Report

	spades_careful_scaffolds	spades_isolate_scaffolds	abyss_k31-scaffolds	abyss_k75-scaffolds	final.contigs
# contigs (>= 0 bp)	57	53	482	29	22
# contigs (>= 1000 bp)	4	3	14	6	9
# contigs (>= 5000 bp)	4	3	11	4	6
# contigs (>= 10000 bp)	3	3	10	3	5
# contigs (>= 25000 bp)	3	3	7	2	5
# contigs (>= 50000 bp)	3	3	4	1	2
Total length (>= 0 bp)	586796	587433	603398	582936	584777
Total length (>= 1000 bp)	576435	577412	575647	577964	580230
Total length (>= 5000 bp)	576435	577412	569590	571706	575137
Total length (>= 10000 bp)	570347	577412	562043	563312	569534
Total length (>= 25000 bp)	570347	577412	511744	547996	569534
Total length (>= 50000 bp)	570347	577412	407095	521282	452879
# contigs	5	4	14	8	11
Largest contig	417388	417388	121138	521282	399763
Total length	577250	578227	575647	579072	581785
Reference length	580076	580076	580076	580076	580076
GC (%)	31.61	31.63	31.47	31.64	31.70
Reference GC (%)	31.69	31.69	31.69	31.69	31.69
N50	417388	417388	88627	521282	399763
NG50	417388	417388	88627	521282	399763
N90	75917	77091	20085	521282	38504
NG90	75917	77091	20085	26714	38504
auN	322129.6	323461.7	81955.6	471054.2	287414.7
auNG	320560.3	322430.7	81329.8	470238.9	288261.5
L50	1	1	3	1	1
LG50	1	1	3	1	1
L90	3	3	8	1	4
LG90	3	3	8	2	4
# misassemblies	1	2	1	3	3
# misassembled contigs	1	2	1	1	1
Misassembled contigs length	417388	500321	82288	521282	399763
# local misassemblies	0	0	0	1	0
# scaffold gap ext. mis.	0	0	1	0	0
# scaffold gap loc. mis.	0	0	6	0	0
# unaligned mis. contigs	0	0	0	0	0
# unaligned contigs	1 + 1 part	1 + 2 part	0 + 2 part	3 + 1 part	3 + 2 part
Unaligned length	2551	3212	2605	9027	9982
Genome fraction (%)	98.872	98.988	97.140	98.144	98.325
Duplication ratio	1.001	1.001	1.005	1.001	1.001
# N's per 100 kbp	0.00	17.29	899.68	19.51	0.00
# mismatches per 100 kbp	570.04	585.41	388.85	549.46	568.45
# indels per 100 kbp	91.67	98.29	31.07	92.48	97.34
Largest alignment	317168	317168	121070	392013	237371
Total aligned length	573823	574806	566545	569834	571205
NA50	317168	317168	84504	392013	79877
NGA50	317168	317168	84504	392013	79877
NA90	75686	76493	20085	26667	38443
NGA90	75686	76493	15556	26667	38443
auNA	211279.0	211145.5	78510.3	281274.4	125619.1
auNGA	210249.7	210472.5	77910.8	280787.6	125989.2
LA50	1	1	3	1	2
LGA50	1	1	3	1	2
LA90	4	4	8	4	7
LGA90	4	4	9	4	7

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

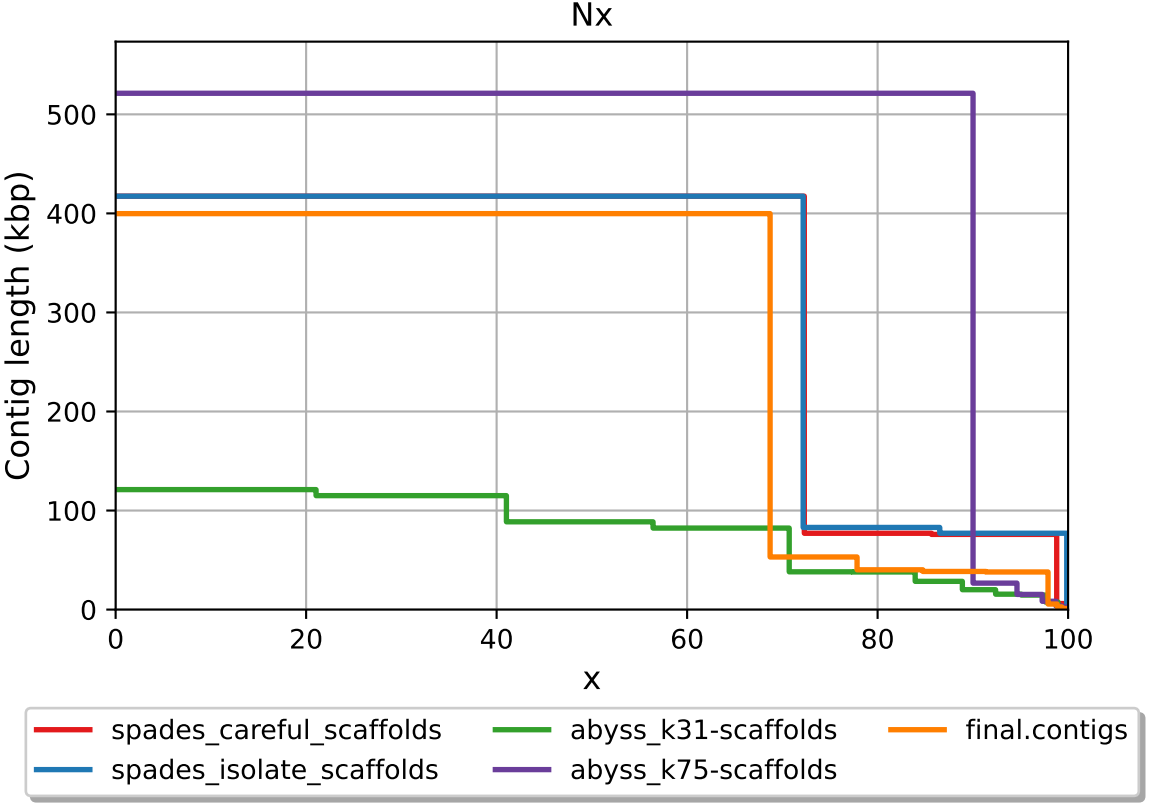
	spades_careful_scaffolds	spades_isolate_scaffolds	abyss_k31-scaffolds	abyss_k75-scaffolds	final.contigs
# misassemblies	1	2	1	3	3
# contig misassemblies	1	2	0	2	3
# c. relocations	1	2	0	2	3
# c. translocations	0	0	0	0	0
# c. inversions	0	0	0	0	0
# scaffold misassemblies	0	0	1	1	0
# s. relocations	0	0	1	1	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	1	2	1	1	1
Misassembled contigs length	417388	500321	82288	521282	399763
# local misassemblies	0	0	0	1	0
# scaffold gap ext. mis.	0	0	1	0	0
# scaffold gap loc. mis.	0	0	6	0	0
# unaligned mis. contigs	0	0	0	0	0
# mismatches	3271	3365	2203	3131	3247
# indels	526	565	176	527	556
# indels (<= 5 bp)	488	526	157	488	514
# indels (> 5 bp)	38	39	19	39	42
Indels length	1547	1804	776	1677	1634

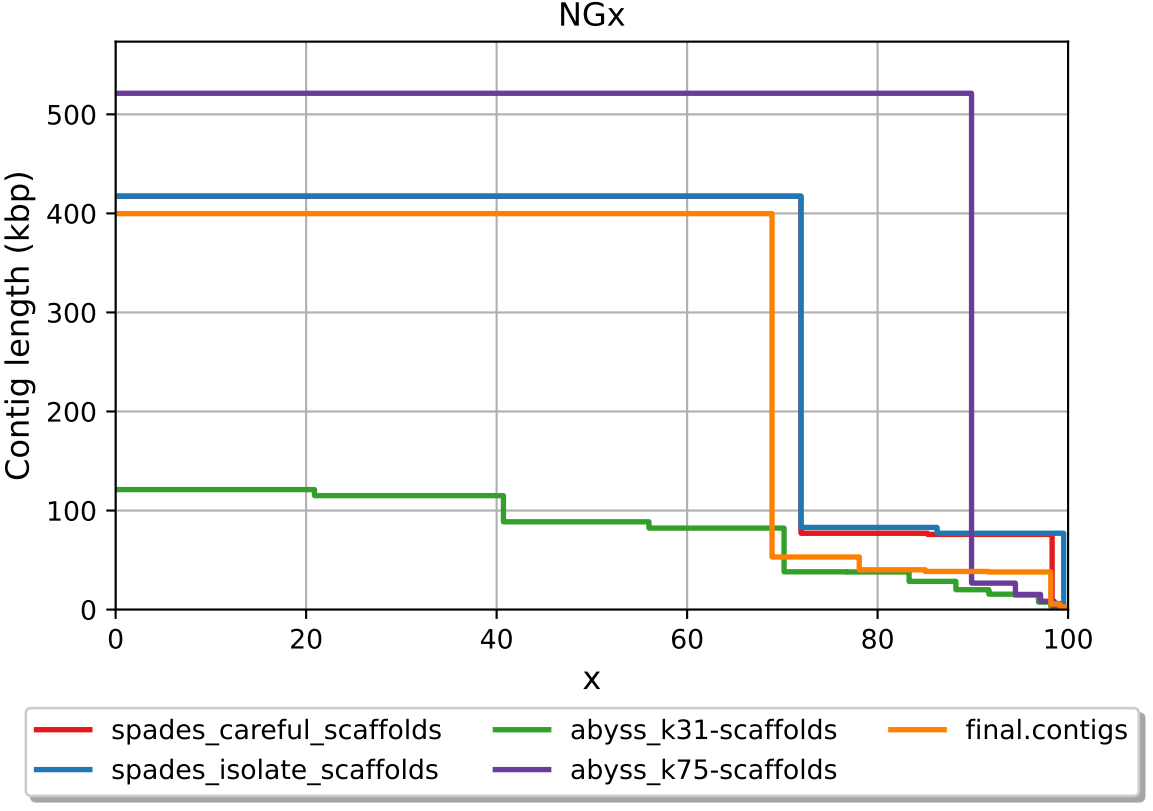
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

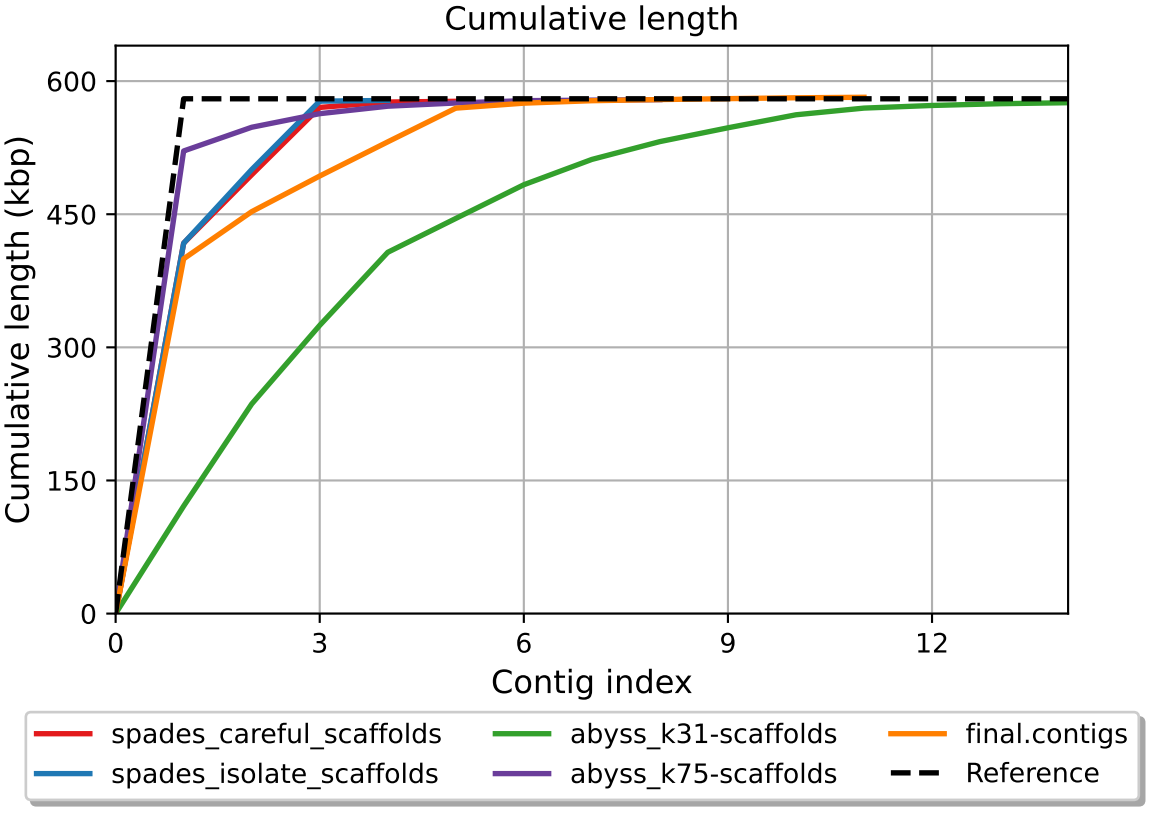
Unaligned report

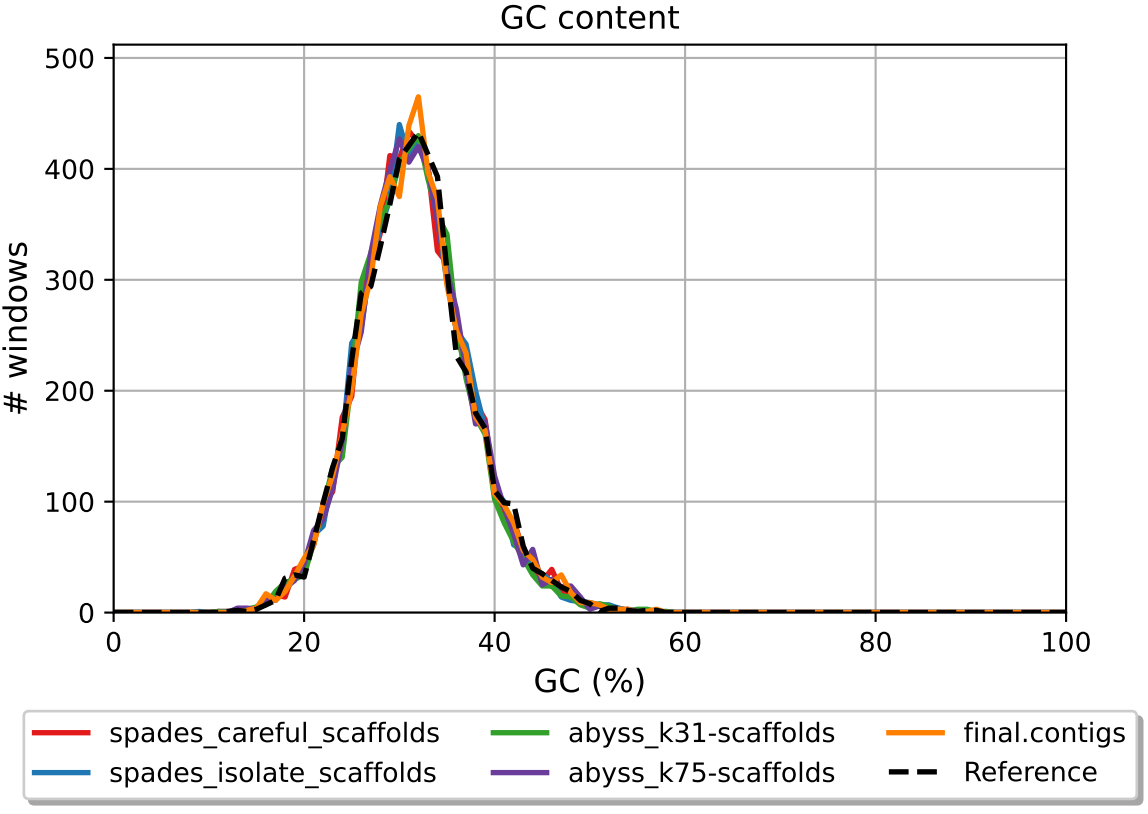
	spades_careful_scaffolds	spades_isolate_scaffolds	abyss_k31-scaffolds	abyss_k75-scaffolds	final.contigs
# fully unaligned contigs	1	1	0	3	3
Fully unaligned length	815	815	0	6783	5039
# partially unaligned contigs	1	2	2	1	2
Partially unaligned length	1736	2397	2605	2244	4943
# N's	0	100	5179	113	0

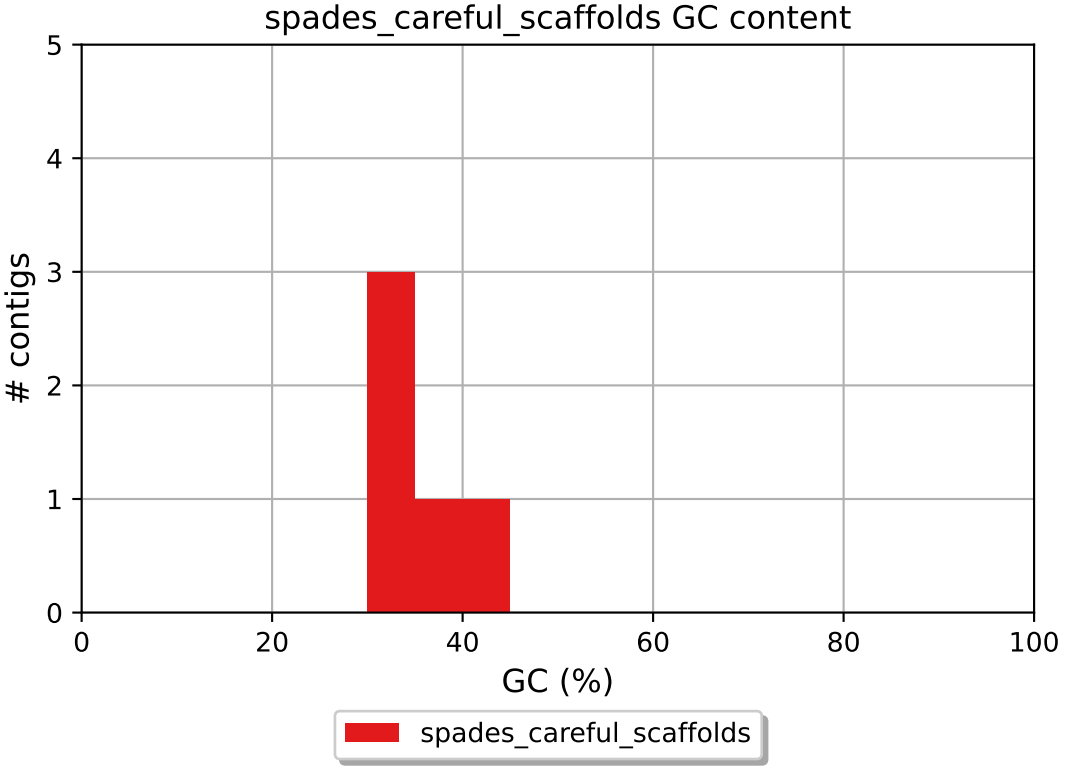
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

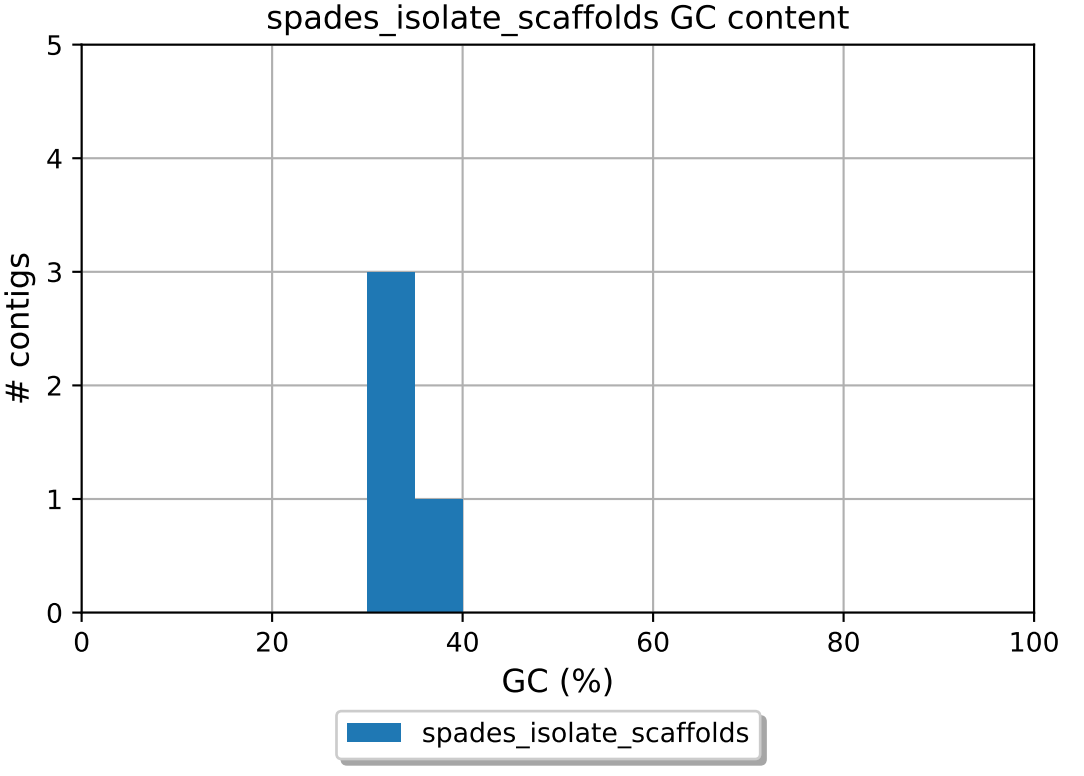

Nx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs

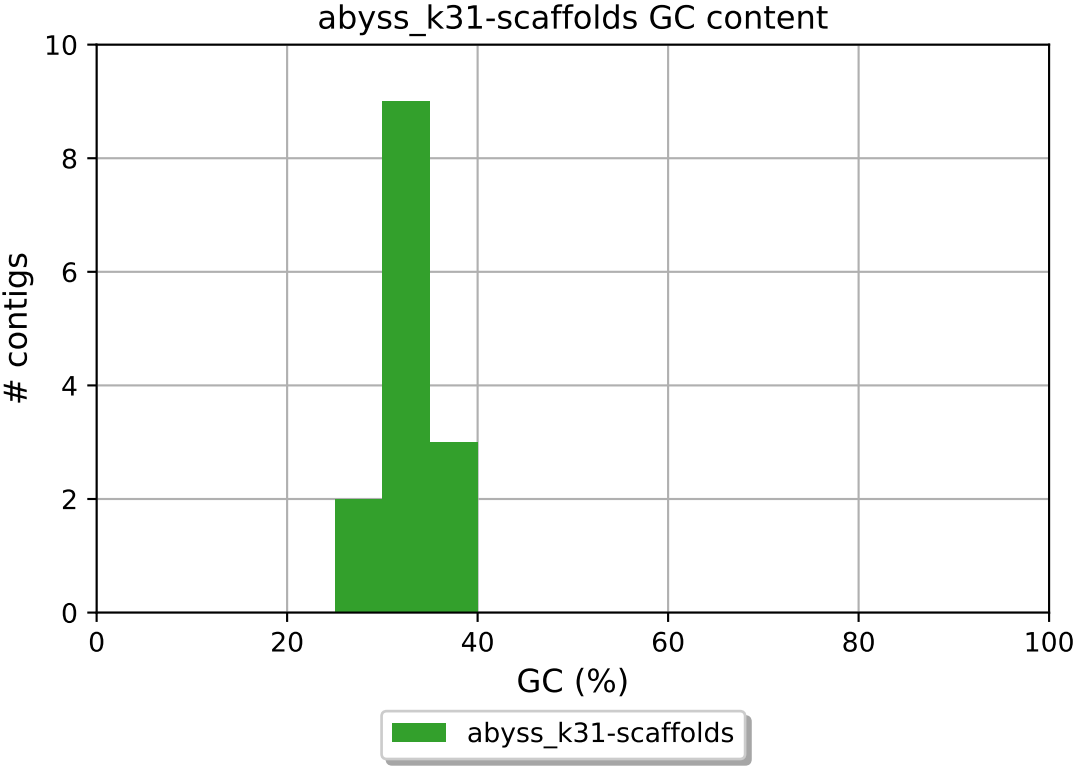

NGx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs

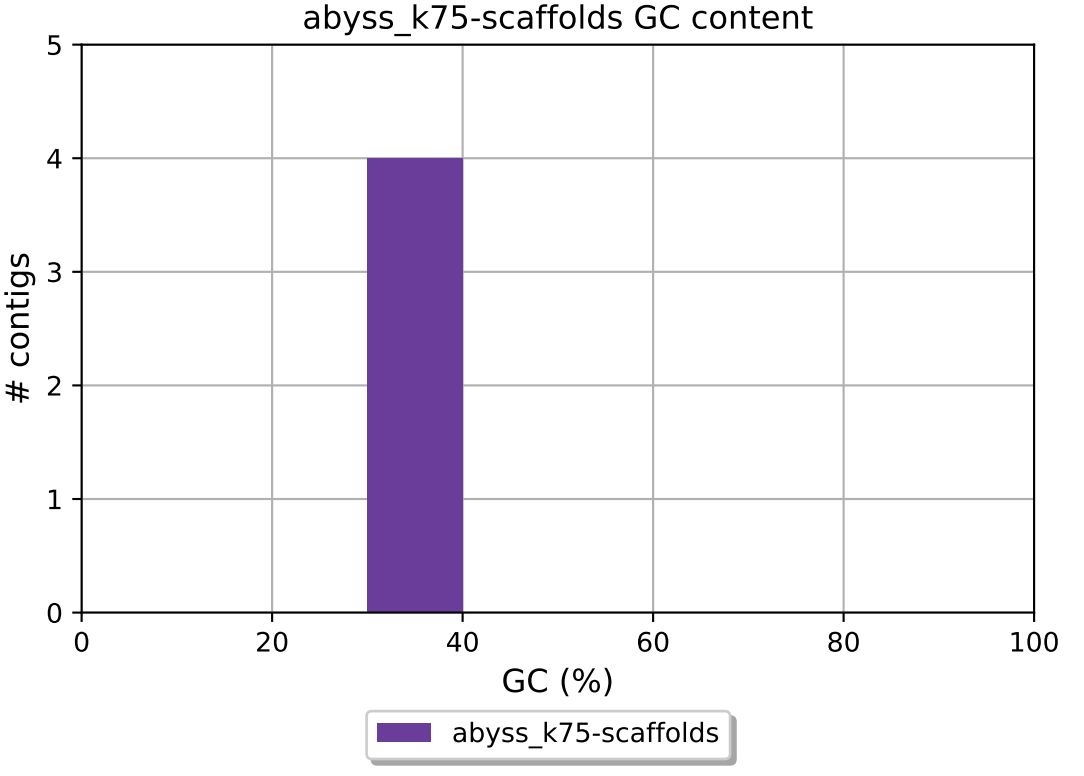

Cumulative length
Cumulative length (kbp)
600
450
300
150
0
0
3
6
9
12
Contig index
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs
Reference

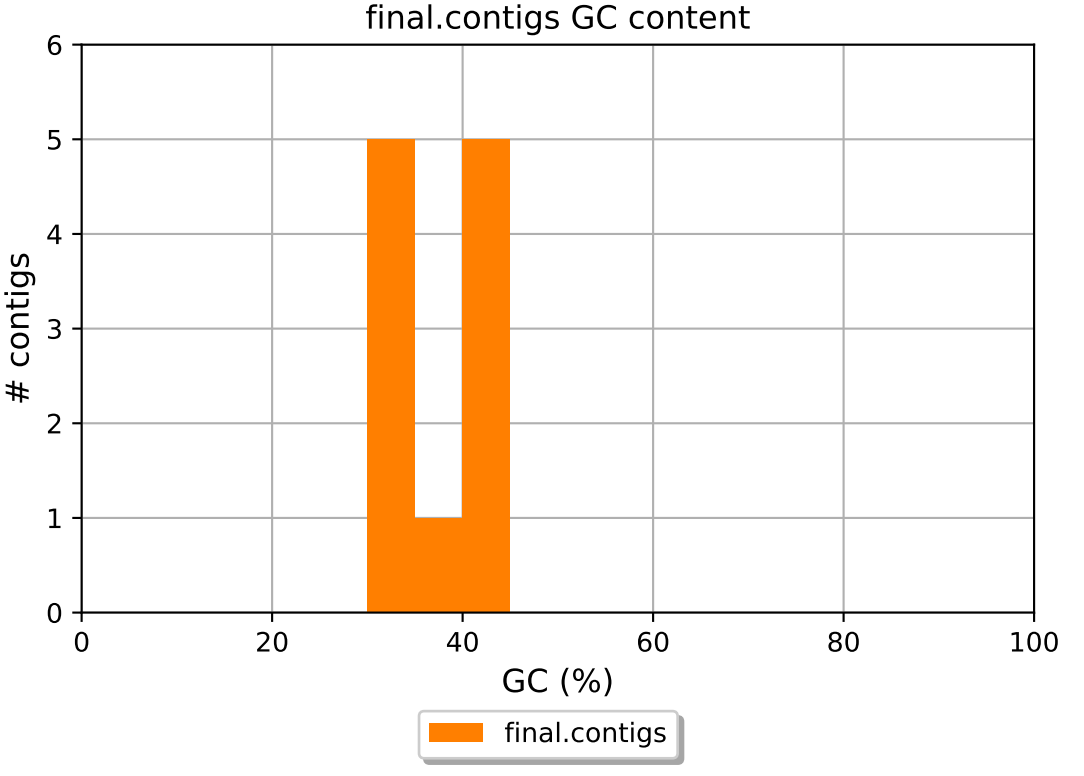

GC content
windows
GC (%)
0
100
200
300
400
500
0
20
40
60
80
100
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs
Reference

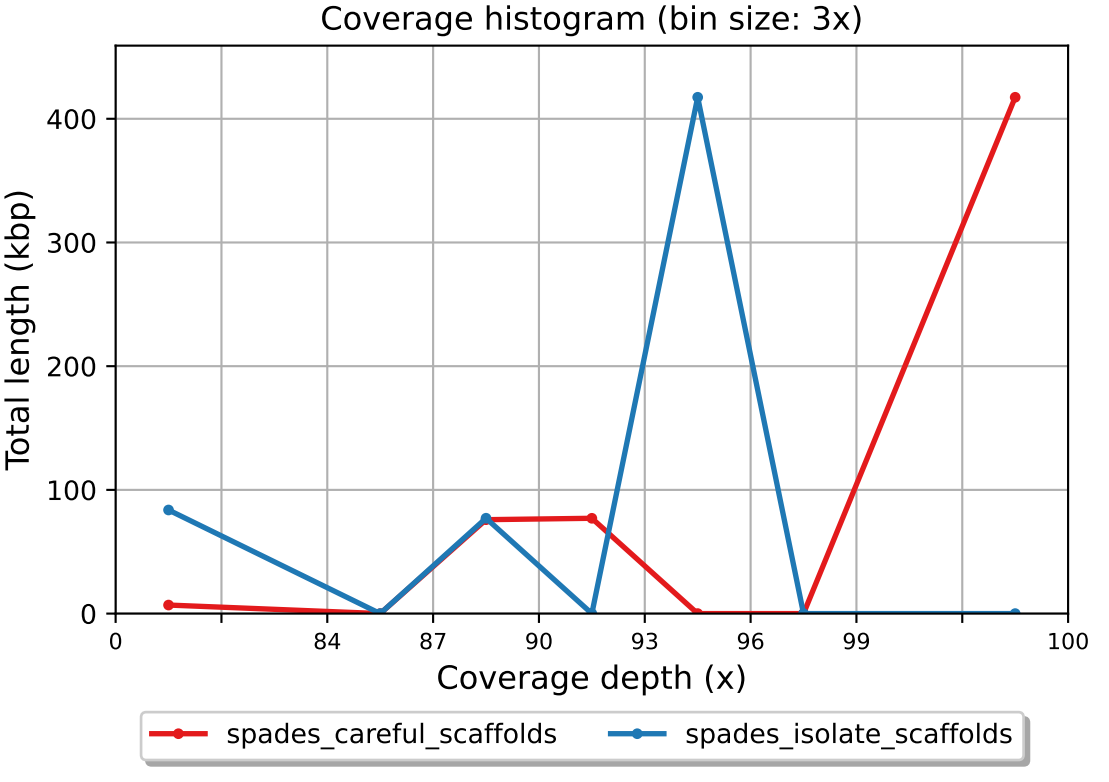

spades_careful_scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
spades_careful_scaffolds

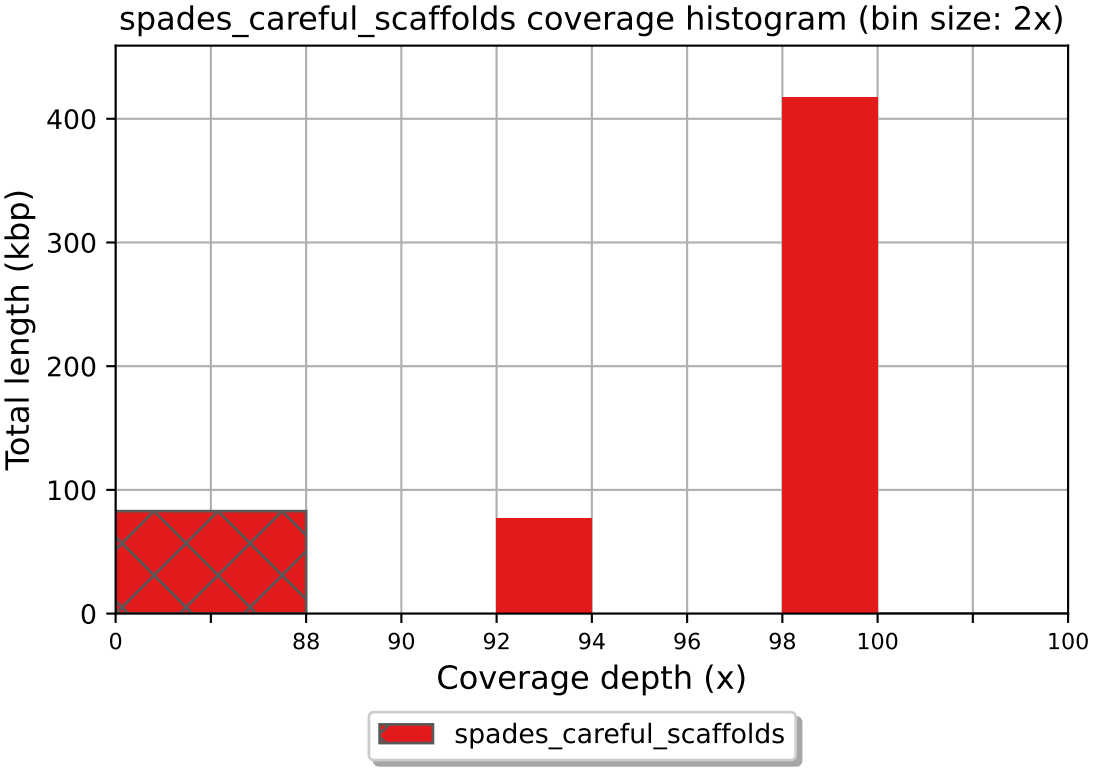

spades_isolate_scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
spades_isolate_scaffolds

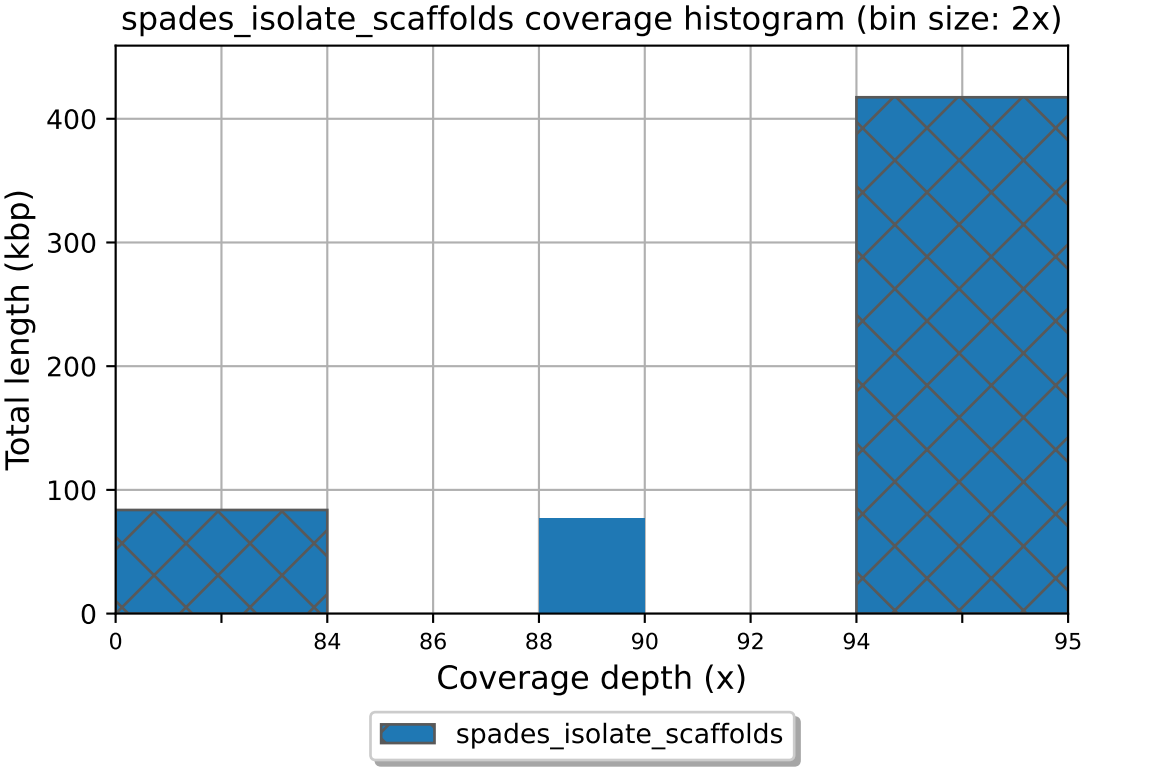

abyss_k31-scaffolds GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
abyss_k31-scaffolds

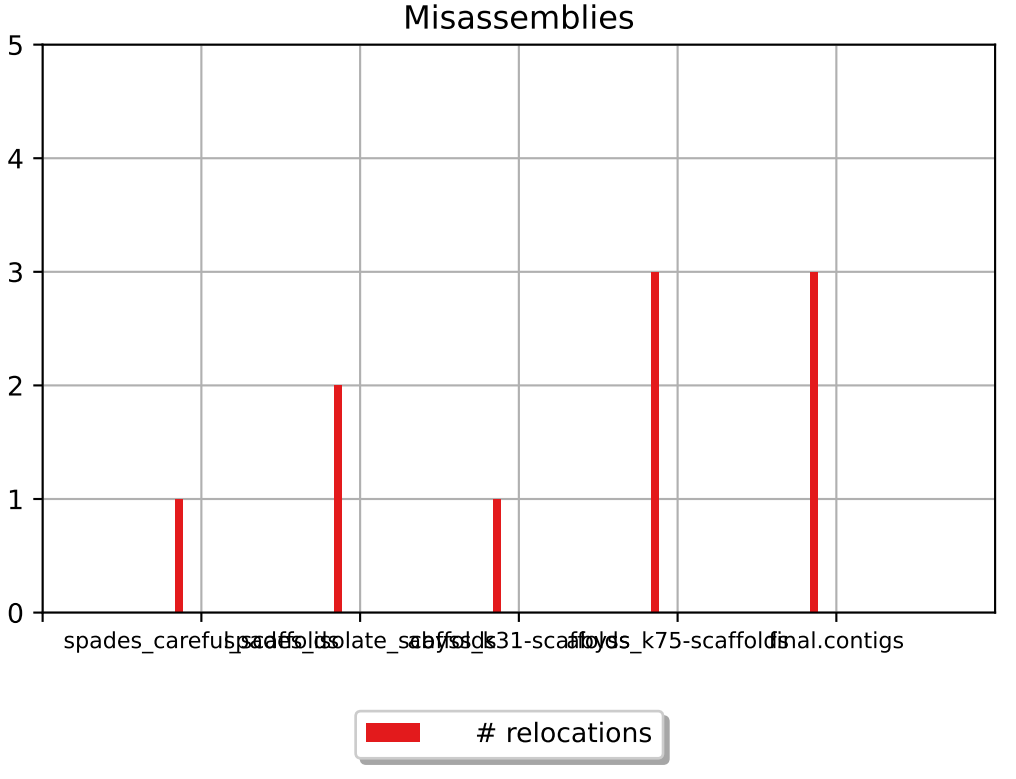

abyss_k75-scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
abyss_k75-scaffolds

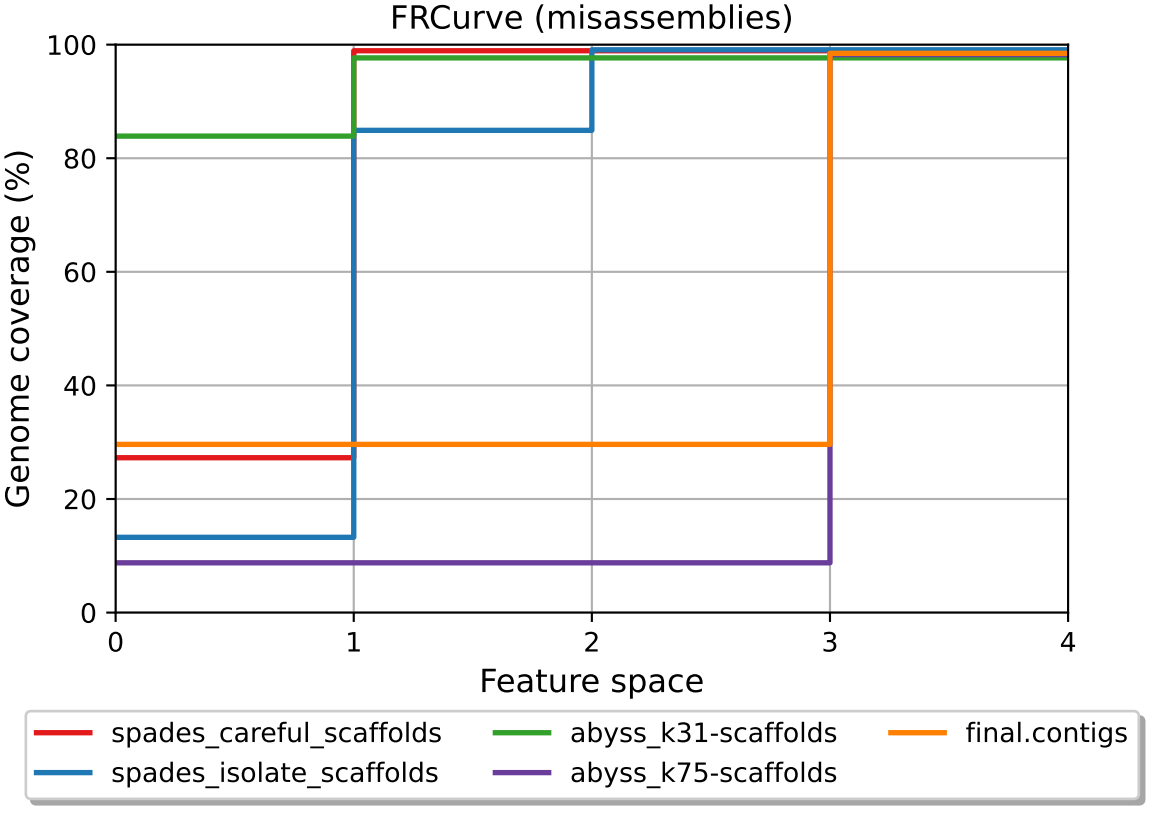

final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs

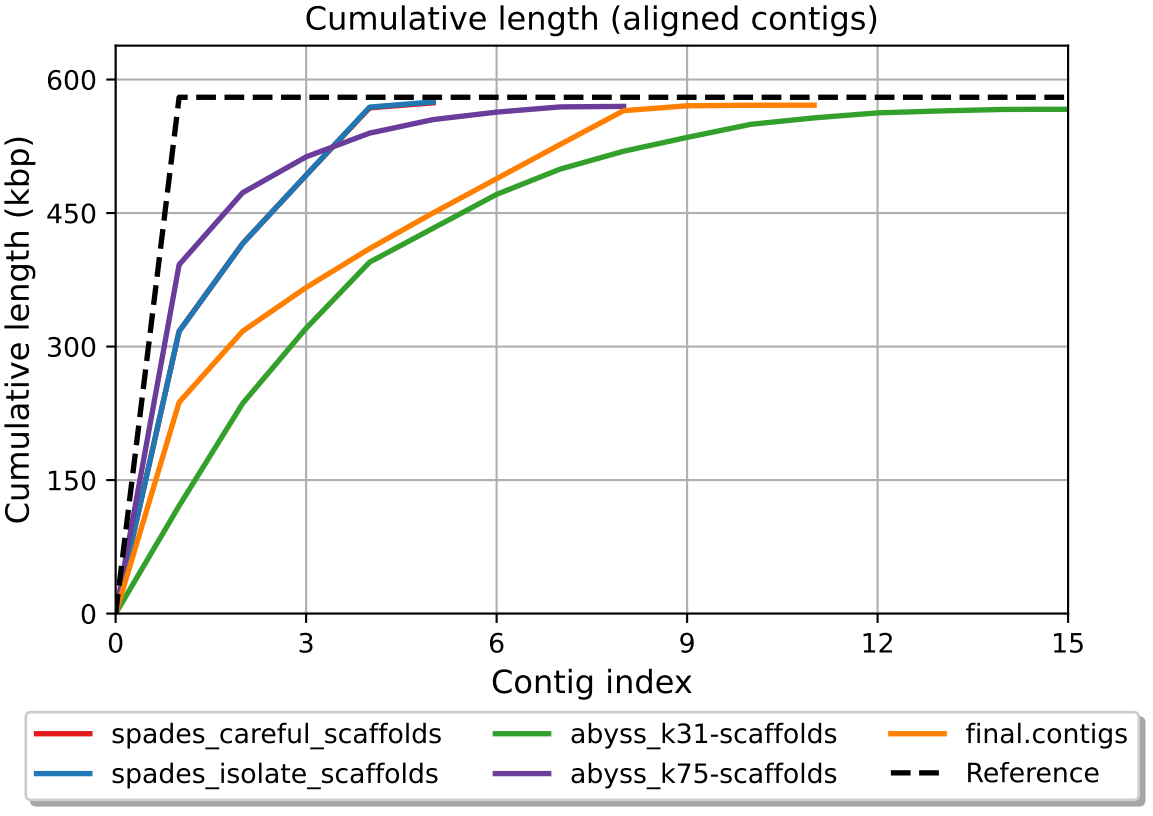

Coverage histogram (bin size: 3x)
Total length (kbp)
0
100
200
300
400
0
84
87
90
93
96
99
100
Coverage depth (x)
spades_careful_scaffolds
spades_isolate_scaffolds

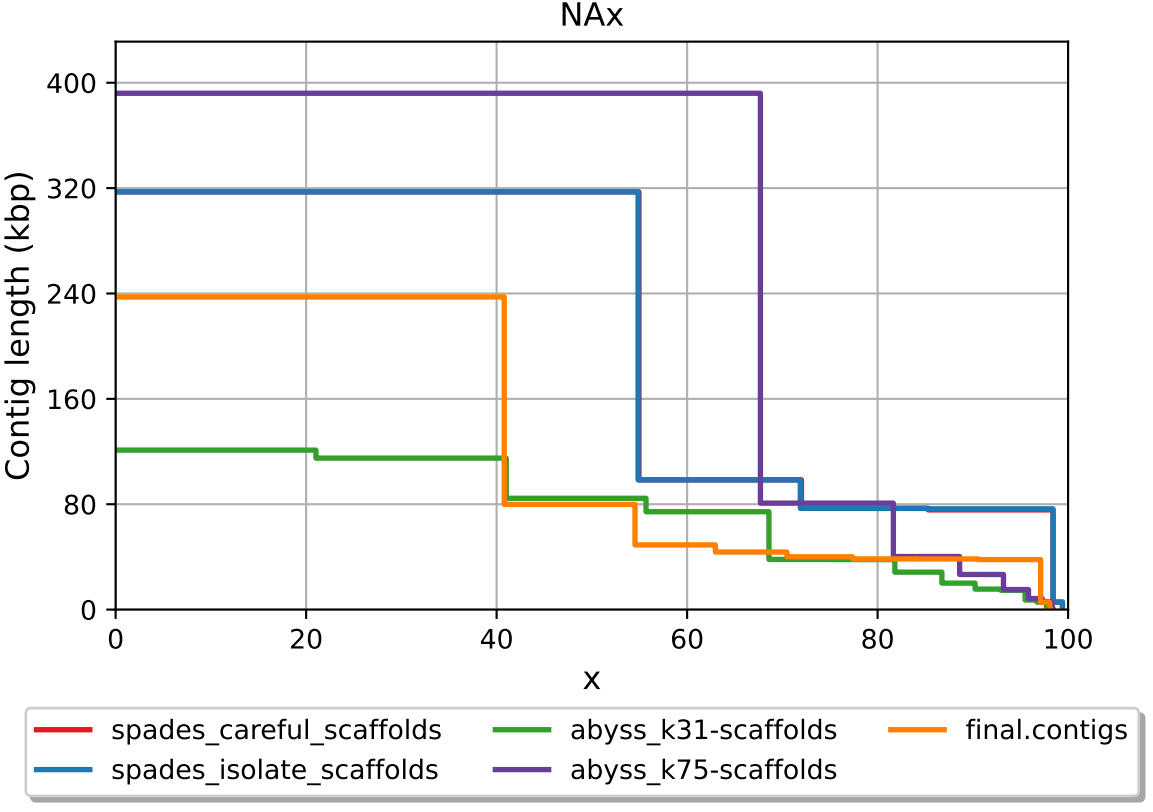

spades_careful_scaffolds coverage histogram (bin size: 2x)
Total length (kbp)
0
100
200
300
400
0
88
90
92
94
96
98
100
100
Coverage depth (x)
spades_careful_scaffolds

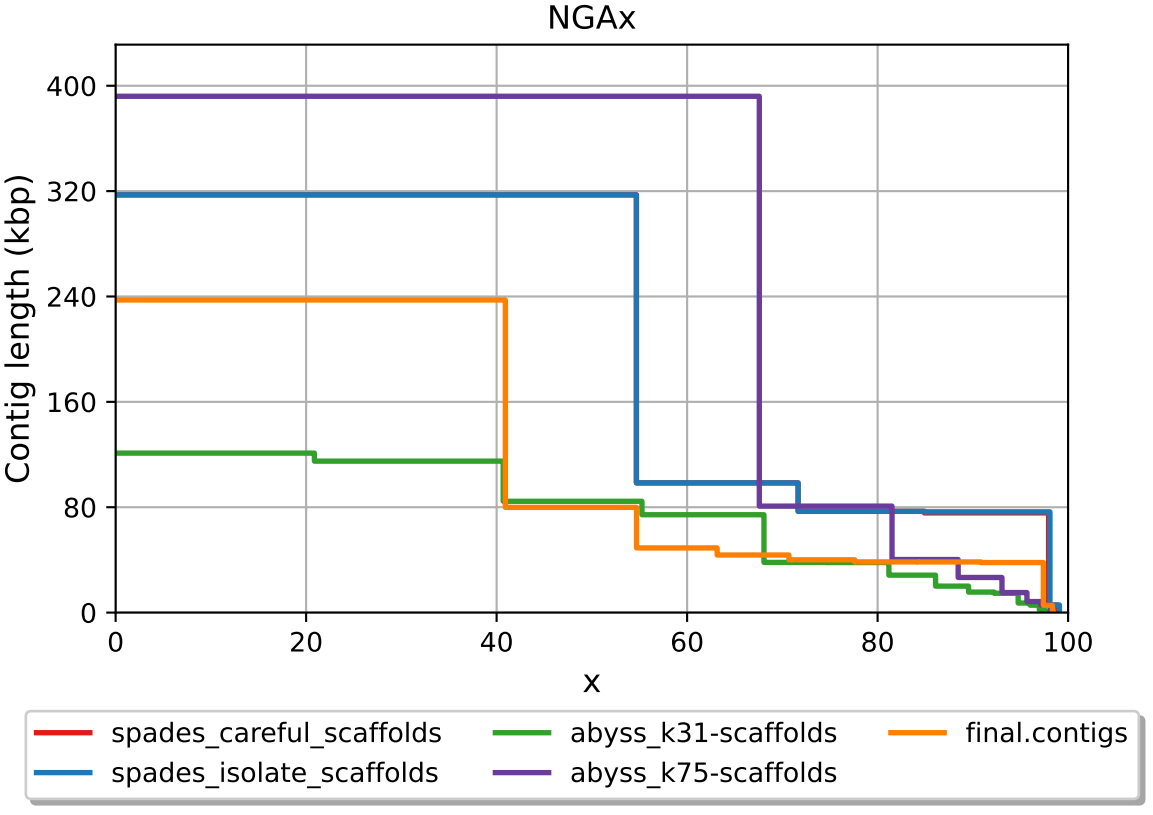

spades_isolate_scaffolds coverage histogram (bin size: 2x)
Total length (kbp)
0
100
200
300
400
0
84
86
88
90
92
94
95
Coverage depth (x)
spades_isolate_scaffolds

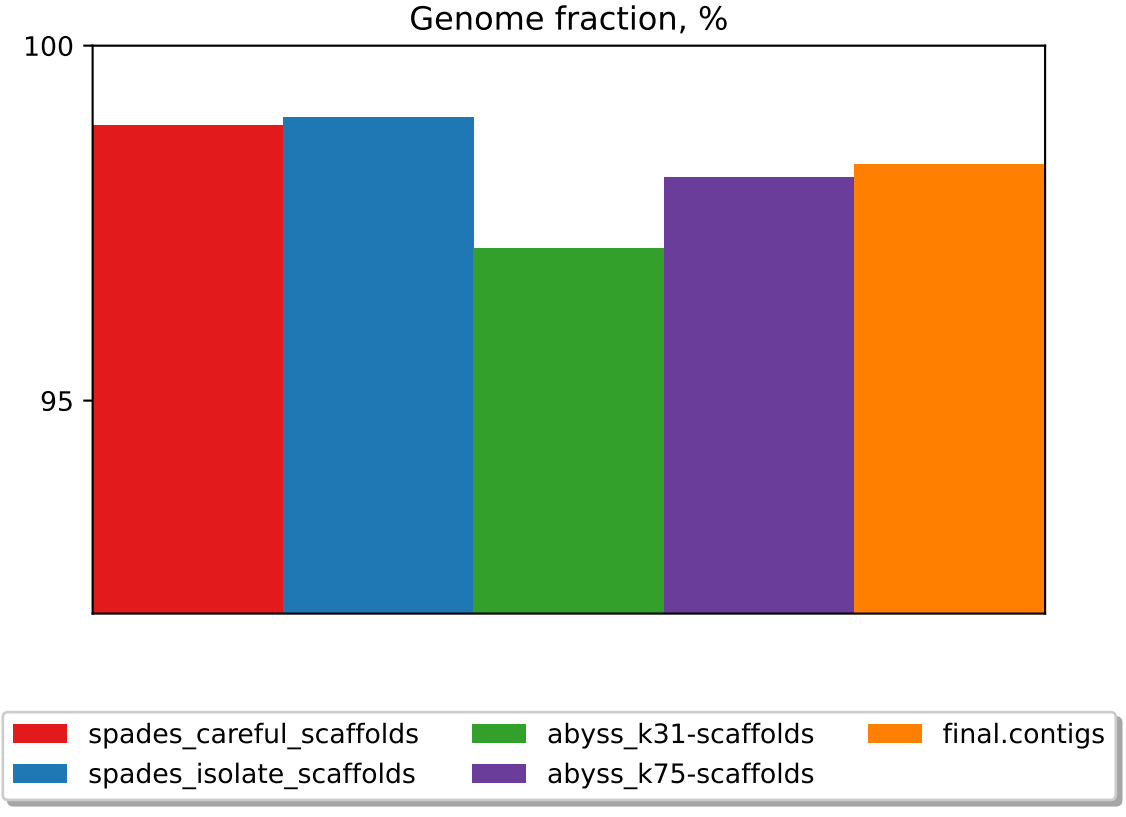

Misassemblies
5
4
3
2
1
0
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
Feature space
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
600
450
300
150
0
0
3
6
9
12
15
Contig index
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs


Genome fraction, %
100
95
spades_careful_scaffolds
spades_isolate_scaffolds
abyss_k31-scaffolds
abyss_k75-scaffolds
final.contigs