

# Report

	SPAdes_on_data_36_and_data_35__Scaffolds	SPAdes_on_data_36_and_data_35__Scaffolds_broken
# contigs (>= 0 bp)	562	-
# contigs (>= 1000 bp)	310	317
Total length (>= 0 bp)	6522694	-
Total length (>= 1000 bp)	6460836	6460136
# contigs	342	349
Largest contig	181675	181675
Total length	6482848	6482148
Reference length	4176973	4176973
GC (%)	45.83	45.83
Reference GC (%)	34.93	34.93
N50	39388	38513
NG50	61365	59122
N90	10721	10690
NG90	35228	34198
auN	49805.9	48009.0
auNG	77301.0	74504.0
L50	49	52
LG50	25	26
L90	162	167
LG90	63	66
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	340 + 2 part	347 + 2 part
Unaligned length	6481999	6481999
Genome fraction (%)	0.007	0.007
Duplication ratio	1.000	1.000
# N's per 100 kbp	10.80	0.00
# mismatches per 100 kbp	4697.99	4697.99
# indels per 100 kbp	0.00	0.00
# genomic features	12 + 0 part	12 + 0 part
Complete BUSCO (%)	89.86	89.86
Partial BUSCO (%)	2.70	2.70
# predicted rRNA genes	2 + 0 part	2 + 0 part
Largest alignment	76	76
Total aligned length	149	149
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	0.0	0.0
auNGA	0.0	0.0
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

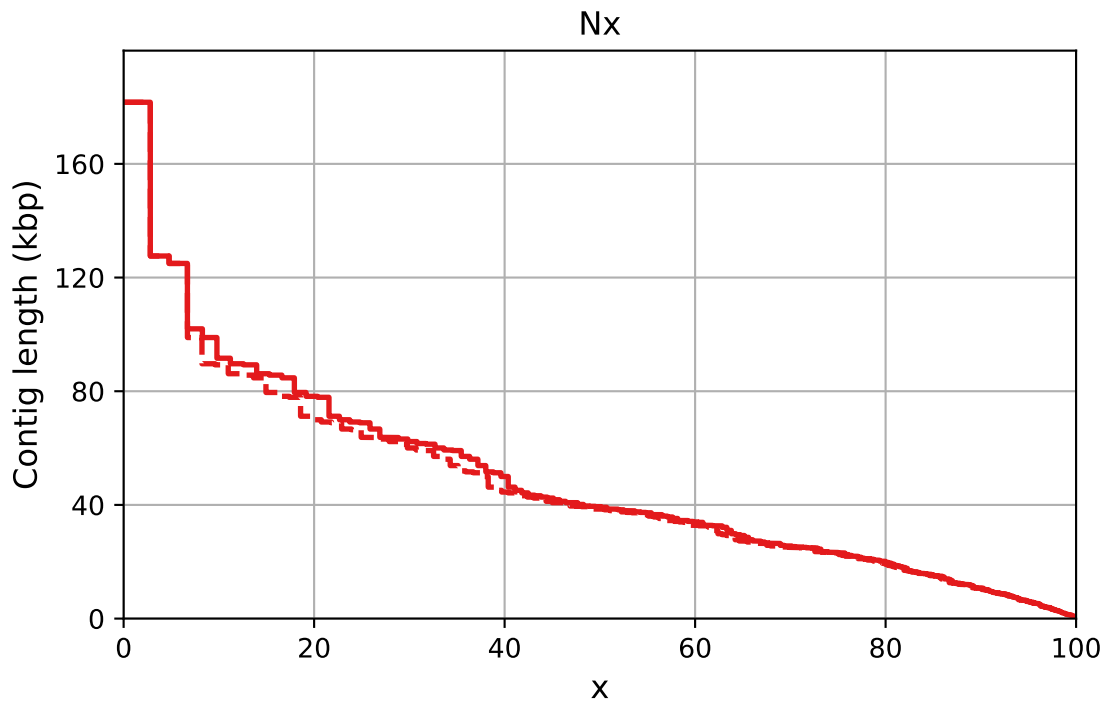
	SPAdes_on_data_36_and_data_35__Scaffolds	SPAdes_on_data_36_and_data_35__Scaffolds_broken
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	7	7
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	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).

## Unaligned report

	SPAdes_on_data_36_and_data_35__Scaffolds	SPAdes_on_data_36_and_data_35__Scaffolds_broken
# fully unaligned contigs	340	347
Fully unaligned length	6466605	6466605
# partially unaligned contigs	2	2
Partially unaligned length	15394	15394
# N's	700	0

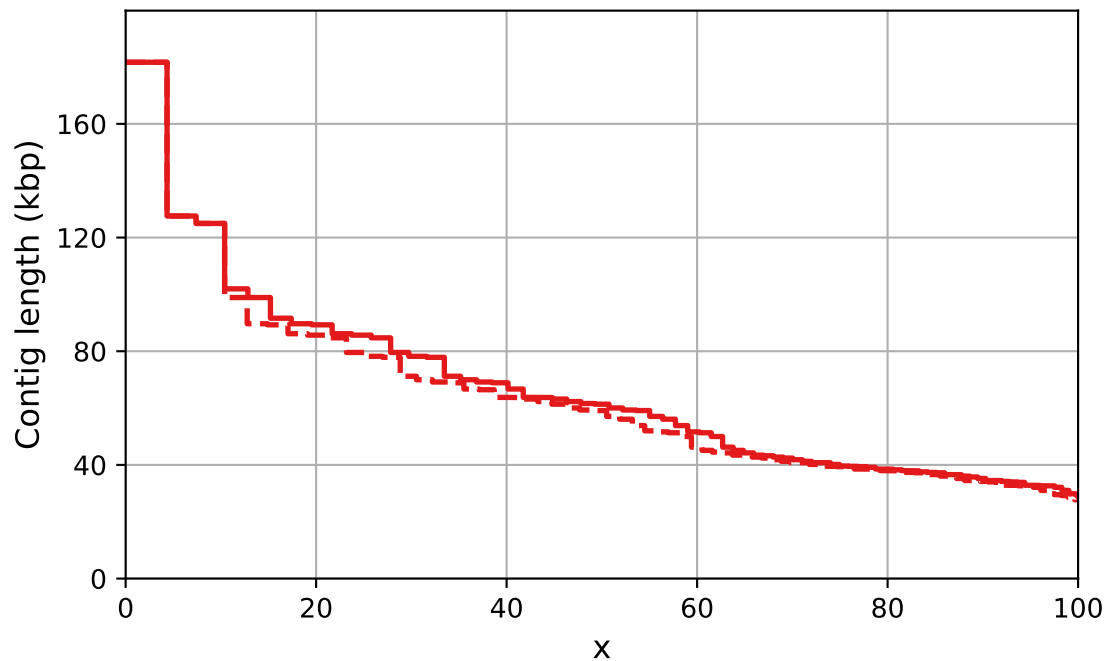
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



des\_on\_data\_36\_and\_data\_35\_\_Scaffolds

-- SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds

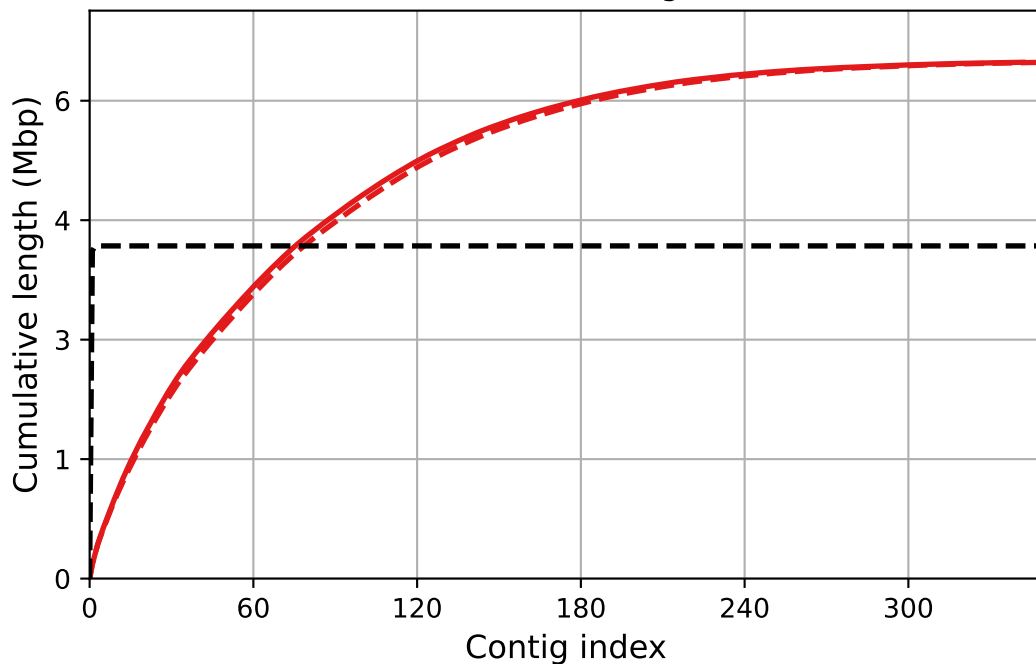
NGx



des\_on\_data\_36\_and\_data\_35\_\_Scaffolds

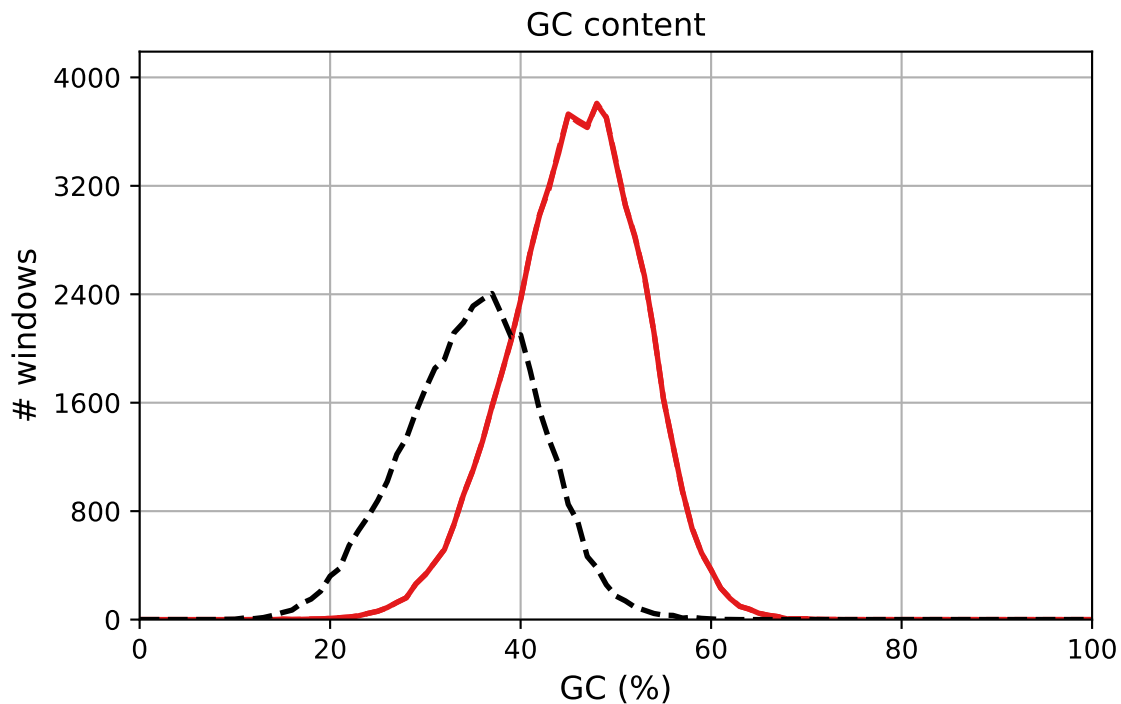
-- SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds

Cumulative length



data\_36\_and\_data\_35\_\_Scaffolds

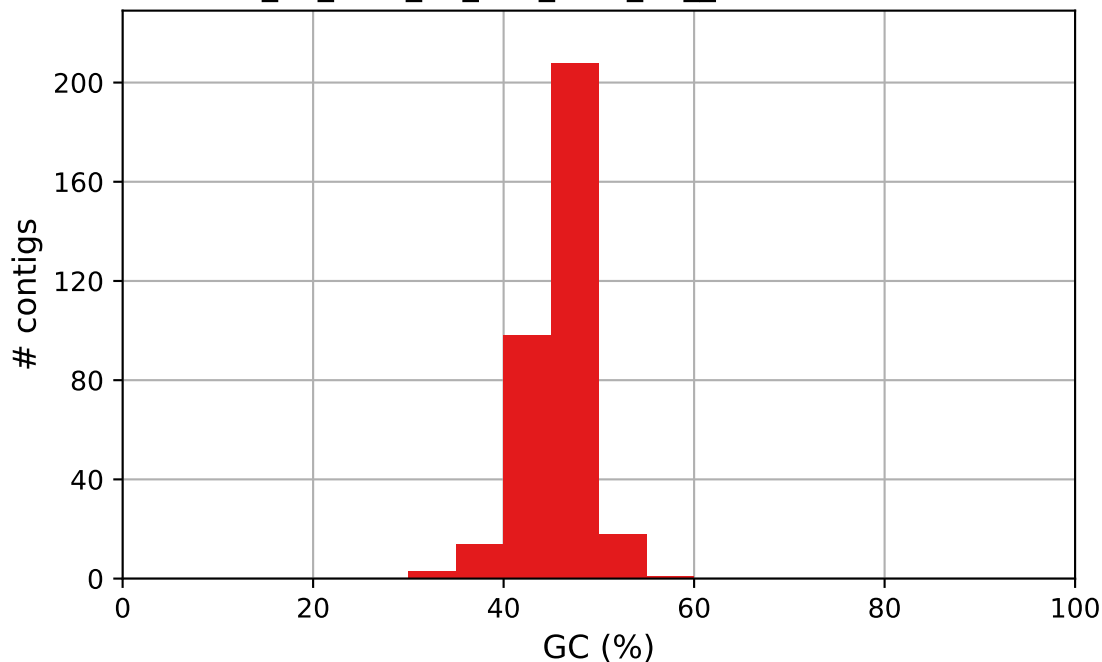
-- SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds\_broken



data\_36\_and\_data\_35\_\_Scaffolds

SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds\_broken

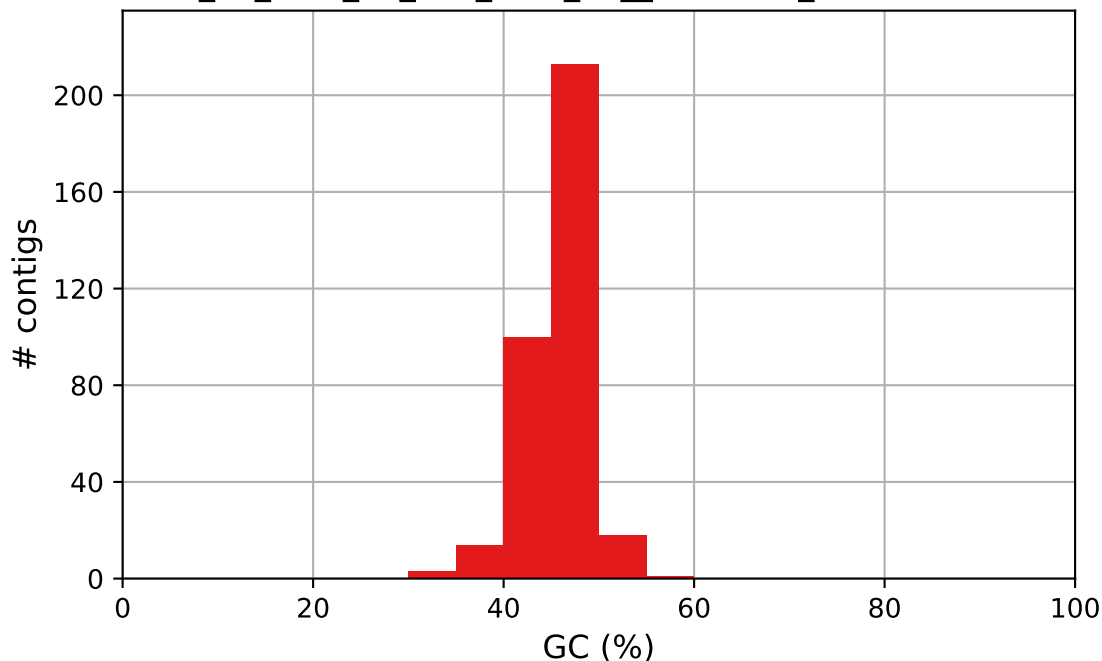
SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds GC content



SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds

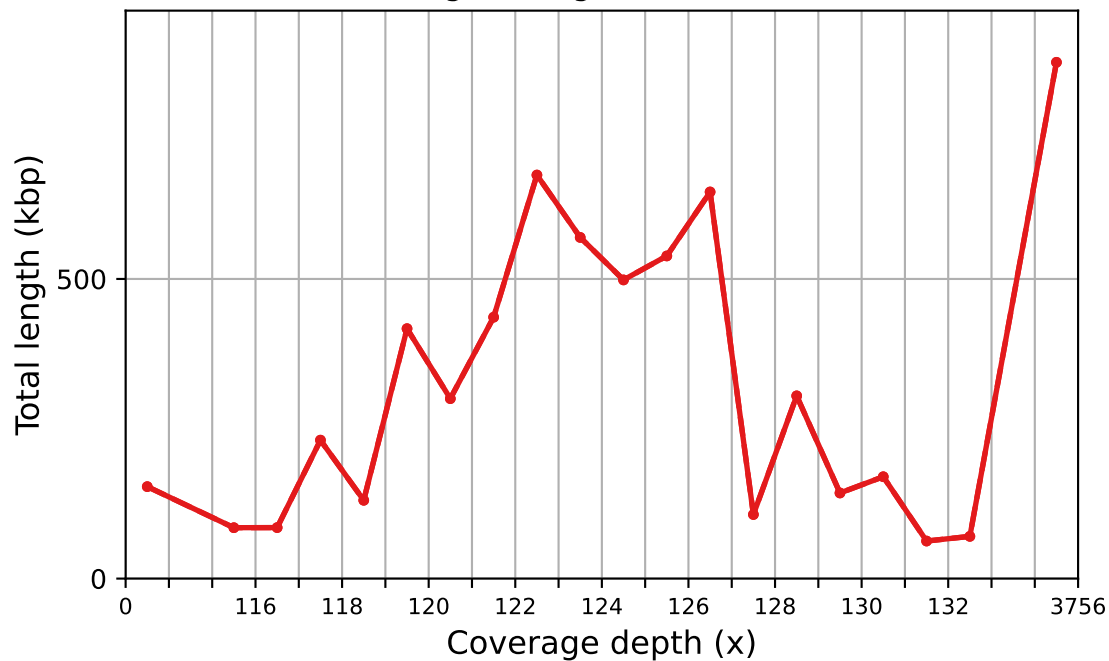


SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds\_broken GC content



SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds\_broken

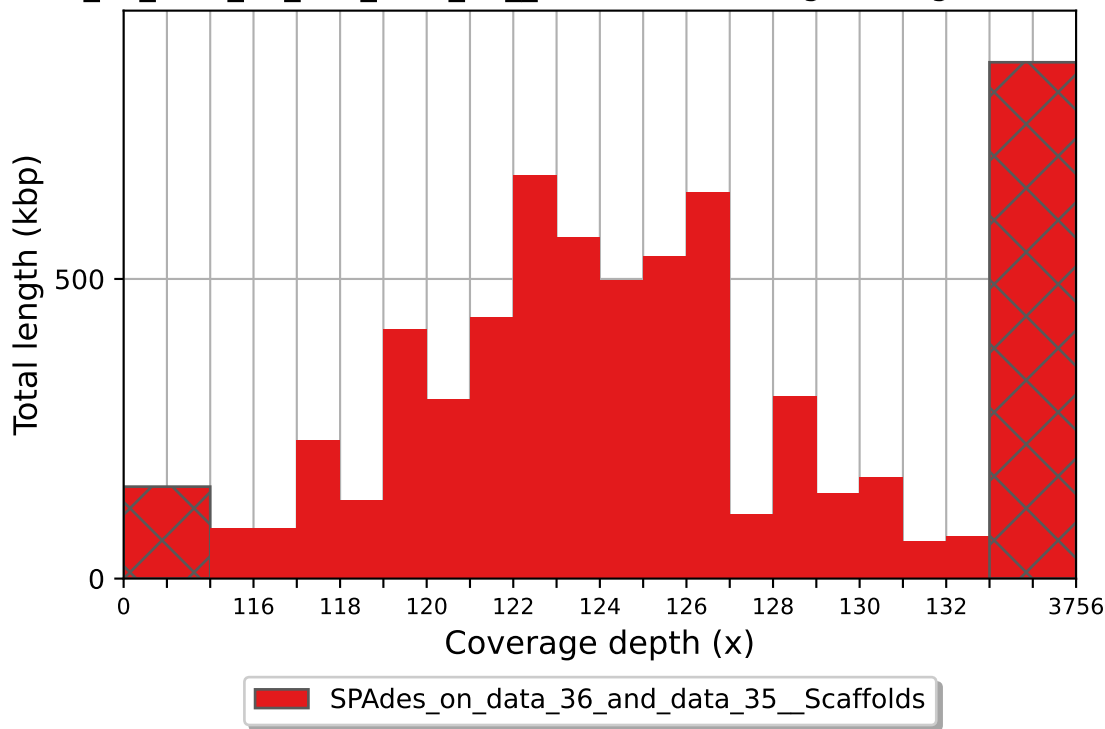
Coverage histogram (bin size: 1x)



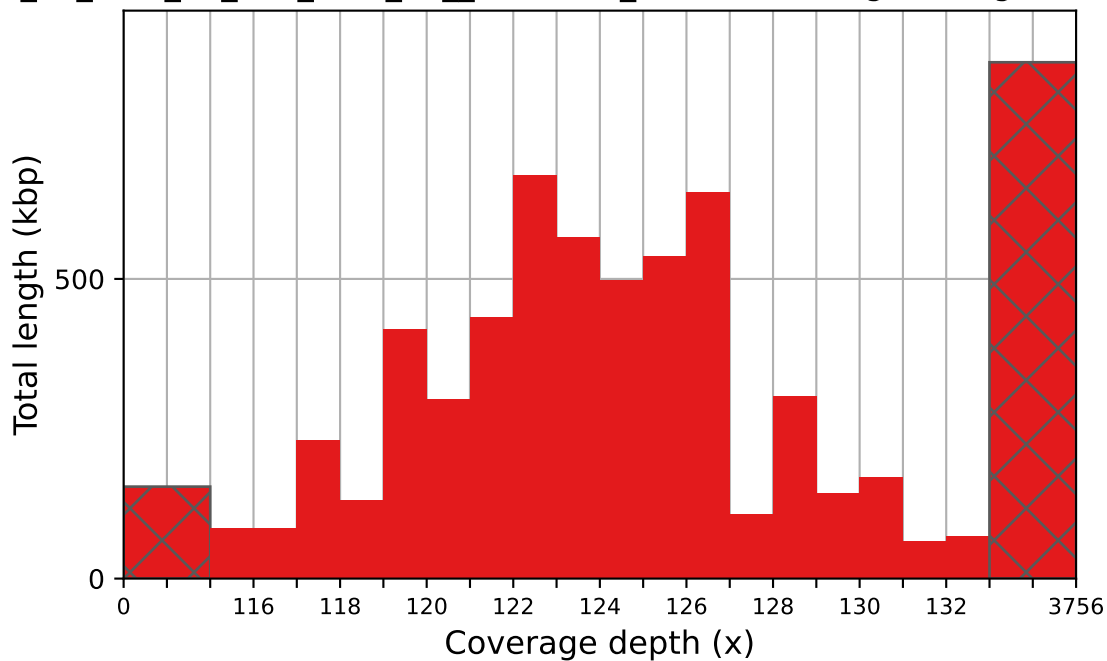
des\_on\_data\_36\_and\_data\_35\_Scaffolds

—•— SPAdes\_on\_data\_36\_and\_data\_35\_Scaffolds

SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds coverage histogram (bin size: 1

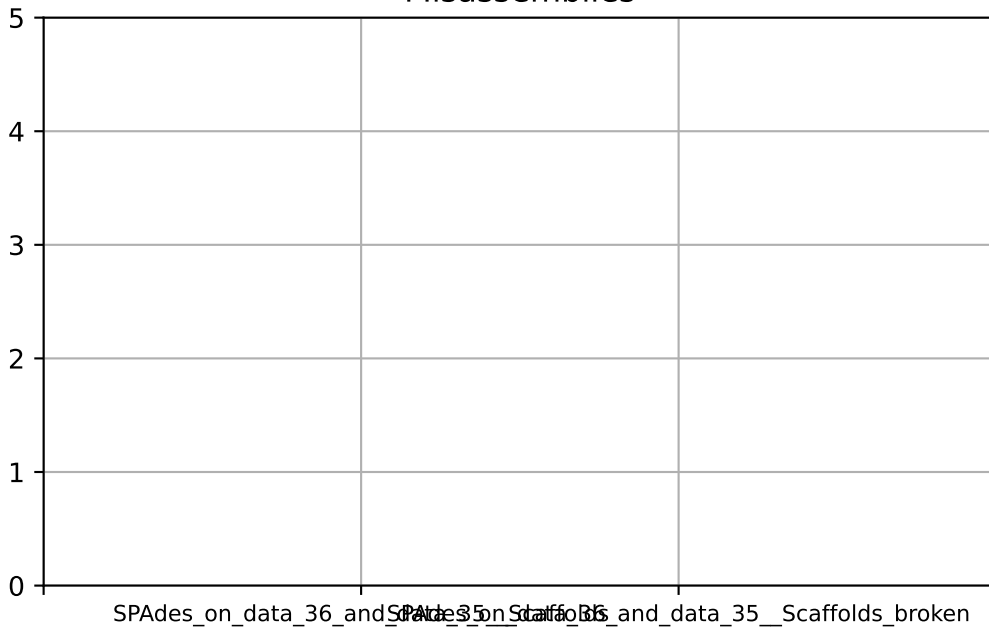


SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds\_broken coverage histogram (bin size 4)



SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds\_broken

## Misassemblies



FRCurve (misassemblies)

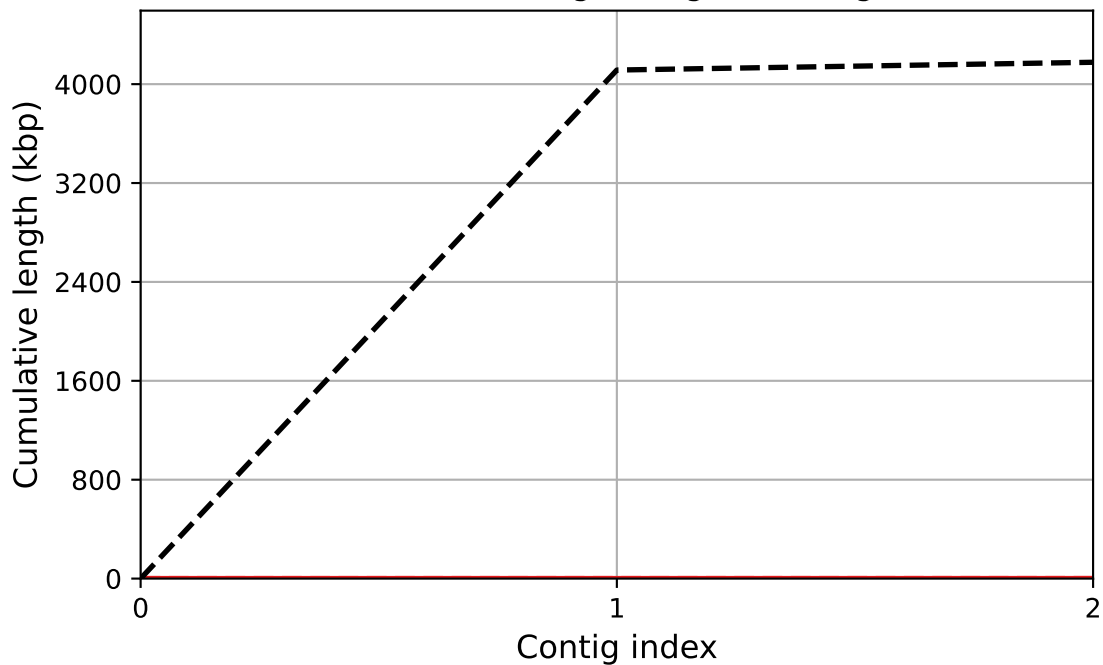


des\_on\_data\_36\_and\_data\_35\_\_Scaffolds



SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds

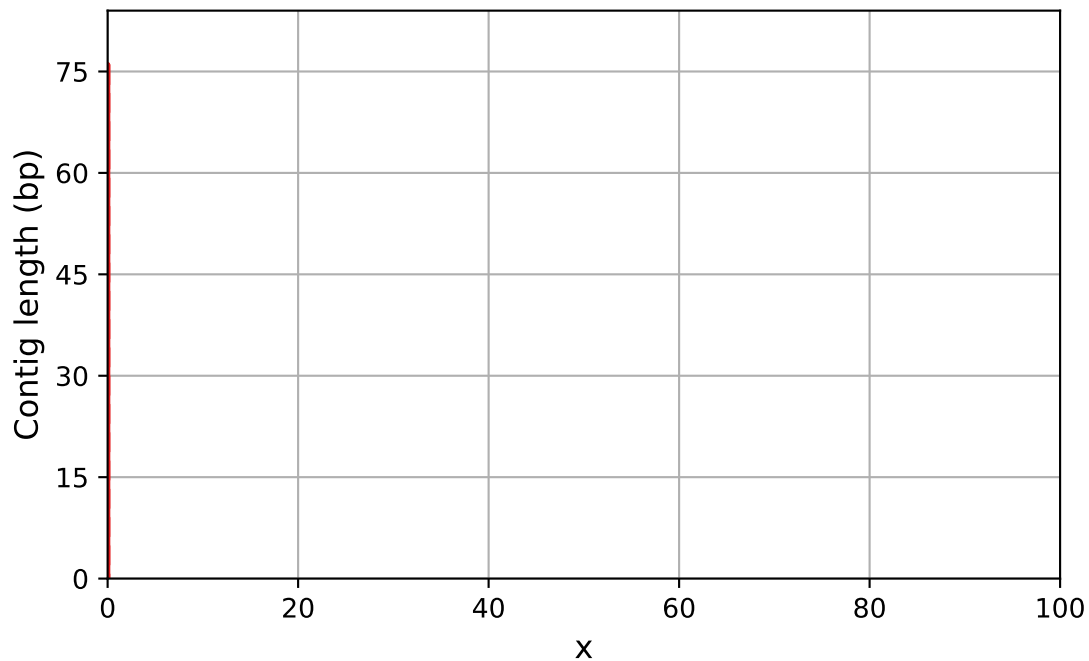
Cumulative length (aligned contigs)



data\_36\_and\_data\_35\_Scaffolds

-- SPAdes\_on\_data\_36\_and\_data\_35\_Scaffolds\_broken

NAx



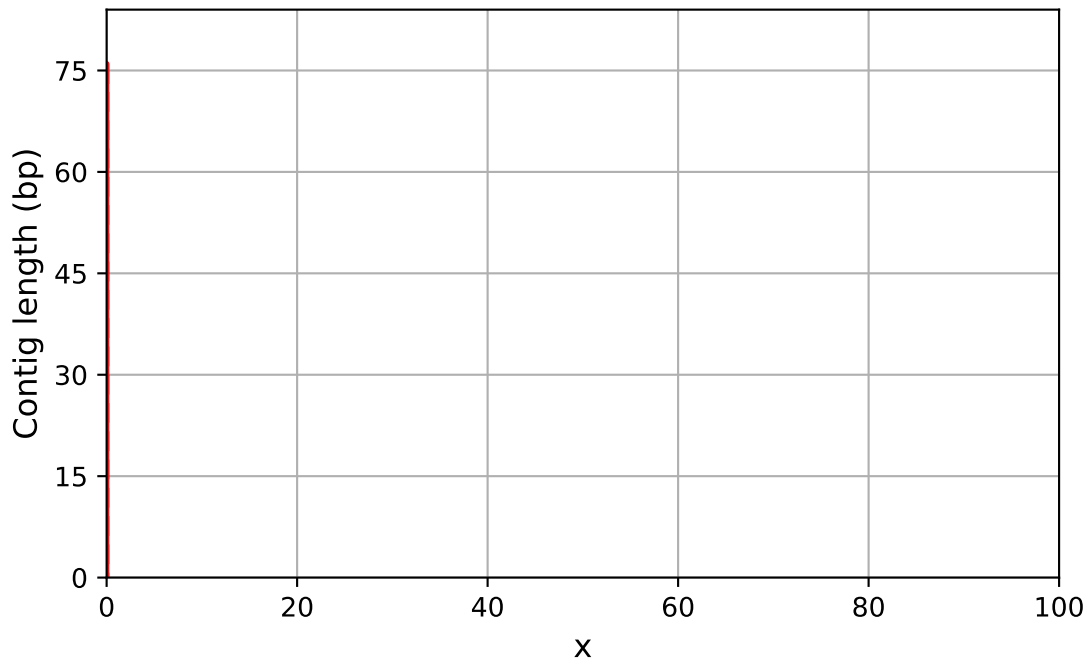
des\_on\_data\_36\_and\_data\_35\_\_Scaffolds

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SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds

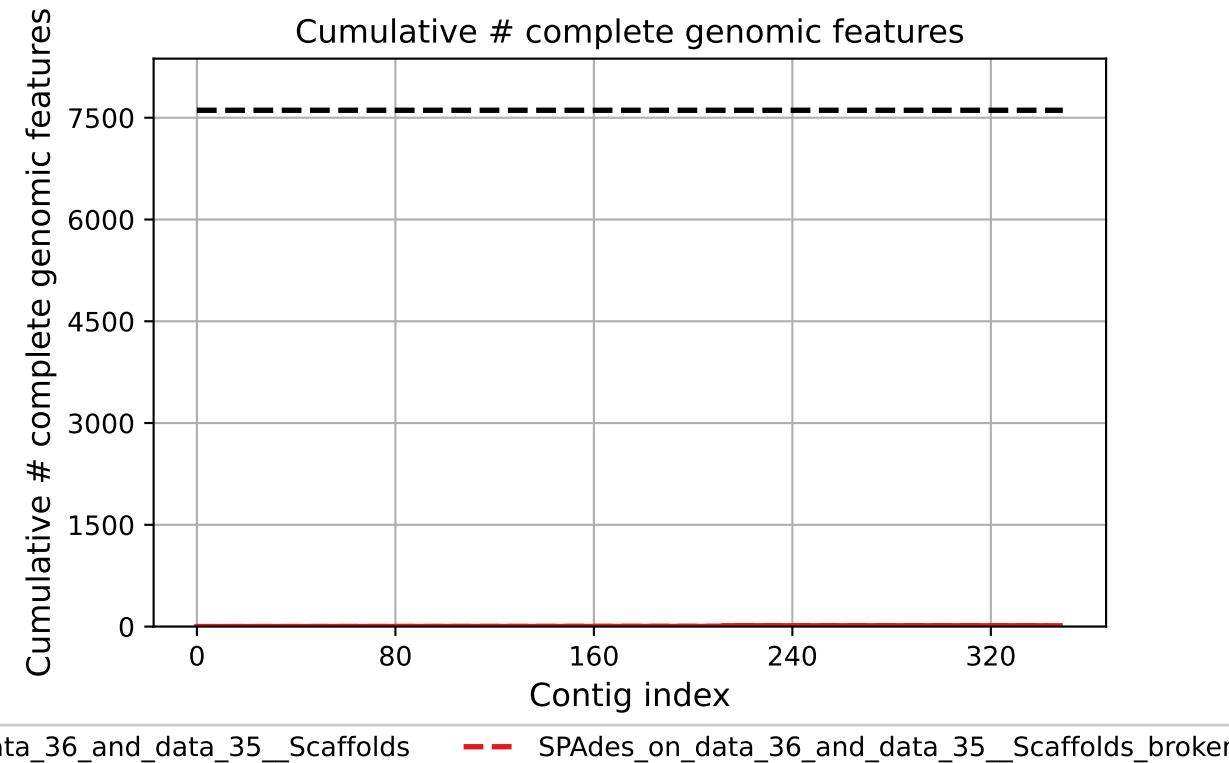


## NGAx

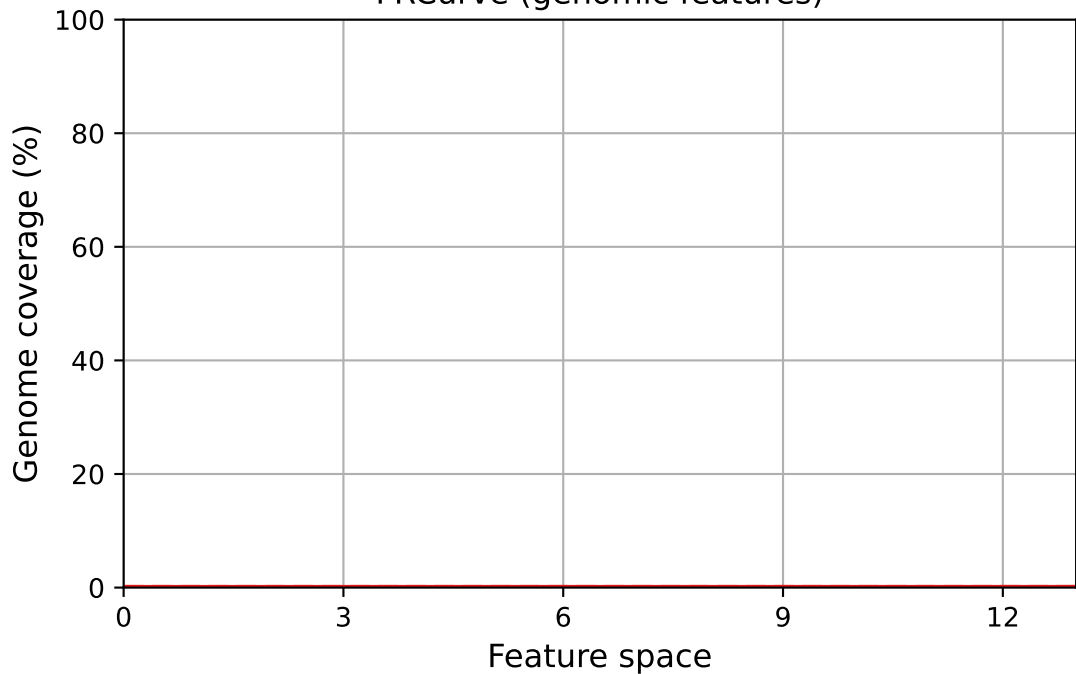


des\_on\_data\_36\_and\_data\_35\_\_Scaffolds

--- SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds



FRCurve (genomic features)



des\_on\_data\_36\_and\_data\_35\_\_Scaffolds



SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds

# complete genomic features



des\_on\_data\_36\_and\_data\_35\_Scaffolds



SPAdes\_on\_data\_36\_and\_data\_35\_Scaffolds

# Genome fraction, %

100

50

des\_on\_data\_36\_and\_data\_35\_\_Scaffolds



SPAdes\_on\_data\_36\_and\_data\_35\_\_Scaffolds