

# Report

	SPAdes_on_data_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# contigs (>= 0 bp)	197	-
# contigs (>= 1000 bp)	66	80
Total length (>= 0 bp)	5511585	-
Total length (>= 1000 bp)	5480096	5478564
# contigs	78	93
Largest contig	465799	388171
Total length	5487980	5486570
Reference length	4951383	4951383
GC (%)	57.21	57.21
Reference GC (%)	52.24	52.24
N50	193741	163595
NG50	195173	172661
N90	73398	55995
NG90	94226	76558
auN	219222.2	160950.6
auNG	242980.0	178347.5
L50	10	13
LG50	9	11
L90	28	37
LG90	22	29
# 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.	2	-
# unaligned mis. contigs	2	2
# unaligned contigs	52 + 24 part	62 + 27 part
Unaligned length	5458250	5458085
Genome fraction (%)	0.685	1.099
Duplication ratio	1.006	1.003
# N's per 100 kbp	25.69	0.00
# mismatches per 100 kbp	3857.16	5534.07
# indels per 100 kbp	452.12	882.50
# genomic features	0 + 0 part	0 + 0 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	13787	13787
Total aligned length	28311	28442
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	41.6	38.9
auNGA	46.1	43.1
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

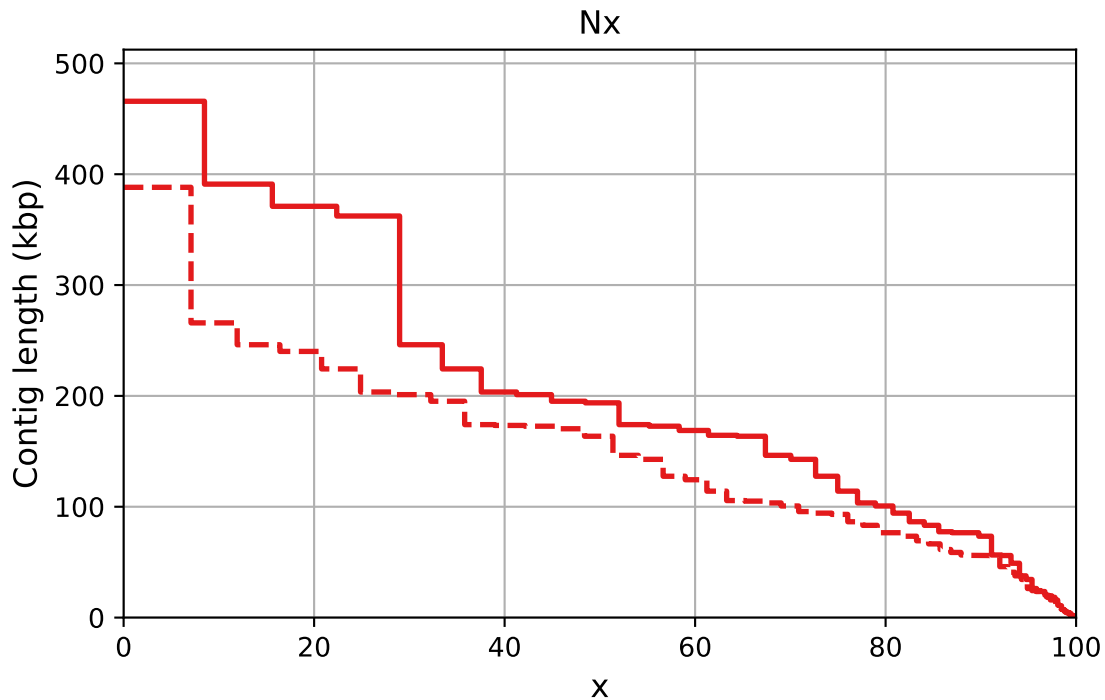
	SPAdes_on_data_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	2	2
# mismatches	1092	1574
# indels	128	251
# indels (<= 5 bp)	124	244
# indels (> 5 bp)	4	7
Indels length	308	541

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_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# fully unaligned contigs	52	62
Fully unaligned length	1576978	2077437
# partially unaligned contigs	24	27
Partially unaligned length	3881272	3380648
# N's	1410	0

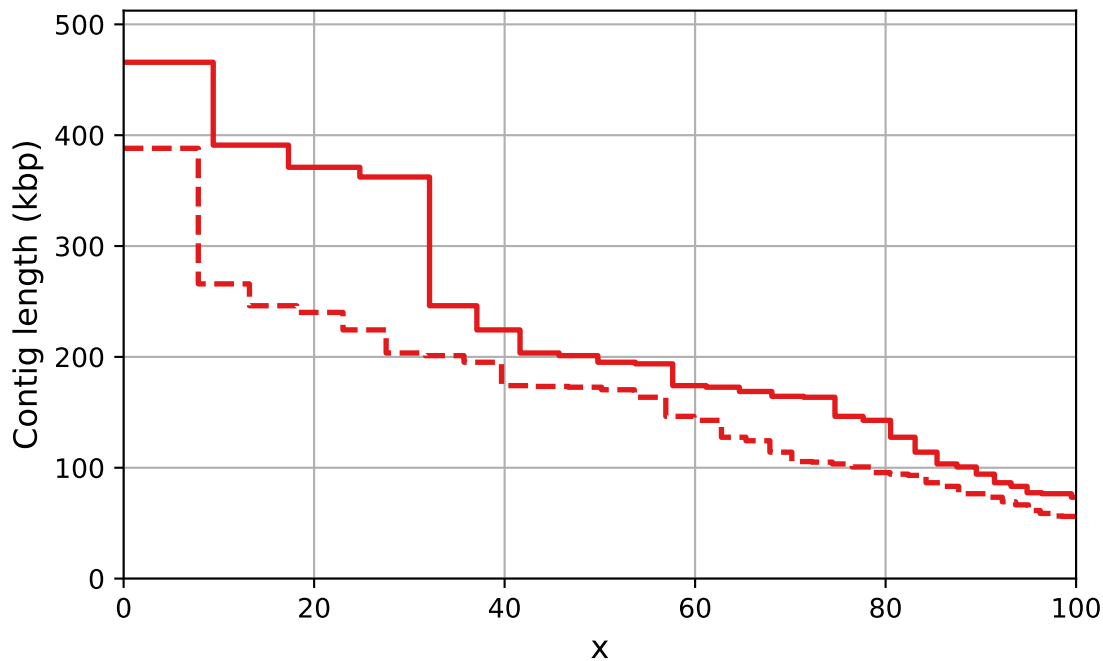
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



des\_on\_data\_15\_and\_data\_14\_Scaffolds

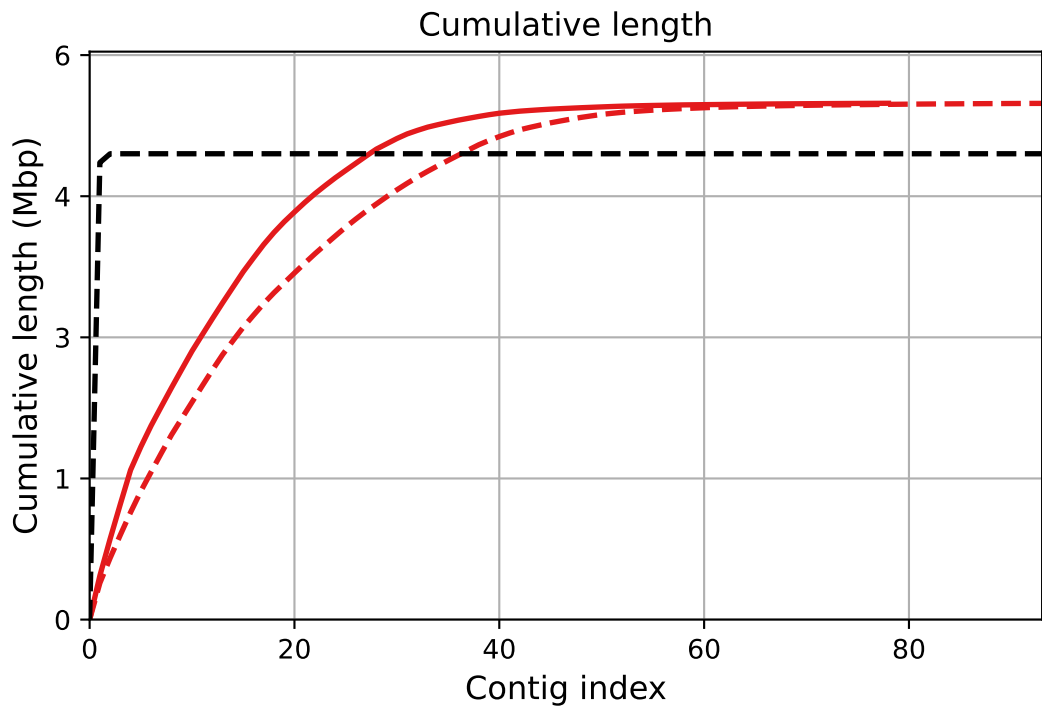
-- SPAdes\_on\_data\_15\_and\_data\_14\_Scaffolds

## NGx



Method on data 15 and data 14 Scaffolds

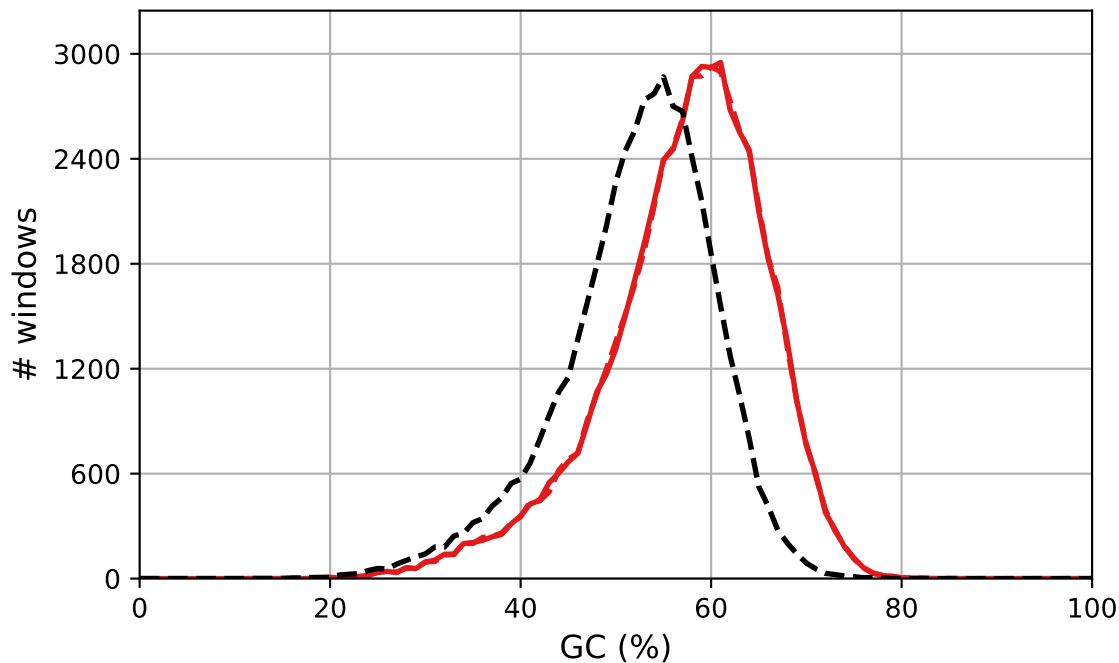
SPAdes on data 15 and data 14 Scaffolds



data\_15\_and\_data\_14\_\_Scaffolds

SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken

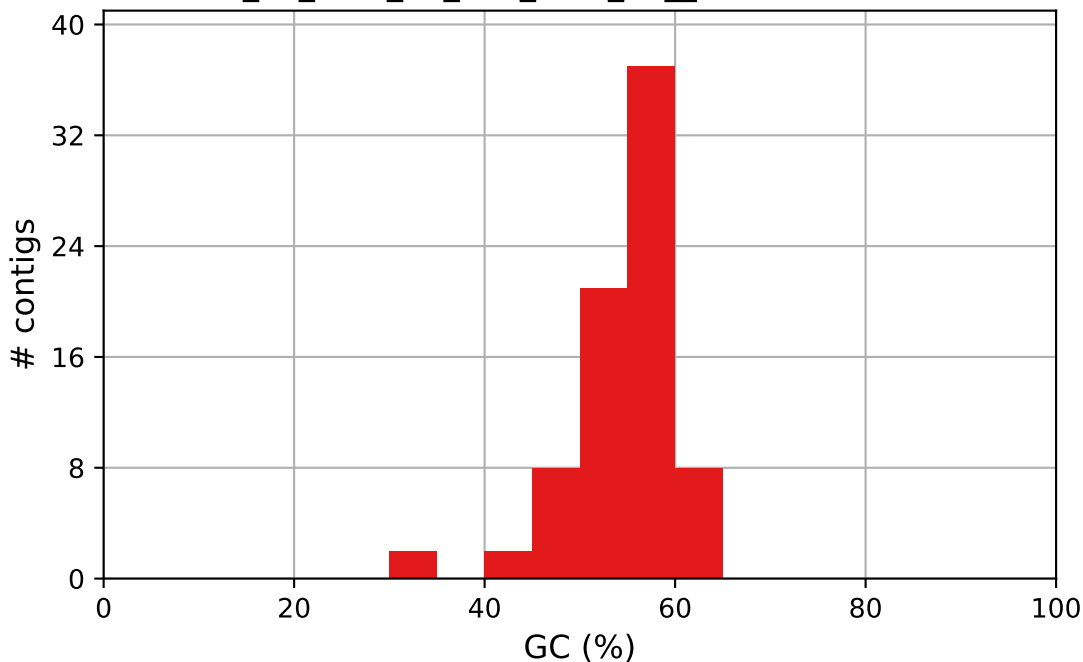
GC content



data\_15\_and\_data\_14\_\_Scaffolds

SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken

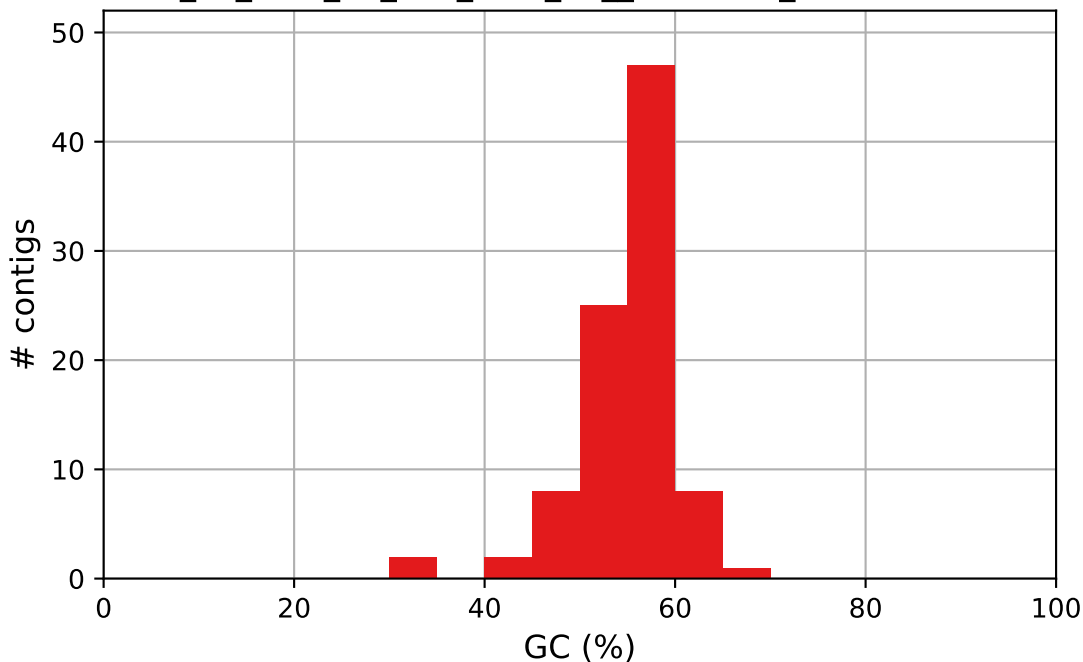
SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds GC content



SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds

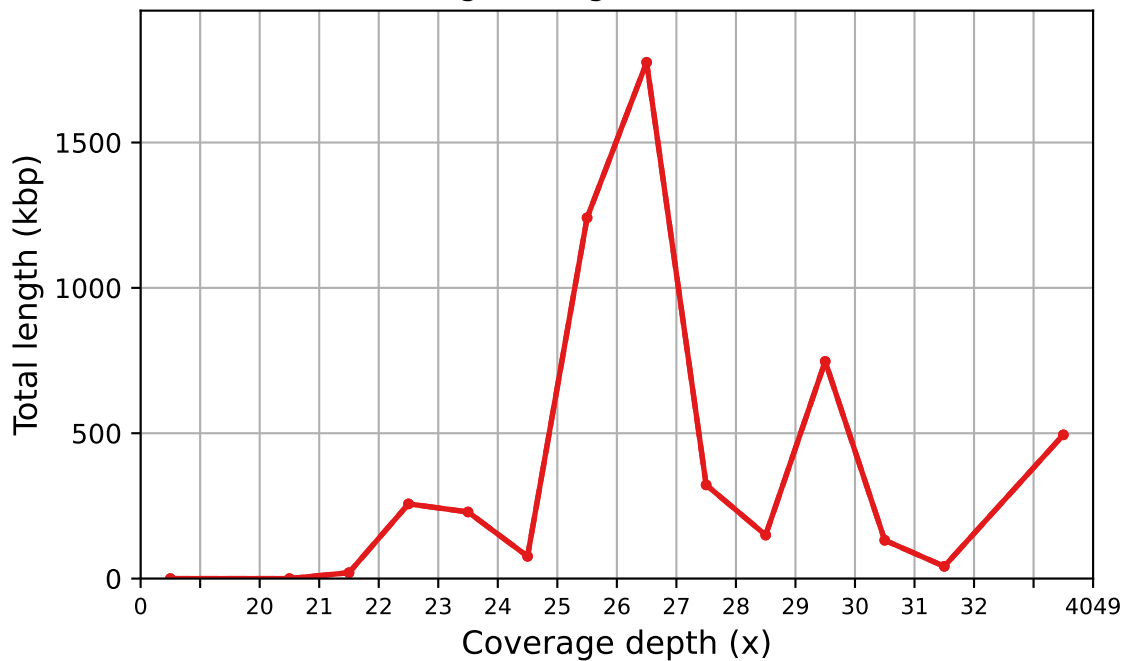


SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken GC content



SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken

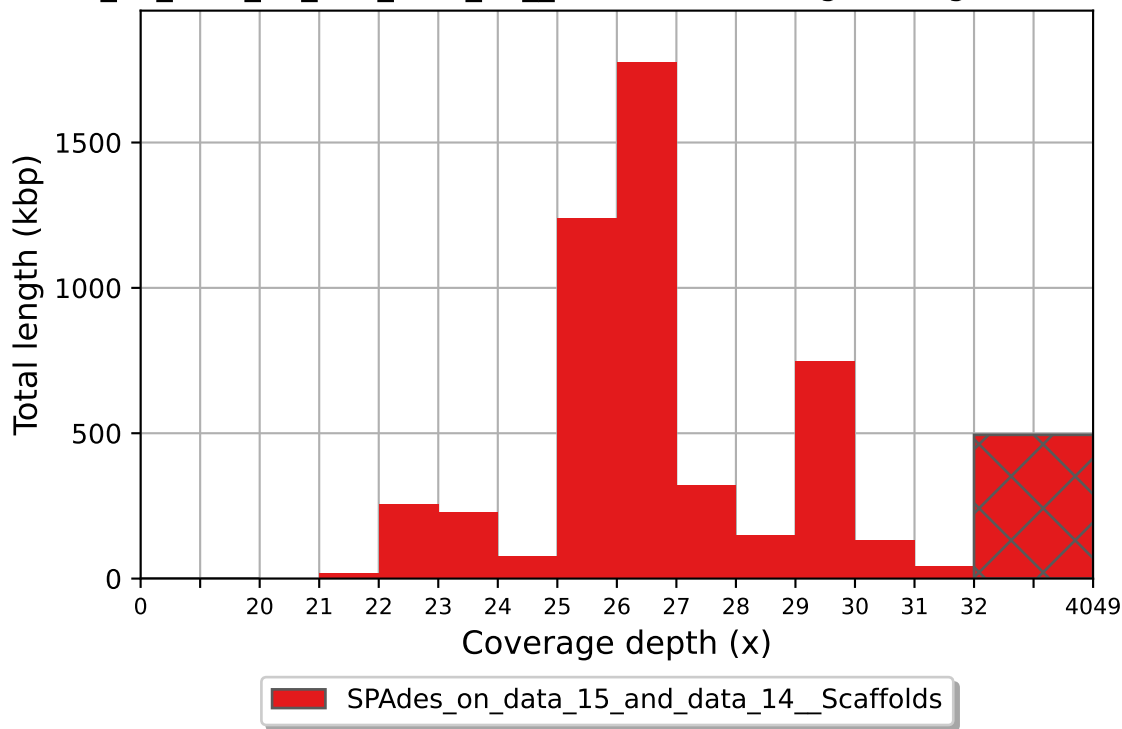
Coverage histogram (bin size: 1x)



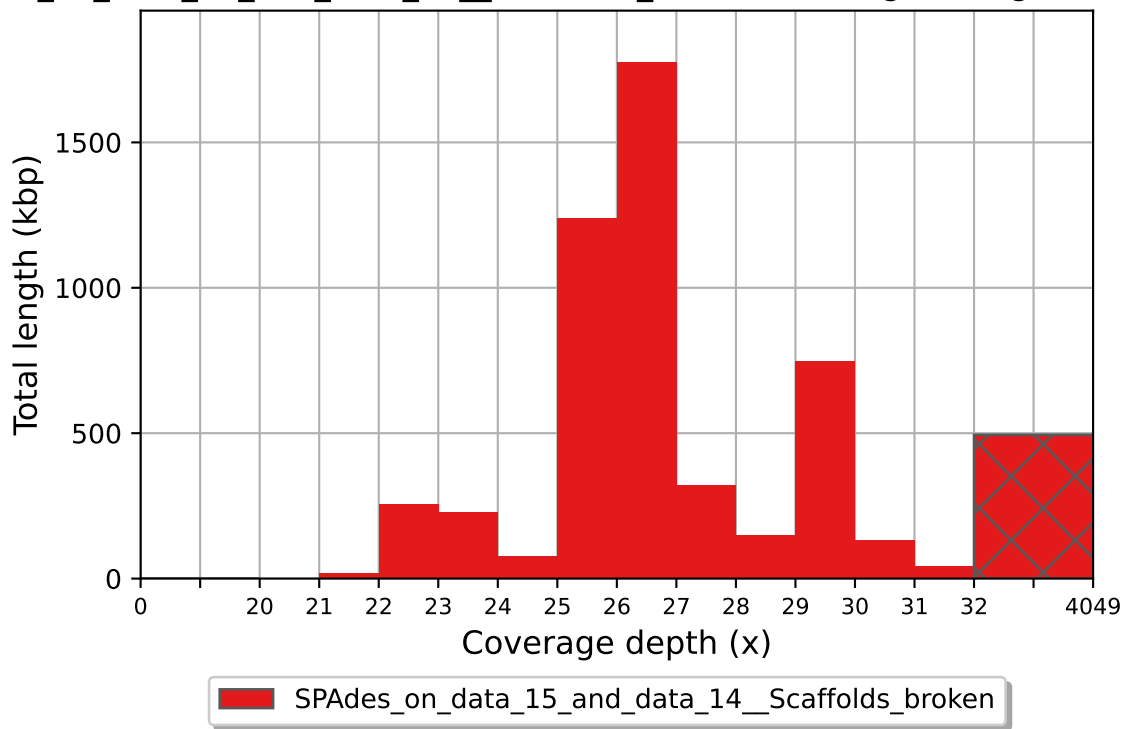
des\_on\_data\_15\_and\_data\_14\_Scaffolds

—•— SPAdes\_on\_data\_15\_and\_data\_14\_Scaffolds

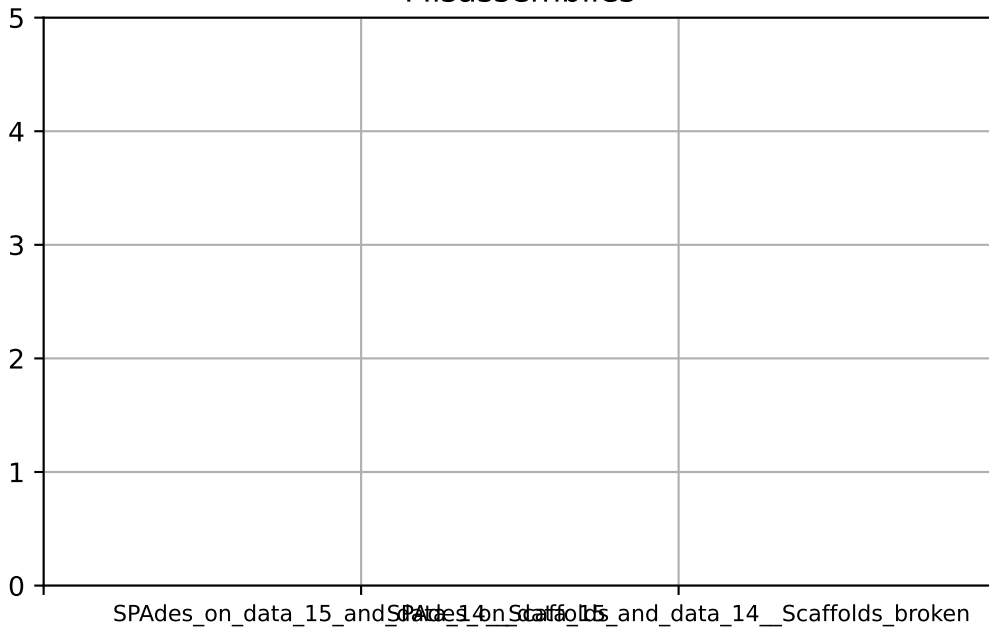
SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds coverage histogram (bin size: 1



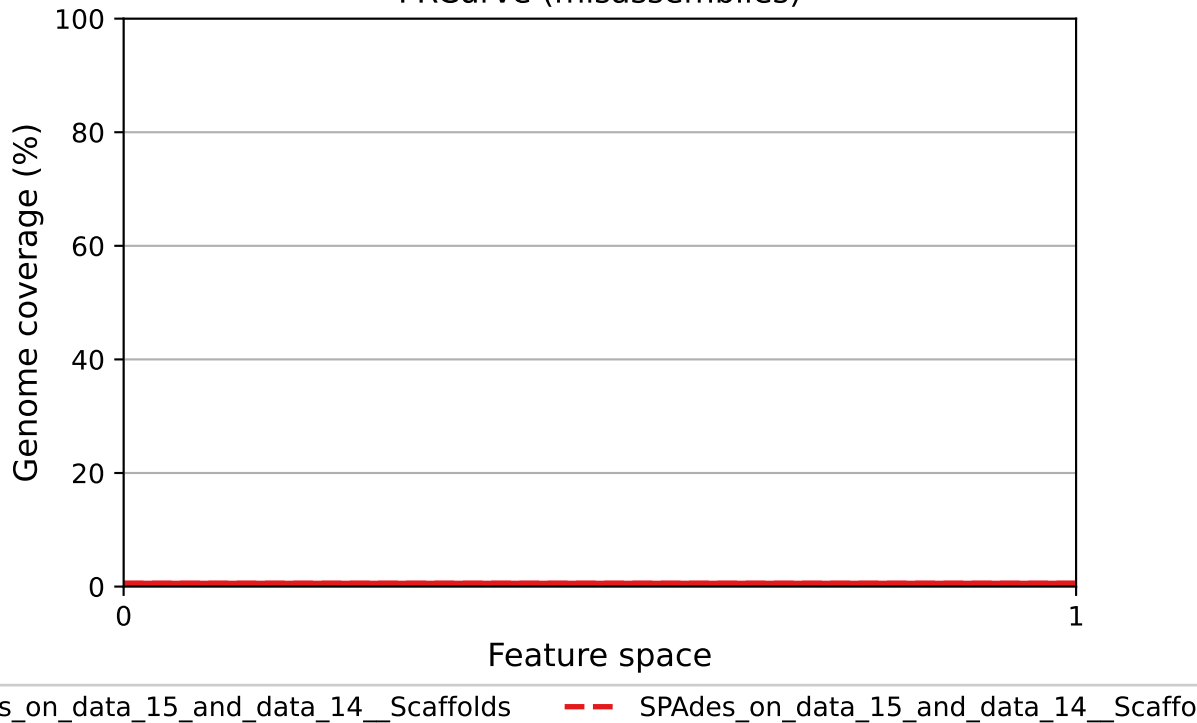
des\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken coverage histogram (bin size



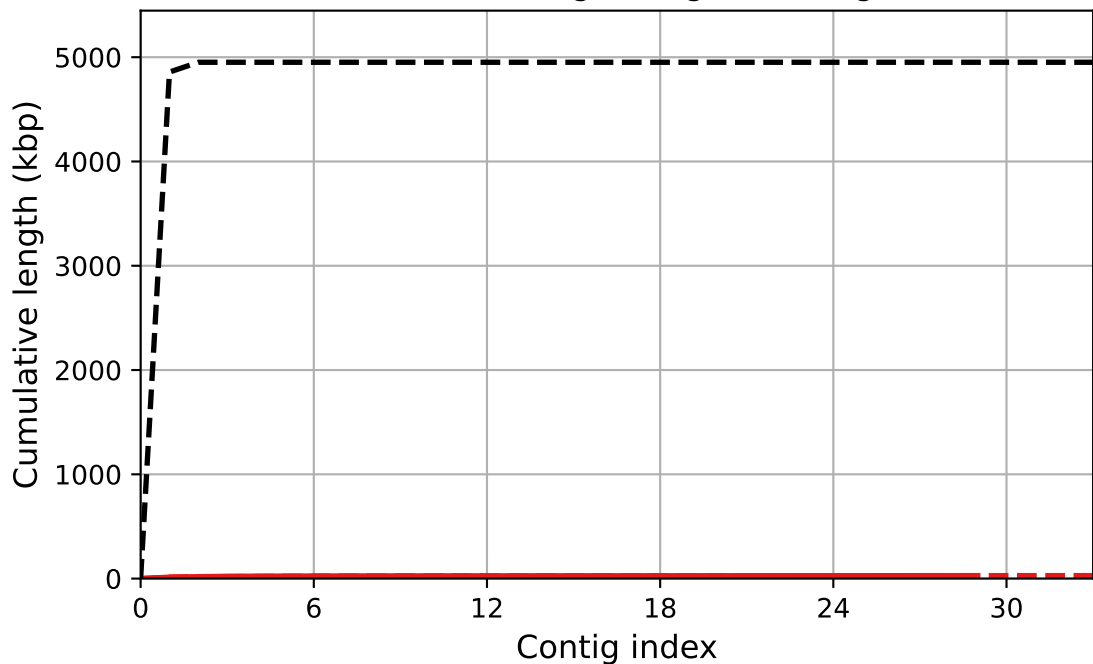
## Misassemblies



FRCurve (misassemblies)



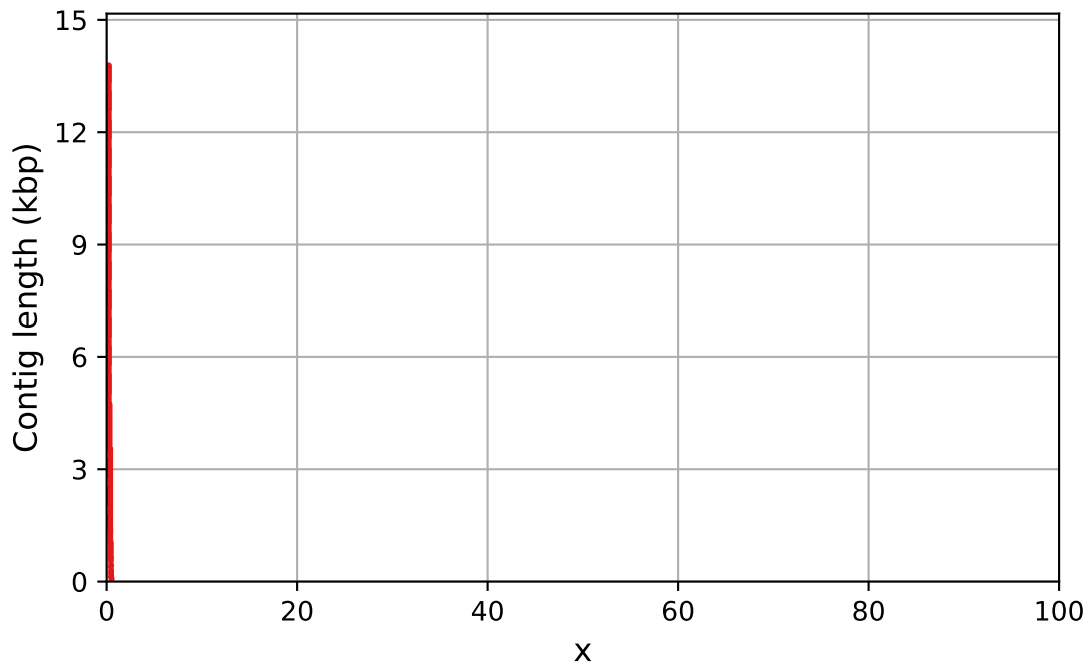
Cumulative length (aligned contigs)



data\_15\_and\_data\_14\_\_Scaffolds

-- SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken

NAx



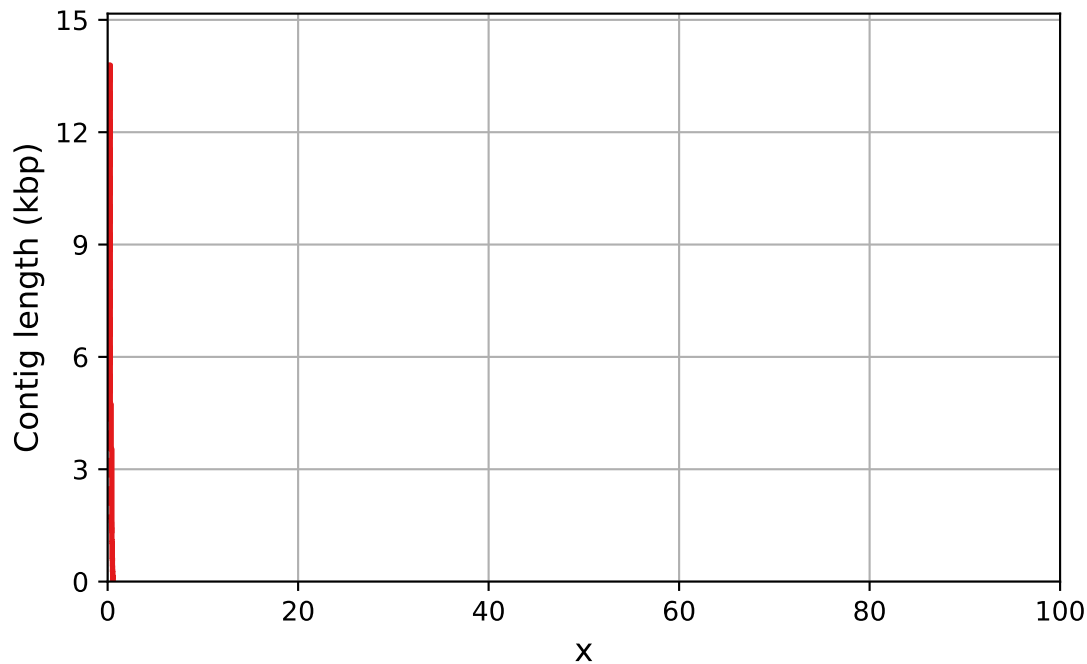
des\_on\_data\_15\_and\_data\_14\_\_Scaffolds

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SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds



# NGAx

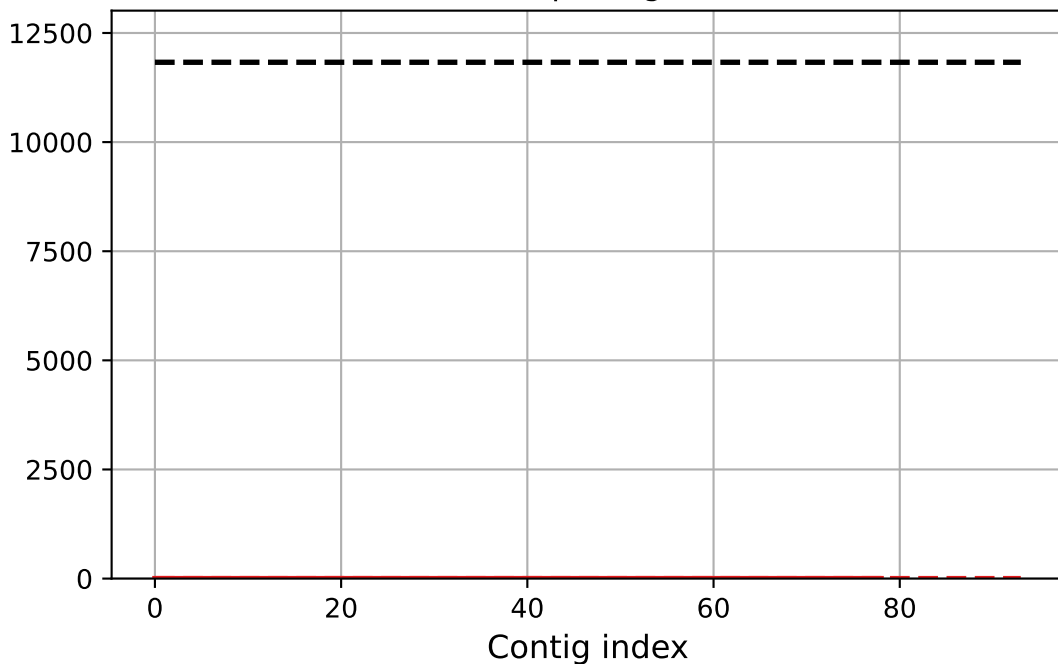


SPAdes\_on\_data\_15\_and\_data\_14\_Scaffolds

-- SPAdes\_on\_data\_15\_and\_data\_14\_Scaffolds

Cumulative # complete genomic features

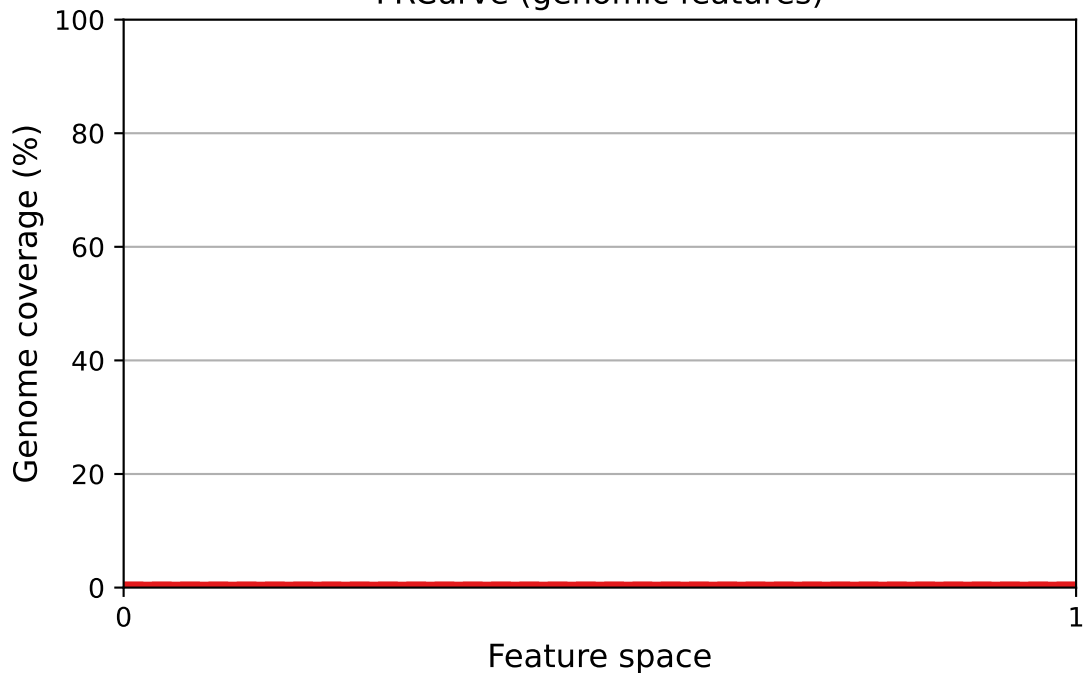
Cumulative # complete genomic features



ta\_15\_and\_data\_14\_\_Scaffolds

-- SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds\_broken

FRCurve (genomic features)



des\_on\_data\_15\_and\_data\_14\_\_Scaffolds

-- SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds

# complete genomic features

1

0

des\_on\_data\_15\_and\_data\_14\_\_Scaffolds



SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds

Genome fraction, %

100

50

des\_on\_data\_15\_and\_data\_14\_\_Scaffolds

SPAdes\_on\_data\_15\_and\_data\_14\_\_Scaffolds