Report

	spades_ctg	mulksg_ctg
# contigs (>= 0 bp)	134	137
# contigs (>= 1000 bp)	61	59
# contigs (>= 5000 bp)	48	47
# contigs (>= 10000 bp)	40	38
# contigs (>= 25000 bp)	34	31
# contigs (>= 50000 bp)	23	22
Total length (>= 0 bp)	4588207	4590313
Total length (>= 1000 bp)	4567216	4567229
Total length (>= 5000 bp)	4540112	4542194
Total length (>= 10000 bp)	4480159	4476066
Total length (>= 25000 bp)	4372834	4346926
Total length (>= 50000 bp)	4002321	4034997
# contigs	66	65
Largest contig	465389	465389
Total length	4571180	4571704
Reference length	114179	114179
GC (%)	68.82	68.82
Reference GC (%)	70.07	70.07
N50	203023	203000
NG50	465389	465389
N75	112756	119428
NG75	465389	465389
L50	8	8
LG50	1	1
L75	16	16
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	0	0
# unaligned contigs	60 + 4 part	59 + 4 part
Unaligned length	4456446	4456970
Genome fraction (%)	100.000	100.000
Duplication ratio	1.005	1.005
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	7.01	7.01
# indels per 100 kbp	2.63	2.63
Largest alignment	112703	112703
Total aligned length	114642	114642
NGA50	112703	112703
NGA75	112703	112703
LGA50	1	1
LGA75	1	1

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

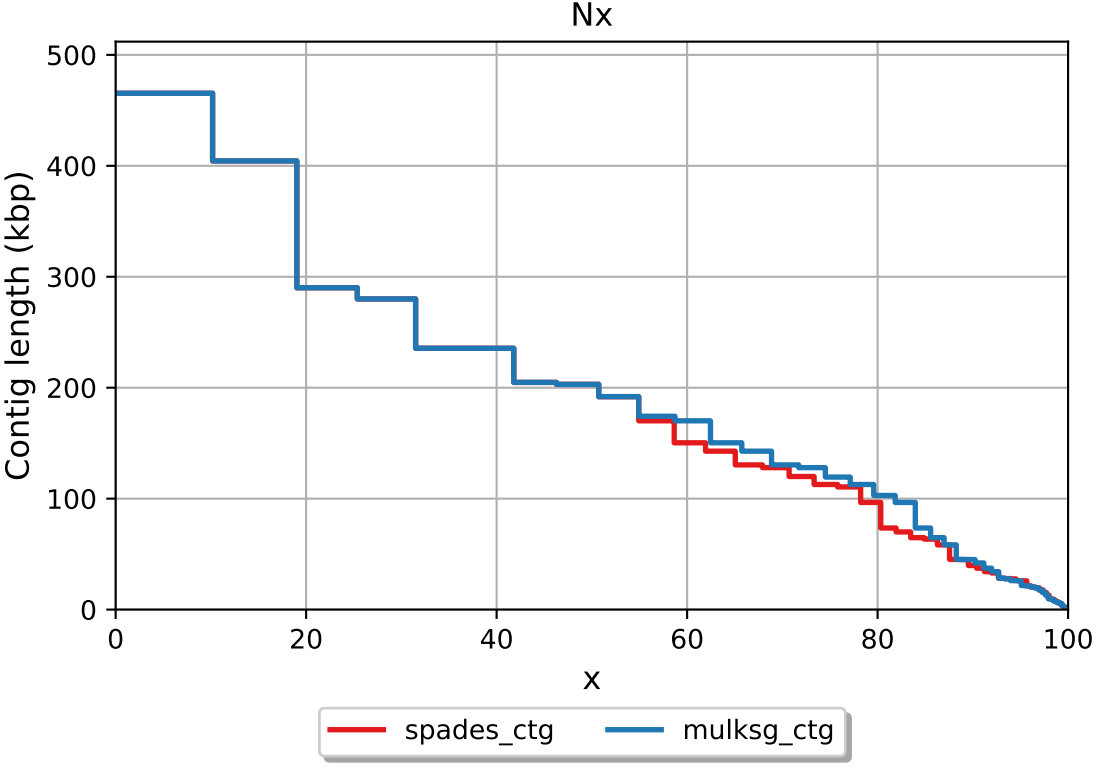
	spades_ctg	mulksg_ctg
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	8	8
# indels	3	3
# indels (<= 5 bp)	3	3
# indels (> 5 bp)	0	0
Indels length	3	3

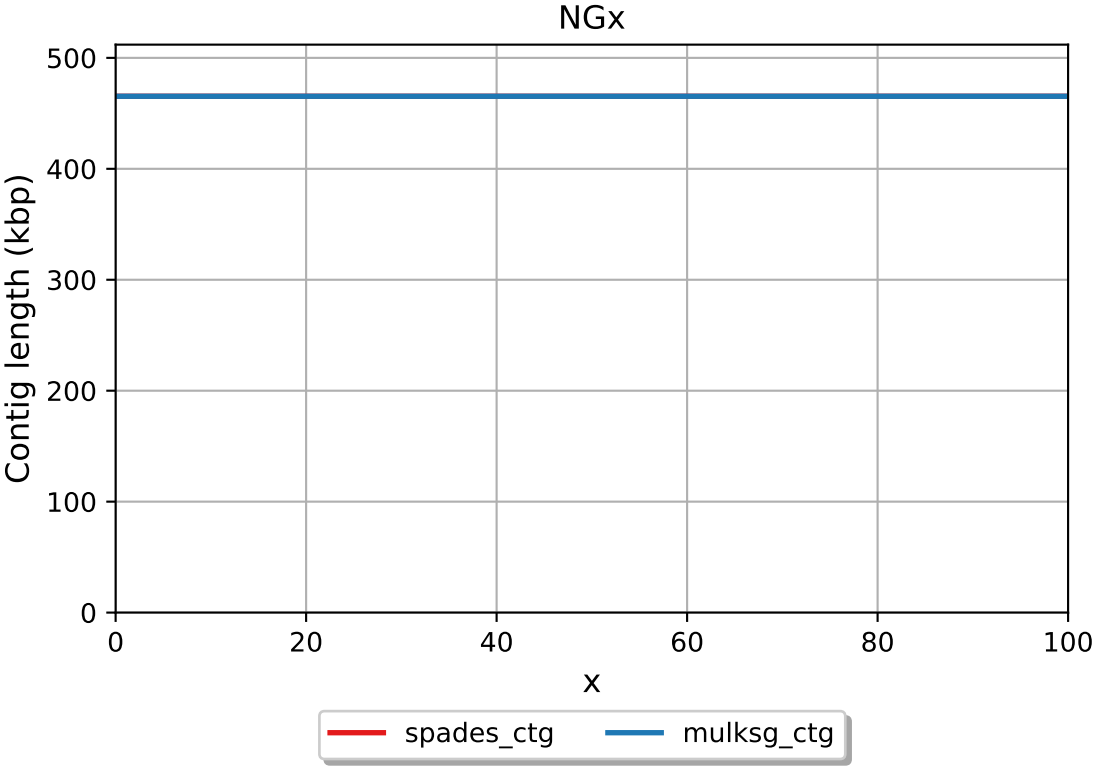
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

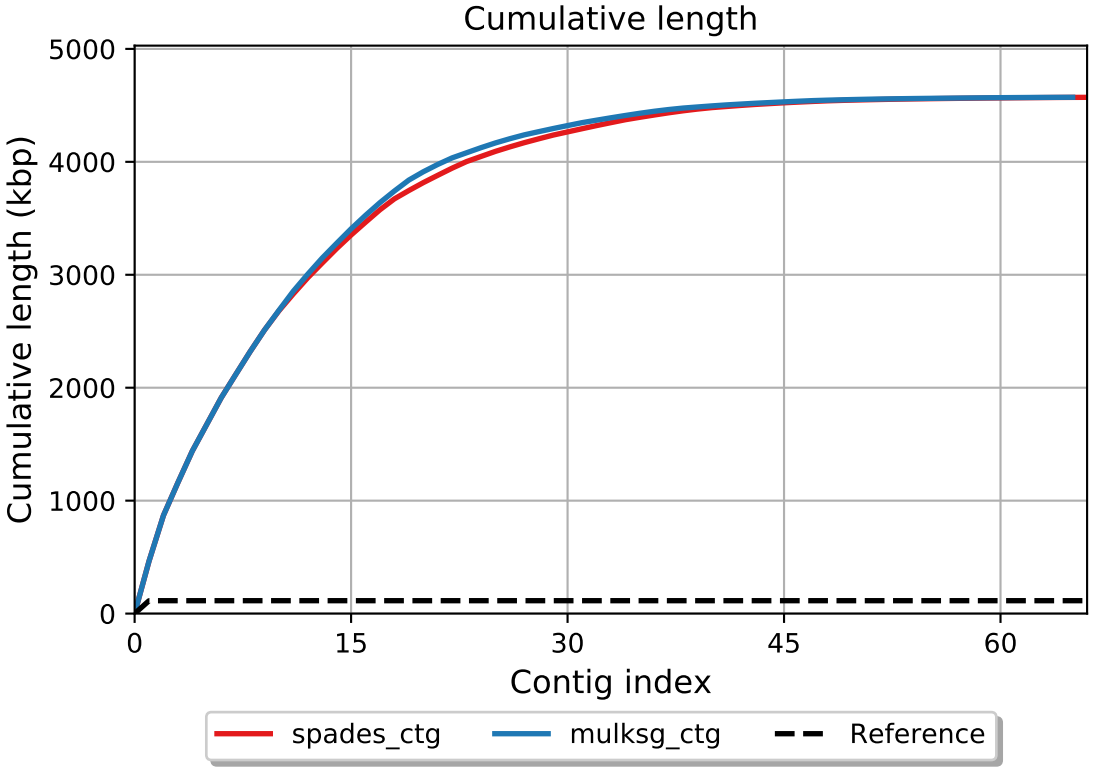
Unaligned report

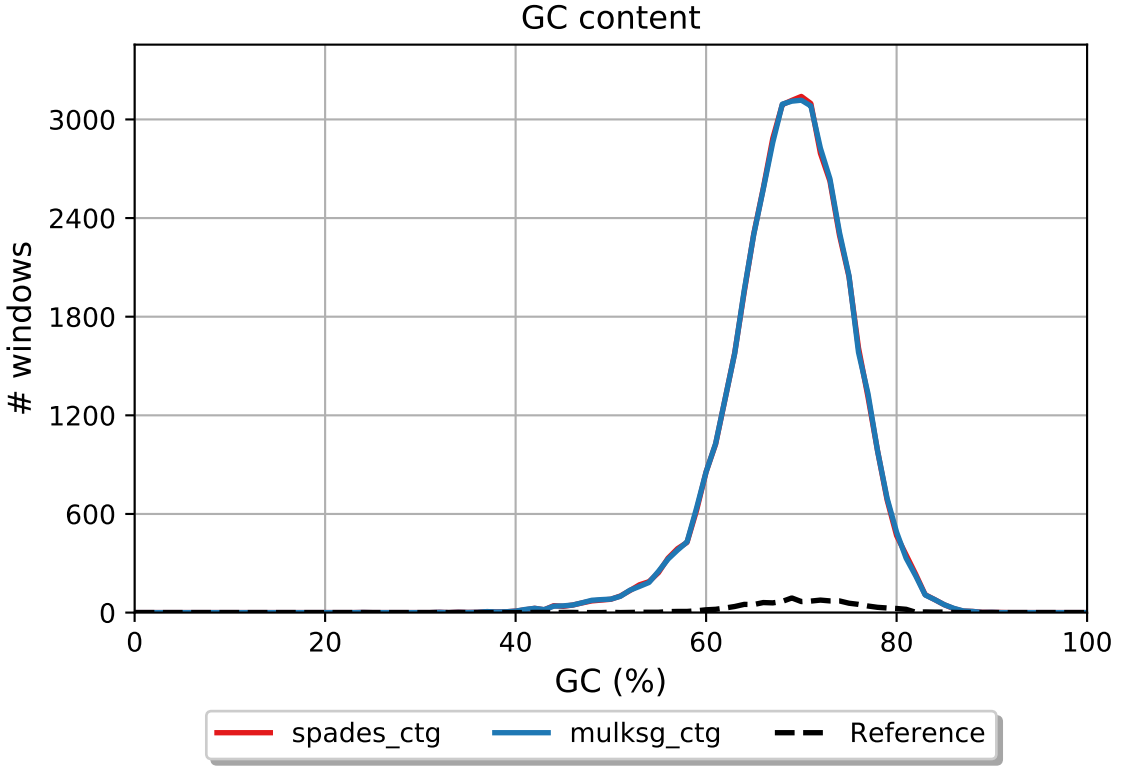
	spades_ctg	mulksg_ctg
# fully unaligned contigs	60	59
Fully unaligned length	3989187	3989734
# partially unaligned contigs	4	4
Partially unaligned length	467259	467236
# N's	0	0

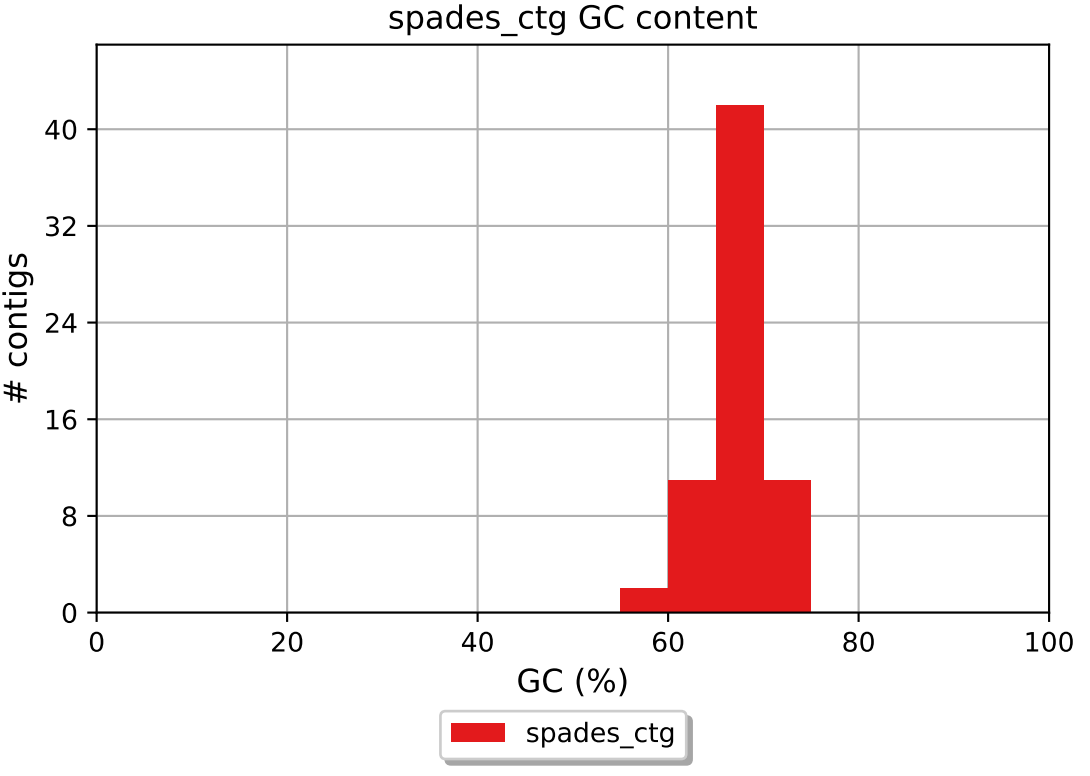
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

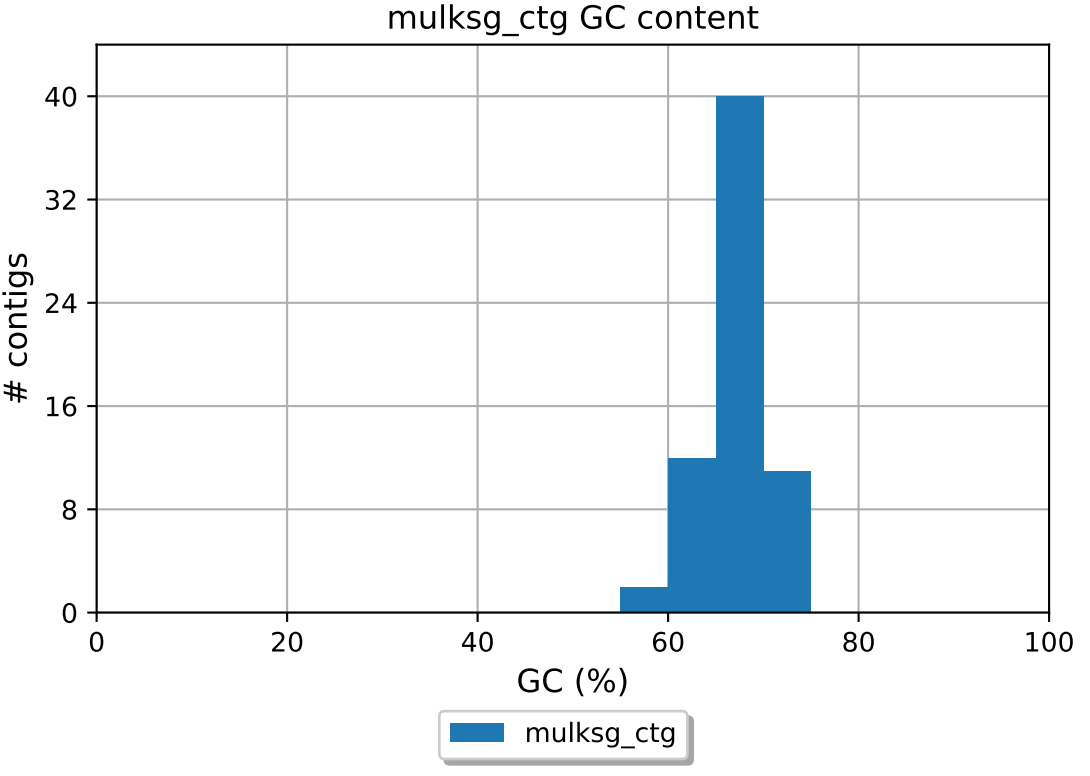

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg

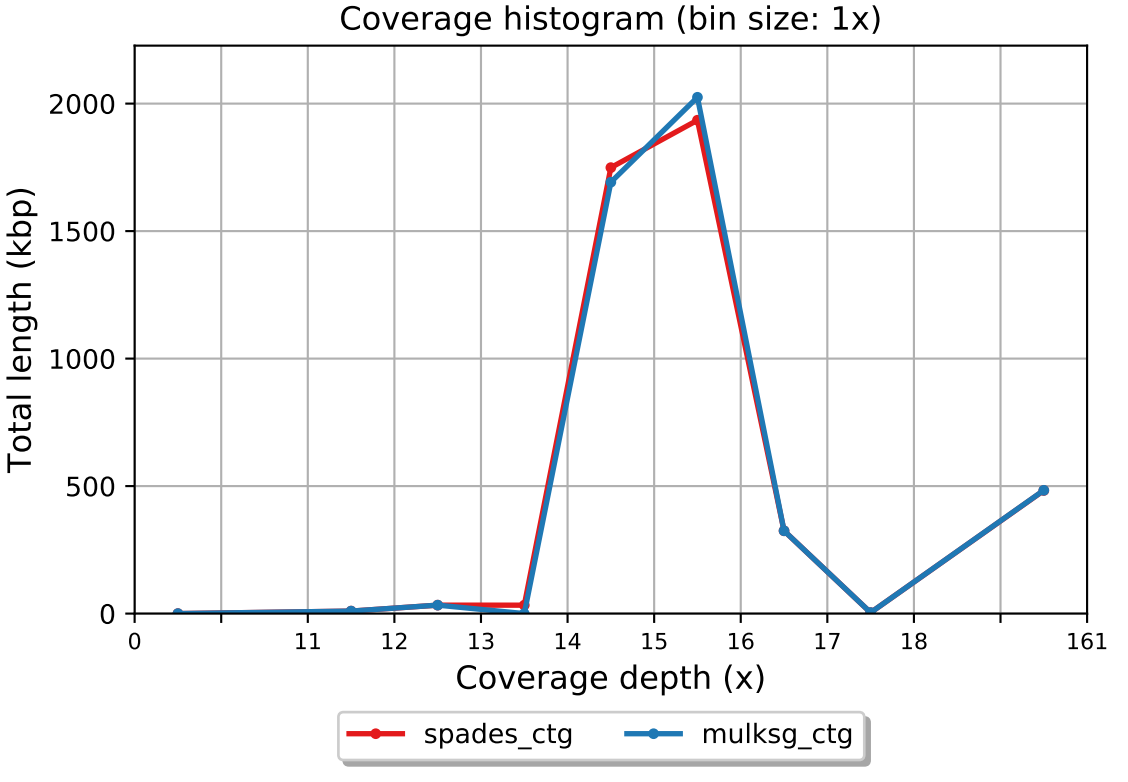

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg

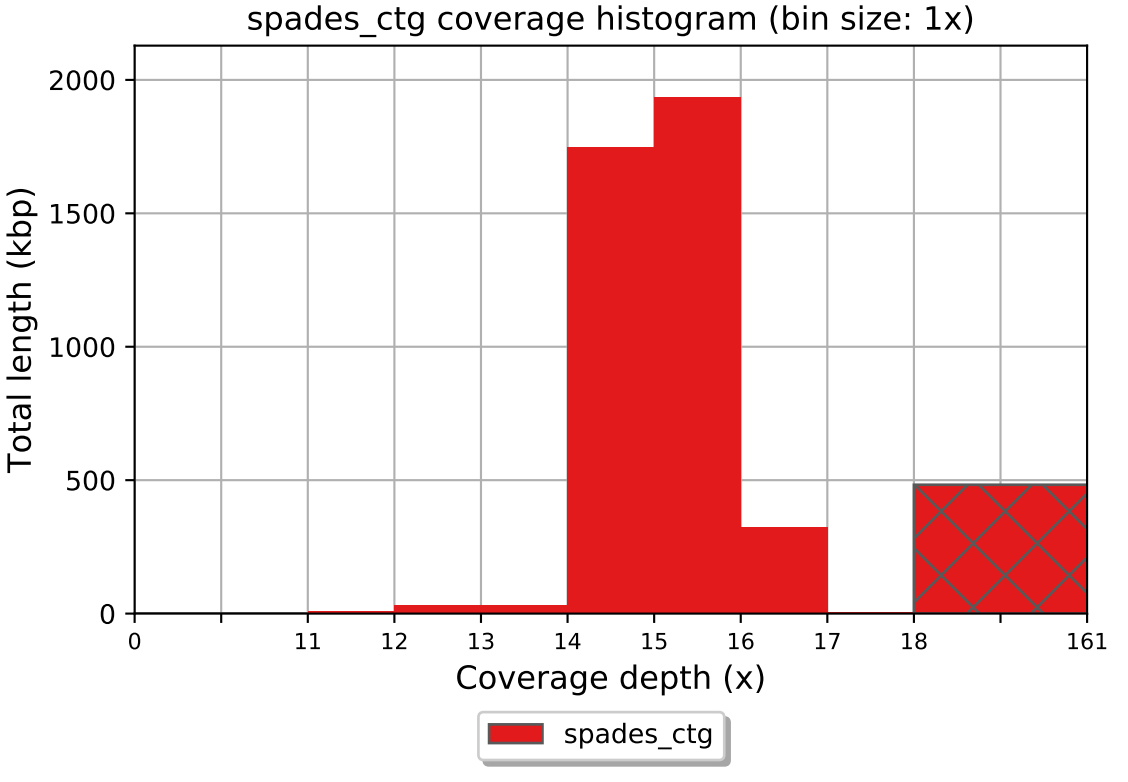

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
15
30
45
60
Contig index
spades_ctg
mulksg_ctg
Reference

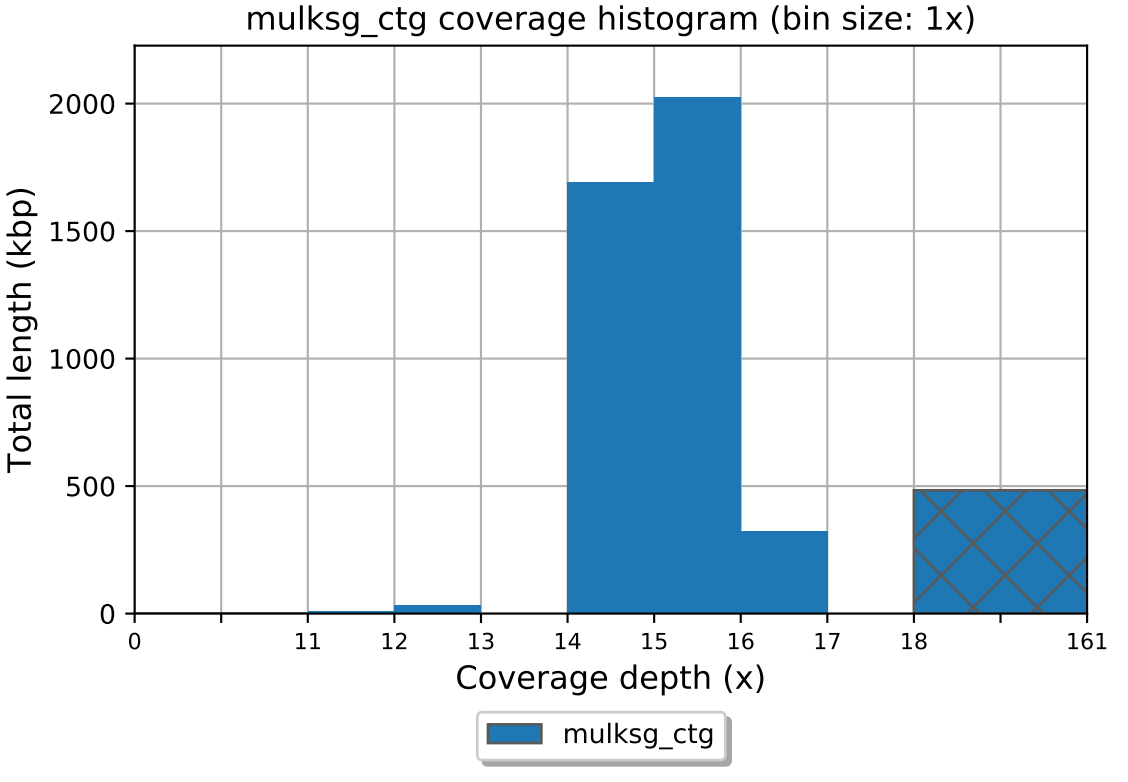

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
spades_ctg
mulksg_ctg
Reference

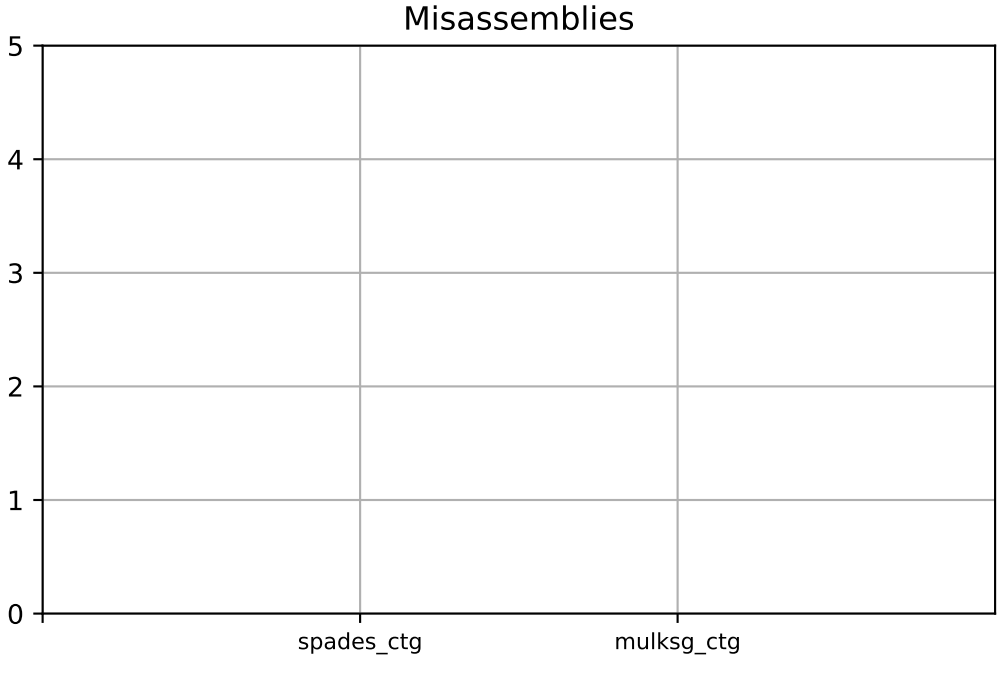

spades_ctg GC content
contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
spades_ctg

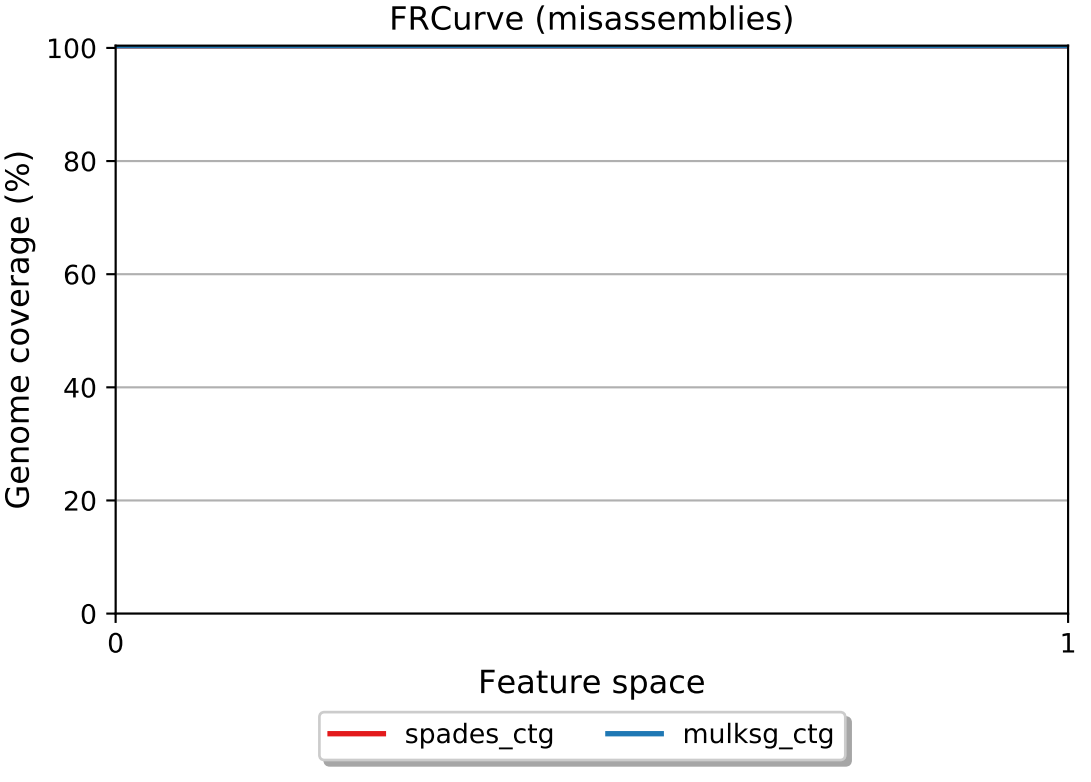

mulksg_ctg GC content
contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
mulksg_ctg

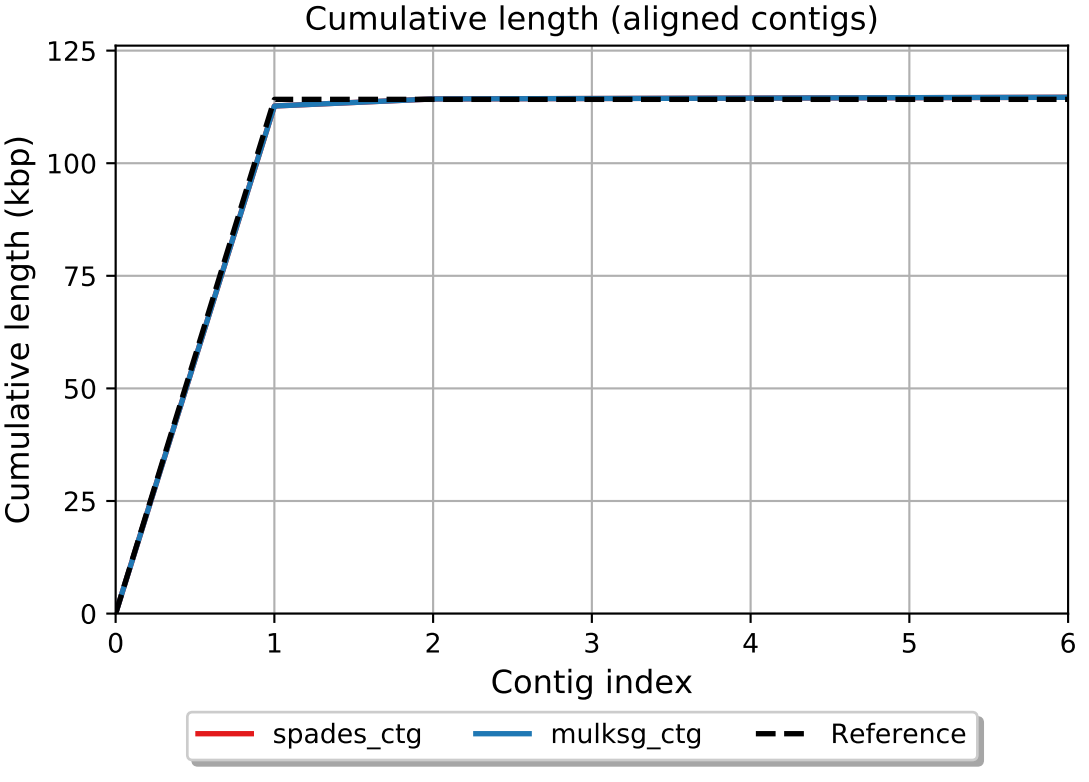

Coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
11
12
13
14
15
16
17
18
161
Coverage depth (x)
spades_ctg
mulksg_ctg

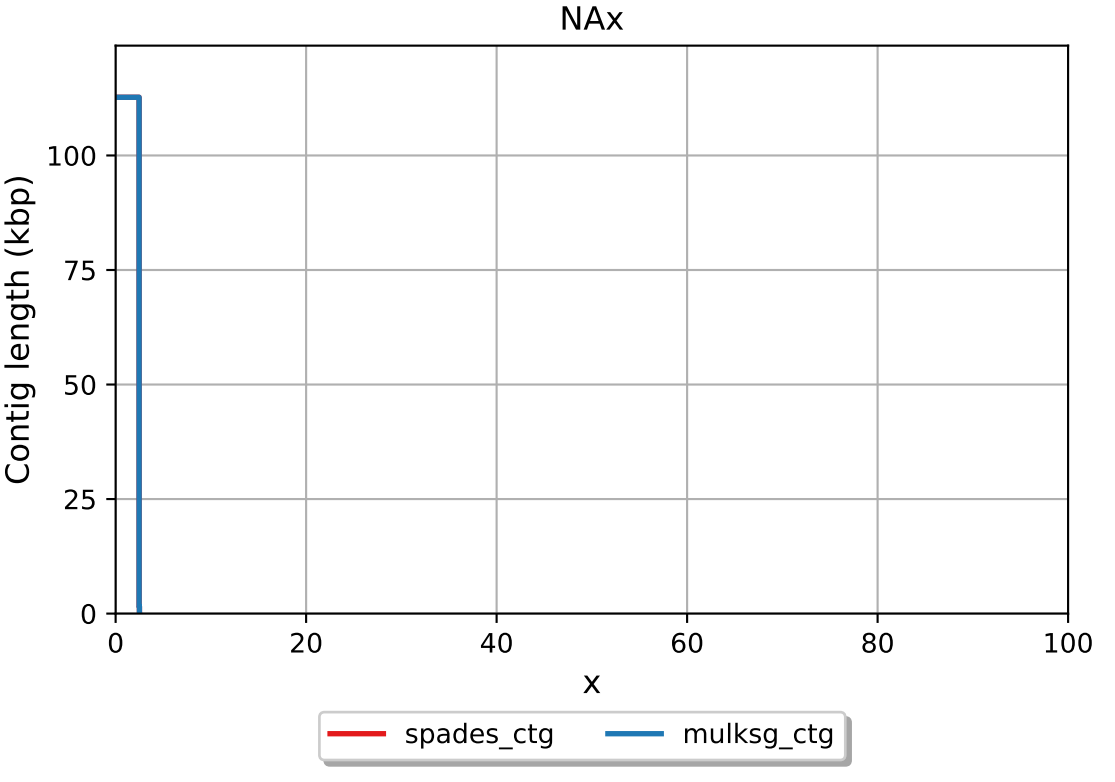

spades_ctg coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
11
12
13
14
15
16
17
18
161
Coverage depth (x)
spades_ctg

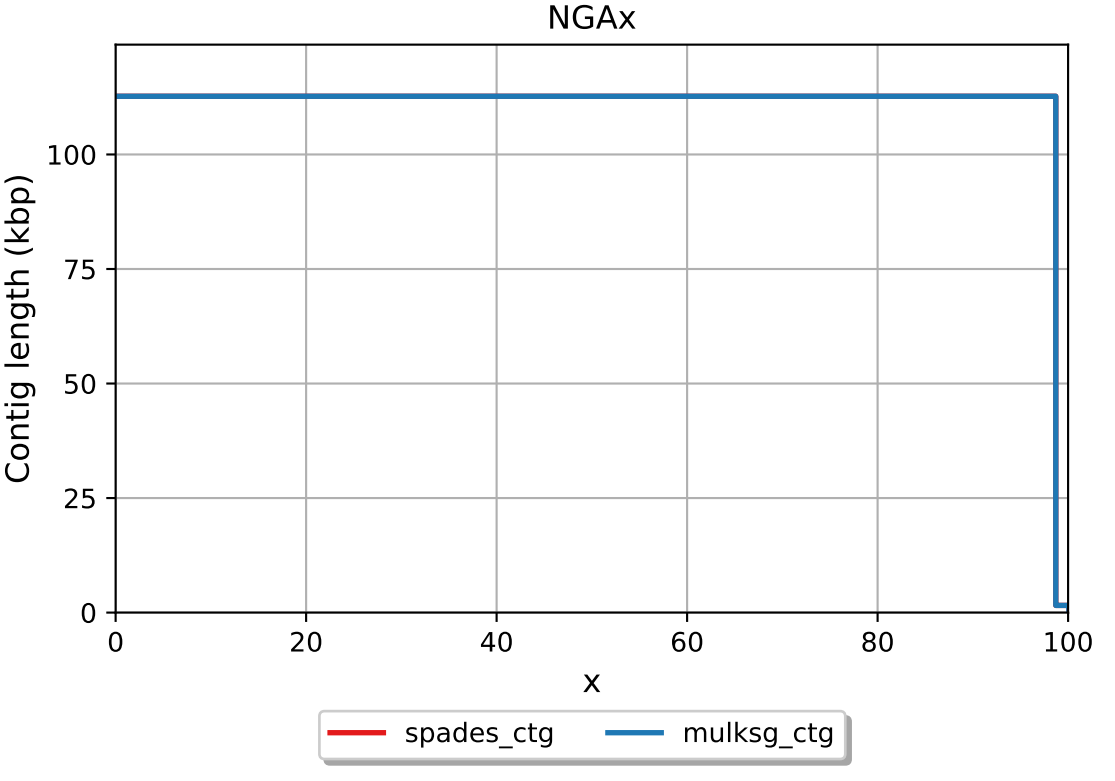

mulksg_ctg coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
11
12
13
14
15
16
17
18
161
Coverage depth (x)
mulksg_ctg

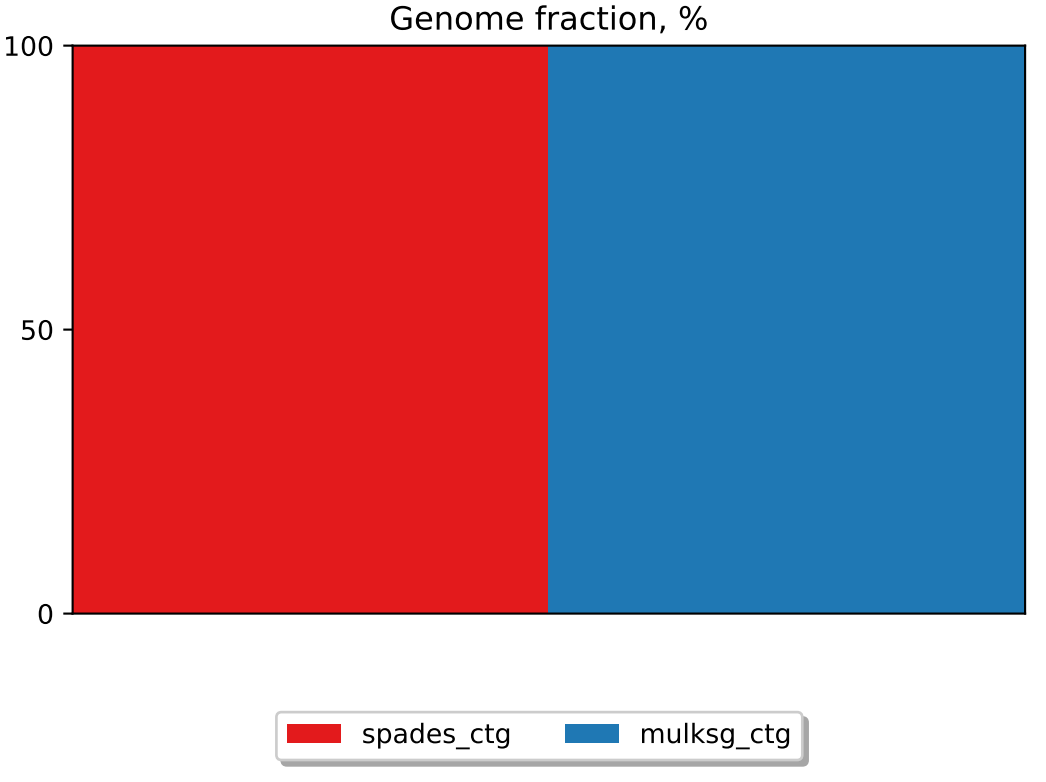

Misassemblies
5
4
3
2
1
0
spades_ctg
mulksg_ctg


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
125
100
75
50
25
0
0
1
2
3
4
5
6
Contig index
spades_ctg
mulksg_ctg
Reference


NAx
Contig length (kbp)
100
75
50
25
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg


NGAx
Contig length (kbp)
0
25
50
75
100
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg


Genome fraction, %
100
50
0
spades_ctg
mulksg_ctg