Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	181	-
# contigs (>= 1000 bp)	65	77
Total length (>= 0 bp)	5509441	-
Total length (>= 1000 bp)	5481124	5480104
# contigs	79	91
Largest contig	465488	390830
Total length	5490296	5489276
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	181027	163855
NG50	174078	146373
N90	76558	56140
NG90	56469	45755
auN	217641.4	159550.4
auNG	210286.5	154130.0
L50	10	13
LG50	11	14
L90	28	37
LG90	31	40
# misassemblies	77	76
# misassembled contigs	28	34
Misassembled contigs length	4555775	4316103
# local misassemblies	29	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	2	2
# unaligned contigs	24 + 31 part	24 + 35 part
Unaligned length	689929	688792
Genome fraction (%)	84.773	85.348
Duplication ratio	1.002	1.002
# N's per 100 kbp	18.58	0.00
# mismatches per 100 kbp	685.98	688.72
# indels per 100 kbp	19.01	19.43
# genomic features	9614 + 174 part	9628 + 204 part
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	205341	205341
Total aligned length	4797934	4797163
NA50	69622	64682
NGA50	69481	60711
NA90	-	-
NGA90	-	-
auNA	81774.5	74905.9
auNGA	79011.0	72361.2
LA50	24	26
LGA50	25	28
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

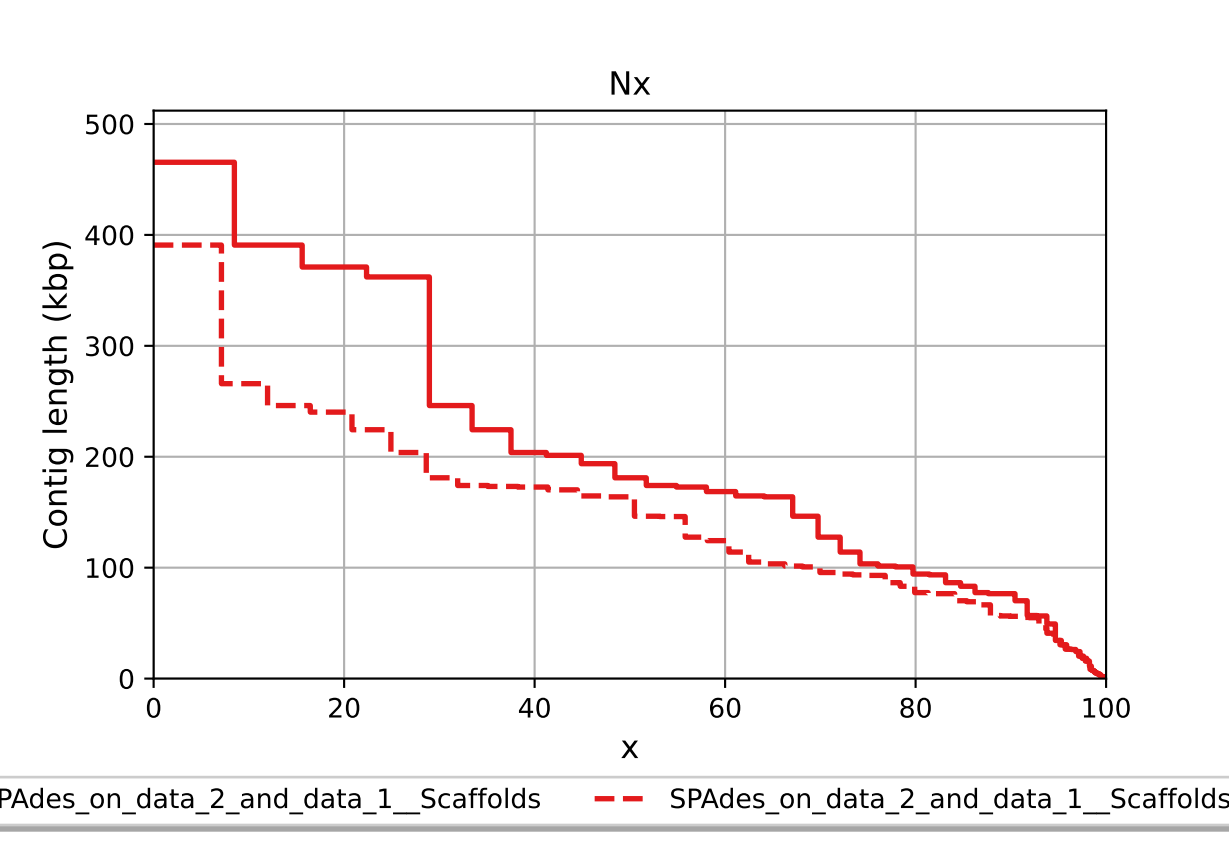
	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# misassemblies	77	76
# contig misassemblies	76	76
# c. relocations	73	73
# c. translocations	3	3
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	28	34
Misassembled contigs length	4555775	4316103
# local misassemblies	29	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	2	2
# mismatches	32913	33039
# indels	912	932
# indels (<= 5 bp)	824	853
# indels (> 5 bp)	88	79
Indels length	7212	6382

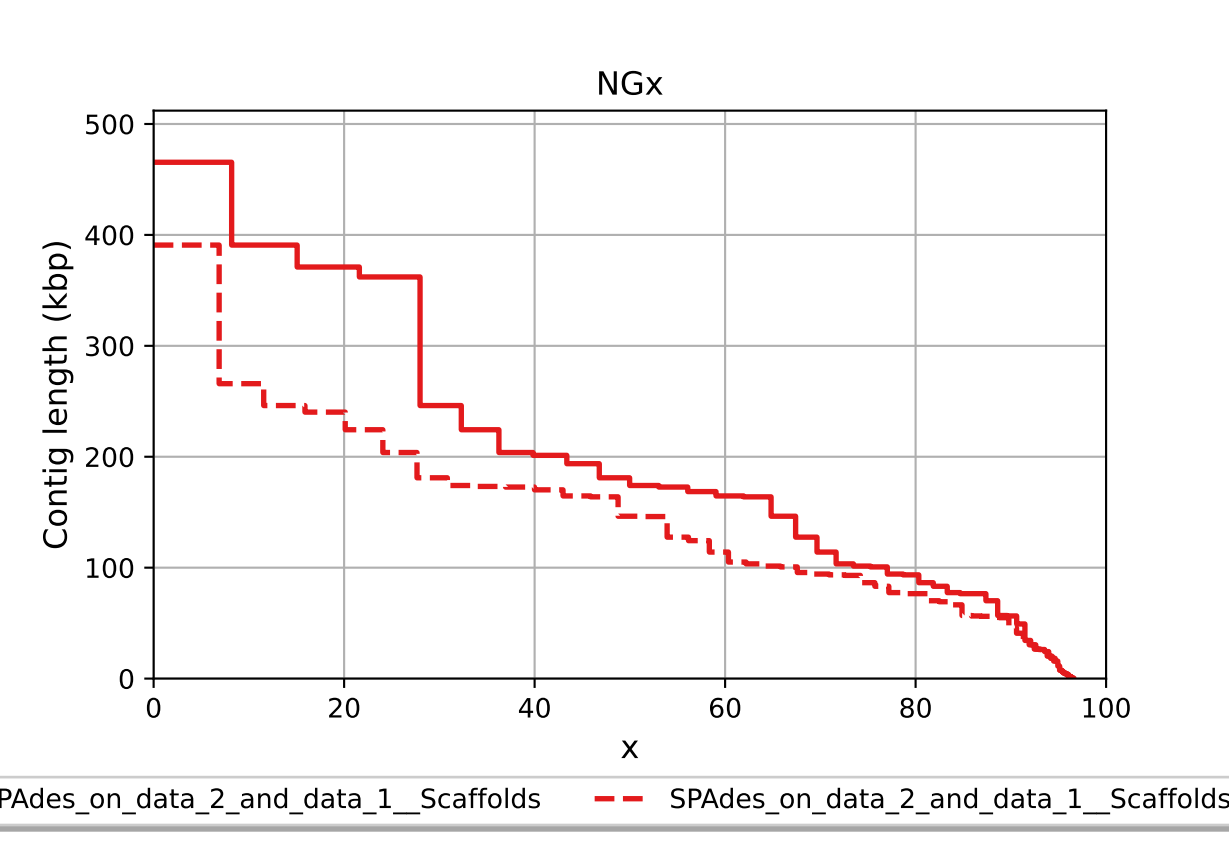
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

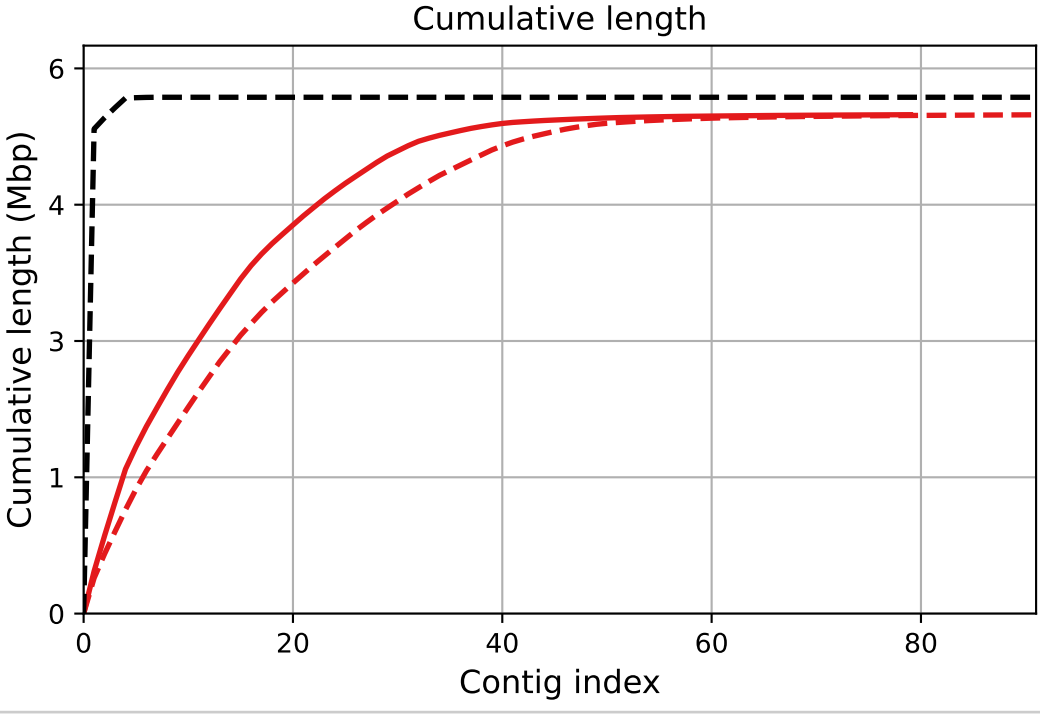
Unaligned report

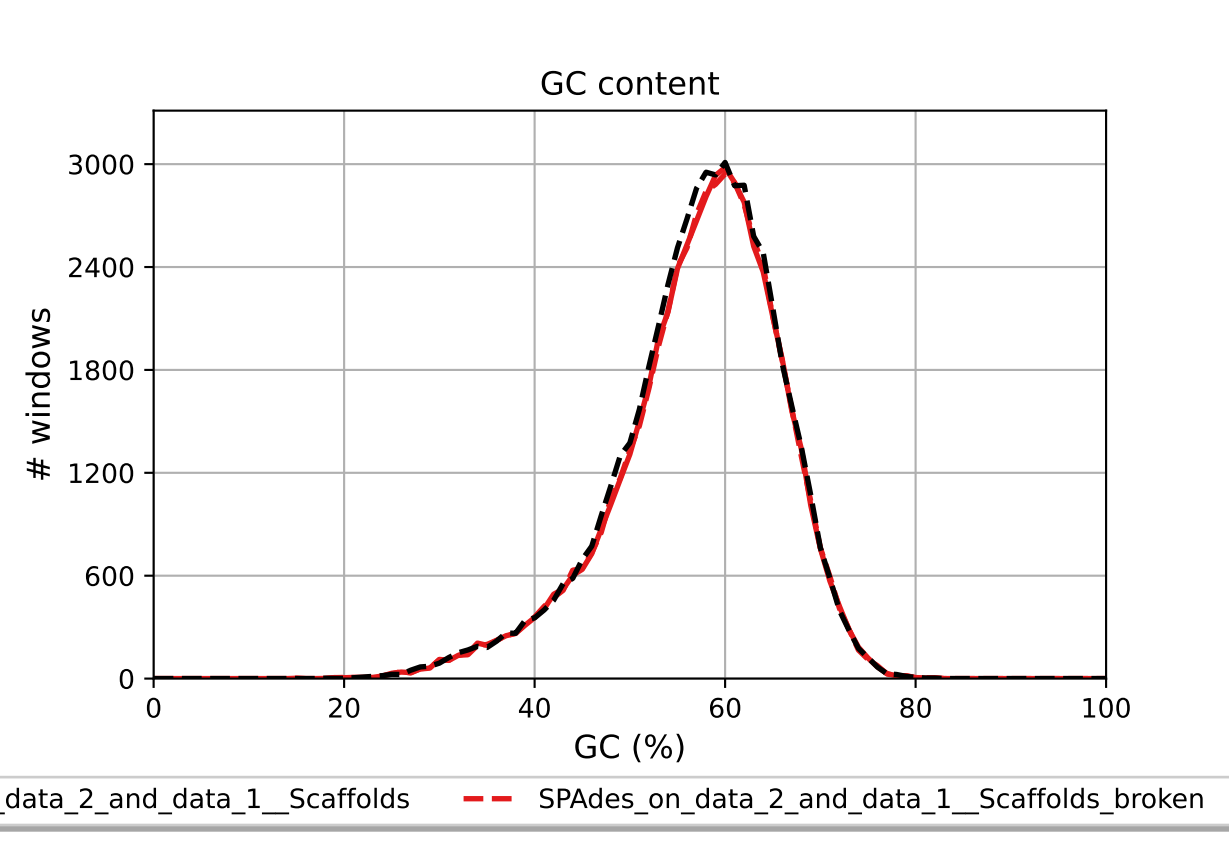
	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# fully unaligned contigs	24	24
Fully unaligned length	85042	85042
# partially unaligned contigs	31	35
Partially unaligned length	604887	603750
# N's	1020	0

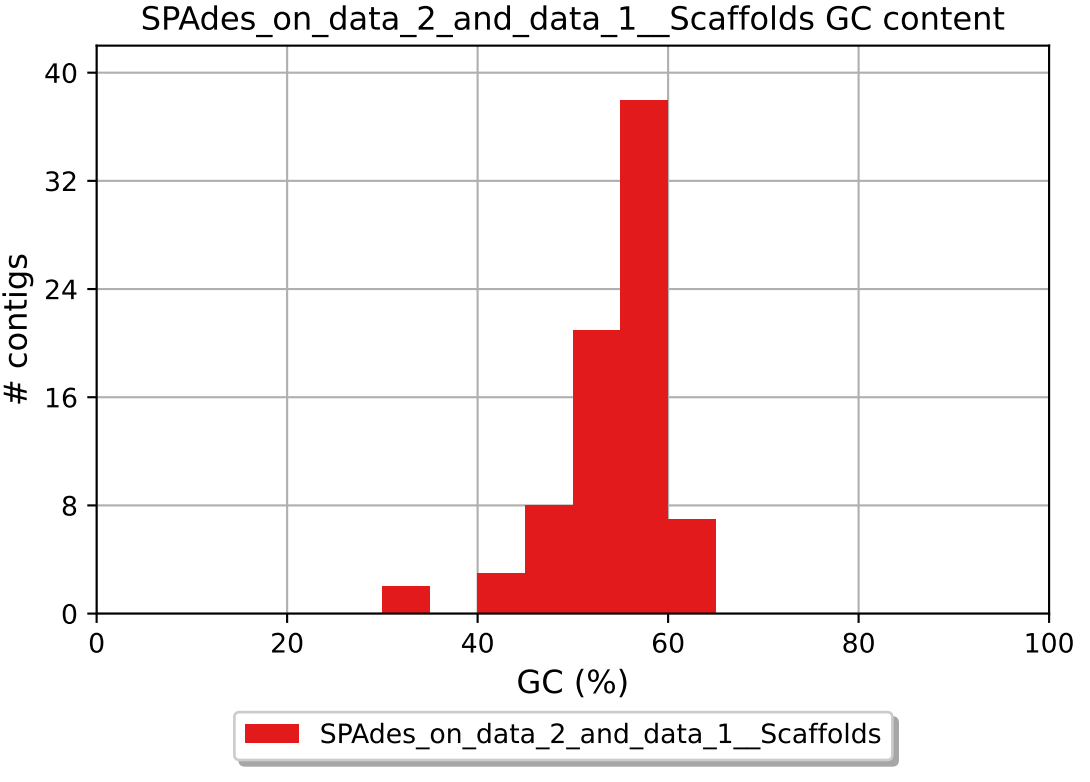
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

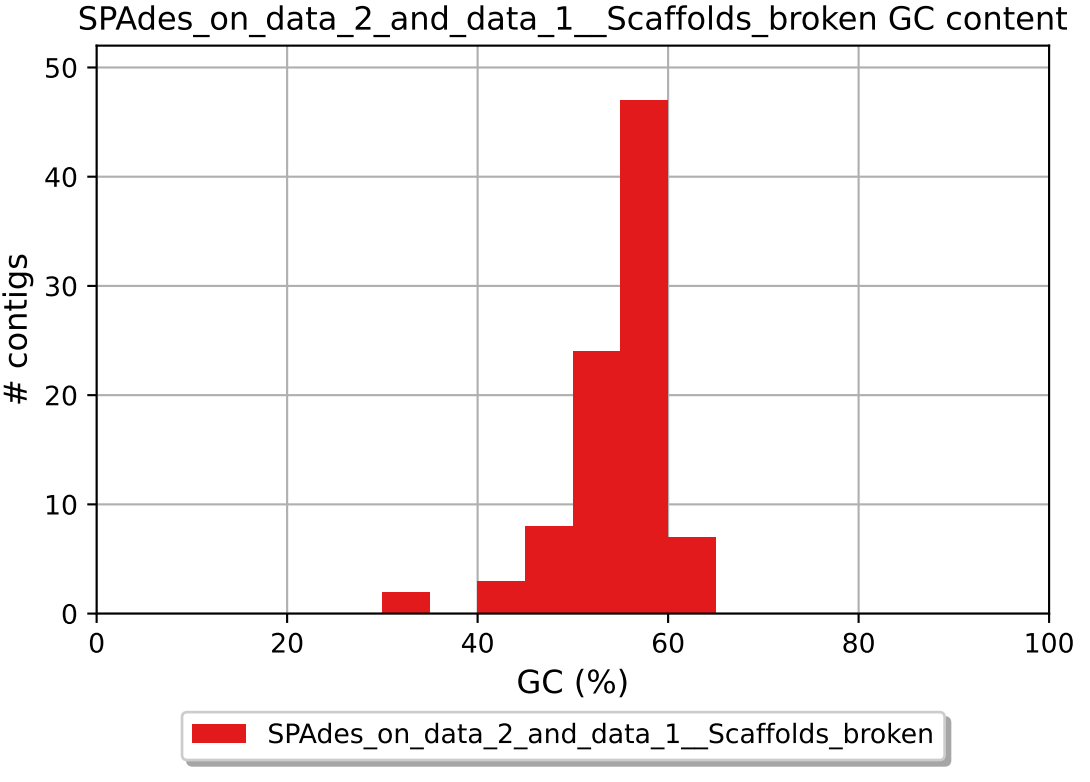

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
SPAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

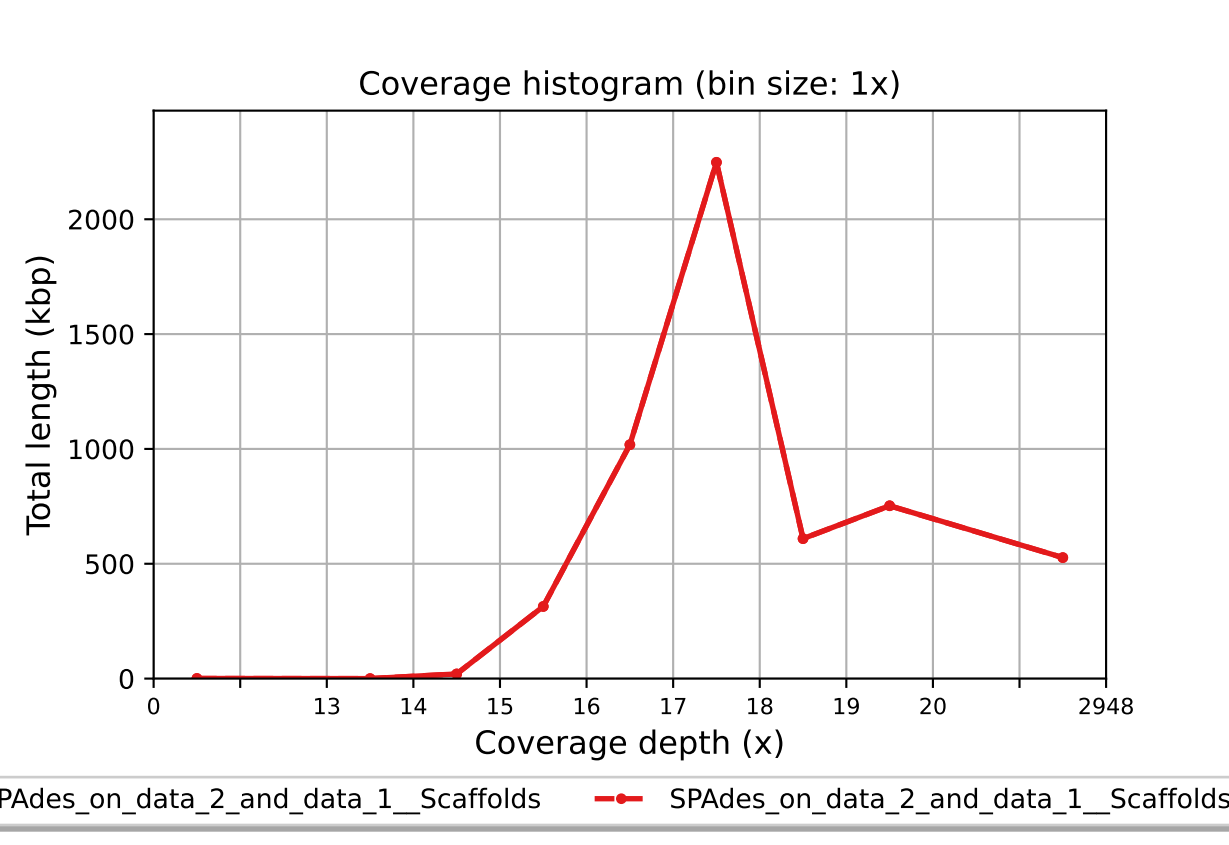

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

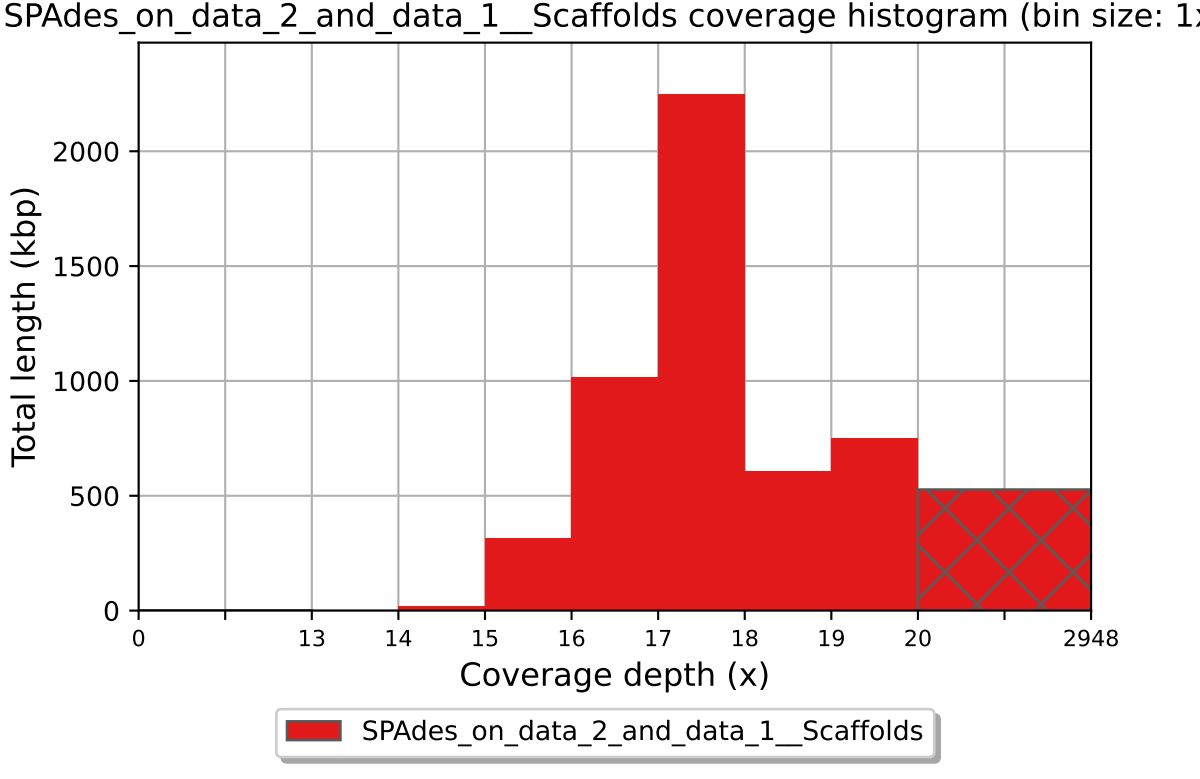

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
3
4
6
0
20
40
60
80
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken

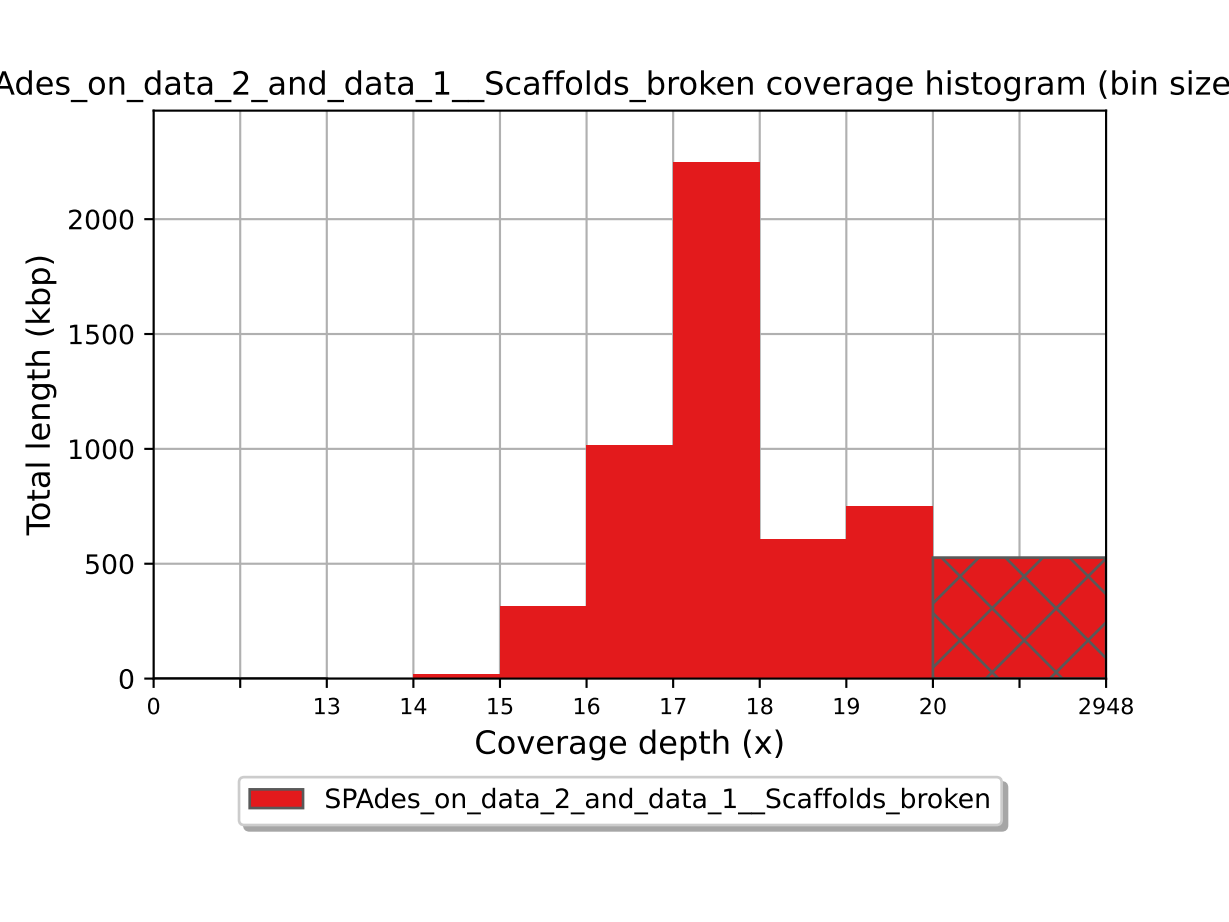

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken

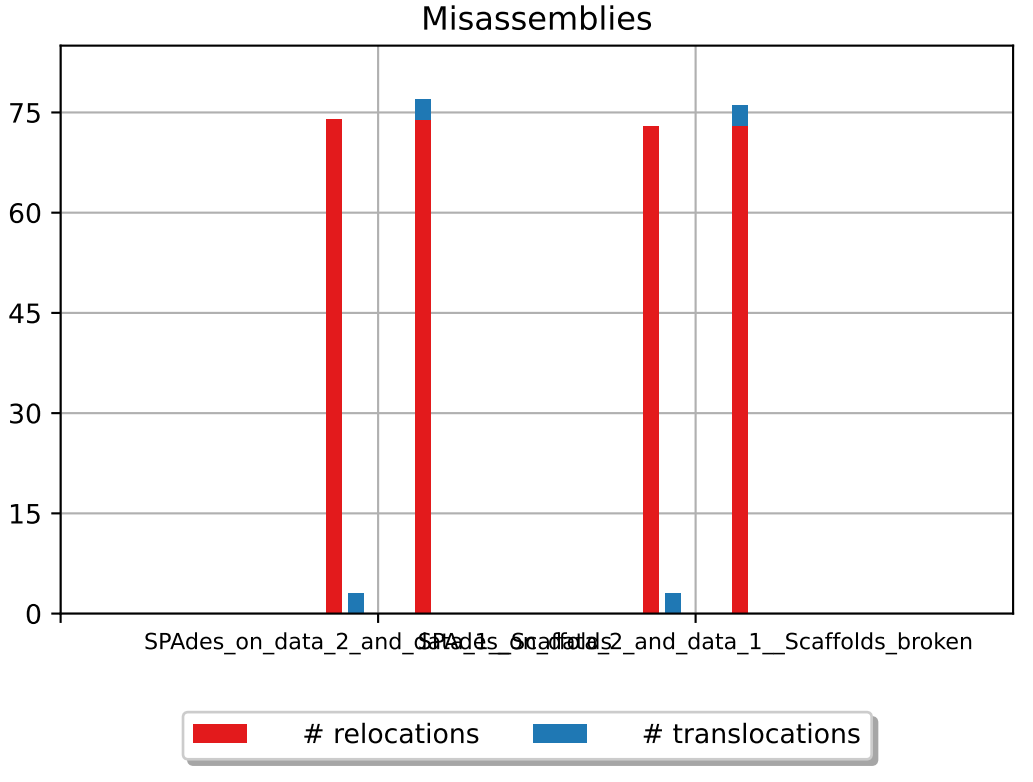

SPAdes_on_data_2_and_data_1__Scaffolds GC content
contigs
GC (%)
0
8
16
24
32
40
0
20
40
60
80
100
SPAdes_on_data_2_and_data_1__Scaffolds

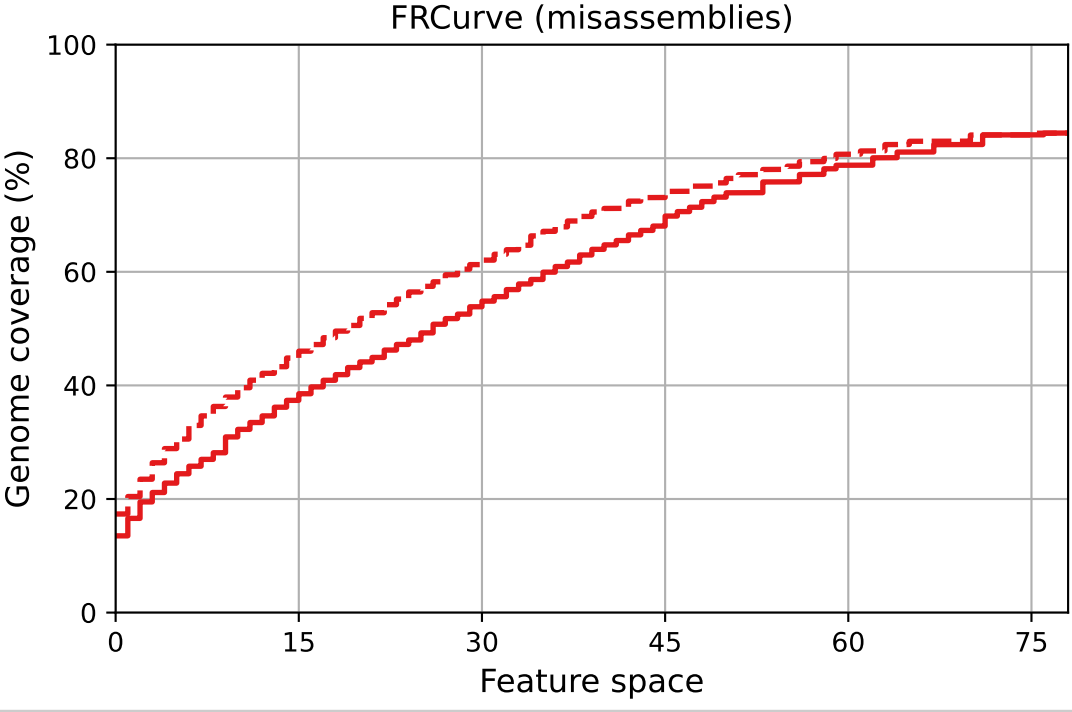

SPAdes_on_data_2_and_data_1__Scaffolds_broken GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
SPAdes_on_data_2_and_data_1__Scaffolds_broken

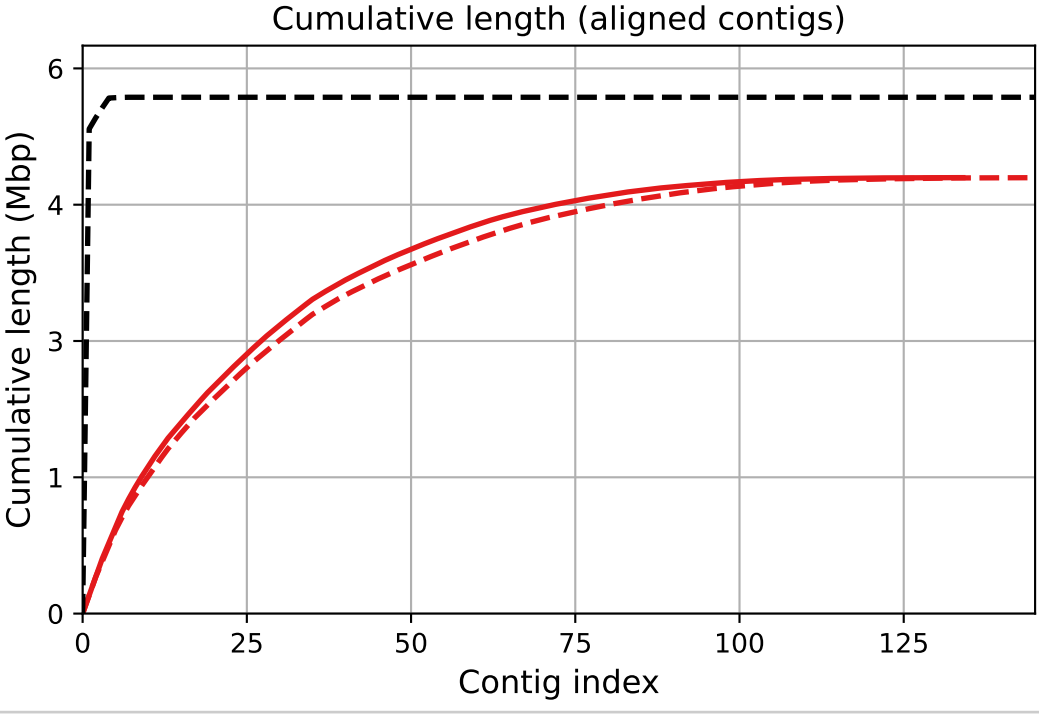

Coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
13
14
15
16
17
18
19
20
2948
Coverage depth (x)
SPAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

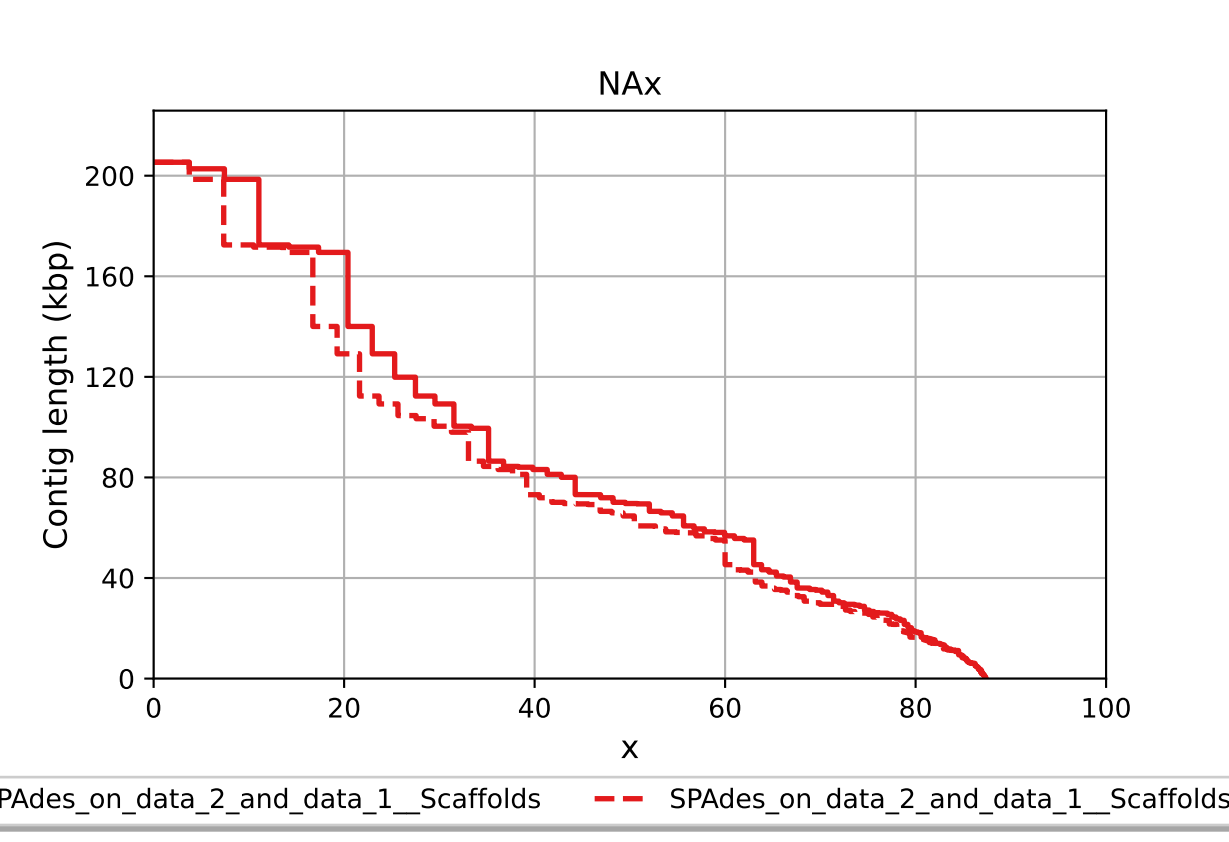

SPAdes_on_data_2_and_data_1__Scaffolds coverage histogram (bin size: 1x
Total length (kbp)
2000
1500
1000
500
0
0
13
14
15
16
17
18
19
20
2948
Coverage depth (x)
SPAdes_on_data_2_and_data_1__Scaffolds

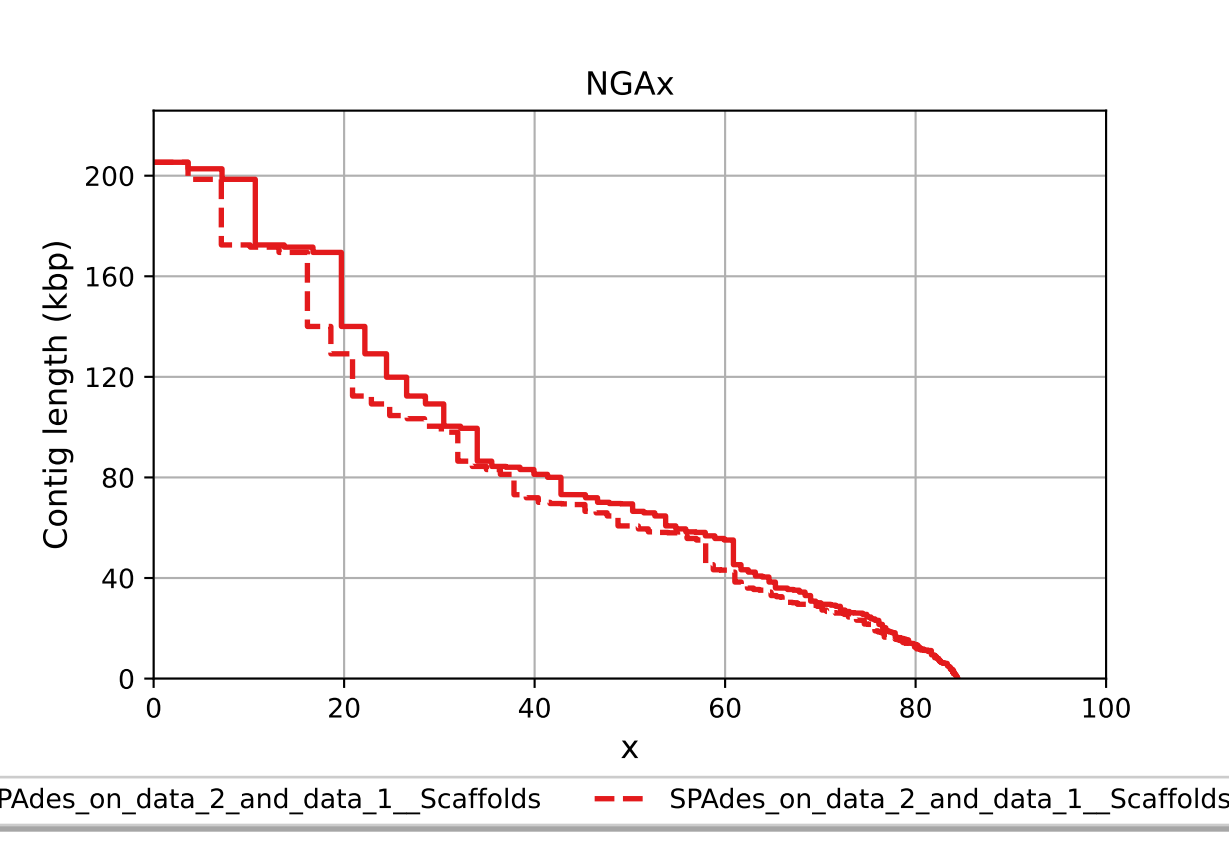

Ades_on_data_2_and_data_1__Scaffolds_broken coverage histogram (bin size
Total length (kbp)
2000
1500
1000
500
0
0
13
14
15
16
17
18
19
20
2948
Coverage depth (x)
SPAdes_on_data_2_and_data_1__Scaffolds_broken

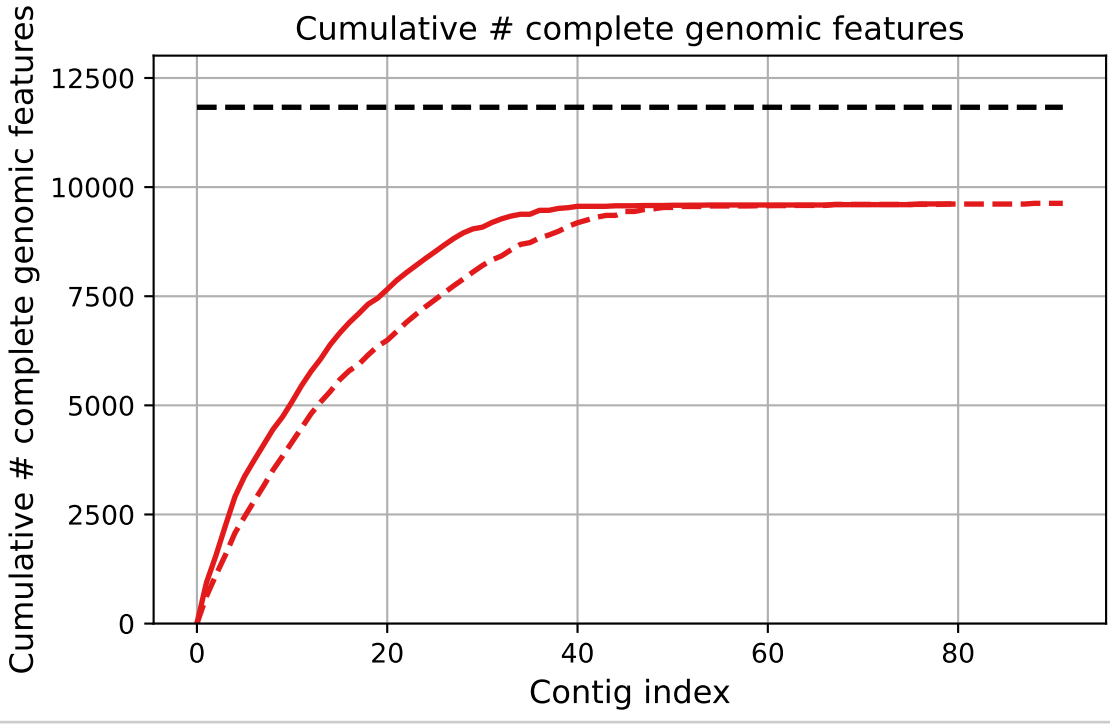

Misassemblies
75
60
45
30
15
0
SPAdes_on_data_2_and_data_1__Scaffolds_broken
relocations
translocations

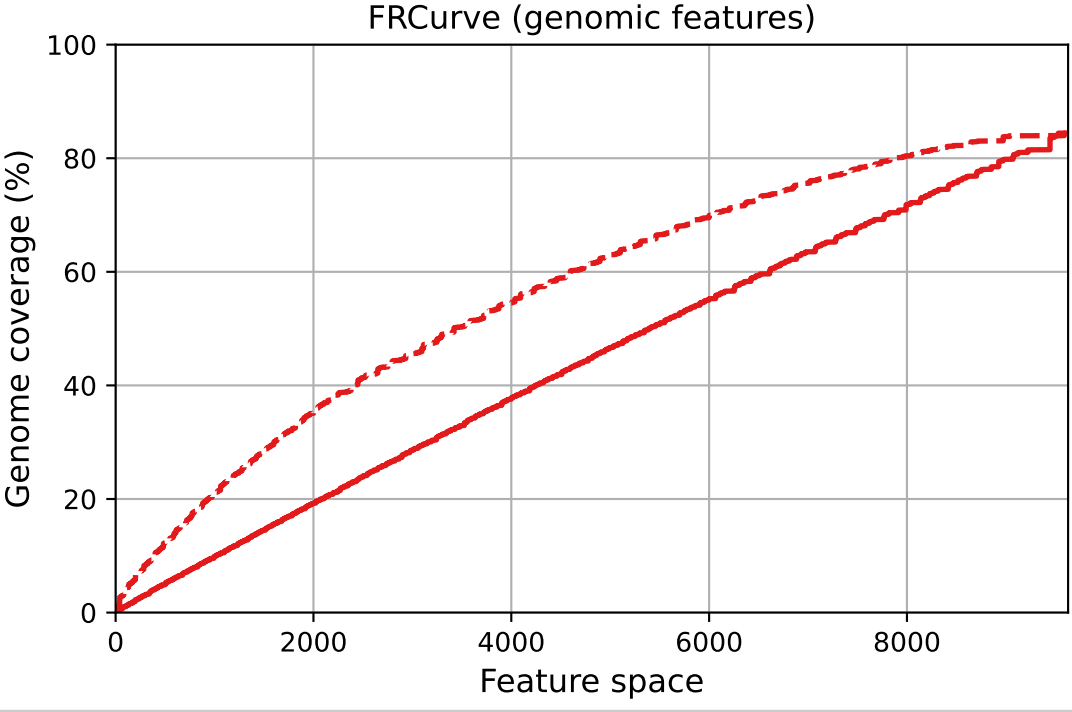

FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
15
30
45
60
75
Feature space
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds

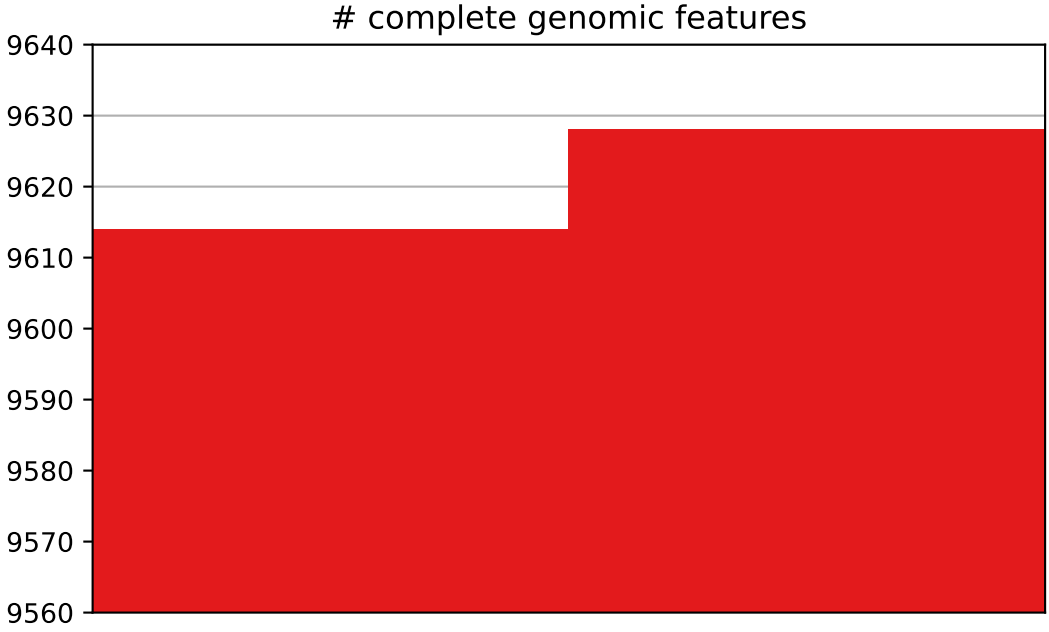

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
3
4
6
0
25
50
75
100
125
_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds_broken

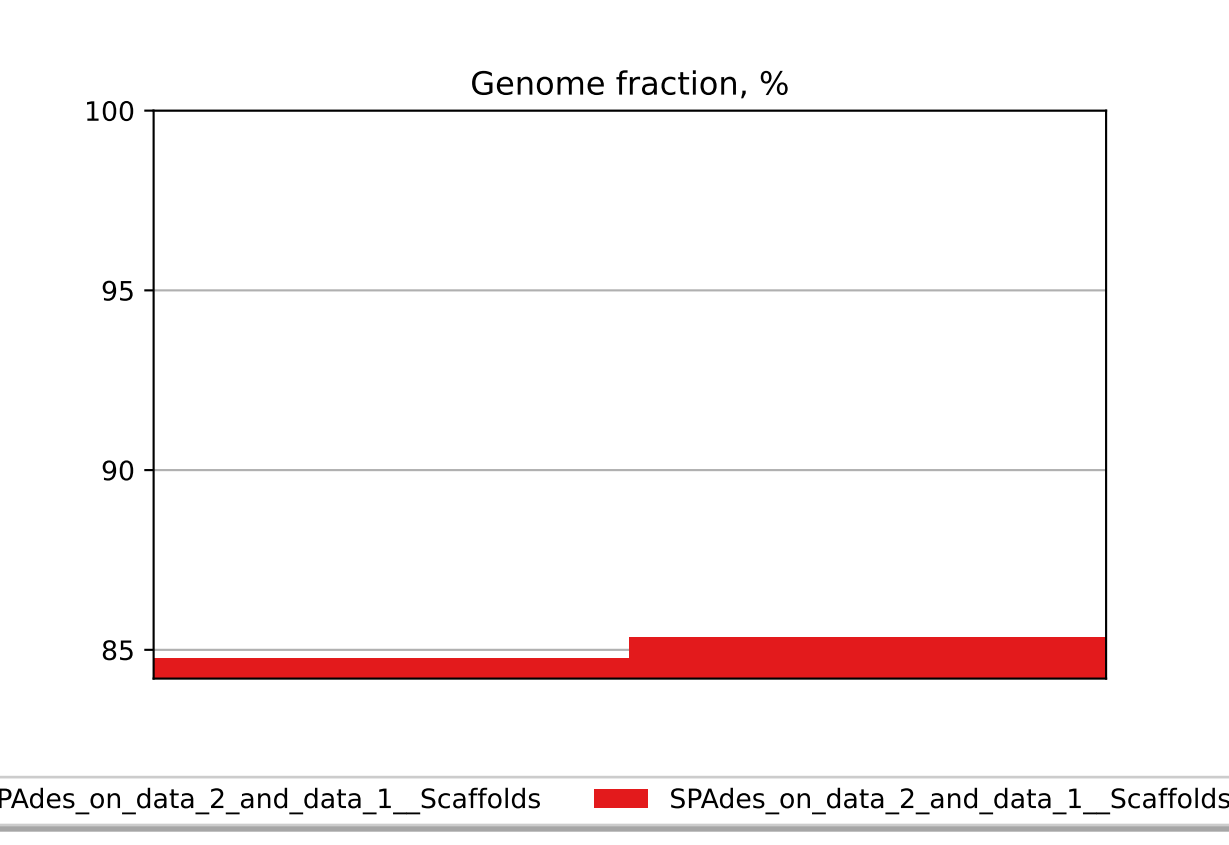

NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
SPAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds


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
9640
9630
9620
9610
9600
9590
9580
9570
9560
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds


Genome fraction, %
100
95
90
85
PAdes_on_data_2_and_data_1__Scaffolds
SPAdes_on_data_2_and_data_1__Scaffolds