

Report

	mystery-8_fa	mystery-8_fa_broken
# contigs (>= 0 bp)	637	-
# contigs (>= 1000 bp)	217	242
Total length (>= 0 bp)	5582960	-
Total length (>= 1000 bp)	5506580	5500963
# contigs	234	266
Largest contig	186641	138914
Total length	5518329	5516709
Reference length	5682322	5682322
GC (%)	57.14	57.14
Reference GC (%)	57.12	57.12
N50	47175	43460
NG50	44873	42779
N90	11063	9823
NG90	9222	8541
auN	59277.0	50813.1
auNG	57566.3	49332.1
L50	33	38
LG50	35	40
L90	122	138
LG90	137	154
# misassemblies	72	70
# misassembled contigs	48	49
Misassembled contigs length	2545545	2283529
# local misassemblies	28	26
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	3	5
# unaligned contigs	17 + 62 part	19 + 63 part
Unaligned length	718920	718633
Genome fraction (%)	84.595	84.960
Duplication ratio	1.003	1.005
# N's per 100 kbp	31.86	2.50
# mismatches per 100 kbp	684.00	686.26
# indels per 100 kbp	23.15	22.87
# genomic features	9355 + 516 part	9321 + 568 part
# predicted rRNA genes	6 + 1 part	6 + 0 part
Largest alignment	100924	95958
Total aligned length	4794575	4792658
NA50	25586	24734
NGA50	24734	22957
NA90	-	-
NGA90	-	-
auNA	33495.4	30468.6
auNGA	32528.7	29580.6
LA50	59	64
LGA50	62	68
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

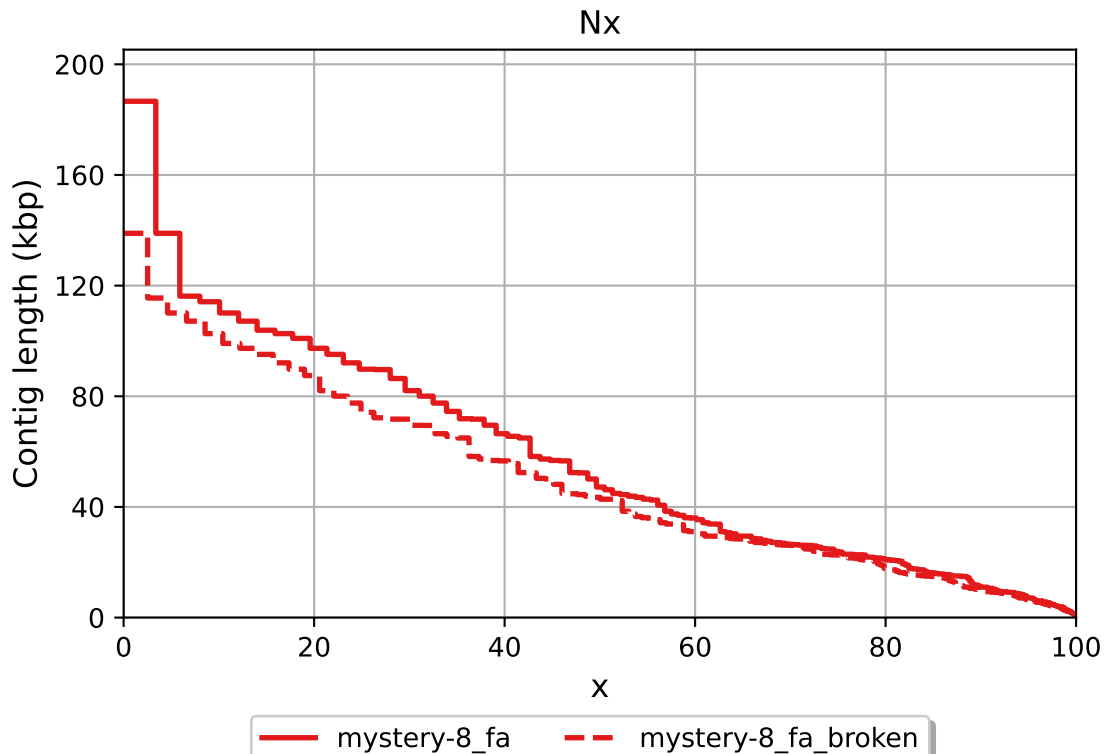
	mystery-8_fa	mystery-8_fa_broken
# misassemblies	72	70
# contig misassemblies	70	70
# c. relocations	67	67
# c. translocations	3	3
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	48	49
Misassembled contigs length	2545545	2283529
# local misassemblies	28	26
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	3	5
# mismatches	32795	32890
# indels	1110	1096
# indels (<= 5 bp)	893	903
# indels (> 5 bp)	217	193
Indels length	14576	12793

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).

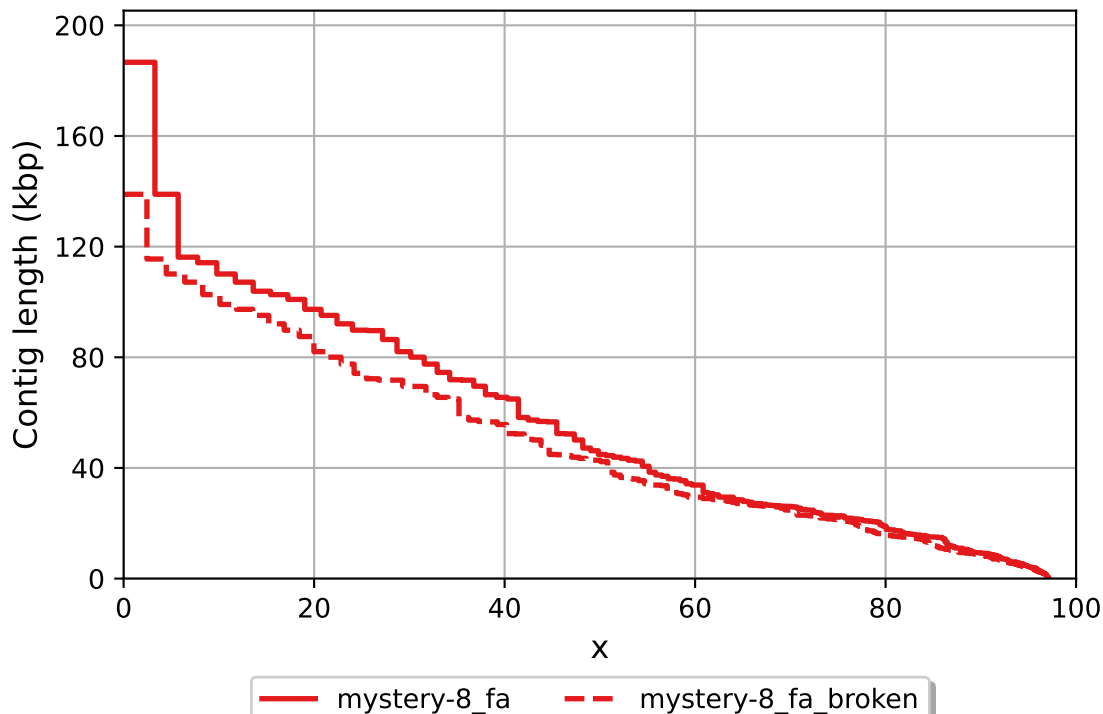
Unaligned report

	mystery-8_fa	mystery-8_fa_broken
# fully unaligned contigs	17	19
Fully unaligned length	90894	93380
# partially unaligned contigs	62	63
Partially unaligned length	628026	625253
# N's	1758	138

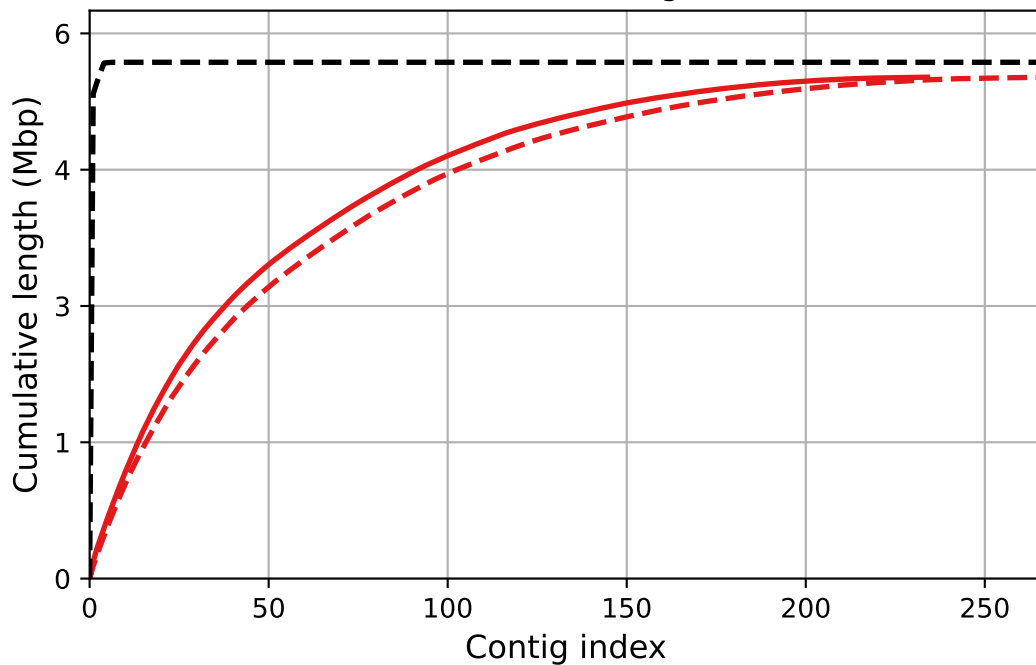
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



NGx

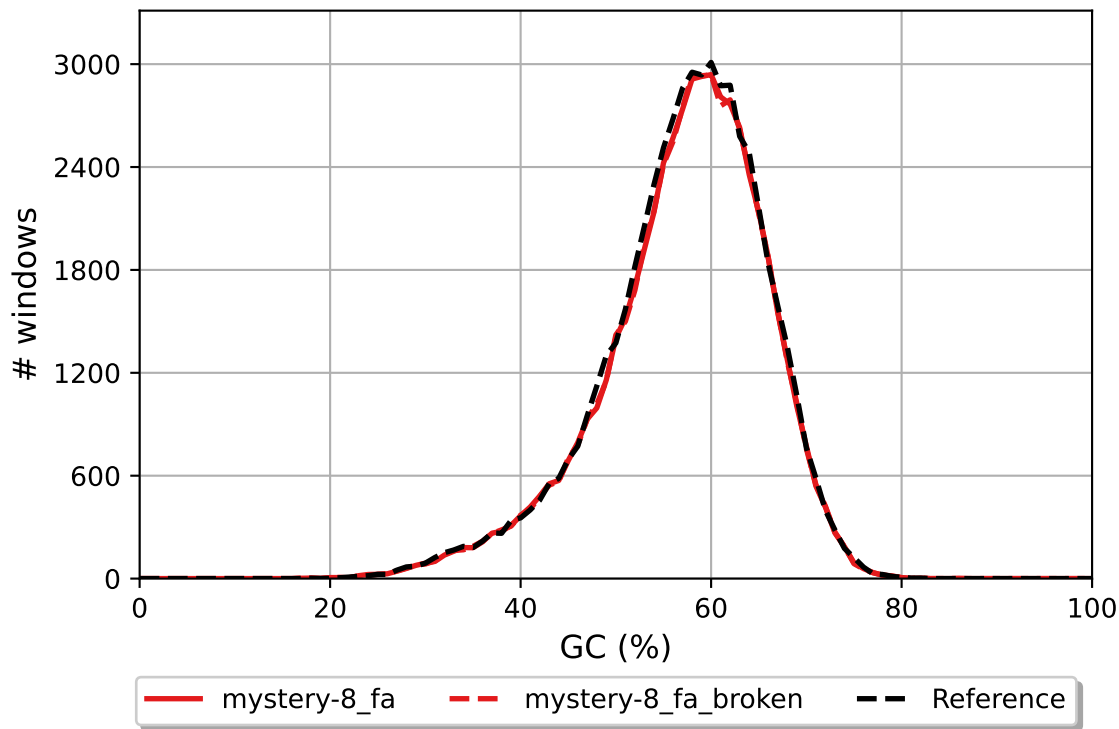


Cumulative length

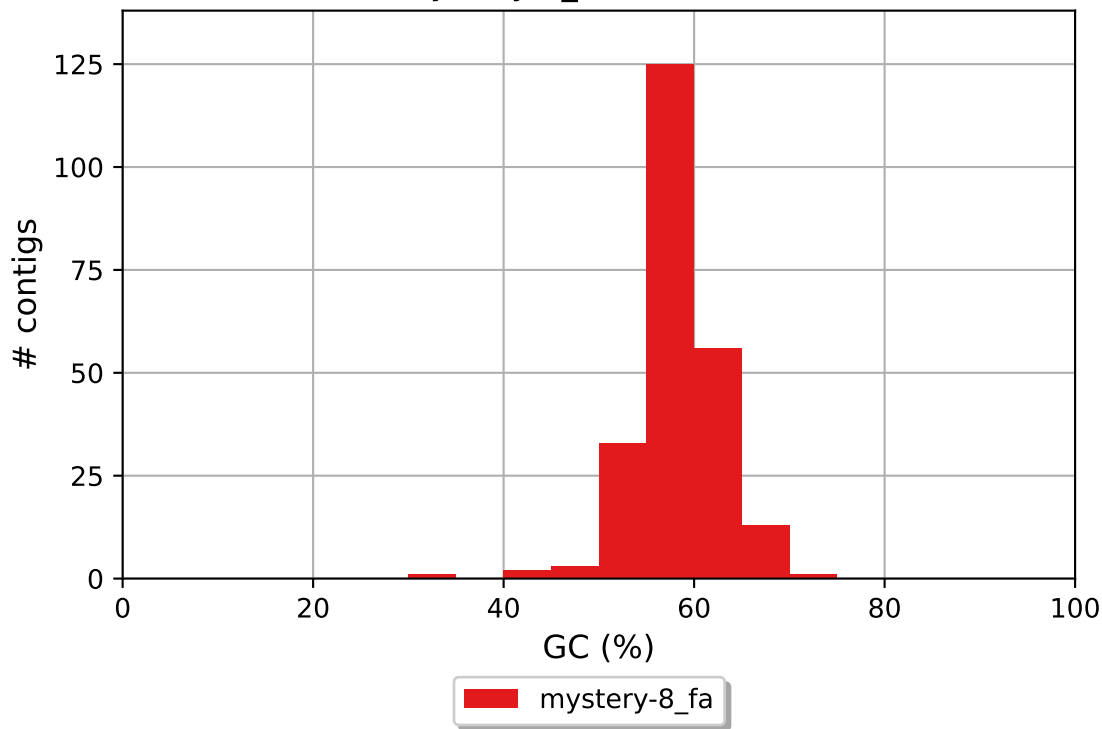


— mystery-8_fa - - - mystery-8_fa_broken - - - Reference

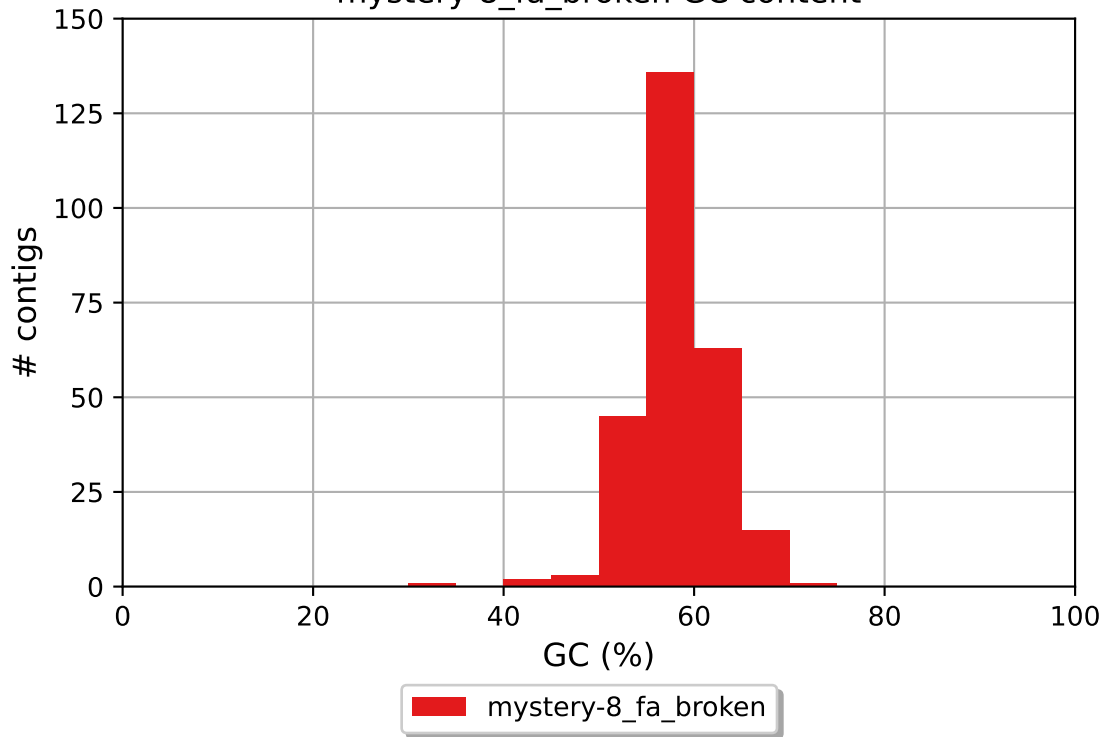
GC content



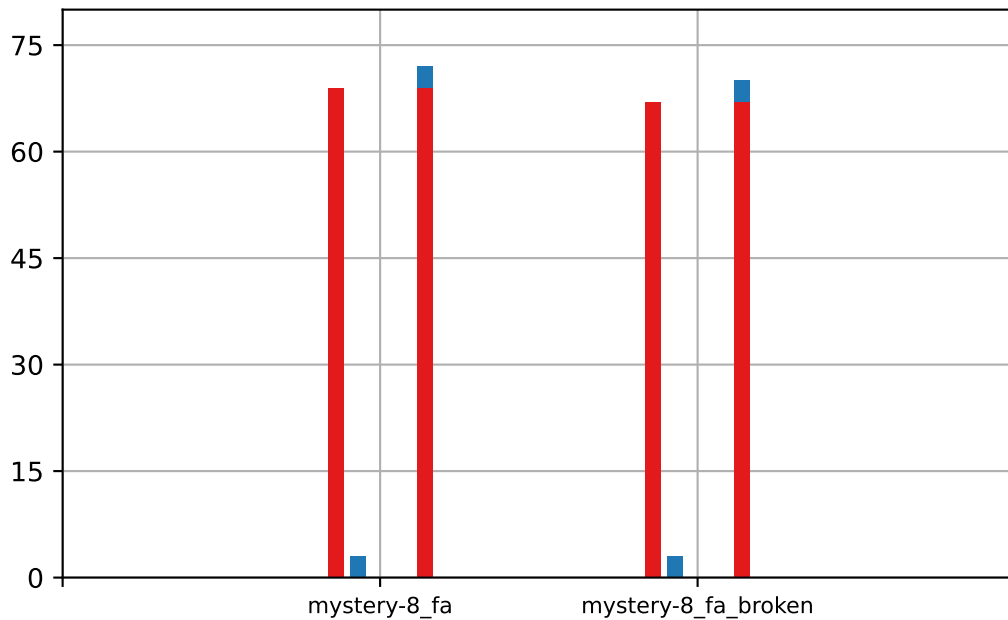
mystery-8_fa GC content



mystery-8_fa_broken GC content



Misassemblies

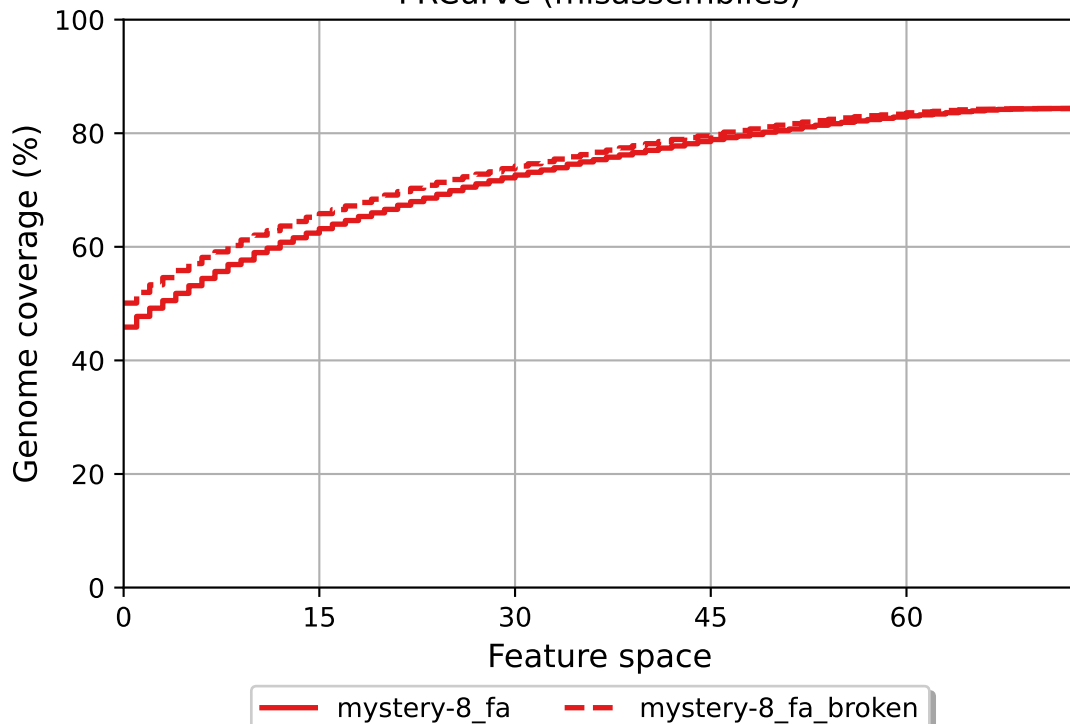


relocations

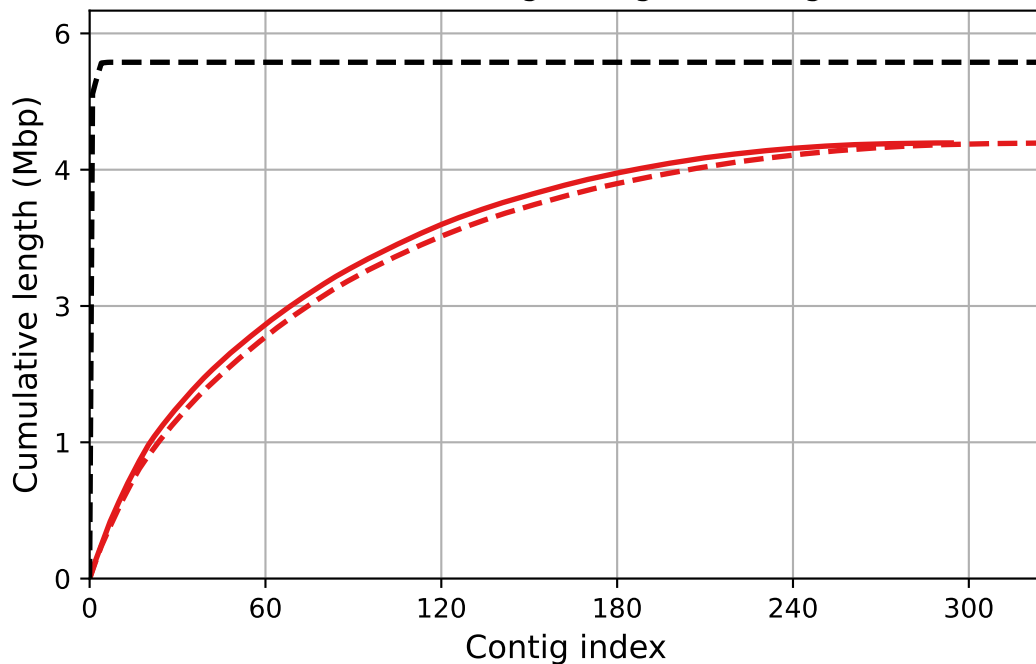


translocations

FRCurve (misassemblies)

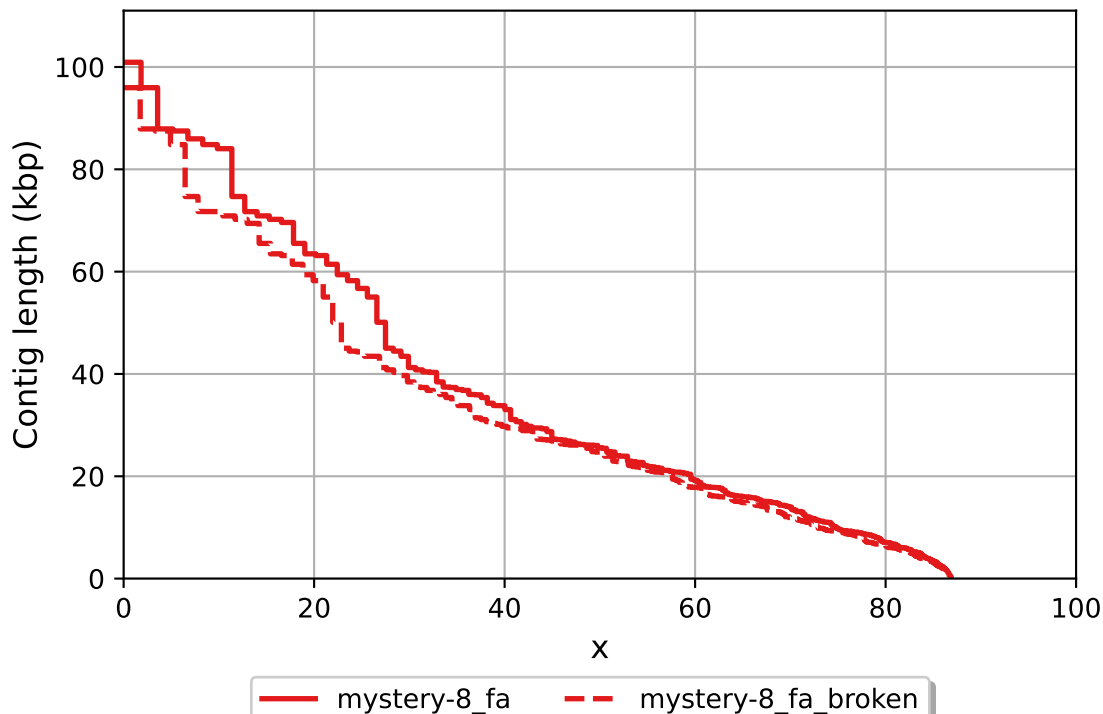


Cumulative length (aligned contigs)

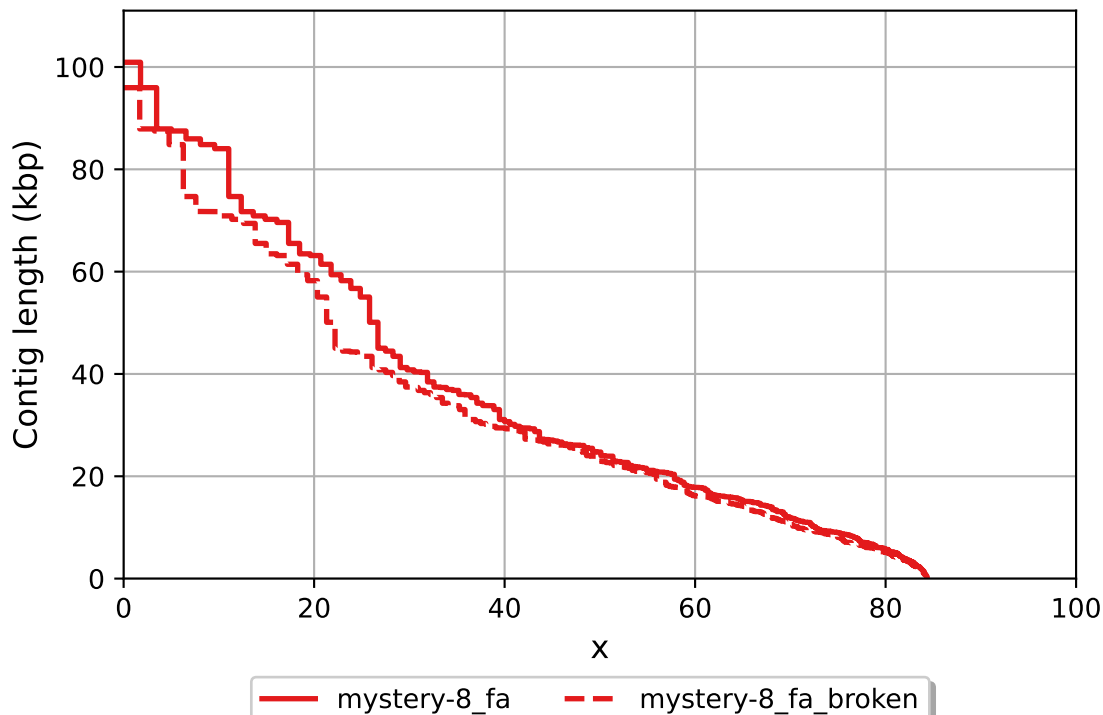


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NAx

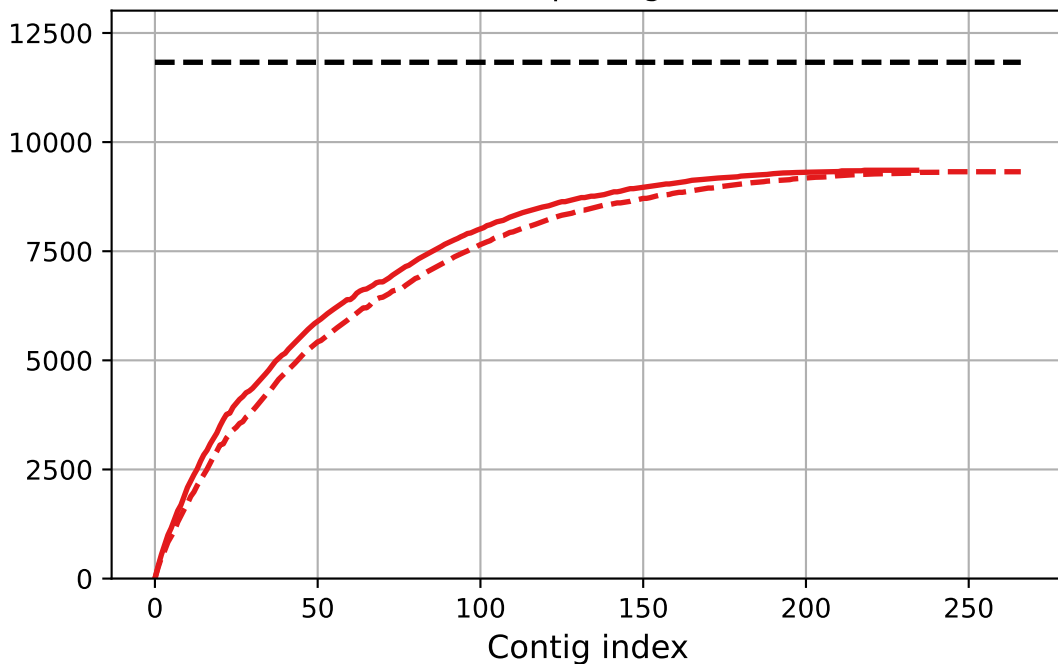


NGAx



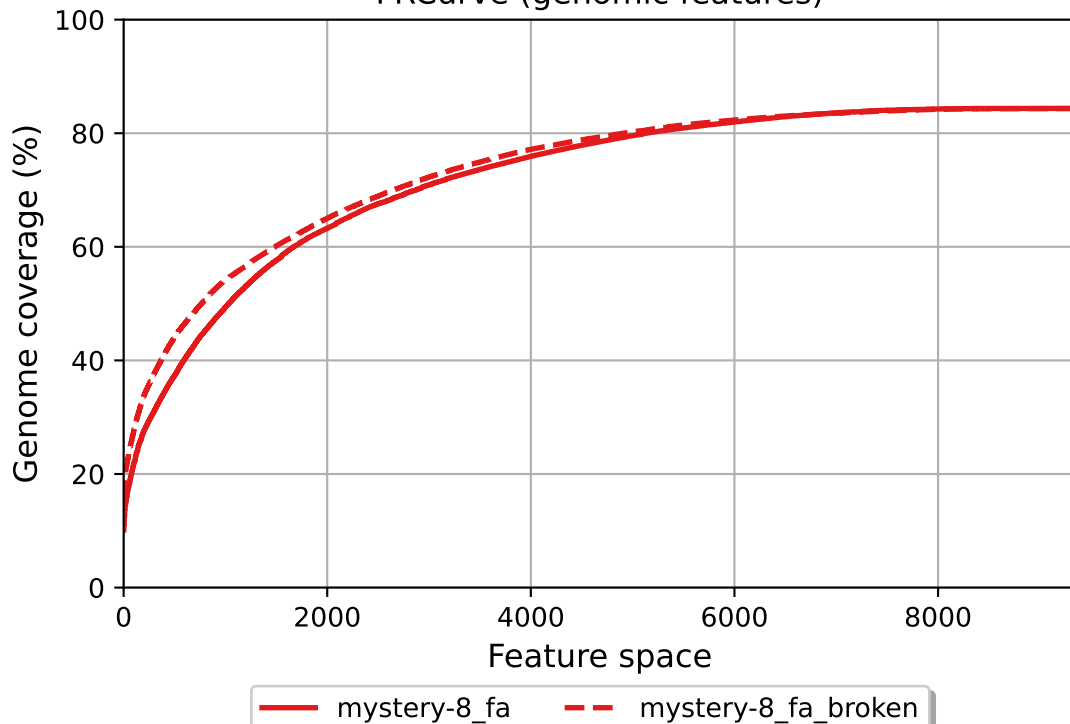
Cumulative # complete genomic features

Cumulative # complete genomic features



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FRCurve (genomic features)



complete genomic features

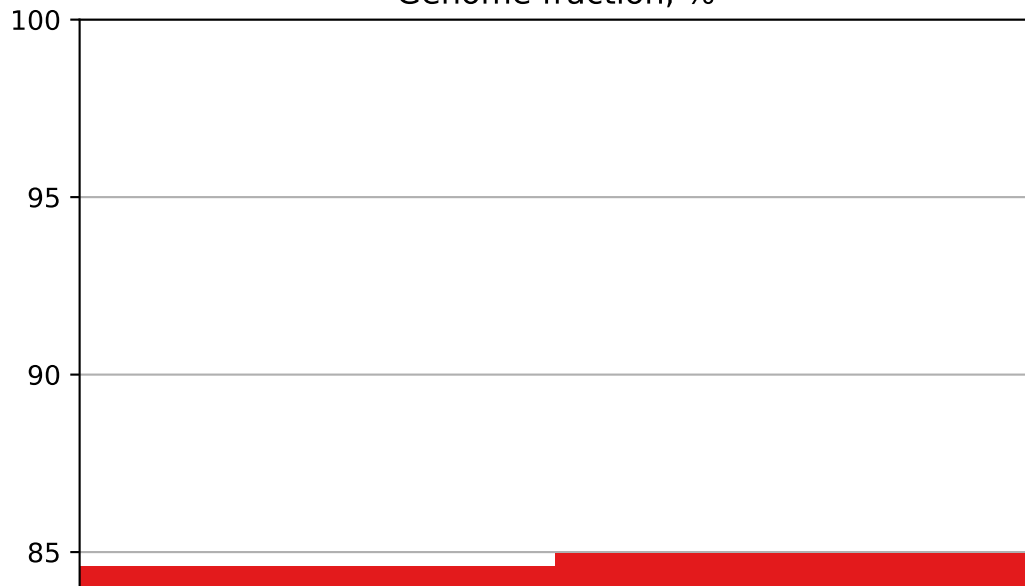


mystery-8_fa



mystery-8_fa_broken

Genome fraction, %



■ mystery-8_fa ■ mystery-8_fa_broken