

Report

	spring-8_fa	spring-8_fa_broken
# contigs (>= 0 bp)	71	-
# contigs (>= 1000 bp)	21	22
Total length (>= 0 bp)	4157030	-
Total length (>= 1000 bp)	4145842	4145032
# contigs	24	27
Largest contig	631096	631096
Total length	4148126	4147976
Reference length	4242130	4242130
GC (%)	43.90	43.90
Reference GC (%)	44.03	44.03
N50	424885	424885
NG50	424885	424885
N90	209092	209092
NG90	88519	88519
auN	408336.1	408242.3
auNG	399287.6	399181.3
L50	4	4
LG50	4	4
L90	10	10
LG90	11	11
# misassemblies	1	1
# misassembled contigs	1	1
Misassembled contigs length	30318	30318
# local misassemblies	1	1
# 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 (%)	98.452	98.622
Duplication ratio	1.000	1.000
# N's per 100 kbp	3.66	0.05
# mismatches per 100 kbp	1.11	1.11
# indels per 100 kbp	0.82	0.41
# genomic features	4473 + 63 part	4473 + 75 part
Complete BUSCO (%)	100.00	100.00
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	7 + 1 part	6 + 2 part
Largest alignment	631084	631084
Total aligned length	4148114	4147964
NA50	424885	424885
NGA50	424885	424885
NA90	209092	209092
NGA90	88519	88519
auNA	408237.6	408143.7
auNGA	399191.2	399085.0
LA50	4	4
LGA50	4	4
LA90	10	10
LGA90	11	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

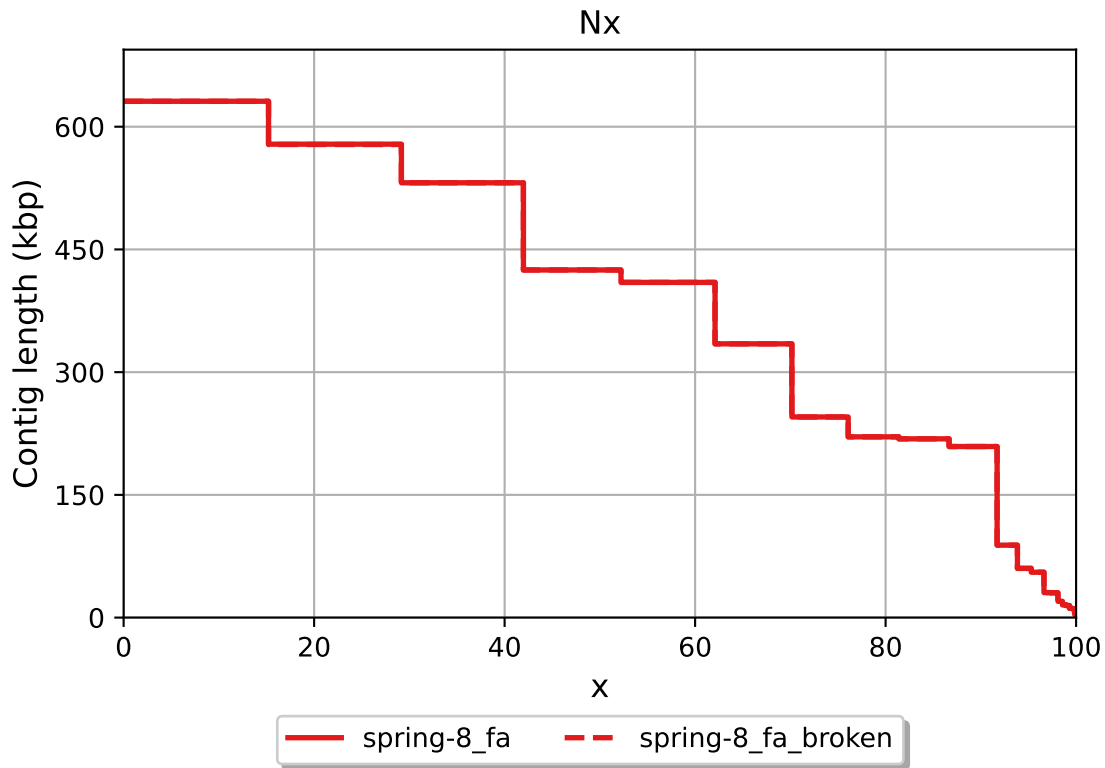
	spring-8_fa	spring-8_fa_broken
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	30318	30318
# local misassemblies	1	1
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	0	0
# mismatches	46	46
# indels	34	17
# indels (<= 5 bp)	12	12
# indels (> 5 bp)	22	5
Indels length	1354	373

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).

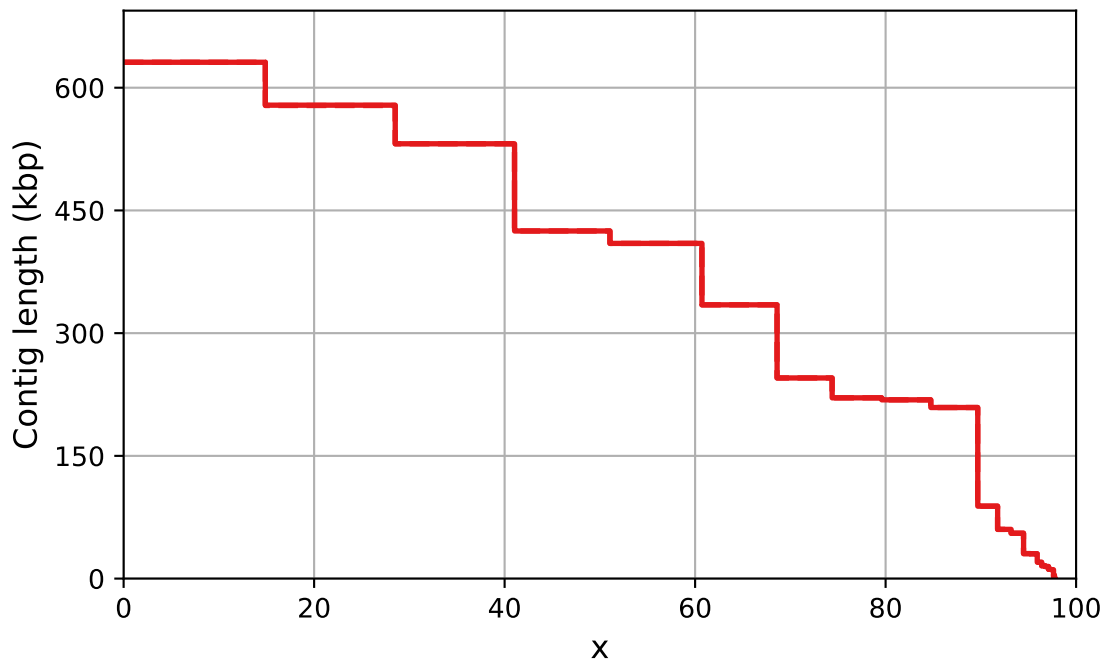
Unaligned report

	spring-8_fa	spring-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	152	2

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).

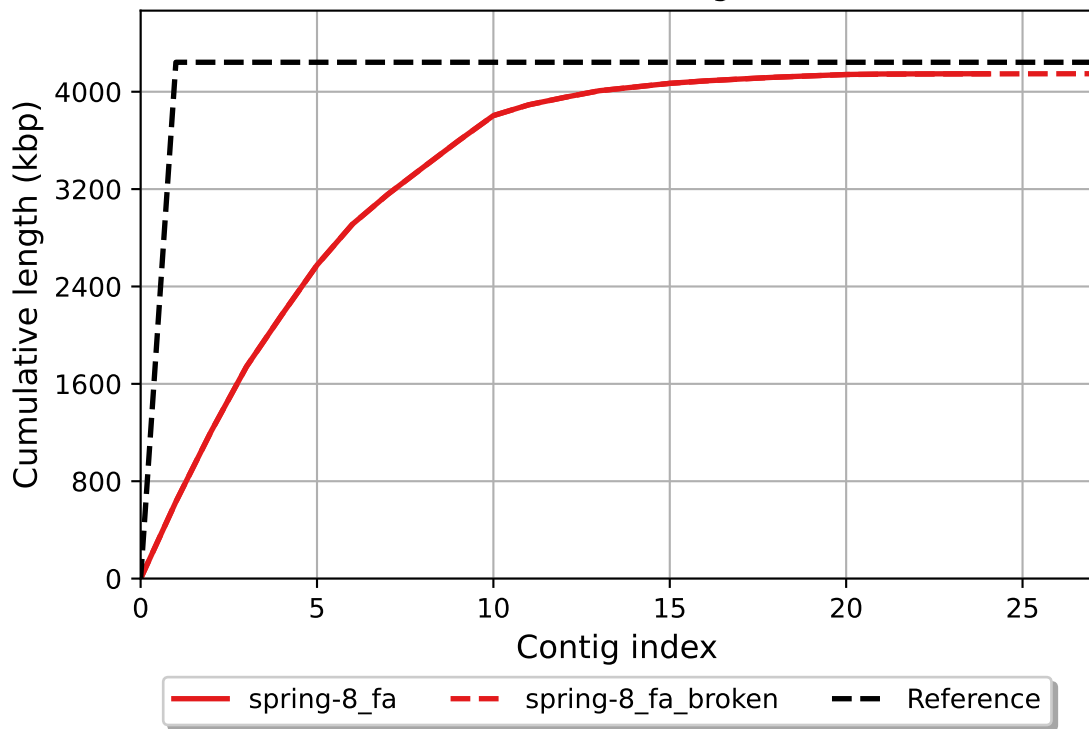


NGx

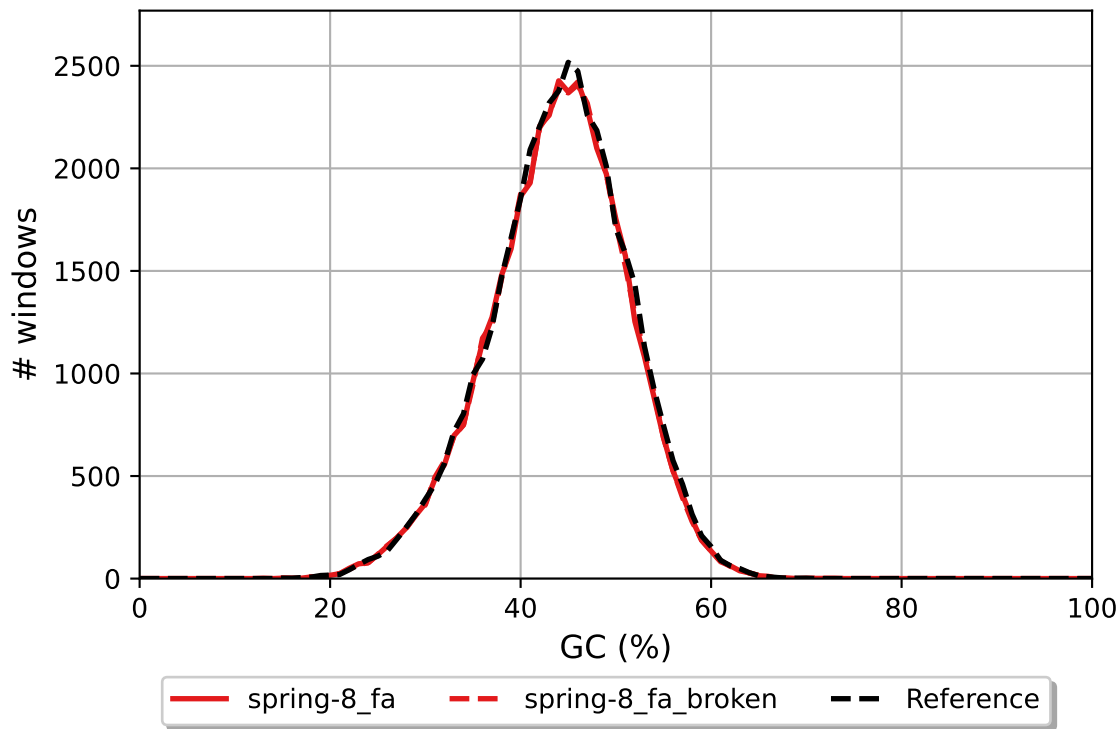


— spring-8_fa - - - spring-8_fa_broken

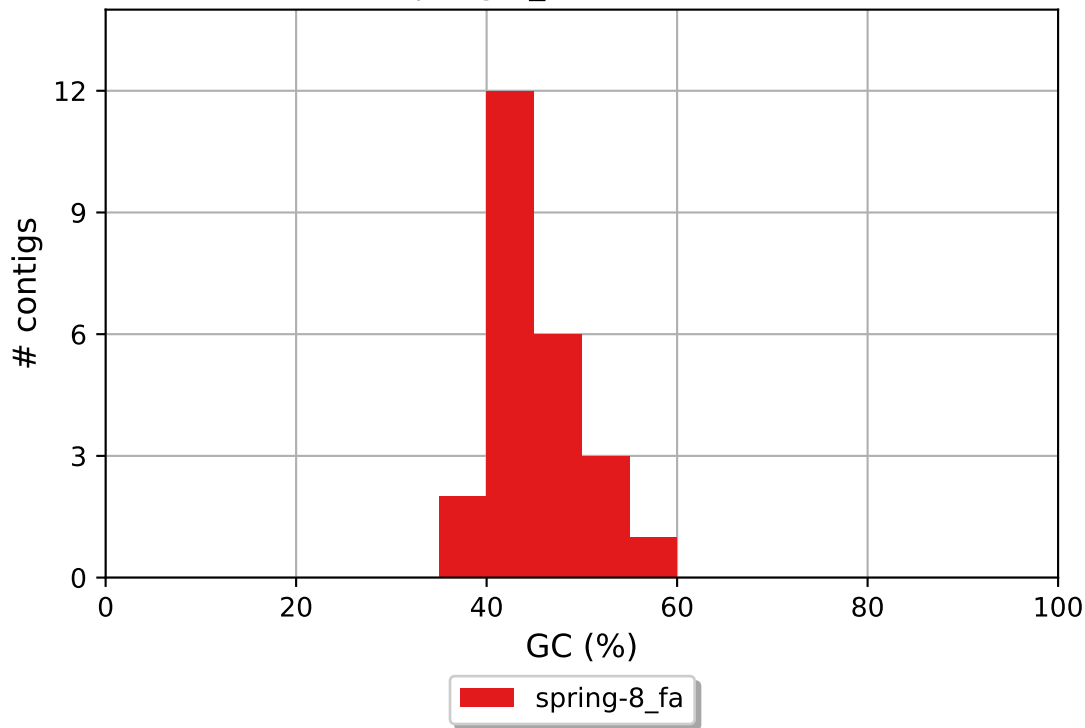
Cumulative length



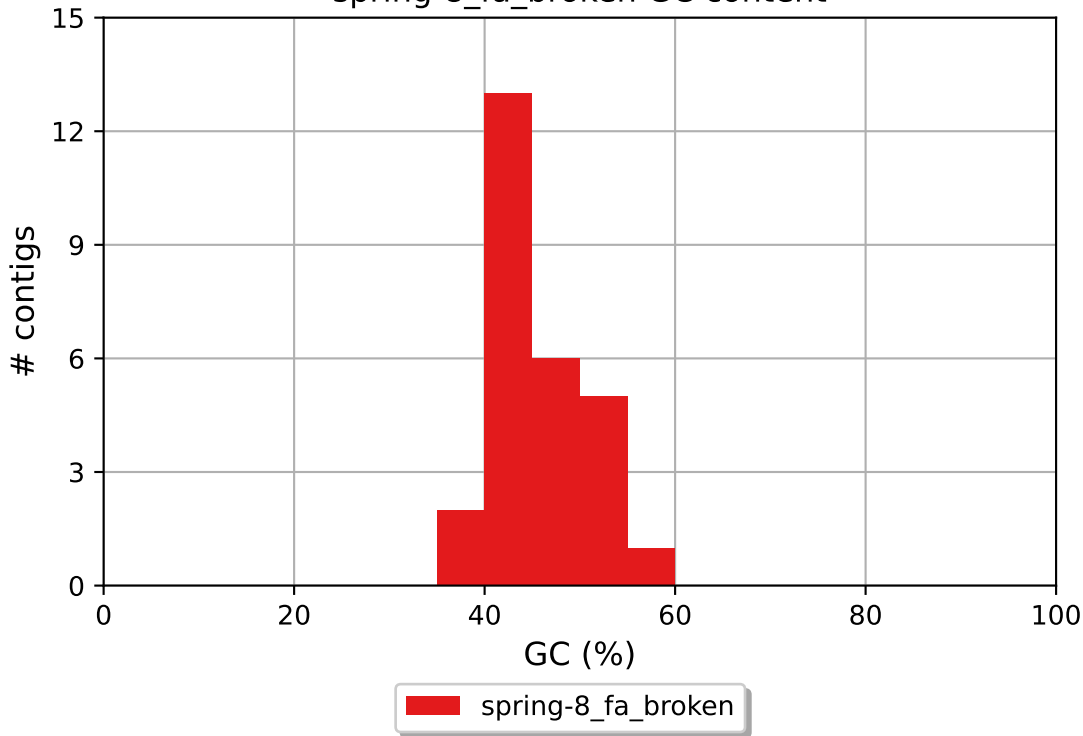
GC content



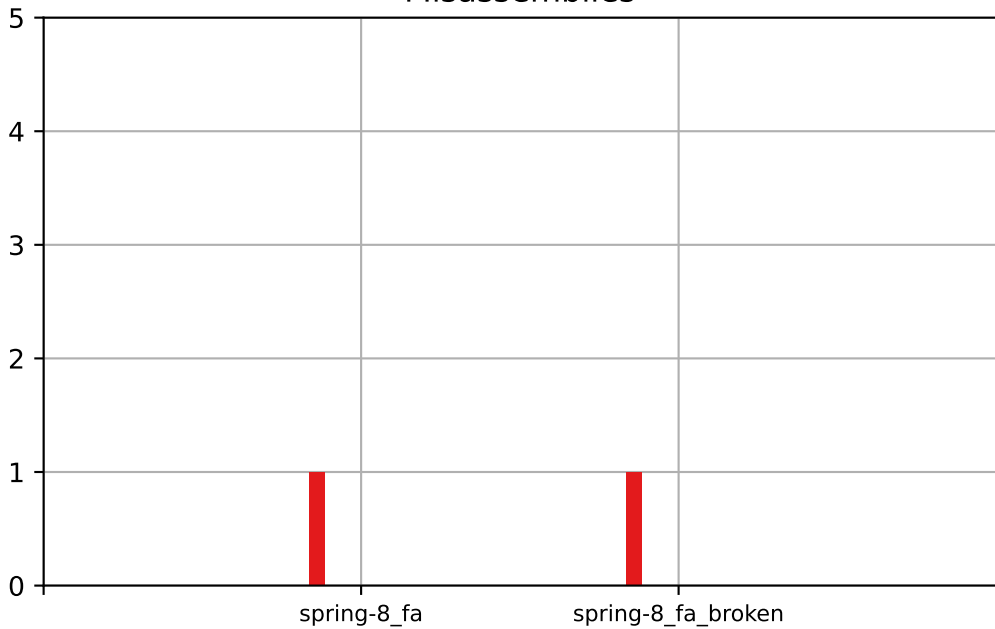
spring-8_fa GC content



spring-8_fa_broken GC content

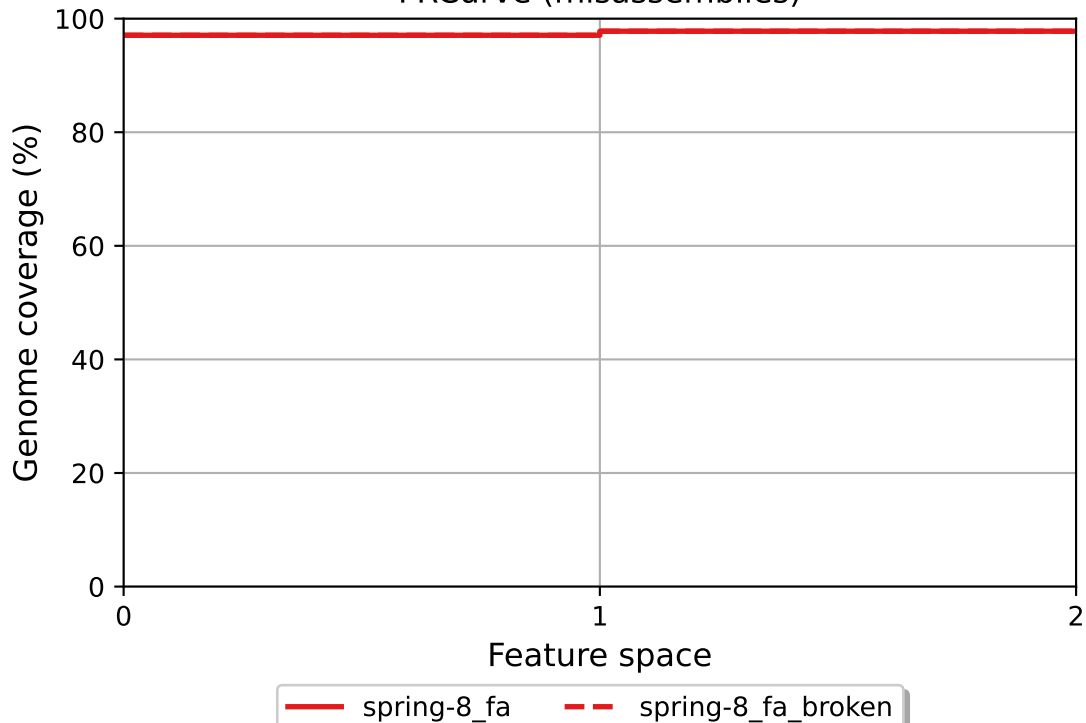


Misassemblies

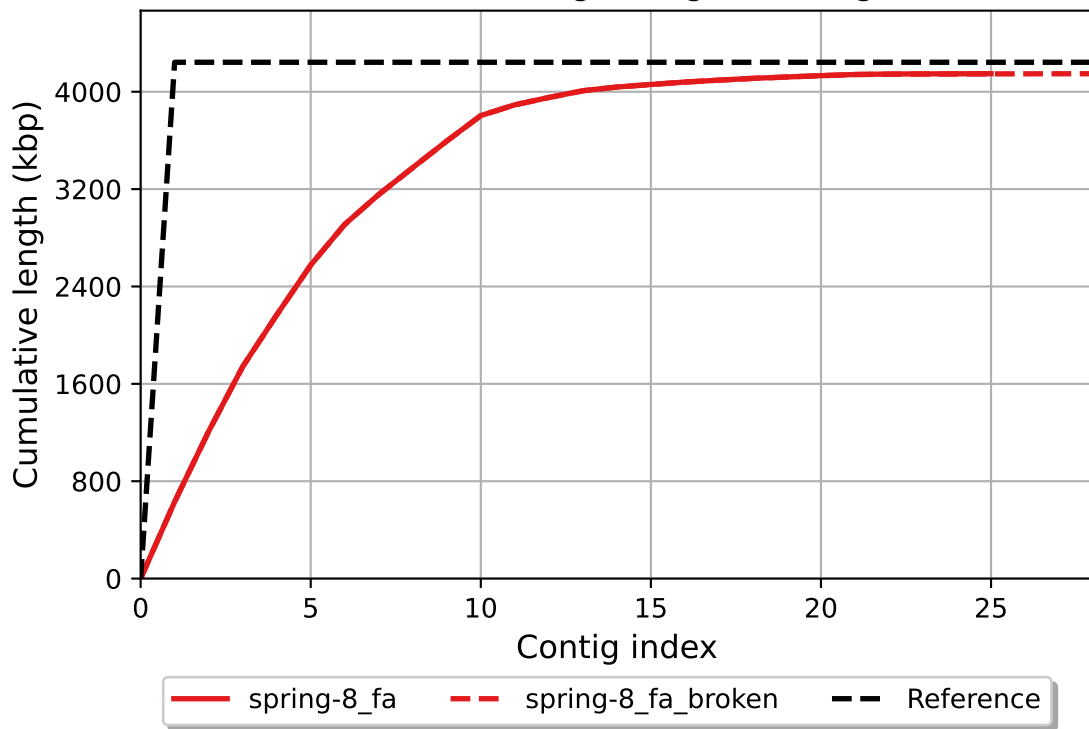


 # relocations

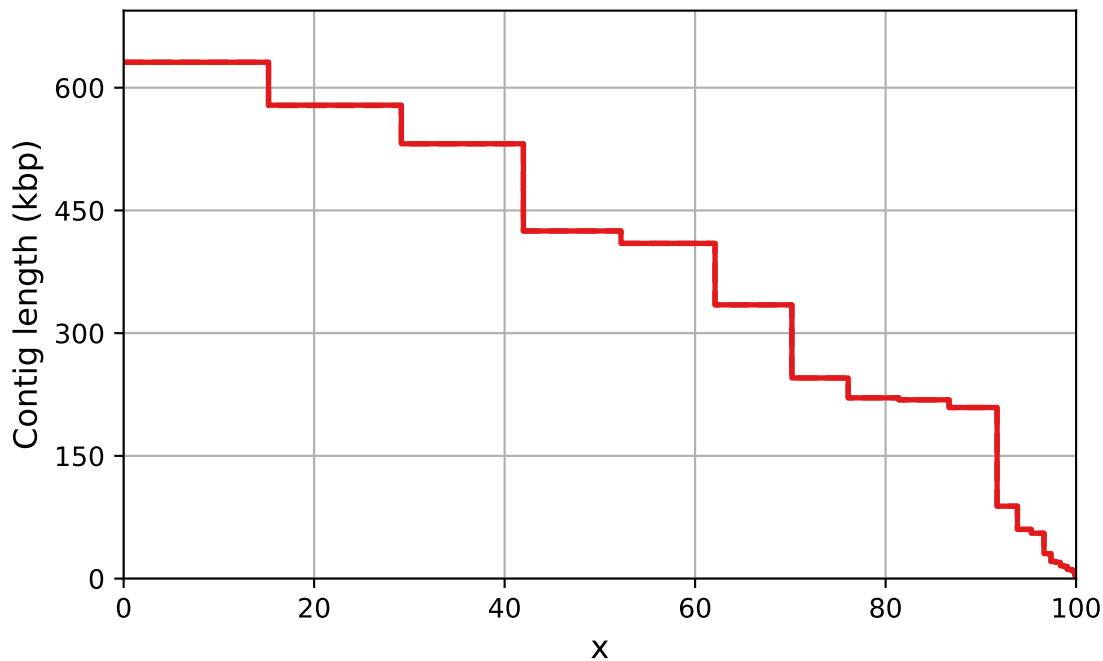
FRCurve (misassemblies)



Cumulative length (aligned contigs)

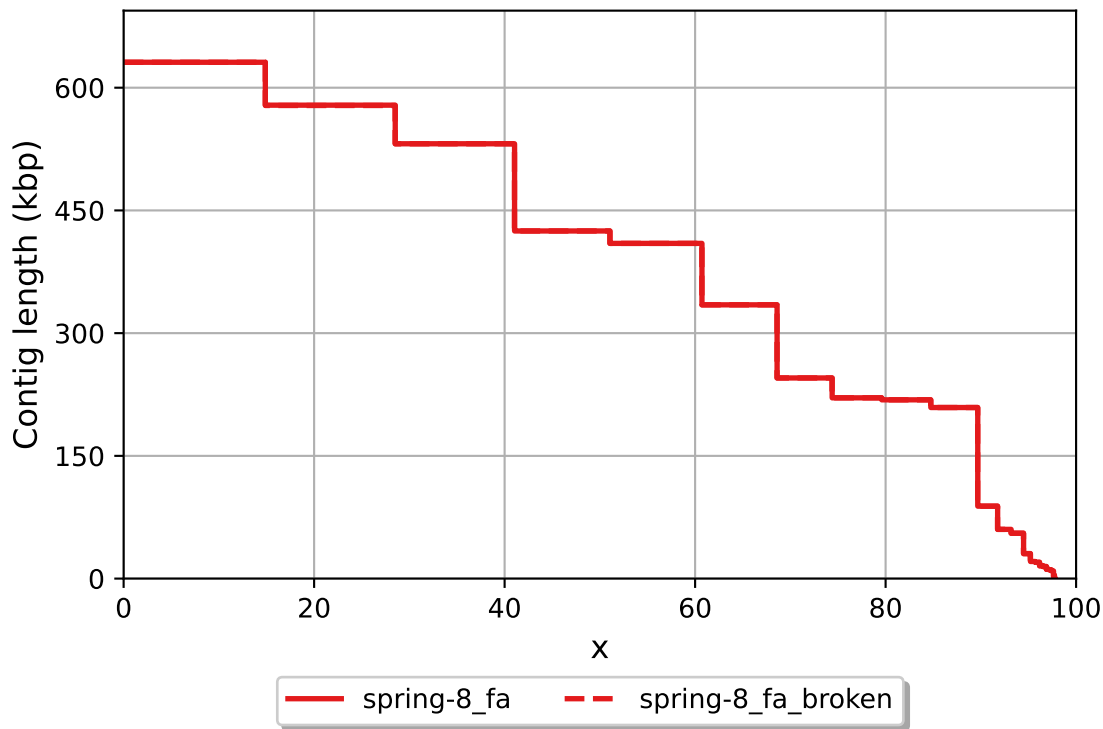


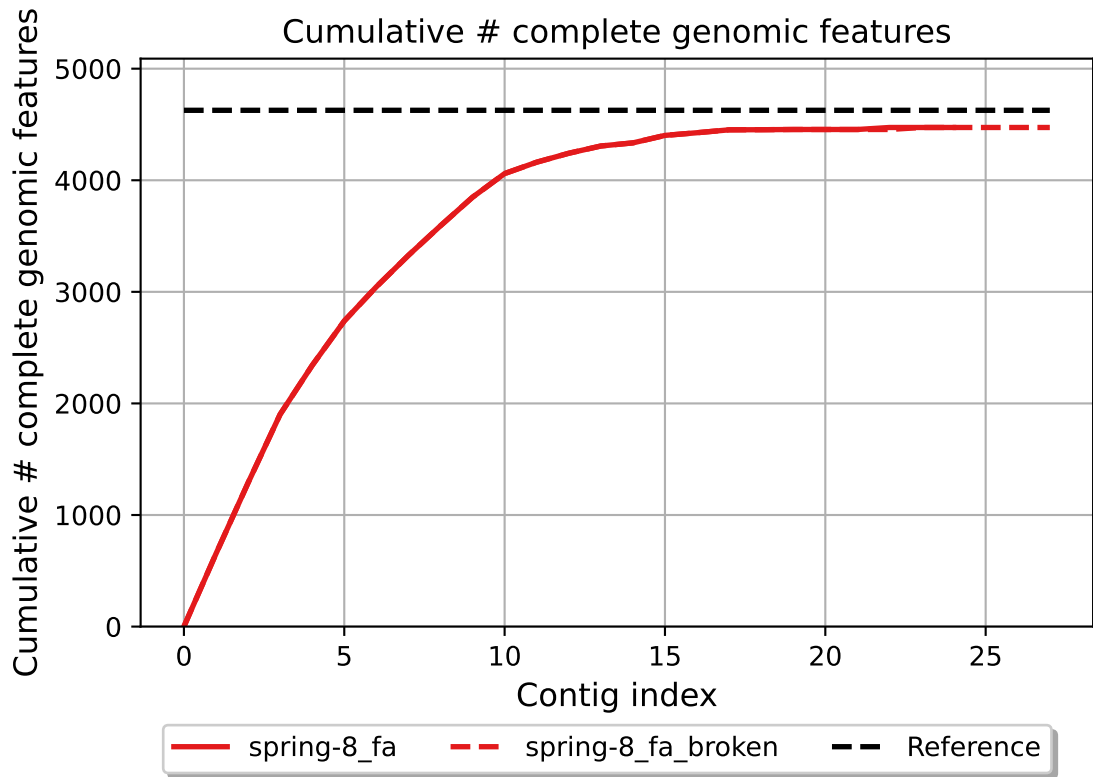
NAx



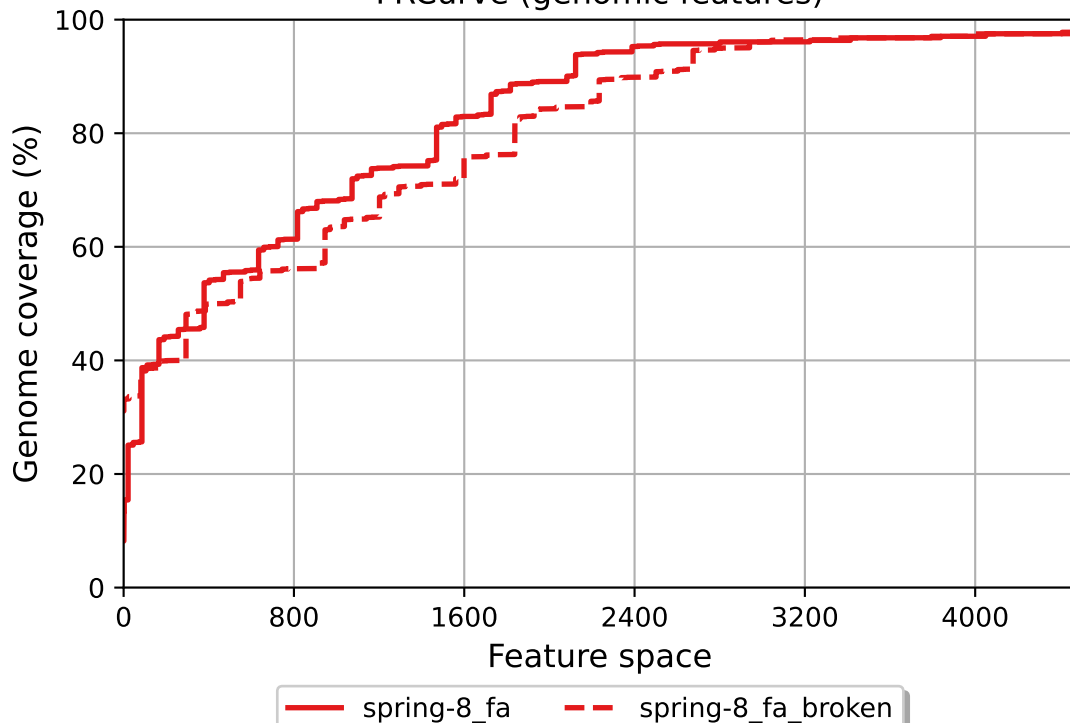
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NGAx

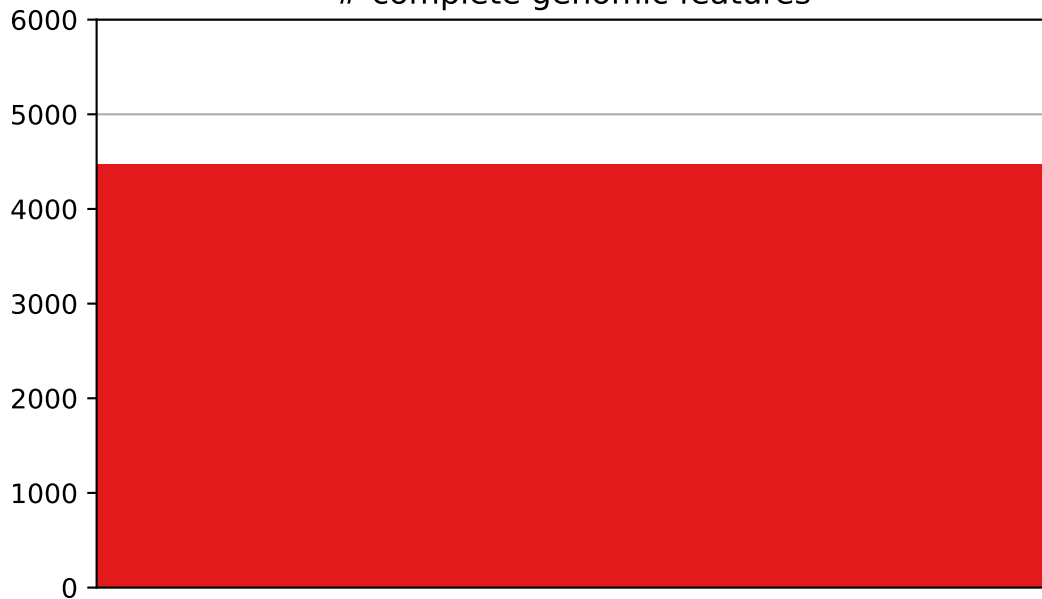




FRCurve (genomic features)



complete genomic features



spring-8_fa



spring-8_fa_broken

Genome fraction, %



spring-8_fa



spring-8_fa_broken