

Report

	unknown-8_fa	unknown-8_fa_broken
# contigs (>= 0 bp)	679	-
# contigs (>= 1000 bp)	60	71
Total length (>= 0 bp)	5633193	-
Total length (>= 1000 bp)	5539003	5537742
# contigs	64	76
Largest contig	565228	565228
Total length	5541523	5540878
Reference length	5682322	5682322
GC (%)	57.20	57.20
Reference GC (%)	57.12	57.12
N50	174111	169829
NG50	174111	169829
N90	73309	45554
NG90	45554	35266
auN	252491.2	229701.6
auNG	246234.9	223983.9
L50	9	10
LG50	9	10
L90	26	31
LG90	28	34
# misassemblies	80	77
# misassembled contigs	27	31
Misassembled contigs length	4568842	4451985
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	2	2
# unaligned contigs	13 + 36 part	13 + 41 part
Unaligned length	723812	724171
Genome fraction (%)	85.116	85.086
Duplication ratio	1.008	1.008
# N's per 100 kbp	11.89	0.25
# mismatches per 100 kbp	686.25	685.92
# indels per 100 kbp	19.89	19.29
# genomic features	9657 + 220 part	9649 + 228 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 2 part	4 + 1 part
Largest alignment	313411	313411
Total aligned length	4816759	4815714
NA50	70102	65917
NGA50	69622	65208
NA90	-	-
NGA90	-	-
auNA	87894.7	86085.2
auNGA	85716.8	83942.4
LA50	23	24
LGA50	24	25
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

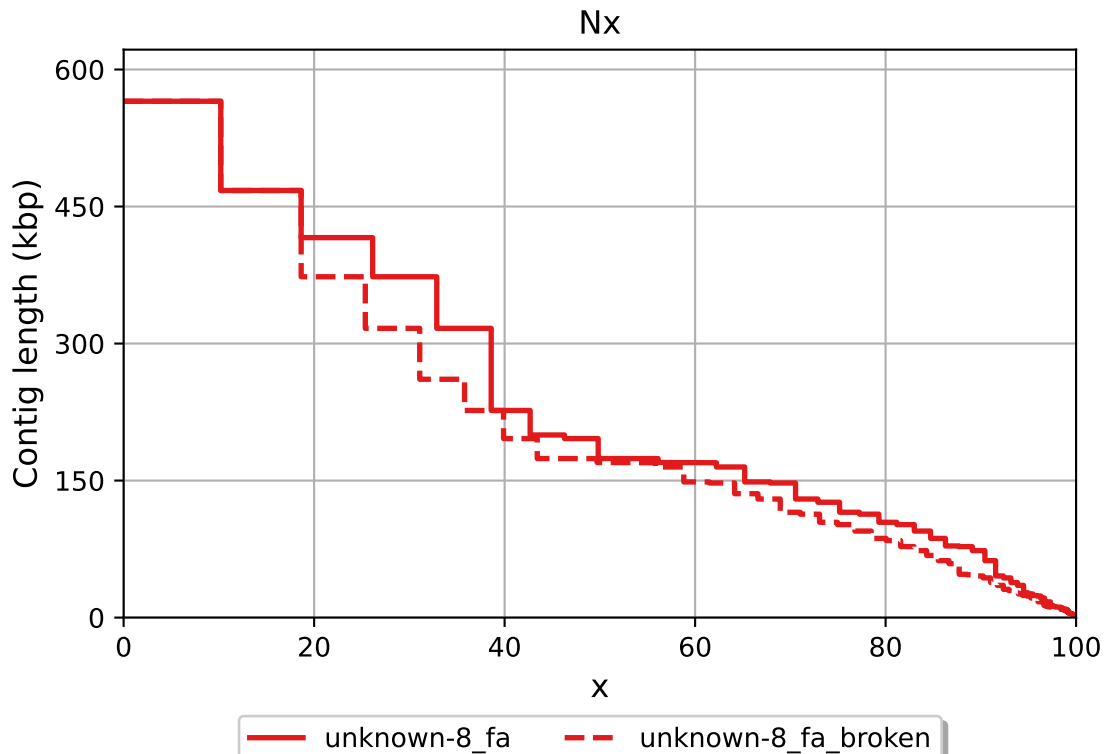
	unknown-8_fa	unknown-8_fa_broken
# misassemblies	80	77
# contig misassemblies	78	77
# c. relocations	74	73
# c. translocations	4	4
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	27	31
Misassembled contigs length	4568842	4451985
# local misassemblies	28	28
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	2	2
# mismatches	33055	33032
# indels	958	929
# indels (<= 5 bp)	846	835
# indels (> 5 bp)	112	94
Indels length	9597	8689

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).

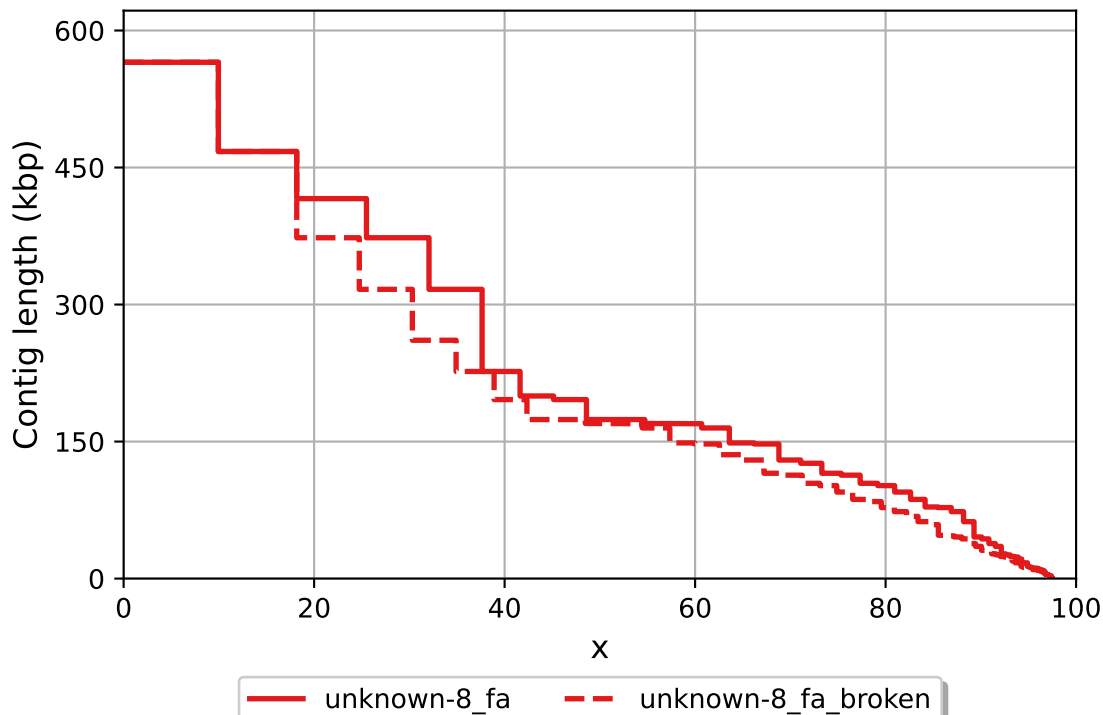
Unaligned report

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# fully unaligned contigs	13	13
Fully unaligned length	83025	83025
# partially unaligned contigs	36	41
Partially unaligned length	640787	641146
# N's	659	14

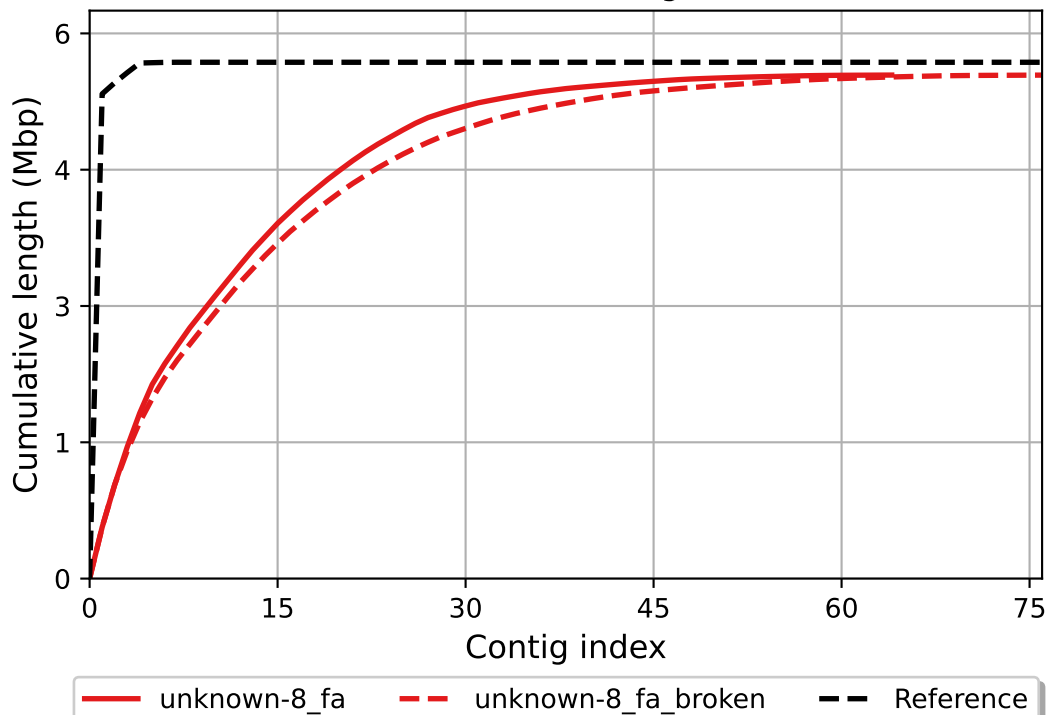
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



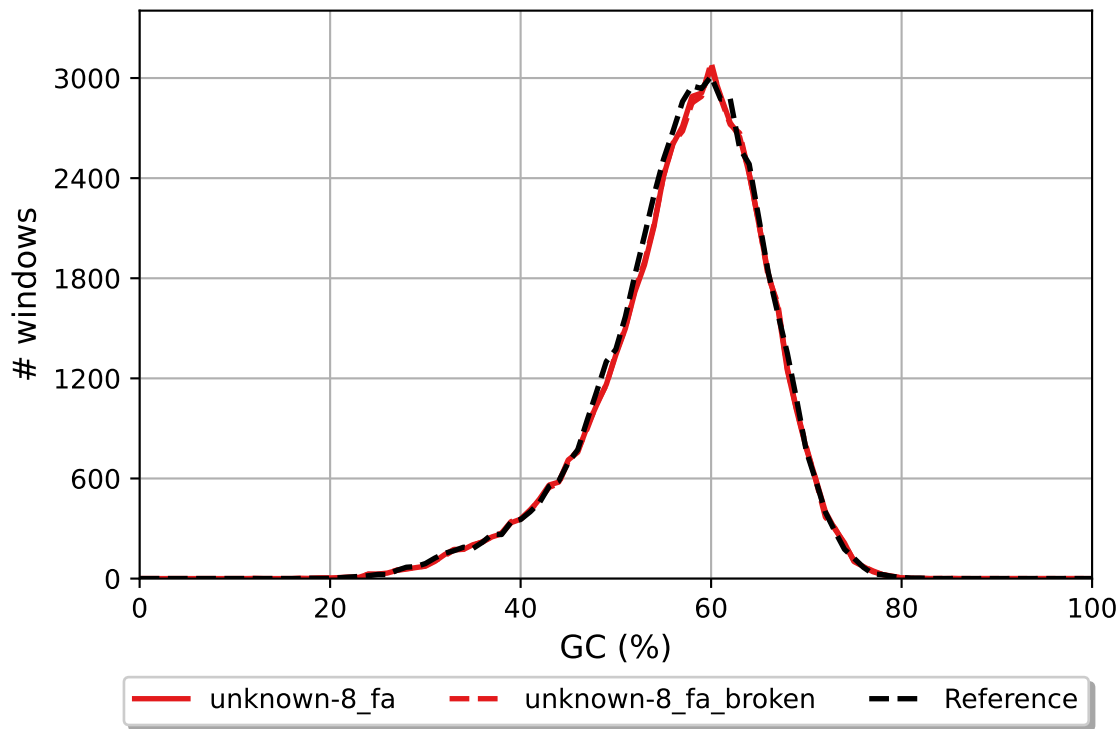
NGx



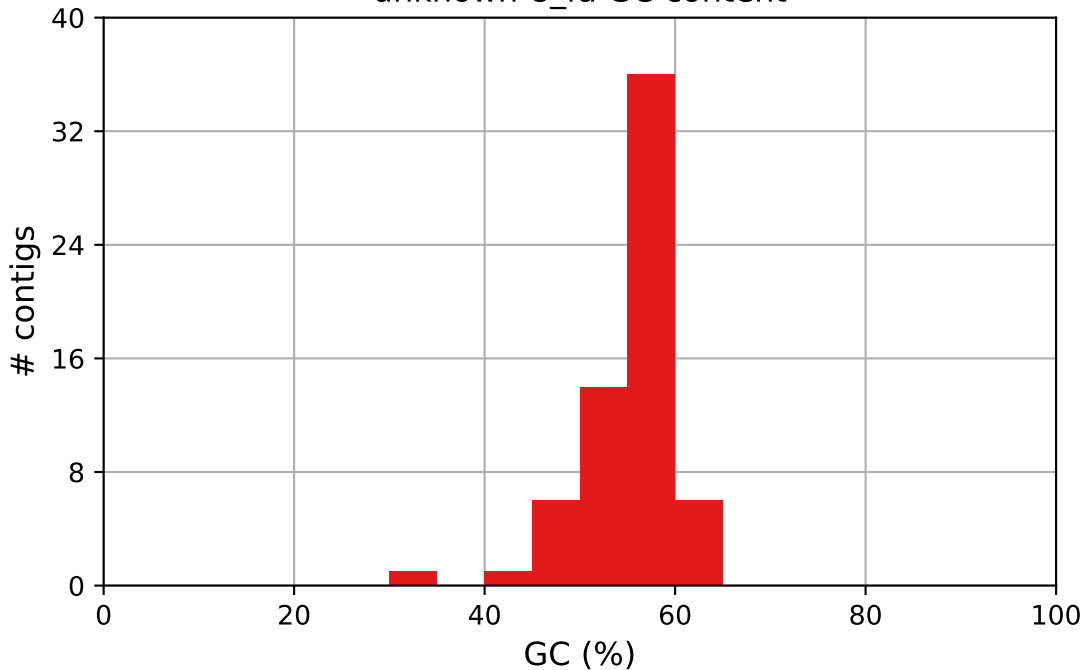
Cumulative length



GC content

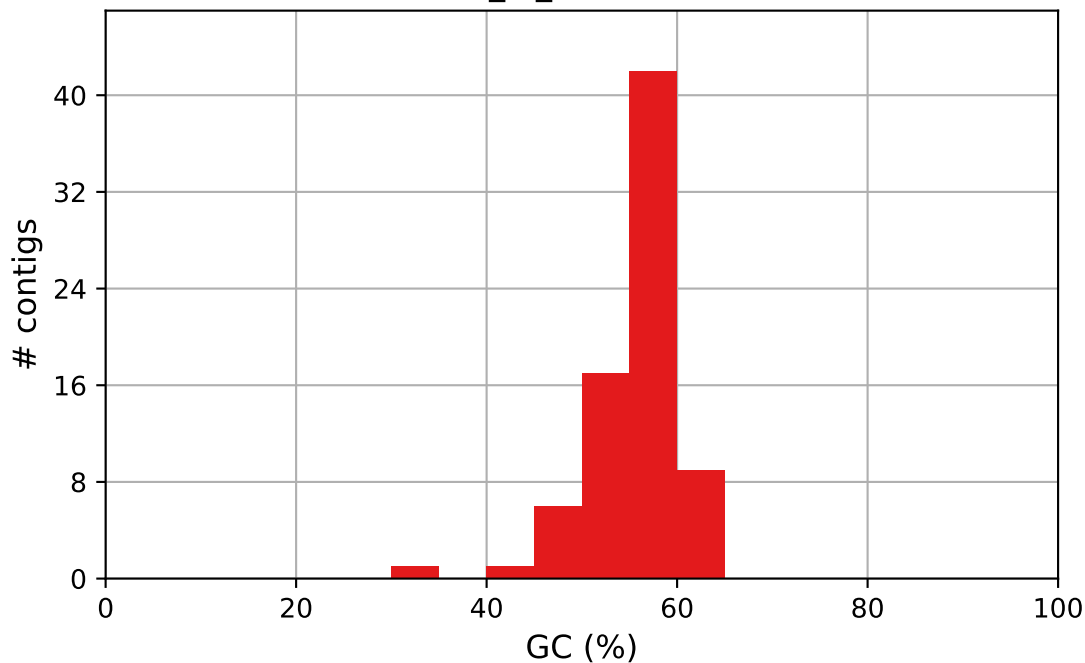


unknown-8_fa GC content



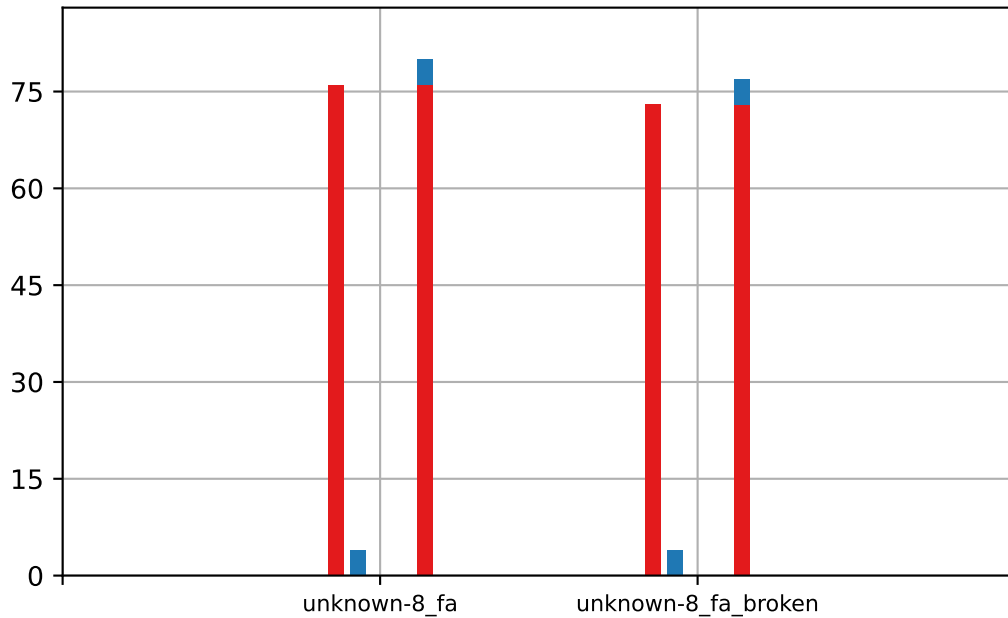
unknown-8_fa

unknown-8_fa_broken GC content



unknown-8_fa_broken

Misassemblies

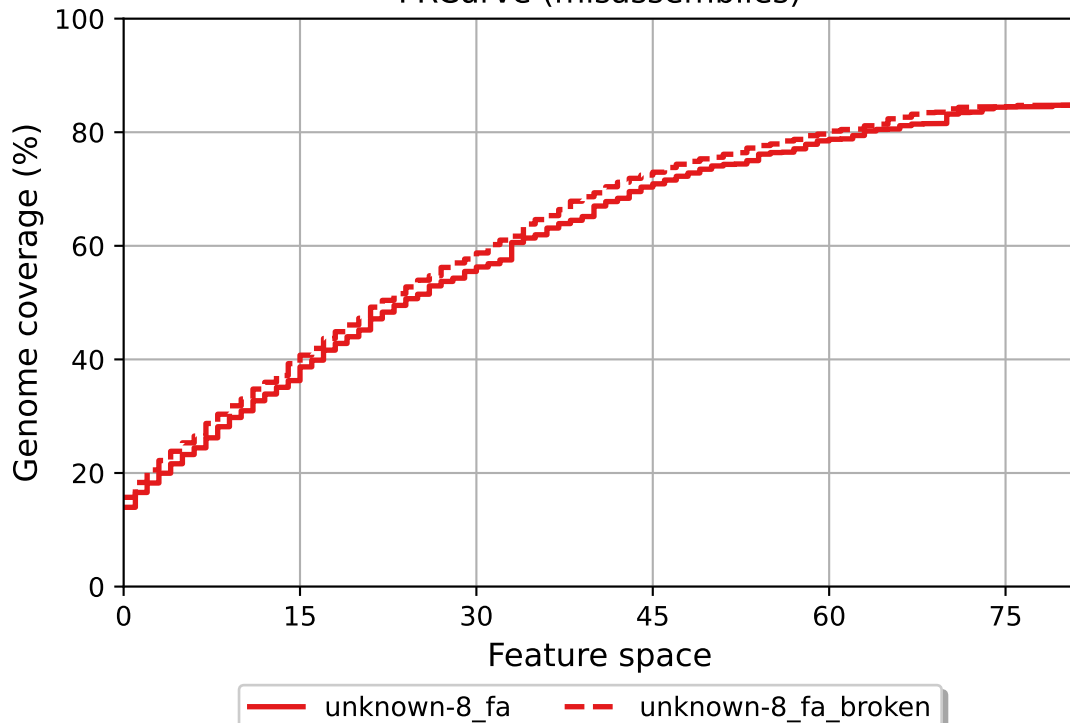


relocations

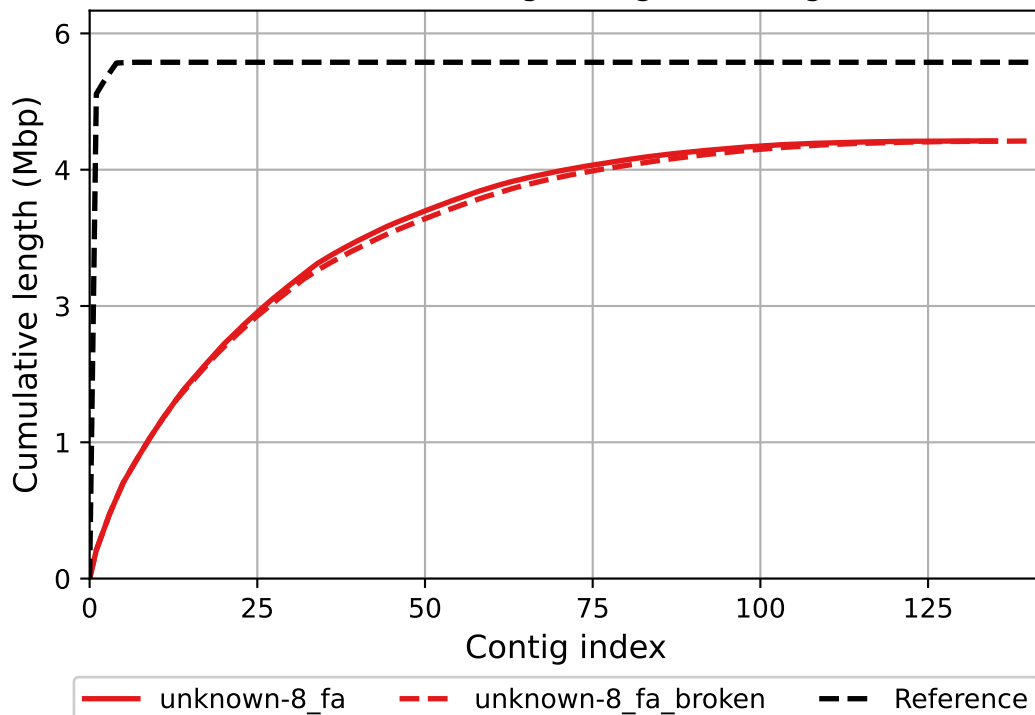


translocations

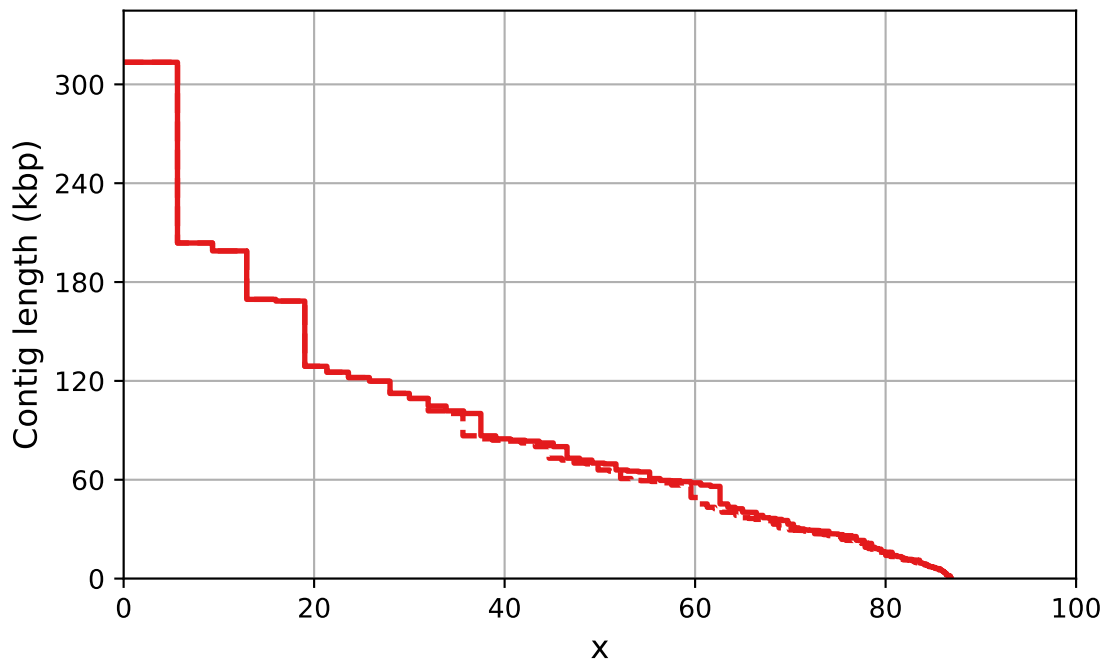
FRCurve (misassemblies)



Cumulative length (aligned contigs)

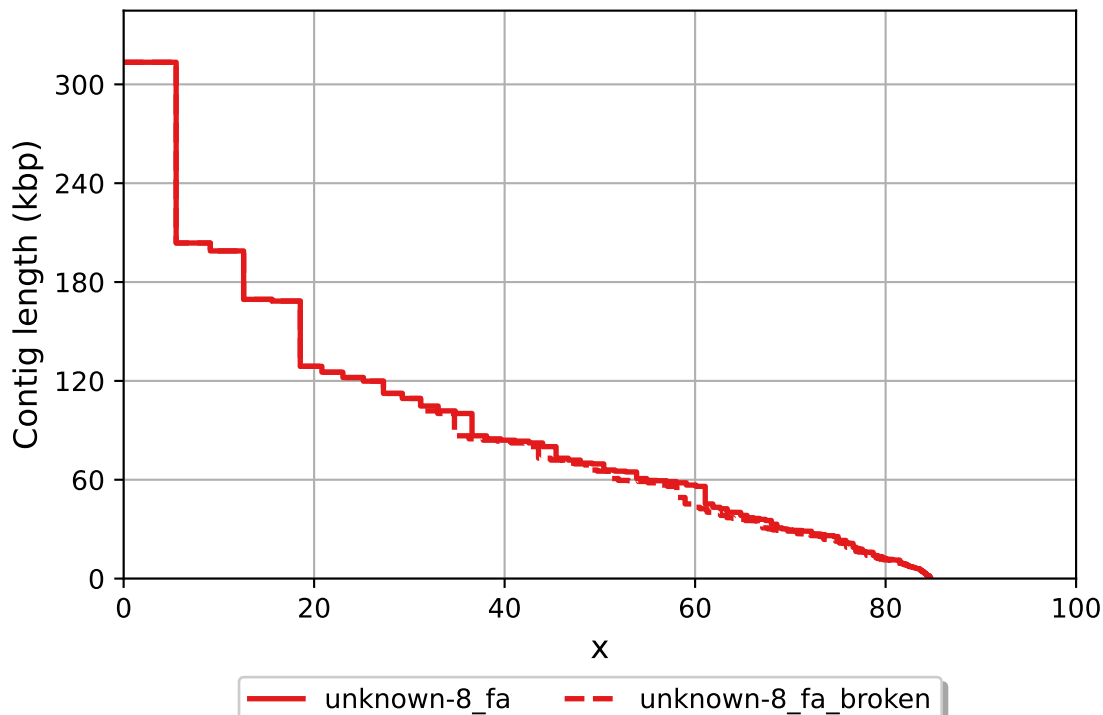


NAx



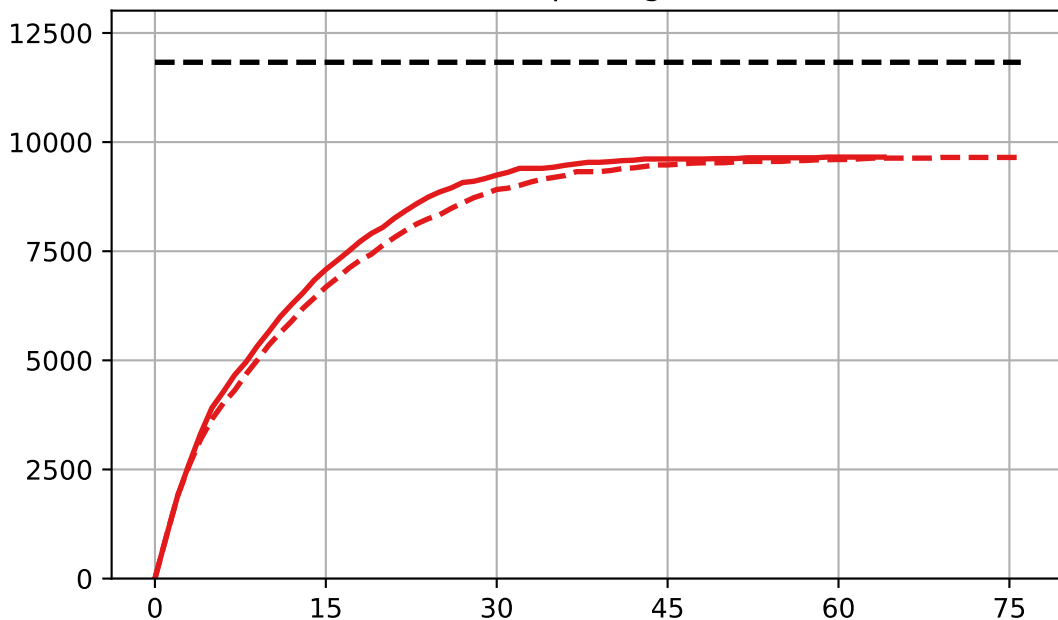
— unknown-8_fa - - - unknown-8_fa_broken

NGAx



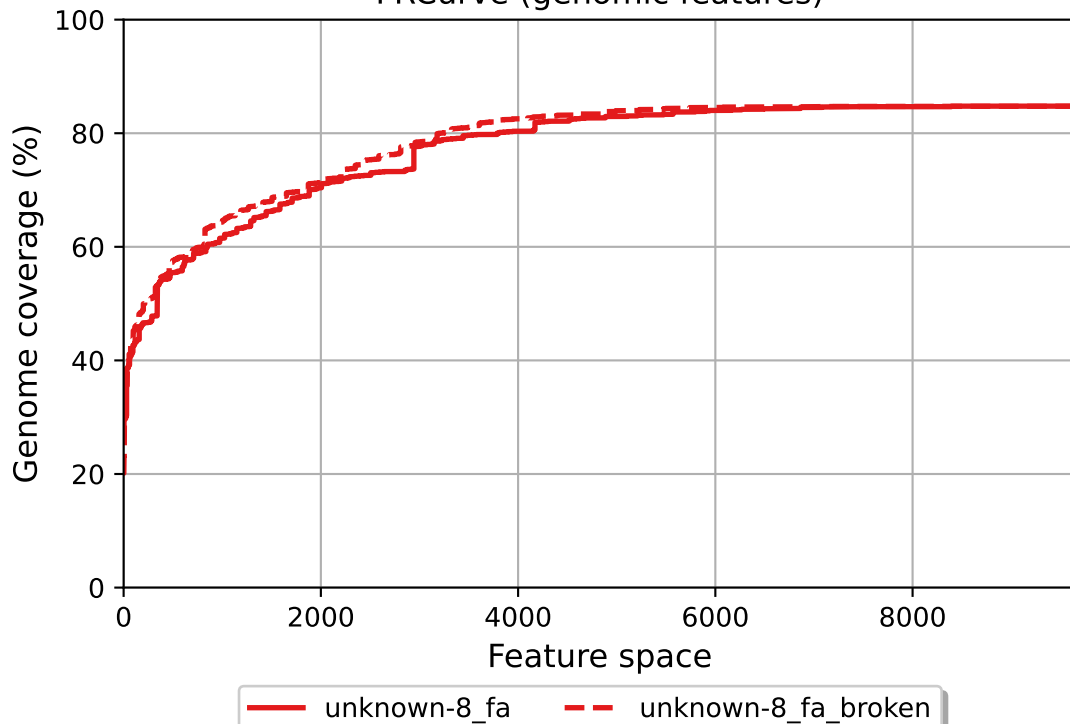
Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)



complete genomic features



unknown-8_fa



unknown-8_fa_broken

Genome fraction, %



unknown-8_fa



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