Report

	SPAdes_on_data_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# contigs (>= 0 bp)	221	-
# contigs (>= 1000 bp)	69	82
Total length (>= 0 bp)	5515534	-
Total length (>= 1000 bp)	5477168	5476048
# contigs	83	96
Largest contig	402605	388171
Total length	5486773	5485653
Reference length	5682322	5682322
GC (%)	57.21	57.21
Reference GC (%)	57.12	57.12
N50	180590	160392
NG50	174078	157941
N90	62724	56469
NG90	45493	34393
auN	209102.2	159538.3
auNG	201906.2	154016.6
L50	10	13
LG50	11	14
L90	29	36
LG90	32	40
# misassemblies	74	73
# misassembled contigs	30	33
Misassembled contigs length	4536494	4011639
# local misassemblies	27	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	2	2
# unaligned contigs	23 + 34 part	23 + 36 part
Unaligned length	688347	686918
Genome fraction (%)	84.769	85.341
Duplication ratio	1.001	1.001
# N's per 100 kbp	20.41	0.00
# mismatches per 100 kbp	685.72	688.80
# indels per 100 kbp	19.31	19.80
# genomic features	9599 + 180 part	9609 + 208 part
# predicted rRNA genes	4 + 0 part	3 + 0 part
Largest alignment	205341	205341
Total aligned length	4794662	4794024
NA50	70102	60829
NGA50	69622	60721
NA90	-	-
NGA90	-	-
auNA	80386.5	72700.4
auNGA	77620.1	70184.2
LA50	24	27
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_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# misassemblies	74	73
# contig misassemblies	73	73
# c. relocations	70	70
# c. translocations	3	3
# c. inversions	0	0
# scaffold misassemblies	1	0
# s. relocations	1	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	30	33
Misassembled contigs length	4536494	4011639
# local misassemblies	27	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	4	-
# unaligned mis. contigs	2	2
# mismatches	32878	33021
# indels	926	949
# indels (<= 5 bp)	835	866
# indels (> 5 bp)	91	83
Indels length	7969	6711

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_2_and_data_1__Scaffolds	SPAdes_on_data_2_and_data_1__Scaffolds_broken
# fully unaligned contigs	23	23
Fully unaligned length	84989	84989
# partially unaligned contigs	34	36
Partially unaligned length	603358	601929
# N's	1120	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
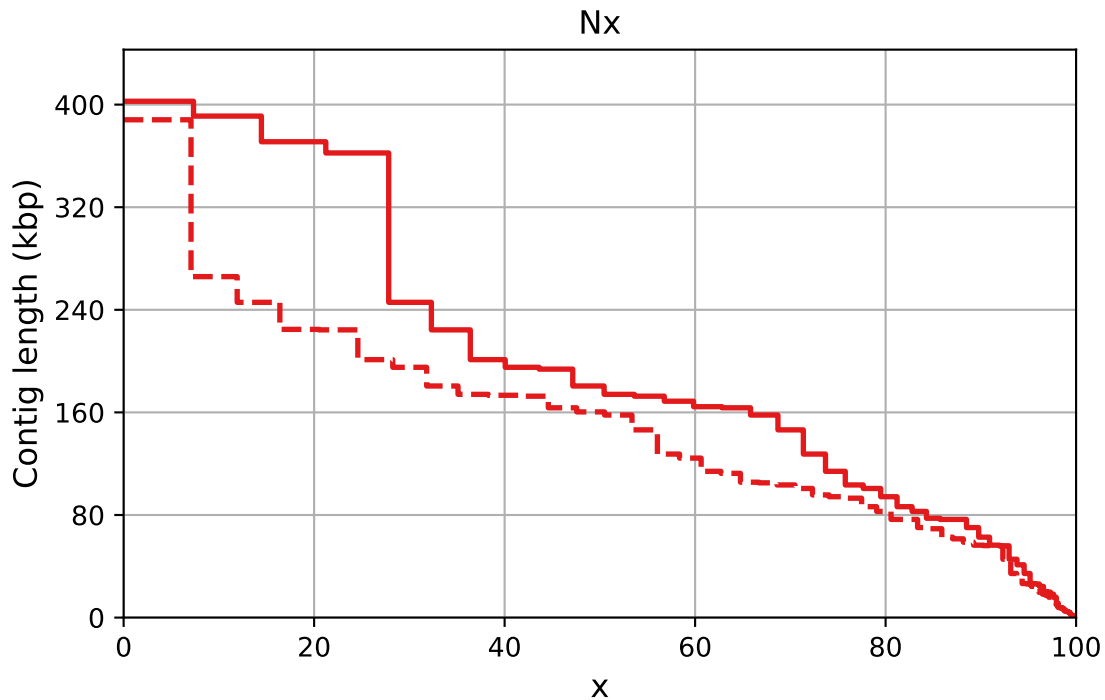
SPAdes_on_data_2_and_data_1__Scaffolds   - - - SPAdes_on_data_2_and_data_1__Scaffolds
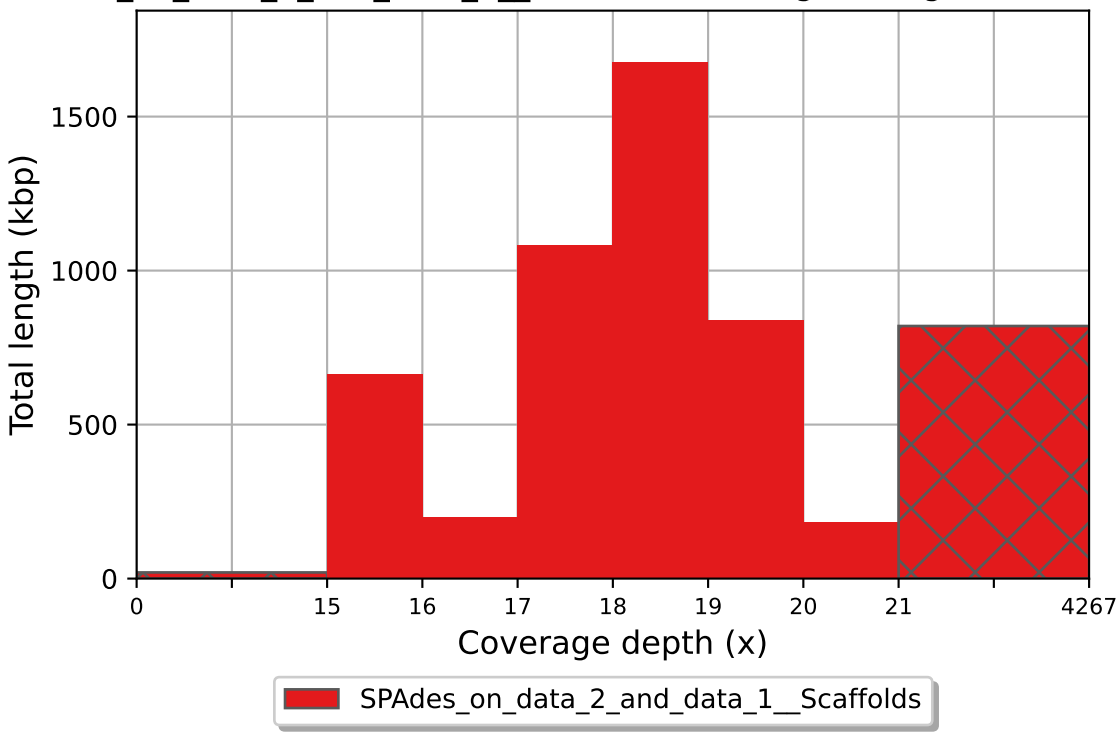
NGx
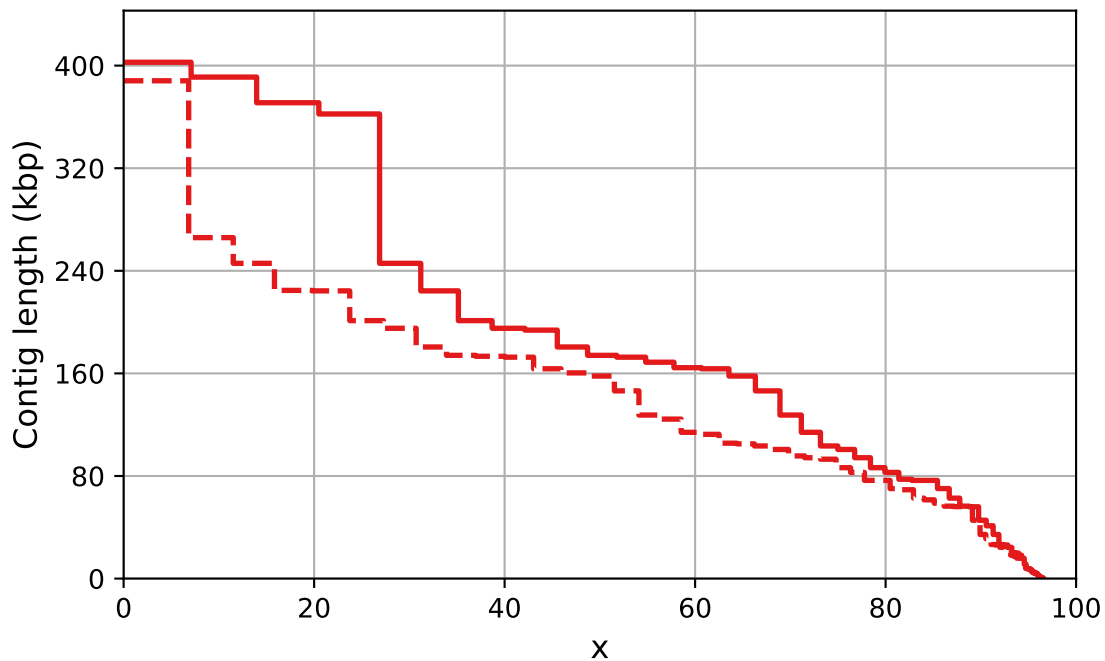
PAdes_on_data_2_and_data_1__Scaffolds   SPAdes_on_data_2_and_data_1__Scaffolds

Cumulative length

Cumulative length (Mbp) vs Contig index
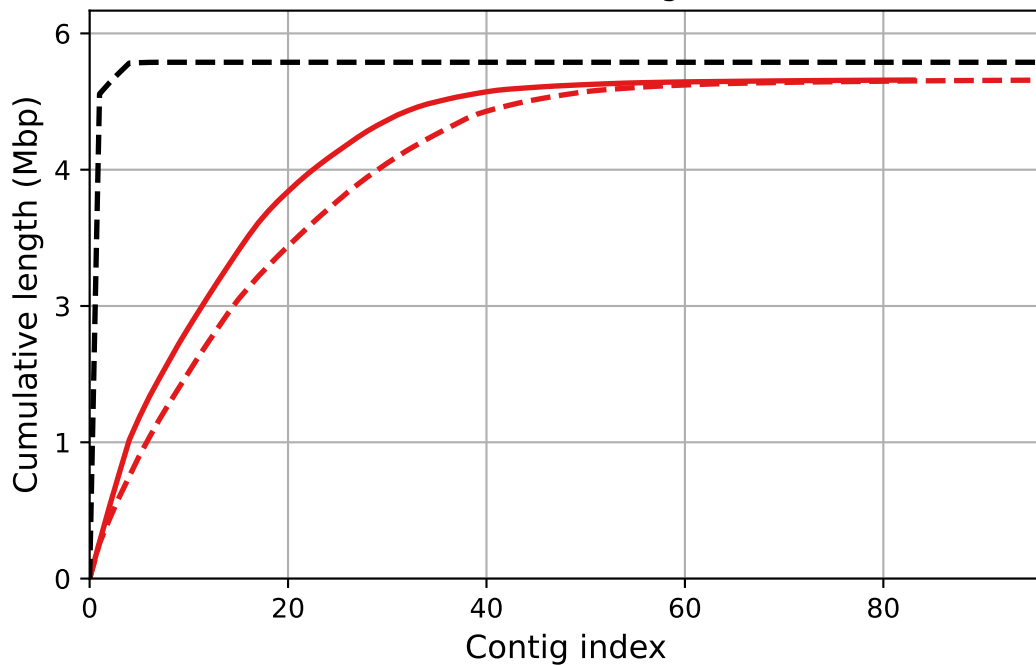
_data_2_and_data_1__Scaffolds   – – – SPAdes_on_data_2_and_data_1__Scaffolds_broken
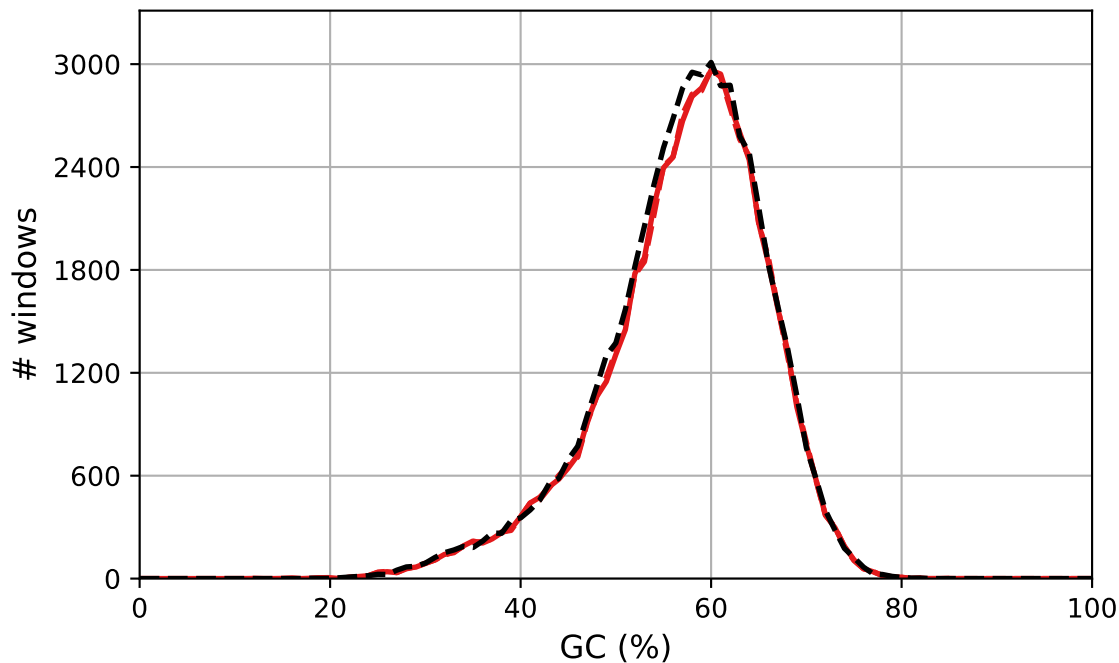
GC content

_data_2_and_data_1__Scaffolds — SPAdes_on_data_2_and_data_1__Scaffolds_broken

SPAdes_on_data_2_and_data_1__Scaffolds GC content
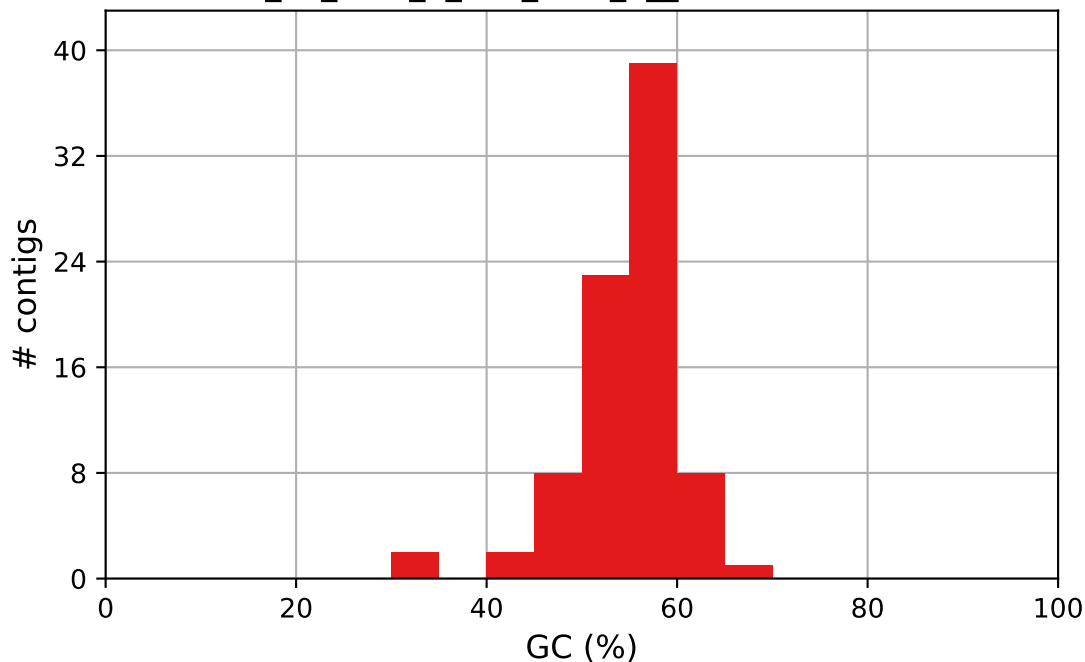
SPAdes_on_data_2_and_data_1__Scaffolds_broken GC content

Coverage histogram (bin size: 1x)

Coverage depth (x) vs Total length (kbp)

SPAdes_on_data_2_and_data_1__Scaffolds coverage histogram (bin size: 1x)
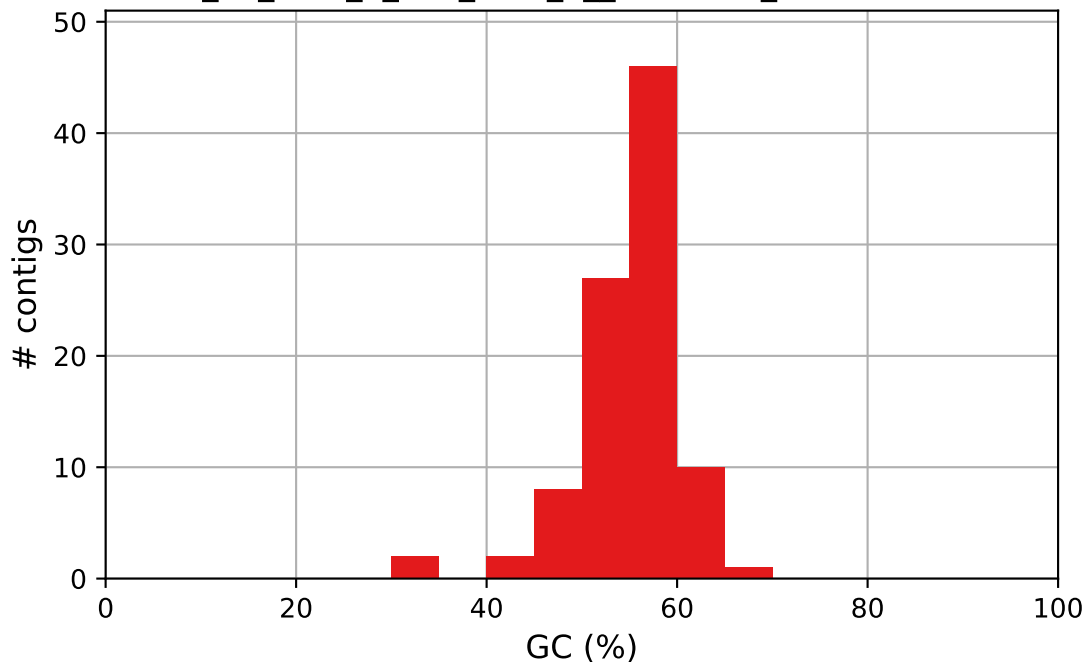
Ades_on_data_2_and_data_1__Scaffolds_broken coverage histogram (bin size
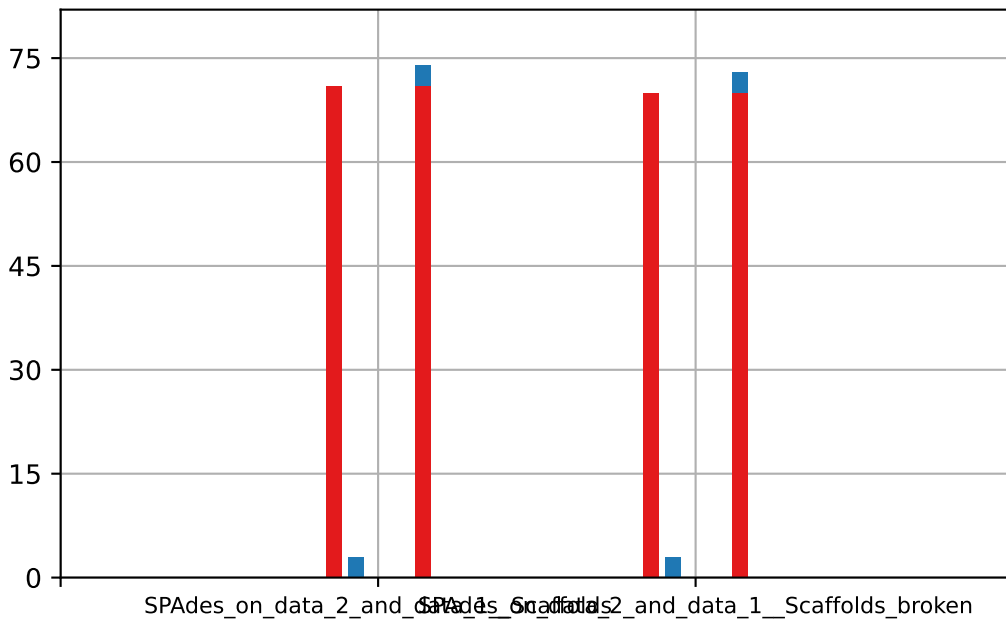
Misassemblies

relocations
translocations

FRCurve (misassemblies)
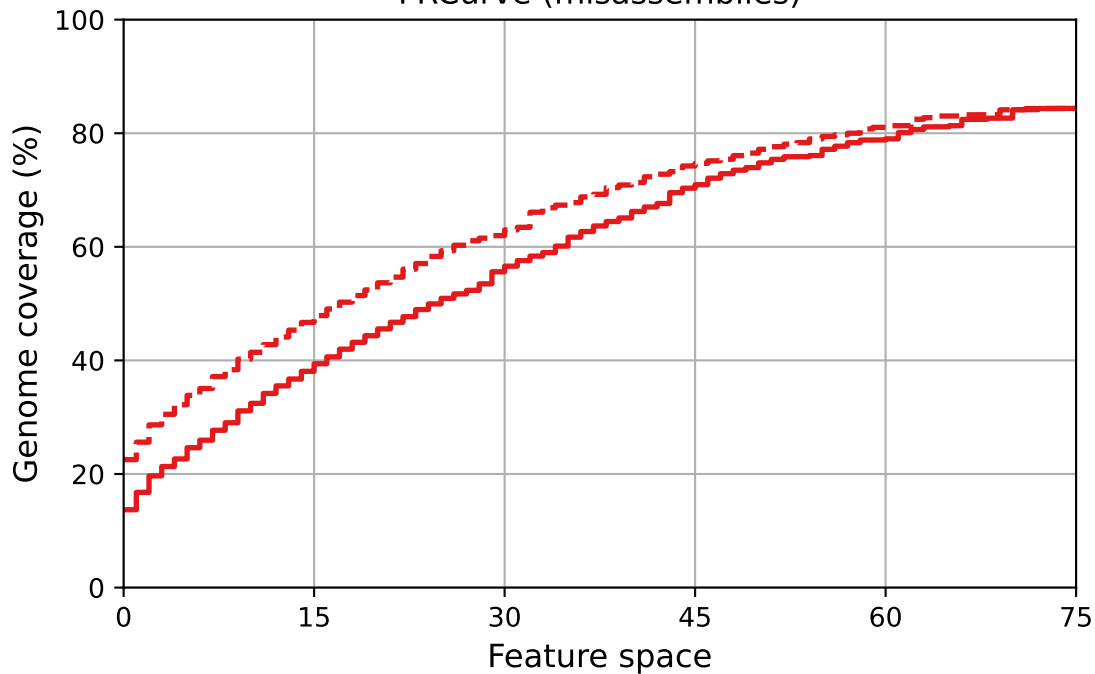
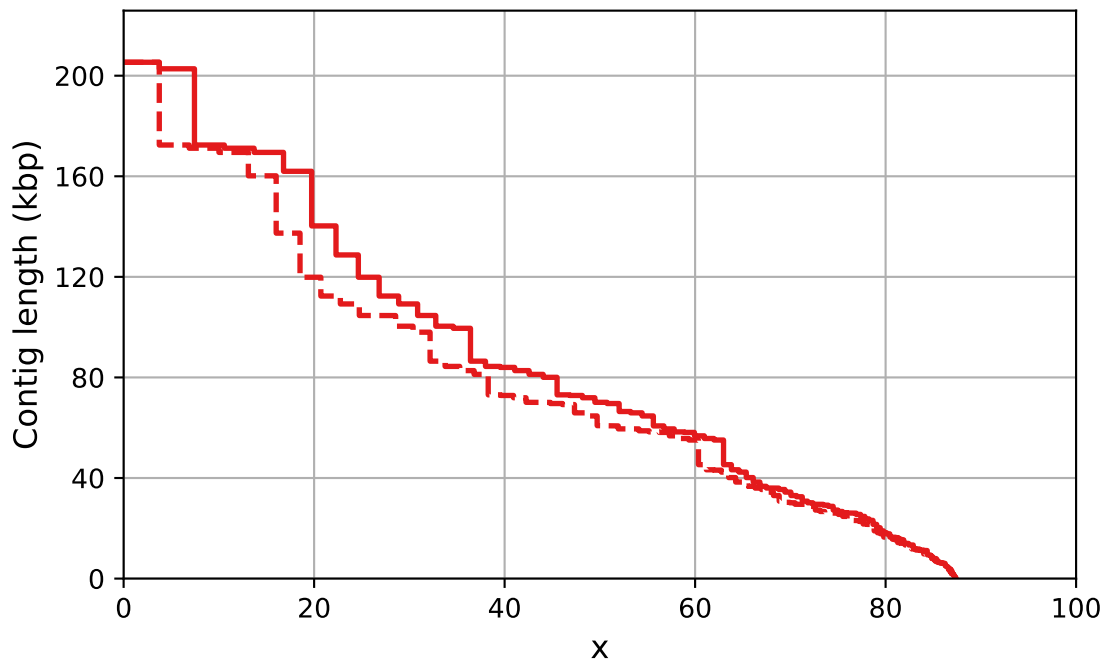PAdes_on_data_2_and_data_1__Scaffolds   - - - SPAdes_on_data_2_and_data_1__Scaffolds

Cumulative length (aligned contigs)
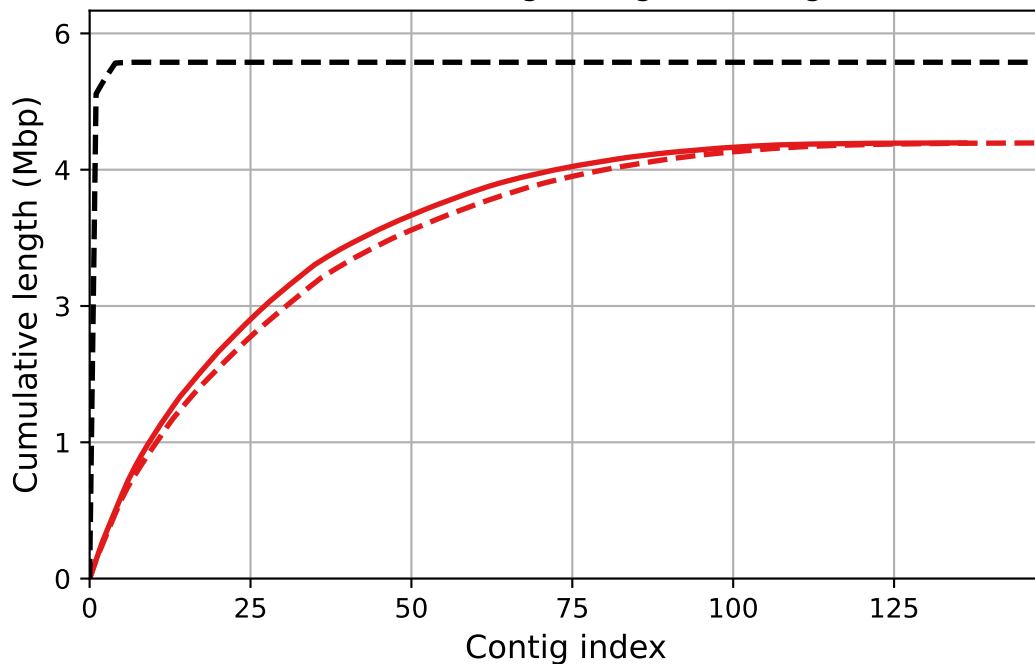
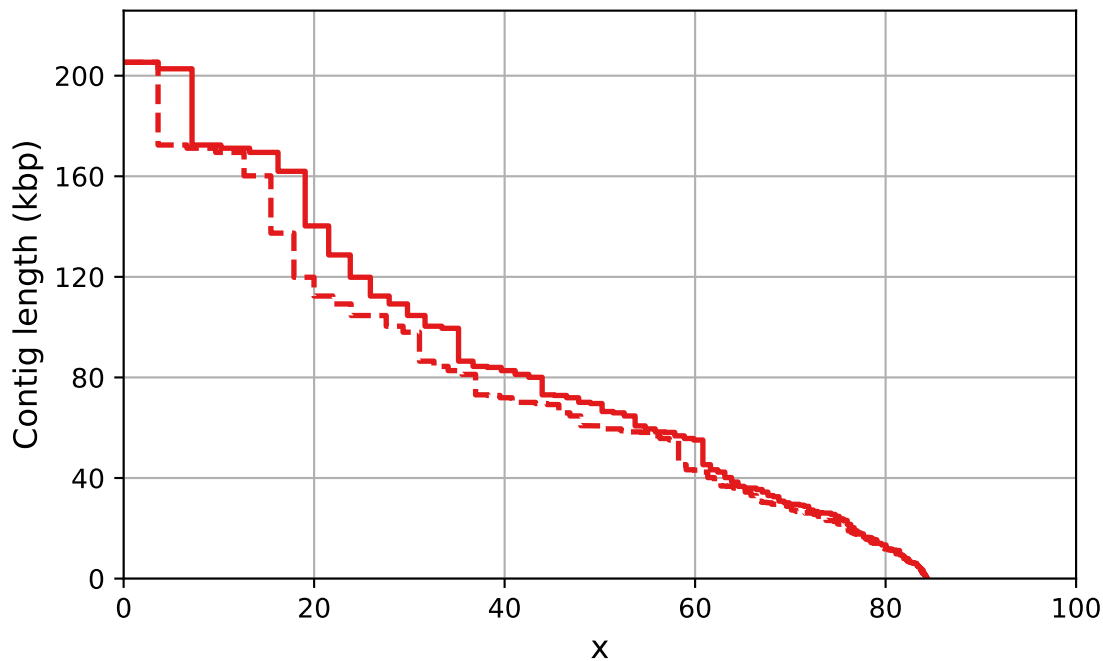_data_2_and_data_1__Scaffolds — — — SPAdes_on_data_2_and_data_1__Scaffolds_broken

NAx

SPAdes_on_data_2_and_data_1__Scaffolds   - - - SPAdes_on_data_2_and_data_1__Scaffolds

NGAx

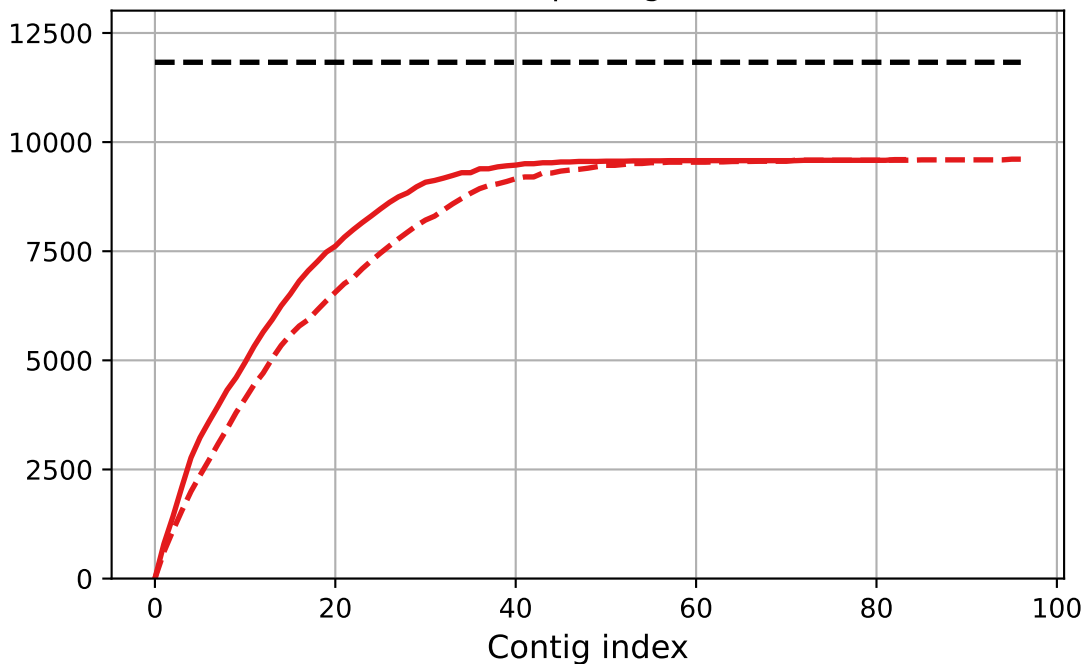SPAdes_on_data_2_and_data_1__Scaffolds   - - -   SPAdes_on_data_2_and_data_1__Scaffolds
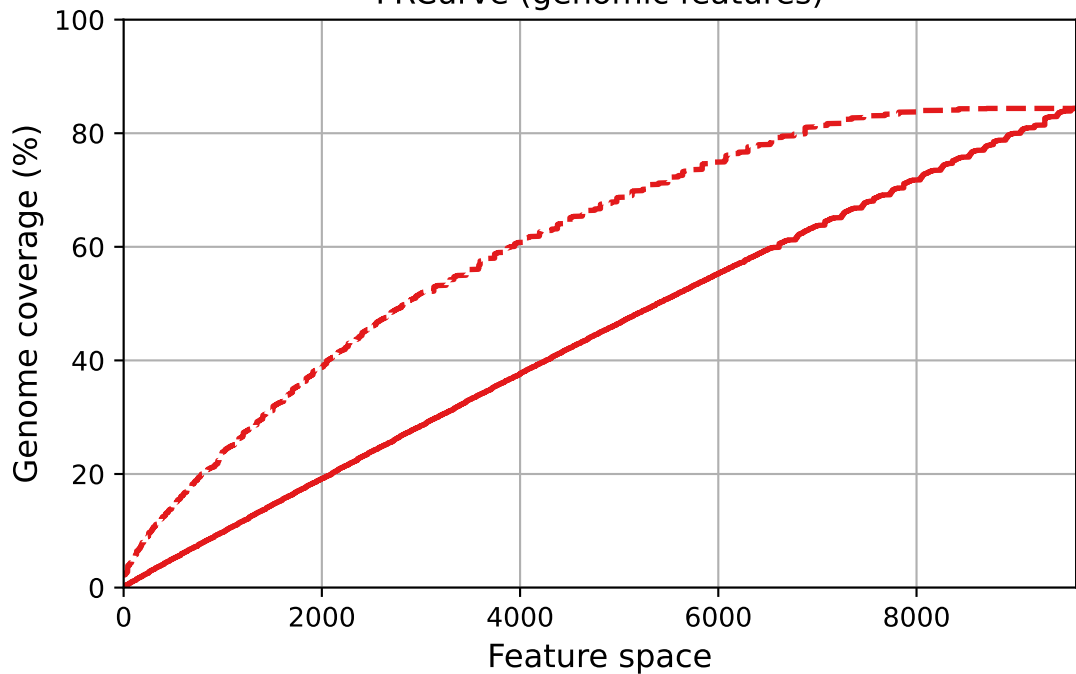
Cumulative # complete genomic features

_data_2_and_data_1__Scaffolds — — — SPAdes_on_data_2_and_data_1__Scaffolds_broken

FRCurve (genomic features)

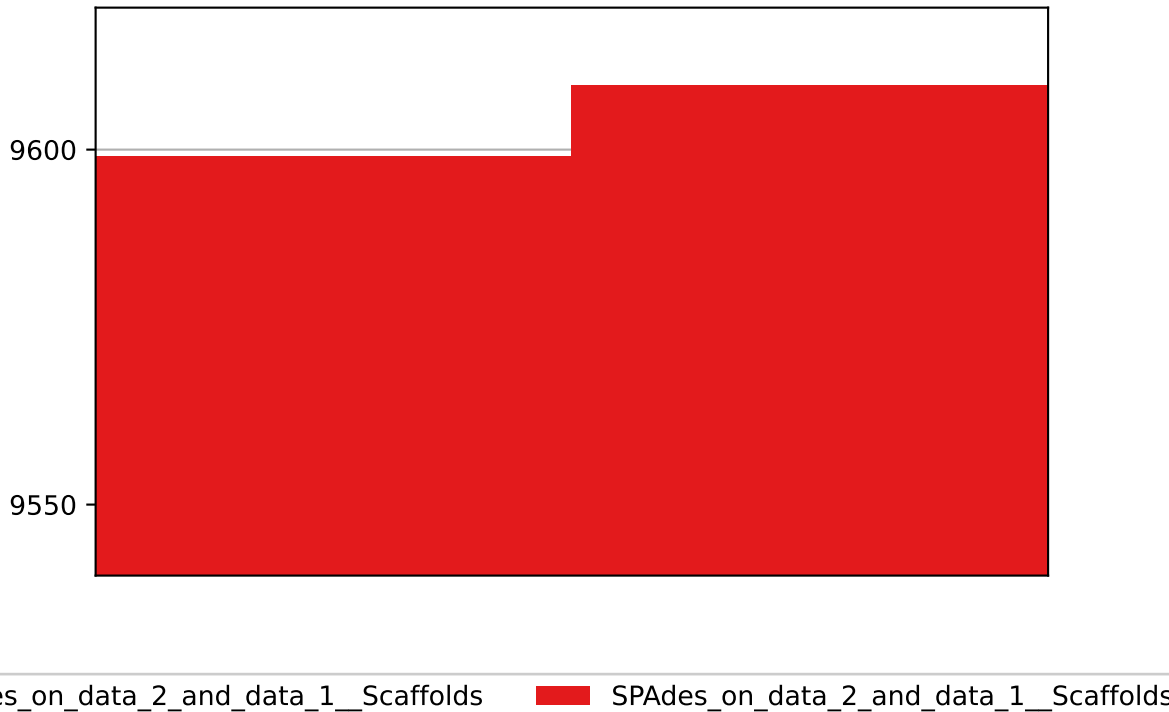# # complete genomic features

| PADes_on_data_2_and_data_1__Scaffolds | ■ SPAdes_on_data_2_and_data_1__Scaffolds |

Genome fraction, %

PAdes_on_data_2_and_data_1__Scaffolds   SPAdes_on_data_2_and_data_1__Scaffolds