

Report

	unknown-8_fa	unknown-8_fa_broken
# contigs (>= 0 bp)	330	-
# contigs (>= 1000 bp)	142	165
Total length (>= 0 bp)	5568030	-
Total length (>= 1000 bp)	5528676	5524386
# contigs	149	176
Largest contig	195464	174746
Total length	5533424	5531759
Reference length	5682322	5682322
GC (%)	57.17	57.17
Reference GC (%)	57.12	57.12
N50	82933	67492
NG50	79928	63196
N90	20950	16616
NG90	17296	14018
auN	81080.8	71216.4
auNG	78956.1	69329.4
L50	25	28
LG50	26	29
L90	79	92
LG90	86	100
# misassemblies	71	66
# misassembled contigs	44	46
Misassembled contigs length	3039726	2686449
# local misassemblies	22	23
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	6	4
# unaligned contigs	15 + 60 part	16 + 61 part
Unaligned length	721649	721774
Genome fraction (%)	84.718	85.095
Duplication ratio	1.007	1.007
# N's per 100 kbp	31.93	1.84
# mismatches per 100 kbp	683.44	685.47
# indels per 100 kbp	21.51	21.16
# genomic features	9498 + 364 part	9464 + 416 part
# predicted rRNA genes	6 + 1 part	5 + 1 part
Largest alignment	169586	169586
Total aligned length	4807318	4805781
NA50	37064	33387
NGA50	35865	32899
NA90	-	-
NGA90	-	-
auNA	45895.5	43414.8
auNGA	44692.9	42264.5
LA50	42	46
LGA50	44	48
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

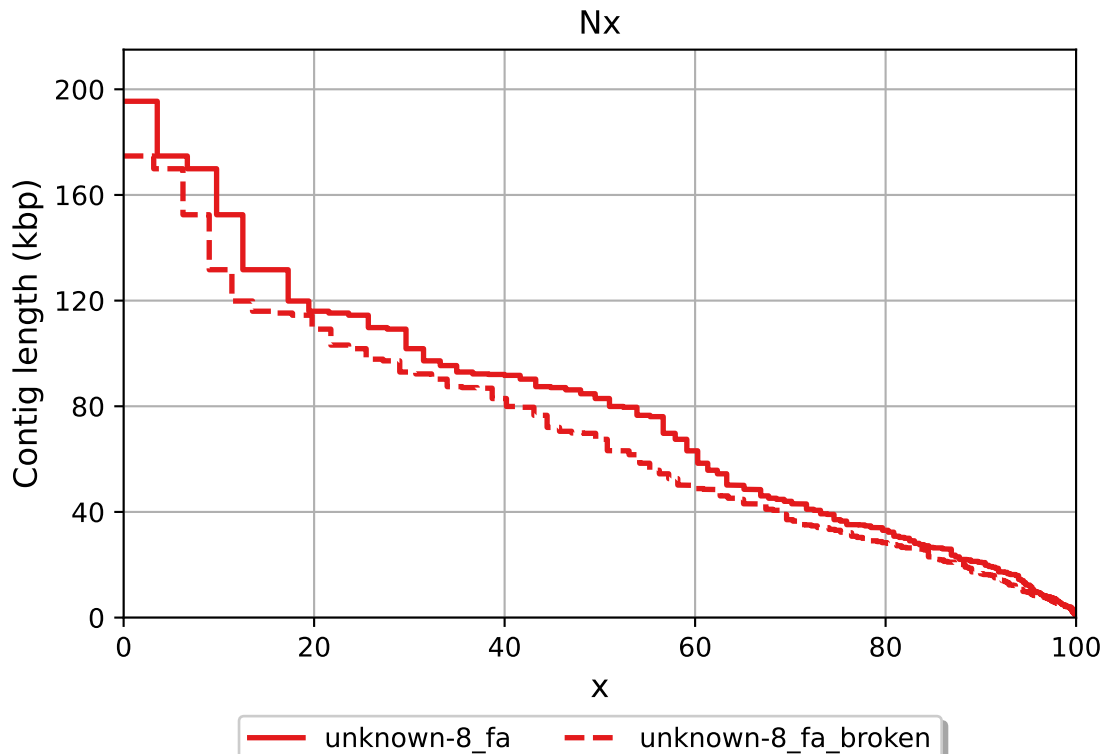
	unknown-8_fa	unknown-8_fa_broken
# misassemblies	71	66
# contig misassemblies	67	66
# c. relocations	63	62
# c. translocations	4	4
# c. inversions	0	0
# scaffold misassemblies	4	0
# s. relocations	4	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	44	46
Misassembled contigs length	3039726	2686449
# local misassemblies	22	23
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	6	4
# mismatches	32855	32942
# indels	1034	1017
# indels (<= 5 bp)	856	857
# indels (> 5 bp)	178	160
Indels length	11975	10939

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).

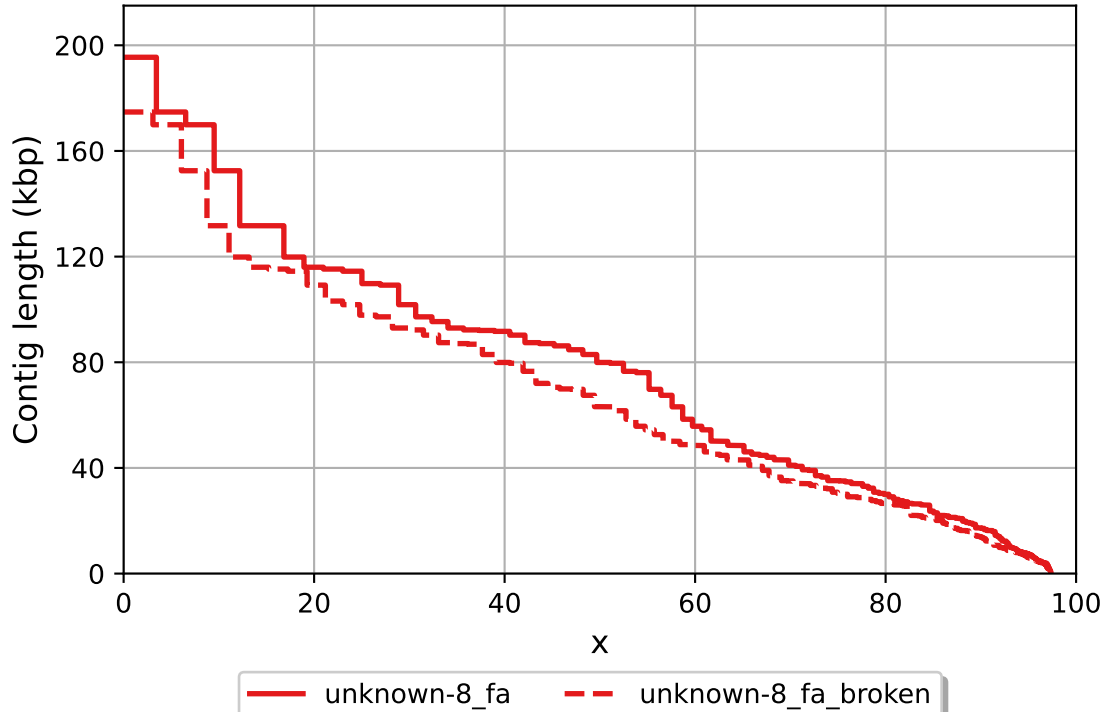
Unaligned report

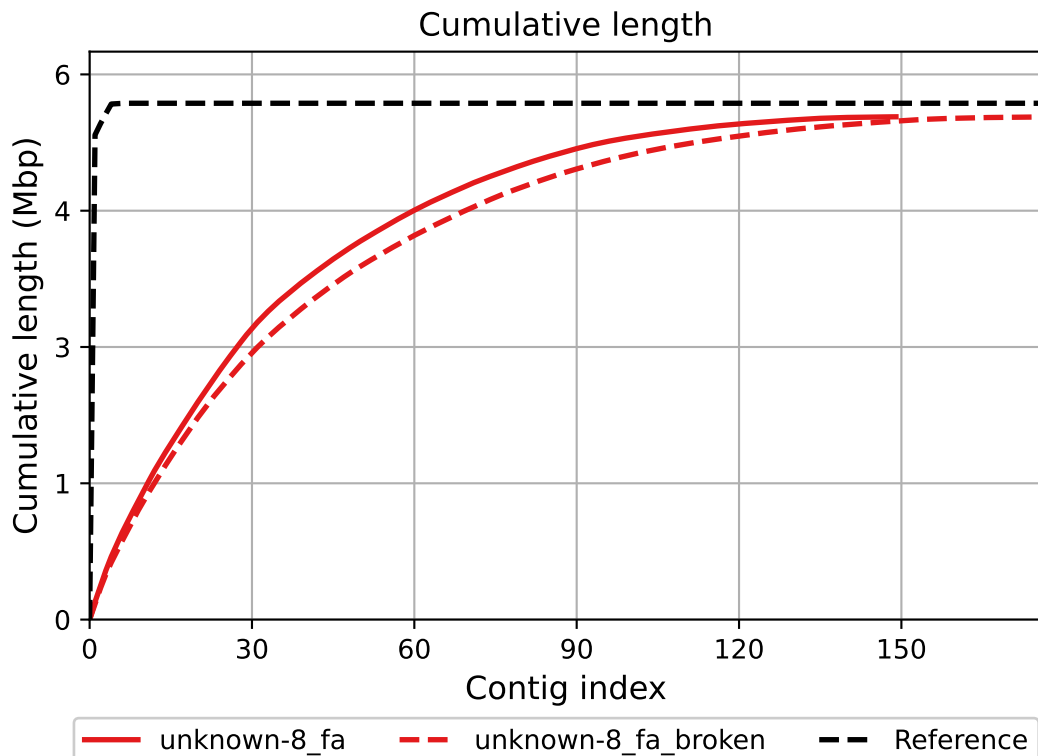
	unknown-8_fa	unknown-8_fa_broken
# fully unaligned contigs	15	16
Fully unaligned length	91786	112813
# partially unaligned contigs	60	61
Partially unaligned length	629863	608961
# N's	1767	102

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).

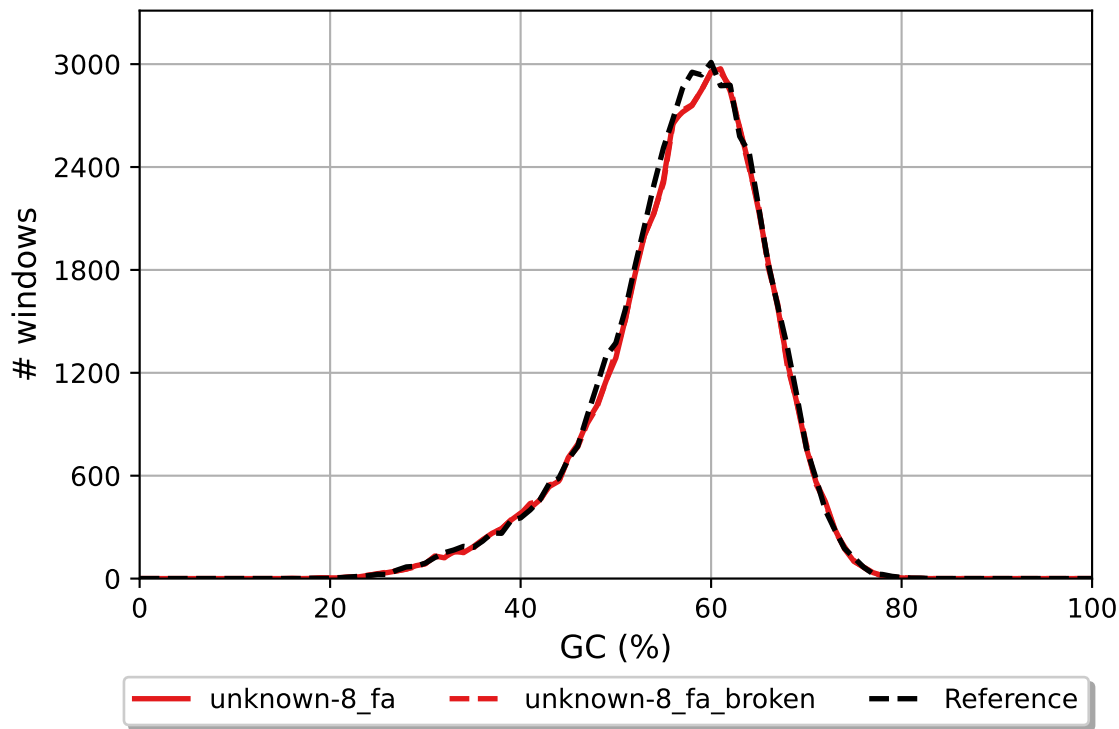


NGx

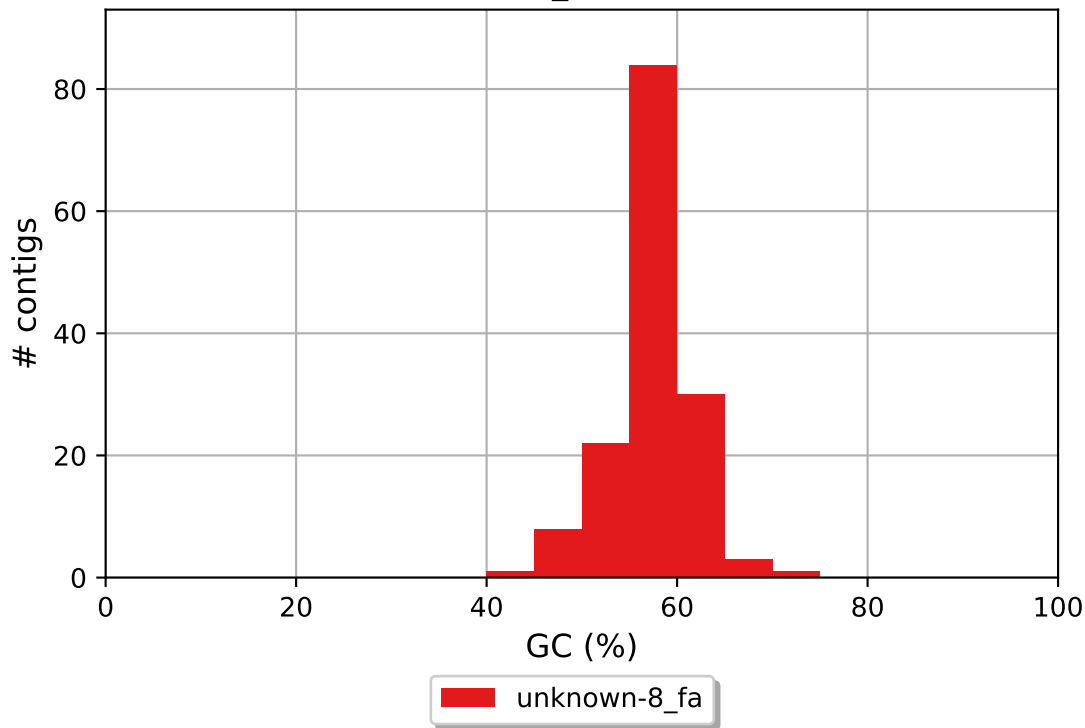




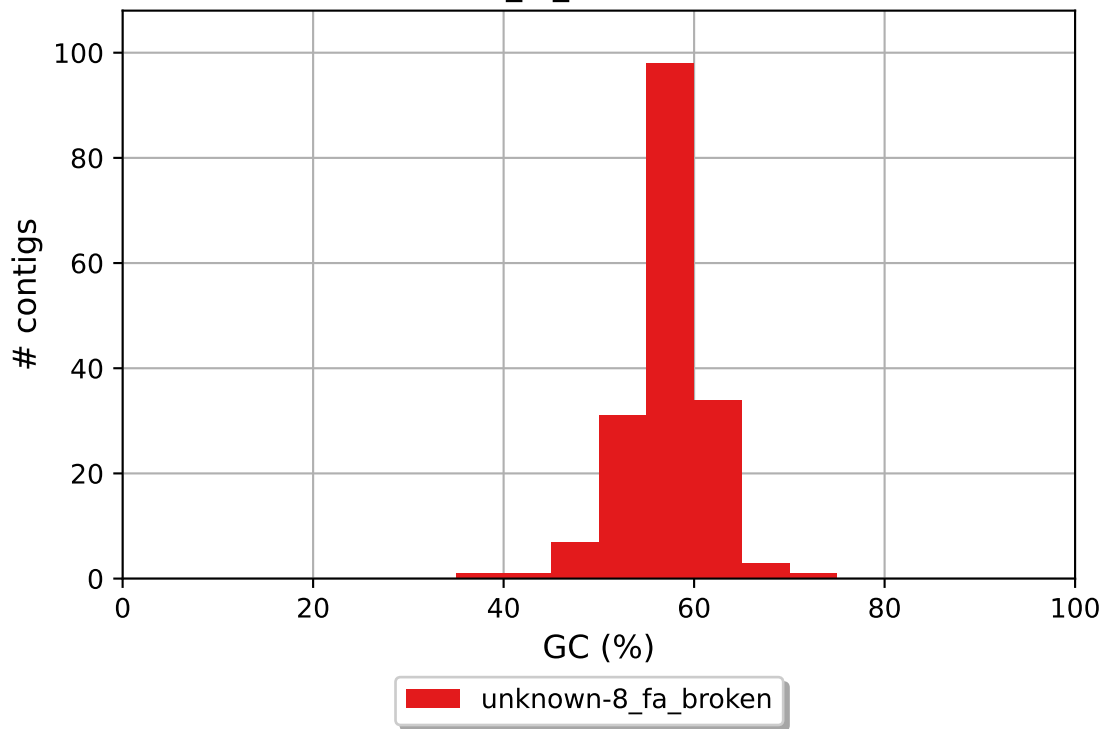
GC content



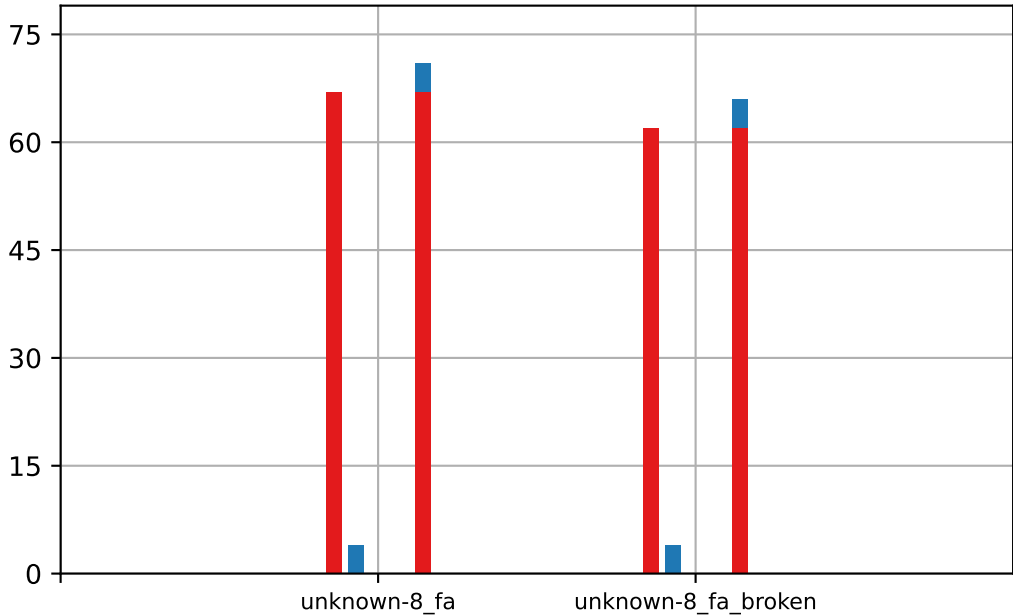
unknown-8_fa GC content



unknown-8_fa_broken GC content



Misassemblies

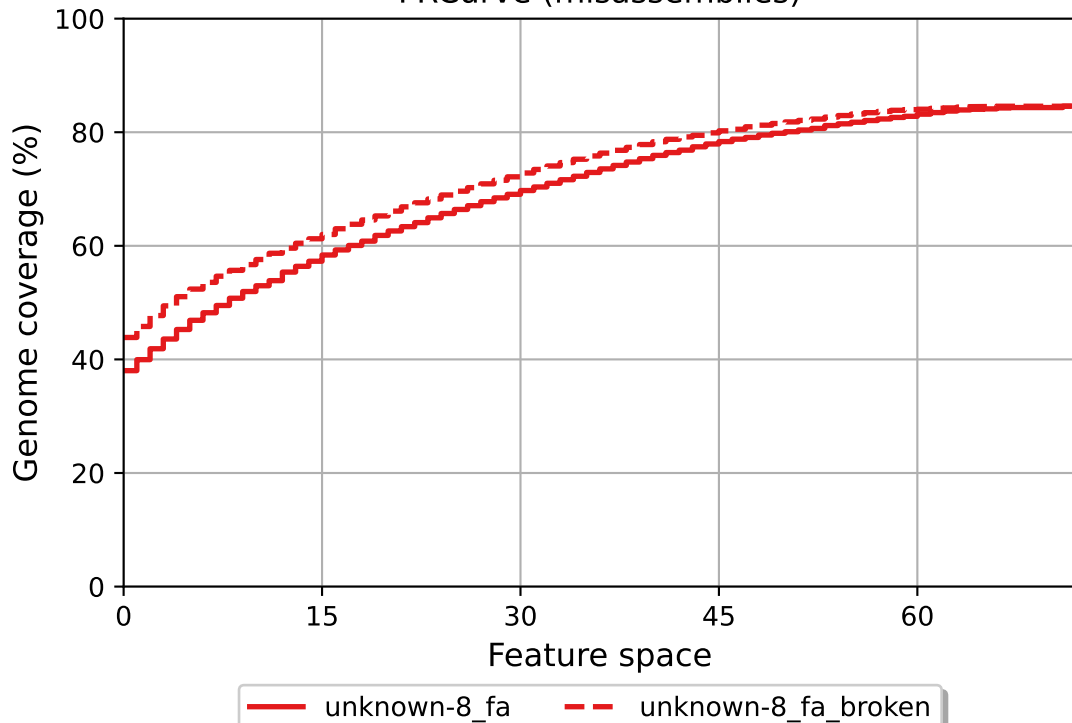


relocations

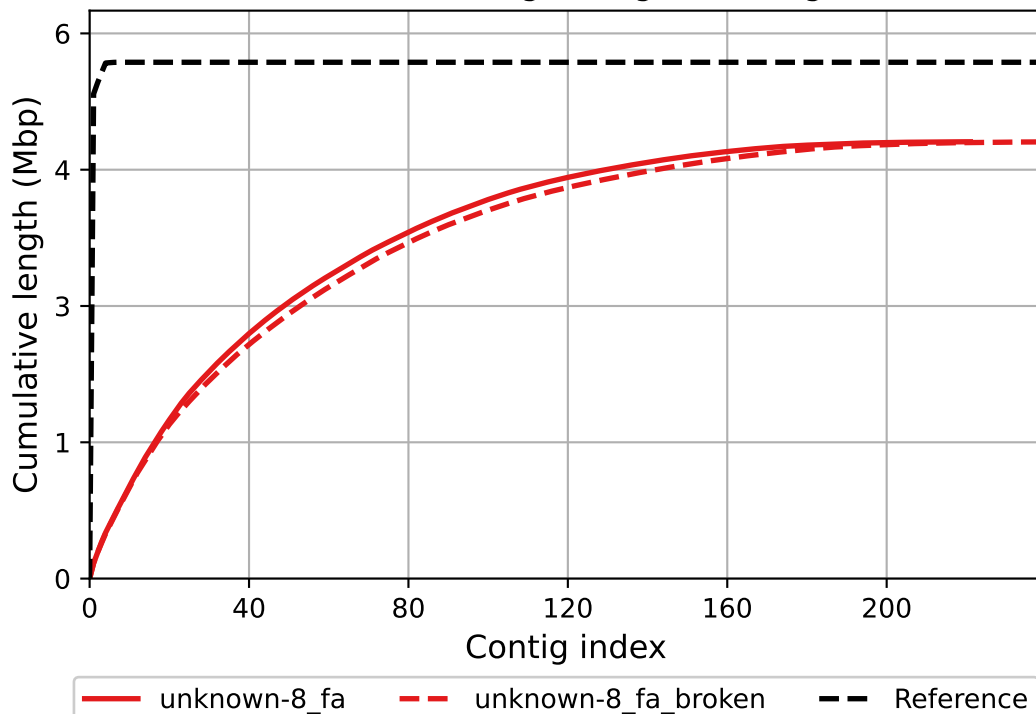


translocations

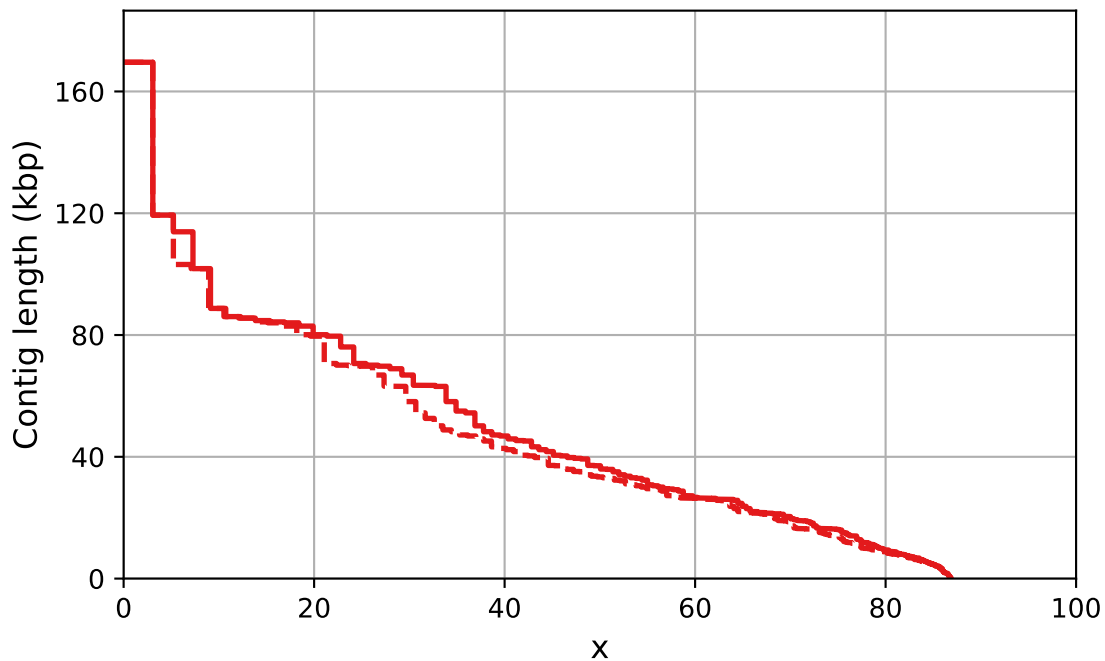
FRCurve (misassemblies)



Cumulative length (aligned contigs)

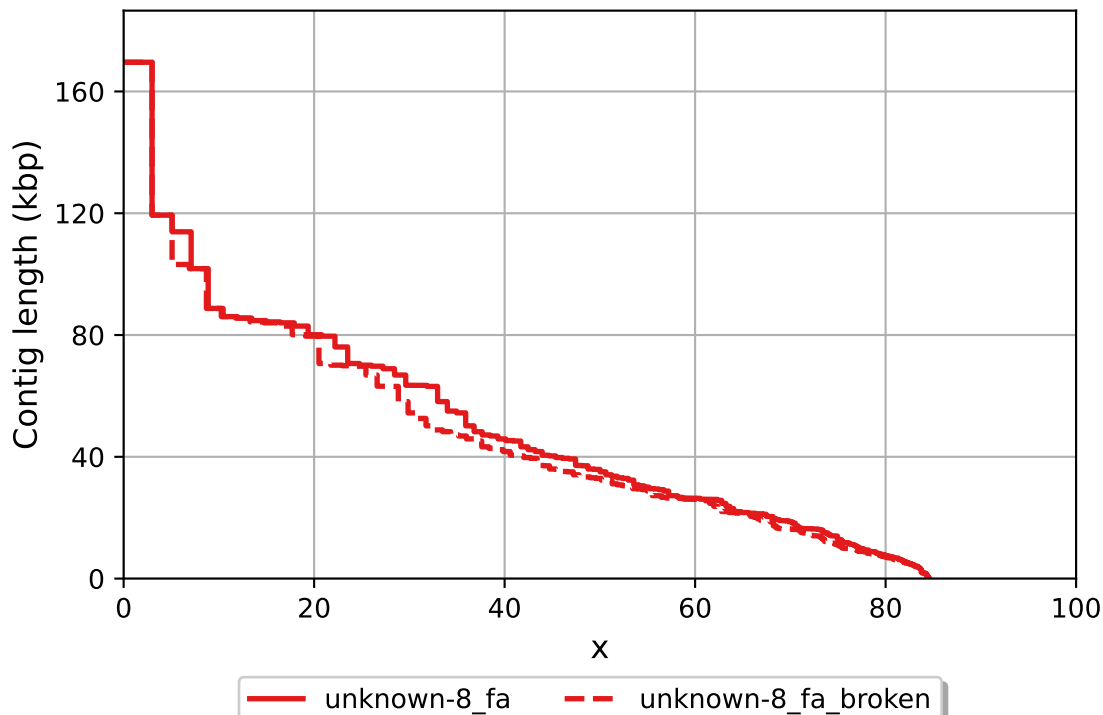


NAx



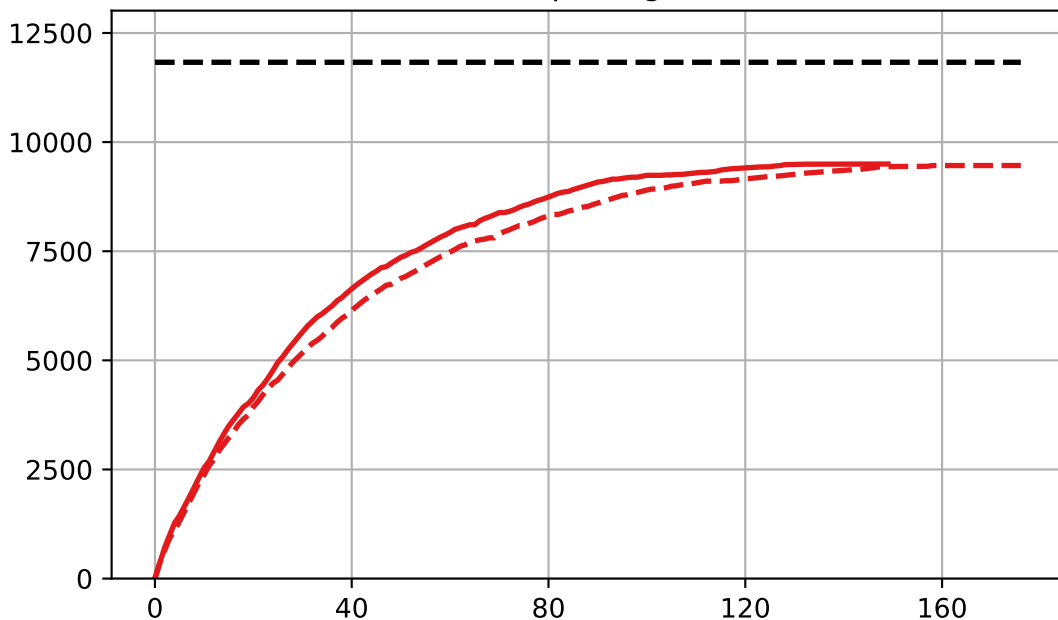
— unknown-8_fa - - - unknown-8_fa_broken

NGAx



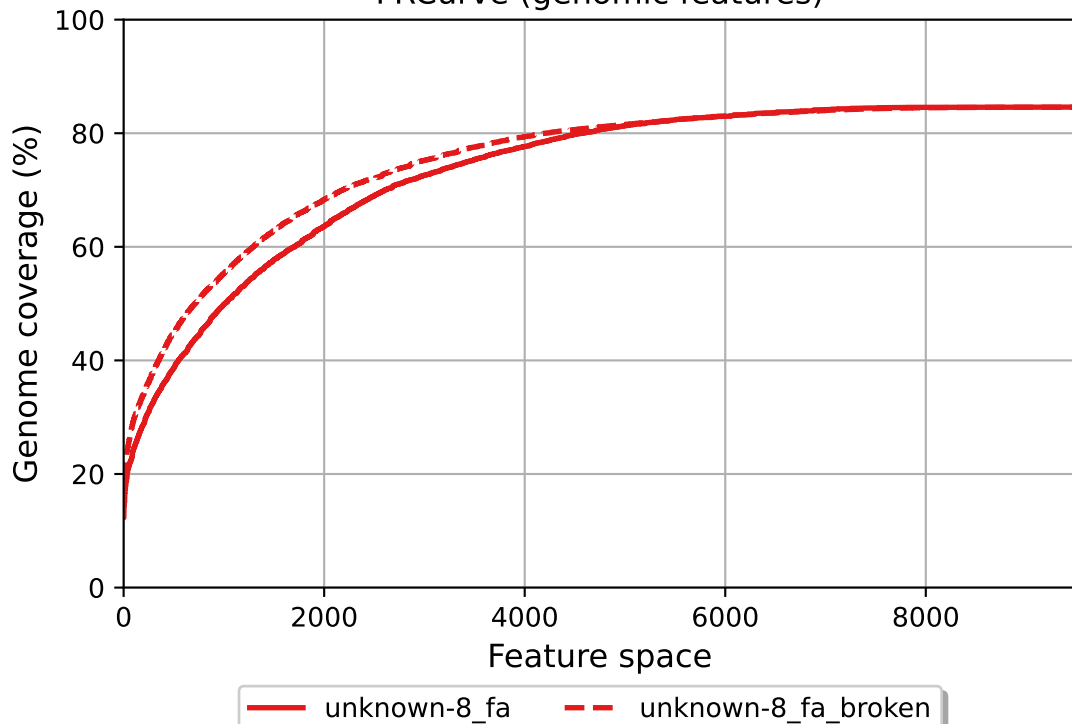
Cumulative # complete genomic features

Cumulative # complete genomic features

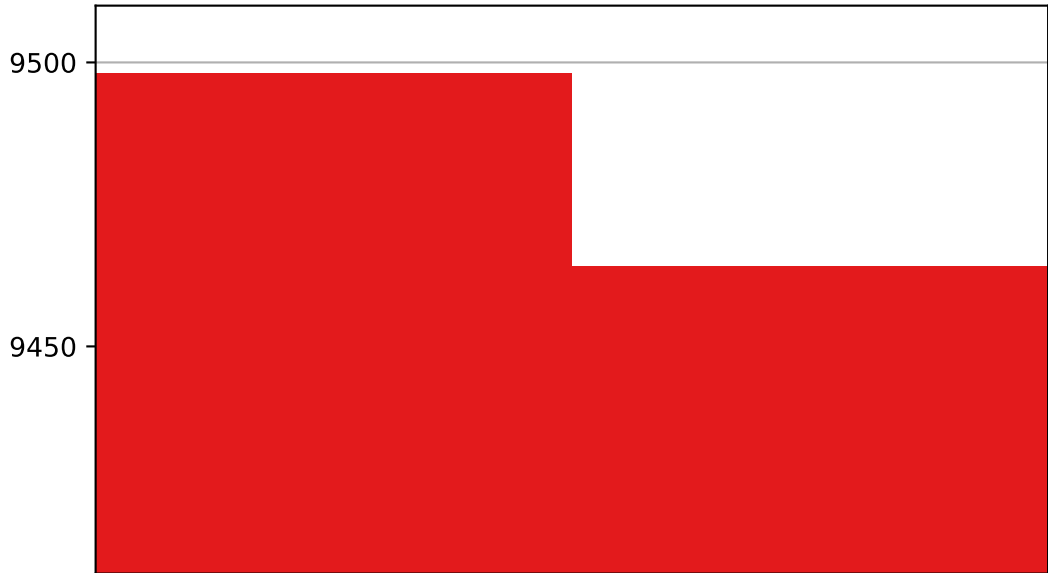


unknown-8_fa unknown-8_fa_broken Reference

FRCurve (genomic features)



complete genomic features

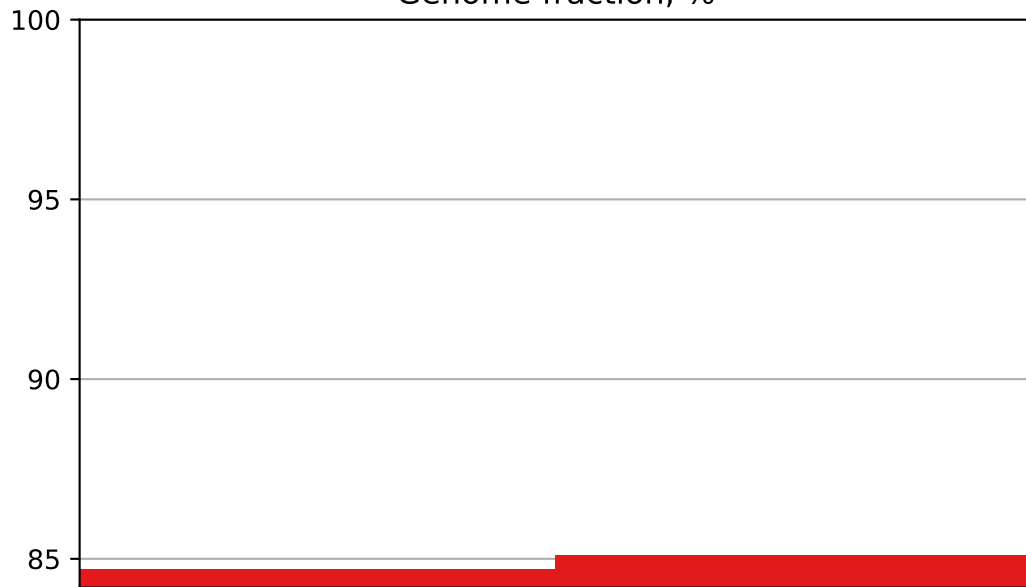


unknown-8_fa



unknown-8_fa_broken

Genome fraction, %



unknown-8_fa



unknown-8_fa_broken