

Report

	SPAdes_on_data_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# contigs (>= 0 bp)	180	-
# contigs (>= 1000 bp)	65	77
Total length (>= 0 bp)	5507955	-
Total length (>= 1000 bp)	5480687	5479403
# contigs	76	89
Largest contig	564161	387978
Total length	5488021	5486811
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	194930	168694
NG50	194930	168694
N90	76558	58773
NG90	49263	45493
auN	246558.6	167616.6
auNG	238127.8	161849.4
L50	9	13
LG50	9	13
L90	26	34
LG90	29	37
# misassemblies	74	73
# misassembled contigs	28	31
Misassembled contigs length	4776562	4301867
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	2	2
# unaligned contigs	22 + 33 part	23 + 35 part
Unaligned length	689531	688966
Genome fraction (%)	84.787	85.357
Duplication ratio	1.001	1.001
# N's per 100 kbp	22.05	0.00
# mismatches per 100 kbp	685.71	688.38
# indels per 100 kbp	19.62	19.94
# genomic features	9605 + 180 part	9620 + 206 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	313376	205341
Total aligned length	4796368	4795350
NA50	71923	65917
NGA50	69622	60829
NA90	-	-
NGA90	-	-
auNA	91671.4	75550.0
auNGA	88536.8	72950.6
LA50	22	26
LGA50	24	28
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

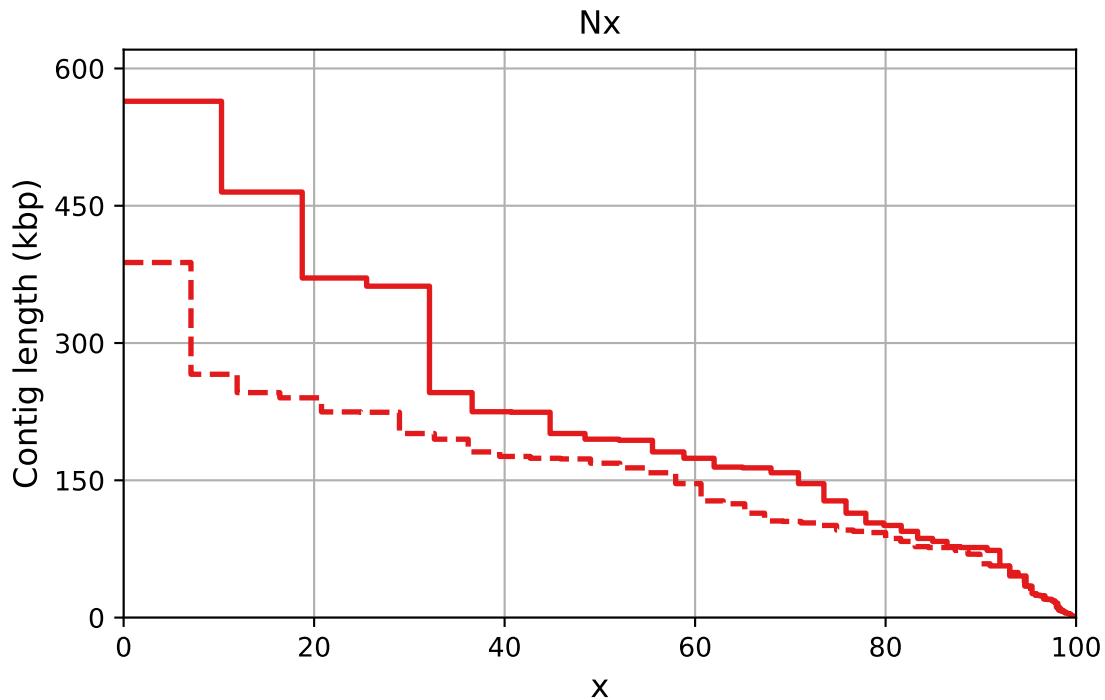
	SPAdes_on_data_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# misassemblies	74	73
# contig misassemblies	73	73
# c. relocations	71	71
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	28	31
Misassembled contigs length	4776562	4301867
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	2	2
# mismatches	32889	33010
# indels	941	956
# indels (<= 5 bp)	846	869
# indels (> 5 bp)	95	87
Indels length	8611	7235

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_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# fully unaligned contigs	22	23
Fully unaligned length	58791	58865
# partially unaligned contigs	33	35
Partially unaligned length	630740	630101
# N's	1210	0

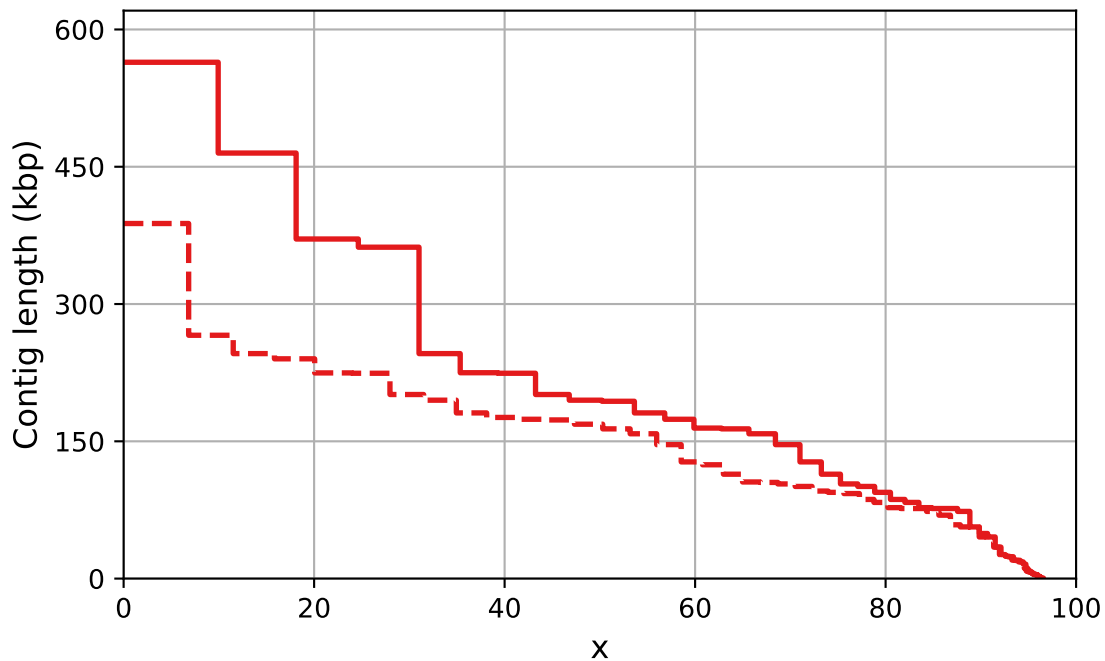
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



des_on_data_15_and_data_14_Scaffolds

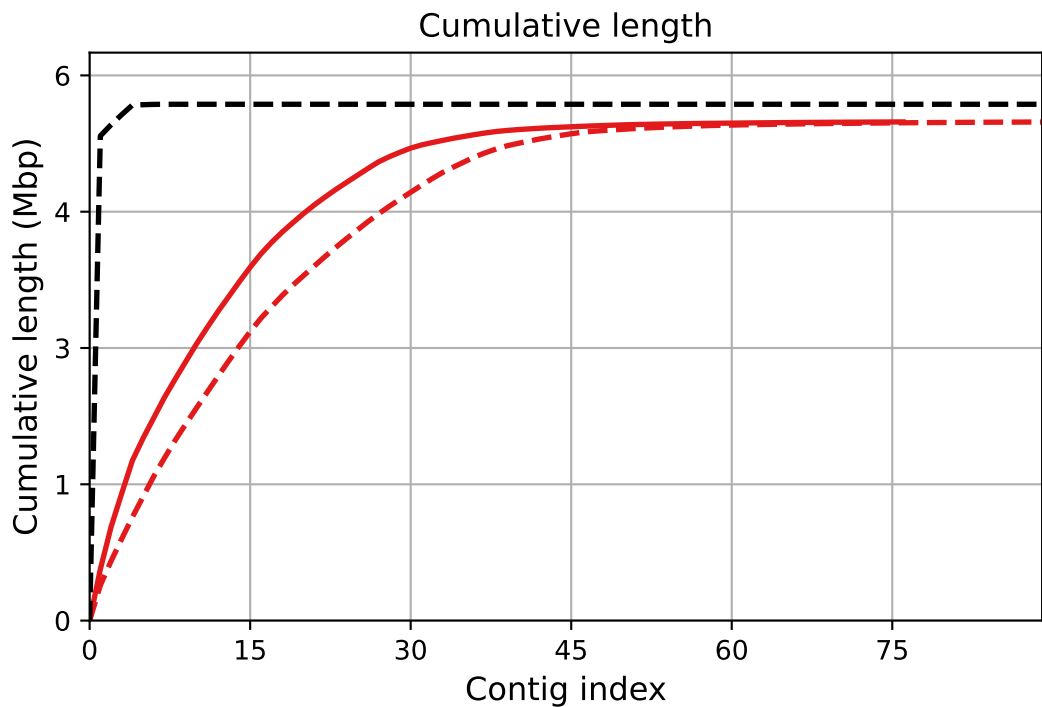
SPAdes_on_data_15_and_data_14_Scaffolds

NGx



des_on_data_15_and_data_14_Scaffolds

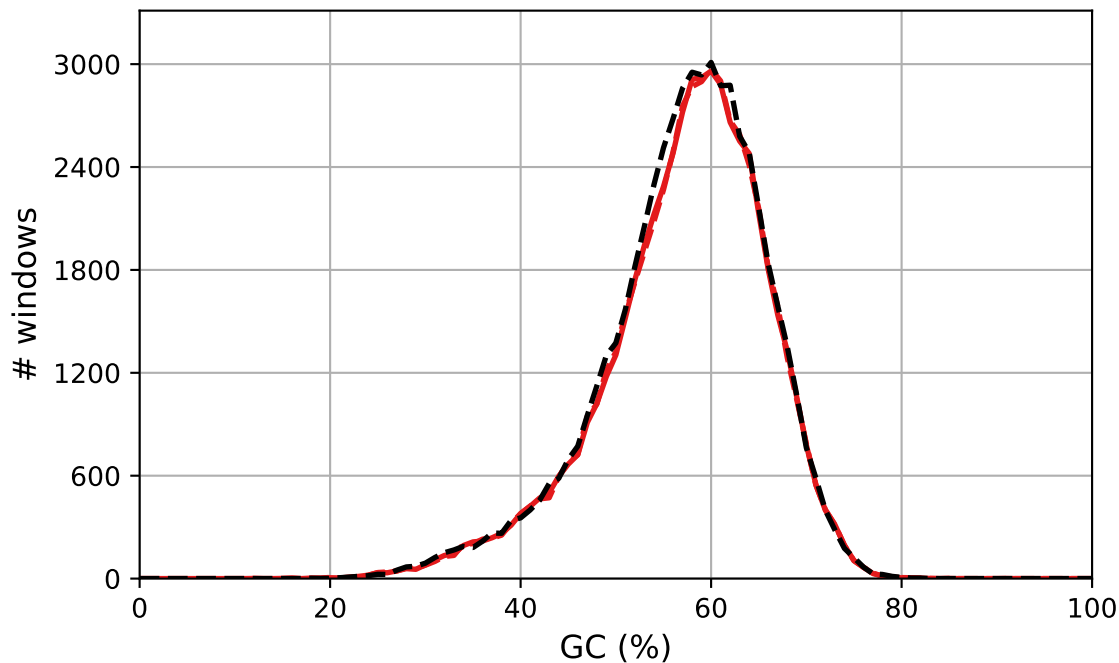
SPAdes_on_data_15_and_data_14_Scaffolds



data_15_and_data_14__Scaffolds

-- SPAdes_on_data_15_and_data_14__Scaffolds_broken

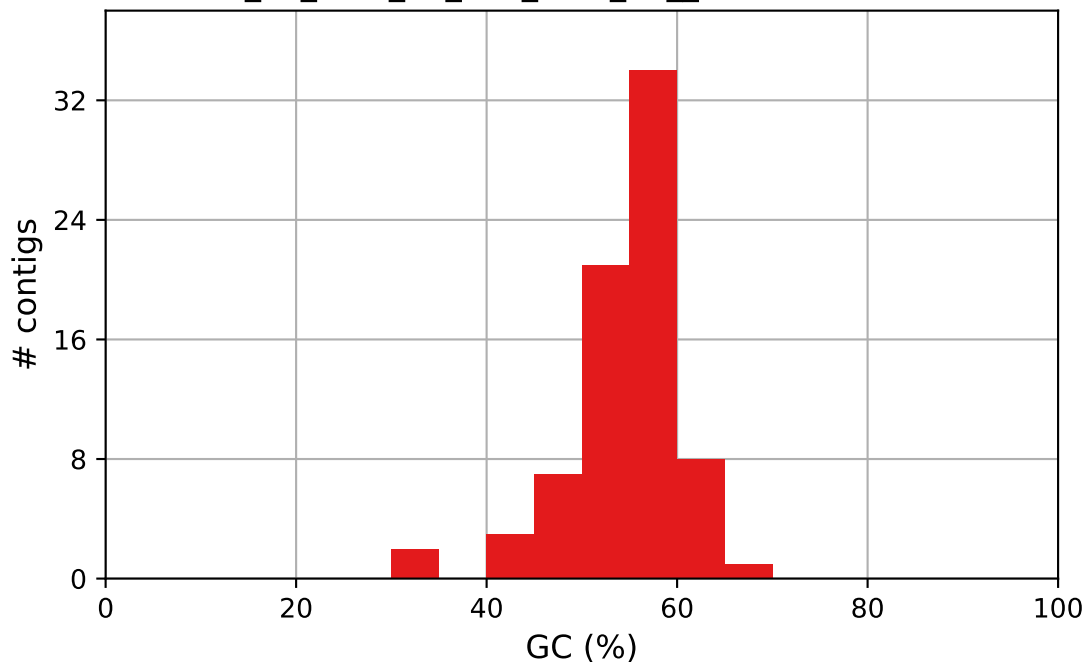
GC content



data_15_and_data_14__Scaffolds

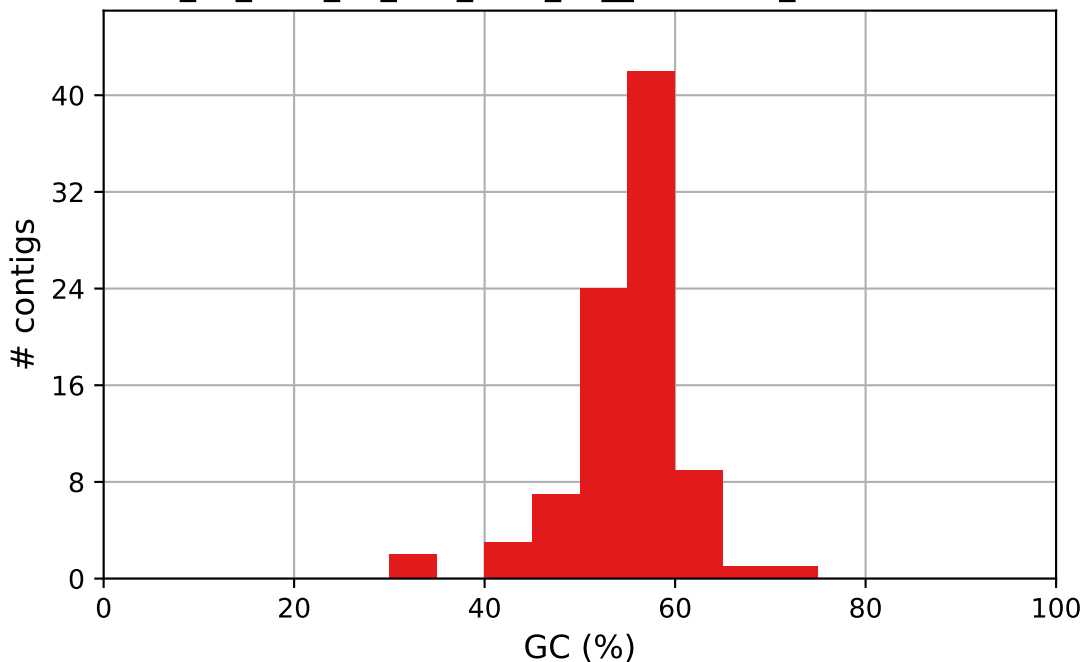
-- SPAdes_on_data_15_and_data_14__Scaffolds_broken

SPAdes_on_data_15_and_data_14__Scaffolds GC content



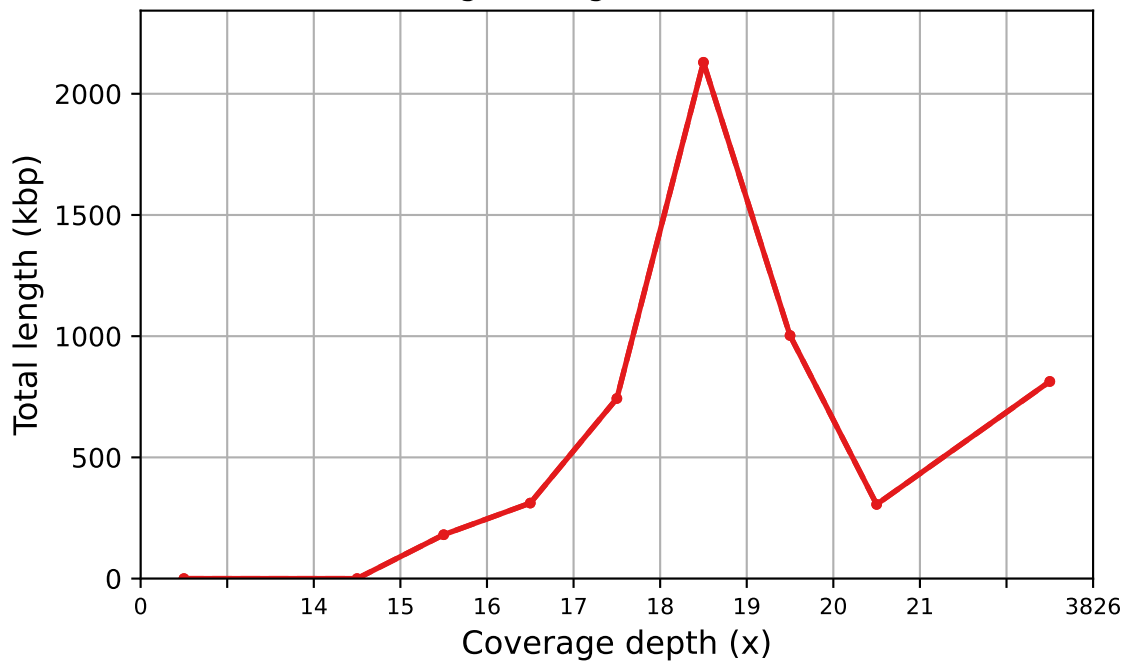
SPAdes_on_data_15_and_data_14__Scaffolds

SPAdes_on_data_15_and_data_14__Scaffolds_broken GC content



SPAdes_on_data_15_and_data_14__Scaffolds_broken

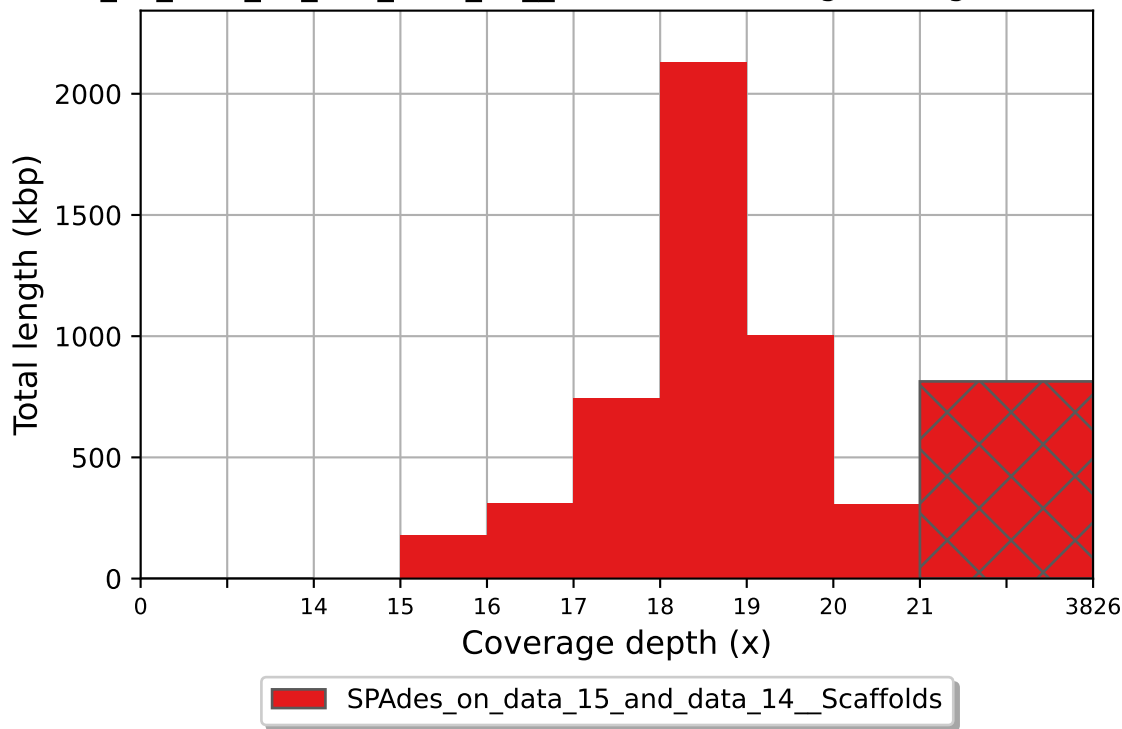
Coverage histogram (bin size: 1x)



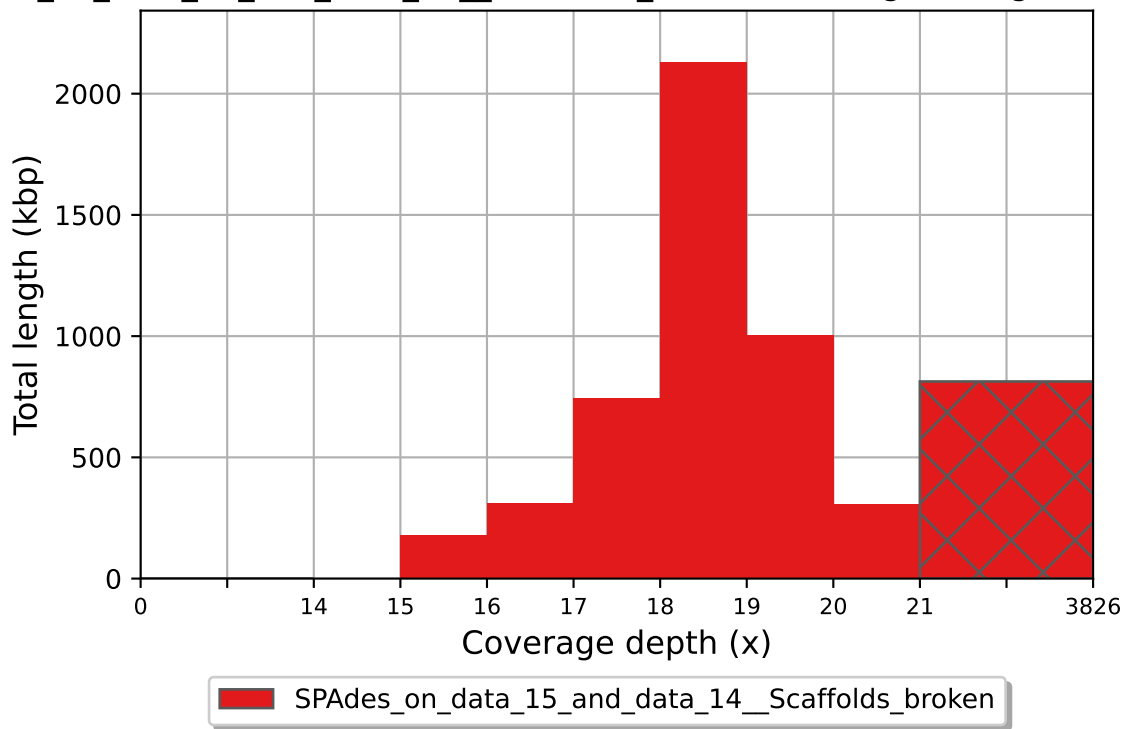
des_on_data_15_and_data_14_Scaffolds

—●— SPAdes_on_data_15_and_data_14_Scaffolds

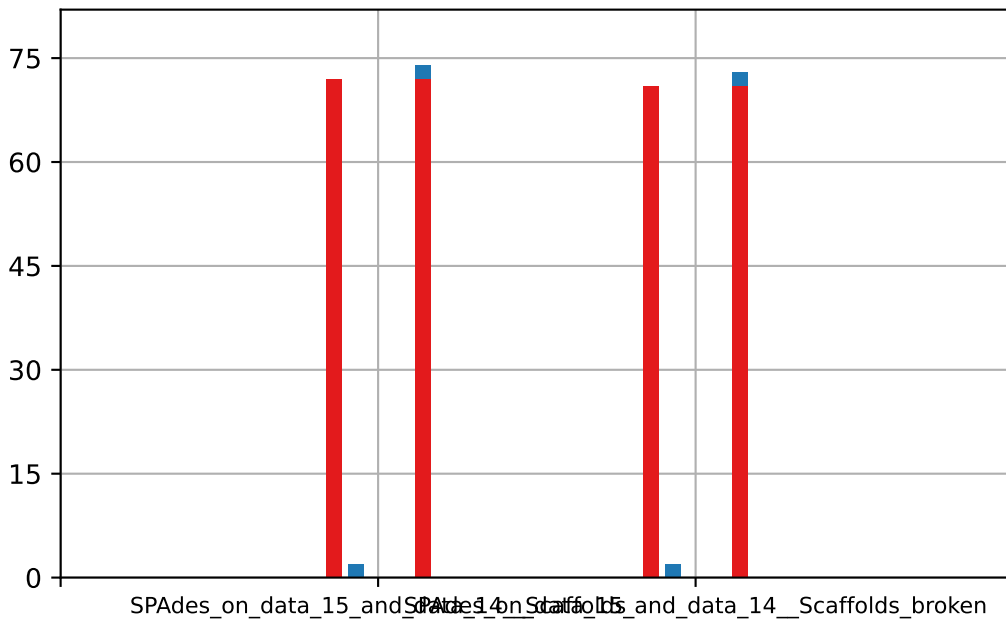
SPAdes_on_data_15_and_data_14__Scaffolds coverage histogram (bin size: 1



des_on_data_15_and_data_14__Scaffolds_broken coverage histogram (bin size



Misassemblies

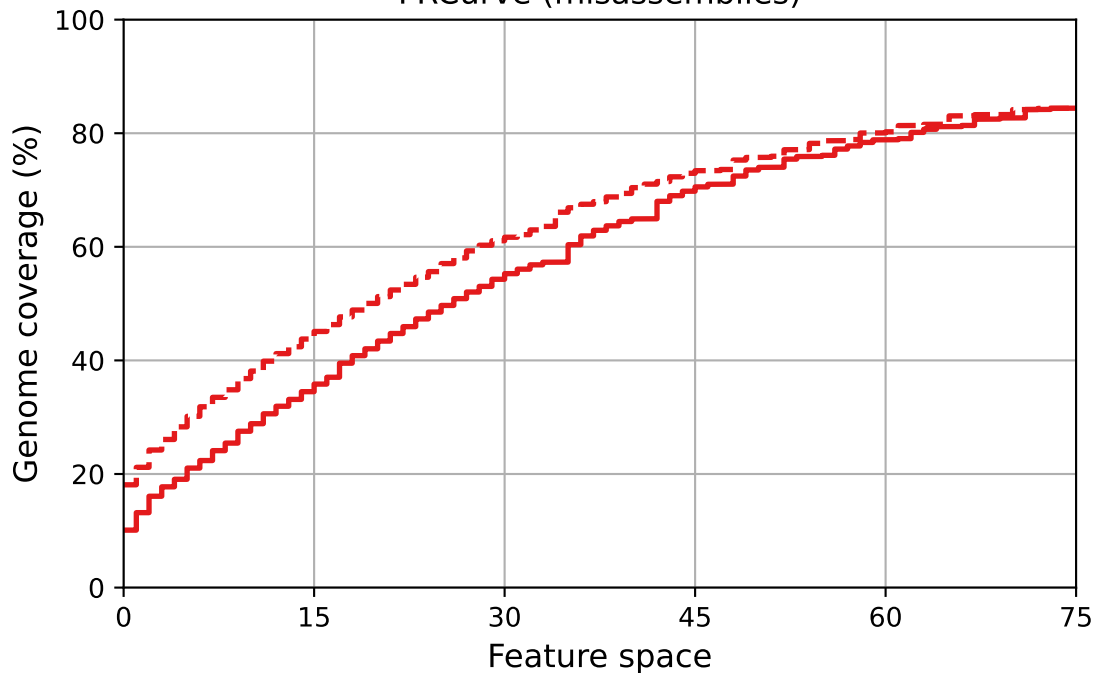


relocations



translocations

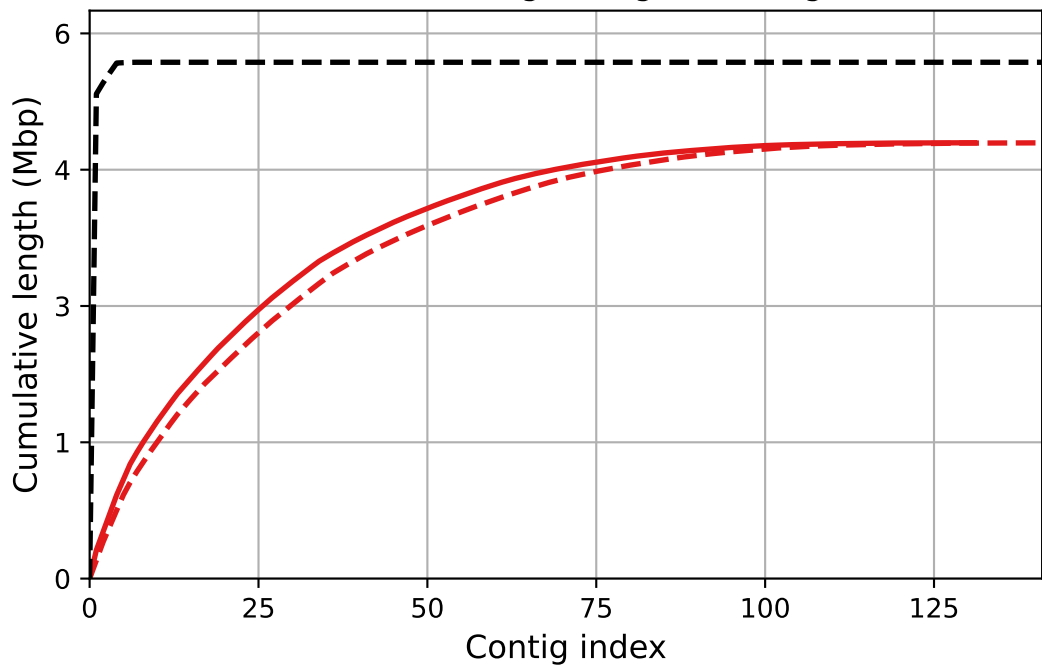
FRCurve (misassemblies)



des_on_data_15_and_data_14_Scaffolds

-- SPAdes_on_data_15_and_data_14_Scaffolds

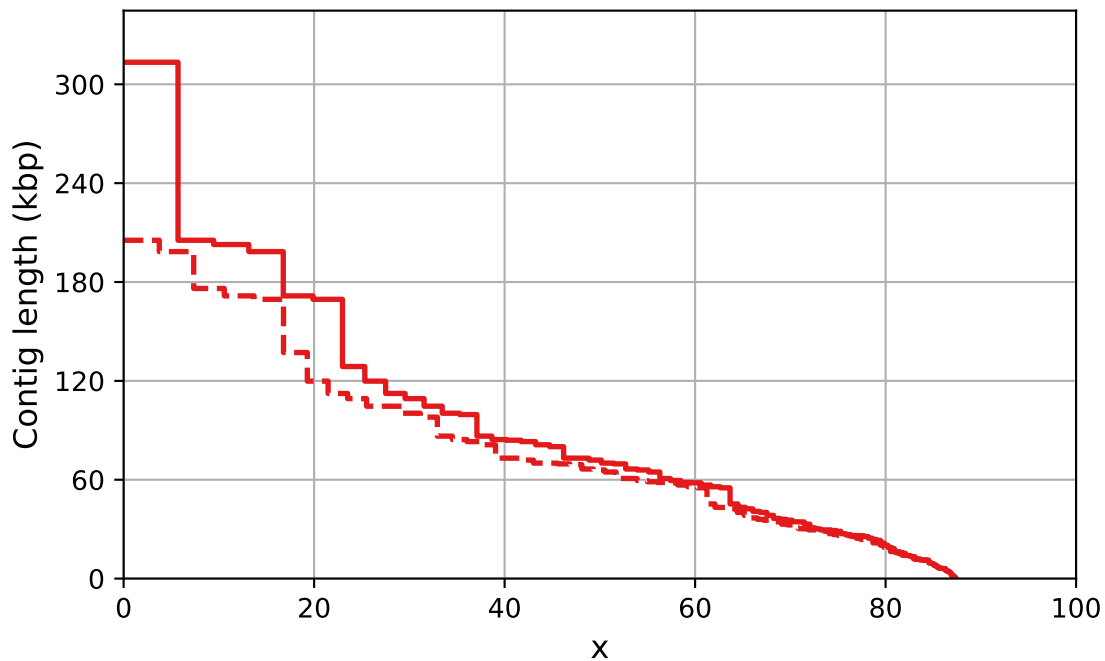
Cumulative length (aligned contigs)



data_15_and_data_14__Scaffolds

-- SPAdes_on_data_15_and_data_14__Scaffolds_broken

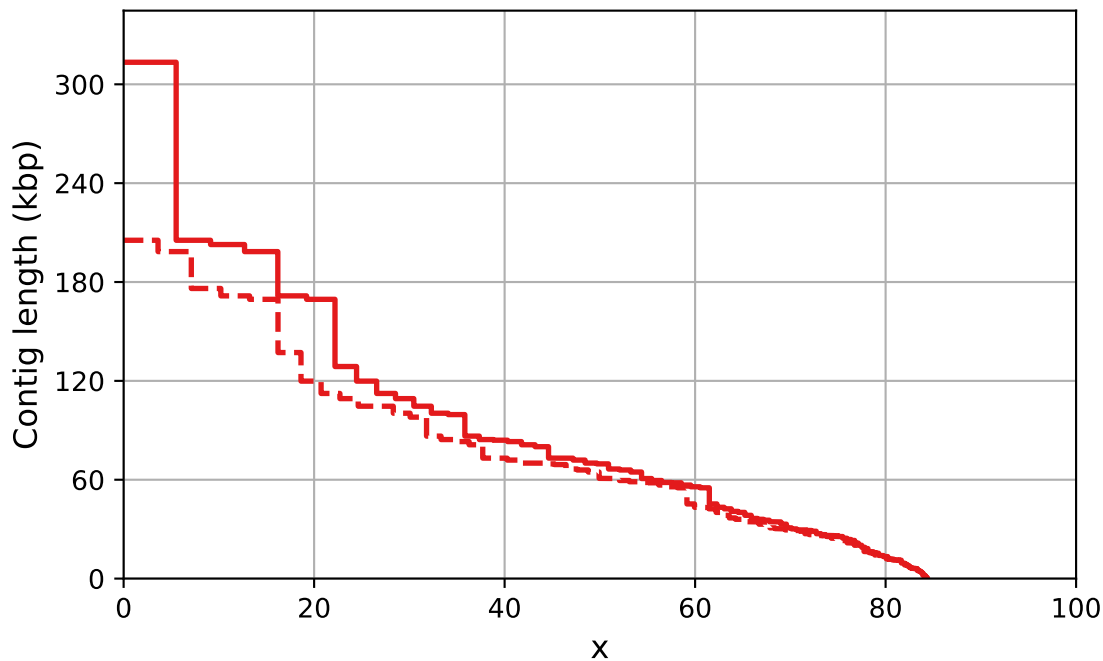
NAx



des_on_data_15_and_data_14_Scaffolds

-- SPAdes_on_data_15_and_data_14_Scaffolds

NGAx

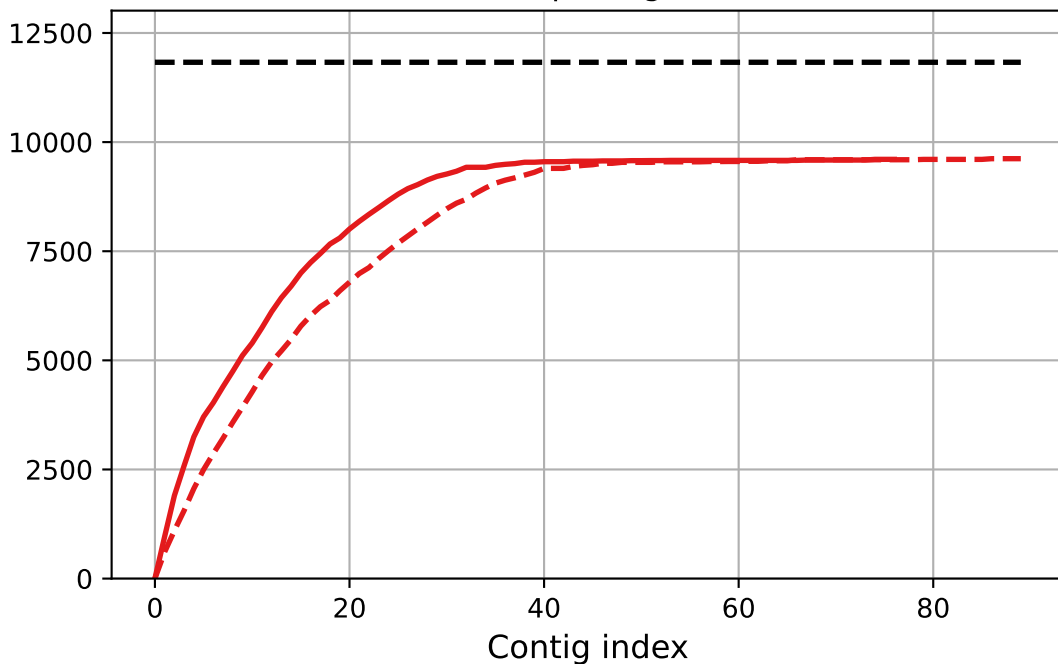


des_on_data_15_and_data_14_Scaffolds

-- SPAdes_on_data_15_and_data_14_Scaffolds

Cumulative # complete genomic features

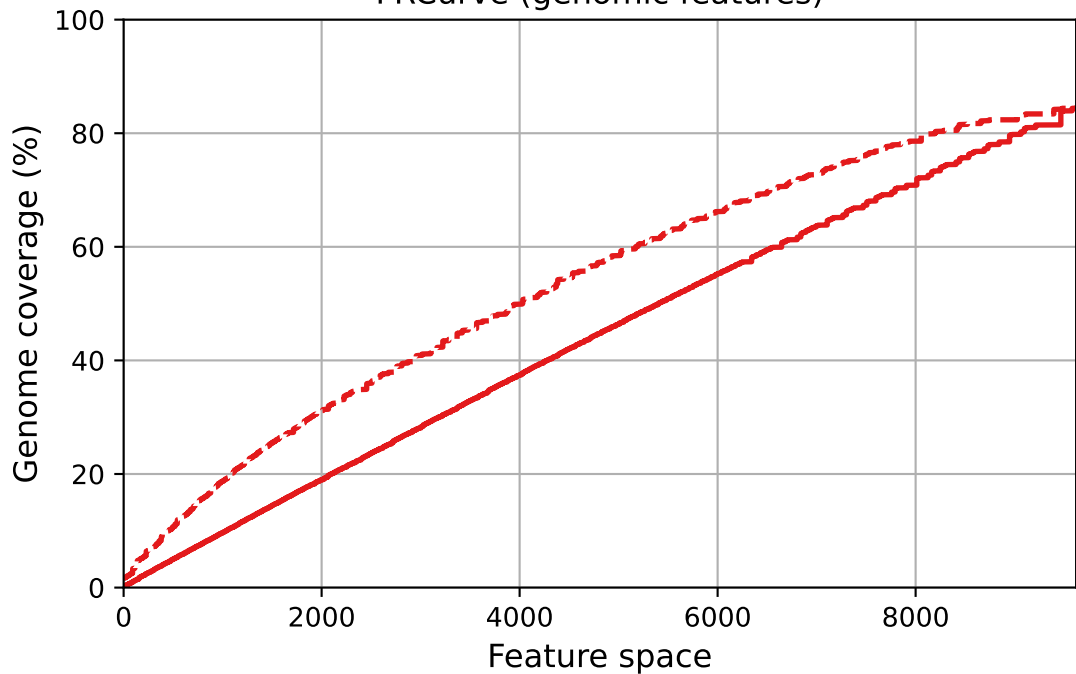
Cumulative # complete genomic features



ta_15_and_data_14__Scaffolds

-- SPAdes_on_data_15_and_data_14__Scaffolds_broken

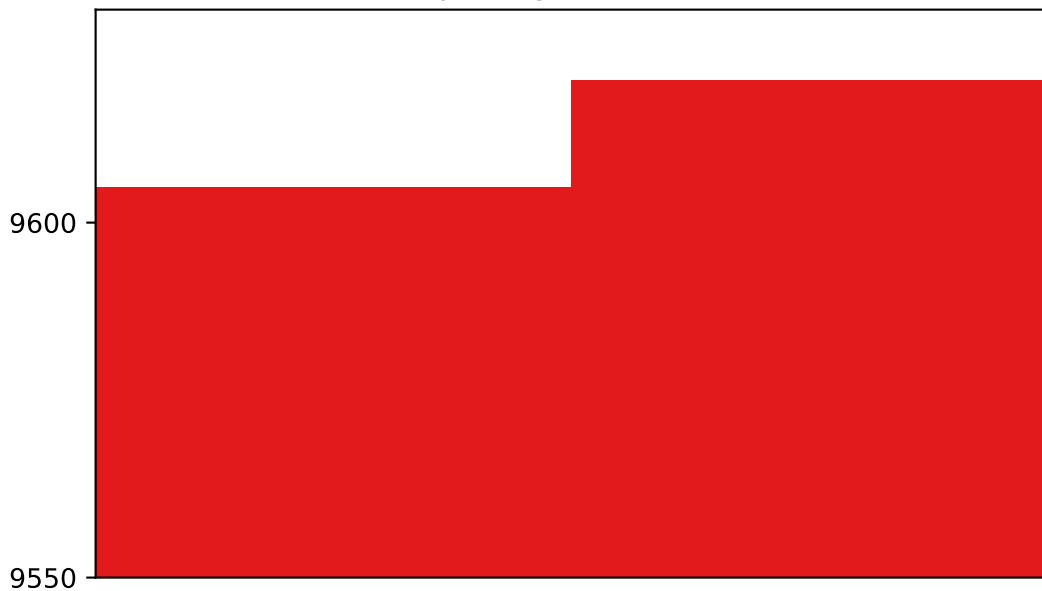
FRCurve (genomic features)



des_on_data_15_and_data_14_Scaffolds

SPAdes_on_data_15_and_data_14_Scaffolds

complete genomic features



des_on_data_15_and_data_14__Scaffolds



SPAdes_on_data_15_and_data_14__Scaffolds

Genome fraction, %

100

95

90

85

des_on_data_15_and_data_14__Scaffolds

SPAdes_on_data_15_and_data_14__Scaffolds

