Report

	SPAdes_on_data_28_and_data_27__Scaffolds	SPAdes_on_data_28_and_data_27__Scaffolds_broken
# contigs (>= 0 bp)	211	-
# contigs (>= 1000 bp)	116	130
Total length (>= 0 bp)	4408870	-
Total length (>= 1000 bp)	4367058	4365370
# contigs	141	157
Largest contig	215247	168121
Total length	4384125	4383065
Reference length	4411532	4411532
GC (%)	65.45	65.45
Reference GC (%)	65.61	65.61
N50	81436	71106
NG50	81436	71106
N90	22832	17640
NG90	22526	17572
auN	91362.7	81253.1
auNG	90795.1	80728.8
L50	18	20
LG50	18	20
L90	54	62
LG90	55	64
# misassemblies	30	28
# misassembled contigs	25	23
Misassembled contigs length	1562513	1148426
# local misassemblies	12	12
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	1
# unaligned contigs	16 + 16 part	16 + 16 part
Unaligned length	46510	46501
Genome fraction (%)	98.435	98.430
Duplication ratio	1.007	1.006
# N's per 100 kbp	24.18	0.00
# mismatches per 100 kbp	60.63	60.84
# indels per 100 kbp	9.11	8.88
# genomic features	8304 + 255 part	8292 + 264 part
Complete BUSCO (%)	97.30	97.30
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 1 part	2 + 1 part
Largest alignment	170119	168121
Total aligned length	4324357	4322984
NA50	66446	63897
NGA50	64320	63897
NA90	17470	16022
NGA90	17031	15501
auNA	76209.8	72059.7
auNGA	75736.3	71594.7
LA50	21	23
LGA50	22	23
LA90	68	75
LGA90	70	77

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).
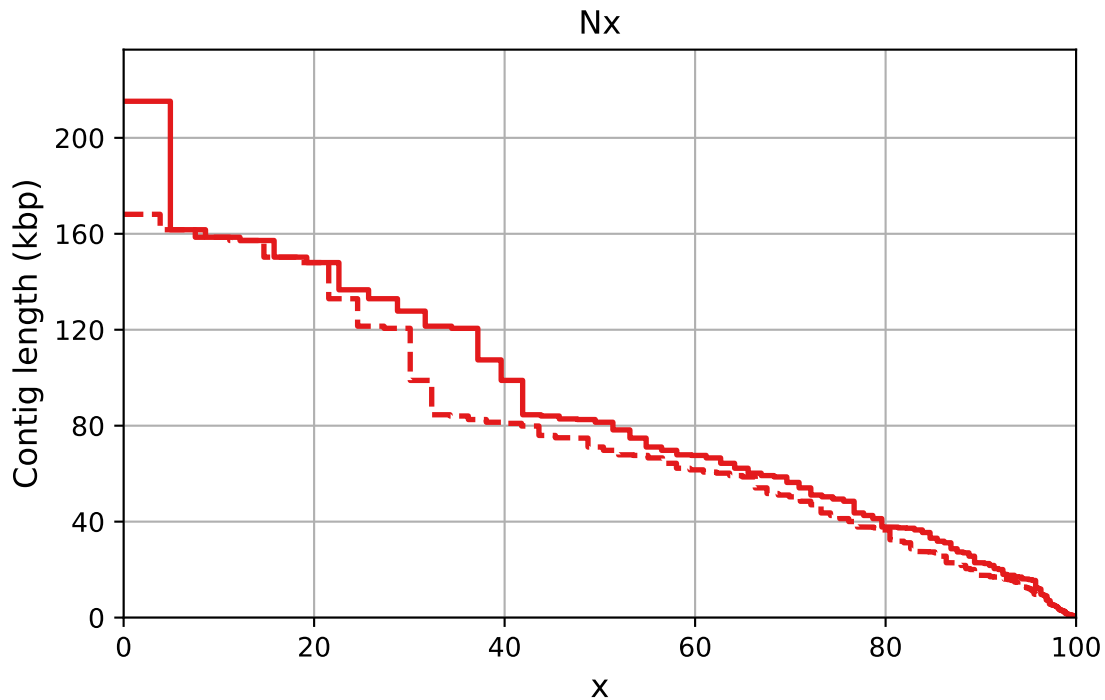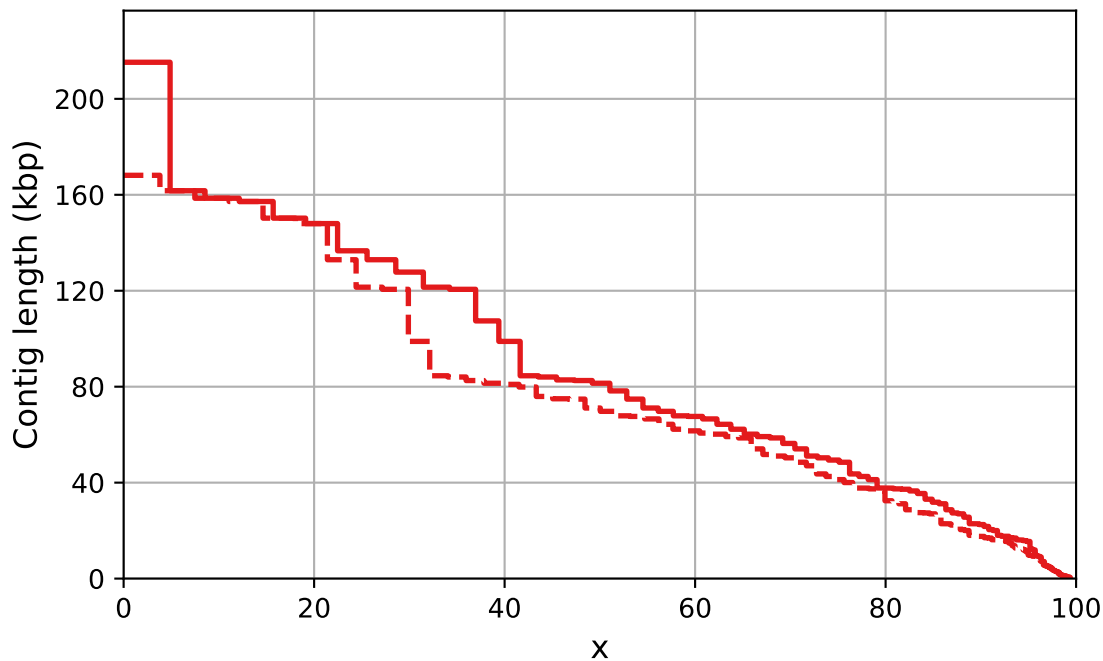
Misassemblies report

	SPAdes_on_data_28_and_data_27__Scaffolds	SPAdes_on_data_28_and_data_27__Scaffolds_broken
# misassemblies	30	28
# contig misassemblies	30	28
# c. relocations	29	27
# c. translocations	0	0
# c. inversions	1	1
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	25	23
Misassembled contigs length	1562513	1148426
# local misassemblies	12	12
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	3	-
# unaligned mis. contigs	0	1
# mismatches	2622	2630
# indels	394	384
# indels (<= 5 bp)	252	254
# indels (> 5 bp)	142	130
Indels length	9417	7328

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_28_and_data_27__Scaffolds	SPAdes_on_data_28_and_data_27__Scaffolds_broken
# fully unaligned contigs	16	16
Fully unaligned length	12321	12321
# partially unaligned contigs	16	16
Partially unaligned length	34189	34180
# N's	1060	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).

Nx

NGx

Contig length (kbp) vs x

des_on_data_28_and_data_27__Scaffolds — — SPAdes_on_data_28_and_data_27__Scaffo

Cumulative length

Contig index (x-axis), **Cumulative length (kbp)** (y-axis)
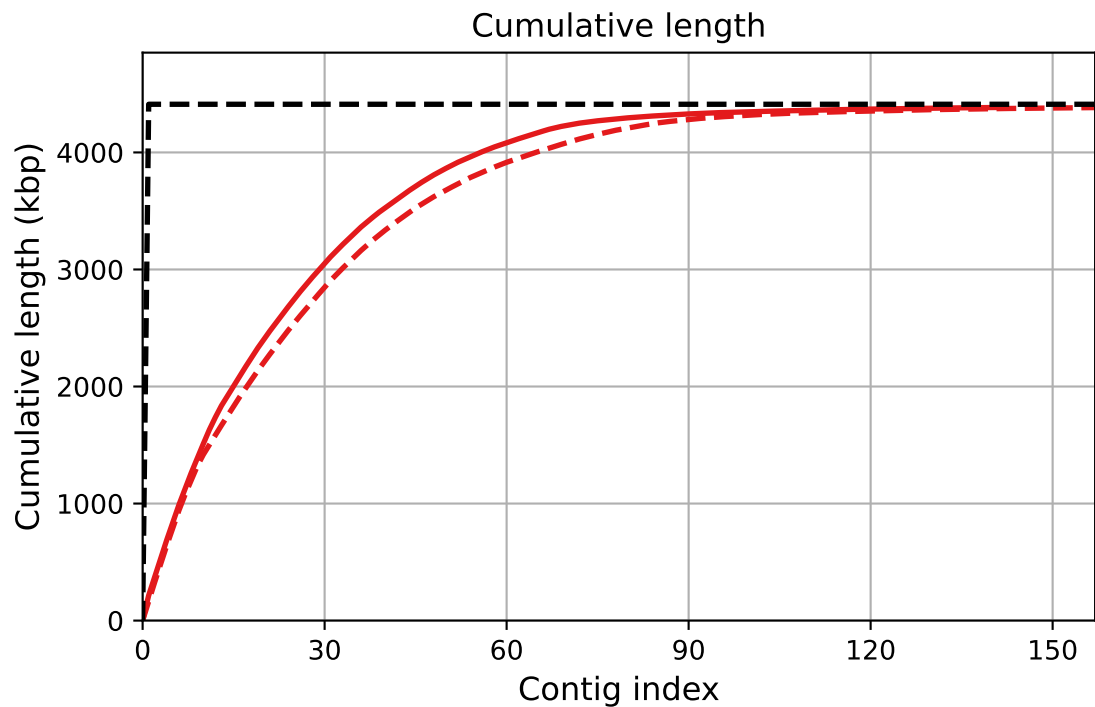
ta_28_and_data_27__Scaffolds   SPAdes_on_data_28_and_data_27__Scaffolds_broken
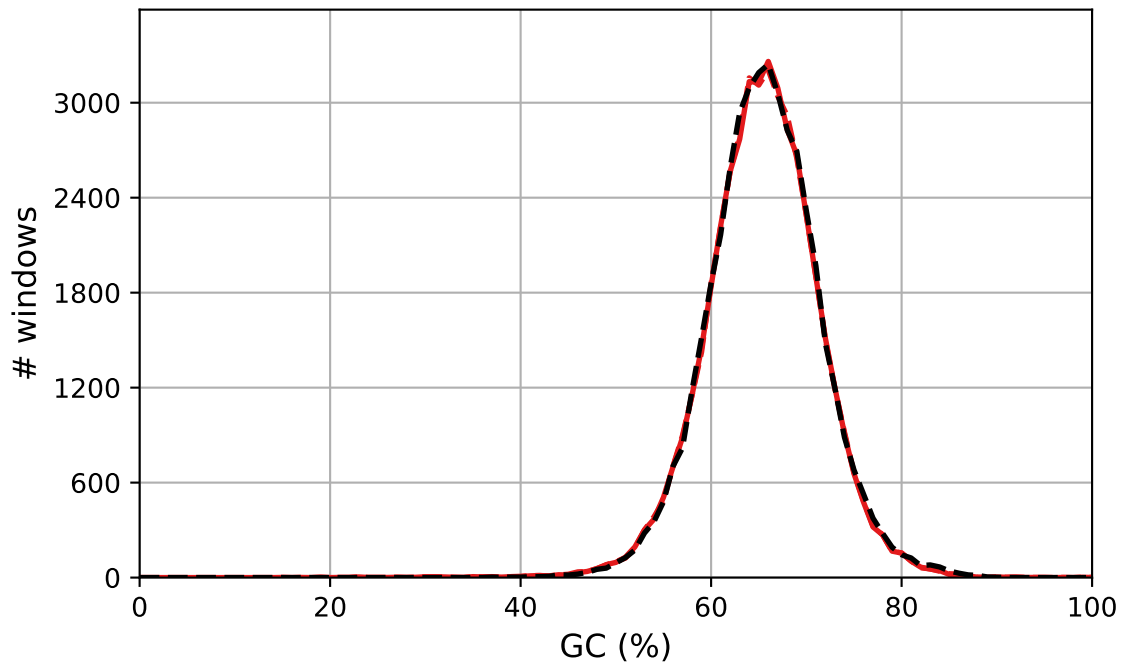
GC content

Legend:
- ta_28_and_data_27__Scaffolds
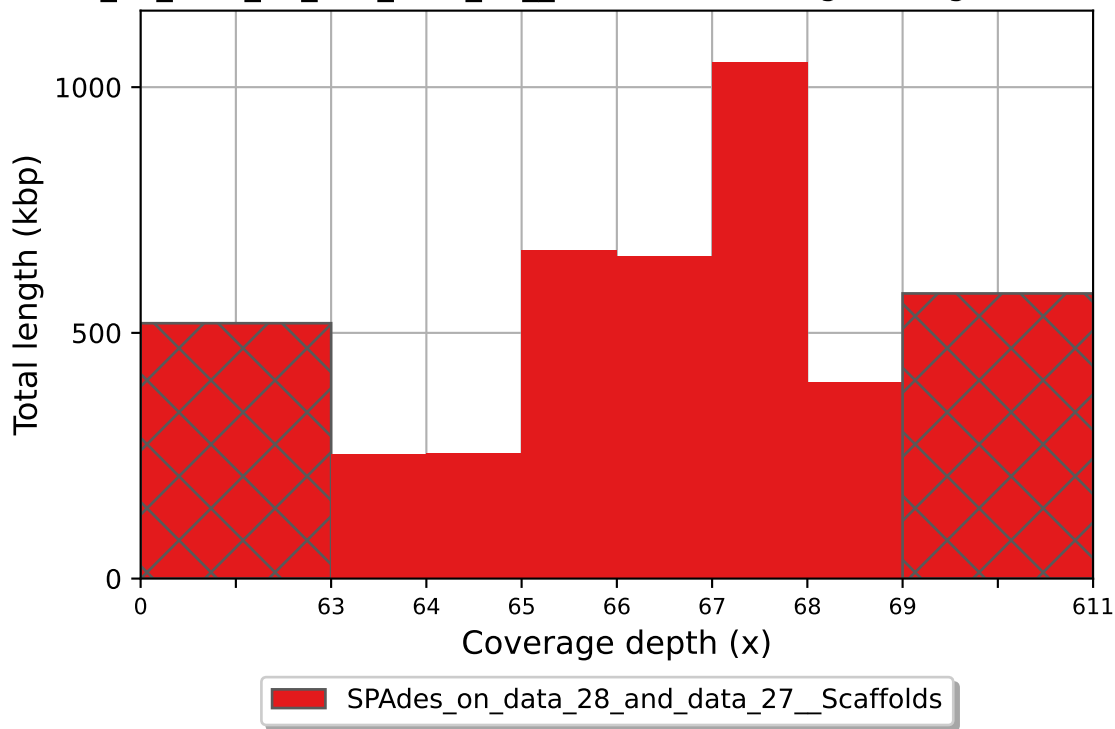- SPAdes_on_data_28_and_data_27__Scaffolds_broken

SPAdes_on_data_28_and_data_27__Scaffolds GC content

SPAdes_on_data_28_and_data_27__Scaffolds_broken GC content

Coverage histogram (bin size: 1x)

SPAdes_on_data_28_and_data_27__Scaffolds coverage histogram (bin size: 1

Total length (kbp) vs Coverage depth (x)
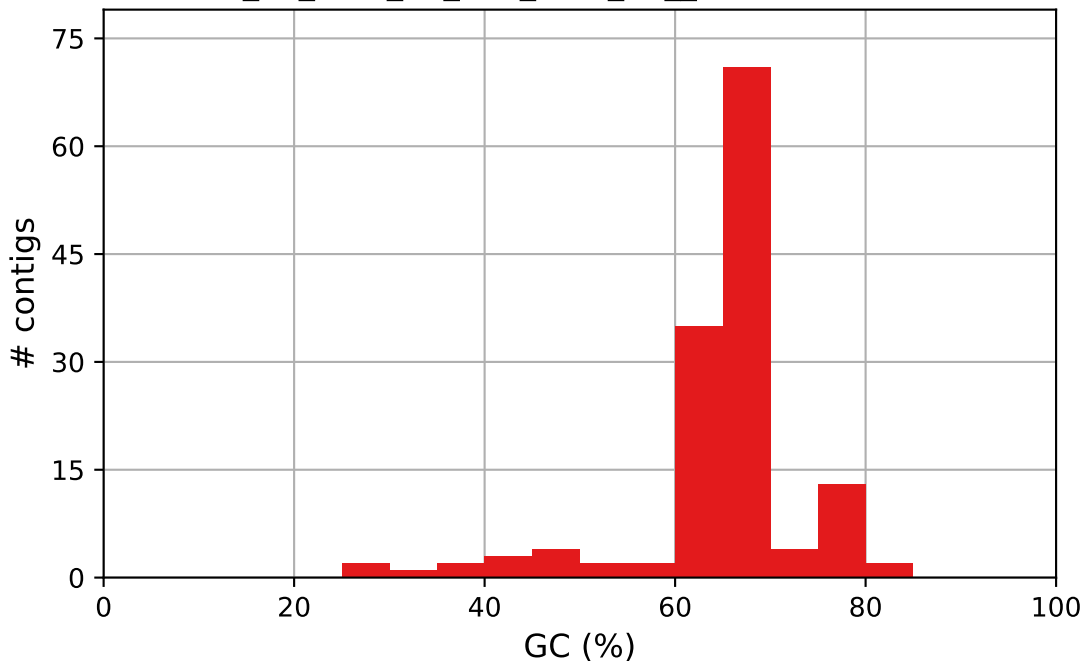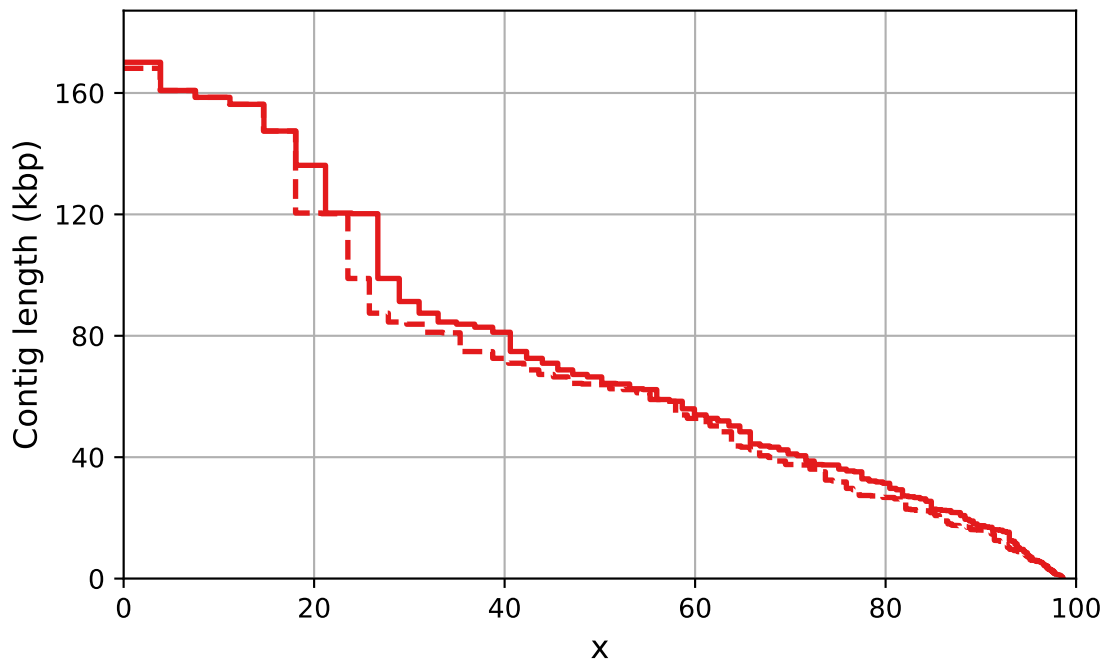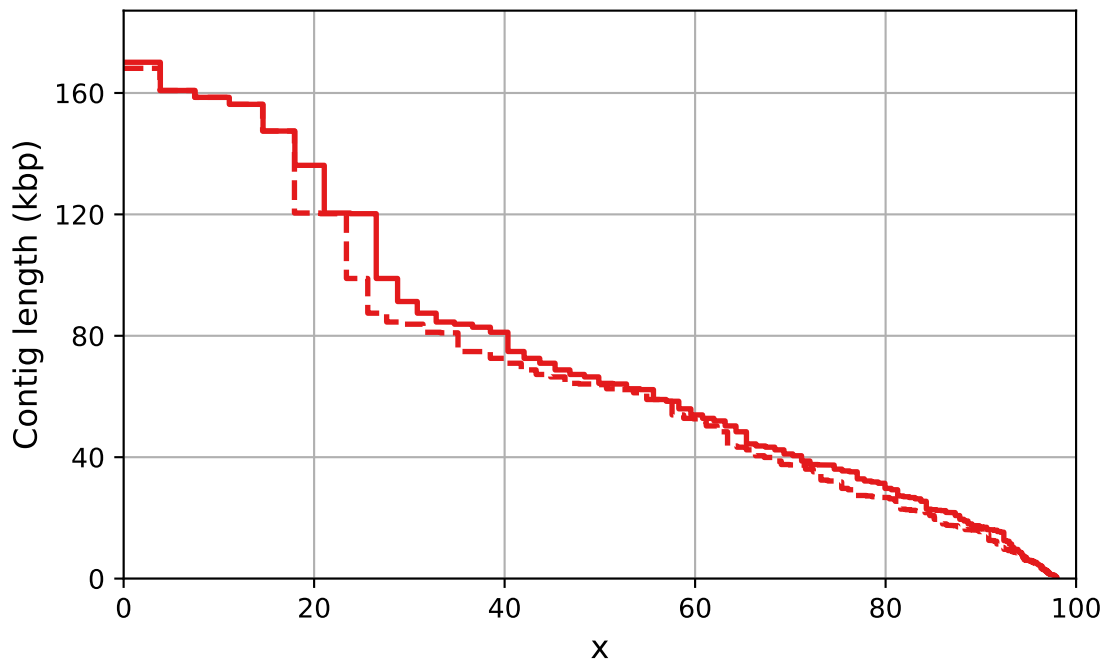
Legend: SPAdes_on_data_28_and_data_27__Scaffolds
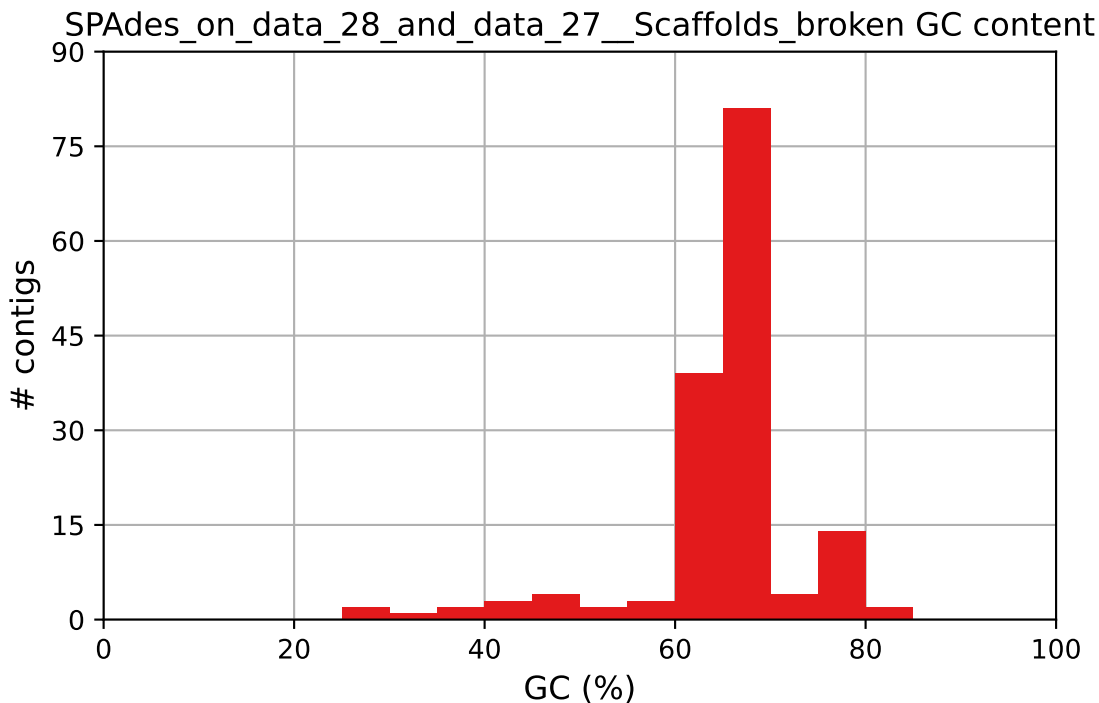
des_on_data_28_and_data_27__Scaffolds_broken coverage histogram (bin siz...
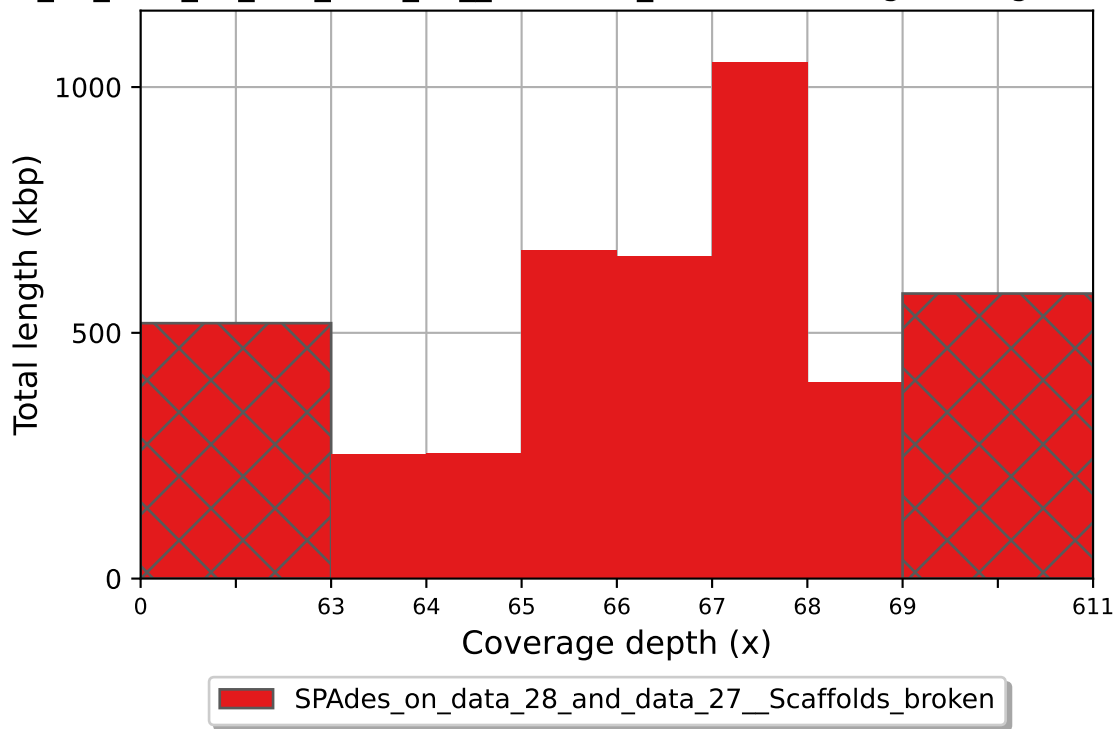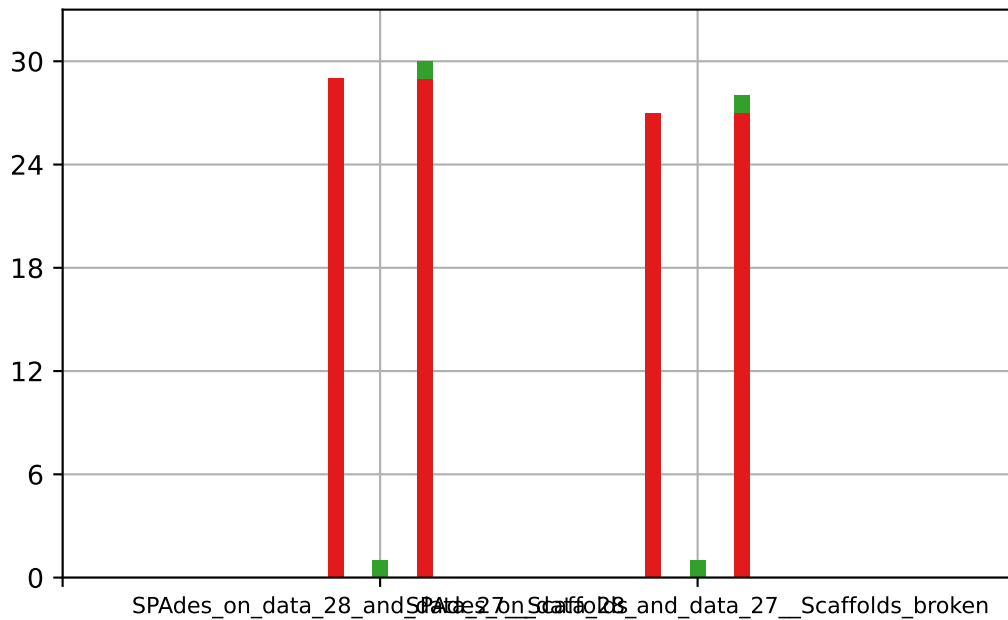
Misassemblies

FRCurve (misassemblies)
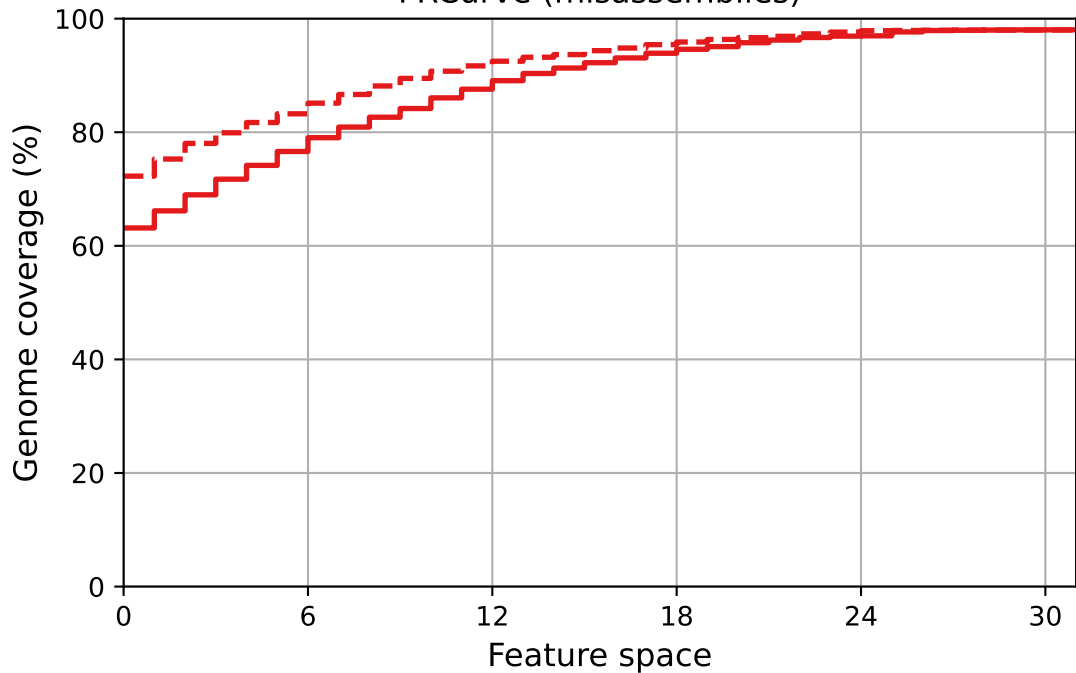
des_on_data_28_and_data_27__Scaffolds   --- SPAdes_on_data_28_and_data_27__Scaffo

Cumulative length (aligned contigs)
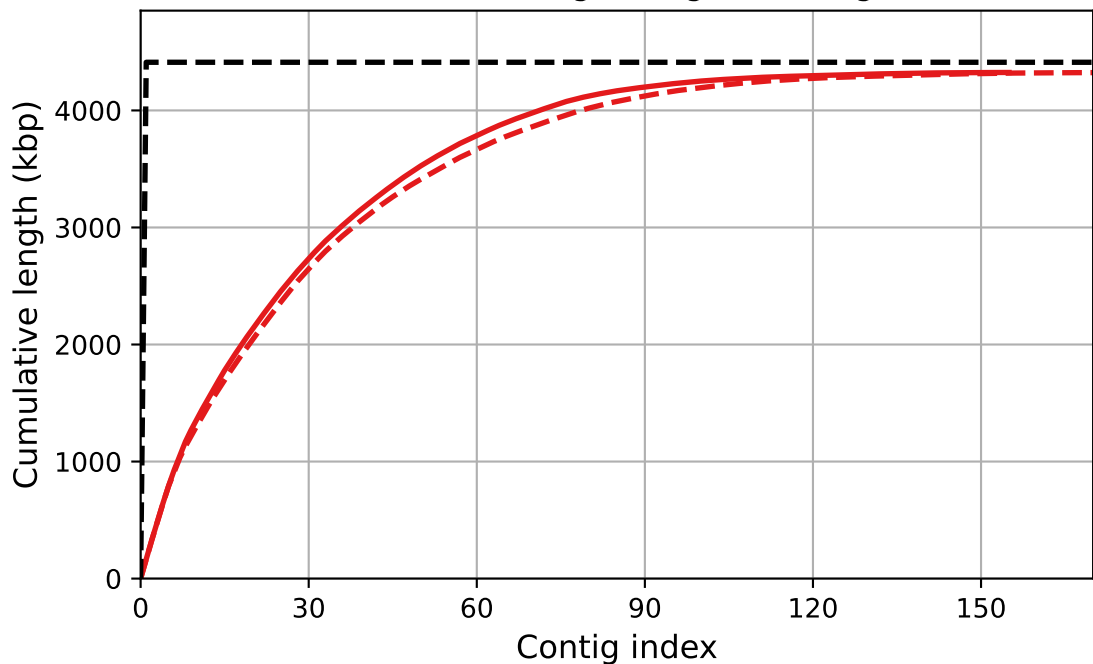
Cumulative length (kbp) vs Contig index

Legend:
- ...ata_28_and_data_27__Scaffolds
- SPAdes_on_data_28_and_data_27__Scaffolds_broken

NAx

SPAdes_on_data_28_and_data_27__Scaffolds
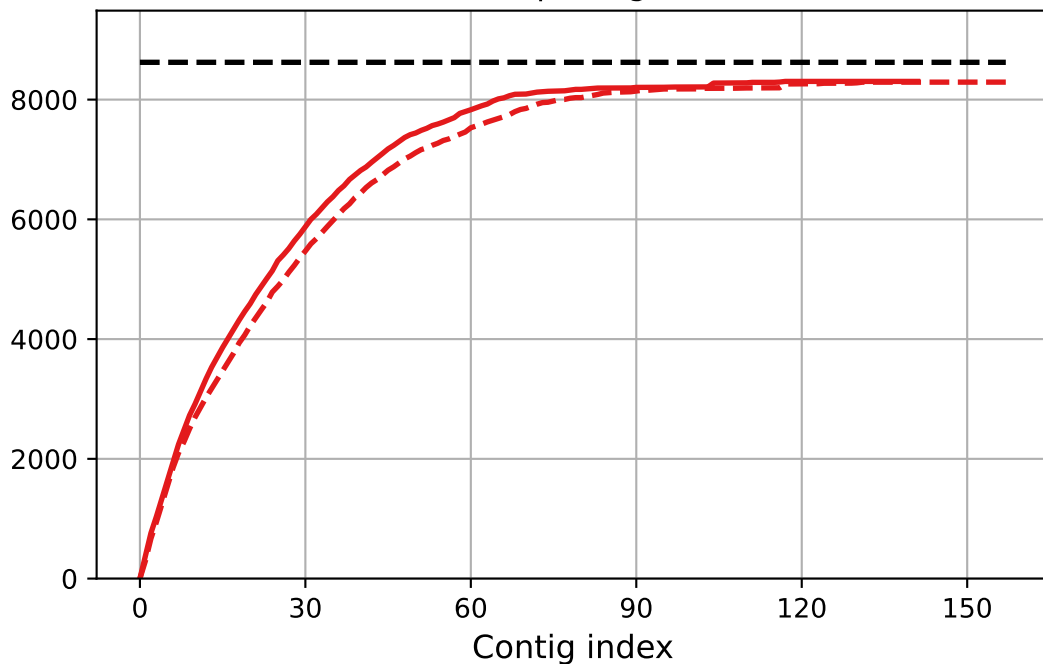
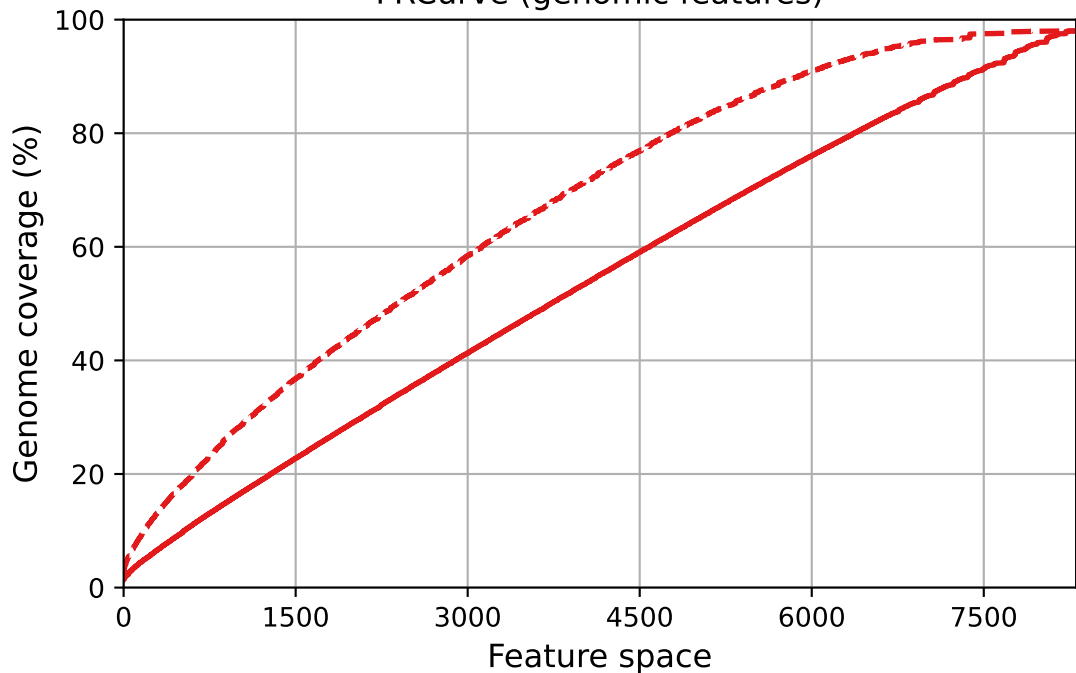SPAdes_on_data_28_and_data_27__Scaffo

NGAx

Cumulative # complete genomic features

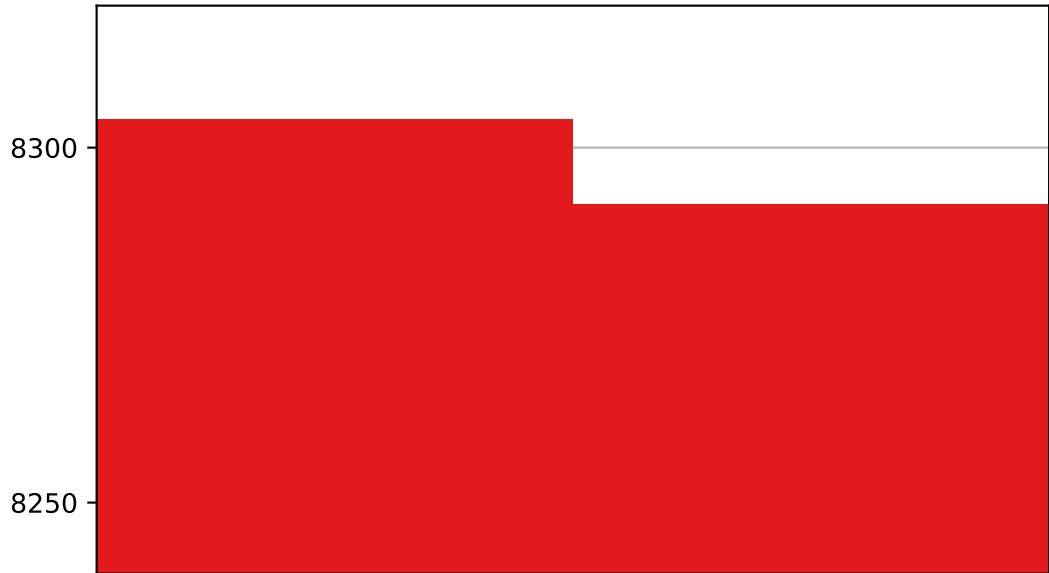ta_28_and_data_27__Scaffolds — — — SPAdes_on_data_28_and_data_27__Scaffolds_broken

FRCurve (genomic features)

Legend:
- ...des_on_data_28_and_data_27__Scaffolds
- SPAdes_on_data_28_and_data_27__Scaffo...

complete genomic features

Genome fraction, %

100

99