

Report

	SPAdes_on_data_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# contigs (>= 0 bp)	207	-
# contigs (>= 1000 bp)	64	78
Total length (>= 0 bp)	5511542	-
Total length (>= 1000 bp)	5479363	5477879
# contigs	76	91
Largest contig	465386	390830
Total length	5487345	5485935
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	195408	170161
NG50	195408	163595
N90	77465	58773
NG90	70690	54891
auN	225987.5	164499.8
auNG	218233.2	158814.5
L50	10	13
LG50	10	14
L90	26	35
LG90	28	38
# misassemblies	75	74
# misassembled contigs	27	33
Misassembled contigs length	4608634	4256756
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	5	-
# unaligned mis. contigs	1	1
# unaligned contigs	22 + 31 part	23 + 37 part
Unaligned length	689148	688112
Genome fraction (%)	84.784	85.354
Duplication ratio	1.001	1.001
# N's per 100 kbp	25.70	0.00
# mismatches per 100 kbp	685.97	688.76
# indels per 100 kbp	19.39	19.75
# genomic features	9605 + 182 part	9618 + 210 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	4795663	4795105
NA50	71923	60829
NGA50	69622	59552
NA90	-	-
NGA90	-	-
auNA	83117.3	74946.7
auNGA	80265.3	72356.5
LA50	23	26
LGA50	25	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

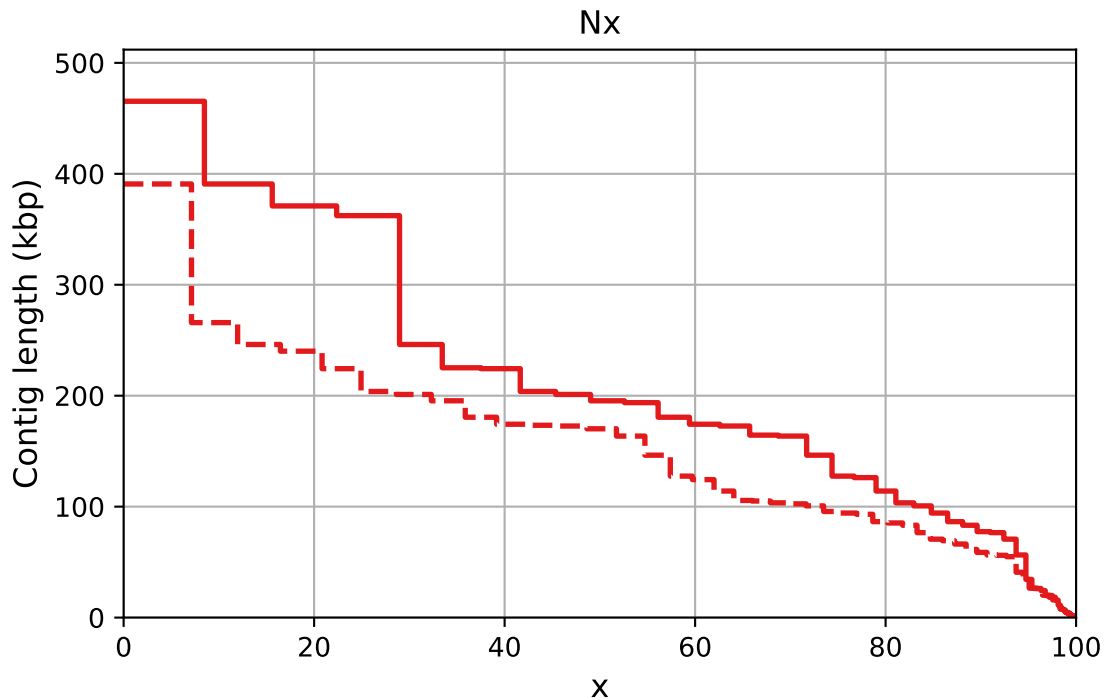
	SPAdes_on_data_15_and_data_14__Scaffolds	SPAdes_on_data_15_and_data_14__Scaffolds_broken
# misassemblies	75	74
# contig misassemblies	74	74
# c. relocations	72	72
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	27	33
Misassembled contigs length	4608634	4256756
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	5	-
# unaligned mis. contigs	1	1
# mismatches	32897	33027
# indels	930	947
# indels (<= 5 bp)	837	862
# indels (> 5 bp)	93	85
Indels length	7516	6317

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	84016	84090
# partially unaligned contigs	31	37
Partially unaligned length	605132	604022
# N's	1410	0

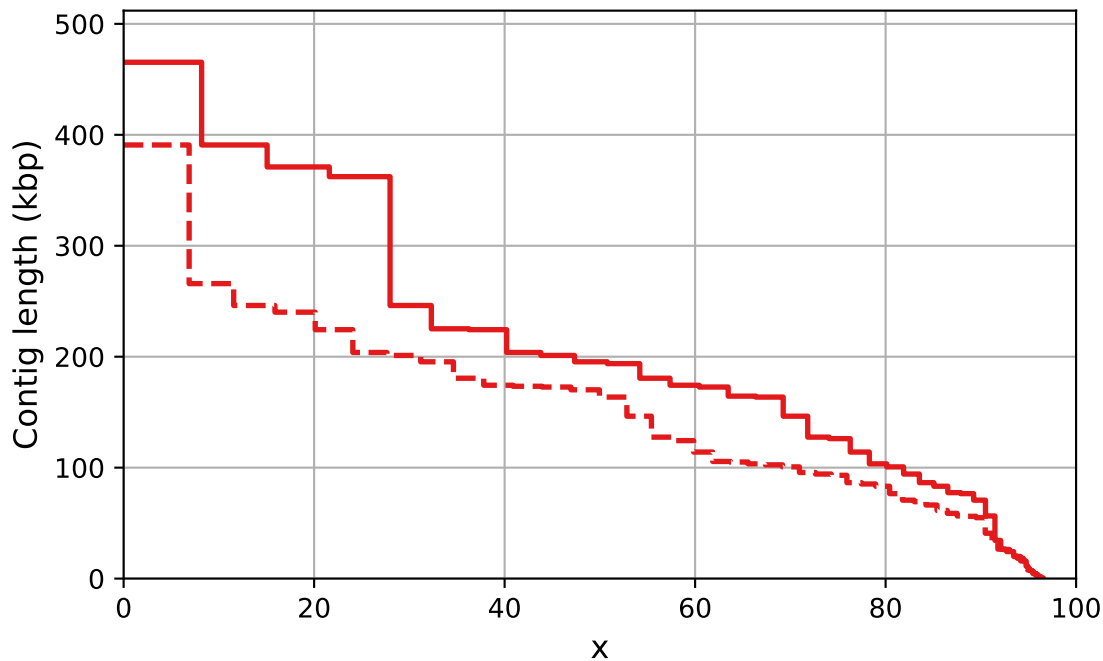
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



des_on_data_15_and_data_14_Scaffolds

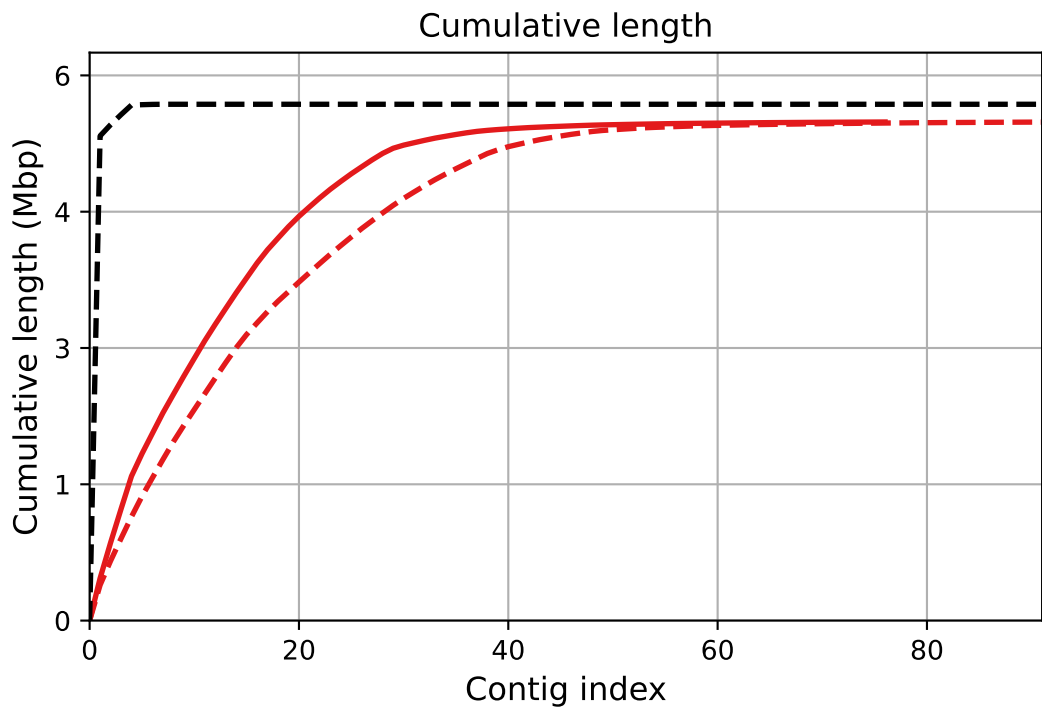
--- SPAdes_on_data_15_and_data_14_Scaffolds

NGx



des_on_data_15_and_data_14_Scaffolds

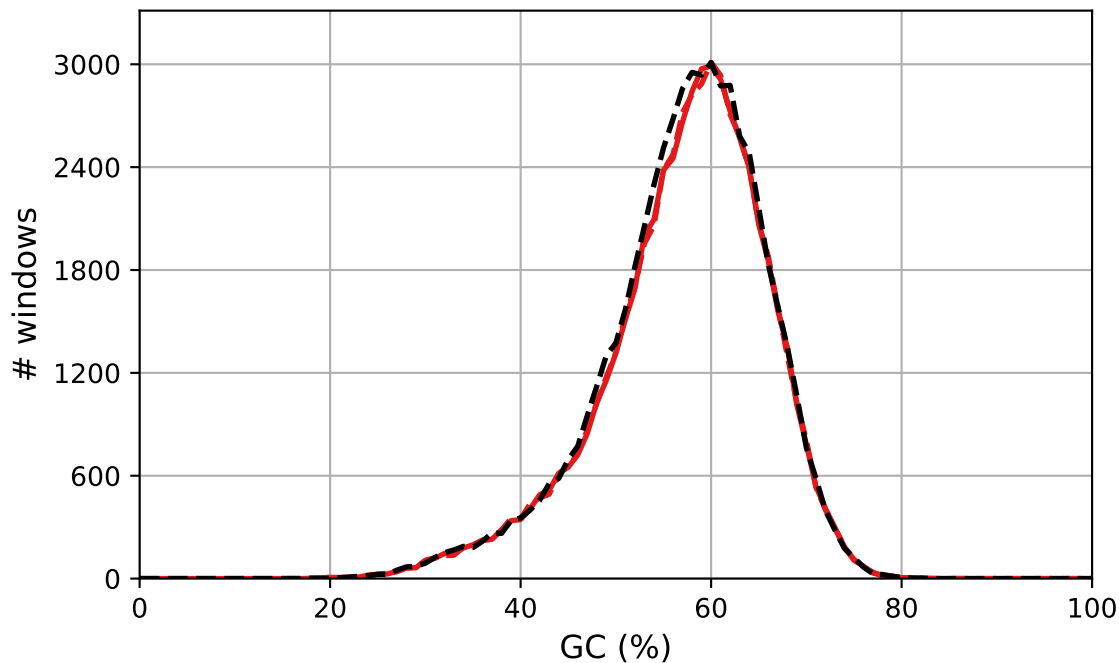
-- SPAdes_on_data_15_and_data_14_Scaffolds



data_15_and_data_14__Scaffolds

SPAdes_on_data_15_and_data_14__Scaffolds_broken

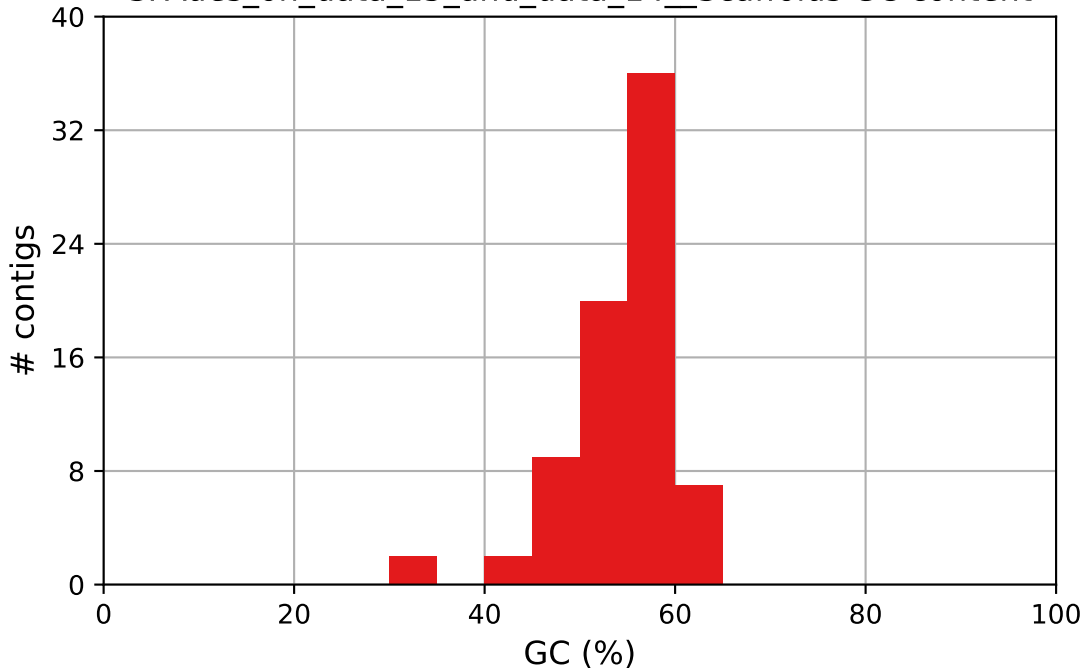
GC content



data_15_and_data_14__Scaffolds

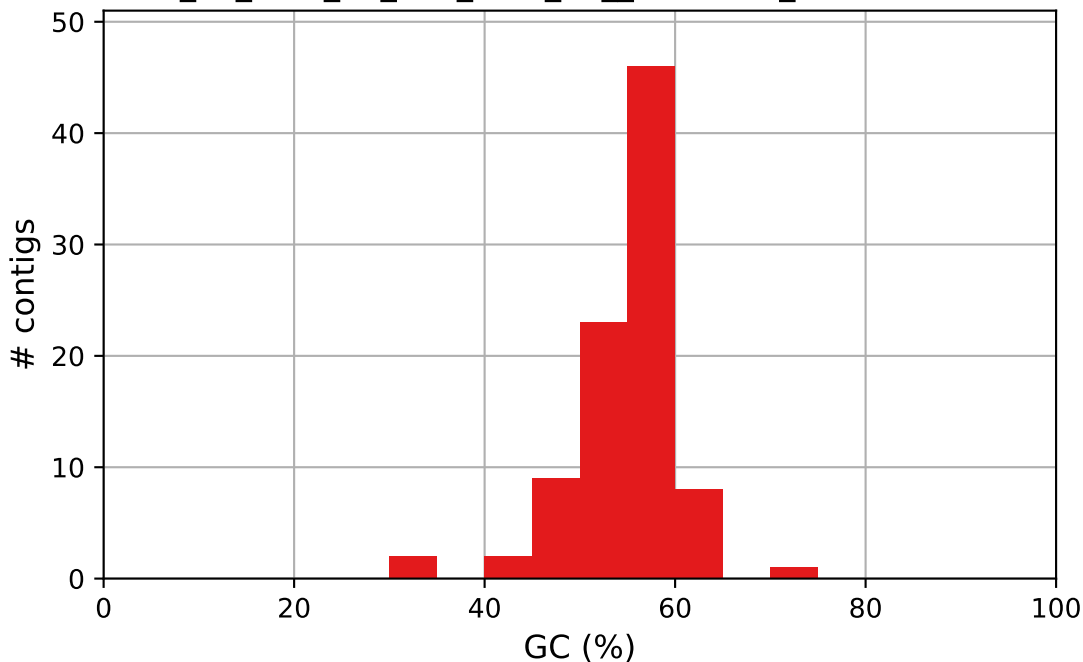
-- SPAdes_on_data_15_and_data_14__Scaffolds_broken

SPAdes_on_data_15_and_data_14__Scaffolds GC content



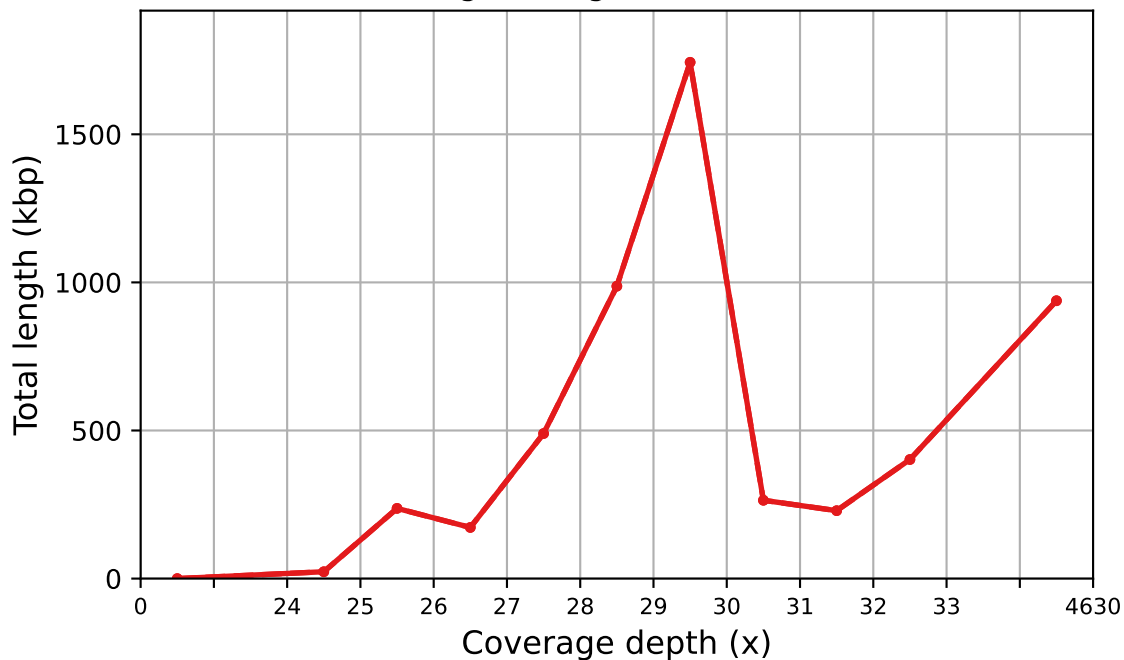
SPAdes_on_data_15_and_data_14__Scaffolds

SPAdes_on_data_15_and_data_14__Scaffolds_broken GC content



SPAdes_on_data_15_and_data_14__Scaffolds_broken

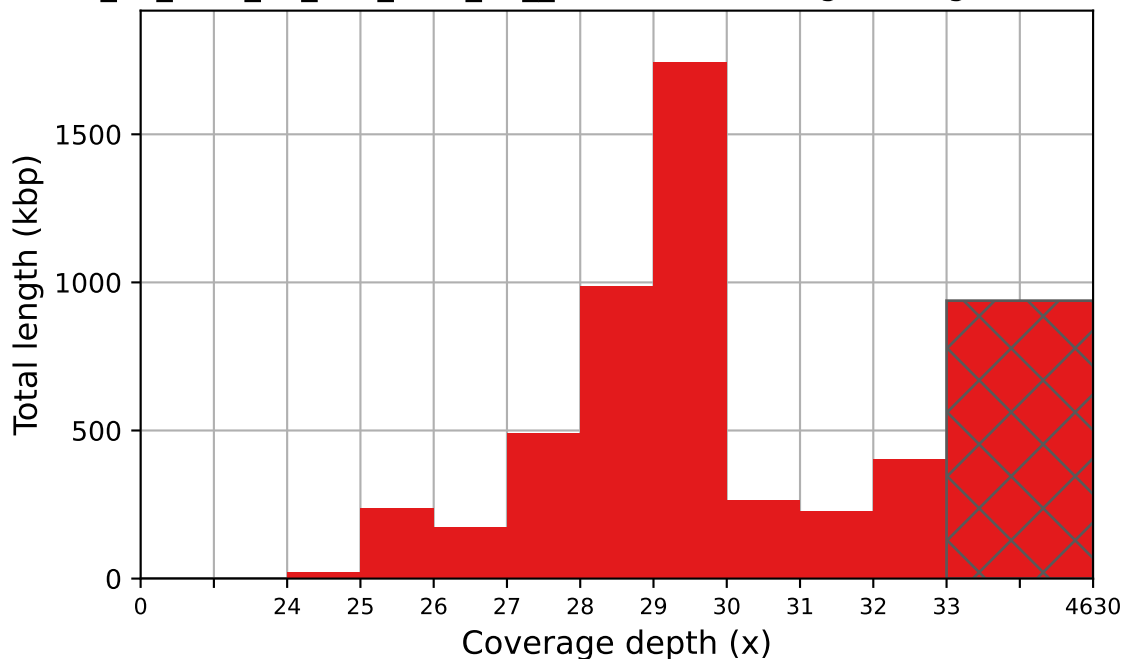
Coverage histogram (bin size: 1x)



des_on_data_15_and_data_14_Scaffolds

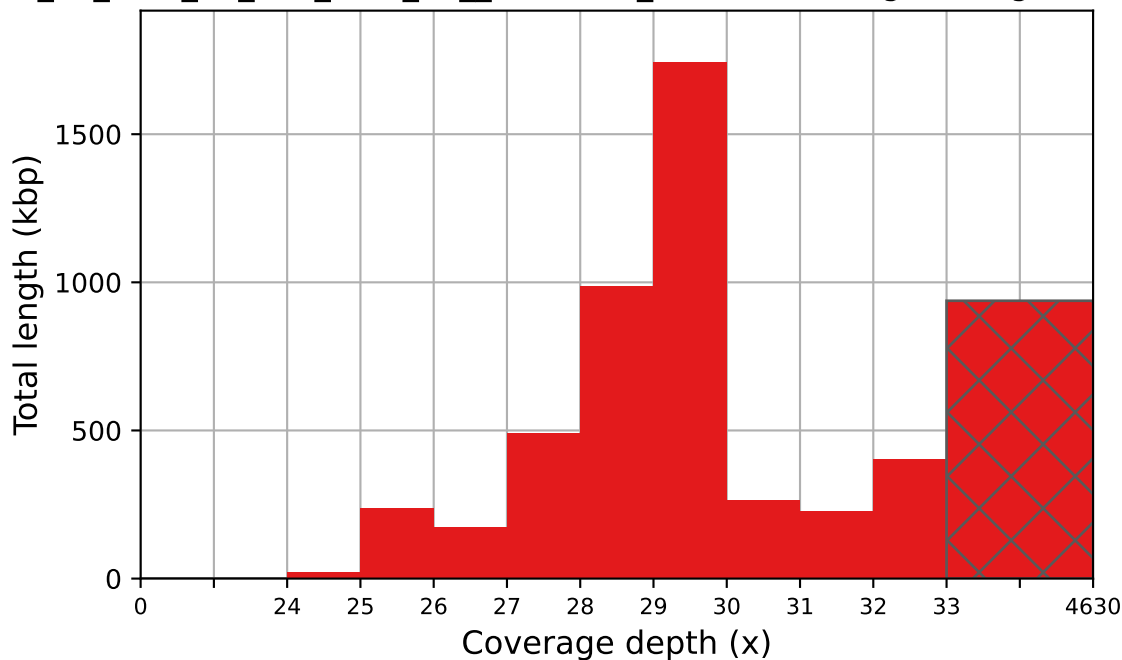
—•— SPAdes_on_data_15_and_data_14_Scaffolds

SPAdes_on_data_15_and_data_14__Scaffolds coverage histogram (bin size: 1



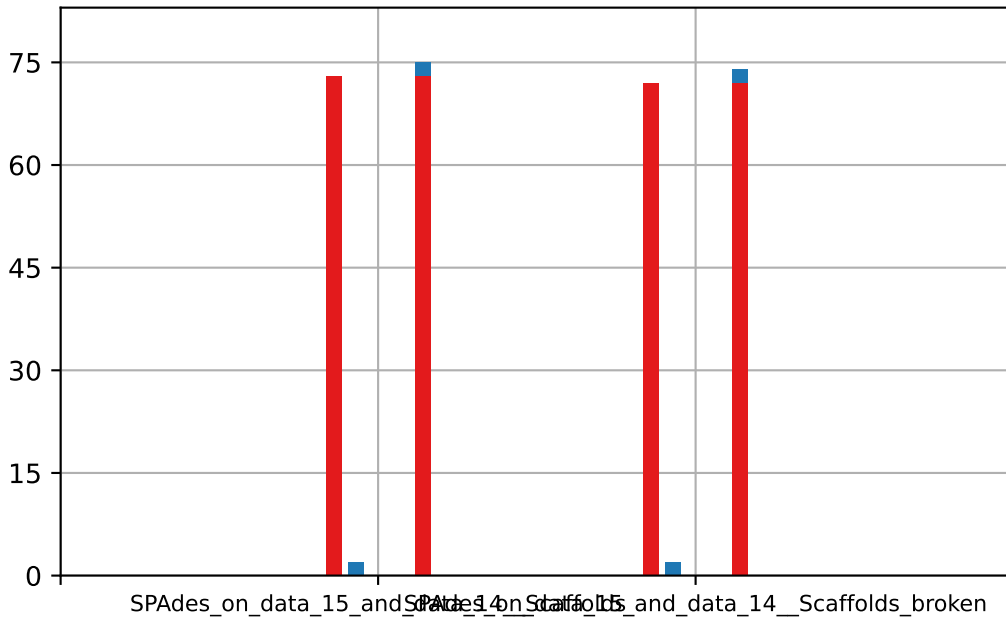
SPAdes_on_data_15_and_data_14__Scaffolds

des_on_data_15_and_data_14__Scaffolds_broken coverage histogram (bin size



SPAdes_on_data_15_and_data_14__Scaffolds_broken

Misassemblies

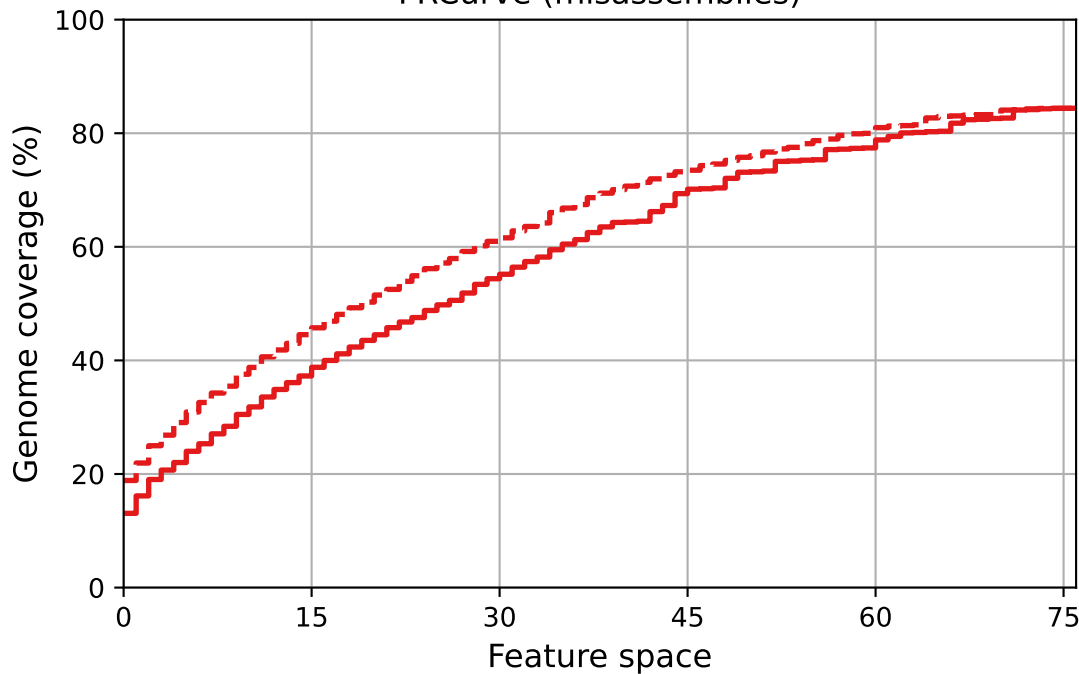


relocations



translocations

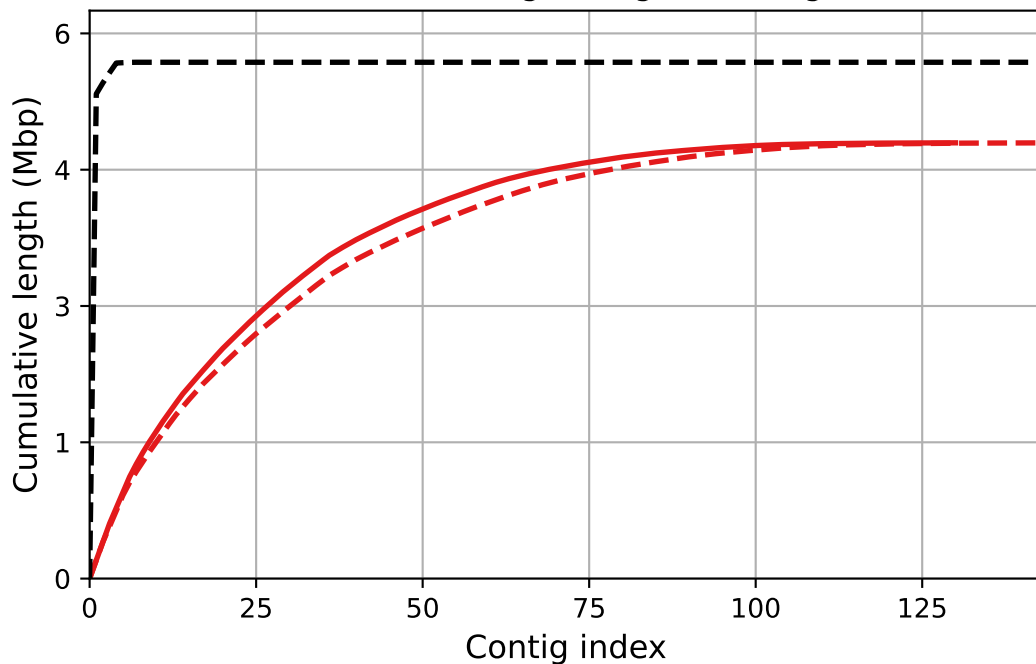
FRCurve (misassemblies)



des_on_data_15_and_data_14_Scaffolds

SPAdes_on_data_15_and_data_14_Scaffolds

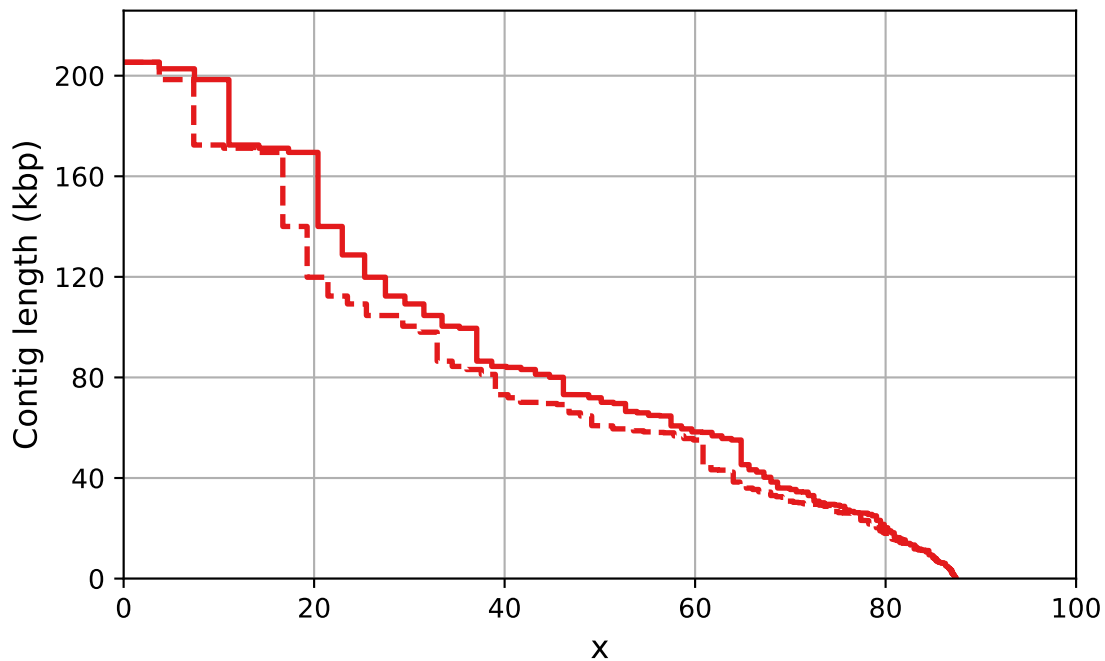
Cumulative length (aligned contigs)



data_15_and_data_14__Scaffolds

-- SPAdes_on_data_15_and_data_14__Scaffolds_broken

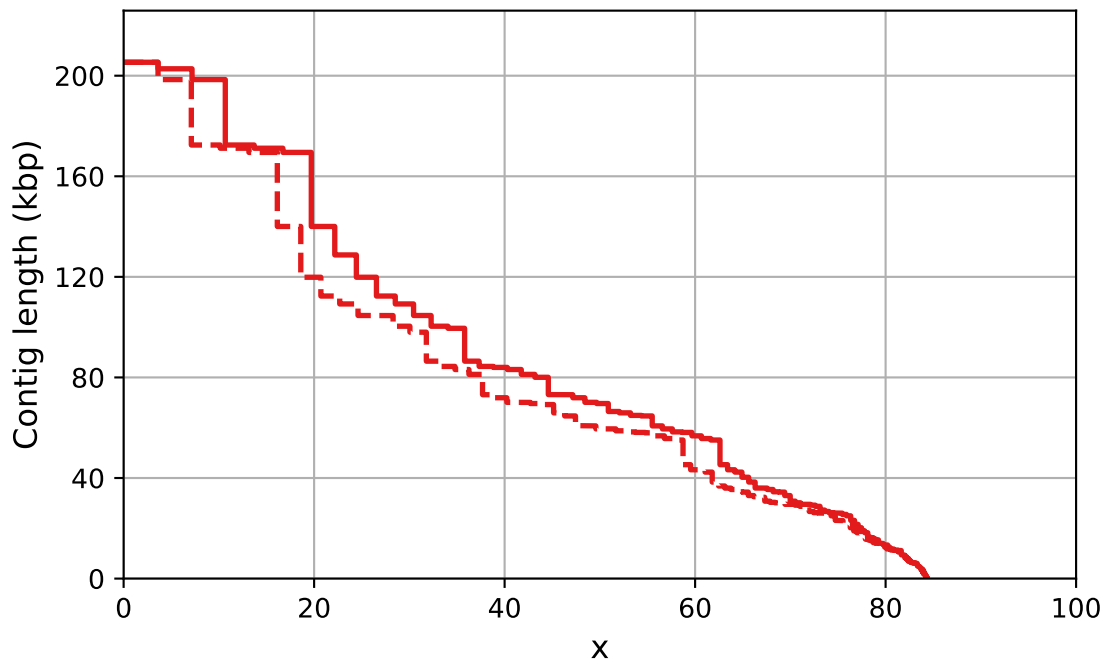
NAx



des_on_data_15_and_data_14_Scaffolds

-- SPAdes_on_data_15_and_data_14_Scaffolds

NGAx

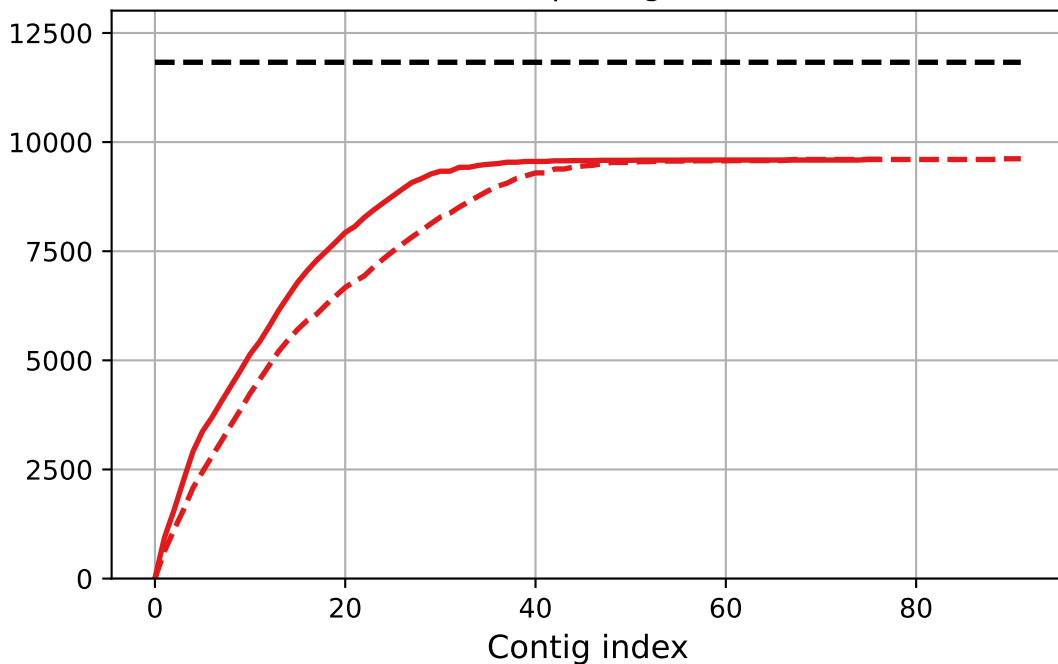


des_on_data_15_and_data_14_Scaffolds

SPAdes_on_data_15_and_data_14_Scaffolds

Cumulative # complete genomic features

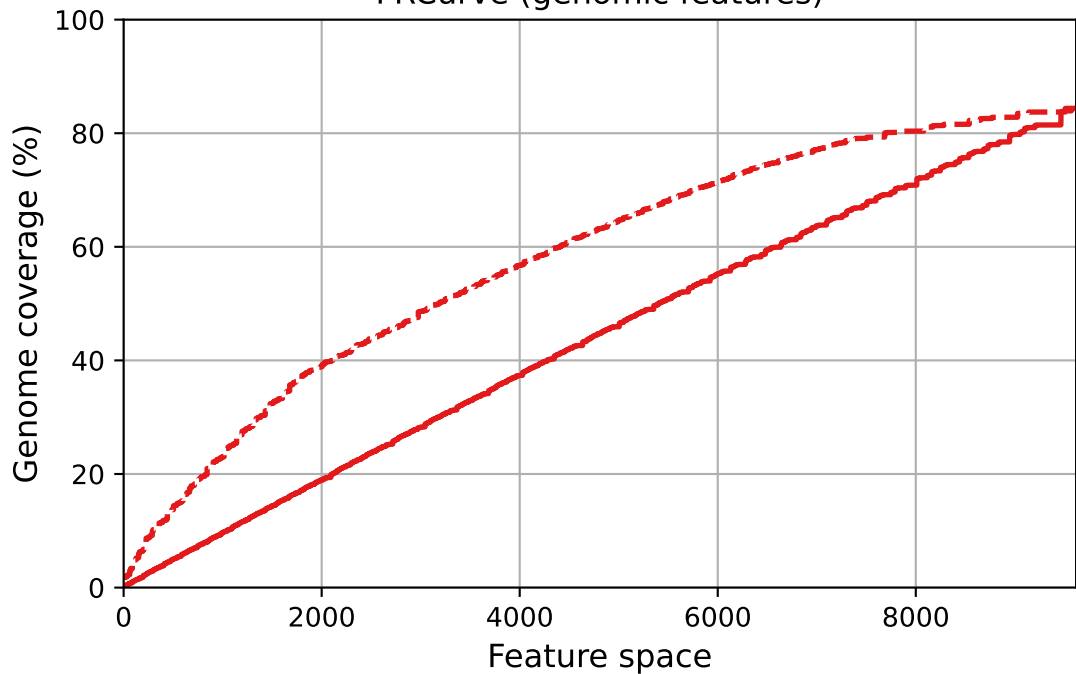
Cumulative # complete genomic features



SPAdes_on_data_15_and_data_14_Scaffolds

SPAdes_on_data_15_and_data_14_Scaffolds_broken

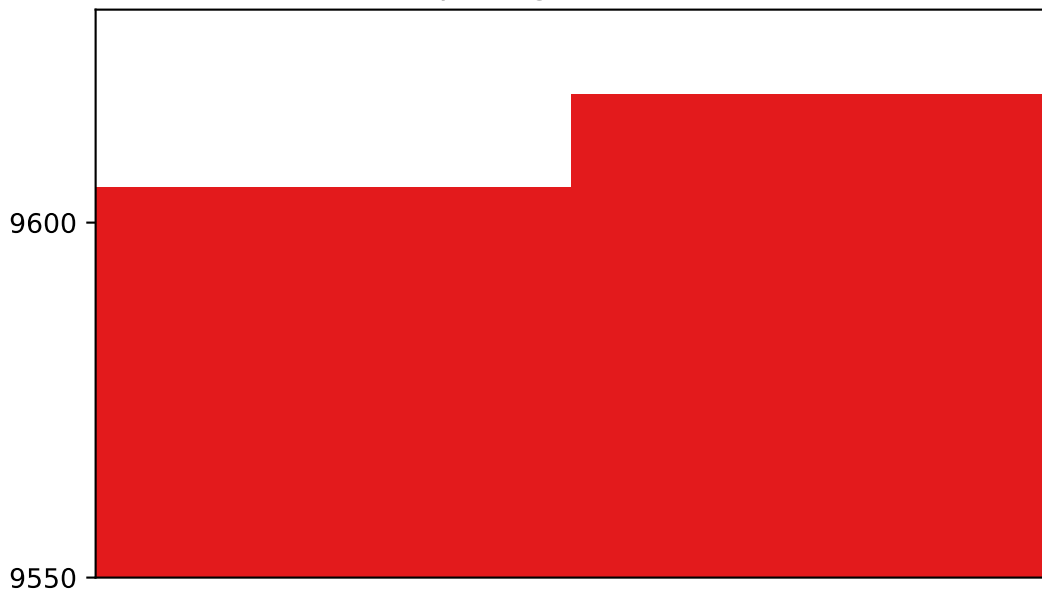
FRCurve (genomic features)



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

