

Report

	unknown-8_fa	unknown-8_fa_broken
# contigs (>= 0 bp)	87	-
# contigs (>= 1000 bp)	15	17
Total length (>= 0 bp)	3905978	-
Total length (>= 1000 bp)	3891876	3891284
# contigs	19	23
Largest contig	1238574	1093836
Total length	3894698	3894498
Reference length	4014440	4014440
GC (%)	46.44	46.44
Reference GC (%)	46.39	46.39
N50	1094105	1011923
NG50	1094105	1011923
N90	150758	150758
NG90	113988	113988
auN	836471.5	718557.2
auNG	811521.4	697088.4
L50	2	2
LG50	2	2
L90	6	7
LG90	7	8
# misassemblies	55	53
# misassembled contigs	8	8
Misassembled contigs length	3706014	3693488
# local misassemblies	38	38
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 9 part	0 + 10 part
Unaligned length	203226	203226
Genome fraction (%)	92.049	92.066
Duplication ratio	1.003	1.003
# N's per 100 kbp	5.16	0.03
# mismatches per 100 kbp	1504.52	1504.64
# indels per 100 kbp	43.64	43.59
# genomic features	7206 + 174 part	7206 + 174 part
# predicted rRNA genes	1 + 8 part	1 + 8 part
Largest alignment	306589	306589
Total aligned length	3691218	3691118
NA50	121608	121608
NGA50	110186	109917
NA90	16829	16829
NGA90	11865	11865
auNA	122986.6	122971.4
auNGA	119318.1	119297.3
LA50	11	11
LGA50	12	12
LA90	45	45
LGA90	53	53

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

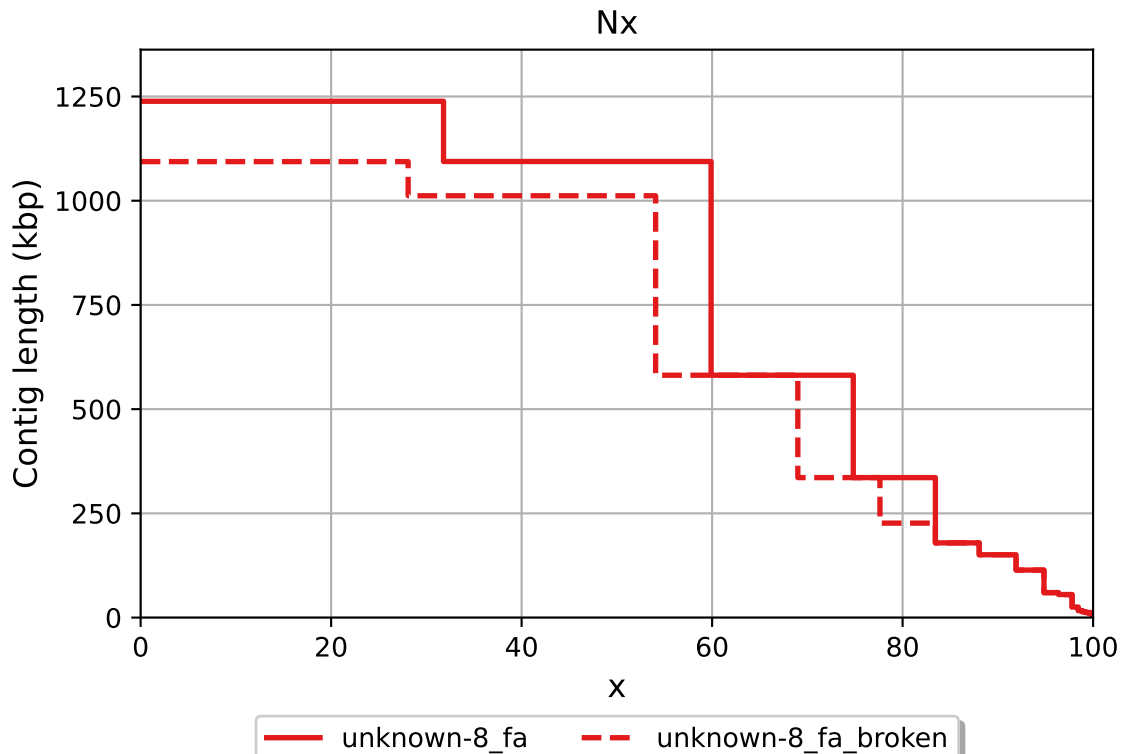
	unknown-8_fa	unknown-8_fa_broken
# misassemblies	55	53
# contig misassemblies	53	53
# c. relocations	51	51
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	8	8
Misassembled contigs length	3706014	3693488
# local misassemblies	38	38
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	55535	55538
# indels	1611	1609
# indels (<= 5 bp)	1416	1416
# indels (> 5 bp)	195	193
Indels length	7691	7587

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).

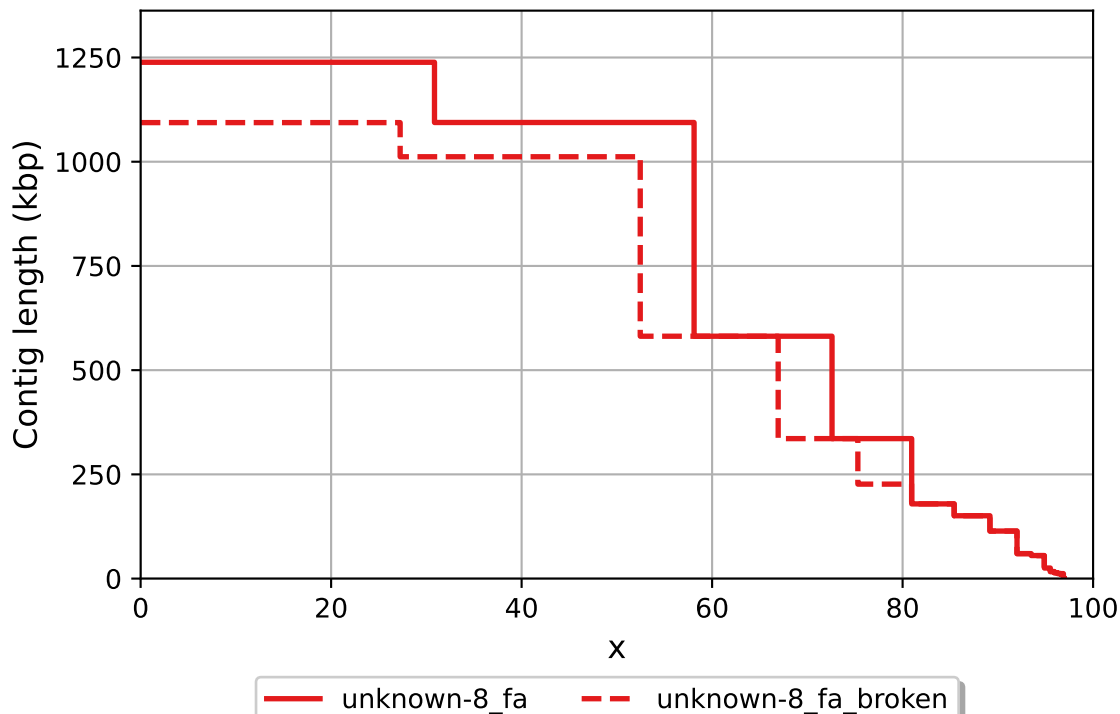
Unaligned report

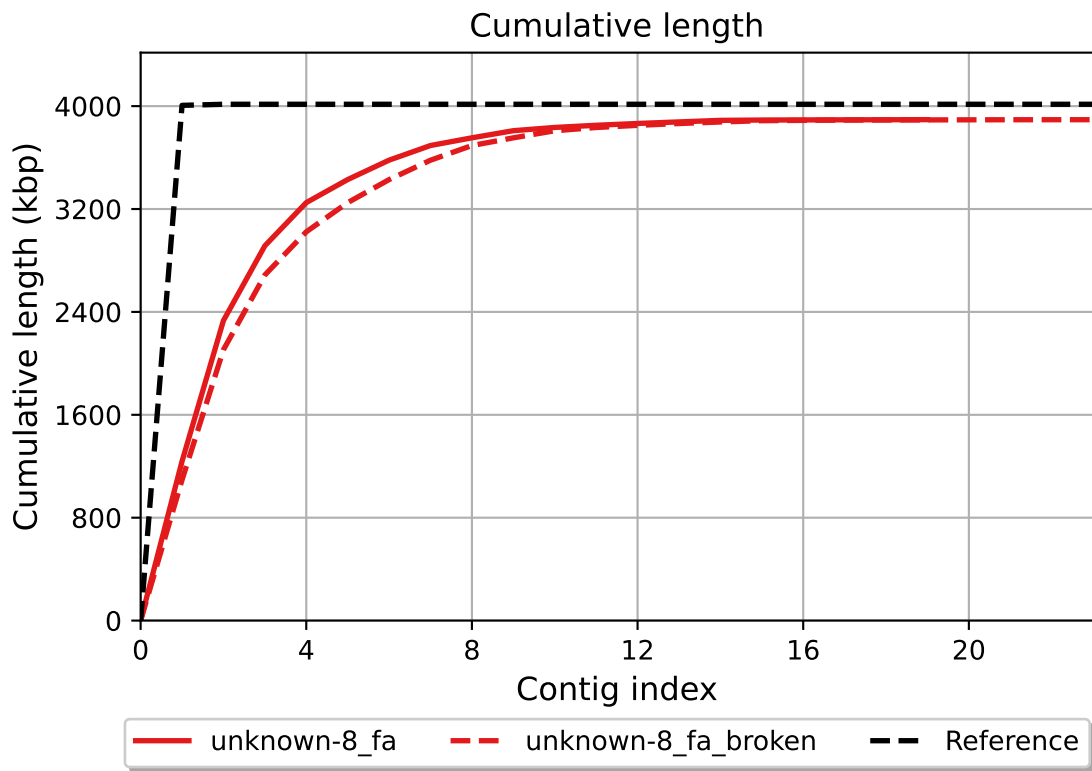
	unknown-8_fa	unknown-8_fa_broken
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	9	10
Partially unaligned length	203226	203226
# N's	201	1

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).

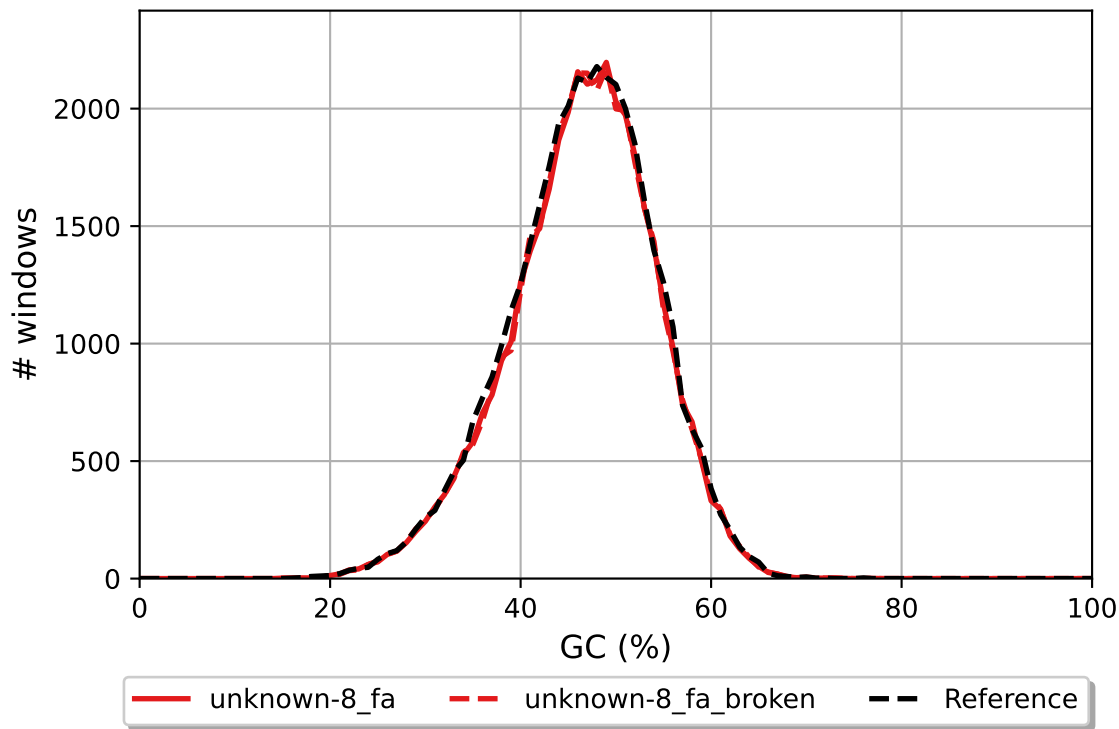


NGx

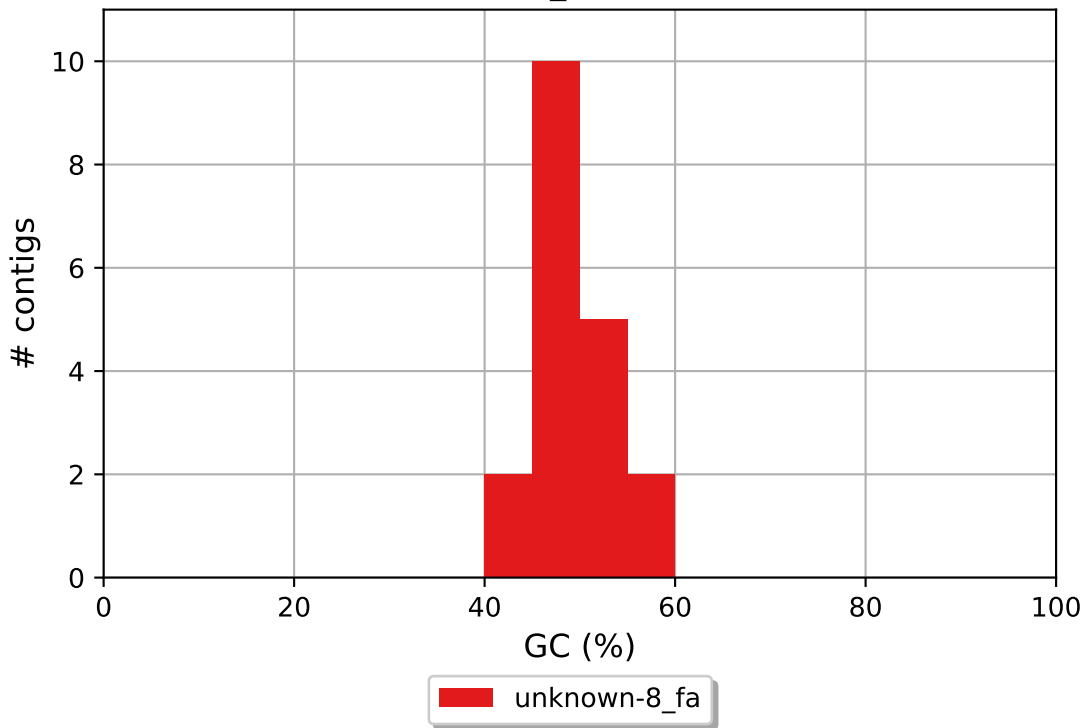




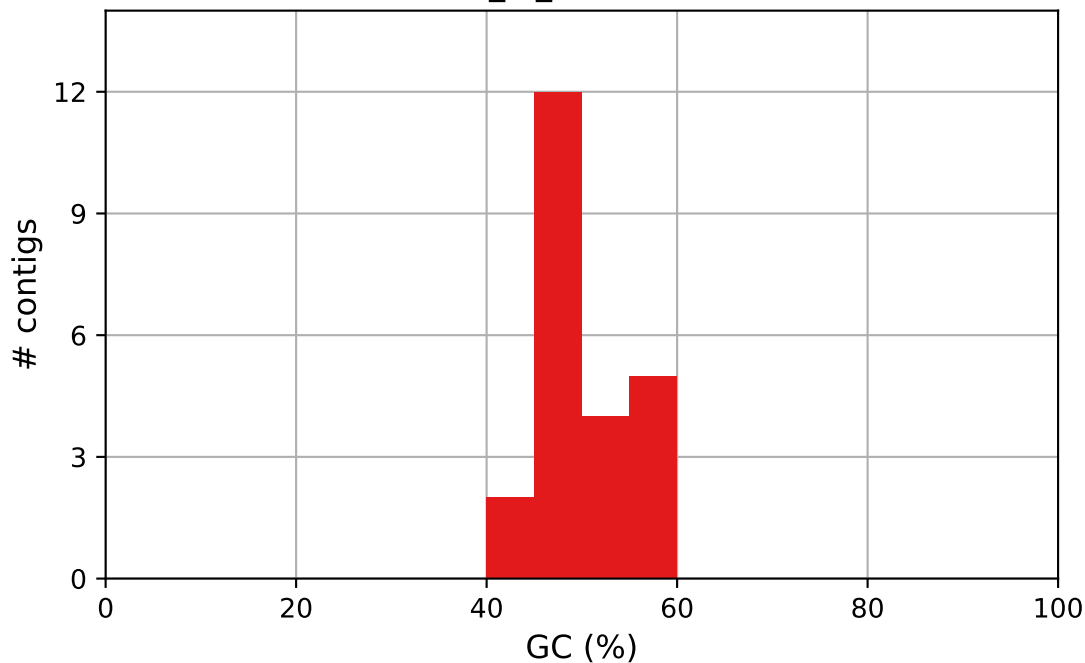
GC content



unknown-8_fa GC content

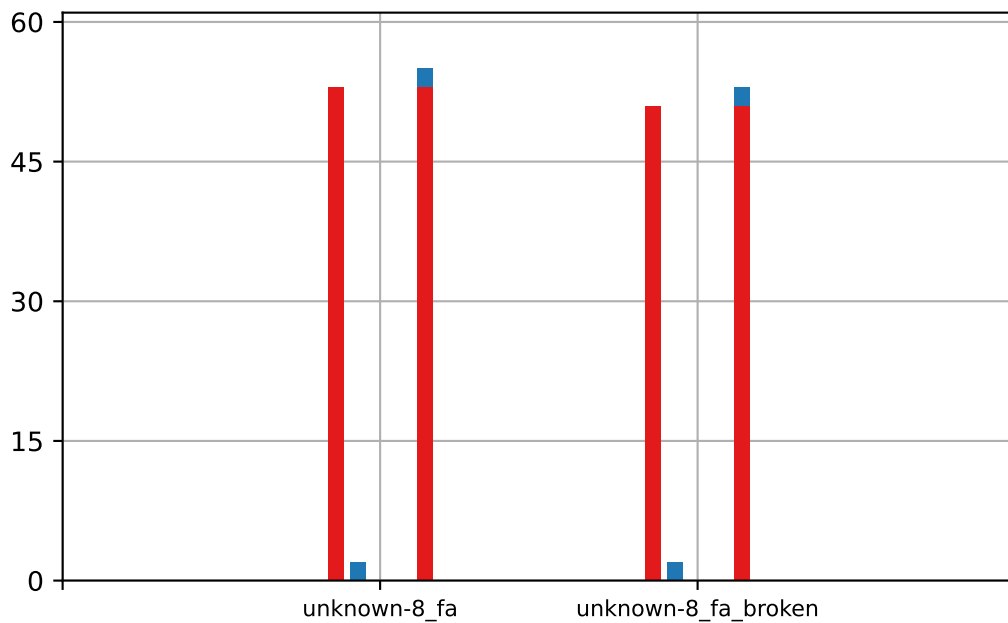


unknown-8_fa_broken GC content



unknown-8_fa_broken

Misassemblies

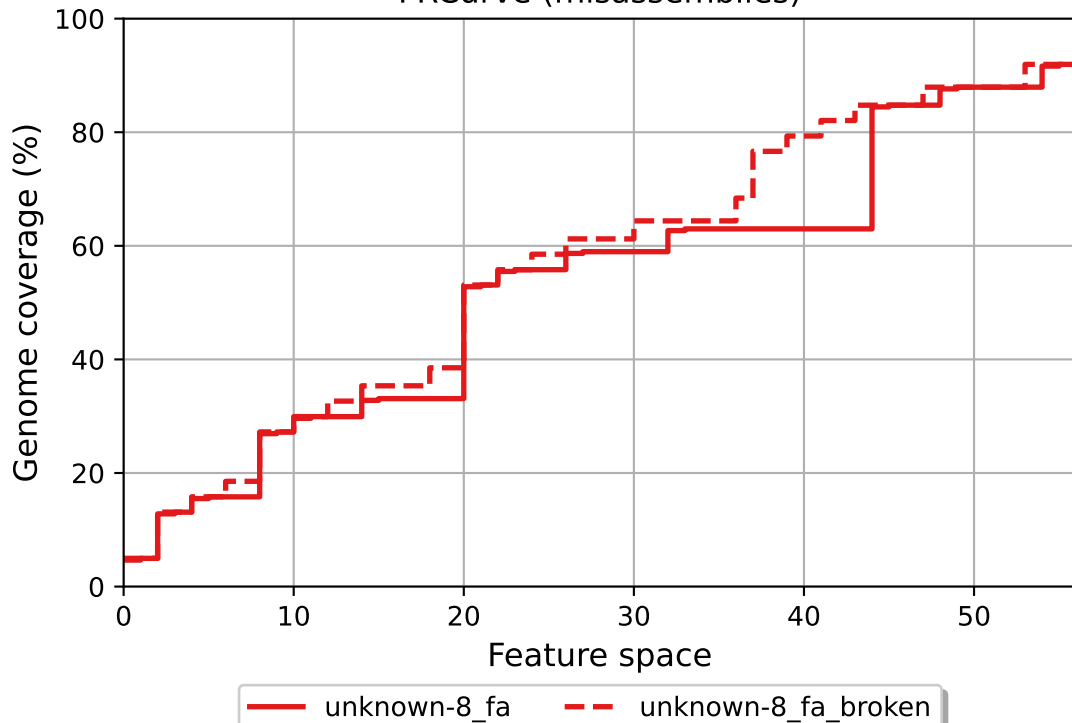


relocations

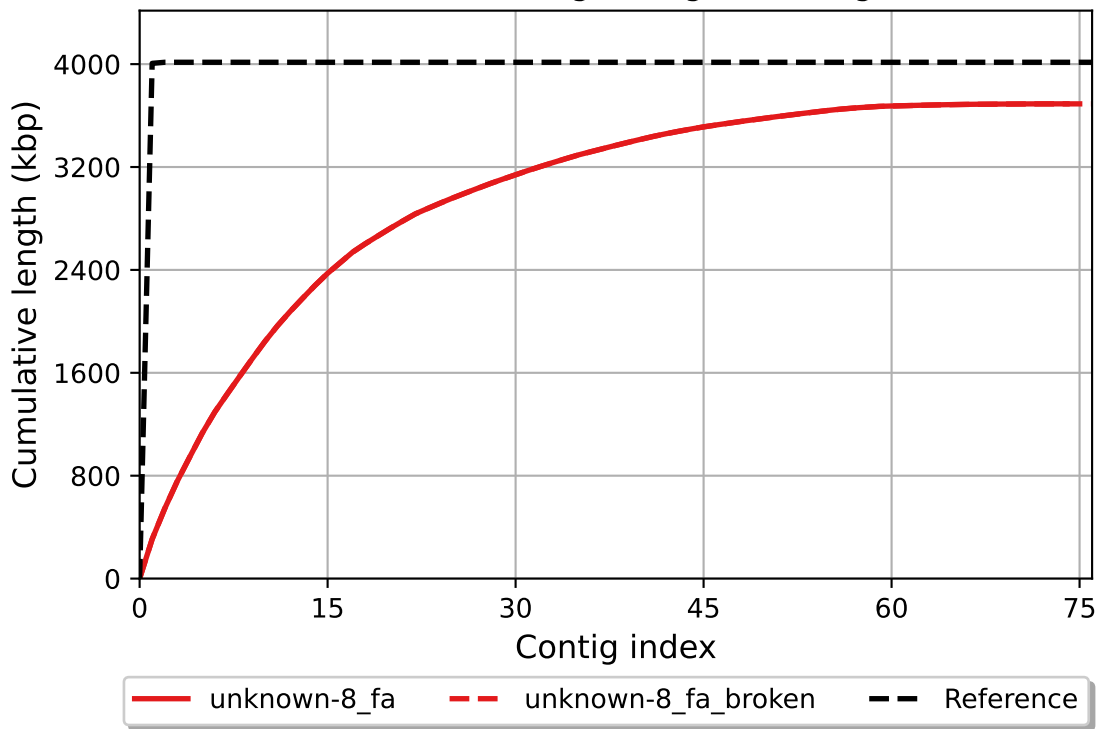


translocations

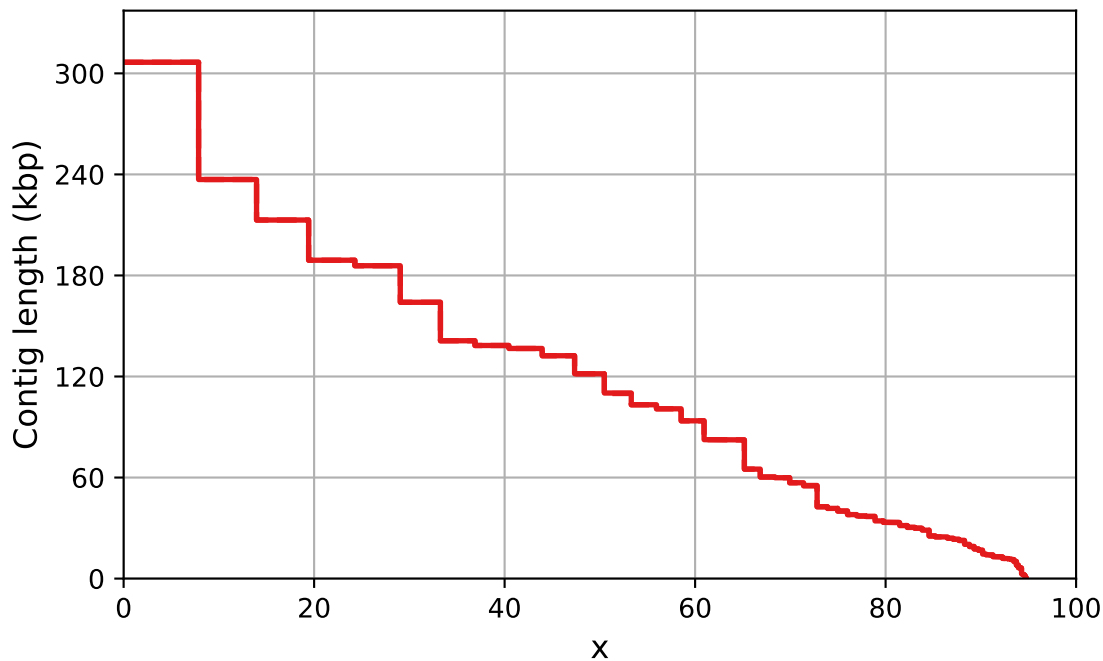
FRCurve (misassemblies)



Cumulative length (aligned contigs)

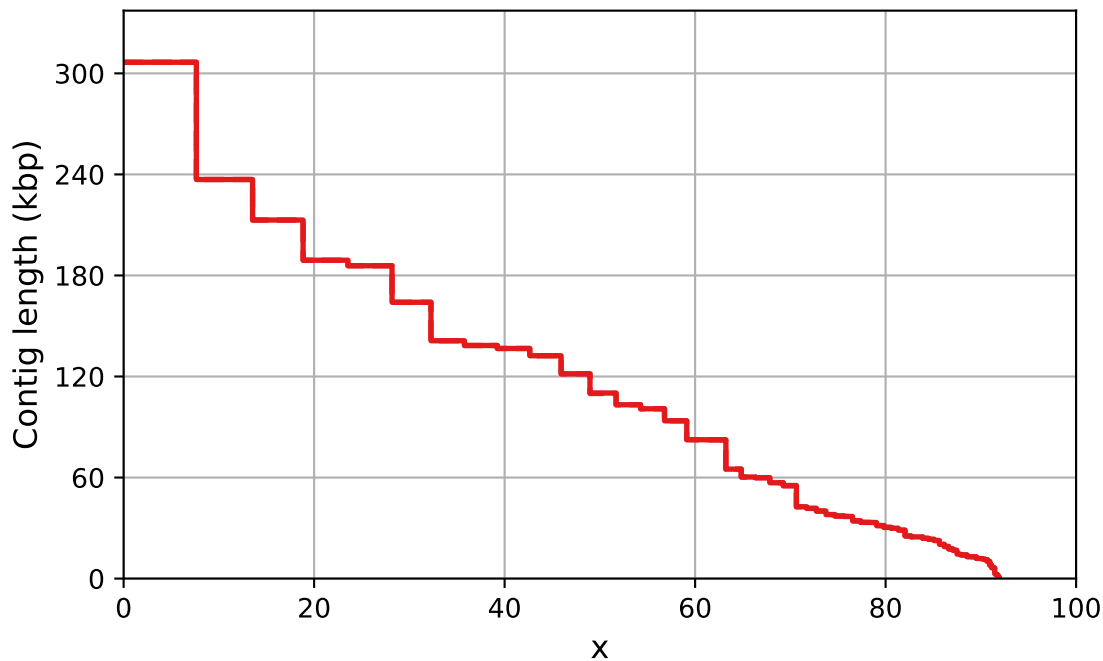


NAx

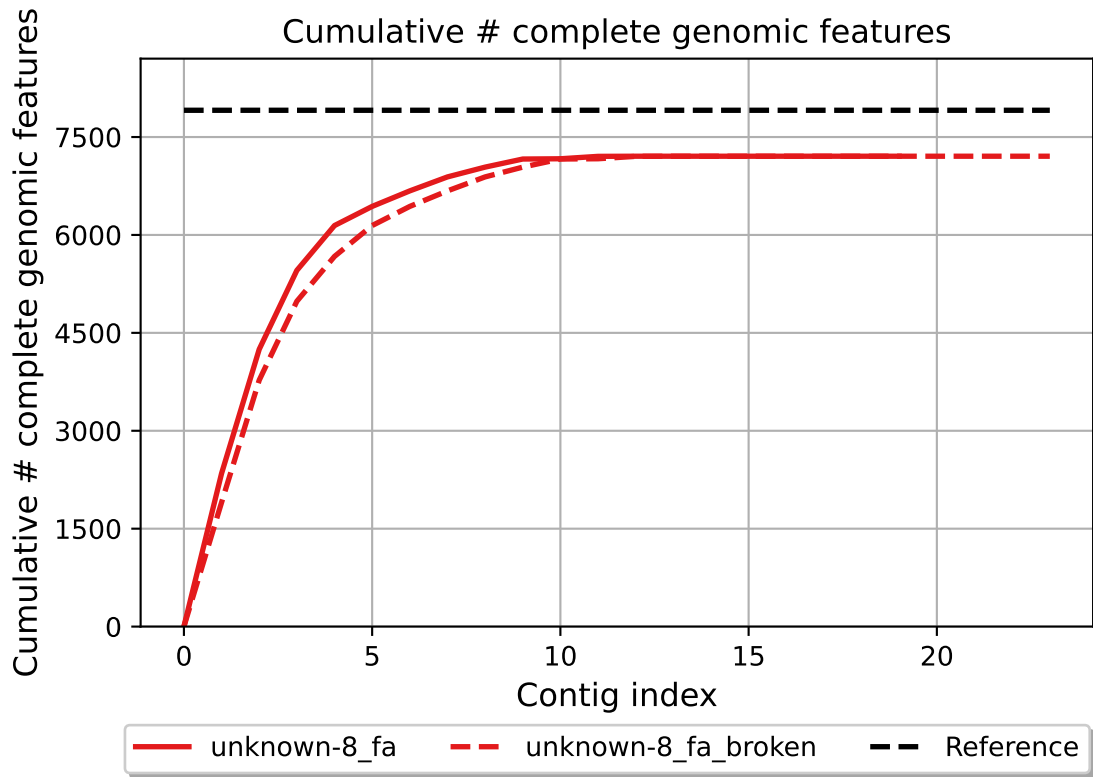


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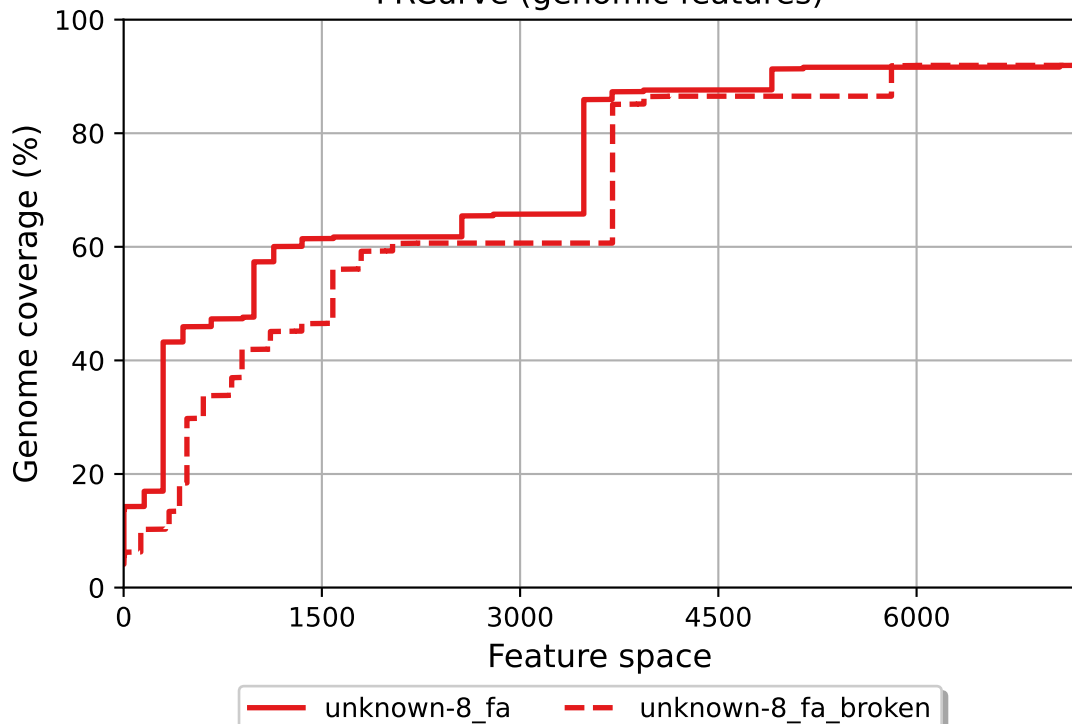
NGAx



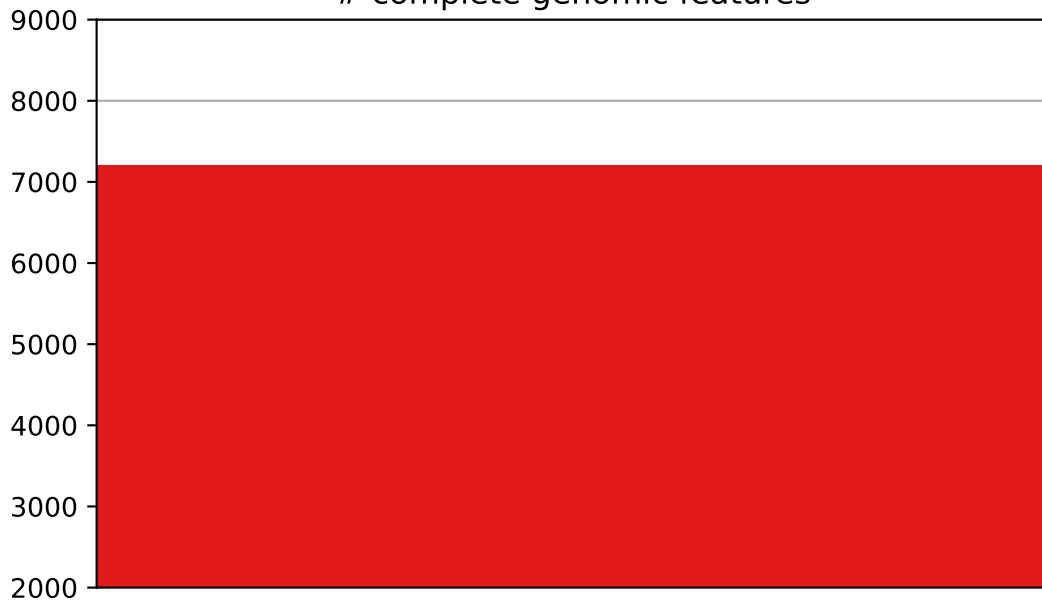
— unknown-8_fa - - - unknown-8_fa_broken



FRCurve (genomic features)



complete genomic features



unknown-8_fa



unknown-8_fa_broken

Genome fraction, %

100

95



unknown-8_fa



unknown-8_fa_broken