Report

	SPAdes_on_data_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# contigs (>= 0 bp)	167	-
# contigs (>= 1000 bp)	58	72
Total length (>= 0 bp)	5453454	-
Total length (>= 1000 bp)	5425313	5423725
# contigs	69	83
Largest contig	465590	309958
Total length	5432836	5431248
Reference length	5682322	5682322
GC (%)	57.24	57.24
Reference GC (%)	57.12	57.12
N50	193741	170161
NG50	181027	146373
N90	76558	56469
NG90	55995	48788
auN	214080.7	153007.6
auNG	204681.3	146246.9
L50	10	13
LG50	11	14
L90	28	37
LG90	31	41
# misassemblies	70	69
# misassembled contigs	25	31
Misassembled contigs length	4446145	4146482
# local misassemblies	29	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	2	2
# unaligned contigs	20 + 29 part	20 + 33 part
Unaligned length	659382	658461
Genome fraction (%)	84.010	84.576
Duplication ratio	1.001	1.001
# N's per 100 kbp	27.61	0.00
# mismatches per 100 kbp	685.44	688.06
# indels per 100 kbp	18.95	19.28
# genomic features	9535 + 153 part	9534 + 183 part
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	205341	205341
Total aligned length	4771381	4770640
NA50	70102	60829
NGA50	66625	59533
NA90	-	-
NGA90	-	-
auNA	81733.0	72909.0
auNGA	78144.5	69687.5
LA50	24	27
LGA50	26	29
LA90	-	-
LGA90	-	-

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

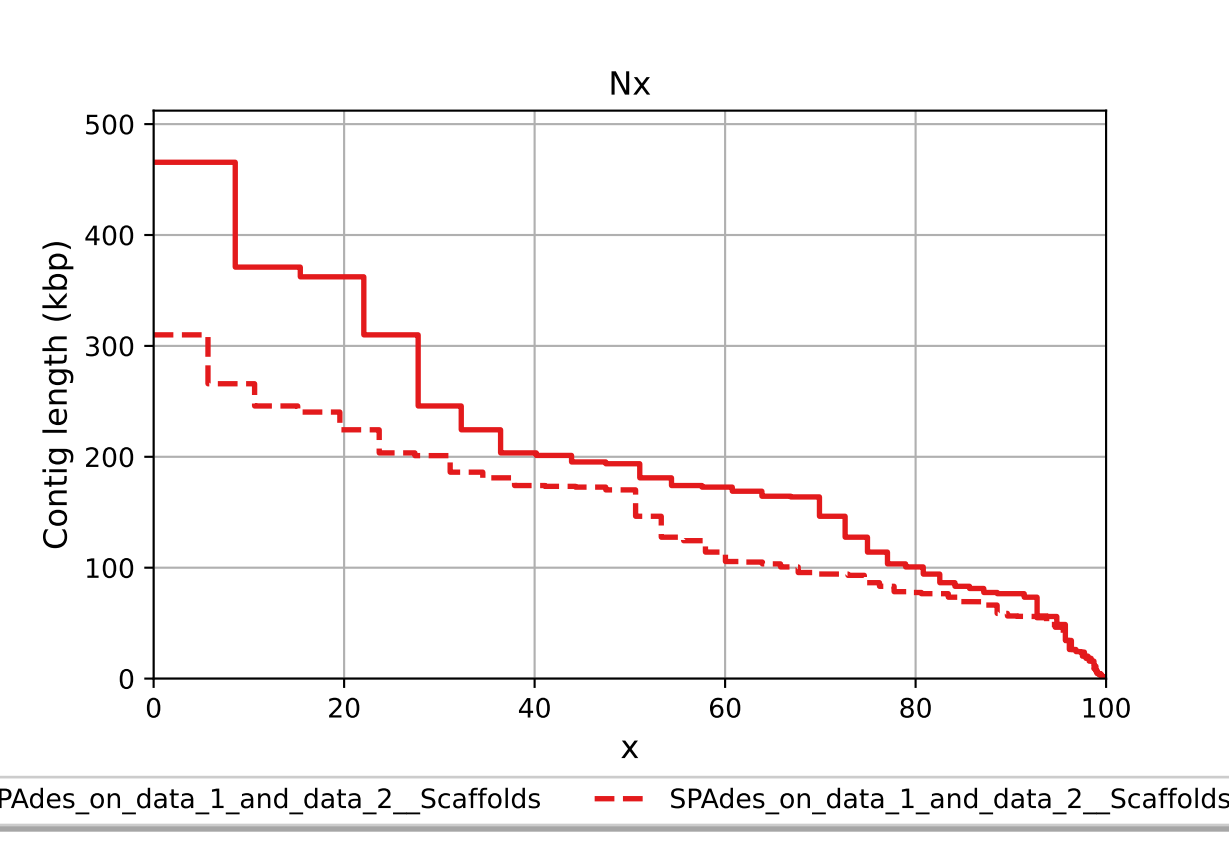
	SPAdes_on_data_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# misassemblies	70	69
# contig misassemblies	69	69
# c. relocations	69	69
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	25	31
Misassembled contigs length	4446145	4146482
# local misassemblies	29	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	2	2
# mismatches	32705	32825
# indels	904	920
# indels (<= 5 bp)	818	842
# indels (> 5 bp)	86	78
Indels length	7062	5915

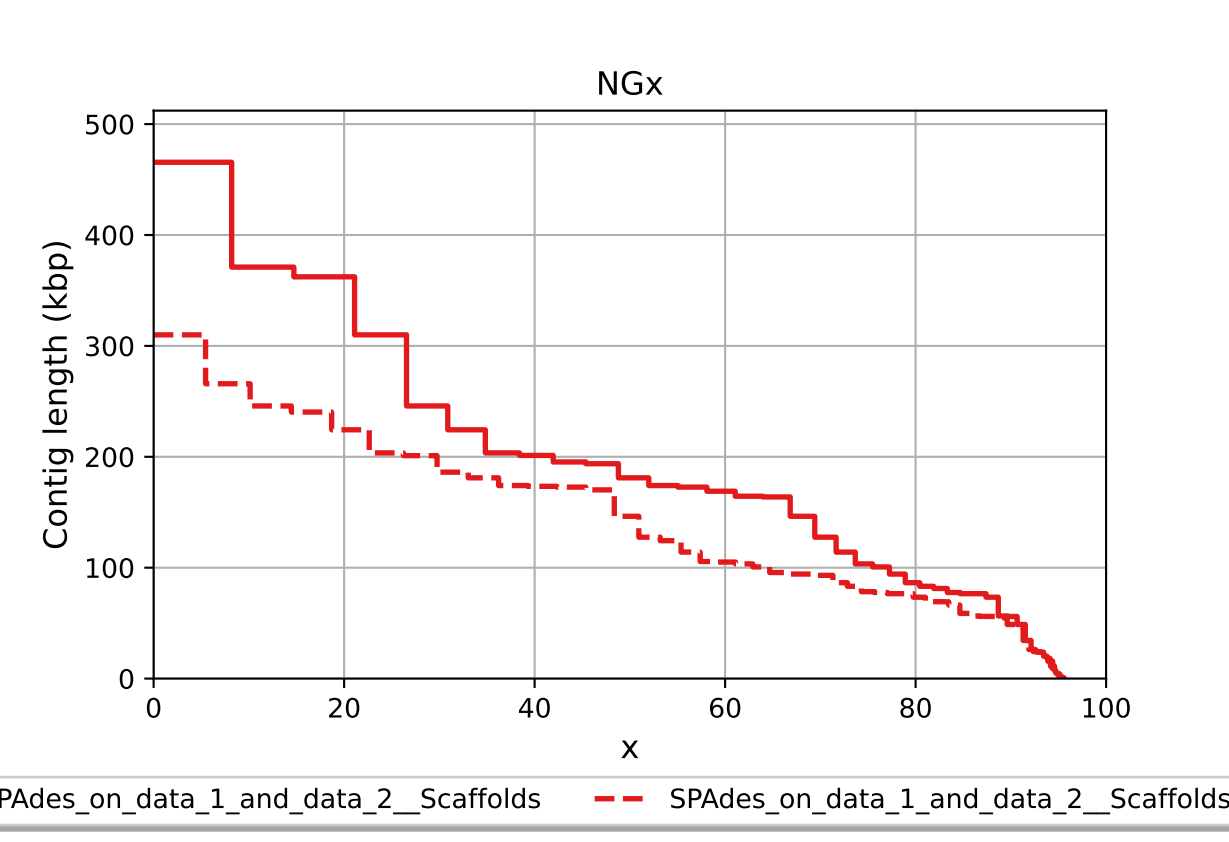
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

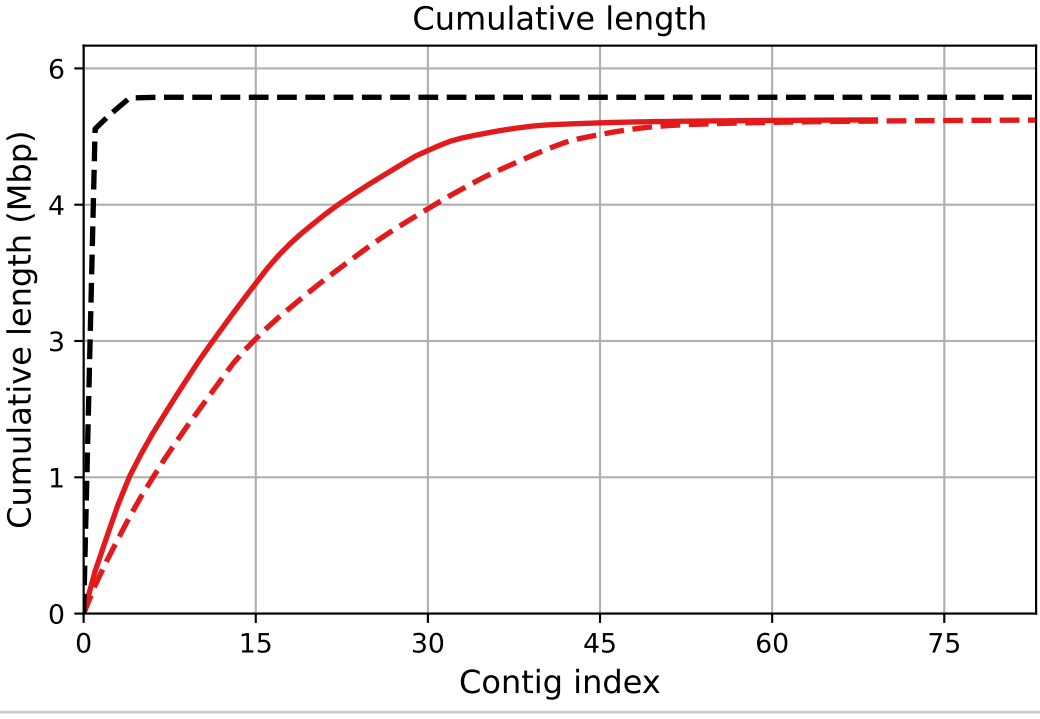
Unaligned report

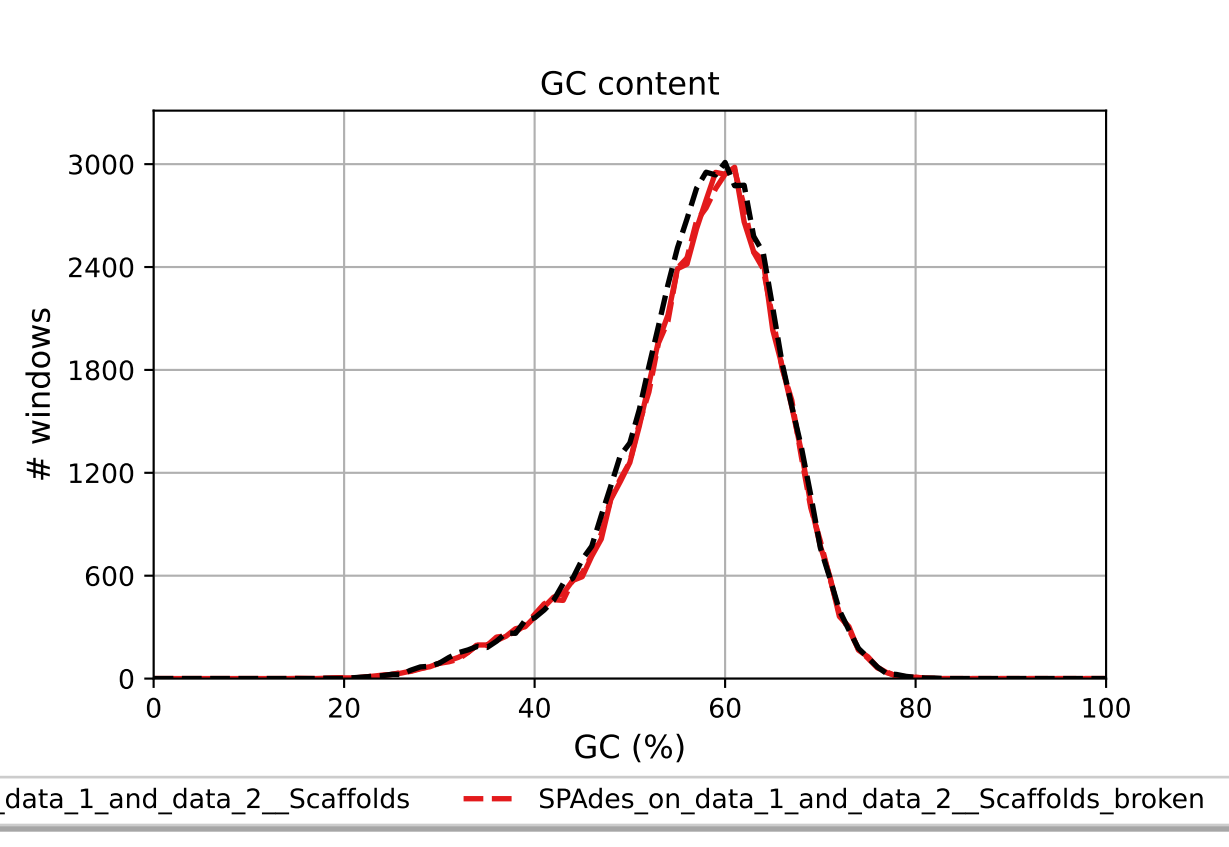
	SPAdes_on_data_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# fully unaligned contigs	20	20
Fully unaligned length	49687	49687
# partially unaligned contigs	29	33
Partially unaligned length	609695	608774
# N's	1500	0

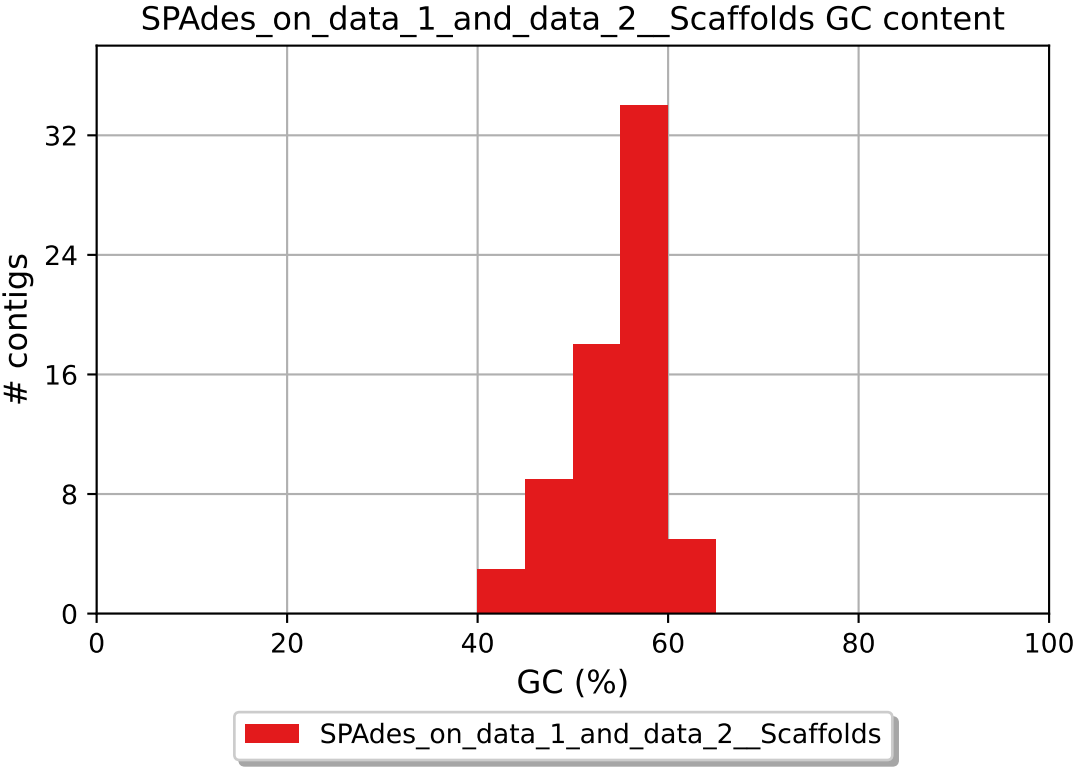
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

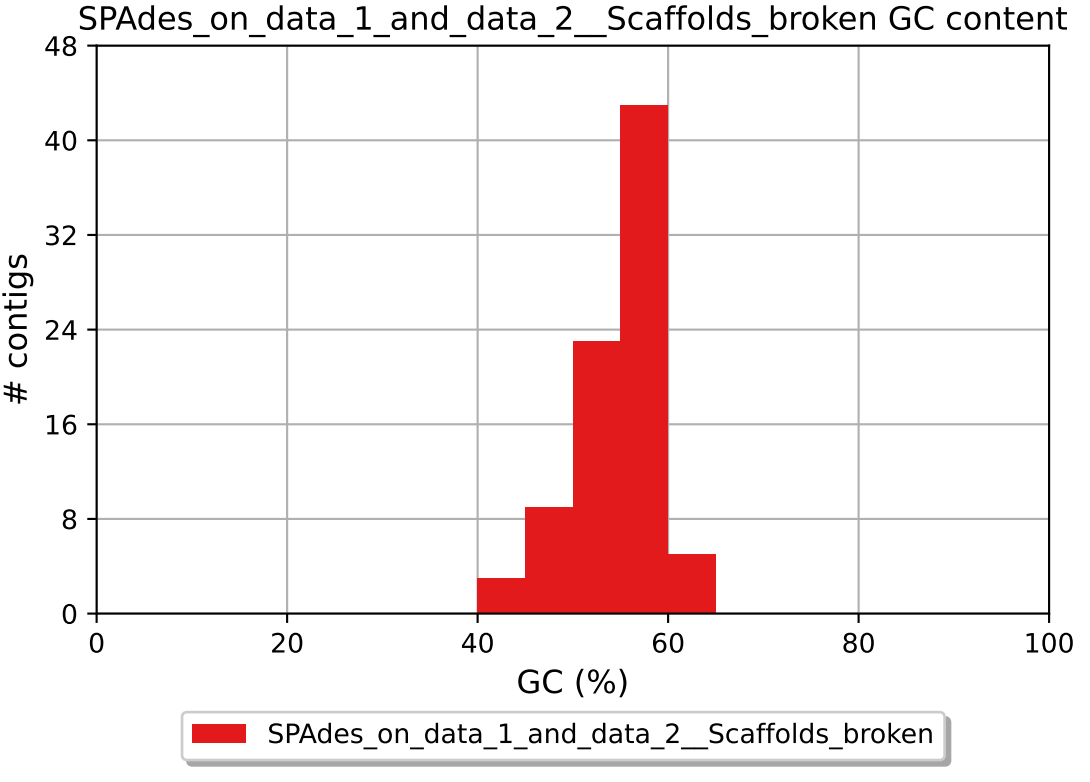

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds

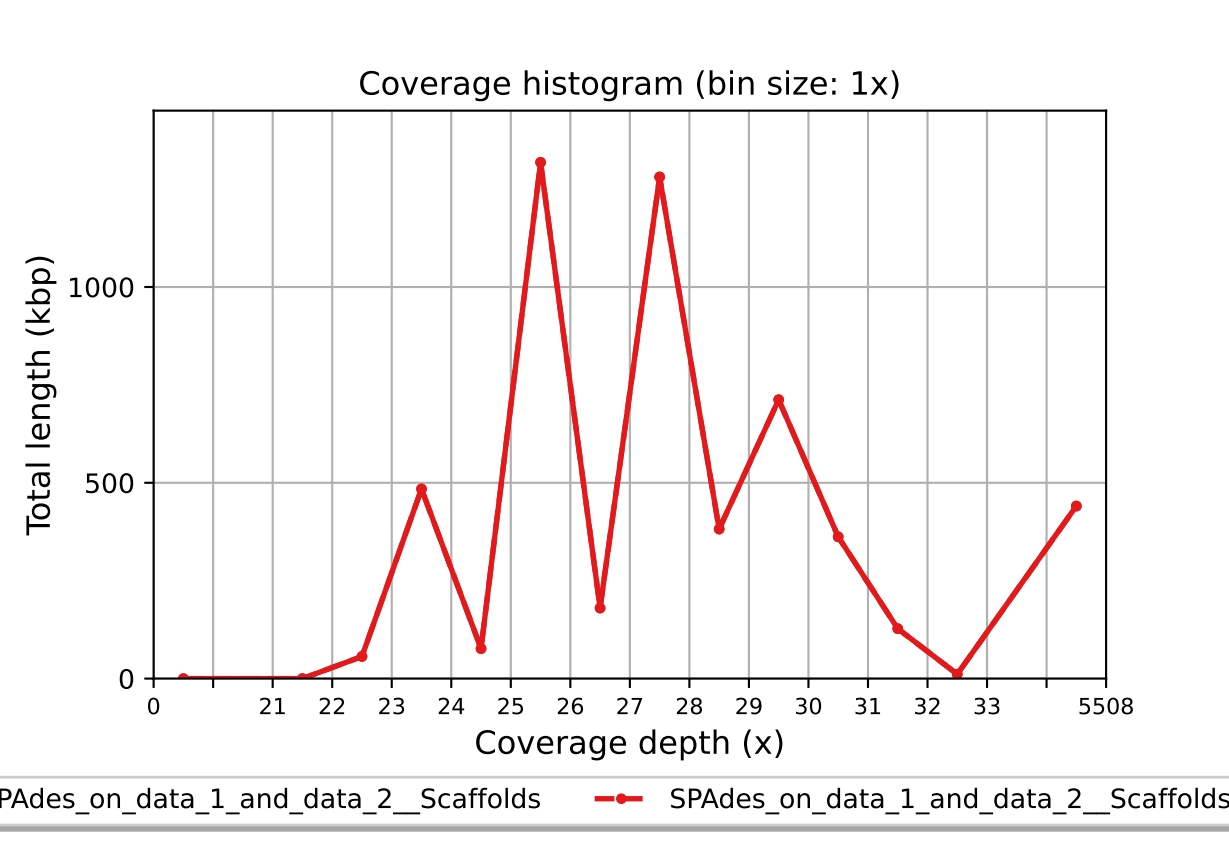

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds

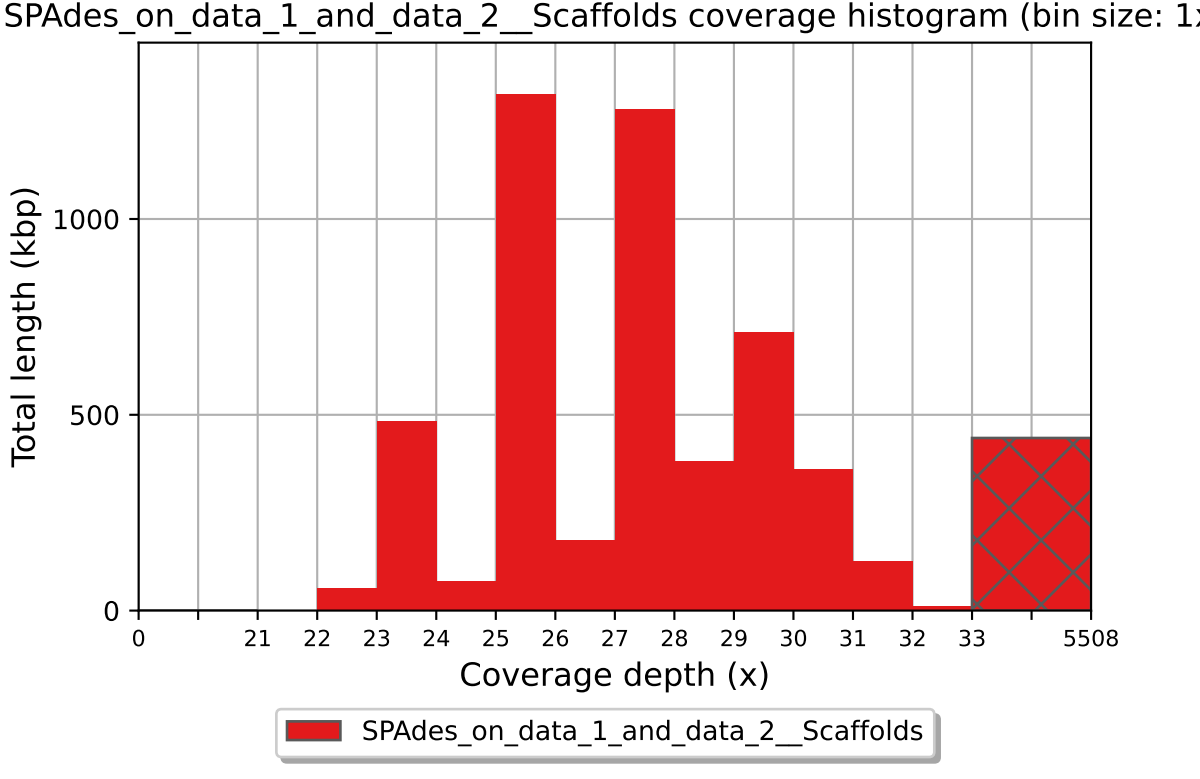

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
3
4
6
0
15
30
45
60
75
_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds_broken

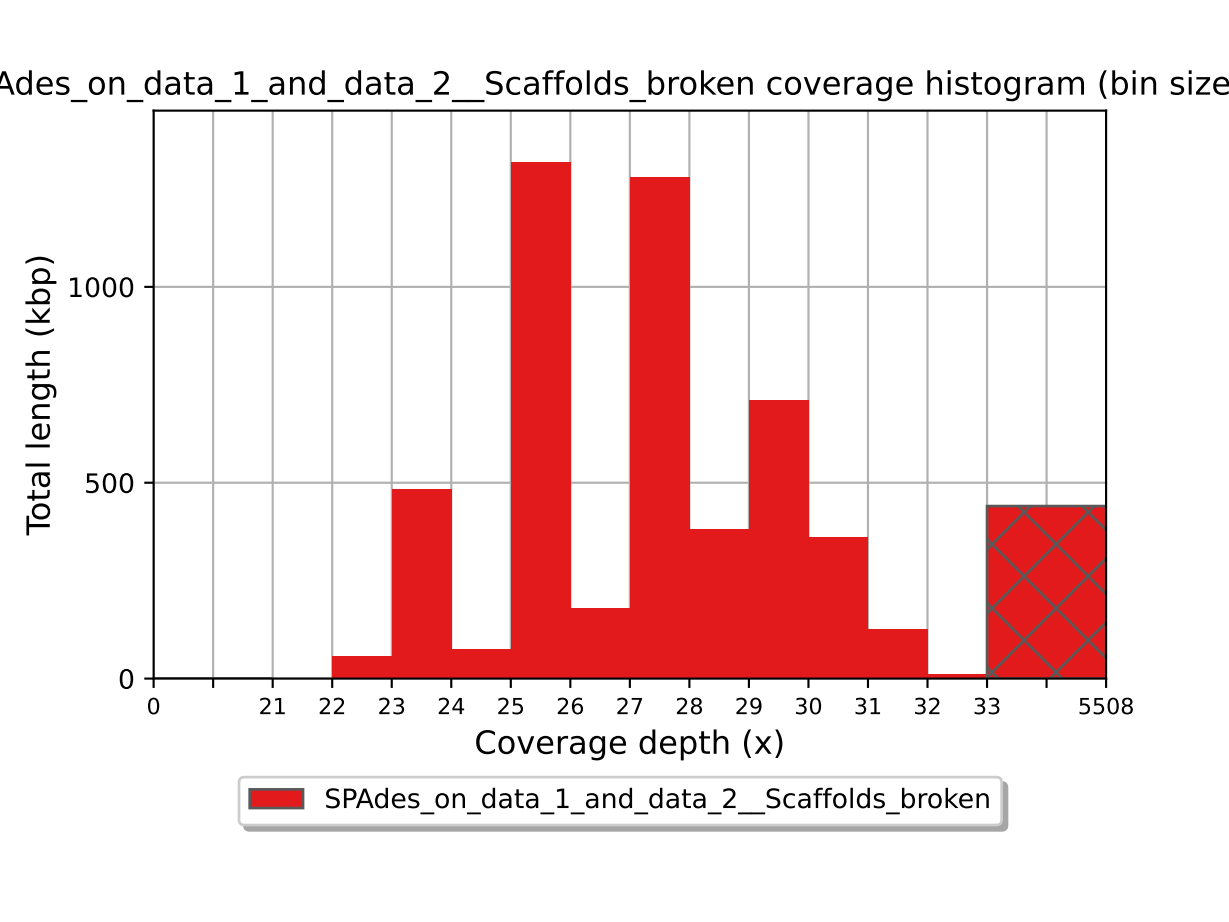

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds_broken

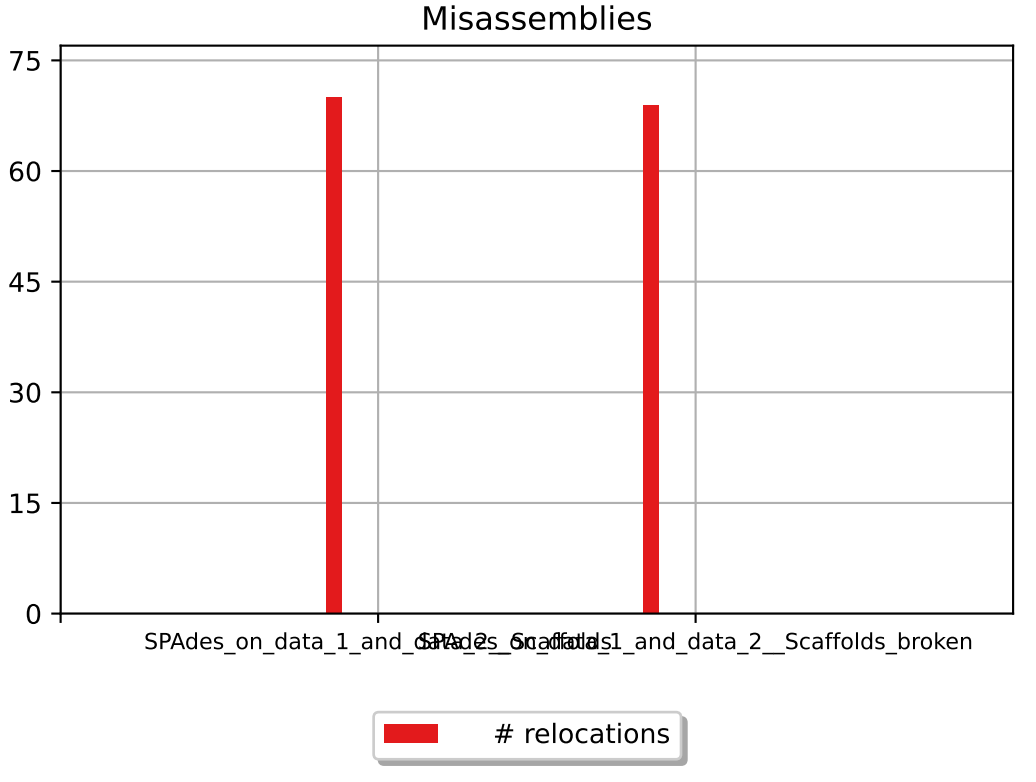

SPAdes_on_data_1_and_data_2__Scaffolds GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
SPAdes_on_data_1_and_data_2__Scaffolds

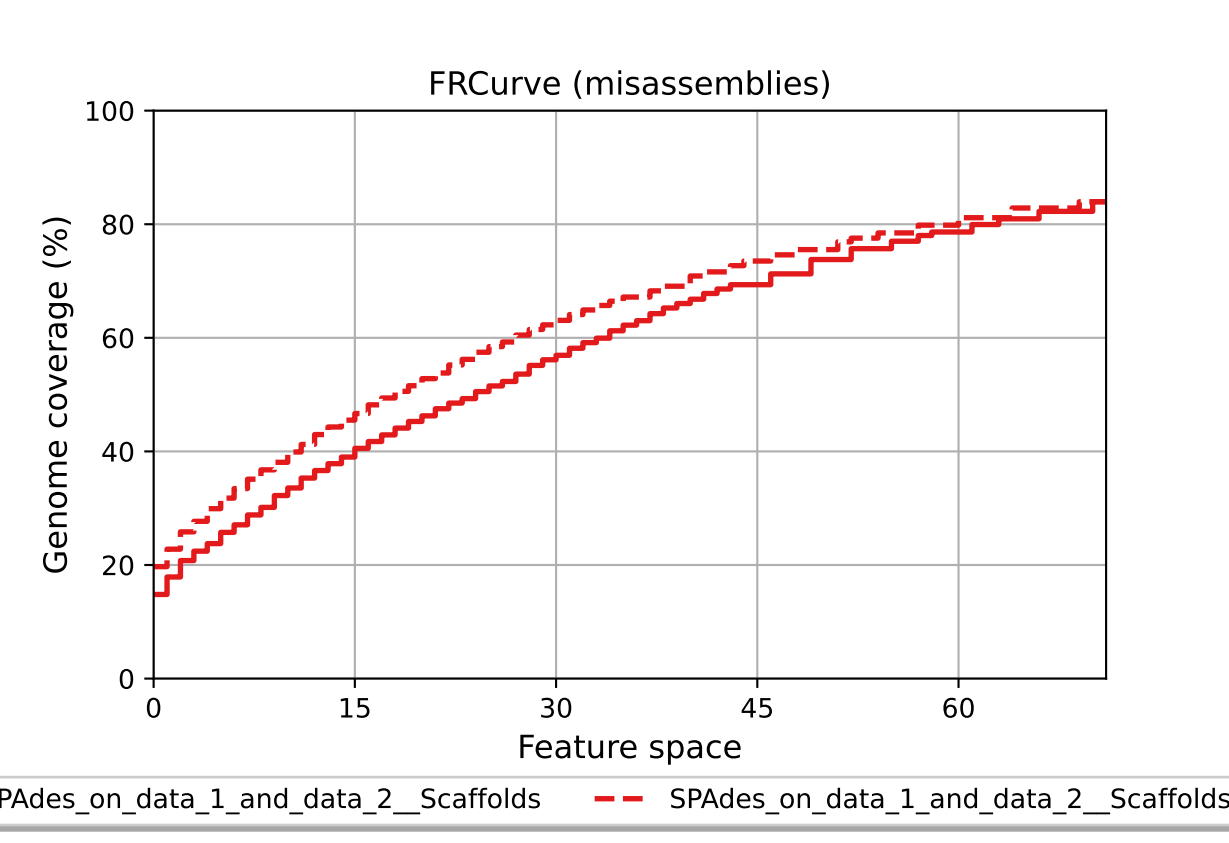

SPAdes_on_data_1_and_data_2__Scaffolds_broken GC content
48
40
32
24
16
8
0
contigs
0
20
40
60
80
100
GC (%)
SPAdes_on_data_1_and_data_2__Scaffolds_broken

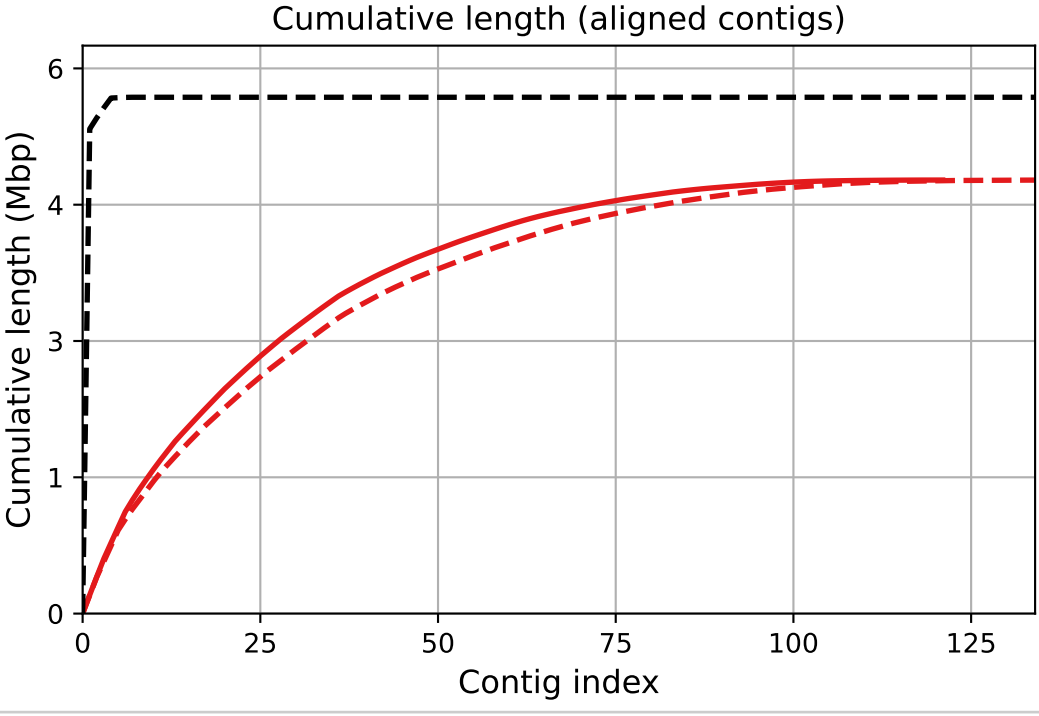

Coverage histogram (bin size: 1x)
Total length (kbp)
1000
500
0
0
21
22
23
24
25
26
27
28
29
30
31
32
33
5508
Coverage depth (x)
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds

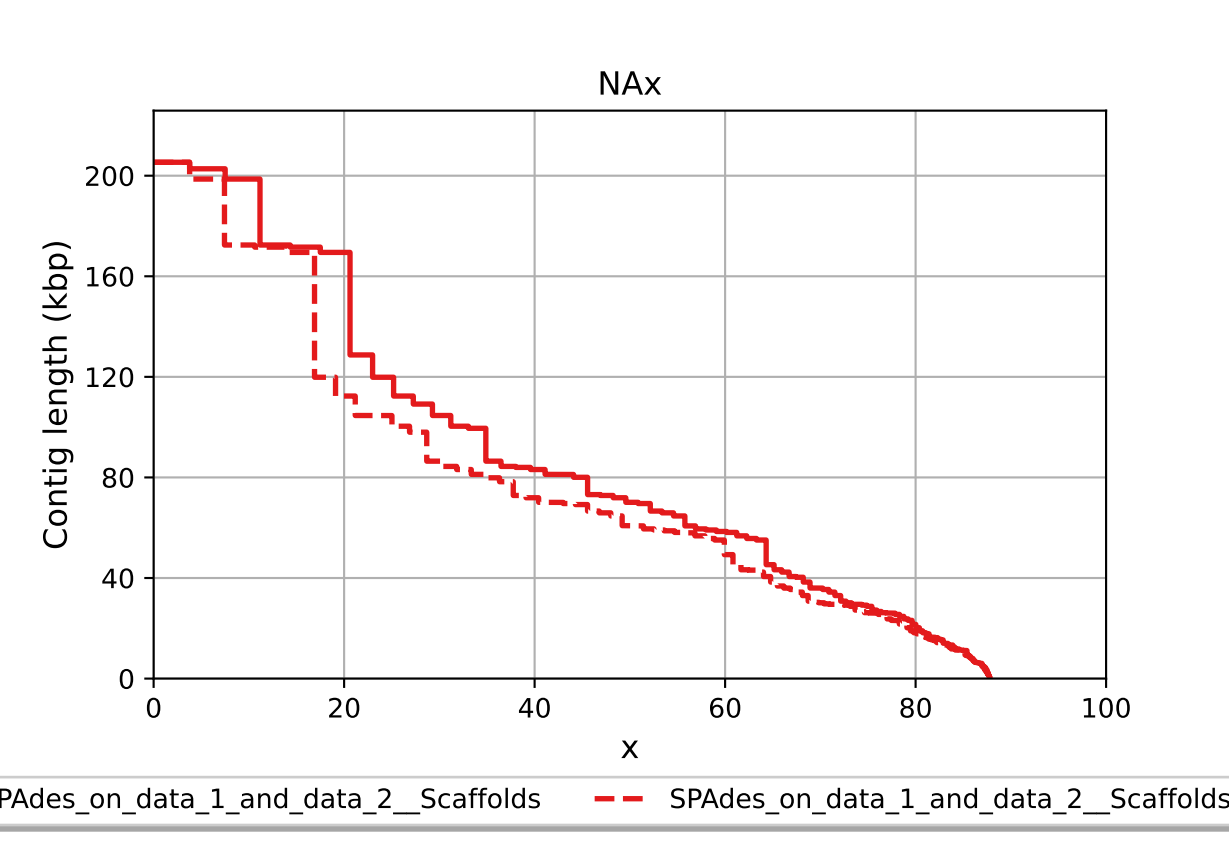

SPAdes_on_data_1_and_data_2__Scaffolds coverage histogram (bin size: 1x
Total length (kbp)
1000
500
0
0
21
22
23
24
25
26
27
28
29
30
31
32
33
5508
Coverage depth (x)
SPAdes_on_data_1_and_data_2__Scaffolds

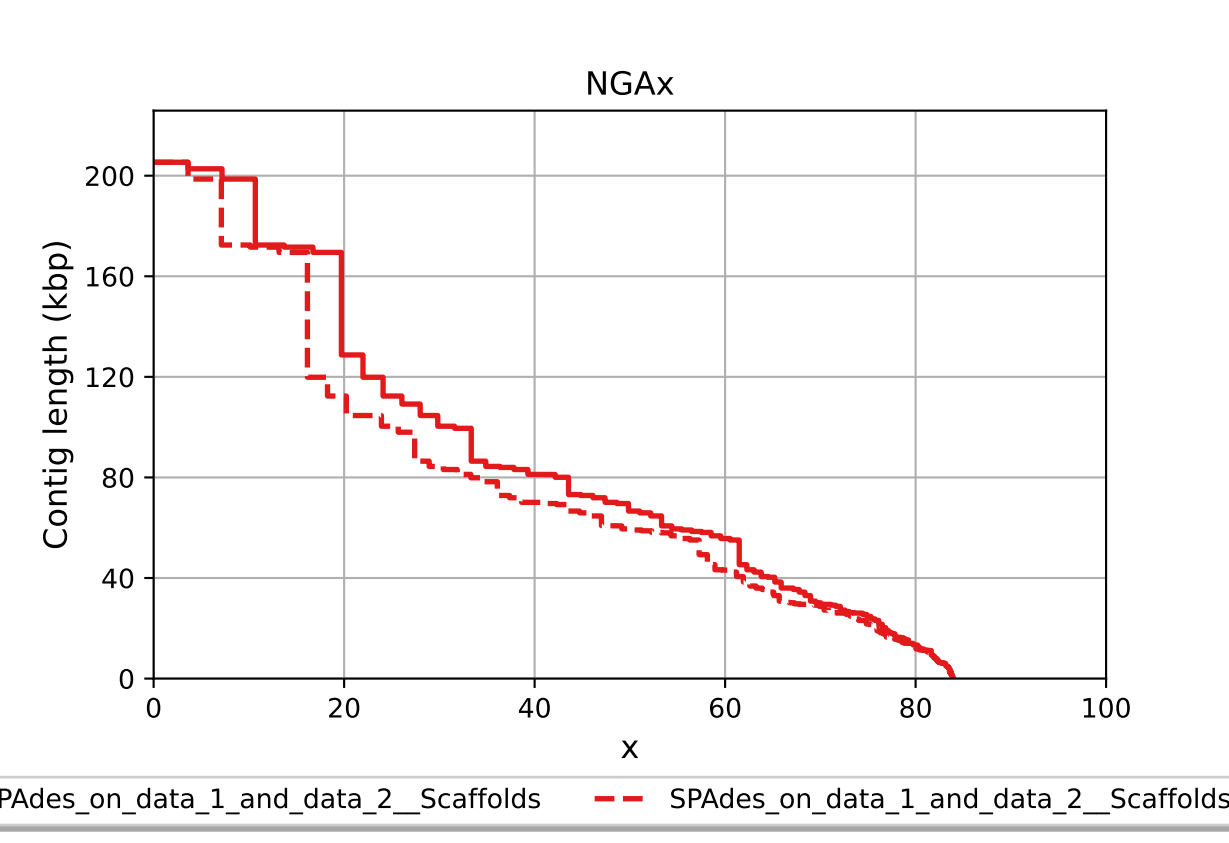

Ades_on_data_1_and_data_2__Scaffolds_broken coverage histogram (bin size
Total length (kbp)
1000
500
0
0
21
22
23
24
25
26
27
28
29
30
31
32
33
5508
Coverage depth (x)
SPAdes_on_data_1_and_data_2__Scaffolds_broken

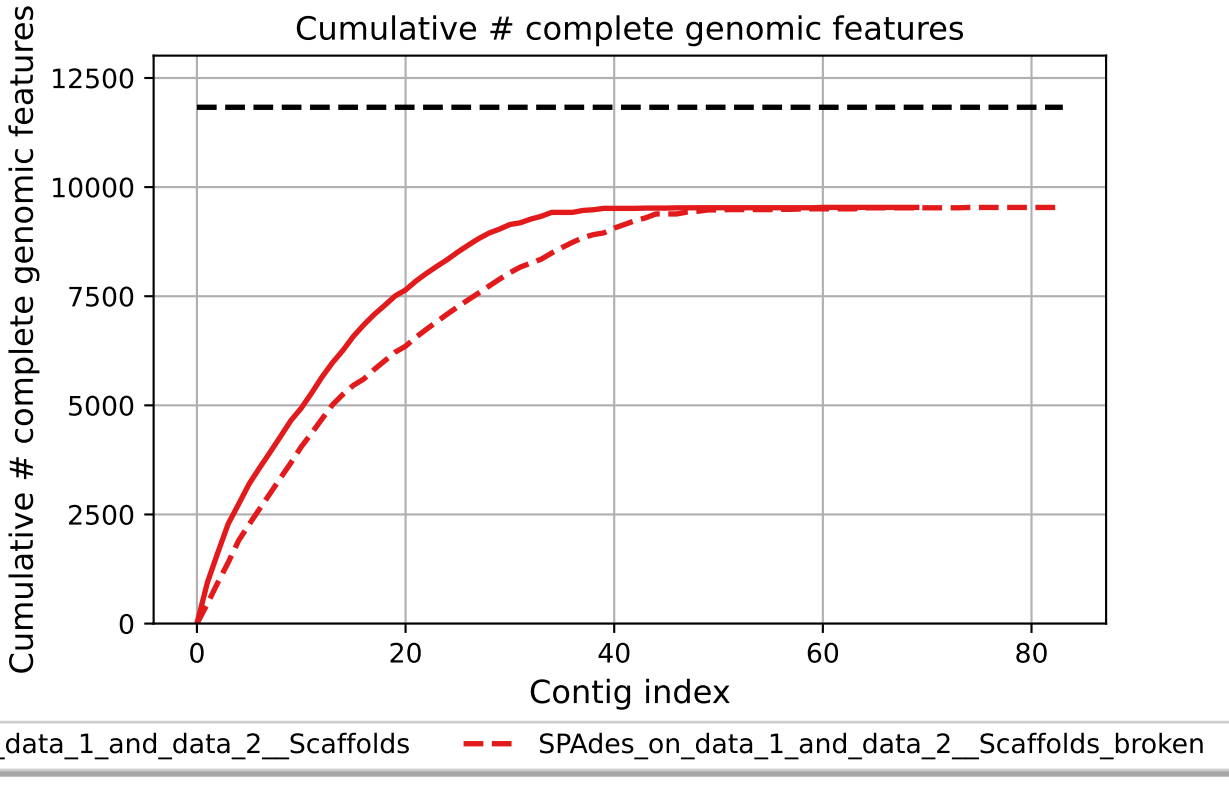

Misassemblies
75
60
45
30
15
0
SPAdes_on_data_1_and_data_2__Scaffolds_broken
relocations

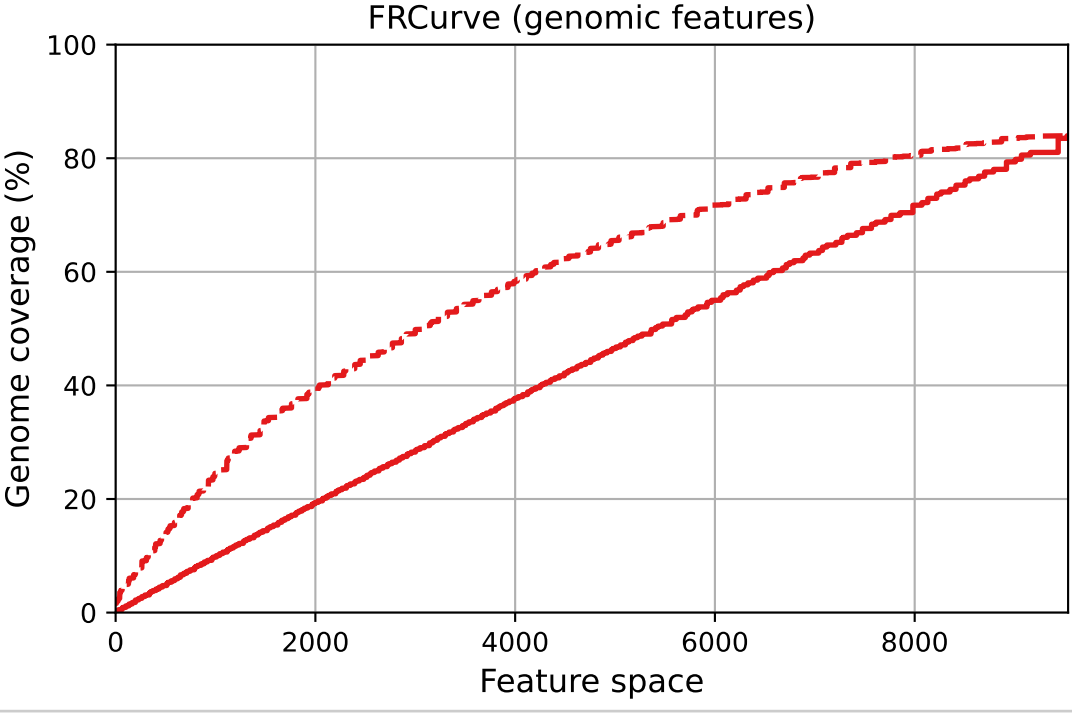

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
Feature space
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds

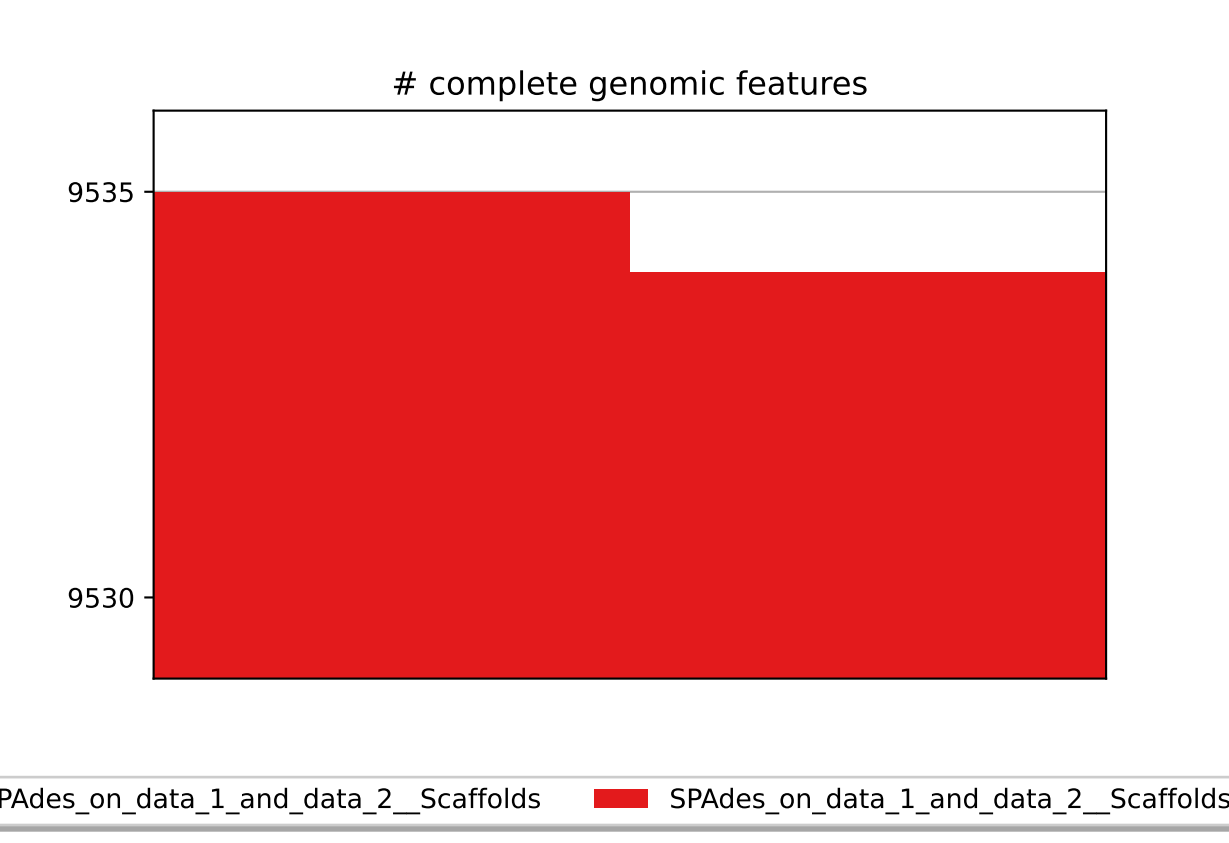

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
25
50
75
100
125
Contig index
_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds_broken

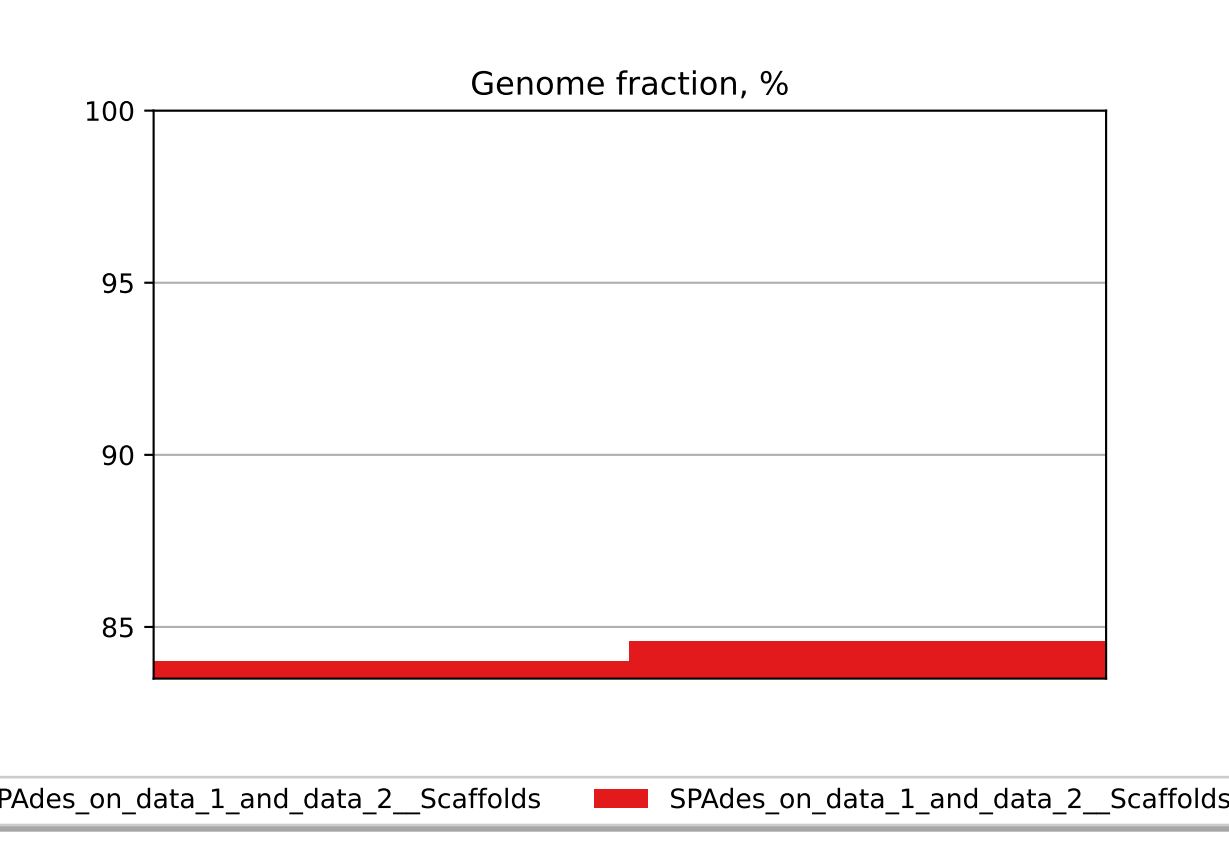

NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds


Cumulative # complete genomic features
Cumulative # complete genomic features
12500
10000
7500
5000
2500
0
0
20
40
60
80
Contig index
_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds_broken


FRCurve (genomic features)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
2000
4000
6000
8000
SPAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds


complete genomic features
9535
9530
PAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds


Genome fraction, %
100
95
90
85
SPAdes_on_data_1_and_data_2__Scaffolds
SPAdes_on_data_1_and_data_2__Scaffolds