Report

	SuziBlue_Hifiasm.contigs.50kb
# contigs (>= 0 bp)	361
# contigs (>= 1000 bp)	361
# contigs (>= 5000 bp)	361
# contigs (>= 10000 bp)	361
# contigs (>= 25000 bp)	361
# contigs (>= 50000 bp)	361
Total length (>= 0 bp)	1179419622
Total length (>= 1000 bp)	1179419622
Total length (>= 5000 bp)	1179419622
Total length (>= 10000 bp)	1179419622
Total length (>= 25000 bp)	1179419622
Total length (>= 50000 bp)	1179419622
# contigs	361
Largest contig	43997265
Total length	1179419622
Reference length	1679081592
GC (%)	38.46
Reference GC (%)	38.48
N50	21732491
NG50	13397844
N90	8353870
NG90	-
auN	22379881.8
auNG	15720065.0
L50	20
LG50	35
L90	55
LG90	-
# misassemblies	140856
# misassembled contigs	262
Misassembled contigs length	1171645992
# local misassemblies	48307
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	97
# unaligned contigs	0 + 358 part
Unaligned length	173656972
Genome fraction (%)	44.263
Duplication ratio	1.336
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1130.81
# indels per 100 kbp	192.93
Largest alignment	1026643
Total aligned length	980472418
NA50	14155
NGA50	4698
NA90	-
NGA90	-
auNA	60242.0
auNGA	42315.2
LA50	15445
LGA50	46063
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

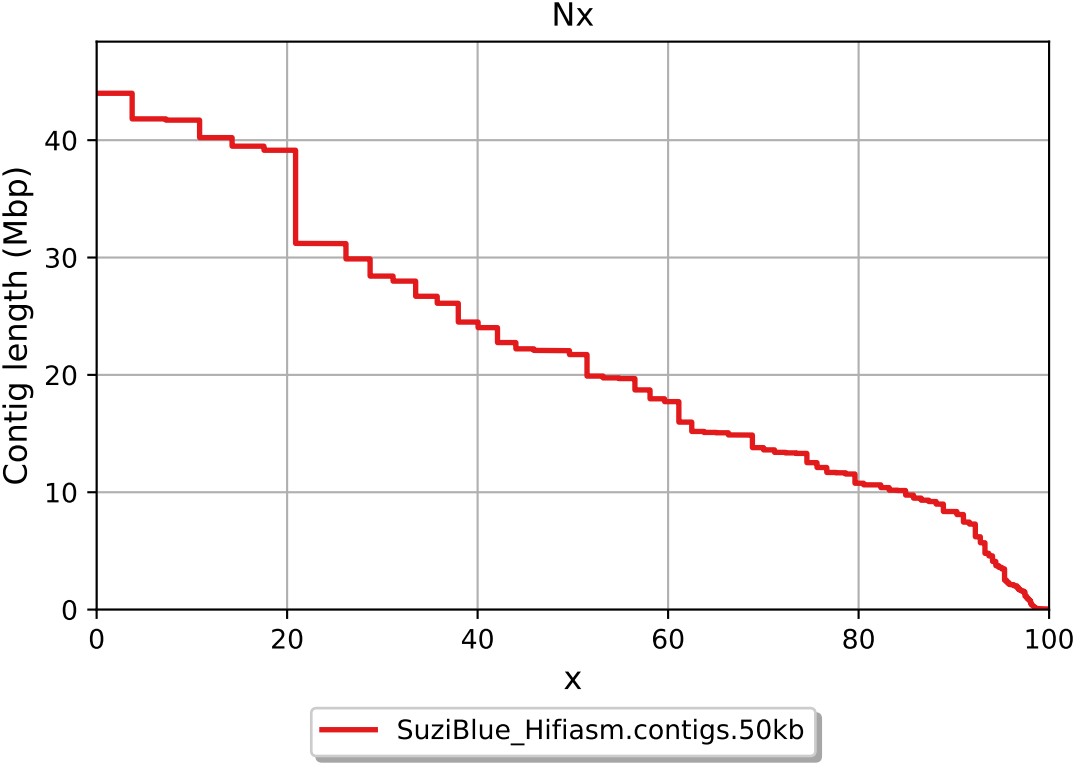
	SuziBlue_Hifiasm.contigs.50kb
# misassemblies	140856
# contig misassemblies	140856
# c. relocations	19911
# c. translocations	120609
# c. inversions	336
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	262
Misassembled contigs length	1171645992
# local misassemblies	48307
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	97
# mismatches	11087249
# indels	1891658
# indels (<= 5 bp)	1439431
# indels (> 5 bp)	452227
Indels length	15954559

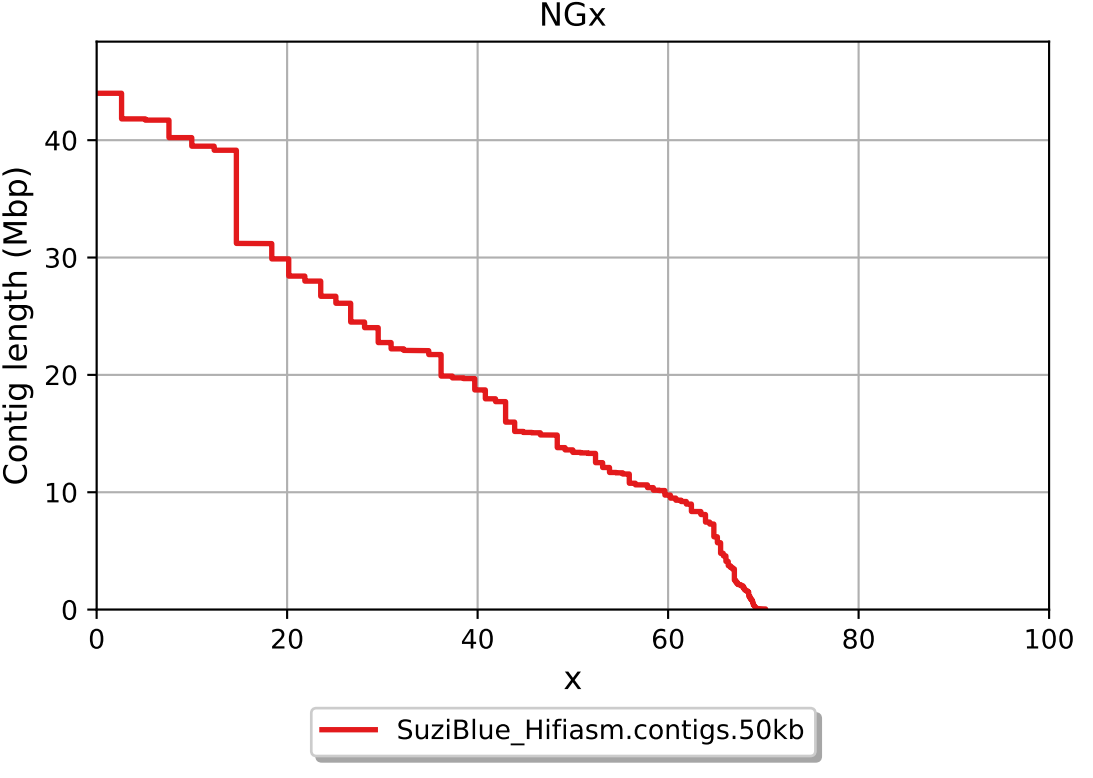
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

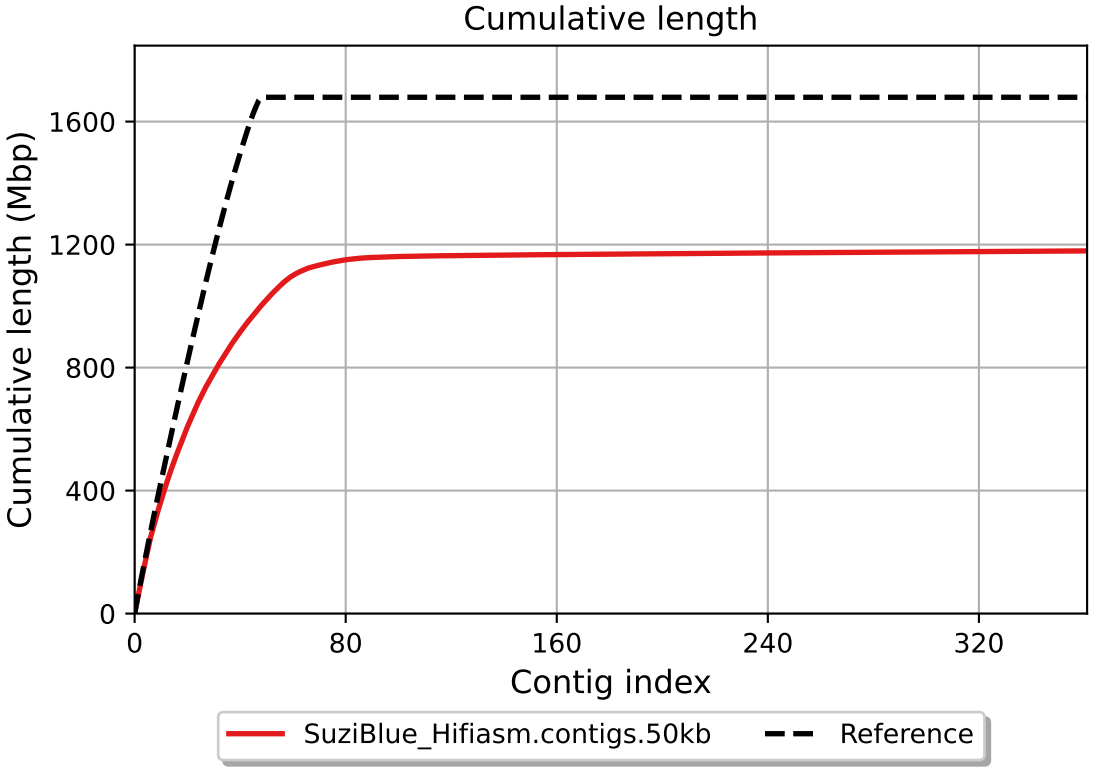
Unaligned report

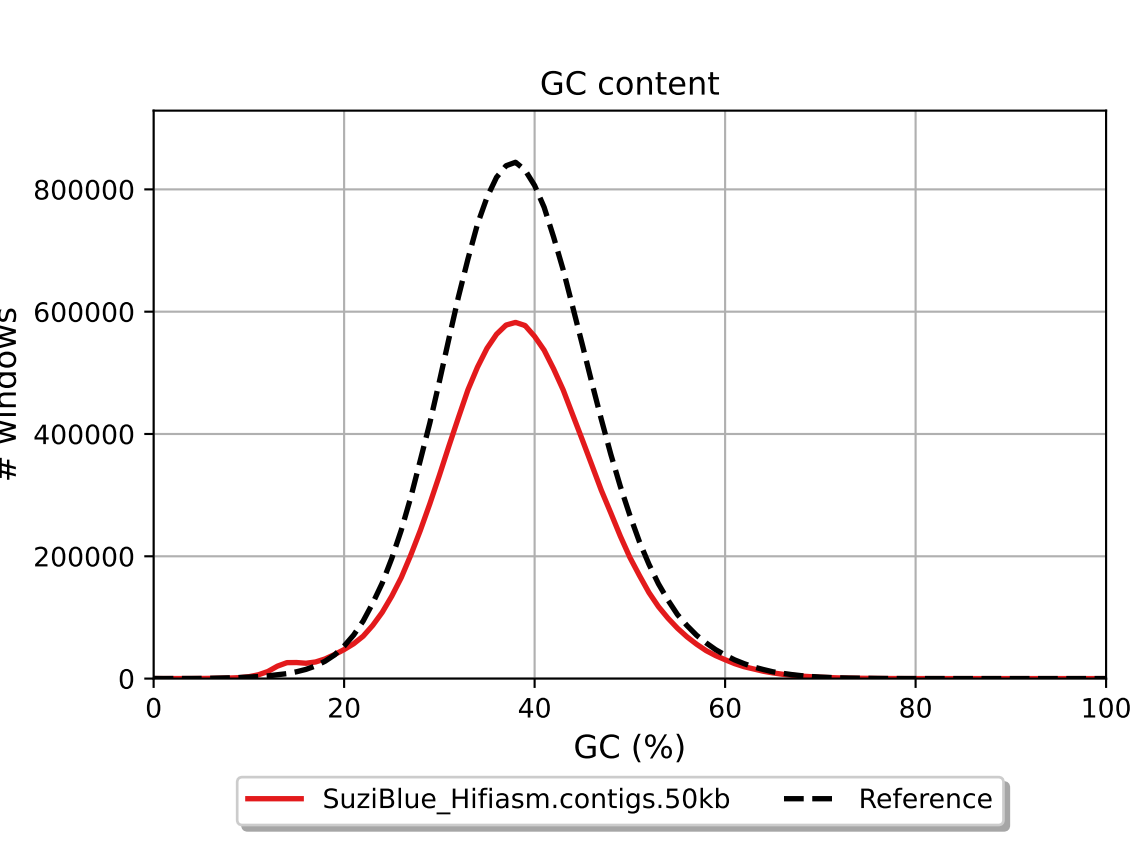
	SuziBlue_Hifiasm.contigs.50kb
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	358
Partially unaligned length	173656972
# N's	0

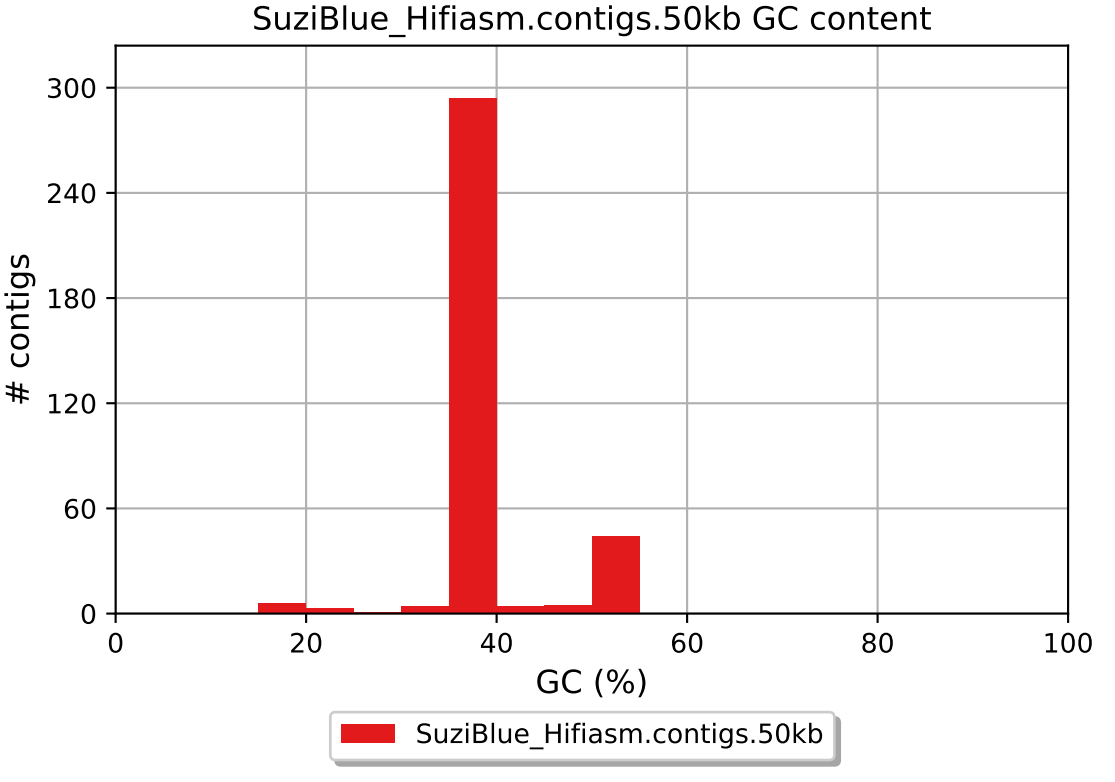
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

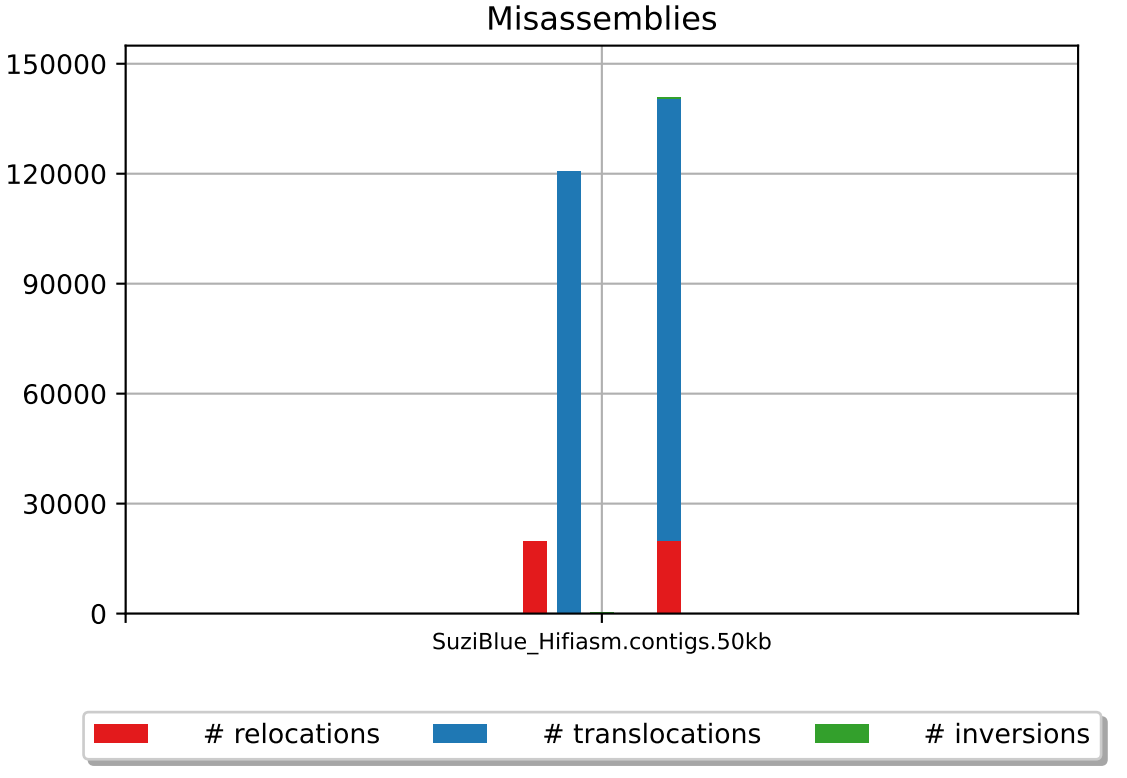

Nx
Contig length (Mbp)
0
10
20
30
40
0
20
40
60
80
100
x
SuziBlue_Hifiasm.contigs.50kb

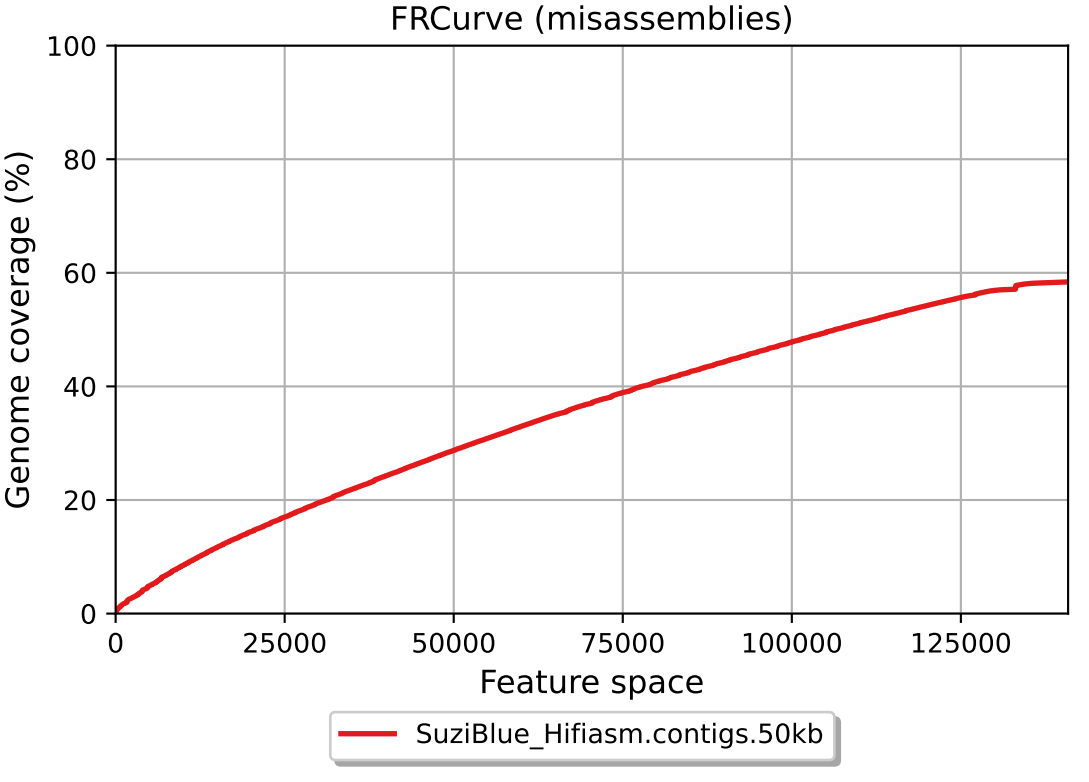

NGx
Contig length (Mbp)
0
10
20
30
40
0
20
40
60
80
100
x
SuziBlue_Hifiasm.contigs.50kb

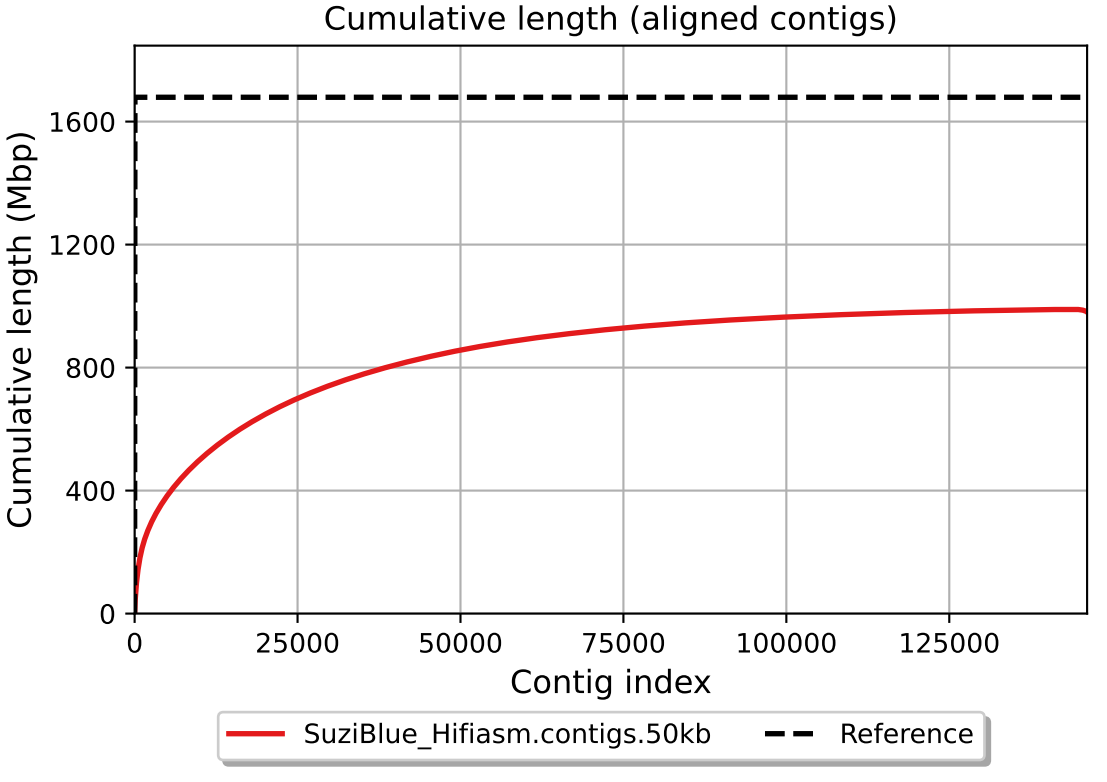

Cumulative length
Cumulative length (Mbp)
1600
1200
800
400
0
0
80
160
240
320
Contig index
SuziBlue_Hifiasm.contigs.50kb
Reference

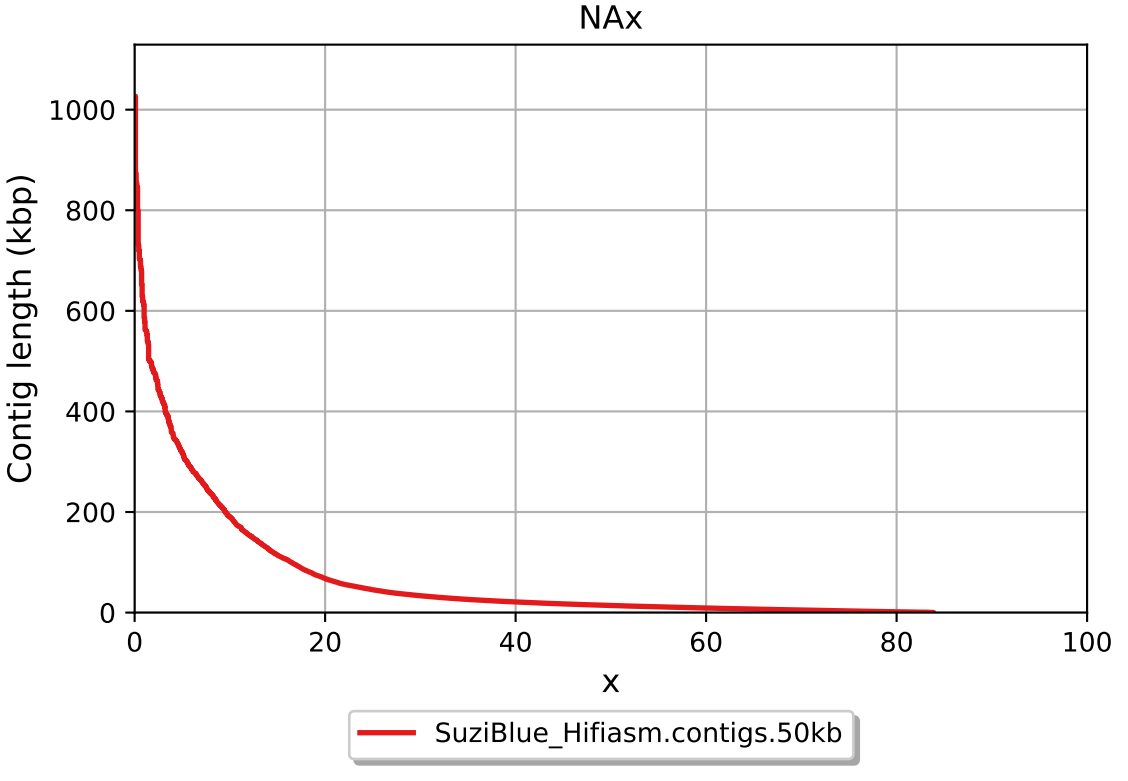

GC content
800000
600000
400000
200000
0
windows
0
20
40
60
80
100
GC (%)
SuziBlue_Hifiasm.contigs.50kb
Reference

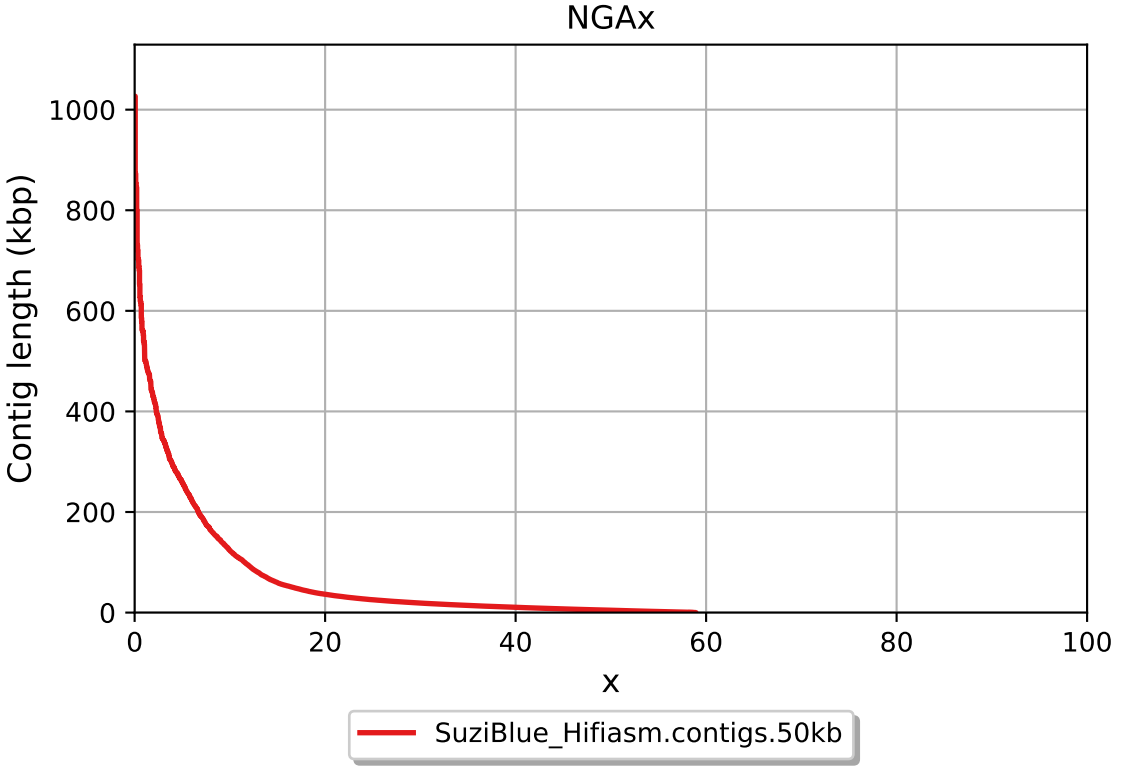

SuziBlue_Hifiasm.contigs.50kb GC content
contigs
GC (%)
0
60
120
180
240
300
0
20
40
60
80
100
SuziBlue_Hifiasm.contigs.50kb


Misassemblies
150000
120000
90000
60000
30000
0
SuziBlue_Hifiasm.contigs.50kb
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
25000
50000
75000
100000
125000
Feature space
SuziBlue_Hifiasm.contigs.50kb


Cumulative length (aligned contigs)
Cumulative length (Mbp)
1600
1200
800
400
0
0
25000
50000
75000
100000
125000
Contig index
SuziBlue_Hifiasm.contigs.50kb
Reference


NAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
SuziBlue_Hifiasm.contigs.50kb


NGAx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
SuziBlue_Hifiasm.contigs.50kb