

# Report

	SPAdes_on_data_59_and_data_58__Scaffolds	SPAdes_on_data_59_and_data_58__Scaffolds_broken
# contigs (>= 0 bp)	22	-
# contigs (>= 1000 bp)	15	17
Total length (>= 0 bp)	1677646	-
Total length (>= 1000 bp)	1675269	1675069
# contigs	17	19
Largest contig	500495	335484
Total length	1676613	1676413
Reference length	1641481	1641481
GC (%)	30.46	30.46
Reference GC (%)	30.55	30.55
N50	224361	218161
NG50	224361	218161
N90	68450	68450
NG90	68450	68450
auN	275826.3	208181.0
auNG	281729.7	212611.3
L50	3	3
LG50	3	3
L90	7	8
LG90	7	8
# misassemblies	19	19
# misassembled contigs	8	8
Misassembled contigs length	1540207	1368996
# local misassemblies	25	25
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 9 part	2 + 10 part
Unaligned length	143719	143719
Genome fraction (%)	94.035	94.033
Duplication ratio	1.001	1.001
# N's per 100 kbp	11.93	0.00
# mismatches per 100 kbp	1211.26	1211.34
# indels per 100 kbp	56.39	56.33
# genomic features	7924 + 118 part	7922 + 120 part
Complete BUSCO (%)	82.43	82.43
Partial BUSCO (%)	2.70	2.70
# predicted rRNA genes	2 + 0 part	2 + 0 part
Largest alignment	233463	196898
Total aligned length	1532122	1532022
NA50	92103	81057
NGA50	92103	81057
NA90	6193	6100
NGA90	12625	12116
auNA	103575.2	89182.9
auNGA	105791.9	91080.8
LA50	6	7
LGA50	6	7
LA90	24	26
LGA90	20	22

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

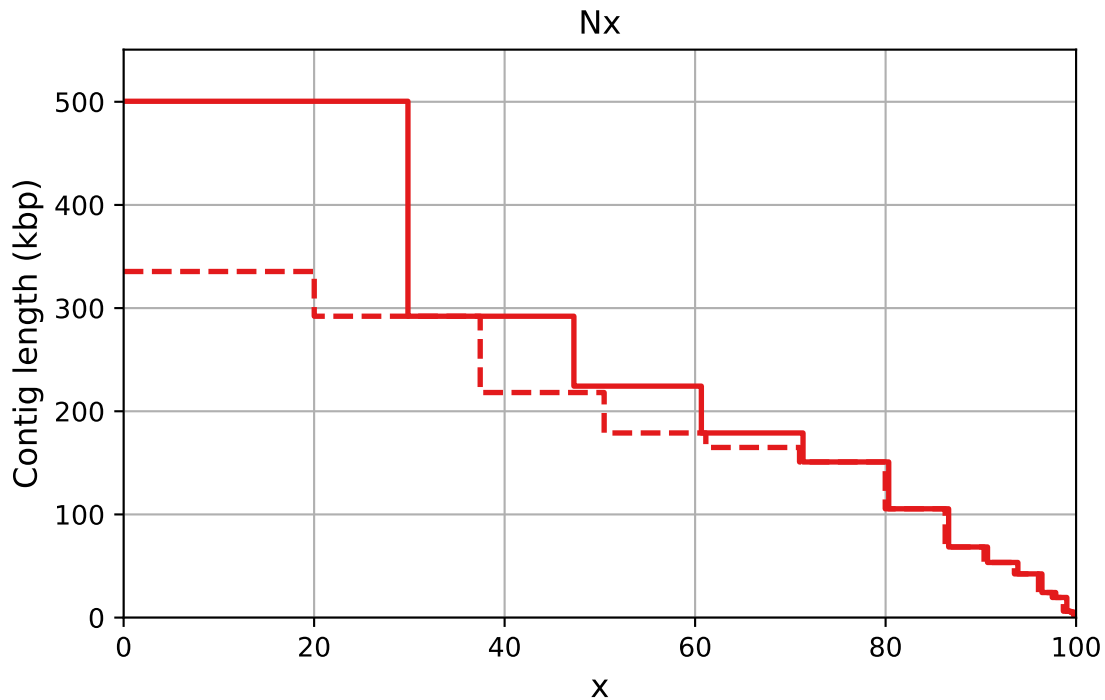
	SPAdes_on_data_59_and_data_58__Scaffolds	SPAdes_on_data_59_and_data_58__Scaffolds_broken
# misassemblies	19	19
# contig misassemblies	19	19
# c. relocations	19	19
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	8	8
Misassembled contigs length	1540207	1368996
# local misassemblies	25	25
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	0	0
# mismatches	18558	18558
# indels	864	863
# indels (<= 5 bp)	794	794
# indels (> 5 bp)	70	69
Indels length	3505	3442

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_59_and_data_58__Scaffolds	SPAdes_on_data_59_and_data_58__Scaffolds_broken
# fully unaligned contigs	2	2
Fully unaligned length	58809	58809
# partially unaligned contigs	9	10
Partially unaligned length	84910	84910
# N's	200	0

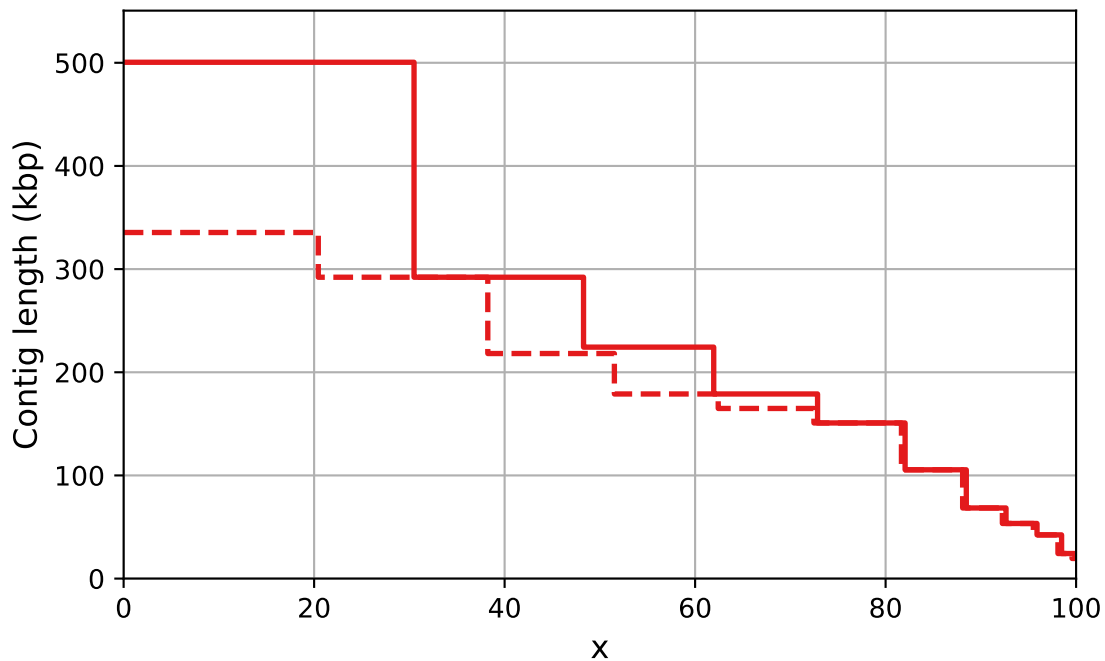
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



des\_on\_data\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds

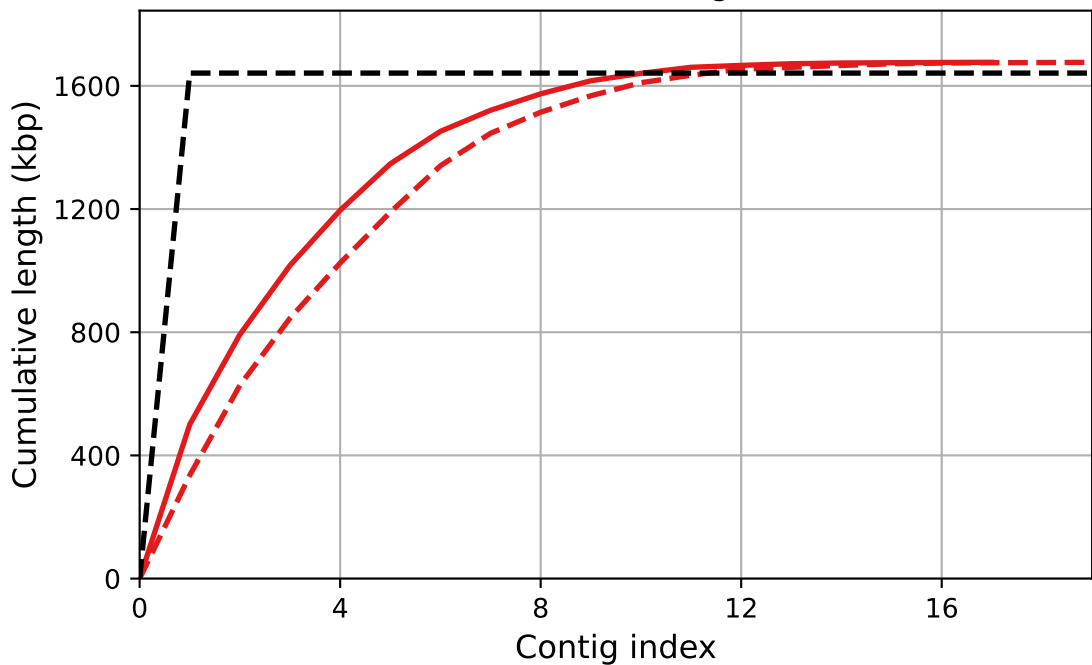
# NGx



des\_on\_data\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds

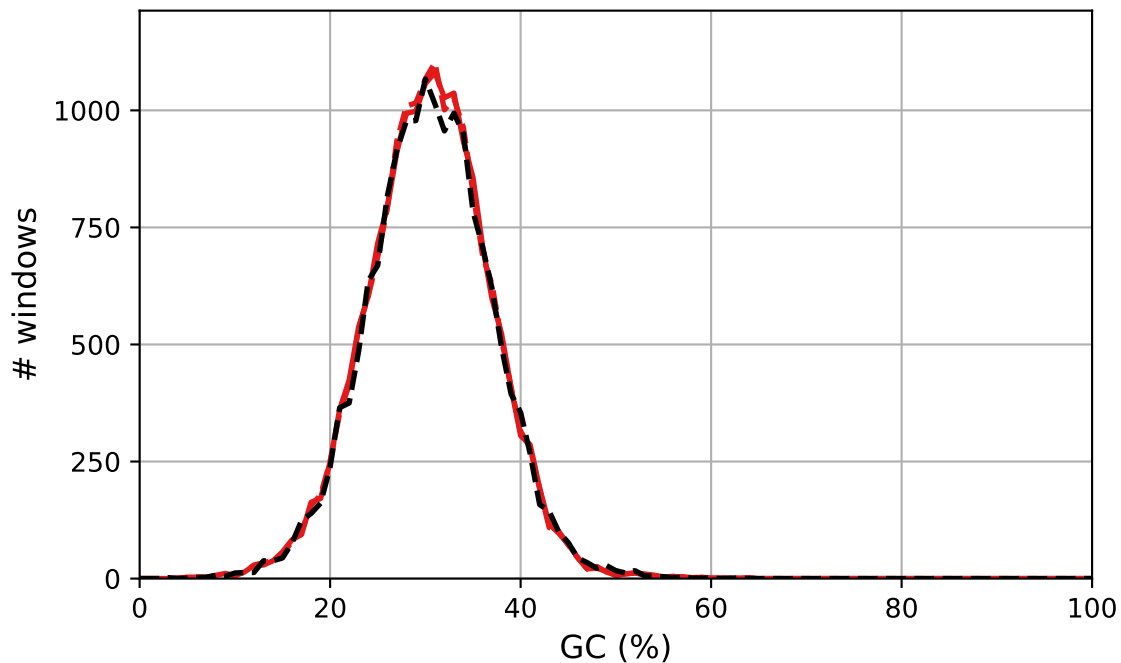
Cumulative length



ta\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds\_broken

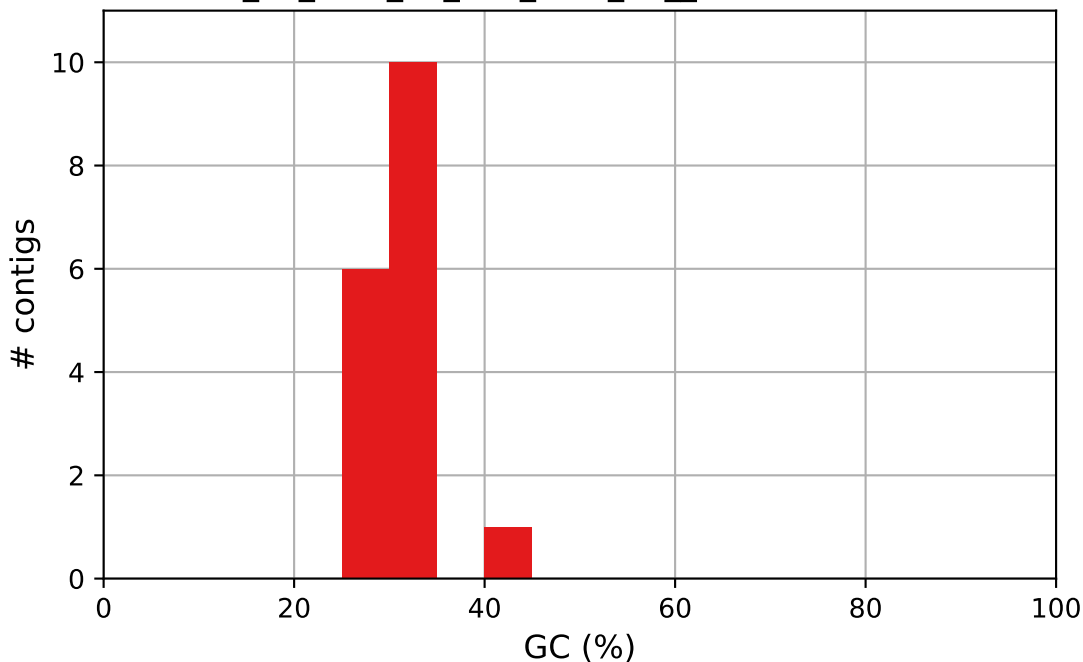
GC content



data\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds\_broken

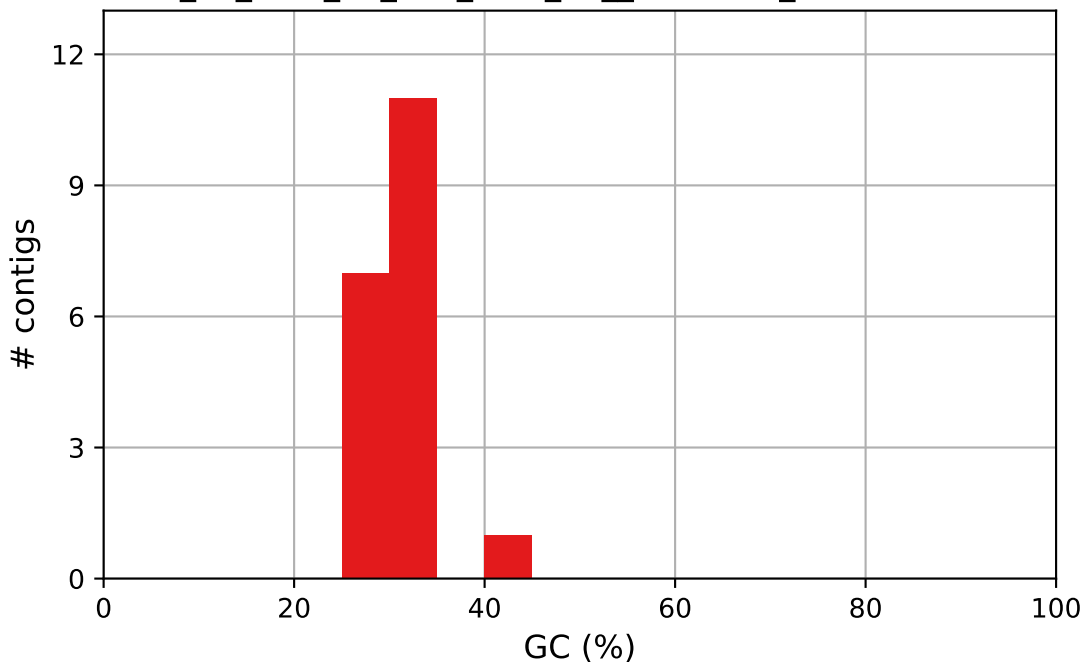
SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds GC content



SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds

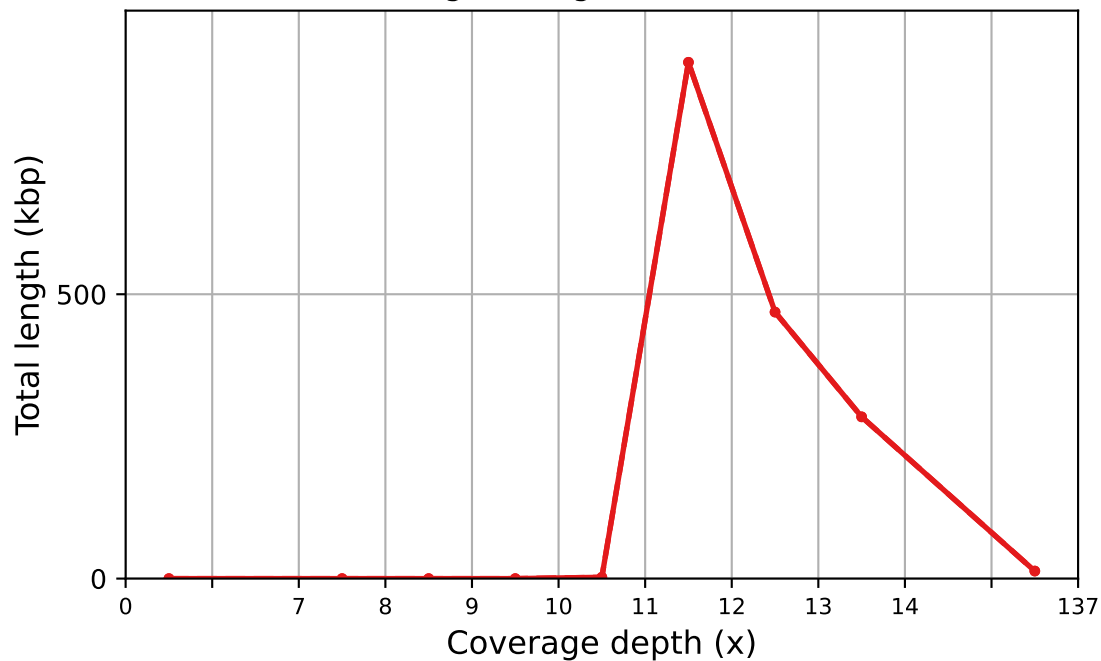


SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds\_broken GC content



SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds\_broken

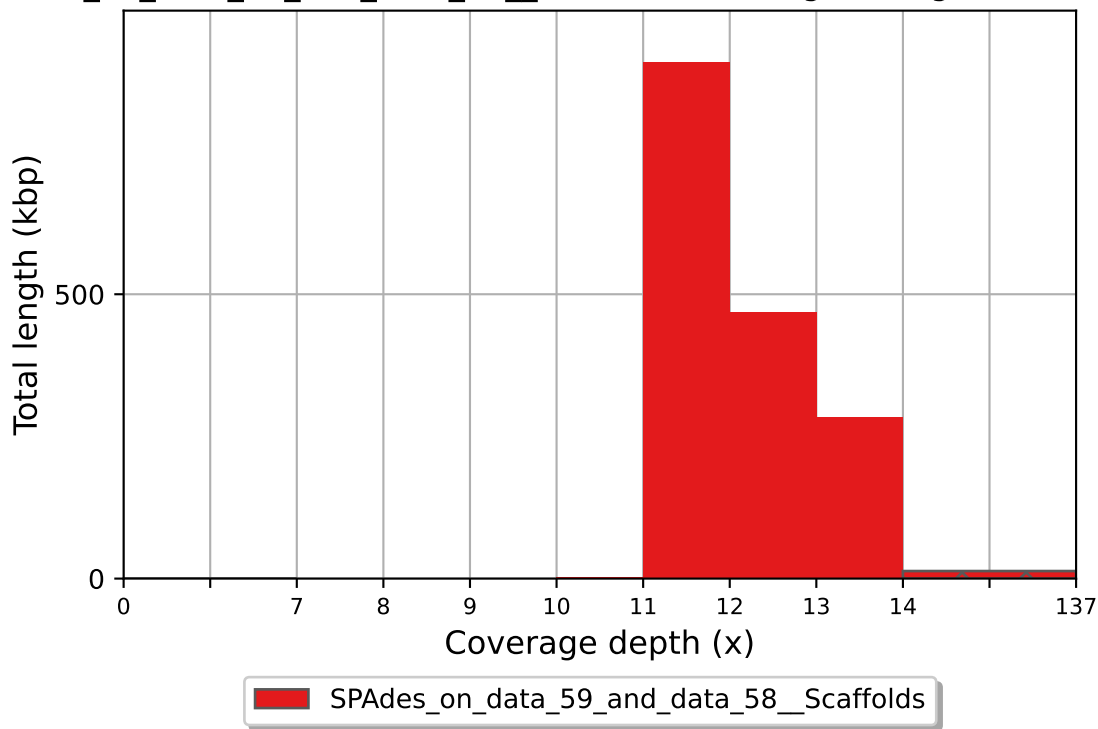
Coverage histogram (bin size: 1x)



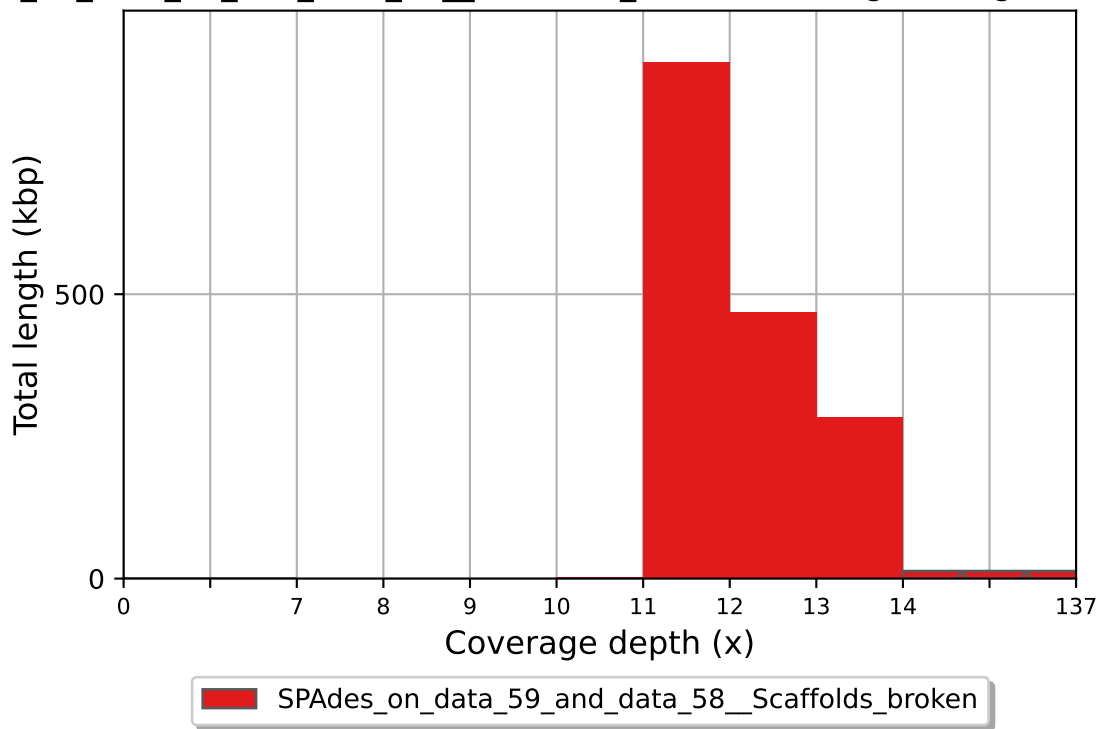
des\_on\_data\_59\_and\_data\_58\_Scaffolds

—•— SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds

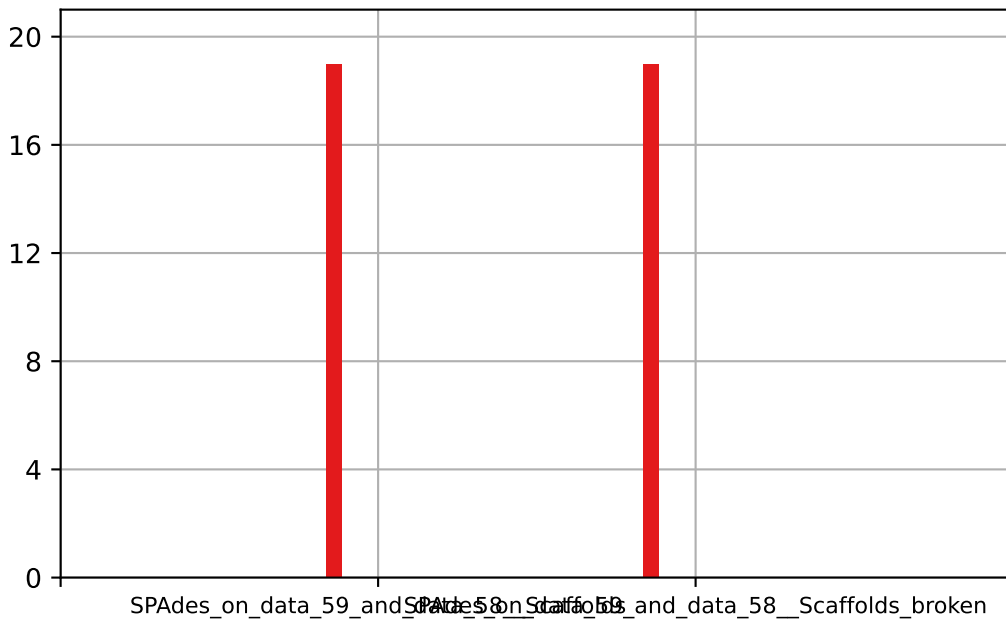
SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds coverage histogram (bin size: 1



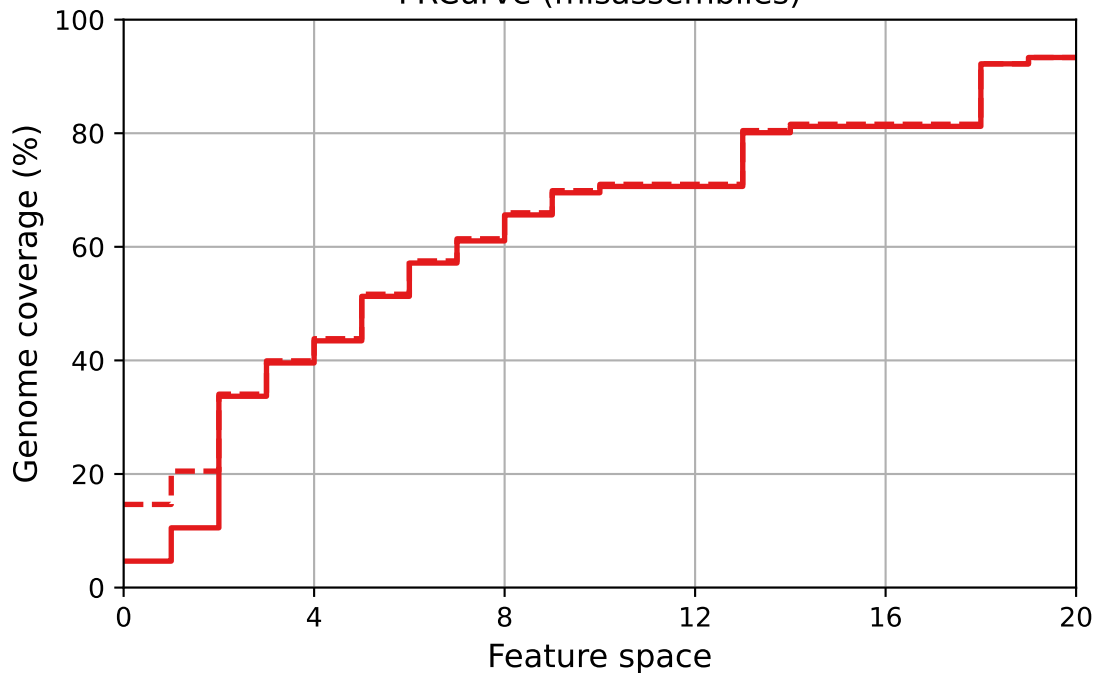
des\_on\_data\_59\_and\_data\_58\_\_Scaffolds\_broken coverage histogram (bin size 1)



## Misassemblies



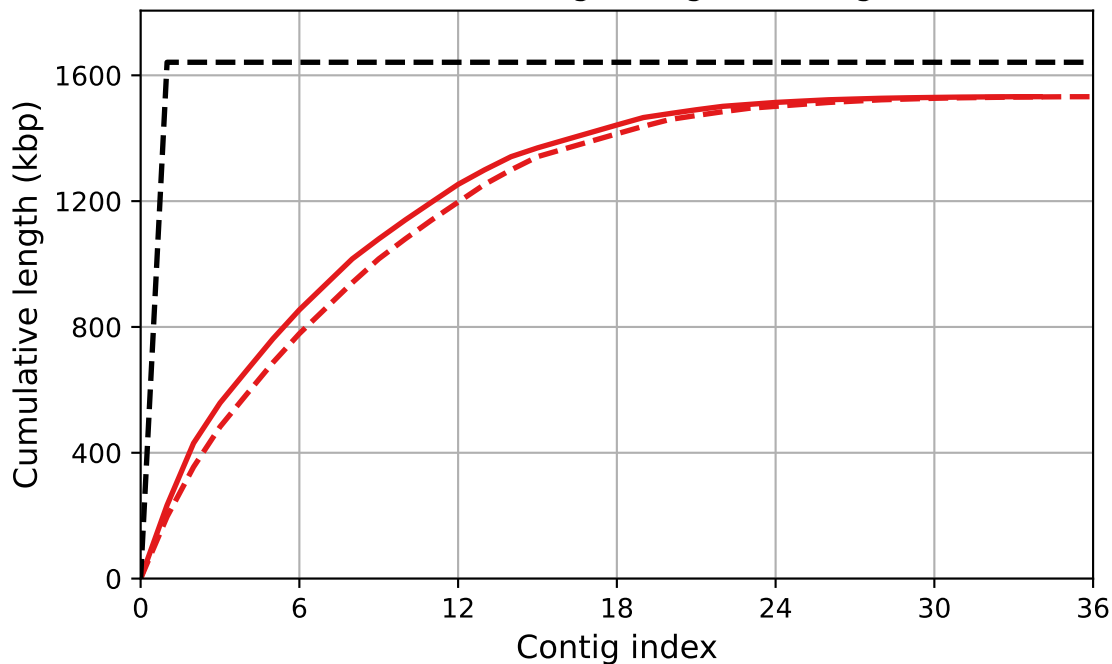
FRCurve (misassemblies)



des\_on\_data\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds

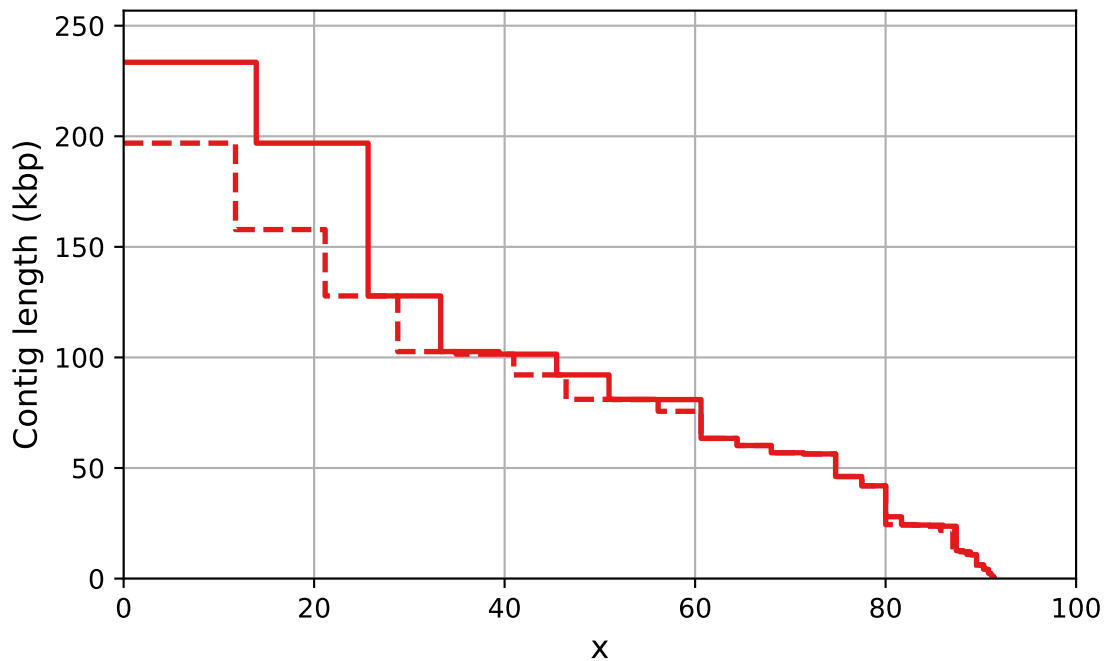
Cumulative length (aligned contigs)



data\_59\_and\_data\_58\_Scaffolds

SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds\_broken

NAx

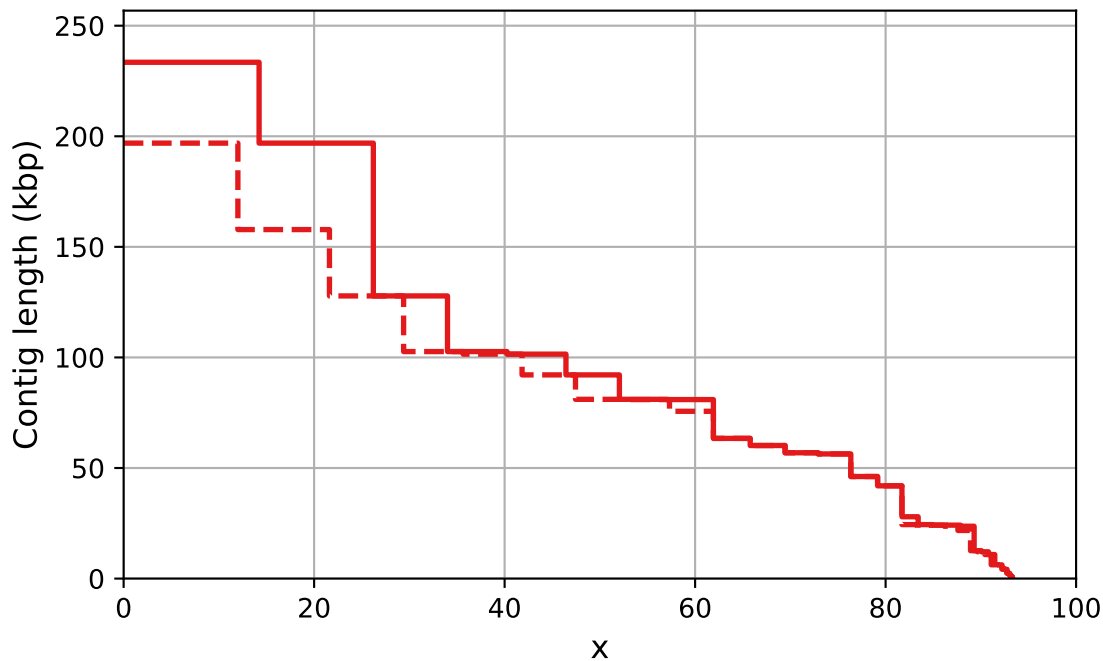


des\_on\_data\_59\_and\_data\_58\_Scaffolds

SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds



# NGAx

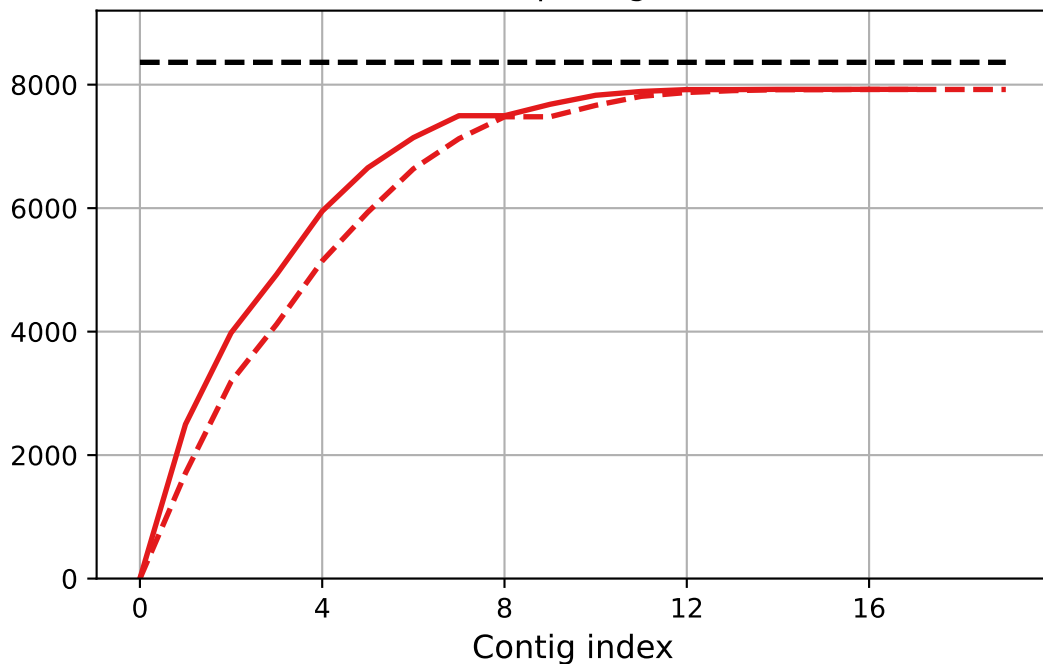


des\_on\_data\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds

Cumulative # complete genomic features

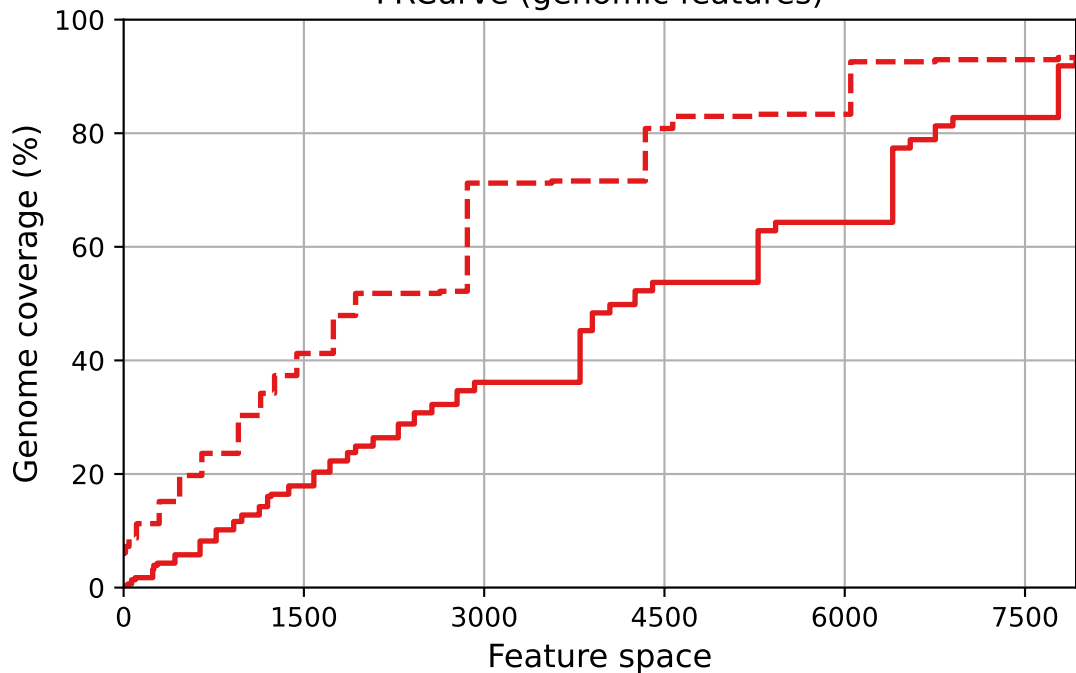
Cumulative # complete genomic features



data\_59\_and\_data\_58\_\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds\_broken

FRCurve (genomic features)



des\_on\_data\_59\_and\_data\_58\_Scaffolds

-- SPAdes\_on\_data\_59\_and\_data\_58\_Scaffolds

# complete genomic features

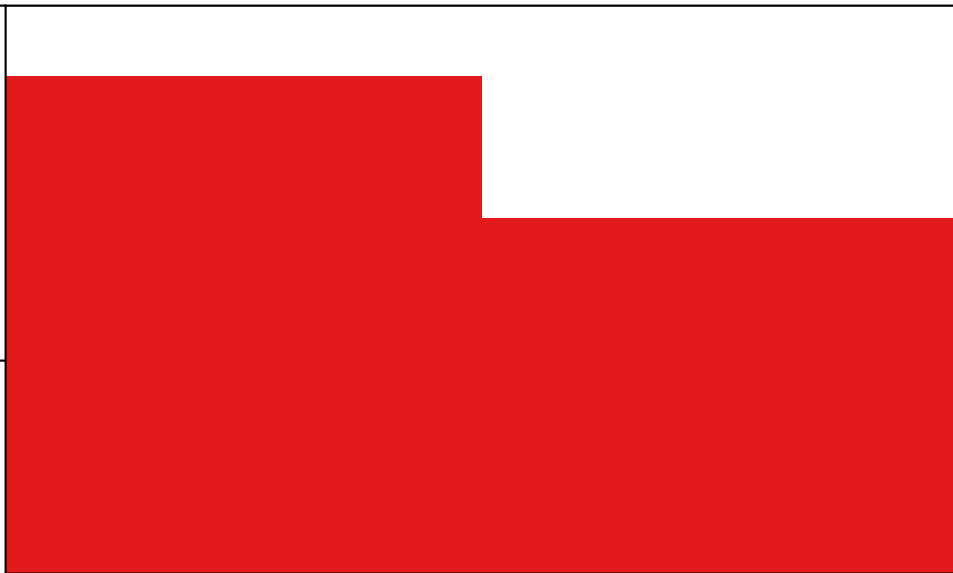
7925

7920

des\_on\_data\_59\_and\_data\_58\_\_Scaffolds



SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds



# Genome fraction, %

100

99

98

97

96

95

des\_on\_data\_59\_and\_data\_58\_\_Scaffolds



SPAdes\_on\_data\_59\_and\_data\_58\_\_Scaffolds