

Report

	SPAdes_on_data_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# contigs (>= 0 bp)	191	-
# contigs (>= 1000 bp)	63	71
Total length (>= 0 bp)	4813654	-
Total length (>= 1000 bp)	4788123	4786289
# contigs	72	82
Largest contig	549770	322638
Total length	4794213	4792805
Reference length	4951383	4951383
GC (%)	52.13	52.13
Reference GC (%)	52.24	52.24
N50	193475	168456
NG50	178662	149367
N90	53847	51504
NG90	44707	44707
auN	224465.2	166813.7
auNG	217340.1	161471.2
L50	8	10
LG50	9	11
L90	27	32
LG90	30	35
# misassemblies	7	7
# misassembled contigs	7	7
Misassembled contigs length	1416504	1035190
# local misassemblies	5	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	0 + 5 part
Unaligned length	81933	81933
Genome fraction (%)	96.032	96.017
Duplication ratio	1.001	1.001
# N's per 100 kbp	22.94	0.00
# mismatches per 100 kbp	28.13	28.20
# indels per 100 kbp	3.65	3.46
# genomic features	13701 + 108 part	13685 + 112 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 0 part	2 + 0 part
Largest alignment	376430	322563
Total aligned length	4710913	4709961
NA50	178662	129564
NGA50	152567	123652
NA90	35969	35969
NGA90	30214	26152
auNA	187266.9	155275.2
auNGA	181322.6	150302.2
LA50	9	11
LGA50	10	12
LA90	32	37
LGA90	36	42

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

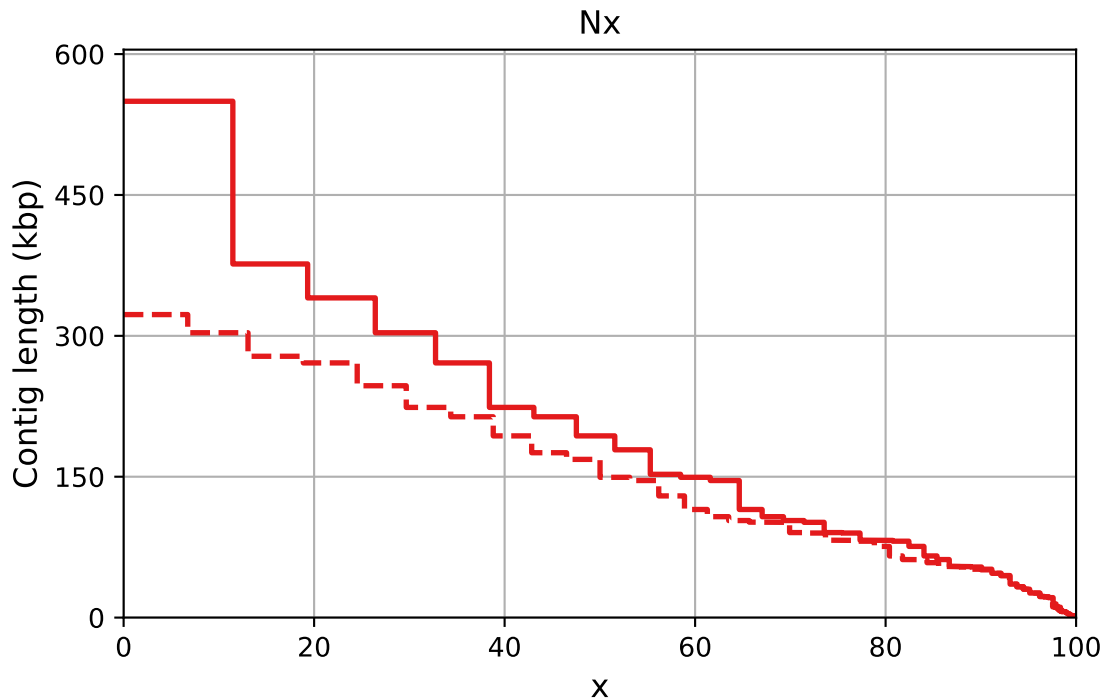
	SPAdes_on_data_1_and_data_2_Scaffolds	SPAdes_on_data_1_and_data_2_Scaffolds_broken
# misassemblies	7	7
# contig misassemblies	7	7
# c. relocations	7	7
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	7	7
Misassembled contigs length	1416504	1035190
# local misassemblies	5	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	0
# mismatches	1325	1328
# indels	172	163
# indels (<= 5 bp)	137	136
# indels (> 5 bp)	35	27
Indels length	3722	2336

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_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	5	5
Partially unaligned length	81933	81933
# N's	1100	0

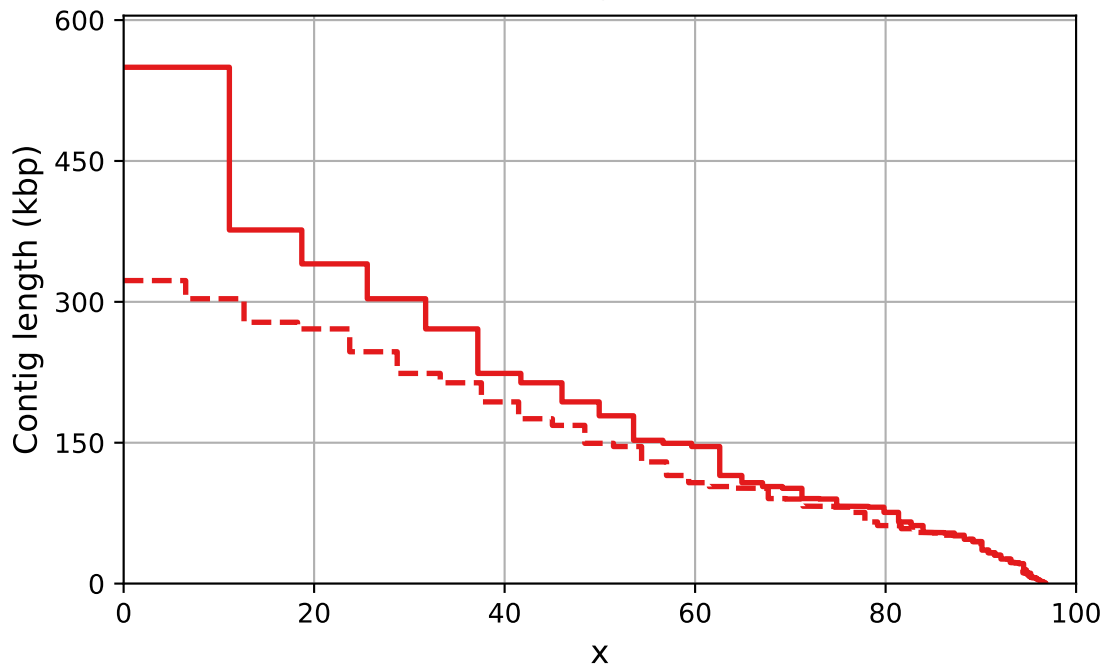
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

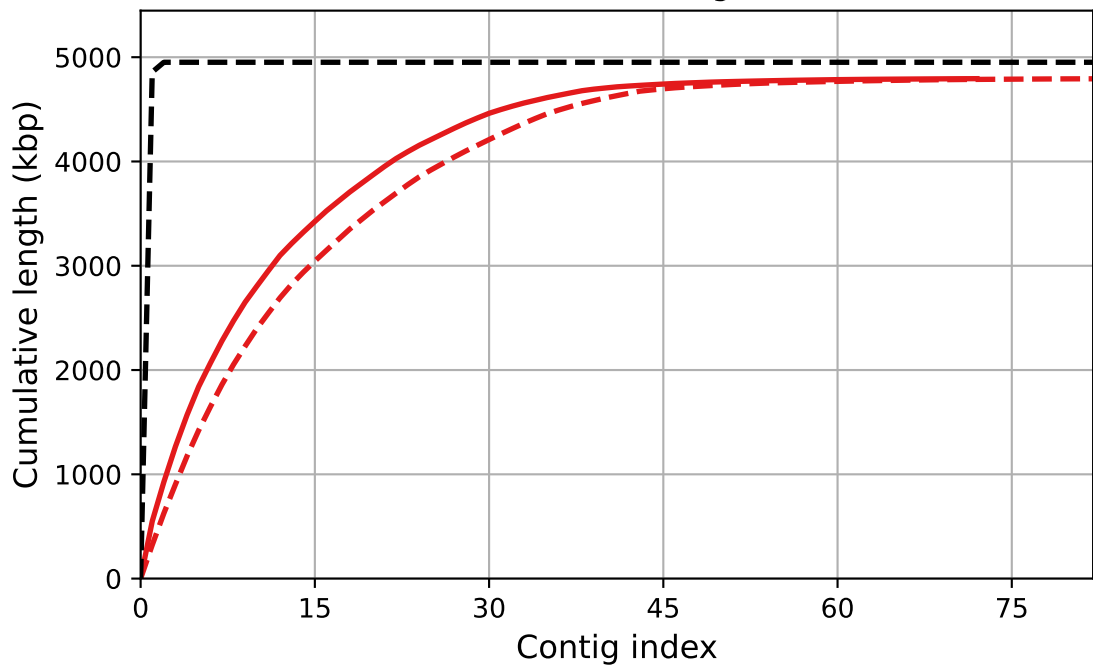
NGx



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

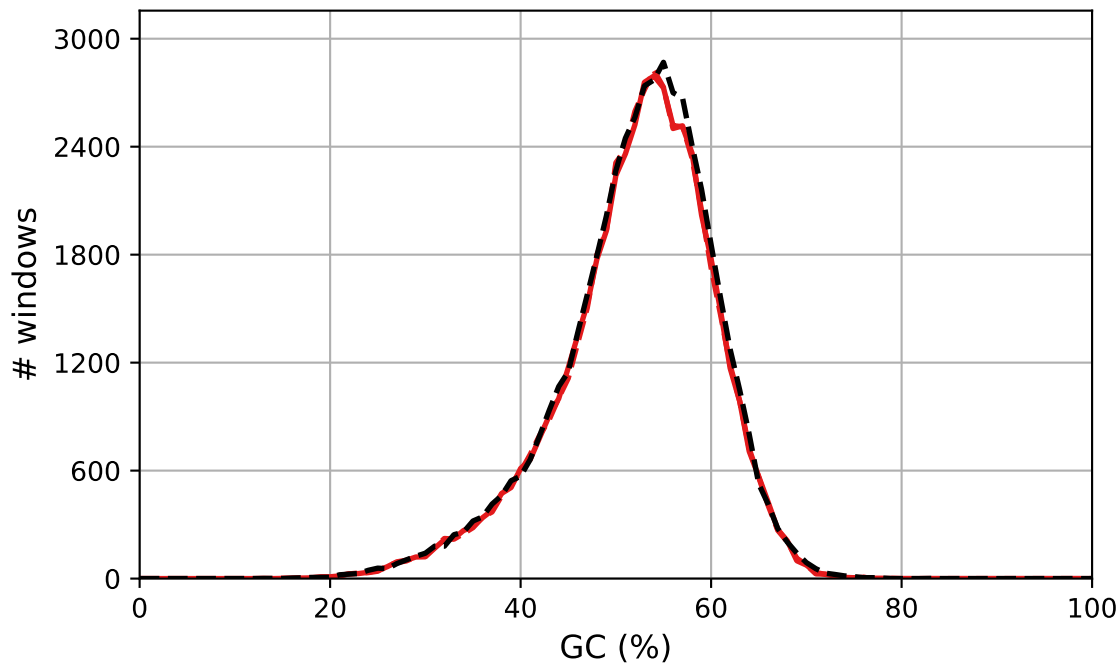
Cumulative length



data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken

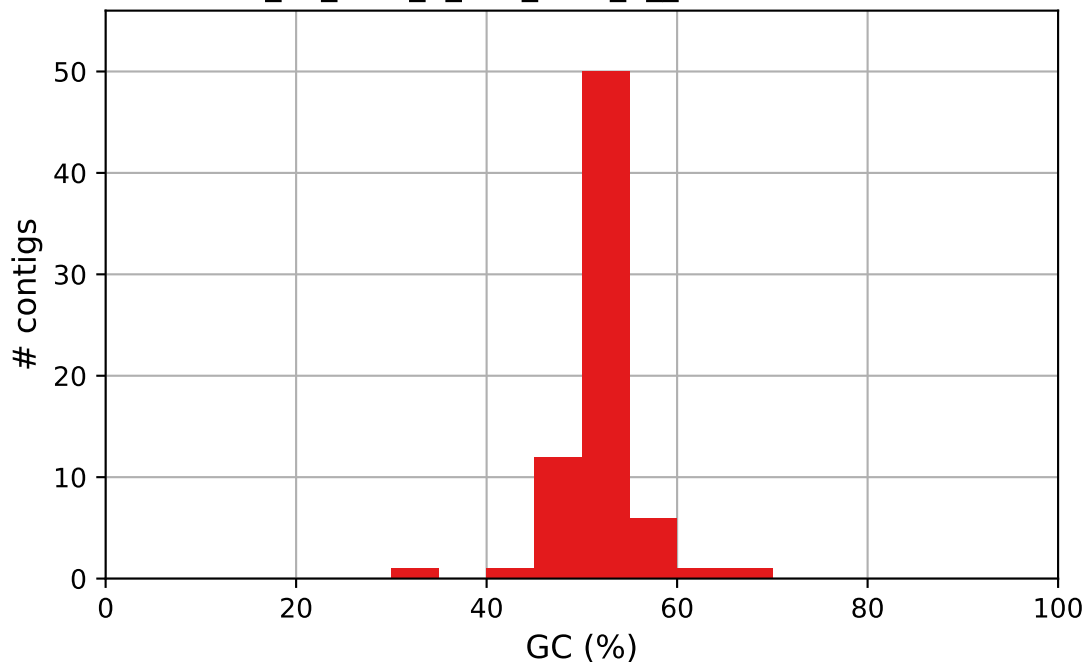
GC content



_data_1_and_data_2__Scaffolds

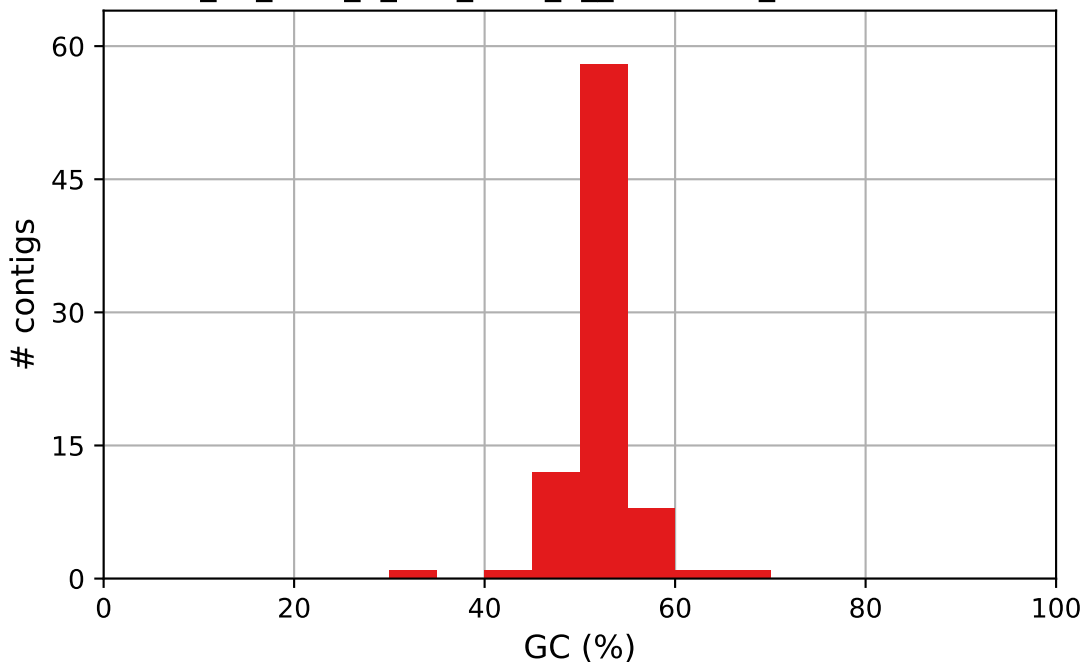
-- SPAdes_on_data_1_and_data_2__Scaffolds_broken

SPAdes_on_data_1_and_data_2__Scaffolds GC content



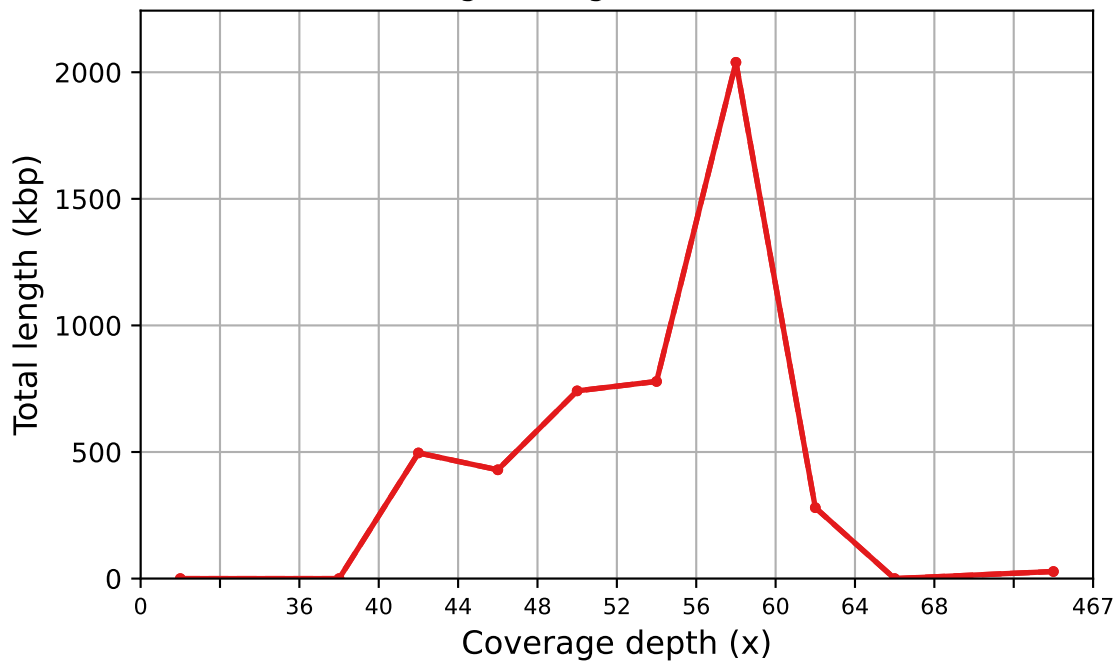
SPAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken GC content



SPAdes_on_data_1_and_data_2__Scaffolds_broken

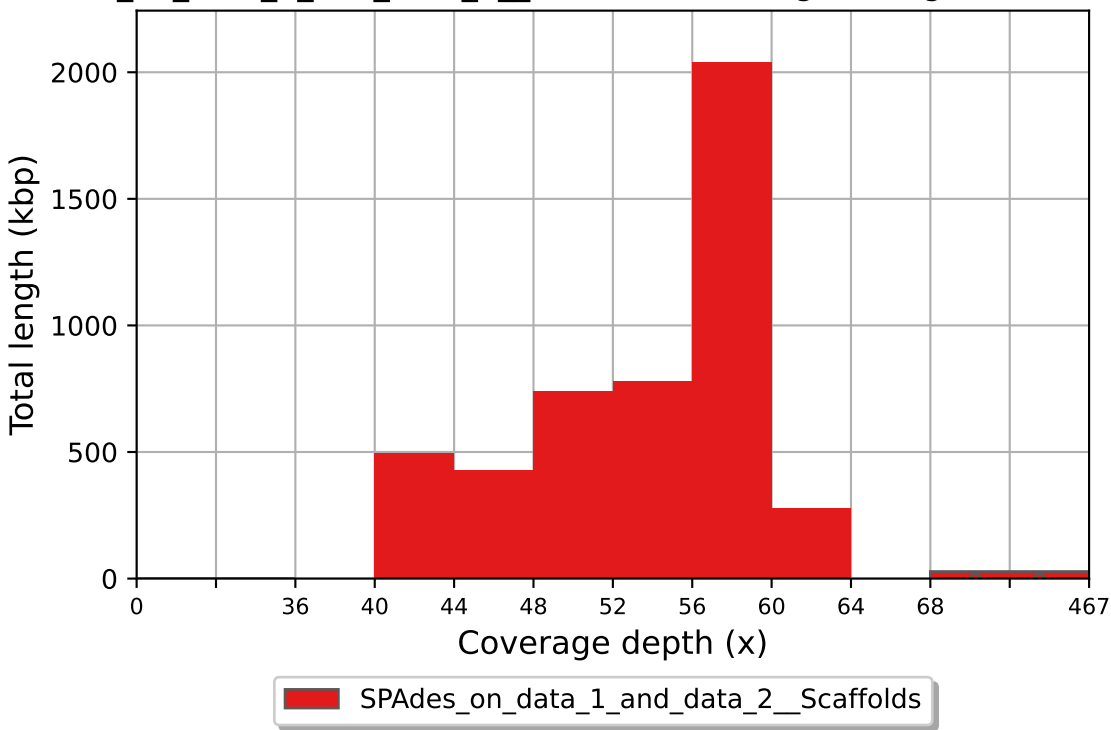
Coverage histogram (bin size: 4x)



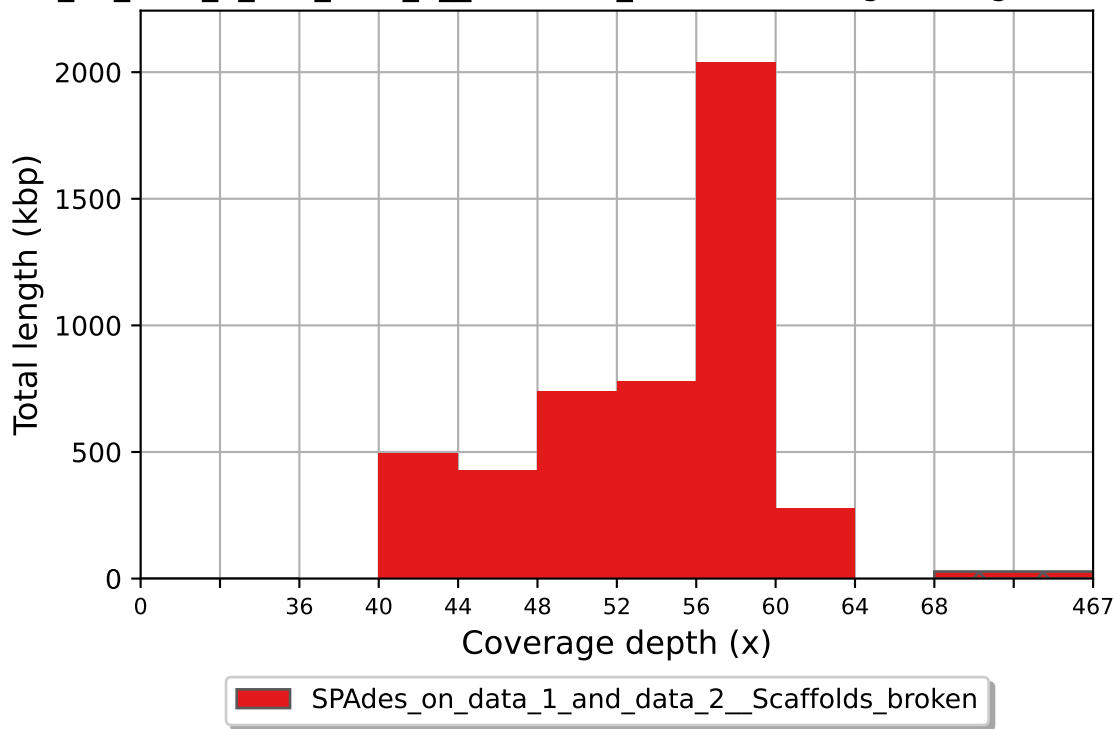
PAdes_on_data_1_and_data_2_Scaffolds

—●— SPAdes_on_data_1_and_data_2_Scaffolds

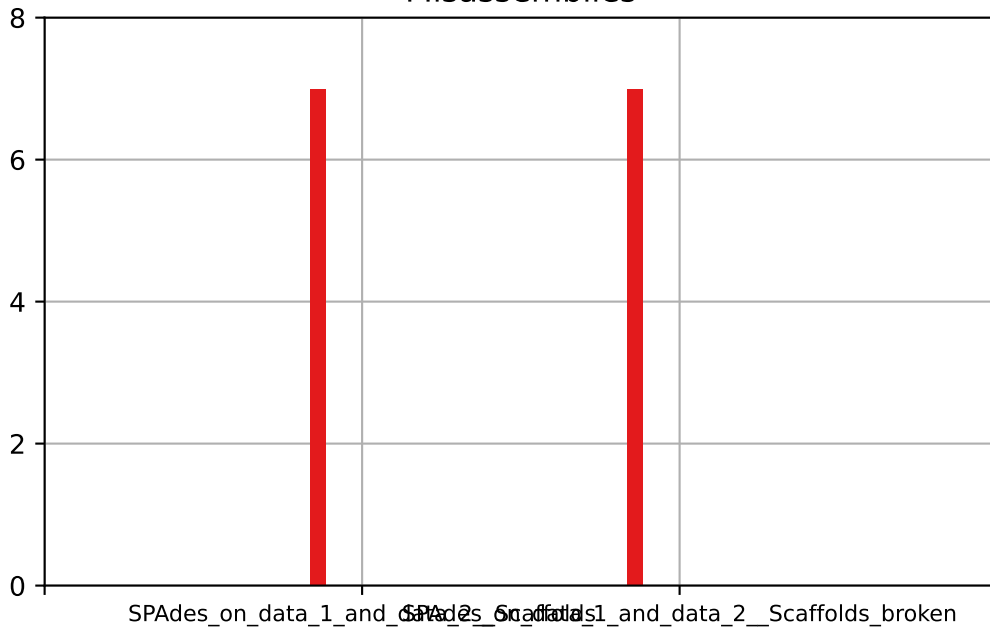
SPAdes_on_data_1_and_data_2__Scaffolds coverage histogram (bin size: 4x)



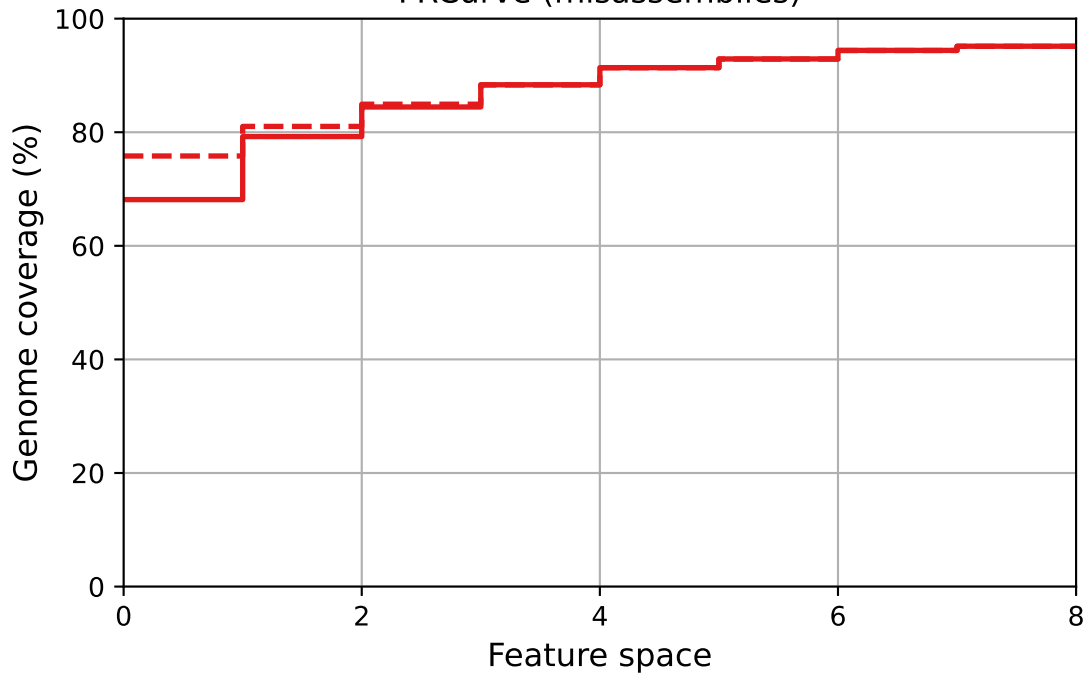
Ades_on_data_1_and_data_2__Scaffolds_broken coverage histogram (bin size



Misassemblies



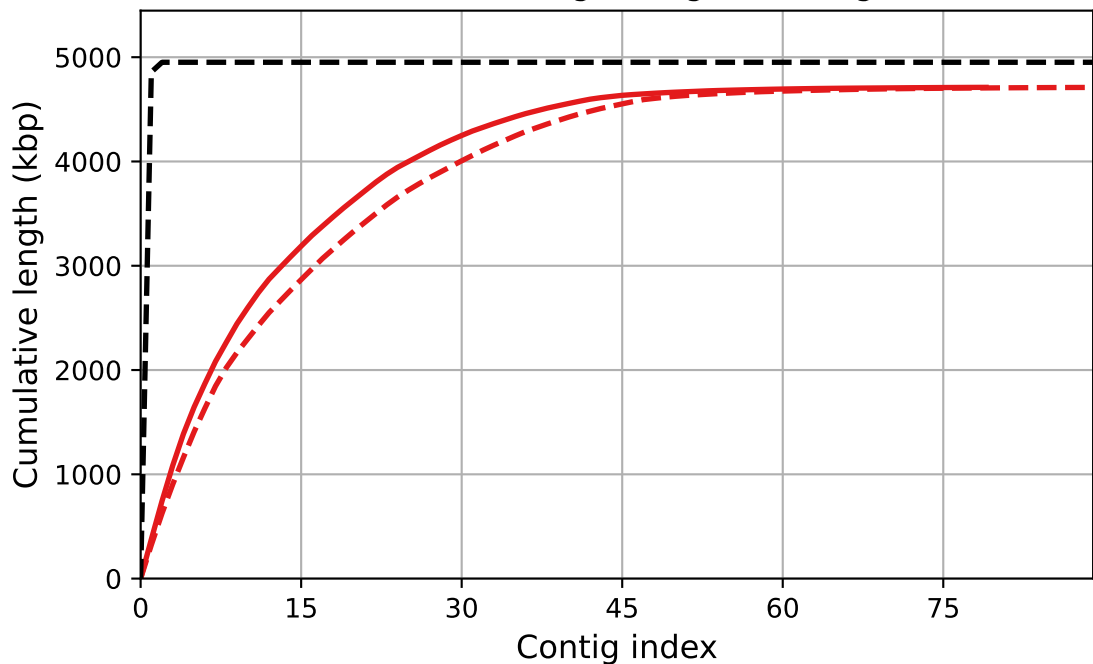
FRCurve (misassemblies)



PAdes_on_data_1_and_data_2_Scaffolds

SPAdes_on_data_1_and_data_2_Scaffolds

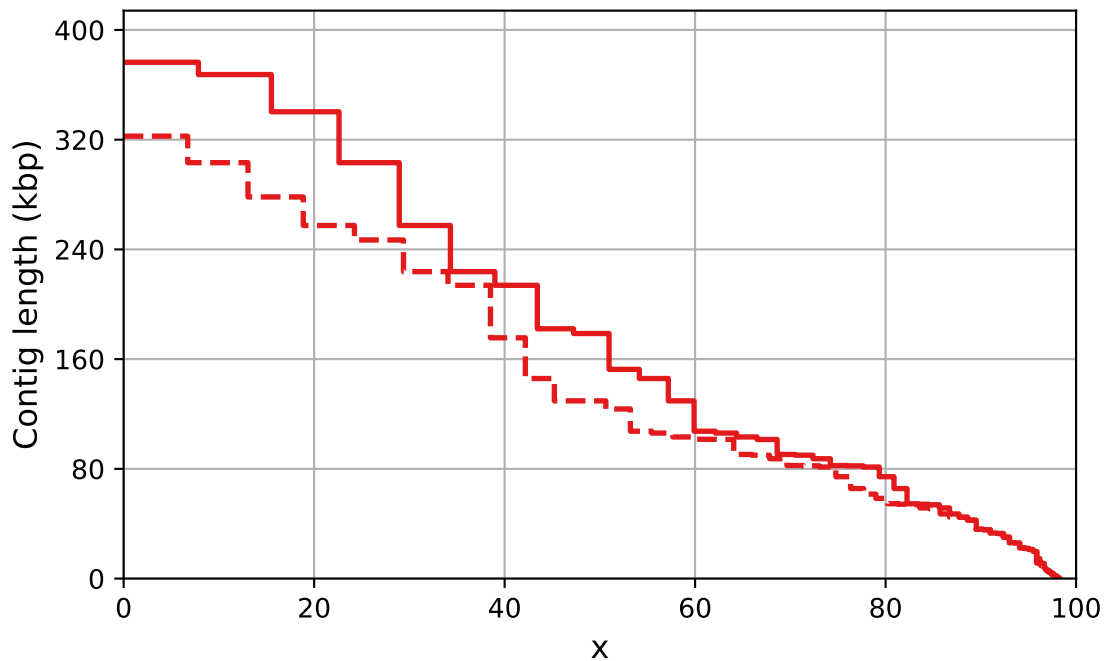
Cumulative length (aligned contigs)



data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken

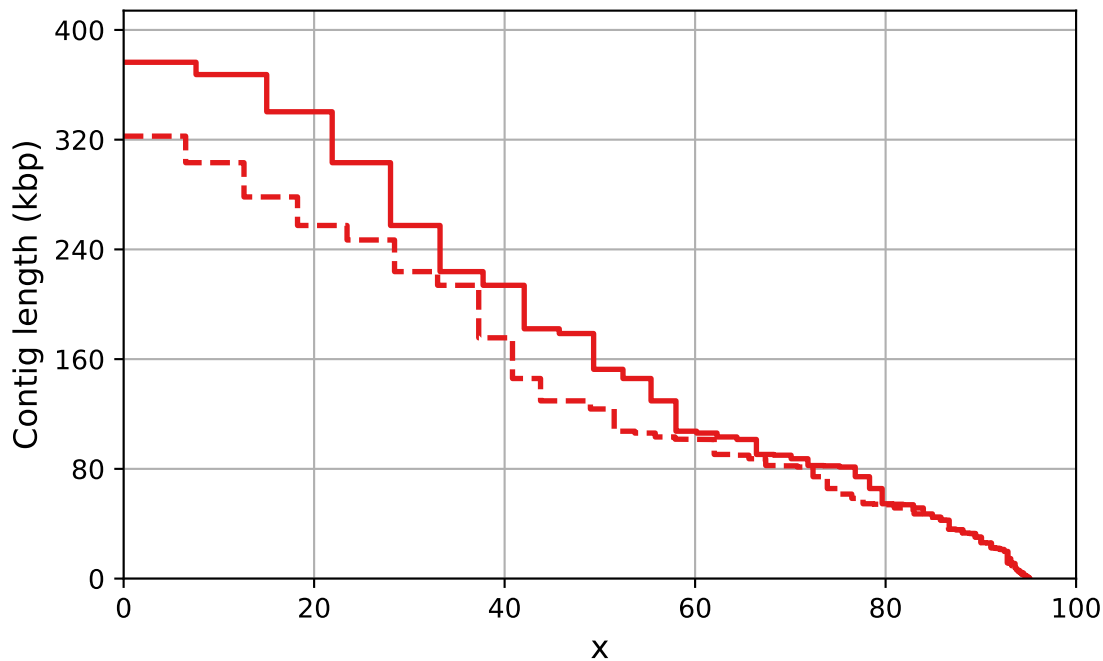
NAx



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

NGAx

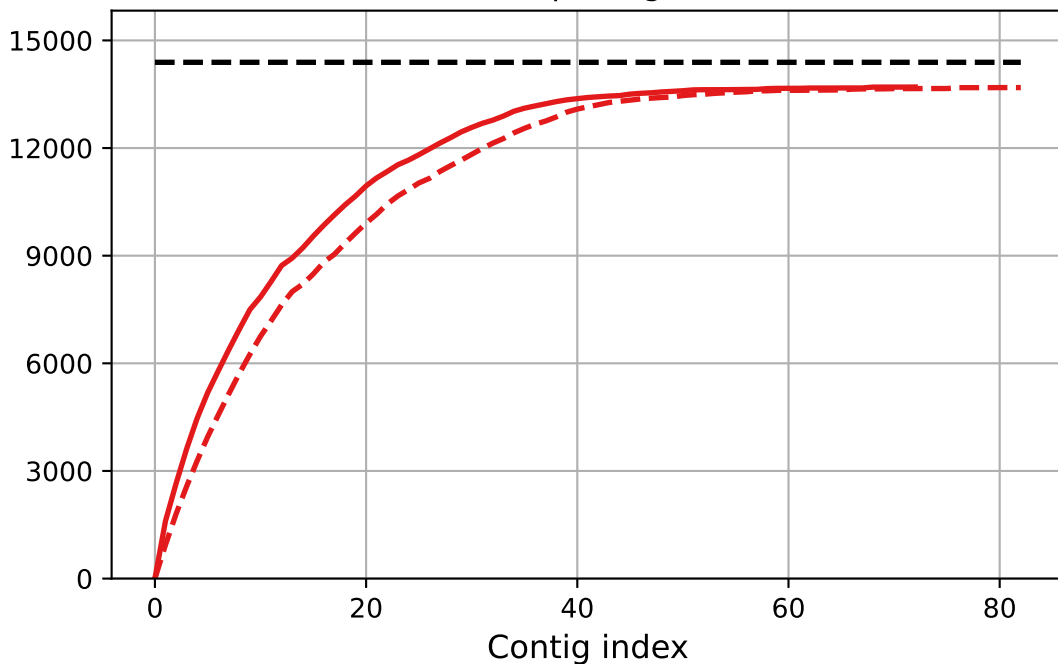


PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

Cumulative # complete genomic features

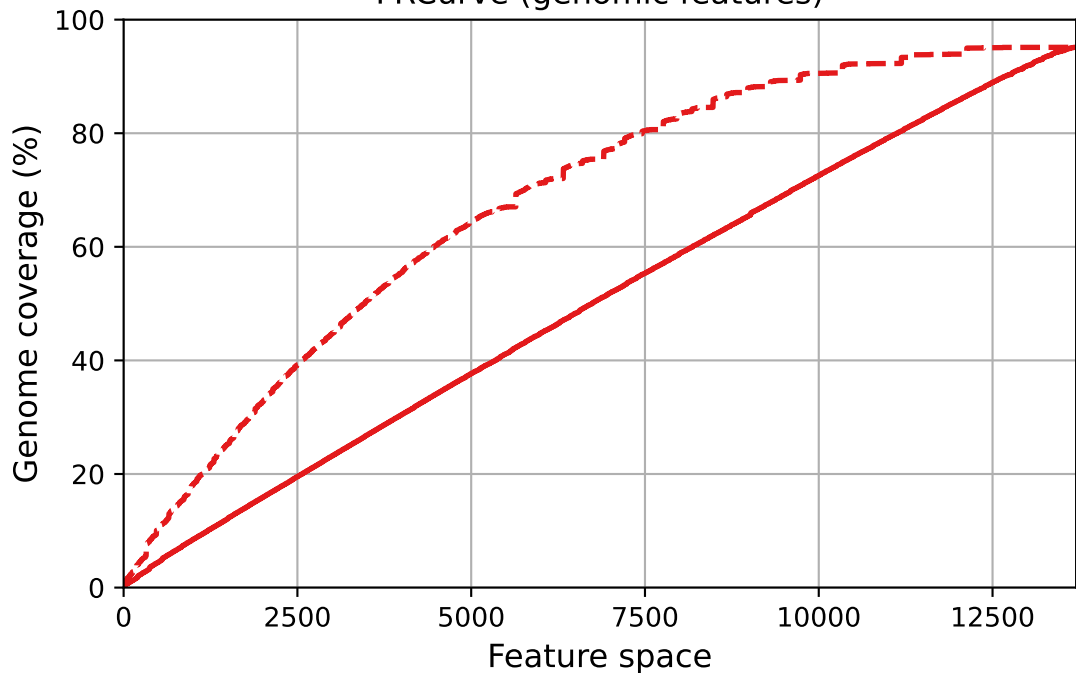
Cumulative # complete genomic features



data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken

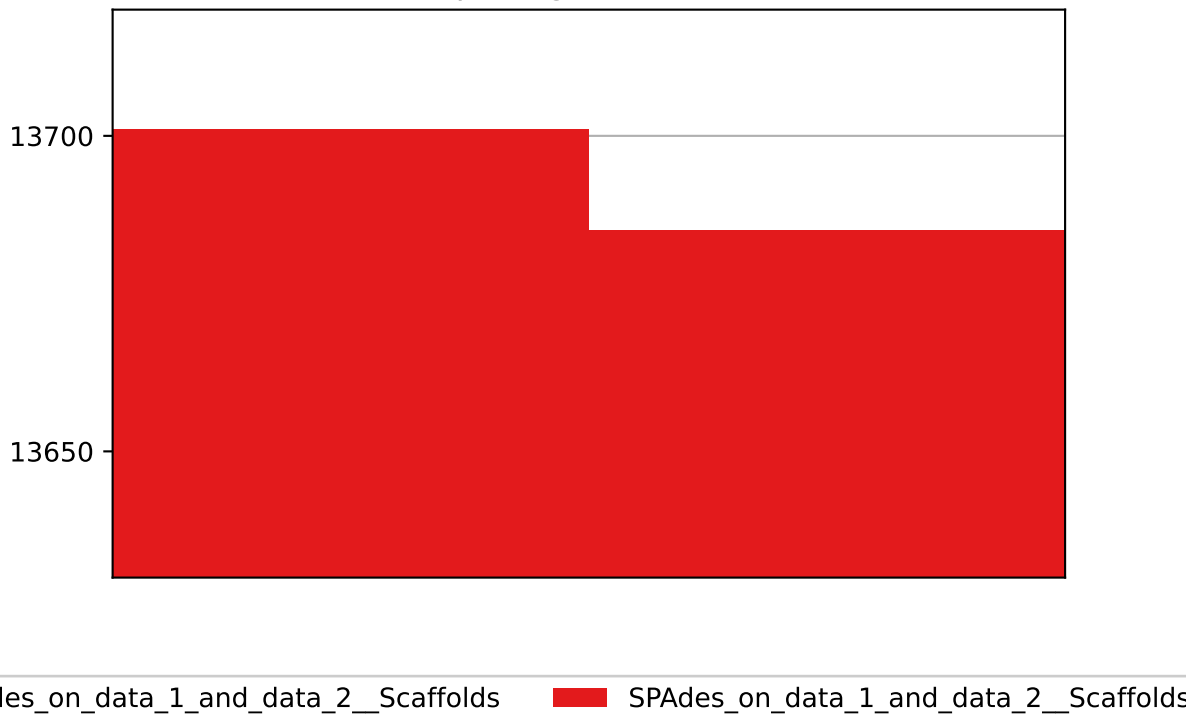
FRCurve (genomic features)



PAdes_on_data_1_and_data_2_Scaffolds

SPAdes_on_data_1_and_data_2_Scaffolds

complete genomic features



Genome fraction, %



PAdes_on_data_1_and_data_2__Scaffolds



SPAdes_on_data_1_and_data_2__Scaffolds