

Report

	SPAdes_on_data_1_and_data_2__Scaffolds	SPAdes_on_data_1_and_data_2__Scaffolds_broken
# contigs (>= 0 bp)	520	-
# contigs (>= 1000 bp)	89	98
Total length (>= 0 bp)	4155498	-
Total length (>= 1000 bp)	4055234	4054164
# contigs	99	109
Largest contig	284620	245272
Total length	4062047	4061047
Reference length	4299632	4299632
GC (%)	43.32	43.32
Reference GC (%)	43.35	43.35
N50	107674	85683
NG50	103100	76609
N90	32404	28350
NG90	15489	15278
auN	114356.7	97440.9
auNG	108037.7	92033.9
L50	13	15
LG50	14	17
L90	41	47
LG90	50	57
# misassemblies	60	57
# misassembled contigs	32	33
Misassembled contigs length	2364792	2127927
# local misassemblies	27	26
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	1	2
# unaligned contigs	35 + 41 part	39 + 47 part
Unaligned length	504222	504307
Genome fraction (%)	83.549	83.549
Duplication ratio	1.000	1.000
# N's per 100 kbp	24.62	0.00
# mismatches per 100 kbp	1241.18	1241.28
# indels per 100 kbp	44.90	44.85
# genomic features	7284 + 184 part	7280 + 188 part
# predicted rRNA genes	3 + 0 part	3 + 0 part
Largest alignment	241424	241424
Total aligned length	3552517	3552233
NA50	44403	44292
NGA50	43313	42728
NA90	-	-
NGA90	-	-
auNA	66055.7	63981.9
auNGA	62405.7	60431.5
LA50	24	25
LGA50	26	27
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

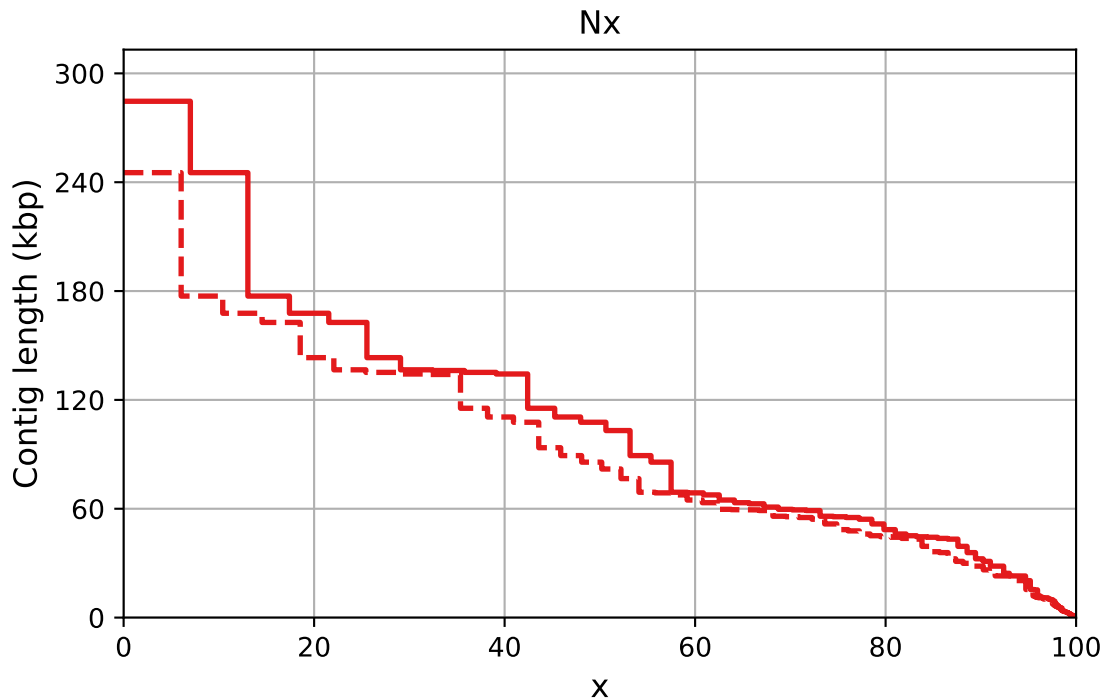
	SPAdes_on_data_1_and_data_2_Scaffolds	SPAdes_on_data_1_and_data_2_Scaffolds_broken
# misassemblies	60	57
# contig misassemblies	57	57
# c. relocations	56	56
# c. translocations	1	1
# c. inversions	0	0
# scaffold misassemblies	3	0
# s. relocations	3	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	32	33
Misassembled contigs length	2364792	2127927
# local misassemblies	27	26
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	1	2
# mismatches	44093	44093
# indels	1595	1593
# indels (<= 5 bp)	1420	1420
# indels (> 5 bp)	175	173
Indels length	7369	7112

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	35	39
Fully unaligned length	165018	165088
# partially unaligned contigs	41	47
Partially unaligned length	339204	339219
# N's	1000	0

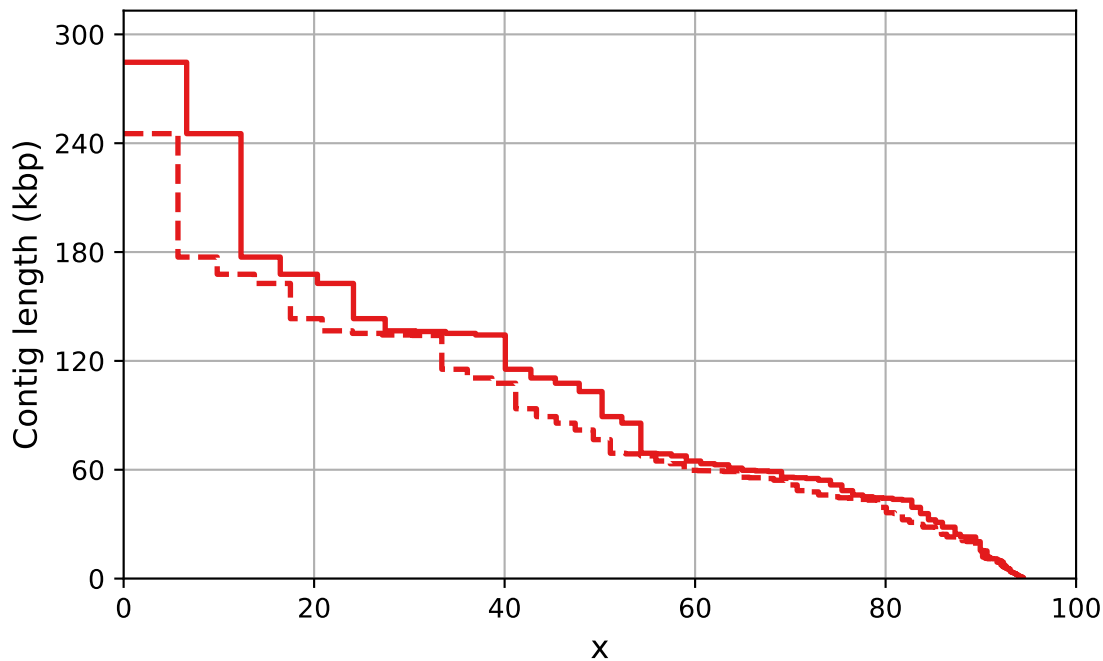
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



PAdes_on_data_1_and_data_2_Scaffolds

SPAdes_on_data_1_and_data_2_Scaffolds

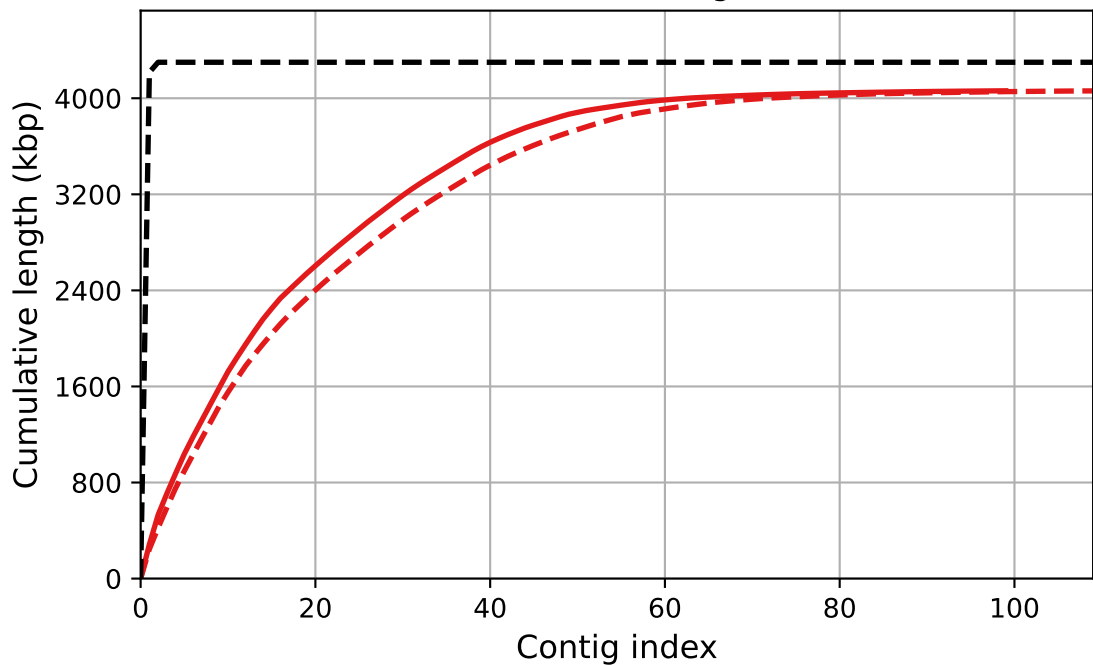
NGx



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

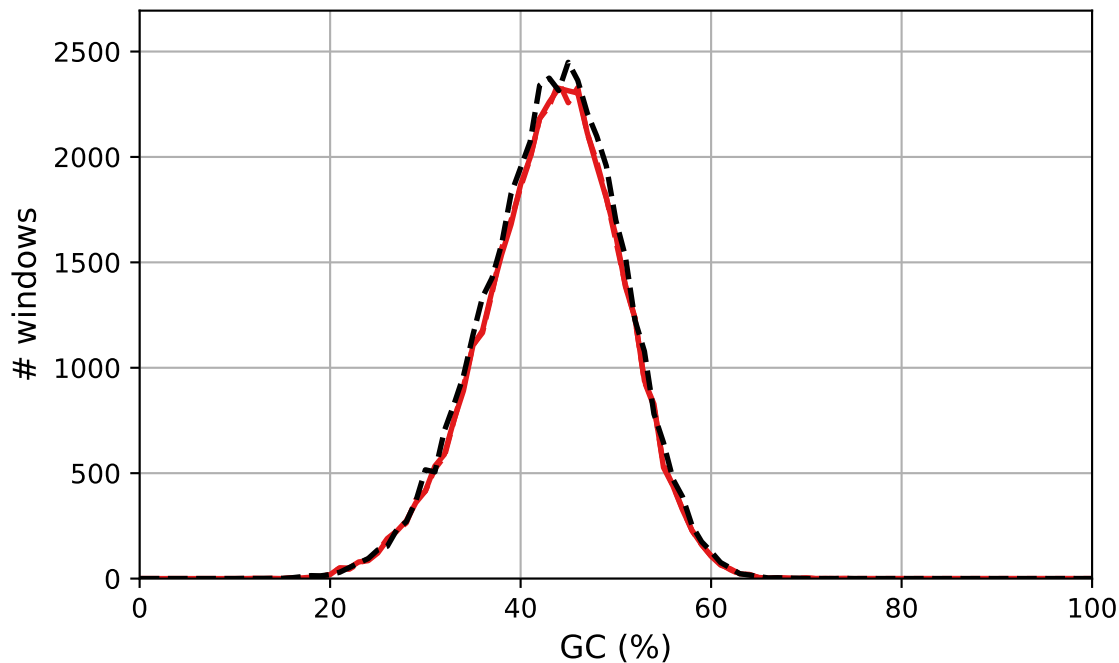
Cumulative length



data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken

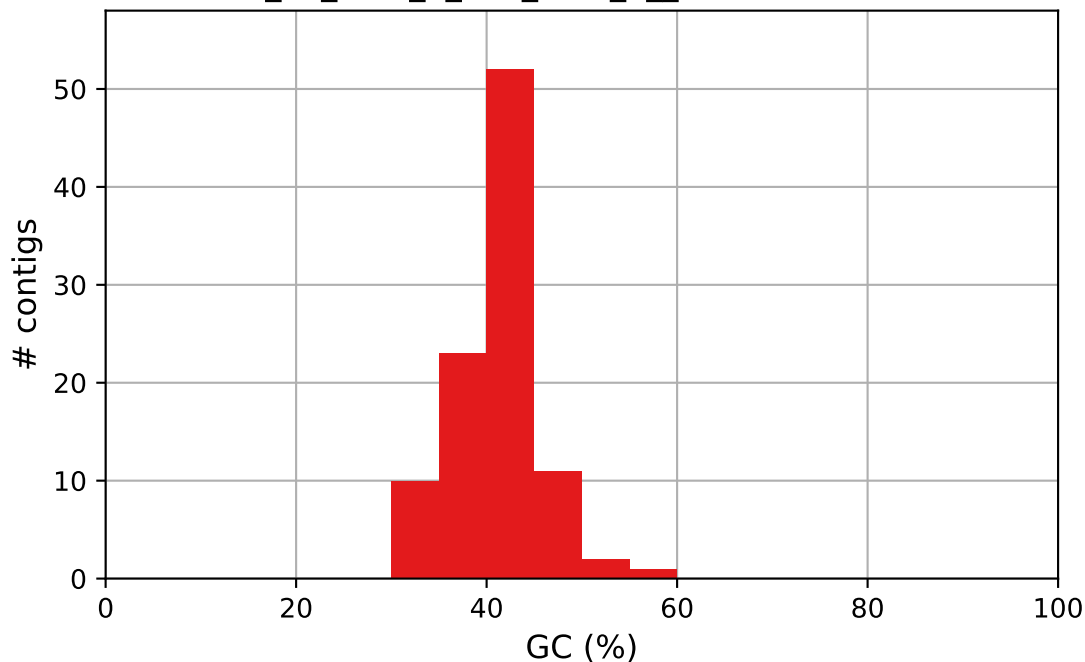
GC content



_data_1_and_data_2__Scaffolds

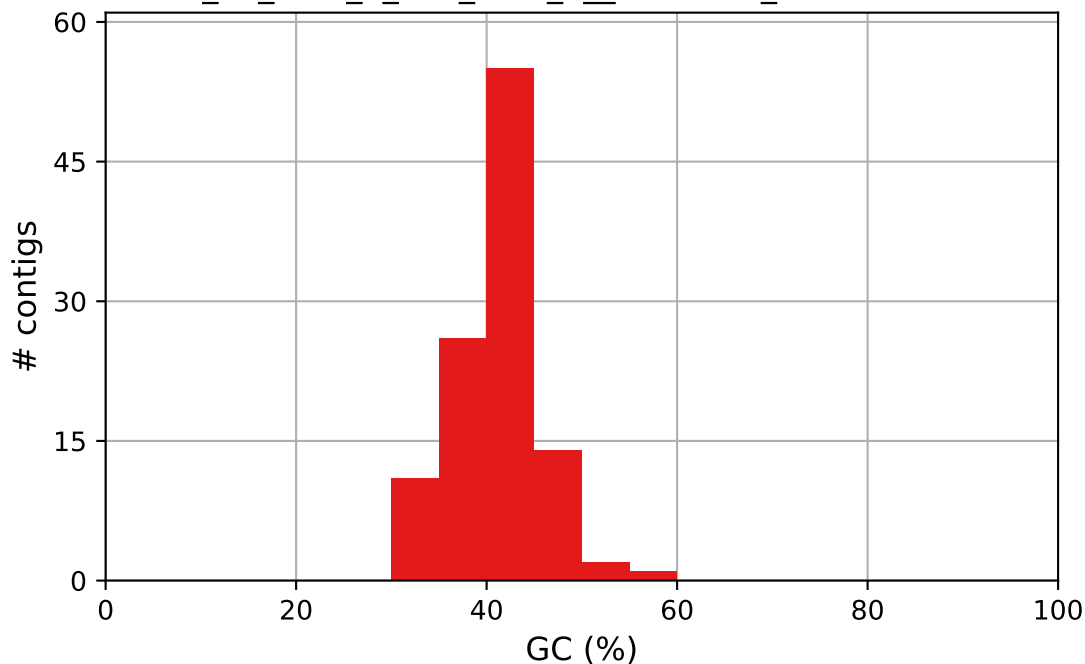
-- SPAdes_on_data_1_and_data_2__Scaffolds_broken

SPAdes_on_data_1_and_data_2__Scaffolds GC content



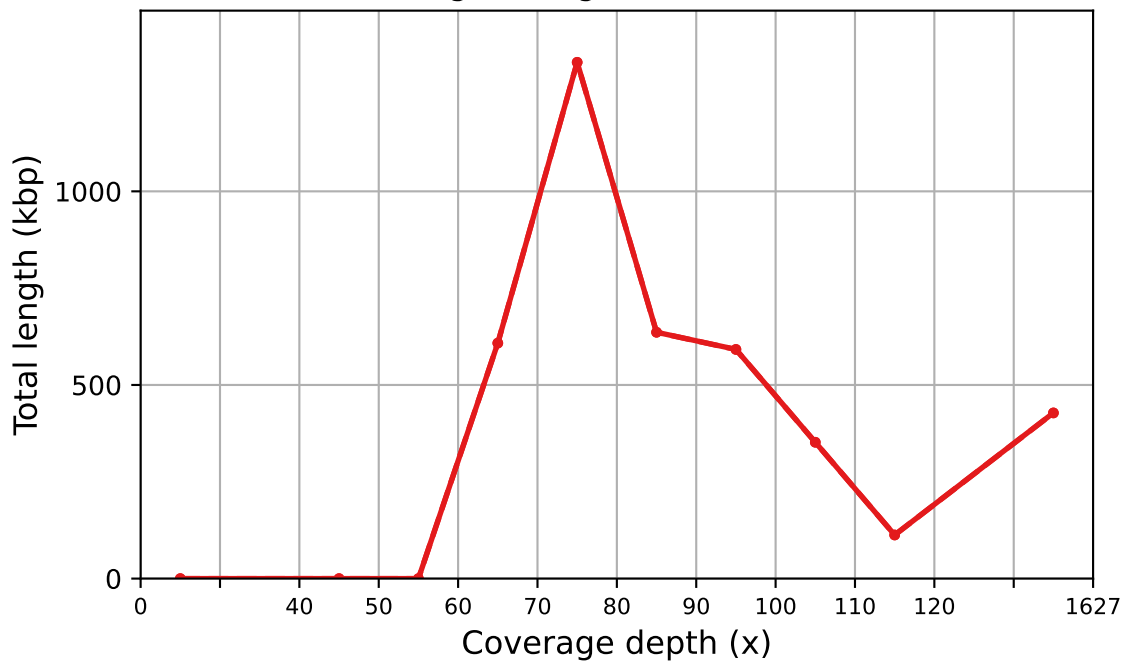
SPAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken GC content



SPAdes_on_data_1_and_data_2__Scaffolds_broken

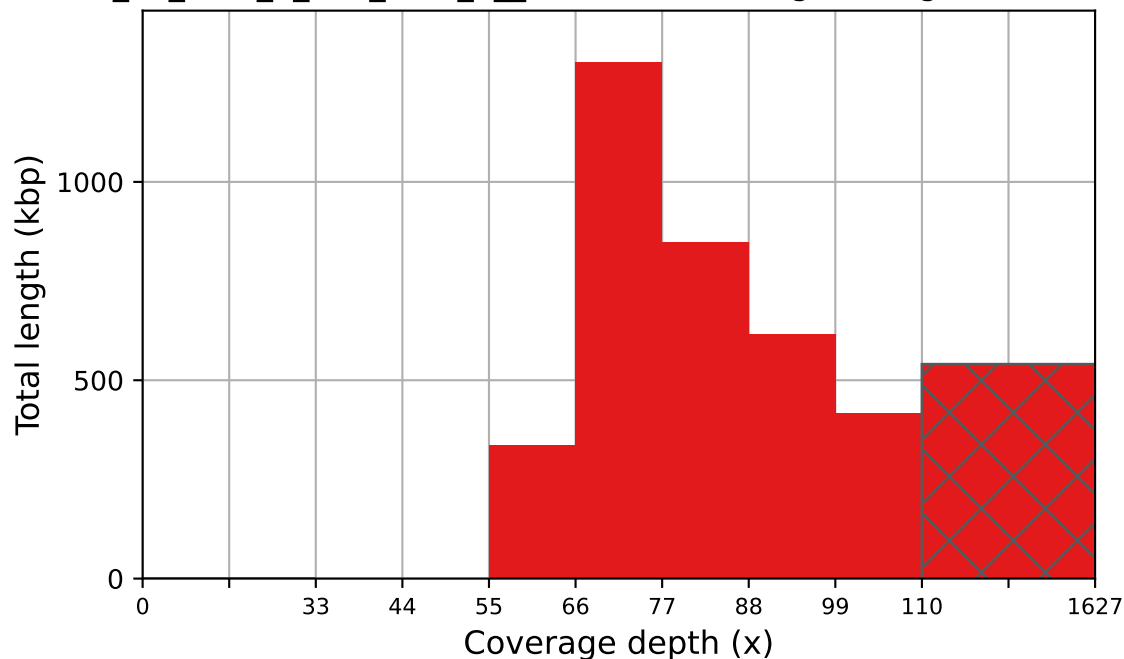
Coverage histogram (bin size: 10x)



PAdes_on_data_1_and_data_2_Scaffolds

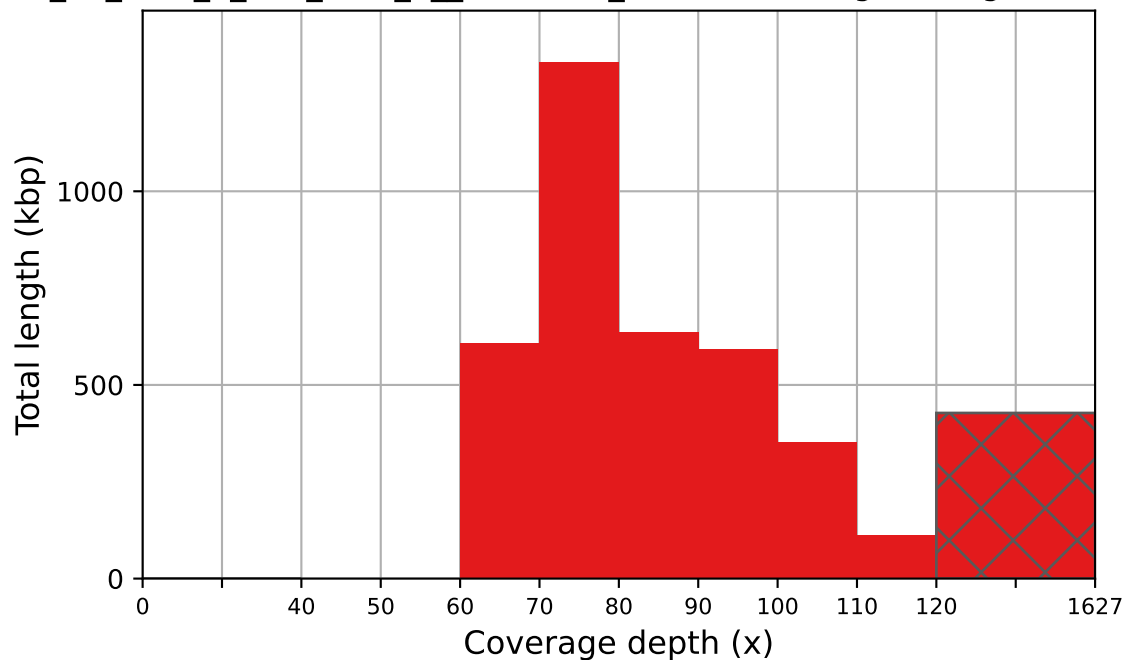
—●— SPAdes_on_data_1_and_data_2_Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds coverage histogram (bin size: 11x)



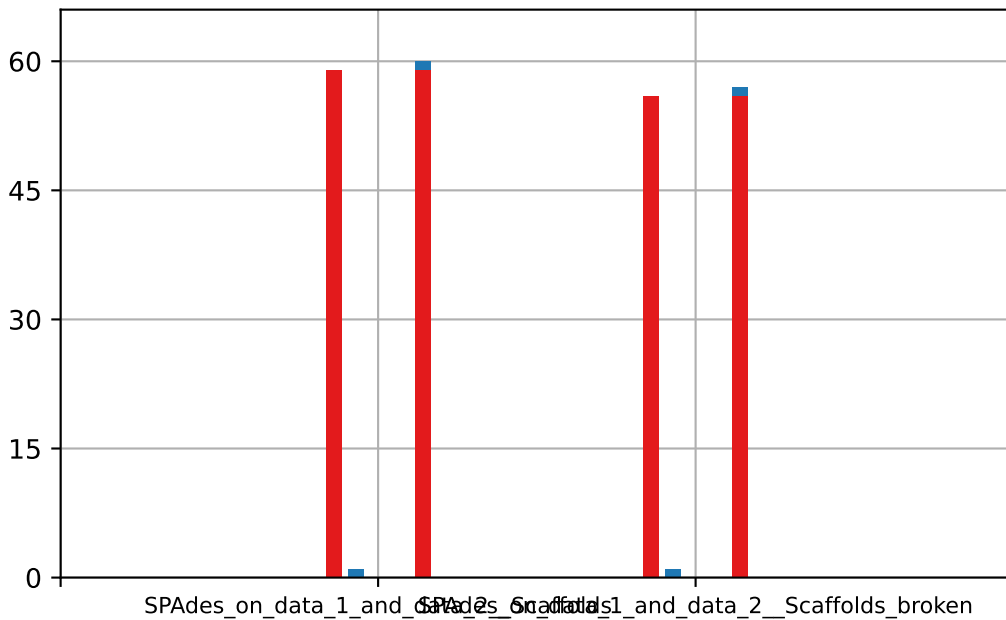
SPAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken coverage histogram (bin size: 10)



SPAdes_on_data_1_and_data_2__Scaffolds_broken

Misassemblies

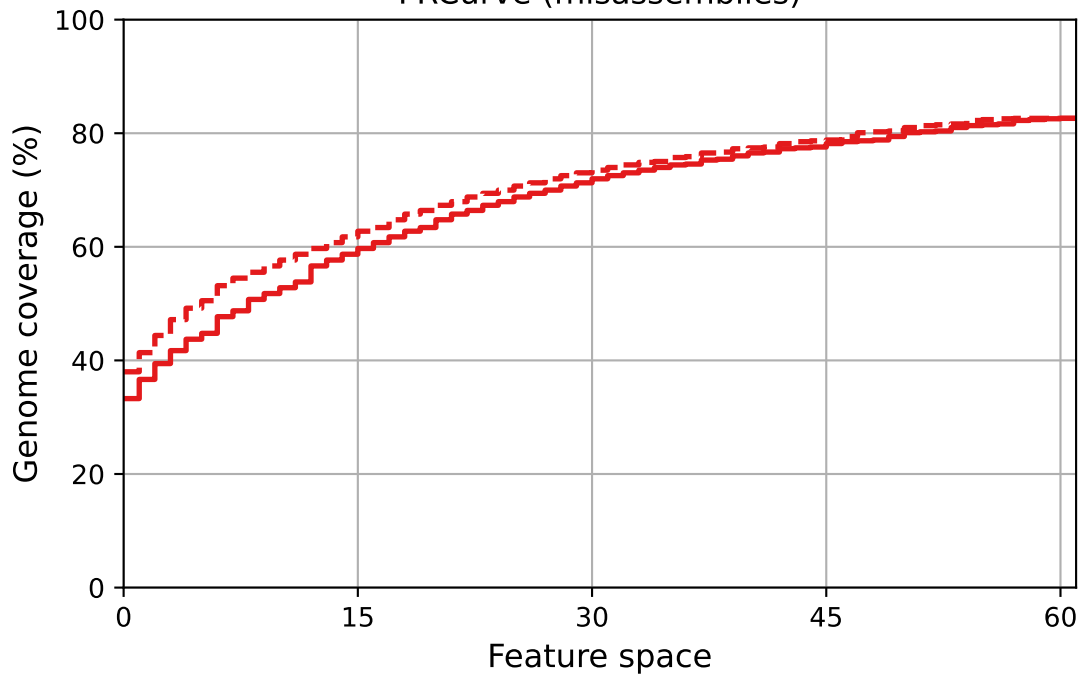


relocations



translocations

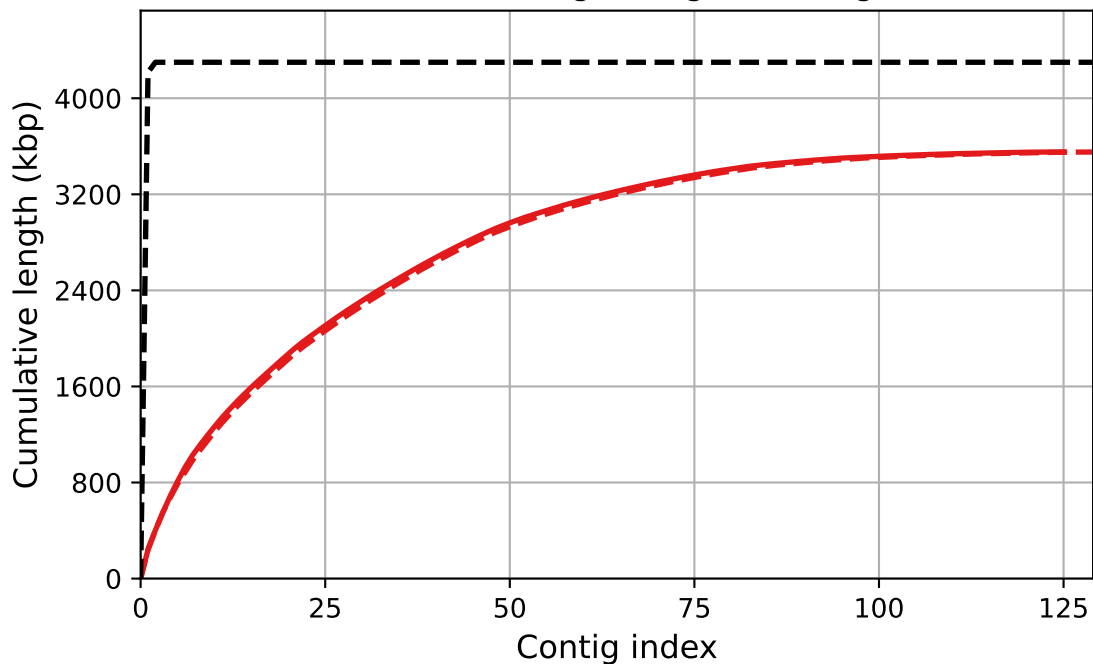
FRCurve (misassemblies)



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

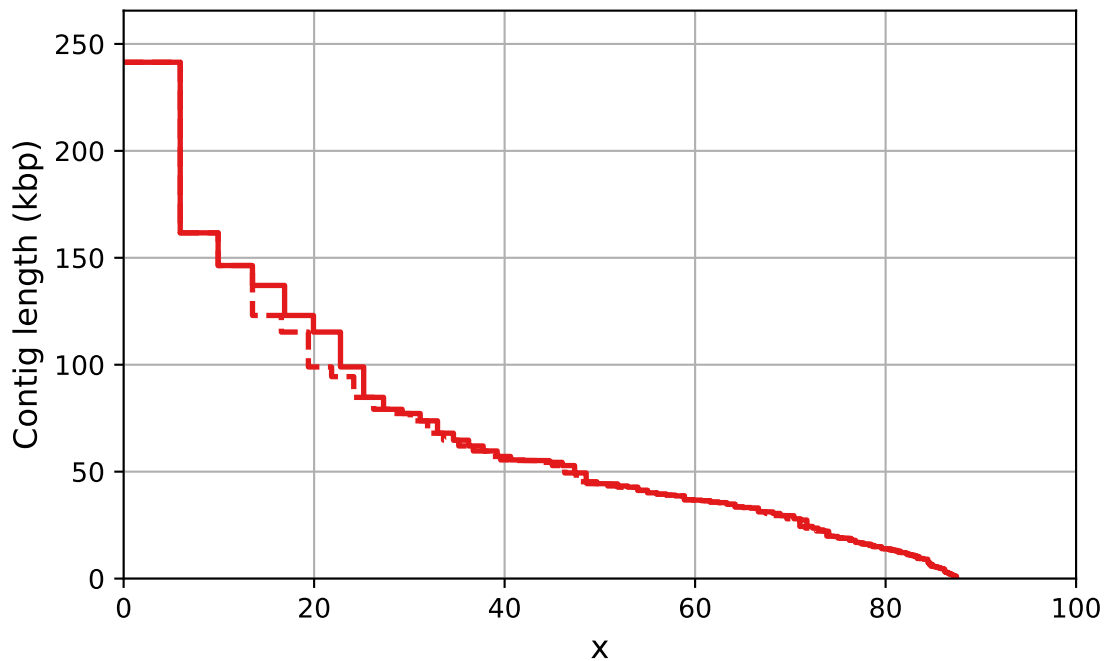
Cumulative length (aligned contigs)



data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds_broken

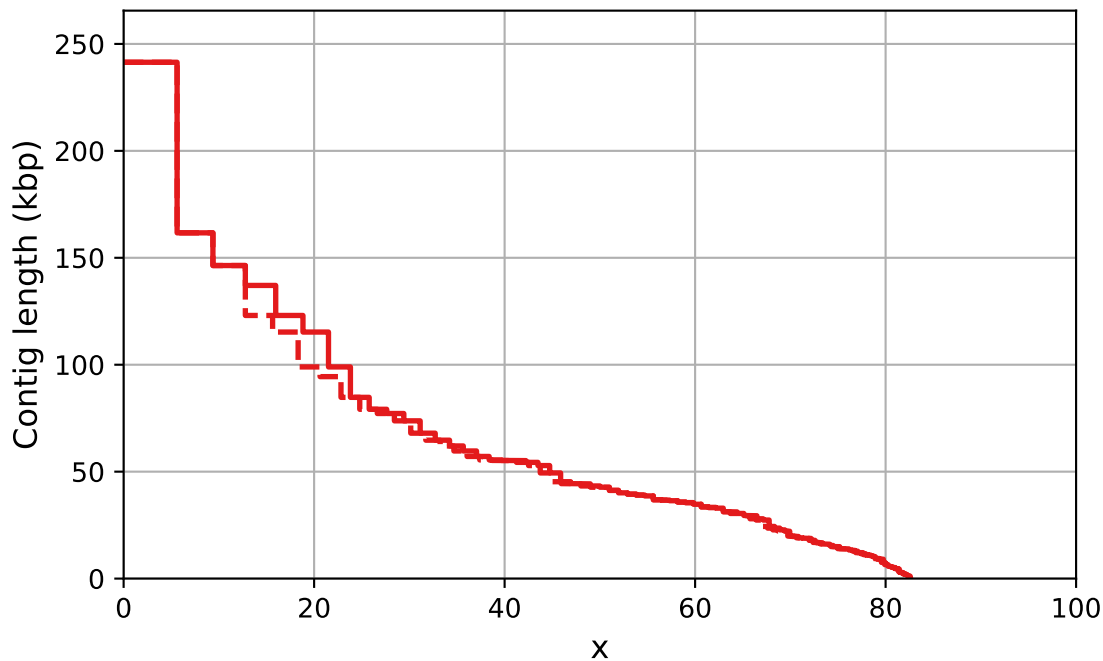
NAx



PAdes_on_data_1_and_data_2__Scaffolds

SPAdes_on_data_1_and_data_2__Scaffolds

NGAx

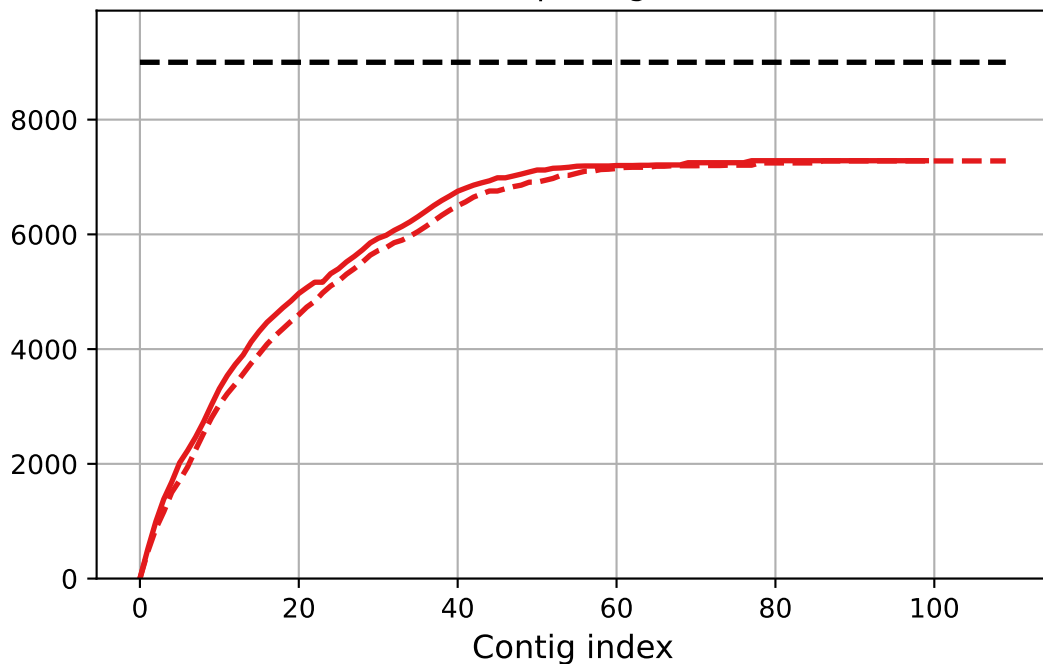


PADES_on_data_1_and_data_2__Scaffolds

-- SPAdes_on_data_1_and_data_2__Scaffolds

Cumulative # complete genomic features

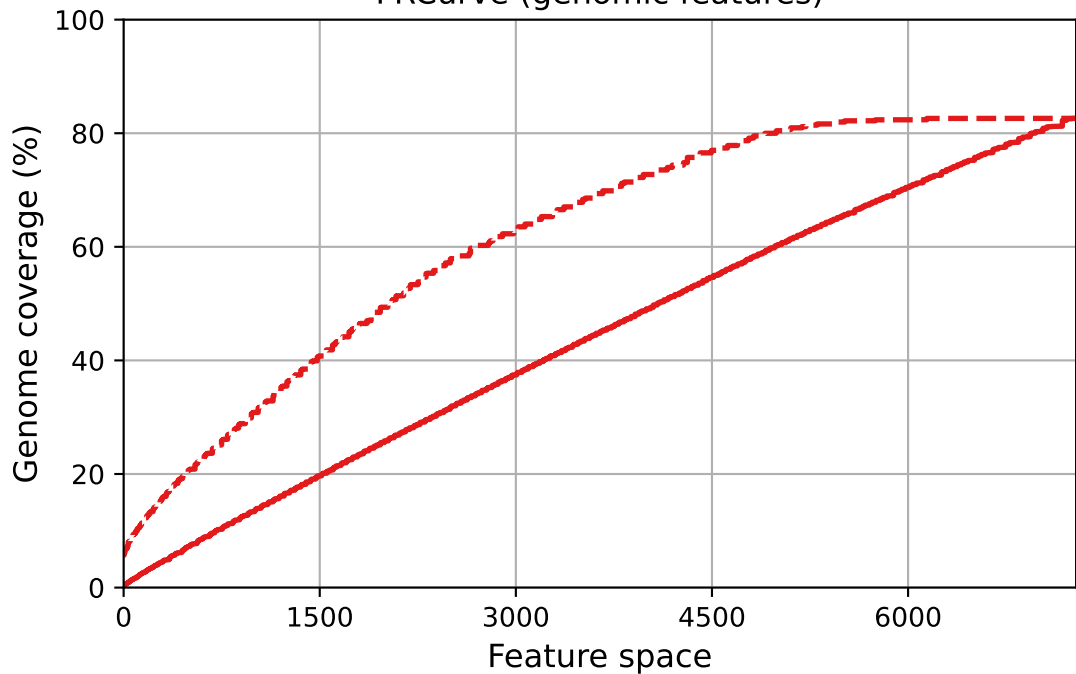
Cumulative # complete genomic features



_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

7285

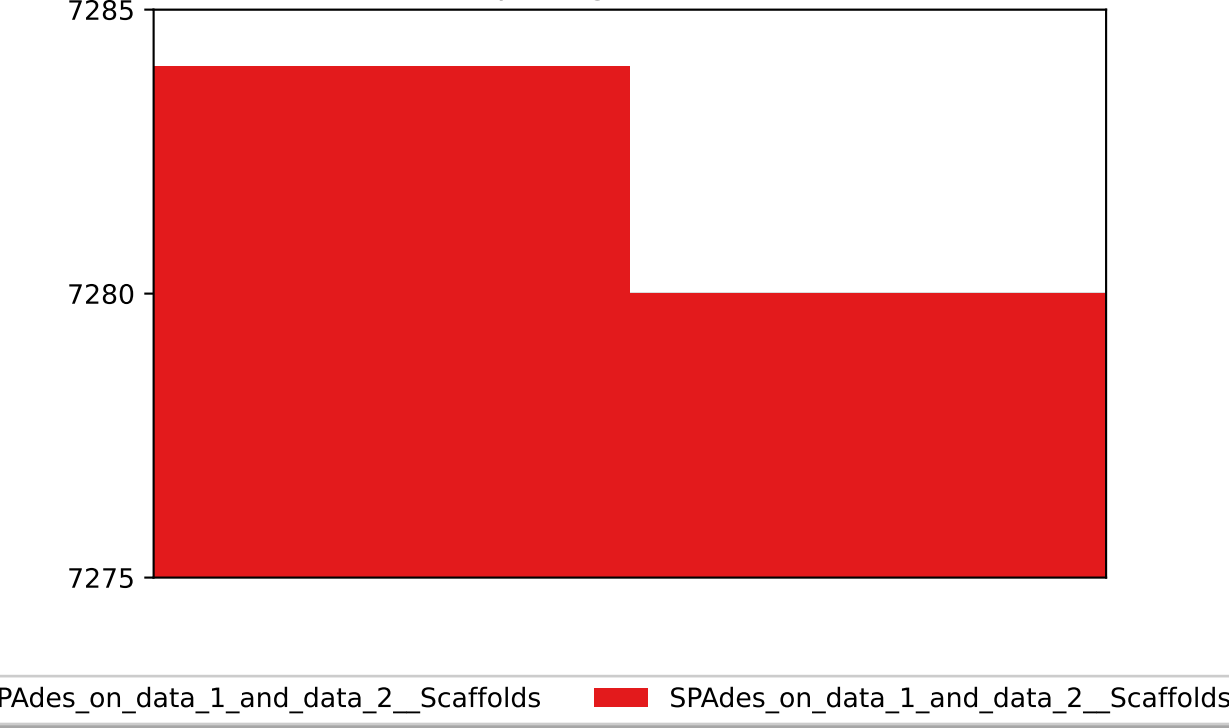
7280

7275

PAdes_on_data_1_and_data_2__Scaffolds



SPAdes_on_data_1_and_data_2__Scaffolds



Genome fraction, %

100

50

PAdes_on_data_1_and_data_2__Scaffolds



SPAdes_on_data_1_and_data_2__Scaffolds