

# Report

	SPAdes_on_data_29_and_data_30__Scaffolds	SPAdes_on_data_29_and_data_30__Scaffolds_broken
# contigs (>= 0 bp)	1354	-
# contigs (>= 1000 bp)	73	86
Total length (>= 0 bp)	5875354	-
Total length (>= 1000 bp)	5504706	5503496
# contigs	104	118
Largest contig	465850	305153
Total length	5524497	5522939
Reference length	5682322	5682322
GC (%)	57.20	57.20
Reference GC (%)	57.12	57.12
N50	193741	146373
NG50	174078	146373
N90	76563	56140
NG90	56144	40867
auN	209796.4	151190.6
auNG	203969.4	146949.8
L50	10	14
LG50	11	14
L90	28	38
LG90	31	41
# misassemblies	78	75
# misassembled contigs	26	32
Misassembled contigs length	4434182	4080183
# local misassemblies	30	29
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	2	2
# unaligned contigs	48 + 31 part	49 + 35 part
Unaligned length	726982	725656
Genome fraction (%)	84.860	85.254
Duplication ratio	1.001	1.001
# N's per 100 kbp	22.26	0.00
# mismatches per 100 kbp	685.87	687.71
# indels per 100 kbp	19.42	19.48
# genomic features	9599 + 204 part	9615 + 208 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	6 + 0 part	6 + 0 part
Largest alignment	205341	205341
Total aligned length	4795044	4794352
NA50	69622	59584
NGA50	66565	59533
NA90	-	-
NGA90	-	-
auNA	78859.1	70849.3
auNGA	76668.8	68862.0
LA50	25	28
LGA50	26	29
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

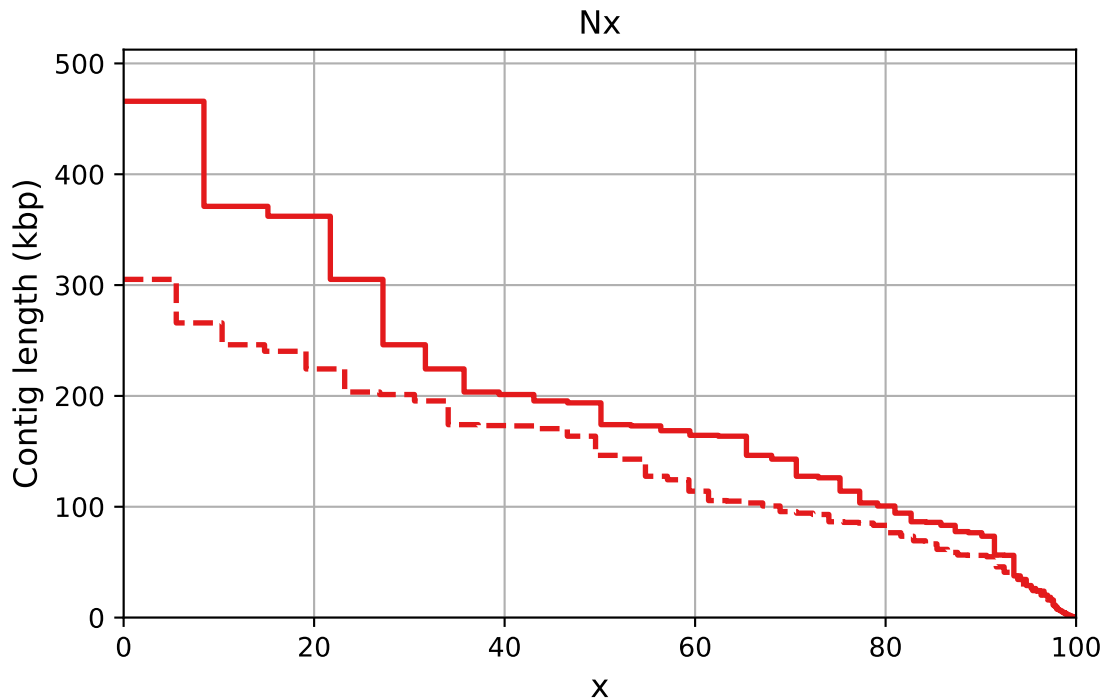
	SPAdes_on_data_29_and_data_30__Scaffolds	SPAdes_on_data_29_and_data_30__Scaffolds_broken
# misassemblies	78	75
# contig misassemblies	75	75
# c. relocations	72	72
# c. translocations	3	3
# c. inversions	0	0
# scaffold misassemblies	3	0
# s. relocations	3	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	26	32
Misassembled contigs length	4434182	4080183
# local misassemblies	30	29
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	2	2
# mismatches	32888	32971
# indels	931	934
# indels (<= 5 bp)	844	856
# indels (> 5 bp)	87	78
Indels length	7354	6108

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_29_and_data_30__Scaffolds	SPAdes_on_data_29_and_data_30__Scaffolds_broken
# fully unaligned contigs	48	49
Fully unaligned length	94681	94353
# partially unaligned contigs	31	35
Partially unaligned length	632301	631303
# N's	1230	0

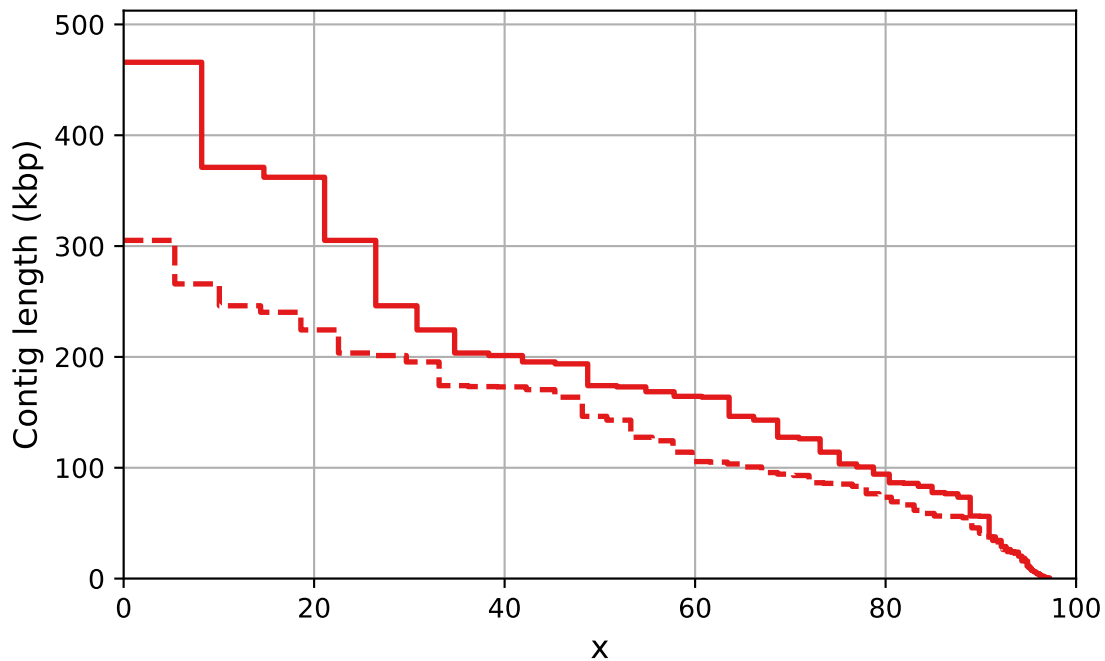
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



des\_on\_data\_29\_and\_data\_30\_Scaffolds

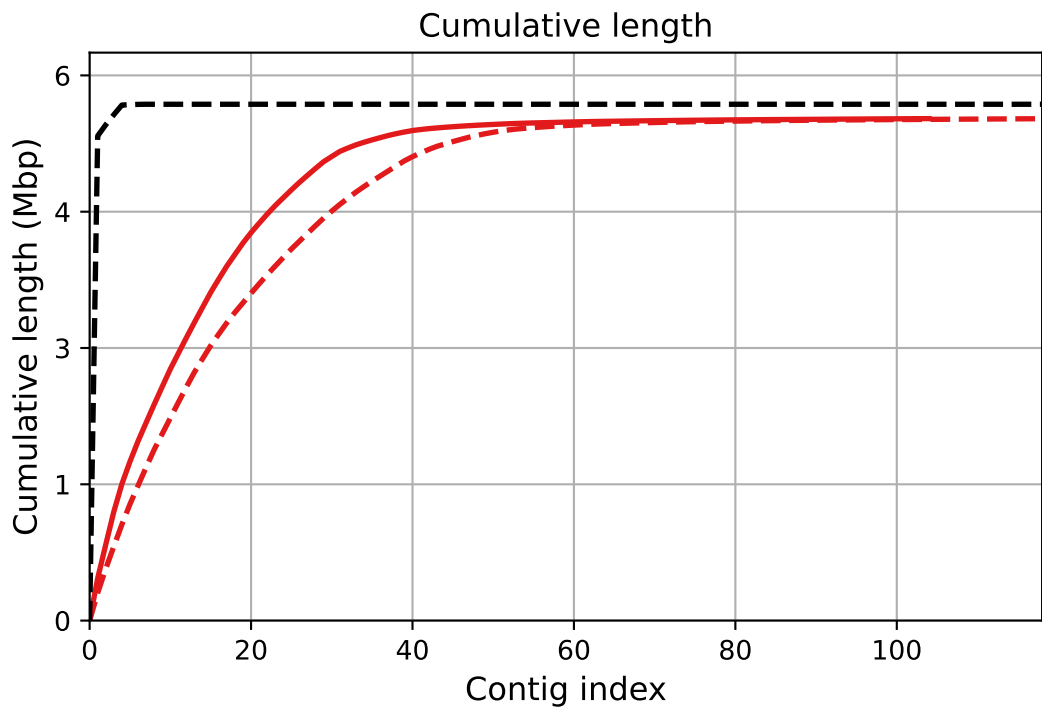
SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds

## NGx



des\_on\_data\_29\_and\_data\_30\_Scaffolds

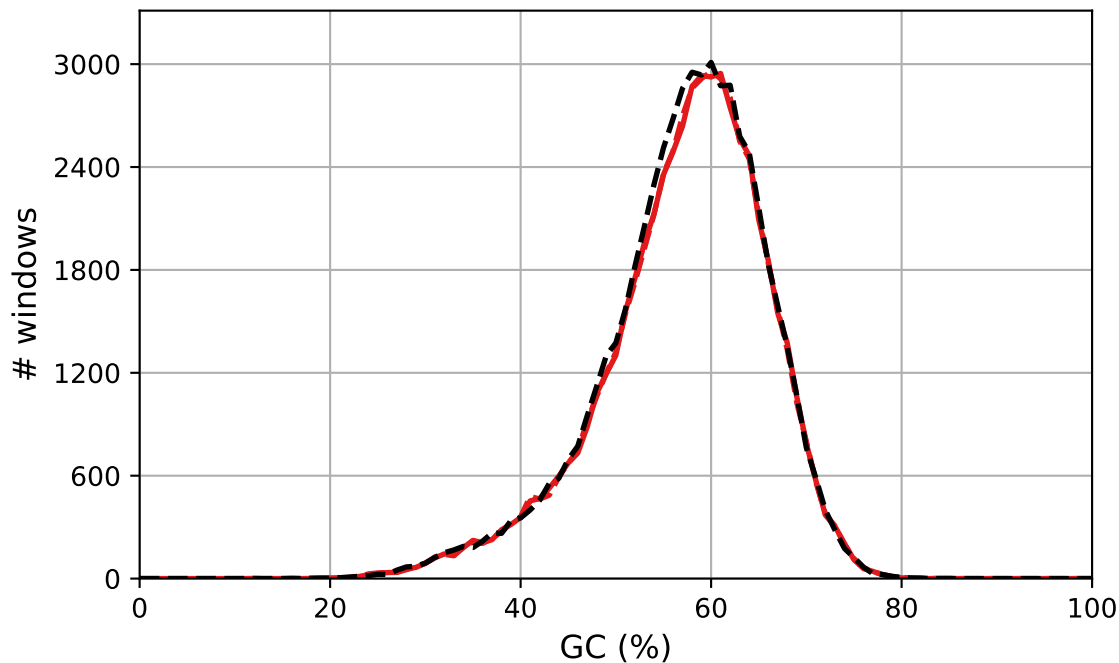
SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds



data\_29\_and\_data\_30\_\_Scaffolds

-- SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken

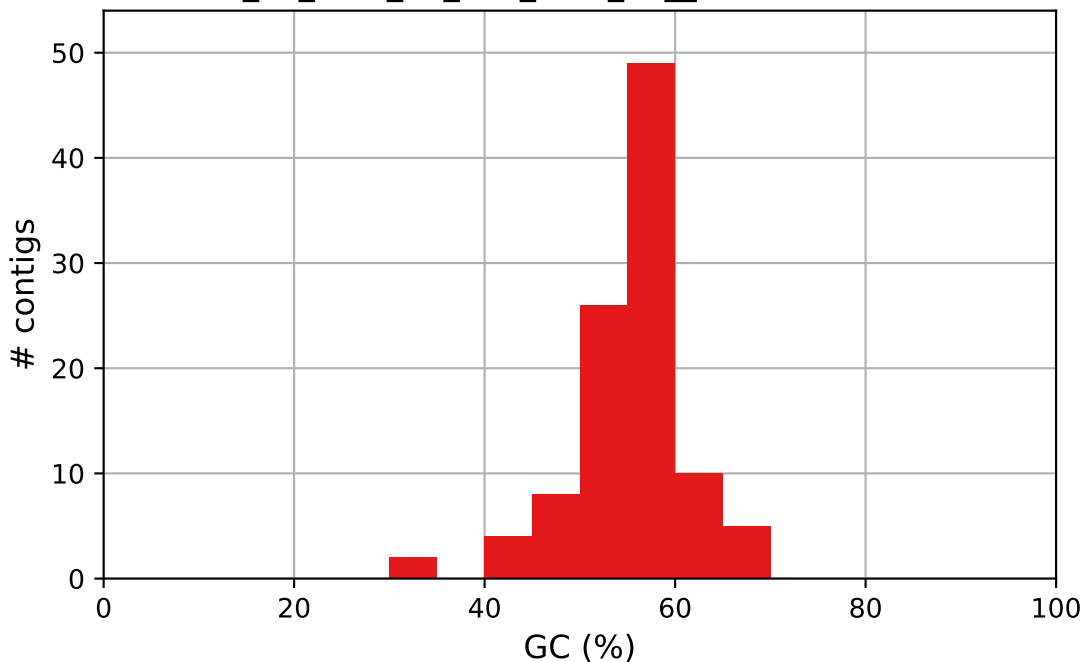
GC content



data\_29\_and\_data\_30\_\_Scaffolds

-- SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken

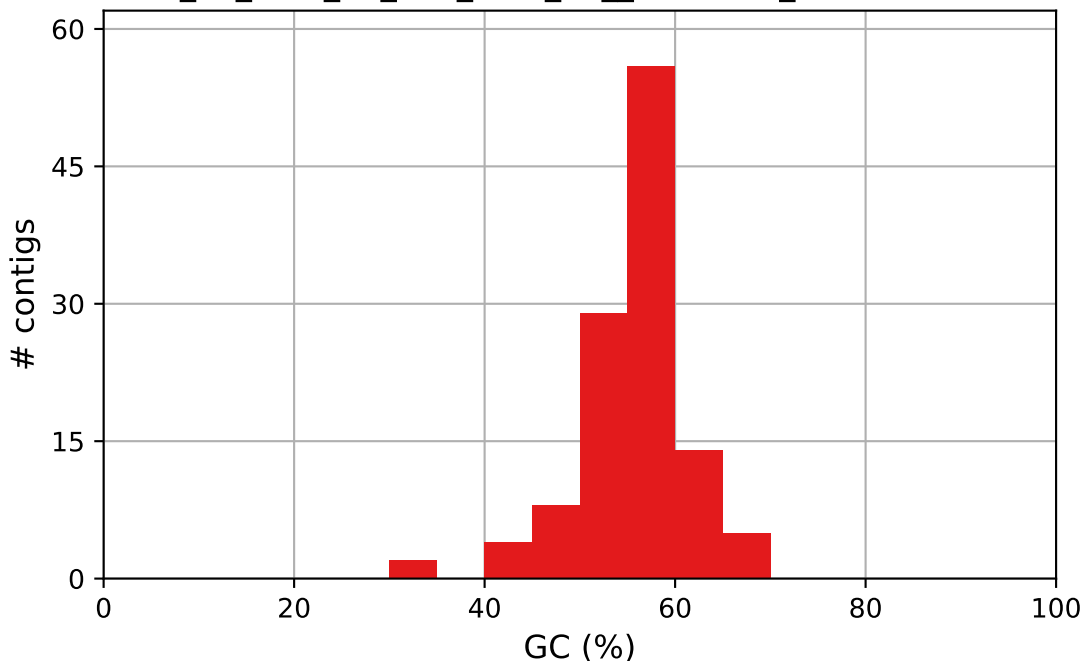
SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds GC content



SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds

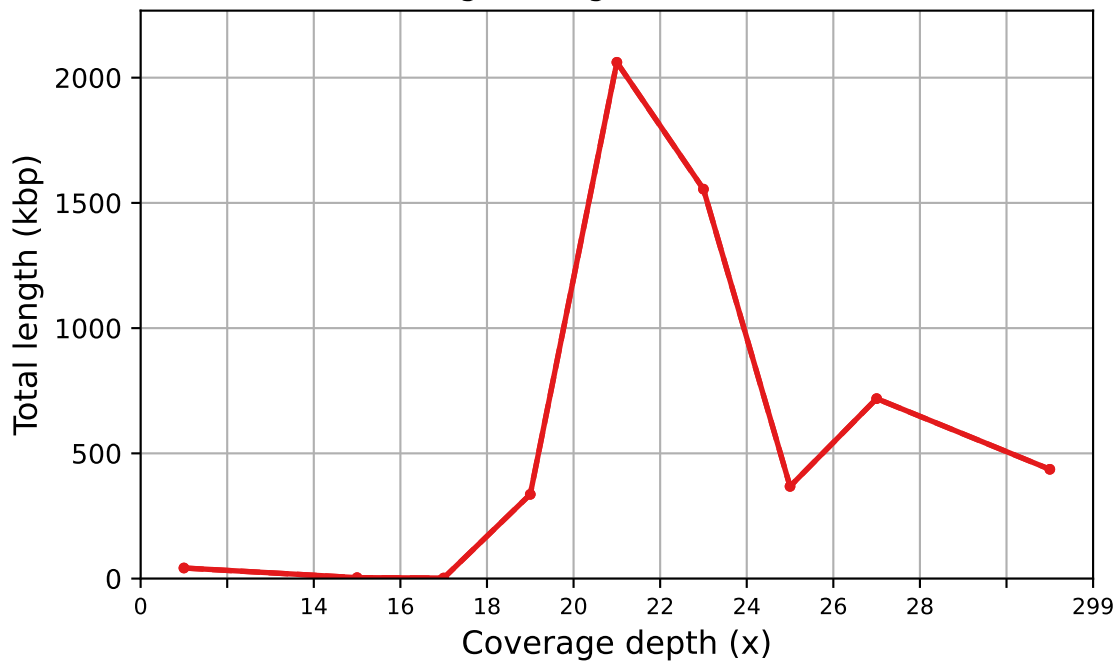


SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken GC content



SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken

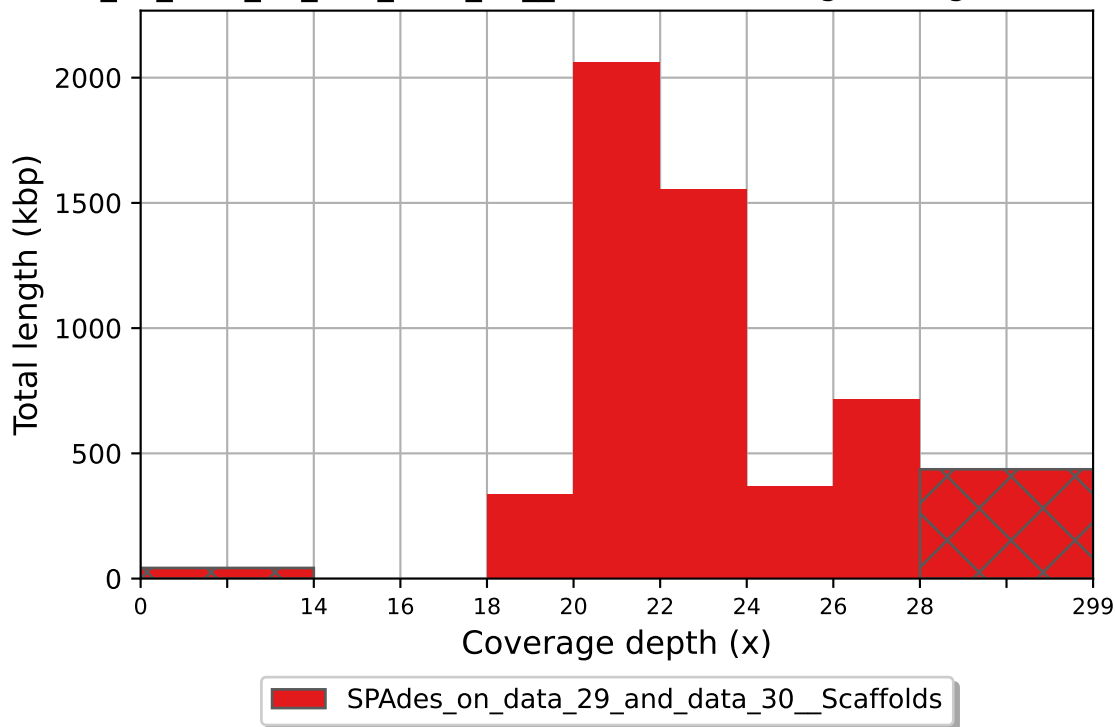
Coverage histogram (bin size: 2x)



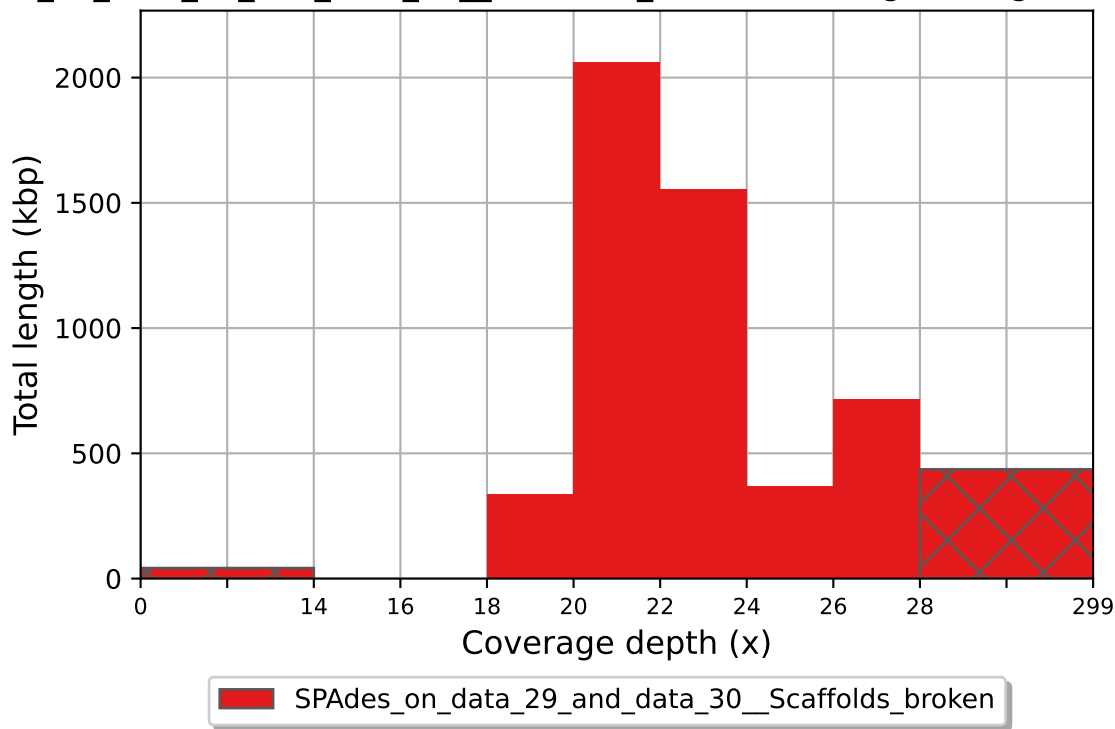
des\_on\_data\_29\_and\_data\_30\_Scaffolds

—•— SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds

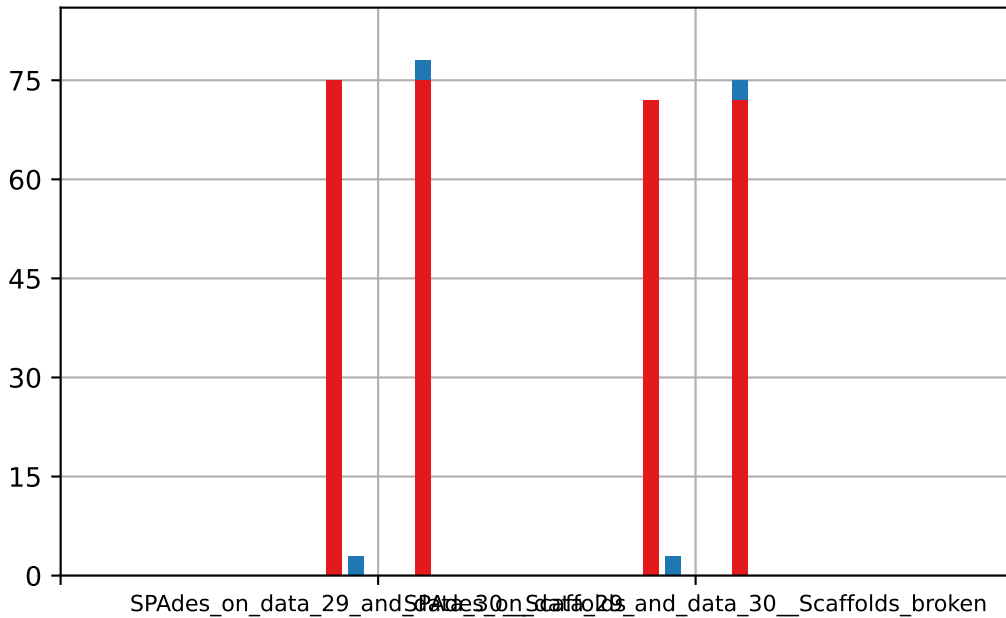
SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds coverage histogram (bin size: 2



des\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken coverage histogram (bin size



## Misassemblies

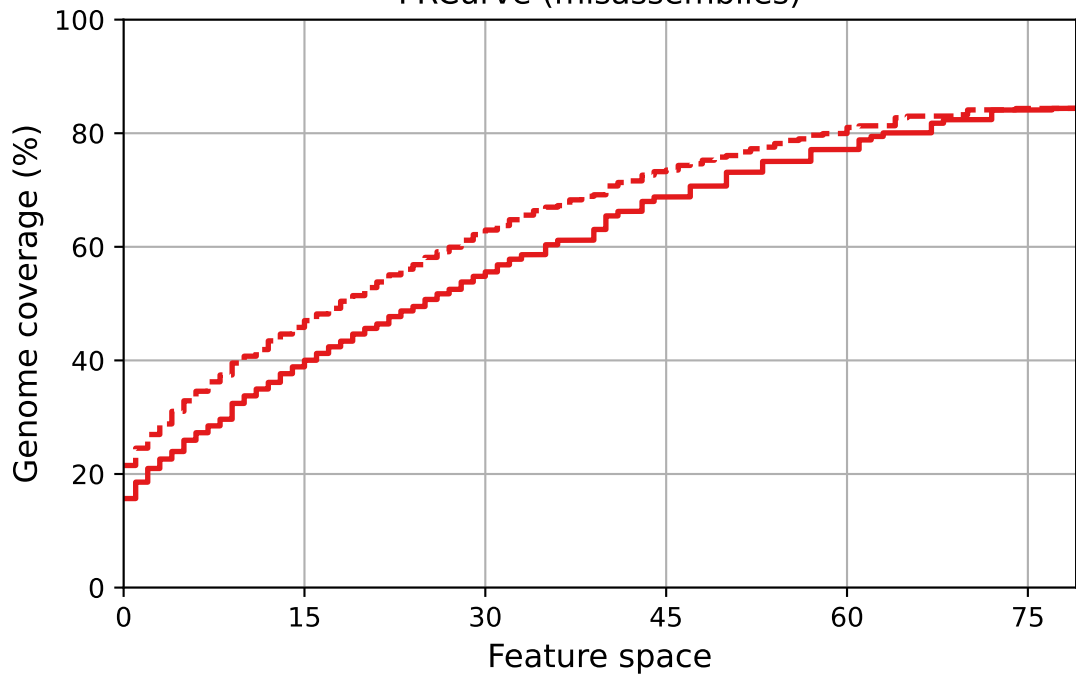


# relocations



# translocations

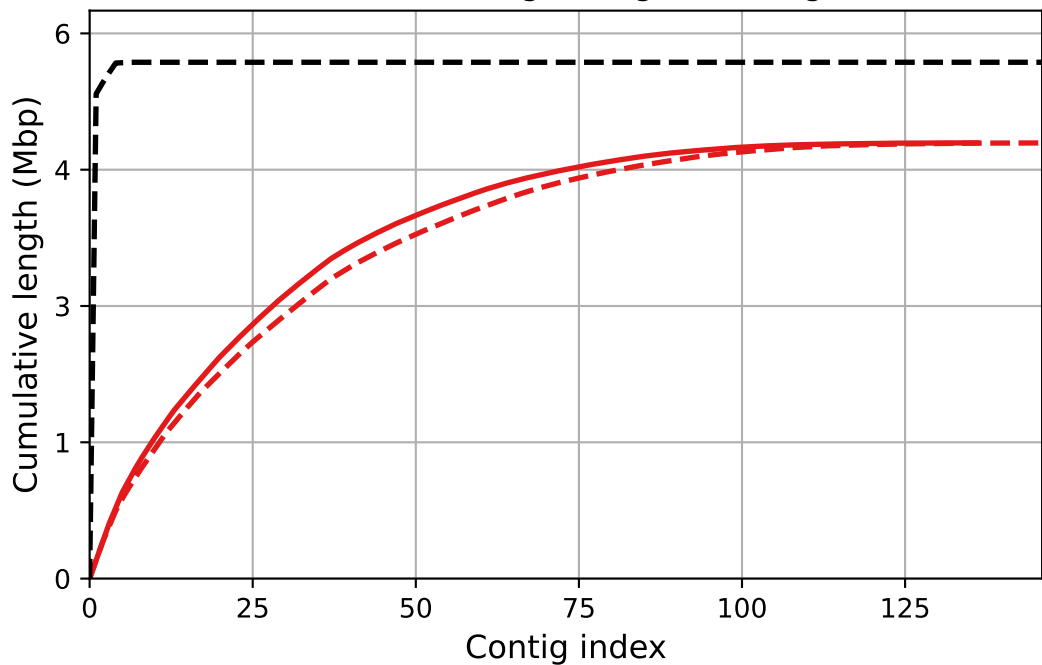
FRCurve (misassemblies)



des\_on\_data\_29\_and\_data\_30\_Scaffolds

SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds

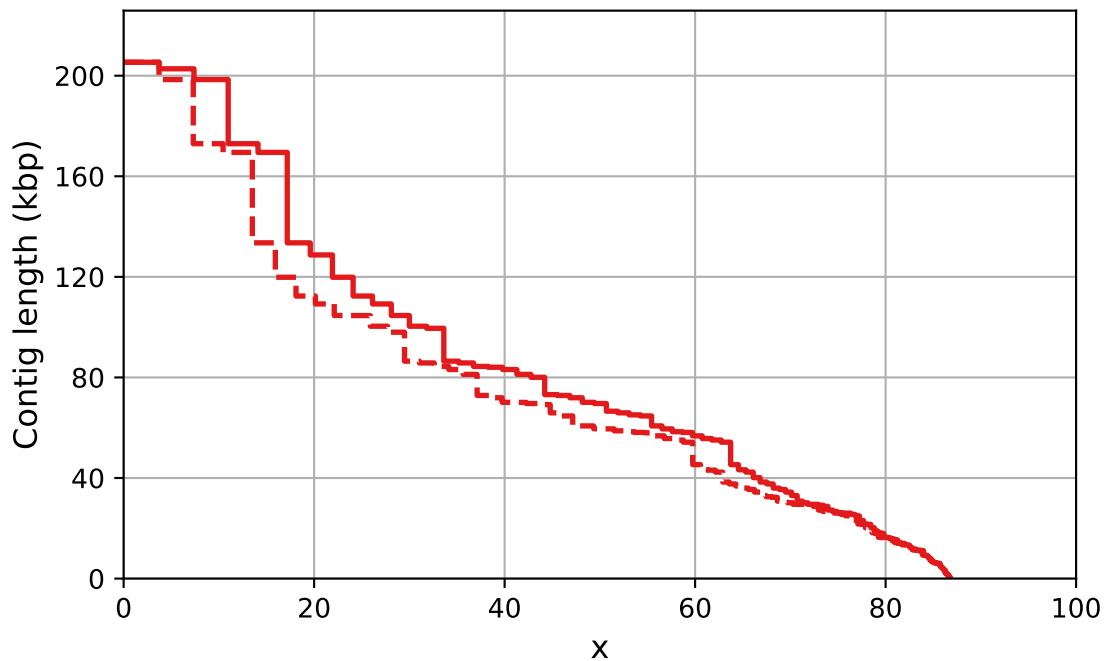
Cumulative length (aligned contigs)



data\_29\_and\_data\_30\_\_Scaffolds

-- SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken

NAx

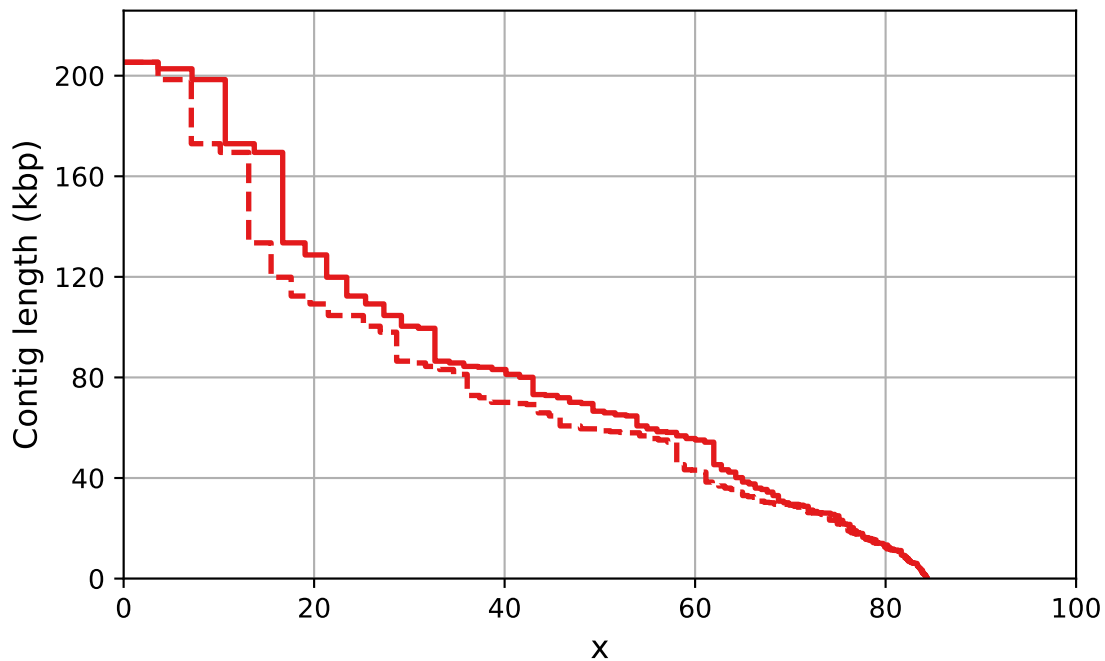


des\_on\_data\_29\_and\_data\_30\_Scaffolds

-- SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds



# NGAx

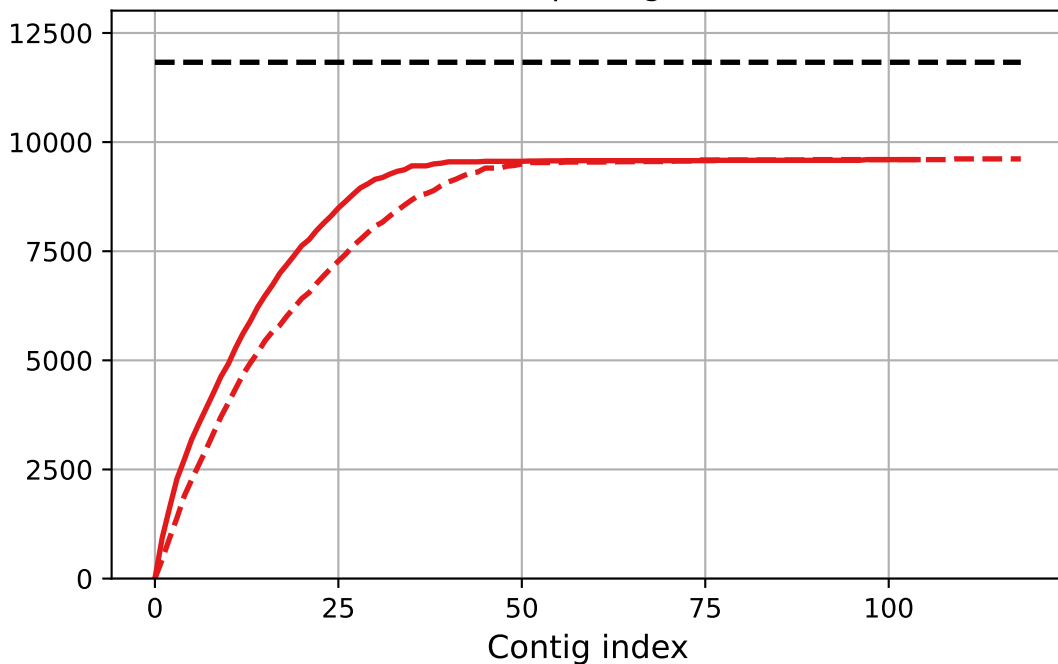


des\_on\_data\_29\_and\_data\_30\_Scaffolds

SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds

Cumulative # complete genomic features

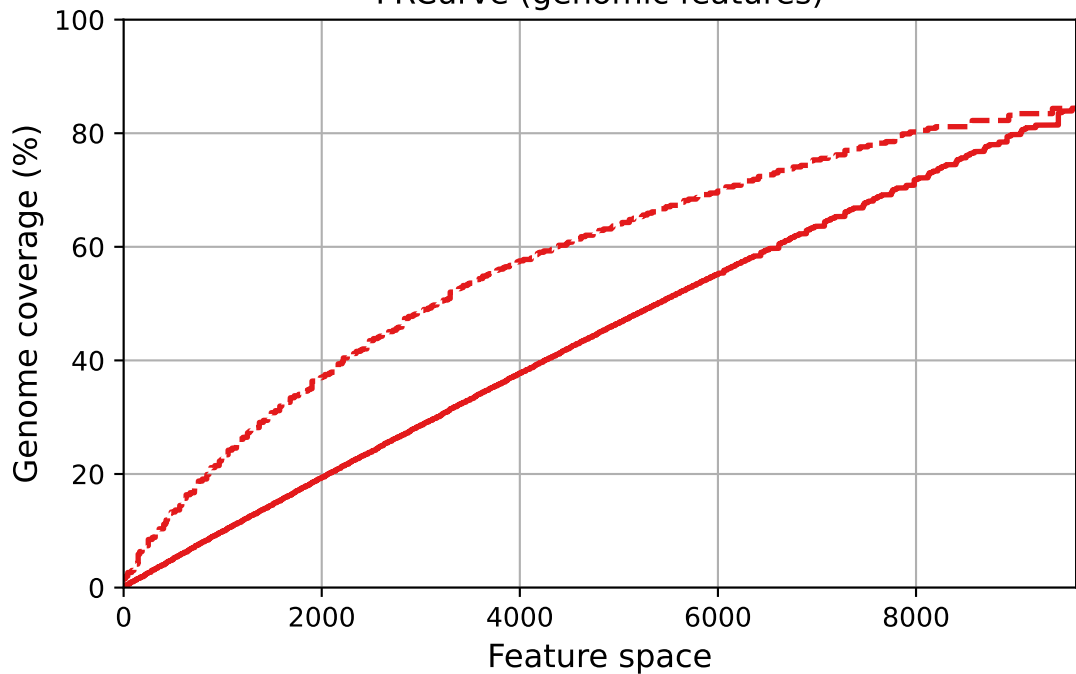
Cumulative # complete genomic features



ta\_29\_and\_data\_30\_\_Scaffolds

-- SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds\_broken

FRCurve (genomic features)



des\_on\_data\_29\_and\_data\_30\_Scaffolds

SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds

# complete genomic features



des\_on\_data\_29\_and\_data\_30\_Scaffolds



SPAdes\_on\_data\_29\_and\_data\_30\_Scaffolds

Genome fraction, %

100

95

90

85

des\_on\_data\_29\_and\_data\_30\_\_Scaffolds

SPAdes\_on\_data\_29\_and\_data\_30\_\_Scaffolds

