

Report

	myspecies-8_fa	myspecies-8_fa_broken
# contigs (>= 0 bp)	795	-
# contigs (>= 1000 bp)	72	81
Total length (>= 0 bp)	5643969	-
Total length (>= 1000 bp)	5535719	5532643
# contigs	78	92
Largest contig	328900	316846
Total length	5539460	5538757
Reference length	5682322	5682322
GC (%)	57.19	57.19
Reference GC (%)	57.12	57.12
N50	146880	146880
NG50	146880	145918
N90	44777	38354
NG90	35266	27080
auN	158442.9	150953.3
auNG	154459.4	147139.4
L50	14	14
LG50	14	15
L90	37	40
LG90	40	44
# misassemblies	76	73
# misassembled contigs	33	34
Misassembled contigs length	4063969	3717853
# local misassemblies	27	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	3	2
# unaligned contigs	13 + 42 part	14 + 47 part
Unaligned length	723223	722823
Genome fraction (%)	85.167	85.234
Duplication ratio	1.007	1.007
# N's per 100 kbp	13.49	0.79
# mismatches per 100 kbp	685.91	685.80
# indels per 100 kbp	20.72	20.18
# genomic features	9664 + 212 part	9628 + 244 part
Complete BUSCO (%)	97.97	97.97
Partial BUSCO (%)	0.00	0.00
# predicted rRNA genes	4 + 1 part	3 + 1 part
Largest alignment	280173	280173
Total aligned length	4812850	4812637
NA50	66509	66509
NGA50	61590	61590
NA90	-	-
NGA90	-	-
auNA	73575.3	73327.2
auNGA	71725.6	71474.6
LA50	26	26
LGA50	28	28
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

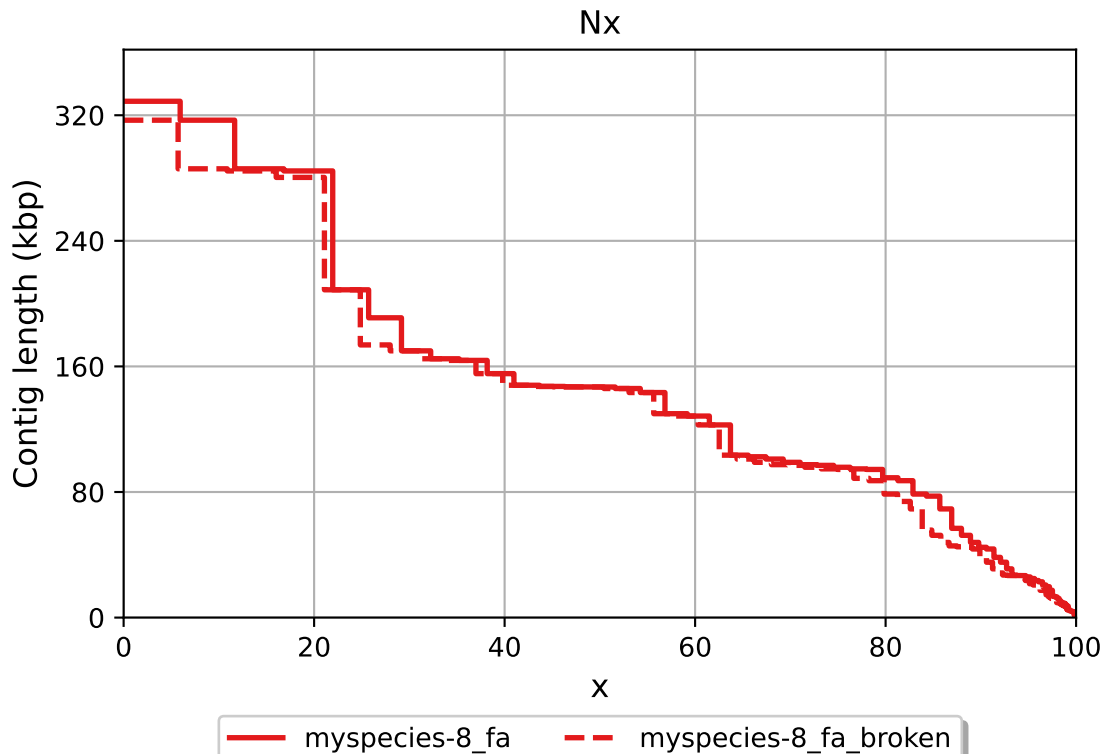
	myspecies-8_fa	myspecies-8_fa_broken
# misassemblies	76	73
# contig misassemblies	72	73
# c. relocations	67	68
# c. translocations	5	5
# c. inversions	0	0
# scaffold misassemblies	4	0
# s. relocations	4	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	33	34
Misassembled contigs length	4063969	3717853
# local misassemblies	27	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	1	-
# unaligned mis. contigs	3	2
# mismatches	33012	33005
# indels	997	971
# indels (<= 5 bp)	864	850
# indels (> 5 bp)	133	121
Indels length	10648	9850

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).

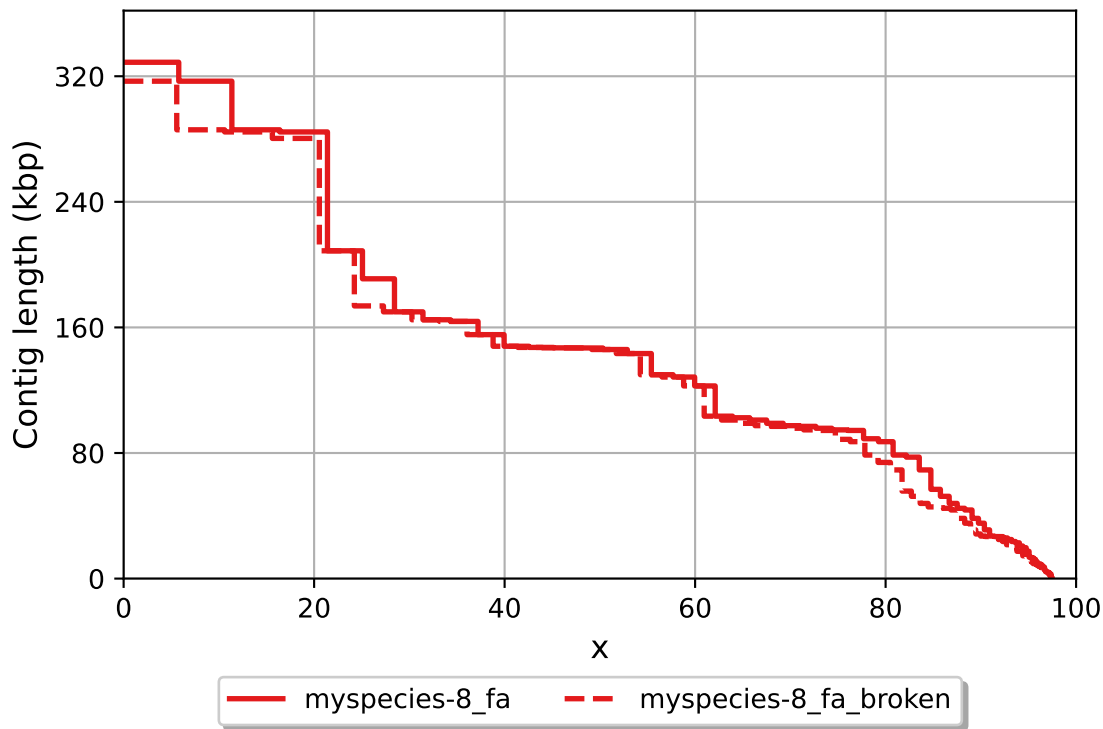
Unaligned report

	myspecies-8_fa	myspecies-8_fa_broken
# fully unaligned contigs	13	14
Fully unaligned length	62938	63271
# partially unaligned contigs	42	47
Partially unaligned length	660285	659552
# N's	747	44

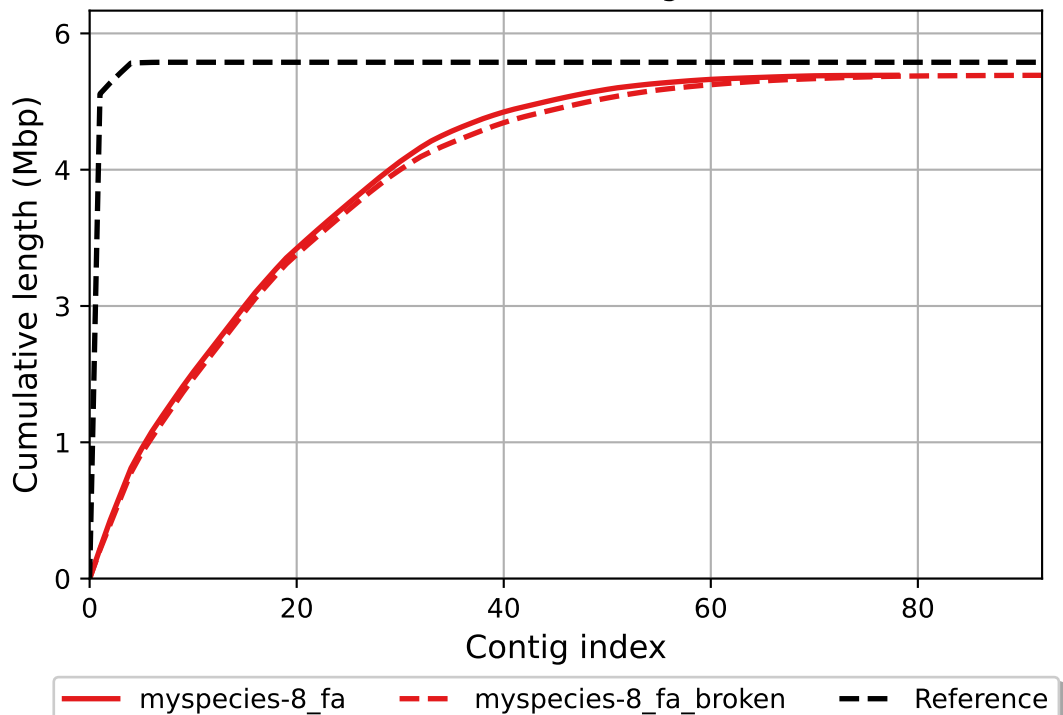
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



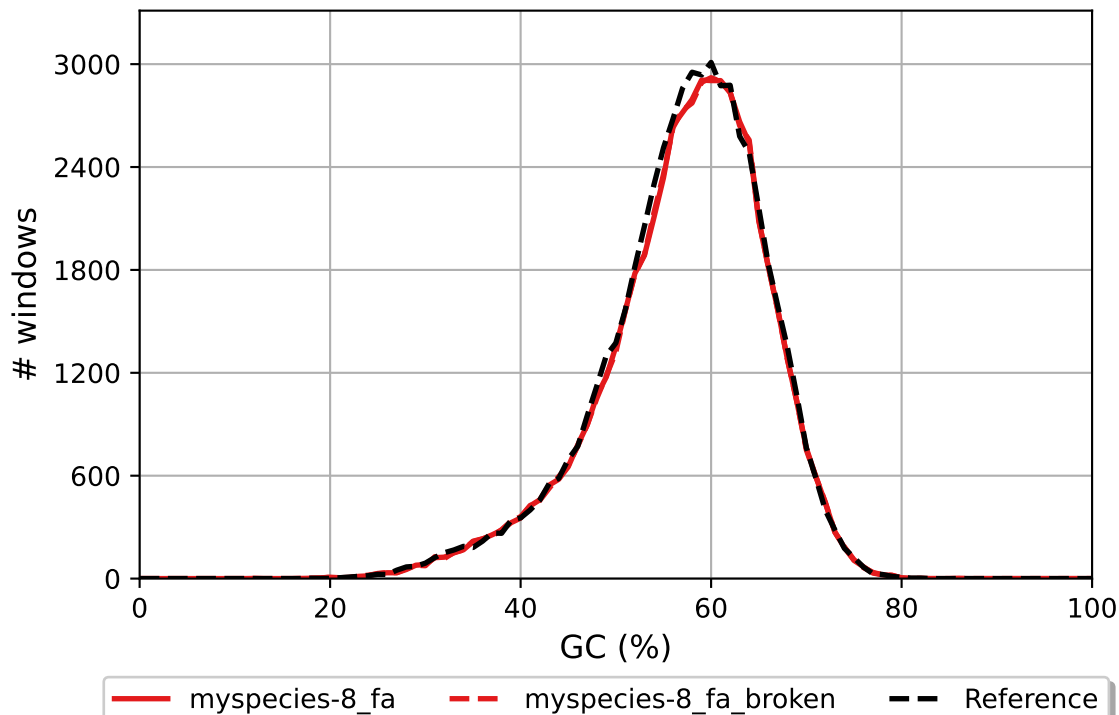
NGx



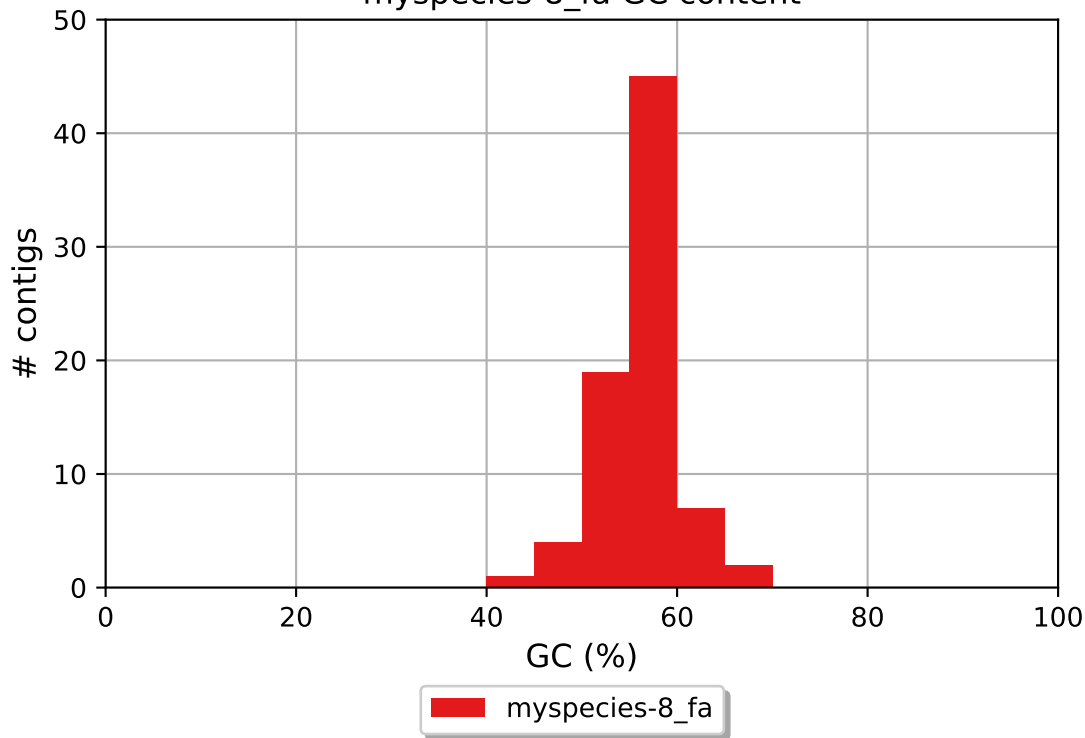
Cumulative length



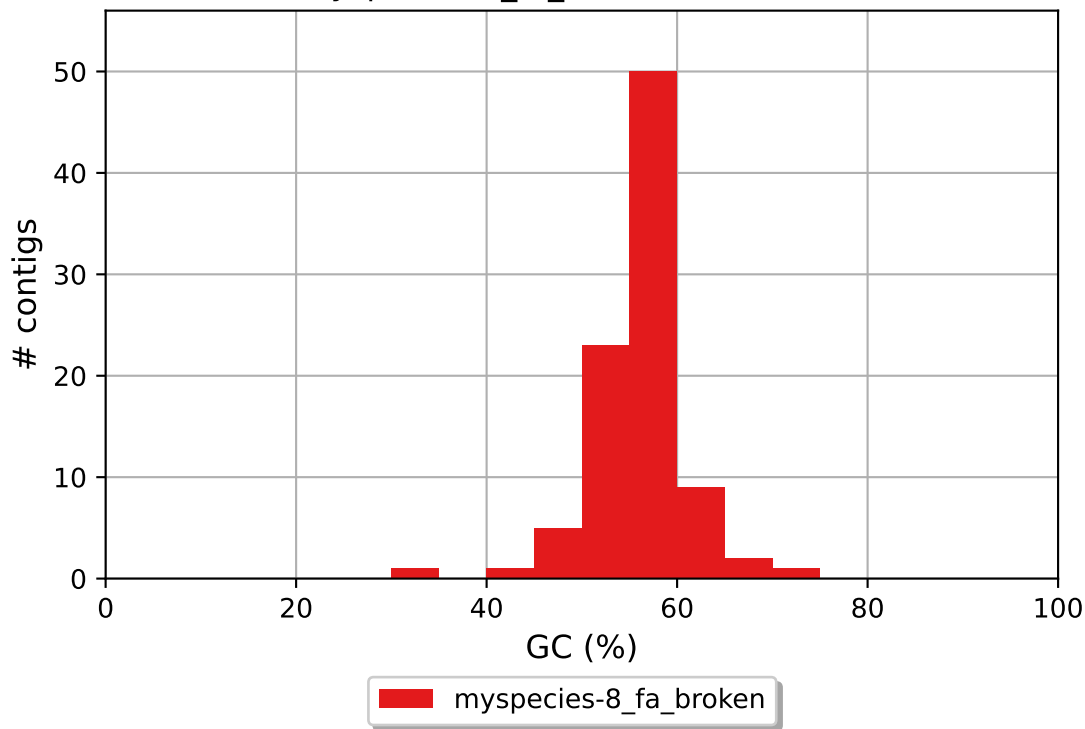
GC content



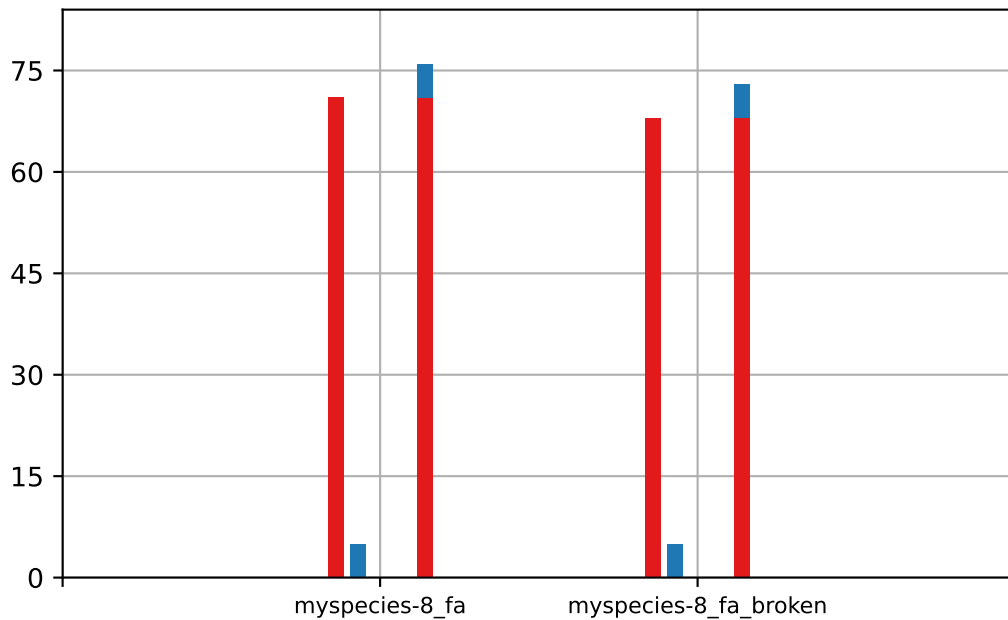
myspecies-8_fa GC content



myspecies-8_fa_broken GC content



Misassemblies

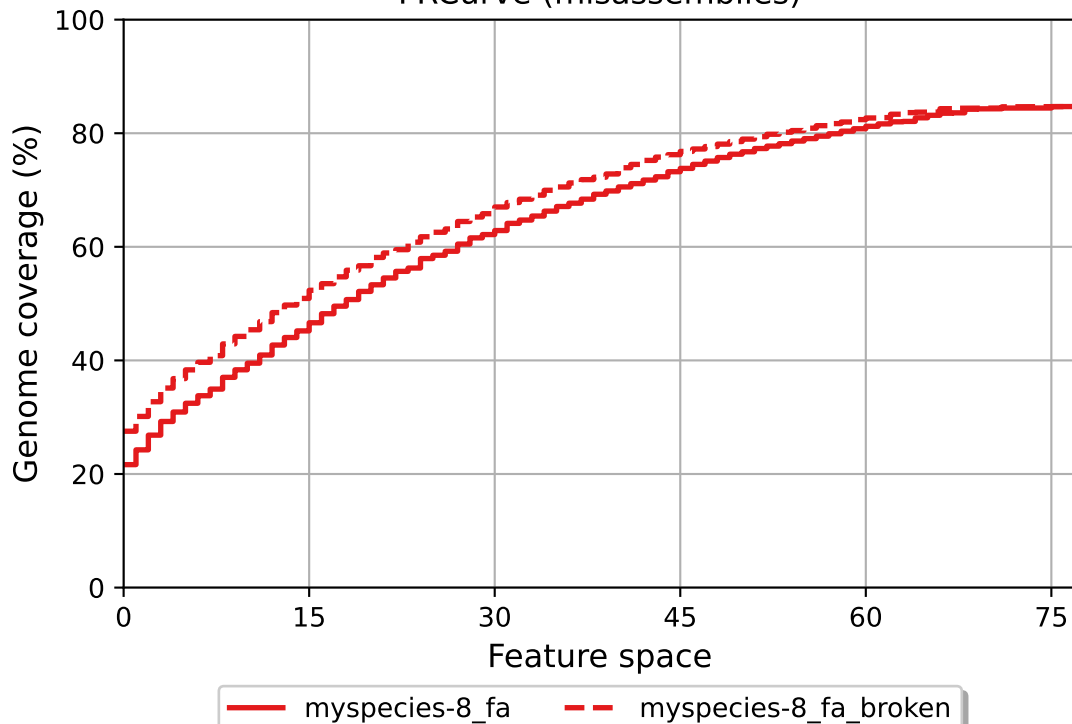


relocations

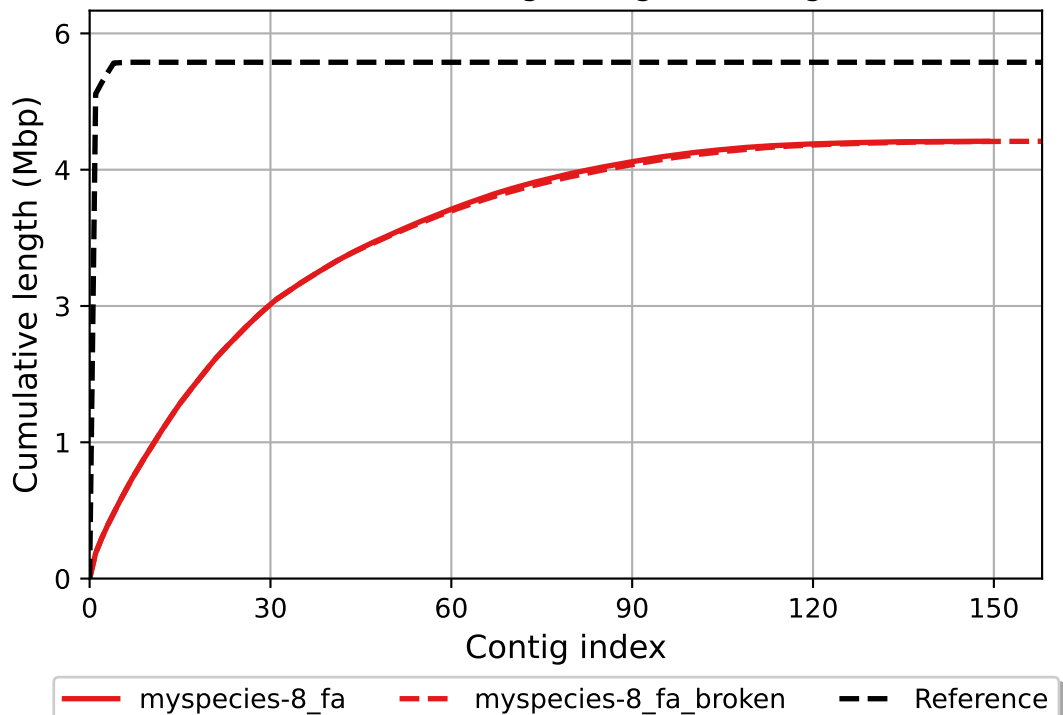


translocations

FRCurve (misassemblies)



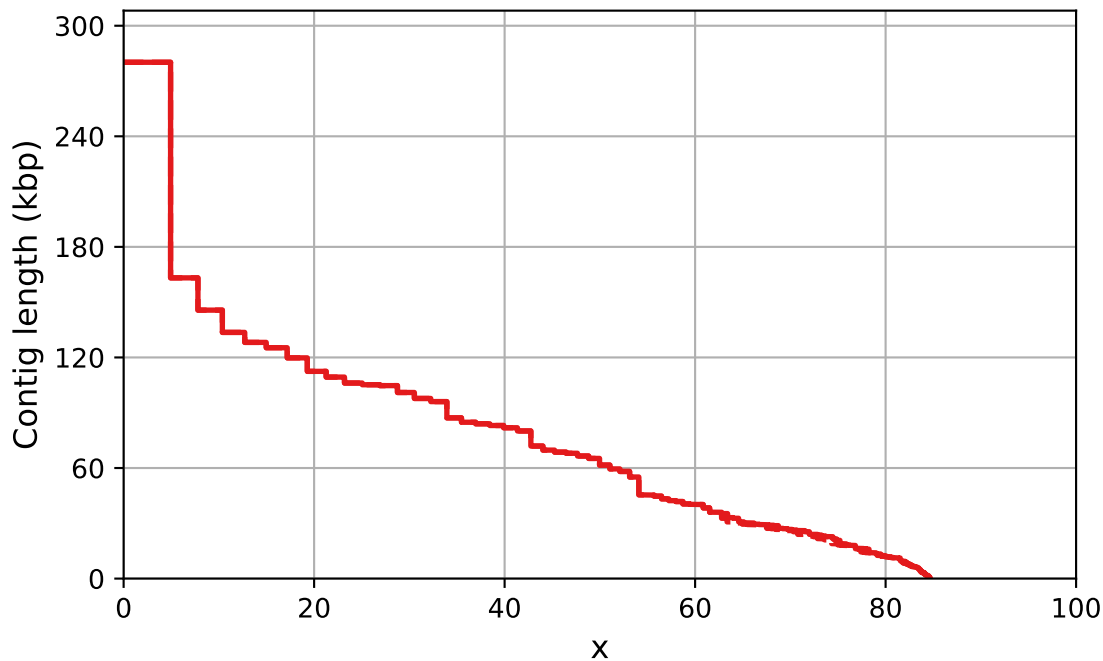
Cumulative length (aligned contigs)



NAx



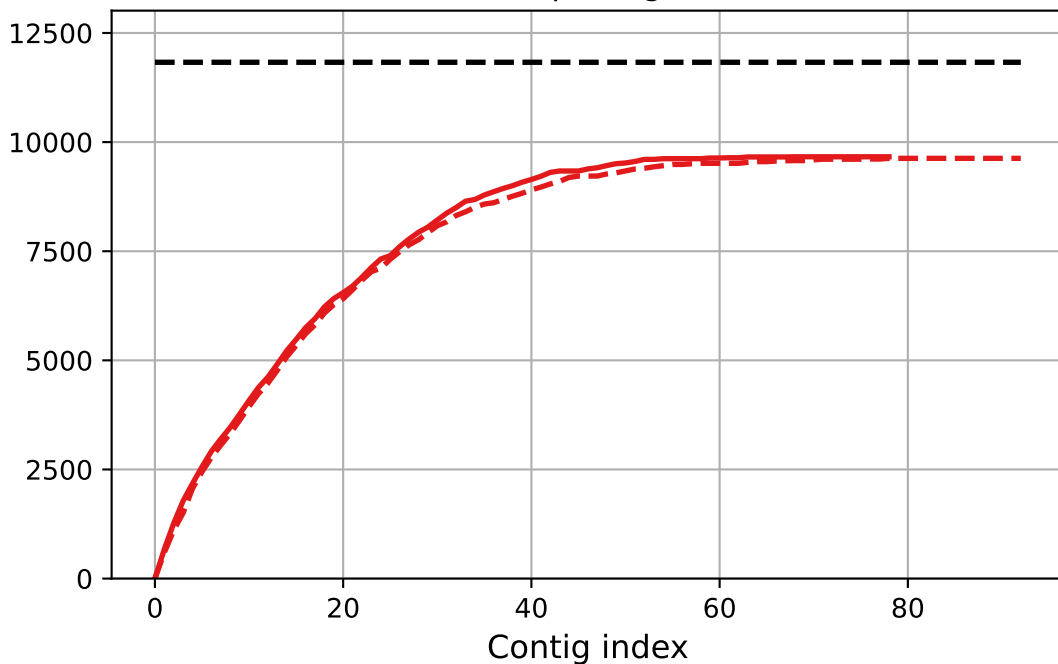
NGAx



myspecies-8_fa myspecies-8_fa_broken

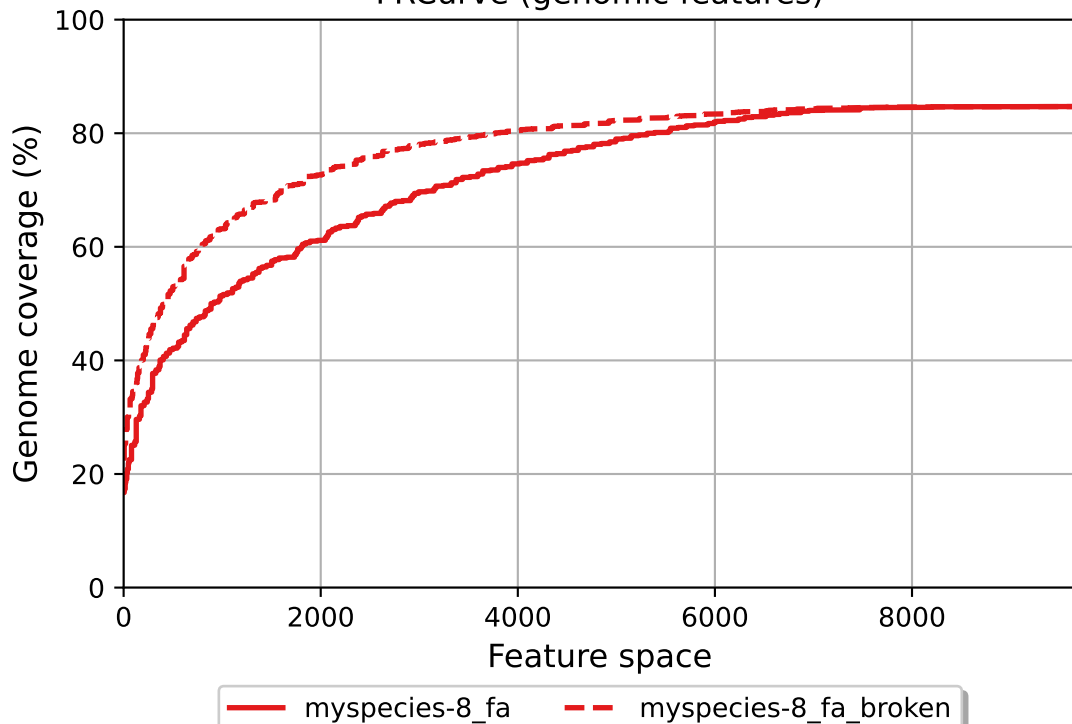
Cumulative # complete genomic features

Cumulative # complete genomic features

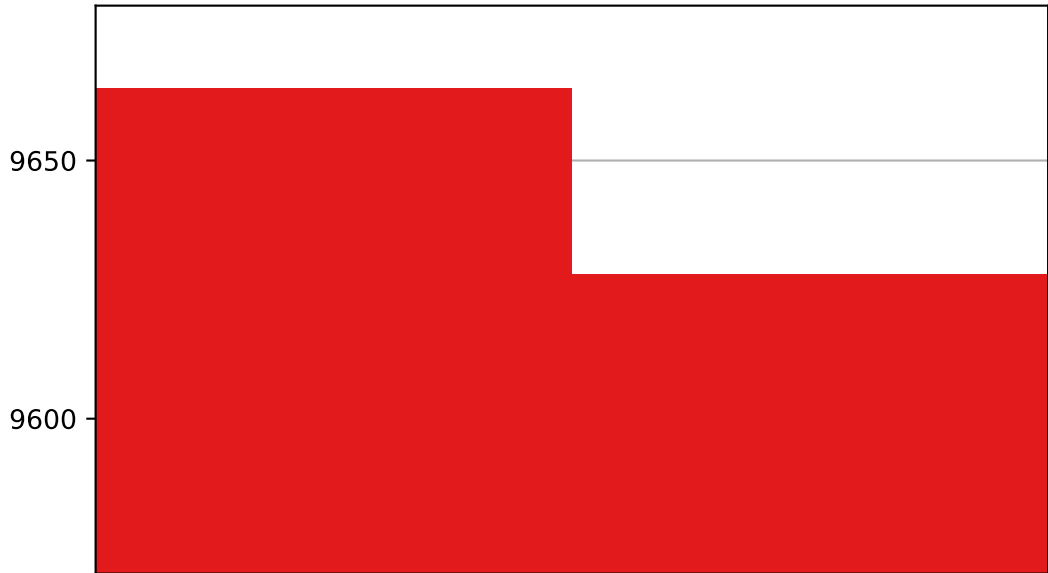


myspecies-8_fa myspecies-8_fa_broken Reference

FRCurve (genomic features)



complete genomic features



myspecies-8_fa



myspecies-8_fa_broken

Genome fraction, %



myspecies-8_fa



myspecies-8_fa_broken