Report

	spades_ctg	mulksg_ctg
# contigs (>= 0 bp)	3729	3982
# contigs (>= 1000 bp)	39	40
# contigs (>= 5000 bp)	20	20
# contigs (>= 10000 bp)	20	20
# contigs (>= 25000 bp)	17	17
# contigs (>= 50000 bp)	16	16
Total length (>= 0 bp)	6202821	6291601
Total length (>= 1000 bp)	4911329	4912210
Total length (>= 5000 bp)	4884310	4884310
Total length (>= 10000 bp)	4884310	4884310
Total length (>= 25000 bp)	4822987	4822987
Total length (>= 50000 bp)	4776910	4776910
# contigs	425	443
Largest contig	1079605	1079605
Total length	5150541	5162891
Reference length	4744448	4744448
GC (%)	61.63	61.65
Reference GC (%)	61.55	61.55
N50	656974	656974
NG50	656974	656974
N75	167320	167320
NG75	189819	189819
L50	3	3
LG50	3	3
L75	9	9
LG75	7	7
# misassemblies	6	6
# misassembled contigs	3	3
Misassembled contigs length	366493	366493
# local misassemblies	45	45
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	17	17
# unaligned contigs	399 + 21 part	418 + 20 part
Unaligned length	3311484	3323954
Genome fraction (%)	38.755	38.753
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	4037.46	4037.62
# indels per 100 kbp	38.02	38.02
Largest alignment	61358	61358
Total aligned length	1839248	1839128
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

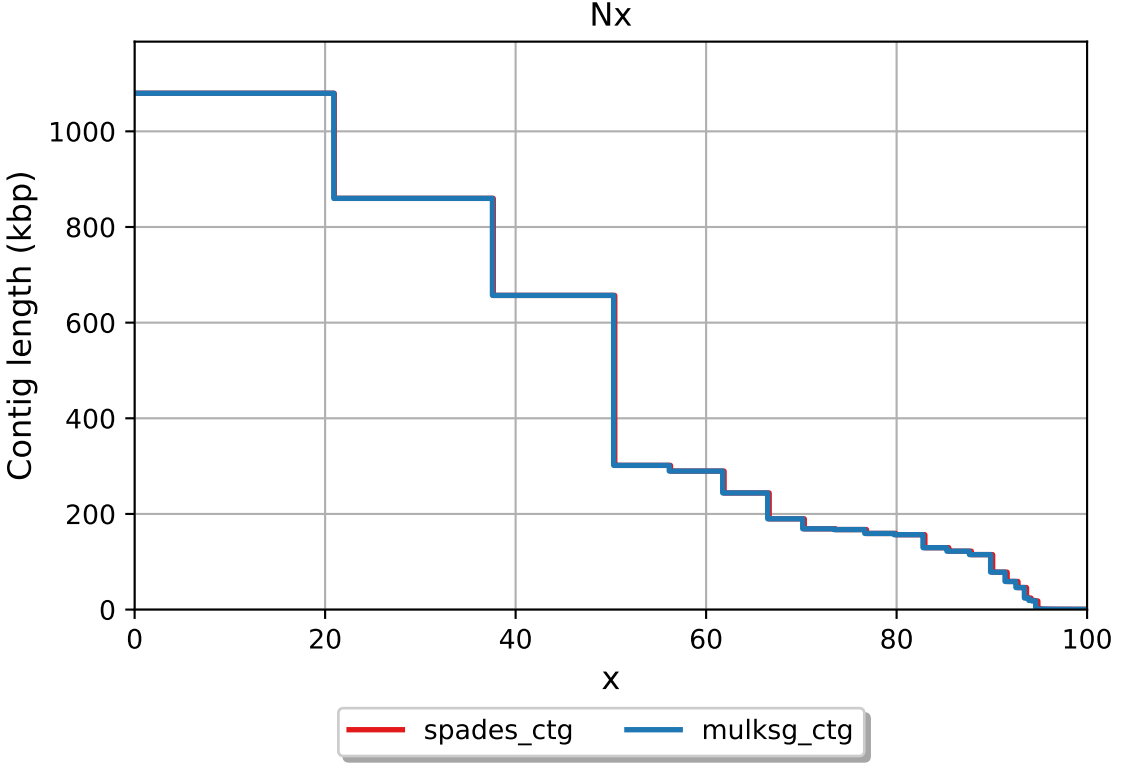
	spades_ctg	mulksg_ctg
# misassemblies	6	6
# contig misassemblies	6	6
# c. relocations	6	6
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	3	3
Misassembled contigs length	366493	366493
# local misassemblies	45	45
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	17	17
# mismatches	74238	74236
# indels	699	699
# indels (<= 5 bp)	637	637
# indels (> 5 bp)	62	62
Indels length	2021	2021

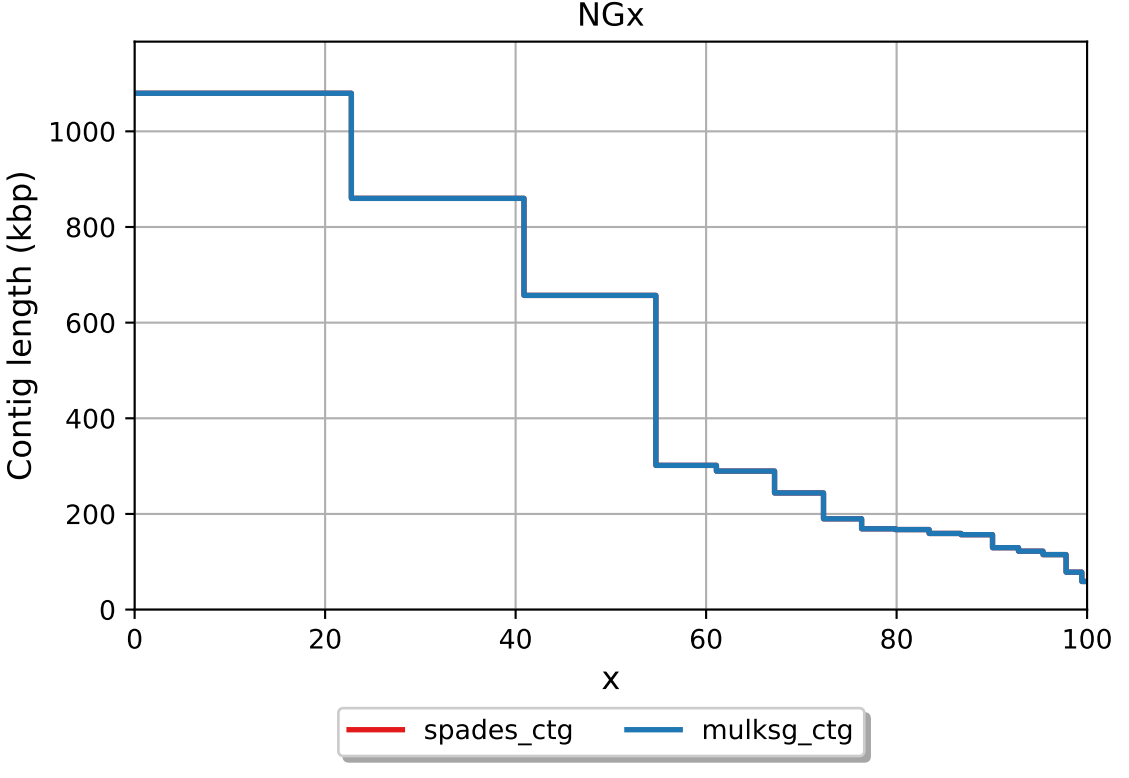
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

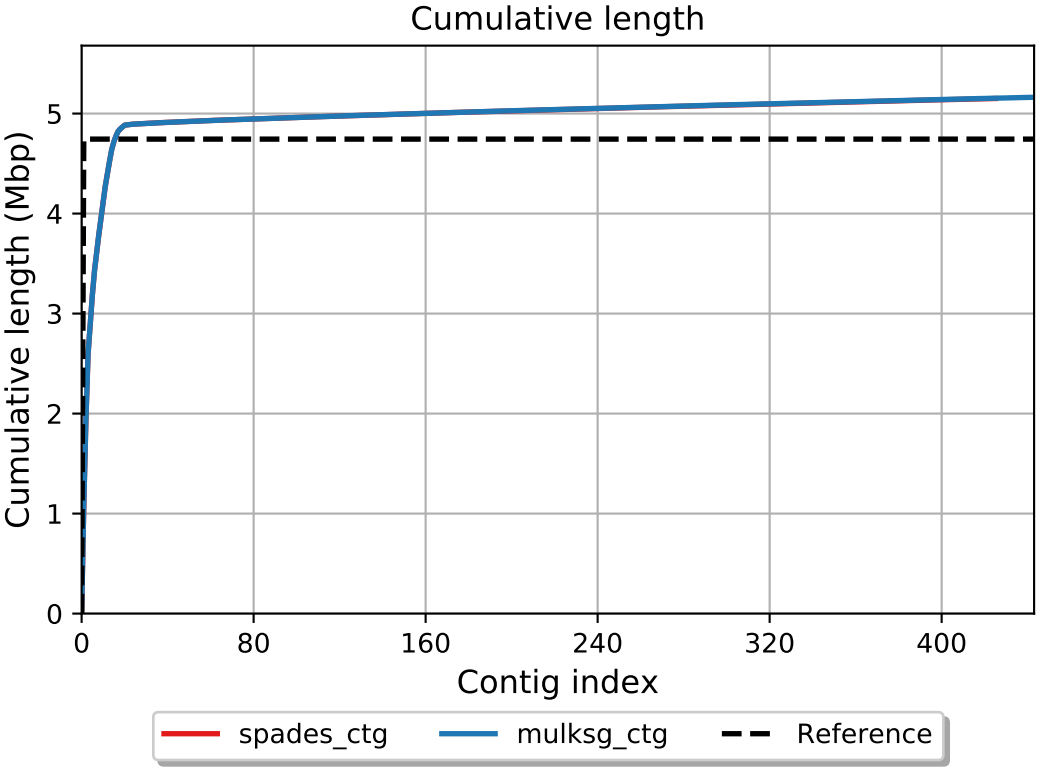
Unaligned report

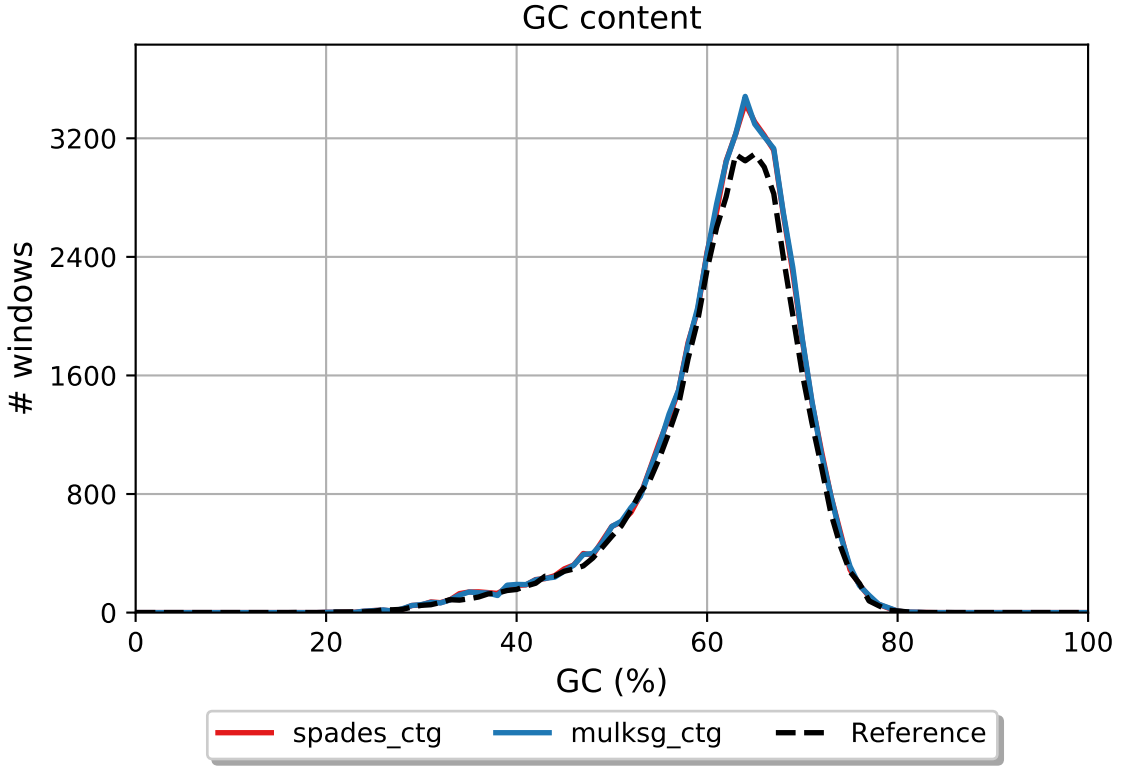
	spades_ctg	mulksg_ctg
# fully unaligned contigs	399	418
Fully unaligned length	259180	272307
# partially unaligned contigs	21	20
Partially unaligned length	3052304	3051647
# N's	0	0

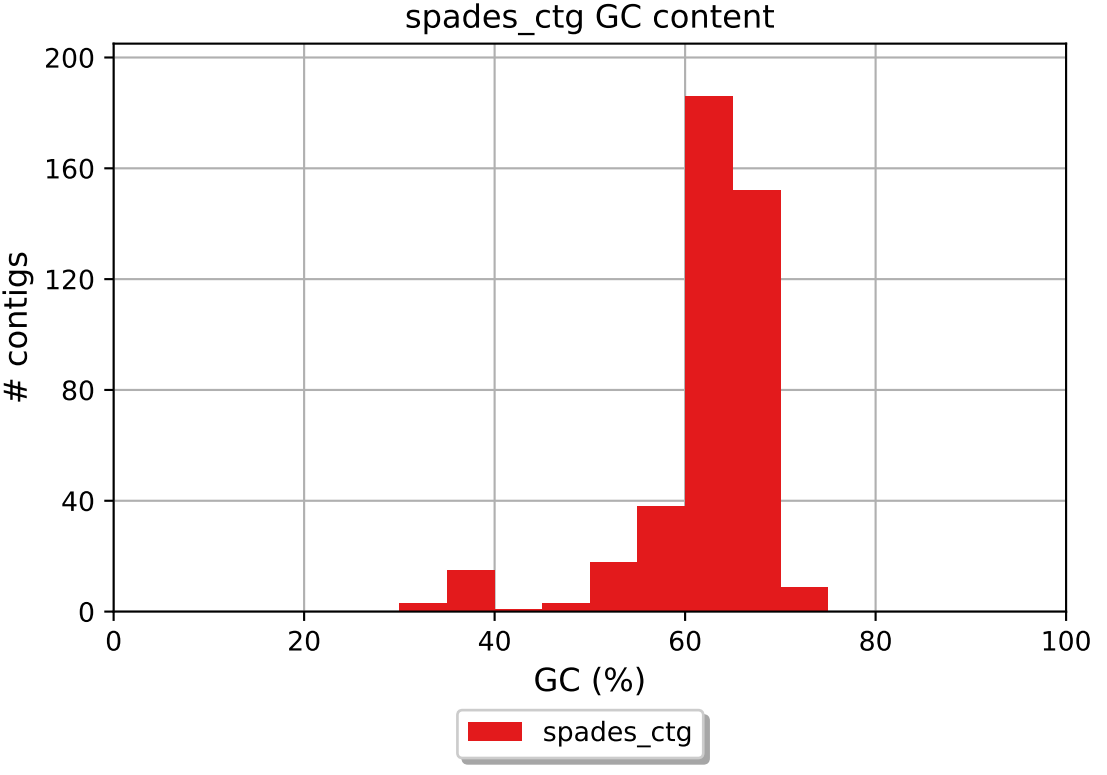
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

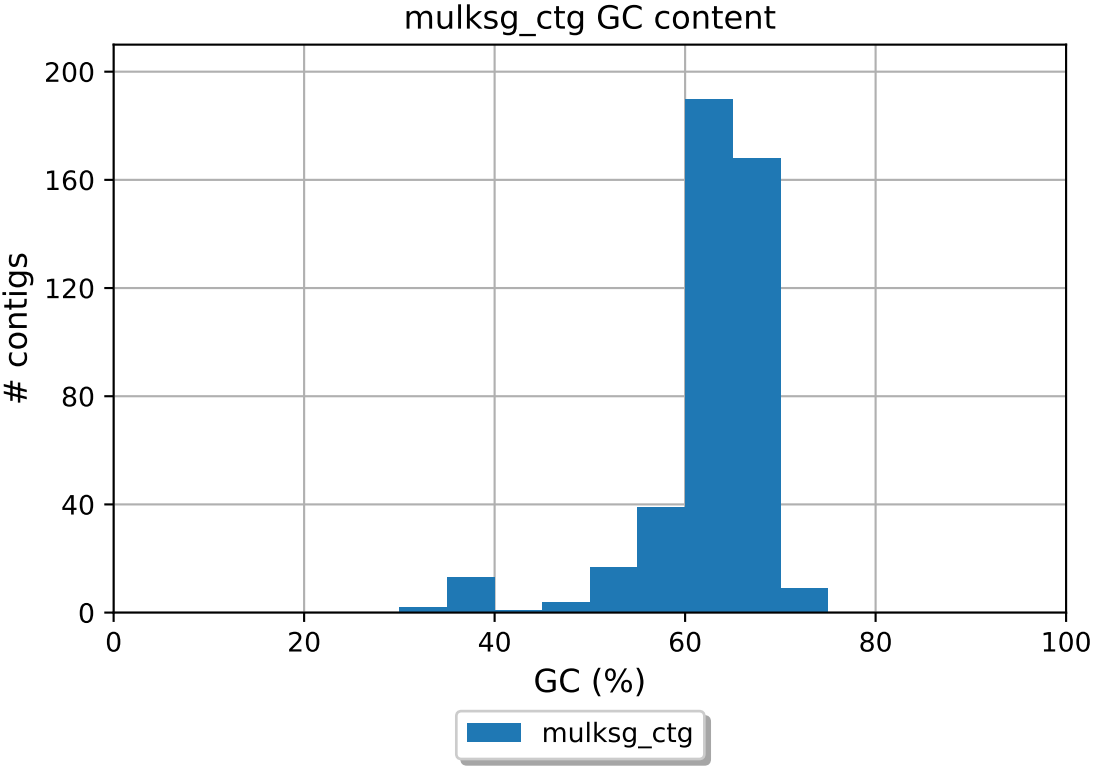

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg

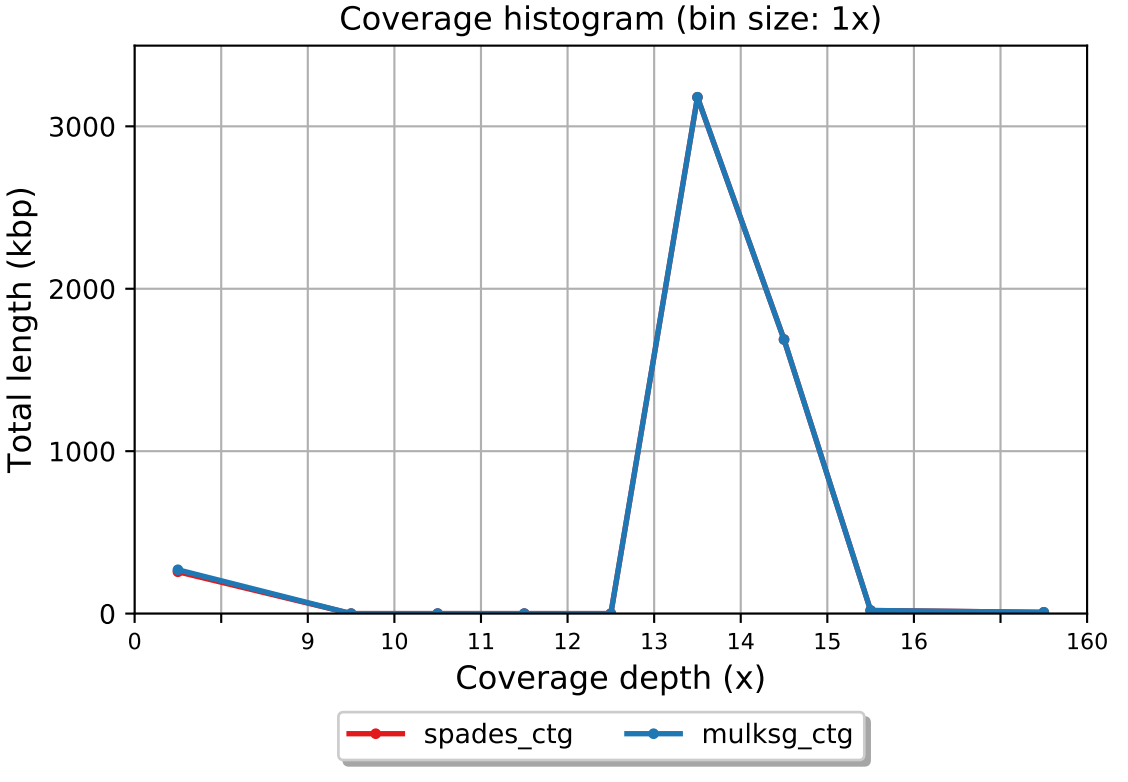

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg

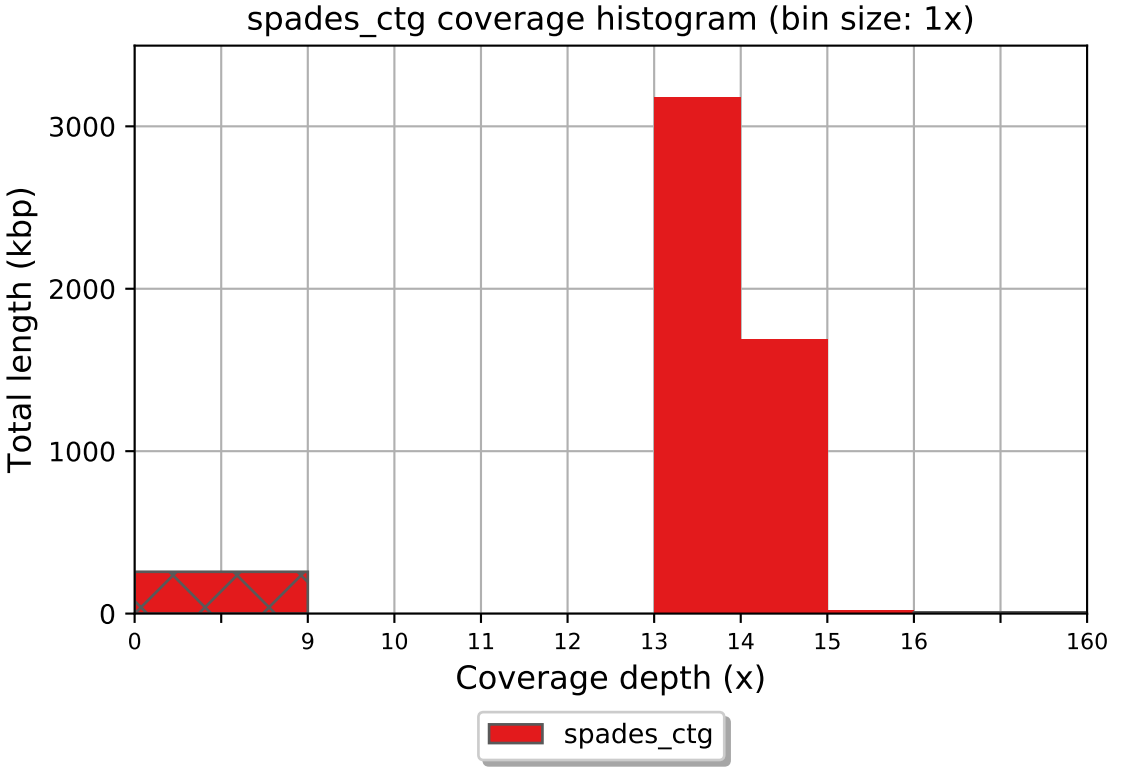

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
80
160
240
320
400
Contig index
spades_ctg
mulksg_ctg
Reference

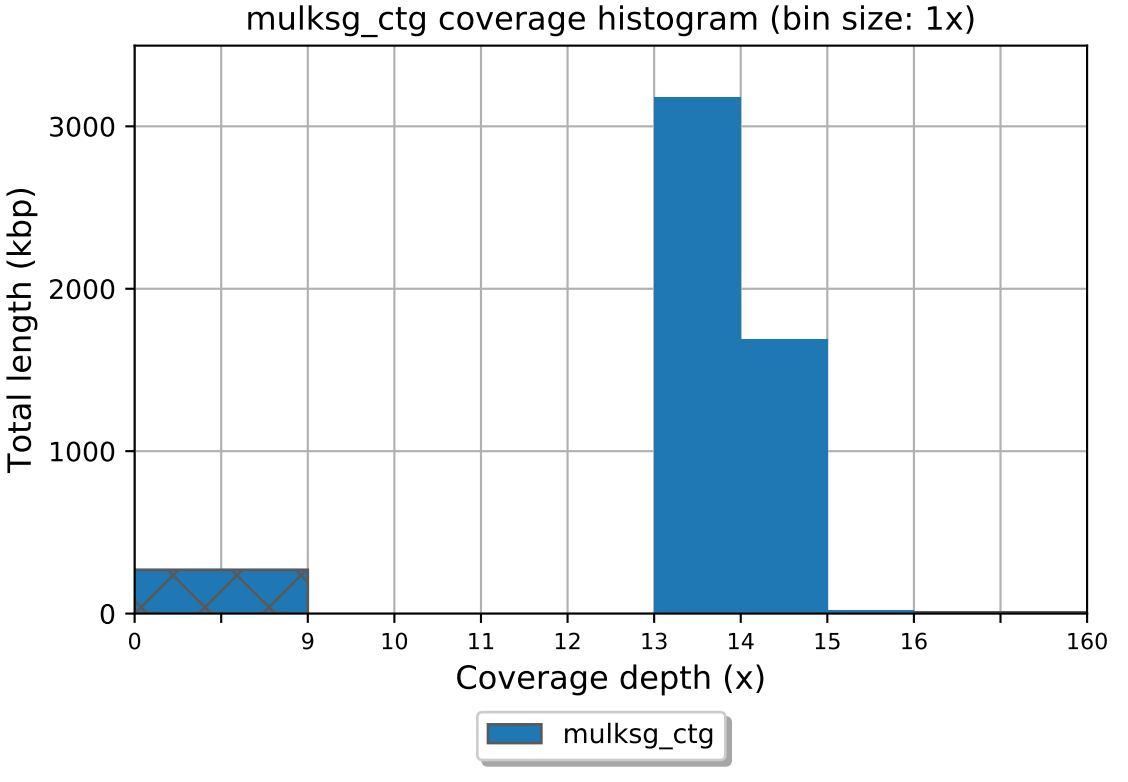

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
spades_ctg
mulksg_ctg
Reference

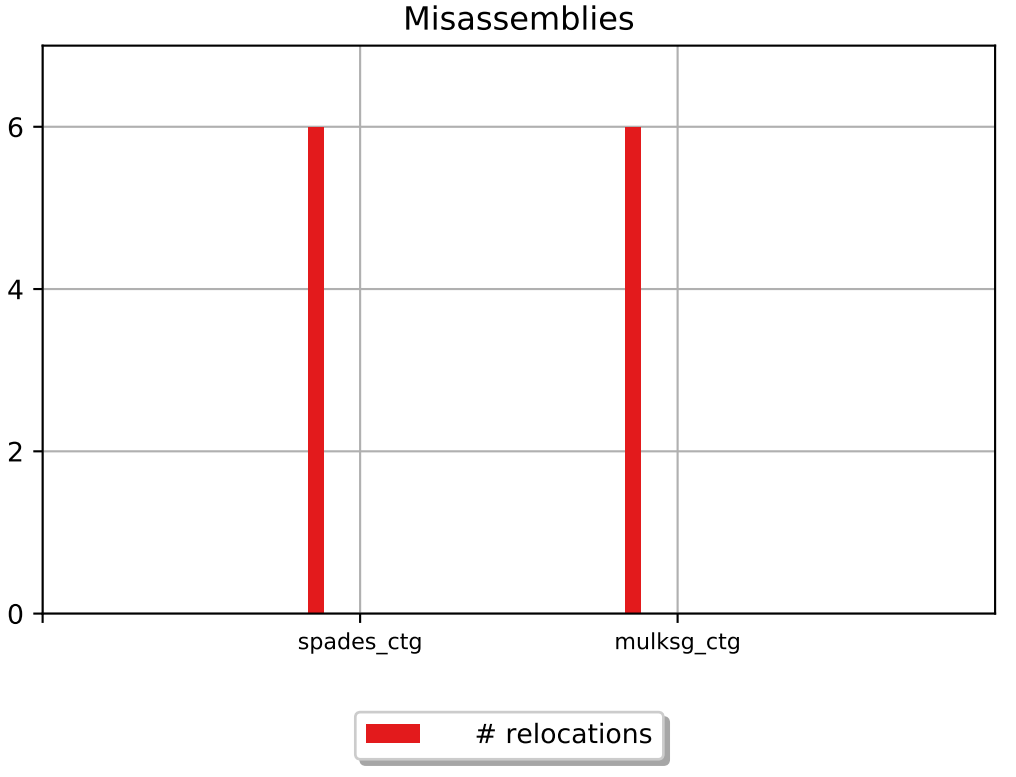

spades_ctg GC content
200
160
120
80
40
0
contigs
0
20
40
60
80
100
GC (%)
spades_ctg

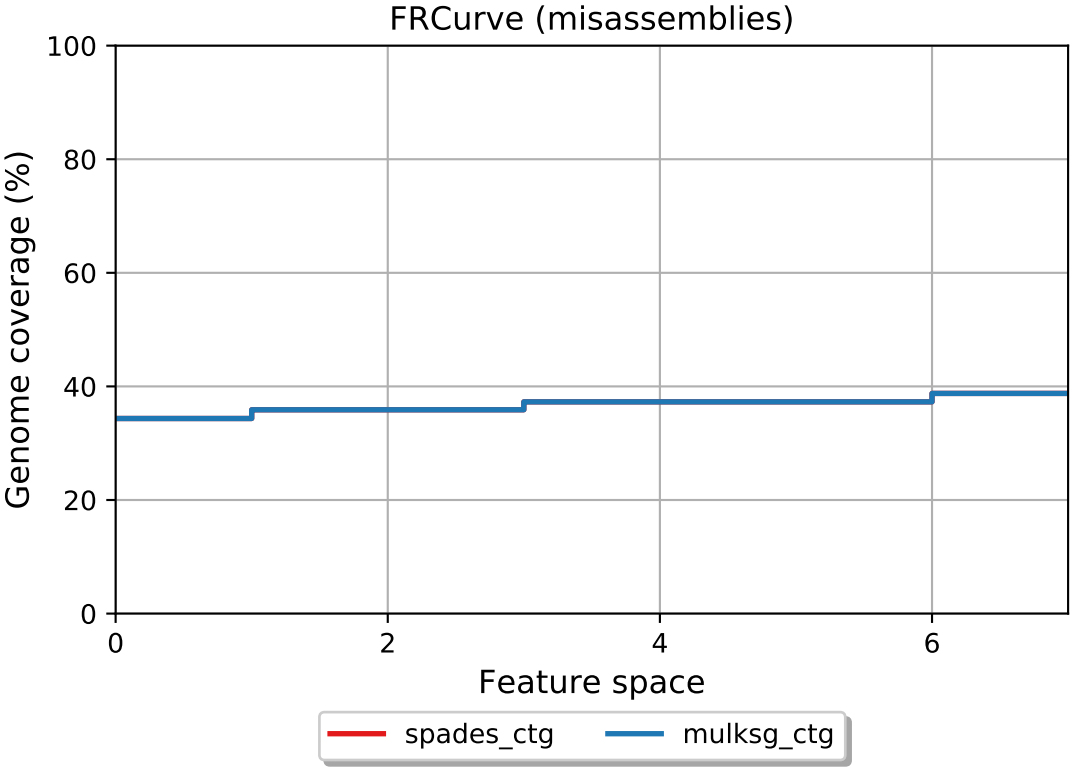

mulksg_ctg GC content
contigs
GC (%)
0
40
80
120
160
200
0
20
40
60
80
100
mulksg_ctg

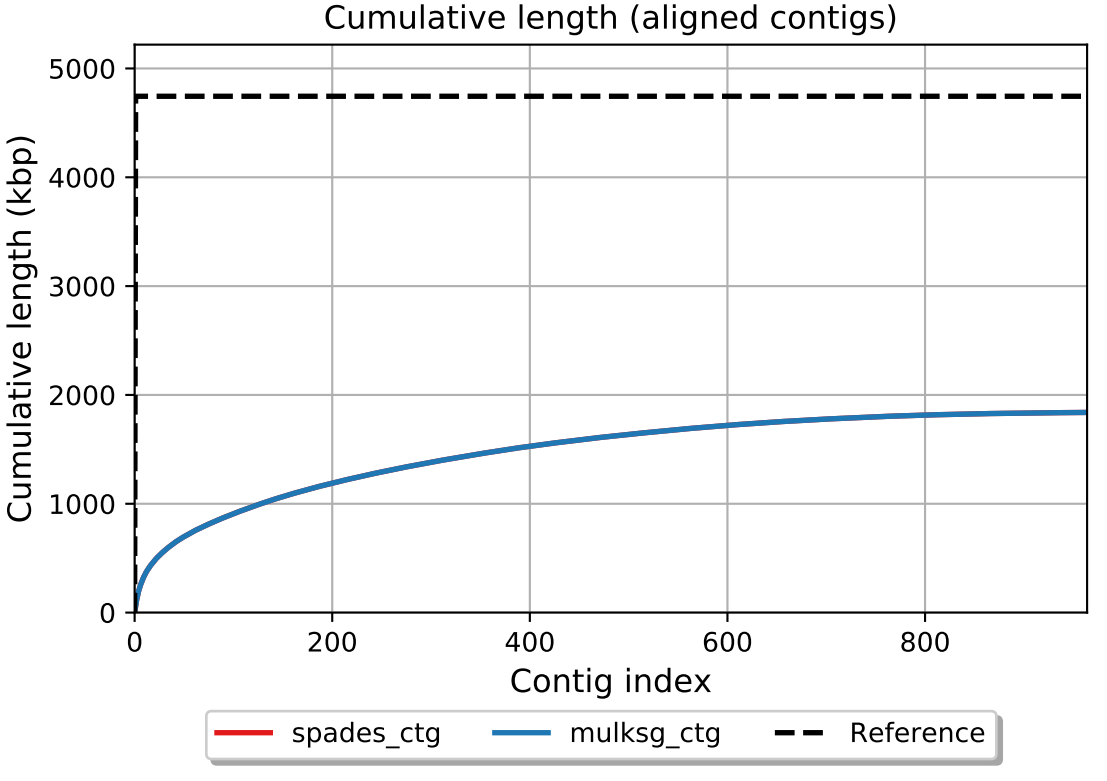

Coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
9
10
11
12
13
14
15
16
160
Coverage depth (x)
spades_ctg
mulksg_ctg

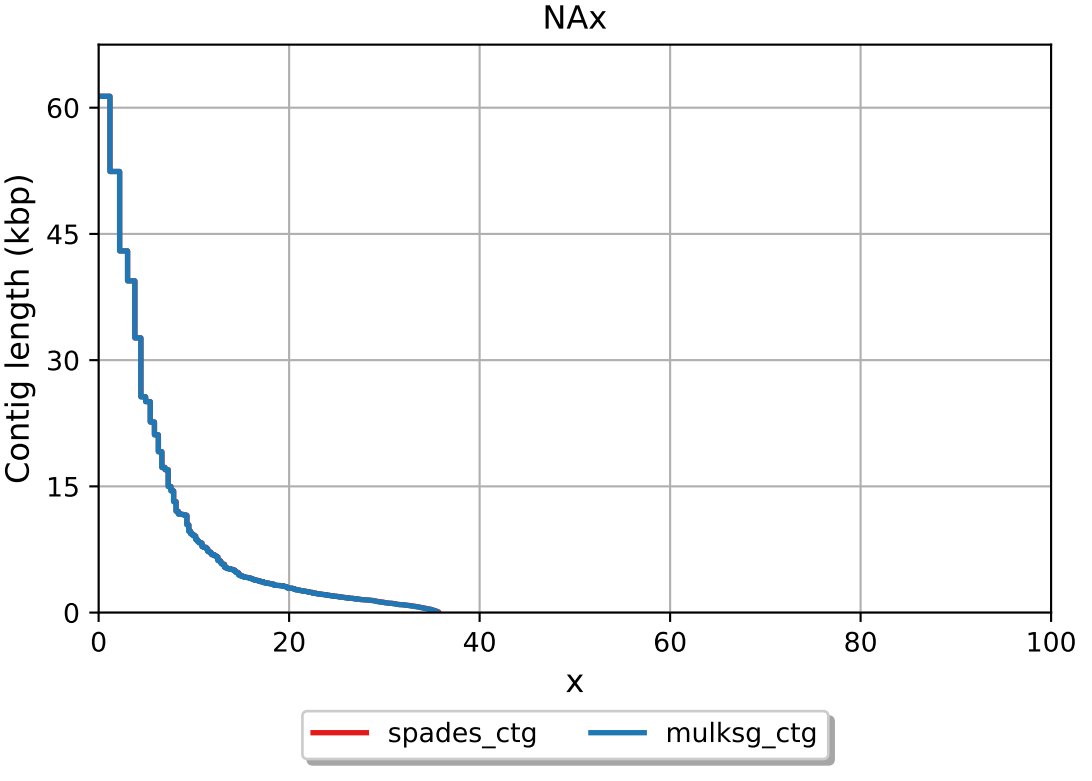

spades_ctg coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
9
10
11
12
13
14
15
16
160
Coverage depth (x)
spades_ctg

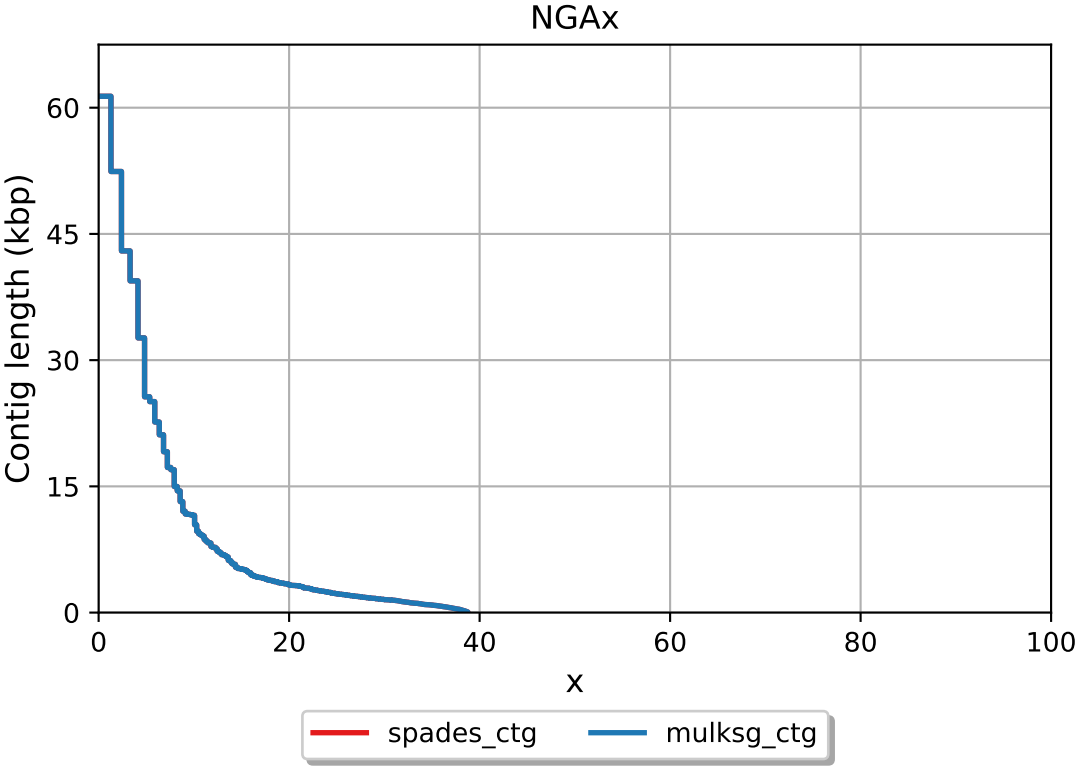

mulksg_ctg coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
9
10
11
12
13
14
15
16
160
Coverage depth (x)
mulksg_ctg

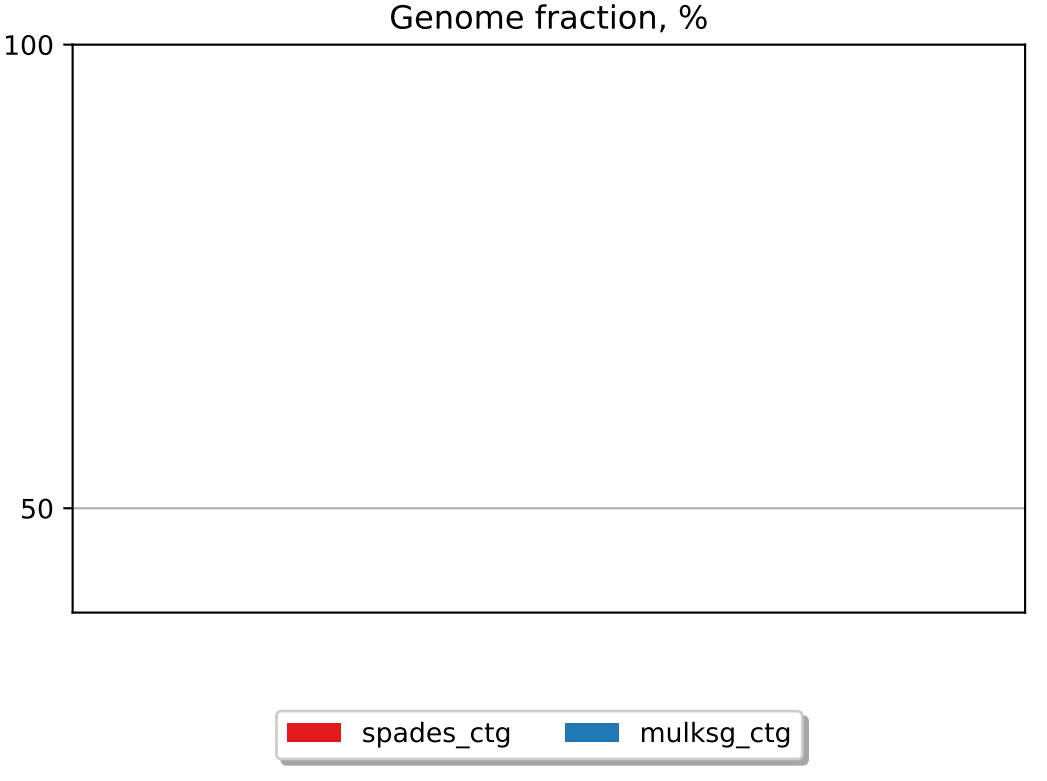

Misassemblies
6
4
2
0
spades_ctg
mulksg_ctg
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
Feature space
spades_ctg
mulksg_ctg


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
spades_ctg
mulksg_ctg
Reference


NAx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg


NGAx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
spades_ctg
mulksg_ctg


Genome fraction, %
100
50
spades_ctg
mulksg_ctg