

	Report
	SuziBlue_Hifiasm.contigs.50kb
# contigs (>= 0 bp)	3887
# contigs (>= 1000 bp)	3887
# contigs (>= 5000 bp)	3887
# contigs (>= 10000 bp)	3887
# contigs (>= 25000 bp)	3887
# contigs (>= 50000 bp)	3887
Total length (>= 0 bp)	1385252742
Total length (>= 1000 bp)	1385252742
Total length (>= 5000 bp)	1385252742
Total length (>= 10000 bp)	1385252742
Total length (>= 25000 bp)	1385252742
Total length (>= 50000 bp)	1385252742
# contigs	3887
Largest contig	10539941
Total length	1385252742
Reference length	1679081592
GC (%)	38.50
Reference GC (%)	38.48
N50	556202
NG50	438770
N90	154681
NG90	-
auN	972684.1
auNG	802470.4
L50	654
LG50	951
L90	2452
LG90	-
# misassemblies	155334
# misassembled contigs	3583
Misassembled contigs length	1327996541
# local misassemblies	54999
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	156
# unaligned contigs	0 + 3489 part
Unaligned length	190568714
Genome fraction (%)	50.534
Duplication ratio	1.392
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1125.76
# indels per 100 kbp	195.20
Largest alignment	799589
Total aligned length	1166163033
NA50	14565
NGA50	9143
NA90	-
NGA90	-
auNA	48210.4
auNGA	39773.9
LA50	18152
LGA50	30885
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.contigs.50kb
# misassemblies	155334
# contig misassemblies	155334
# c. relocations	20462
# c. translocations	134515
# c. inversions	357
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3583
Misassembled contigs length	1327996541
# local misassemblies	54999
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	156
# mismatches	13128161
# indels	2276333
# indels (<= 5 bp)	1749297
# indels (> 5 bp)	527036
Indels length	18205040

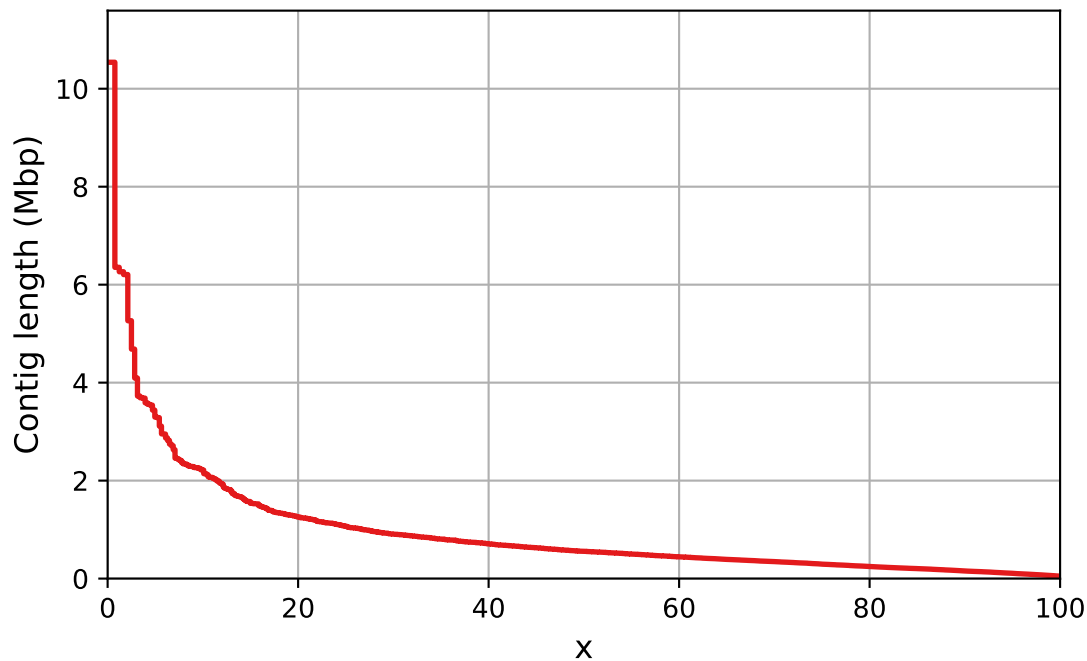
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SuziBlue_Hifiasm.contigs.50kb
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3489
Partially unaligned length	190568714
# N's	0

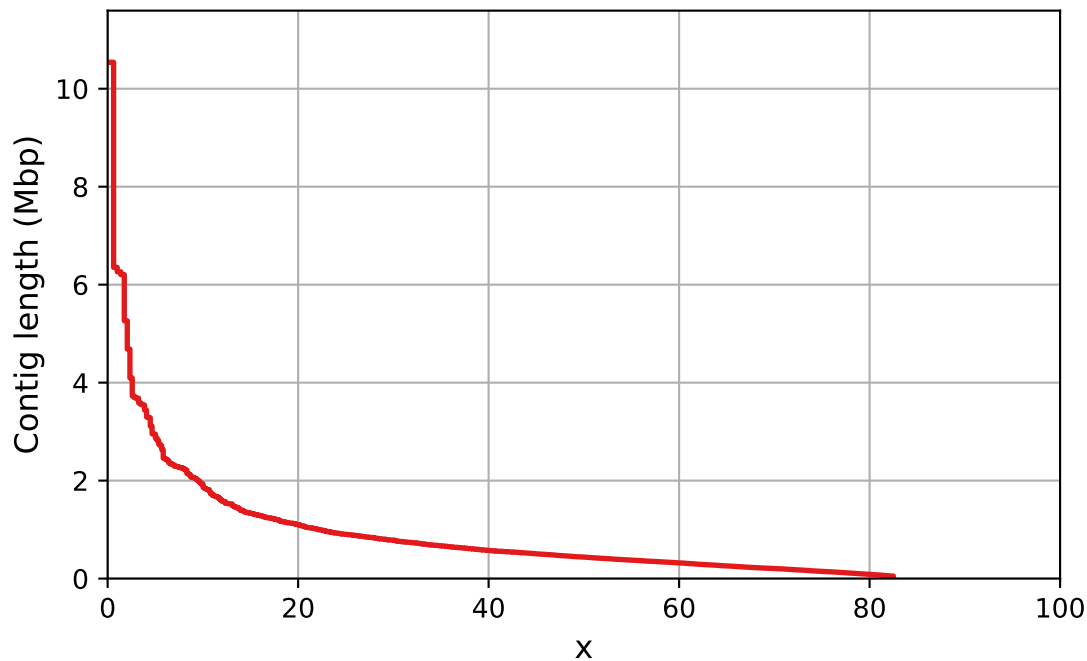
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

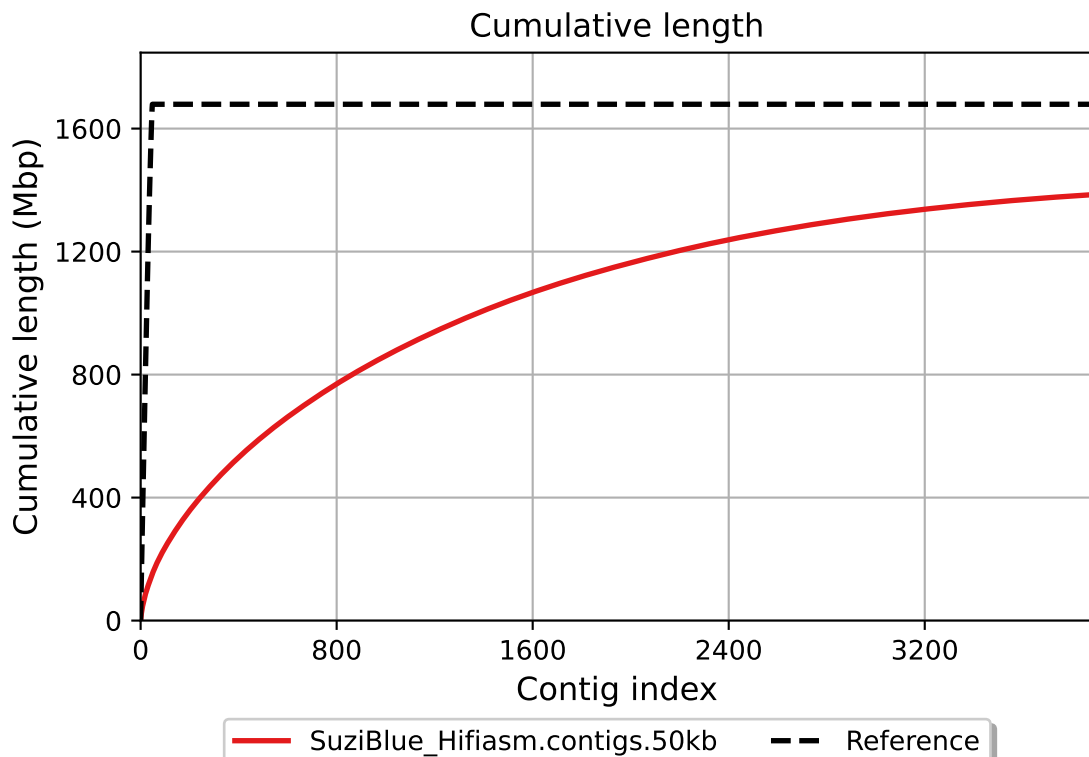


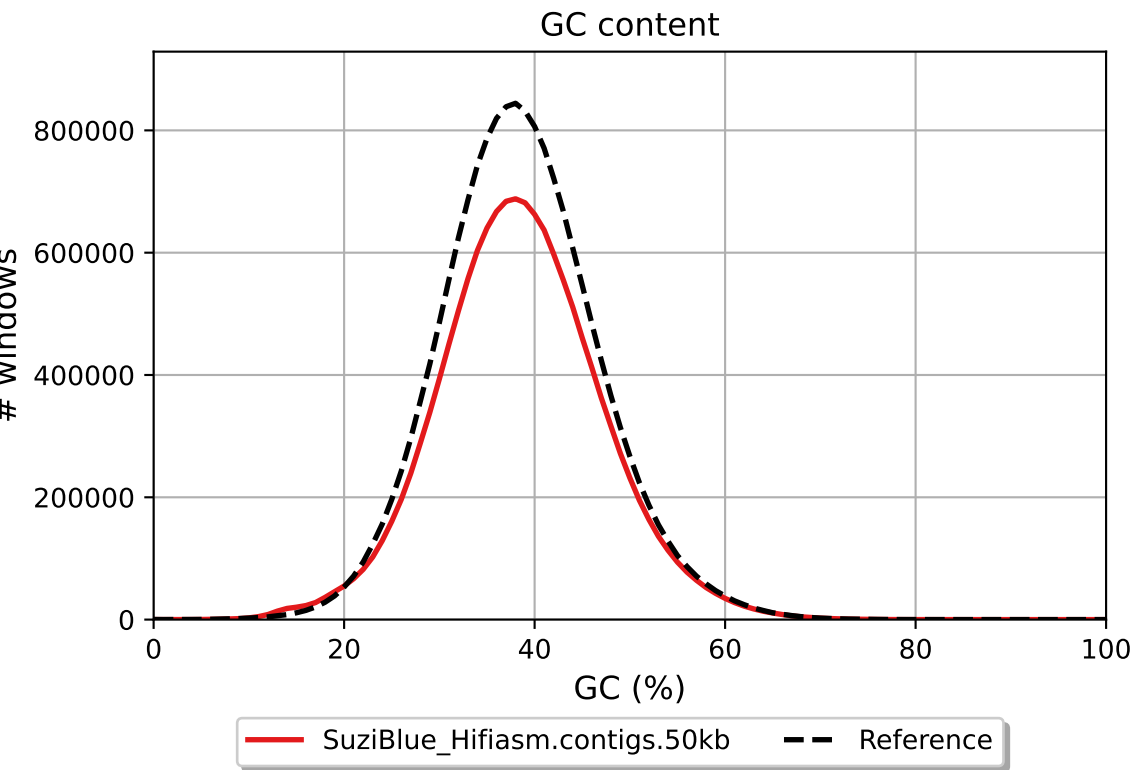
SuziBlue_Hifiasm.contigs.50kb

NGx

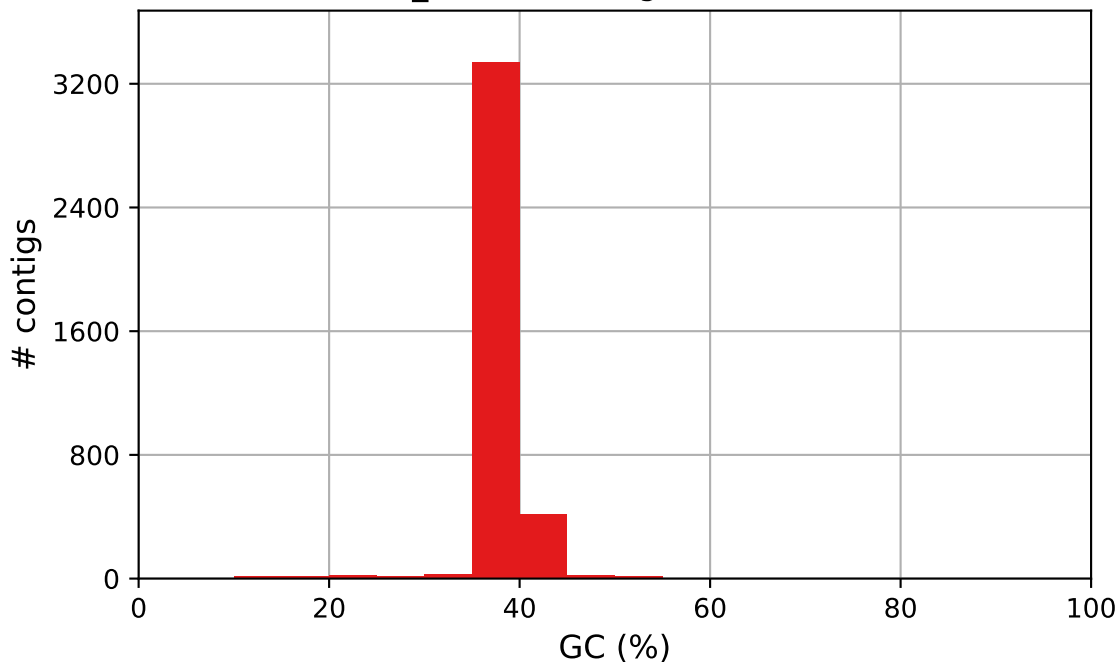


— SuziBlue_Hifiasm.contigs.50kb



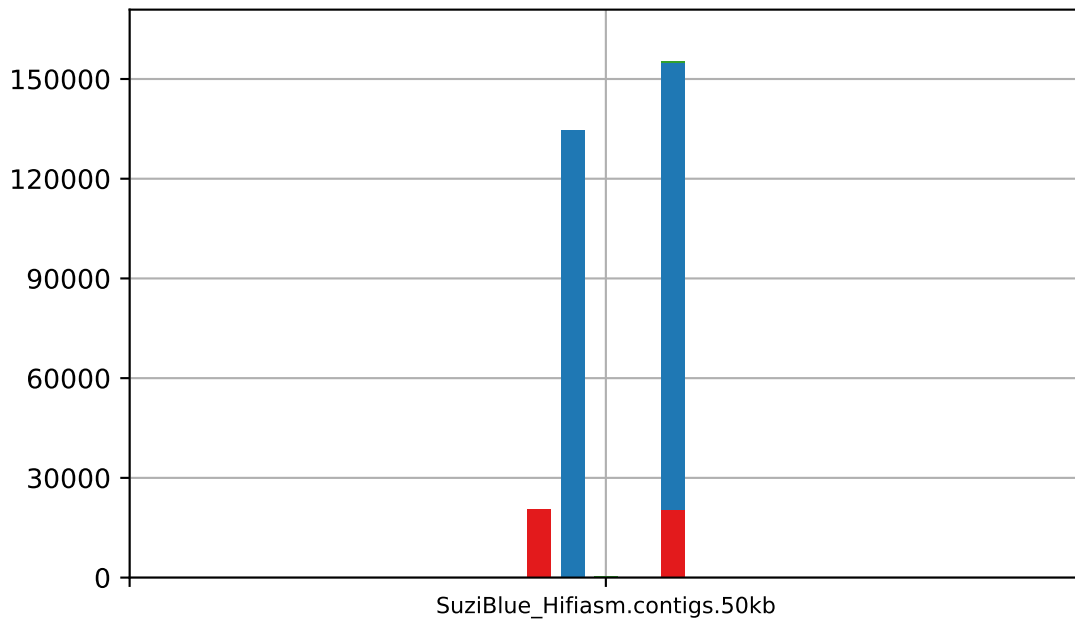


SuziBlue_Hifiasm.contigs.50kb GC content



SuziBlue_Hifiasm.contigs.50kb

Misassemblies



relocations

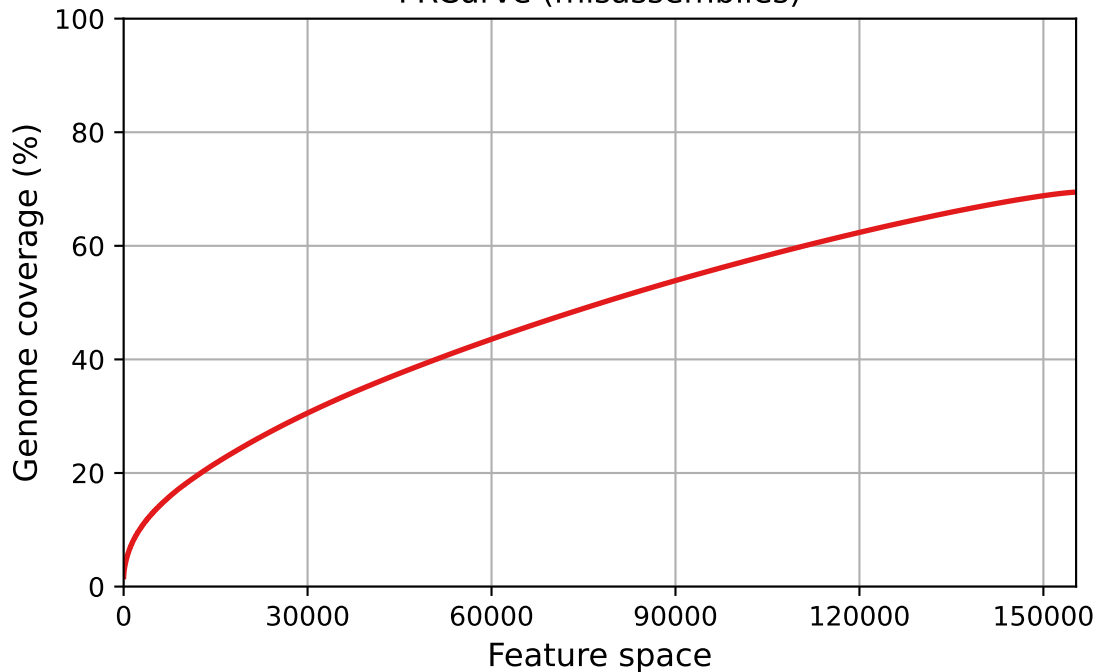


translocations



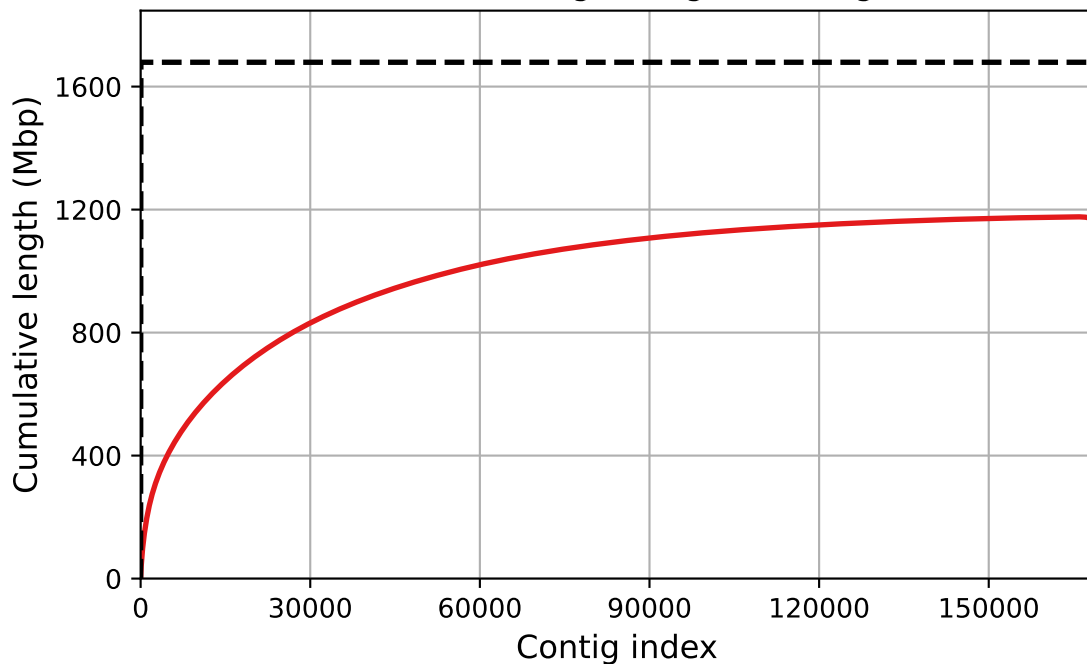
inversions

FRCurve (misassemblies)



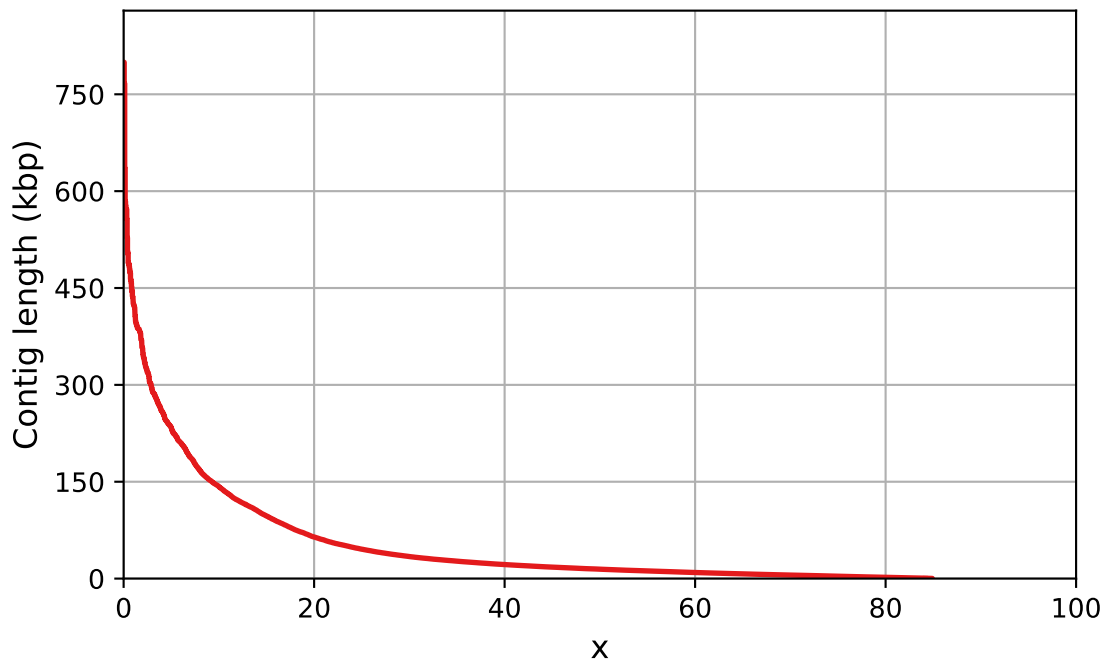
SuziBlue_Hifiasm.contigs.50kb

Cumulative length (aligned contigs)



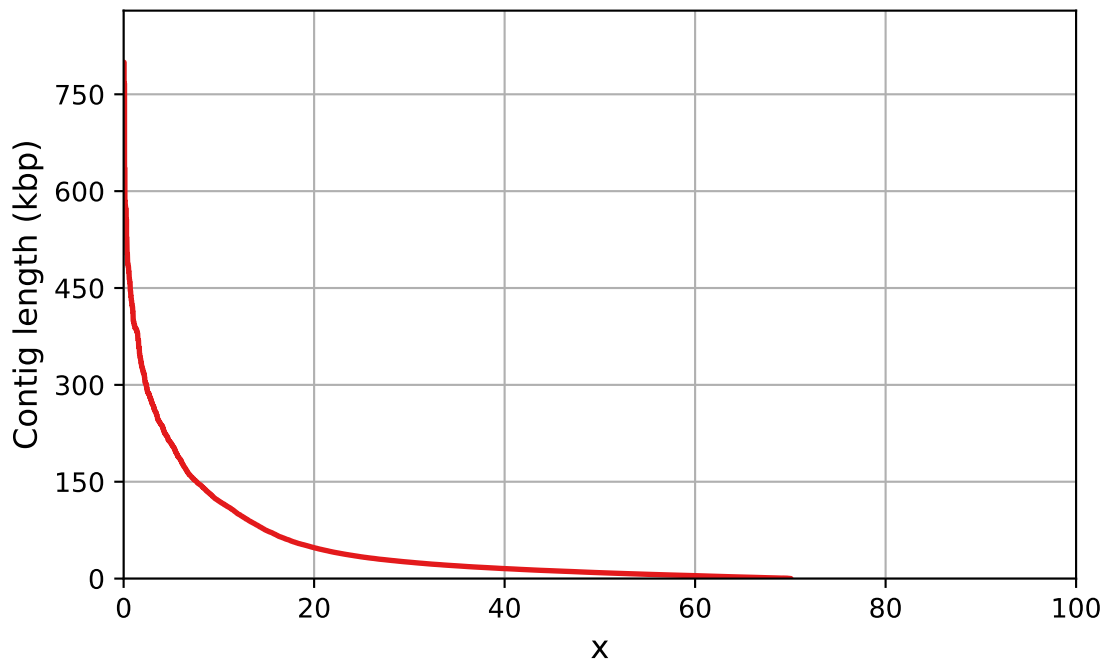
SuziBlue_Hifiasm.contigs.50kb Reference

NAx



SuziBlue_Hifiasm.contigs.50kb

NGAx



— SuziBlue_Hifiasm.contigs.50kb