

Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	220	-
# contigs (>= 1000 bp)	45	46
Total length (>= 0 bp)	3784679	-
Total length (>= 1000 bp)	3751985	3751885
# contigs	58	59
Largest contig	454053	436152
Total length	3761325	3761225
Reference length	3901694	3901694
GC (%)	66.04	66.04
Reference GC (%)	65.70	65.70
N50	352385	352385
NG50	352385	251613
N90	42200	42200
NG90	30133	30133
auN	267841.7	262243.2
auNG	258205.7	252801.9
L50	5	5
LG50	5	6
L90	18	18
LG90	21	21
# misassemblies	50	49
# misassembled contigs	18	18
Misassembled contigs length	2894910	2870372
# local misassemblies	39	39
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	3
# unaligned contigs	12 + 25 part	12 + 26 part
Unaligned length	431545	431545
Genome fraction (%)	85.321	85.321
Duplication ratio	1.002	1.002
# N's per 100 kbp	2.66	0.00
# mismatches per 100 kbp	855.79	855.79
# indels per 100 kbp	40.18	40.18
# genomic features	3106 + 109 part	3106 + 109 part
Largest alignment	349790	349790
Total aligned length	3327441	3327441
NA50	82240	82240
NGA50	82240	82240
NA90	-	-
NGA90	-	-
auNA	109251.5	109254.4
auNGA	105321.0	105321.0
LA50	13	13
LGA50	13	13
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

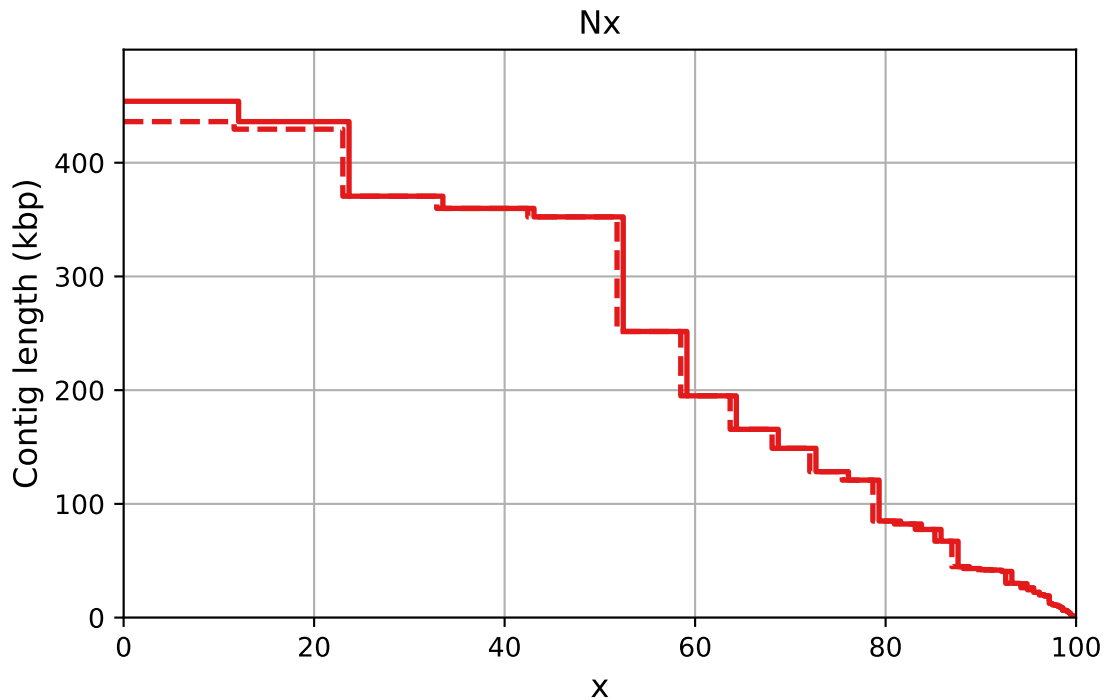
	SPAdes_on_data_2_and_data_1_Scaffolds	SPAdes_on_data_2_and_data_1_Scaffolds_broken
# misassemblies	50	49
# contig misassemblies	49	49
# c. relocations	48	48
# c. translocations	1	1
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	18	18
Misassembled contigs length	2894910	2870372
# local misassemblies	39	39
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	3
# mismatches	28476	28476
# indels	1337	1337
# indels (<= 5 bp)	1109	1109
# indels (> 5 bp)	228	228
Indels length	8293	8293

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_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# fully unaligned contigs	12	12
Fully unaligned length	25865	25865
# partially unaligned contigs	25	26
Partially unaligned length	405680	405680
# N's	100	0

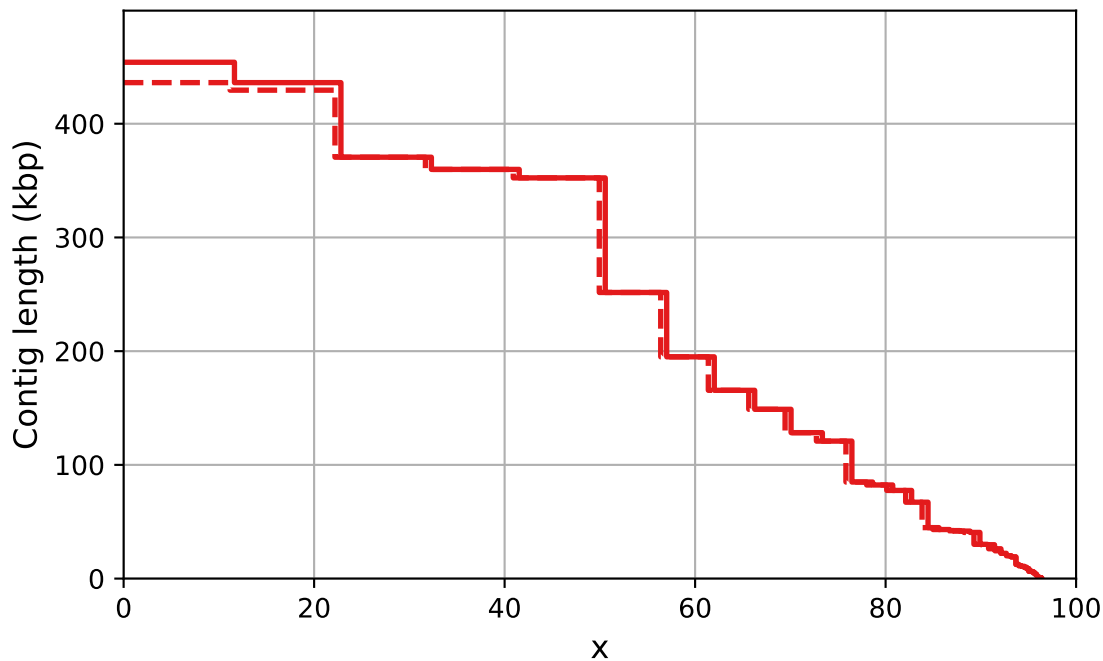
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



PAdes_on_data_2_and_data_1__Scaffolds

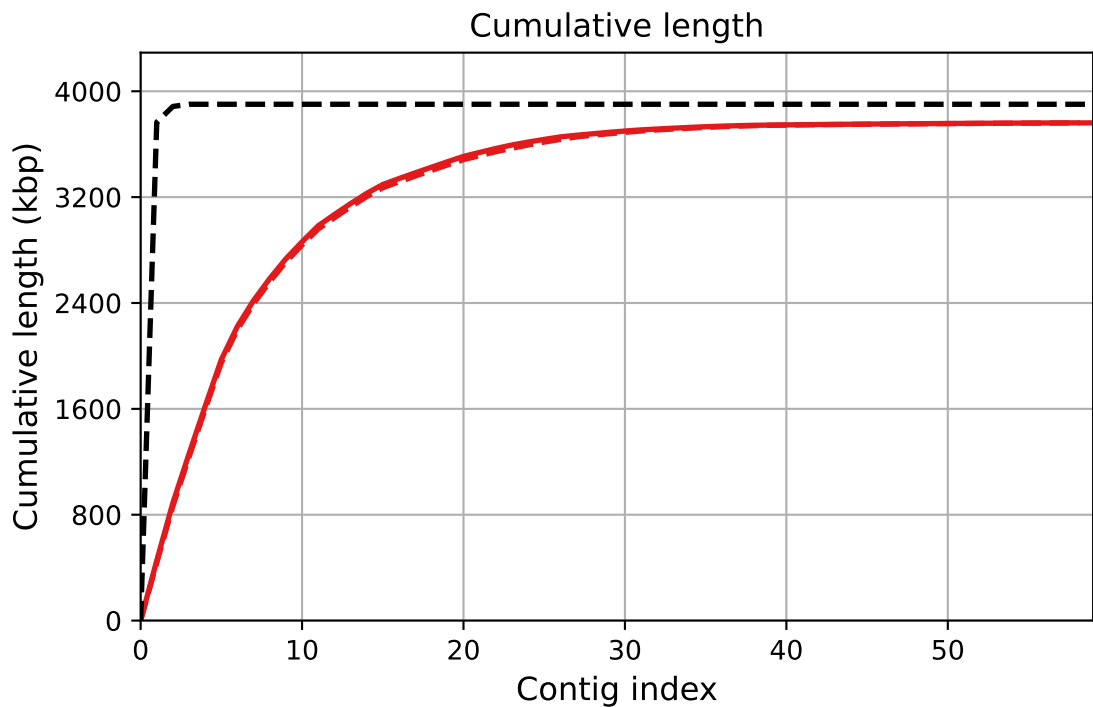
SPAdes_on_data_2_and_data_1__Scaffolds

NGx



PAdes_on_data_2_and_data_1_Scaffolds

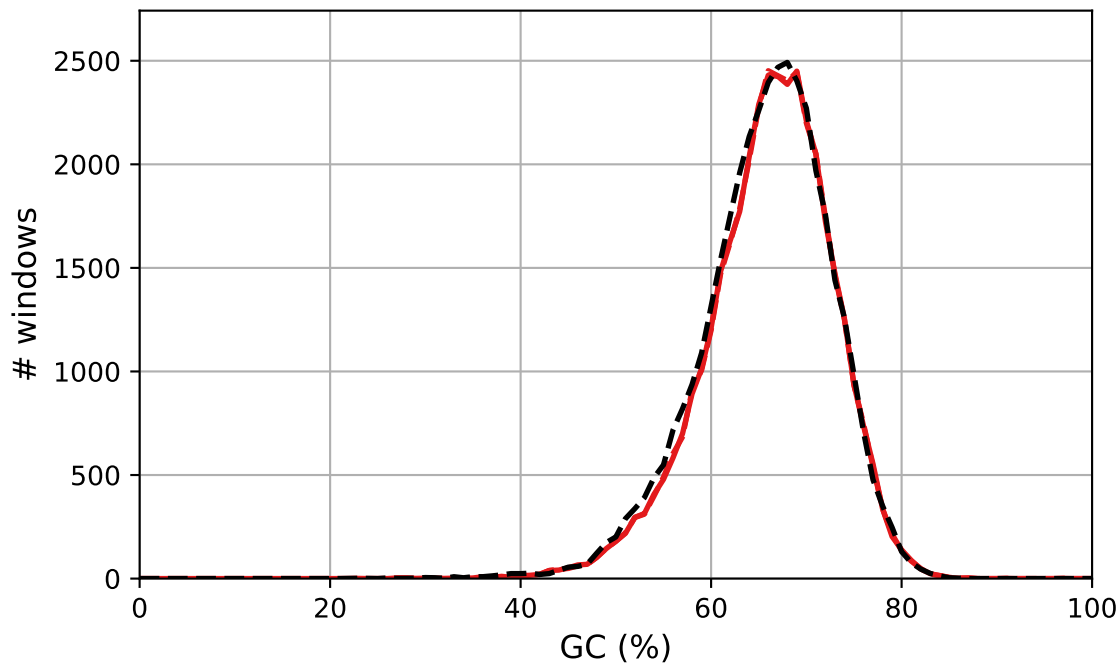
SPAdes_on_data_2_and_data_1_Scaffolds



data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1_Scaffolds_broken

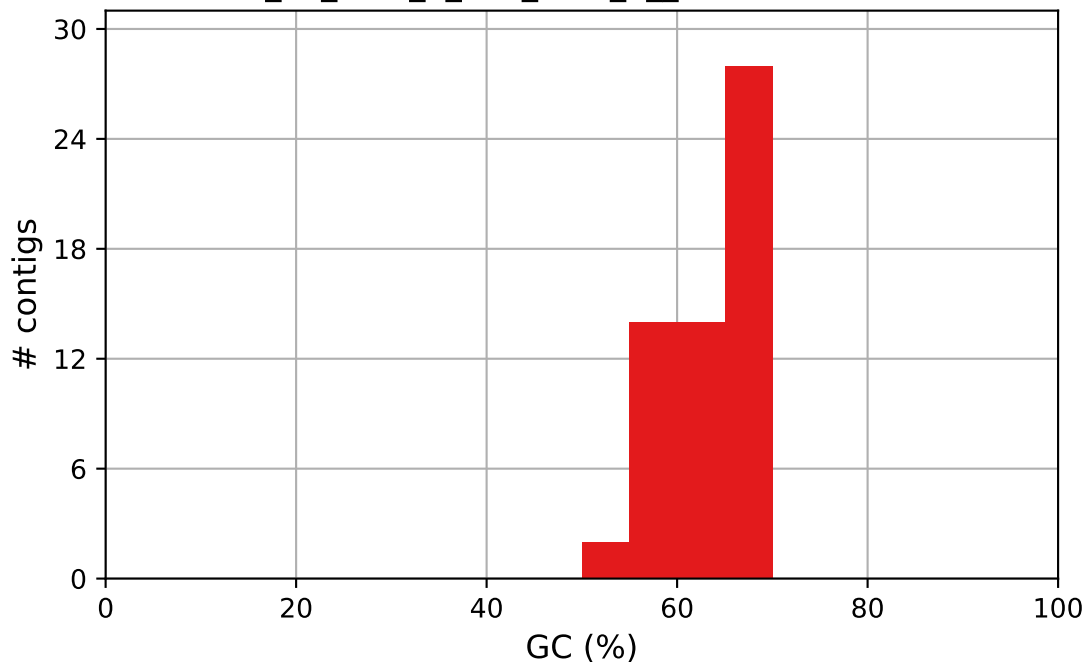
GC content



_data_2_and_data_1__Scaffolds

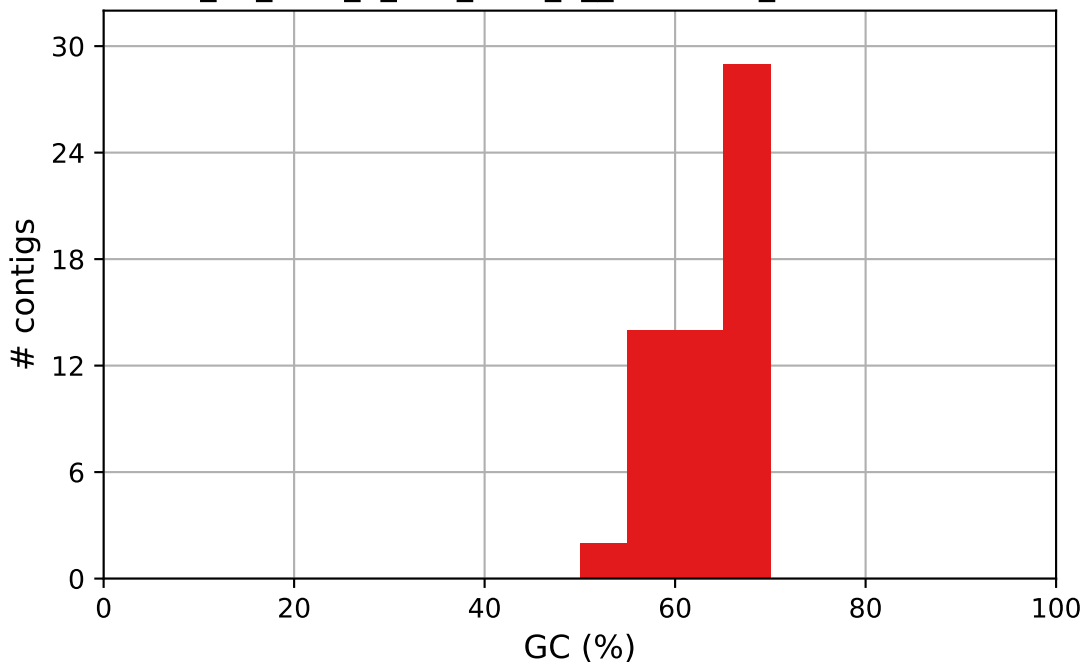
-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

SPAdes_on_data_2_and_data_1__Scaffolds GC content



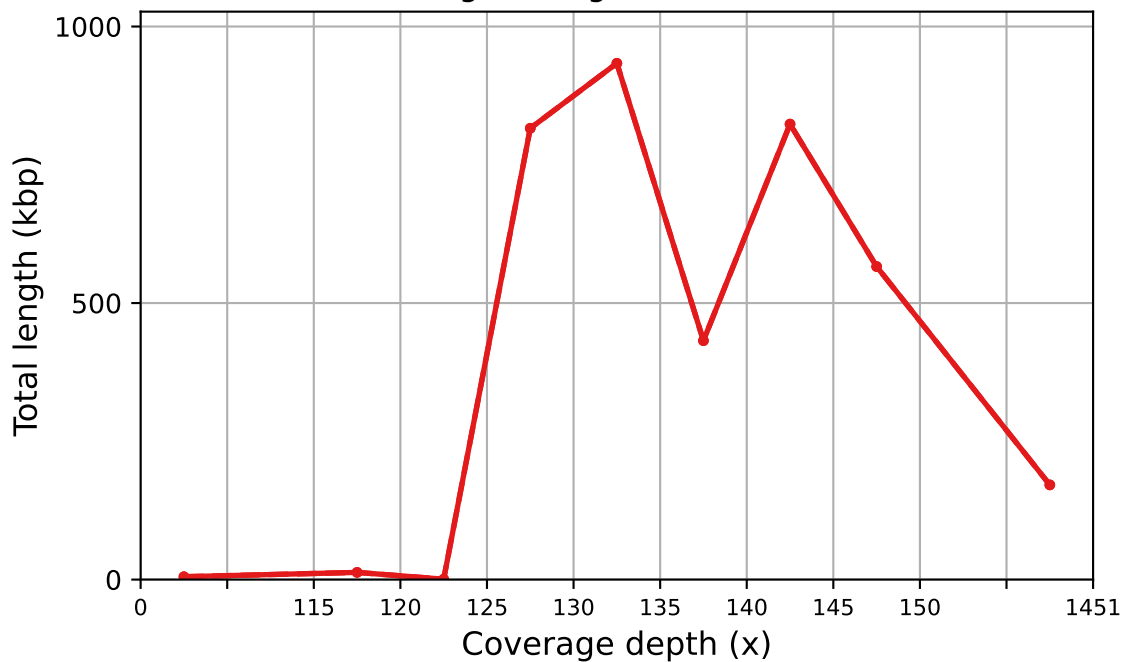
SPAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds_broken GC content



SPAdes_on_data_2_and_data_1__Scaffolds_broken

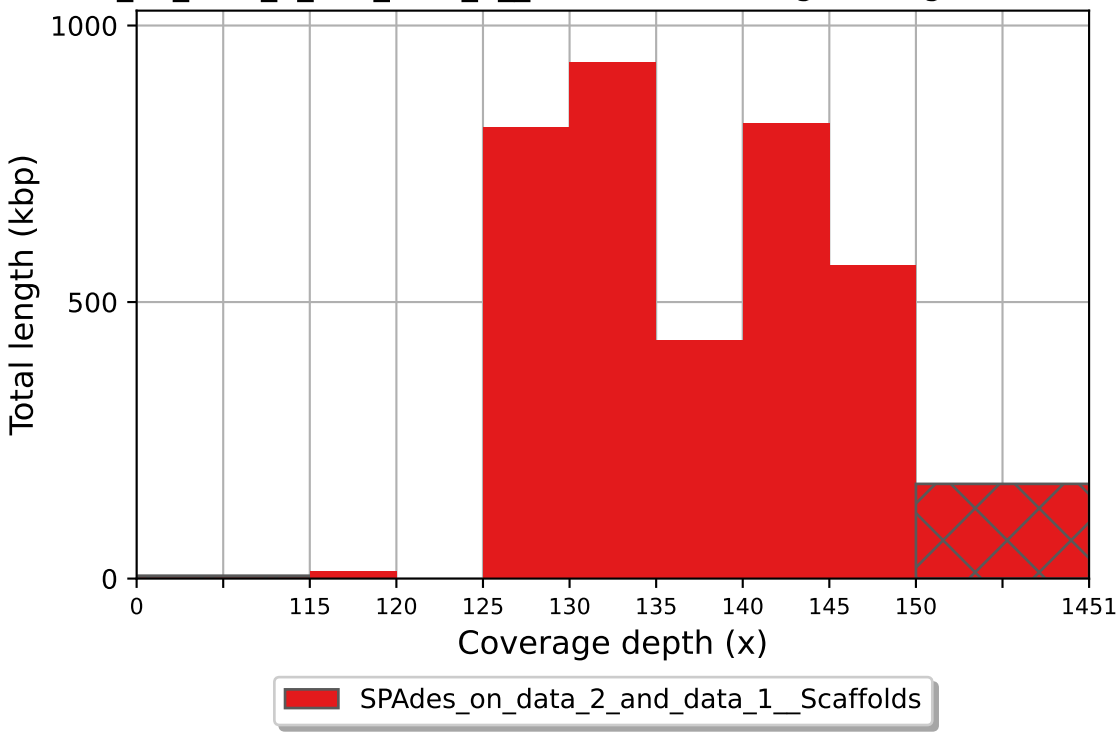
Coverage histogram (bin size: 5x)



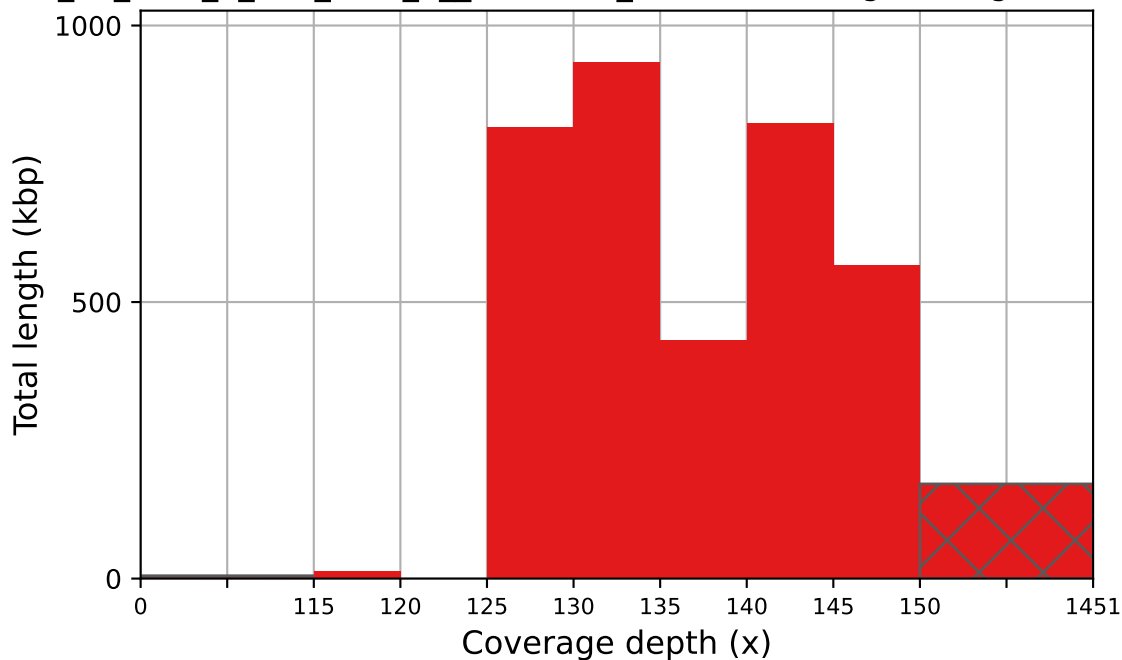
PAdes_on_data_2_and_data_1_Scaffolds

—●— SPAdes_on_data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds coverage histogram (bin size: 5x

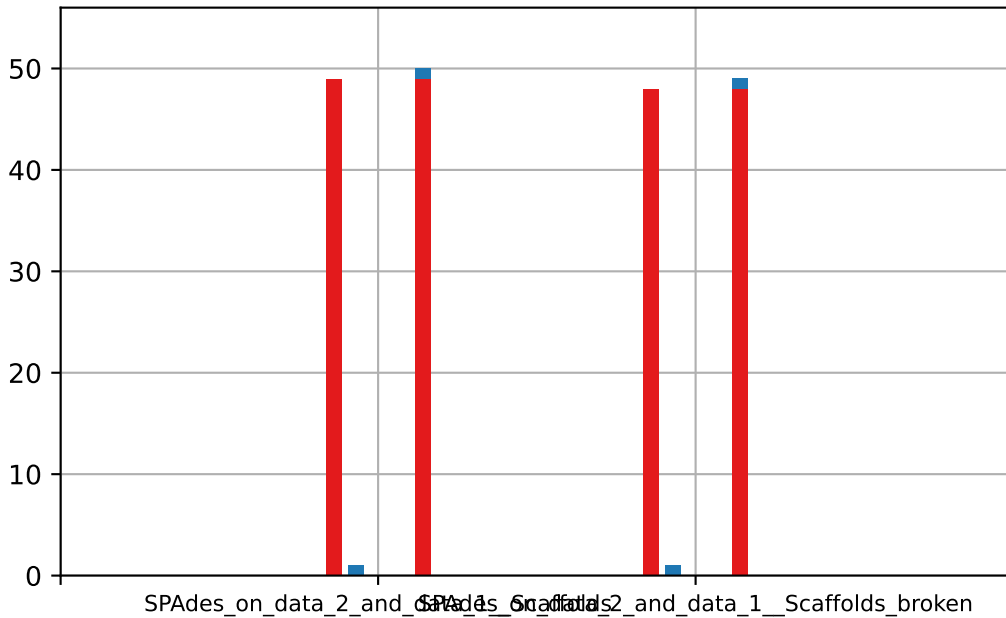


SPAdes_on_data_2_and_data_1__Scaffolds_broken coverage histogram (bin size



SPAdes_on_data_2_and_data_1__Scaffolds_broken

Misassemblies

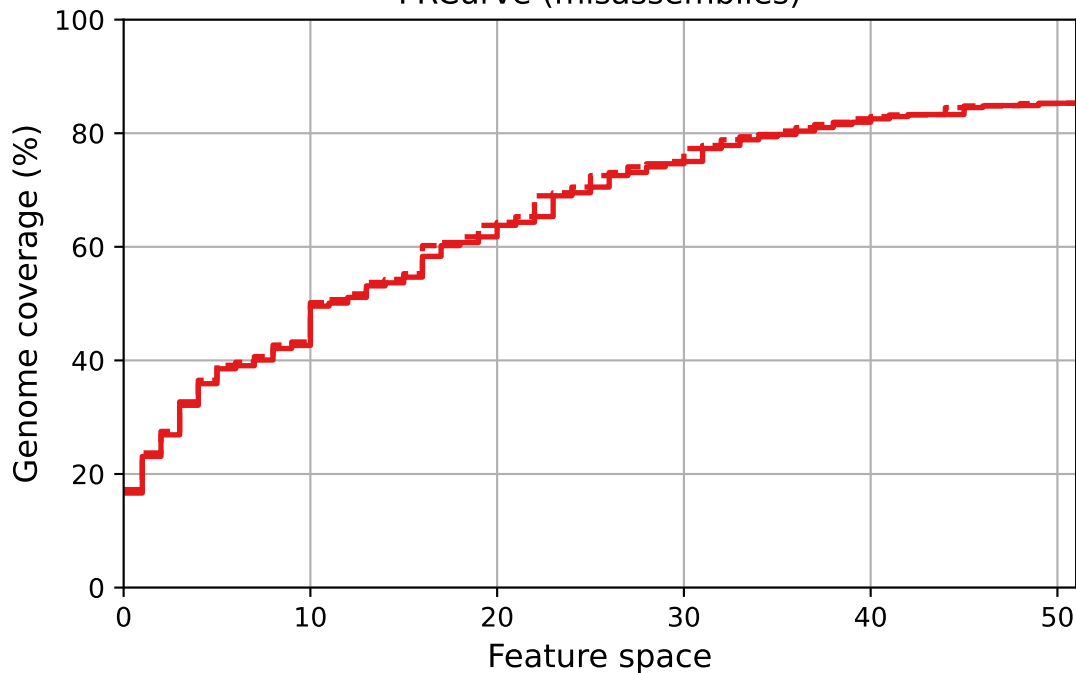


relocations



translocations

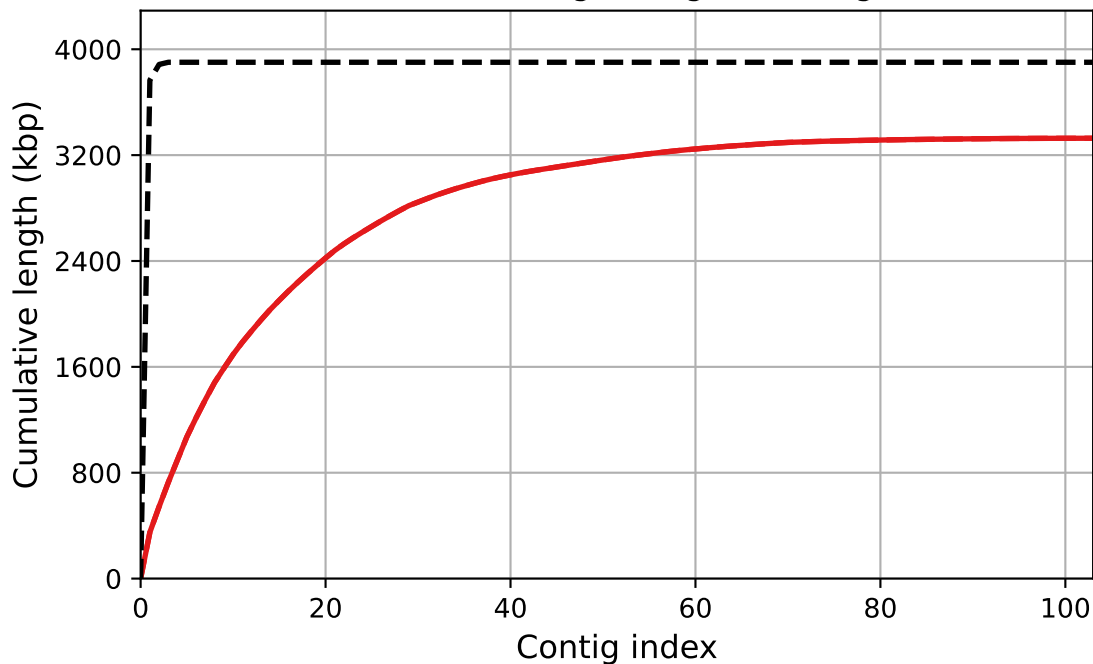
FRCurve (misassemblies)



PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

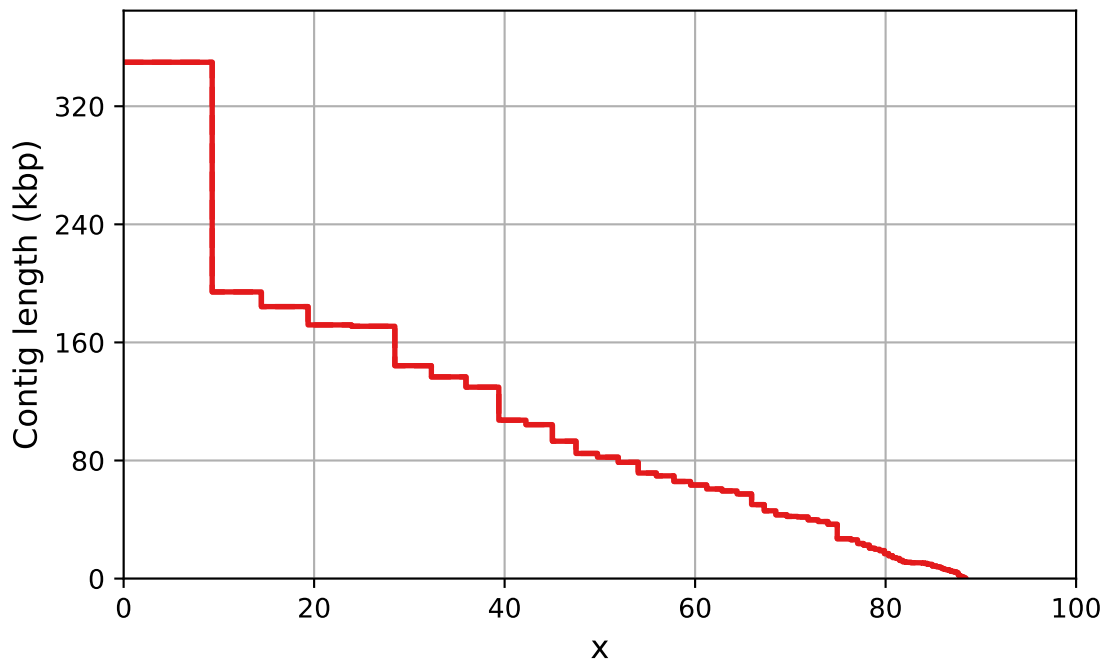
Cumulative length (aligned contigs)



data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1_Scaffolds_broken

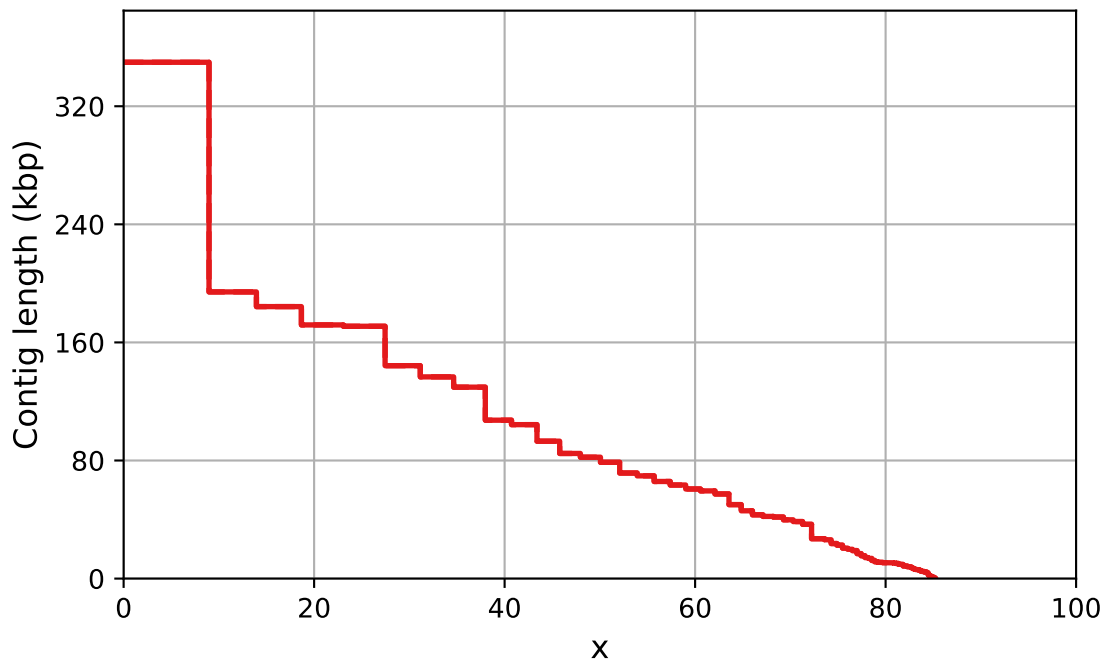
NAx



PAdes_on_data_2_and_data_1_Scaffolds

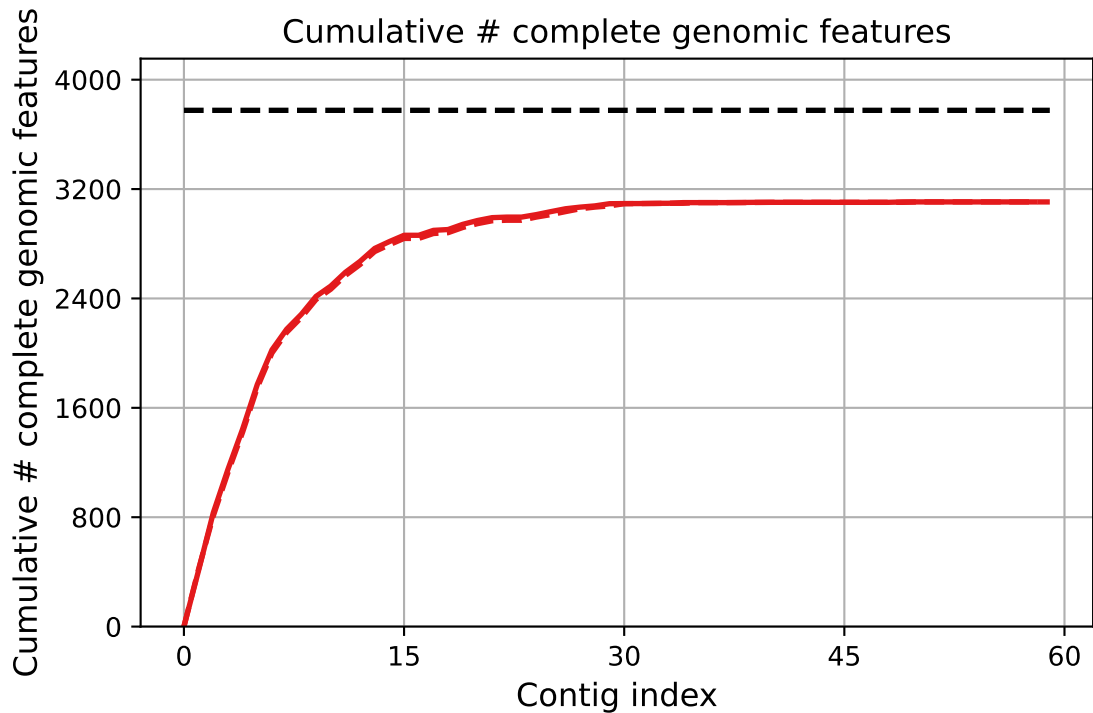
SPAdes_on_data_2_and_data_1_Scaffolds

NGAx



PAdes_on_data_2_and_data_1__Scaffolds

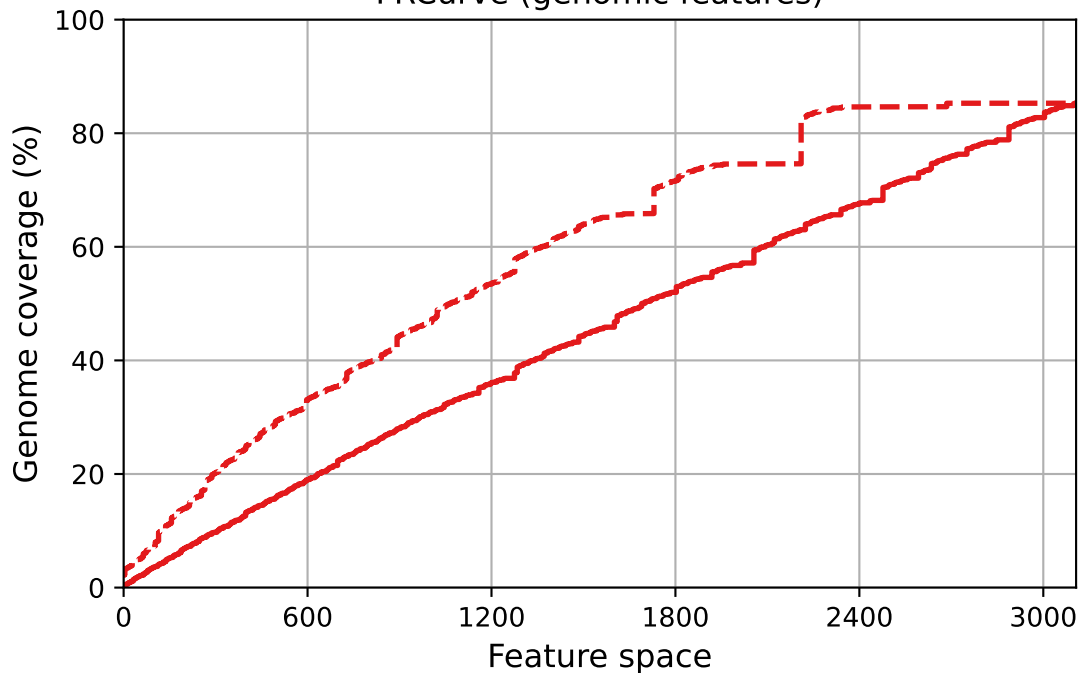
SPAdes_on_data_2_and_data_1__Scaffolds



_data_2_and_data_1__Scaffolds

-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

FRCurve (genomic features)



PAdes_on_data_2_and_data_1_Scaffolds

SPAdes_on_data_2_and_data_1_Scaffolds

complete genomic features



PAdes_on_data_2_and_data_1__Scaffolds



SPAdes_on_data_2_and_data_1__Scaffolds

Genome fraction, %

100

50

PAdes_on_data_2_and_data_1__Scaffolds



SPAdes_on_data_2_and_data_1__Scaffolds