Report

	Cbotulinum-8_fa	Cbotulinum-8_fa_broken
# contigs (>= 0 bp)	84	-
# contigs (>= 1000 bp)	20	24
Total length (>= 0 bp)	4355919	-
Total length (>= 1000 bp)	4342817	4341089
# contigs	24	32
Largest contig	1095256	941021
Total length	4345261	4344861
Reference length	4355919	4355919
GC (%)	27.78	27.78
Reference GC (%)	27.81	27.81
N50	550747	367466
NG50	550747	367466
N90	149783	146911
NG90	149783	146911
auN	586166.7	482435.8
auNG	584732.5	481211.1
L50	3	4
LG50	3	4
L90	9	11
LG90	9	11
# 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	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	99.755	99.755
Duplication ratio	1.000	1.000
# N's per 100 kbp	9.21	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
# genomic features	0 + 0 part	0 + 0 part
Complete BUSCO (%)	98.65	98.65
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	2 + 7 part	2 + 7 part
Largest alignment	1095256	941021
Total aligned length	4345261	4344861
NA50	550747	367466
NGA50	550747	367466
NA90	149783	146911
NGA90	149783	146911
auNA	586166.7	482435.8
auNGA	584732.5	481211.1
LA50	3	4
LGA50	3	4
LA90	9	11
LGA90	9	11

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).
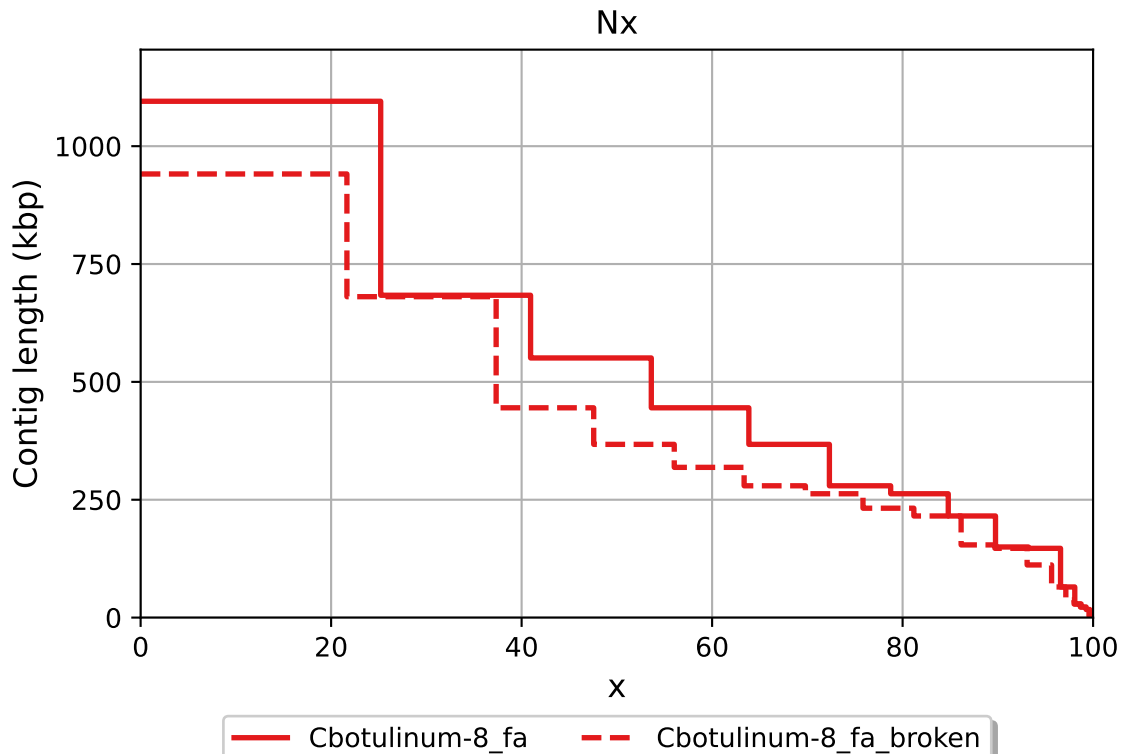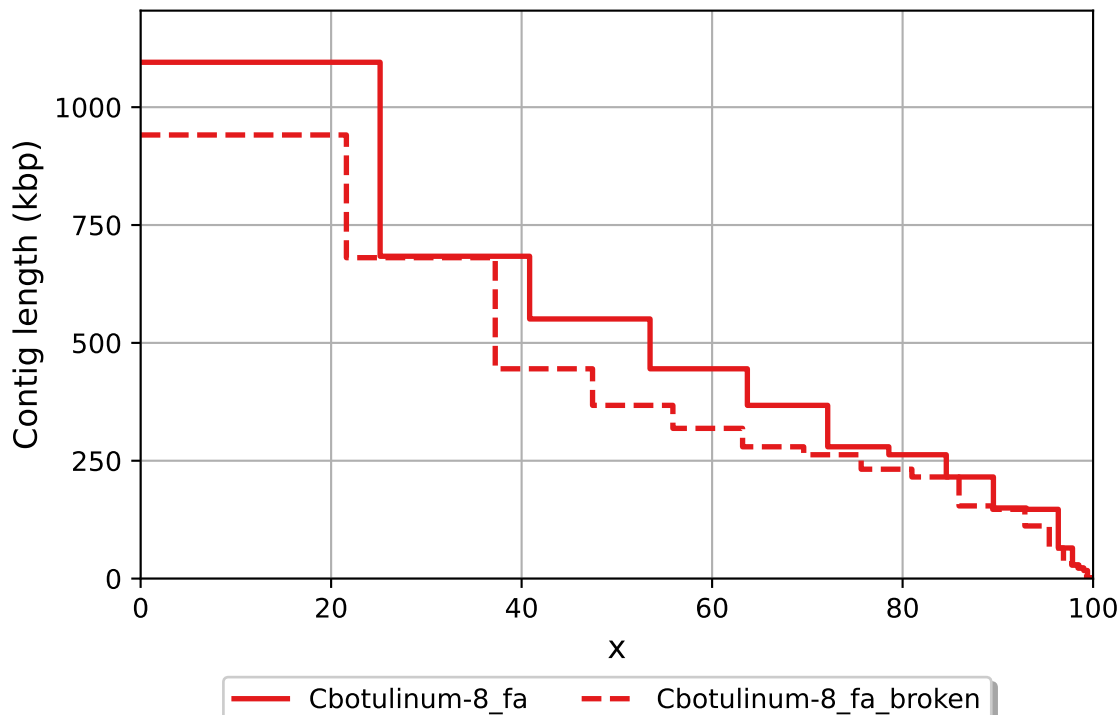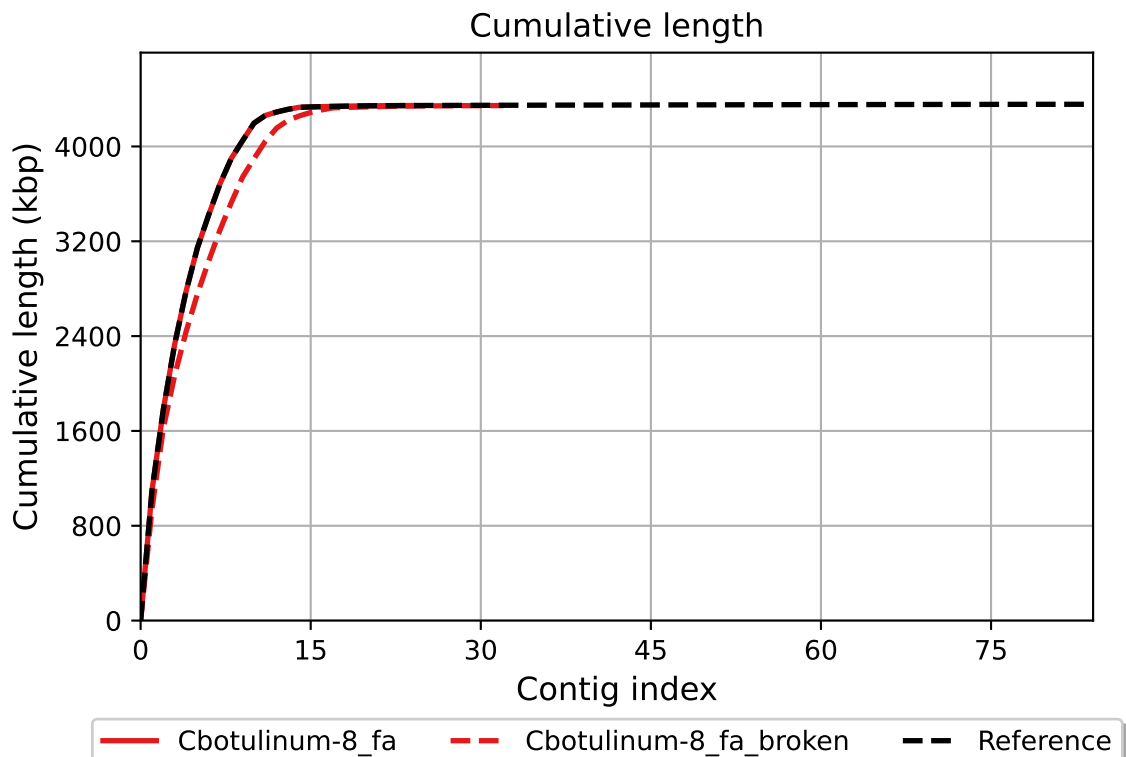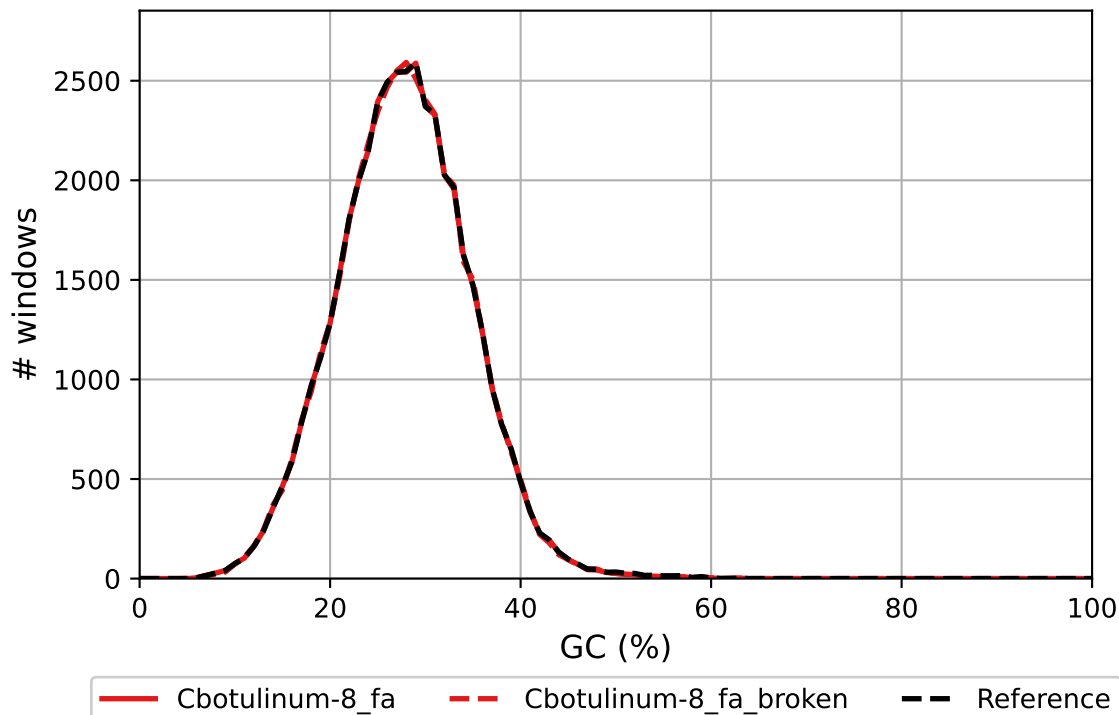
Misassemblies report

	Cbotulinum-8_fa	Cbotulinum-8_fa_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	0	0
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

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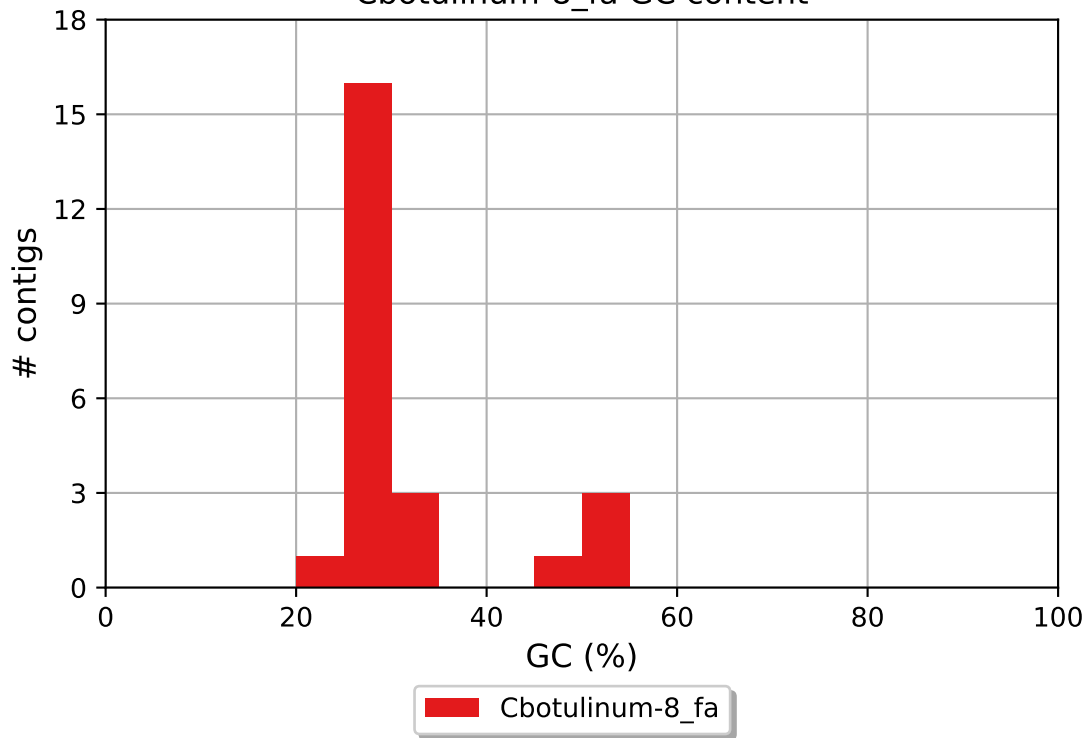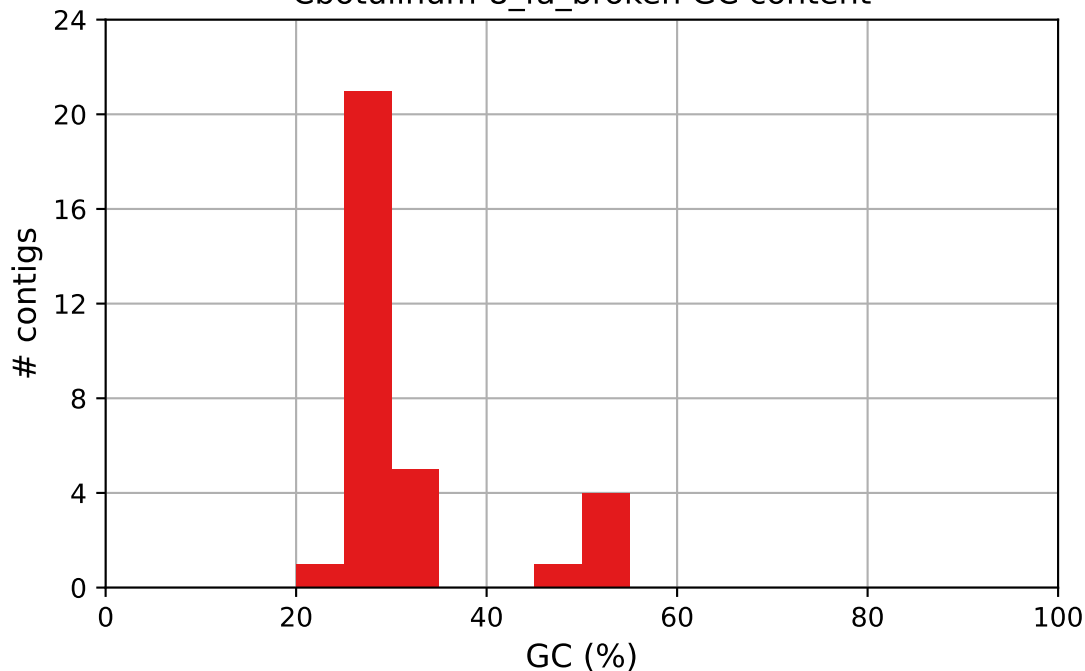(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	Cbotulinum-8_fa	Cbotulinum-8_fa_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	400	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

Cumulative length

GC content

windows vs GC (%)

Cbotulinum-8_fa — Cbotulinum-8_fa_broken — Reference

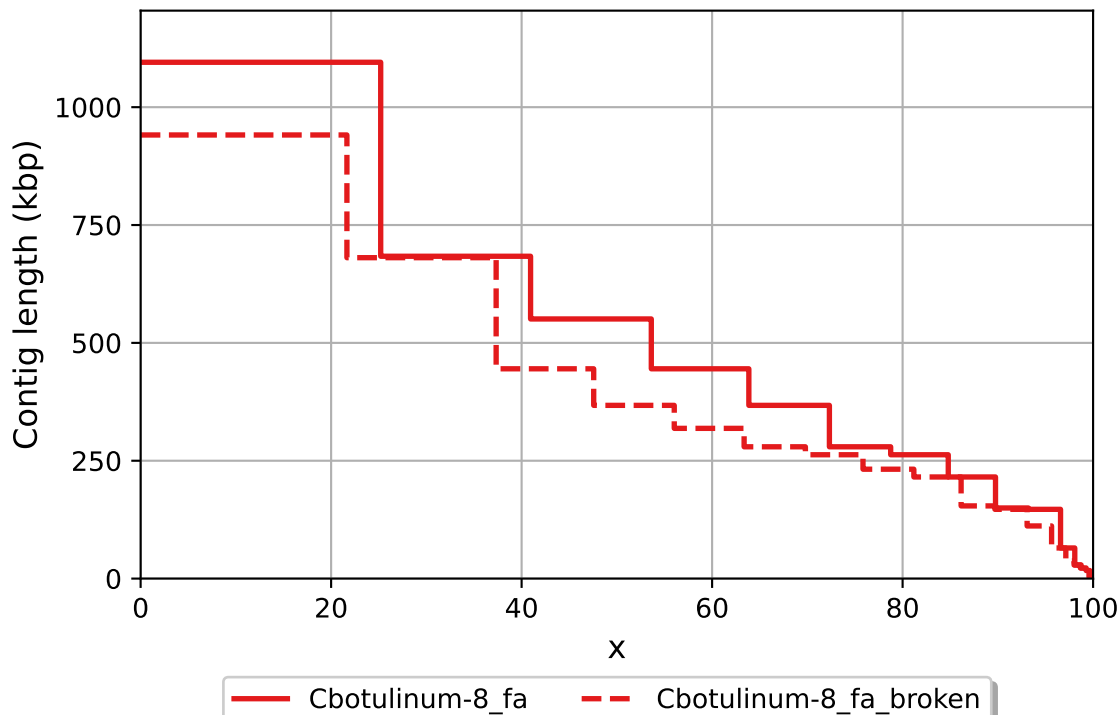Cbotulinum-8_fa GC content

Cbotulinum-8_fa_broken GC content

Misassemblies

FRCurve (misassemblies)
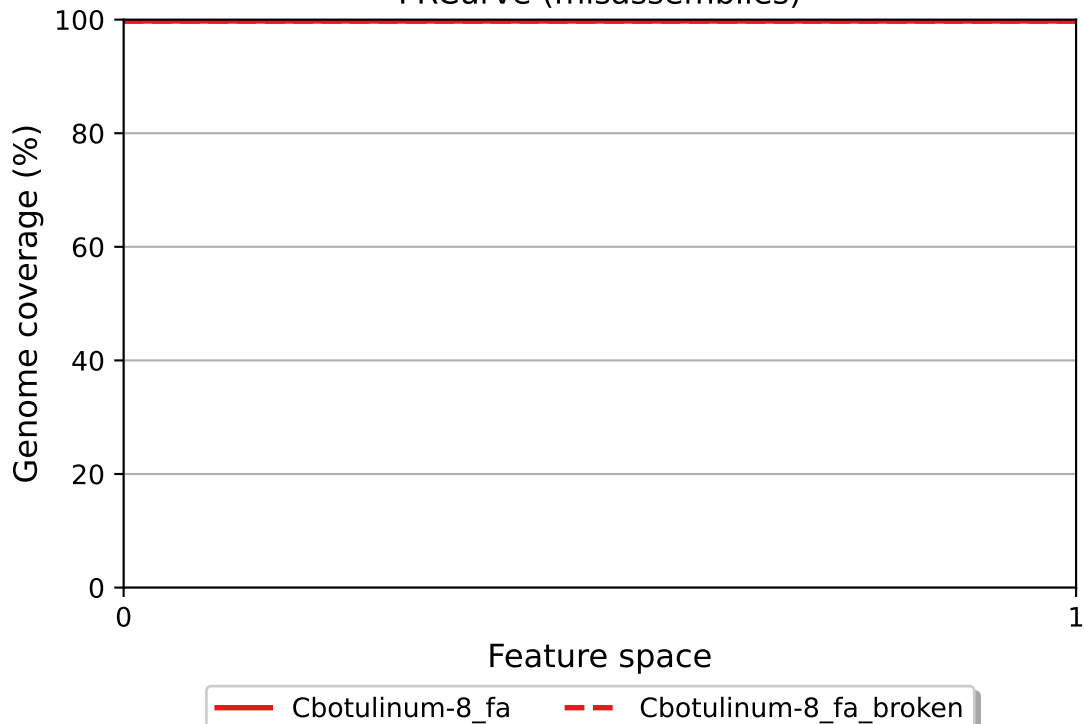
Cumulative length (aligned contigs)

NAx

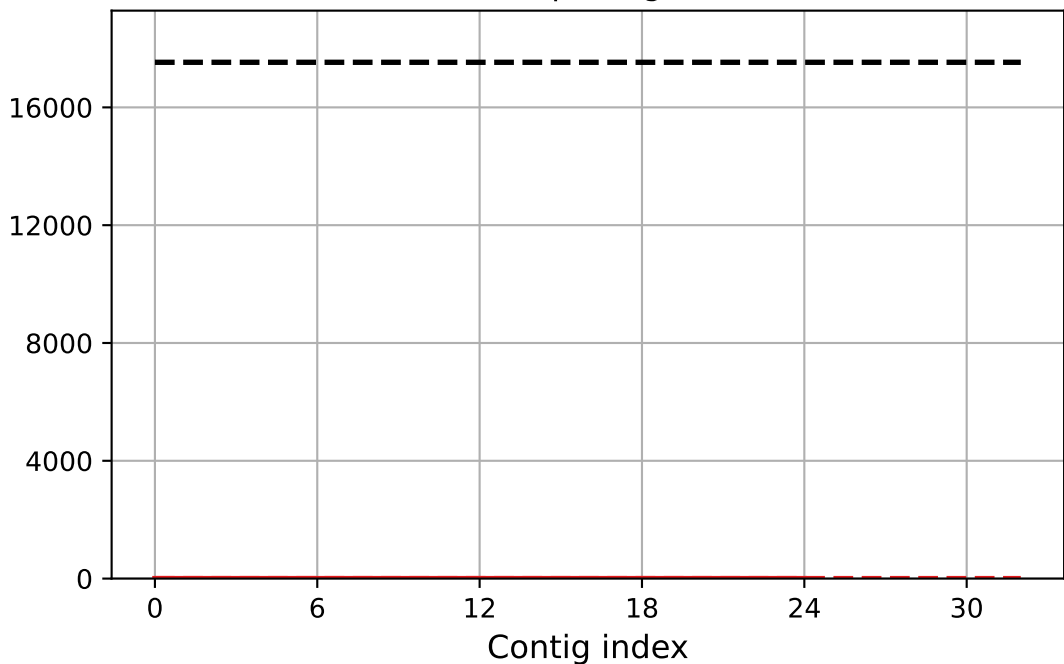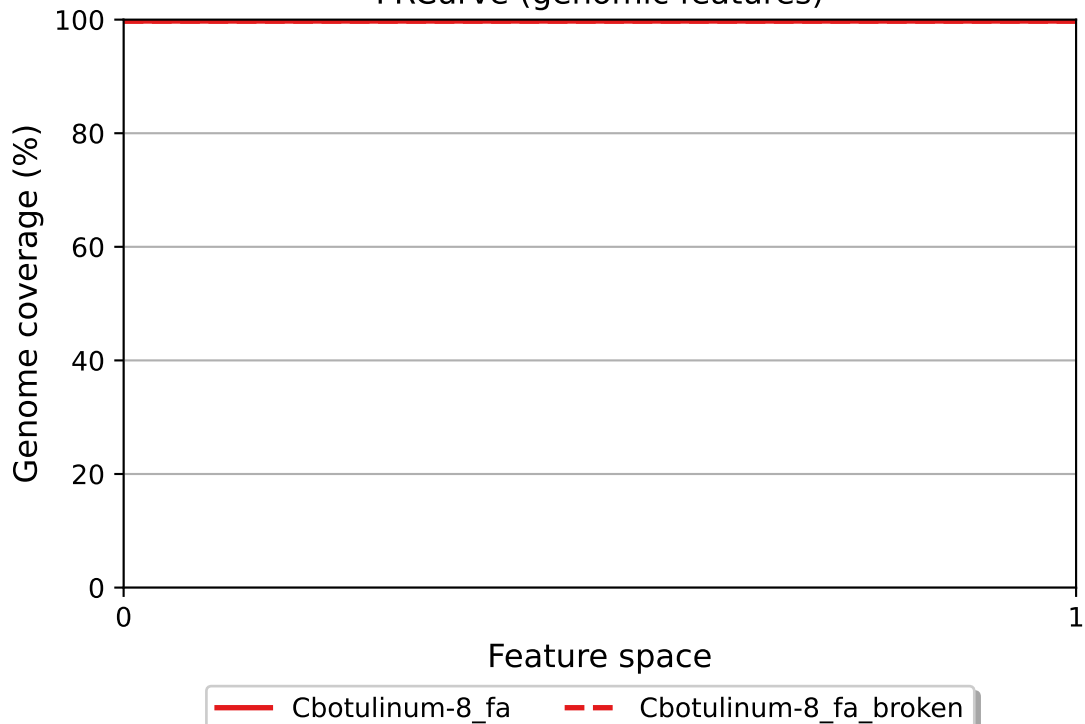Cbotulinum-8_fa — — — Cbotulinum-8_fa_broken
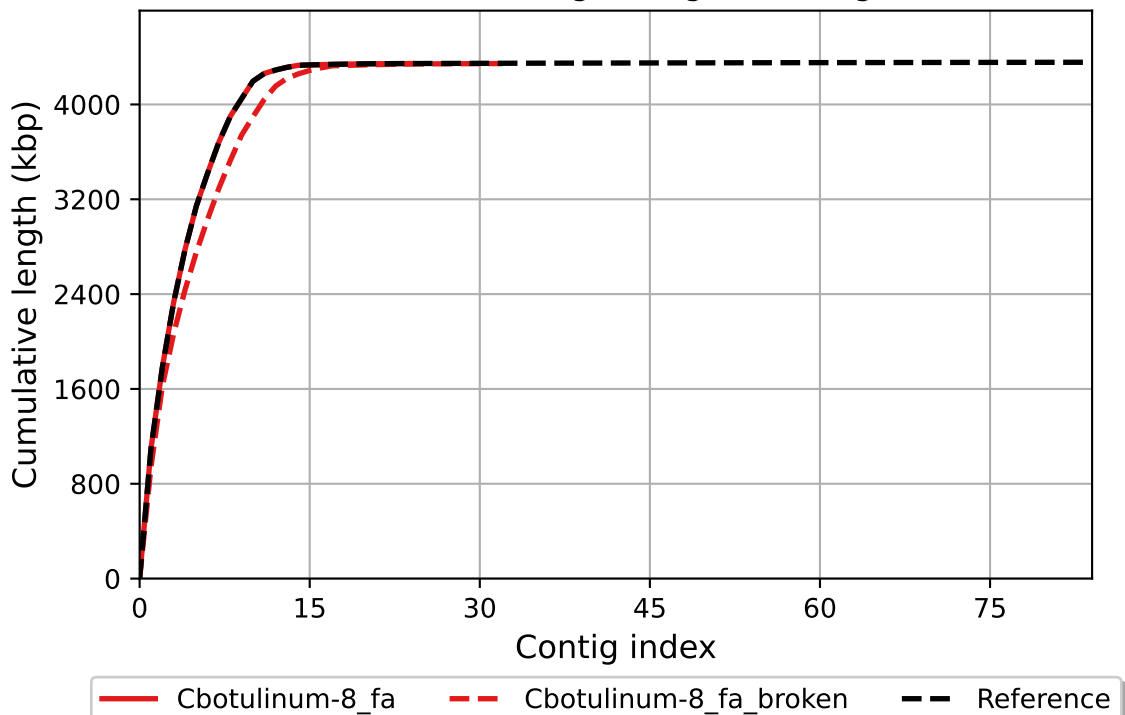
NGAx
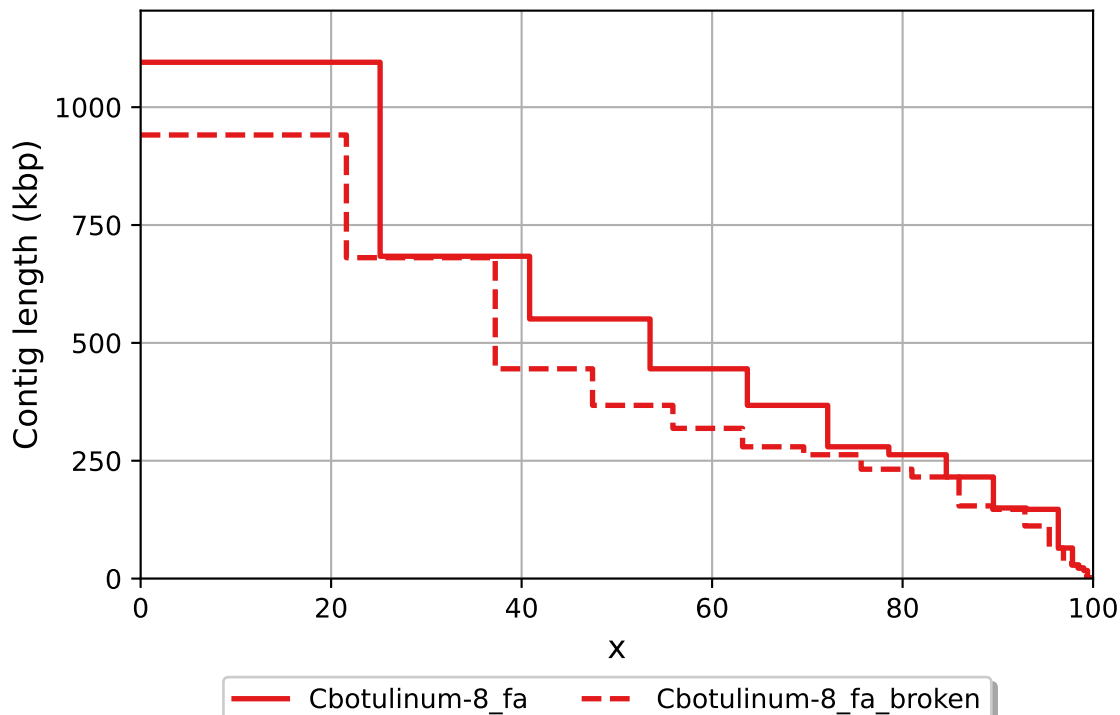
Cumulative # complete genomic features

FRCurve (genomic features)

complete genomic features

Genome fraction, %

Cbotulinum-8_fa   Cbotulinum-8_fa_broken