Report

	abyss_ecoli_ass	spades_ecoli_ass	spades_hyb_ecoli_ass
# contigs (>= 0 bp)	836	553	267
# contigs (>= 1000 bp)	93	61	53
# contigs (>= 5000 bp)	73	48	42
# contigs (>= 10000 bp)	66	43	39
# contigs (>= 25000 bp)	53	39	39
# contigs (>= 50000 bp)	31	25	25
Total length (>= 0 bp)	4609549	4686608	4622092
Total length (>= 1000 bp)	4545358	4566892	4571654
Total length (>= 5000 bp)	4497901	4539340	4545628
Total length (>= 10000 bp)	4445550	4504123	4524192
Total length (>= 25000 bp)	4243269	4440561	4524192
Total length (>= 50000 bp)	3468085	3914996	3993598
# contigs	107	69	58
Largest contig	268126	414005	433760
Total length	4555493	4572278	4575014
Reference length	4641652	4641652	4641652
GC (%)	50.75	50.74	50.74
Reference GC (%)	50.79	50.79	50.79
N50	112479	178300	178278
NG50	112479	178300	178278
N90	29440	40969	41649
NG90	26282	40204	40911
auN	114322.4	185100.3	195798.8
auNG	112200.4	182333.8	192987.8
L50	15	9	9
LG50	15	9	9
L90	48	30	28
LG90	51	32	30
# misassemblies	5	1	1
# misassembled contigs	4	1	1
Misassembled contigs length	427622	297149	297513
# local misassemblies	4	2	2
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	29	3	2
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	1 + 0 part	1 + 0 part
Unaligned length	0	5463	5463
Genome fraction (%)	97.774	98.345	98.396
Duplication ratio	1.003	1.000	1.000
# N's per 100 kbp	234.62	30.62	24.94
# mismatches per 100 kbp	3.89	0.33	0.46
# indels per 100 kbp	6.57	0.28	0.48
# genomic features	8948 + 181 part	9159 + 75 part	9199 + 47 part
Largest alignment	268126	414005	433760
Total aligned length	4551342	4566381	4569357
NA50	95367	175988	178278
NGA50	87887	175988	178278
NA90	28756	40969	41649
NGA90	26089	40204	40911
auNA	109790.0	176640.7	187349.5
auNGA	107752.0	174000.6	184659.8
LA50	15	10	9
LGA50	16	10	9
LA90	51	31	29
LGA90	54	33	31

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

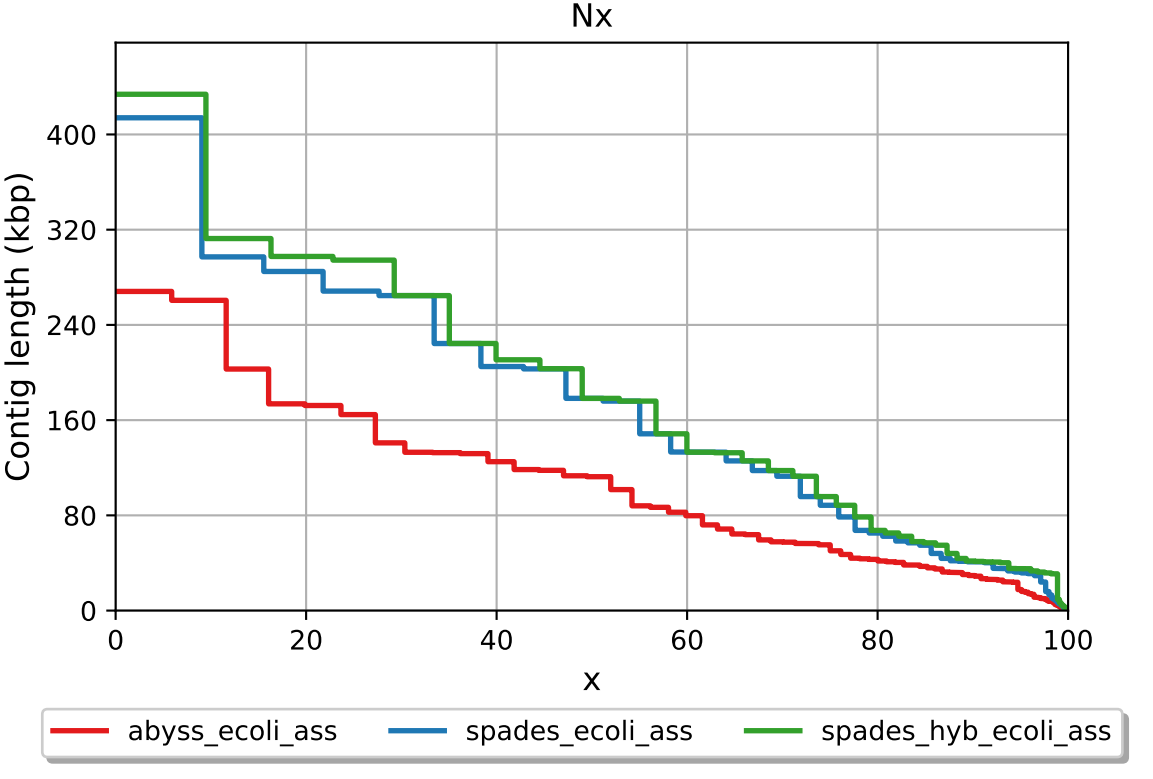
	abyss_ecoli_ass	spades_ecoli_ass	spades_hyb_ecoli_ass
# misassemblies	5	1	1
# contig misassemblies	1	1	1
# c. relocations	1	1	1
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	4	0	0
# s. relocations	4	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	4	1	1
Misassembled contigs length	427622	297149	297513
# local misassemblies	4	2	2
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	29	3	2
# unaligned mis. contigs	0	0	0
# mismatches	177	15	21
# indels	299	13	22
# indels (<= 5 bp)	167	2	5
# indels (> 5 bp)	132	11	17
Indels length	4579	1024	1628

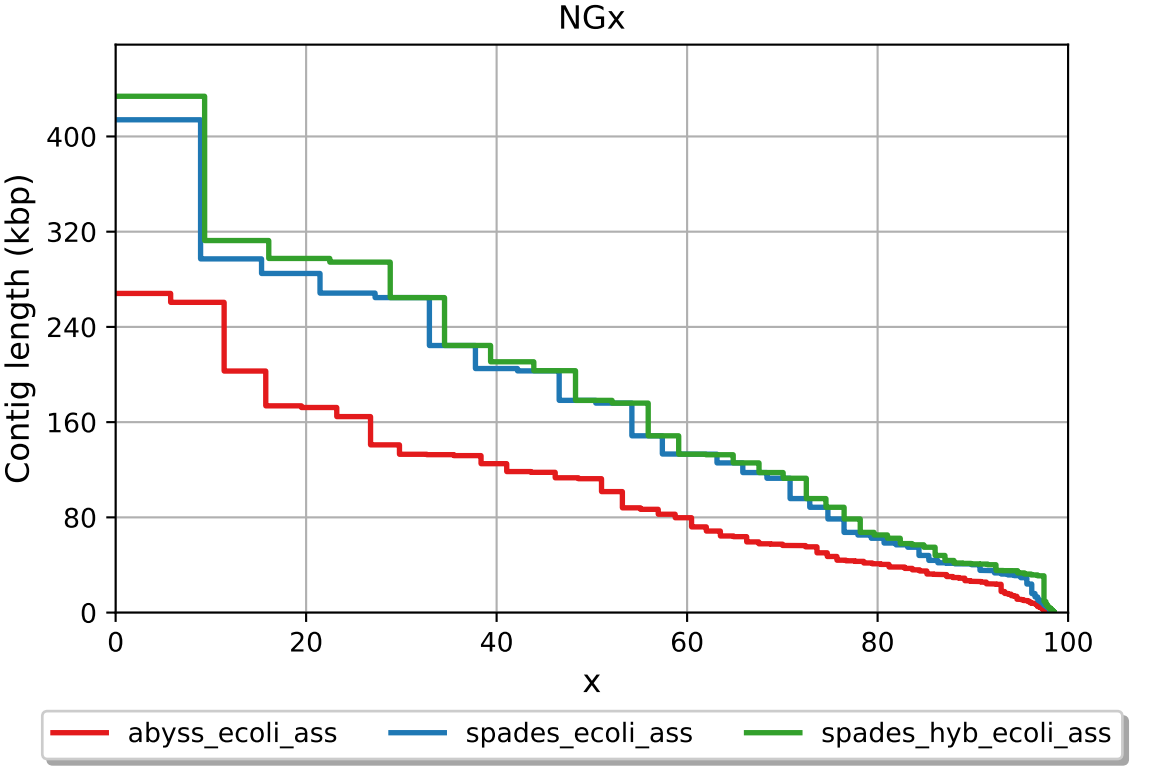
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

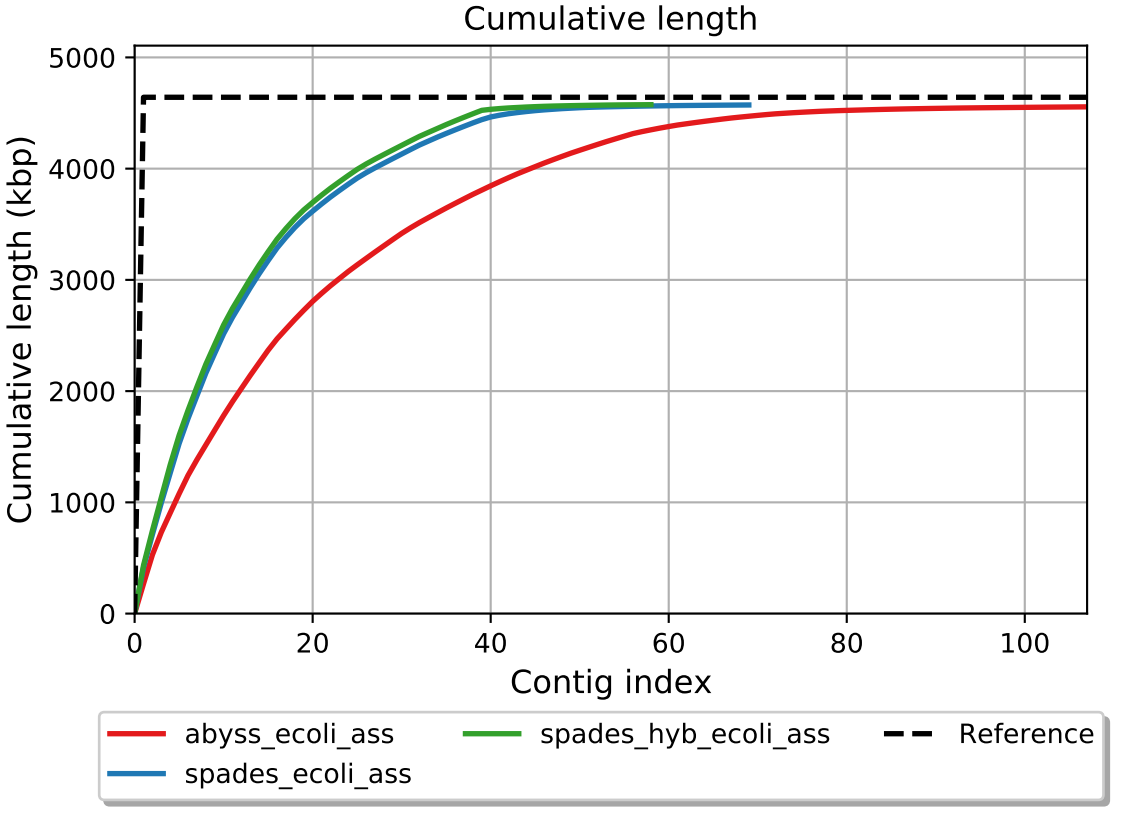
Unaligned report

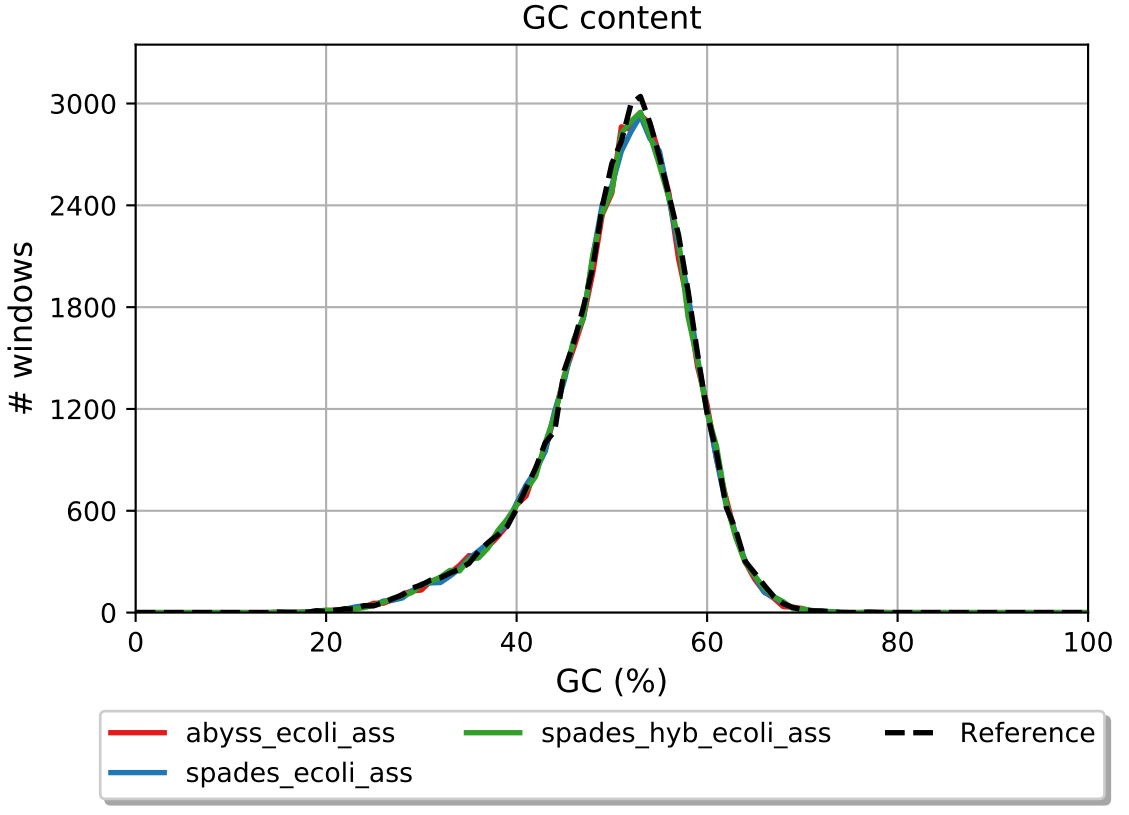
	abyss_ecoli_ass	spades_ecoli_ass	spades_hyb_ecoli_ass
# fully unaligned contigs	0	1	1
Fully unaligned length	0	5463	5463
# partially unaligned contigs	0	0	0
Partially unaligned length	0	0	0
# N's	10688	1400	1141

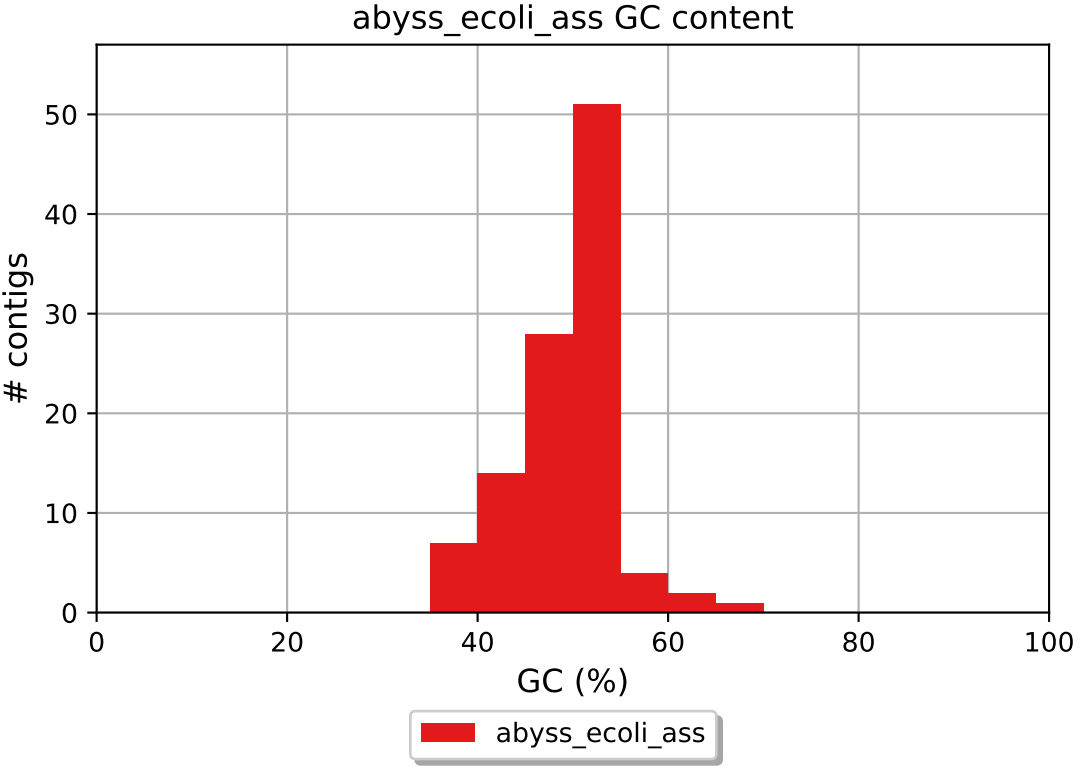
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

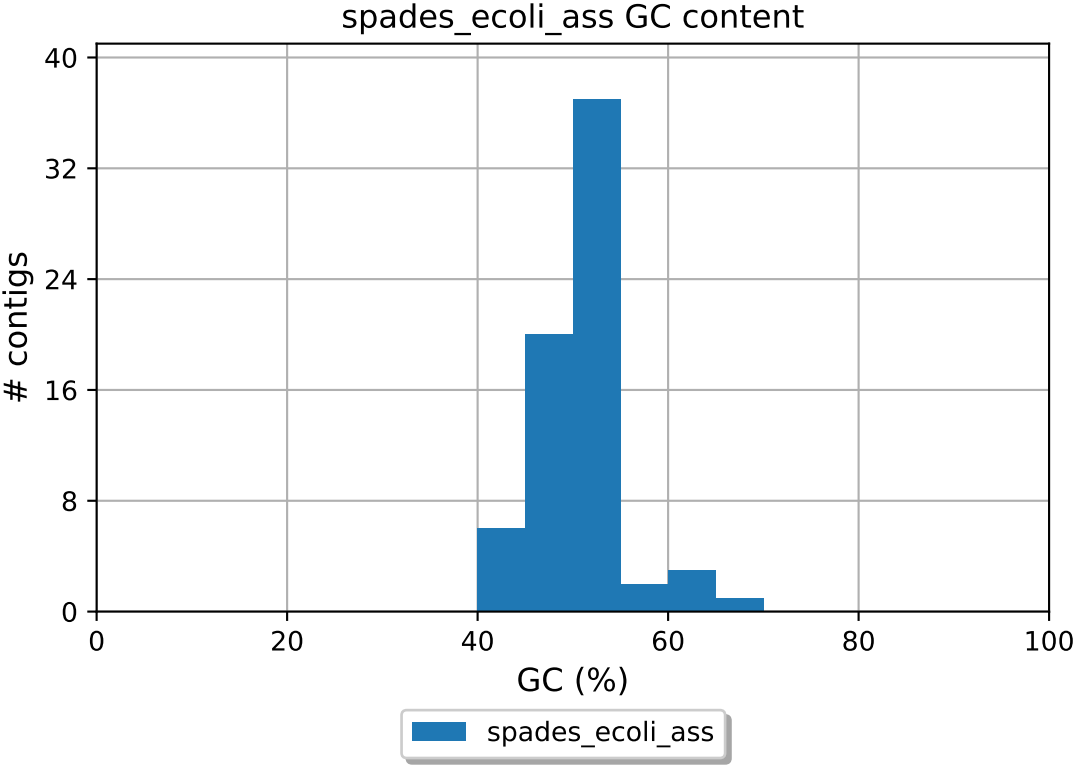

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass

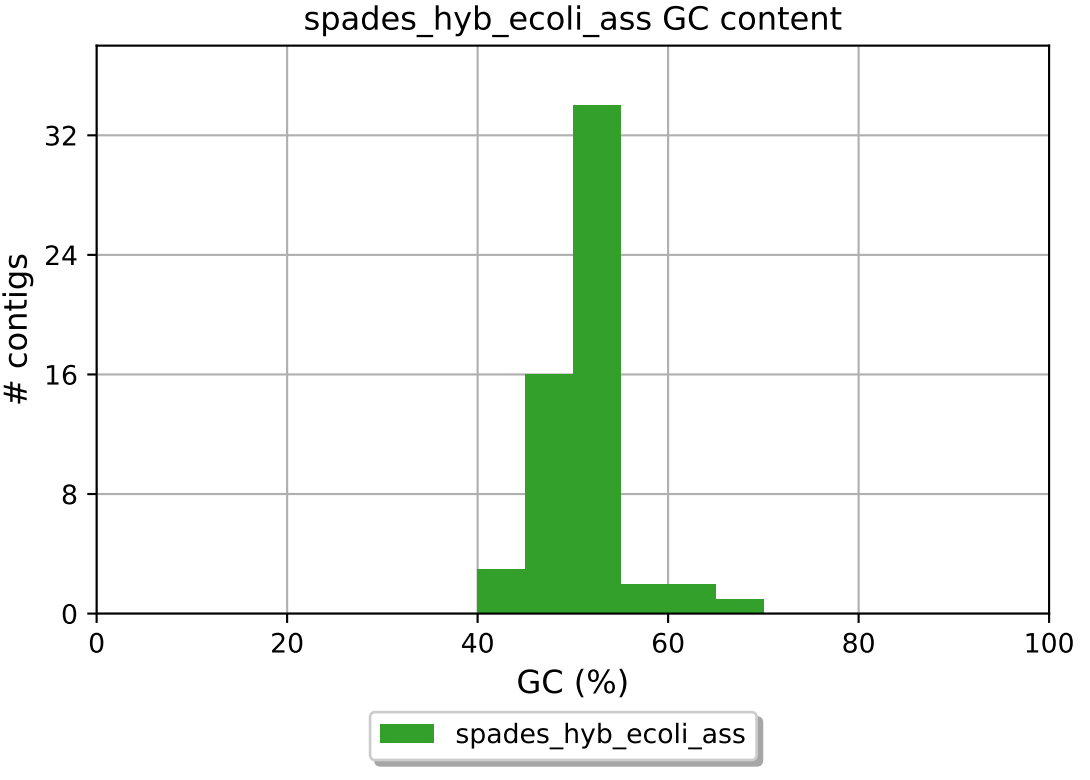

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass

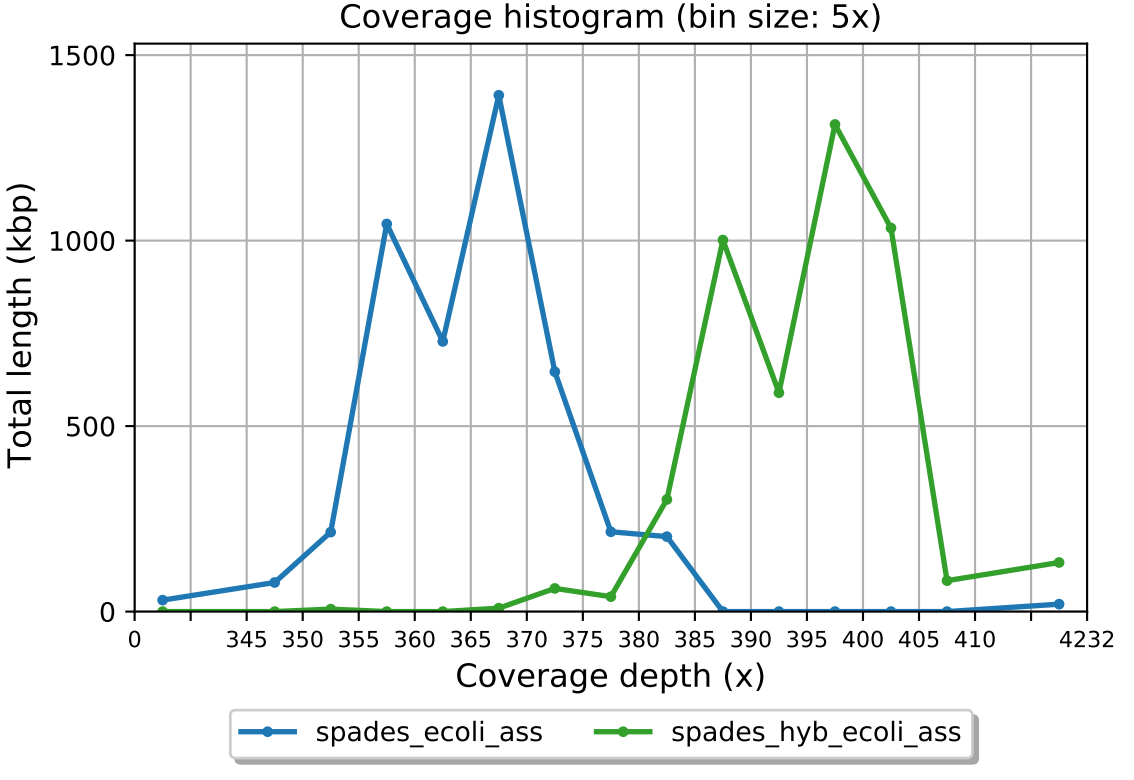

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass
Reference

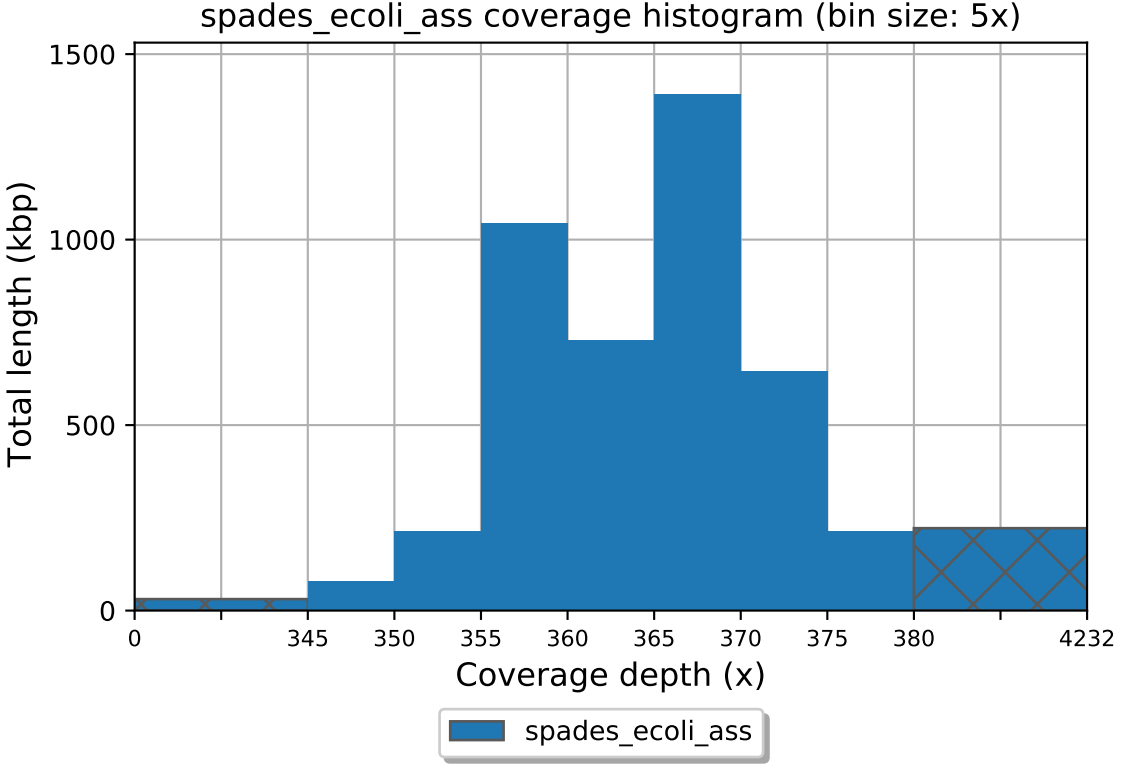

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass
Reference

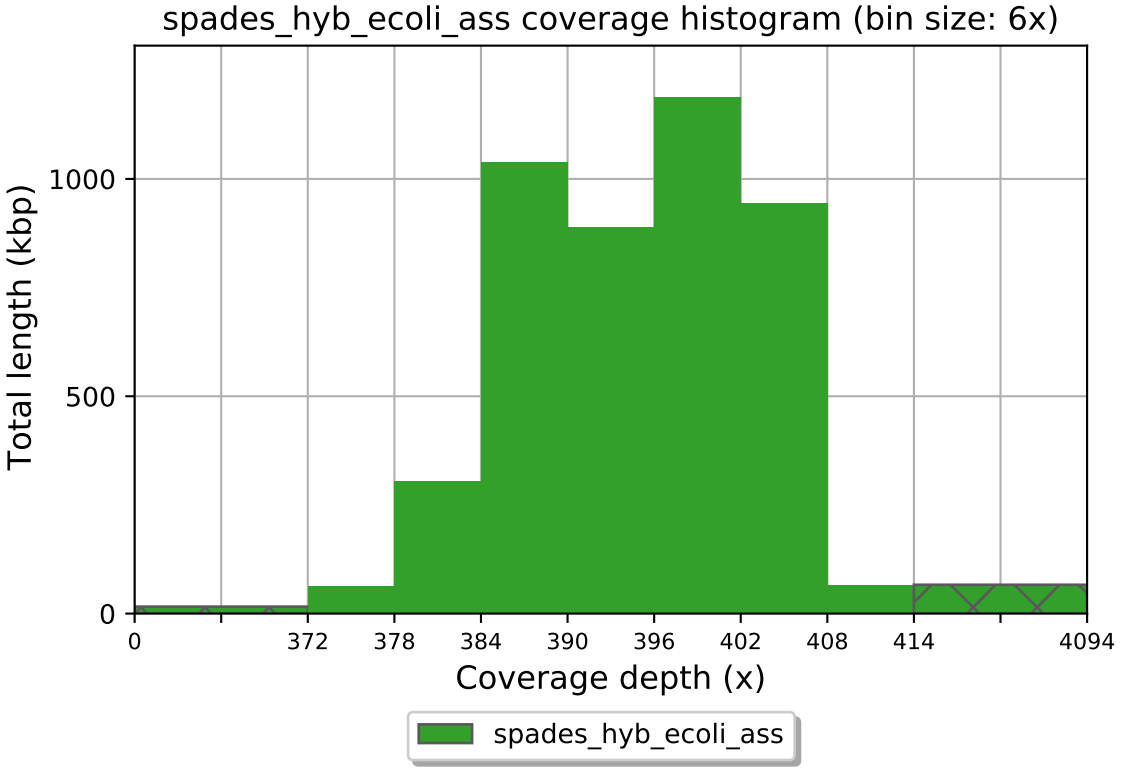

abyss_ecoli_ass GC content
contigs
0
10
20
30
40
50
0
20
40
60
80
100
GC (%)
abyss_ecoli_ass

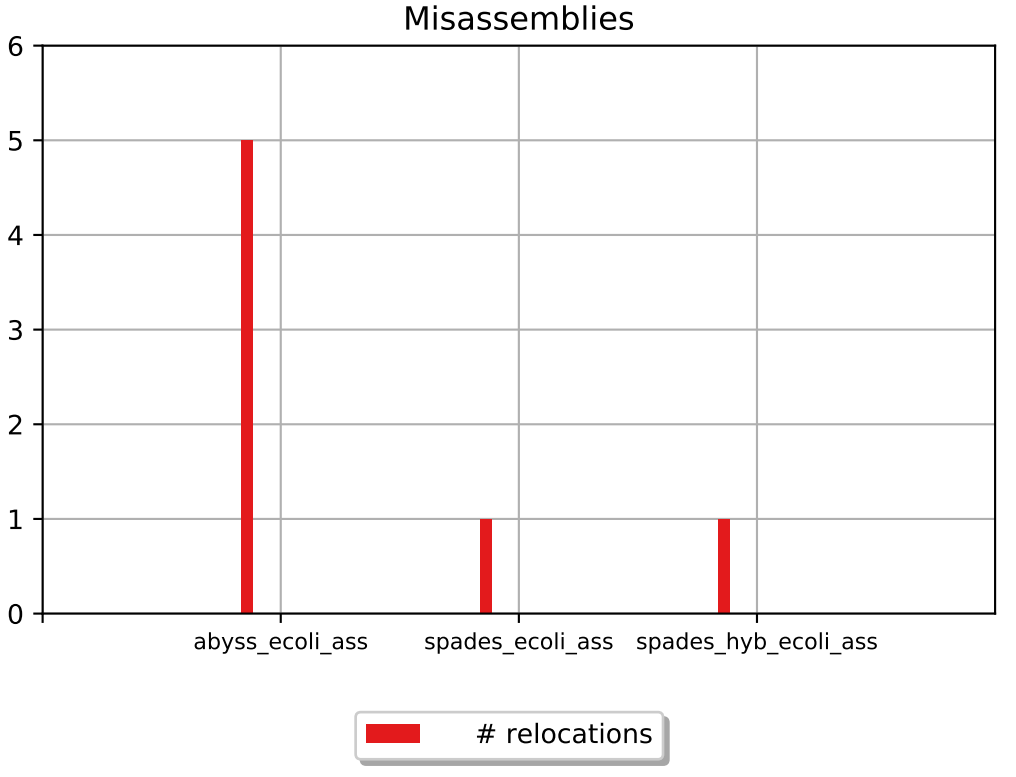

spades_ecoli_ass GC content
40
32
24
16
8
0
contigs
0
20
40
60
80
100
GC (%)
spades_ecoli_ass

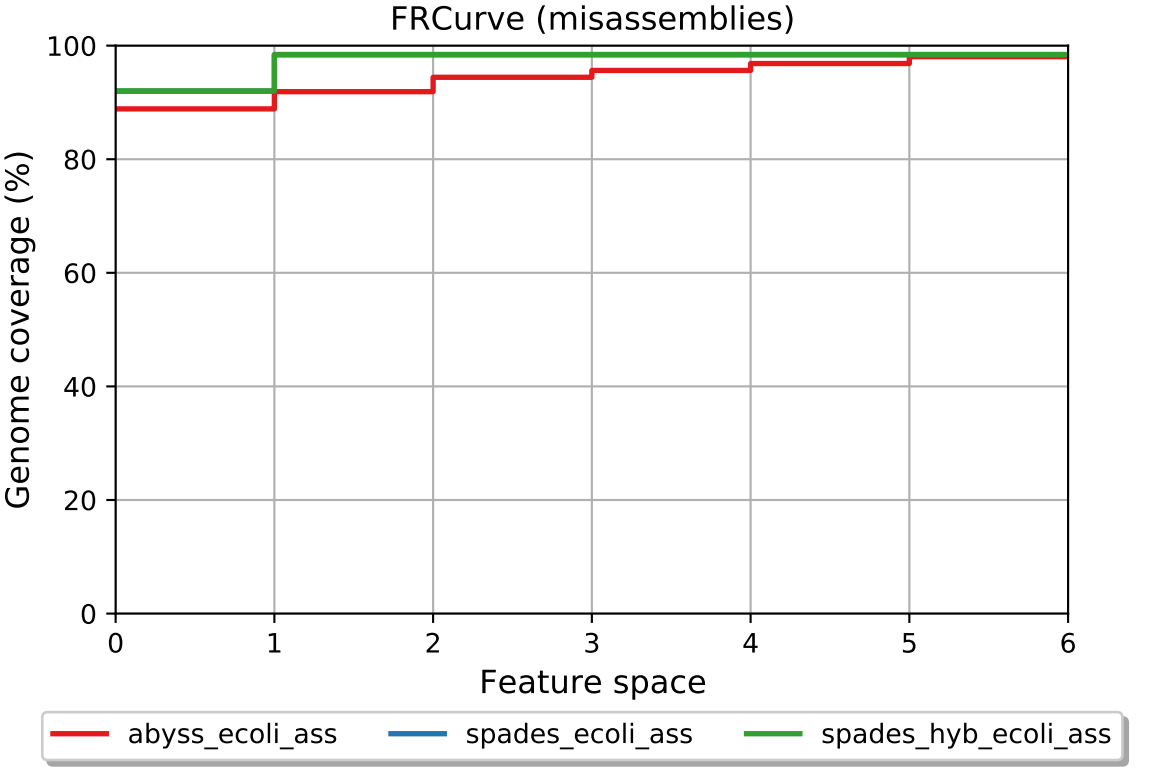

spades_hyb_ecoli_ass GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
spades_hyb_ecoli_ass

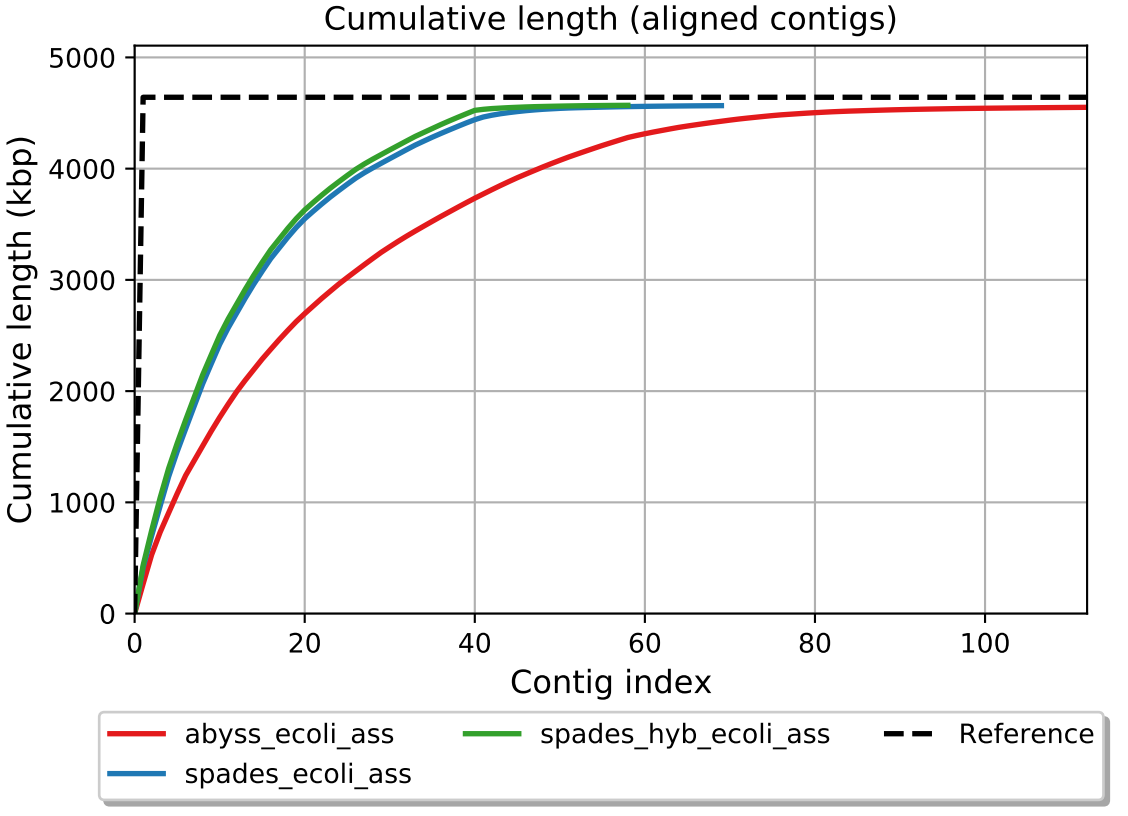

Coverage histogram (bin size: 5x)
Total length (kbp)
1500
1000
500
0
0
345
350
355
360
365
370
375
380
385
390
395
400
405
410
4232
Coverage depth (x)
spades_ecoli_ass
spades_hyb_ecoli_ass

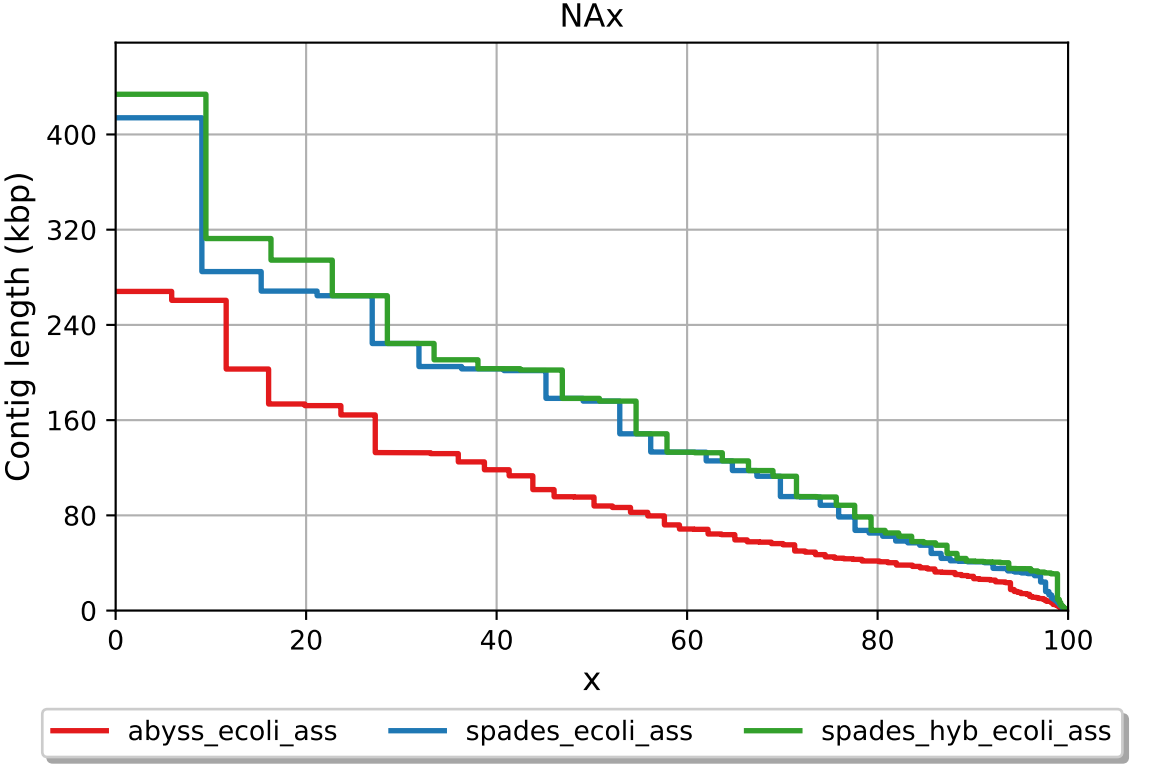

spades_ecoli_ass coverage histogram (bin size: 5x)
Total length (kbp)
1500
1000
500
0
0
345
350
355
360
365
370
375
380
4232
Coverage depth (x)
spades_ecoli_ass

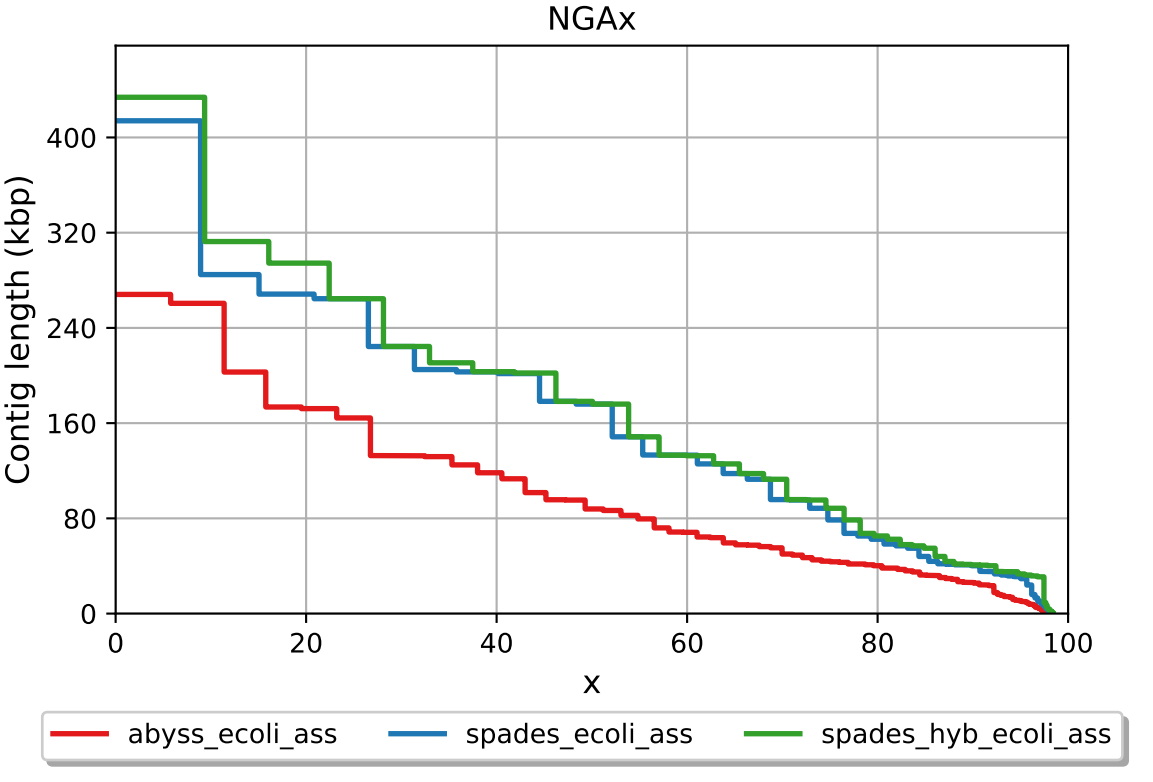

spades_hyb_ecoli_ass coverage histogram (bin size: 6x)
Total length (kbp)
1000
500
0
0
372
378
384
390
396
402
408
414
4094
Coverage depth (x)
spades_hyb_ecoli_ass

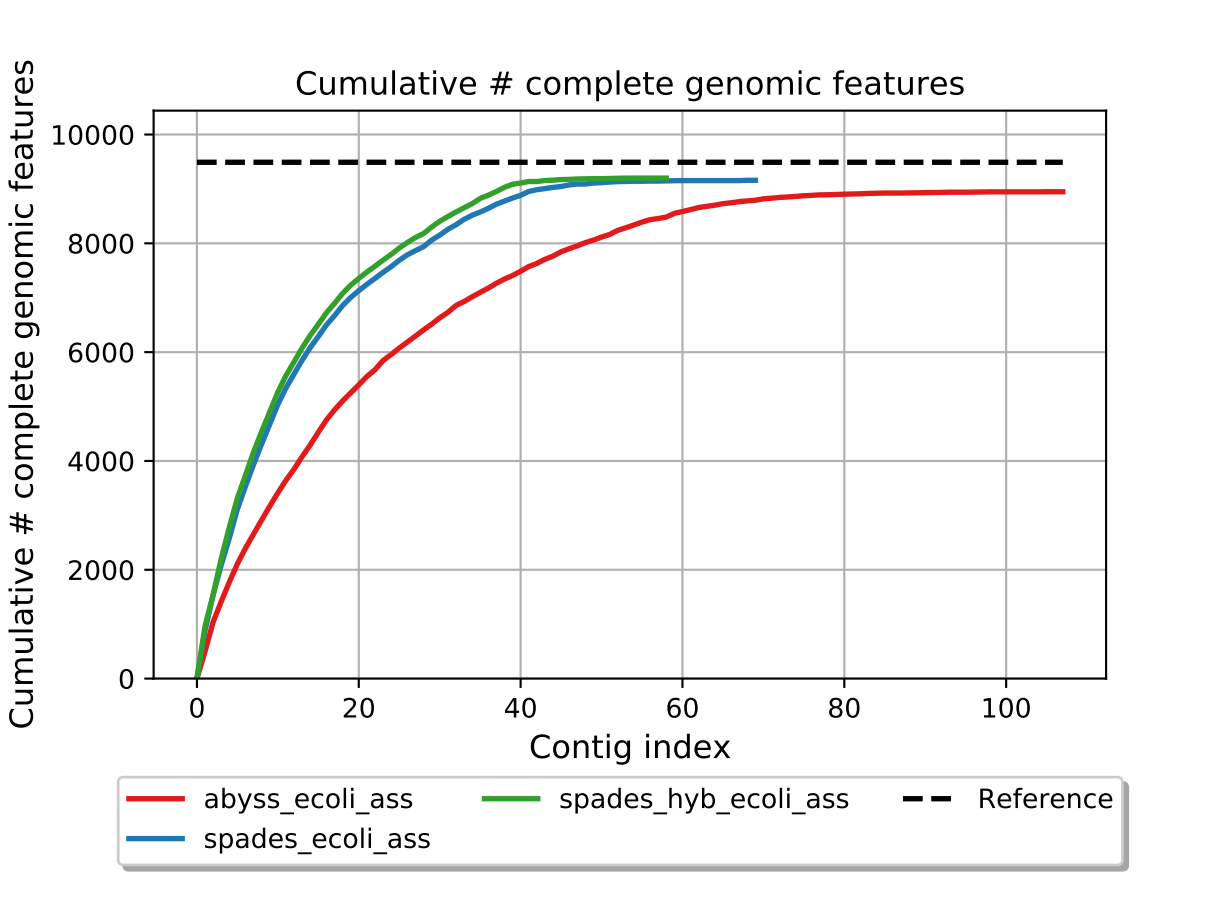

Misassemblies
6
5
4
3
2
1
0
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass
relocations

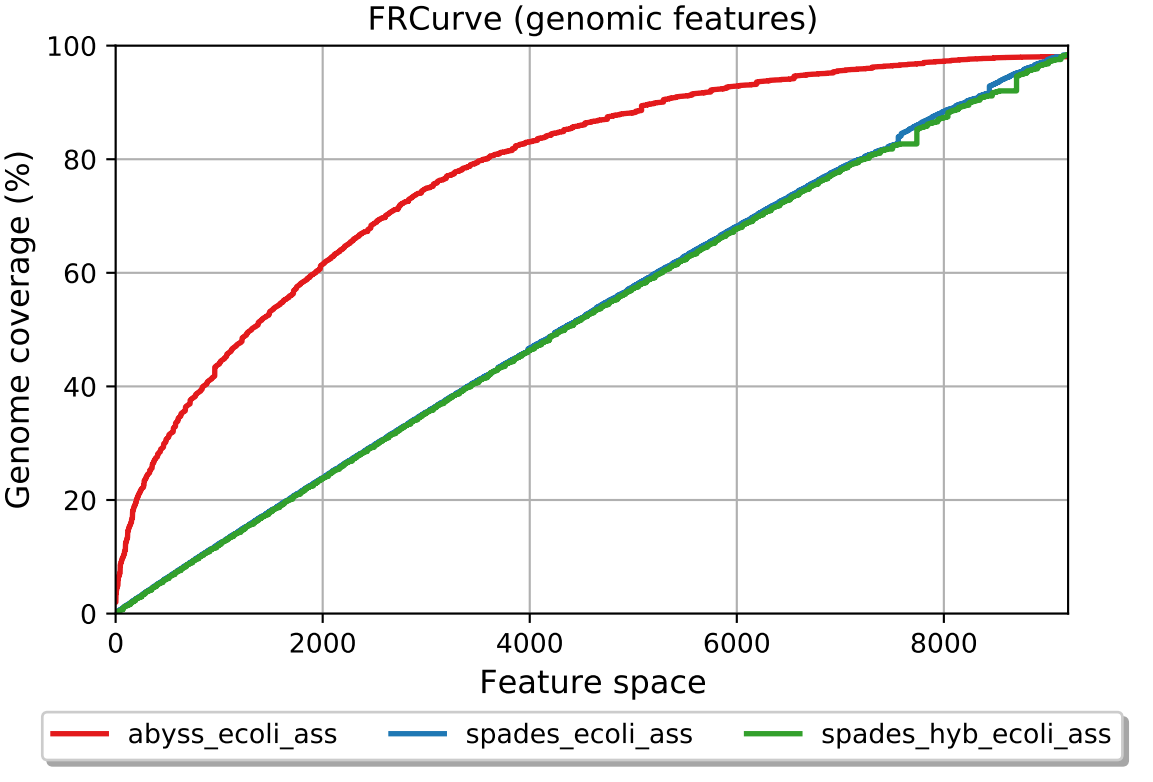

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
Feature space
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass

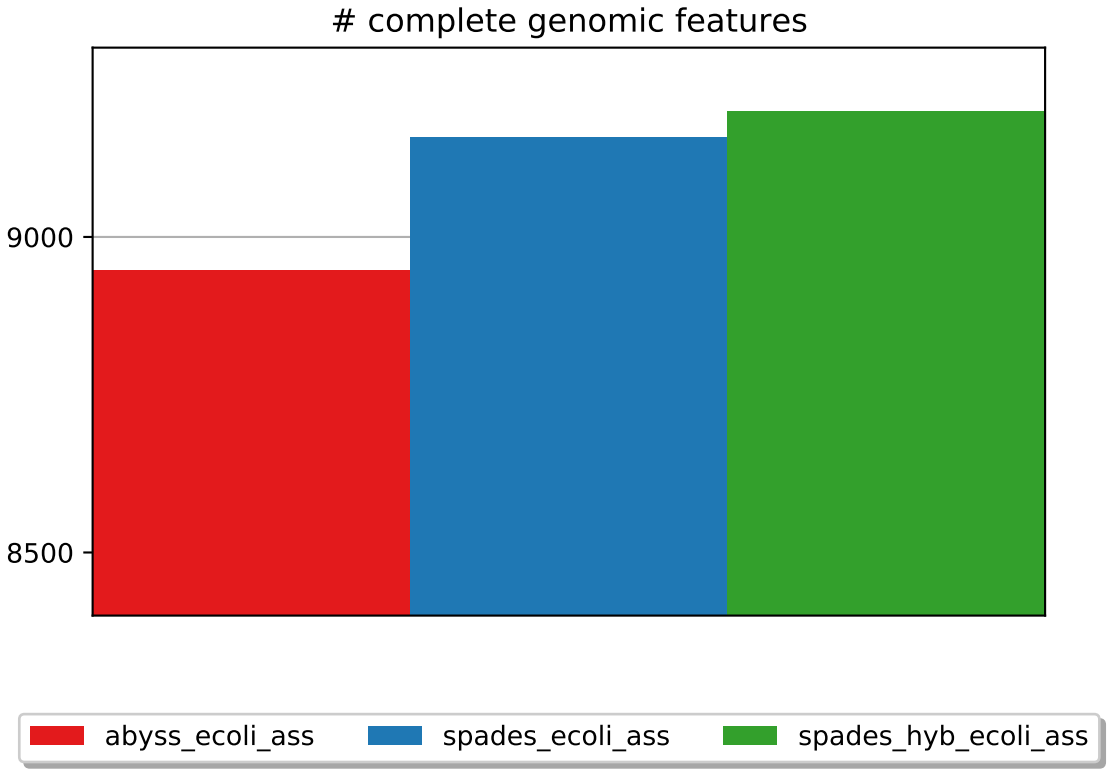

Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass
Reference

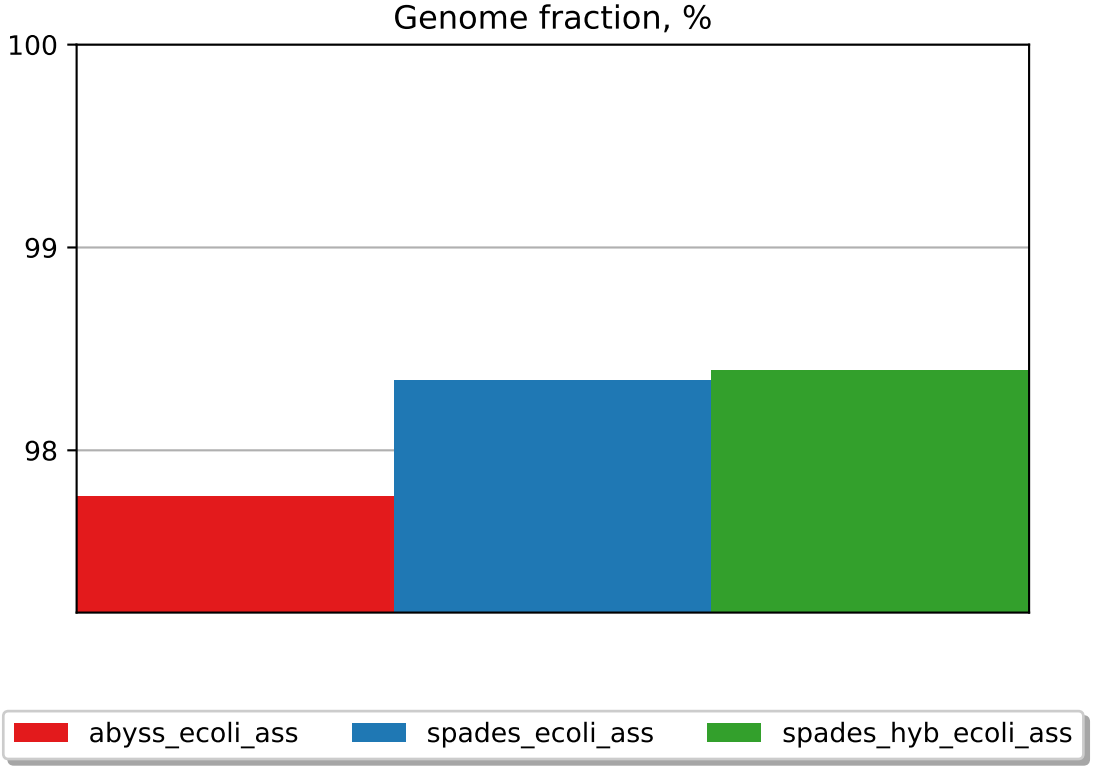

NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass


Cumulative # complete genomic features
Cumulative # complete genomic features
10000
8000
6000
4000
2000
0
0
20
40
60
80
100
Contig index
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass
Reference


FRCurve (genomic features)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
2000
4000
6000
8000
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass


complete genomic features
9000
8500
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass


Genome fraction, %
100
99
98
abyss_ecoli_ass
spades_ecoli_ass
spades_hyb_ecoli_ass