

Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	110	-
# contigs (>= 1000 bp)	16	20
Total length (>= 0 bp)	4134070	-
Total length (>= 1000 bp)	4115976	4115576
# contigs	21	25
Largest contig	1061268	991853
Total length	4119144	4118744
Reference length	4215606	4215606
GC (%)	43.66	43.66
Reference GC (%)	43.51	43.51
N50	1023085	638625
NG50	991853	638625
N90	200153	99944
NG90	200153	99944
auN	816281.6	565178.0
auNG	797603.4	552191.9
L50	2	3
LG50	3	3
L90	6	9
LG90	6	9
# misassemblies	54	52
# misassembled contigs	6	9
Misassembled contigs length	3807906	3767949
# local misassemblies	32	32
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	0	0
# unaligned contigs	2 + 6 part	2 + 10 part
Unaligned length	342151	342151
Genome fraction (%)	90.558	90.558
Duplication ratio	1.001	1.001
# N's per 100 kbp	9.71	0.00
# mismatches per 100 kbp	1282.11	1282.14
# indels per 100 kbp	41.28	41.25
# genomic features	7938 + 208 part	7936 + 210 part
Complete BUSCO (%)	100.00	100.00
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	1 + 1 part	1 + 1 part
Largest alignment	397615	397615
Total aligned length	3776665	3776565
NA50	104924	104924
NGA50	93345	93345
NA90	8988	8677
NGA90	-	-
auNA	150223.1	149931.7
auNGA	146785.7	146486.7
LA50	10	10
LGA50	11	11
LA90	52	53
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

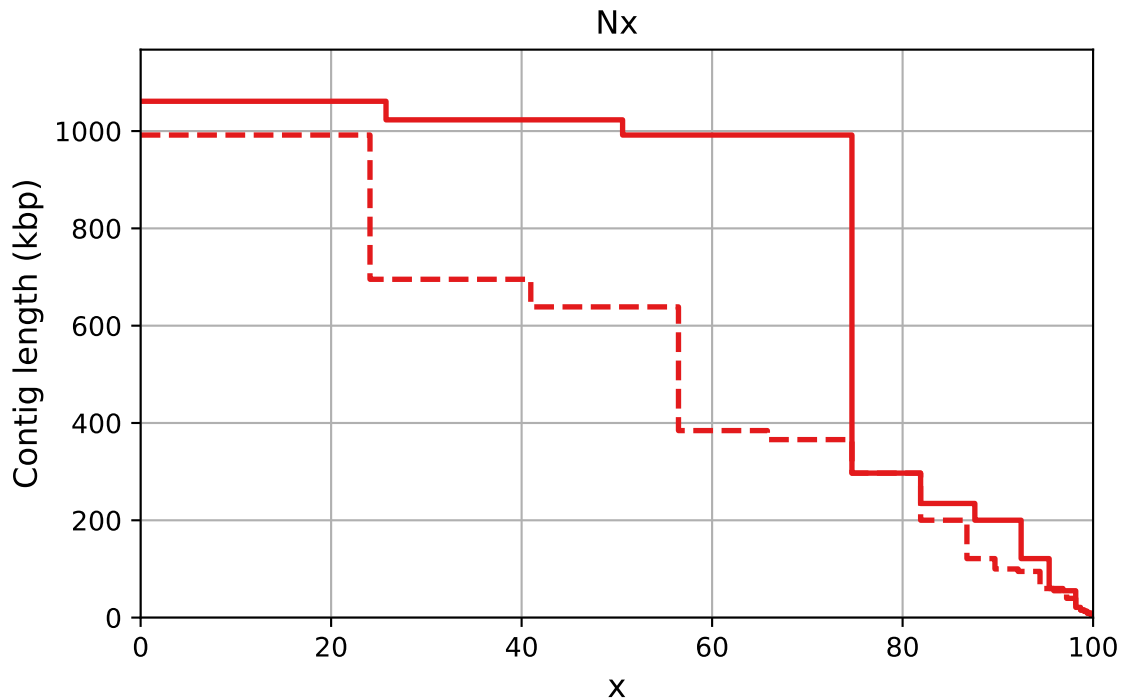
	SPAdes_on_data_2_and_data_1_Scaffolds	SPAdes_on_data_2_and_data_1_Scaffolds_broken
# misassemblies	54	52
# contig misassemblies	52	52
# c. relocations	52	52
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	6	9
Misassembled contigs length	3807906	3767949
# local misassemblies	32	32
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	0	0
# mismatches	48421	48421
# indels	1559	1558
# indels (<= 5 bp)	1363	1363
# indels (> 5 bp)	196	195
Indels length	6786	6686

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	2	2
Fully unaligned length	142224	142224
# partially unaligned contigs	6	10
Partially unaligned length	199927	199927
# N's	400	0

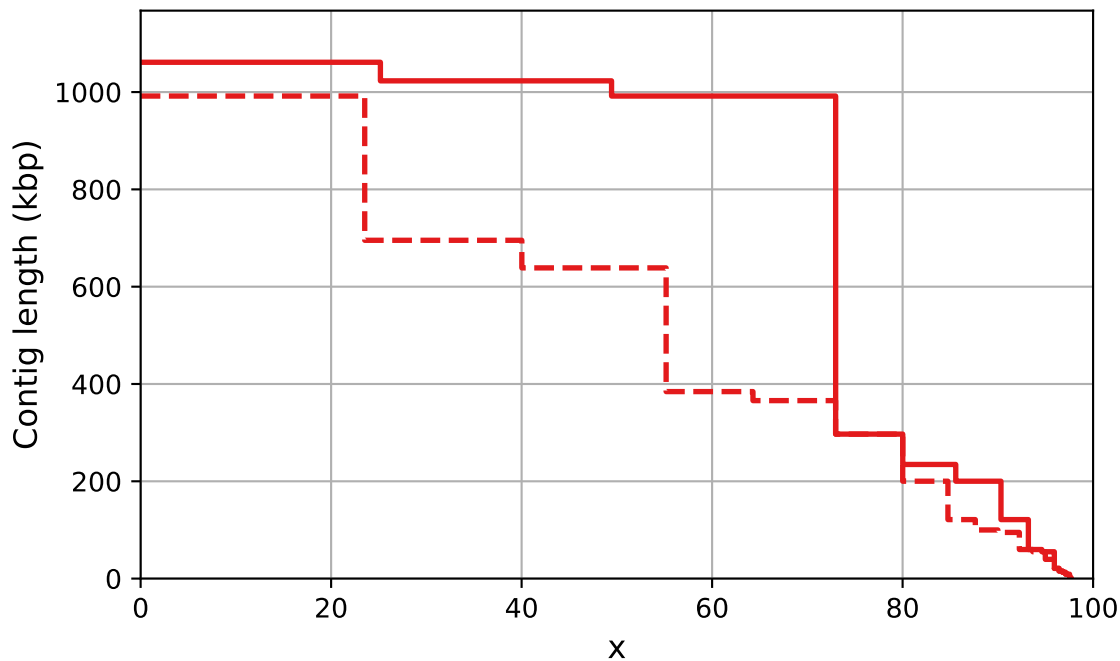
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

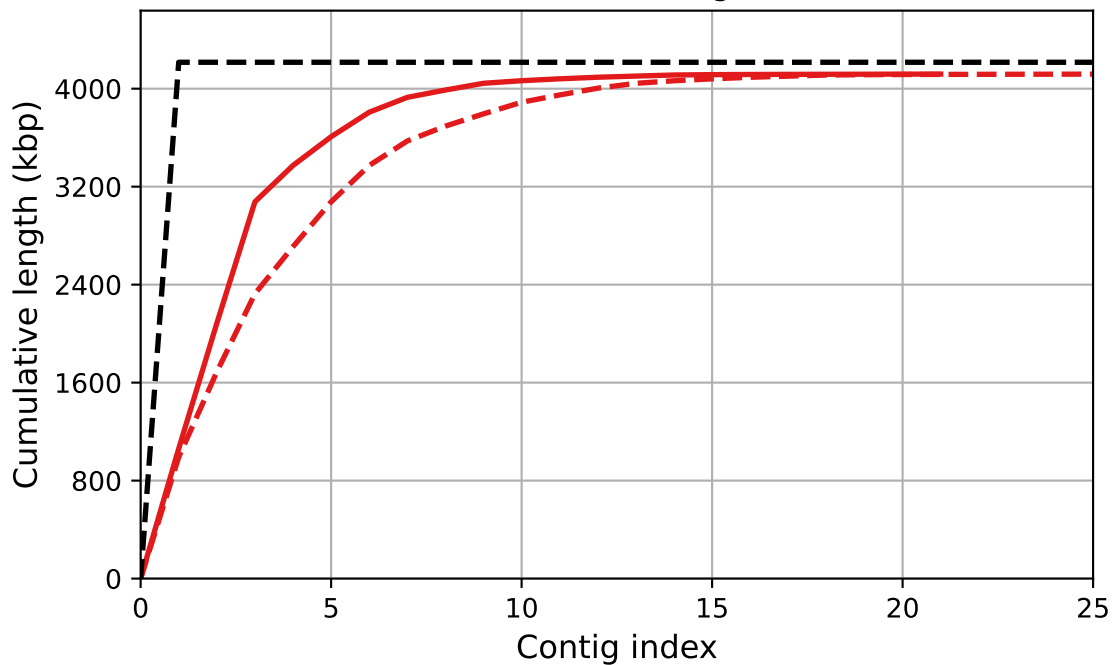
NGx



PAdes_on_data_2_and_data_1_Scaffolds

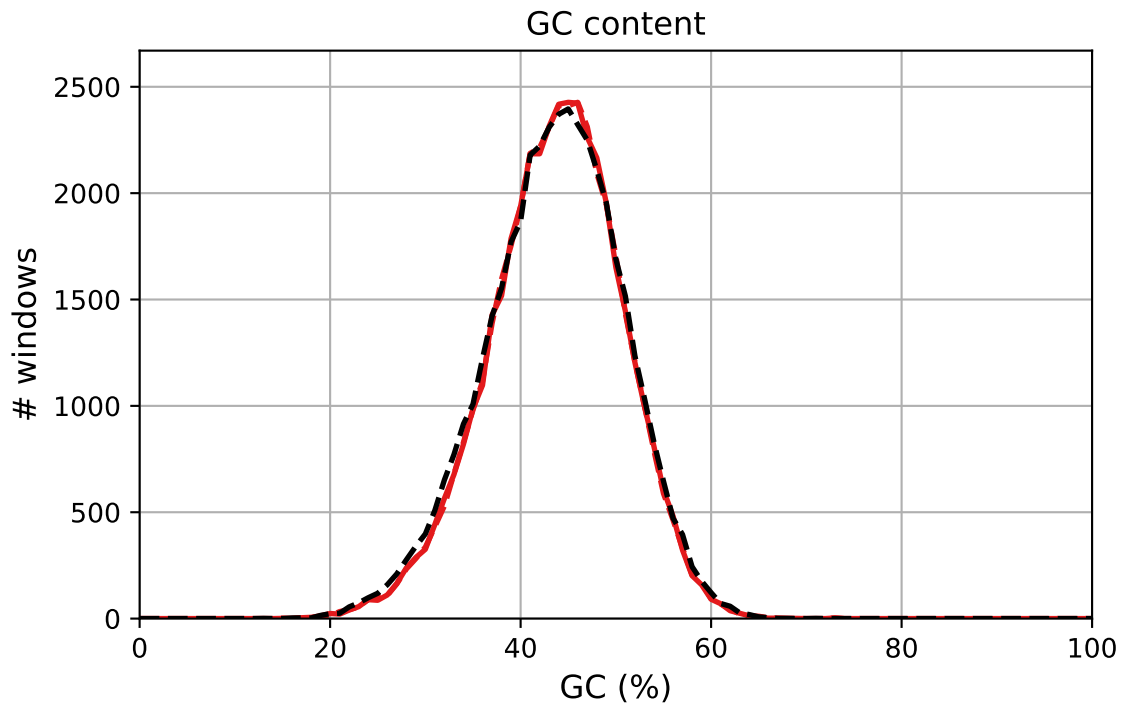
SPAdes_on_data_2_and_data_1_Scaffolds

Cumulative length



_data_2_and_data_1__Scaffolds

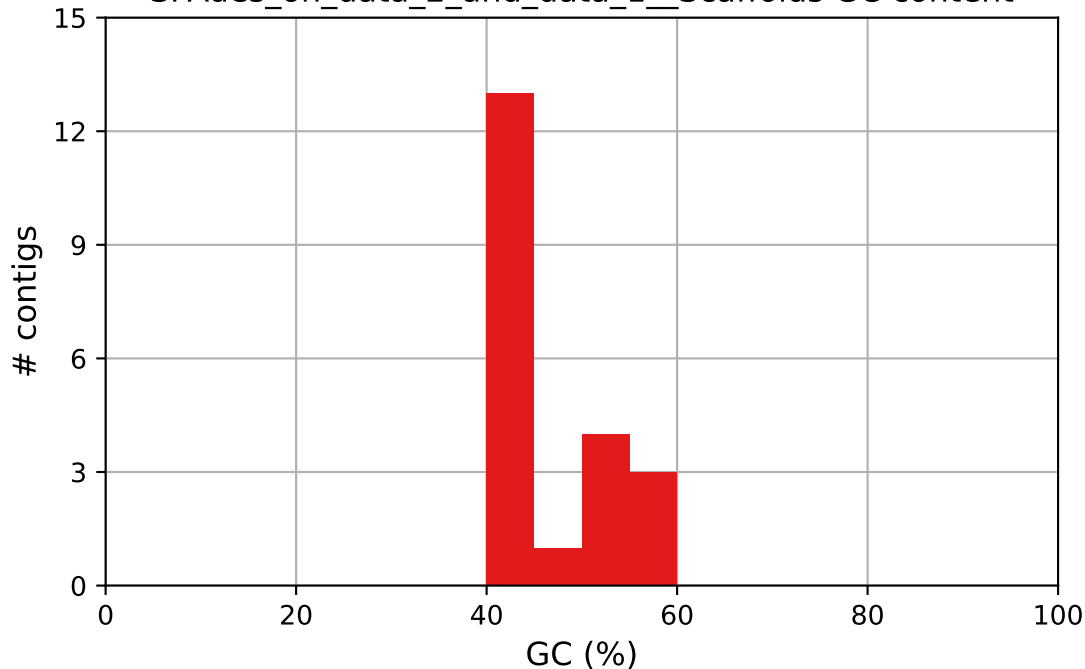
-- SPAdes_on_data_2_and_data_1__Scaffolds_broken



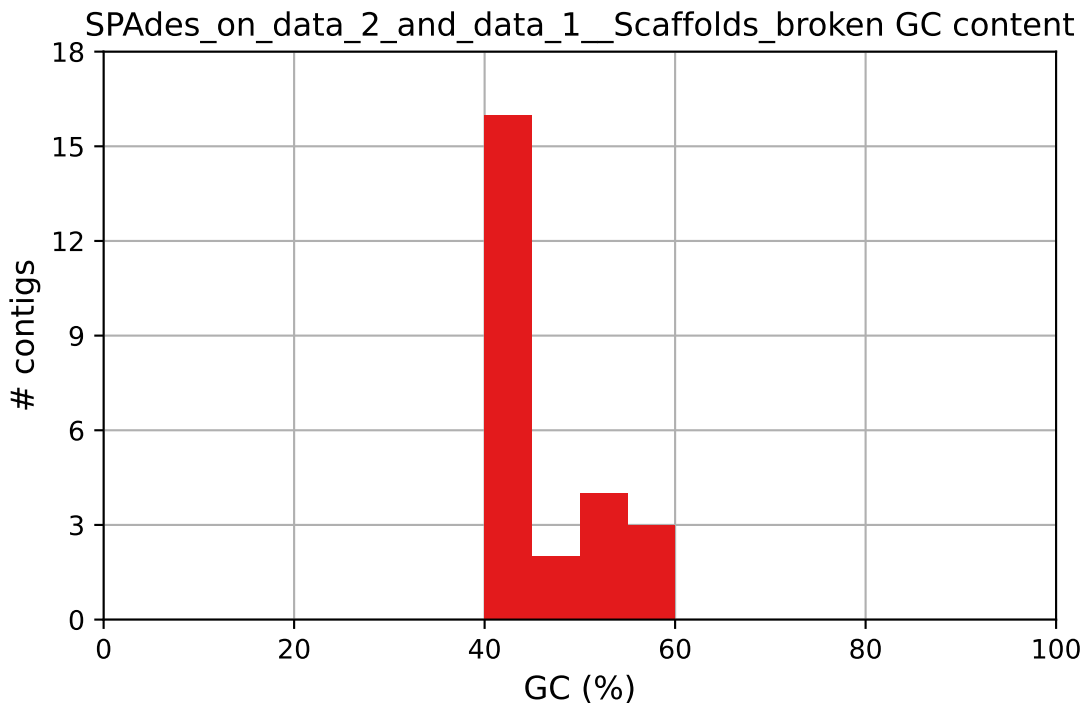
_data_2_and_data_1__Scaffolds

-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

SPAdes_on_data_2_and_data_1__Scaffolds GC content

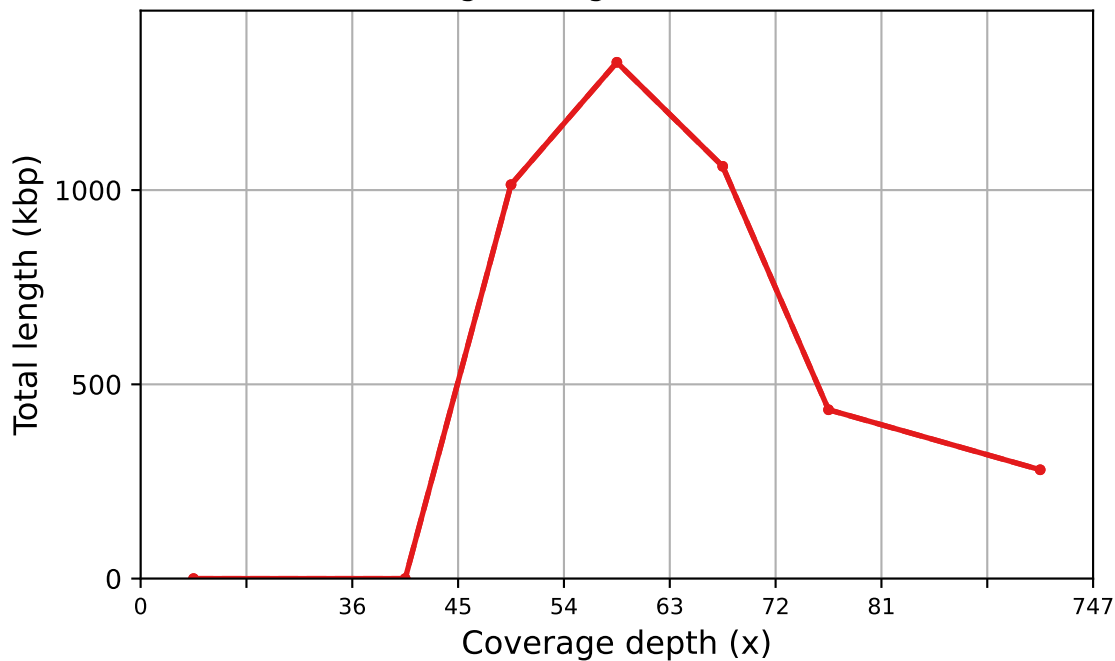


SPAdes_on_data_2_and_data_1__Scaffolds



SPAdes_on_data_2_and_data_1__Scaffolds_broken

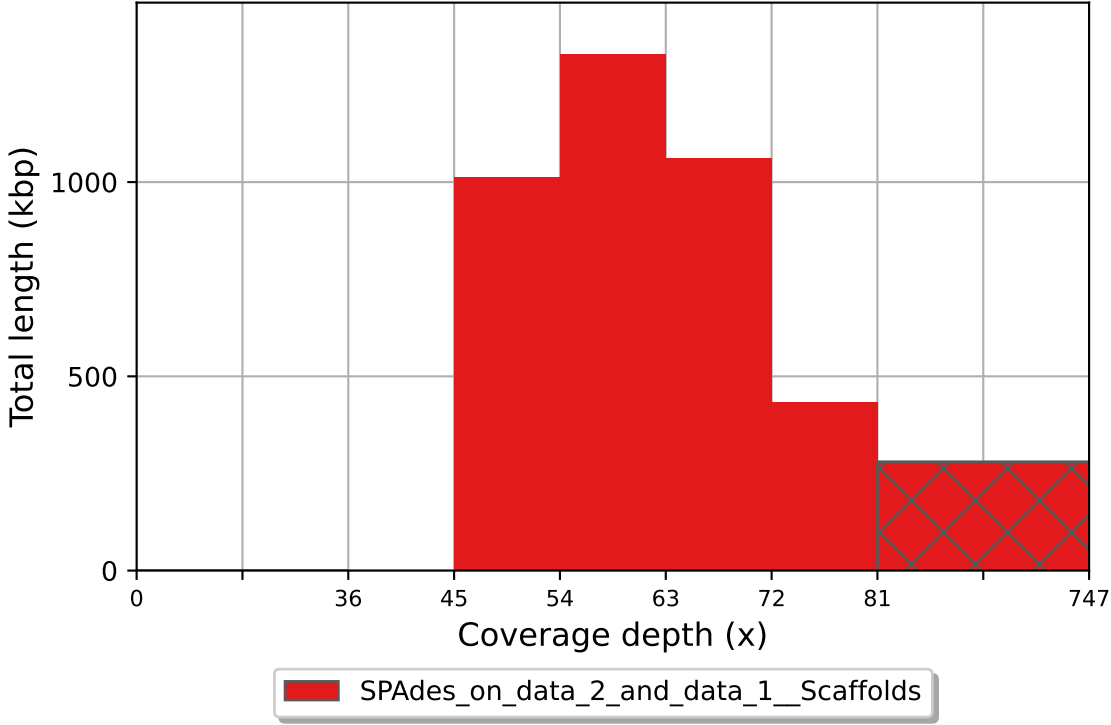
Coverage histogram (bin size: 9x)



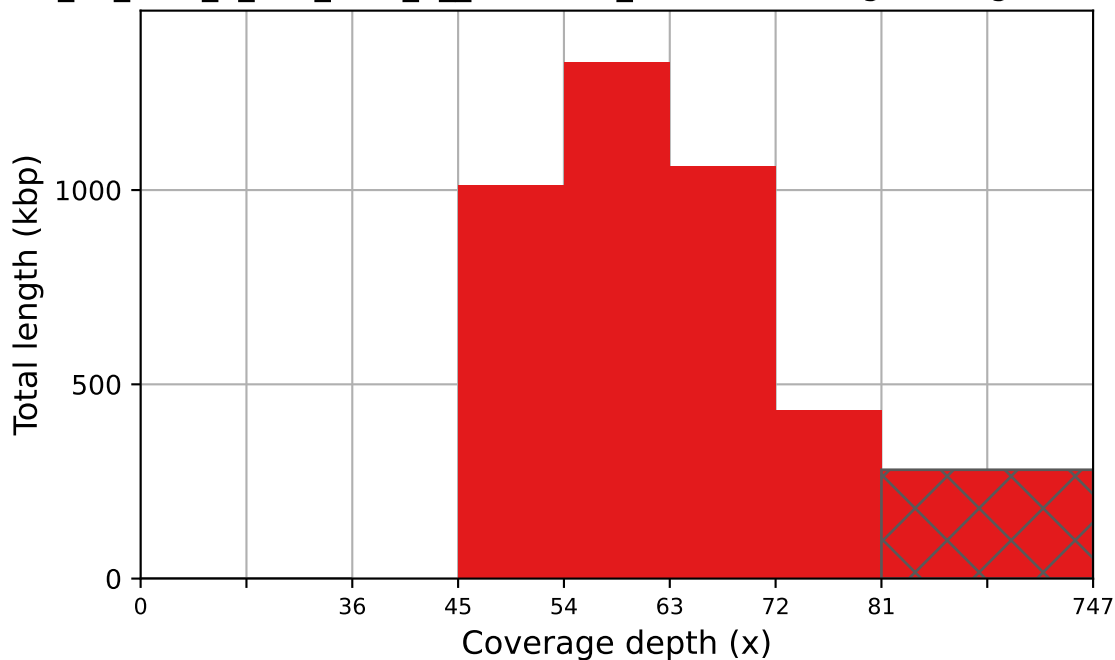
PAdes_on_data_2_and_data_1__Scaffolds

—●— SPAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds coverage histogram (bin size: 9x

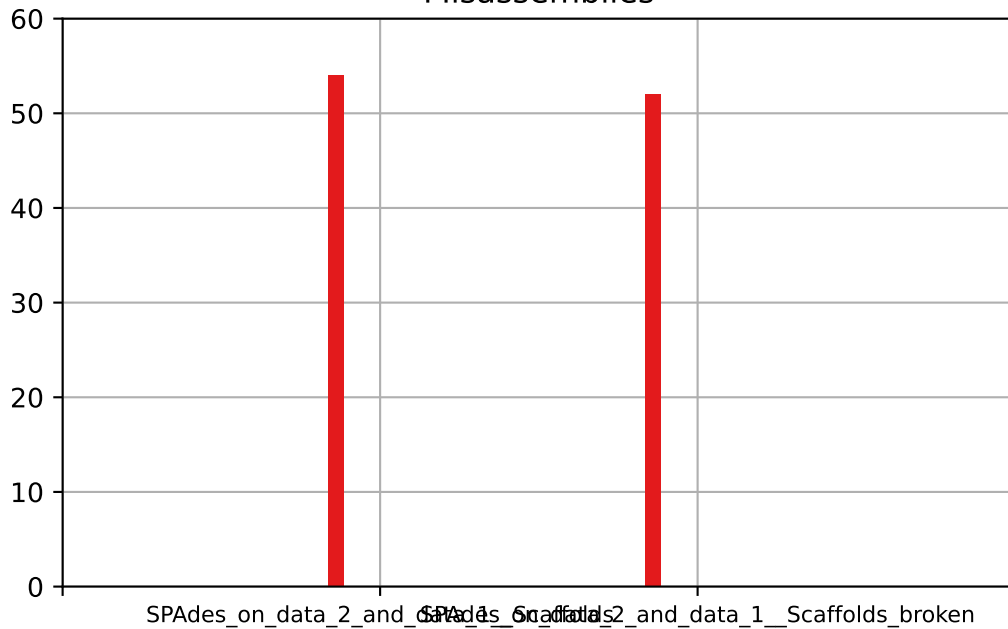


SPAdes_on_data_2_and_data_1__Scaffolds_broken coverage histogram (bin size

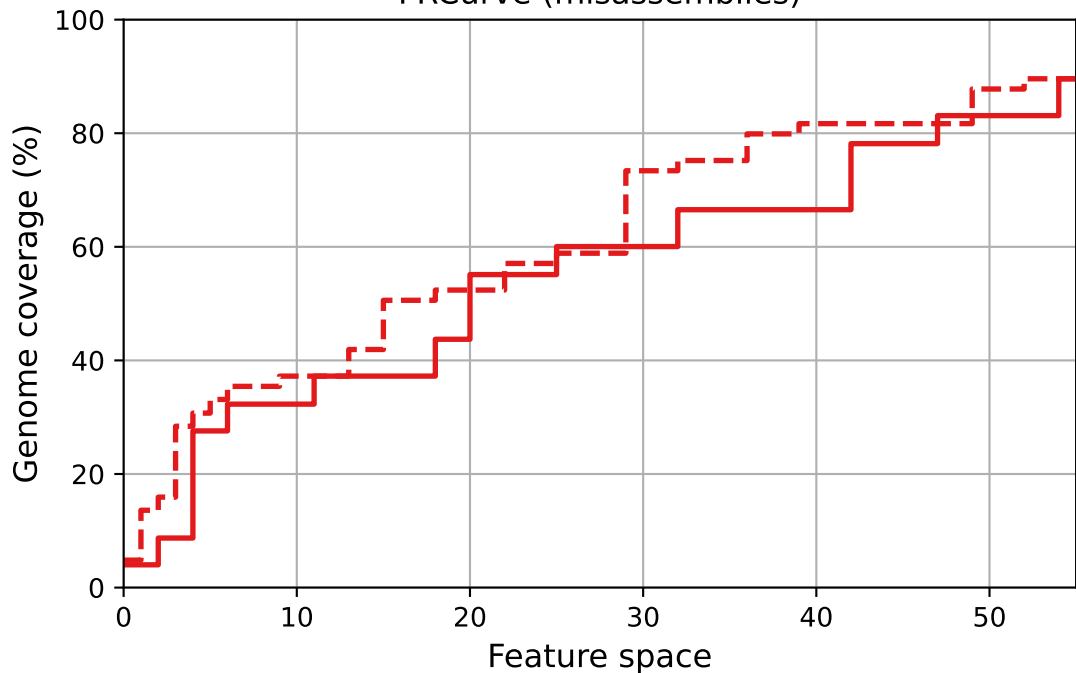


SPAdes_on_data_2_and_data_1__Scaffolds_broken

Misassemblies



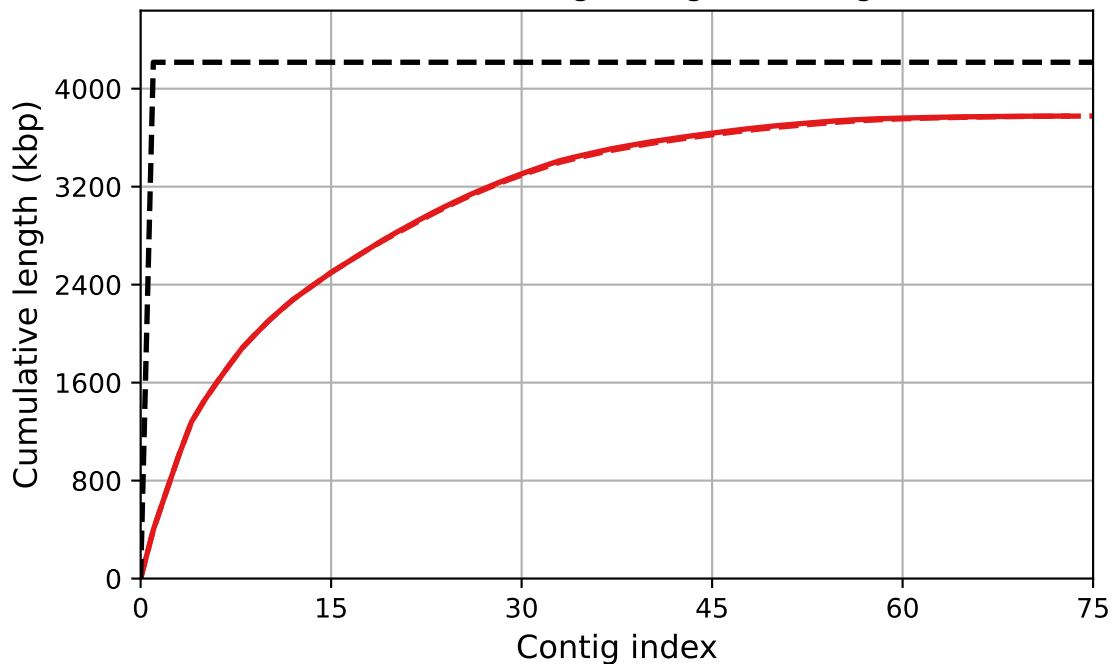
FRCurve (misassemblies)



PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

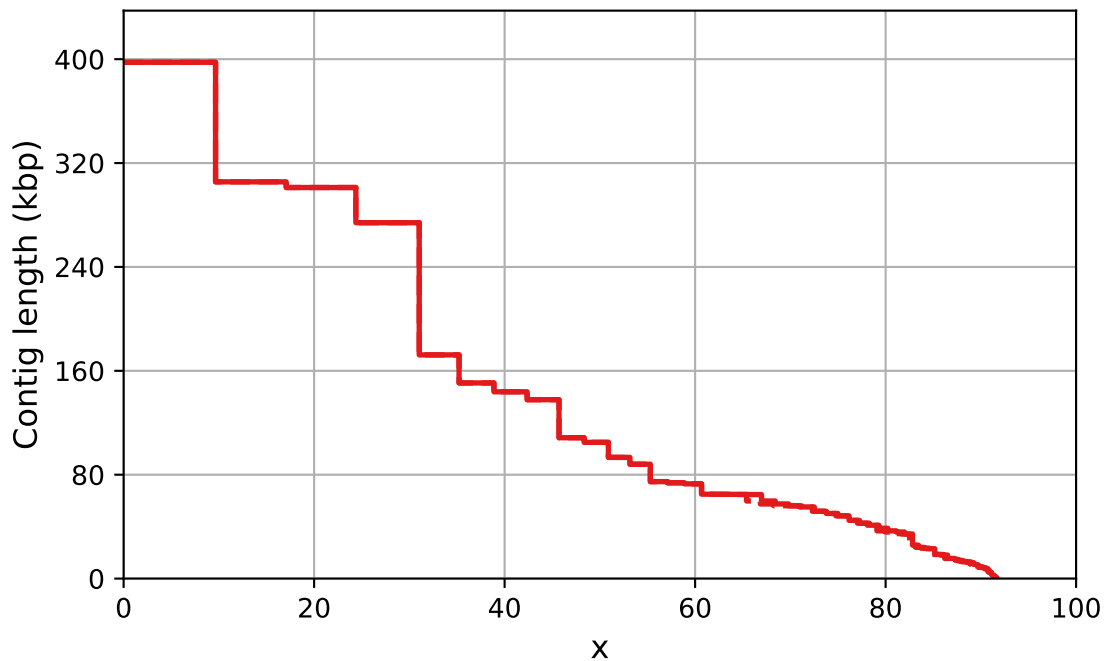
Cumulative length (aligned contigs)



_data_2_and_data_1__Scaffolds

-- SPAdes_on_data_2_and_data_1__Scaffolds_broken

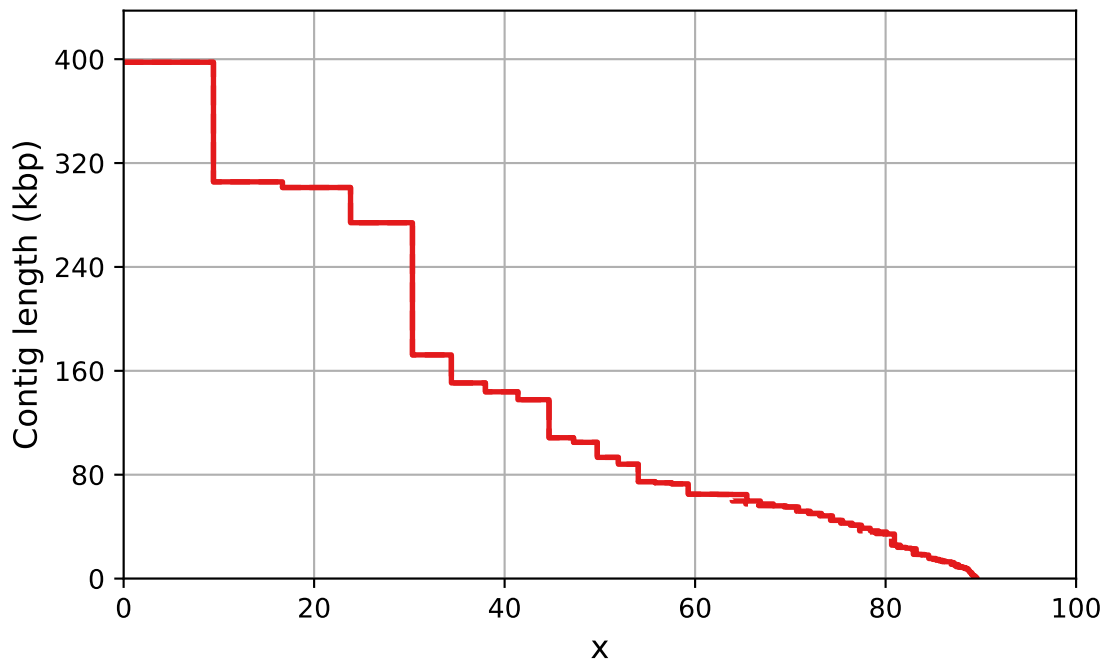
NAx



PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

NGAx

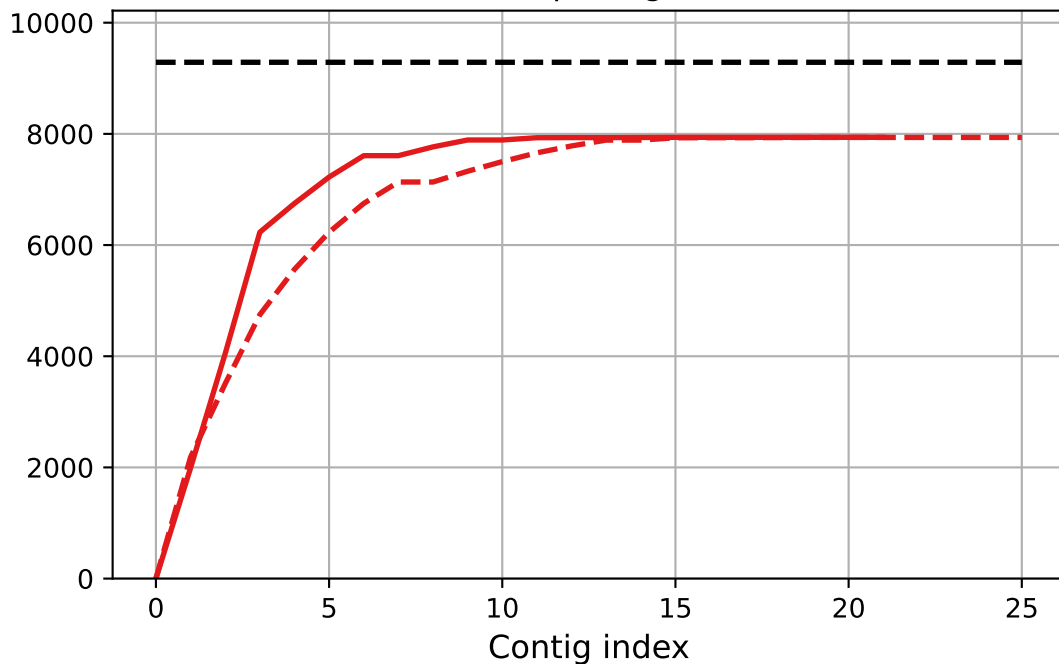


PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

Cumulative # complete genomic features

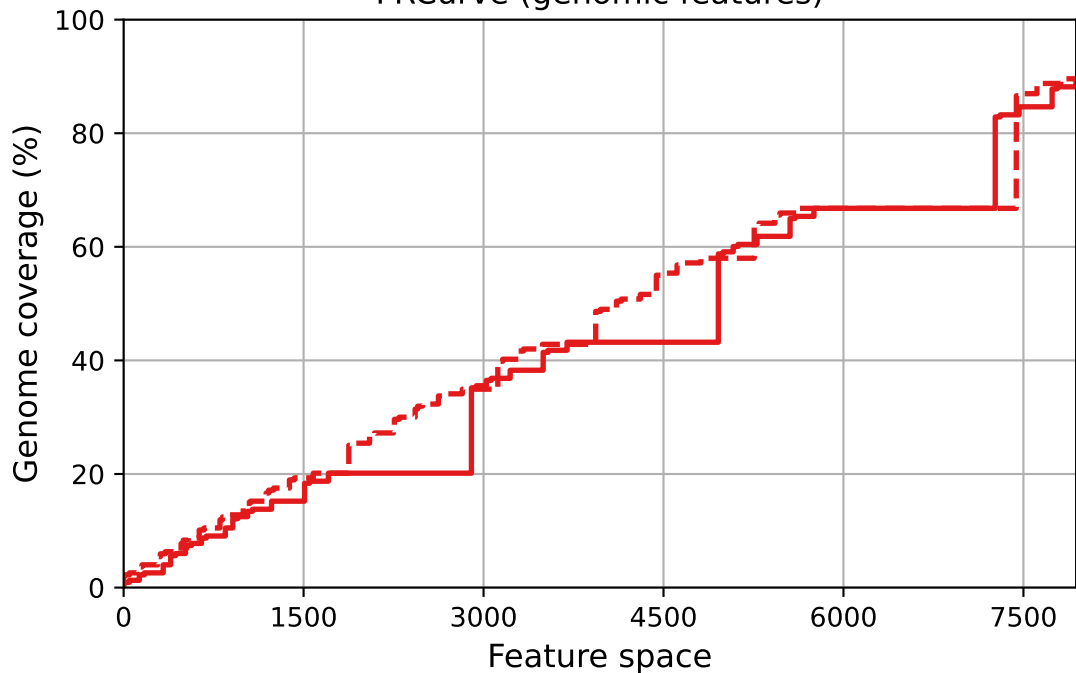
Cumulative # complete genomic features



data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds_broken

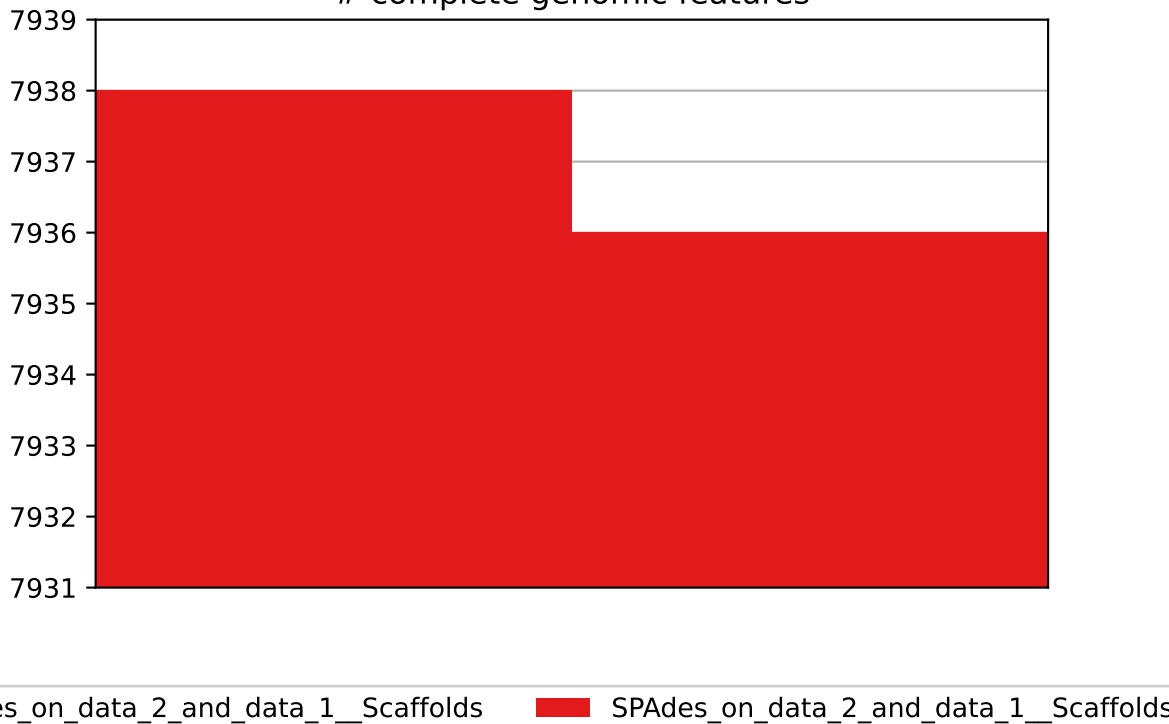
FRCurve (genomic features)



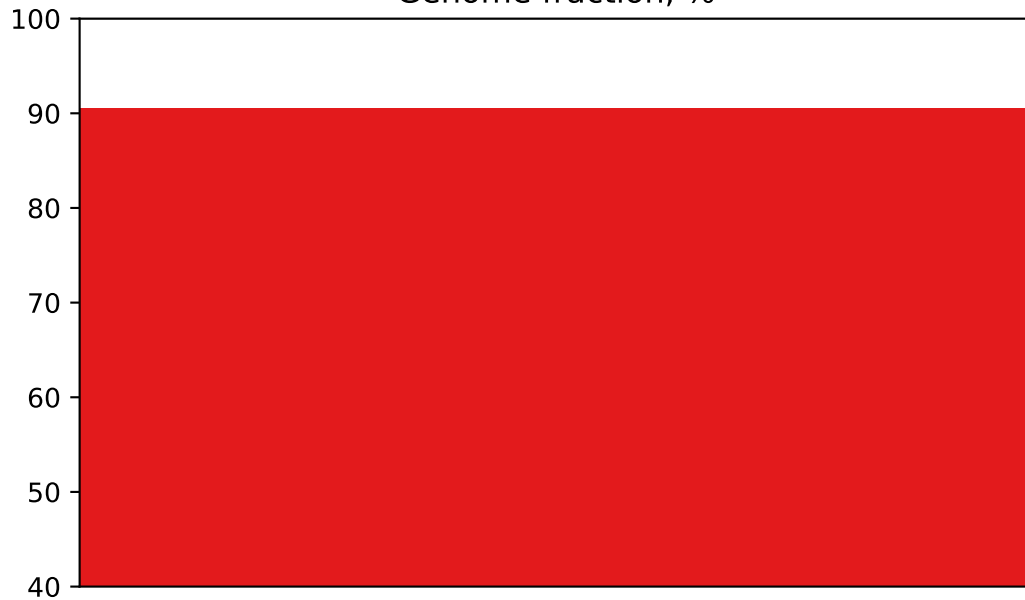
PAdes_on_data_2_and_data_1__Scaffolds

SPAdes_on_data_2_and_data_1__Scaffolds

complete genomic features



Genome fraction, %



PAdes_on_data_2_and_data_1__Scaffolds



SPAdes_on_data_2_and_data_1__Scaffolds