

# Report

	SPAdes_on_data_47_and_data_46__Scaffolds	SPAdes_on_data_47_and_data_46__Scaffolds_broken
# contigs (>= 0 bp)	106	-
# contigs (>= 1000 bp)	23	31
Total length (>= 0 bp)	4343162	-
Total length (>= 1000 bp)	4327123	4325816
# contigs	26	34
Largest contig	993415	468275
Total length	4328810	4327503
Reference length	3903260	3903260
GC (%)	27.75	27.75
Reference GC (%)	28.24	28.24
N50	467820	315988
NG50	468275	318195
N90	119565	101638
NG90	211212	158965
auN	504988.0	289416.4
auNG	560043.9	320872.9
L50	4	6
LG50	3	5
L90	10	15
LG90	8	12
# misassemblies	1	1
# misassembled contigs	1	1
Misassembled contigs length	44289	44289
# local misassemblies	1	1
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	12	16
# unaligned contigs	6 + 16 part	8 + 22 part
Unaligned length	3619474	3619252
Genome fraction (%)	19.311	19.303
Duplication ratio	1.009	1.007
# N's per 100 kbp	20.79	0.00
# mismatches per 100 kbp	3818.71	3809.75
# indels per 100 kbp	147.32	146.71
# genomic features	3434 + 152 part	3431 + 151 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	3 + 1 part	3 + 1 part
Largest alignment	95222	95222
Total aligned length	707961	708183
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	3329.5	3330.6
auNGA	3692.5	3692.5
LA50	-	-
LGA50	-	-
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

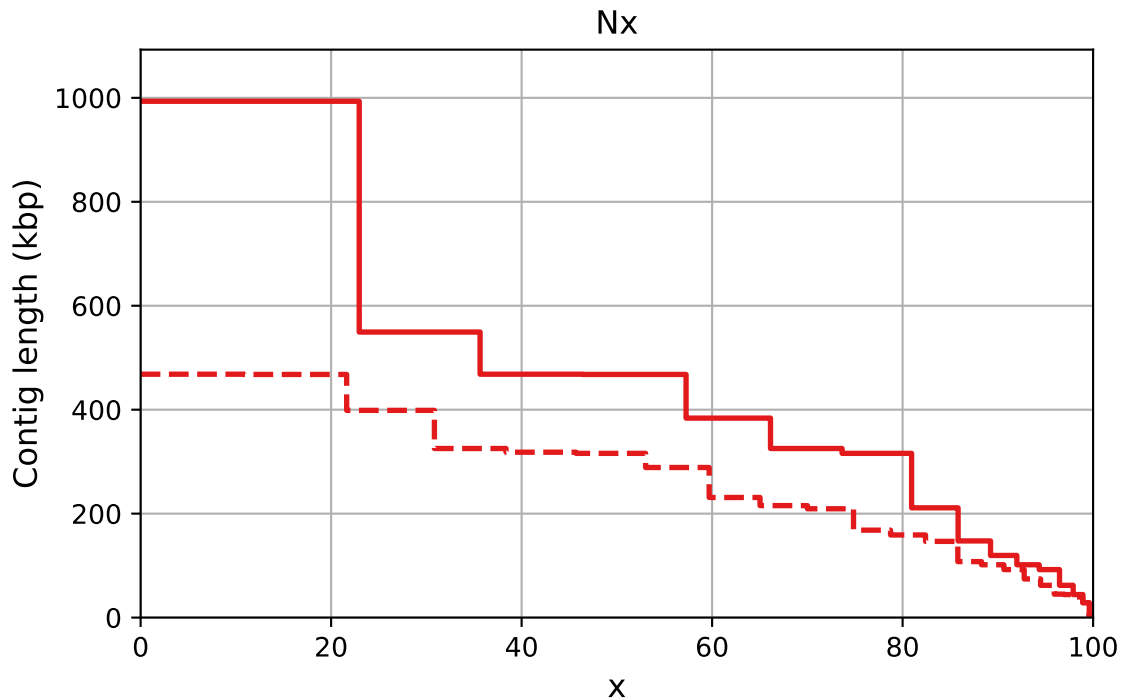
	SPAdes_on_data_47_and_data_46__Scaffolds	SPAdes_on_data_47_and_data_46__Scaffolds_broken
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	44289	44289
# local misassemblies	1	1
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	12	16
# mismatches	27035	26980
# indels	1043	1039
# indels (<= 5 bp)	954	950
# indels (> 5 bp)	89	89
Indels length	3413	3408

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_47_and_data_46__Scaffolds	SPAdes_on_data_47_and_data_46__Scaffolds_broken
# fully unaligned contigs	6	8
Fully unaligned length	8370	49789
# partially unaligned contigs	16	22
Partially unaligned length	3611104	3569463
# N's	900	0

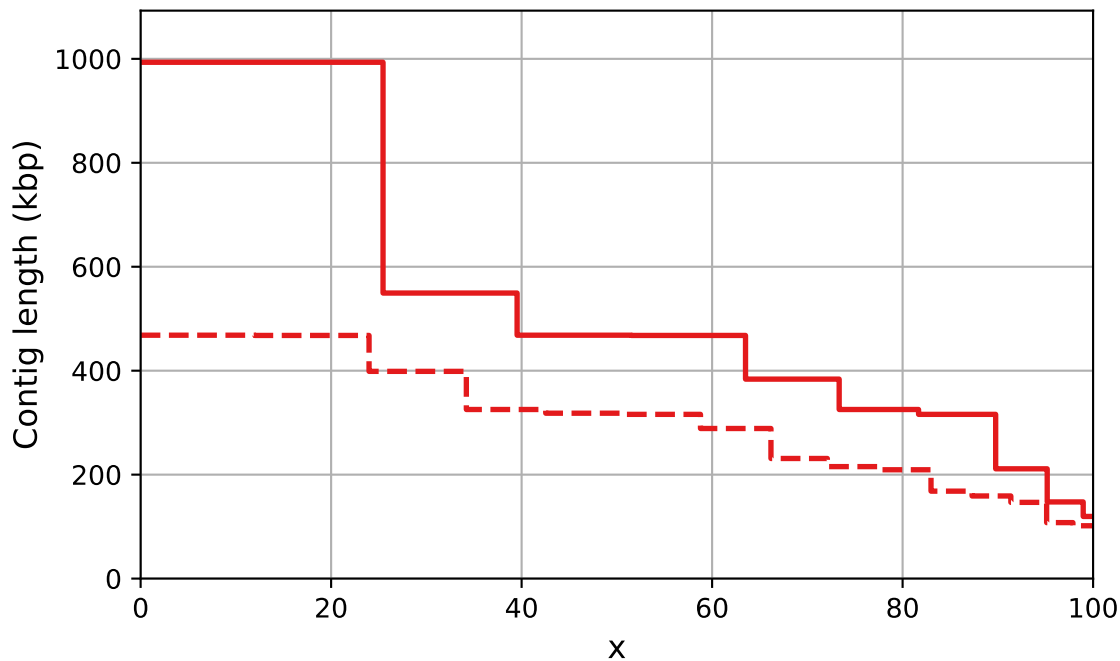
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

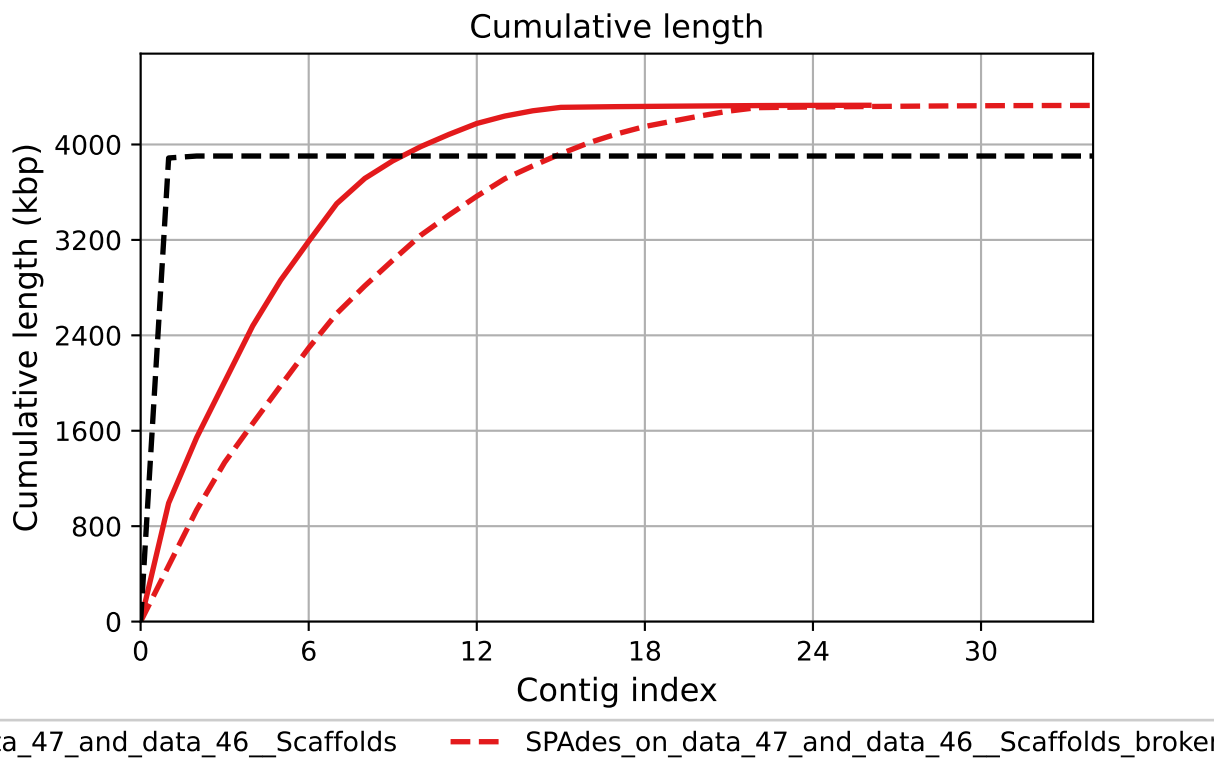
SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

# NGx

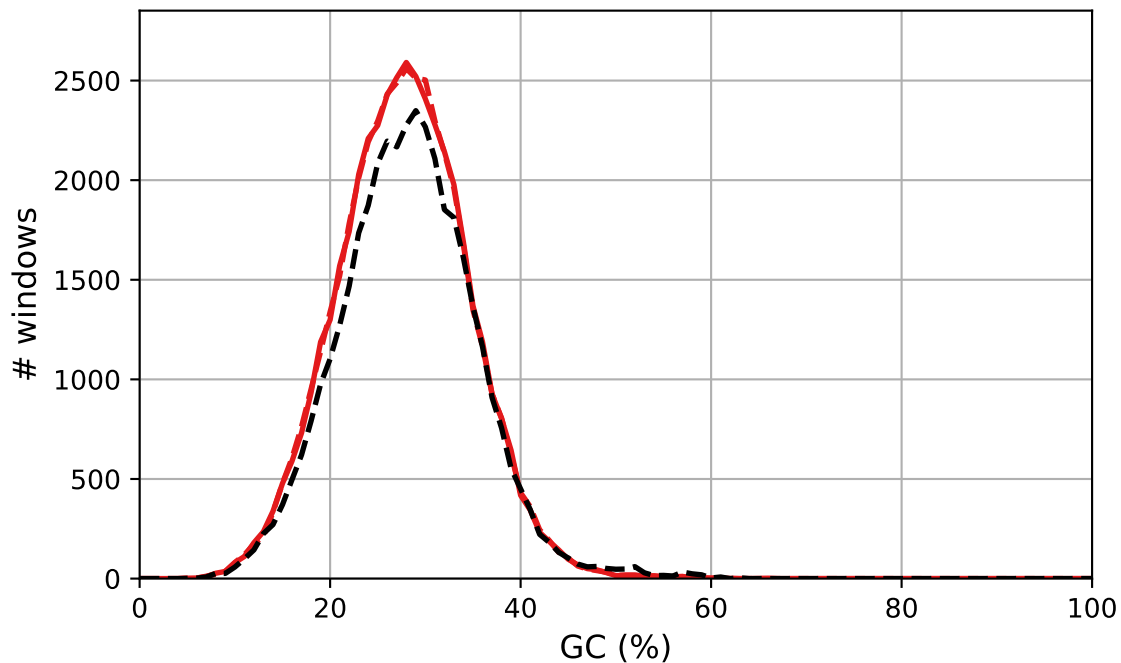


des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds



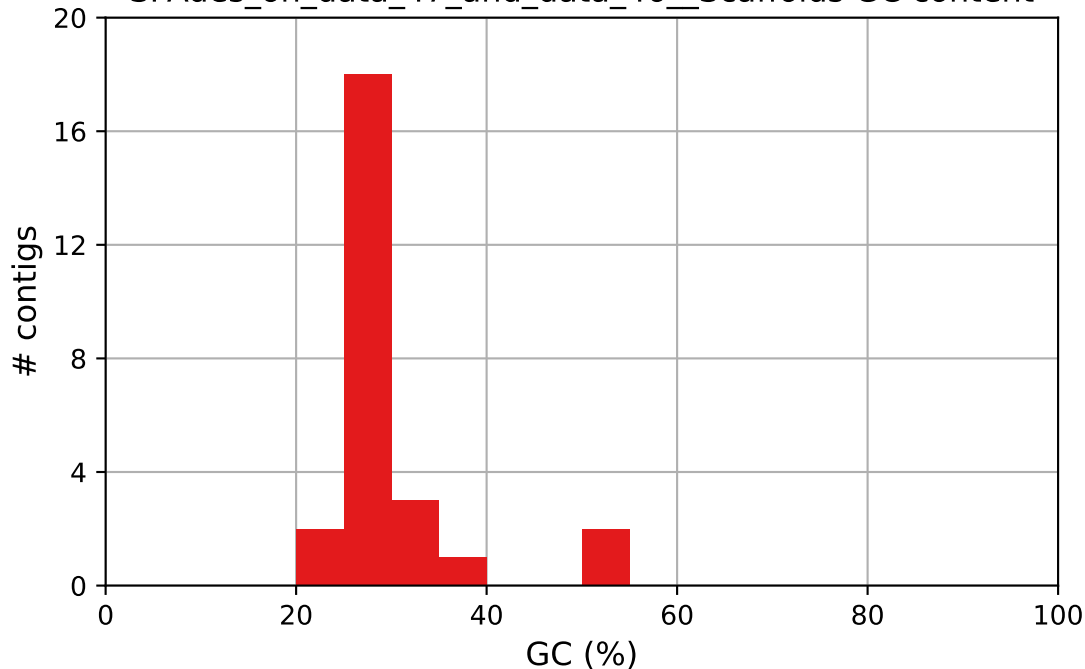
GC content



data\_47\_and\_data\_46\_\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds\_broken

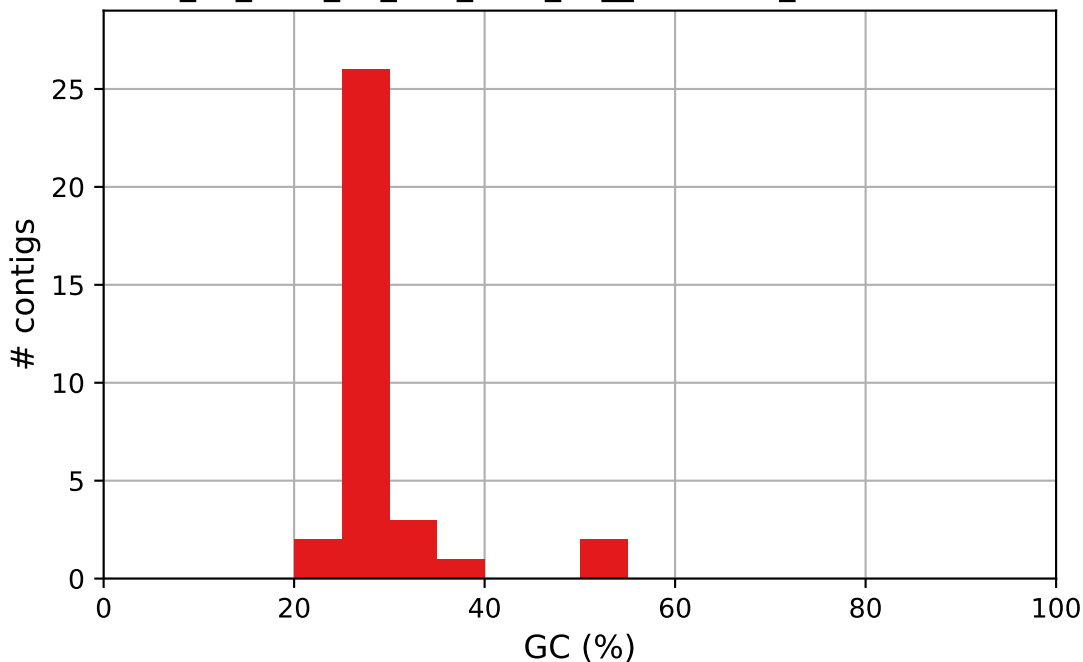
SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds GC content



SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

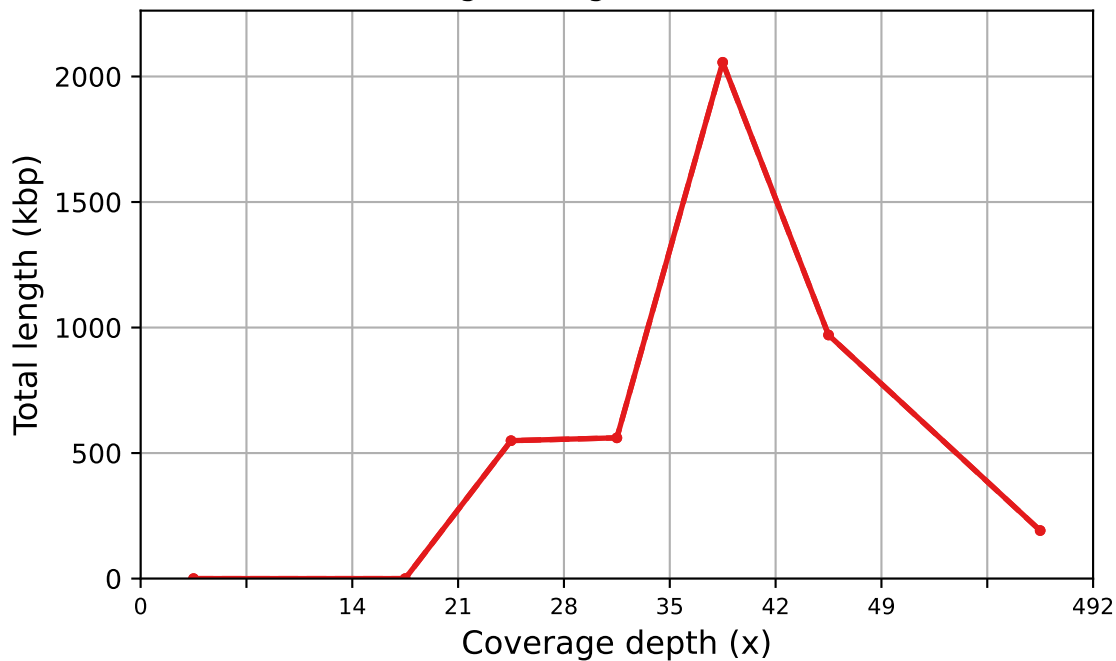


SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds\_broken GC content



SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds\_broken

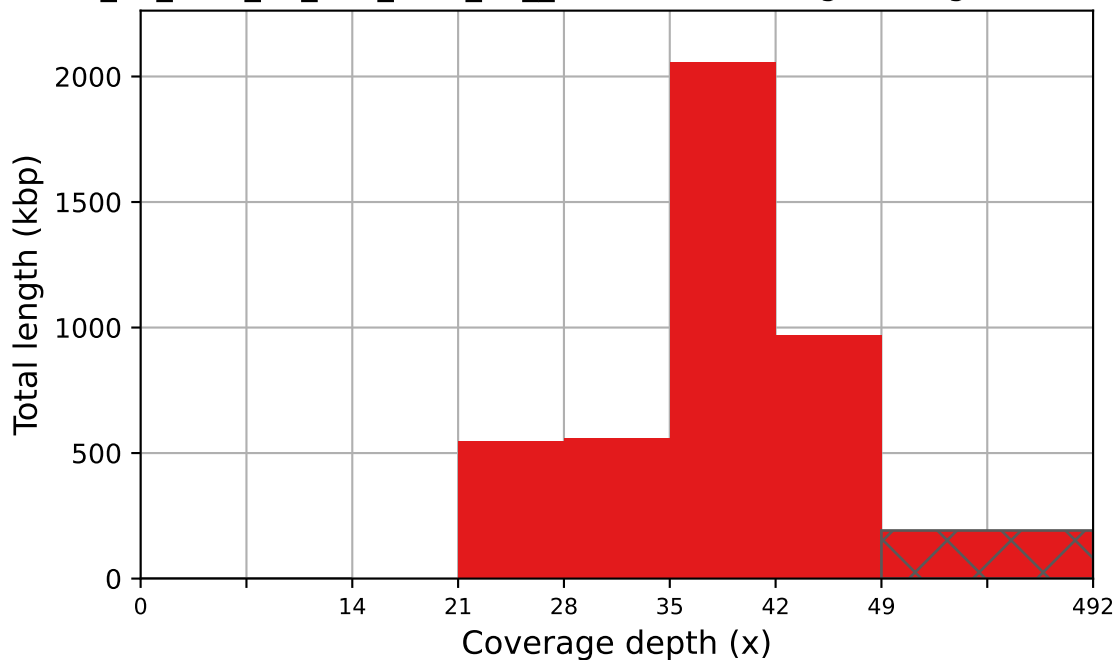
Coverage histogram (bin size: 7x)



des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

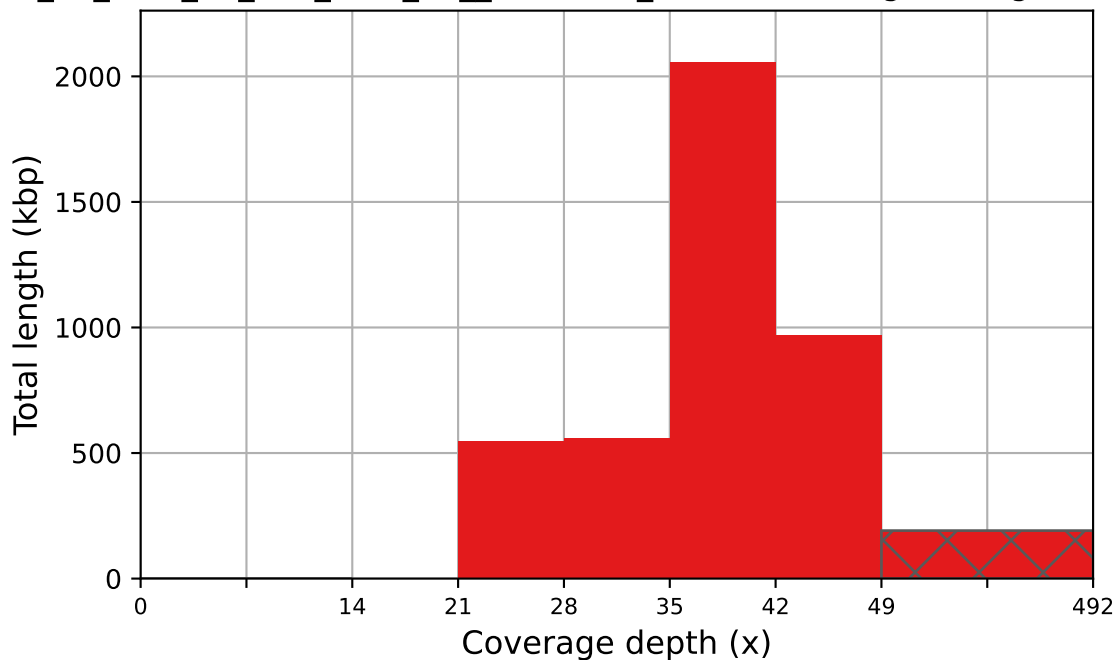
—•— SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds coverage histogram (bin size: 7



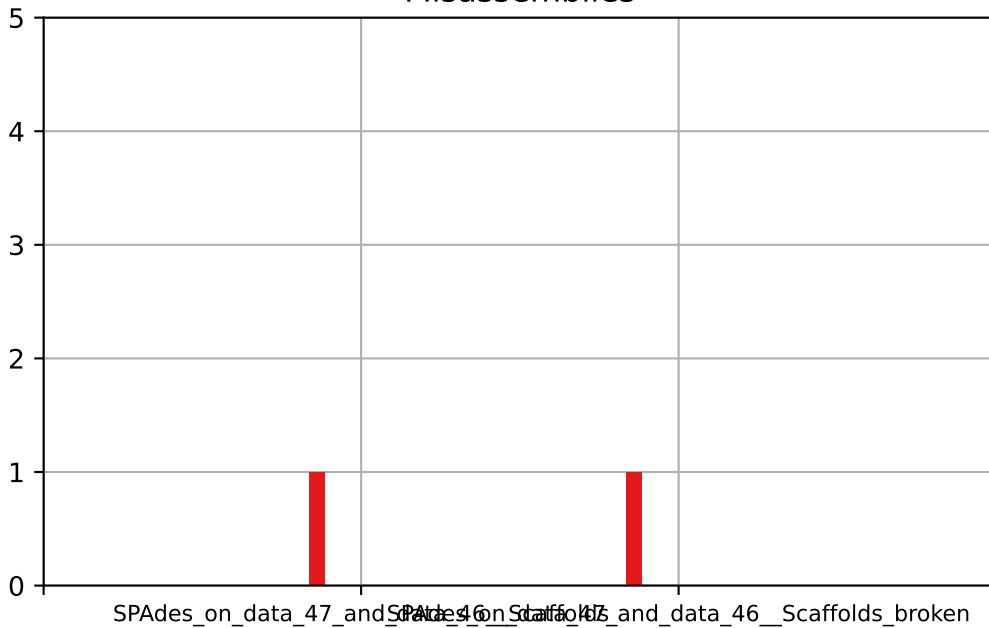
SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds\_broken coverage histogram (bin size 7)

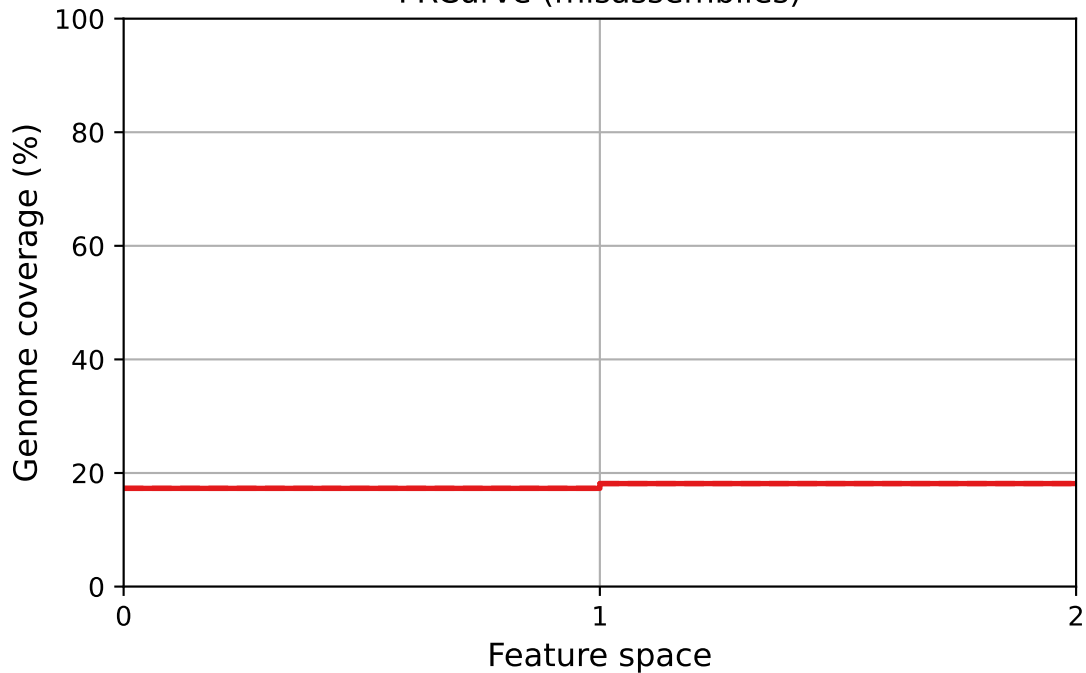


SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds\_broken

## Misassemblies



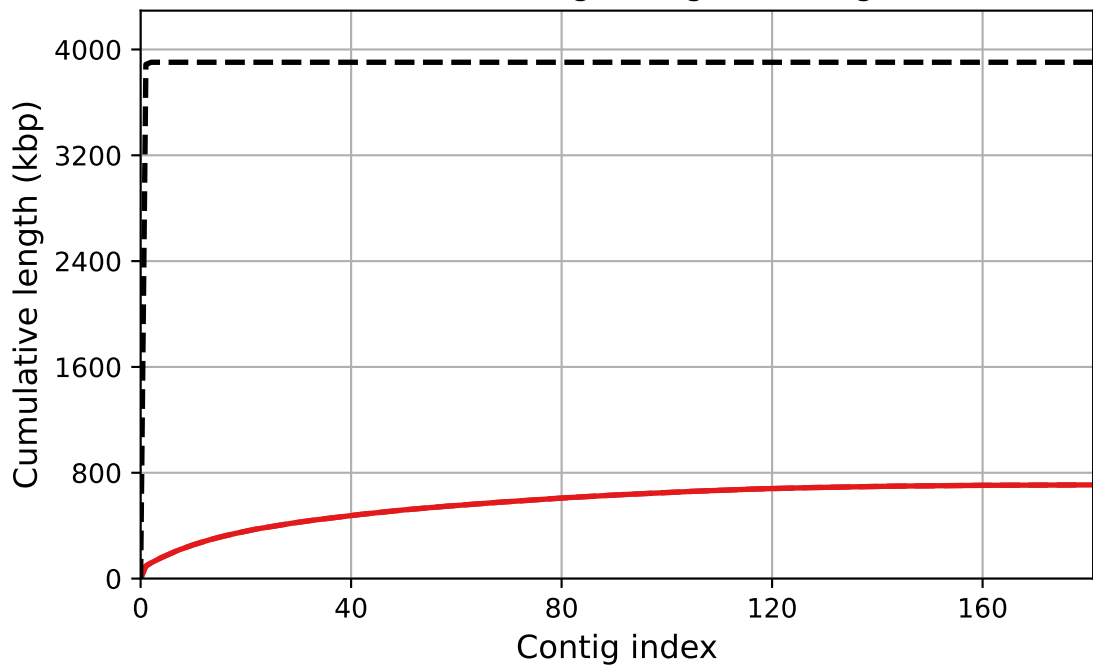
FRCurve (misassemblies)



des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

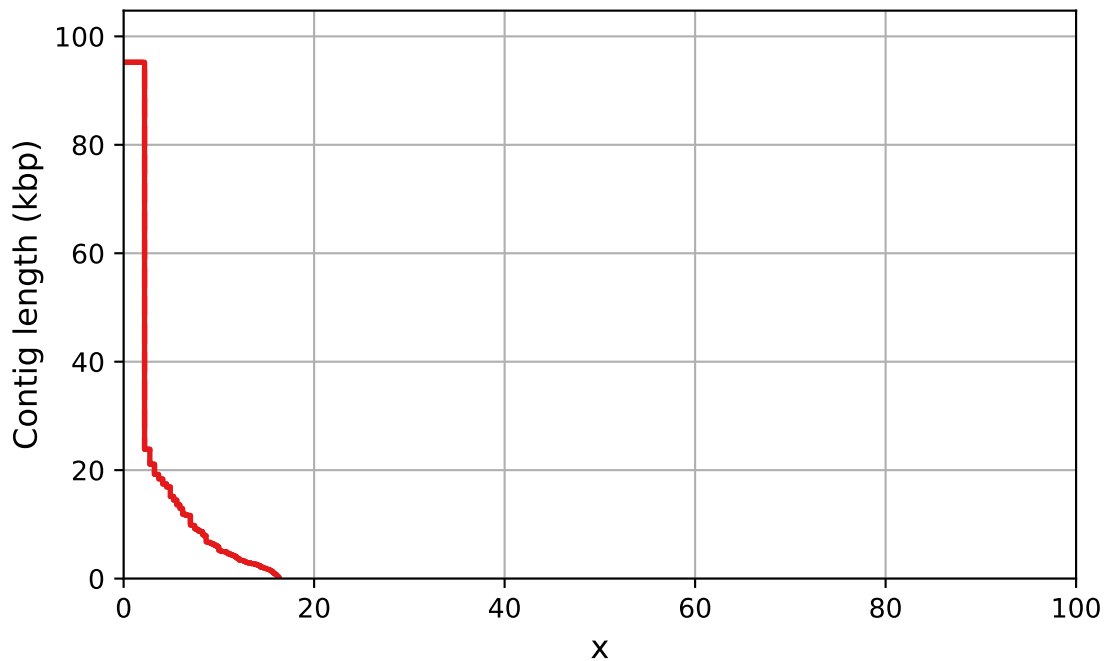
Cumulative length (aligned contigs)



data\_47\_and\_data\_46\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_Scaffolds\_broken

NAx

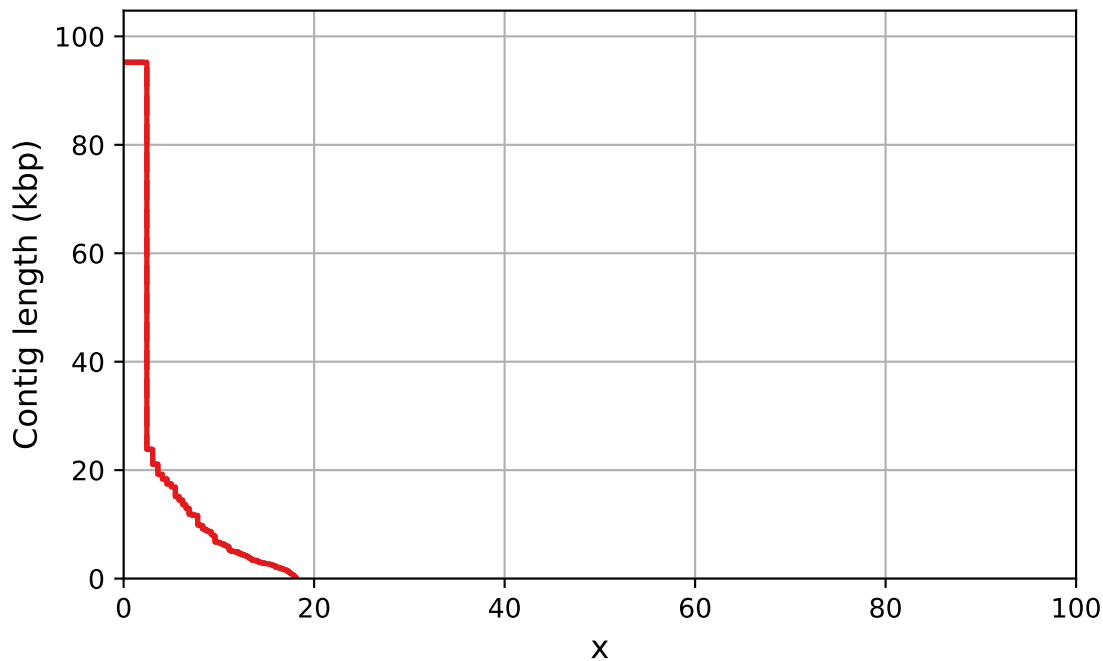


des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds



# NGAx

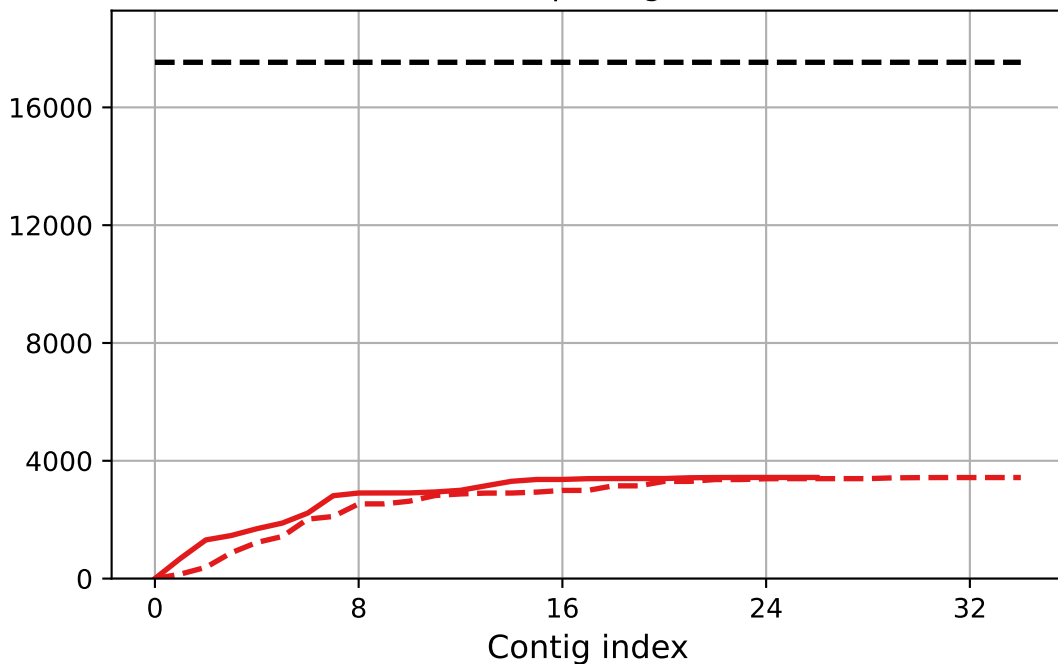


des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

Cumulative # complete genomic features

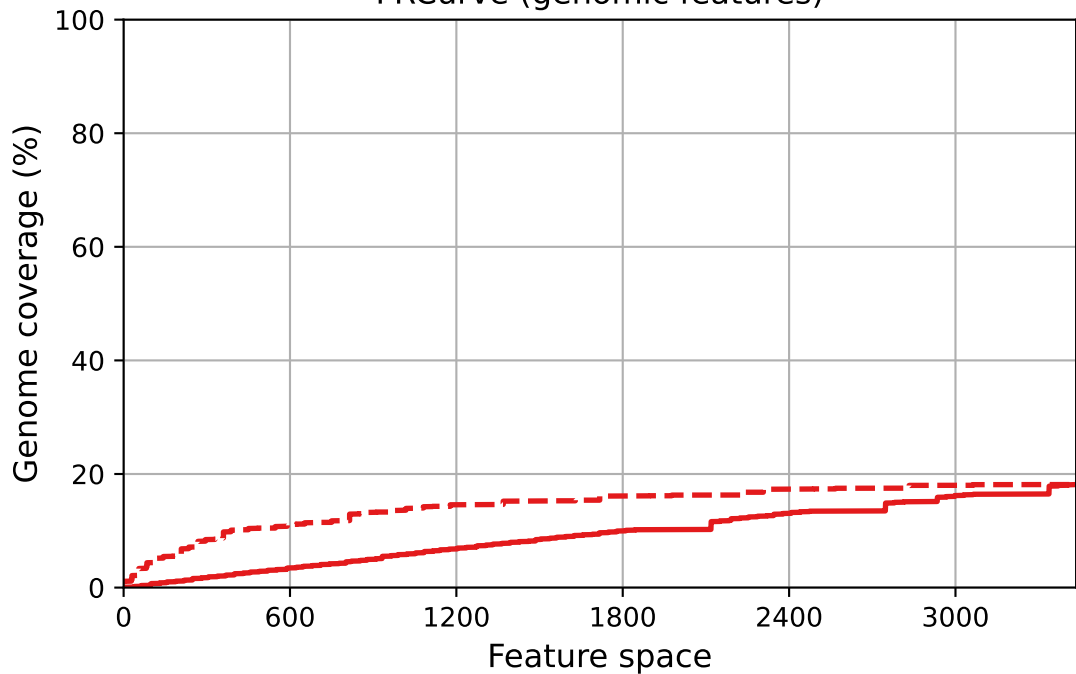
Cumulative # complete genomic features



ta\_47\_and\_data\_46\_\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds\_broken

FRCurve (genomic features)



des\_on\_data\_47\_and\_data\_46\_\_Scaffolds

-- SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds

# complete genomic features

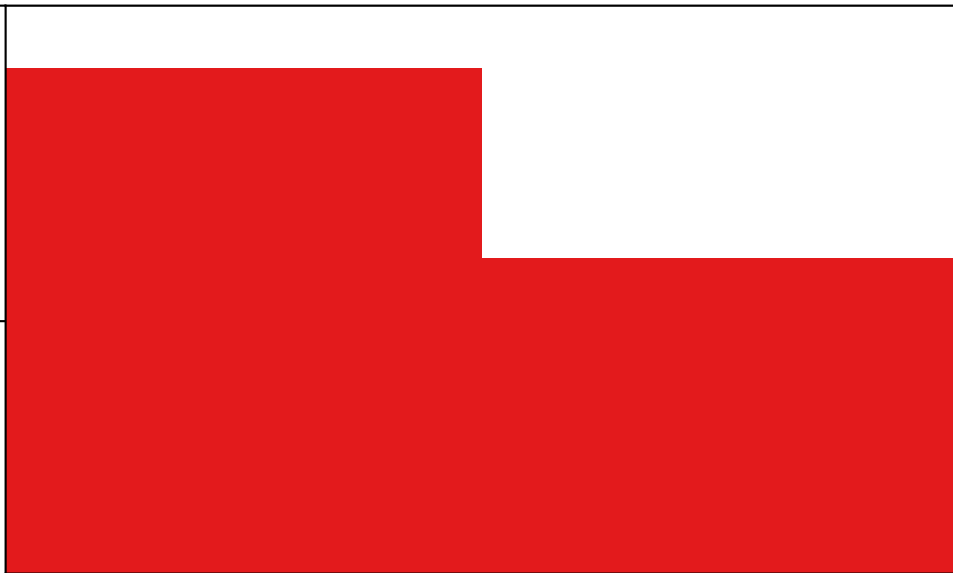
3435

3430

des\_on\_data\_47\_and\_data\_46\_\_Scaffolds



SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds



# Genome fraction, %

100

50

des\_on\_data\_47\_and\_data\_46\_\_Scaffolds



SPAdes\_on\_data\_47\_and\_data\_46\_\_Scaffolds