

	Report	
	mtuberculosis-8_fa	mtuberculosis-8_fa_broken
# contigs (>= 0 bp)	1624	-
# contigs (>= 1000 bp)	231	355
Total length (>= 0 bp)	4628404	-
Total length (>= 1000 bp)	4365612	4348846
# contigs	262	402
Largest contig	121210	72614
Total length	4388009	4379722
Reference length	4411532	4411532
GC (%)	65.48	65.48
Reference GC (%)	65.61	65.61
N50	30952	19477
NG50	30952	19342
N90	8548	5728
NG90	8204	5366
auN	36591.0	23649.1
auNG	36395.9	23478.6
L50	45	70
LG50	45	71
L90	139	227
LG90	142	232
# misassemblies	27	27
# misassembled contigs	26	27
Misassembled contigs length	458385	370600
# local misassemblies	9	9
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	1	1
# unaligned contigs	1 + 14 part	2 + 14 part
Unaligned length	31246	31246
Genome fraction (%)	97.901	97.743
Duplication ratio	1.018	1.017
# N's per 100 kbp	160.14	1.10
# mismatches per 100 kbp	55.99	56.20
# indels per 100 kbp	10.96	8.06
# genomic features	8076 + 475 part	7827 + 721 part
Complete BUSCO (%)	94.59	93.24
Partial BUSCO (%)	0.00	0.68
# predicted rRNA genes	2 + 1 part	2 + 1 part
Largest alignment	120012	72613
Total aligned length	4350965	4343665
NA50	28344	18855
NGA50	28344	18848
NA90	7498	5114
NGA90	7370	4760
auNA	35263.0	22699.1
auNGA	35075.0	22535.4
LA50	47	72
LGA50	47	73
LA90	150	241
LGA90	153	247

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

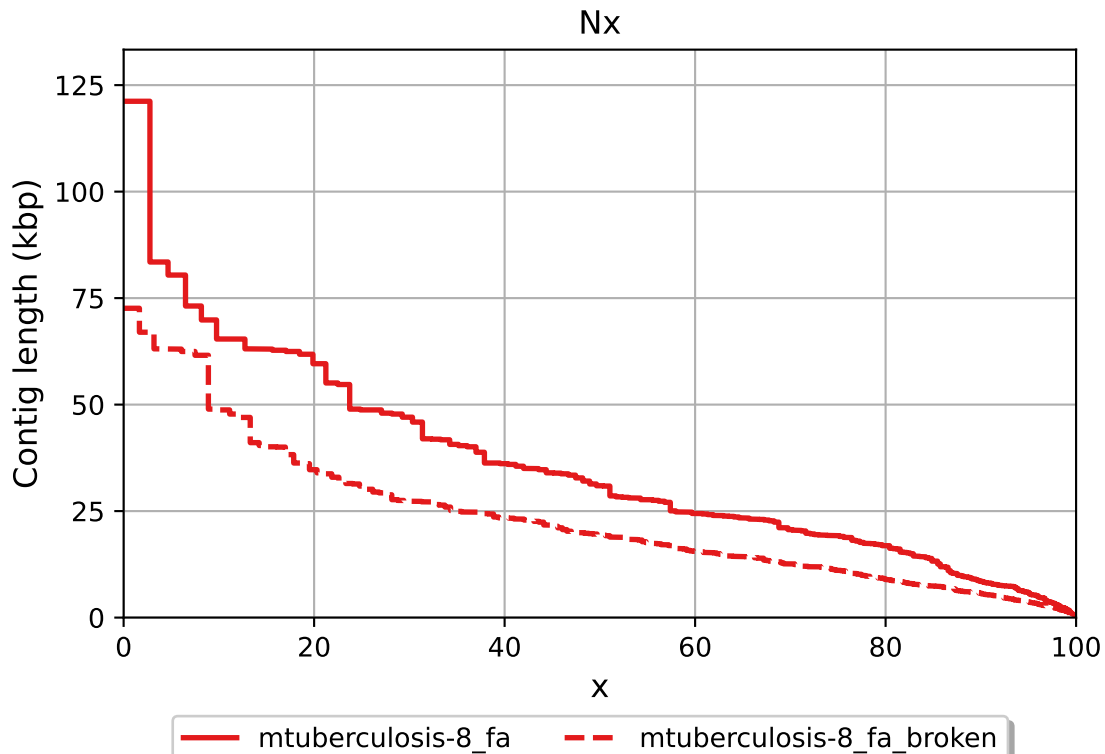
	mtuberculosis-8_fa	mtuberculosis-8_fa_broken
# misassemblies	27	27
# contig misassemblies	27	27
# c. relocations	27	27
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	26	27
Misassembled contigs length	458385	370600
# local misassemblies	9	9
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	2	-
# unaligned mis. contigs	1	1
# mismatches	2436	2441
# indels	477	350
# indels (<= 5 bp)	245	233
# indels (> 5 bp)	232	117
Indels length	10699	6145

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).

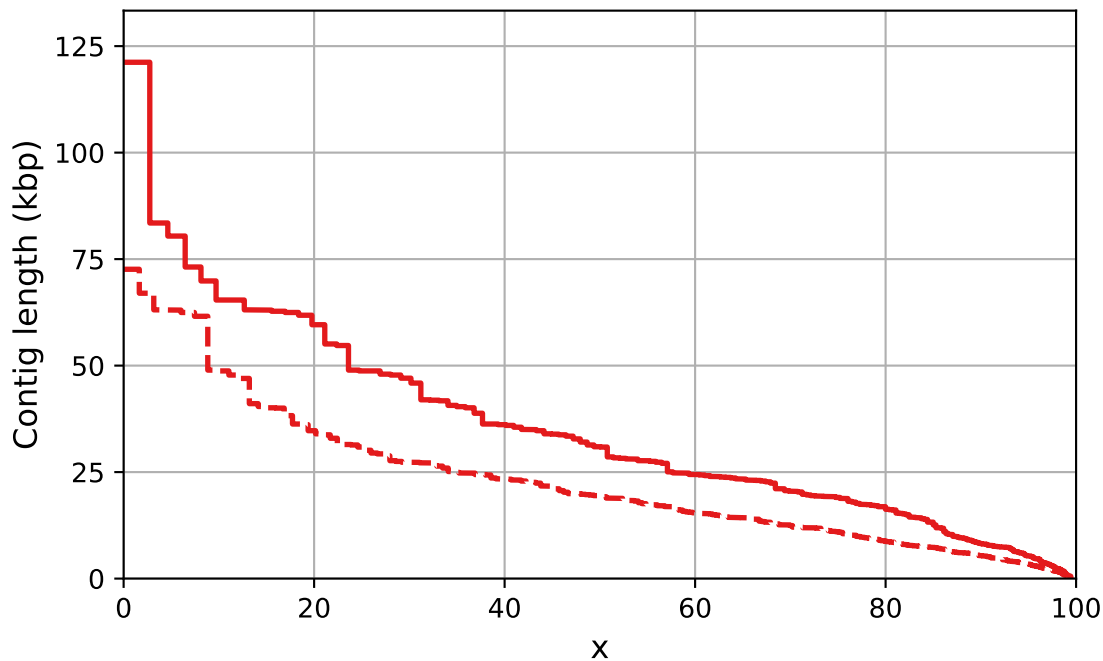
Unaligned report

	mtuberculosis-8_fa	mtuberculosis-8_fa_broken
# fully unaligned contigs	1	2
Fully unaligned length	523	725
# partially unaligned contigs	14	14
Partially unaligned length	30723	30521
# N's	7027	48

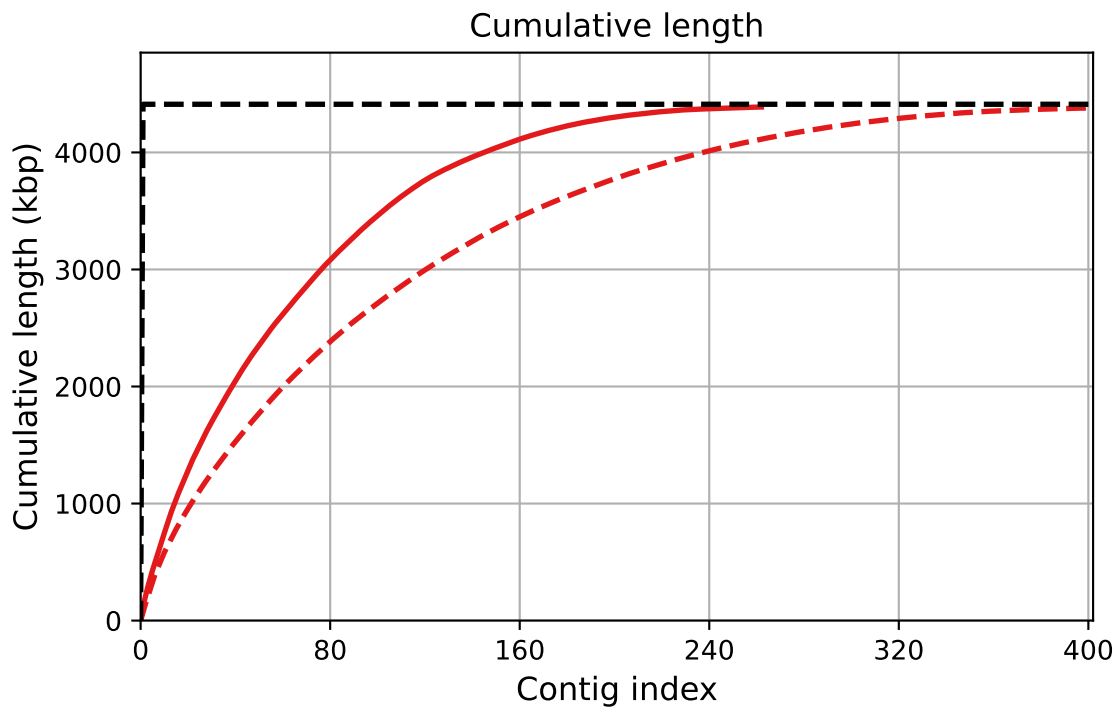
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



NGx

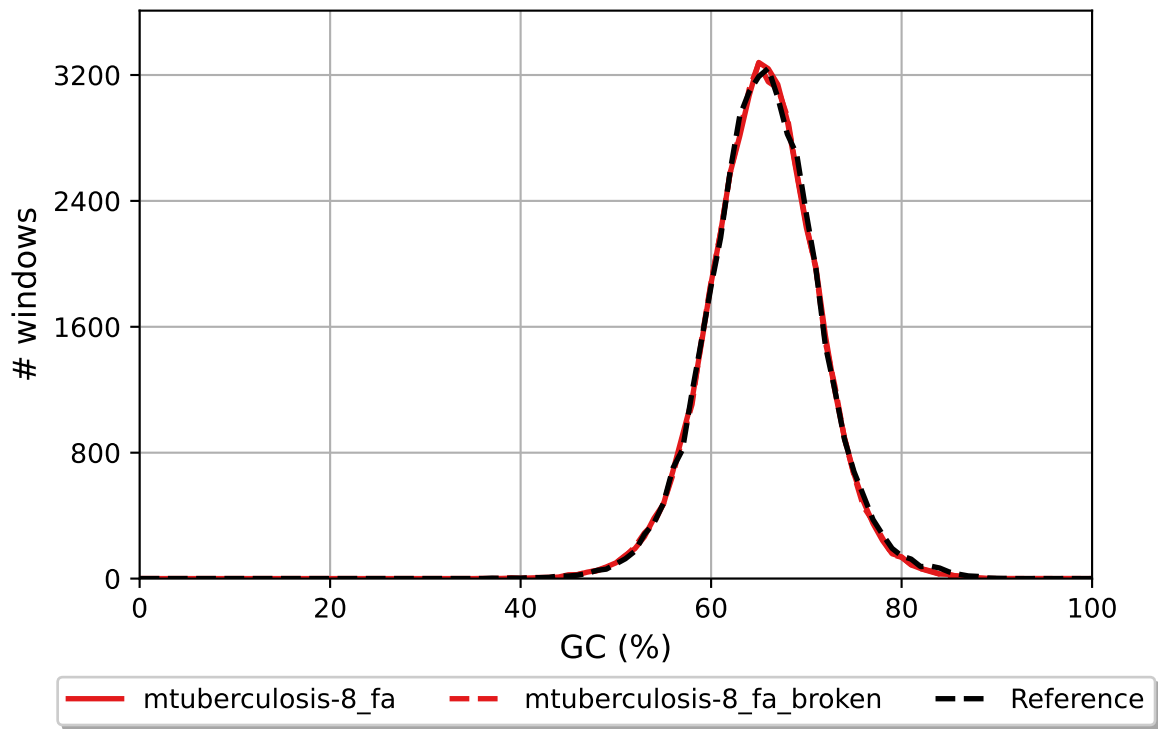


— mtuberculosis-8_fa - - - mtuberculosis-8_fa_broken

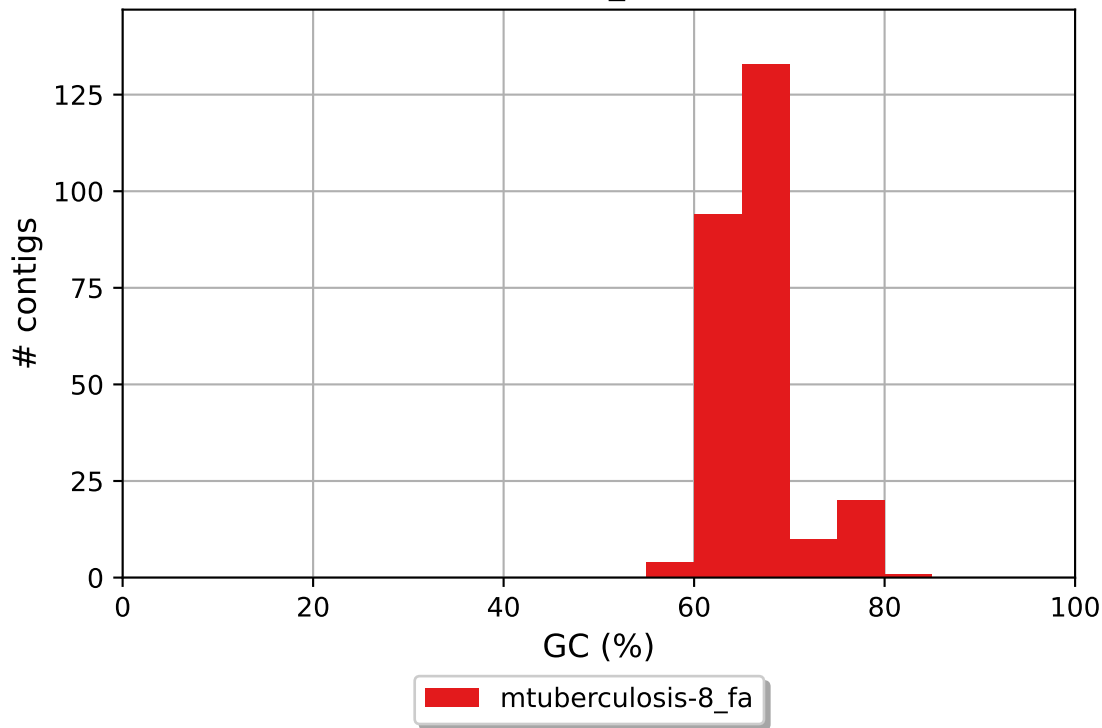


— mtuberculosis-8_fa - - - mtuberculosis-8_fa_broken - - - Reference

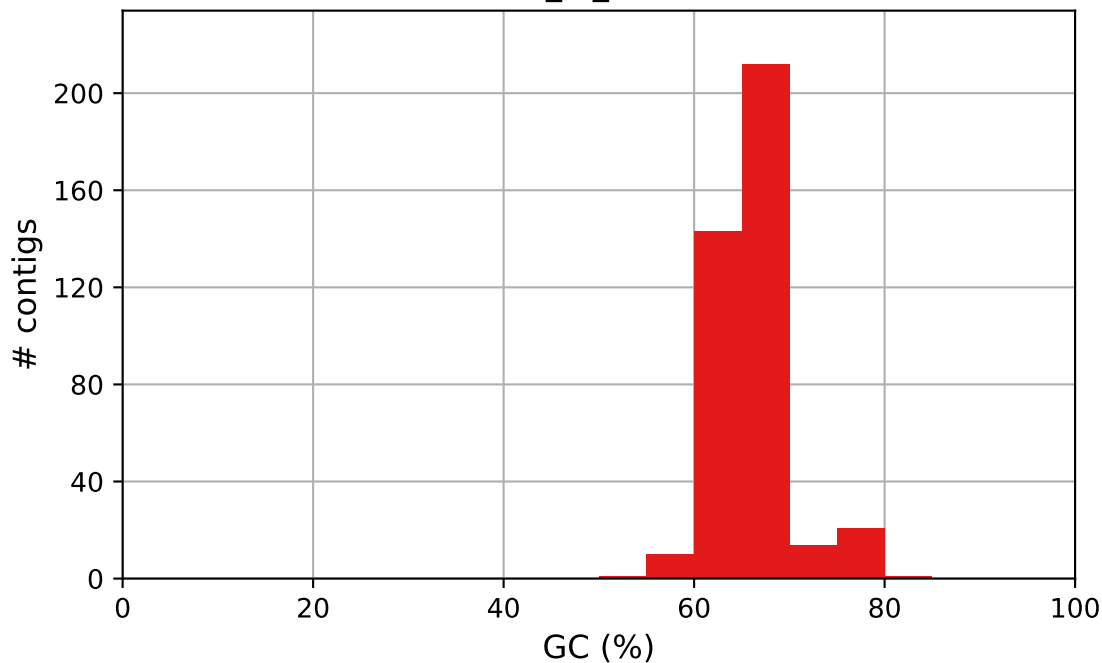
GC content



mtuberculosis-8_fa GC content

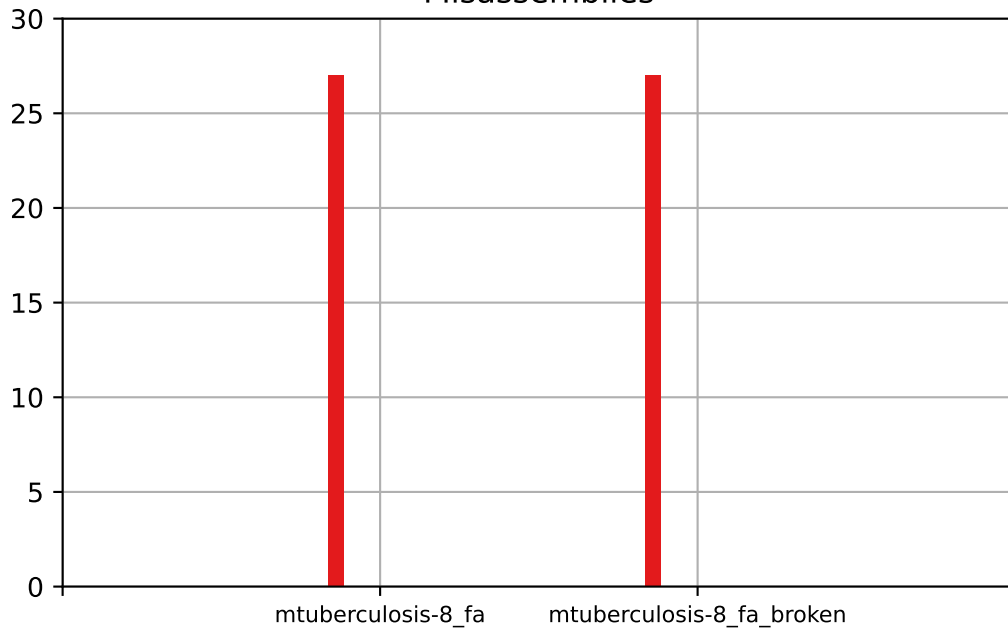


mtuberculosis-8_fa_broken GC content



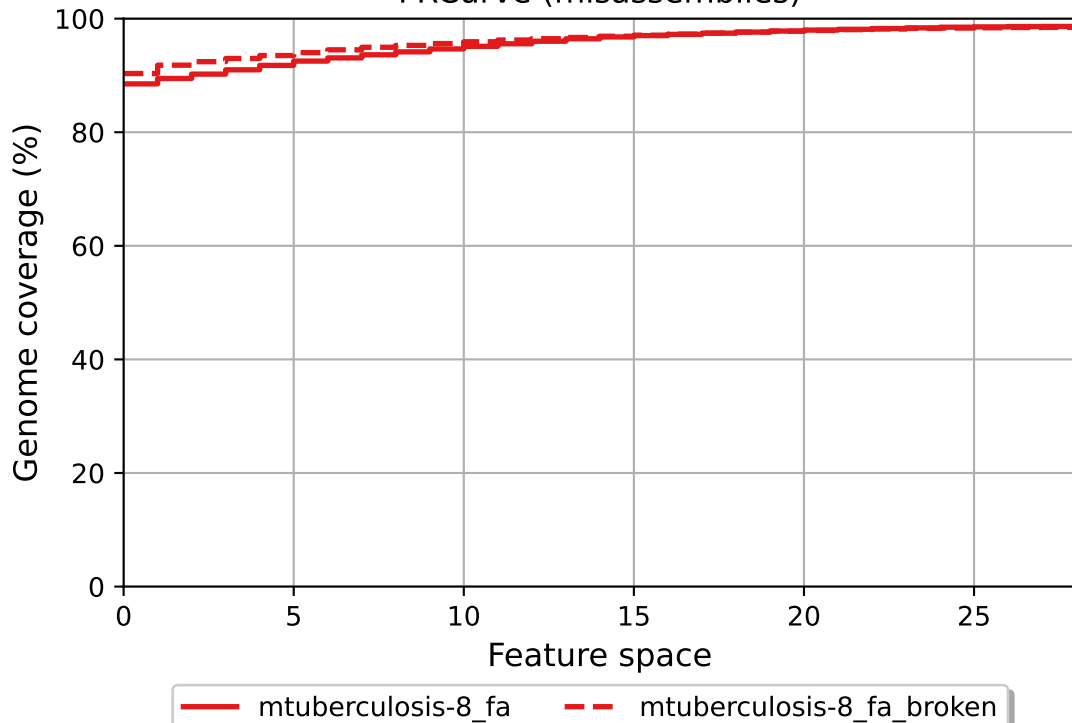
mtuberculosis-8_fa_broken

Misassemblies

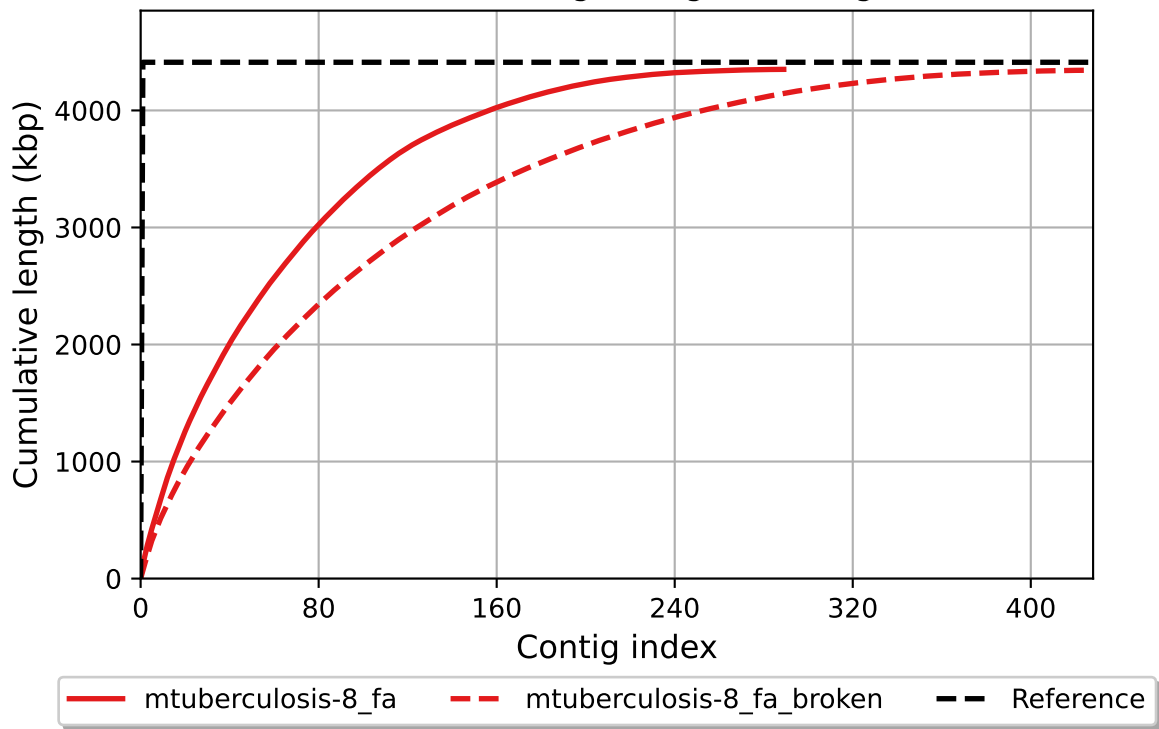


 # relocations

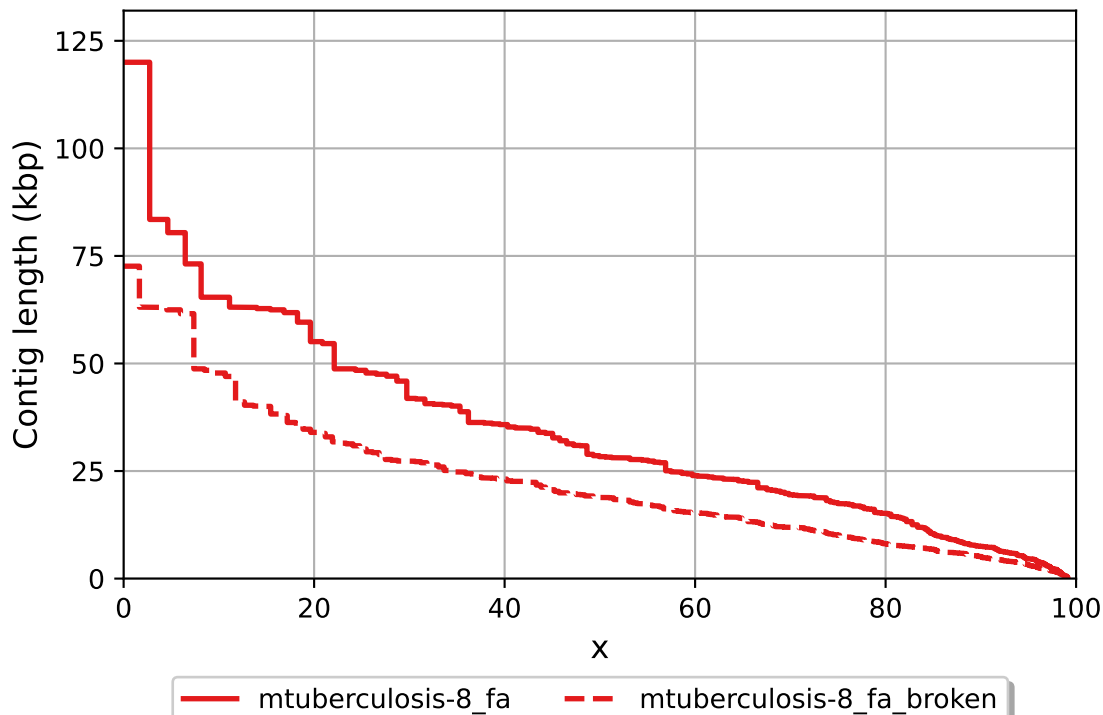
FRCurve (misassemblies)



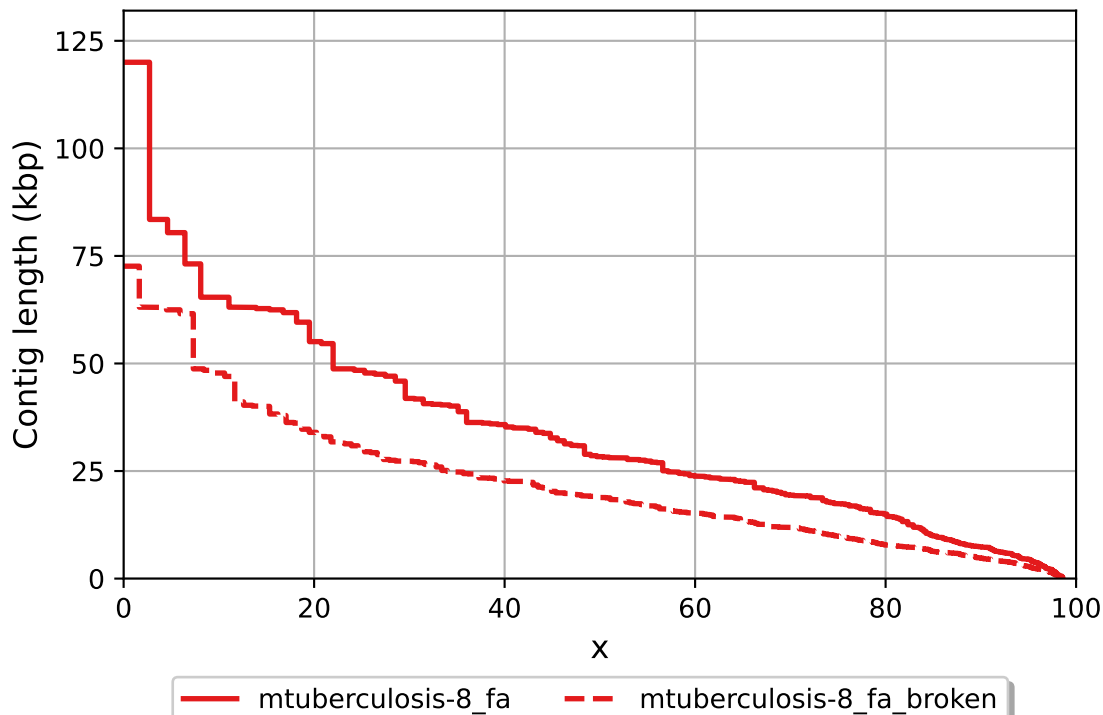
Cumulative length (aligned contigs)

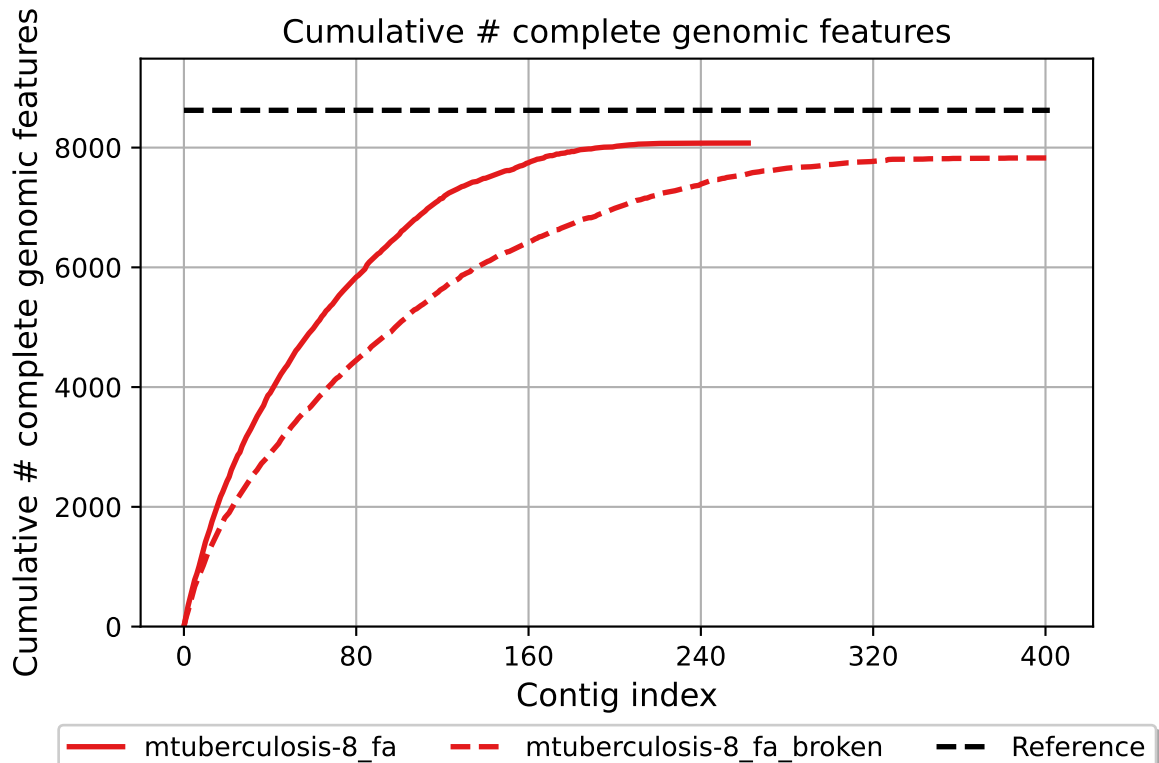


NAx

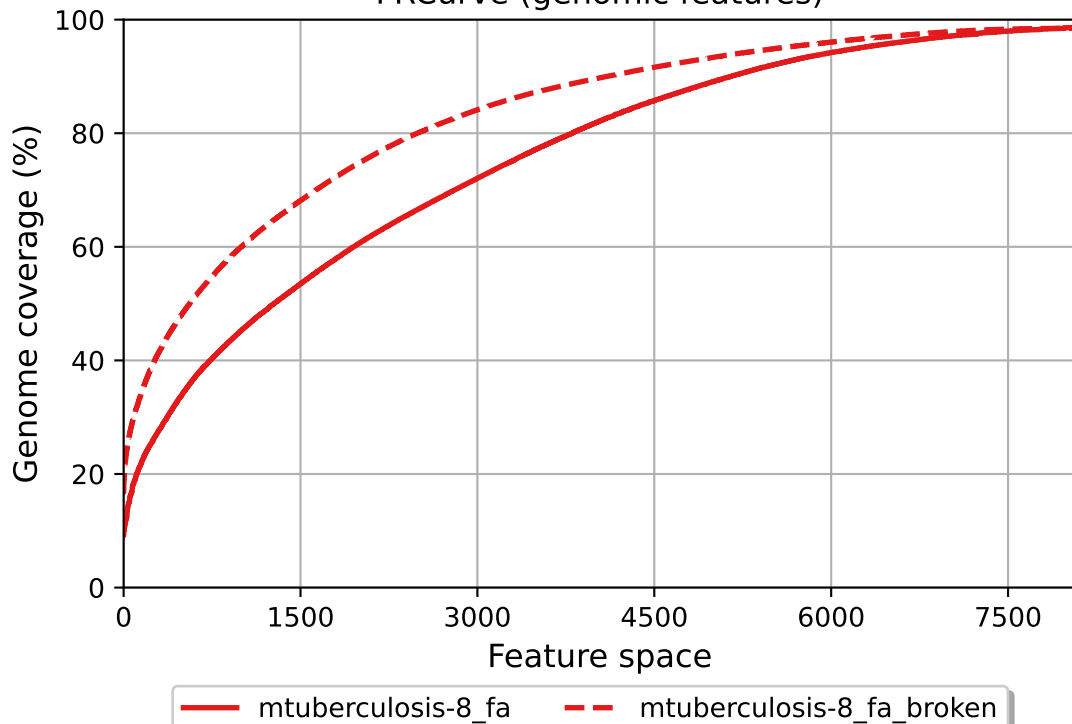


NGAx





FRCurve (genomic features)



complete genomic features

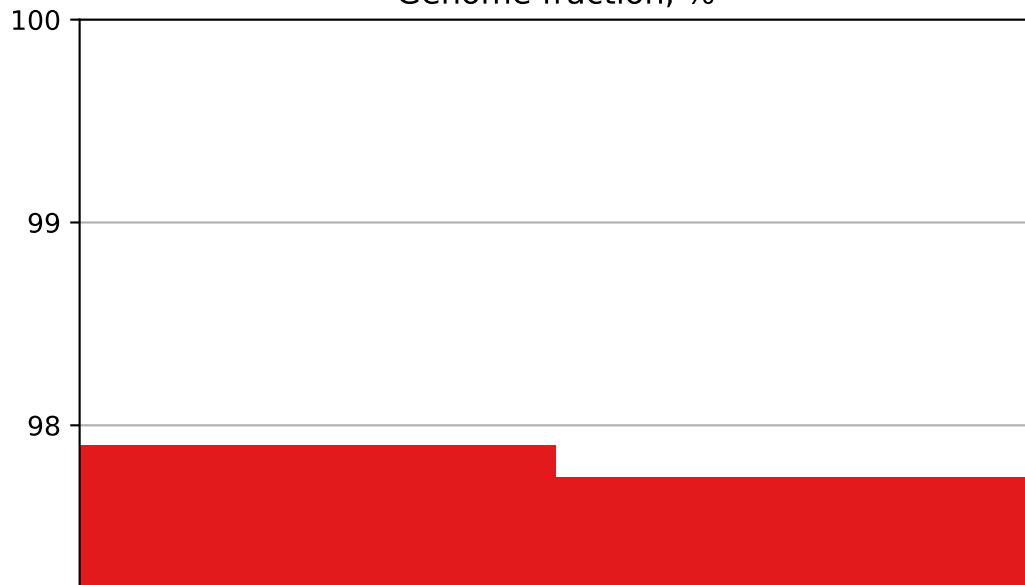


mtuberculosis-8_fa



mtuberculosis-8_fa_broken

Genome fraction, %



mtuberculosis-8_fa



mtuberculosis-8_fa_broken