

Report

	SPAdes_on_data_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# contigs (>= 0 bp)	434	-
# contigs (>= 1000 bp)	19	25
Total length (>= 0 bp)	3971164	-
Total length (>= 1000 bp)	3878235	3877635
# contigs	22	28
Largest contig	1090939	1011820
Total length	3880436	3879836
Reference length	4014440	4014440
GC (%)	46.41	46.41
Reference GC (%)	46.39	46.39
N50	1011820	333697
NG50	1011820	333697
N90	224960	113849
NG90	155939	59699
auN	725712.1	526927.0
auNG	701487.5	509259.2
L50	2	3
LG50	2	3
L90	6	10
LG90	7	11
# misassemblies	54	52
# misassembled contigs	7	11
Misassembled contigs length	3664542	3635992
# local misassemblies	38	38
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	1	1
# unaligned contigs	1 + 7 part	1 + 11 part
Unaligned length	202252	202308
Genome fraction (%)	91.997	92.001
Duplication ratio	1.000	1.000
# N's per 100 kbp	15.46	0.00
# mismatches per 100 kbp	1499.29	1499.87
# indels per 100 kbp	43.51	43.35
# genomic features	7141 + 137 part	7137 + 141 part
# predicted rRNA genes	3 + 0 part	3 + 0 part
Largest alignment	306589	306589
Total aligned length	3677136	3676862
NA50	121608	105732
NGA50	109883	105732
NA90	16754	14560
NGA90	9771	9488
auNA	122905.3	119728.7
auNGA	118802.7	115714.2
LA50	11	12
LGA50	12	12
LA90	45	48
LGA90	55	58

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

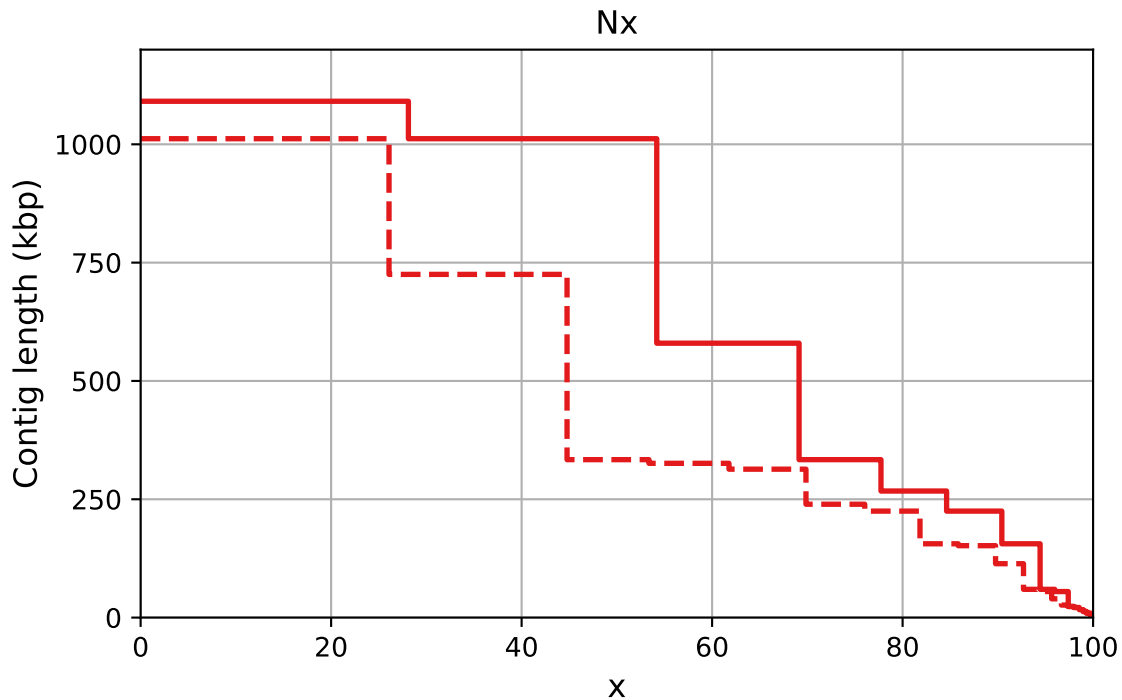
	SPAdes_on_data_1_and_data_2_Scaffolds	SPAdes_on_data_1_and_data_2_Scaffolds_broken
# misassemblies	54	52
# contig misassemblies	52	52
# c. relocations	50	50
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	7	11
Misassembled contigs length	3664542	3635992
# local misassemblies	38	38
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	1	1
# mismatches	55131	55148
# indels	1600	1594
# indels (<= 5 bp)	1407	1404
# indels (> 5 bp)	193	190
Indels length	7889	7607

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	1	1
Fully unaligned length	541	541
# partially unaligned contigs	7	11
Partially unaligned length	201711	201767
# N's	600	0

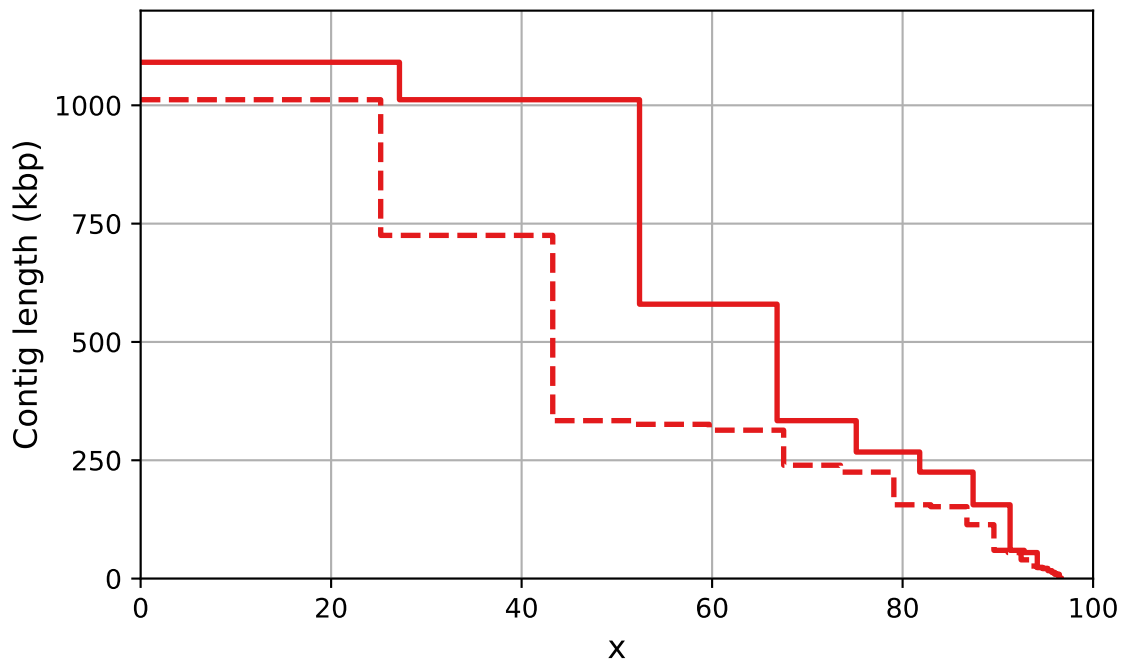
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

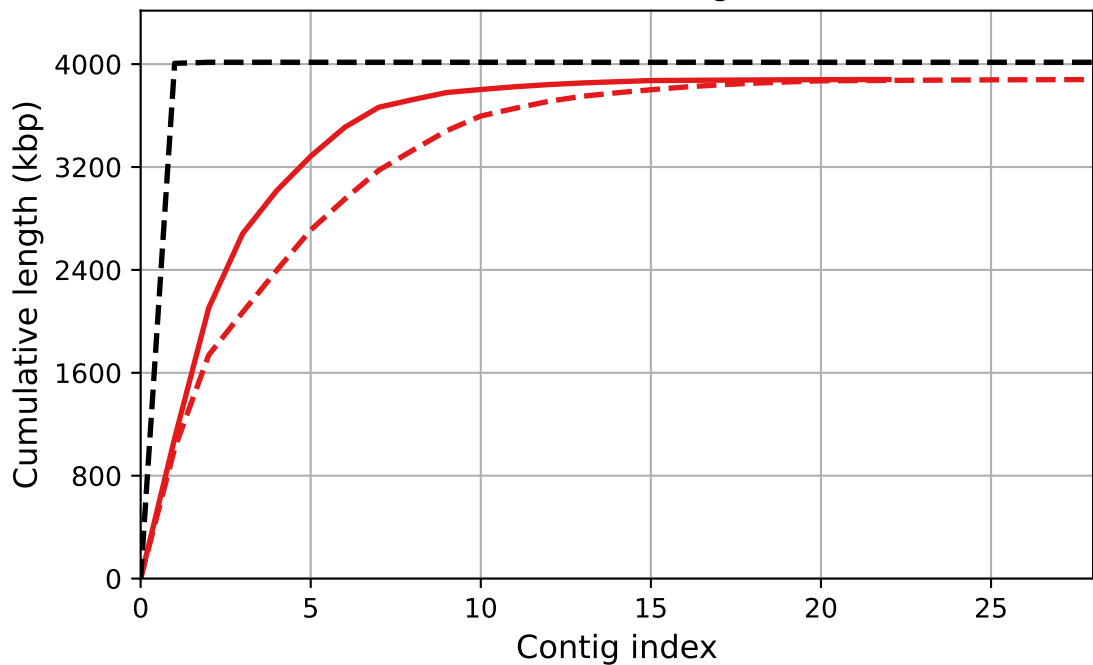
NGx



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

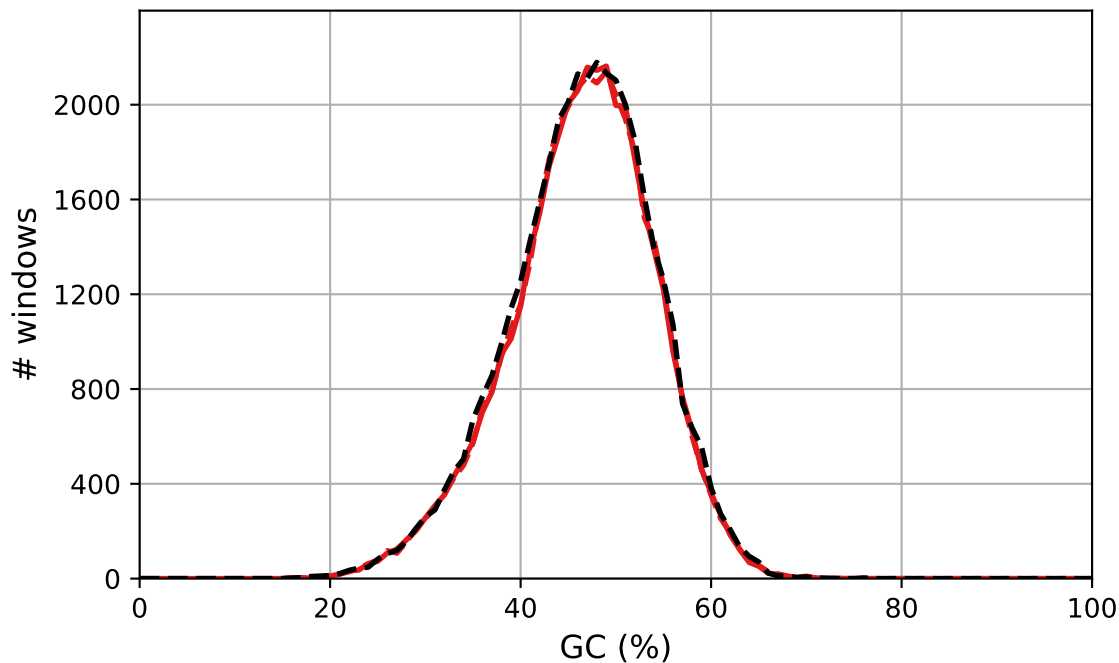
Cumulative length



_data_1_and_data_2__Scaffolds

-- SPAdes_on_data_1_and_data_2__Scaffolds_broken

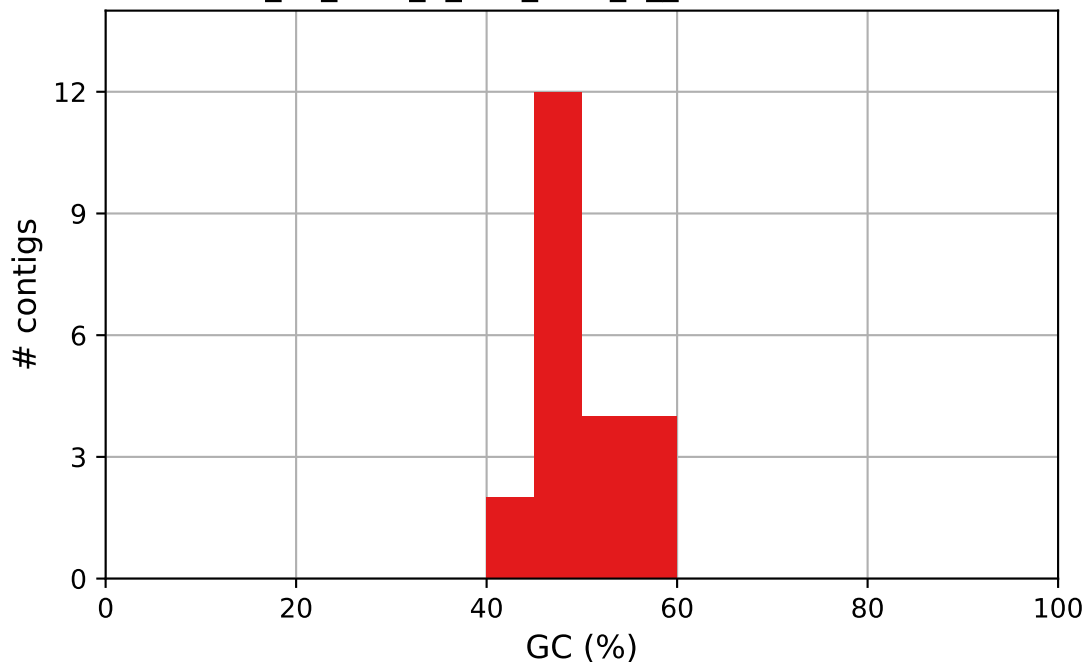
GC content



data_1_and_data_2__Scaffolds

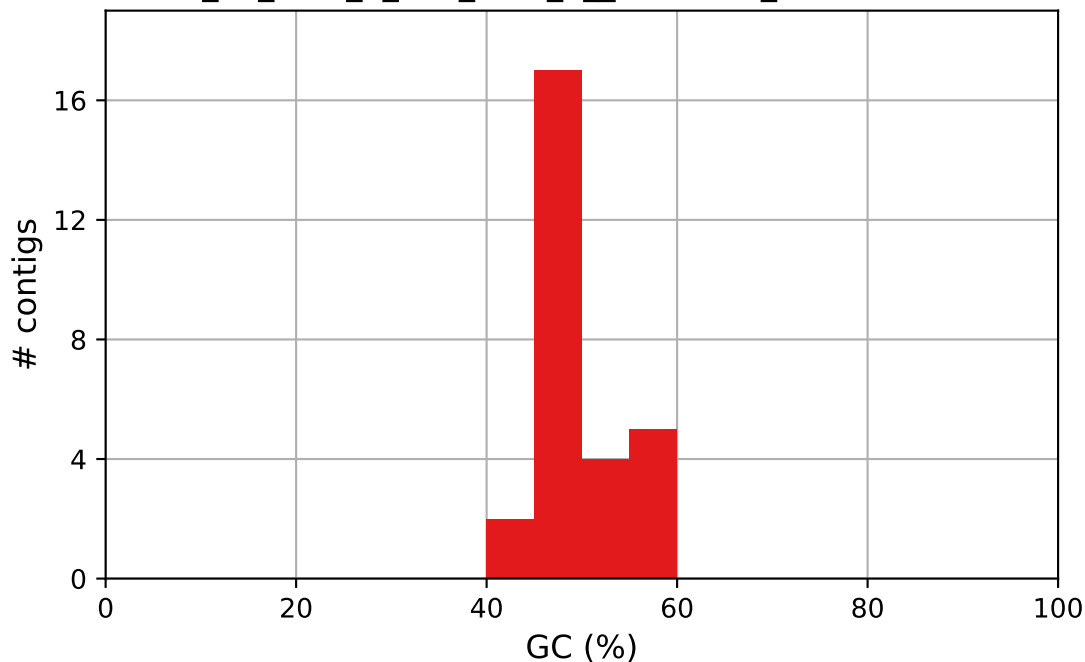
-- SPAdes_on_data_1_and_data_2__Scaffolds_broken

SPAdes_on_data_1_and_data_2__Scaffolds GC content



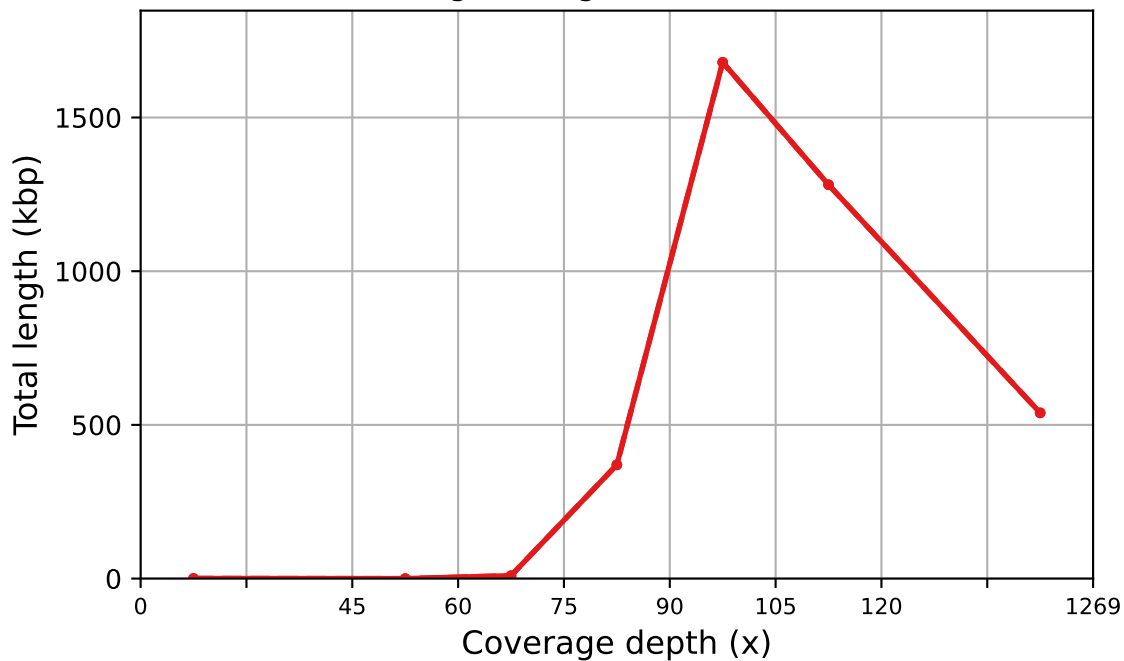
SPAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken GC content



SPAdes_on_data_1_and_data_2__Scaffolds_broken

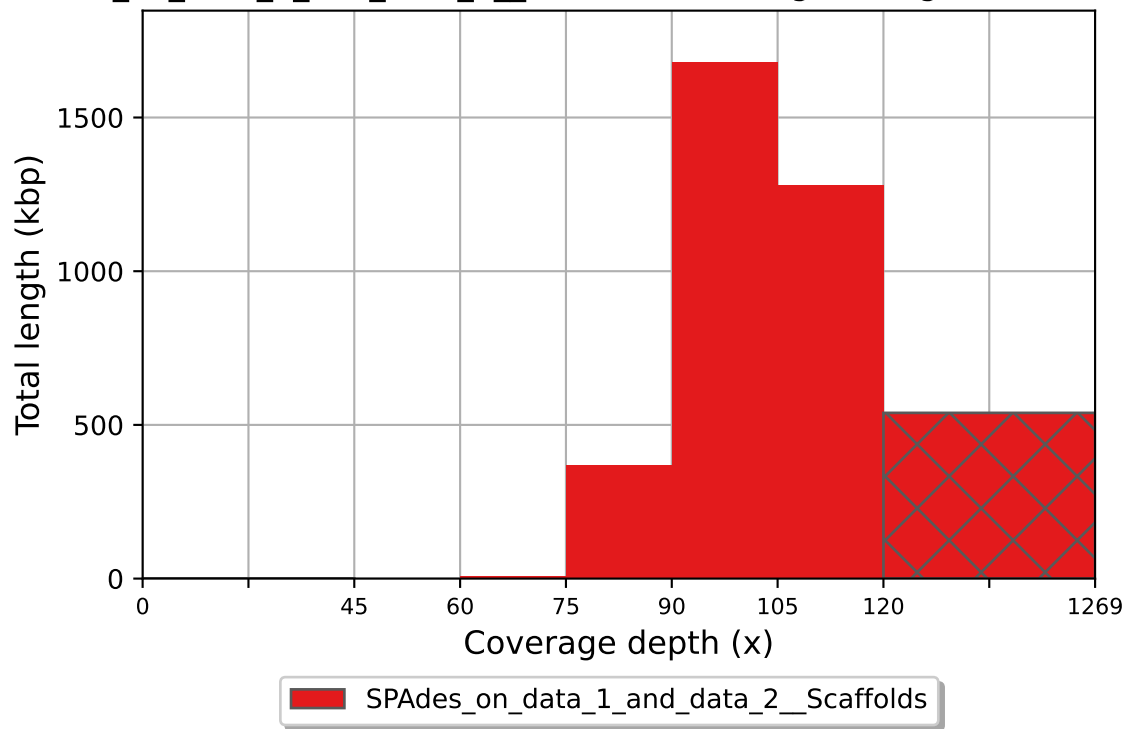
Coverage histogram (bin size: 15x)



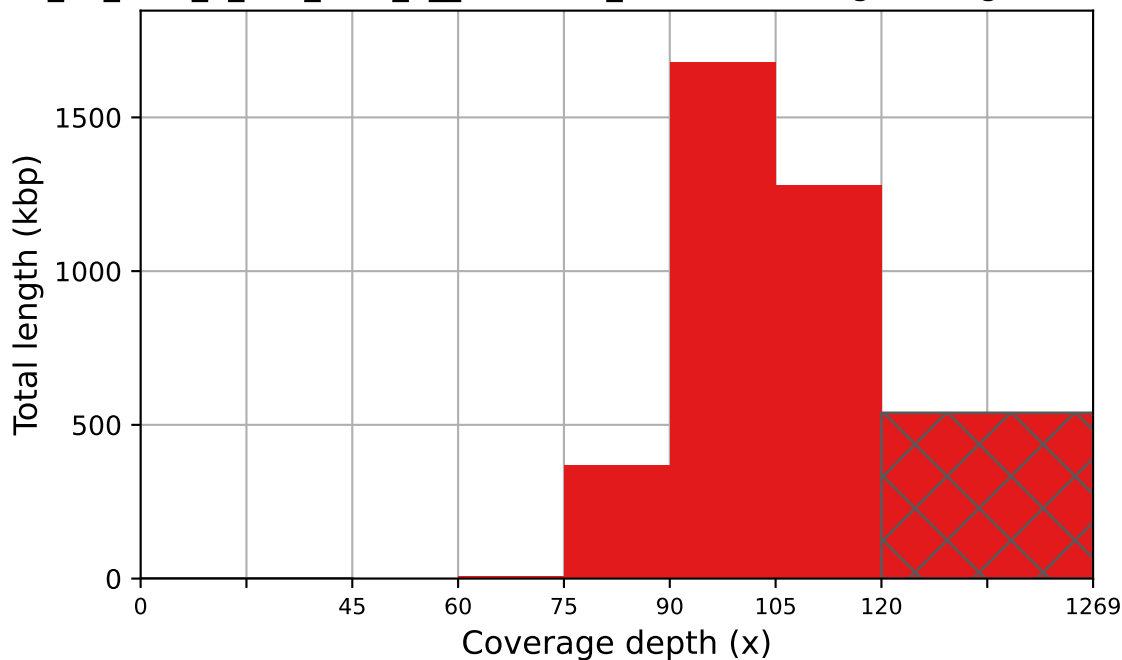
PAdes_on_data_1_and_data_2__Scaffolds

—●— SPAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds coverage histogram (bin size: 15x)

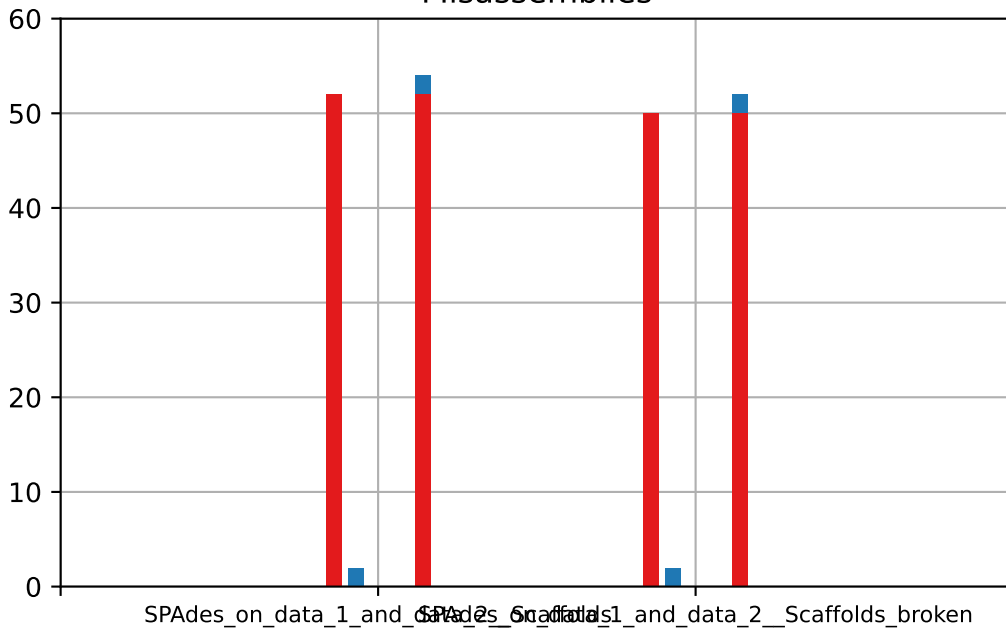


SPAdes_on_data_1_and_data_2__Scaffolds_broken coverage histogram (bin size: 15)



SPAdes_on_data_1_and_data_2__Scaffolds_broken

Misassemblies

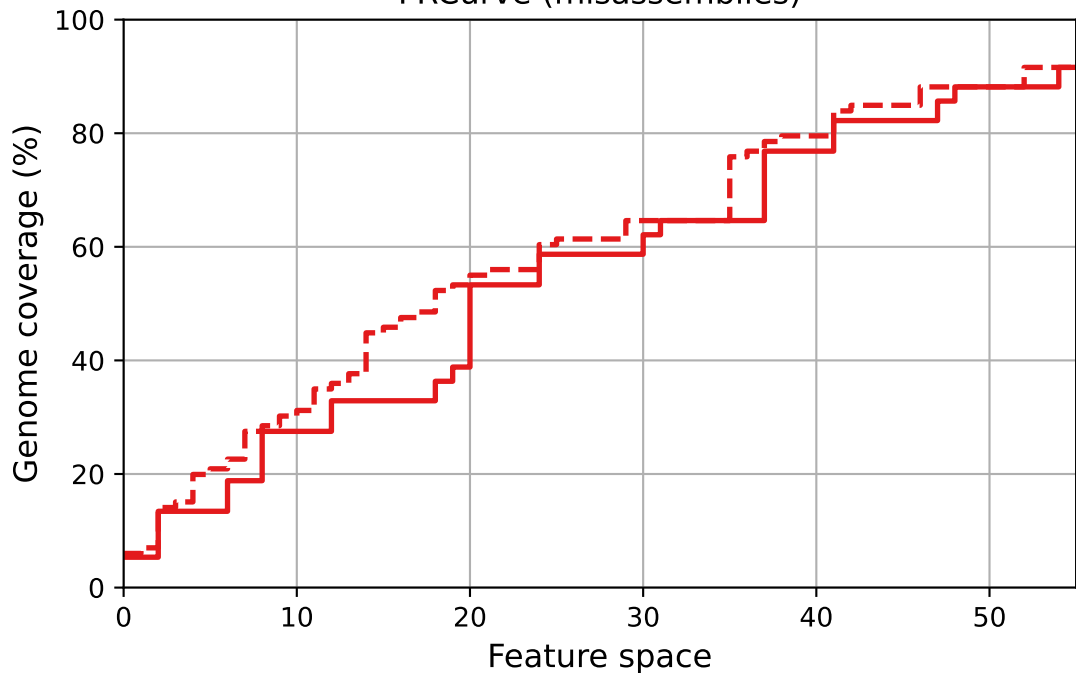


relocations



translocations

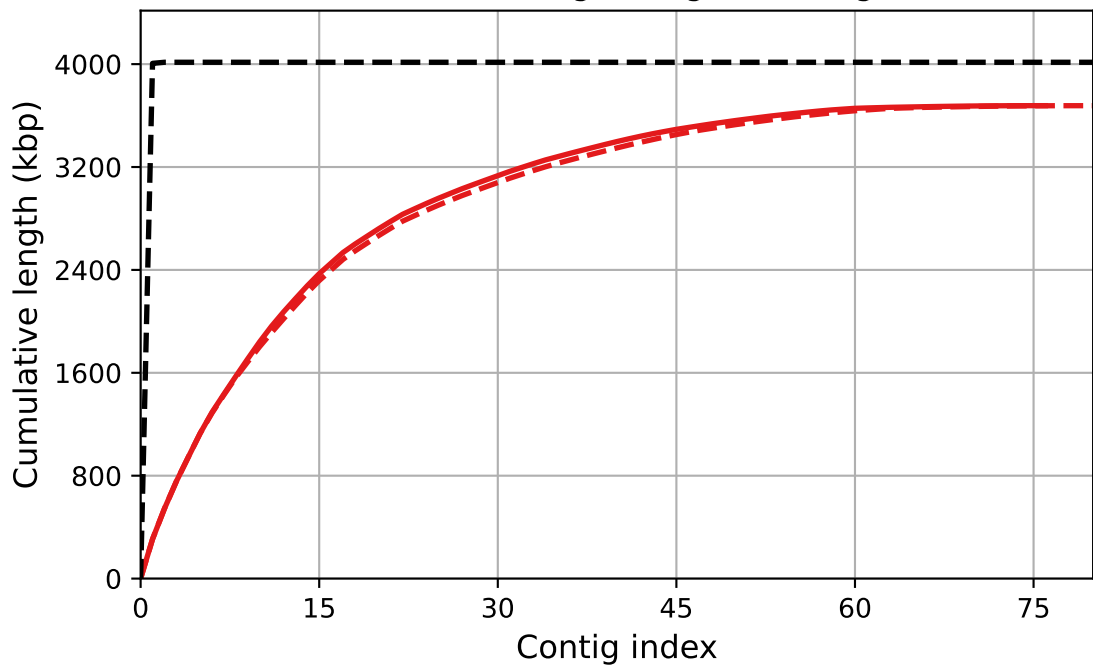
FRCurve (misassemblies)



PAdes_on_data_1_and_data_2_Scaffolds

SPAdes_on_data_1_and_data_2_Scaffolds

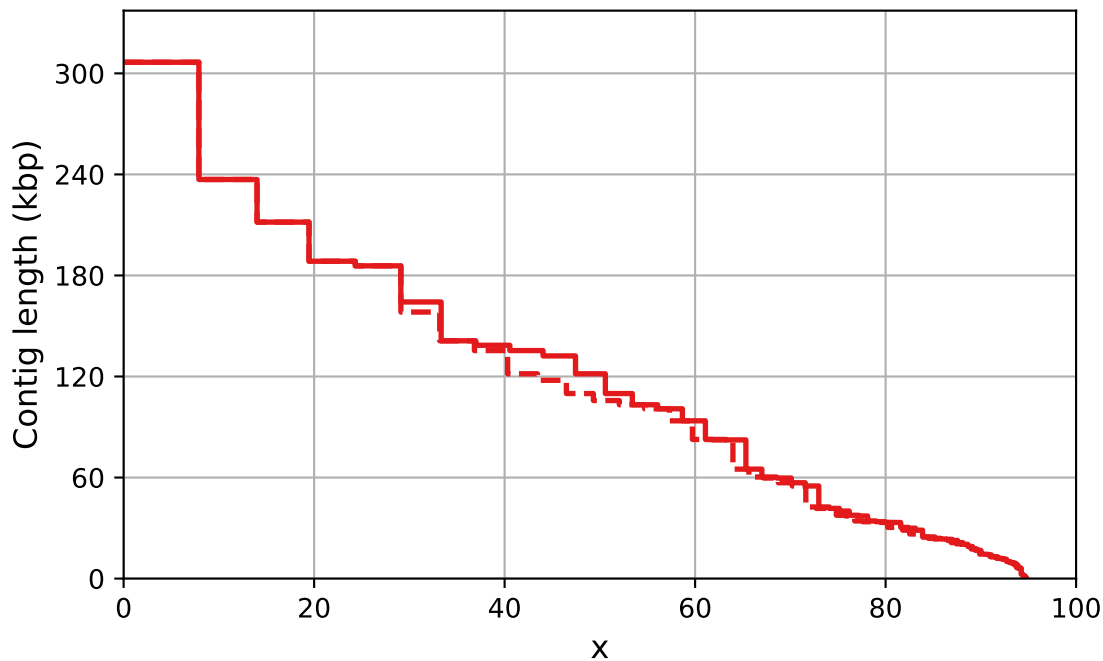
Cumulative length (aligned contigs)



data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken

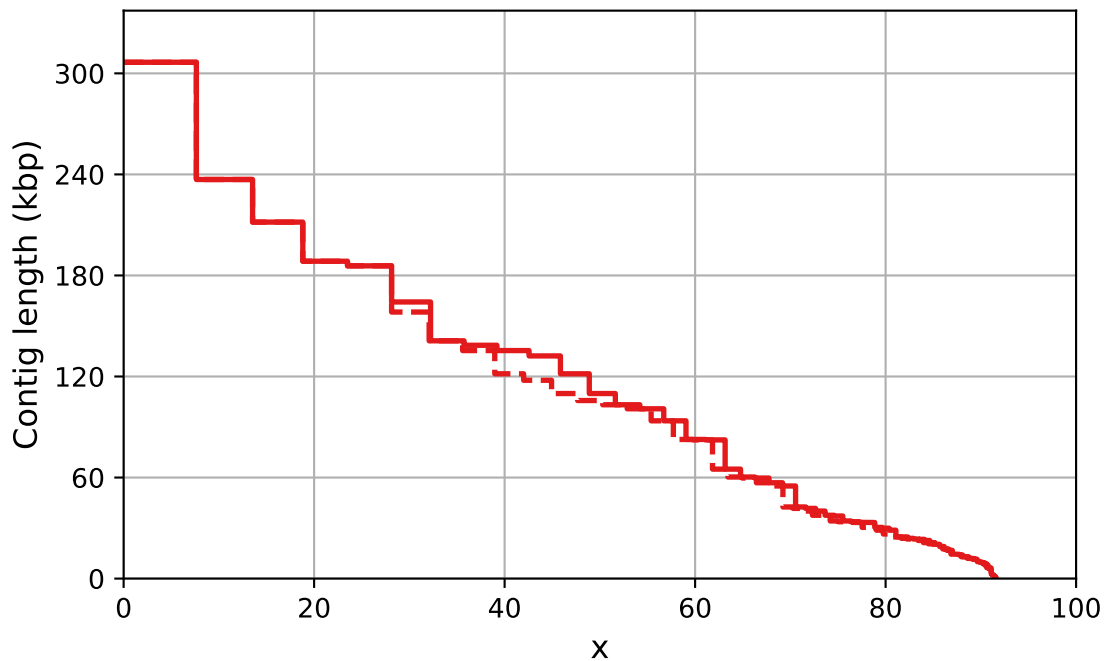
NAx



PAdes_on_data_1_and_data_2__Scaffolds

-- SPAdes_on_data_1_and_data_2__Scaffolds

NGAx

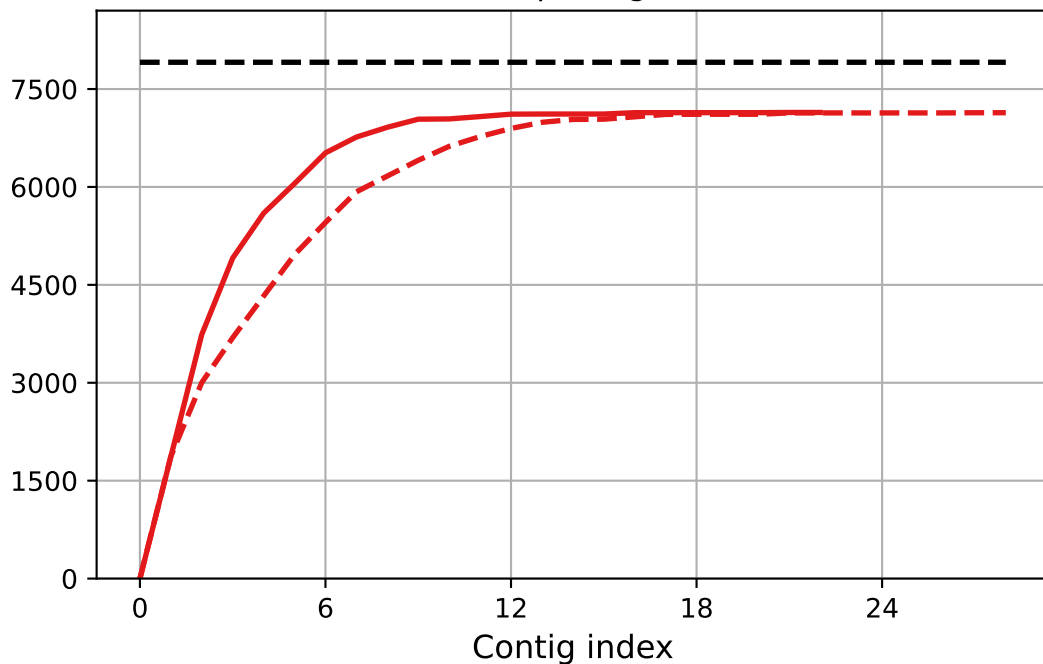


PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

Cumulative # complete genomic features

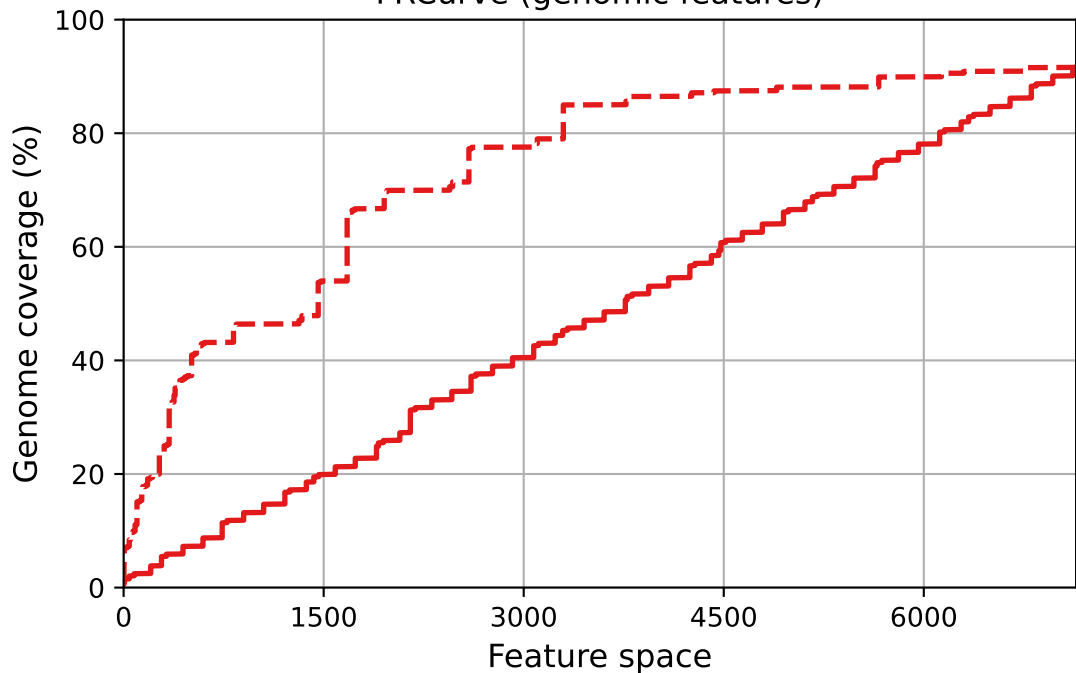
Cumulative # complete genomic features



_data_1_and_data_2__Scaffolds

-- SPAdes_on_data_1_and_data_2__Scaffolds_broken

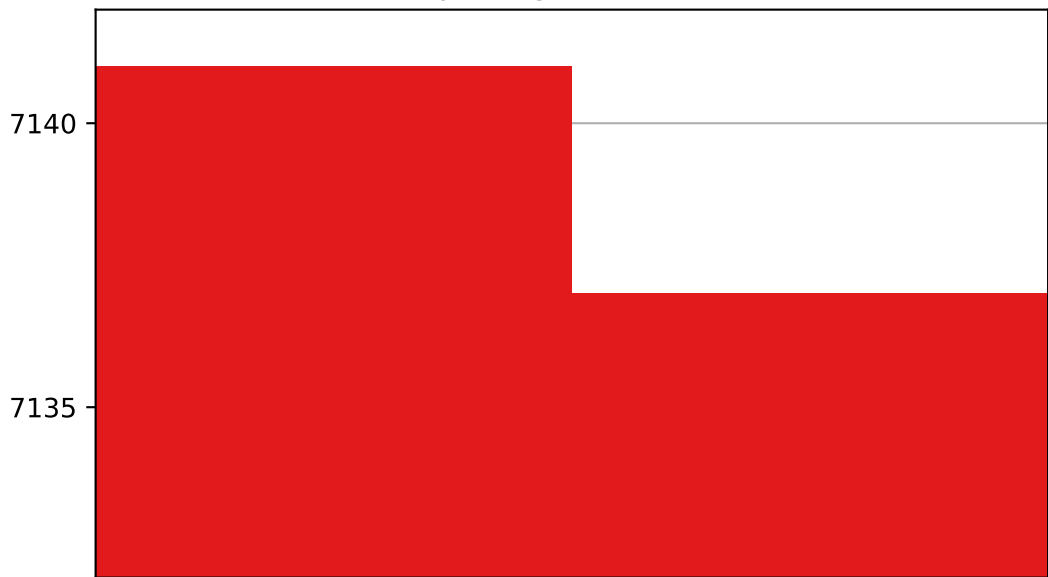
FRCurve (genomic features)



PAdes_on_data_1_and_data_2_Scaffolds

SPAdes_on_data_1_and_data_2_Scaffolds

complete genomic features



PAdes_on_data_1_and_data_2_Scaffolds



SPAdes_on_data_1_and_data_2_Scaffolds

Genome fraction, %

100

95

PAdes_on_data_1_and_data_2__Scaffolds



SPAdes_on_data_1_and_data_2__Scaffolds