

Report

	SPAdes_on_data_19_and_data_18__Scaffolds	SPAdes_on_data_19_and_data_18__Scaffolds_broken
# contigs (>= 0 bp)	1422	-
# contigs (>= 1000 bp)	72	82
Total length (>= 0 bp)	5871034	-
Total length (>= 1000 bp)	5473339	5472429
# contigs	123	133
Largest contig	465117	398488
Total length	5503784	5502505
Reference length	5391123	5391123
GC (%)	57.25	57.25
Reference GC (%)	57.85	57.85
N50	193741	163595
NG50	201241	168694
N90	76558	58305
NG90	77460	61419
auN	221802.6	167260.3
auNG	226437.7	170715.9
L50	10	13
LG50	9	12
L90	28	35
LG90	26	33
# misassemblies	6	8
# misassembled contigs	3	4
Misassembled contigs length	257257	316030
# local misassemblies	2	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	19	19
# unaligned contigs	78 + 35 part	80 + 43 part
Unaligned length	4312368	4311941
Genome fraction (%)	22.748	22.750
Duplication ratio	1.005	1.005
# N's per 100 kbp	16.72	0.00
# mismatches per 100 kbp	4208.45	4208.97
# indels per 100 kbp	93.00	93.08
# genomic features	1196 + 80 part	1196 + 80 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 2 part	4 + 2 part
Largest alignment	87446	100791
Total aligned length	1190271	1190339
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	5715.2	6179.6
auNGA	5834.6	6307.3
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

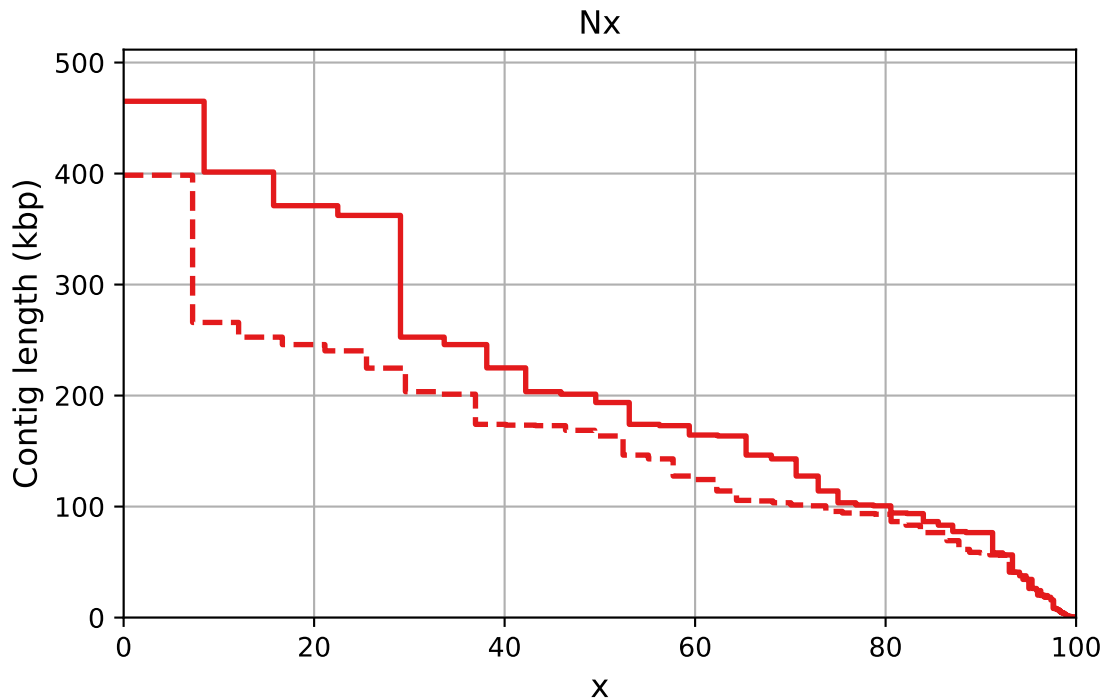
	SPAdes_on_data_19_and_data_18_Scaffolds	SPAdes_on_data_19_and_data_18_Scaffolds_broken
# misassemblies	6	8
# contig misassemblies	6	8
# c. relocations	6	8
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	3	4
Misassembled contigs length	257257	316030
# local misassemblies	2	5
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	19	19
# mismatches	50092	50101
# indels	1107	1108
# indels (<= 5 bp)	1057	1058
# indels (> 5 bp)	50	50
Indels length	3069	3070

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_19_and_data_18__Scaffolds	SPAdes_on_data_19_and_data_18__Scaffolds_broken
# fully unaligned contigs	78	80
Fully unaligned length	235453	237870
# partially unaligned contigs	35	43
Partially unaligned length	4076915	4074071
# N's	920	0

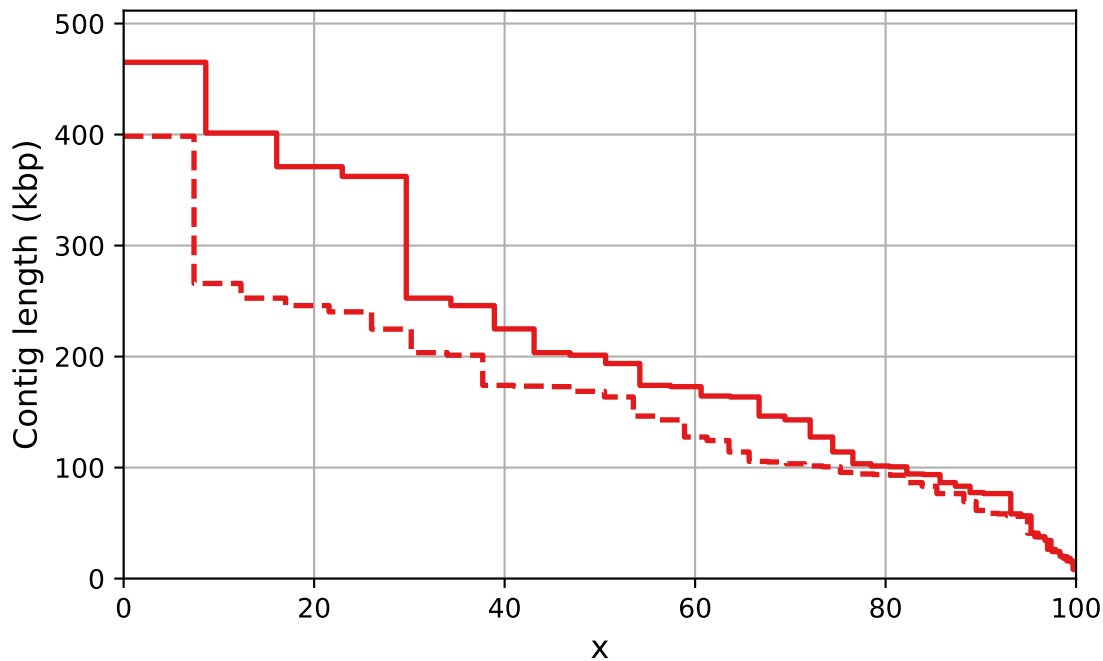
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



SPAdes_on_data_19_and_data_18_Scaffolds

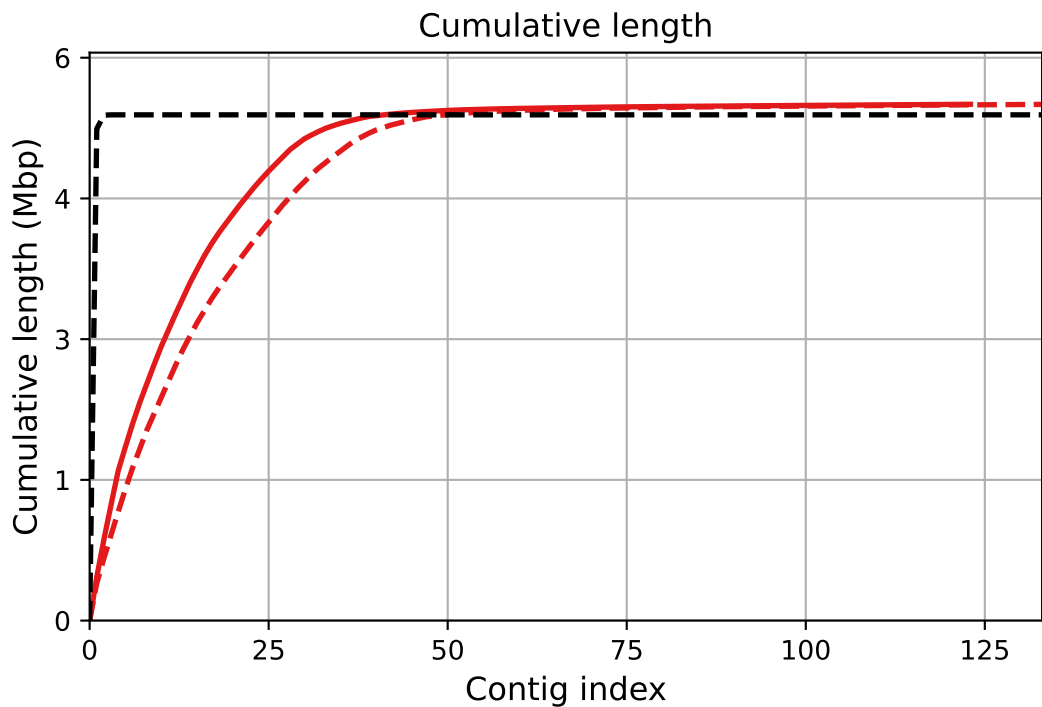
SPAdes_on_data_19_and_data_18_Scaffolds

NGx



des_on_data_19_and_data_18_Scaffolds

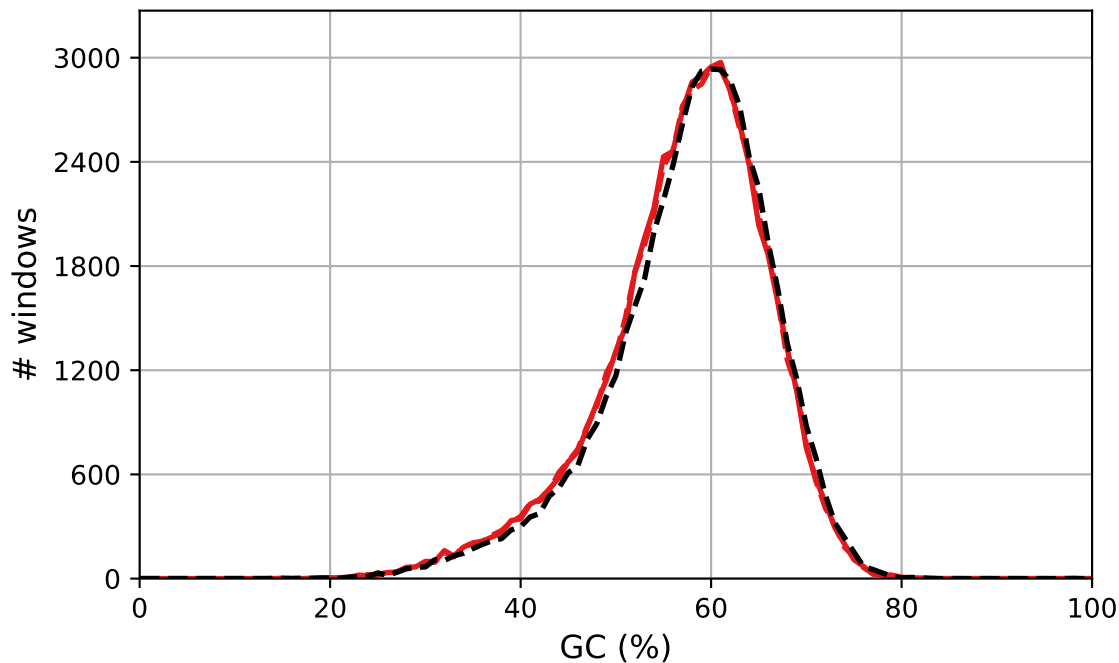
SPAdes_on_data_19_and_data_18_Scaffolds



data_19_and_data_18__Scaffolds

--- SPAdes_on_data_19_and_data_18__Scaffolds_broken

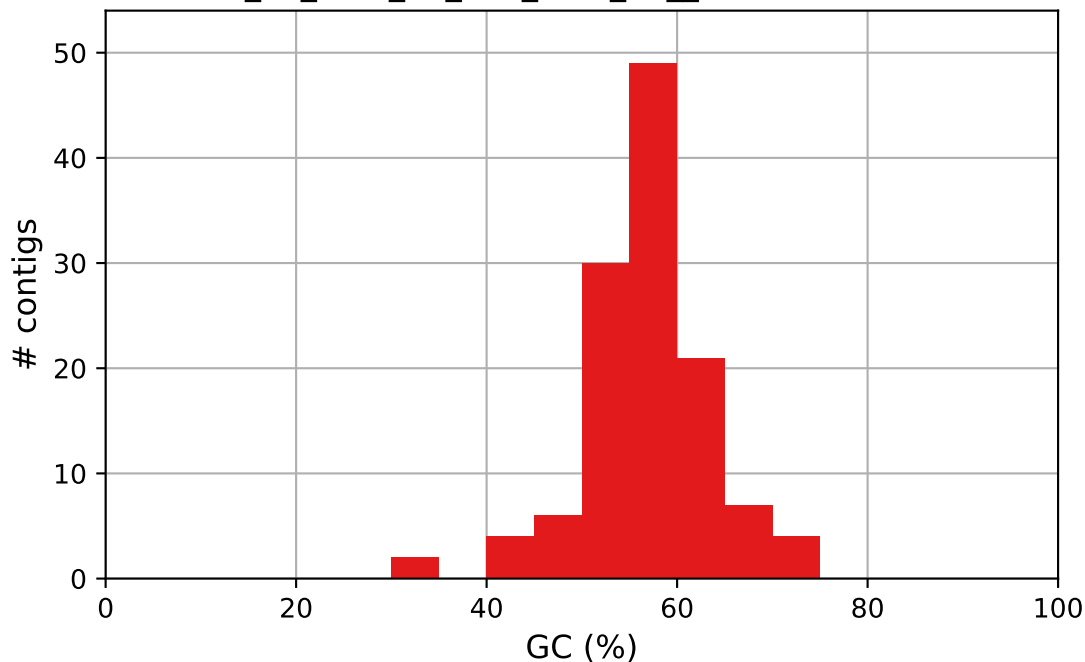
GC content



data_19_and_data_18__Scaffolds

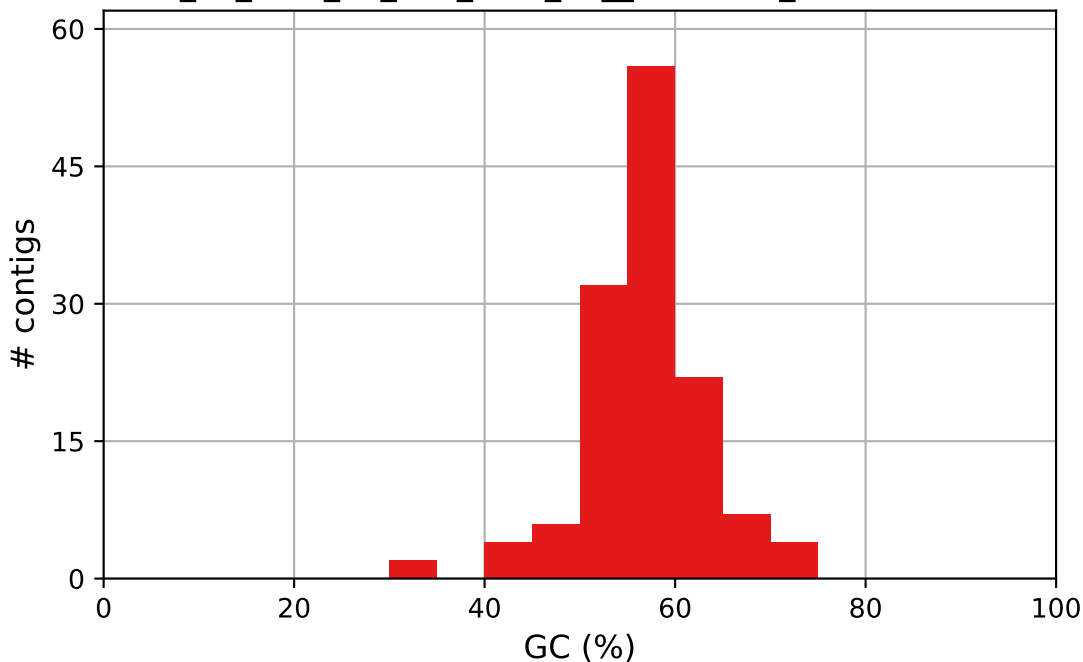
-- SPAdes_on_data_19_and_data_18__Scaffolds_broken

SPAdes_on_data_19_and_data_18__Scaffolds GC content



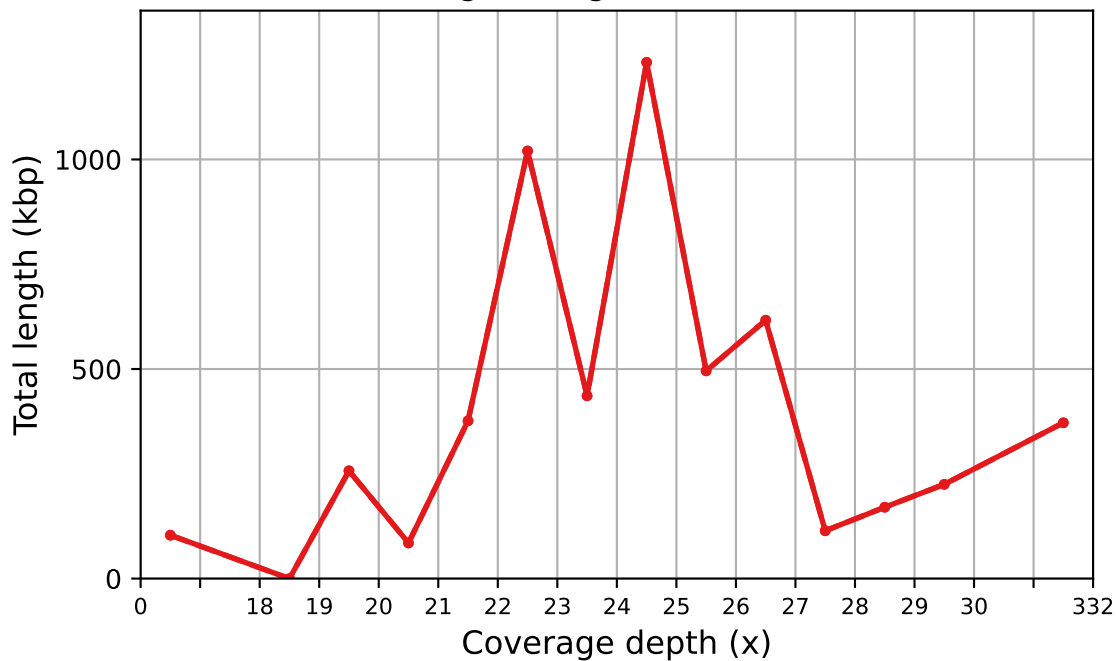
SPAdes_on_data_19_and_data_18__Scaffolds

SPAdes_on_data_19_and_data_18__Scaffolds_broken GC content



SPAdes_on_data_19_and_data_18__Scaffolds_broken

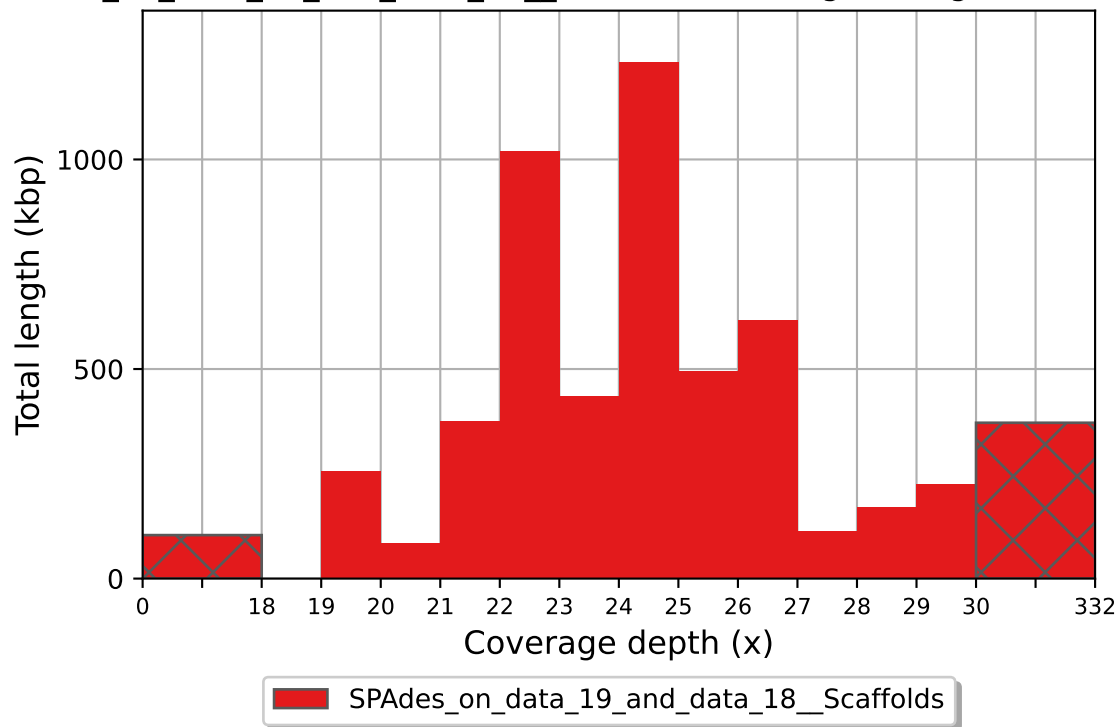
Coverage histogram (bin size: 1x)



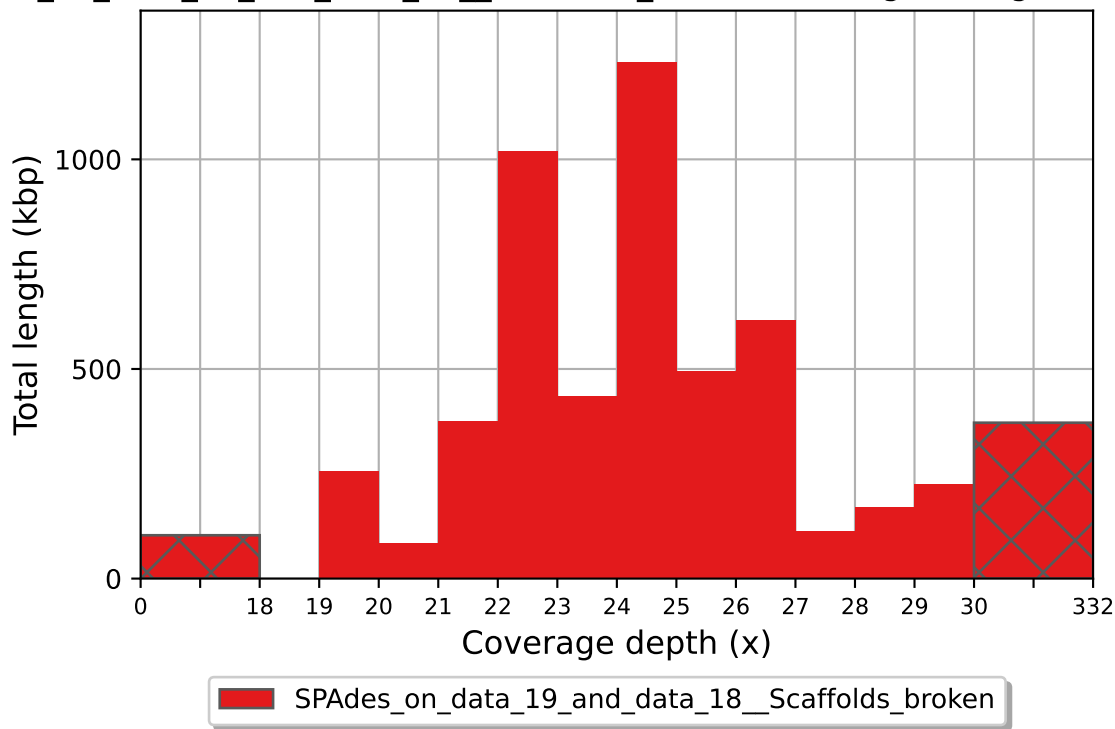
des_on_data_19_and_data_18_Scaffolds

—●— SPAdes_on_data_19_and_data_18_Scaffolds

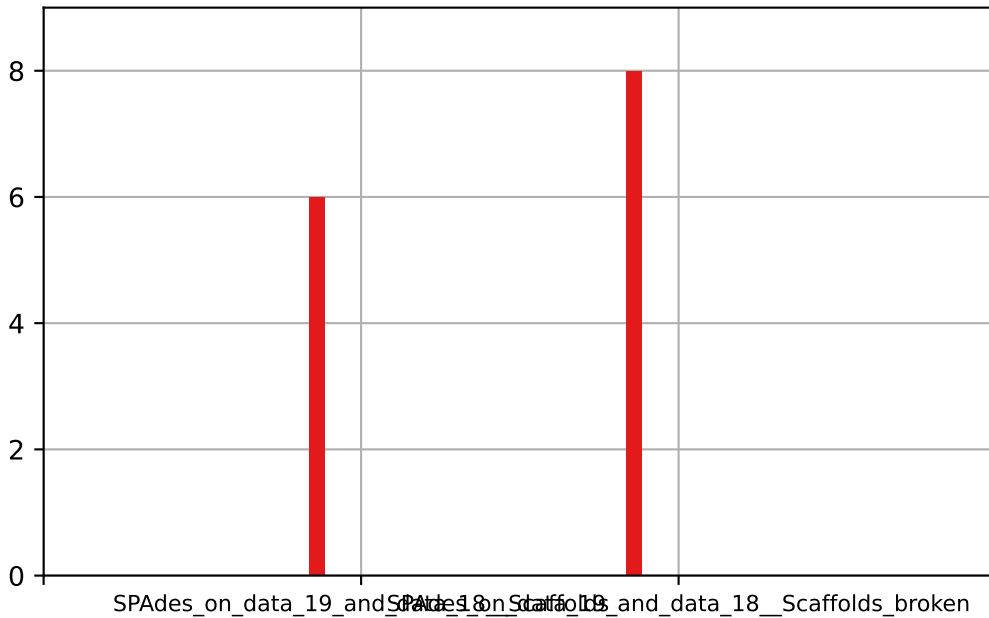
SPAdes_on_data_19_and_data_18__Scaffolds coverage histogram (bin size: 1



des_on_data_19_and_data_18__Scaffolds_broken coverage histogram (bin size

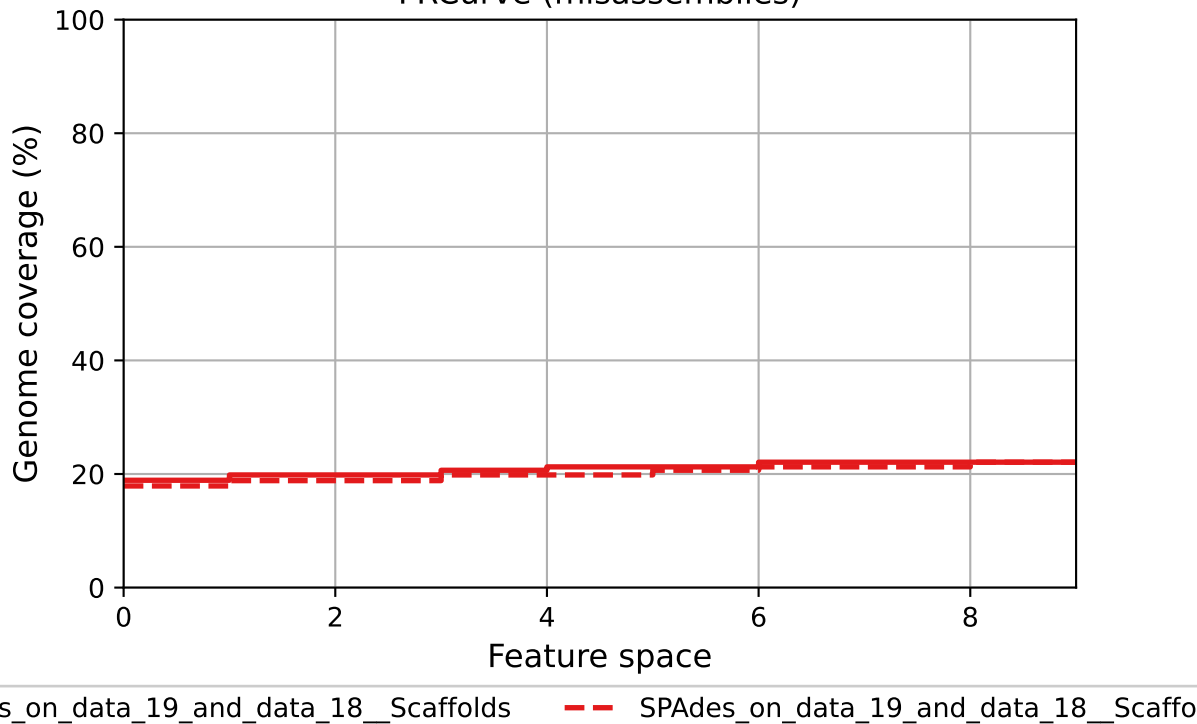


Misassemblies

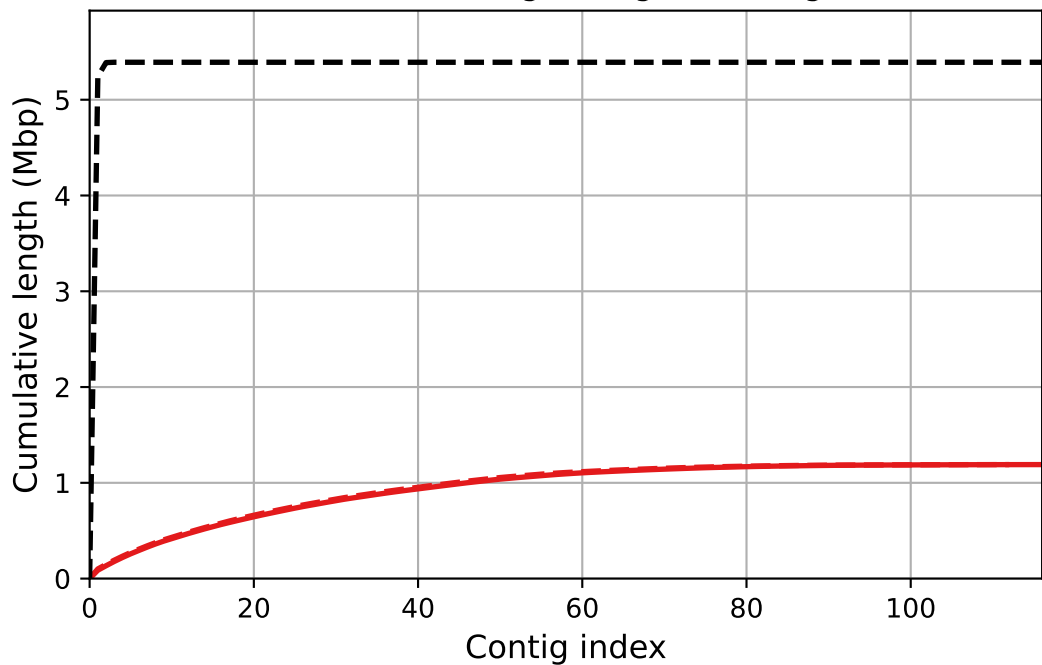


 # relocations

FRCurve (misassemblies)



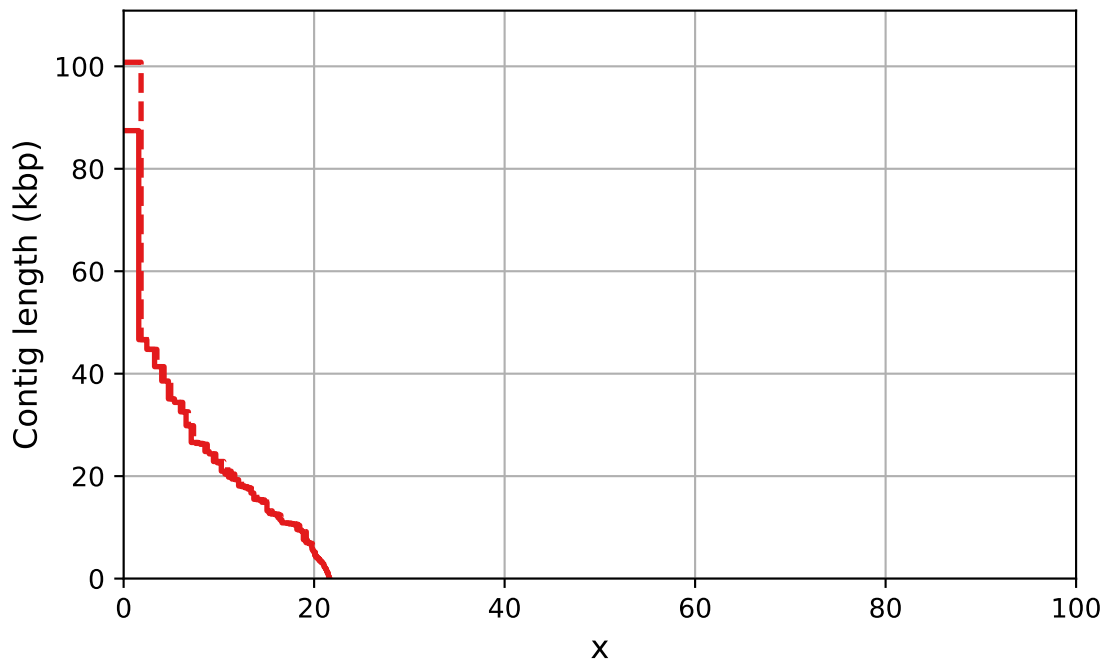
Cumulative length (aligned contigs)



data_19_and_data_18_Scaffolds

SPAdes_on_data_19_and_data_18_Scaffolds_broken

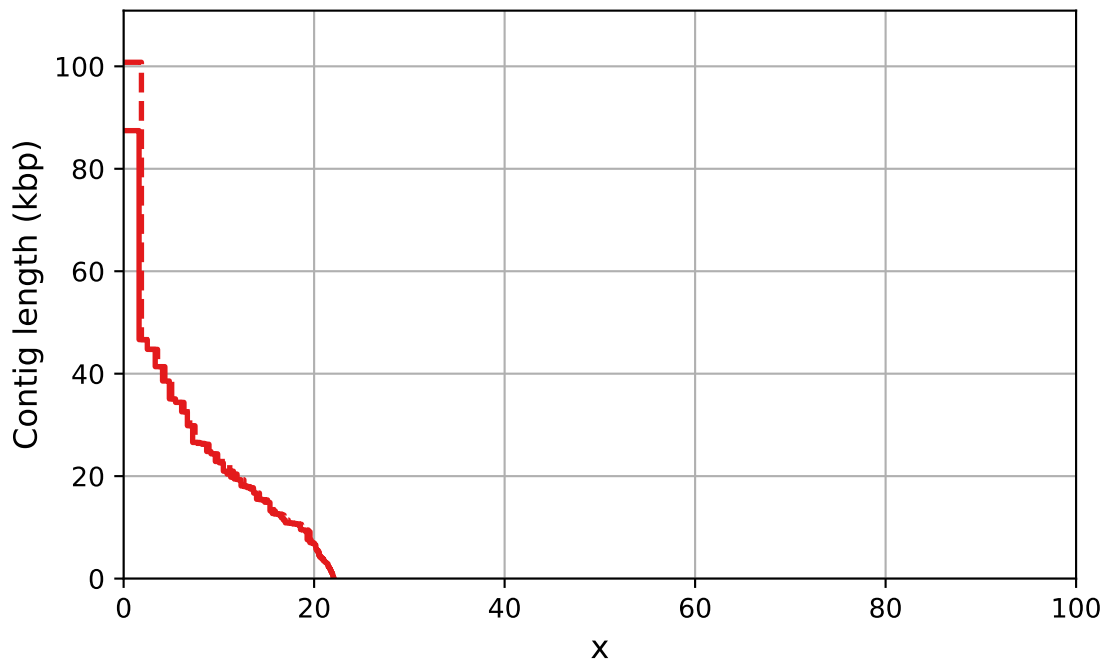
NAx



des_on_data_19_and_data_18__Scaffolds

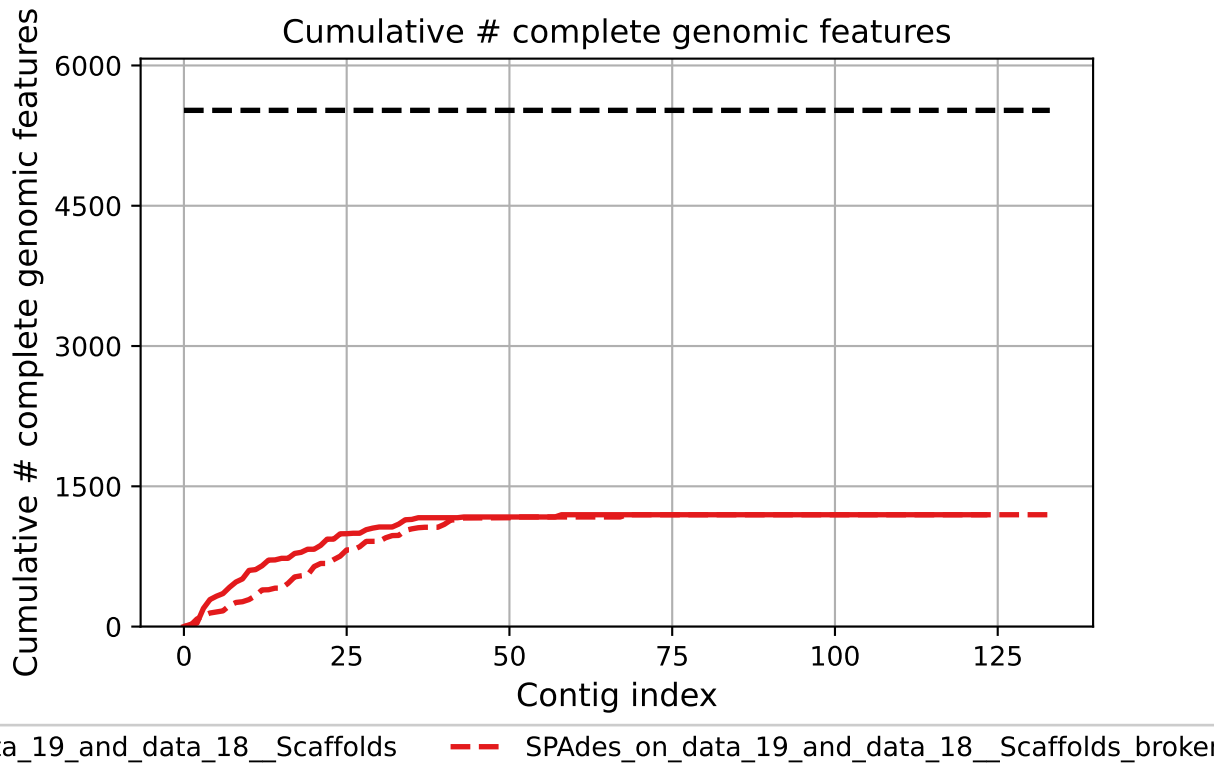
-- SPAdes_on_data_19_and_data_18__Scaffolds

NGAx

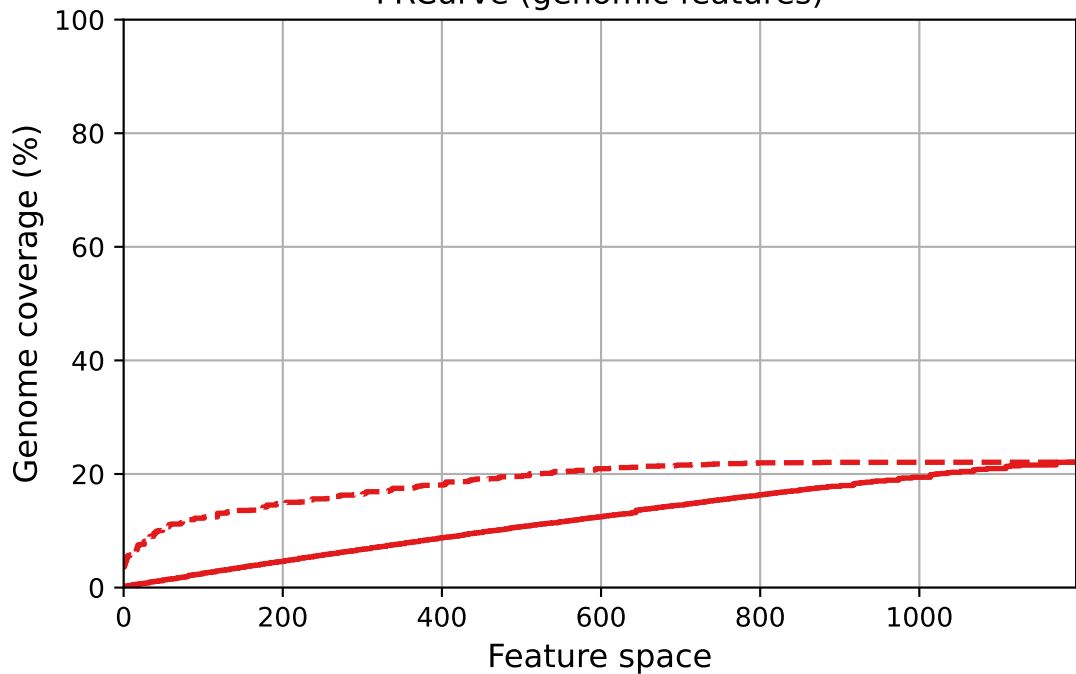


des_on_data_19_and_data_18_Scaffolds

-- SPAdes_on_data_19_and_data_18_Scaffolds



FRCurve (genomic features)



des_on_data_19_and_data_18__Scaffolds

-- SPAdes_on_data_19_and_data_18__Scaffolds

complete genomic features



des_on_data_19_and_data_18_Scaffolds



SPAdes_on_data_19_and_data_18_Scaffolds

Genome fraction, %

100

50

des_on_data_19_and_data_18__Scaffolds



SPAdes_on_data_19_and_data_18__Scaffolds