Report

	SRR11425846_plasmid_scaffolds	SRR1686737_plasmid_scaffolds	SRR1686740_plasmid_scaffolds	SRR3712208_plasmid_scaffolds	SRR8282855_plasmid_scaffolds	SRR9050348_plasmid_scaffolds
# contigs (>= 0 bp)	13	11	16	35	9	2
# contigs (>= 1000 bp)	10	7	12	7	7	2
# contigs (>= 5000 bp)	5	6	8	4	5	0
# contigs (>= 10000 bp)	2	3	6	4	3	0
# contigs (>= 25000 bp)	1	2	3	4	0	0
# contigs (>= 50000 bp)	1	1	0	2	0	0
Total length (>= 0 bp)	102903	160635	189596	294783	54659	4515
Total length (>= 1000 bp)	101593	159671	186988	289314	53326	4515
Total length (>= 5000 bp)	90883	157142	175659	284878	50863	0
Total length (>= 10000 bp)	74317	134625	161202	284878	37375	0
Total length (>= 25000 bp)	59289	120011	110255	284878	0	0
Total length (>= 50000 bp)	59289	91650	0	215517	0	0
# contigs	11	7	15	8	9	2
Largest contig	59289	91650	44200	138486	15125	2269
Total length	102398	159671	189111	290085	54659	4515
Reference length	4951383	4951383	4951383	4951383	4951383	4951383
GC (%)	52.89	50.45	44.80	50.89	49.03	48.75
Reference GC (%)	52.24	52.24	52.24	52.24	52.24	52.24
N50	59289	91650	32900	77031	10698	2269
N75	5768	28361	19106	37774	8138	2246
L50	1	1	3	2	3	1
L75	3	2	5	3	4	2
# misassemblies	0	-	0	5	0	-
# misassembled contigs	0	-	0	3	0	-
Misassembled contigs length	0	-	0	247104	0	-
# local misassemblies	0	-	0	2	0	-
# scaffold gap ext. mis.	0	-	0	0	0	-
# scaffold gap loc. mis.	0	-	0	0	0	-
# unaligned mis. contigs	1	-	1	0	0	-
# unaligned contigs	10 + 1 part	7 + 0 part	10 + 4 part	1 + 1 part	8 + 1 part	2 + 0 part
Unaligned length	102218	159671	166230	43241	54576	4515
Genome fraction (%)	0.004	-	0.444	4.982	0.002	-
Duplication ratio	1.000	-	1.041	1.001	1.000	-
# N's per 100 kbp	0.00	0.00	52.88	0.00	0.00	0.00
# mismatches per 100 kbp	1666.67	-	2657.20	742.63	0.00	-
# indels per 100 kbp	0.00	-	45.50	9.73	0.00	-
# genomic features	0 + 3 part	-	40 + 9 part	800 + 27 part	0 + 0 part	-
Largest alignment	106	-	17854	92668	83	-
Total aligned length	180	-	22773	246715	83	-
NA50	-	-	-	31055	-	-
NGA50	-	-	-	-	-	-
NA75	-	-	-	18077	-	-
LA50	-	-	-	3	-	-
LA75	-	-	-	6	-	-

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

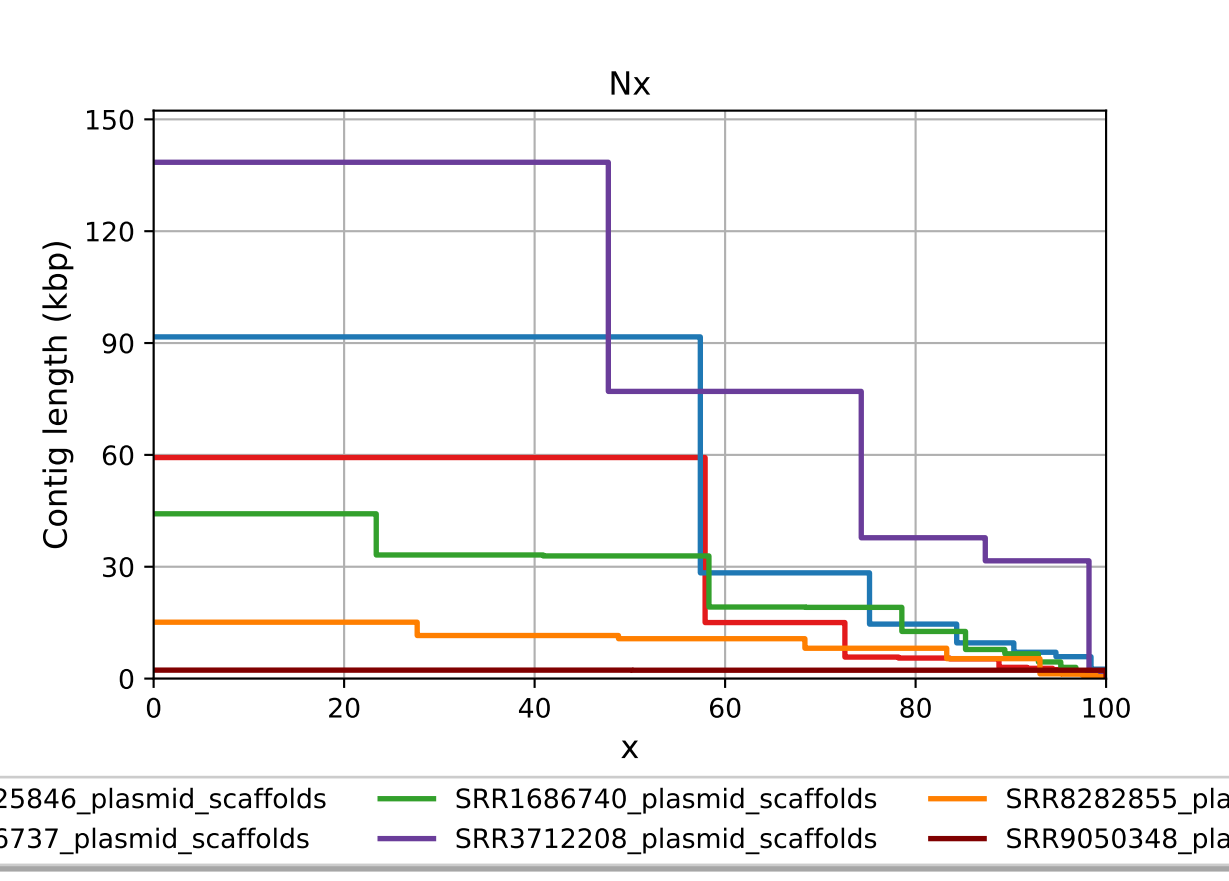
	SRR11425846_plasmid_scaffolds	SRR1686737_plasmid_scaffolds	SRR1686740_plasmid_scaffolds	SRR3712208_plasmid_scaffolds	SRR8282855_plasmid_scaffolds	SRR9050348_plasmid_scaffolds
# misassemblies	0	-	0	5	0	-
# contig misassemblies	0	-	0	5	0	-
# c. relocations	0	-	0	5	0	-
# c. translocations	0	-	0	0	0	-
# c. inversions	0	-	0	0	0	-
# scaffold misassemblies	0	-	0	0	0	-
# s. relocations	0	-	0	0	0	-
# s. translocations	0	-	0	0	0	-
# s. inversions	0	-	0	0	0	-
# misassembled contigs	0	-	0	3	0	-
Misassembled contigs length	0	-	0	247104	0	-
# local misassemblies	0	-	0	2	0	-
# scaffold gap ext. mis.	0	-	0	0	0	-
# scaffold gap loc. mis.	0	-	0	0	0	-
# unaligned mis. contigs	1	-	1	0	0	-
# mismatches	3	-	584	1832	0	-
# indels	0	-	10	24	0	-
# indels (<= 5 bp)	0	-	10	22	0	-
# indels (> 5 bp)	0	-	0	2	0	-
Indels length	0	-	16	75	0	-

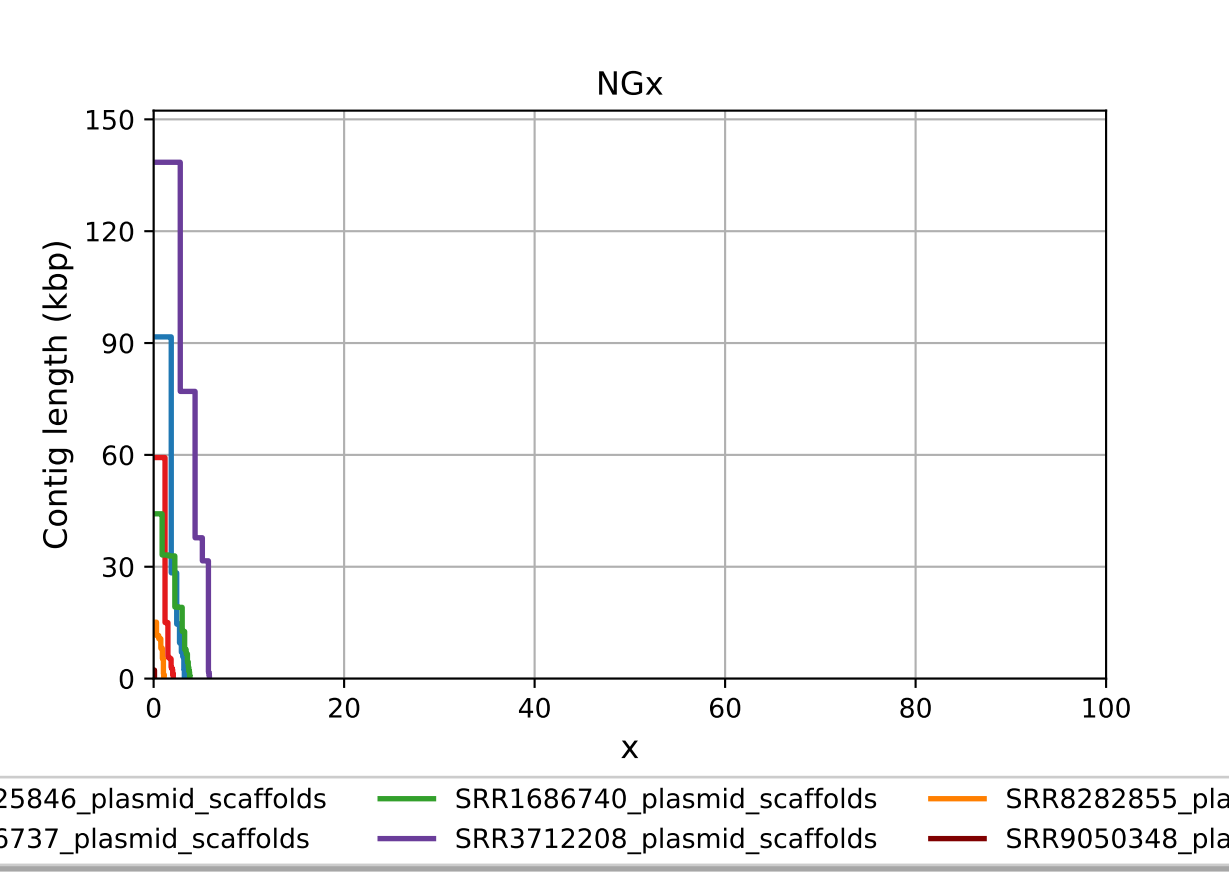
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

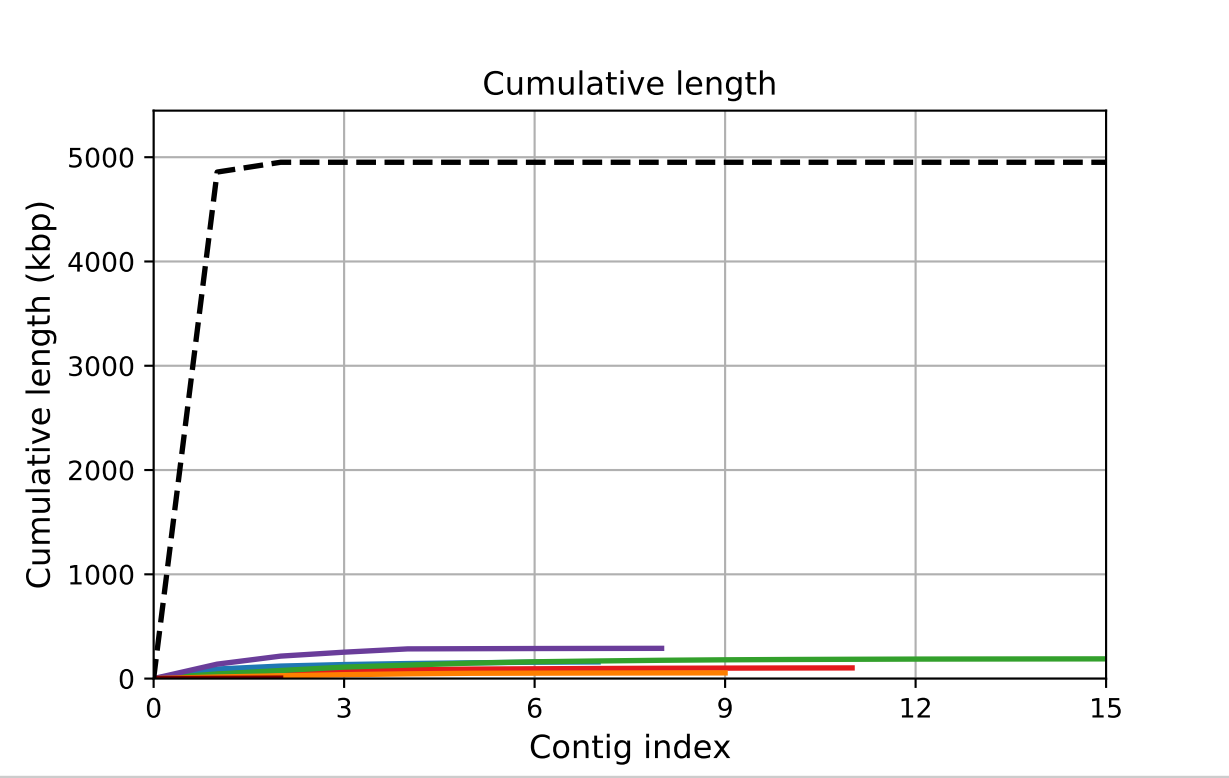
Unaligned report

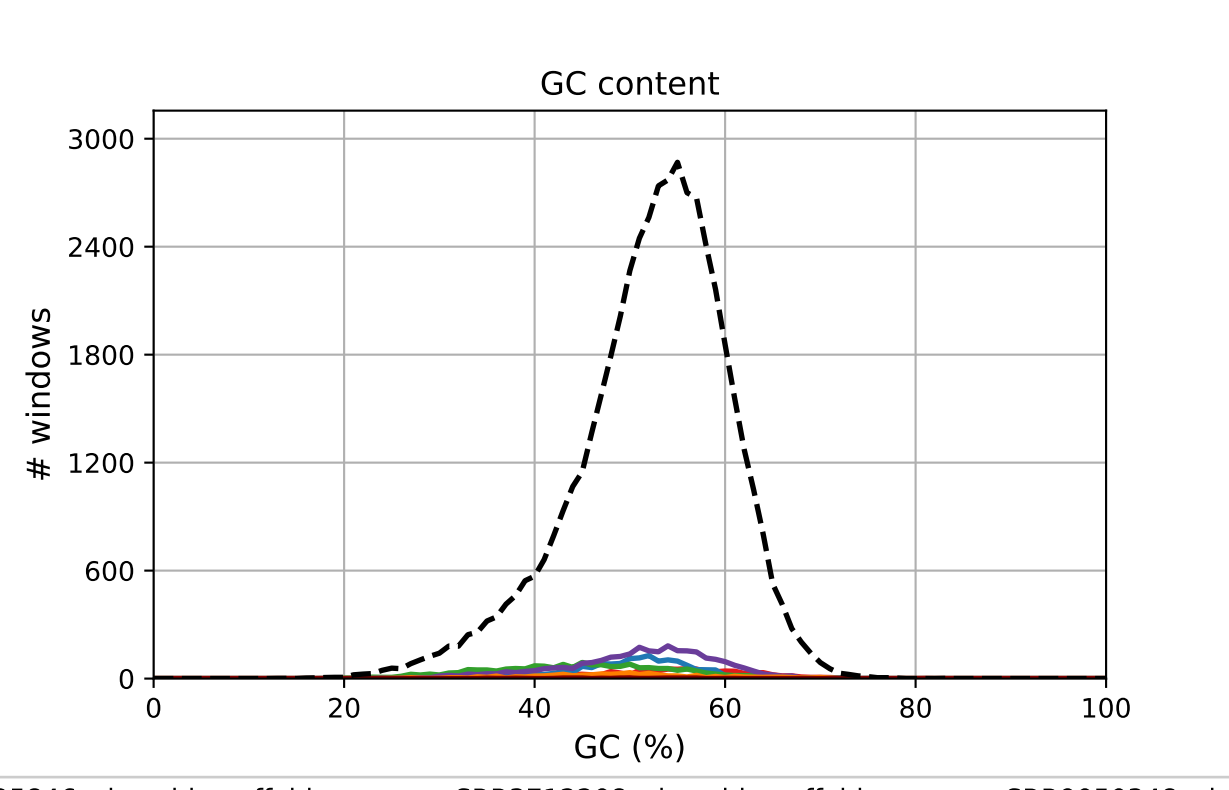
	SRR11425846_plasmid_scaffolds	SRR1686737_plasmid_scaffolds	SRR1686740_plasmid_scaffolds	SRR3712208_plasmid_scaffolds	SRR8282855_plasmid_scaffolds	SRR9050348_plasmid_scaffolds
# fully unaligned contigs	10	7	10	1	8	2
Fully unaligned length	43109	159671	83935	37774	39534	4515
# partially unaligned contigs	1	-	4	1	1	-
Partially unaligned length	59109	-	82295	5467	15042	-
# N's	0	0	100	0	0	0

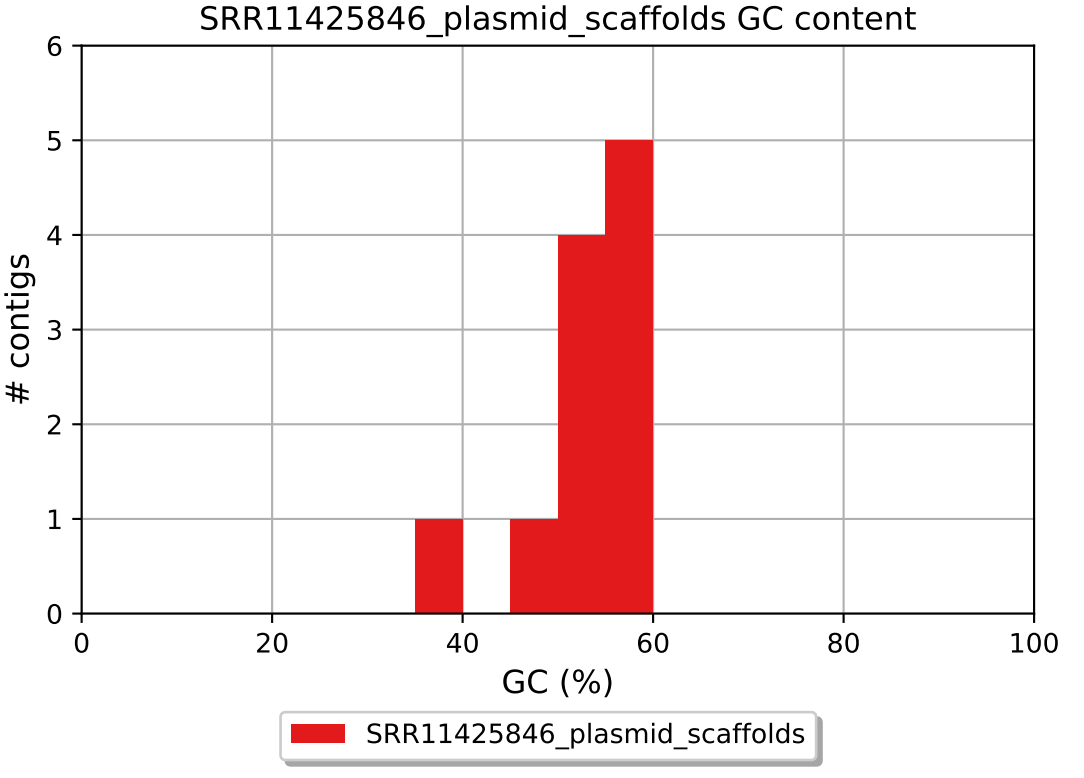
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

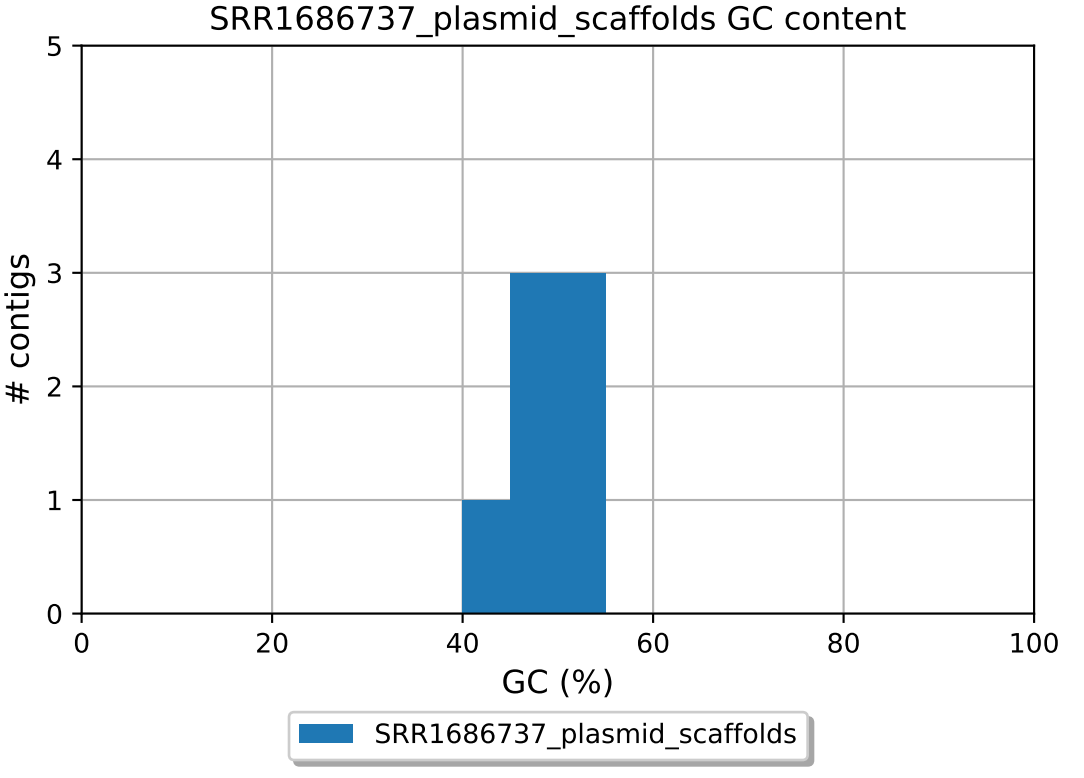

Nx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
25846_plasmid_scaffolds
SRR1686740_plasmid_scaffolds
SRR8282855_pla
6737_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR9050348_pla

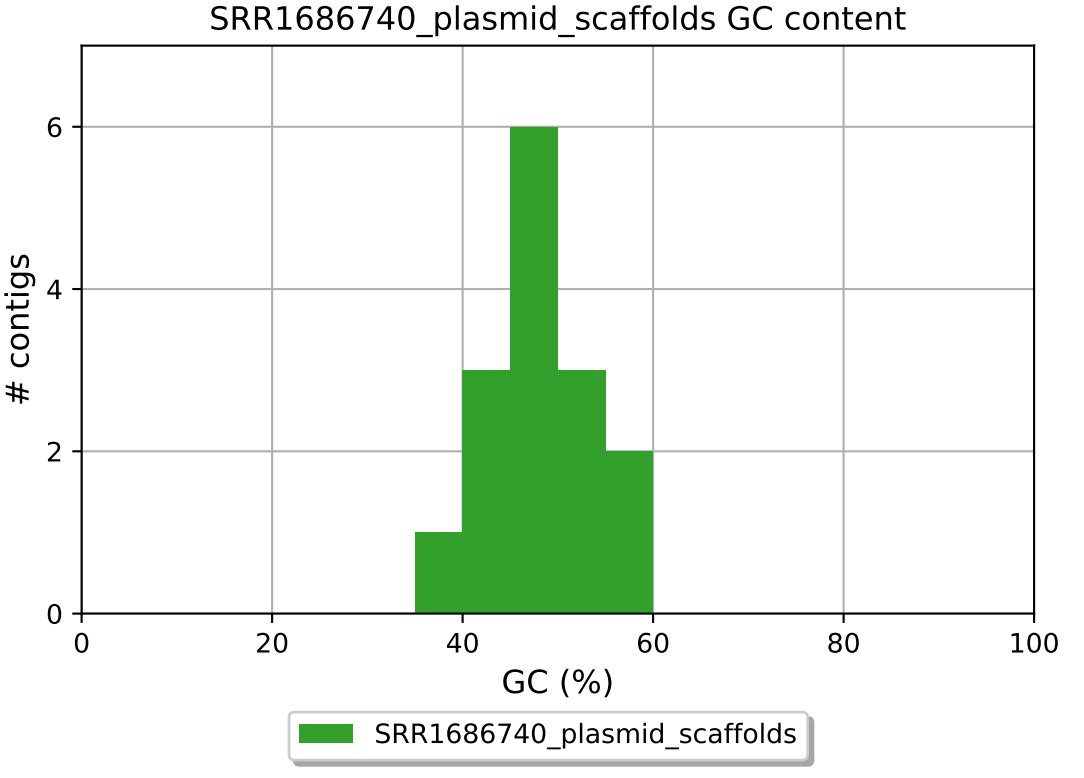

NGx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
25846_plasmid_scaffolds
SRR1686740_plasmid_scaffolds
SRR8282855_pla
6737_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR9050348_pla

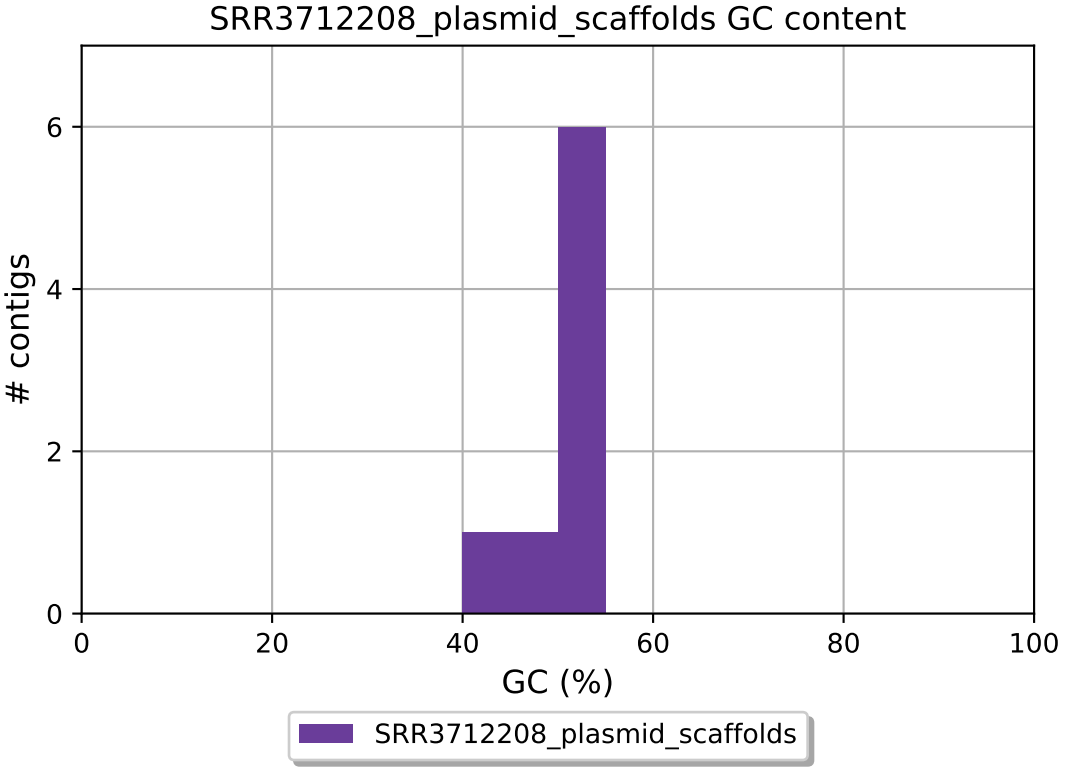

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
25846_plasmid_scaffolds
6737_plasmid_scaffolds
6740_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_plasmid_scaffolds
SRR9050348_pla
Reference

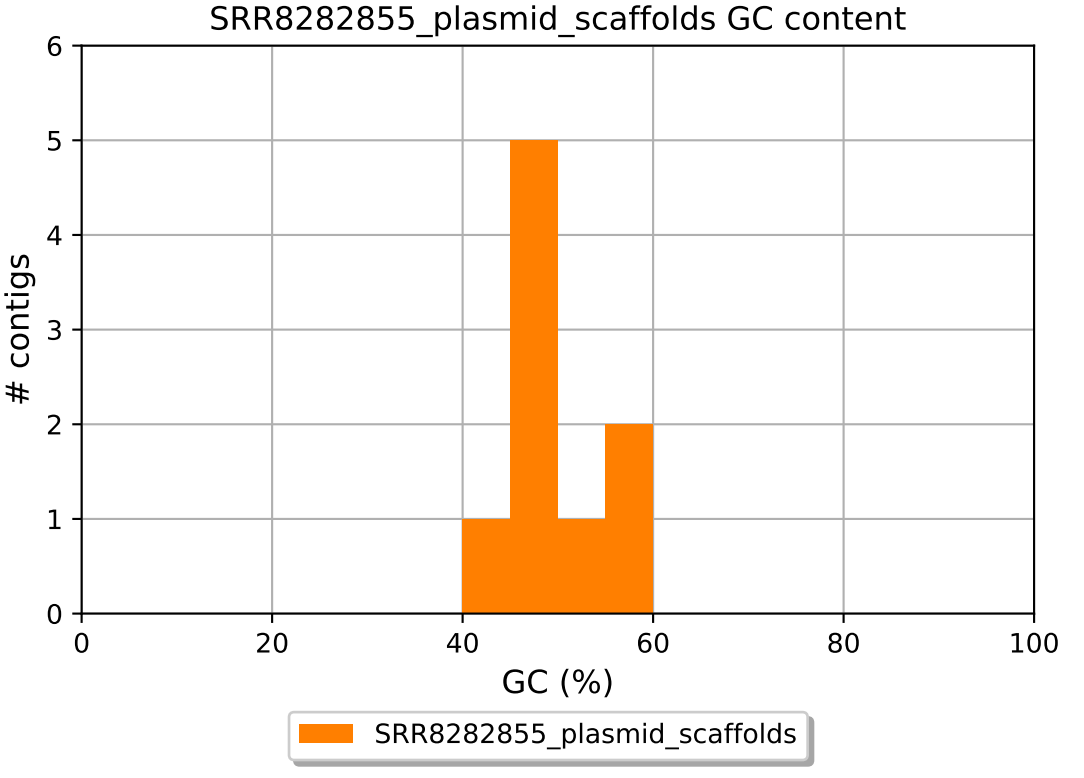

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
25846_plasmid_scaffolds
6737_plasmid_scaffolds
6740_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_plasmid_scaffolds
SRR9050348_pla
Reference

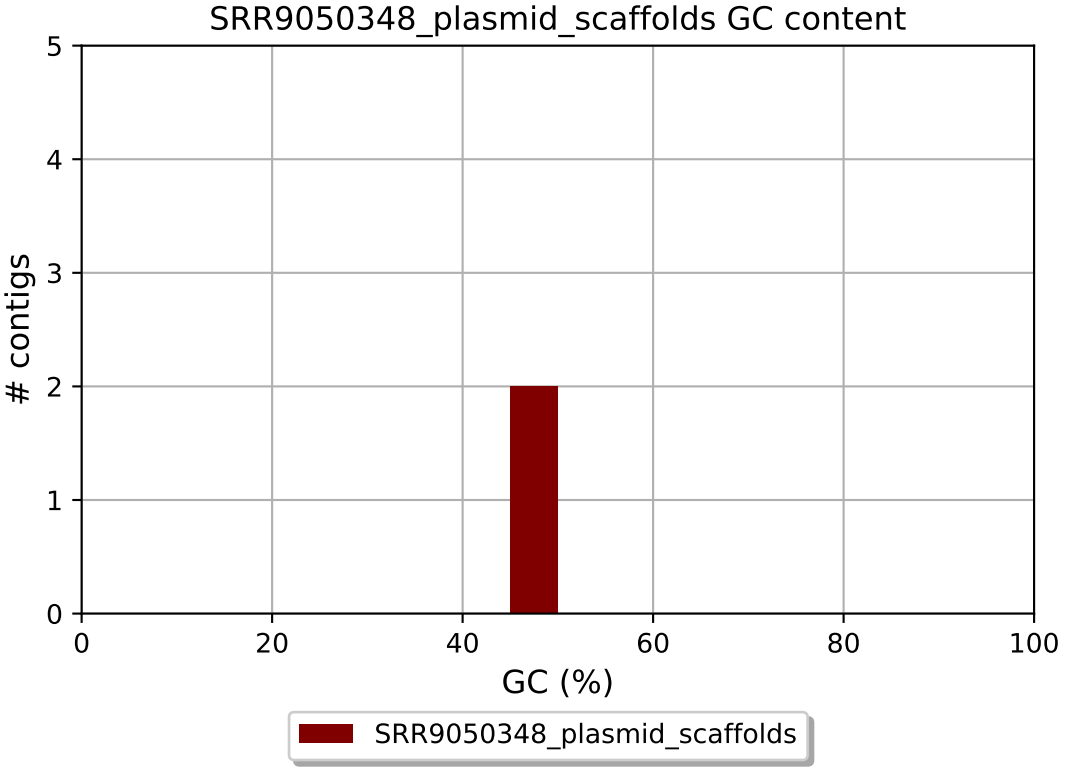

SRR11425846_plasmid_scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
SRR11425846_plasmid_scaffolds

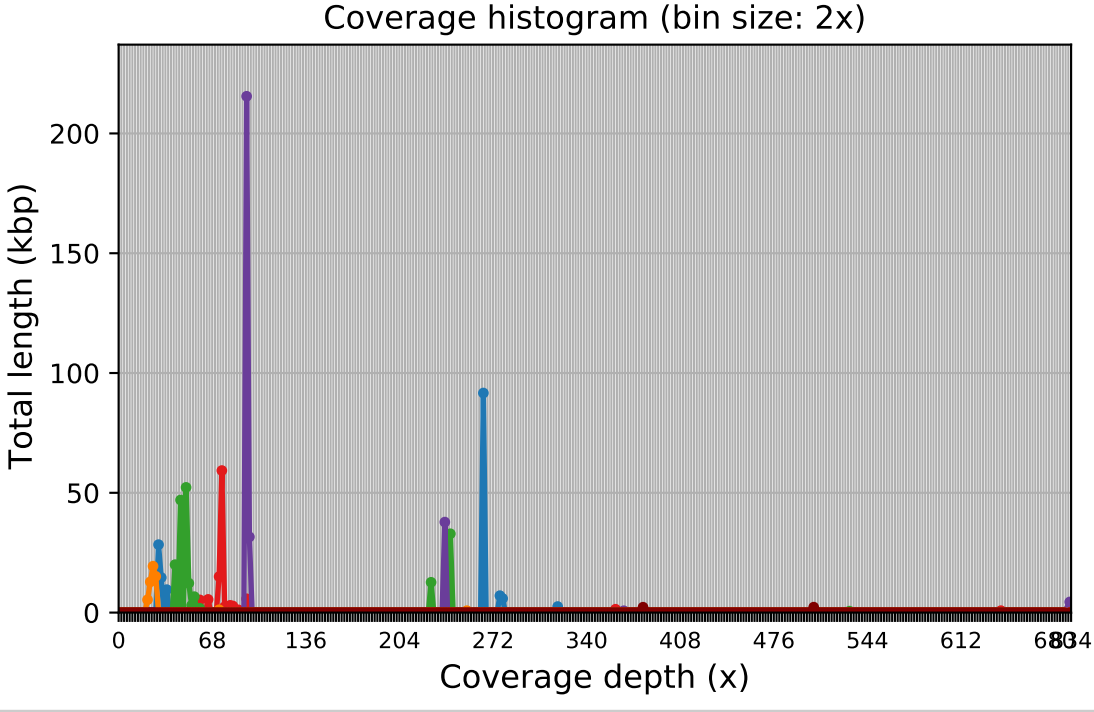

SRR1686737_plasmid_scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SRR1686737_plasmid_scaffolds

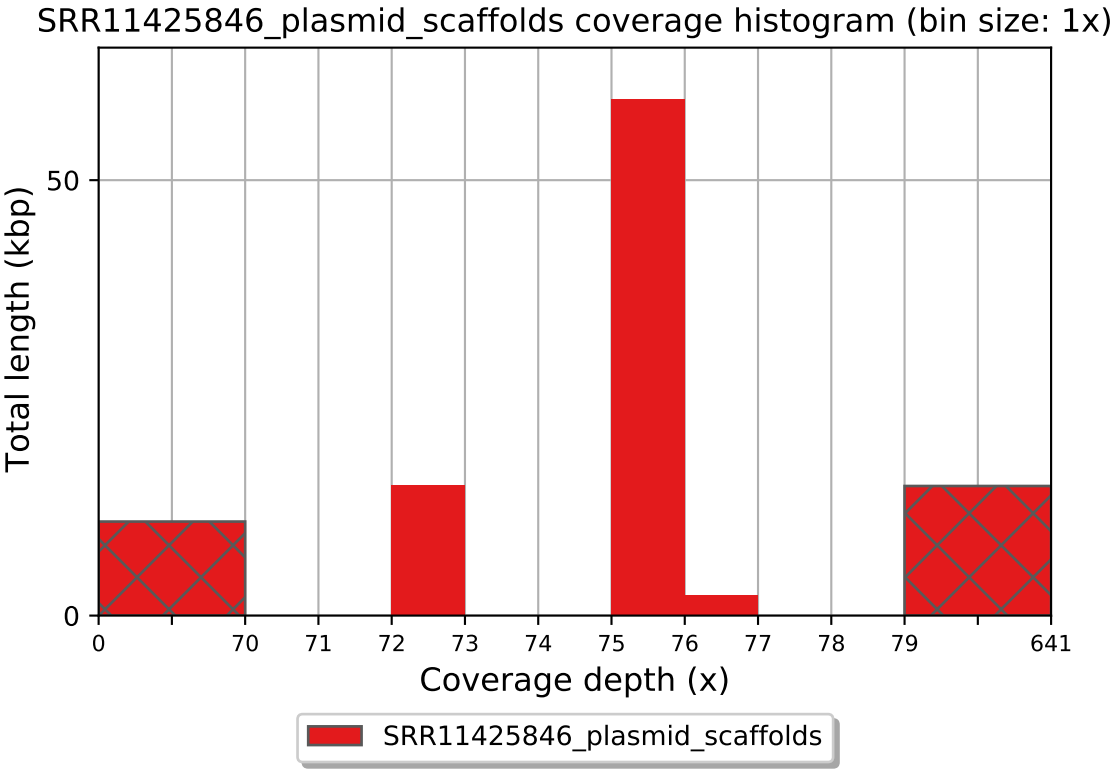

SRR1686740_plasmid_scaffolds GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
SRR1686740_plasmid_scaffolds

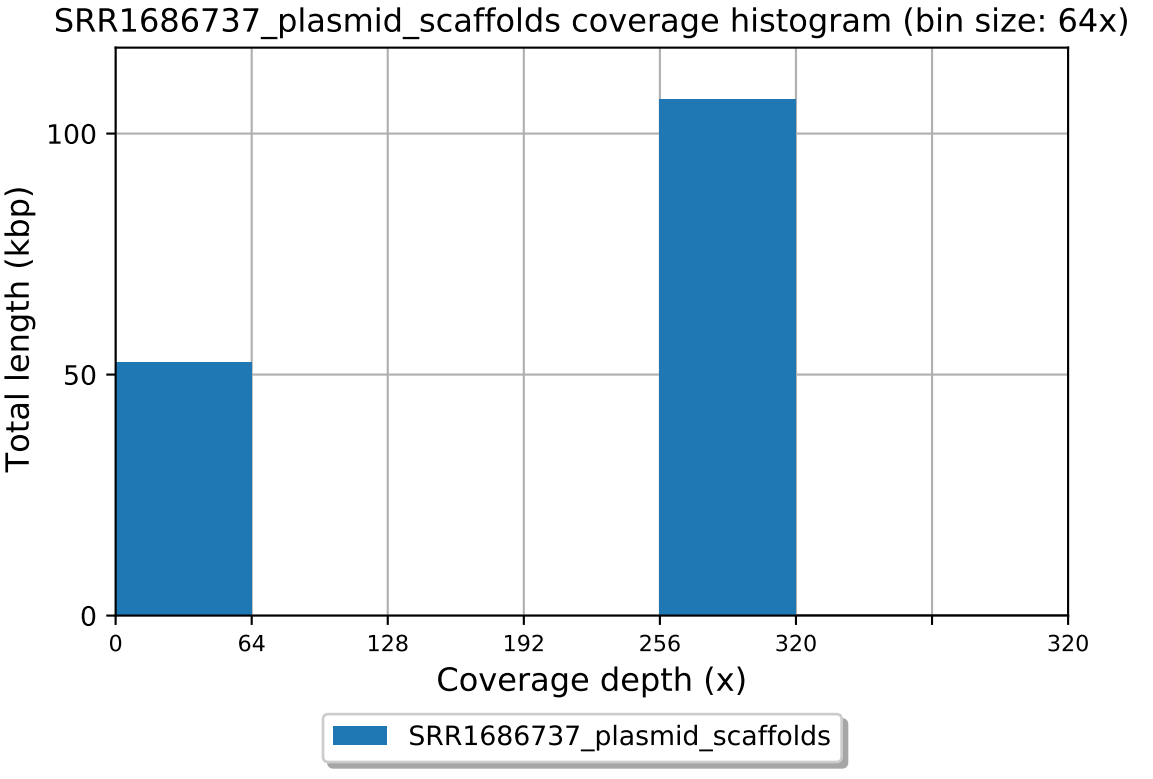

SRR3712208_plasmid_scaffolds GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
SRR3712208_plasmid_scaffolds

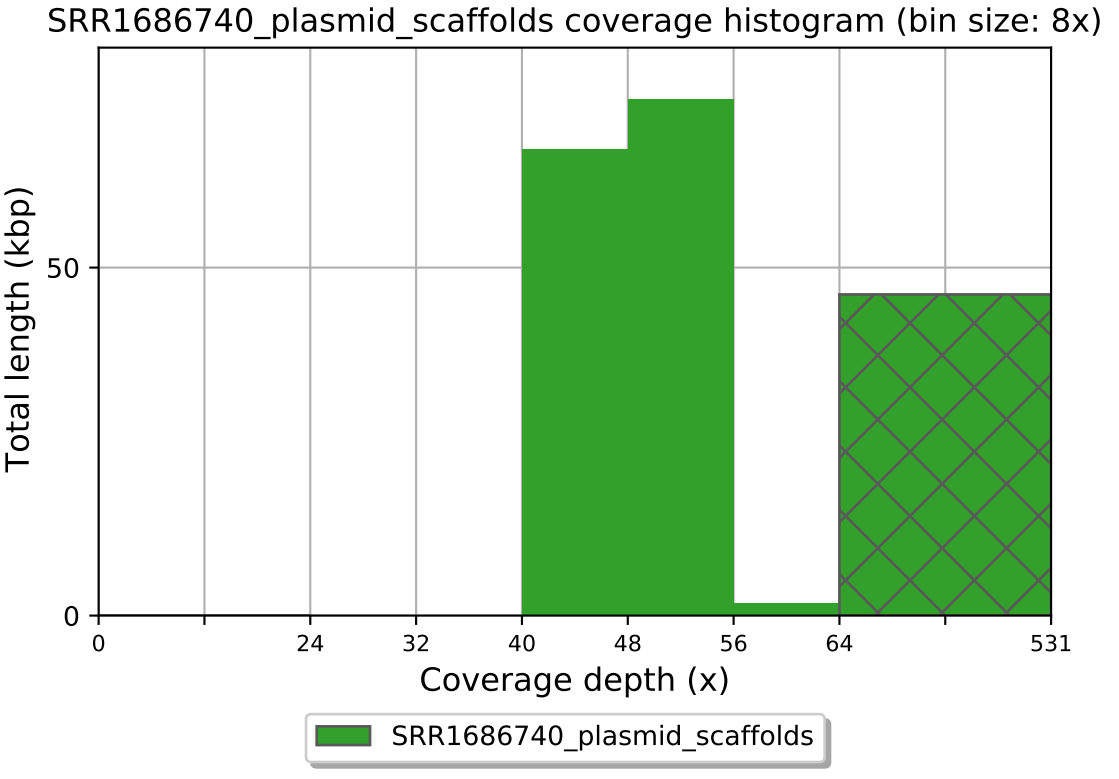

SRR8282855_plasmid_scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
6
0
20
40
60
80
100
SRR8282855_plasmid_scaffolds

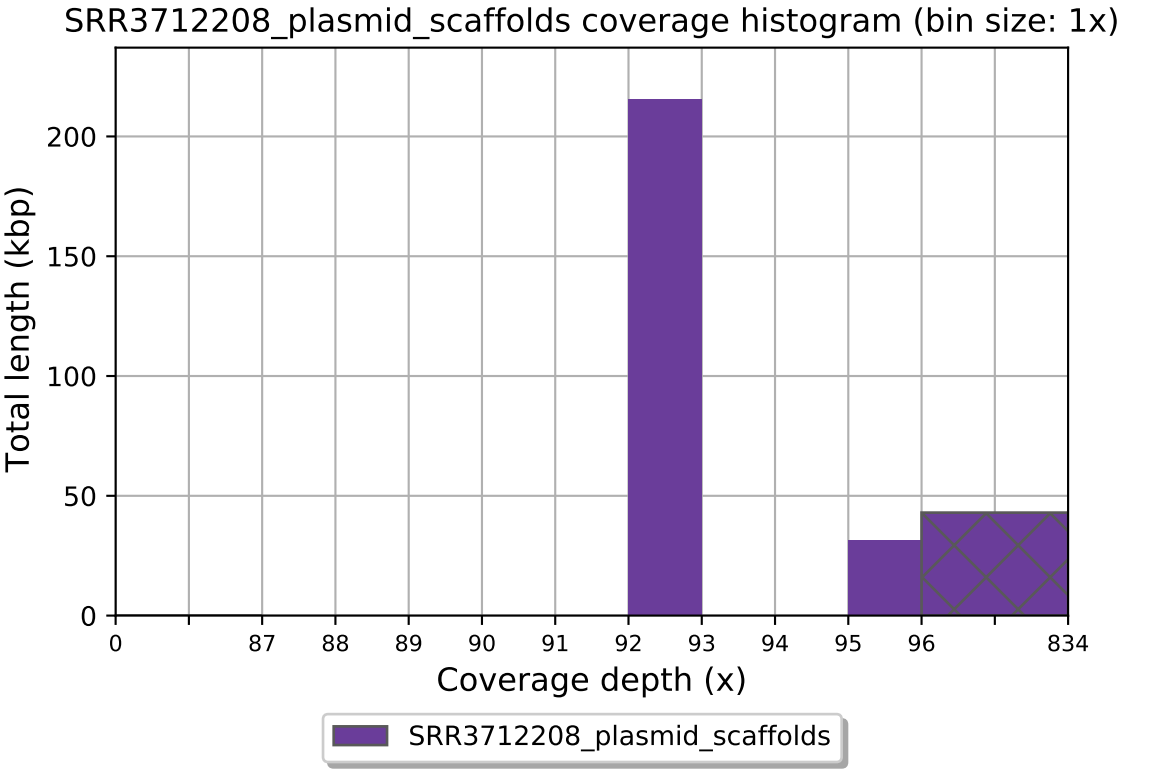

SRR9050348_plasmid_scaffolds GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
SRR9050348_plasmid_scaffolds

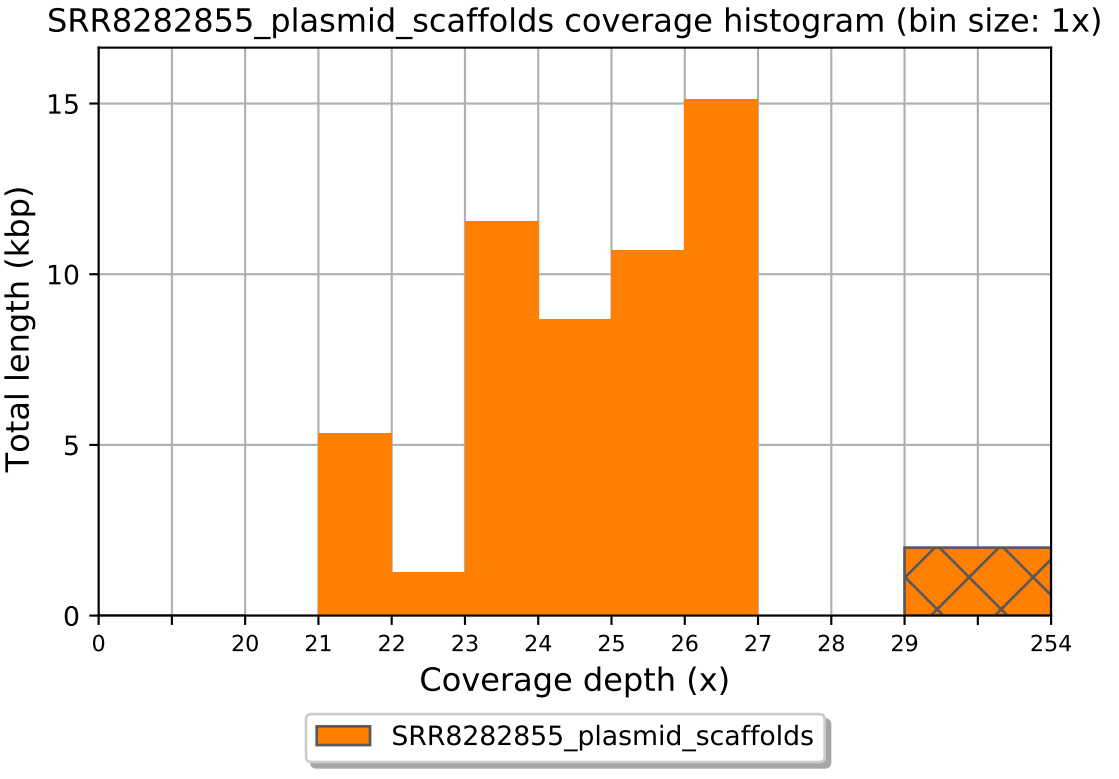

Coverage histogram (bin size: 2x)
Total length (kbp)
200
150
100
50
0
0
68
136
204
272
340
408
476
544
612
680
Coverage depth (x)
25846_plasmid_scaffolds
SRR1686740_plasmid_scaffolds
SRR8282855_pla
6737_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR9050348_pla

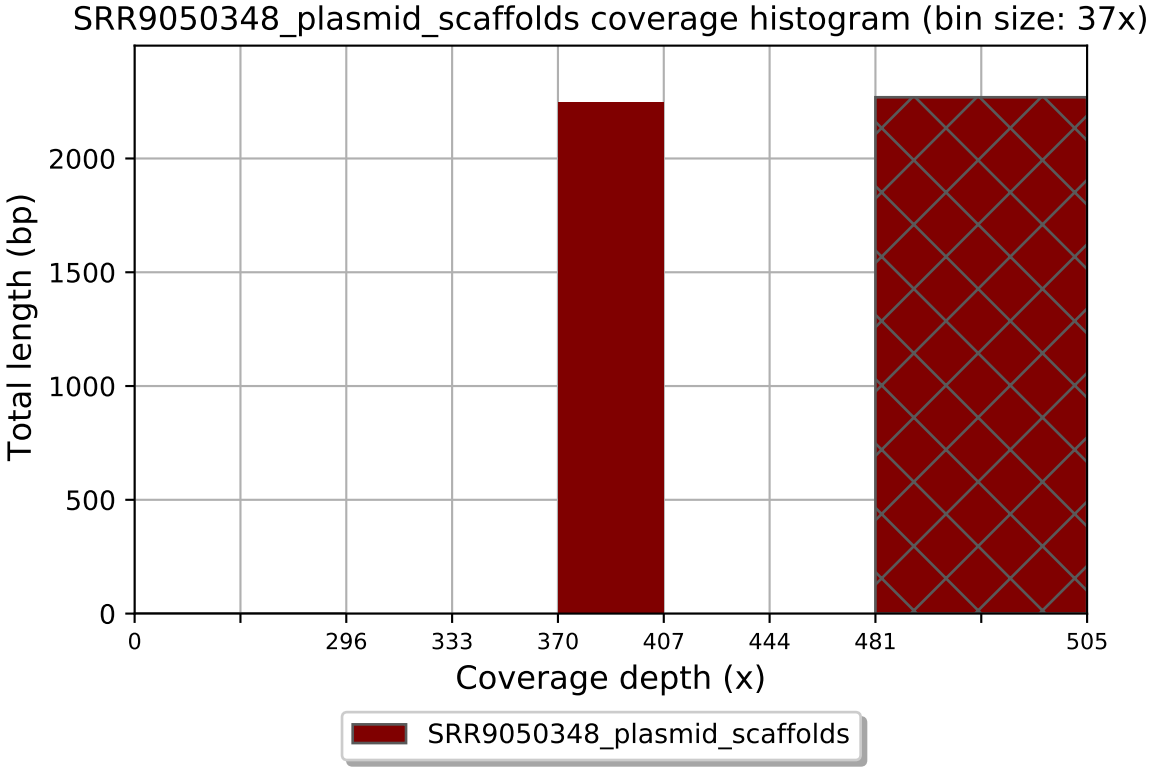

SRR11425846_plasmid_scaffolds coverage histogram (bin size: 1x)
Total length (kbp)
50
0
0
70
71
72
73
74
75
76
77
78
79
641
Coverage depth (x)
SRR11425846_plasmid_scaffolds

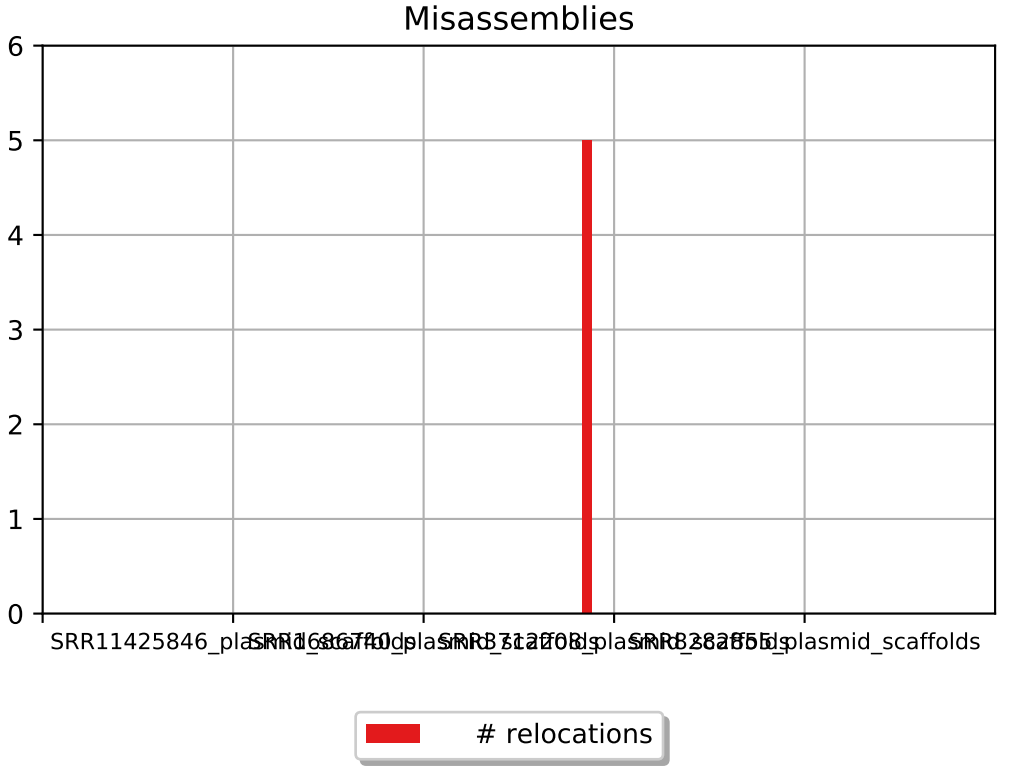

SRR1686737_plasmid_scaffolds coverage histogram (bin size: 64x)
Total length (kbp)
100
50
0
0
64
128
192
256
320
320
Coverage depth (x)
SRR1686737_plasmid_scaffolds

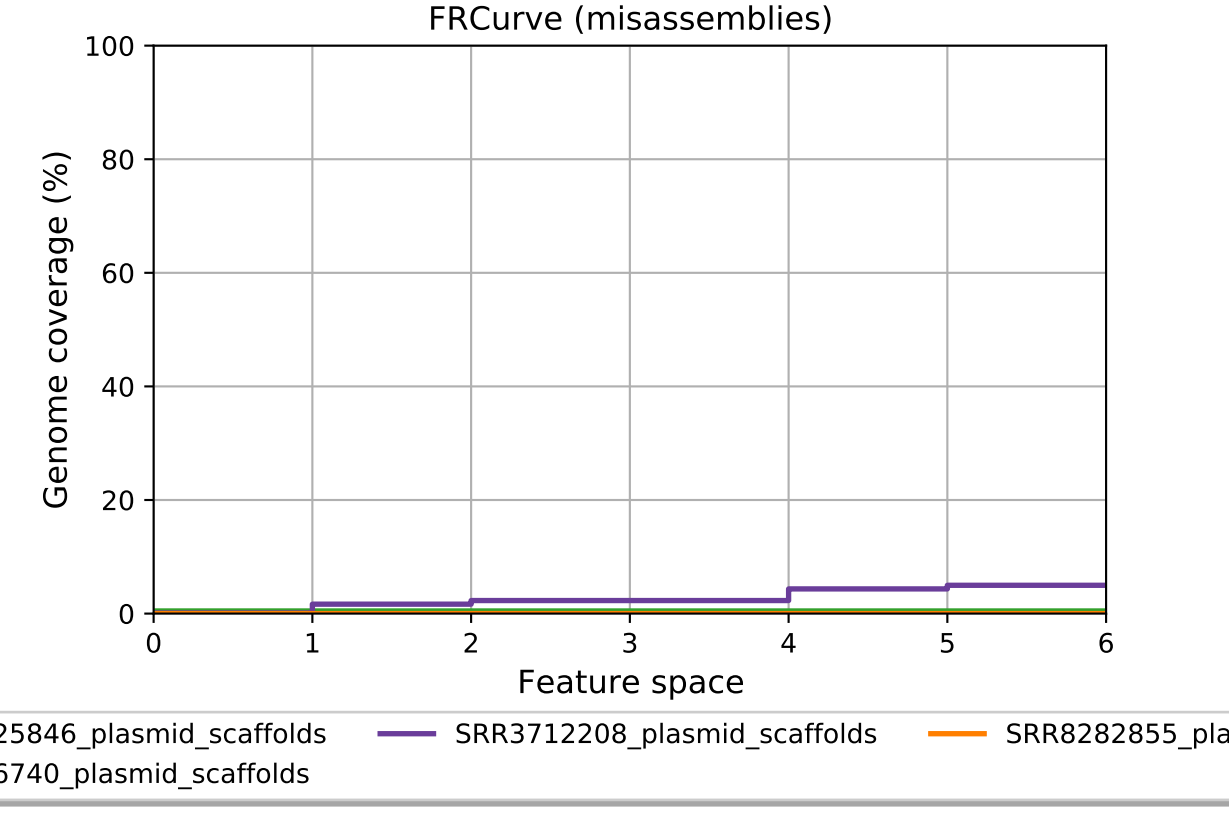

SRR1686740_plasmid_scaffolds coverage histogram (bin size: 8x)
Total length (kbp)
50
0
0
24
32
40
48
56
64
531
Coverage depth (x)
SRR1686740_plasmid_scaffolds

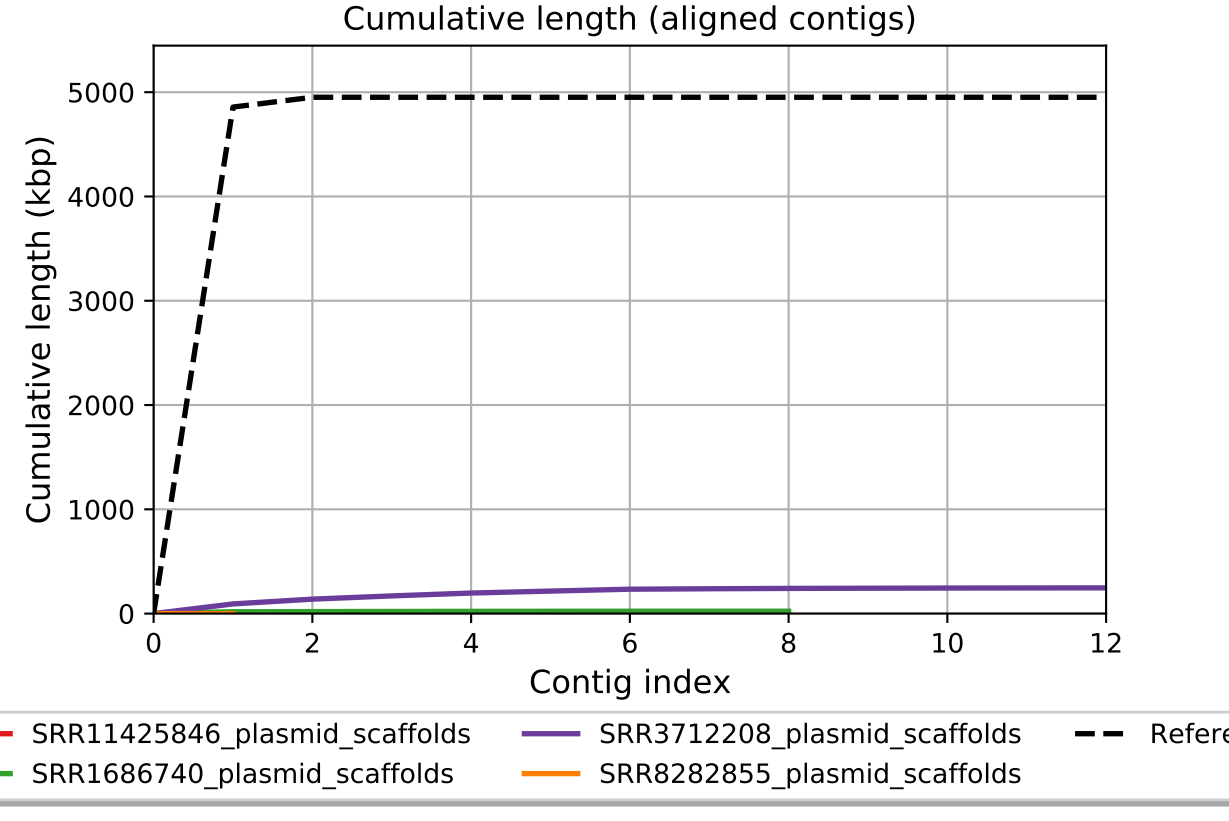

SRR3712208_plasmid_scaffolds coverage histogram (bin size: 1x)
Total length (kbp)
0
50
100
150
200
0
87
88
89
90
91
92
93
94
95
96
834
Coverage depth (x)
SRR3712208_plasmid_scaffolds

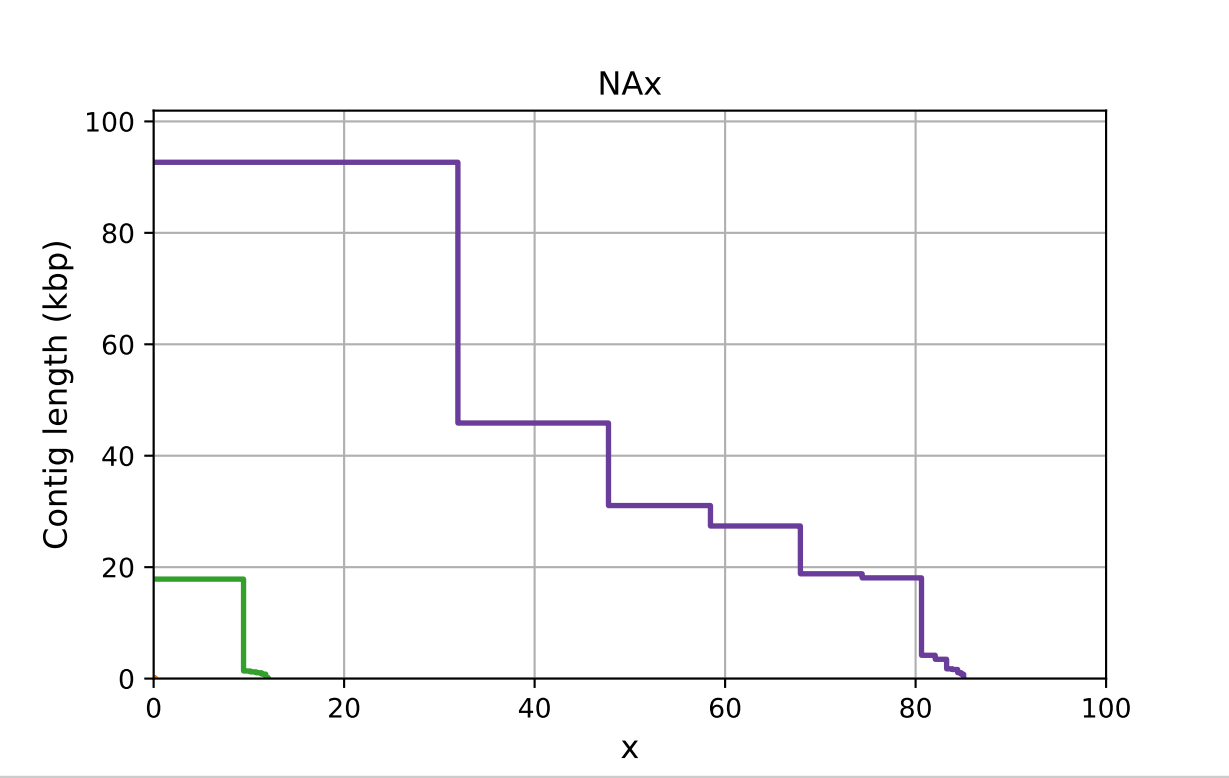

SRR8282855_plasmid_scaffolds coverage histogram (bin size: 1x)
Total length (kbp)
0
5
10
15
0
20
21
22
23
24
25
26
27
28
29
254
Coverage depth (x)
SRR8282855_plasmid_scaffolds

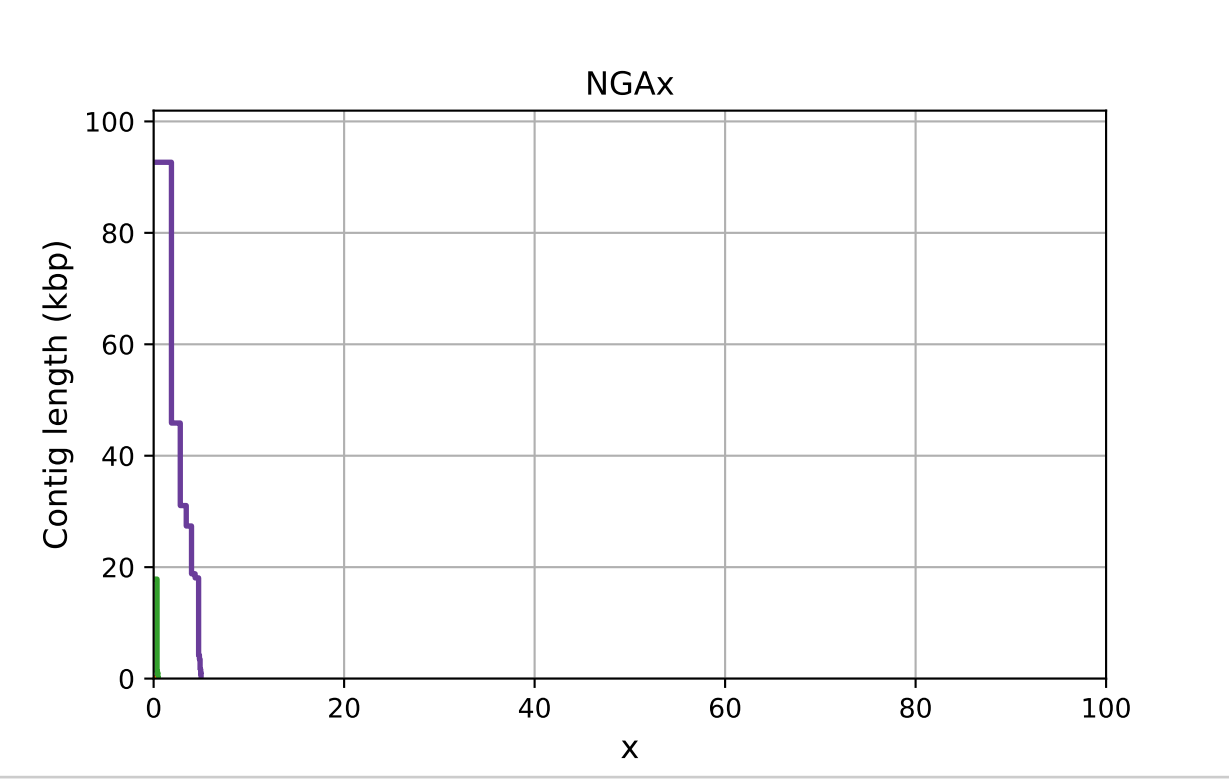

SRR9050348_plasmid_scaffolds coverage histogram (bin size: 37x)
Total length (bp)
2000
1500
1000
500
0
0
296
333
370
407
444
481
505
Coverage depth (x)
SRR9050348_plasmid_scaffolds

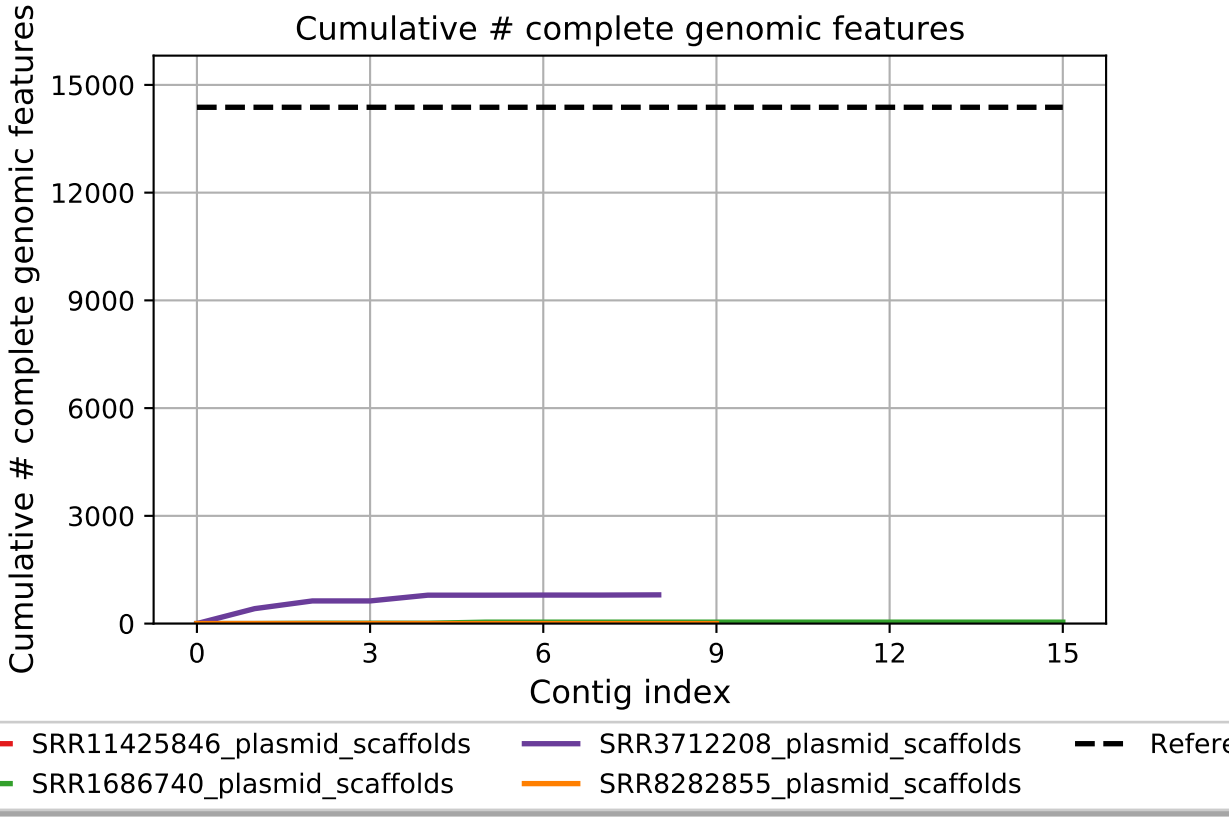

Misassemblies
6
5
4
3
2
1
0
SRR11425846_plasmid_scaffolds
SRR11686740_plasmid_scaffolds
SRR37122708_plasmid_scaffolds
SRR3282855_plasmid_scaffolds
relocations

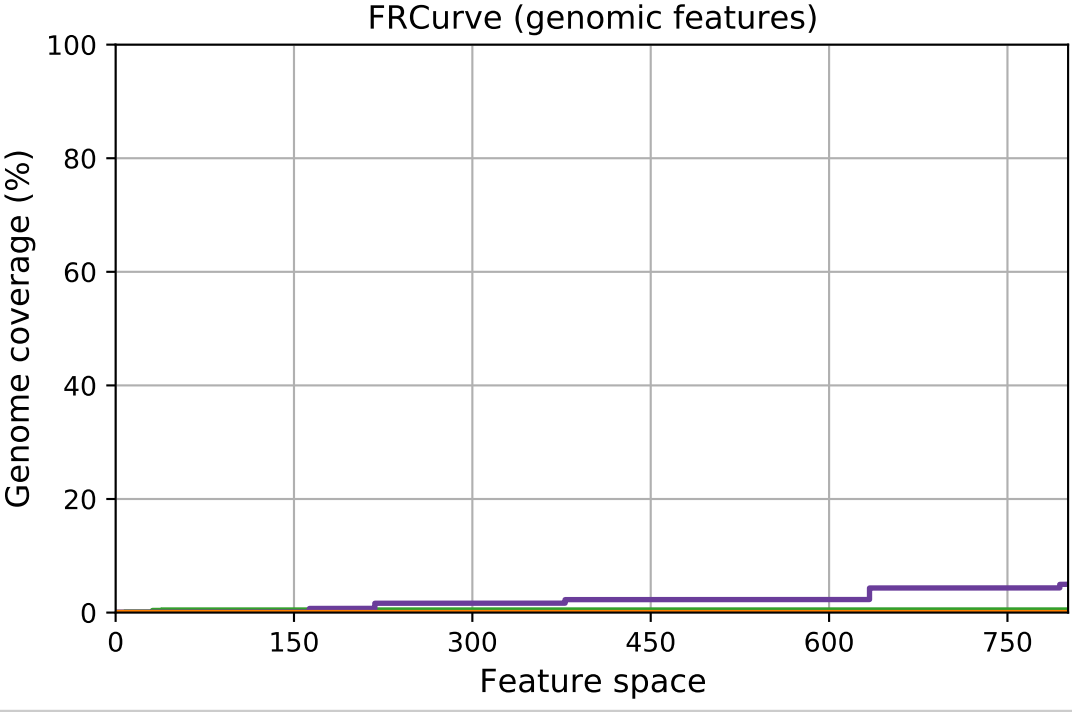

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
Feature space
25846_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_pla
6740_plasmid_scaffolds

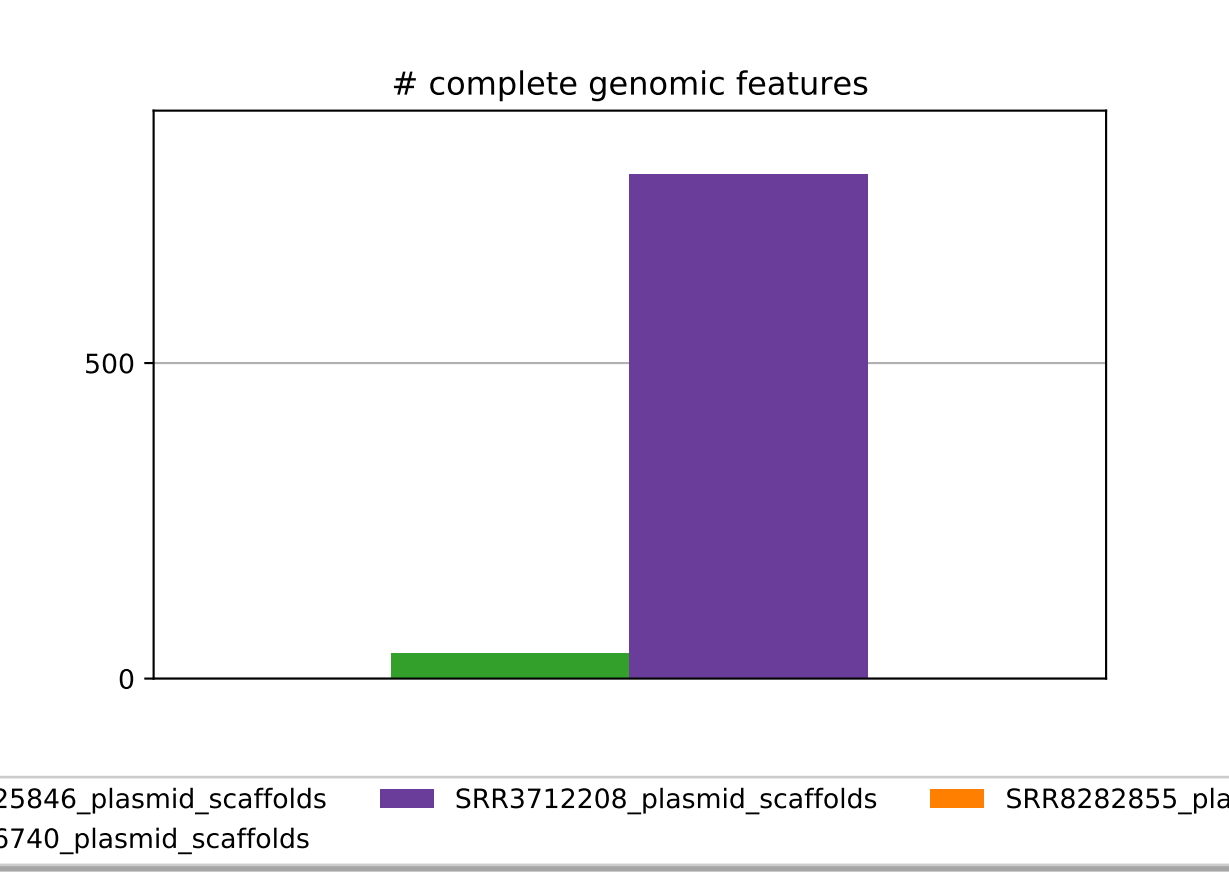

Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
2
4
6
8
10
12
Contig index
SRR11425846_plasmid_scaffolds
SRR1686740_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_plasmid_scaffolds
Refere

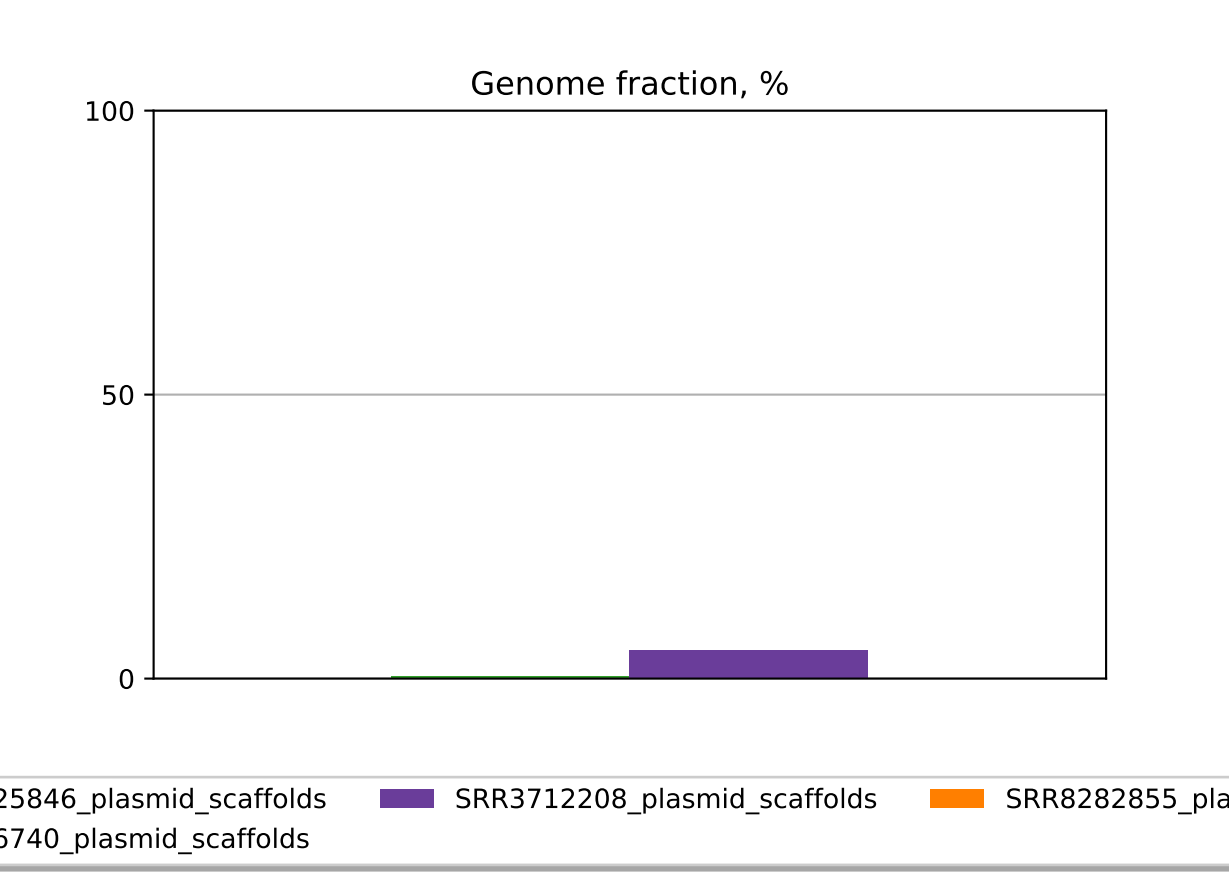

NAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
25846_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_pla
6740_plasmid_scaffolds


NGAx
Contig length (kbp)
0
20
40
60
80
100
x
25846_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_pla
6740_plasmid_scaffolds


Cumulative # complete genomic features
Cumulative # complete genomic features
15000
12000
9000
6000
3000
0
0
3
6
9
12
15
Contig index
SRR11425846_plasmid_scaffolds
SRR1686740_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_plasmid_scaffolds
Refere


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
150
300
450
600
750
Feature space
25846_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_pla
6740_plasmid_scaffolds


complete genomic features
500
0
25846_plasmid_scaffolds
SRR3712208_plasmid_scaffolds
SRR8282855_pla
6740_plasmid_scaffolds


Genome fraction, %
100
50
0
25846_plasmid_scaffolds
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