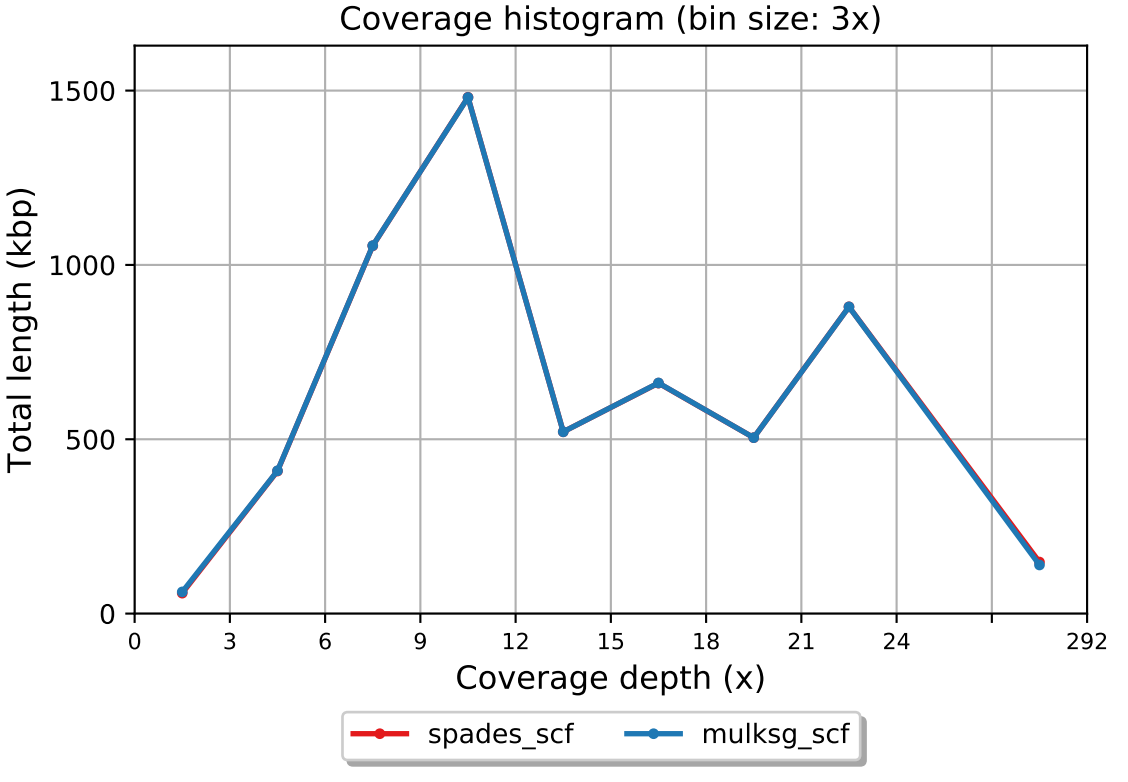

NGx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf

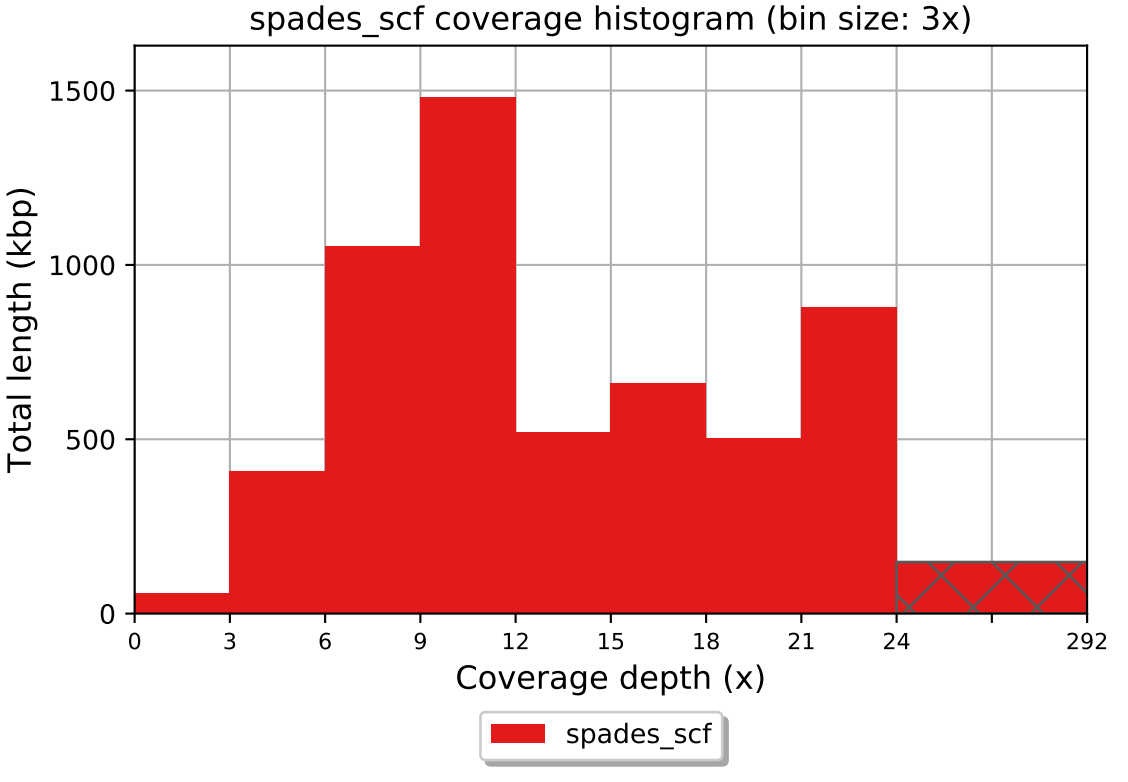

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
40
80
120
160
200
Contig index
spades_scf
mulksg_scf
Reference

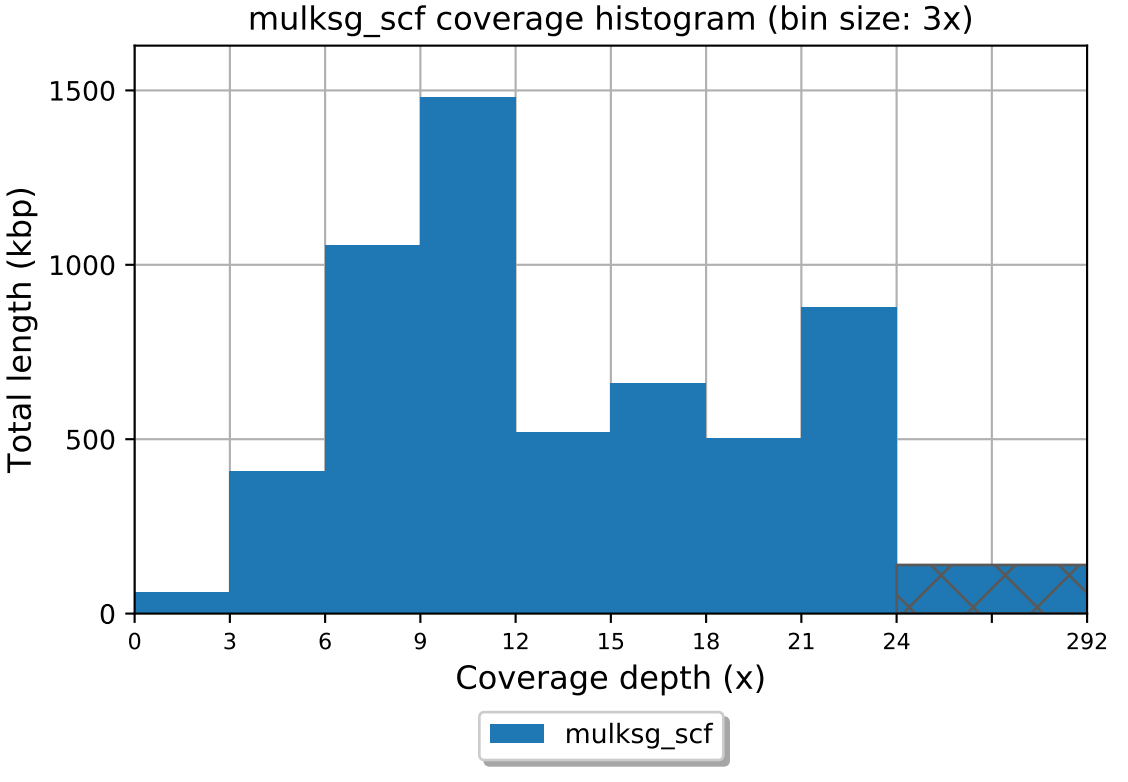

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
spades_scf
mulksg_scf
Reference

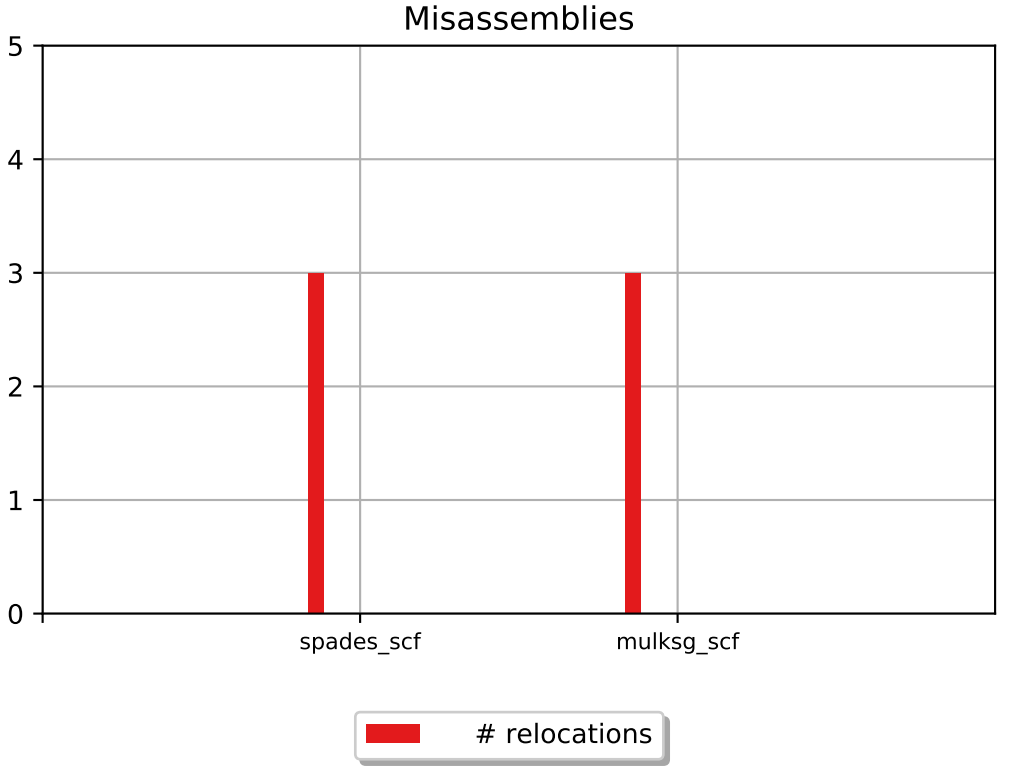

spades_scf GC content
contigs
GC (%)
0
20
40
60
80
100
spades_scf

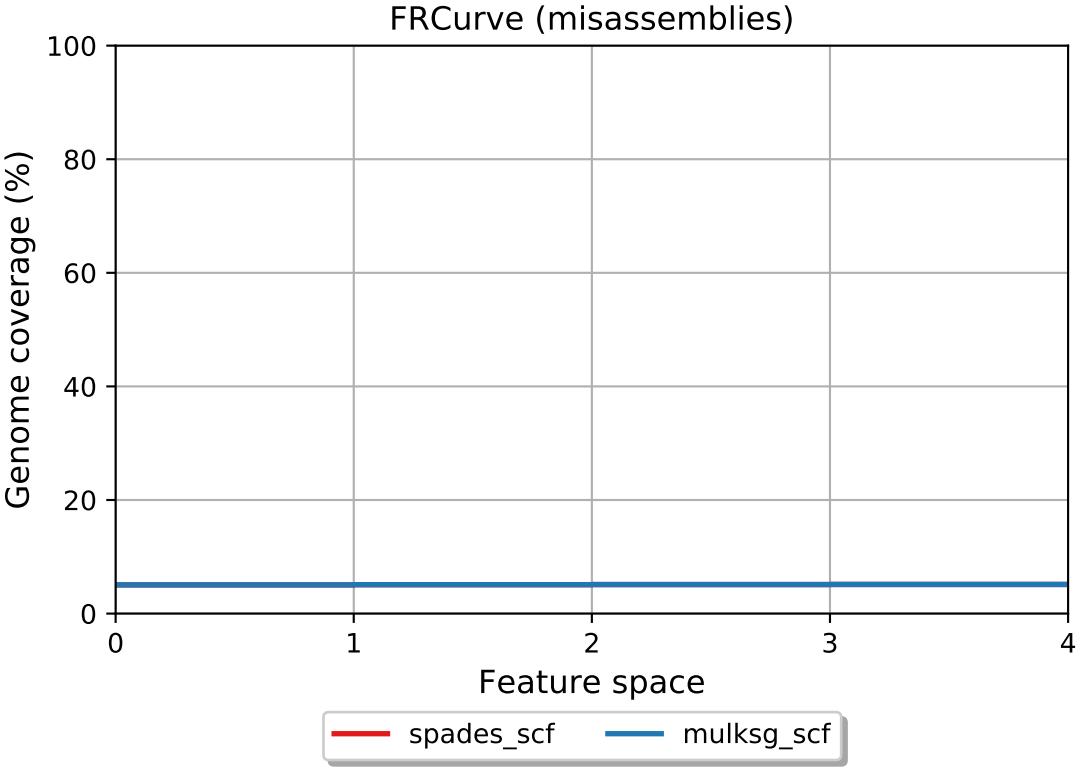

mulksg_scf GC content
contigs
GC (%)
0
20
40
60
80
100
mulksg_scf

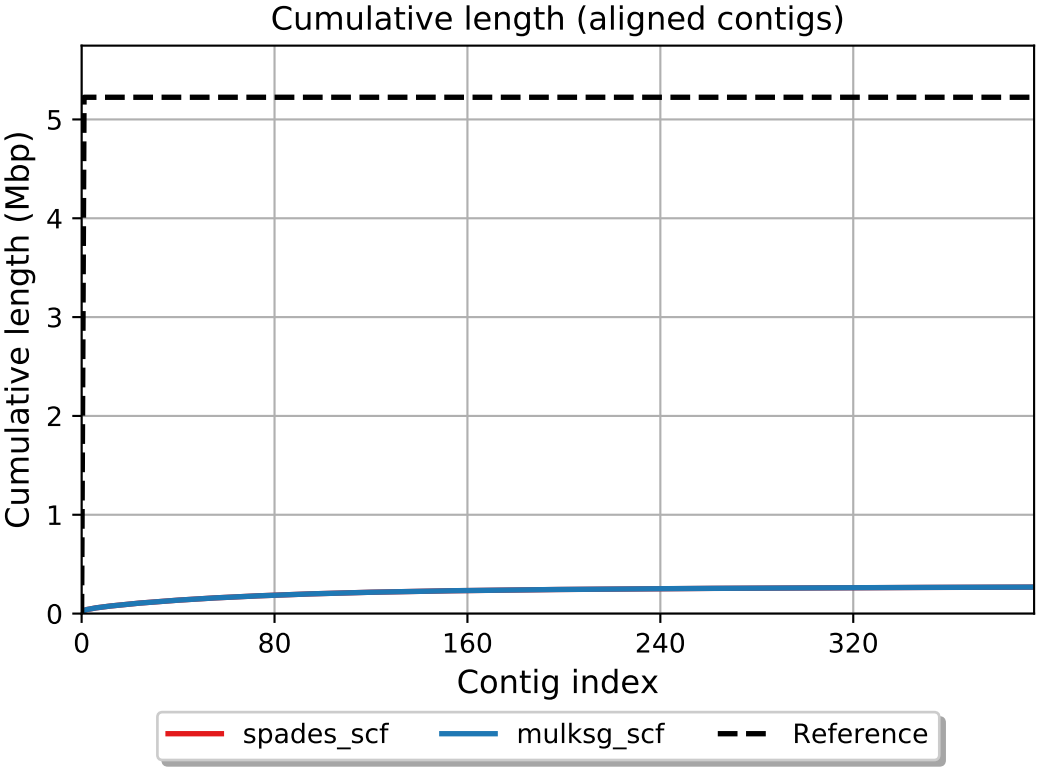

Coverage histogram (bin size: 3x)
Total length (kbp)
1500
1000
500
0
0
3
6
9
12
15
18
21
24
292
Coverage depth (x)
spades_scf
mulksg_scf

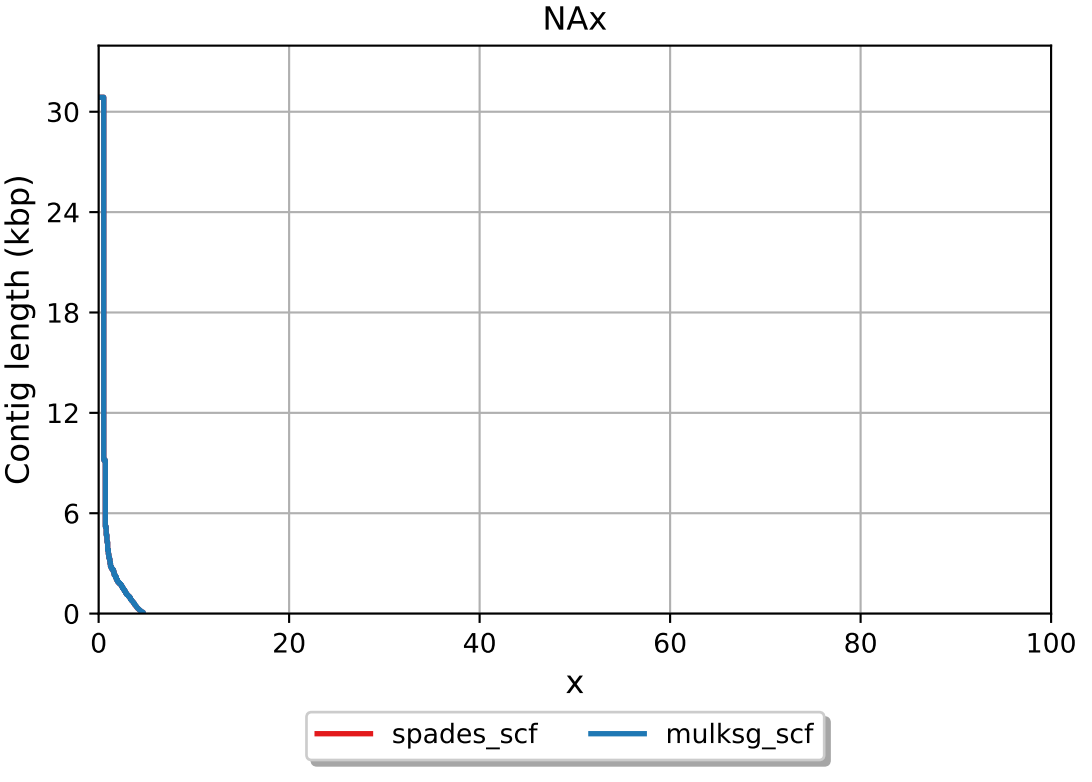

spades_scf coverage histogram (bin size: 3x)
Total length (kbp)
1500
1000
500
0
0
3
6
9
12
15
18
21
24
292
Coverage depth (x)
spades_scf

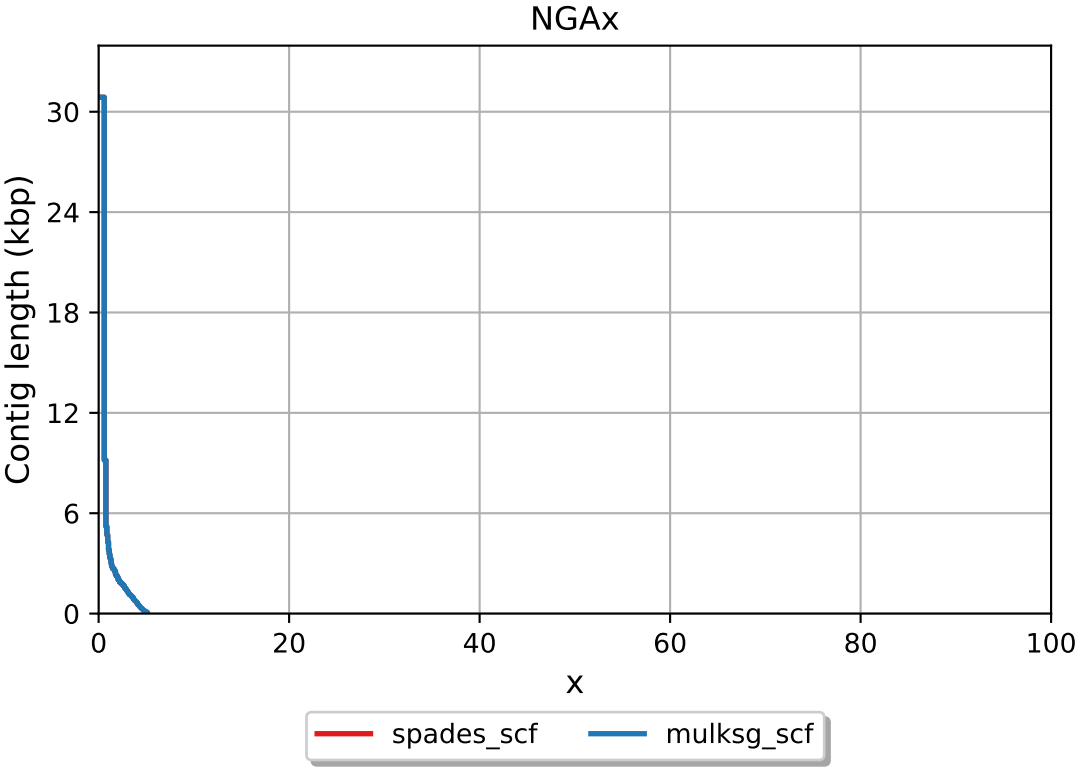

mulksg_scf coverage histogram (bin size: 3x)
Total length (kbp)
1500
1000
500
0
0
3
6
9
12
15
18
21
24
292
Coverage depth (x)
mulksg_scf


Misassemblies
5
4
3
2
1
0
spades_scf
mulksg_scf
relocations


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
80
160
240
320
Contig index
spades_scf
mulksg_scf
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
spades_scf
mulksg_scf

Genome fraction, %
100
50
spades_scf
mulksg_scf