Report

	abyssoutput_April9-8_fa	abyssoutput_April9-8_fa_broken
# contigs (>= 0 bp)	87	-
# contigs (>= 1000 bp)	15	15
Total length (>= 0 bp)	4140847	-
Total length (>= 1000 bp)	4124163	4123854
# contigs	22	23
Largest contig	1060944	1060944
Total length	4128861	4128811
Reference length	4215606	4215606
GC (%)	43.68	43.68
Reference GC (%)	43.51	43.51
N50	1024464	1024464
NG50	991598	991598
N90	201291	201291
NG90	201291	201291
auN	816341.4	816351.1
auNG	799543.5	799543.2
L50	2	2
LG50	3	3
L90	6	6
LG90	6	6
# misassemblies	54	54
# misassembled contigs	6	6
Misassembled contigs length	3811335	3811335
# local misassemblies	33	33
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	1 + 6 part	1 + 6 part
Unaligned length	342710	342710
Genome fraction (%)	90.332	90.327
Duplication ratio	1.001	1.001
# N's per 100 kbp	1.21	0.00
# mismatches per 100 kbp	1282.14	1282.16
# indels per 100 kbp	41.68	41.47
# genomic features	8060 + 194 part	8060 + 194 part
Complete BUSCO (%)	100.00	100.00
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	3 + 5 part	3 + 5 part
Largest alignment	397615	397615
Total aligned length	3785776	3785726
NA50	104924	104924
NGA50	93746	93746
NA90	10504	10504
NGA90	-	-
auNA	150090.0	150091.6
auNGA	147001.6	147001.3
LA50	10	10
LGA50	11	11
LA90	52	52
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).
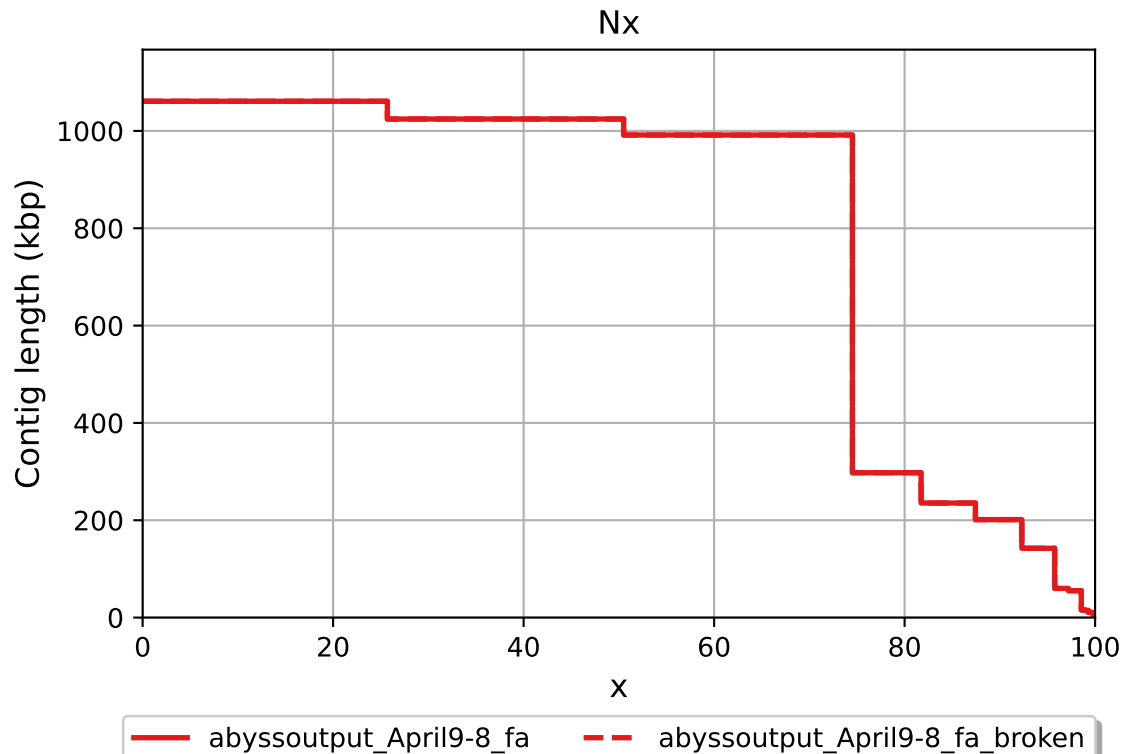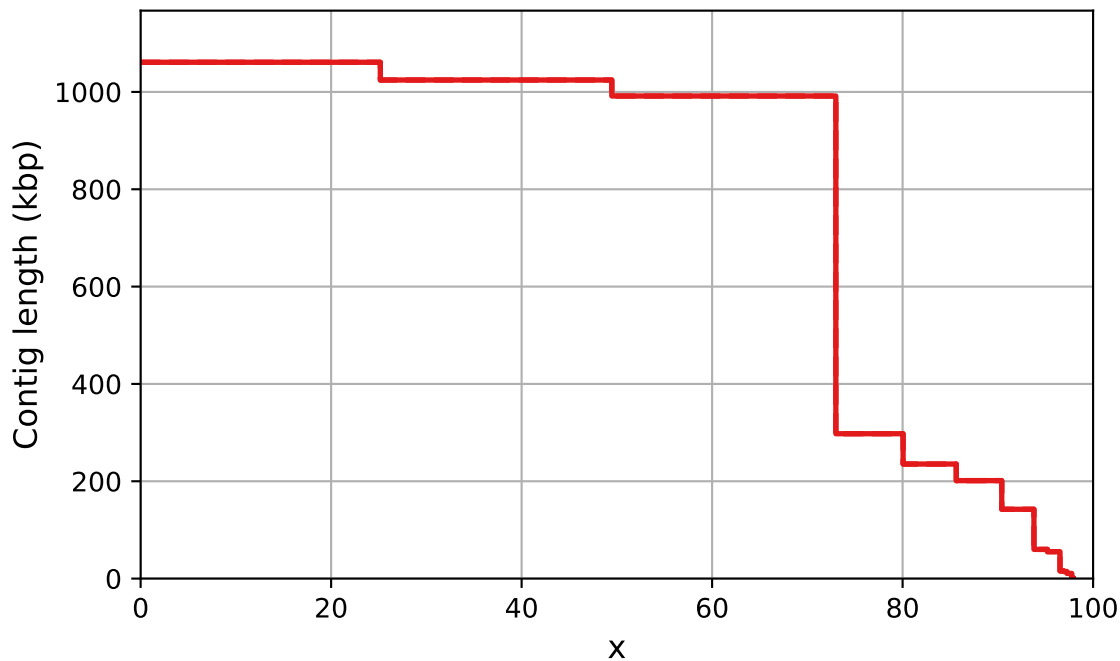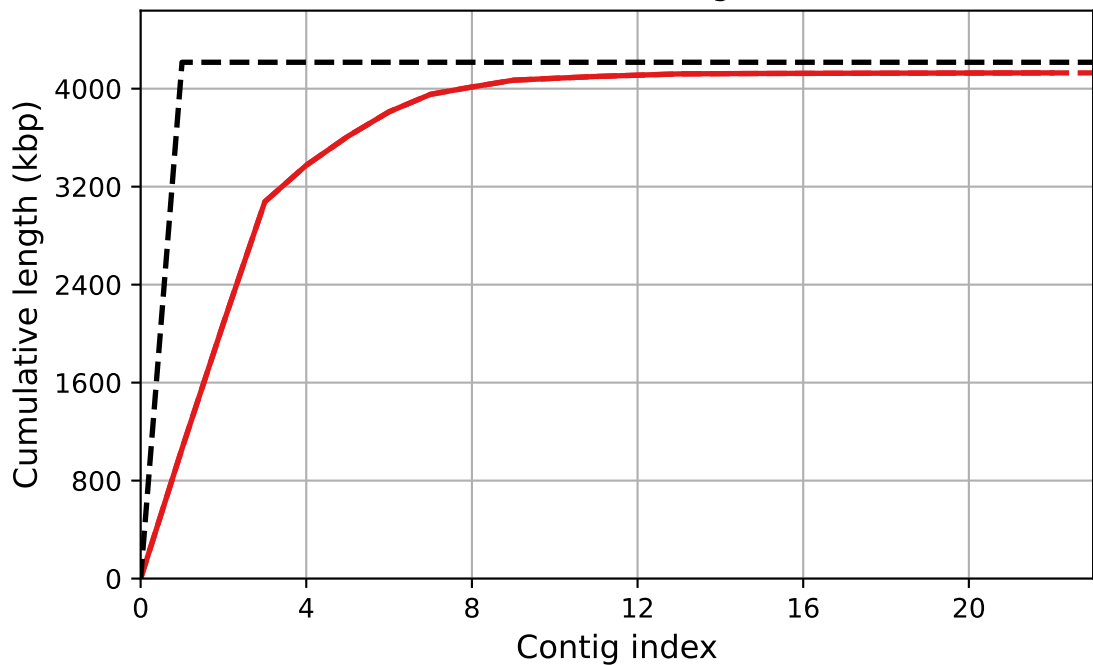
Misassemblies report

	abyssoutput_April9-8_fa	abyssoutput_April9-8_fa_broken
# misassemblies	54	54
# contig misassemblies	54	54
# c. relocations	54	54
# 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	6	6
Misassembled contigs length	3811335	3811335
# local misassemblies	33	33
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	48539	48539
# indels	1578	1570
# indels (<= 5 bp)	1376	1376
# indels (> 5 bp)	202	194
Indels length	6801	6665

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

	abyssoutput_April9-8_fa	abyssoutput_April9-8_fa_broken
# fully unaligned contigs	1	1
Fully unaligned length	142436	142436
# partially unaligned contigs	6	6
Partially unaligned length	200274	200274
# N's	50	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

abyssoutput_April9-8_fa   abyssoutput_April9-8_fa_broken

Cumulative length

Legend:
- abyssoutput_April9-8_fa
- abyssoutput_April9-8_fa_broken
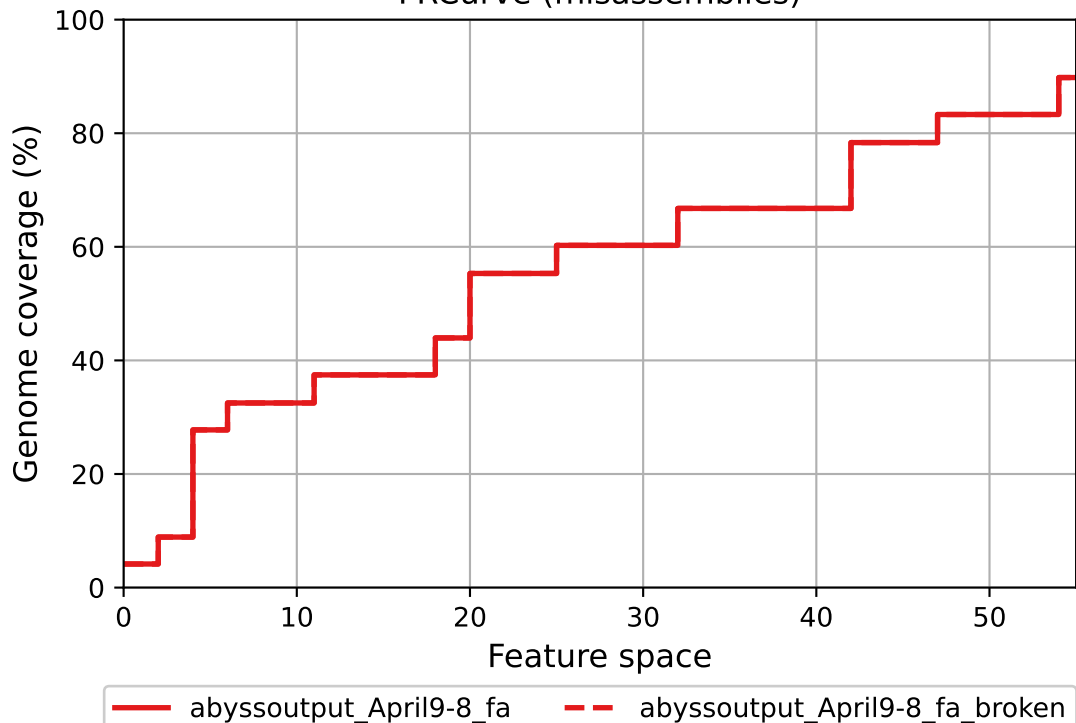- Reference

GC content
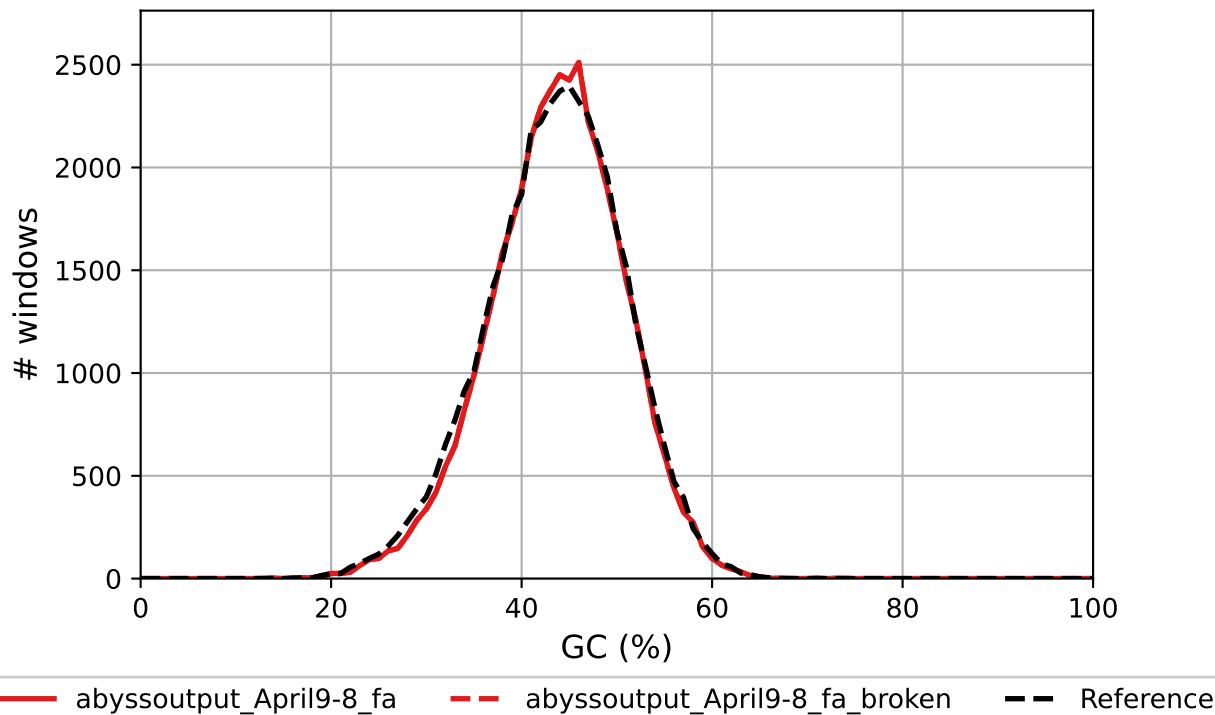
abyssoutput_April9-8_fa GC content
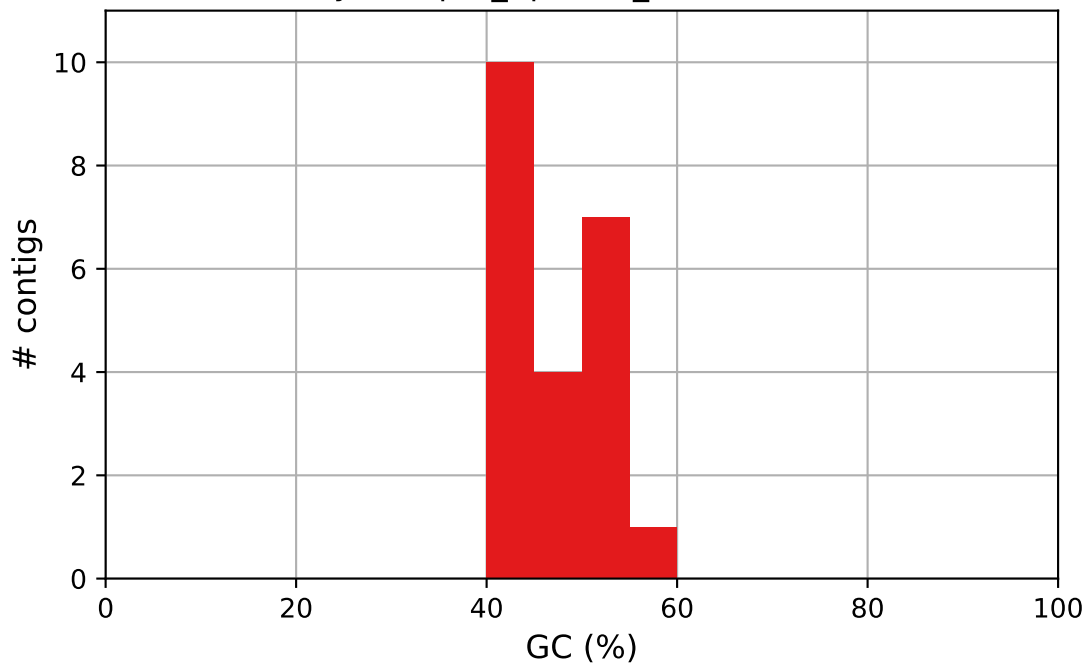
abyssoutput_April9-8_fa_broken GC content

Misassemblies

FRCurve (misassemblies)

Cumulative length (aligned contigs)
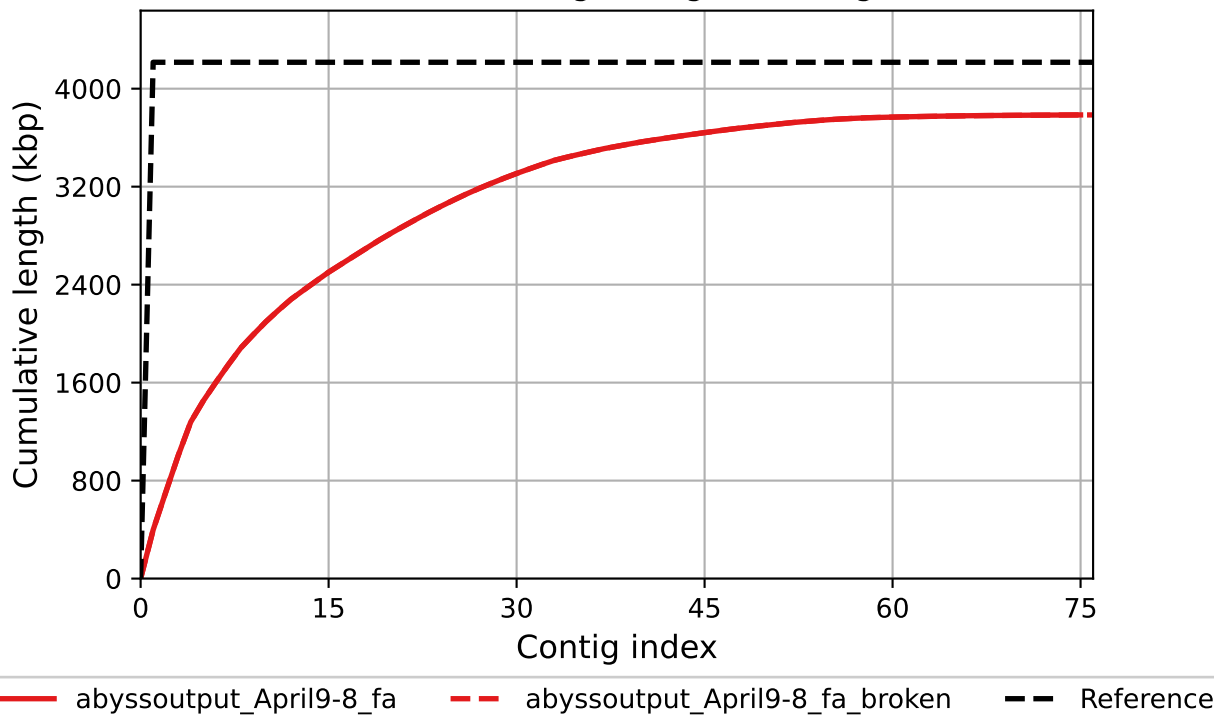
NAx
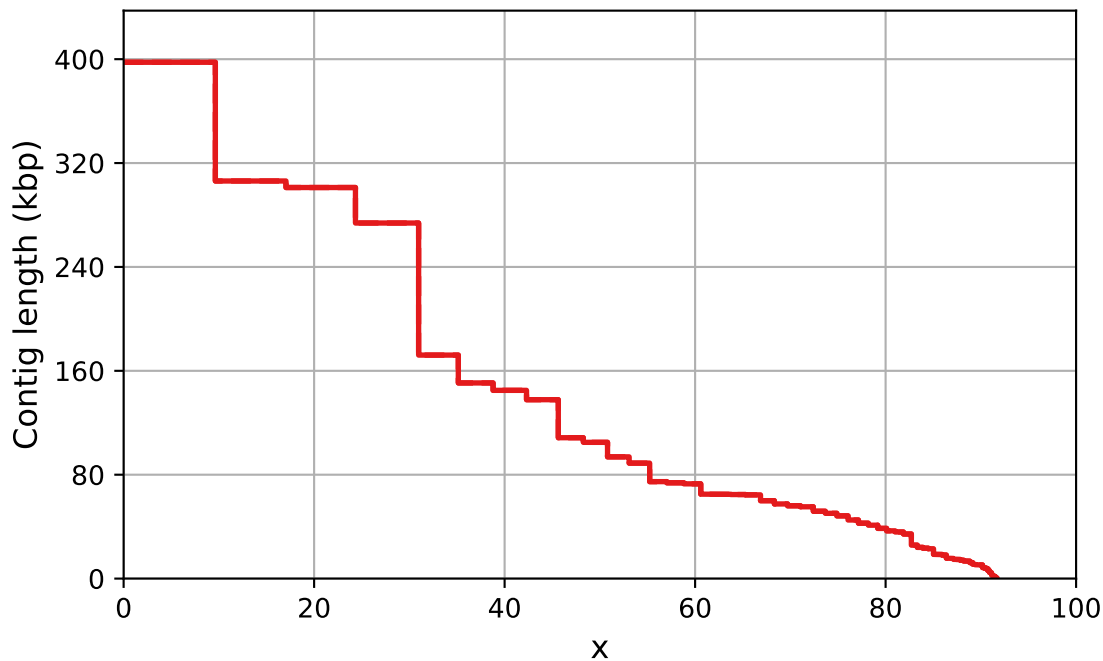
NGAx

| x | Contig length (kbp) |
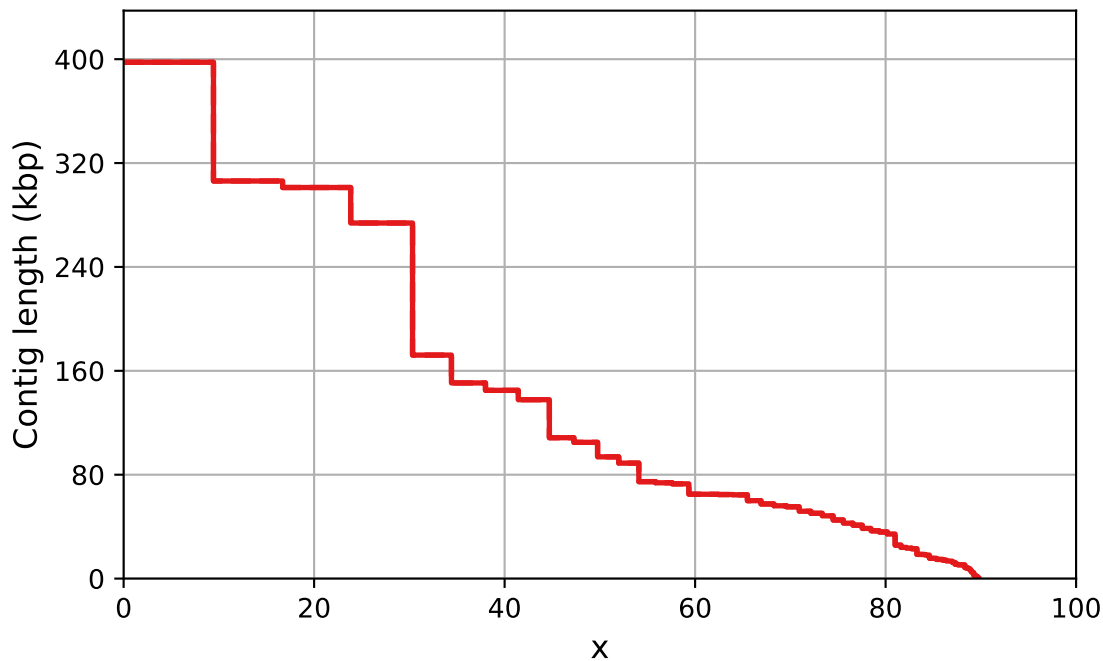
Legend: abyssoutput_April9-8_fa — abyssoutput_April9-8_fa_broken
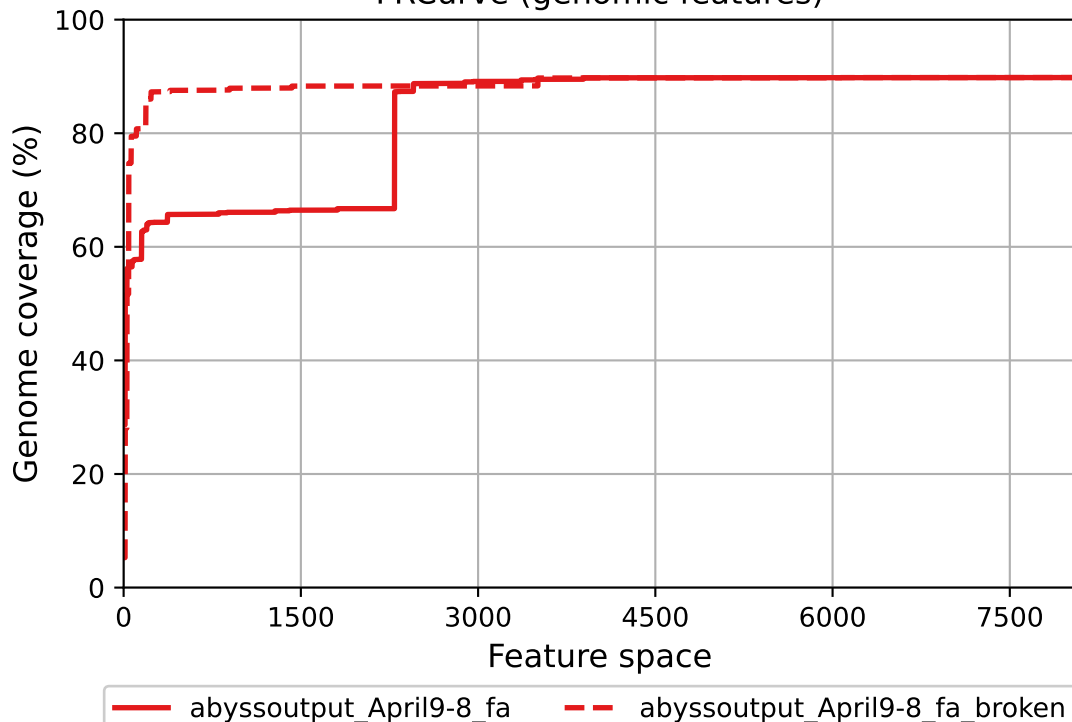
Cumulative # complete genomic features
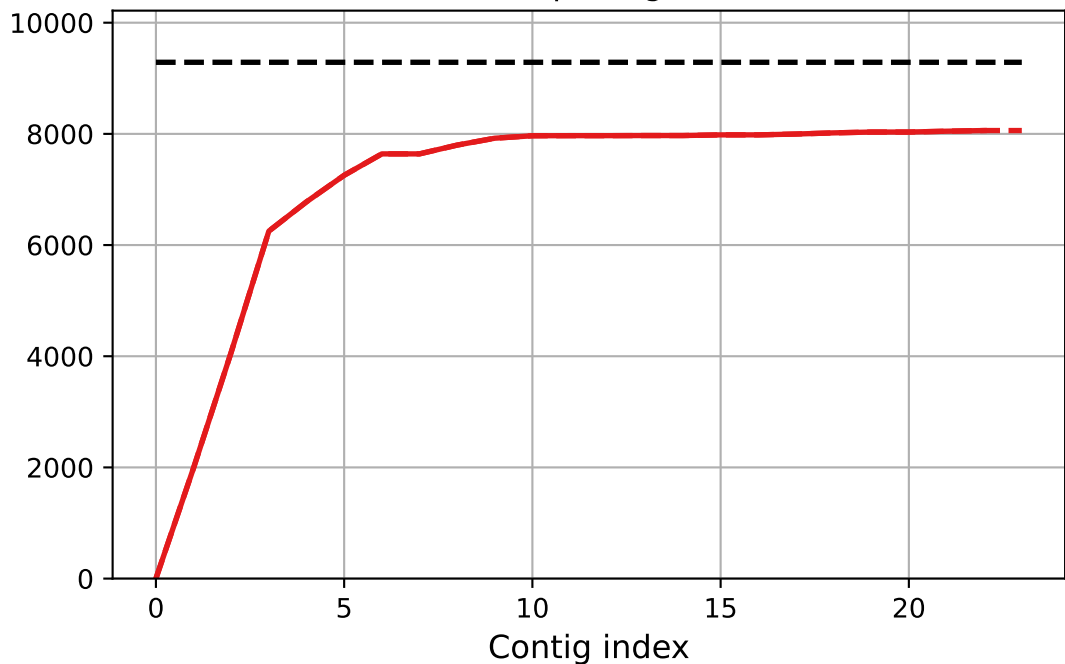
- abyssoutput_April9-8_fa
- abyssoutput_April9-8_fa_broken
- Reference

FRCurve (genomic features)

complete genomic features

abyssoutput_April9-8_fa	abyssoutput_April9-8_fa_broken

Genome fraction, %

100 —

95 —

▮ abyssoutput_April9-8_fa	▮ abyssoutput_April9-8_fa_broken