

Report

	SPAdes_on_data_15__Scaffolds	SPAdes_on_data_15__Scaffolds_broken
# contigs (≥ 0 bp)	1501	-
# contigs (≥ 1000 bp)	208	215
Total length (≥ 0 bp)	4962494	-
Total length (≥ 1000 bp)	4589645	4588945
# contigs	267	274
Largest contig	146719	146719
Total length	4626322	4625622
Reference length	4411608	4411608
GC (%)	73.47	73.47
Reference GC (%)	74.43	74.43
N50	37075	36224
NG50	39690	37174
N90	11502	11129
NG90	14717	14442
auN	48596.8	45951.1
auNG	50962.1	48180.3
L50	37	38
LG50	34	35
L90	121	127
LG90	106	111
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	241 + 22 part	247 + 23 part
Unaligned length	4603854	4603751
Genome fraction (%)	0.710	0.713
Duplication ratio	1.012	1.012
# N's per 100 kbp	15.13	0.00
# mismatches per 100 kbp	4146.42	4149.85
# indels per 100 kbp	721.73	718.24
# genomic features	43 + 15 part	43 + 15 part
Complete BUSCO (%)	89.86	89.86
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	3 + 3 part	3 + 3 part
Largest alignment	3915	3915
Total aligned length	21199	21302
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	10.3	10.3
auNGA	10.8	10.8
LA50	-	-
LGA50	-	-
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

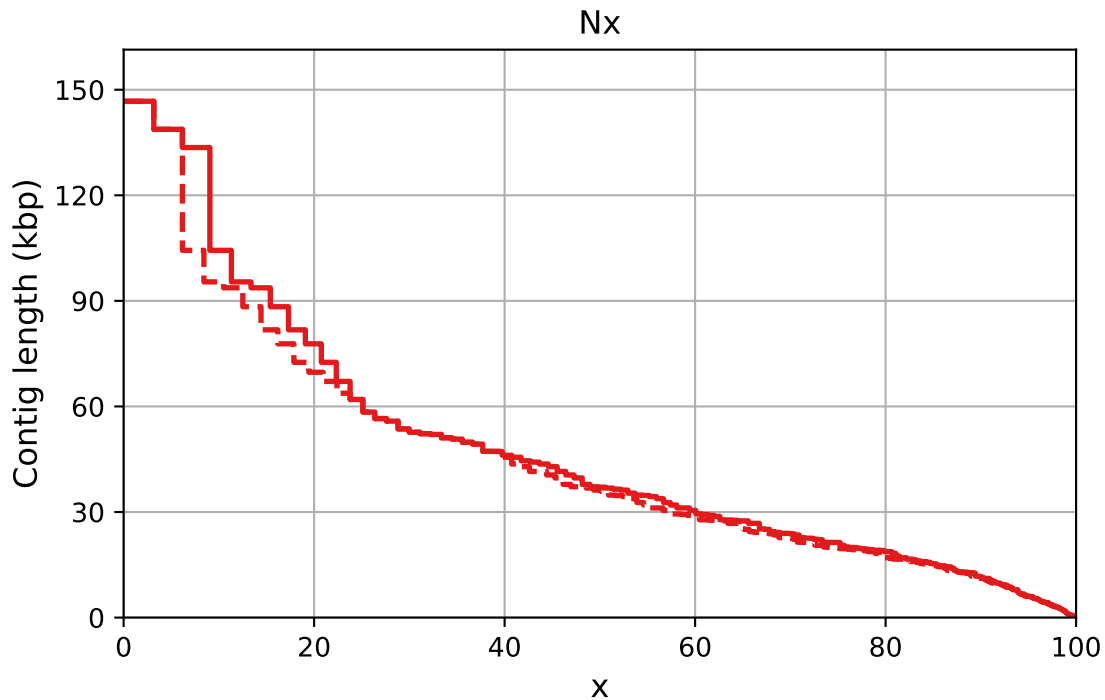
	SPAdes_on_data_15__Scaffolds	SPAdes_on_data_15__Scaffolds_broken
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	879	884
# indels	153	153
# indels (<= 5 bp)	143	143
# indels (> 5 bp)	10	10
Indels length	386	386

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__Scaffolds	SPAdes_on_data_15__Scaffolds_broken
# fully unaligned contigs	241	247
Fully unaligned length	3749159	3749159
# partially unaligned contigs	22	23
Partially unaligned length	854695	854592
# N's	700	0

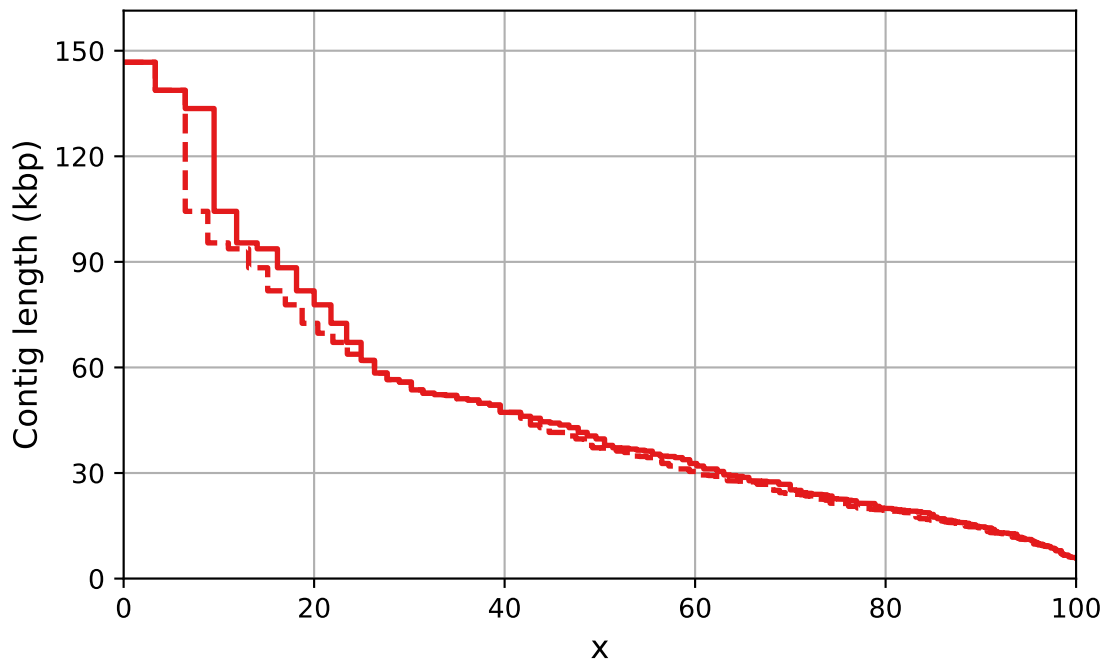
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



— SPAdes_on_data_15__Scaffolds

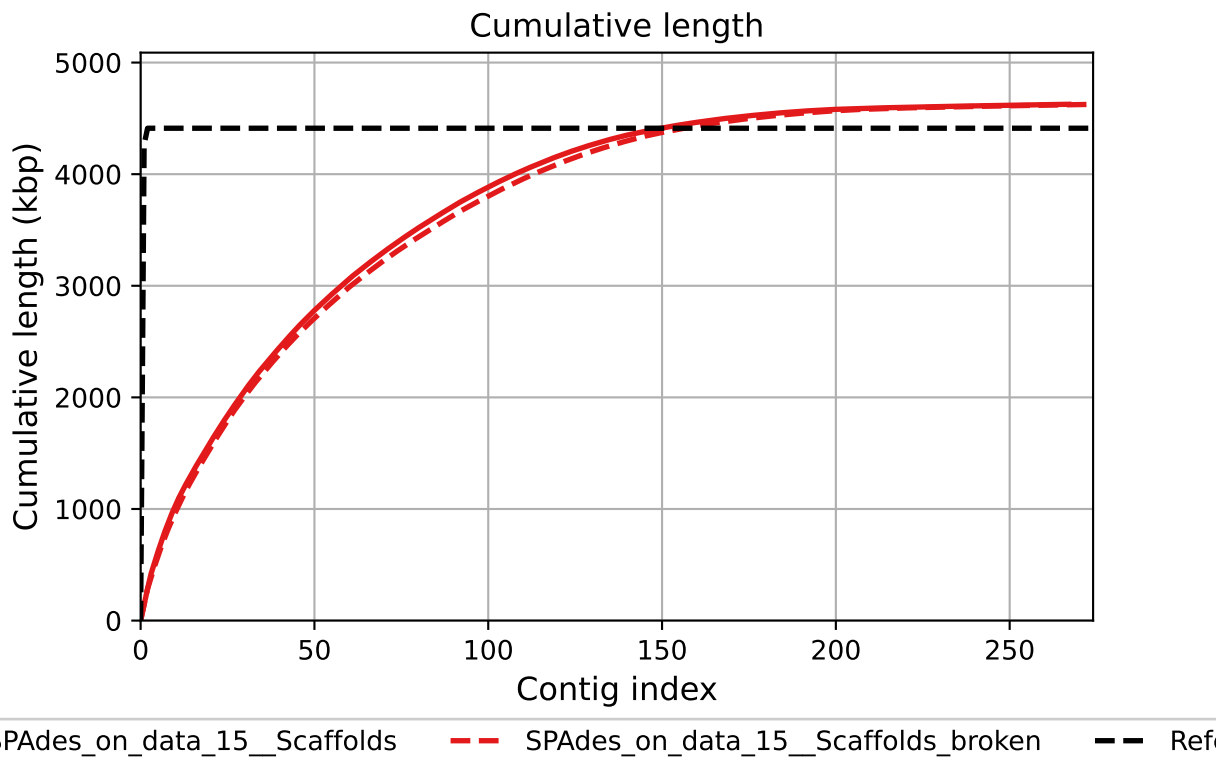
- - SPAdes_on_data_15__Scaffolds_broken

NGx

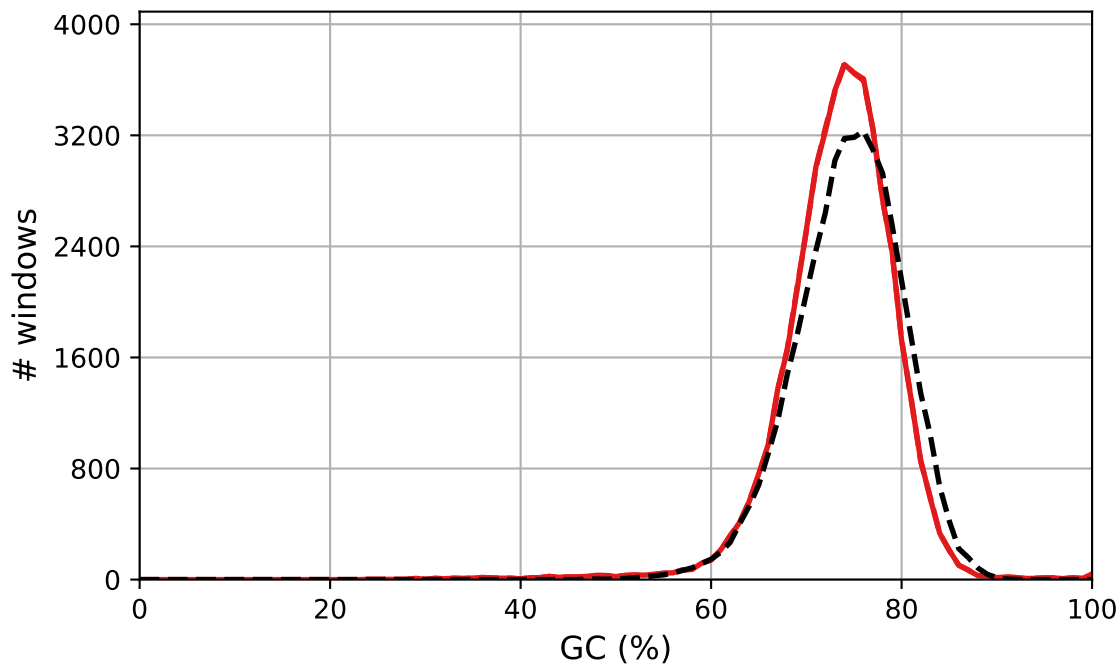


— SPAdes_on_data_15__Scaffolds

- - SPAdes_on_data_15__Scaffolds_broken



GC content

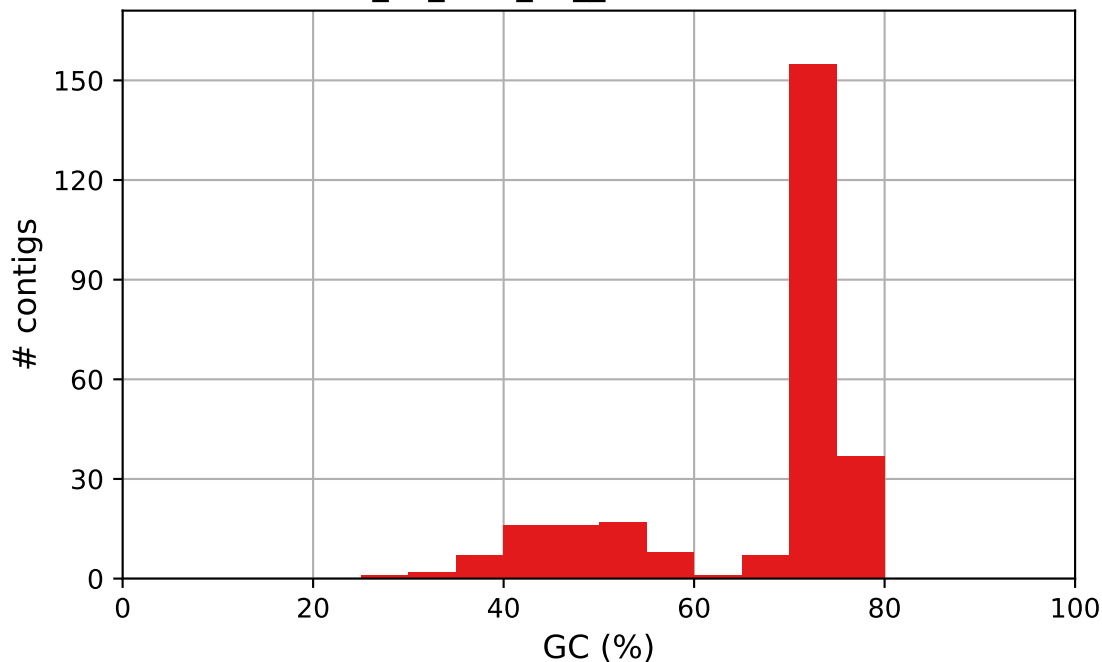


SPAdes_on_data_15_Scaffolds

SPAdes_on_data_15_Scaffolds_broken

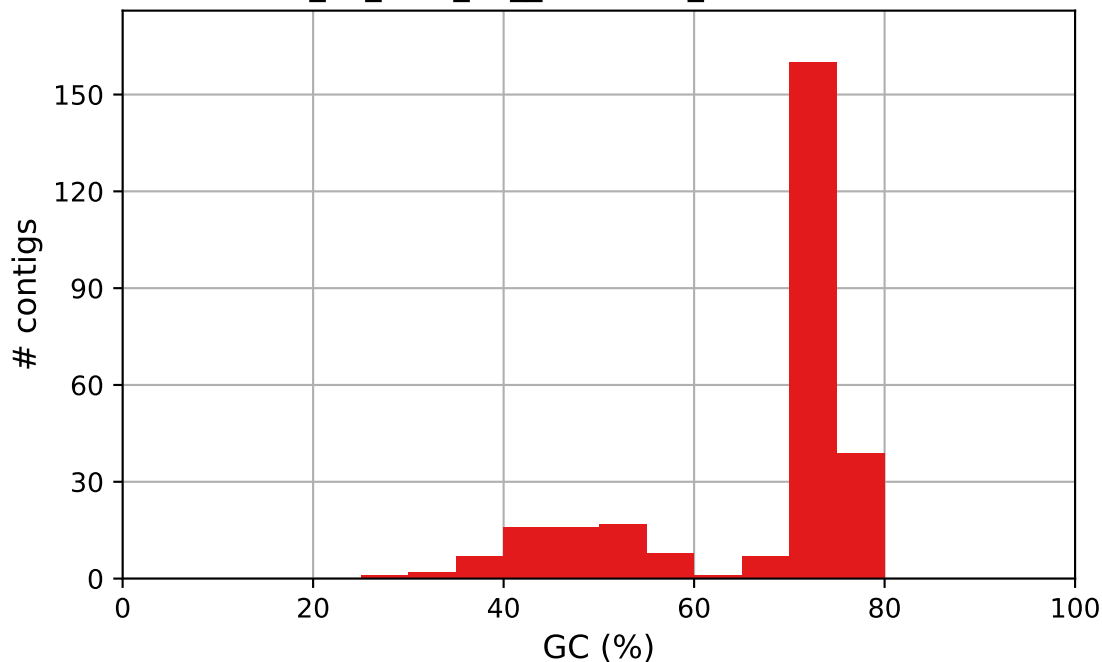
Ref

SPAdes_on_data_15__Scaffolds GC content



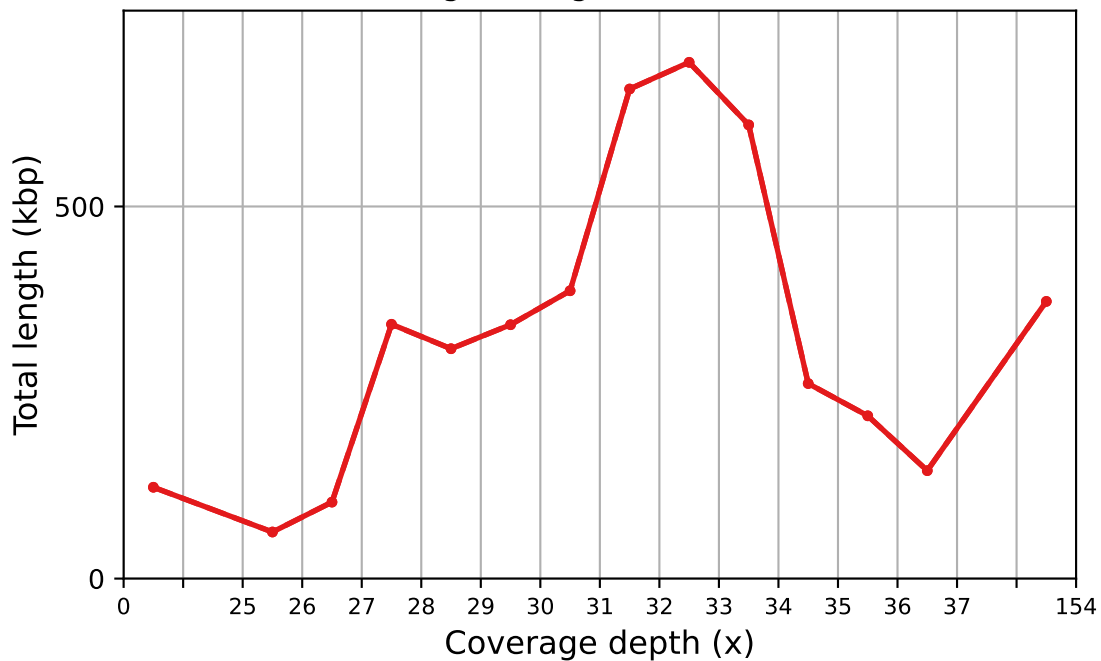
SPAdes_on_data_15__Scaffolds

SPAdes_on_data_15__Scaffolds_broken GC content



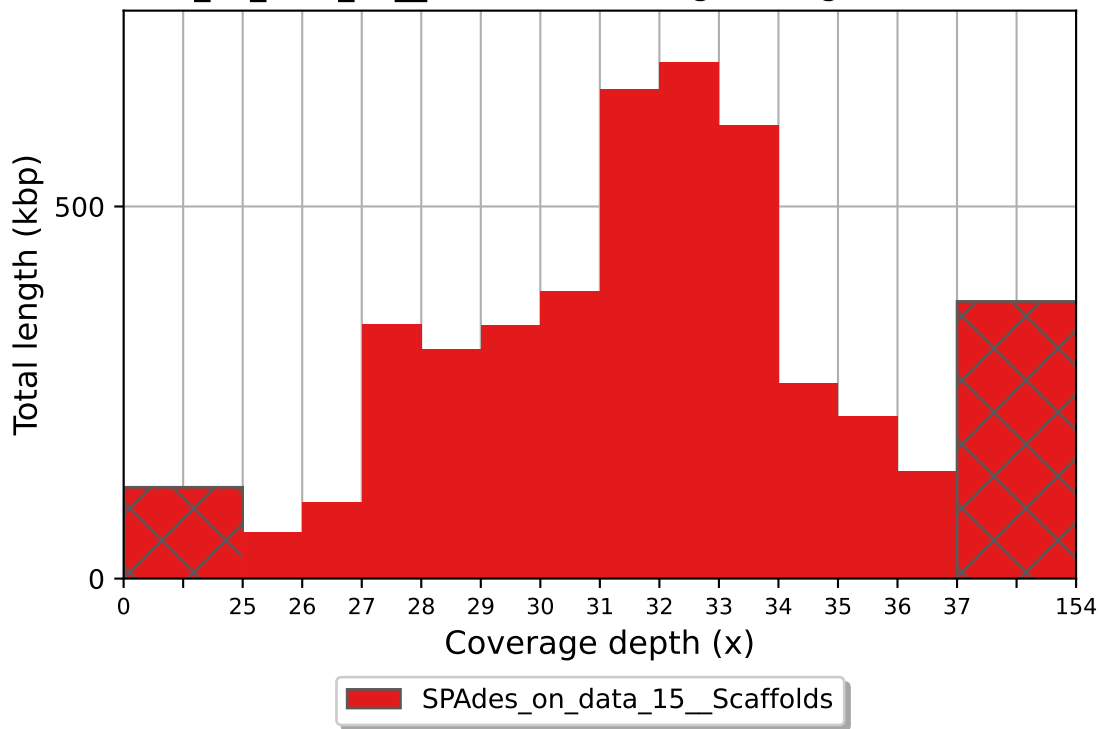
SPAdes_on_data_15__Scaffolds_broken

Coverage histogram (bin size: 1x)

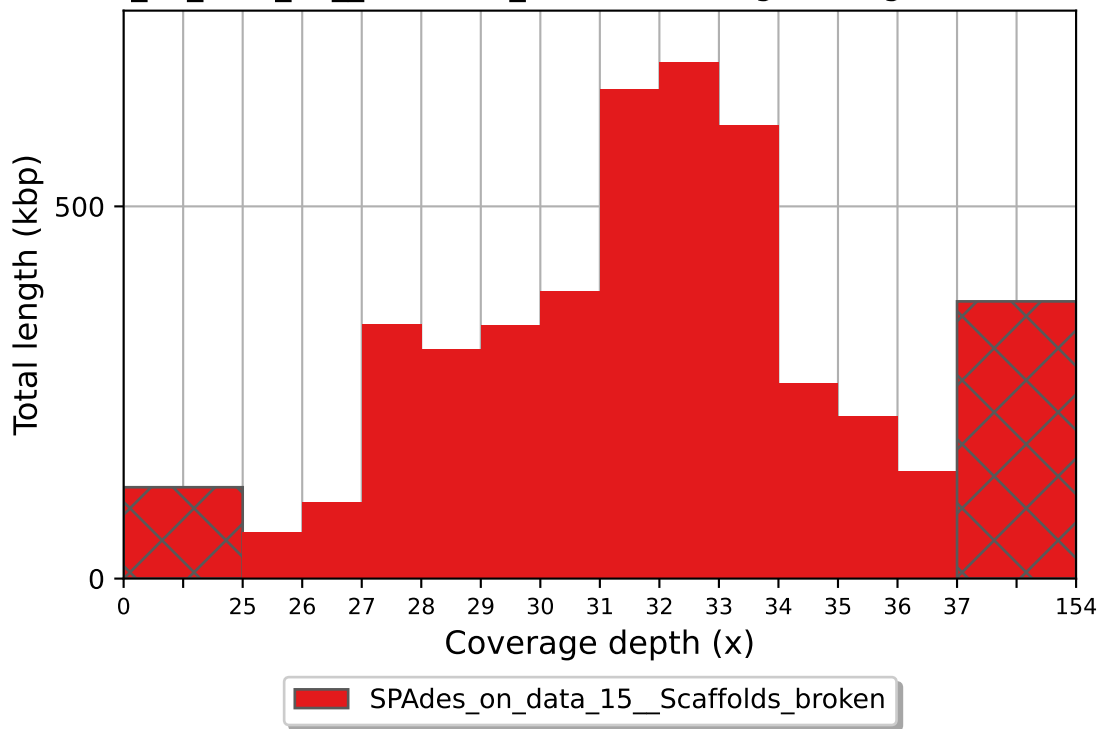


SPAdes_on_data_15__Scaffolds SPAdes_on_data_15__Scaffolds_broken

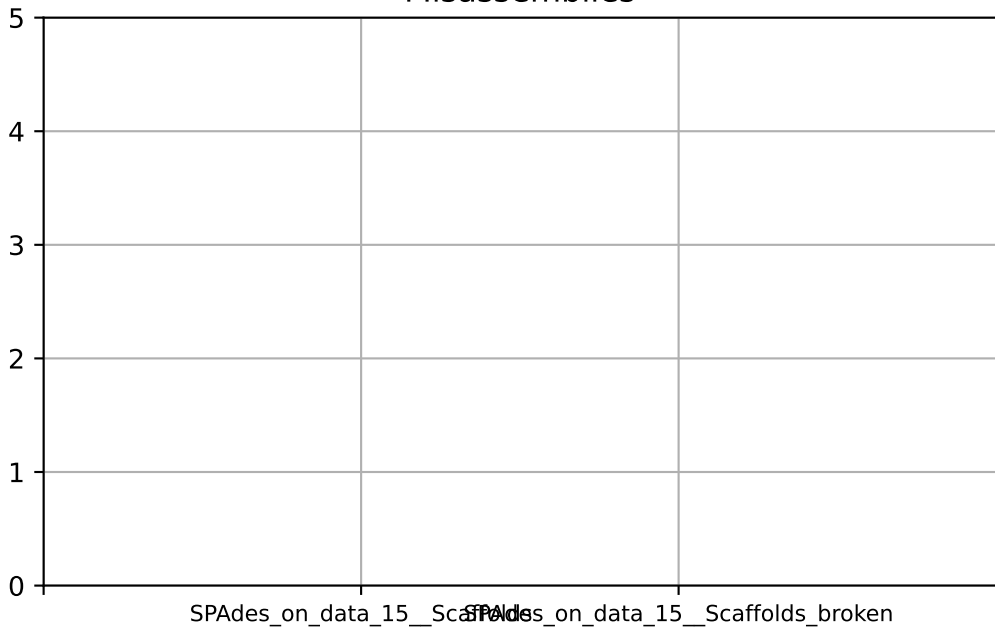
SPAdes_on_data_15__Scaffolds coverage histogram (bin size: 1x)



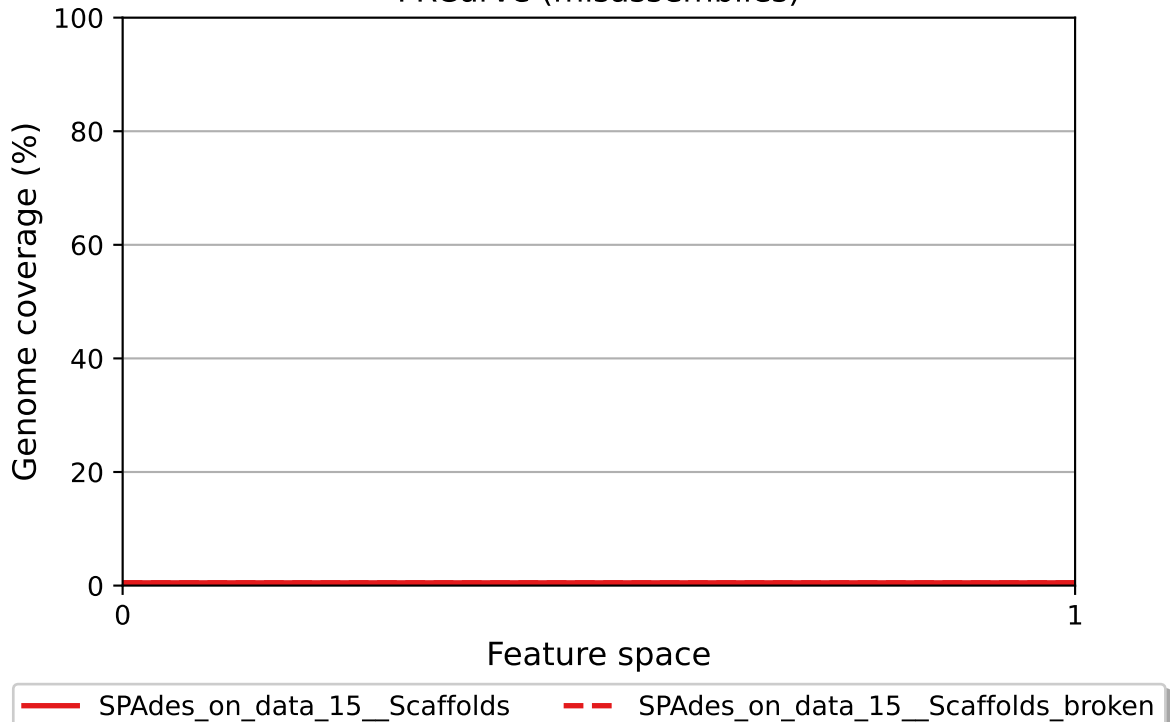
SPAdes_on_data_15__Scaffolds_broken coverage histogram (bin size: 1x)



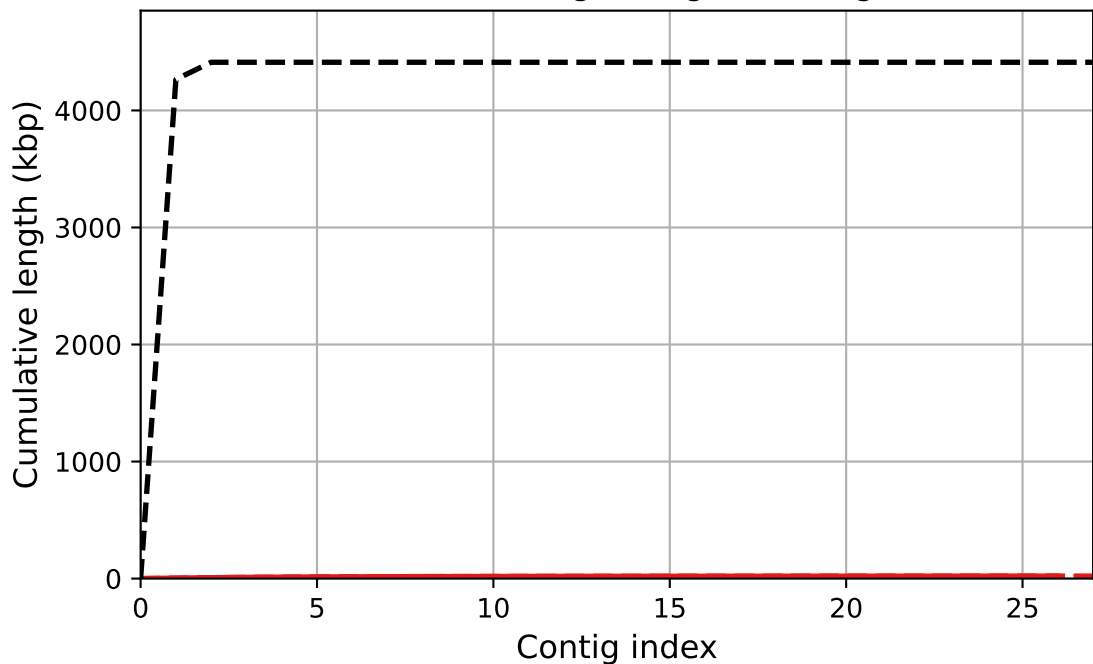
Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)

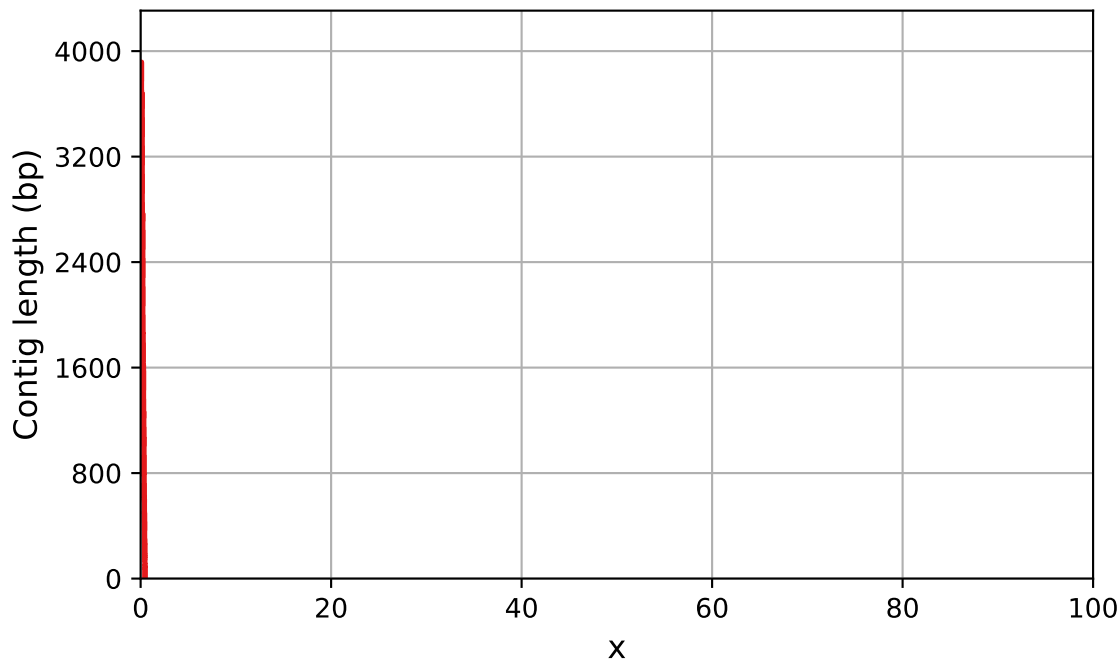


SPAdes_on_data_15_Scaffolds

SPAdes_on_data_15_Scaffolds_broken

Ref

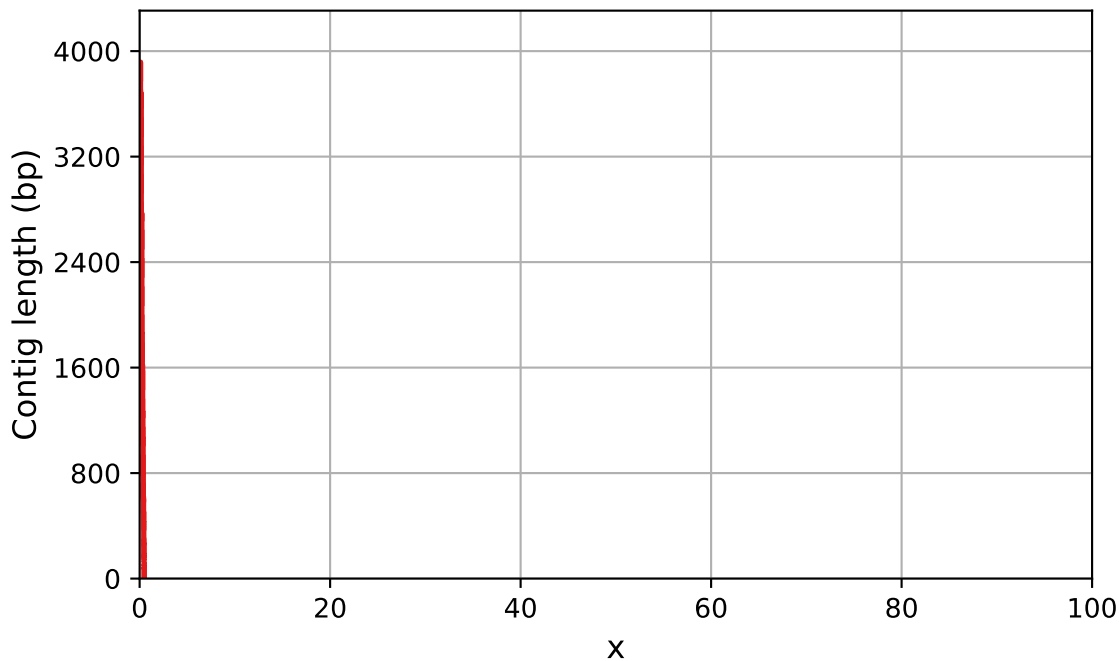
NAx



— SPAdes_on_data_15__Scaffolds

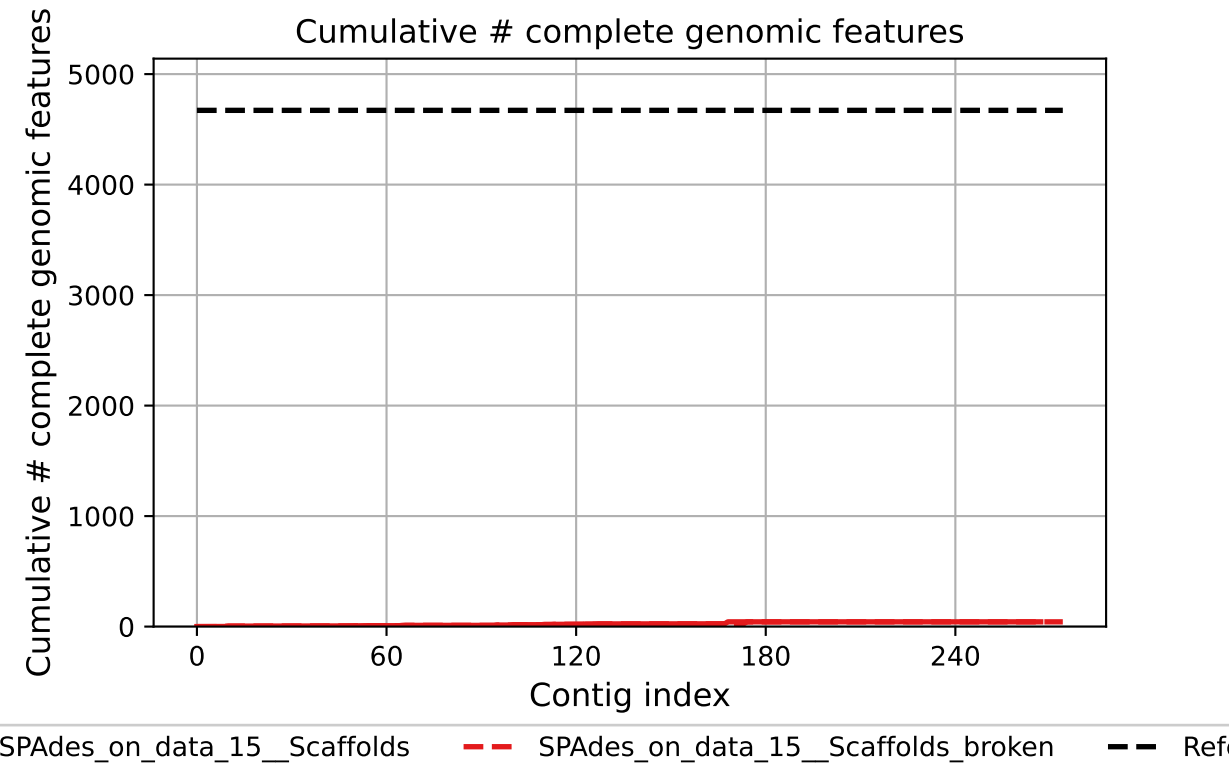
- - SPAdes_on_data_15__Scaffolds_broken

NGAx

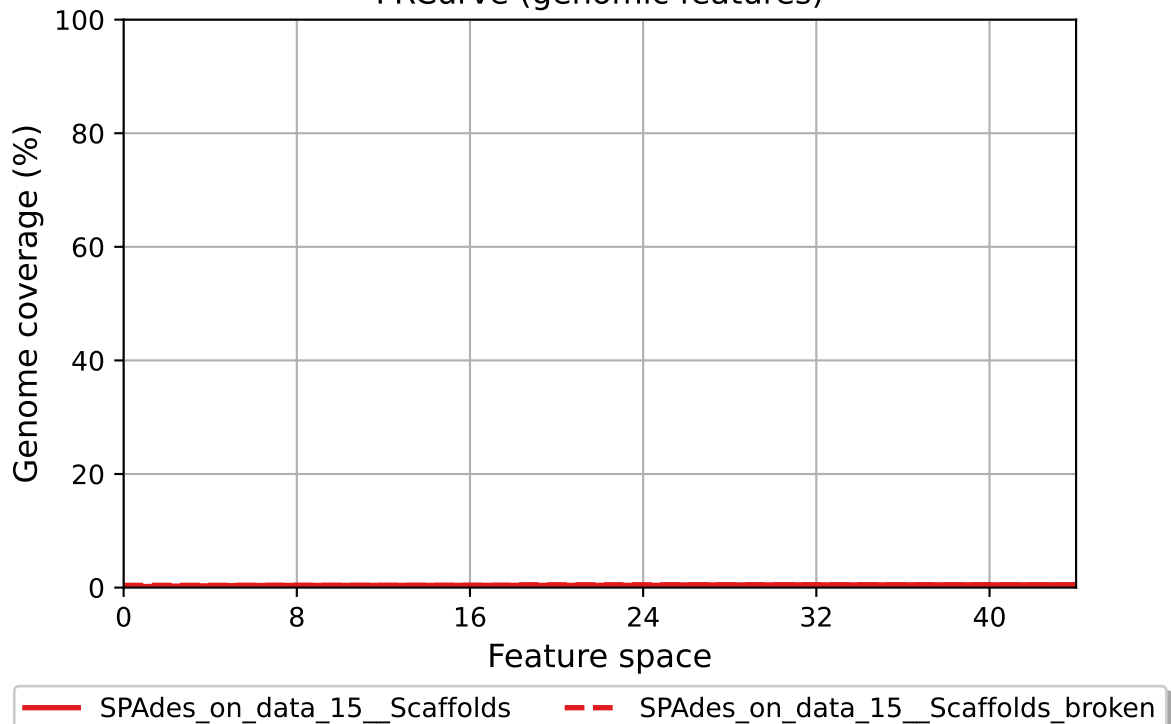


SPAdes_on_data_15__Scaffolds

SPAdes_on_data_15__Scaffolds_broken



FRCurve (genomic features)



complete genomic features



SPAdes_on_data_15__Scaffolds

SPAdes_on_data_15__Scaffolds_broken

Genome fraction, %

100

50

SPAdes_on_data_15__Scaffolds SPAdes_on_data_15__Scaffolds_broken