

Report

	SPAdes_on_data_27_and_data_26__Scaffolds	SPAdes_on_data_27_and_data_26__Scaffolds_broken
# contigs (>= 0 bp)	208	-
# contigs (>= 1000 bp)	66	79
Total length (>= 0 bp)	5511966	-
Total length (>= 1000 bp)	5479410	5477978
# contigs	79	93
Largest contig	465607	390831
Total length	5488114	5486804
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	193741	163595
NG50	193741	146373
N90	73396	56140
NG90	49002	40884
auN	219143.0	161297.7
auNG	211653.2	155747.8
L50	10	13
LG50	10	14
L90	28	36
LG90	31	40
# misassemblies	77	75
# misassembled contigs	29	34
Misassembled contigs length	4520761	4160732
# local misassemblies	28	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	2	2
# unaligned contigs	21 + 33 part	22 + 36 part
Unaligned length	689104	687960
Genome fraction (%)	84.760	85.332
Duplication ratio	1.002	1.002
# N's per 100 kbp	23.87	0.00
# mismatches per 100 kbp	685.63	688.24
# indels per 100 kbp	19.33	19.64
# genomic features	9603 + 176 part	9616 + 204 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	205341	205341
Total aligned length	4796180	4795686
NA50	70102	60726
NGA50	69622	59533
NA90	-	-
NGA90	-	-
auNA	80652.4	72883.8
auNGA	77895.8	70376.0
LA50	24	27
LGA50	25	29
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

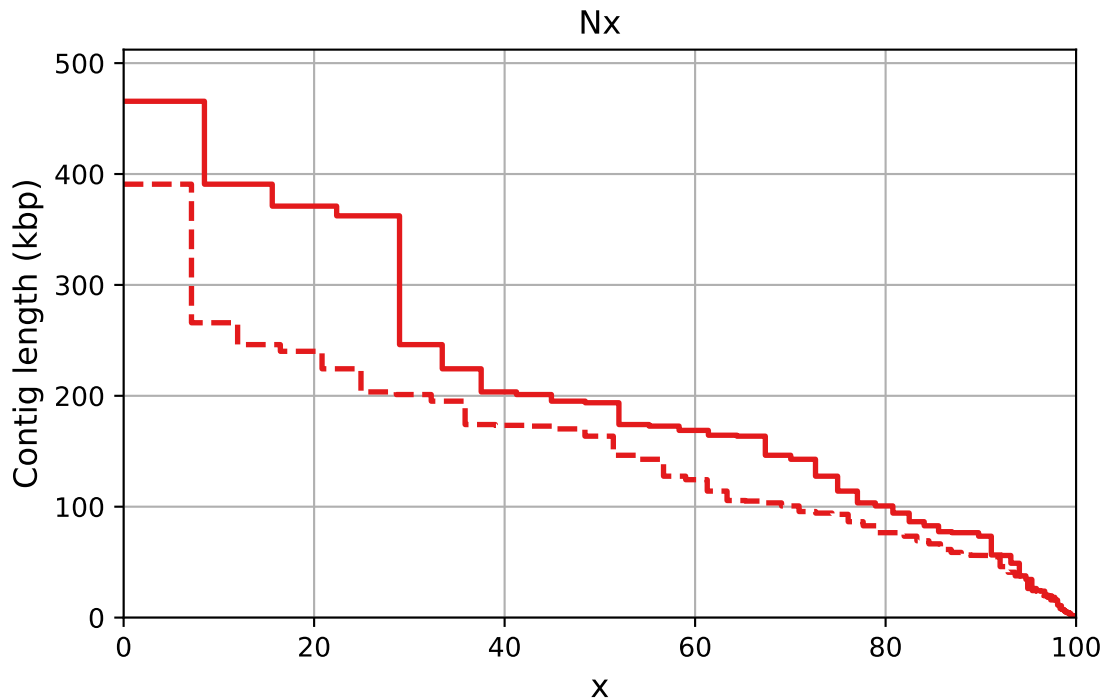
	SPAdes_on_data_27_and_data_26__Scaffolds	SPAdes_on_data_27_and_data_26__Scaffolds_broken
# misassemblies	77	75
# contig misassemblies	75	75
# c. relocations	71	71
# c. translocations	4	4
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	29	34
Misassembled contigs length	4520761	4160732
# local misassemblies	28	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	2	2
# mismatches	32884	33006
# indels	927	942
# indels (<= 5 bp)	833	856
# indels (> 5 bp)	94	86
Indels length	7697	6532

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_27_and_data_26__Scaffolds	SPAdes_on_data_27_and_data_26__Scaffolds_broken
# fully unaligned contigs	21	22
Fully unaligned length	57461	57583
# partially unaligned contigs	33	36
Partially unaligned length	631643	630377
# N's	1310	0

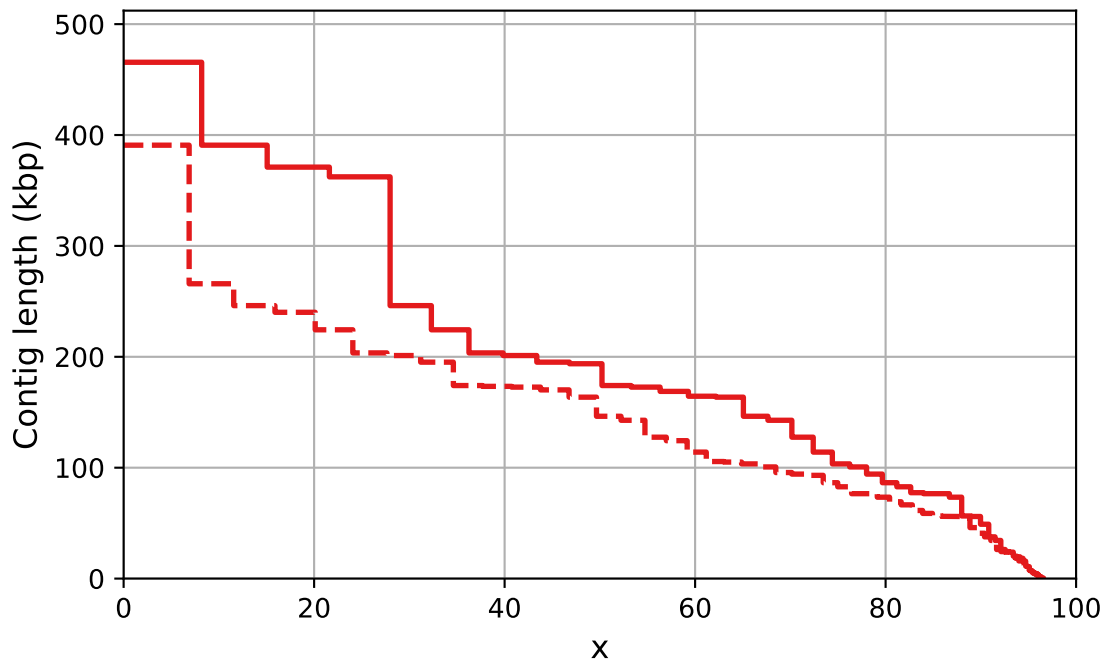
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



des_on_data_27_and_data_26_Scaffolds

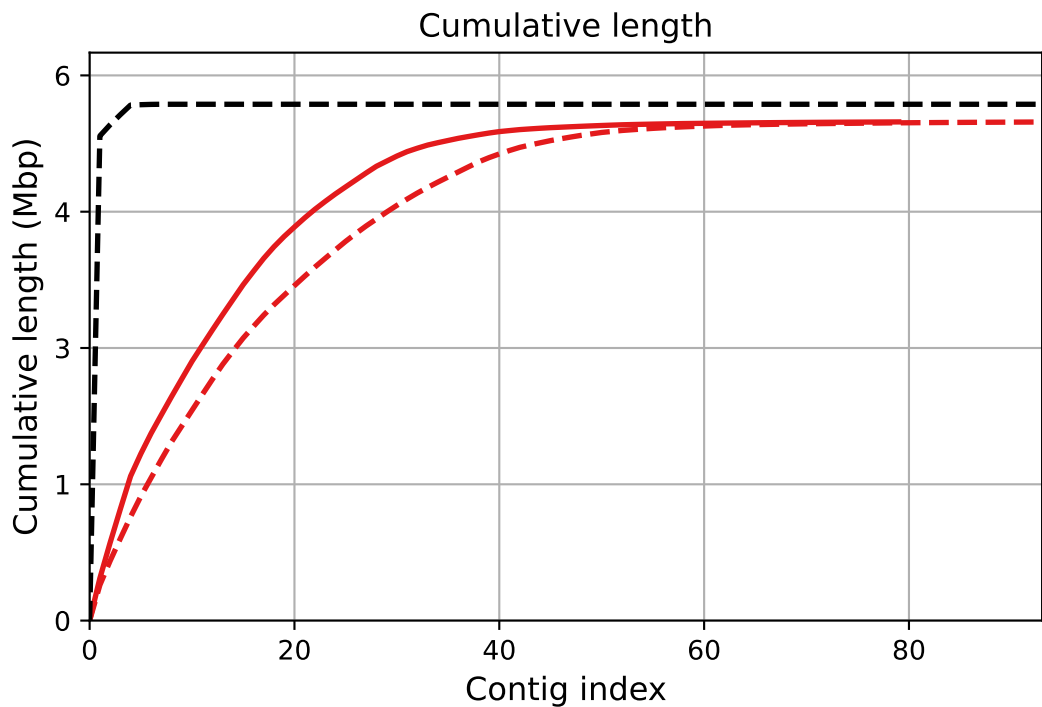
-- SPAdes_on_data_27_and_data_26_Scaffolds

NGx



des_on_data_27_and_data_26_Scaffolds

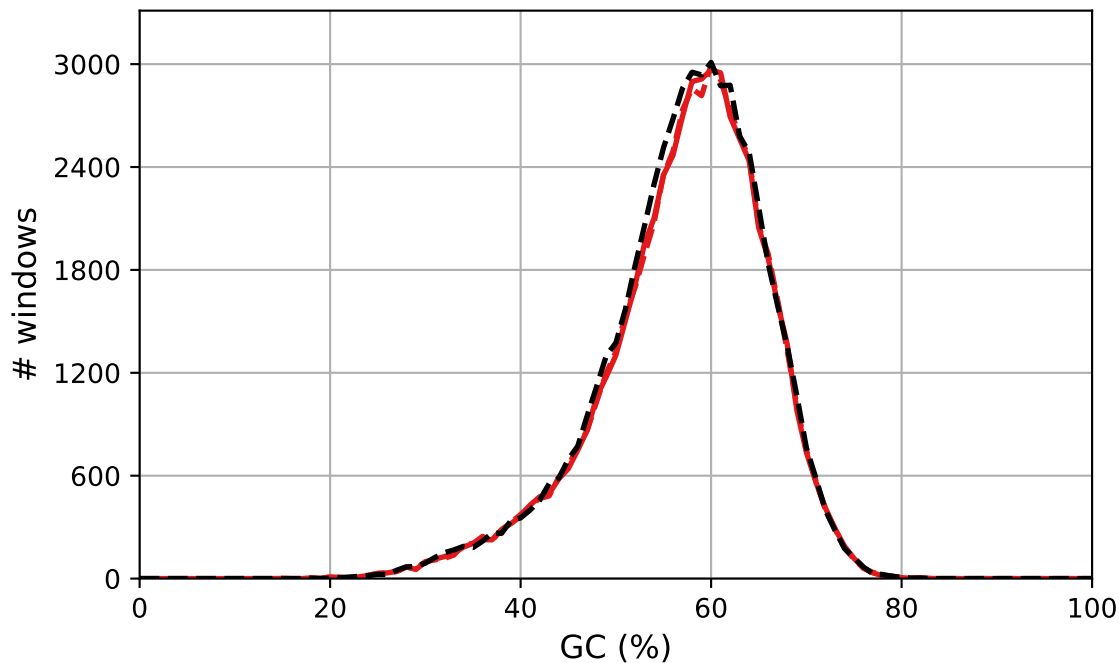
SPAdes_on_data_27_and_data_26_Scaffolds



data_27_and_data_26__Scaffolds

--- SPAdes_on_data_27_and_data_26__Scaffolds_broken

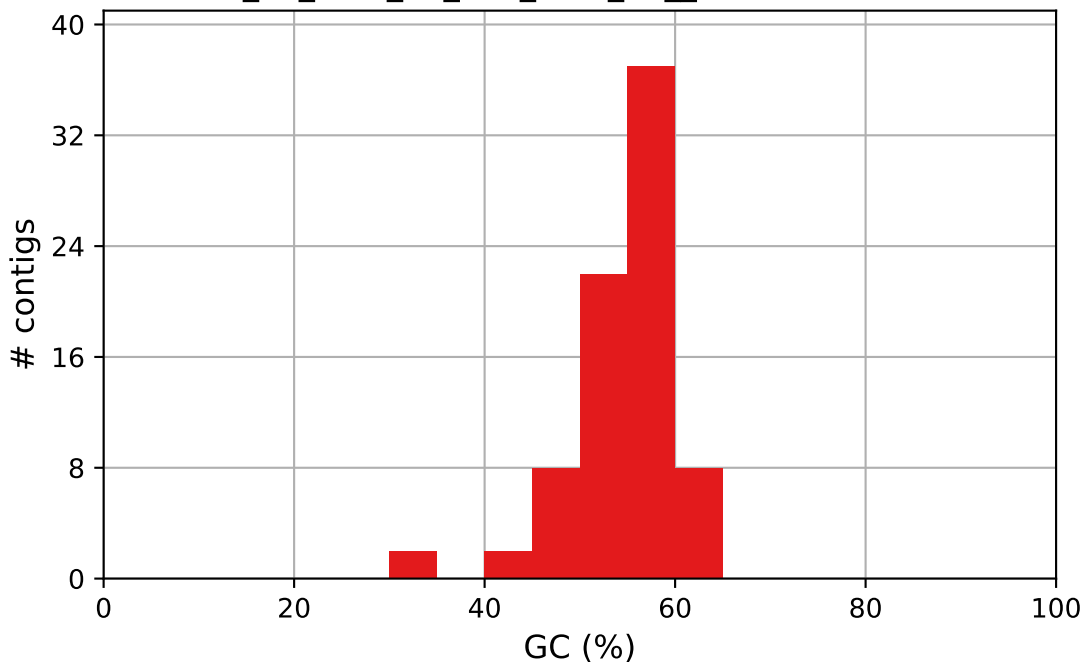
GC content



data_27_and_data_26__Scaffolds

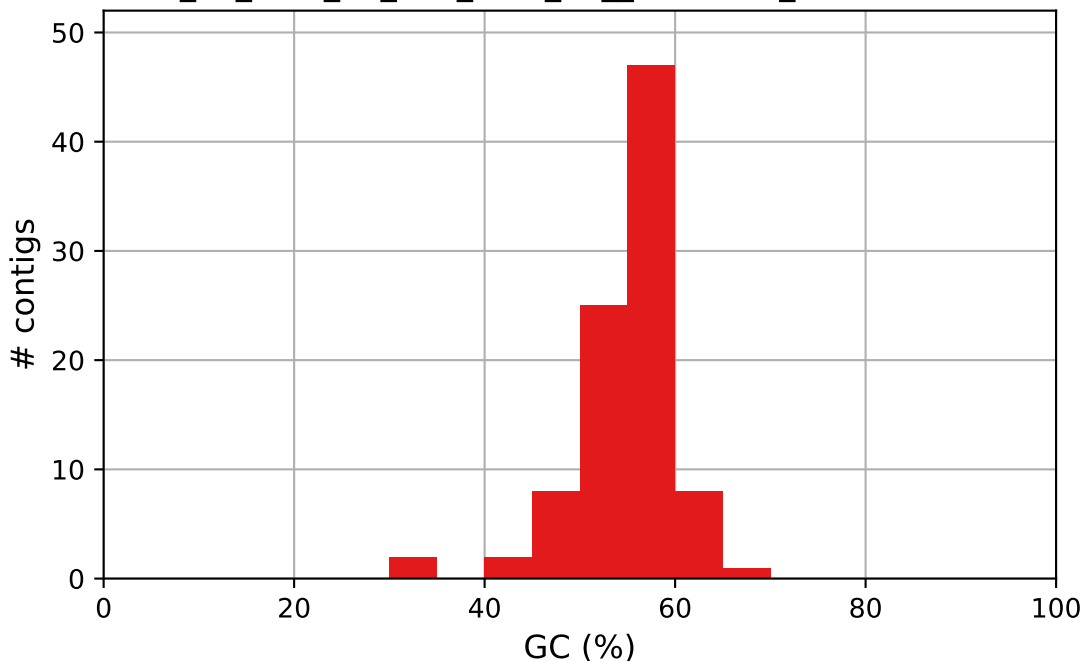
-- SPAdes_on_data_27_and_data_26__Scaffolds_broken

SPAdes_on_data_27_and_data_26__Scaffolds GC content



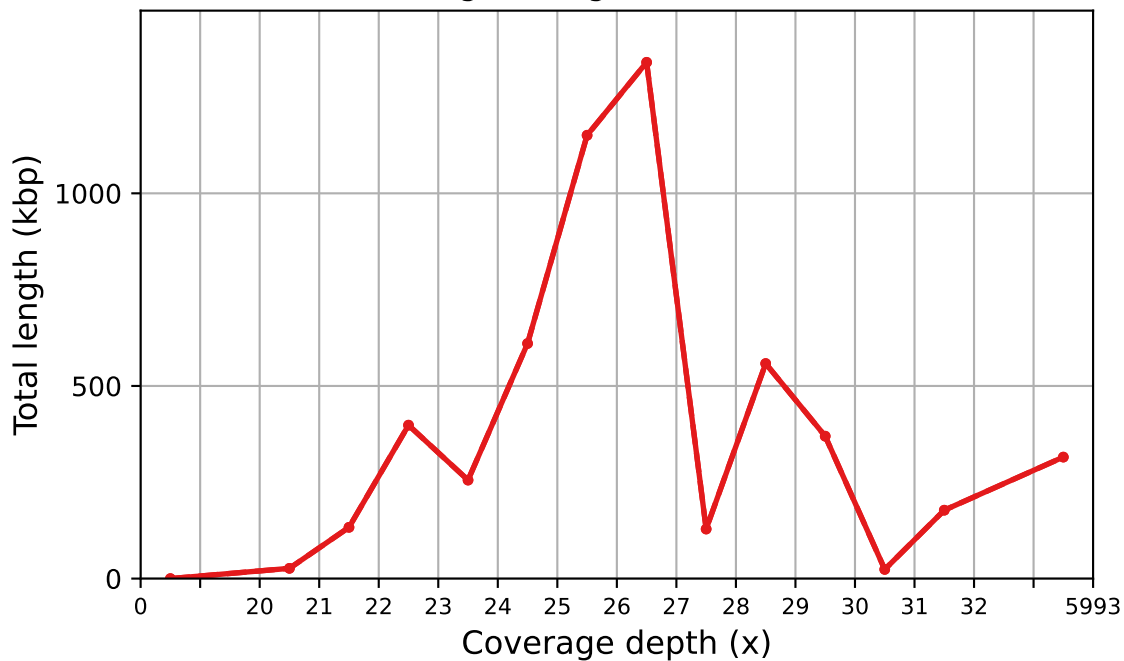
SPAdes_on_data_27_and_data_26__Scaffolds

SPAdes_on_data_27_and_data_26__Scaffolds_broken GC content



SPAdes_on_data_27_and_data_26__Scaffolds_broken

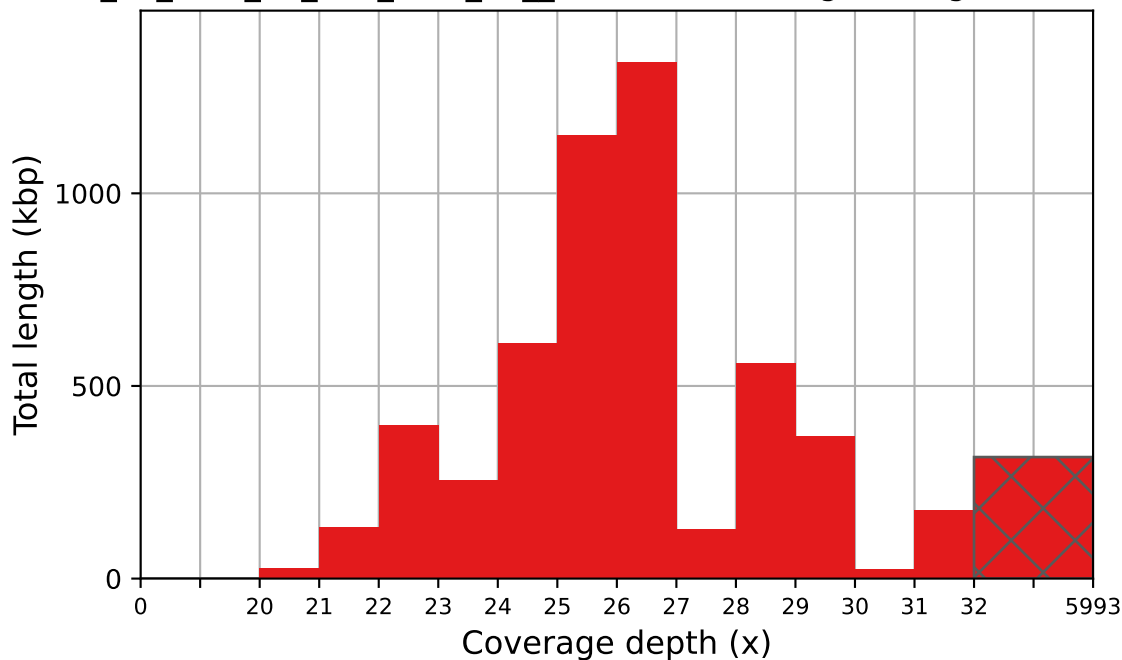
Coverage histogram (bin size: 1x)



des_on_data_27_and_data_26__Scaffolds

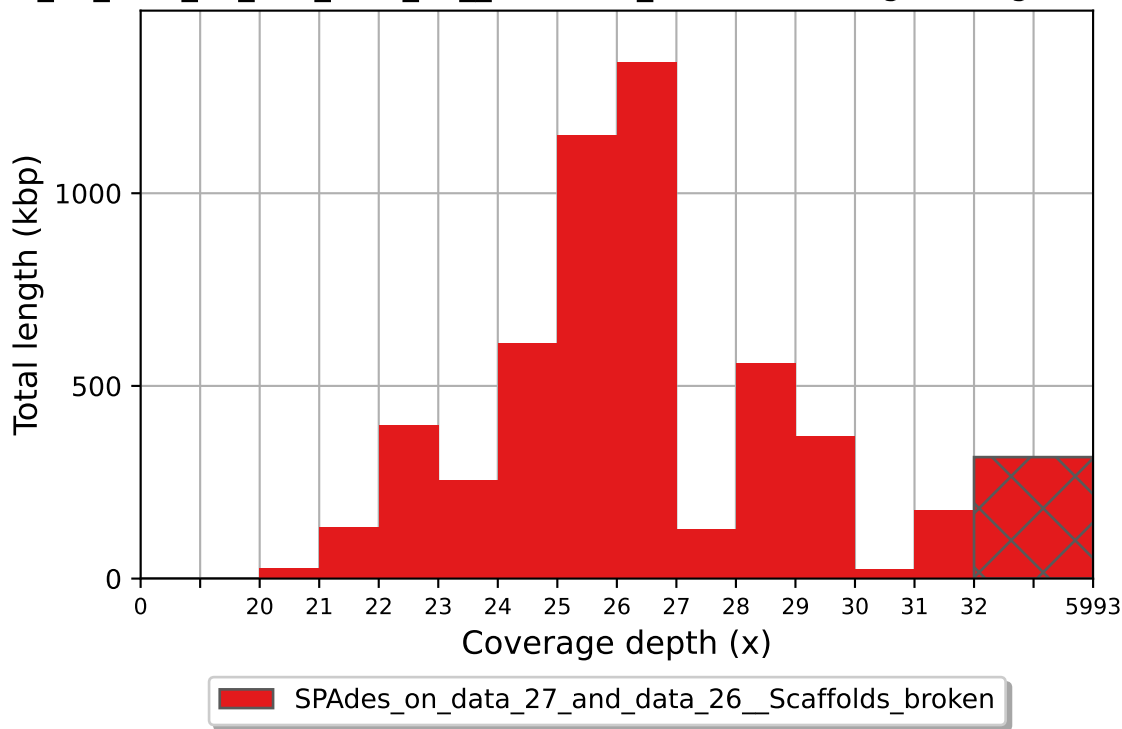
—•— SPAdes_on_data_27_and_data_26__Scaffolds

SPAdes_on_data_27_and_data_26__Scaffolds coverage histogram (bin size: 1

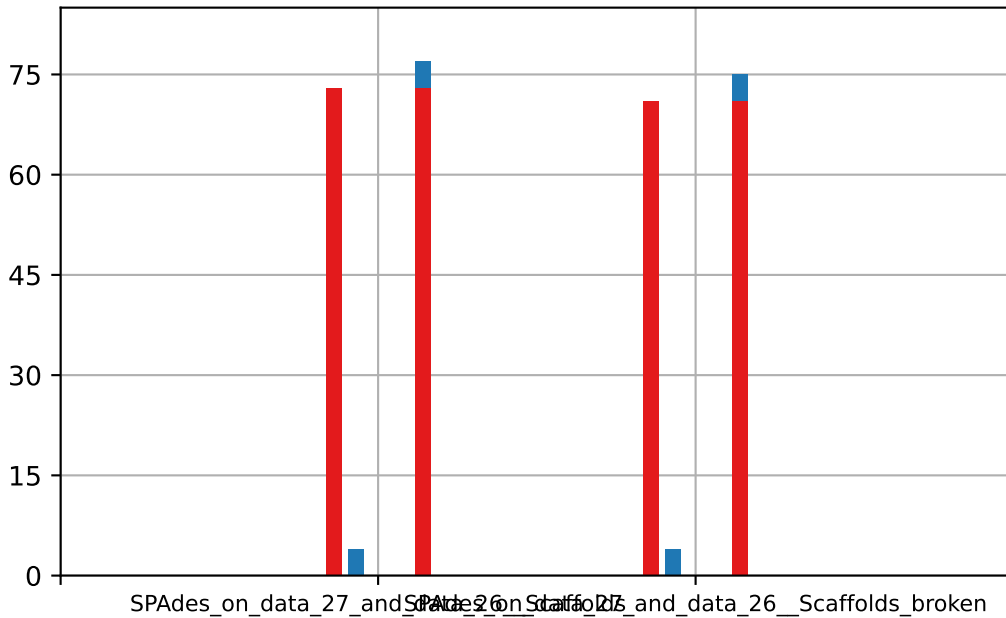


SPAdes_on_data_27_and_data_26__Scaffolds

SPAdes_on_data_27_and_data_26__Scaffolds_broken coverage histogram (bin size 1)



Misassemblies

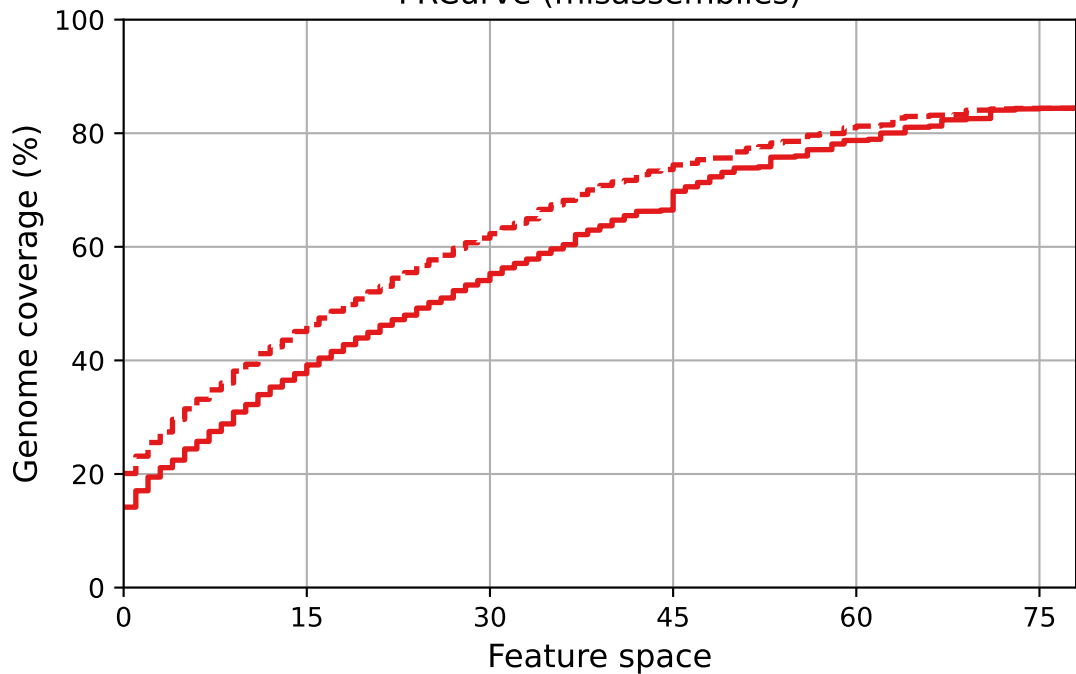


relocations



translocations

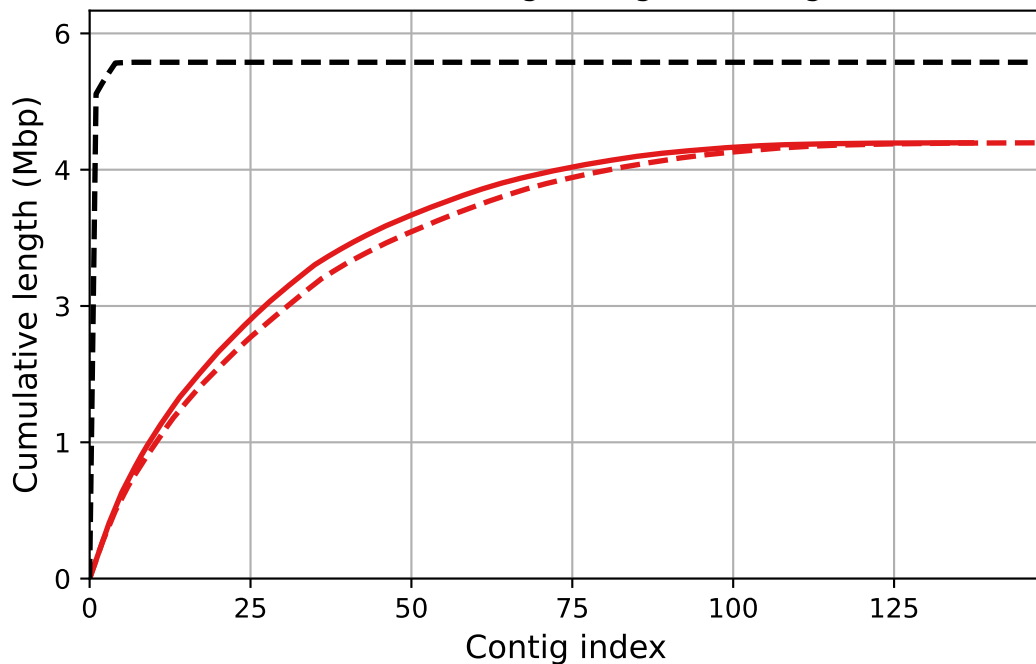
FRCurve (misassemblies)



des_on_data_27_and_data_26__Scaffolds

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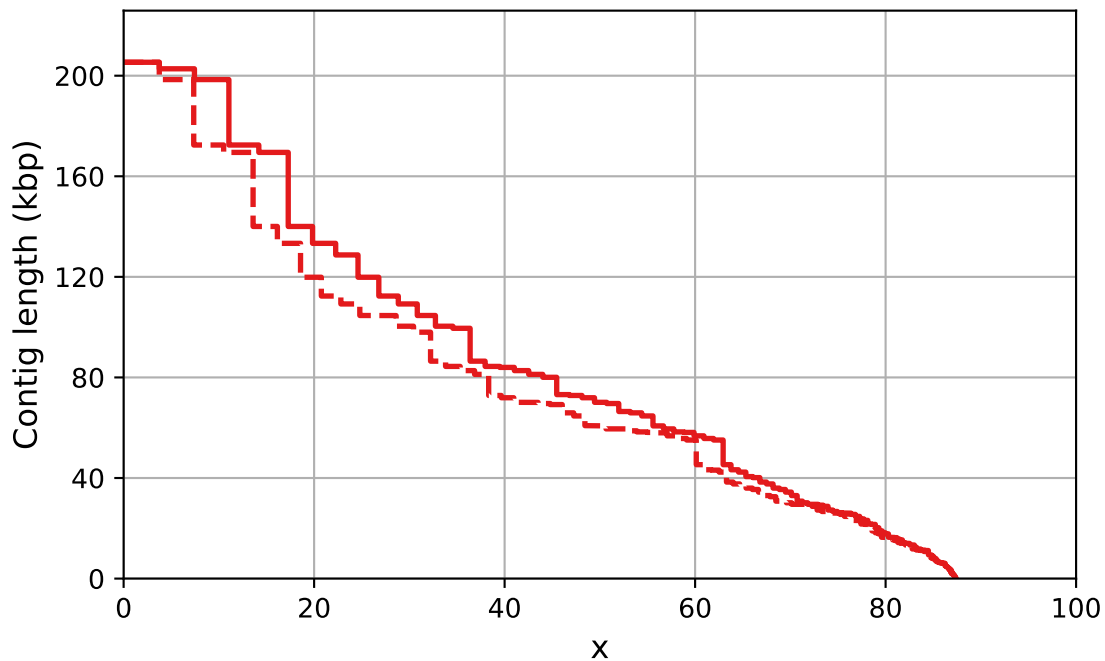
Cumulative length (aligned contigs)



data_27_and_data_26__Scaffolds

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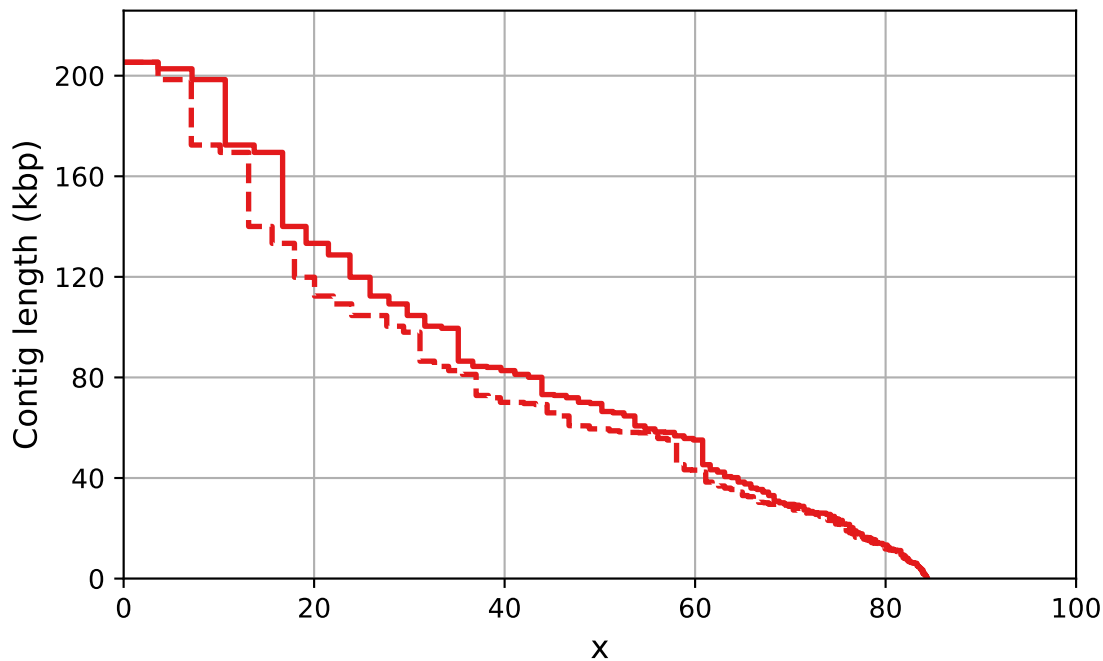
NAx



des_on_data_27_and_data_26__Scaffolds

-- SPAdes_on_data_27_and_data_26__Scaffolds

NGAx

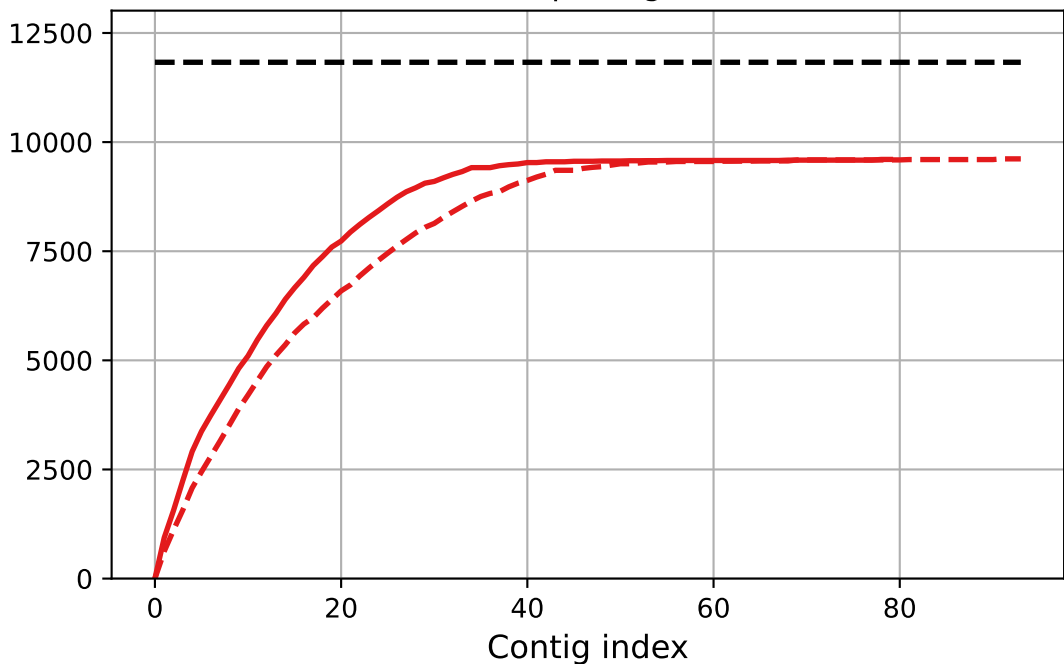


des_on_data_27_and_data_26_Scaffolds

-- SPAdes_on_data_27_and_data_26_Scaffolds

Cumulative # complete genomic features

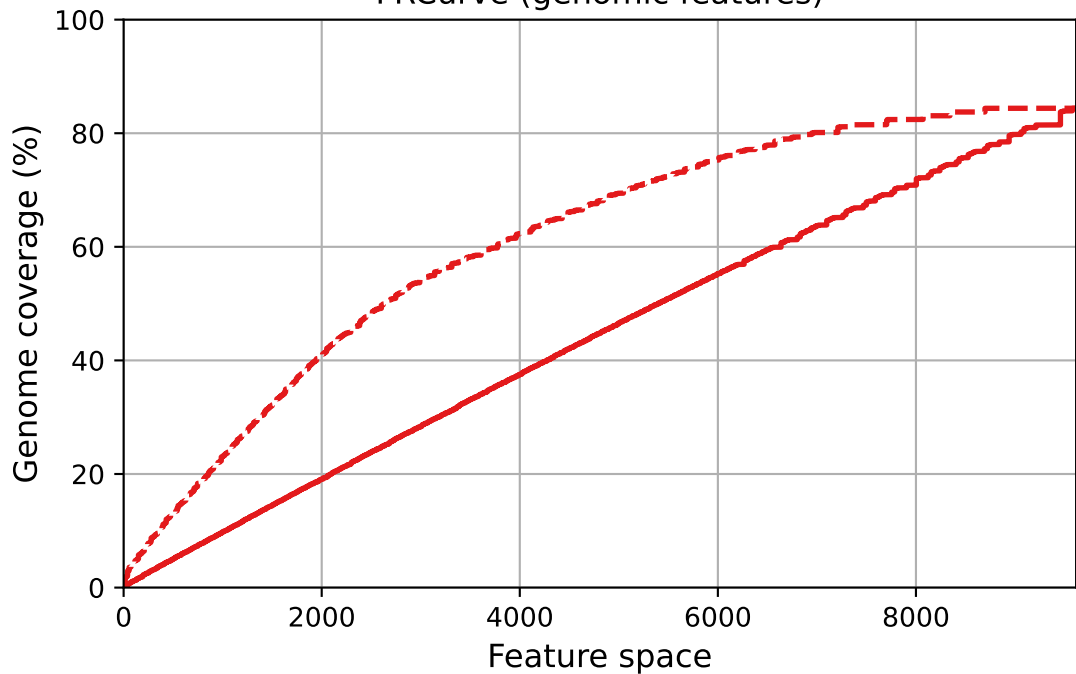
Cumulative # complete genomic features



ta_27_and_data_26__Scaffolds

-- SPAdes_on_data_27_and_data_26__Scaffolds_broken

FRCurve (genomic features)



des_on_data_27_and_data_26__Scaffolds

SPAdes_on_data_27_and_data_26__Scaffolds

complete genomic features



des_on_data_27_and_data_26__Scaffolds



SPAdes_on_data_27_and_data_26__Scaffolds

Genome fraction, %

100

95

90

85

des_on_data_27_and_data_26__Scaffolds

SPAdes_on_data_27_and_data_26__Scaffolds

