Report

	SPAdes_on_data_8_and_data_7__Scaffolds	SPAdes_on_data_8_and_data_7__Scaffolds_broken
# contigs (>= 0 bp)	78	-
# contigs (>= 1000 bp)	46	52
Total length (>= 0 bp)	5053809	-
Total length (>= 1000 bp)	5040390	5038607
# contigs	59	67
Largest contig	570518	506009
Total length	5049193	5048393
Reference length	4641652	4641652
GC (%)	50.61	50.61
Reference GC (%)	50.79	50.79
N50	390869	312376
NG50	408096	312376
N90	94800	88270
NG90	150929	130956
auN	343882.1	276231.0
auNG	374075.2	300436.8
L50	6	7
LG50	5	7
L90	15	19
LG90	12	16
# misassemblies	120	113
# misassembled contigs	16	19
Misassembled contigs length	4640133	4483792
# local misassemblies	66	65
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	3	4
# unaligned contigs	16 + 33 part	17 + 36 part
Unaligned length	1013298	1012949
Genome fraction (%)	87.507	87.911
Duplication ratio	1.004	1.004
# N's per 100 kbp	15.84	0.00
# mismatches per 100 kbp	2239.37	2242.43
# indels per 100 kbp	44.54	45.29
# genomic features	7950 + 320 part	7953 + 341 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	9 + 1 part	8 + 2 part
Largest alignment	188758	188758
Total aligned length	4034211	4033800
NA50	37783	37213
NGA50	44299	41861
NA90	-	-
NGA90	-	-
auNA	51347.4	50328.5
auNGA	55855.8	54738.7
LA50	35	36
LGA50	30	31
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

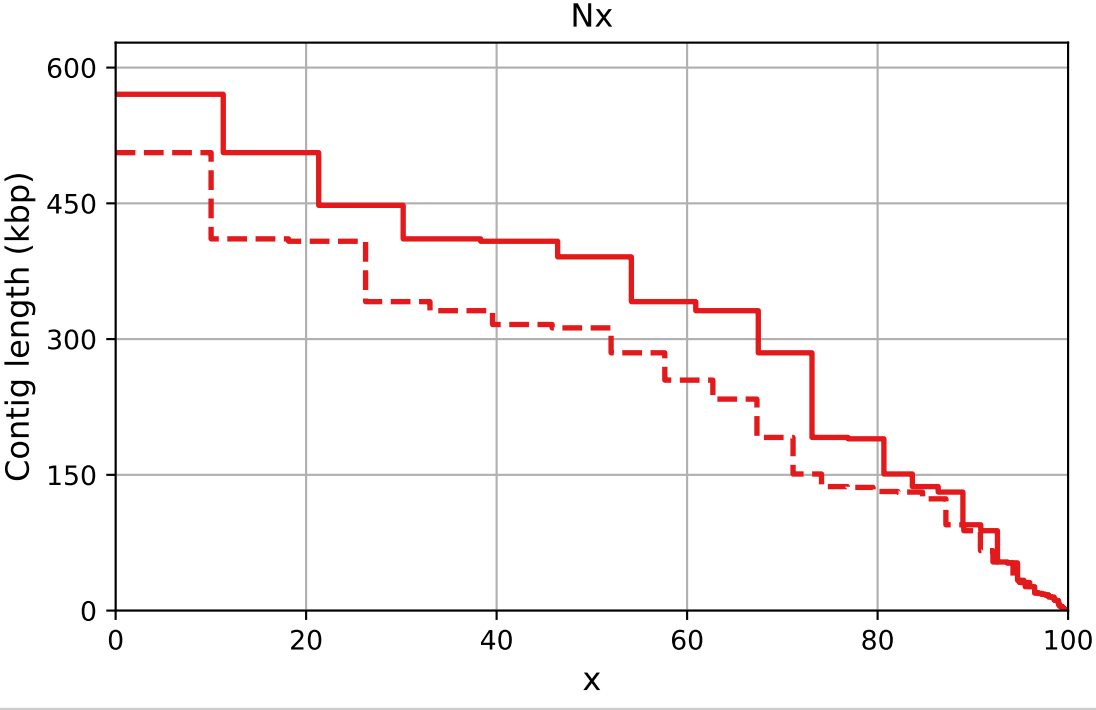
	SPAdes_on_data_8_and_data_7__Scaffolds	SPAdes_on_data_8_and_data_7__Scaffolds_broken
# misassemblies	120	113
# contig misassemblies	119	113
# c. relocations	119	113
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	16	19
Misassembled contigs length	4640133	4483792
# local misassemblies	66	65
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	3	4
# mismatches	90341	90455
# indels	1797	1827
# indels (<= 5 bp)	1532	1567
# indels (> 5 bp)	265	260
Indels length	18799	18244

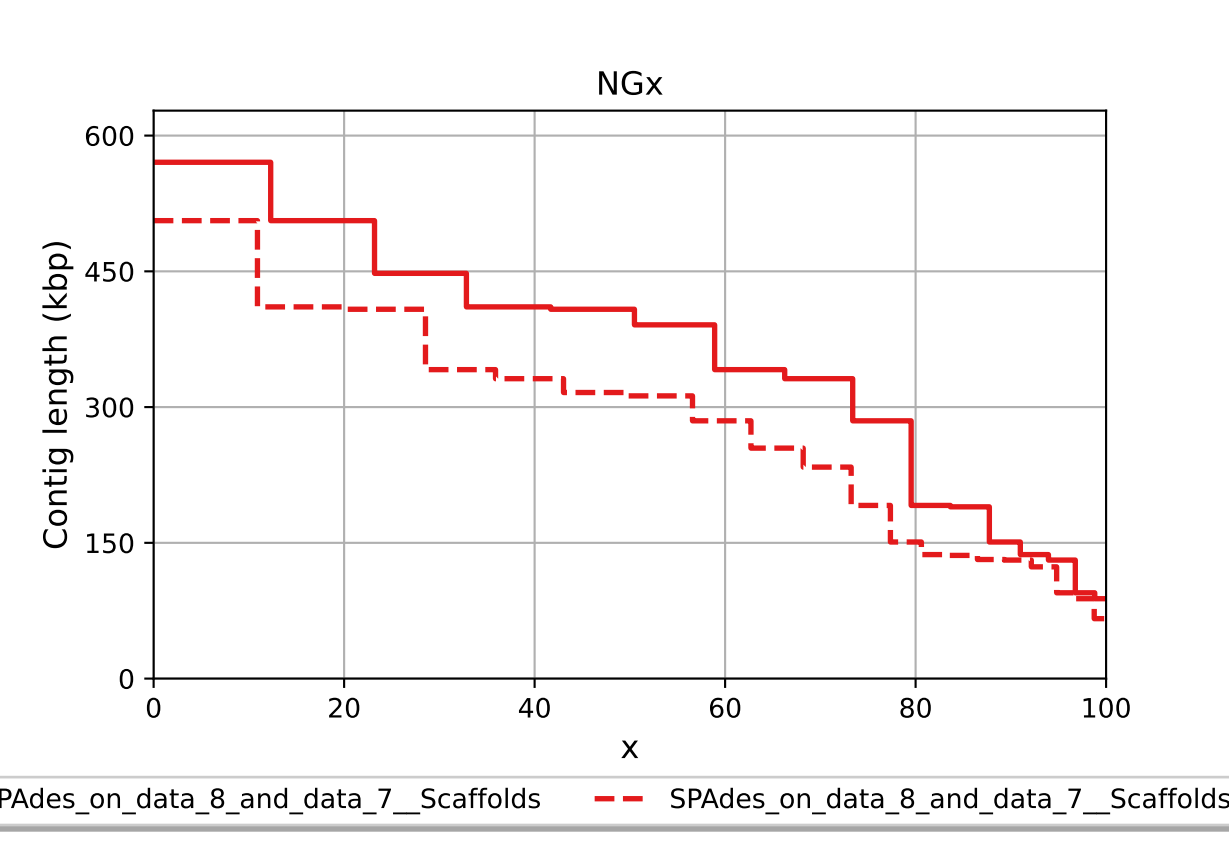
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

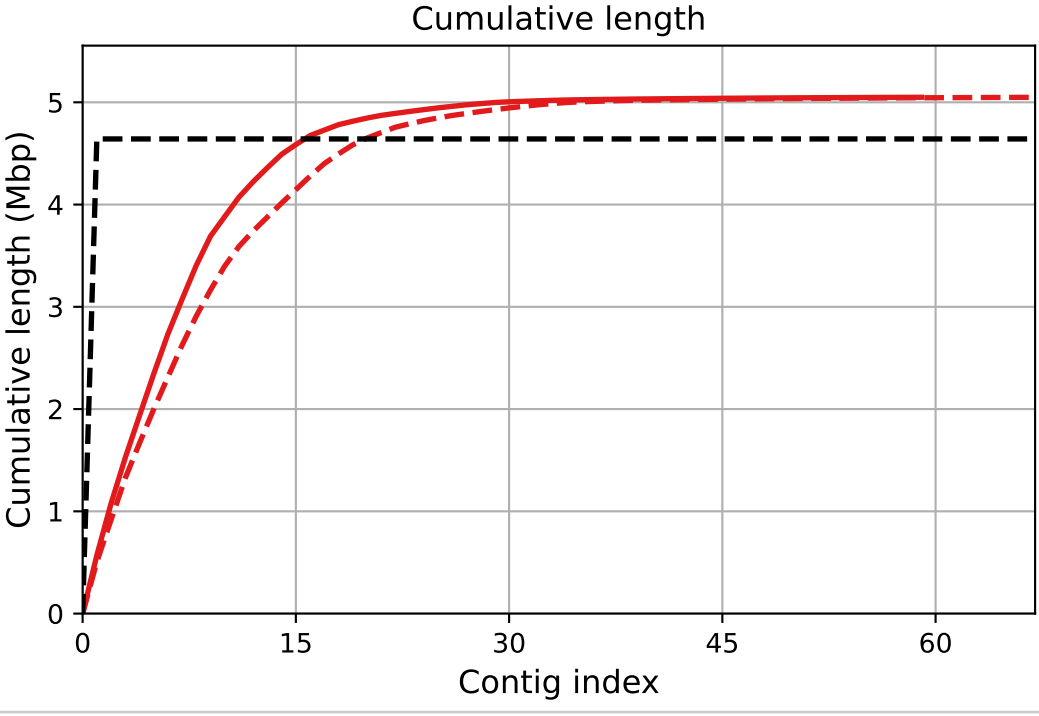
Unaligned report

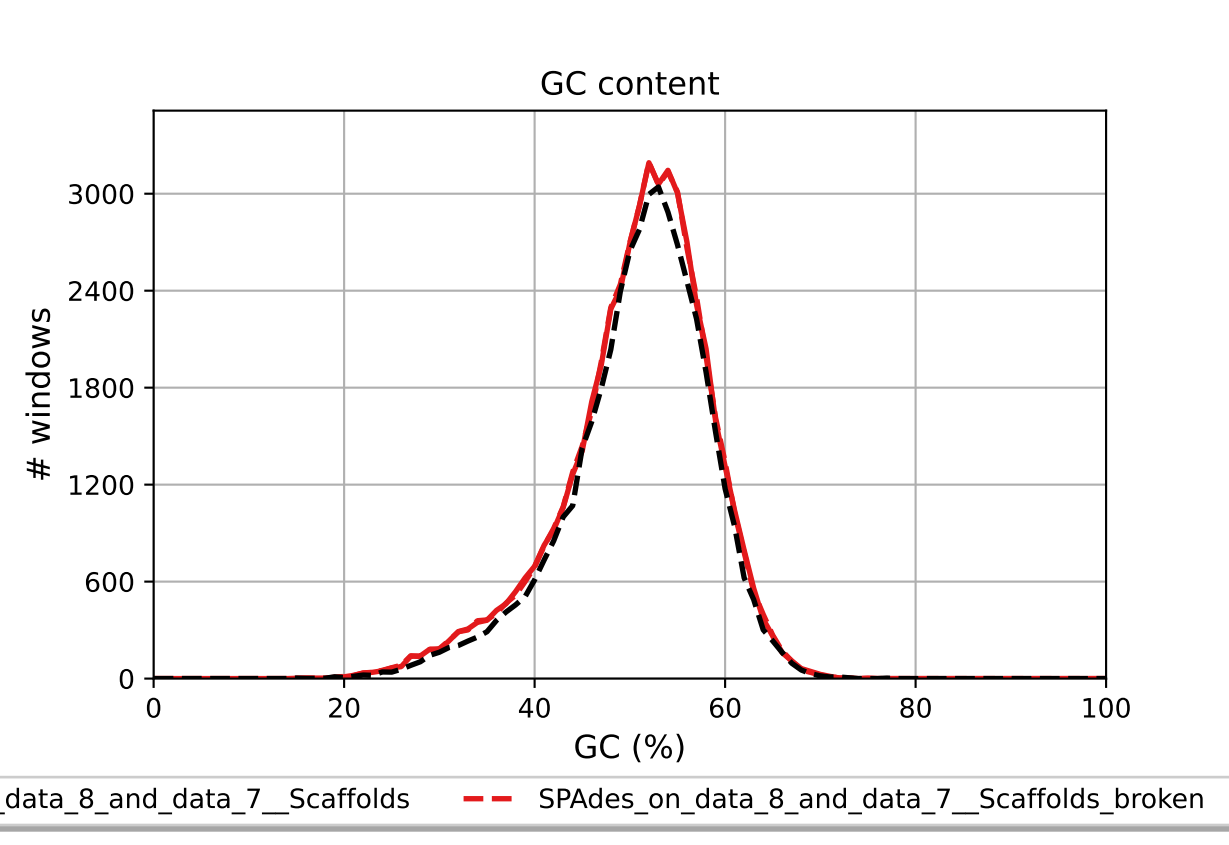
	SPAdes_on_data_8_and_data_7__Scaffolds	SPAdes_on_data_8_and_data_7__Scaffolds_broken
# fully unaligned contigs	16	17
Fully unaligned length	35403	35478
# partially unaligned contigs	33	36
Partially unaligned length	977895	977471
# N's	800	0

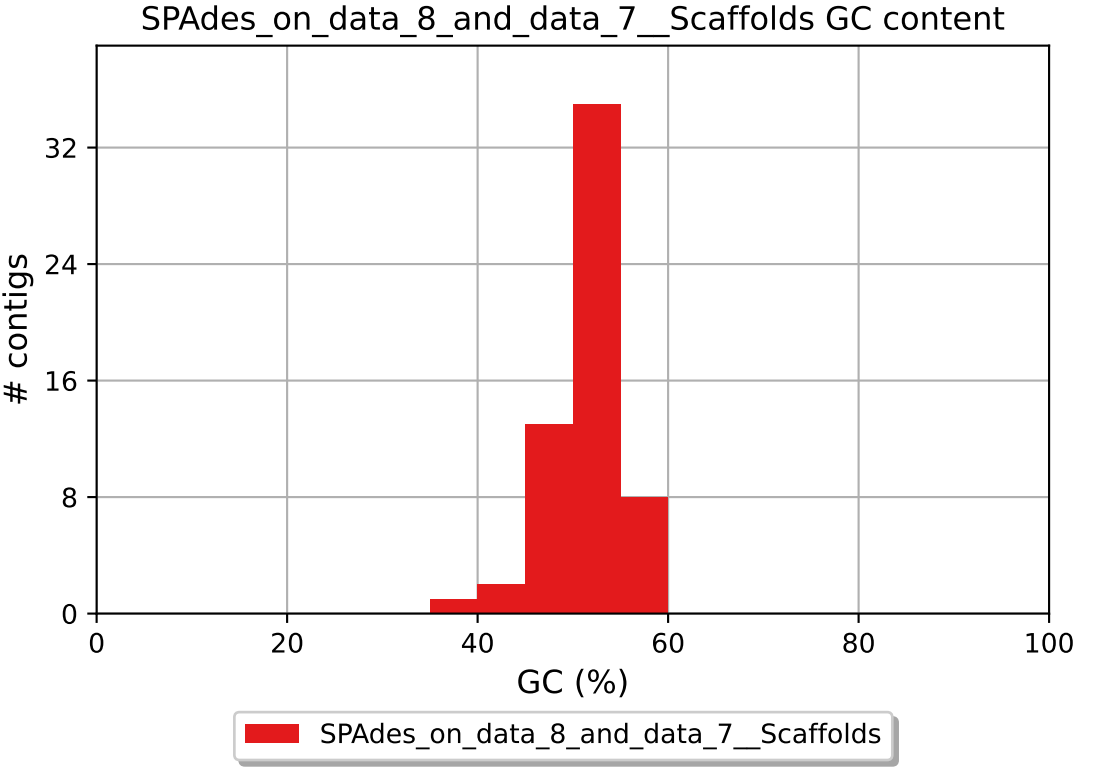
All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

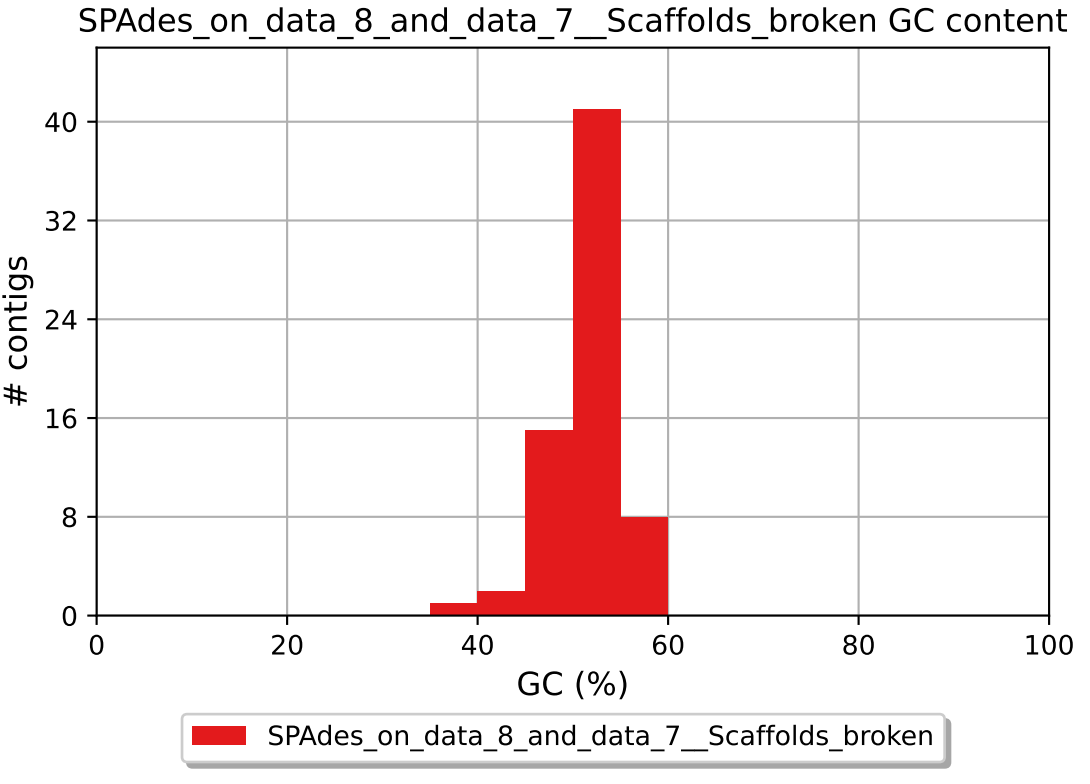

Nx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds

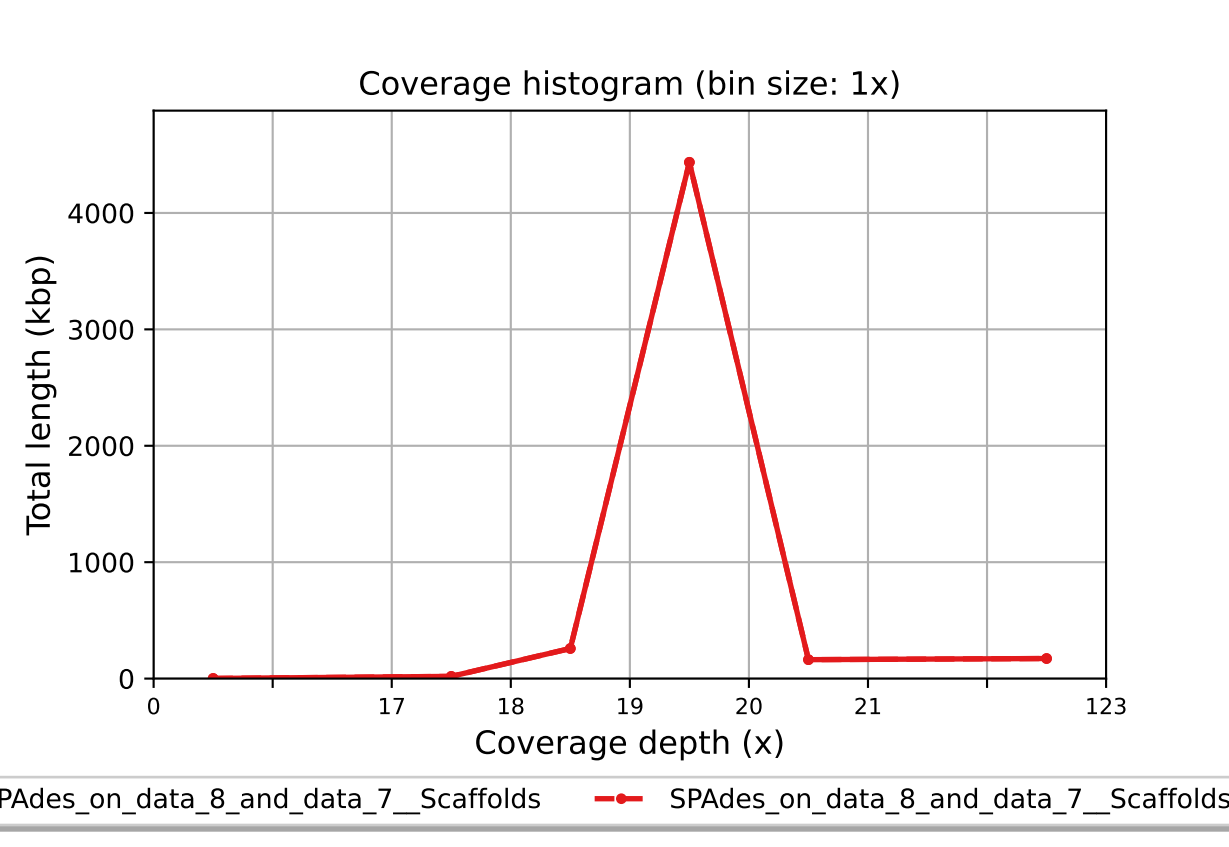

NGx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds

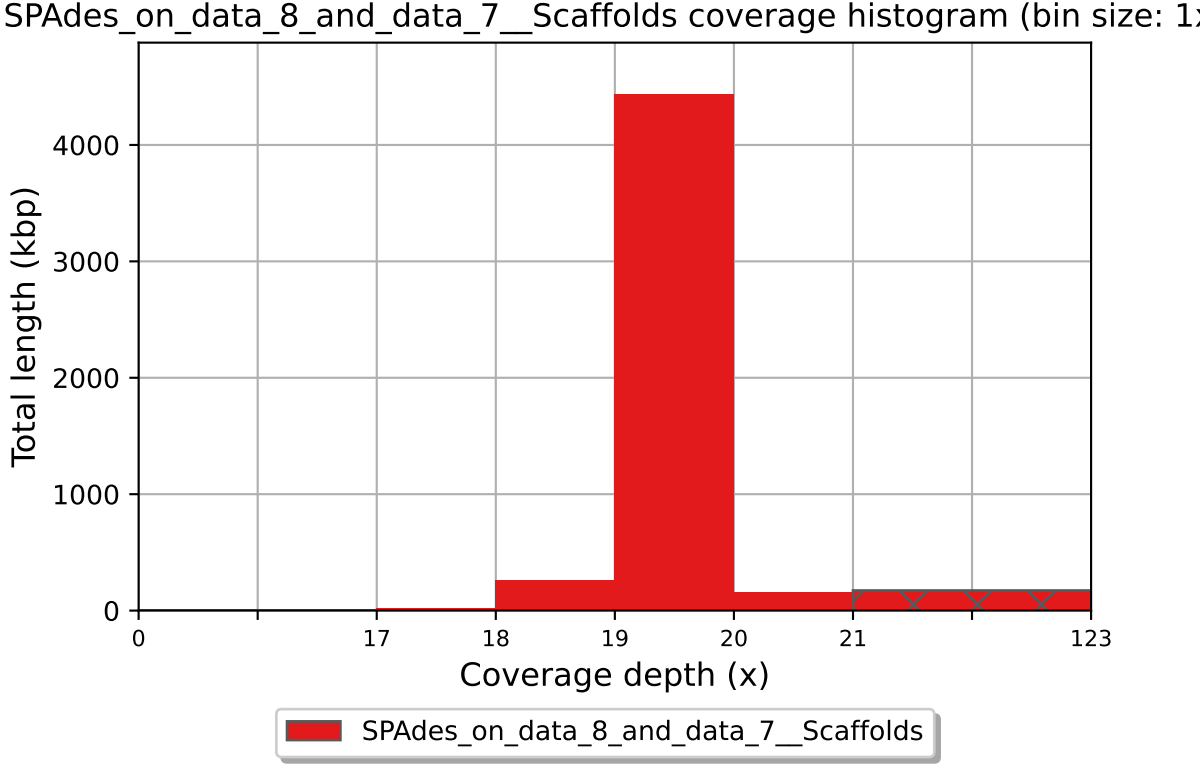

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
0
15
30
45
60
Contig index
_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds_broken

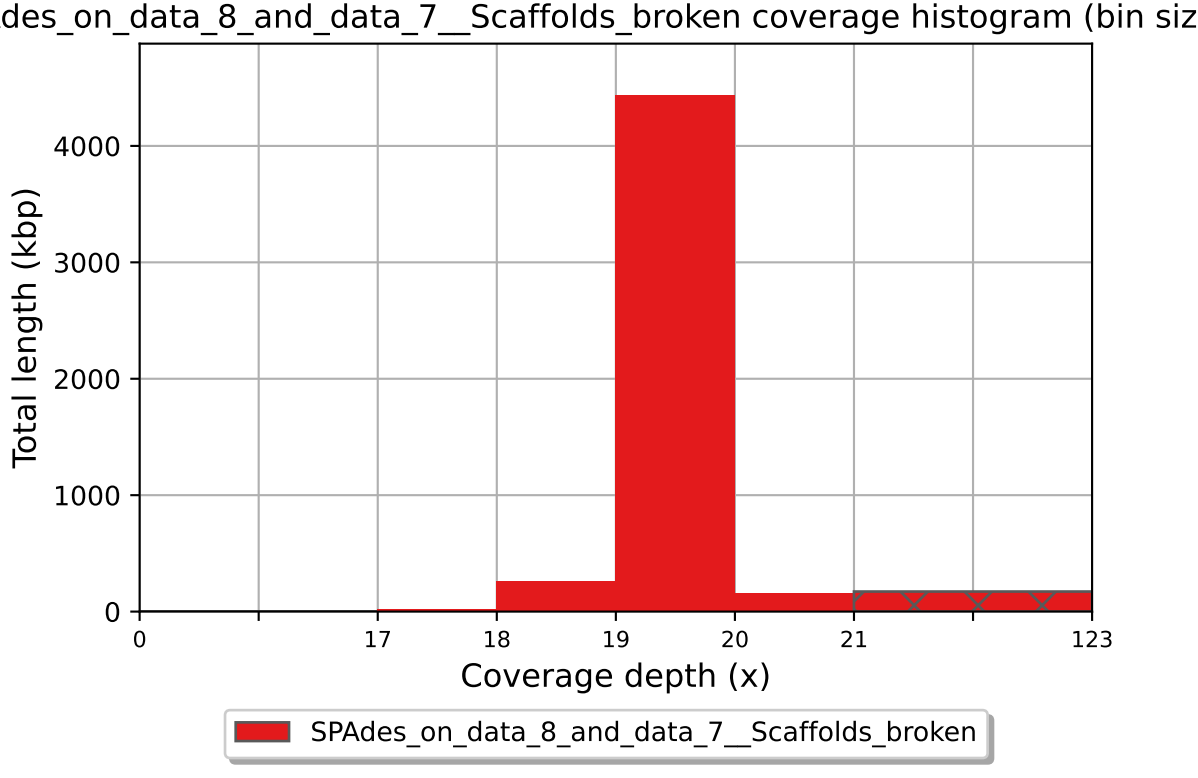

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds_broken

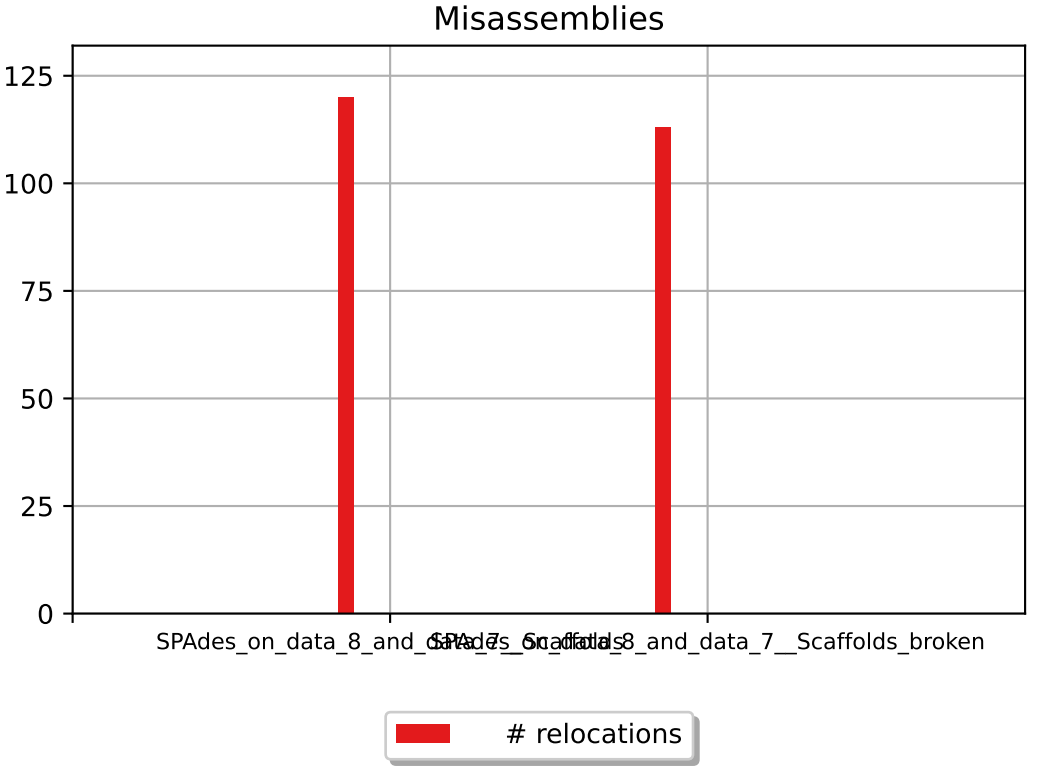

SPAdes_on_data_8_and_data_7__Scaffolds GC content
contigs
0
8
16
24
32
0
20
40
60
80
100
GC (%)
SPAdes_on_data_8_and_data_7__Scaffolds

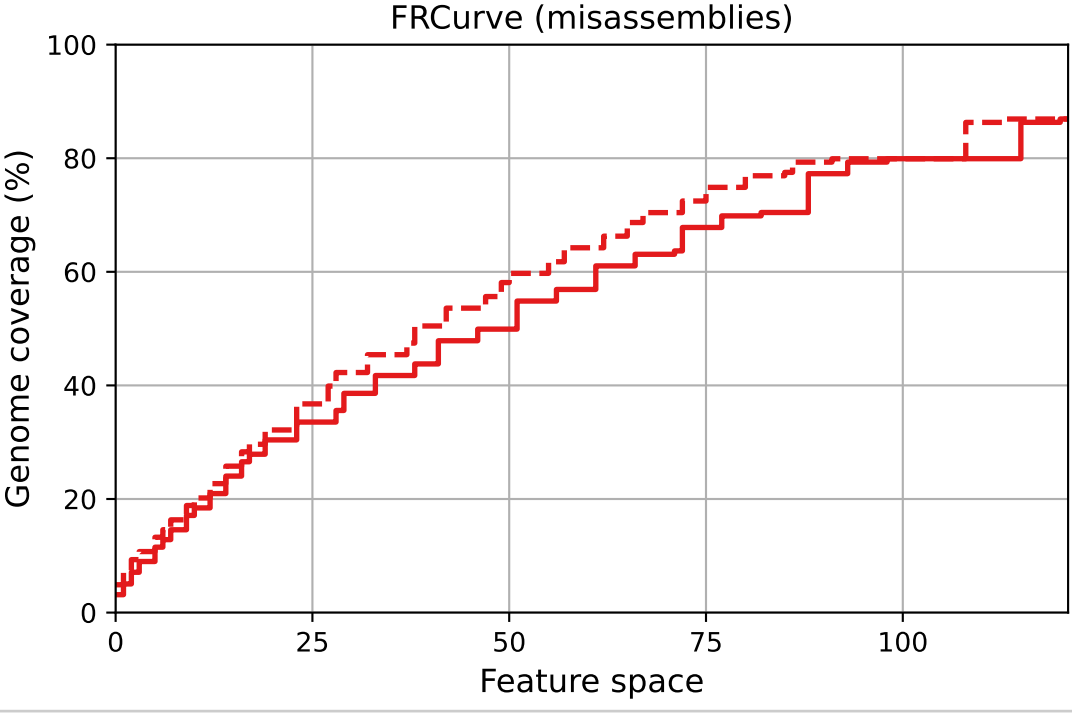

SPAdes_on_data_8_and_data_7__Scaffolds_broken GC content
contigs
0
8
16
24
32
40
0
20
40
60
80
100
GC (%)
SPAdes_on_data_8_and_data_7__Scaffolds_broken

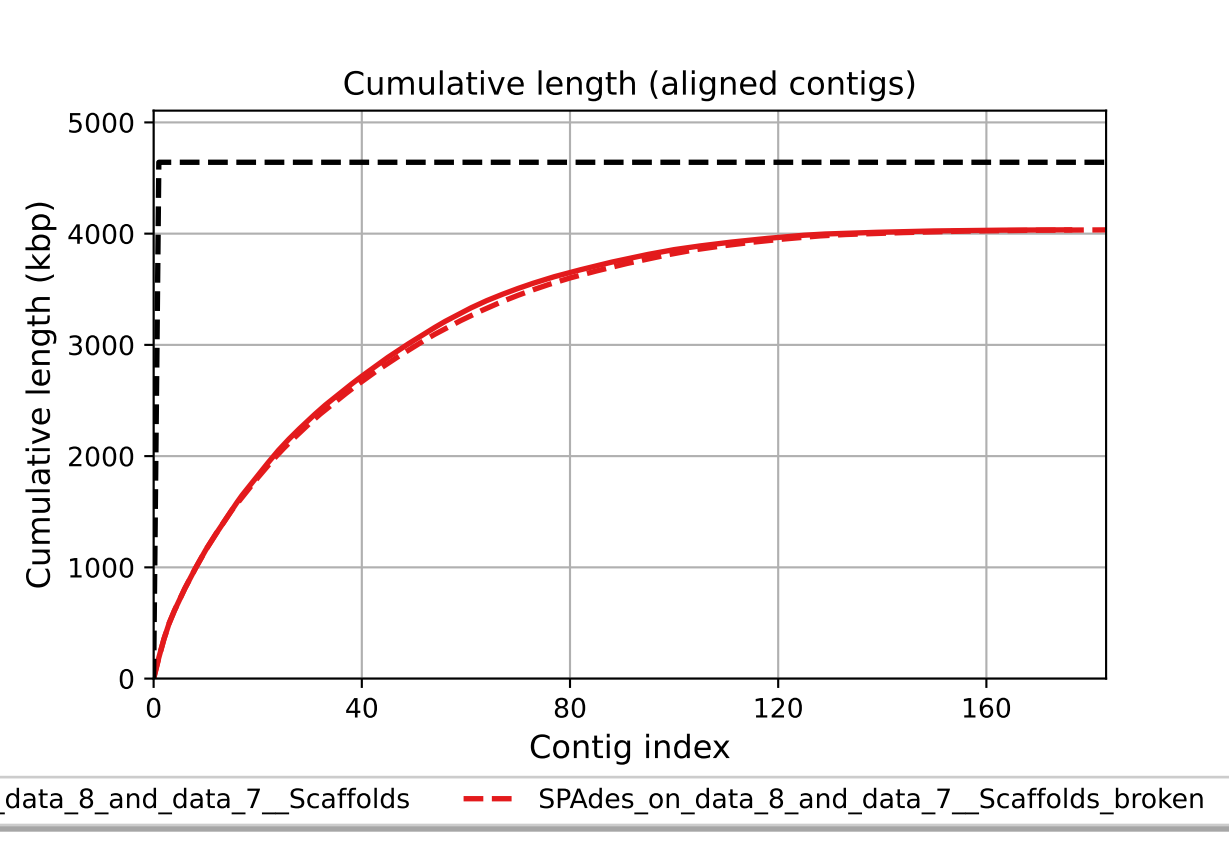

Coverage histogram (bin size: 1x)
Total length (kbp)
4000
3000
2000
1000
0
0
17
18
19
20
21
123
Coverage depth (x)
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds

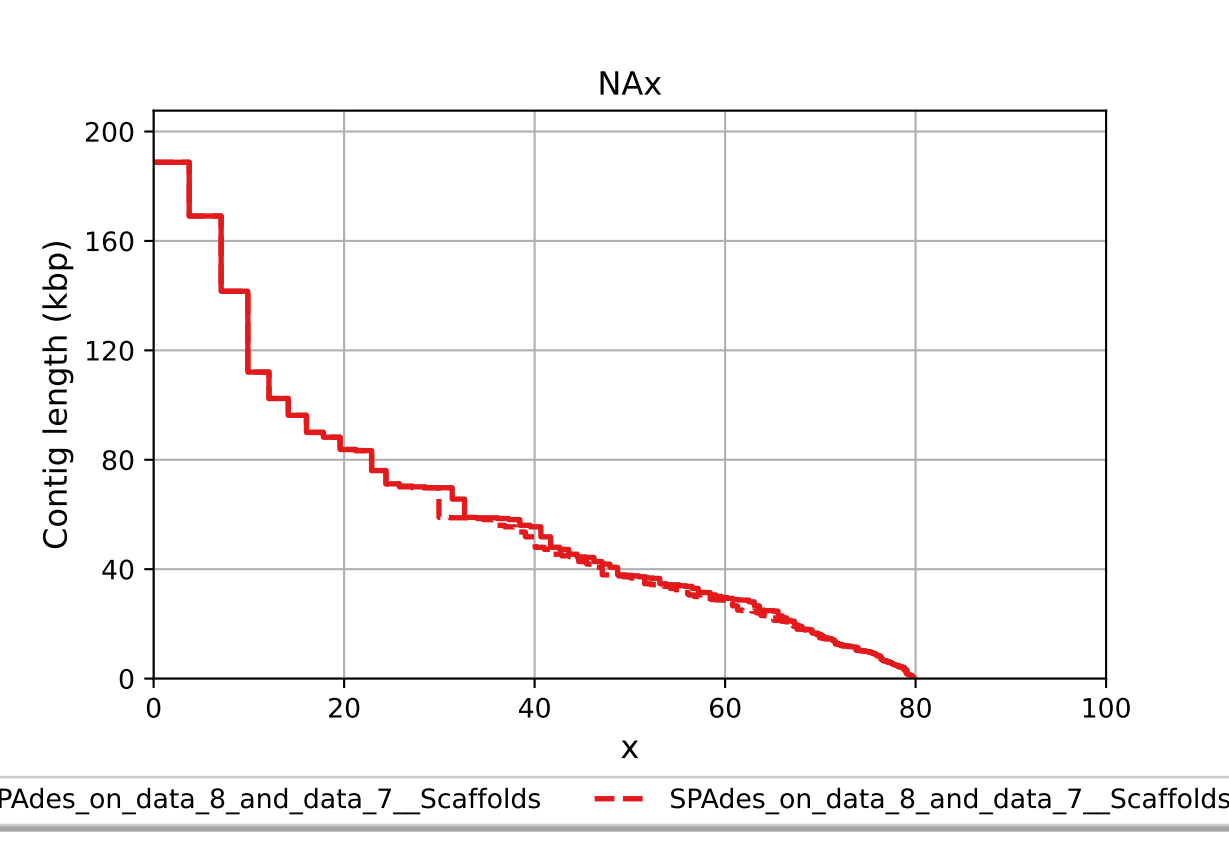

SPAdes_on_data_8_and_data_7__Scaffolds coverage histogram (bin size: 1x
Total length (kbp)
4000
3000
2000
1000
0
0
17
18
19
20
21
123
Coverage depth (x)
SPAdes_on_data_8_and_data_7__Scaffolds

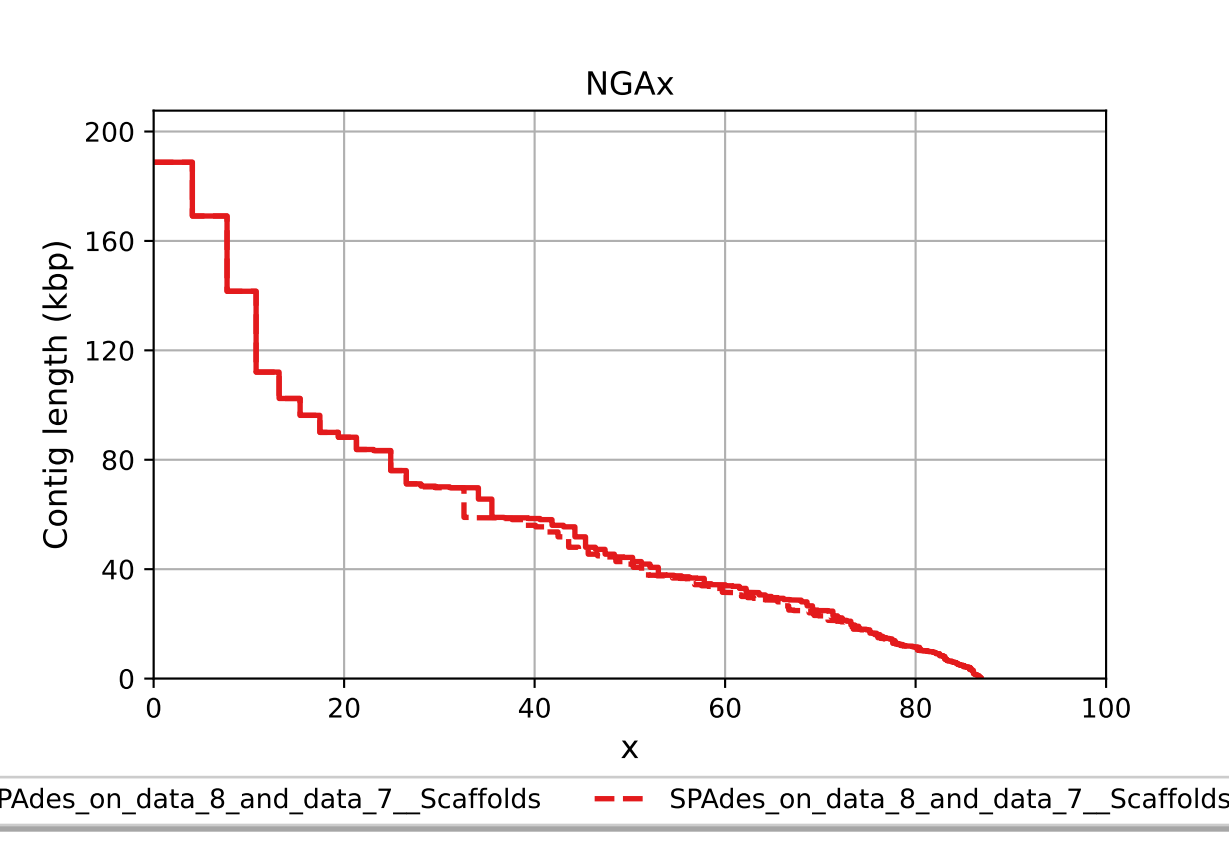

Ades_on_data_8_and_data_7__Scaffolds_broken coverage histogram (bin size
Total length (kbp)
4000
3000
2000
1000
0
0
17
18
19
20
21
123
Coverage depth (x)
SPAdes_on_data_8_and_data_7__Scaffolds_broken

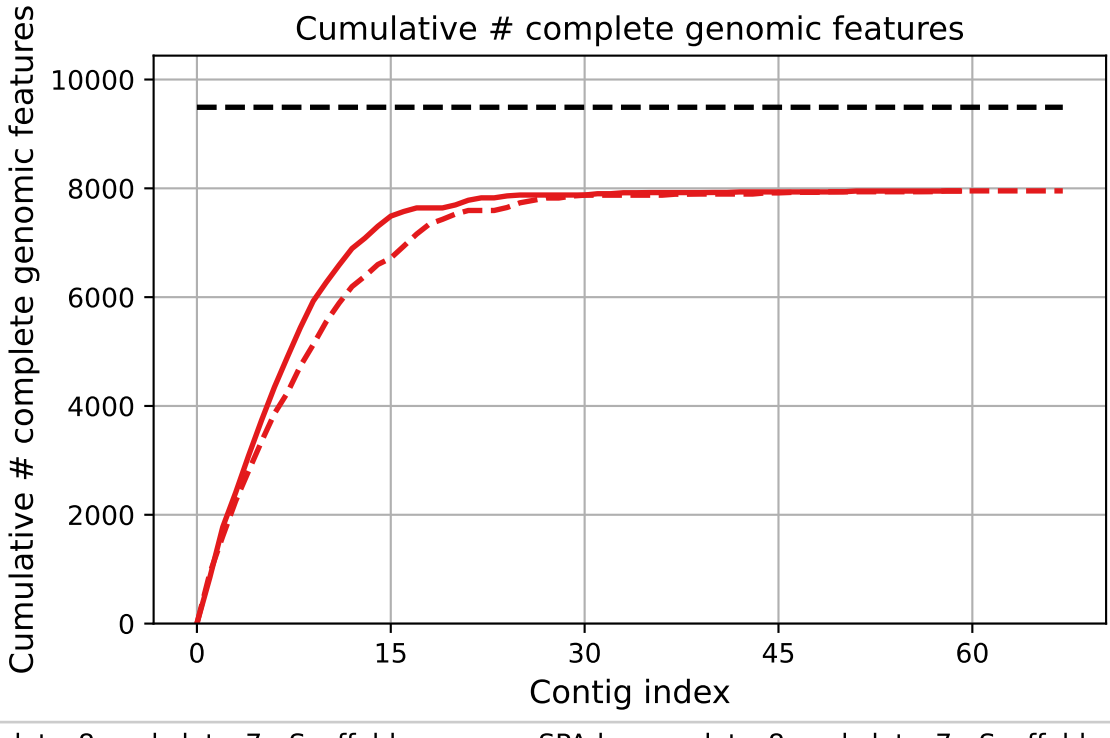

Misassemblies
125
100
75
50
25
0
SPAdes_on_data_8_and_data_7__Scaffolds_broken
relocations

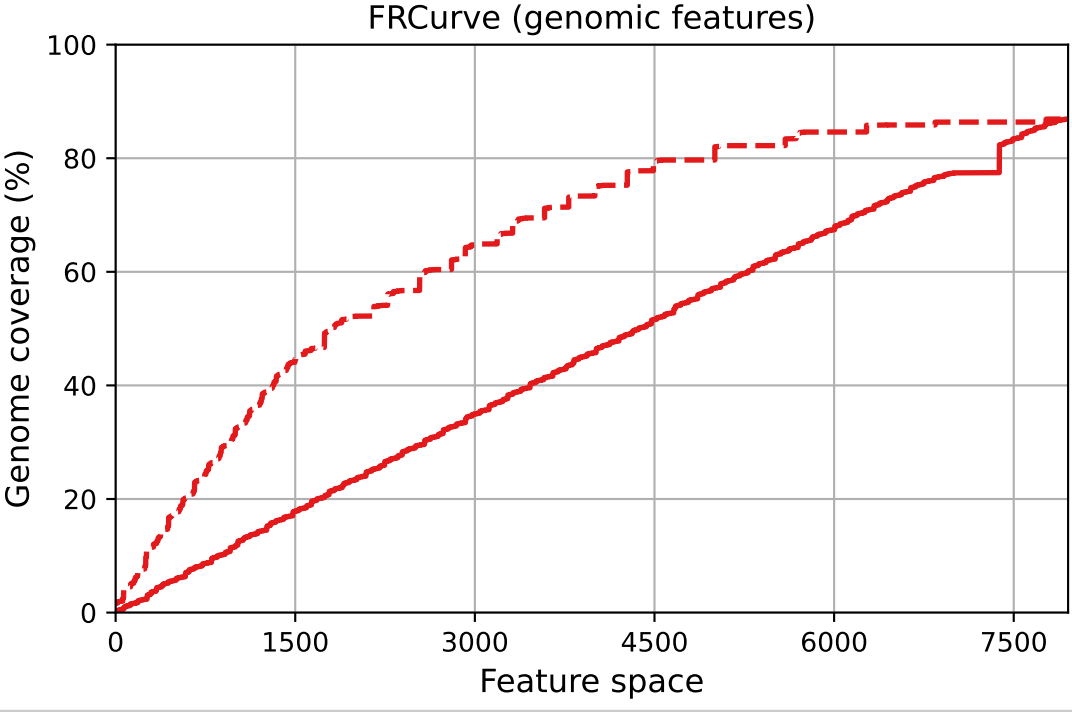

FRCurve (misassemblies)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
25
50
75
100
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds

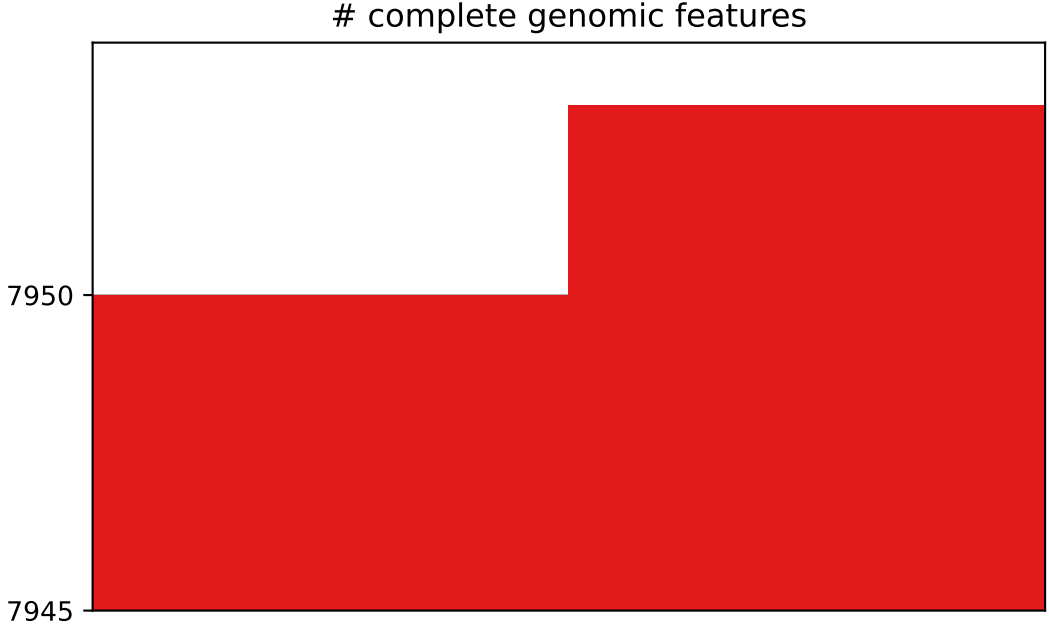

Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
40
80
120
160
Contig index
_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds_broken

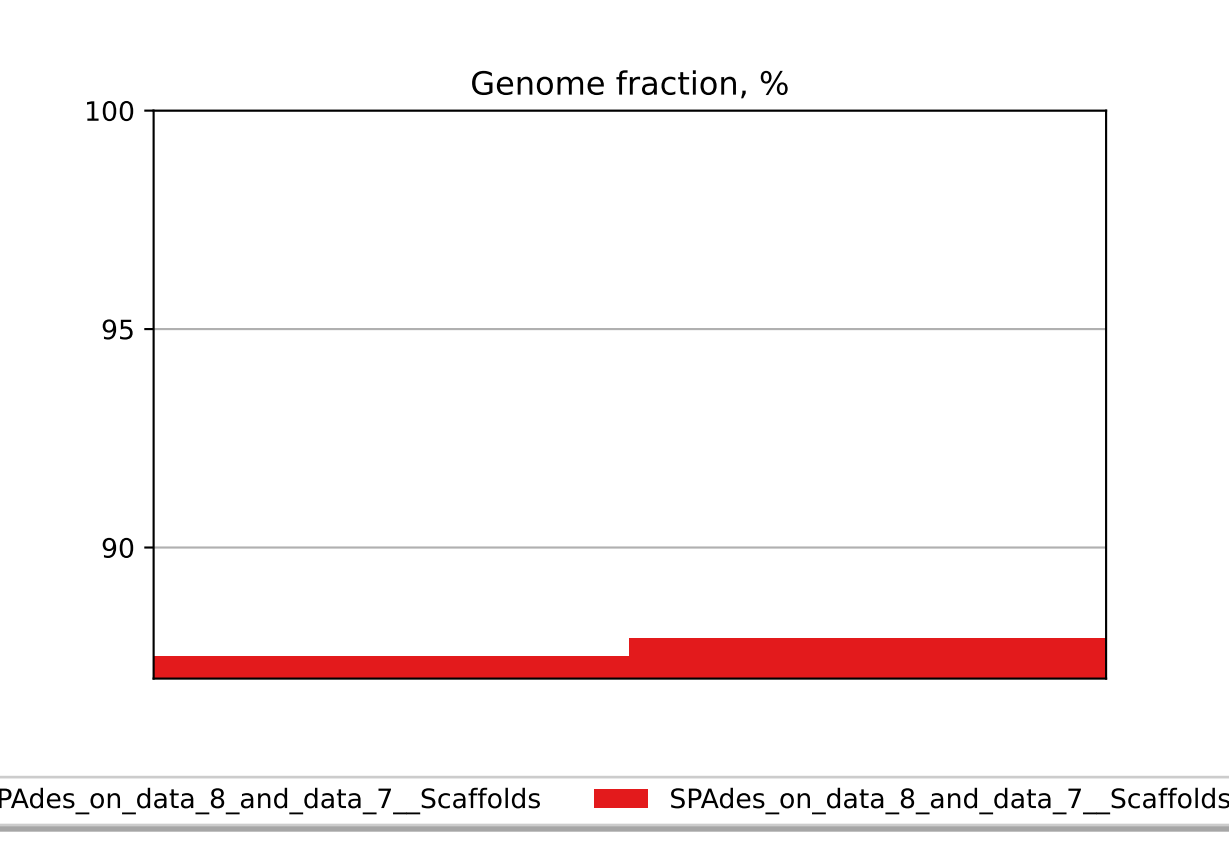

NAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds


NGAx
Contig length (kbp)
200
160
120
80
40
0
0
20
40
60
80
100
x
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds


Cumulative # complete genomic features
Cumulative # complete genomic features
10000
8000
6000
4000
2000
0
0
15
30
45
60
Contig index
_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds_broken


FRCurve (genomic features)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
1500
3000
4500
6000
7500
PAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds


complete genomic features
7950
7945
SPAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds


Genome fraction, %
100
95
90
SPAdes_on_data_8_and_data_7__Scaffolds
SPAdes_on_data_8_and_data_7__Scaffolds