

# Report

	unknowngenome-8_fa	unknowngenome-8_fa_broken
# contigs (>= 0 bp)	1048	-
# contigs (>= 1000 bp)	69	78
Total length (>= 0 bp)	5683518	-
Total length (>= 1000 bp)	5539611	5536528
# contigs	75	89
Largest contig	373123	373123
Total length	5543441	5542709
Reference length	5682322	5682322
GC (%)	57.19	57.19
Reference GC (%)	57.12	57.12
N50	161156	147550
NG50	159655	147360
N90	48056	43008
NG90	43008	35391
auN	161223.6	153413.2
auNG	157283.2	149643.9
L50	13	14
LG50	14	15
L90	38	42
LG90	41	45
# misassemblies	77	76
# misassembled contigs	33	37
Misassembled contigs length	4178329	4080427
# local misassemblies	27	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	2
# unaligned contigs	14 + 45 part	15 + 49 part
Unaligned length	724735	724275
Genome fraction (%)	84.856	85.248
Duplication ratio	1.007	1.007
# N's per 100 kbp	13.87	0.67
# mismatches per 100 kbp	683.66	685.36
# indels per 100 kbp	19.76	19.76
# genomic features	9645 + 214 part	9639 + 242 part
# predicted rRNA genes	5 + 2 part	4 + 2 part
Largest alignment	203607	203607
Total aligned length	4816835	4816863
NA50	58788	58555
NGA50	58555	58133
NA90	-	-
NGA90	-	-
auNA	70290.1	69302.8
auNGA	68572.2	67600.0
LA50	27	28
LGA50	28	29
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

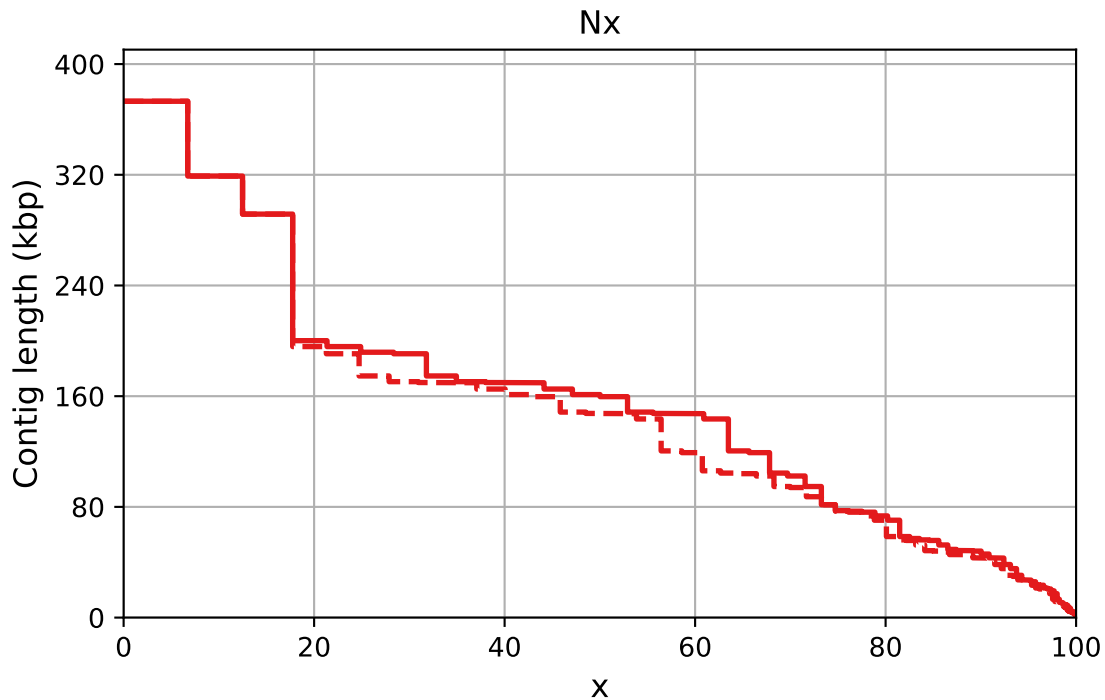
	unknowngenome-8_fa	unknowngenome-8_fa_broken
# misassemblies	77	76
# contig misassemblies	75	76
# c. relocations	71	72
# c. translocations	4	4
# c. inversions	0	0
# scaffold misassemblies	2	0
# s. relocations	2	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	33	37
Misassembled contigs length	4178329	4080427
# local misassemblies	27	27
# scaffold gap ext. mis.	0	-
# scaffold gap loc. mis.	0	-
# unaligned mis. contigs	3	2
# mismatches	32931	33013
# indels	952	952
# indels (<= 5 bp)	834	840
# indels (> 5 bp)	118	112
Indels length	10285	9768

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

## Unaligned report

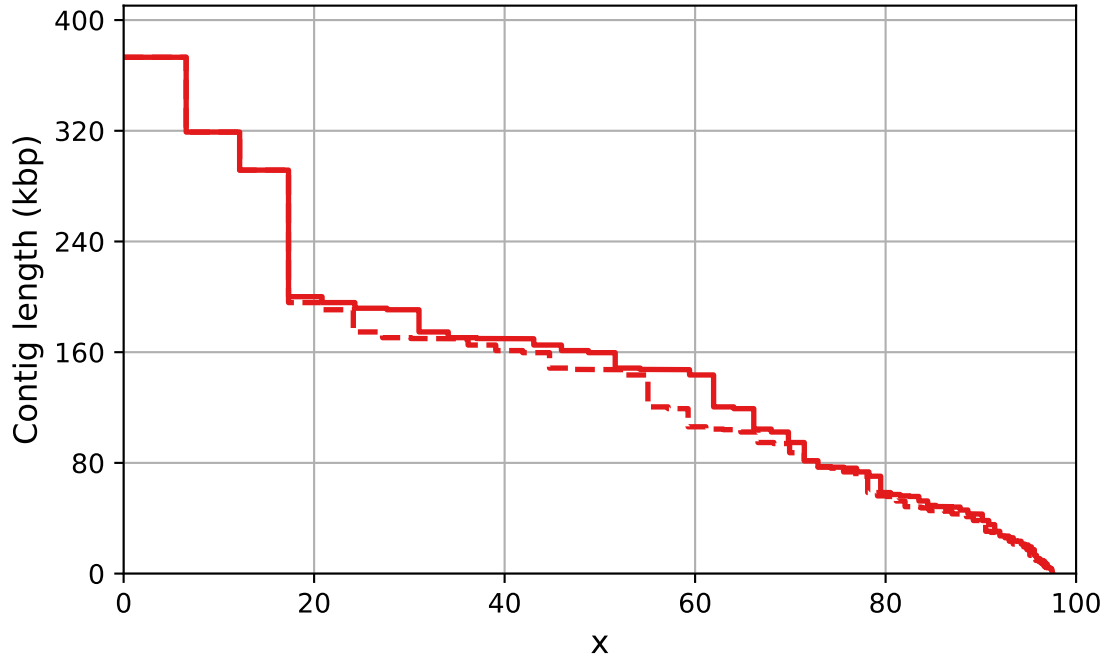
	unknowngenome-8_fa	unknowngenome-8_fa_broken
# fully unaligned contigs	14	15
Fully unaligned length	87686	88019
# partially unaligned contigs	45	49
Partially unaligned length	637049	636256
# N's	769	37

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



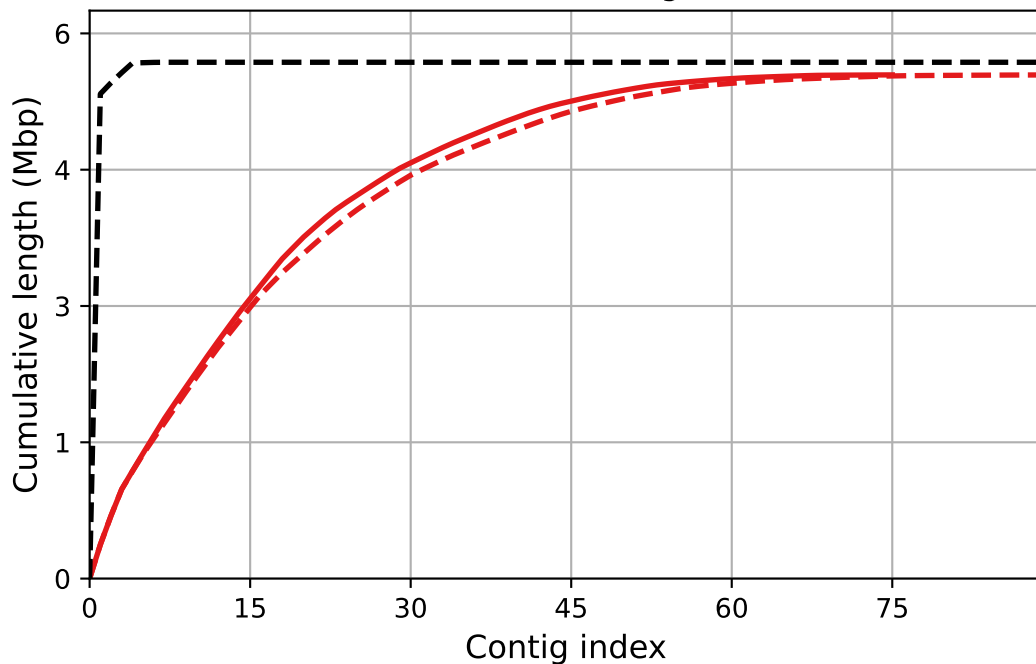
— unknowngenome-8\_fa      - - - unknowngenome-8\_fa\_broken

# NGx



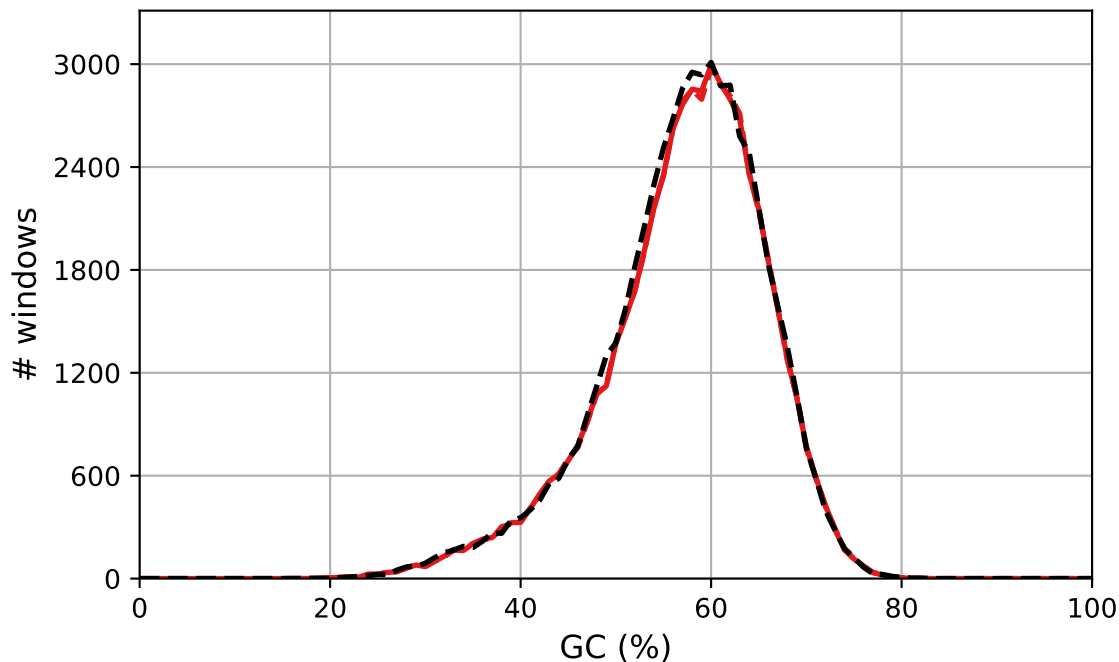
unknowngenome-8\_fa      unknowngenome-8\_fa\_broken

Cumulative length



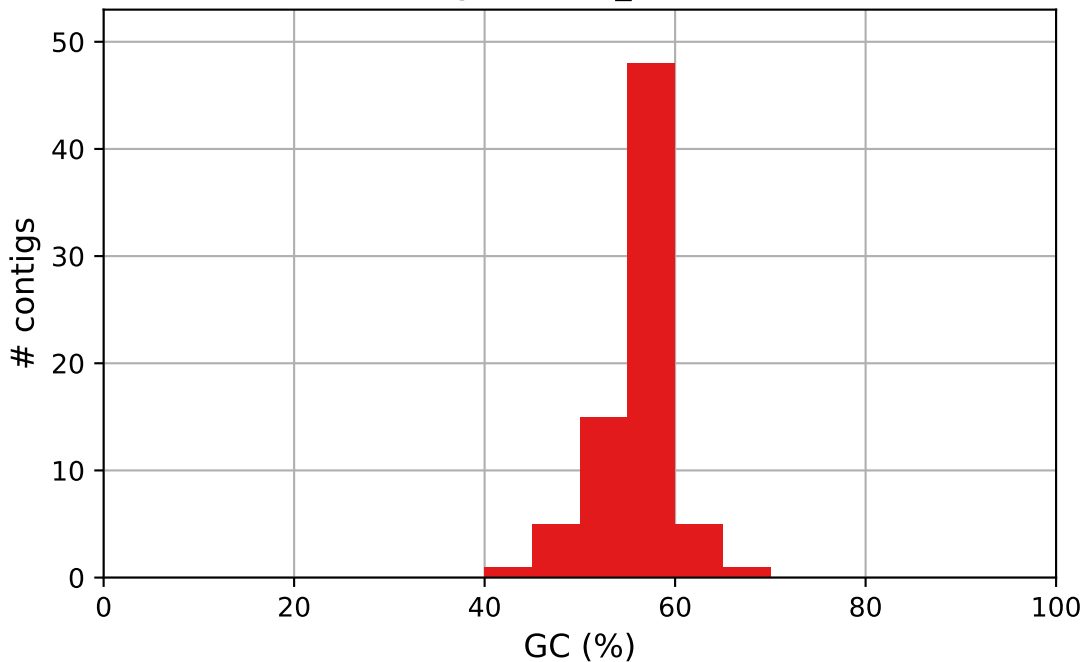
unknowngenome-8\_fa    unknowngenome-8\_fa\_broken    Reference

GC content



unknowngenome-8\_fa    unknowngenome-8\_fa\_broken    Reference

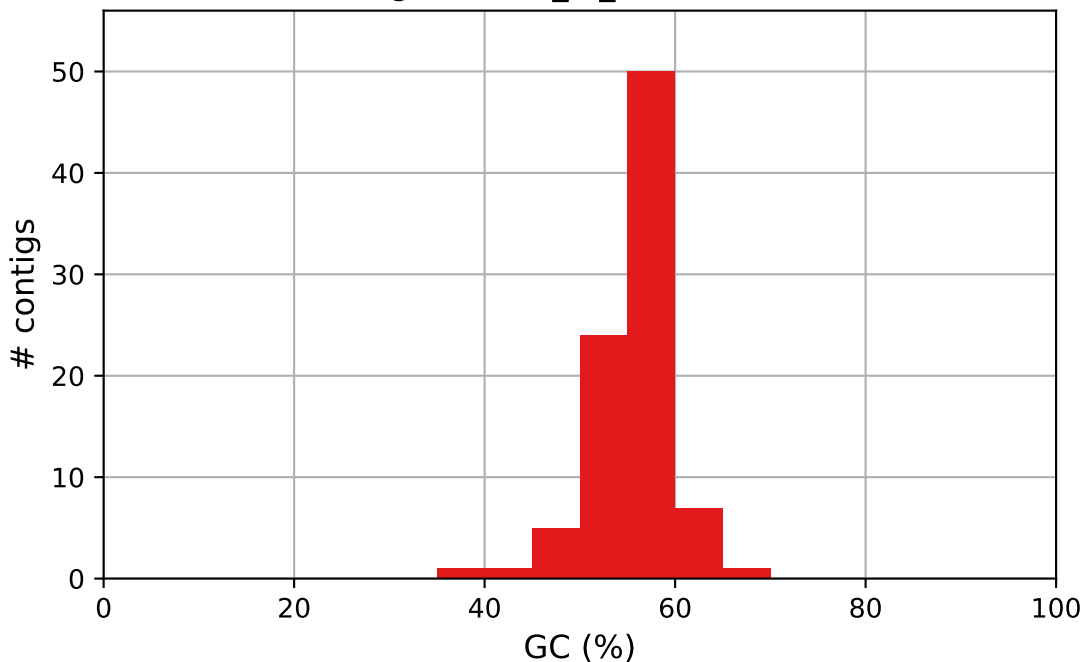
unknowngenome-8\_fa GC content



unknowngenome-8\_fa

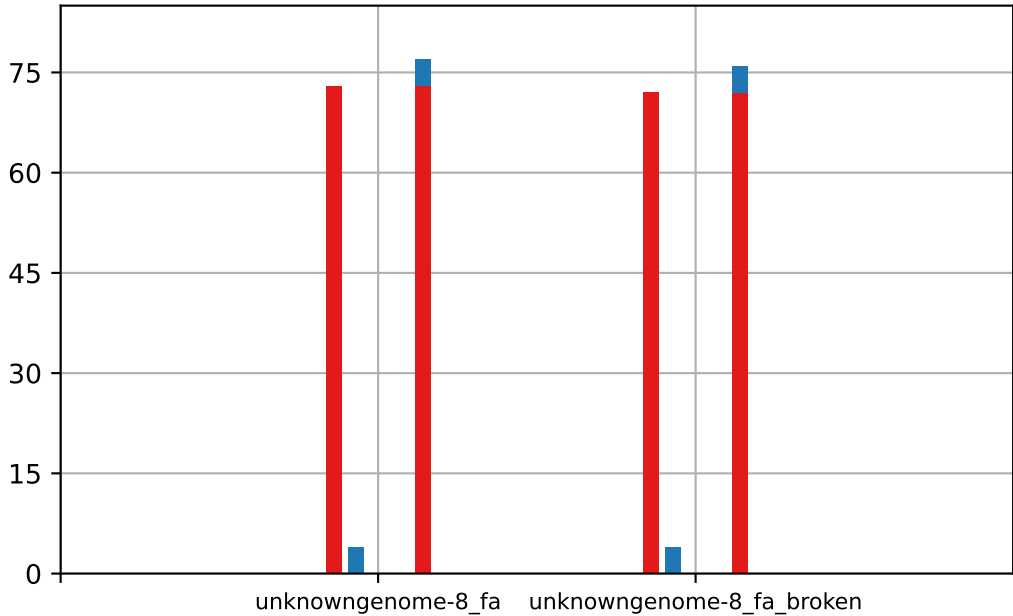


unknowngenome-8\_fa\_broken GC content



unknowngenome-8\_fa\_broken

## Misassemblies

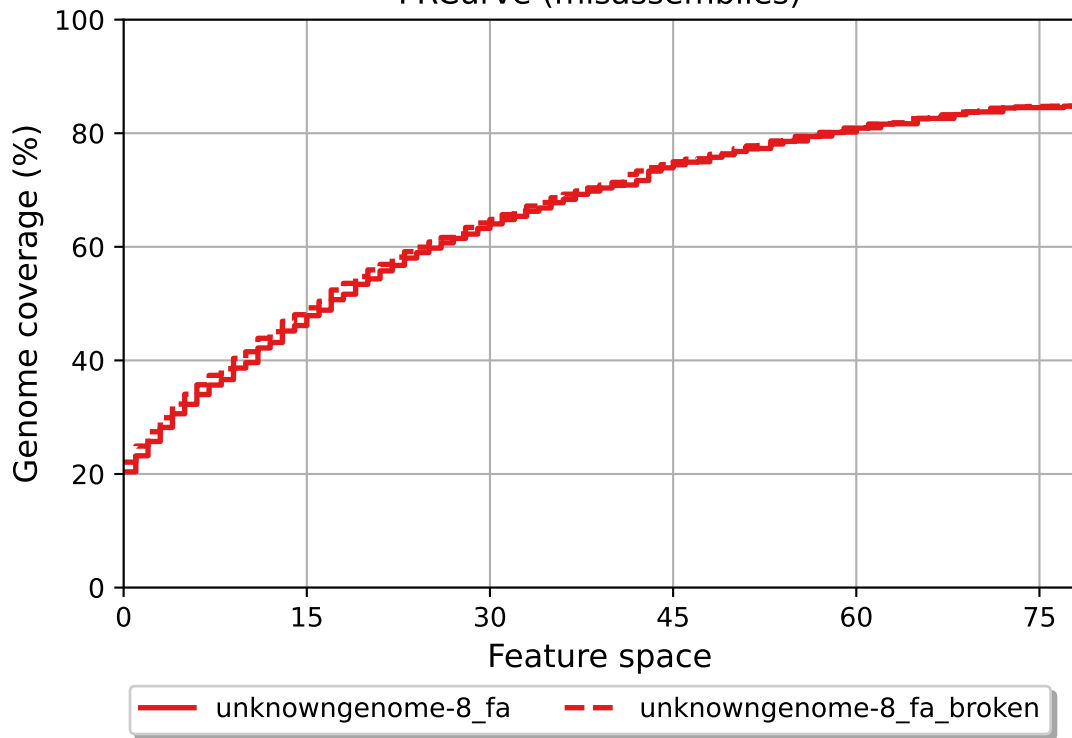


# relocations

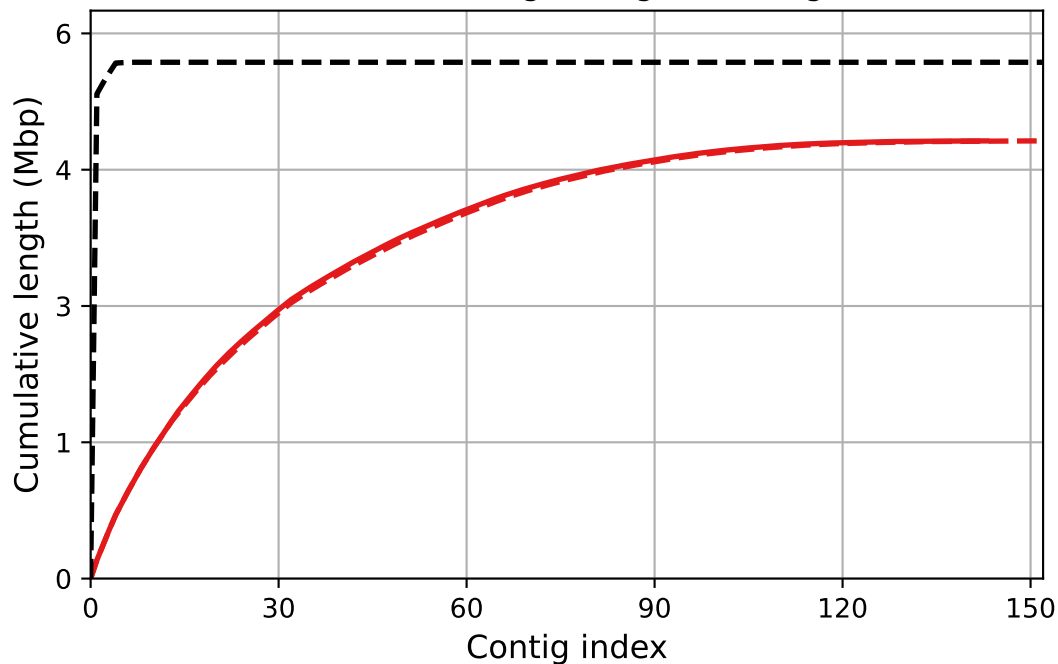


# translocations

FRCurve (misassemblies)

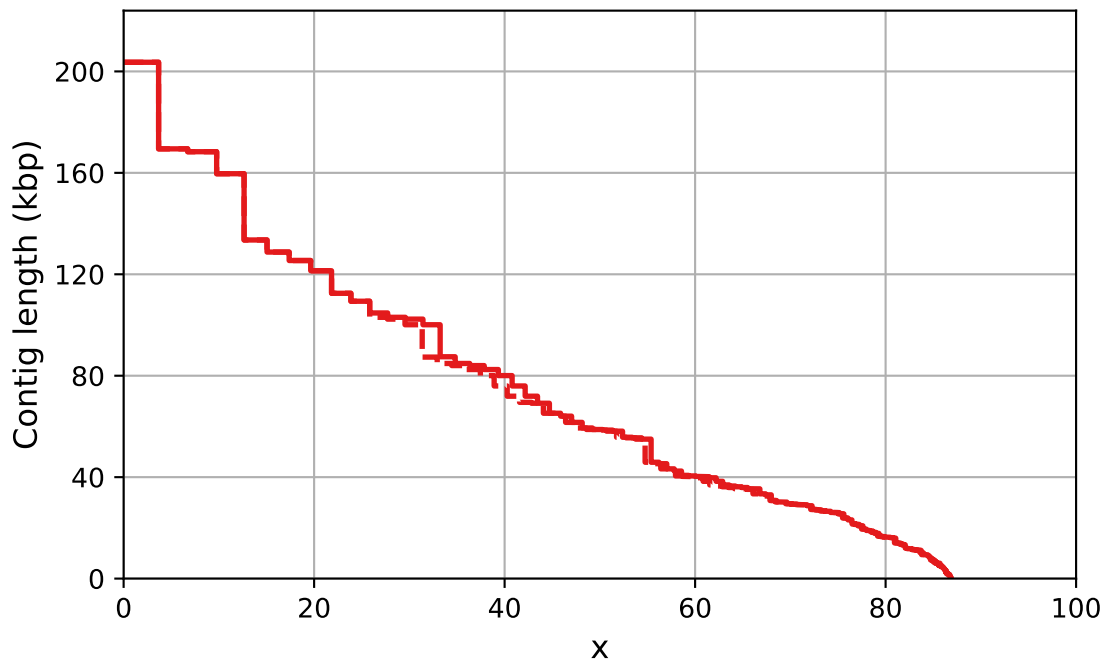


Cumulative length (aligned contigs)



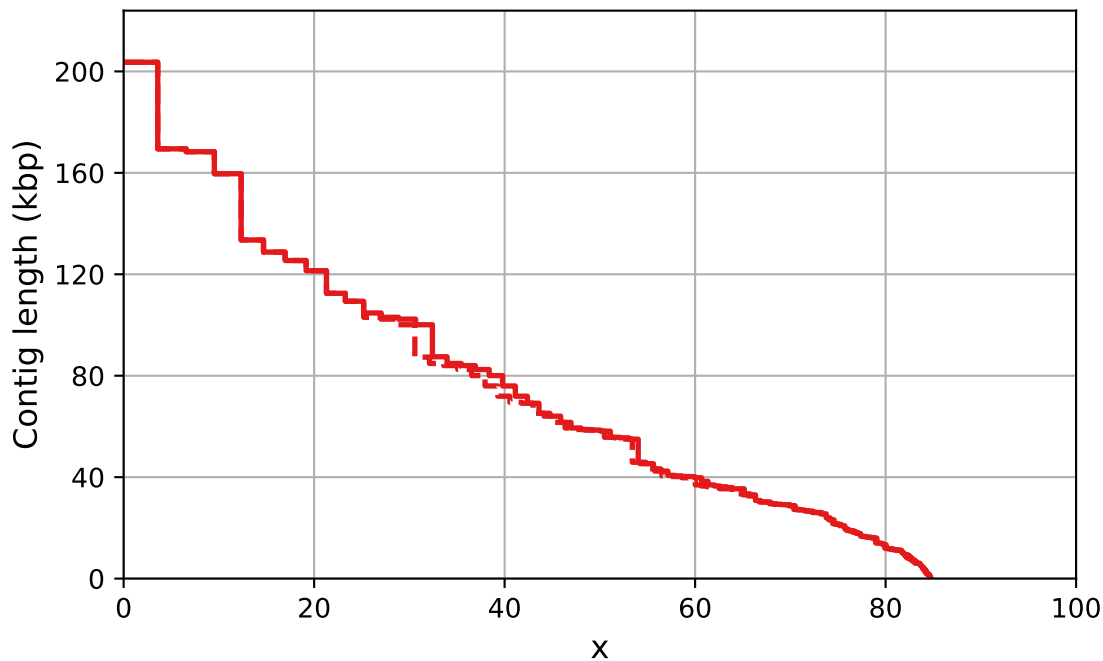
unknowngenome-8\_fa    unknowngenome-8\_fa\_broken    Reference

NAx



— unknowngenome-8\_fa      - - - unknowngenome-8\_fa\_broken

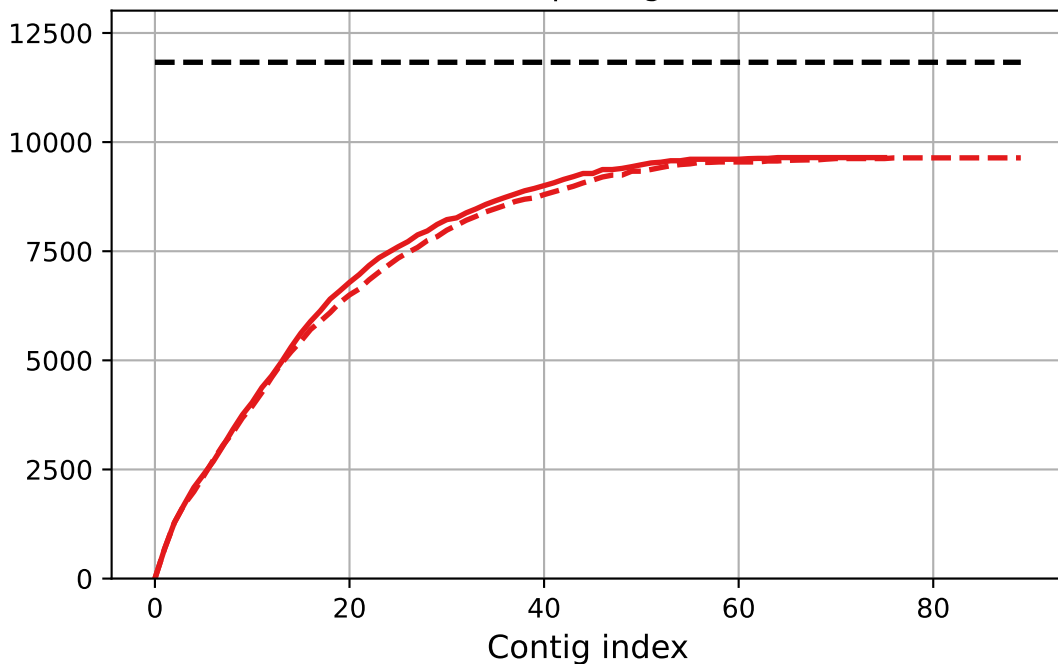
# NGAx



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Cumulative # complete genomic features

Cumulative # complete genomic features

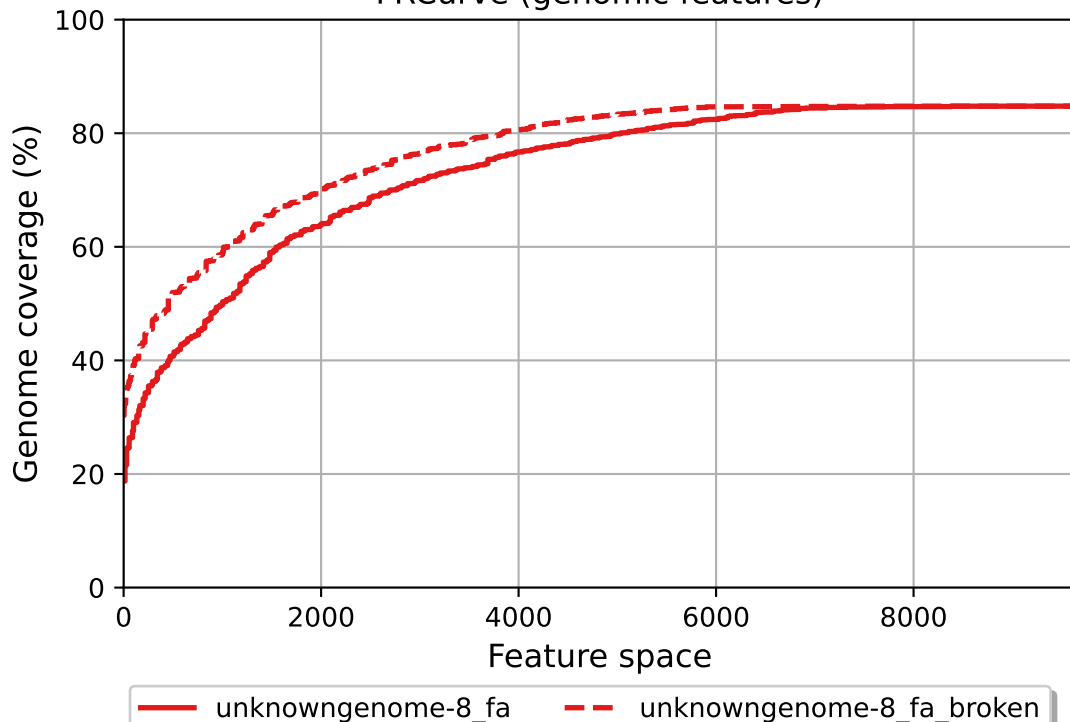


unknowngenome-8\_fa

unknowngenome-8\_fa\_broken

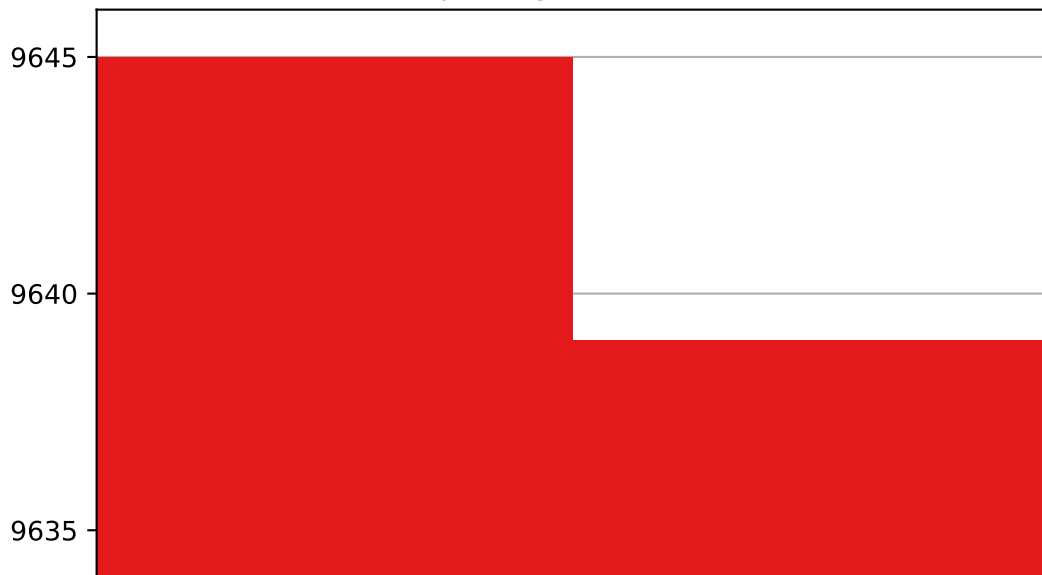
Reference

FRCurve (genomic features)





# # complete genomic features

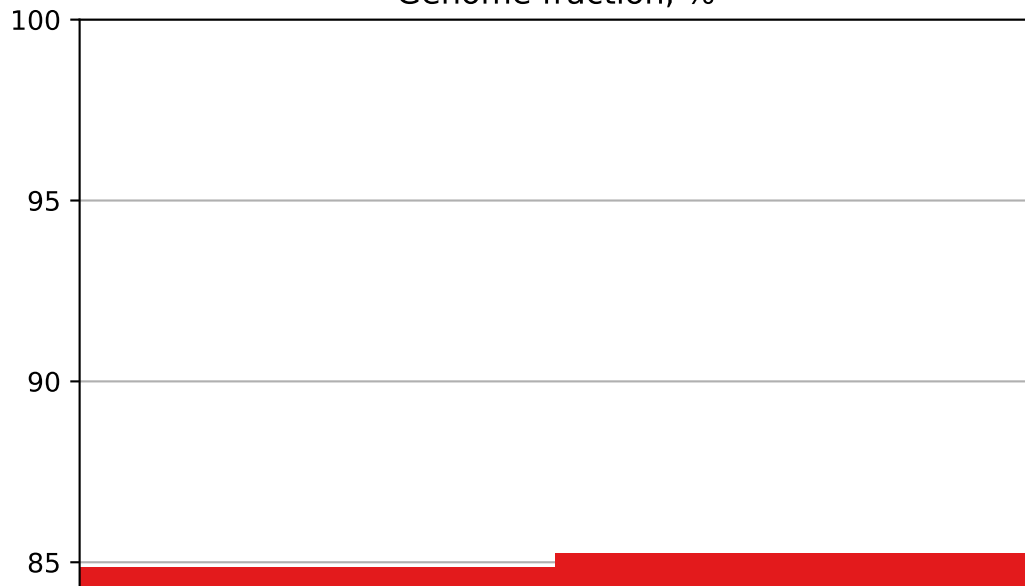


unknowngenome-8\_fa



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Genome fraction, %



unknowngenome-8\_fa



unknowngenome-8\_fa\_broken