Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	237	-
# contigs (>= 1000 bp)	64	79
Total length (>= 0 bp)	5517067	-
Total length (>= 1000 bp)	5479392	5477586
# contigs	76	93
Largest contig	465799	388171
Total length	5487567	5485957
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	193741	146373
NG50	193741	142842
N90	76563	56140
NG90	55995	40890
auN	220595.5	158781.9
auNG	213034.8	153294.8
L50	10	13
LG50	10	14
L90	27	37
LG90	30	41
# misassemblies	76	74
# misassembled contigs	27	34
Misassembled contigs length	4518608	4163537
# local misassemblies	30	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	1	1
# unaligned contigs	23 + 31 part	25 + 36 part
Unaligned length	689367	688332
Genome fraction (%)	84.708	85.280
Duplication ratio	1.002	1.002
# N's per 100 kbp	29.34	0.00
# mismatches per 100 kbp	685.79	688.40
# indels per 100 kbp	19.31	19.60
# genomic features	9597 + 174 part	9607 + 202 part
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	205341	205341
Total aligned length	4795479	4794885
NA50	70102	60721
NGA50	69622	59533
NA90	-	-
NGA90	-	-
auNA	81050.5	71998.6
auNGA	78272.6	69510.6
LA50	24	27
LGA50	25	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

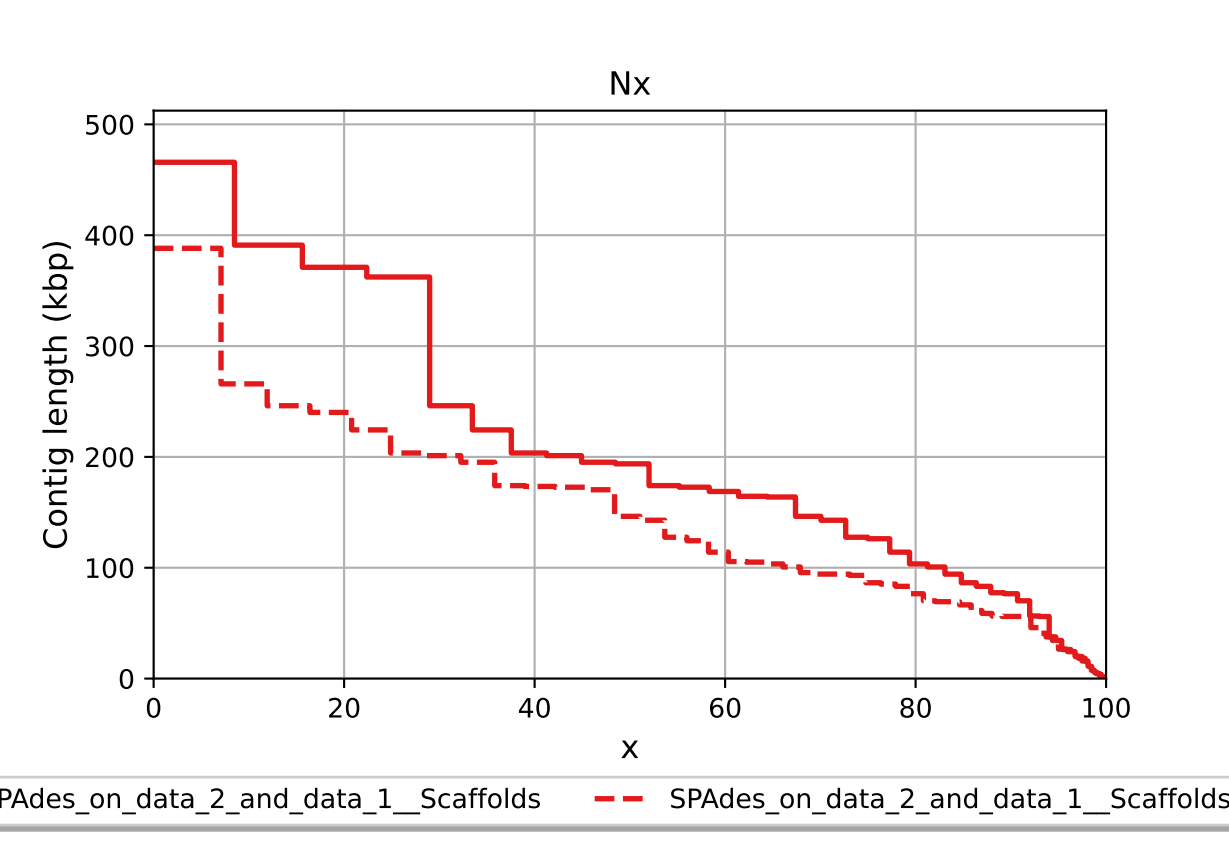
	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# misassemblies	76	74
# contig misassemblies	74	74
# c. relocations	71	71
# c. translocations	3	3
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	27	34
Misassembled contigs length	4518608	4163537
# local misassemblies	30	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	1	1
# mismatches	32887	33008
# indels	926	940
# indels (<= 5 bp)	834	857
# indels (> 5 bp)	92	83
Indels length	7335	6067

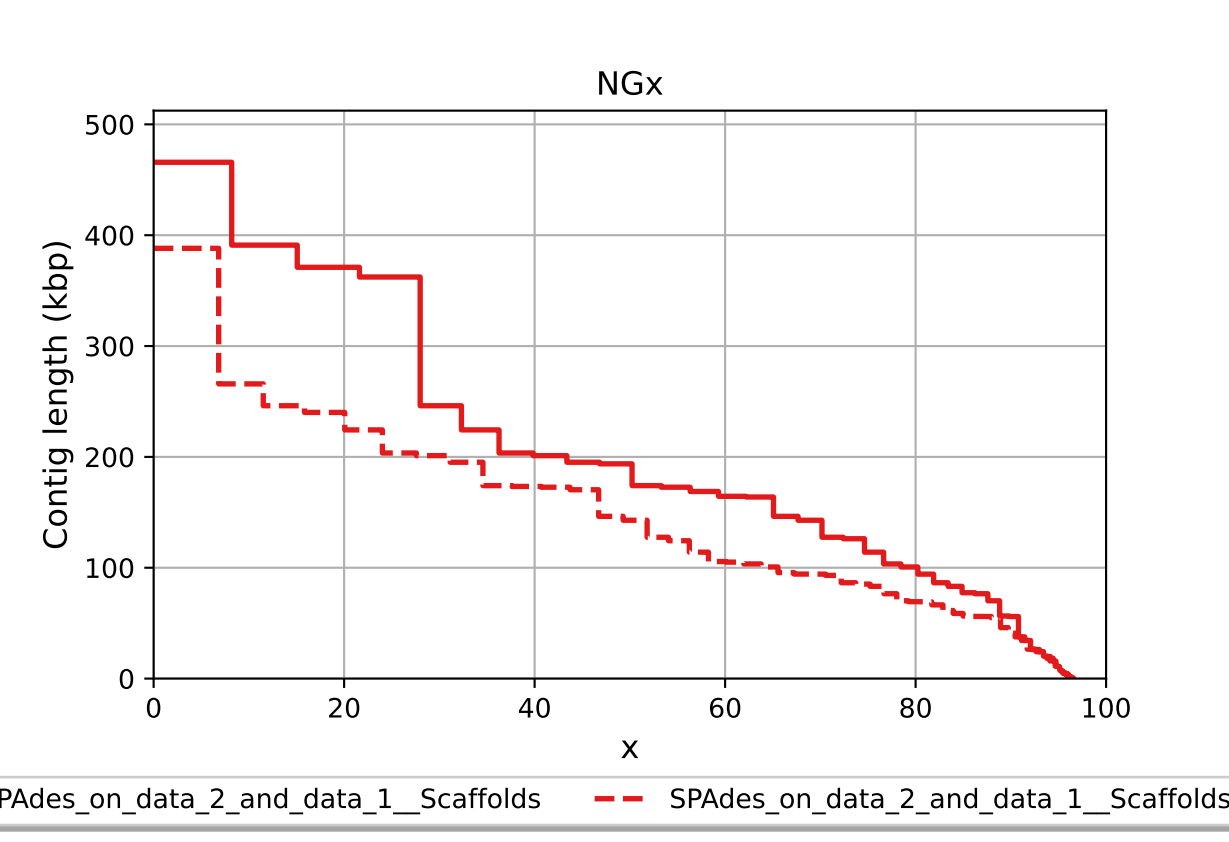
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

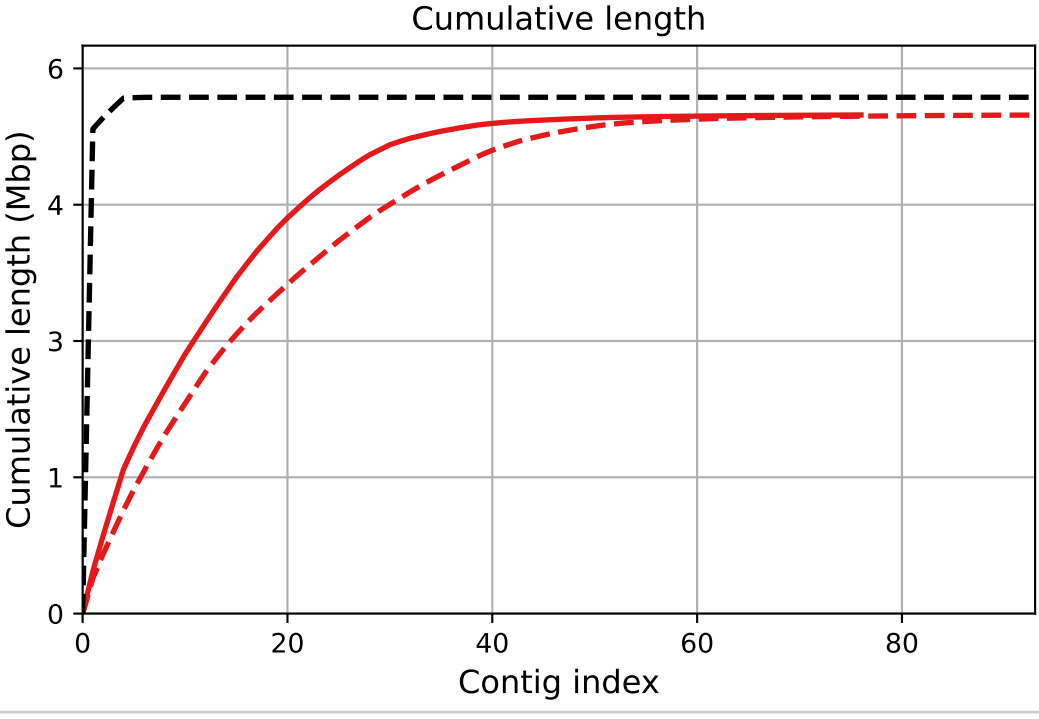
Unaligned report

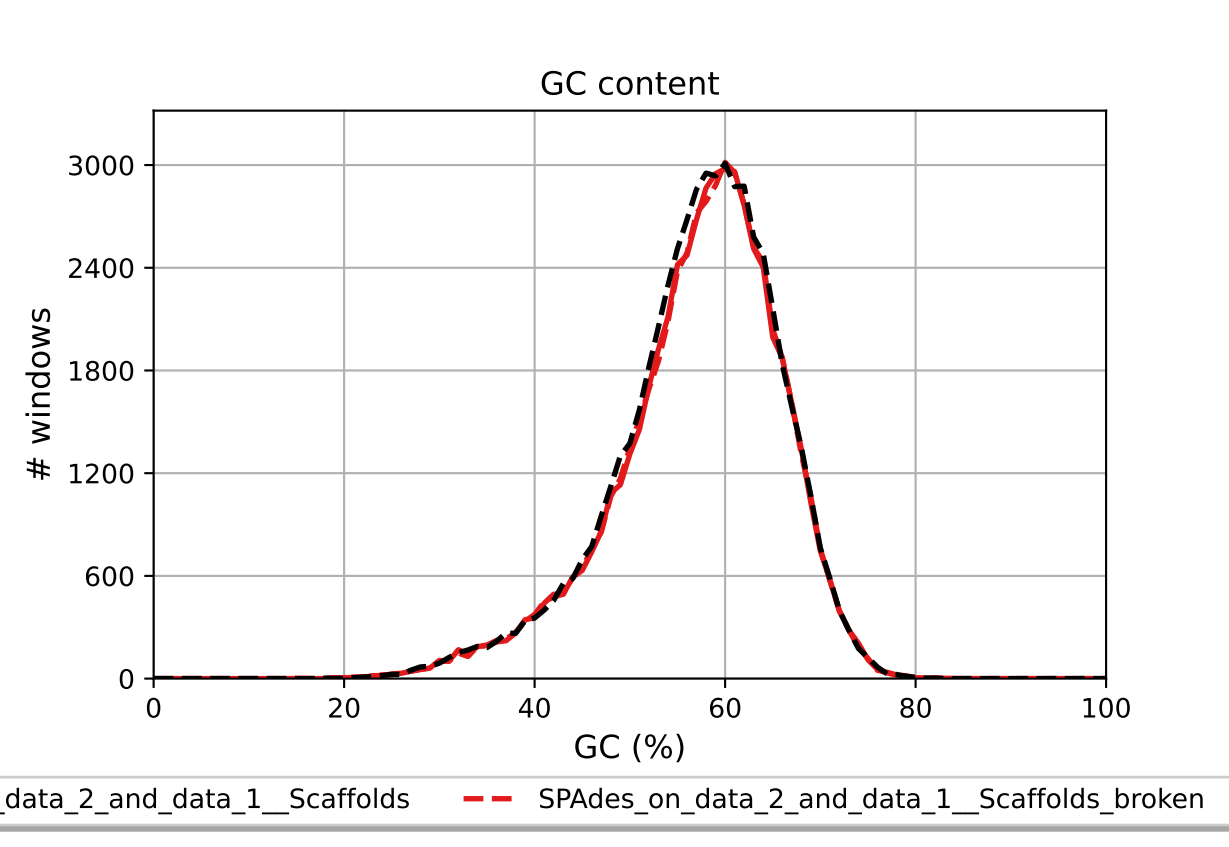
	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# fully unaligned contigs	23	25
Fully unaligned length	84331	84527
# partially unaligned contigs	31	36
Partially unaligned length	605036	603805
# N's	1610	0

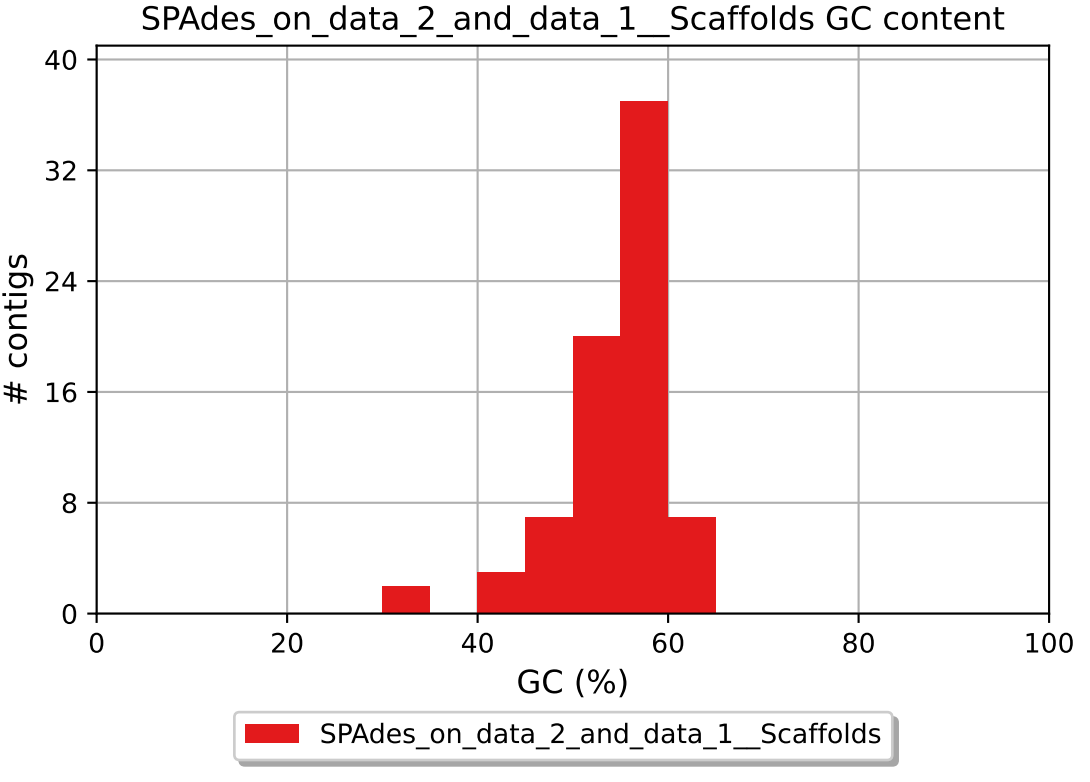
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

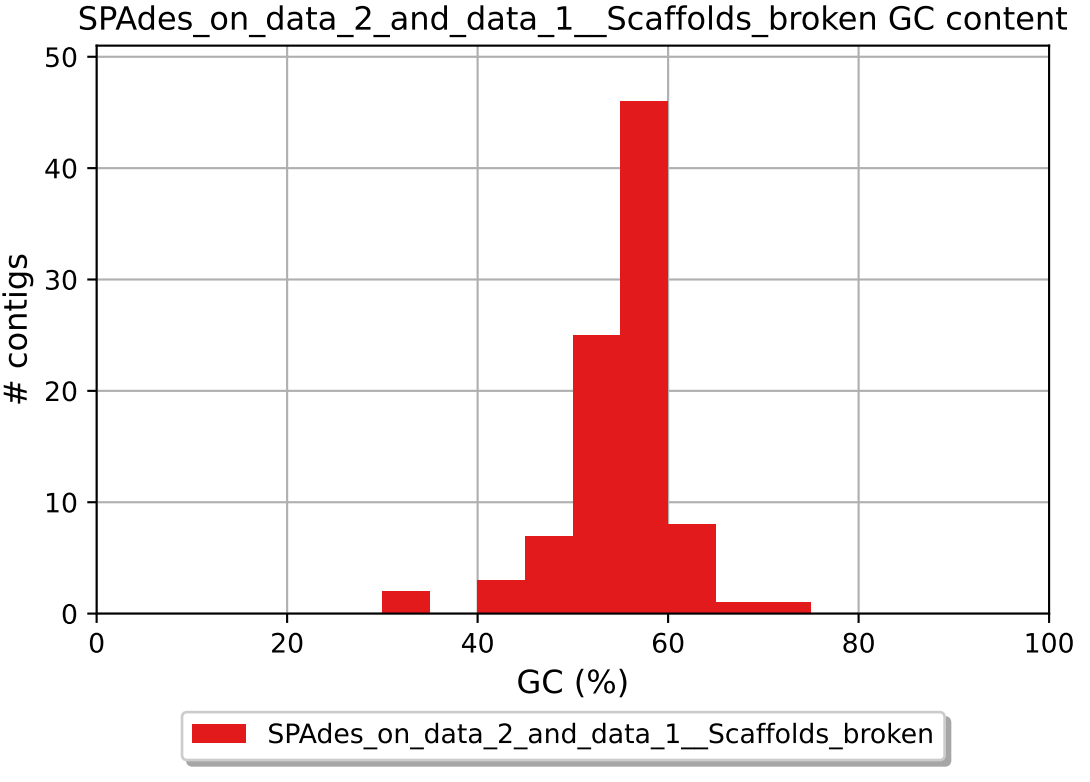

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

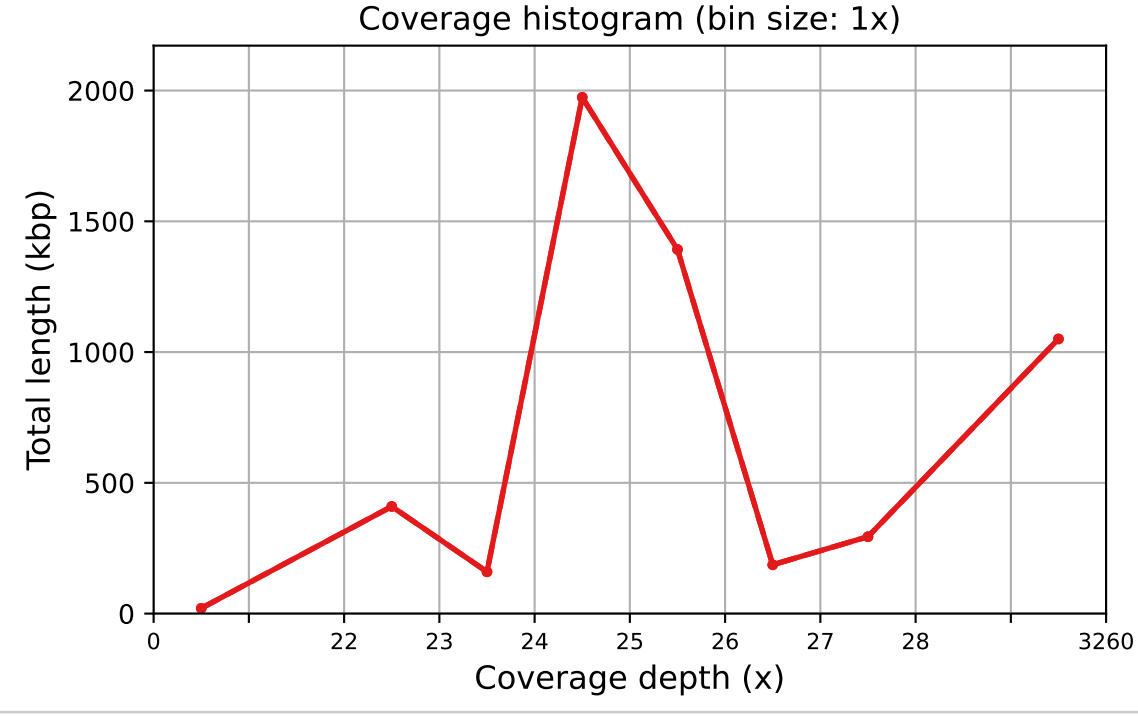

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

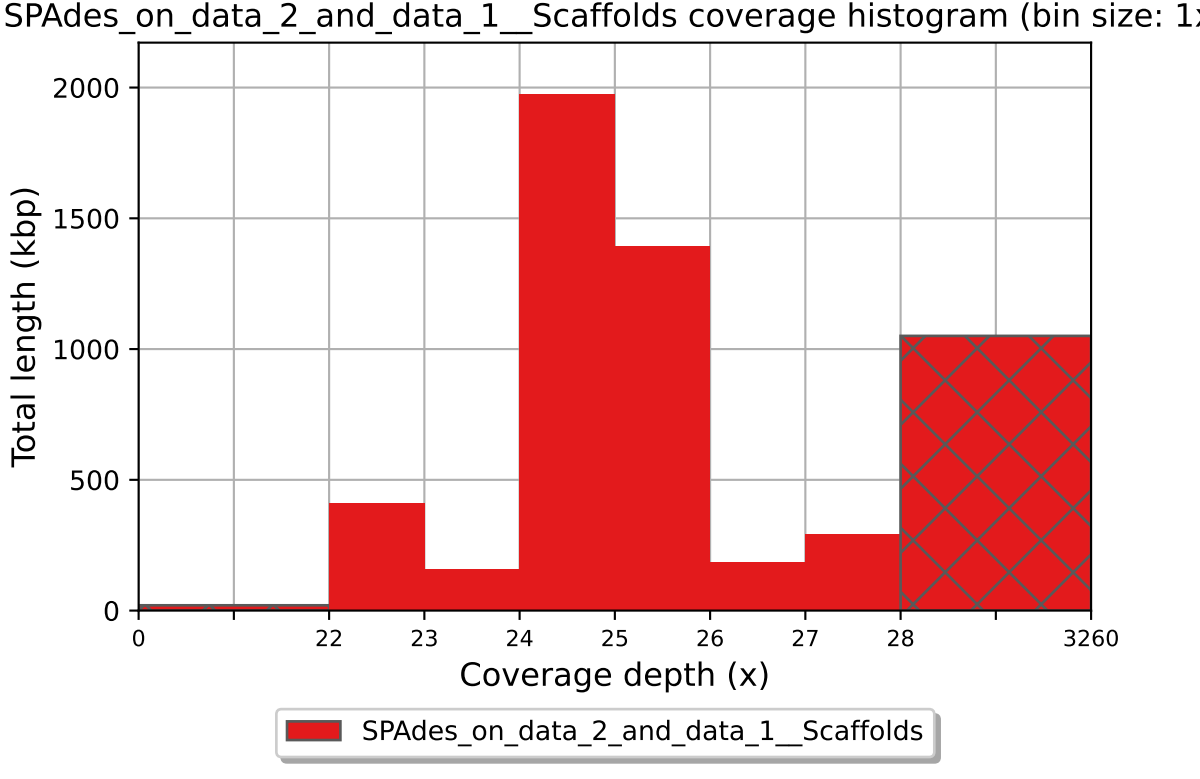

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
3
4
6
0
20
40
60
80
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken

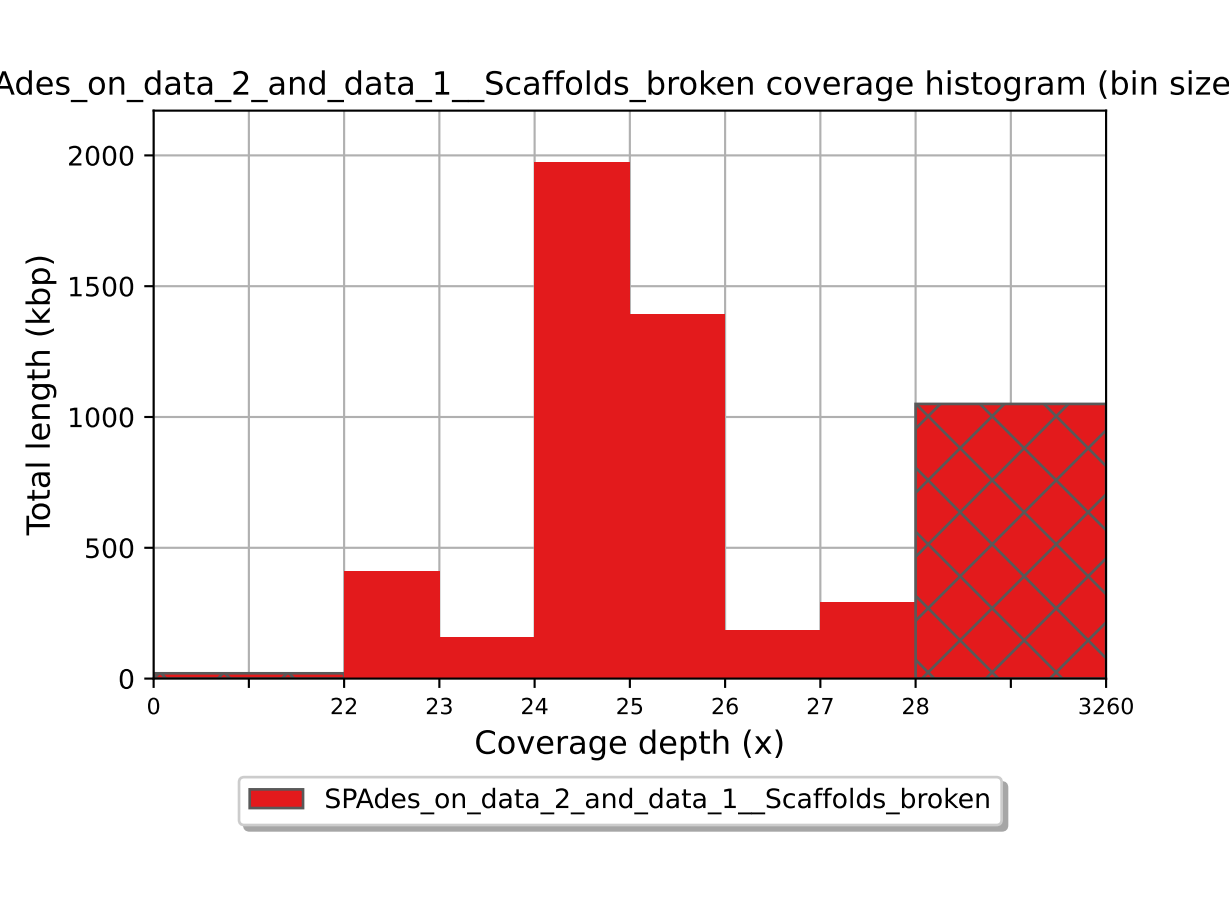

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken


SPAdes_on_data_2_and_data_1__Scaffolds GC content
contigs
GC (%)
0
8
16
24
32
40
0
20
40
60
80
100
SPAdes_on_data_2_and_data_1__Scaffolds

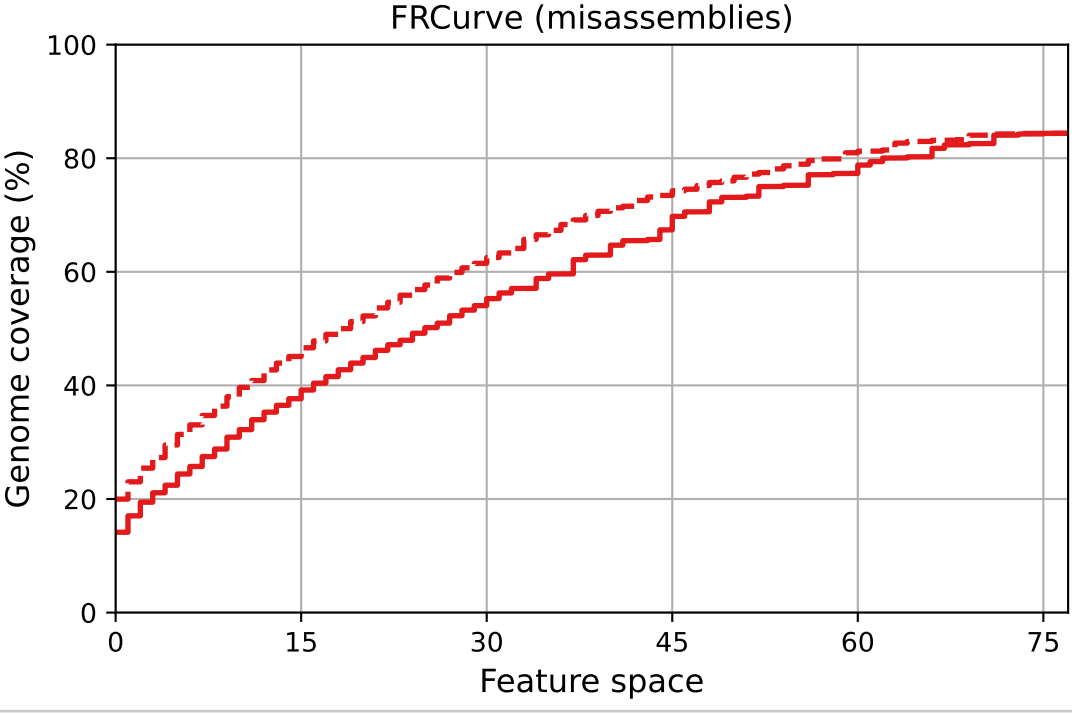

SPAdes_on_data_2_and_data_1__Scaffolds_broken GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
SPAdes_on_data_2_and_data_1__Scaffolds_broken

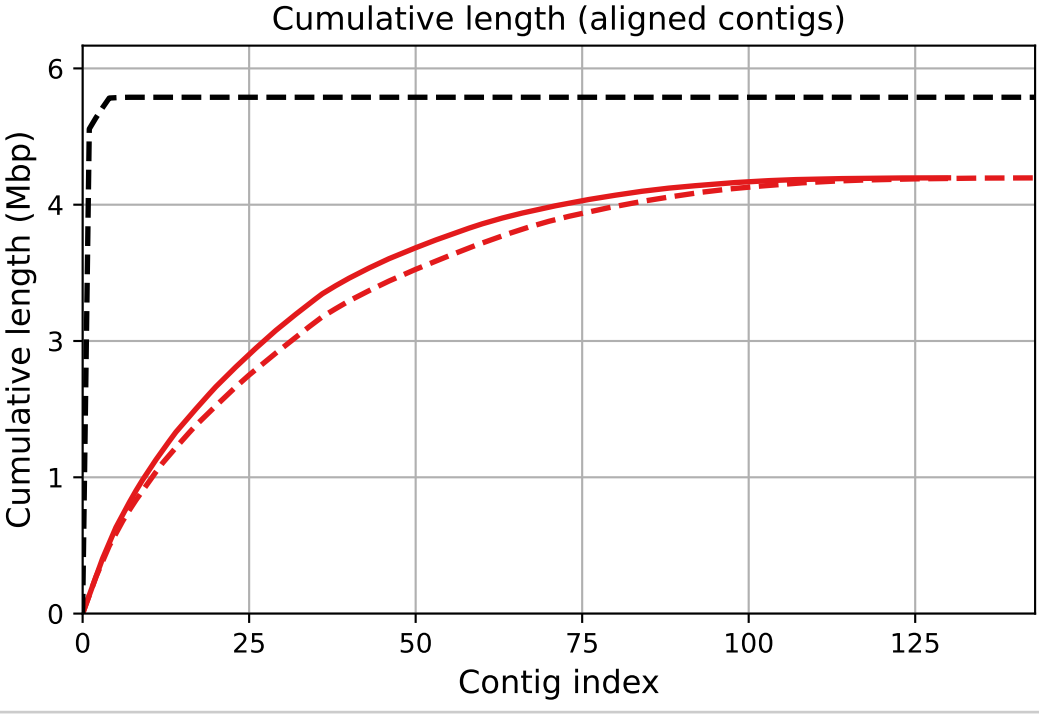

Coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
22
23
24
25
26
27
28
3260
Coverage depth (x)
SPAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

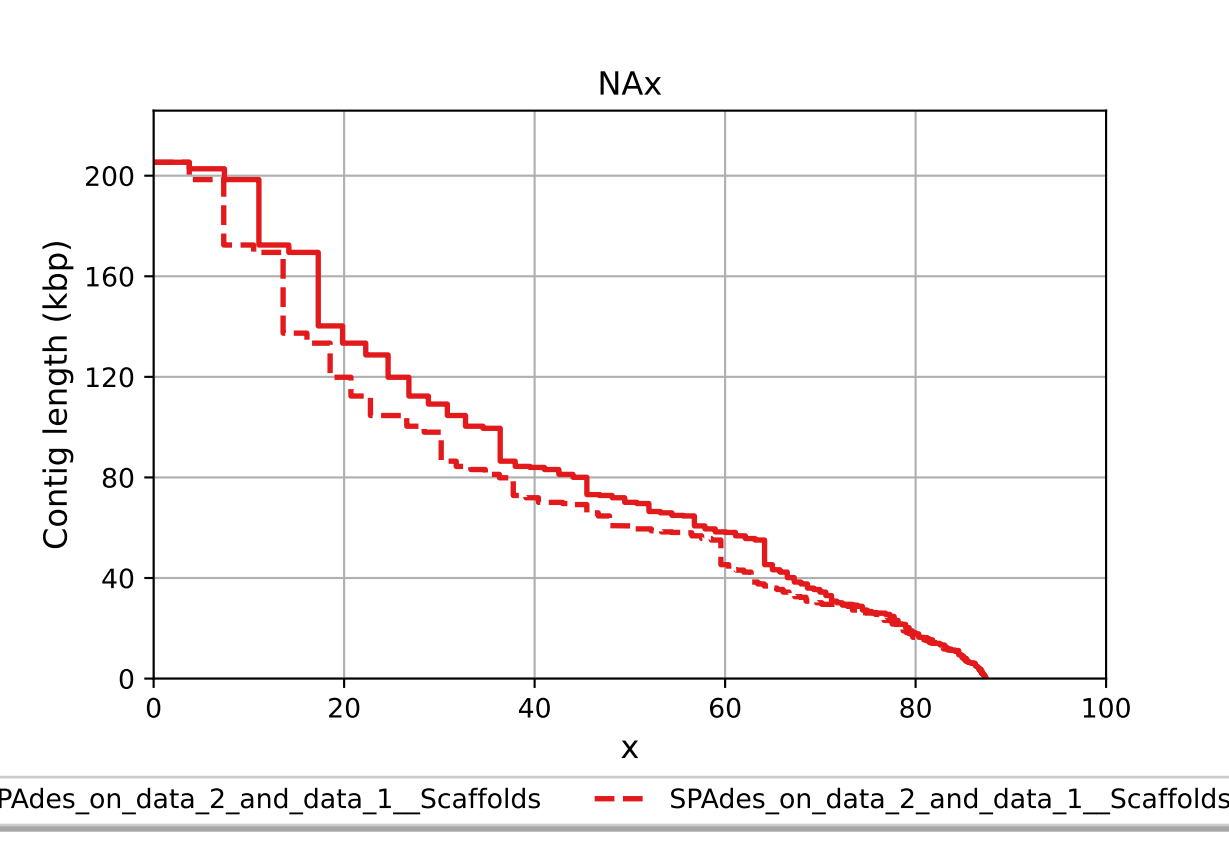

SPAdes_on_data_2_and_data_1__Scaffolds coverage histogram (bin size: 1x
Total length (kbp)
2000
1500
1000
500
0
0
22
23
24
25
26
27
28
3260
Coverage depth (x)
SPAdes_on_data_2_and_data_1__Scaffolds

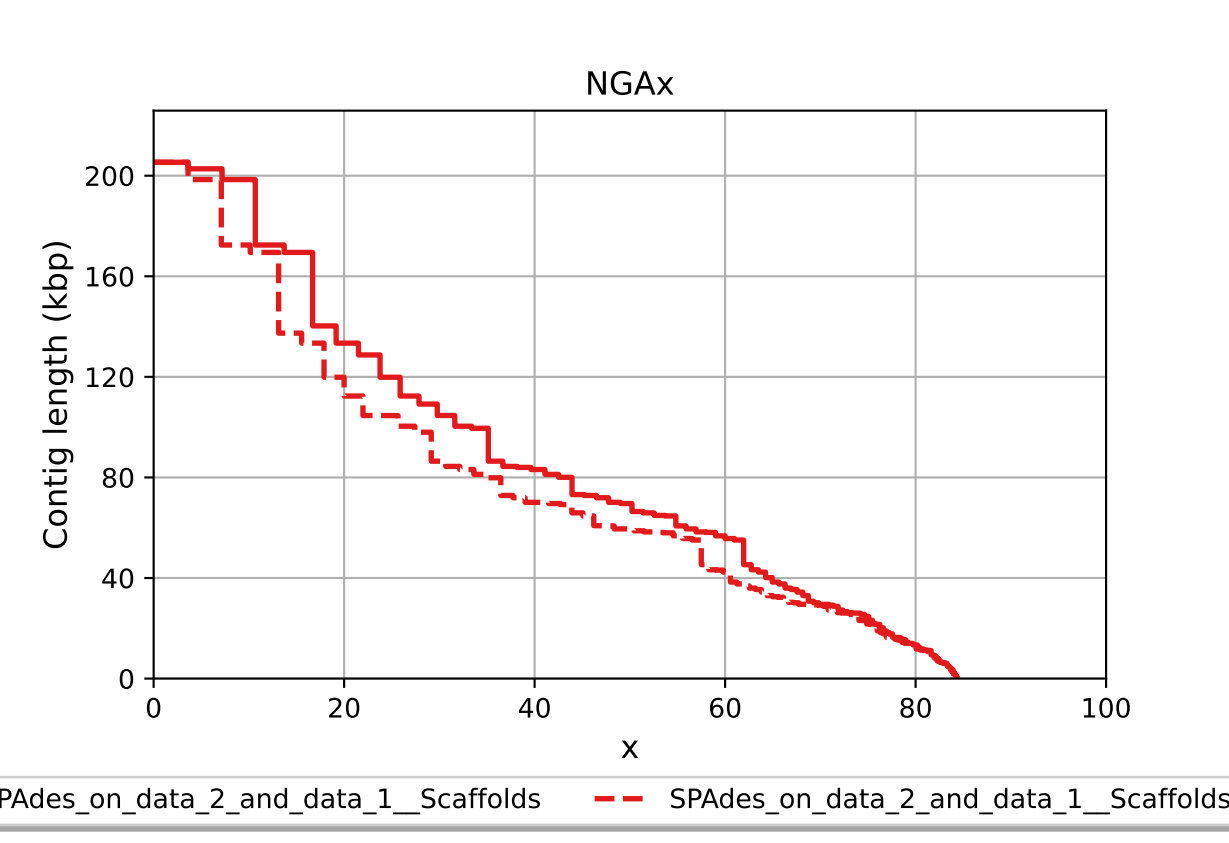

Ades_on_data_2_and_data_1__Scaffolds_broken coverage histogram (bin size
Total length (kbp)
2000
1500
1000
500
0
0
22
23
24
25
26
27
28
3260
Coverage depth (x)
SPAdes_on_data_2_and_data_1__Scaffolds_broken

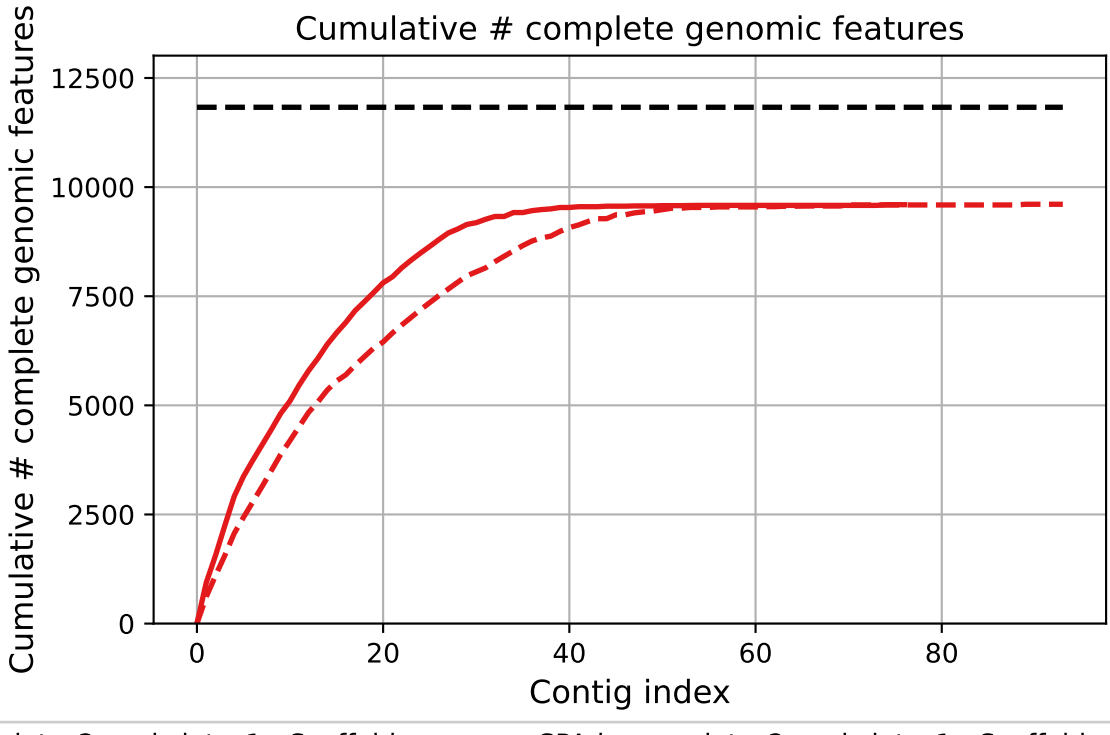
Misassemblies
75
60
45
30
15
0
SPAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken
relocations
translocations

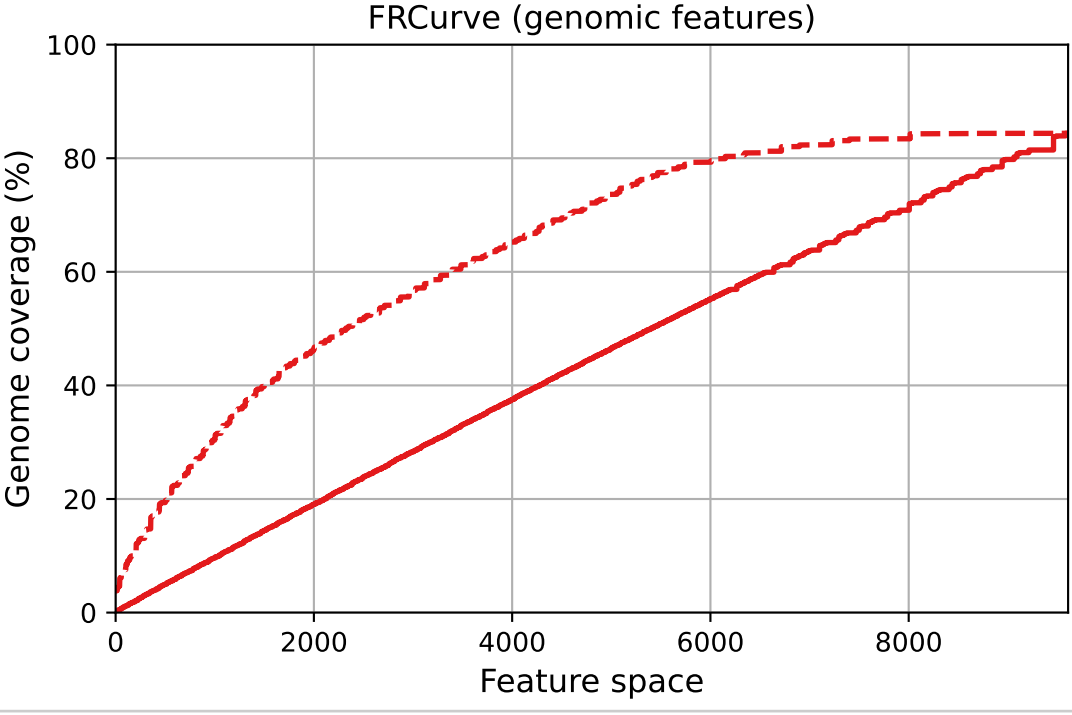

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
75
Feature space
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

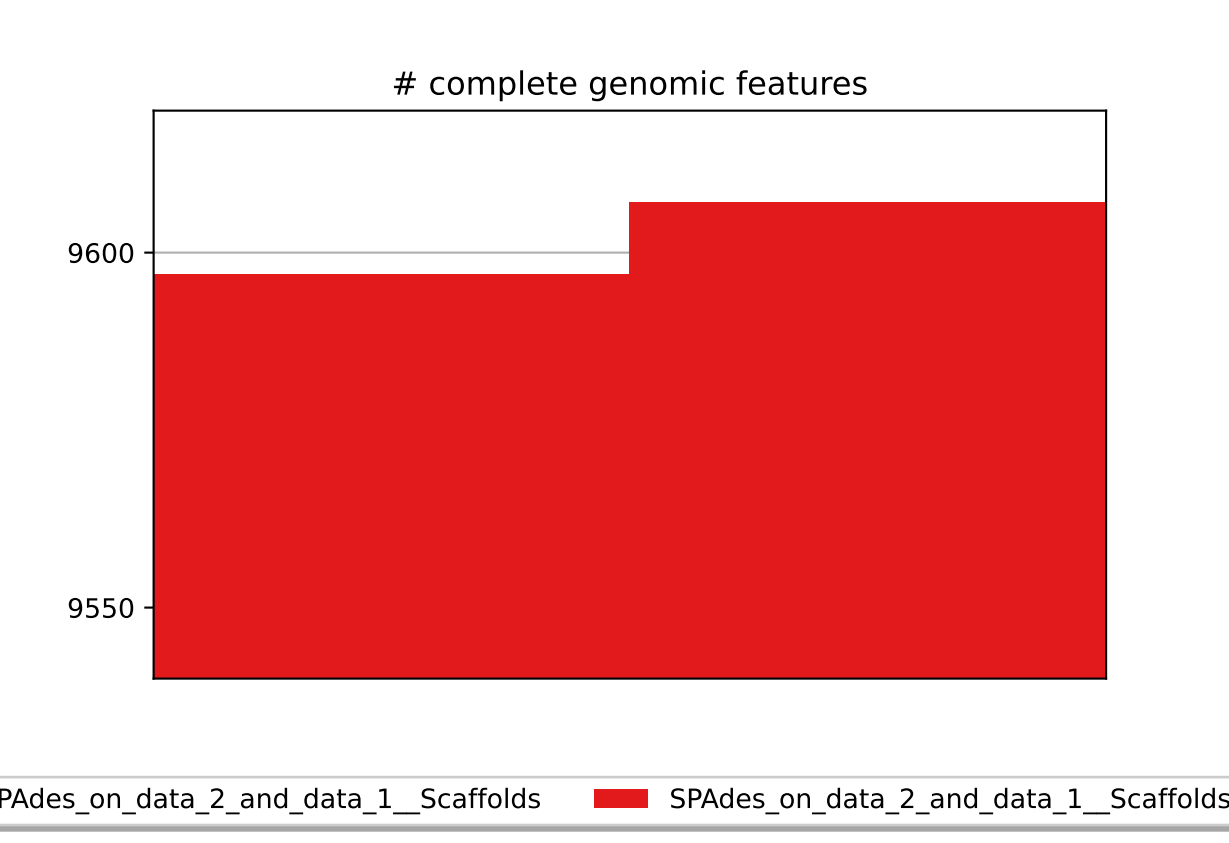

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
3
4
6
0
25
50
75
100
125
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken

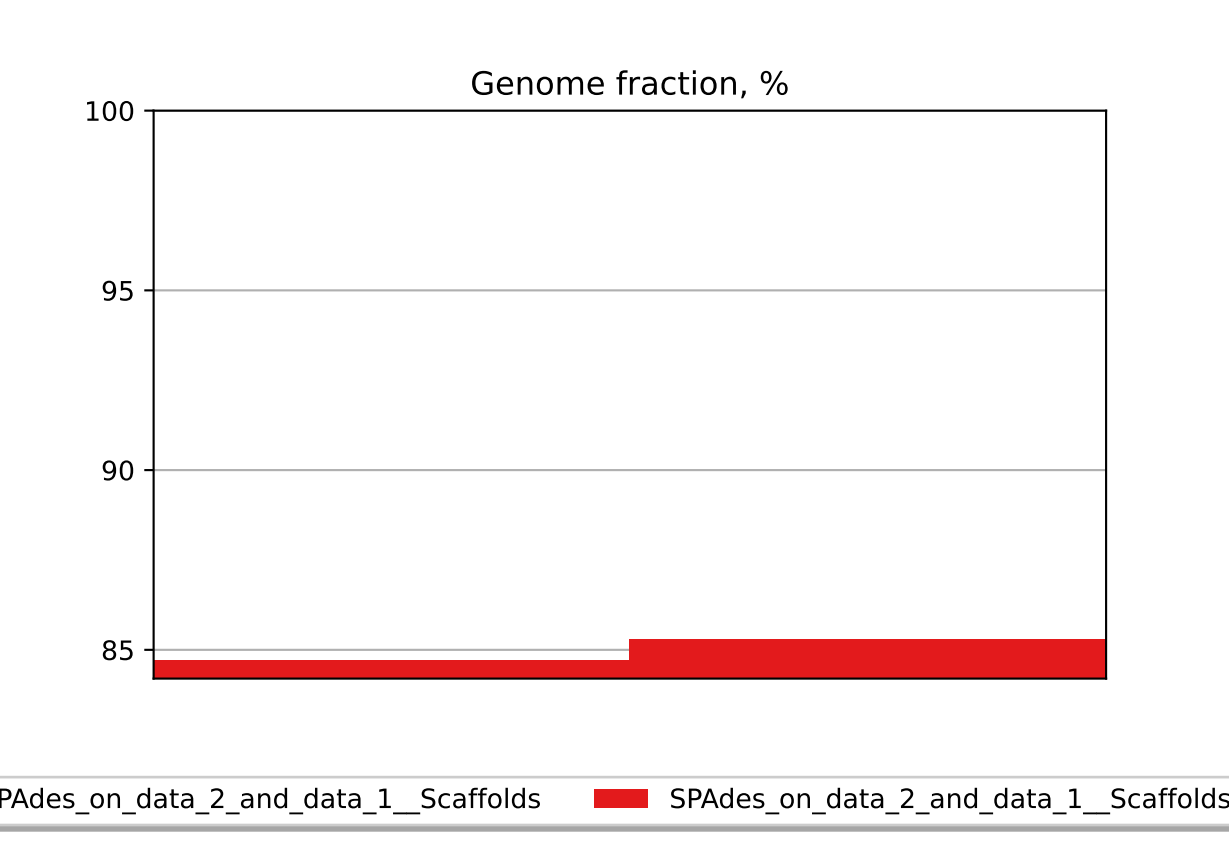

NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds


Cumulative # complete genomic features
Cumulative # complete genomic features
12500
10000
7500
5000
2500
0
0
20
40
60
80
Contig index
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken


FRCurve (genomic features)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
2000
4000
6000
8000
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds


complete genomic features
9600
9550
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds


Genome fraction, %
100
95
90
85
SPAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds