

Report

	SPAdes_on_data_16_and_data_14__Scaffolds	SPAdes_on_data_16_and_data_14__Scaffolds_broken
# contigs (>= 0 bp)	225	-
# contigs (>= 1000 bp)	24	26
Total length (>= 0 bp)	4173566	-
Total length (>= 1000 bp)	4132059	4131014
# contigs	26	32
Largest contig	577673	577673
Total length	4133612	4133012
Reference length	4242130	4242130
GC (%)	43.87	43.87
Reference GC (%)	44.03	44.03
N50	408434	334366
NG50	408434	325288
N90	208464	127987
NG90	127987	117518
auN	377099.8	325847.6
auNG	367453.2	317466.0
L50	5	5
LG50	5	6
L90	10	12
LG90	11	13
# misassemblies	1	1
# misassembled contigs	1	1
Misassembled contigs length	28821	28821
# local misassemblies	1	1
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.524	98.522
Duplication ratio	1.000	1.000
# N's per 100 kbp	14.52	0.00
# mismatches per 100 kbp	2.61	2.66
# indels per 100 kbp	0.56	0.41
# genomic features	4422 + 16 part	4420 + 18 part
Complete BUSCO (%)	100.00	100.00
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	3 + 0 part	3 + 0 part
Largest alignment	577673	577673
Total aligned length	4133611	4132987
NA50	408434	334366
NGA50	408434	325288
NA90	208464	127987
NGA90	127987	117518
auNA	377011.8	325758.4
auNGA	367367.5	317379.1
LA50	5	5
LGA50	5	6
LA90	10	12
LGA90	11	13

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

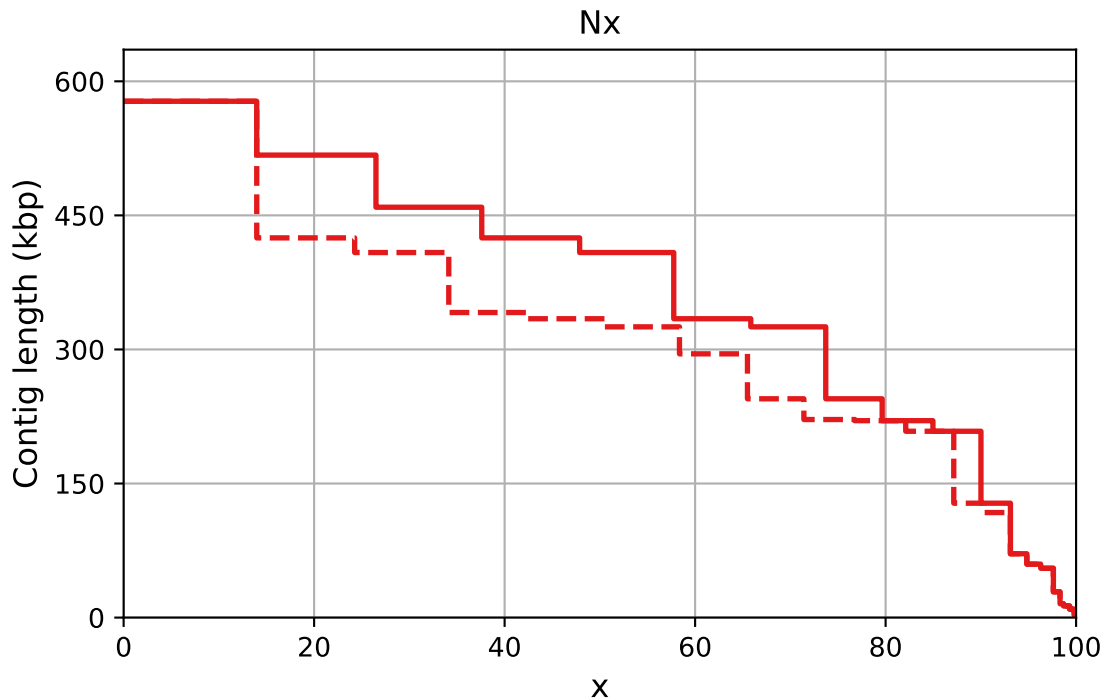
	SPAdes_on_data_16_and_data_14__Scaffolds	SPAdes_on_data_16_and_data_14__Scaffolds_broken
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	28821	28821
# local misassemblies	1	1
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	108	110
# indels	23	17
# indels (<= 5 bp)	14	14
# indels (> 5 bp)	9	3
Indels length	870	170

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).

Unaligned report

	SPAdes_on_data_16_and_data_14__Scaffolds	SPAdes_on_data_16_and_data_14__Scaffolds_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	600	0

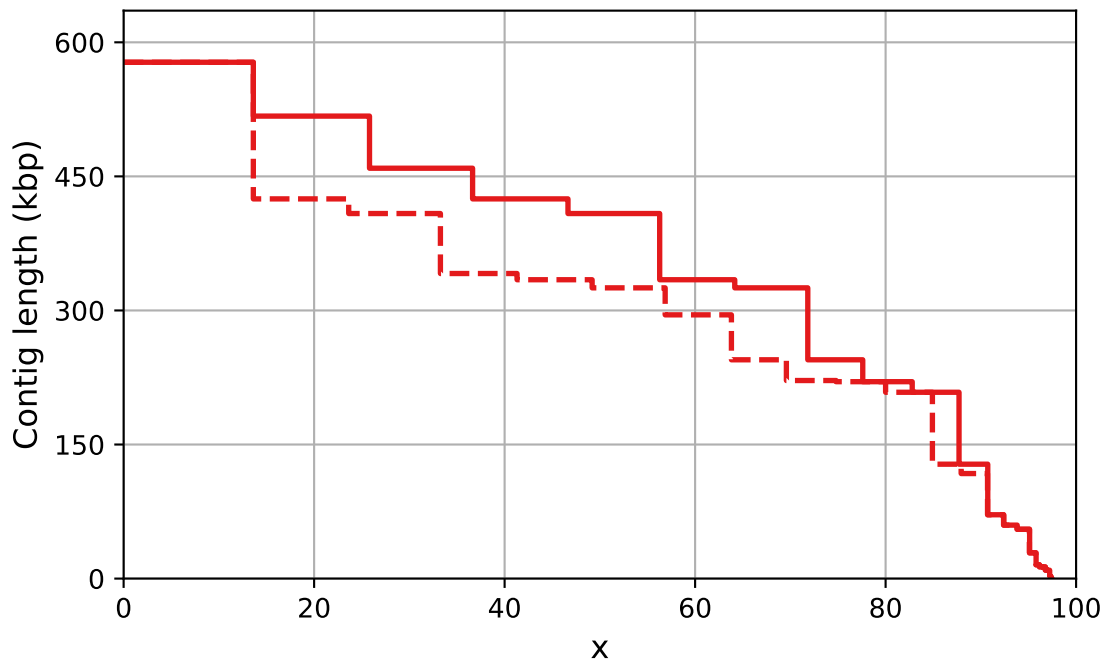
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



des_on_data_16_and_data_14_Scaffolds

-- SPAdes_on_data_16_and_data_14_Scaffolds

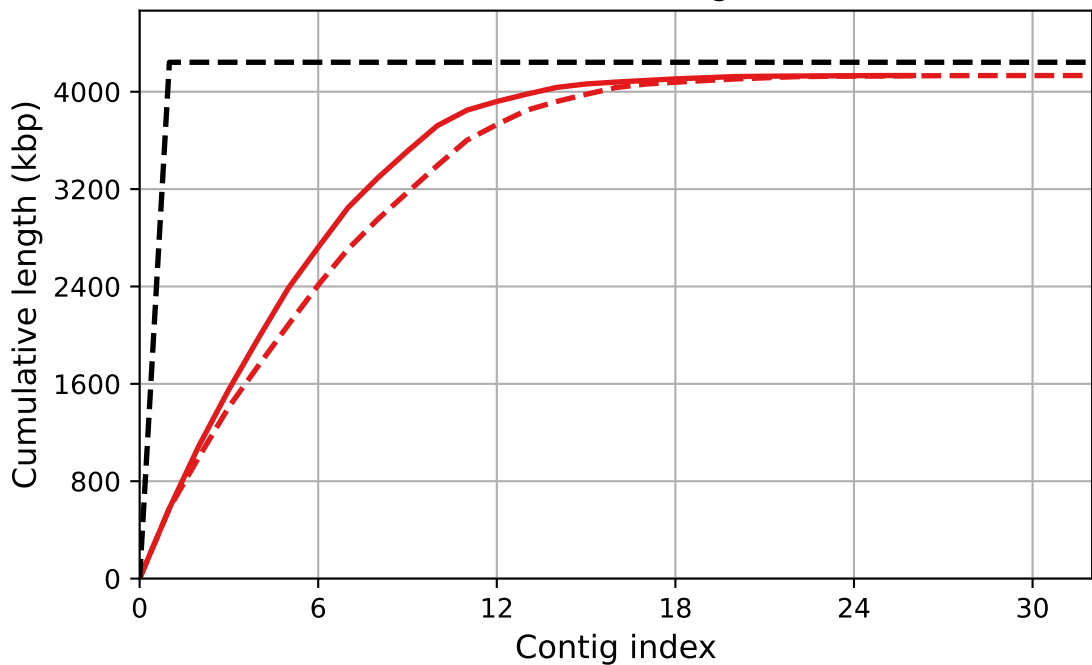
NGx



des_on_data_16_and_data_14_Scaffolds

-- SPAdes_on_data_16_and_data_14_Scaffolds

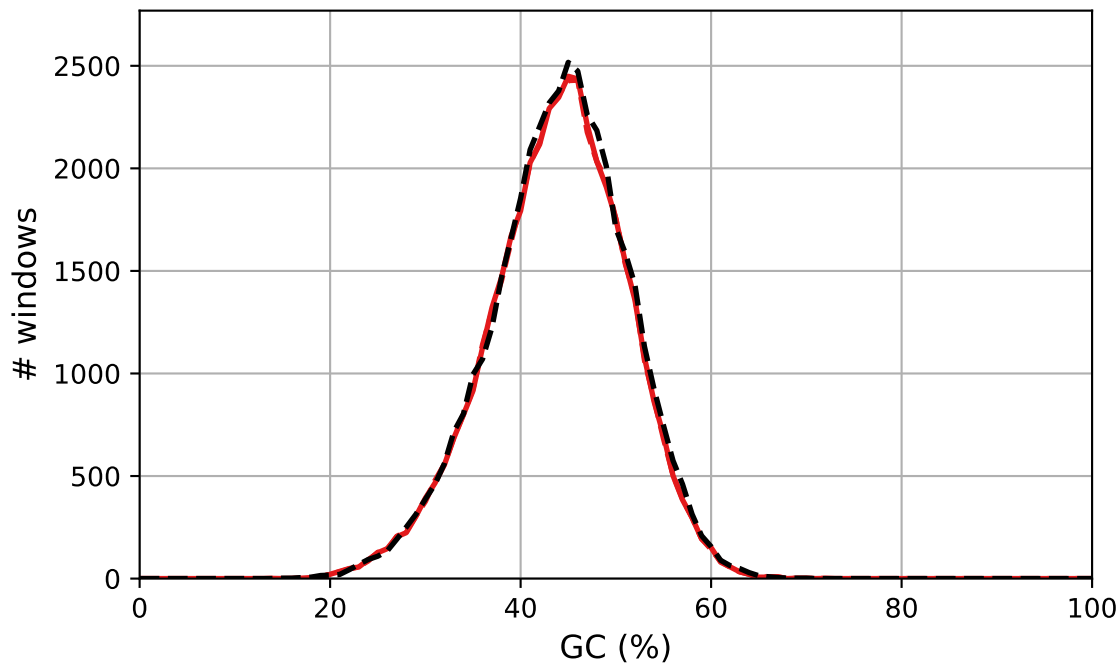
Cumulative length



data_16_and_data_14__Scaffolds

-- SPAdes_on_data_16_and_data_14__Scaffolds_broken

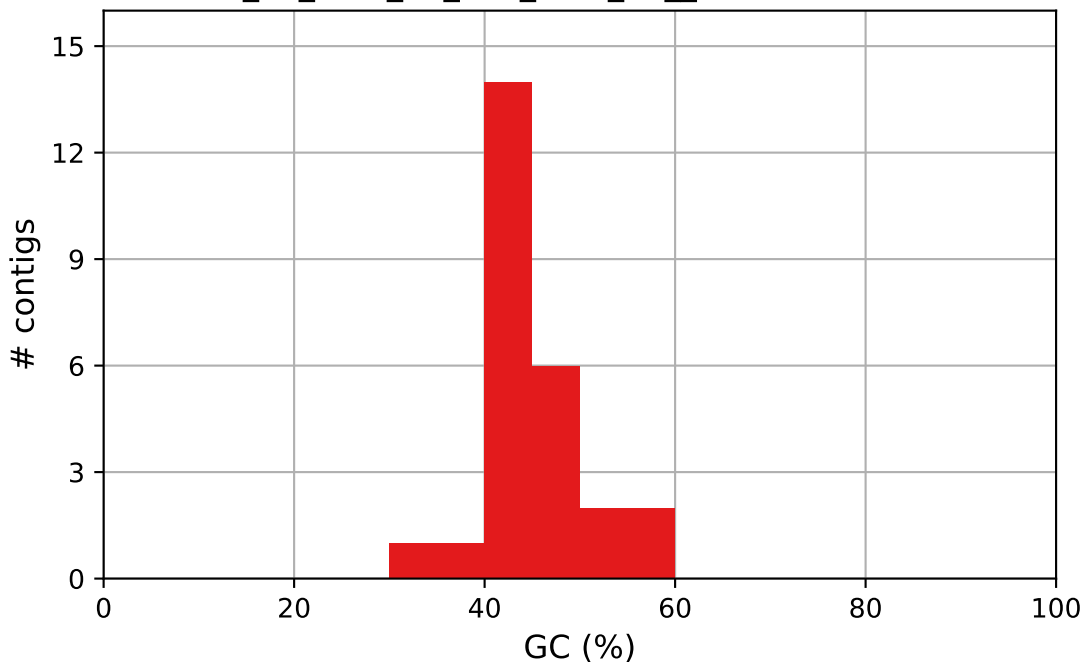
GC content



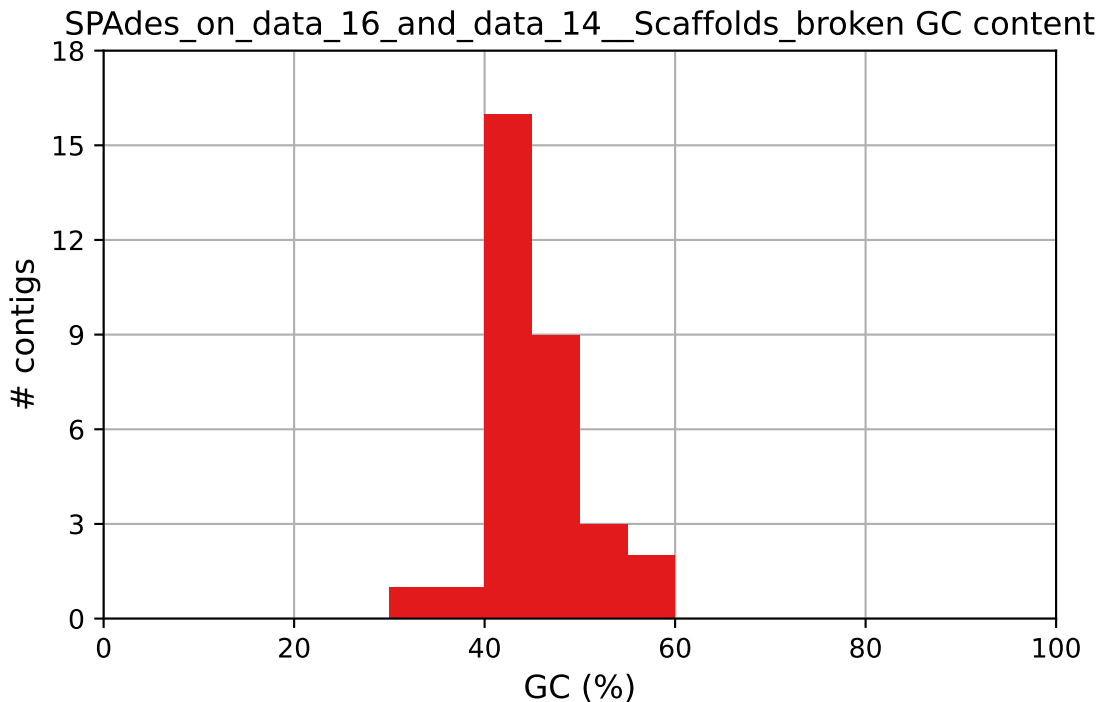
data_16_and_data_14__Scaffolds

-- SPAdes_on_data_16_and_data_14__Scaffolds_broken

SPAdes_on_data_16_and_data_14__Scaffolds GC content

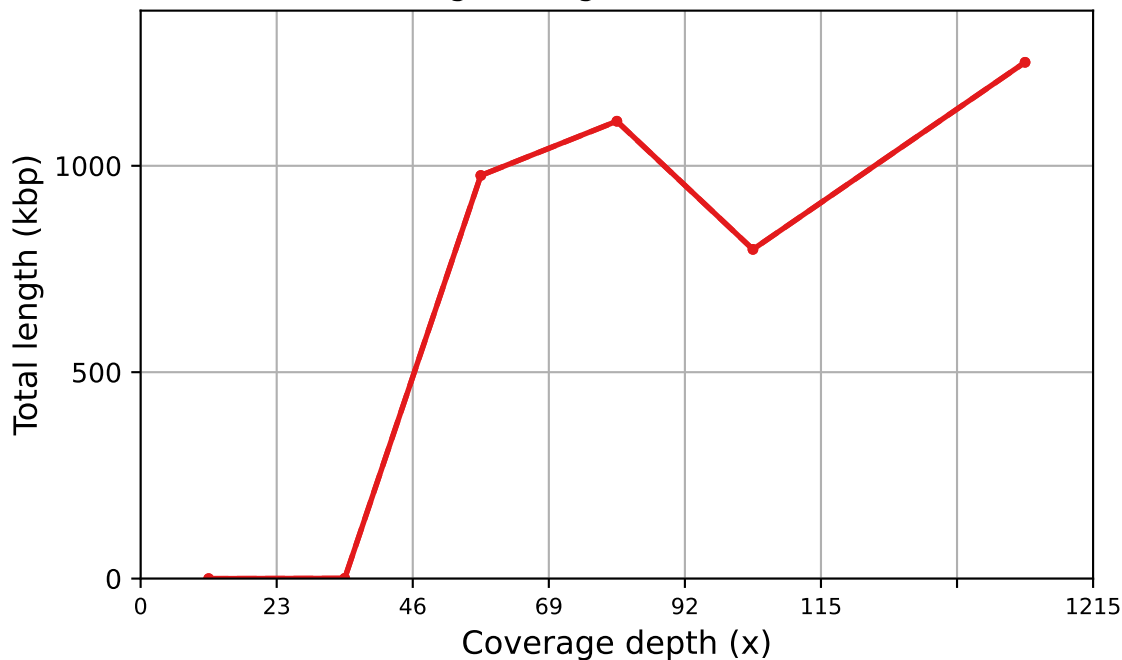


SPAdes_on_data_16_and_data_14__Scaffolds



SPAdes_on_data_16_and_data_14__Scaffolds_broken

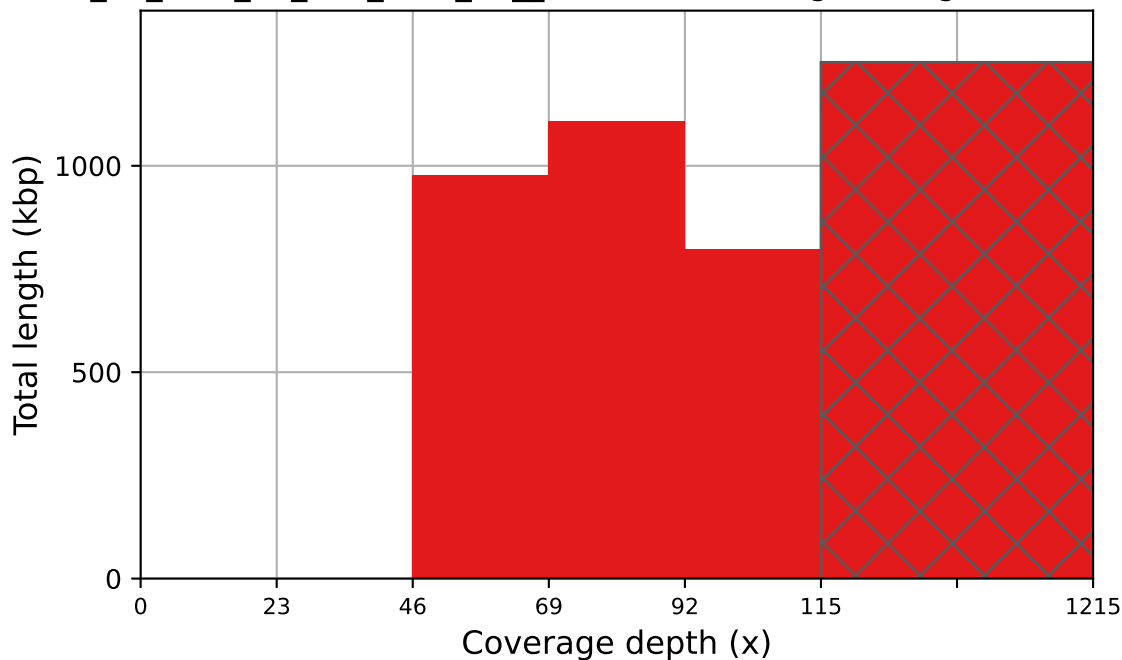
Coverage histogram (bin size: 23x)



des_on_data_16_and_data_14__Scaffolds

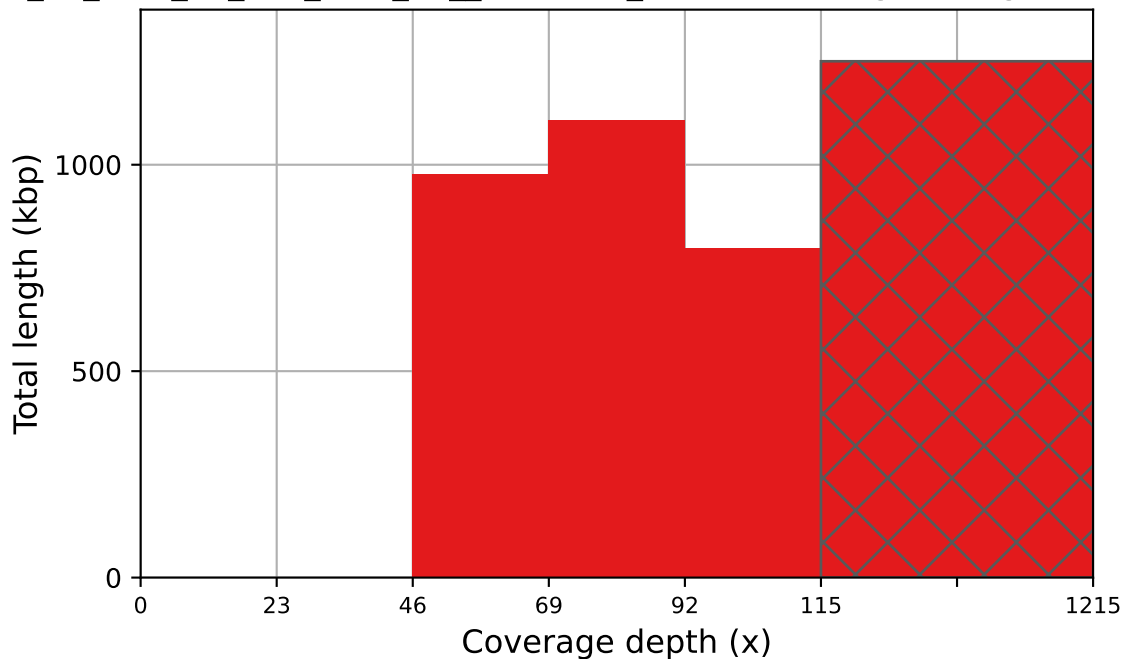
—•— SPAdes_on_data_16_and_data_14__Scaffolds

SPAdes_on_data_16_and_data_14__Scaffolds coverage histogram (bin size: 23)



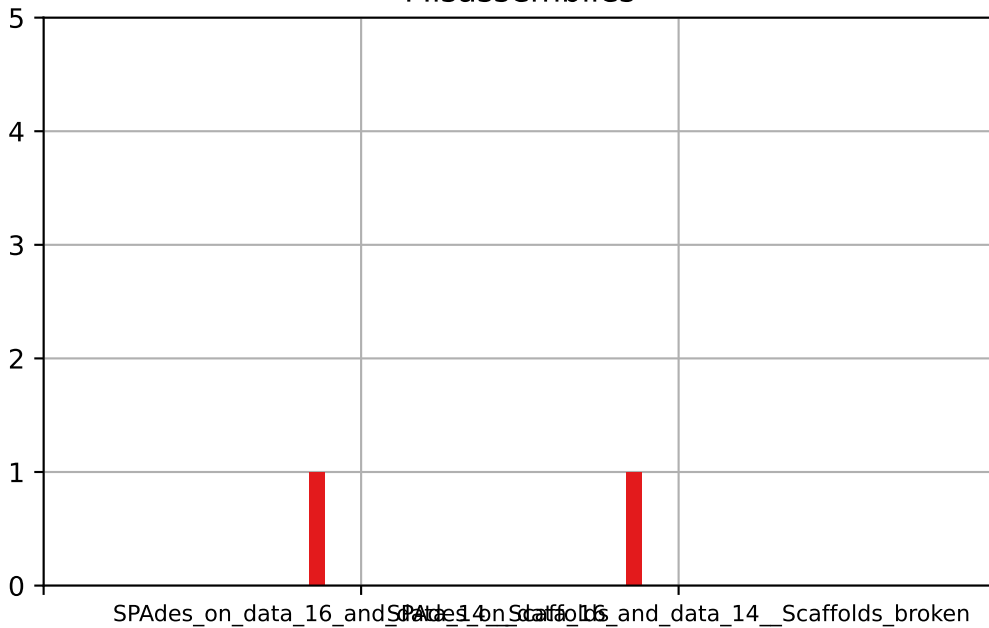
SPAdes_on_data_16_and_data_14__Scaffolds

SPAdes_on_data_16_and_data_14__Scaffolds_broken coverage histogram (bin size 23)

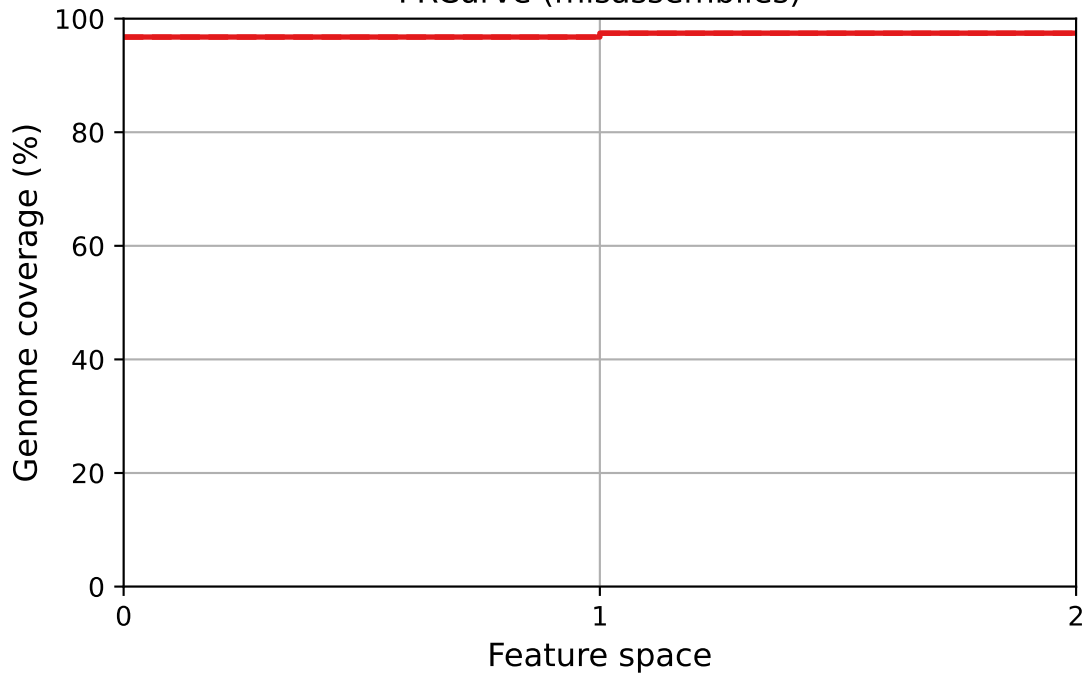


SPAdes_on_data_16_and_data_14__Scaffolds_broken

Misassemblies



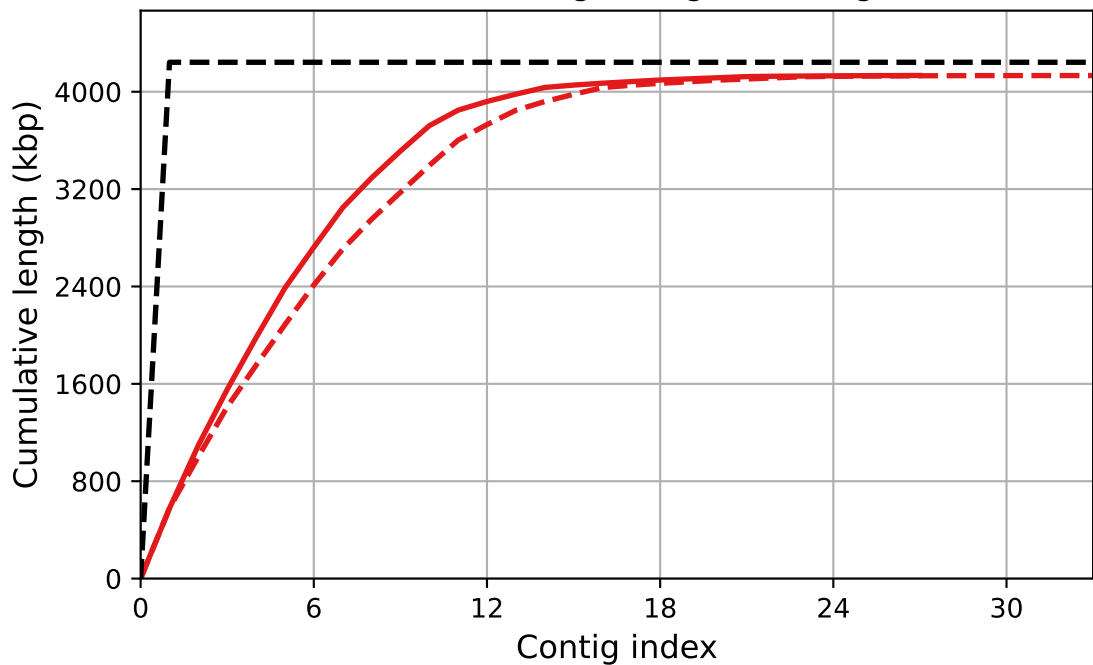
FRCurve (misassemblies)



des_on_data_16_and_data_14__Scaffolds

-- SPAdes_on_data_16_and_data_14__Scaffolds

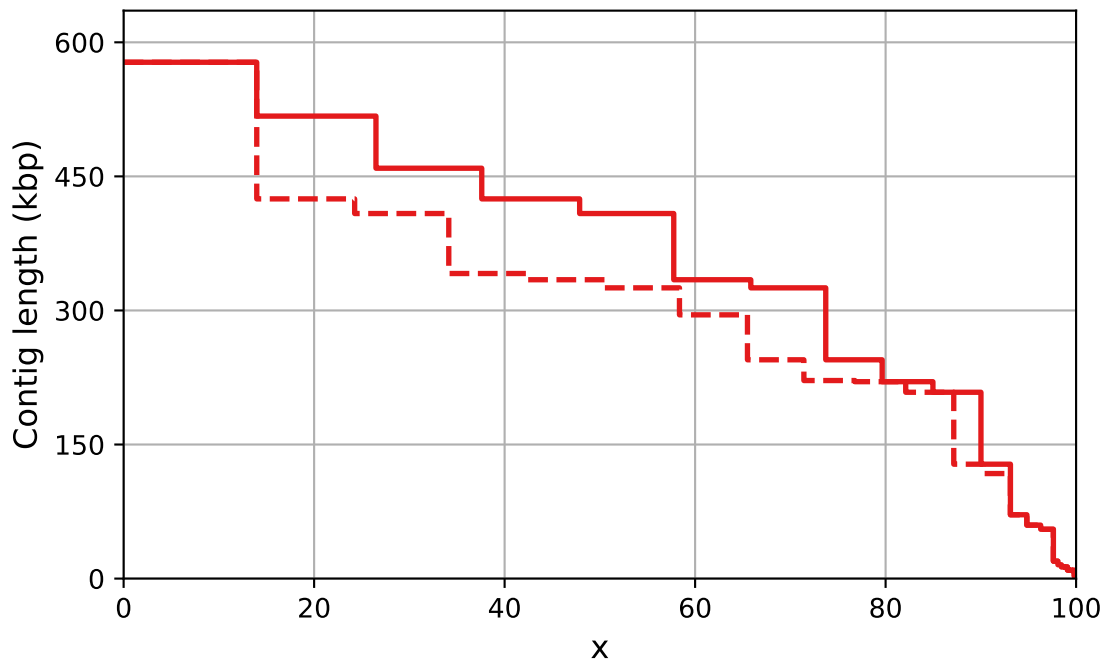
Cumulative length (aligned contigs)



data_16_and_data_14__Scaffolds

SPAdes_on_data_16_and_data_14__Scaffolds_broken

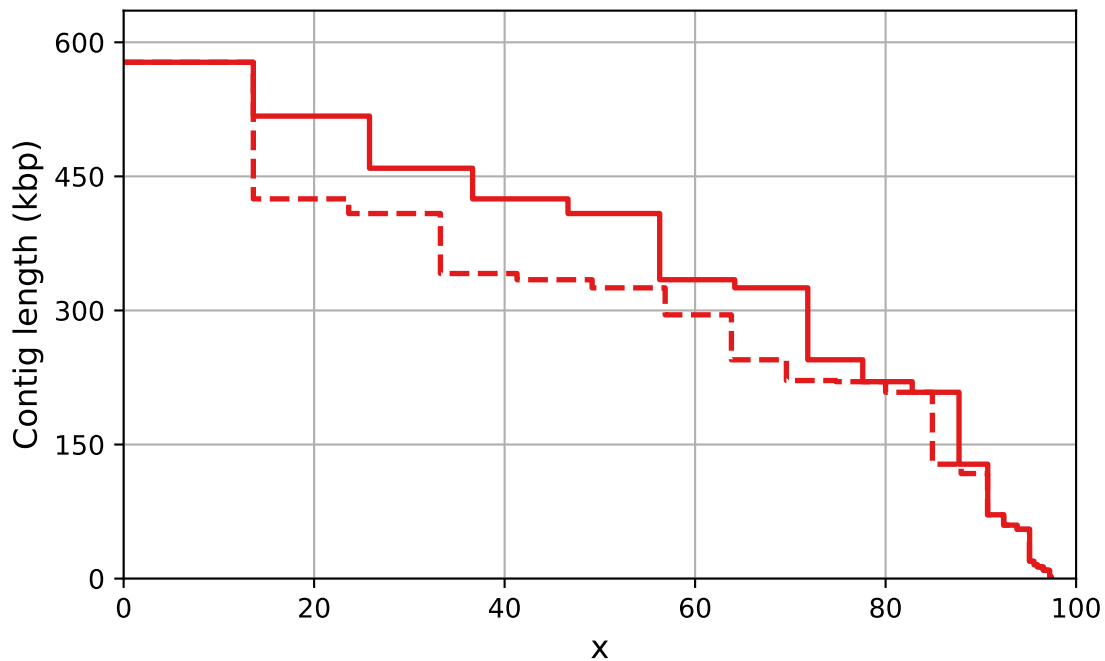
NAx



SPAdes_on_data_16_and_data_14_Scaffolds

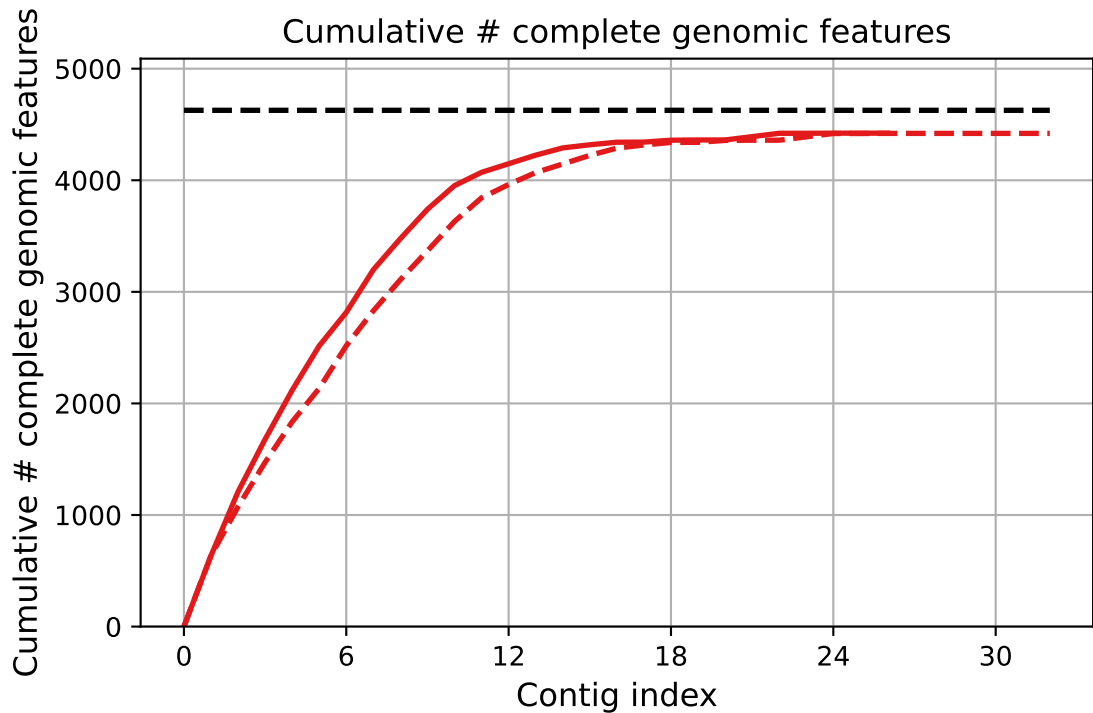
SPAdes_on_data_16_and_data_14_Scaffolds

NGAx



des_on_data_16_and_data_14_Scaffolds

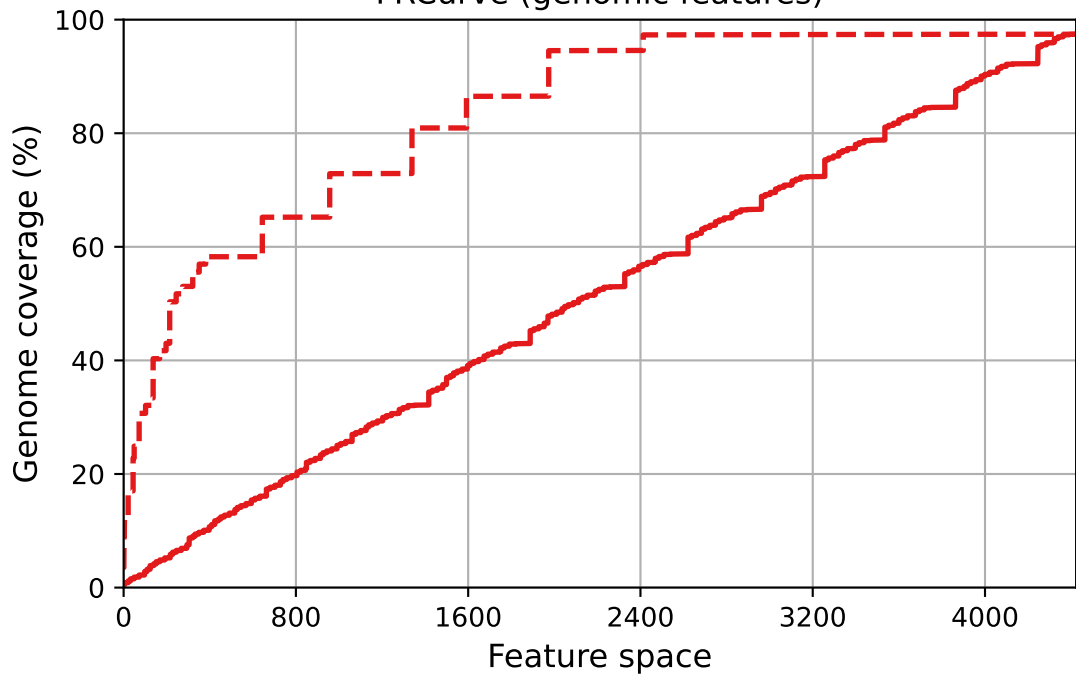
SPAdes_on_data_16_and_data_14_Scaffolds



data_16_and_data_14__Scaffolds

SPAdes_on_data_16_and_data_14__Scaffolds_broken

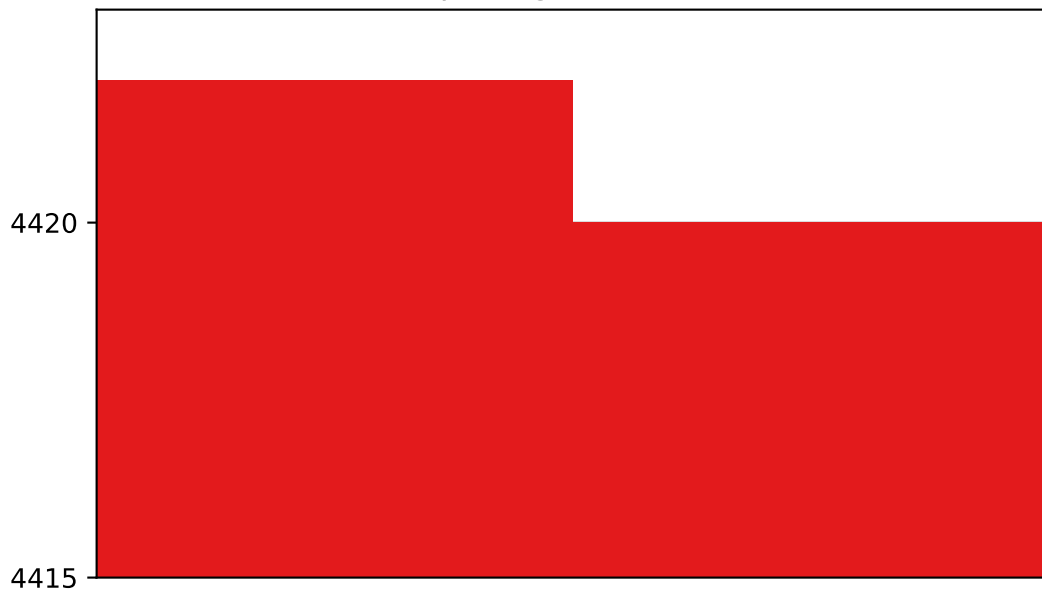
FRCurve (genomic features)



des_on_data_16_and_data_14_Scaffolds

SPAdes_on_data_16_and_data_14_Scaffolds

complete genomic features



des_on_data_16_and_data_14__Scaffolds



SPAdes_on_data_16_and_data_14__Scaffolds

Genome fraction, %

100

99

des_on_data_16_and_data_14__Scaffolds



SPAdes_on_data_16_and_data_14__Scaffolds