Report

	SPAdes_on_data_40_and_data_39__Scaffolds	SPAdes_on_data_40_and_data_39__Scaffolds_broken
# contigs (>= 0 bp)	28	-
# contigs (>= 1000 bp)	10	12
Total length (>= 0 bp)	1854485	-
Total length (>= 1000 bp)	1850319	1850119
# contigs	11	13
Largest contig	657161	657161
Total length	1851119	1850919
Reference length	2649137	2649137
GC (%)	41.57	41.57
Reference GC (%)	43.54	43.54
N50	448281	394588
NG50	357232	357232
N90	219945	76017
NG90	-	-
auN	447244.3	419372.0
auNG	312517.8	293010.0
L50	2	2
LG50	3	3
L90	4	5
LG90	-	-
# 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	6 + 5 part	8 + 5 part
Unaligned length	1848028	1848028
Genome fraction (%)	0.109	0.109
Duplication ratio	1.002	1.002
# N's per 100 kbp	10.80	0.00
# mismatches per 100 kbp	3182.29	3182.29
# indels per 100 kbp	933.93	933.93
# genomic features	9 + 7 part	9 + 7 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 1 part	2 + 1 part
Largest alignment	2555	2555
Total aligned length	2891	2891
NA50	-	-
NGA50	-	-
NA90	-	-
NGA90	-	-
auNA	3.5	3.5
auNGA	2.5	2.5
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).
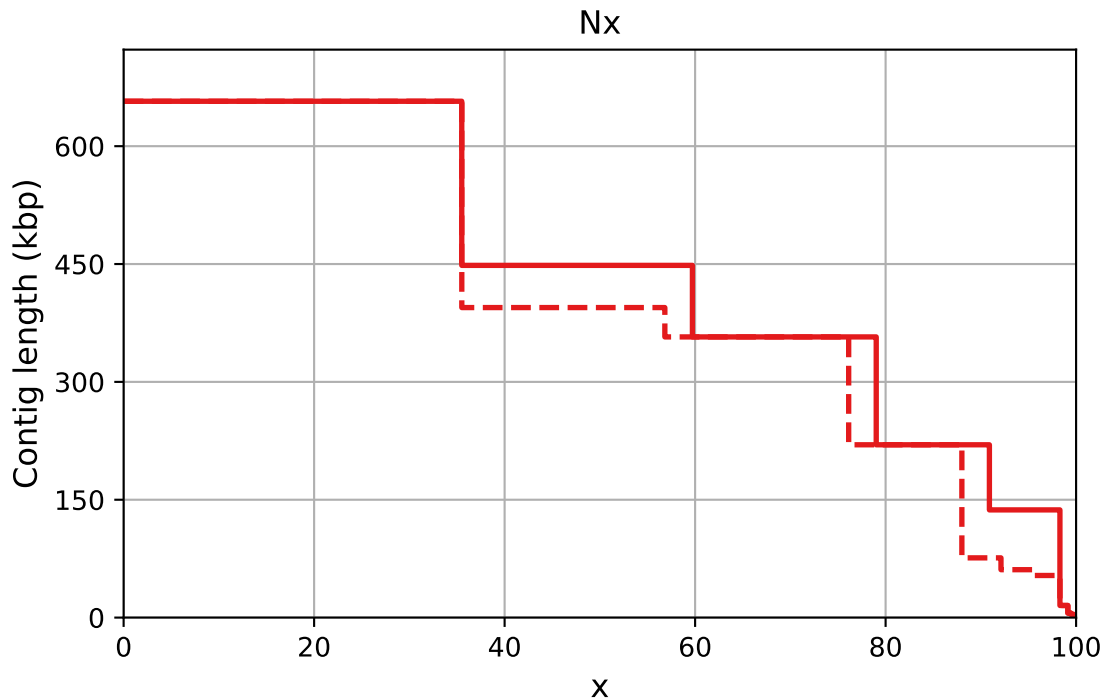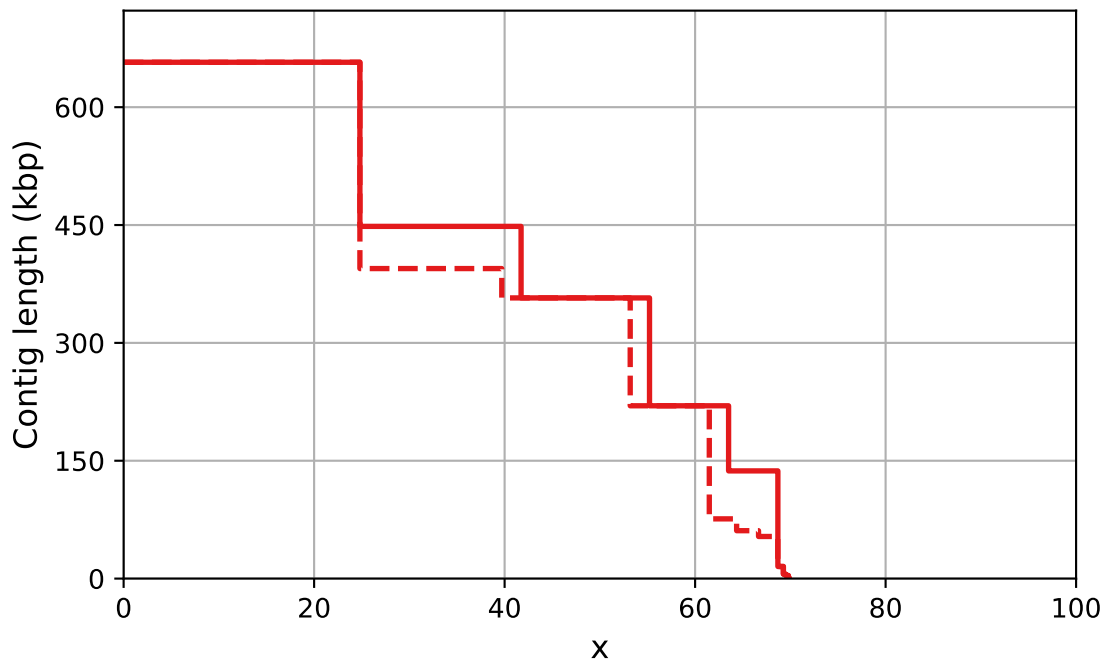
Misassemblies report

	SPAdes_on_data_40_and_data_39__Scaffolds	SPAdes_on_data_40_and_data_39__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	92	92
# indels	27	27
# indels (<= 5 bp)	26	26
# indels (> 5 bp)	1	1
Indels length	68	68

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_40_and_data_39__Scaffolds	SPAdes_on_data_40_and_data_39__Scaffolds_broken
# fully unaligned contigs	6	8
Fully unaligned length	382925	497475
# partially unaligned contigs	5	5
Partially unaligned length	1465103	1350553
# N's	200	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

SPAdes_on_data_40_and_data_39__Scaffolds

SPAdes_on_data_40_and_data_39__Scaffo...

NGx

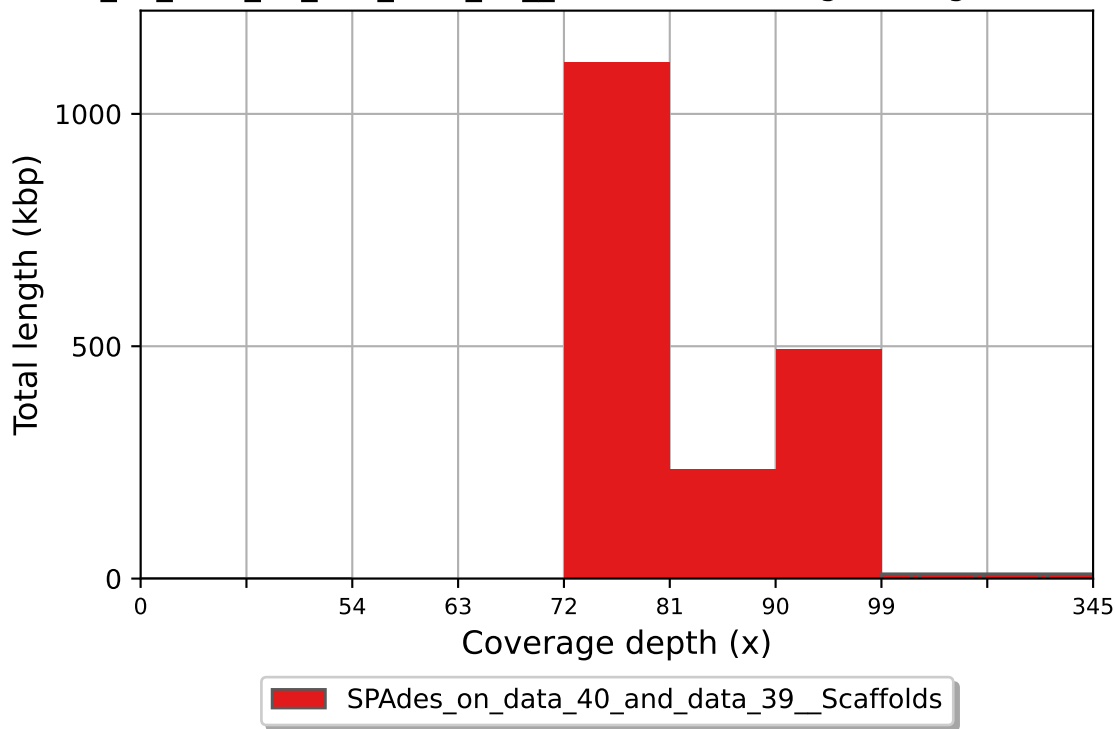Contig length (kbp)

x

des_on_data_40_and_data_39__Scaffolds   SPAdes_on_data_40_and_data_39__Scaffo

Cumulative length

Cumulative length (kbp) vs Contig index
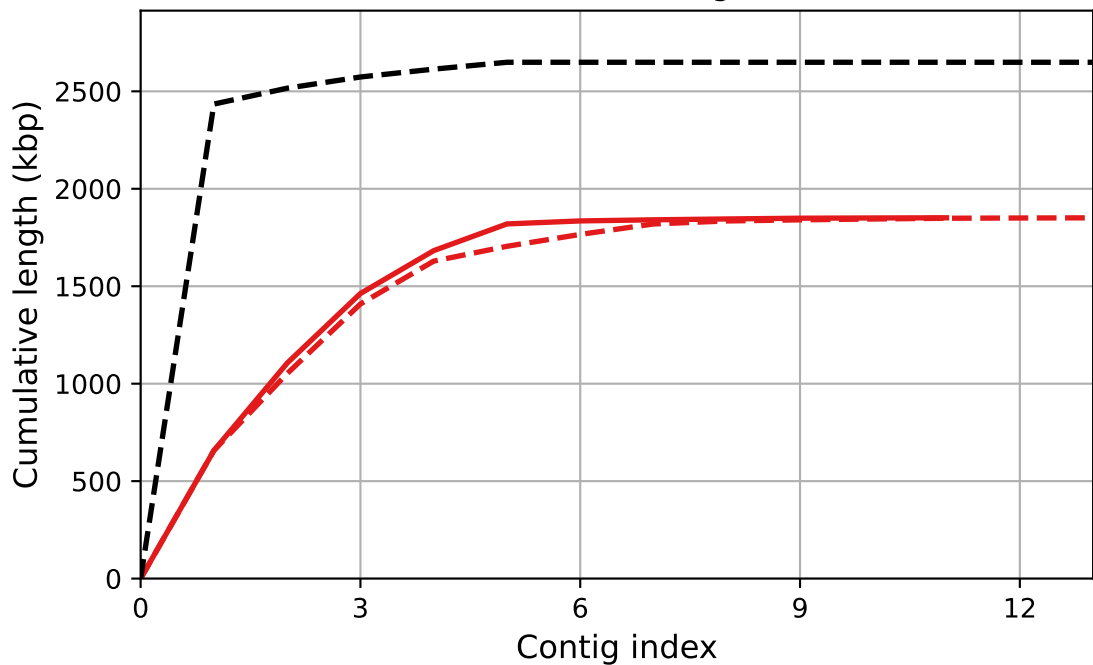
ta_40_and_data_39__Scaffolds   - - -   SPAdes_on_data_40_and_data_39__Scaffolds_broken
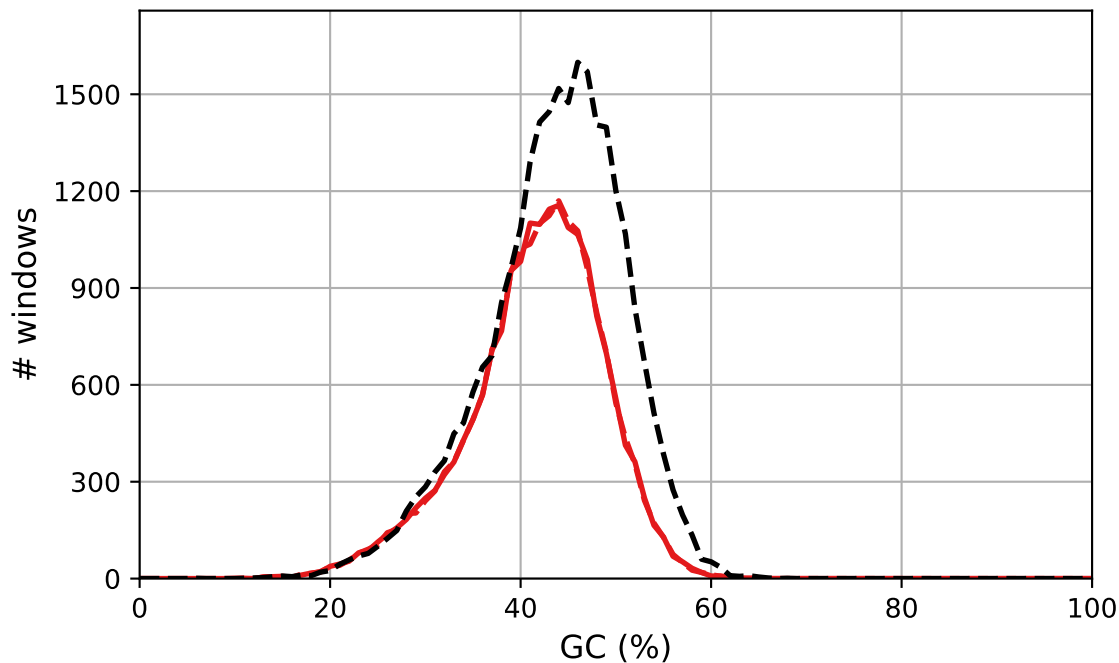
GC content

Legend:
- — — data_40_and_data_39__Scaffolds
- — — SPAdes_on_data_40_and_data_39__Scaffolds_broken

SPAdes_on_data_40_and_data_39__Scaffolds GC content
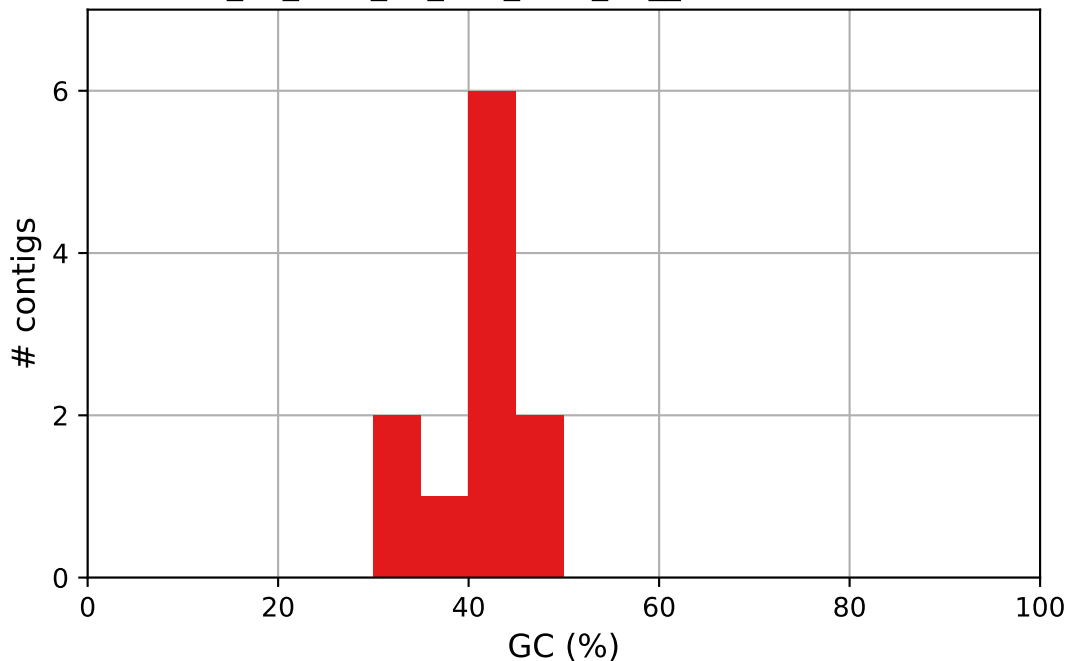
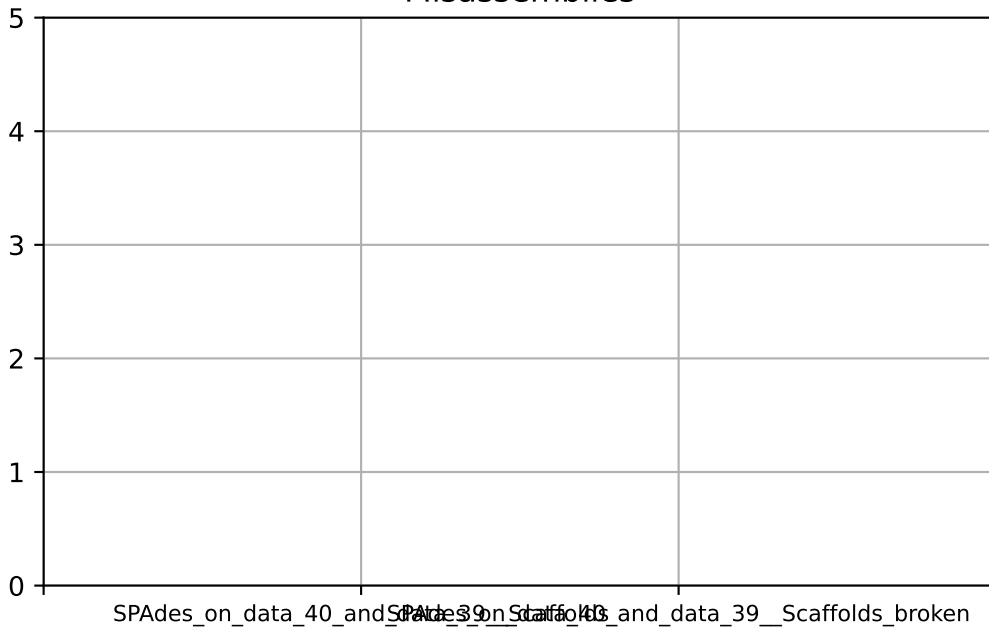SPAdes_on_data_40_and_data_39__Scaffolds_broken GC content

Coverage histogram (bin size: 9x)
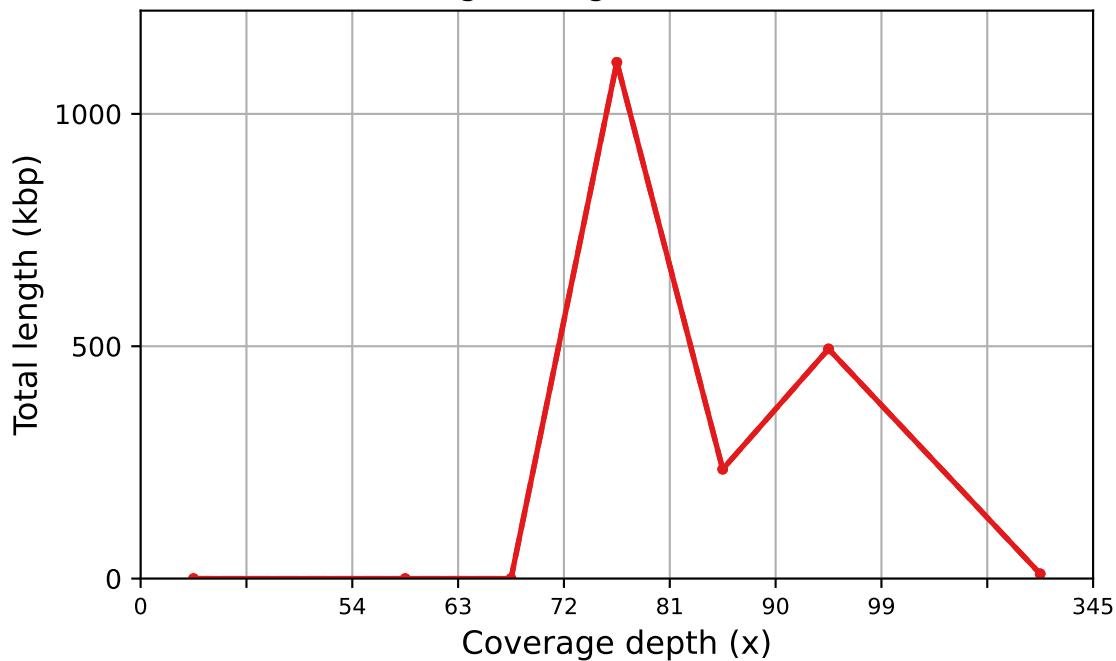
SPAdes_on_data_40_and_data_39__Scaffolds coverage histogram (bin size: 9)

SPAdes_on_data_40_and_data_39__Scaffolds_broken coverage histogram (bin siz...

Total length (kbp) vs Coverage depth (x)

Legend: SPAdes_on_data_40_and_data_39__Scaffolds_broken

Misassemblies

SPAdes_on_data_40_and_data_39__Scaffolds SPAdes_on_data_40_and_data_39__Scaffolds_broken
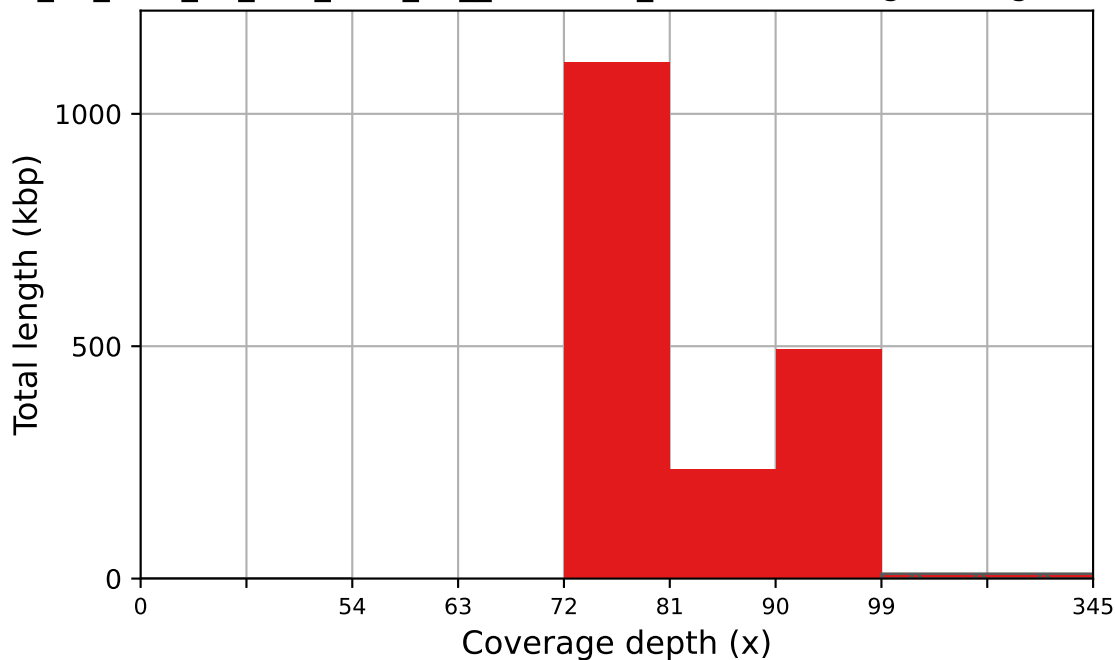
FRCurve (misassemblies)

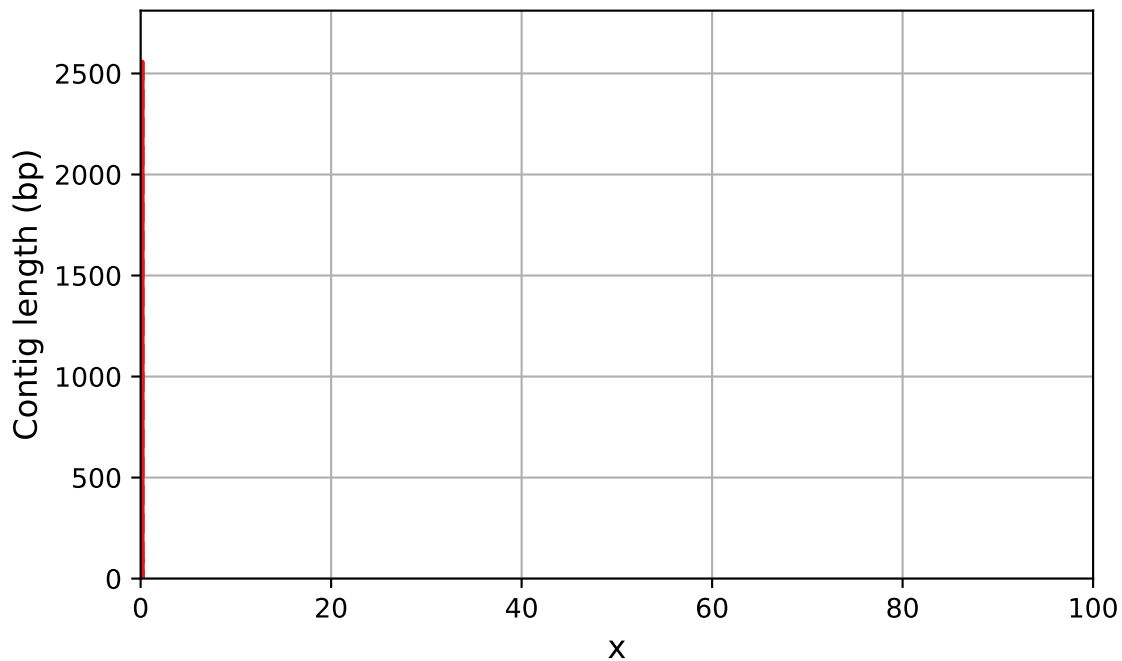des_on_data_40_and_data_39__Scaffolds — — SPAdes_on_data_40_and_data_39__Scaffo

Cumulative length (aligned contigs)
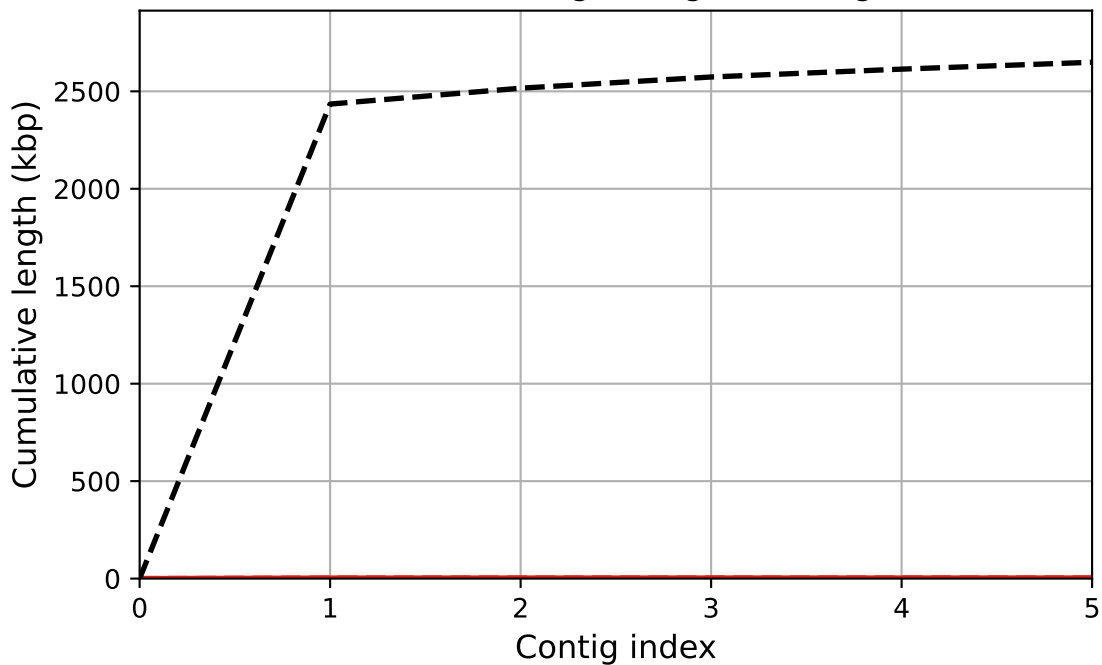
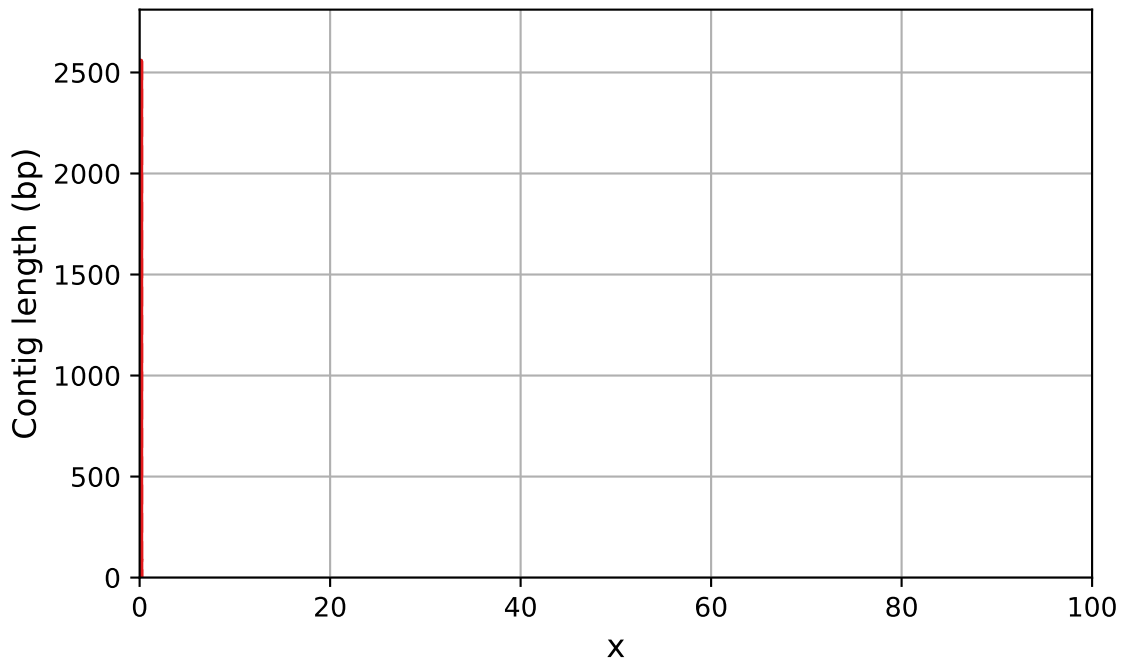ta_40_and_data_39__Scaffolds   — — SPAdes_on_data_40_and_data_39__Scaffolds_broken

NAx

Contig length (bp)

x

des_on_data_40_and_data_39__Scaffolds — — SPAdes_on_data_40_and_data_39__Scaffo
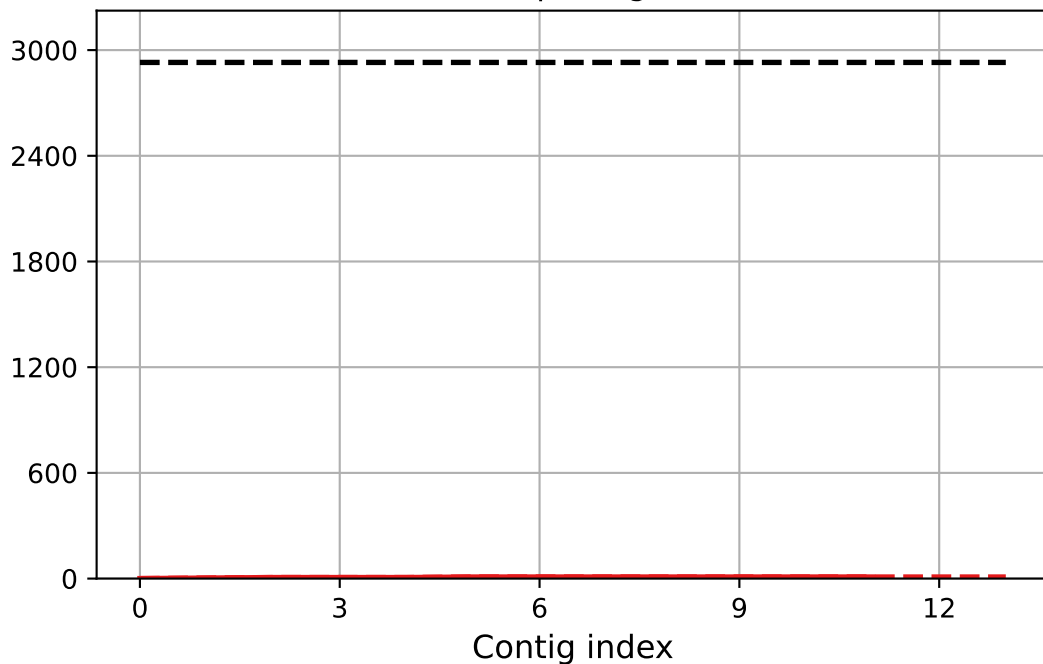
NGAx

Contig length (bp) vs x

des_on_data_40_and_data_39__Scaffolds   — — SPAdes_on_data_40_and_data_39__Scaffo
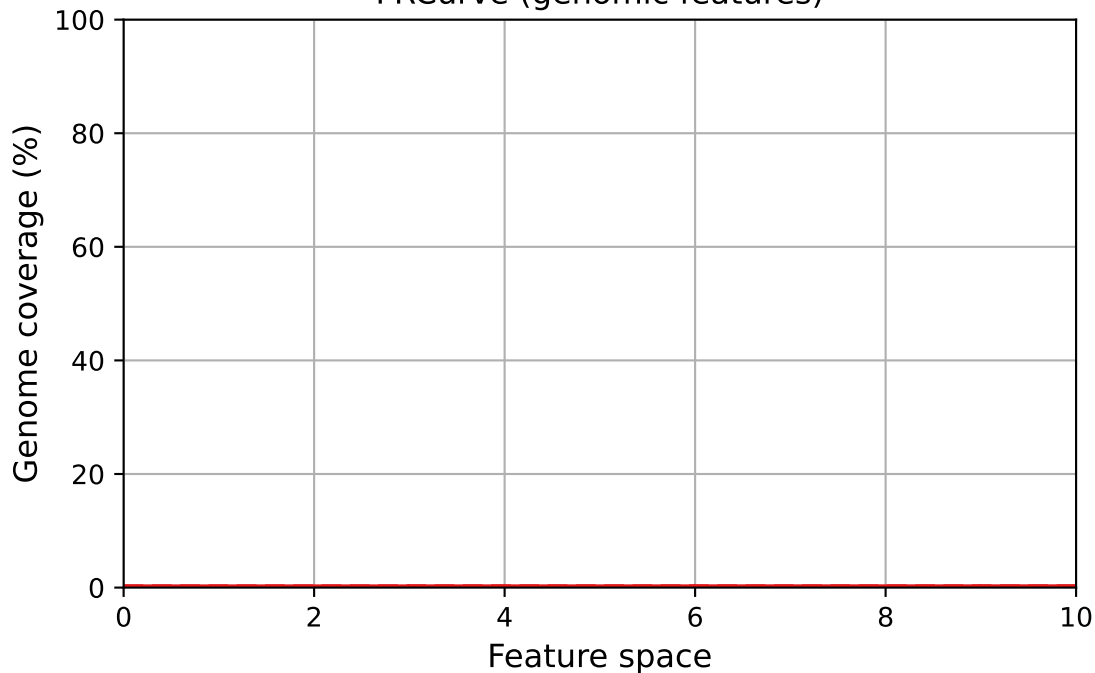
Cumulative # complete genomic features

FRCurve (genomic features)

des_on_data_40_and_data_39__Scaffolds   **— —** SPAdes_on_data_40_and_data_39__Scaffo

complete genomic features

Genome fraction, %

des_on_data_40_and_data_39__Scaffolds   ▉ SPAdes_on_data_40_and_data_39__Scaffo