

Report

	SuziBlue_Hifiasm.bp.p_ctg
# contigs (>= 0 bp)	4426
# contigs (>= 1000 bp)	4426
# contigs (>= 5000 bp)	4426
# contigs (>= 10000 bp)	4426
# contigs (>= 25000 bp)	4357
# contigs (>= 50000 bp)	3887
Total length (>= 0 bp)	1404759771
Total length (>= 1000 bp)	1404759771
Total length (>= 5000 bp)	1404759771
Total length (>= 10000 bp)	1404759771
Total length (>= 25000 bp)	1403318536
Total length (>= 50000 bp)	1385252742
# contigs	4426
Largest contig	10539941
Total length	1404759771
Reference length	1679081592
GC (%)	38.48
Reference GC (%)	38.48
N50	549838
NG50	438770
N90	144295
NG90	-
auN	959708.9
auNG	802915.4
L50	672
LG50	951
L90	2569
LG90	-
# misassemblies	158583
# misassembled contigs	3956
Misassembled contigs length	1341707239
# local misassemblies	56058
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	243
# unaligned contigs	0 + 3886 part
Unaligned length	195071578
Genome fraction (%)	50.883
Duplication ratio	1.400
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1128.64
# indels per 100 kbp	195.73
Largest alignment	799589
Total aligned length	1180958273
NA50	14387
NGA50	9387
NA90	-
NGA90	-
auNA	47698.3
auNGA	39905.5
LA50	18644
LGA50	30433
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

	SuziBlue_Hifiasm.bp.p_ctg
# misassemblies	158583
# contig misassemblies	158583
# c. relocations	21054
# c. translocations	137167
# c. inversions	362
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3956
Misassembled contigs length	1341707239
# local misassemblies	56058
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	243
# mismatches	13328733
# indels	2311460
# indels (<= 5 bp)	1777184
# indels (> 5 bp)	534276
Indels length	18496053

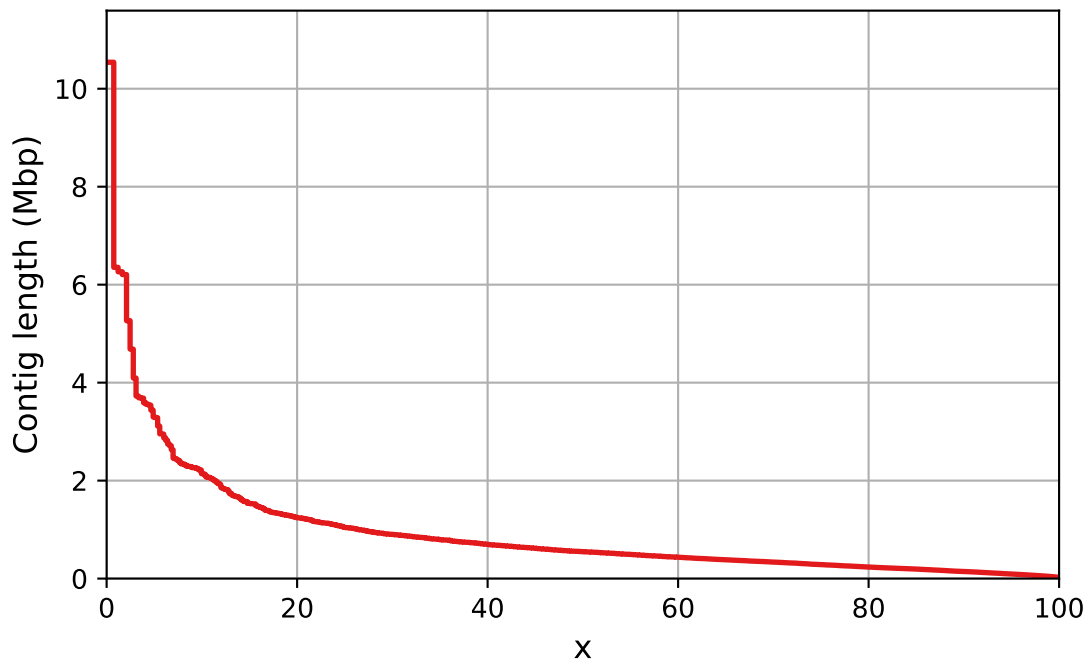
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	SuziBlue_Hifiasm.bp.p_ctg
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3886
Partially unaligned length	195071578
# N's	0

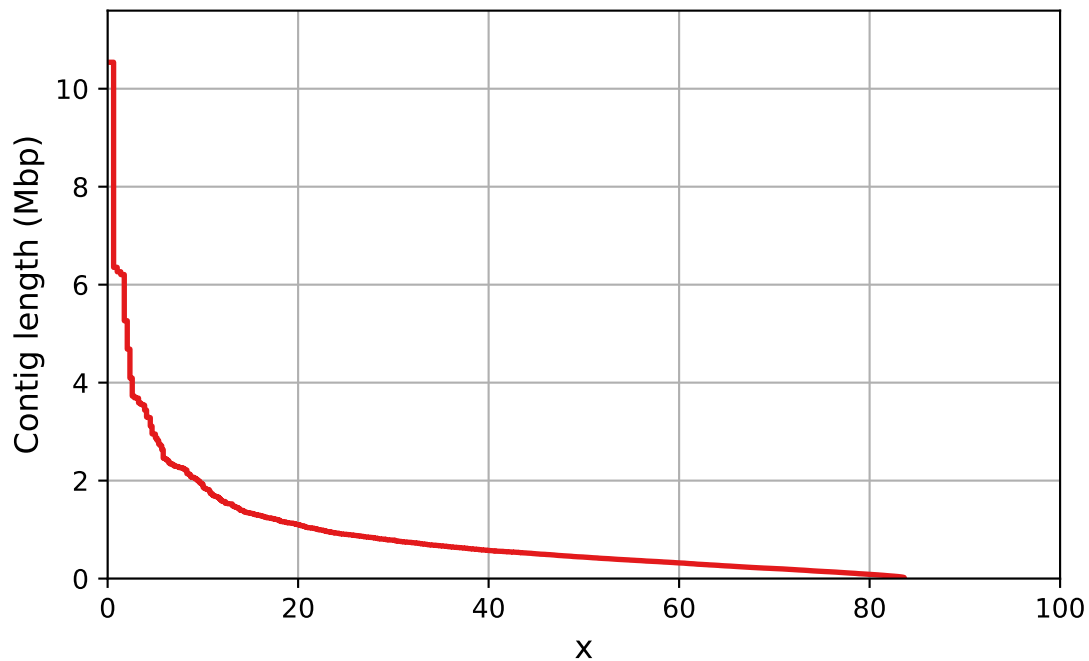
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



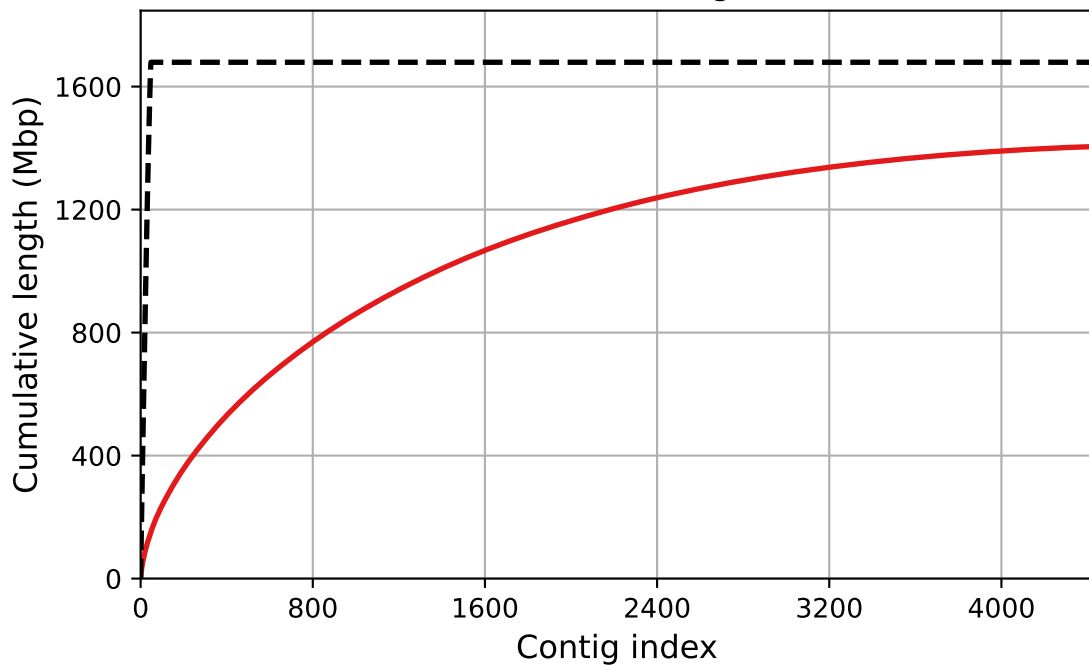
SuziBlue\_Hifiasm.bp.p\_ctg

NGx



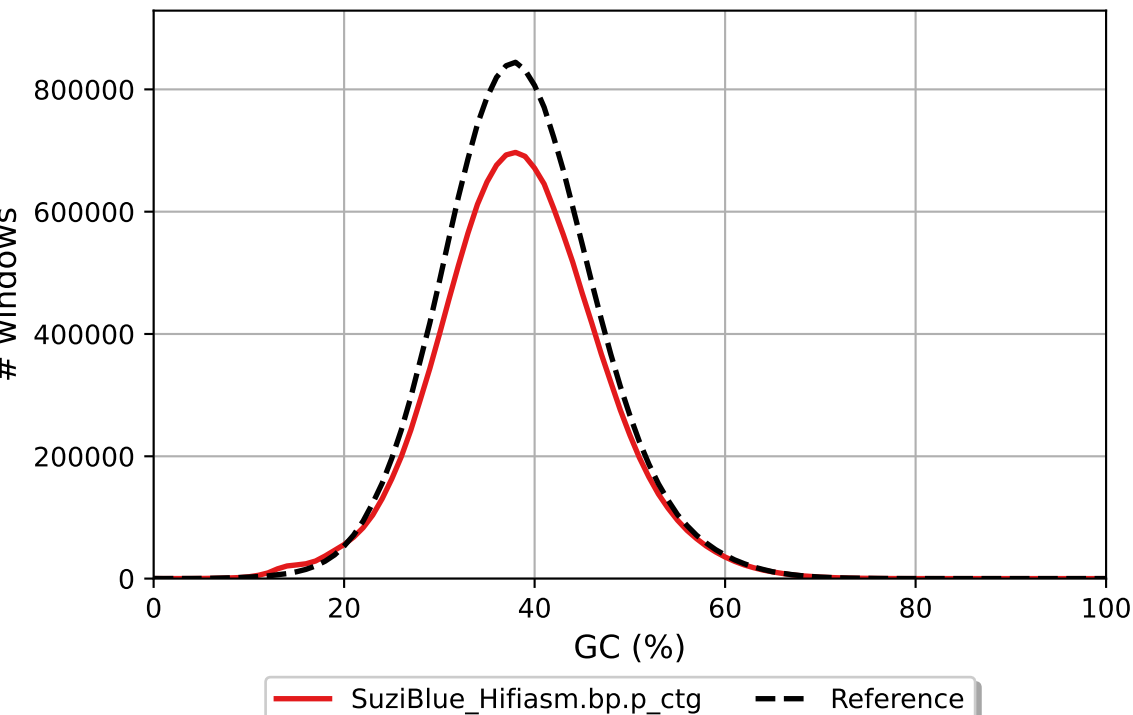
SuziBlue\_Hifiasm.bp.p\_ctg

Cumulative length

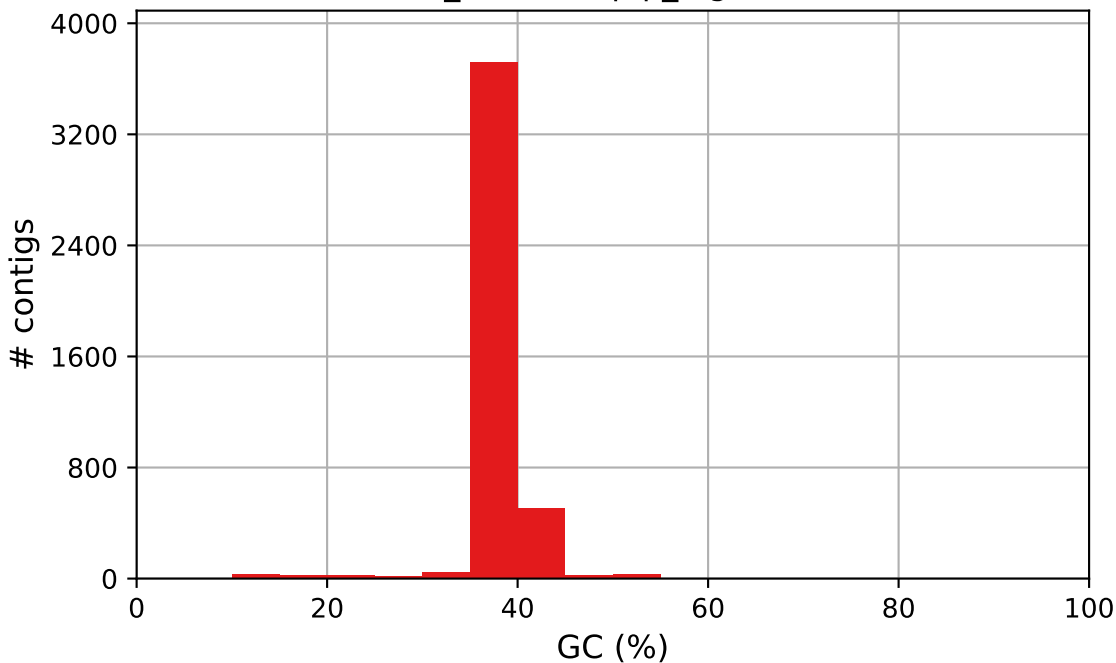


— SuziBlue\_Hifiasm.bp.p\_ctg    - - Reference

GC content



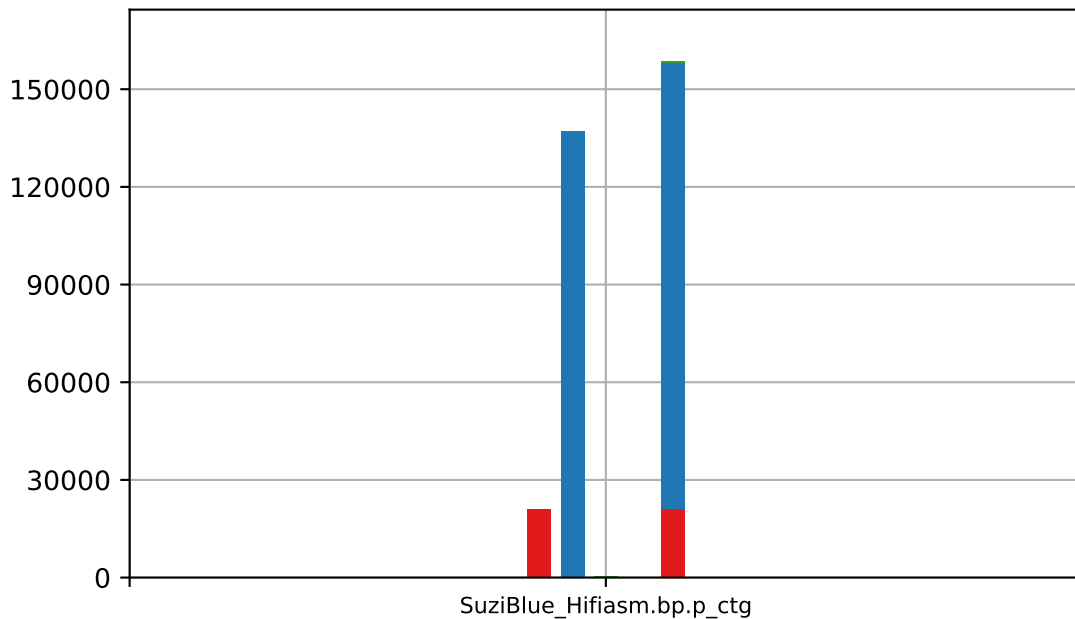
SuziBlue\_Hifi.asm.bp.p\_ctg GC content



SuziBlue\_Hifi.asm.bp.p\_ctg



## Misassemblies



# relocations

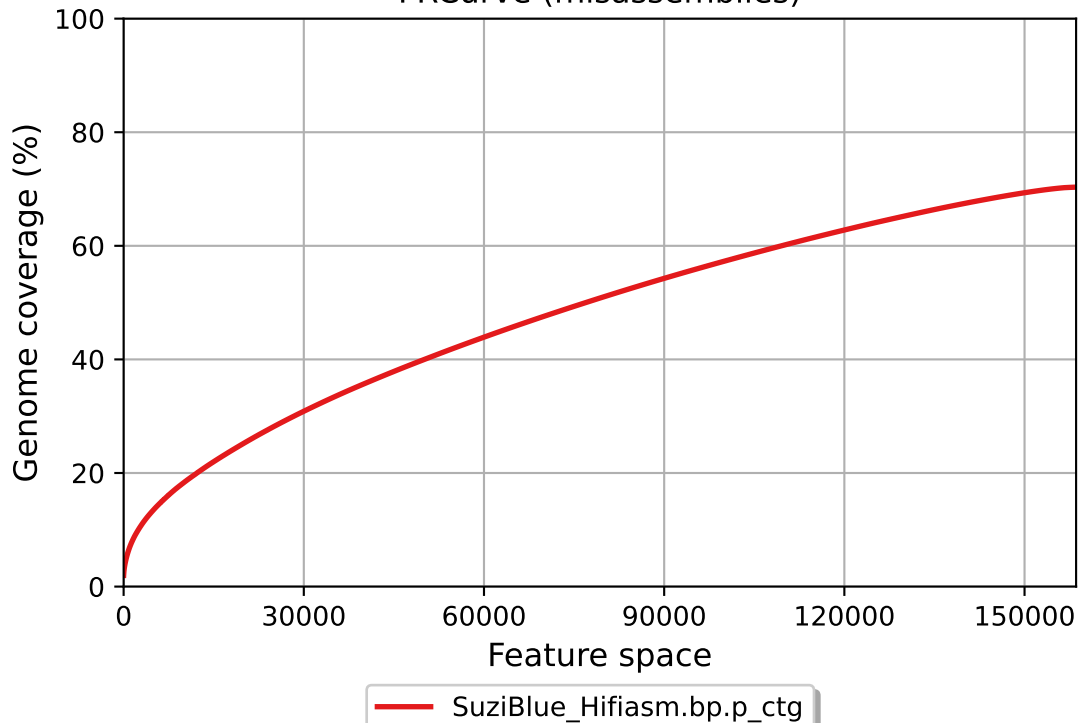


# translocations

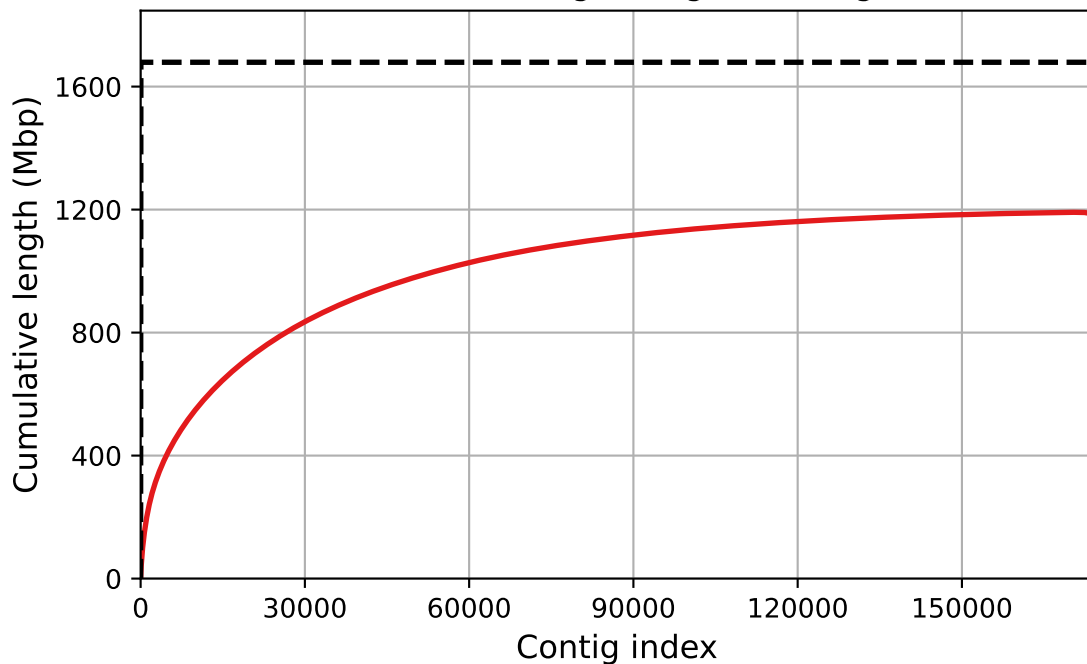


# inversions

FRCurve (misassemblies)

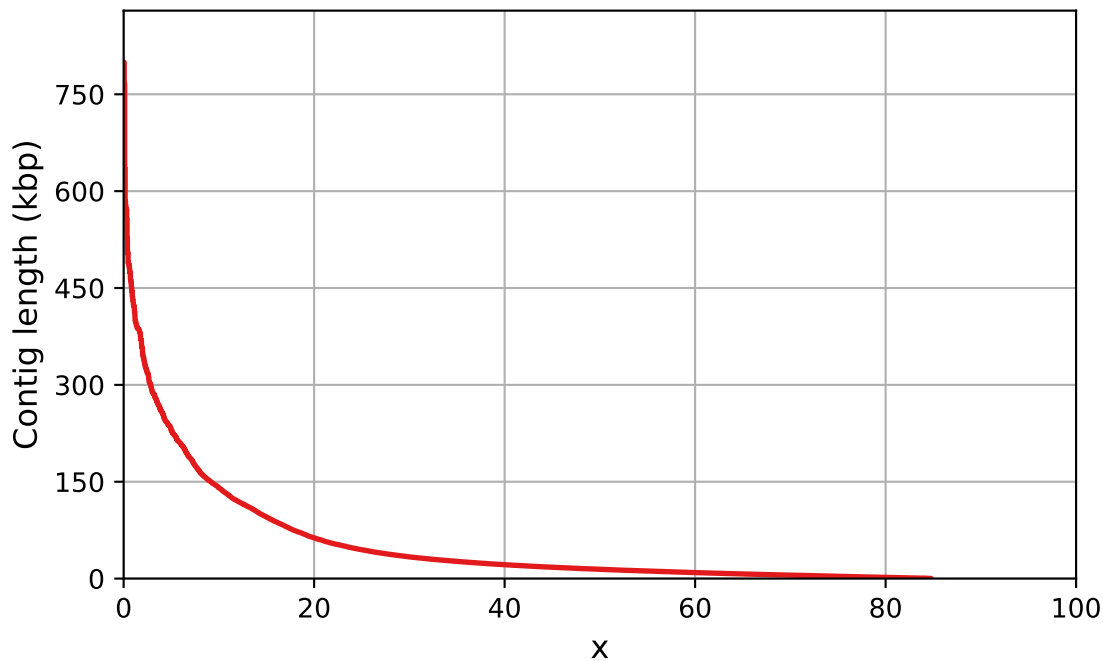


Cumulative length (aligned contigs)



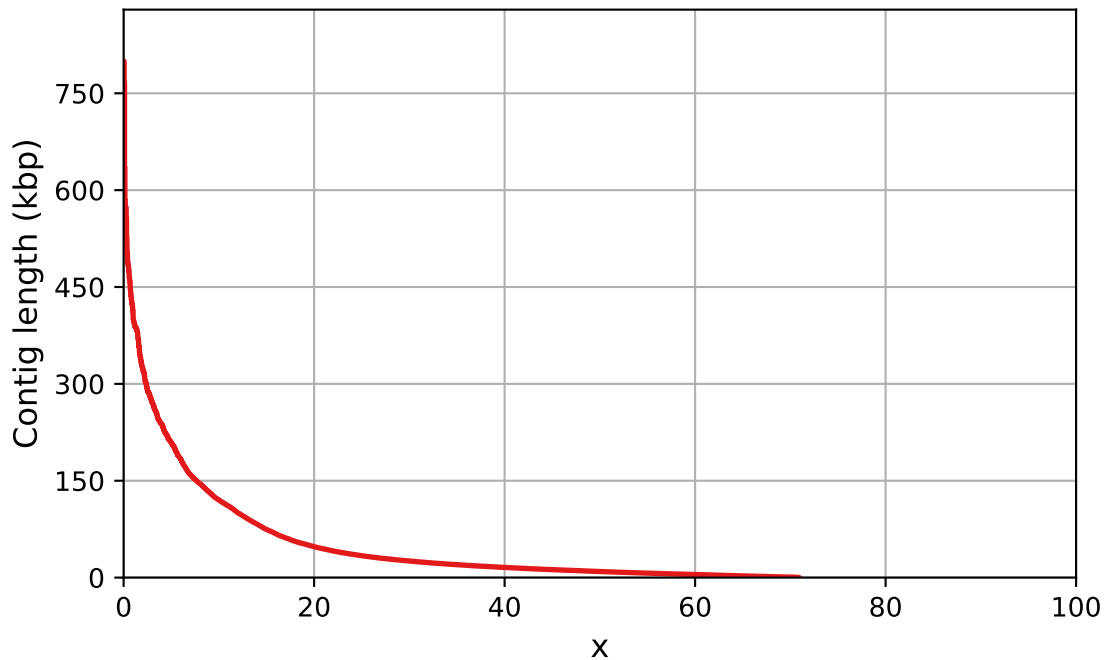
— SuziBlue\_Hifiasm.bp.p\_ctg      - - Reference

NAx



SuziBlue\_Hifiasm.bp.p\_ctg

## NGAx



— SuziBlue\_Hifiasm.bp.p\_ctg