

## Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	191	-
# contigs (>= 1000 bp)	63	71
Total length (>= 0 bp)	4813654	-
Total length (>= 1000 bp)	4788123	4786289
# contigs	72	82
Largest contig	549770	322638
Total length	4794213	4792805
Reference length	4951383	4951383
GC (%)	52.13	52.13
Reference GC (%)	52.24	52.24
N50	193475	168456
NG50	178662	149367
N90	53847	51504
NG90	44707	44707
auN	224465.2	166813.7
auNG	217340.1	161471.2
L50	8	10
LG50	9	11
L90	27	32
LG90	30	35
# misassemblies	7	7
# misassembled contigs	7	7
Misassembled contigs length	1416504	1035190
# local misassemblies	5	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	0 + 5 part
Unaligned length	81933	81933
Genome fraction (%)	96.032	96.017
Duplication ratio	1.001	1.001
# N's per 100 kbp	22.94	0.00
# mismatches per 100 kbp	28.13	28.20
# indels per 100 kbp	3.65	3.46
# genomic features	0 + 0 part	0 + 0 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 0 part	2 + 0 part
Largest alignment	376430	322563
Total aligned length	4710913	4709961
NA50	178662	129564
NGA50	152567	123652
NA90	35969	35969
NGA90	30214	26152
auNA	187266.9	155275.2
auNGA	181322.6	150302.2
LA50	9	11
LGA50	10	12
LA90	32	37
LGA90	36	42

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

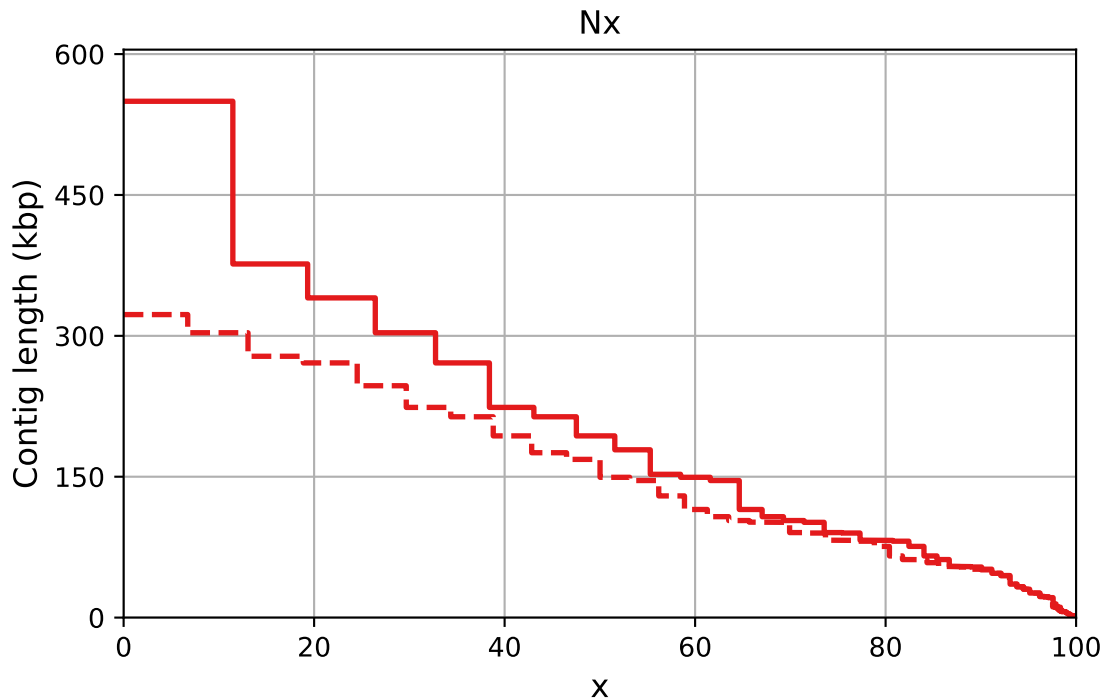
	SPAdes_on_data_2_and_data_1_Scaffolds	SPAdes_on_data_2_and_data_1_Scaffolds_broken
# misassemblies	7	7
# contig misassemblies	7	7
# c. relocations	7	7
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	7	7
Misassembled contigs length	1416504	1035190
# local misassemblies	5	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	0
# mismatches	1325	1328
# indels	172	163
# indels (<= 5 bp)	137	136
# indels (> 5 bp)	35	27
Indels length	3722	2336

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  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	0	0
Fully unaligned length	0	0
# partially unaligned contigs	5	5
Partially unaligned length	81933	81933
# N's	1100	0

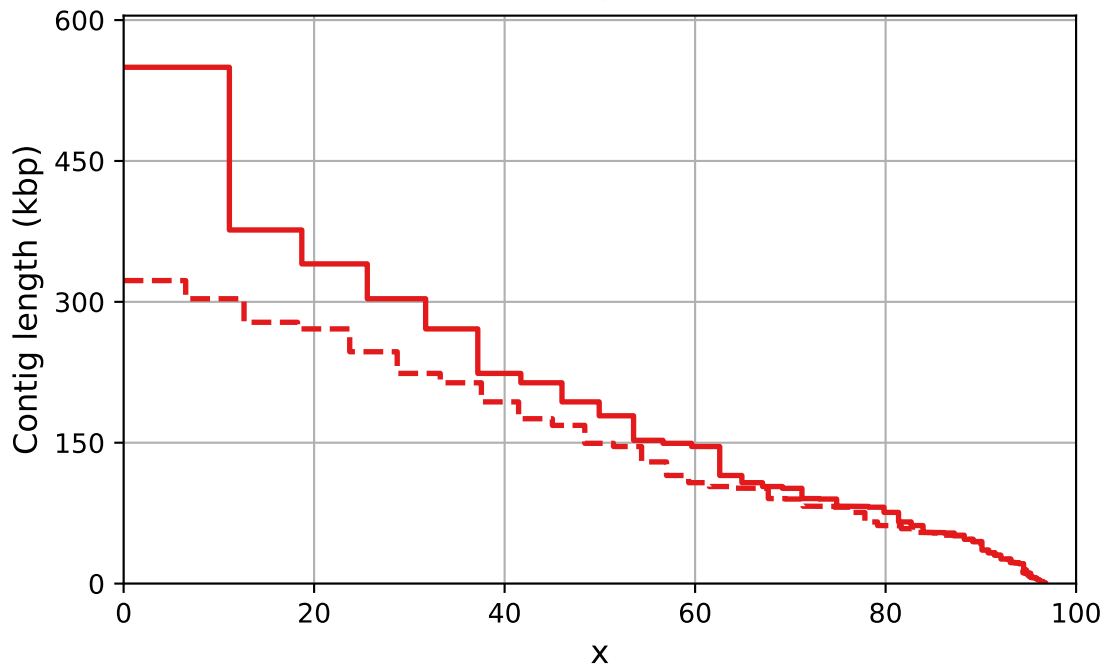
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



PAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds

SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds

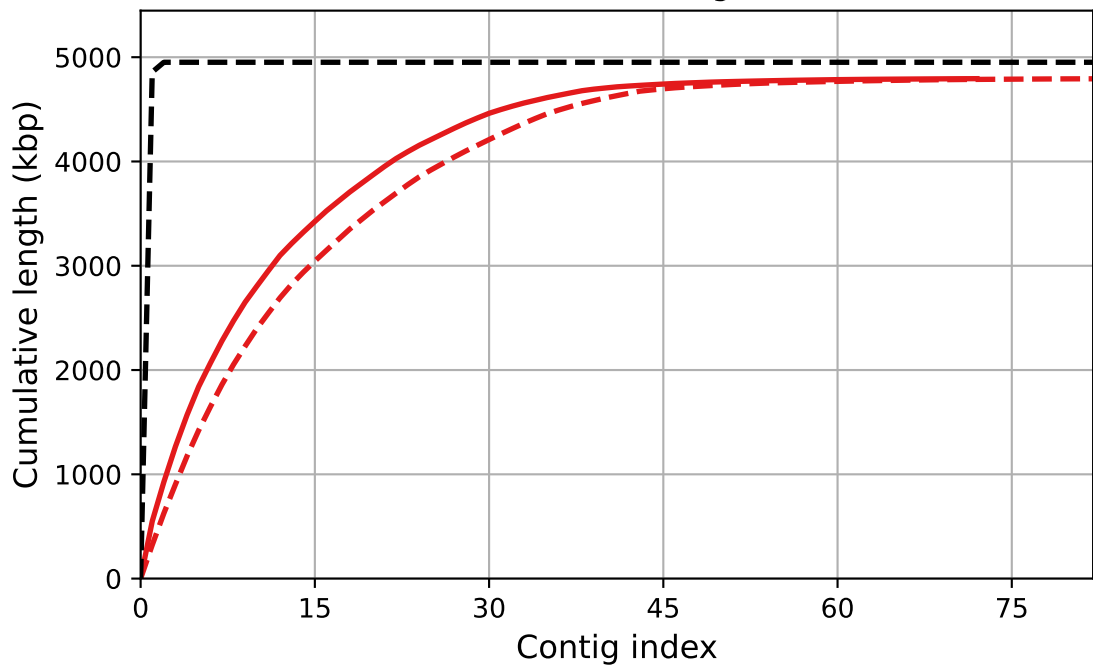
# NGx



PAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

SPAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

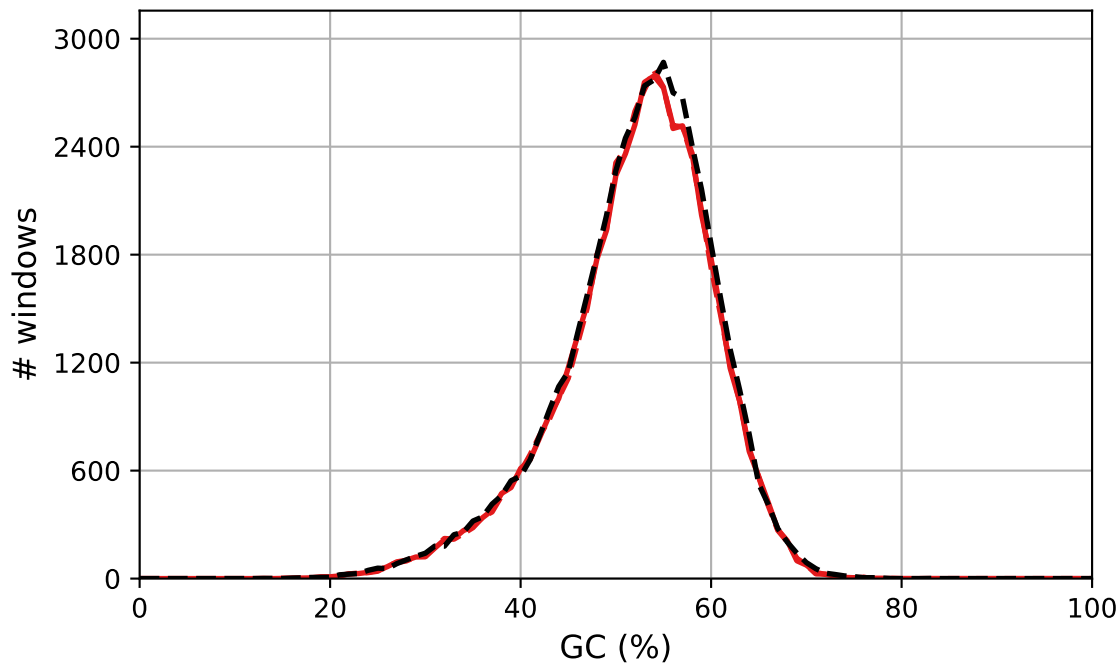
Cumulative length



\_data\_2\_and\_data\_1\_\_Scaffolds

-- SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken

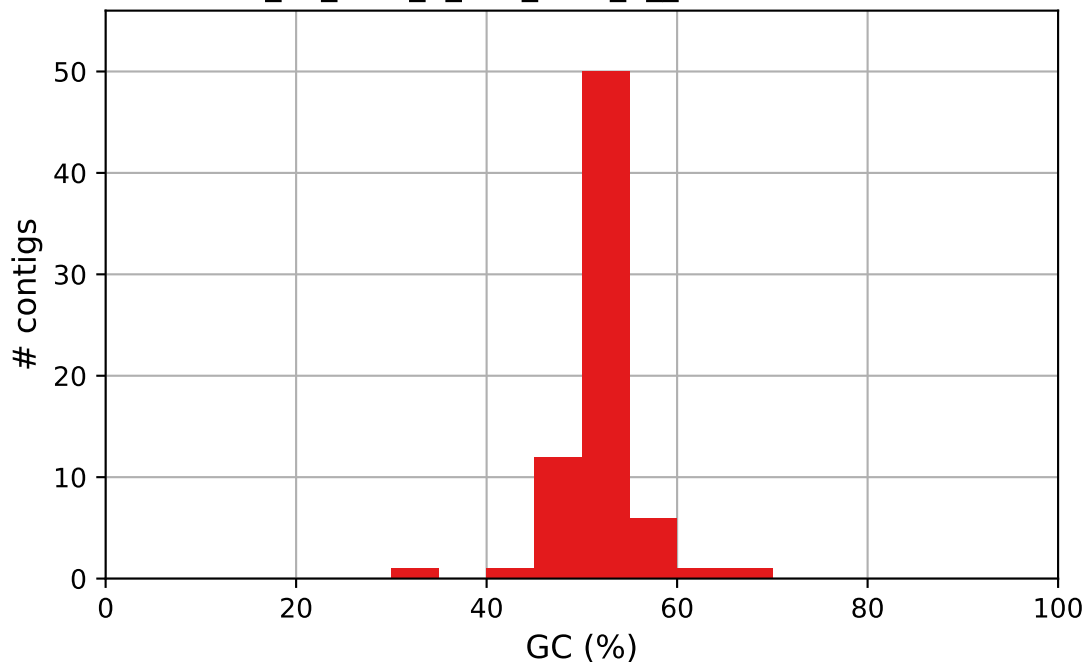
GC content



\_data\_2\_and\_data\_1\_\_Scaffolds

-- SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken

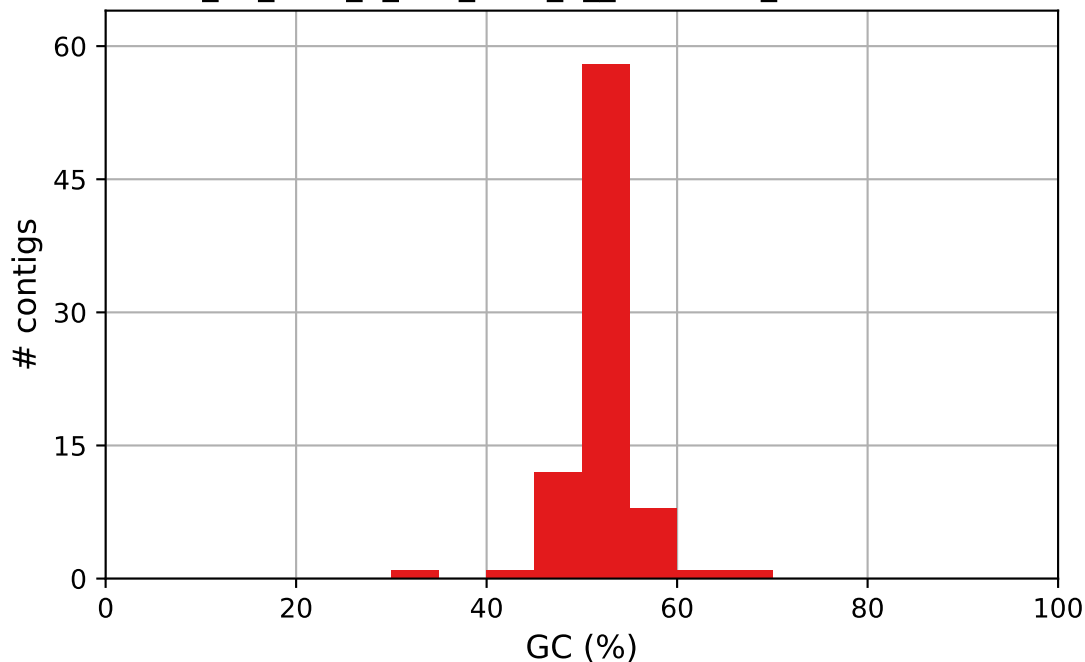
SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds GC content



SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds

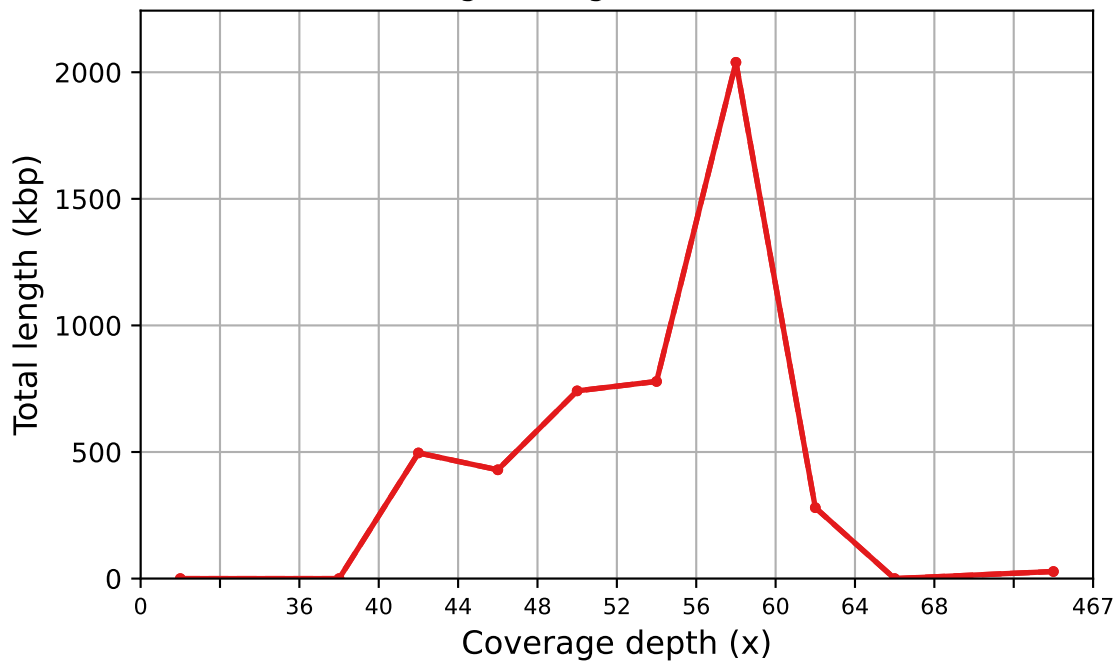


SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken GC content



SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken

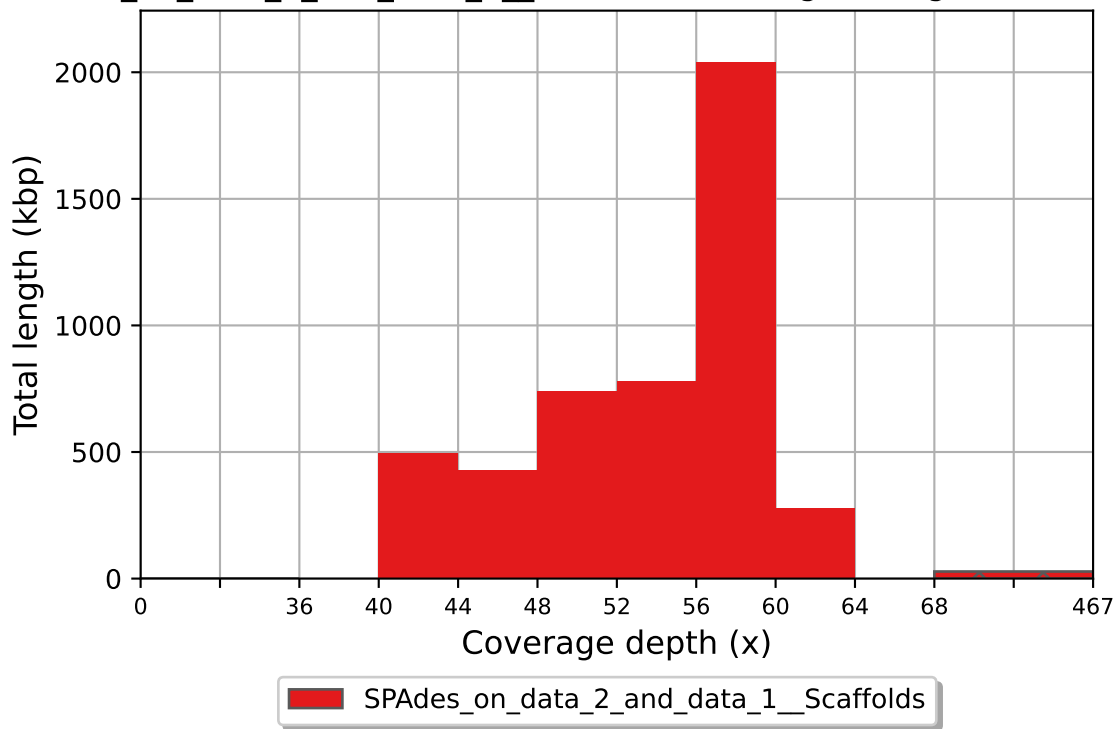
Coverage histogram (bin size: 4x)



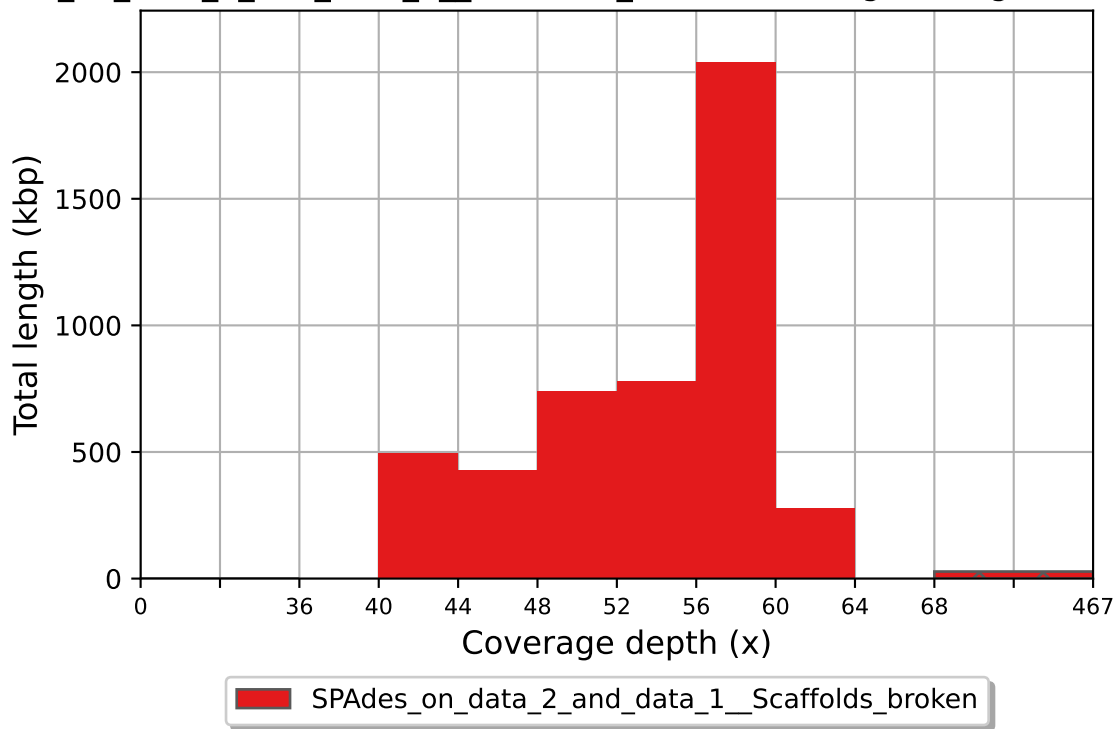
PAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

—●— SPAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

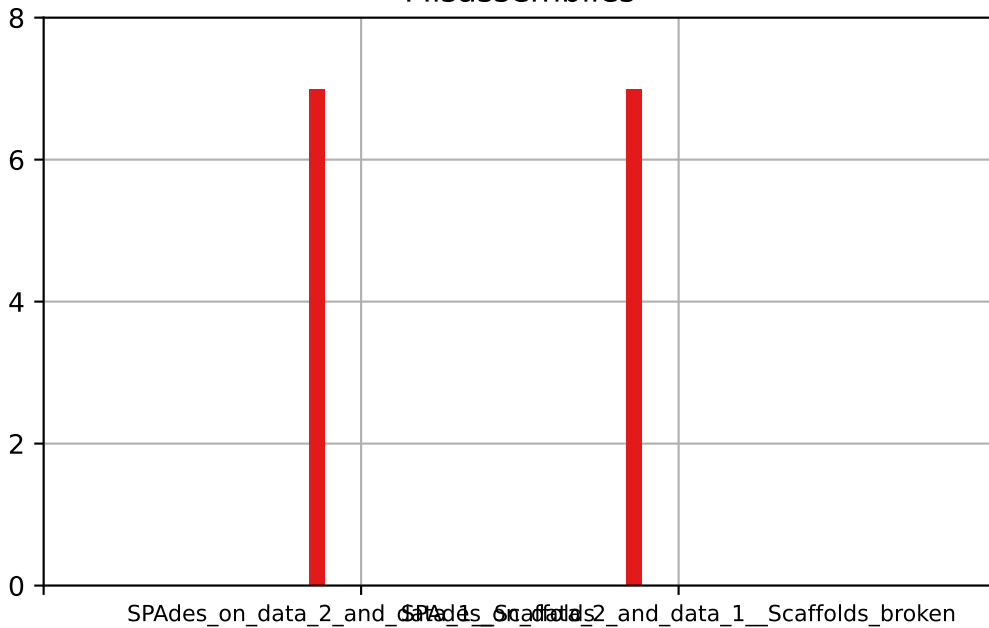
SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds coverage histogram (bin size: 4x)



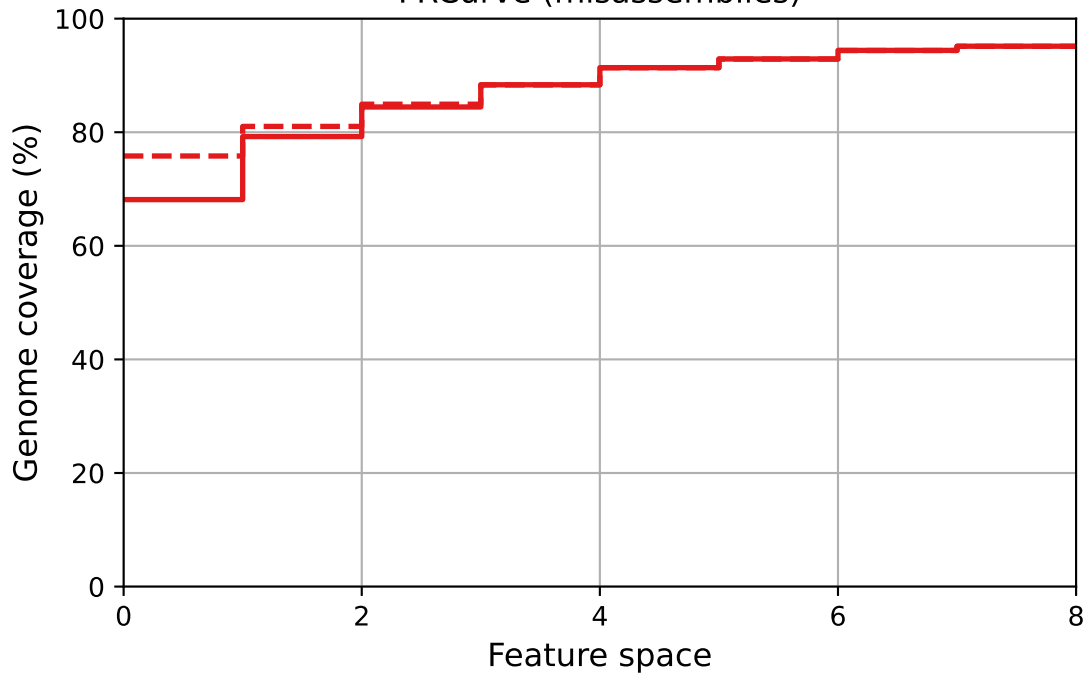
Ades\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken coverage histogram (bin size



## Misassemblies



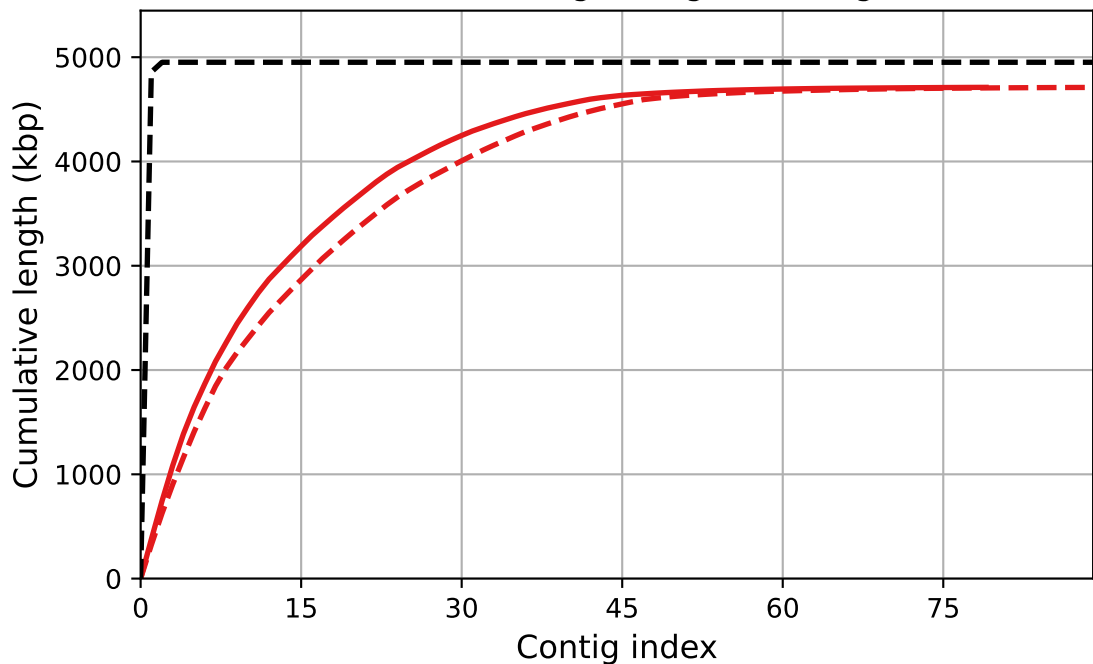
FRCurve (misassemblies)



PAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

-- SPAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

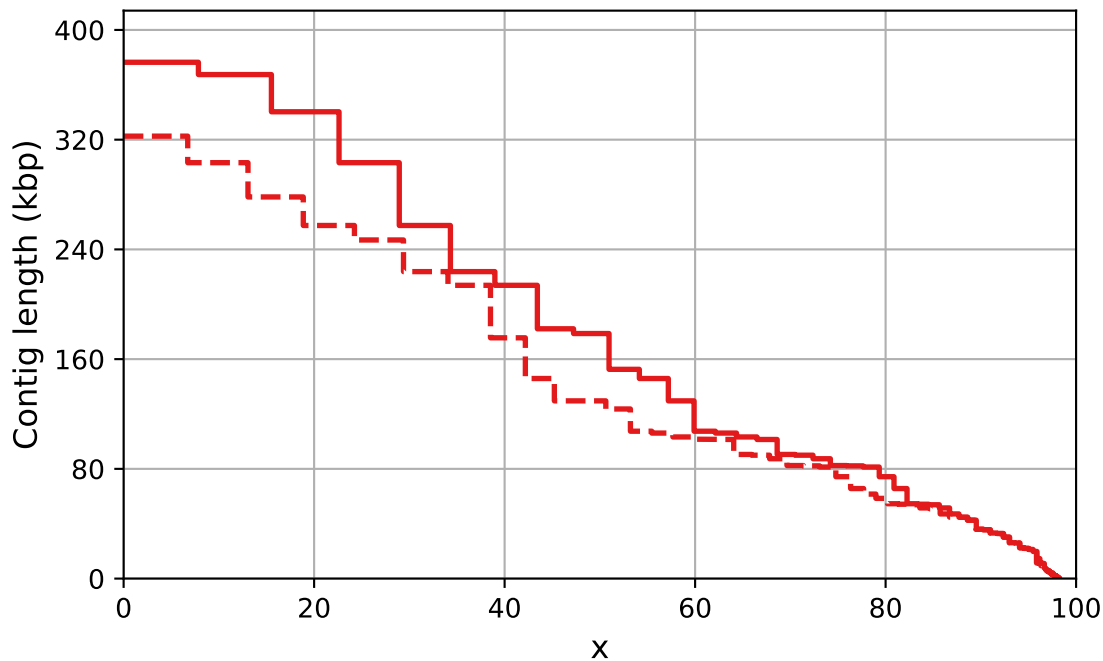
Cumulative length (aligned contigs)



data\_2\_and\_data\_1\_\_Scaffolds

SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken

NAx

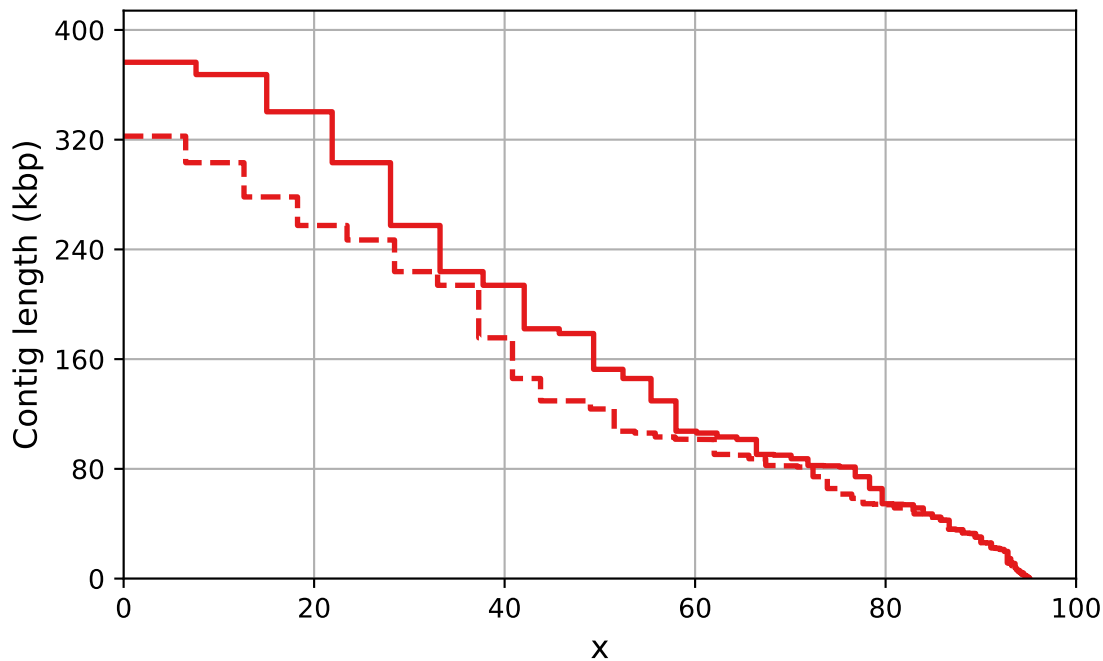


PADES\_on\_data\_2\_and\_data\_1\_Scaffolds

SPADES\_on\_data\_2\_and\_data\_1\_Scaffolds



# NGAx

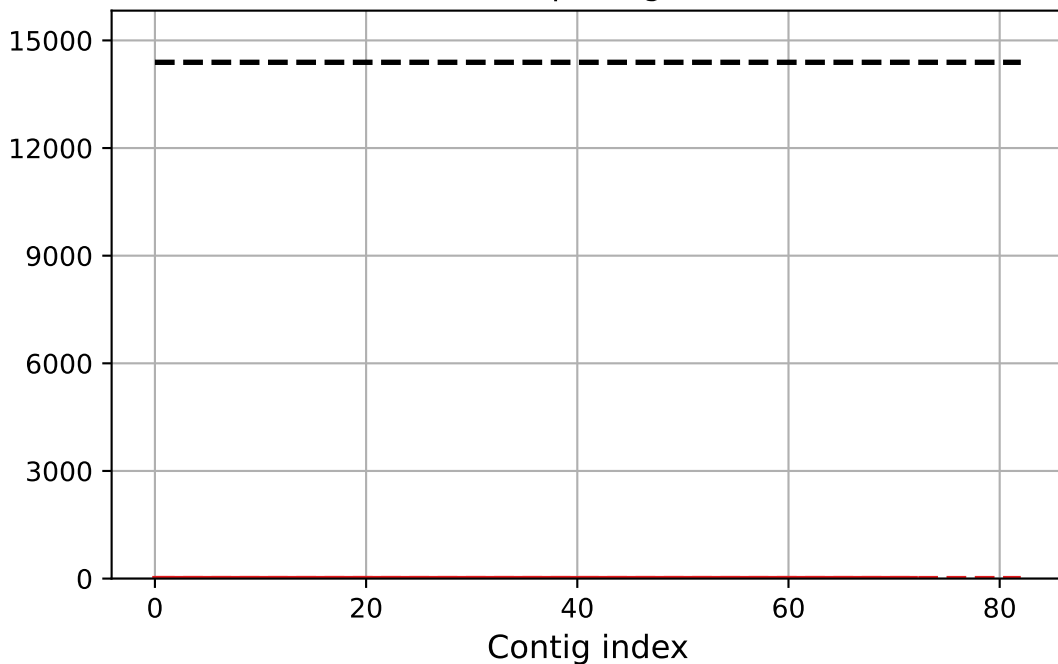


PAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds

SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds

Cumulative # complete genomic features

Cumulative # complete genomic features



data\_2\_and\_data\_1\_\_Scaffolds

SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds\_broken

FRCurve (genomic features)



SPAdes\_on\_data\_2\_and\_data\_1\_Scaffolds



SPAdes\_on\_data\_2\_and\_data\_1\_Scaffolds

# complete genomic features

1

0

PAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds



SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds

Genome fraction, %



PAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds



SPAdes\_on\_data\_2\_and\_data\_1\_\_Scaffolds