

Report

	Scerevisiae-INSC1019_flye_30x_fa	Scerevisiae-INSC1019_hifiasm_30x_fa
# contigs (>= 0 bp)	26	19
# contigs (>= 1000 bp)	26	19
Total length (>= 0 bp)	12237056	9325826
Total length (>= 1000 bp)	12237056	9325826
# contigs	26	19
Largest contig	1438238	1795653
Total length	12237056	9325826
Reference length	12071326	12071326
GC (%)	38.18	38.07
Reference GC (%)	38.30	38.30
N50	929061	956944
NG50	929061	746623
N90	429765	477748
NG90	429765	-
auN	844863.2	990334.7
auNG	856462.5	765093.1
L50	6	4
LG50	6	6
L90	14	10
LG90	14	-
# total reads	45000	45000
# left	0	0
# right	0	0
Mapped (%)	110.14	140.8
Reference mapped (%)	110.66	110.66
Properly paired (%)	0.0	0.0
Reference properly paired (%)	0.0	0.0
Avg. coverage depth	35	49
Reference avg. coverage depth	36	36
Coverage >= 1x (%)	100.0	100.0
Reference coverage >= 1x (%)	99.97	99.97
# misassemblies	38	23
# misassembled contigs	12	10
Misassembled contigs length	9399201	6695194
# local misassemblies	7	4
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 8 part	3 + 8 part
Unaligned length	92782	150045
Genome fraction (%)	99.588	75.083
Duplication ratio	1.067	1.029
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	137.74	49.83
# indels per 100 kbp	11.61	6.41
Largest alignment	1051578	1051572
Total aligned length	12128269	9164662
NA50	528374	666826
NGA50	528374	468868
NA90	216384	190049
NGA90	220684	-
auNA	532744.4	584458.7
auNGA	540058.6	451529.5
LA50	9	6
LGA50	9	9
LA90	23	16
LGA90	22	-

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).

Reads report

	Scerevisiae-INSC1019_flye_30x_fa	Scerevisiae-INSC1019_hifiasm_30x_fa
# total reads	45000	45000
# left	0	0
# right	0	0
# mapped	49561	63361
Mapped (%)	110.14	140.8
# properly paired	0	0
Properly paired (%)	0.0	0.0
# singletons	0	0
Singletons (%)	0.0	0.0
# misjoint mates	0	0
Misjoint mates (%)	0.0	0.0
Avg. coverage depth	35	49
Coverage >= 1x (%)	100.0	100.0
Coverage >= 5x (%)	99.99	99.84
Coverage >= 10x (%)	99.98	99.63
# reference mapped	49797	49797
Reference mapped (%)	110.66	110.66
# reference properly paired	0	0
Reference properly paired (%)	0.0	0.0
# reference singletons	0	0
Reference singletons (%)	0.0	0.0
# reference misjoint mates	0	0
Reference misjoint mates (%)	0.0	0.0
Reference avg. coverage depth	36	36
Reference coverage >= 1x (%)	99.97	99.97
Reference coverage >= 5x (%)	99.97	99.97
Reference coverage >= 10x (%)	99.91	99.91

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

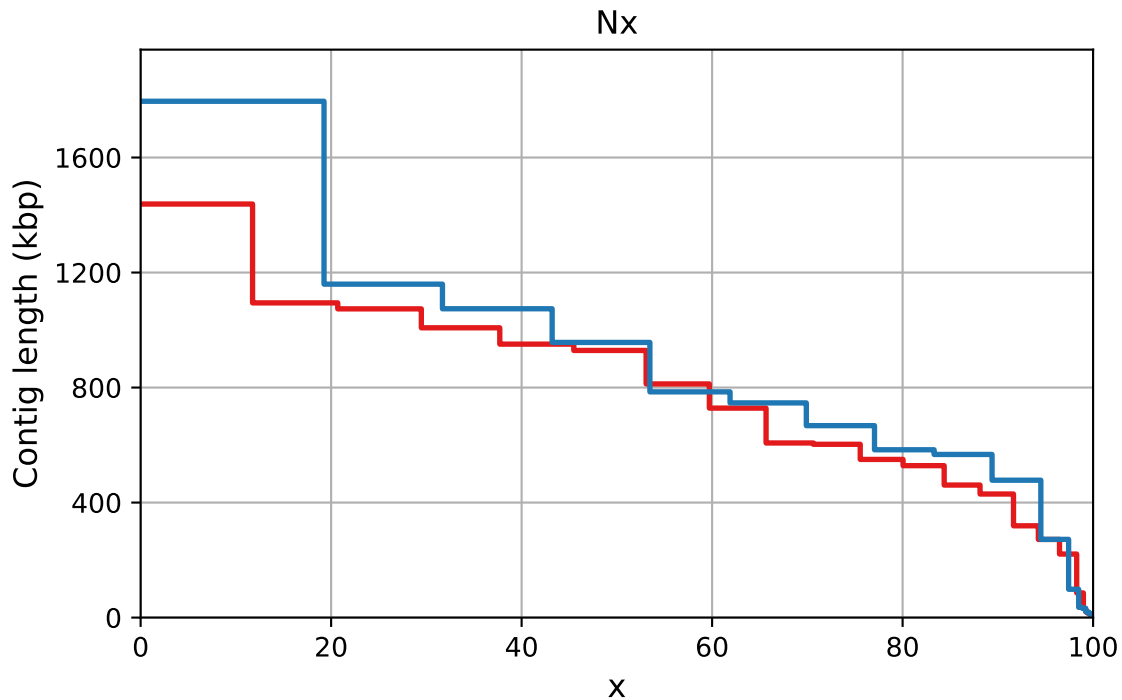
	Scerevisiae-INSC1019_flye_30x_fa	Scerevisiae-INSC1019_hifiasm_30x_fa
# misassemblies	38	23
# contig misassemblies	38	23
# c. relocations	17	16
# c. translocations	21	7
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	12	10
Misassembled contigs length	9399201	6695194
# local misassemblies	7	4
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	16706	4567
# indels	1408	587
# indels (<= 5 bp)	1285	503
# indels (> 5 bp)	123	84
Indels length	8479	3431

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

	Scerevisiae-INSC1019_flye_30x_fa	Scerevisiae-INSC1019_hifiasm_30x_fa
# fully unaligned contigs	0	3
Fully unaligned length	0	43578
# partially unaligned contigs	8	8
Partially unaligned length	92782	106467
# N's	0	0

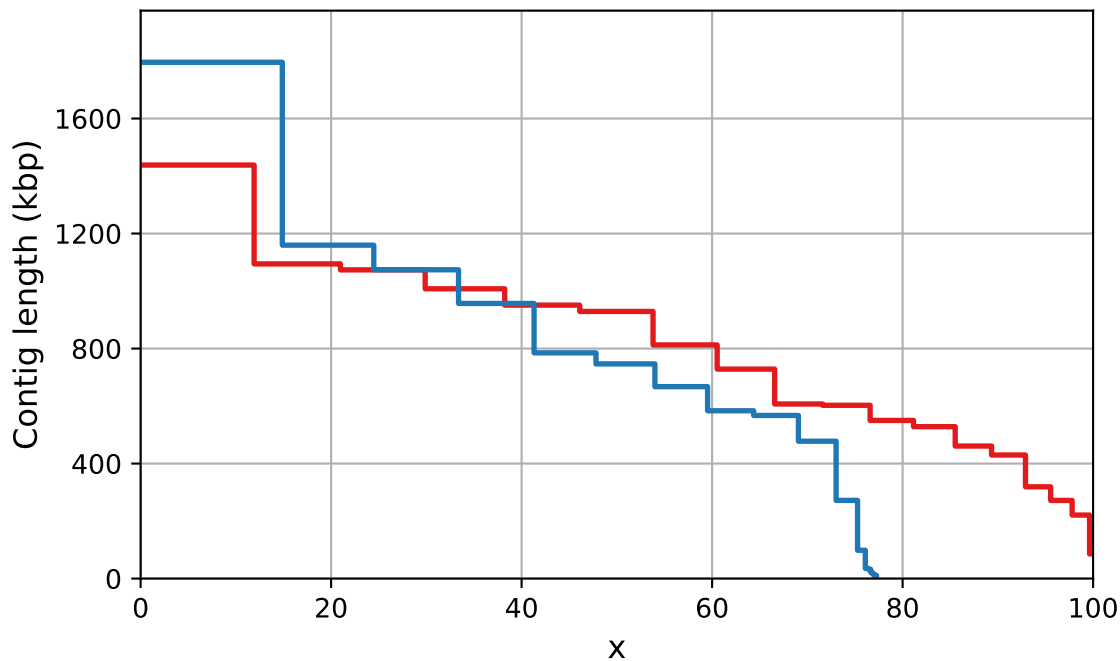
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



— Scerevisiae-INSC1019_flye_30x_fa

— Scerevisiae-INSC1019_hifiasm_30x_fa

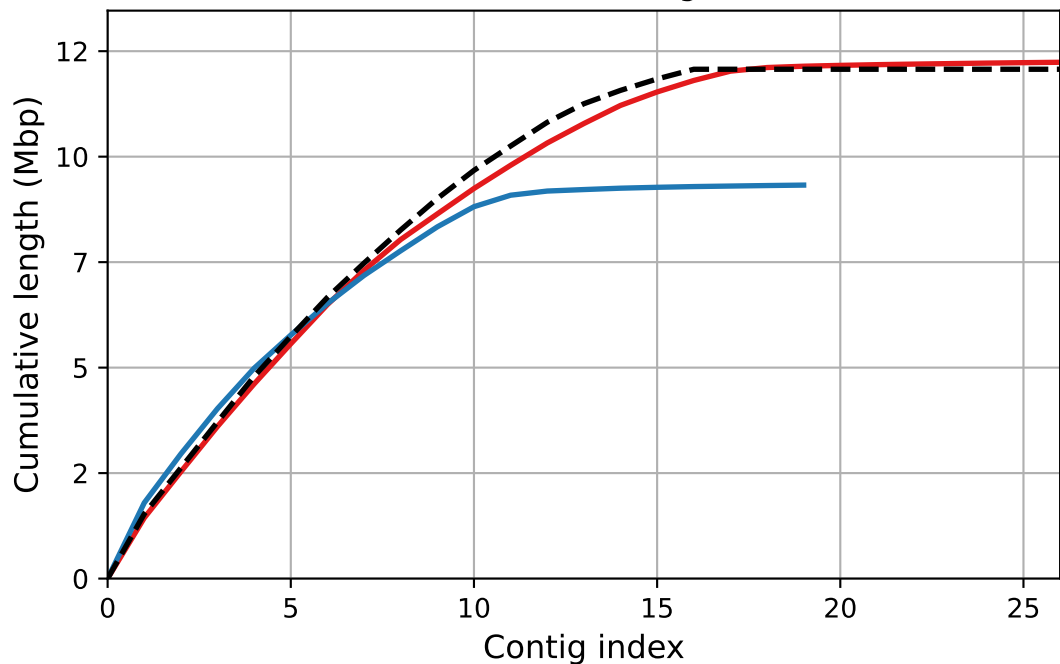
NGx



— Scerevisiae-INSC1019_flye_30x_fa

— Scerevisiae-INSC1019_hifiasm_30x_fa

Cumulative length

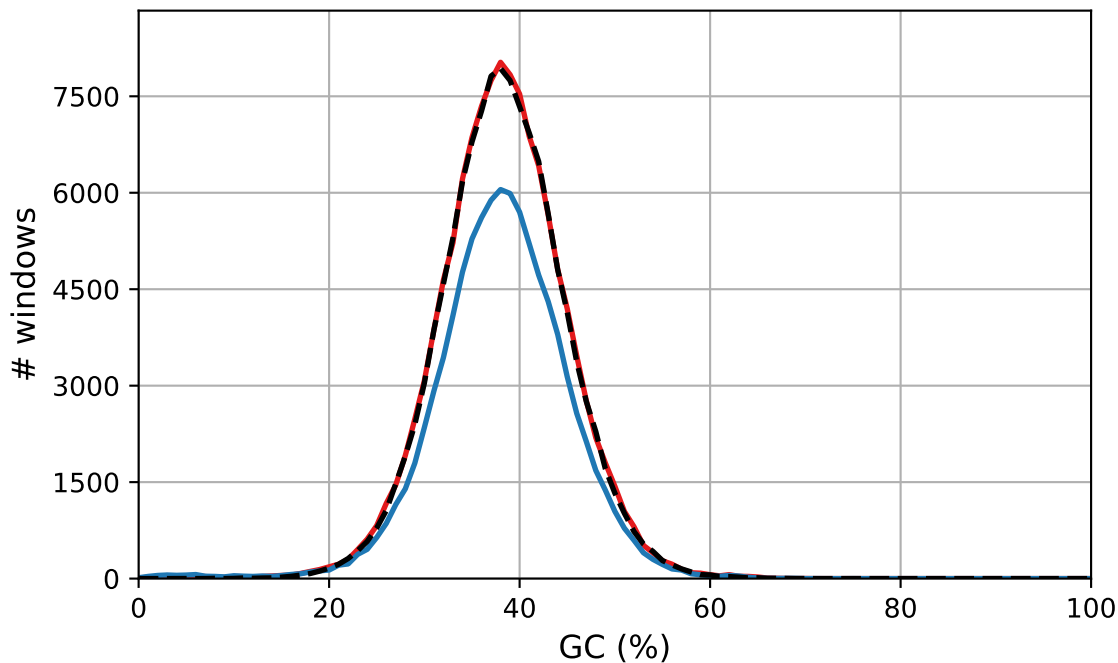


cerevisiae-INSC1019_flye_30x_fa

— Scerevisiae-INSC1019_hifiasm_30x_fa

- - Reference

GC content

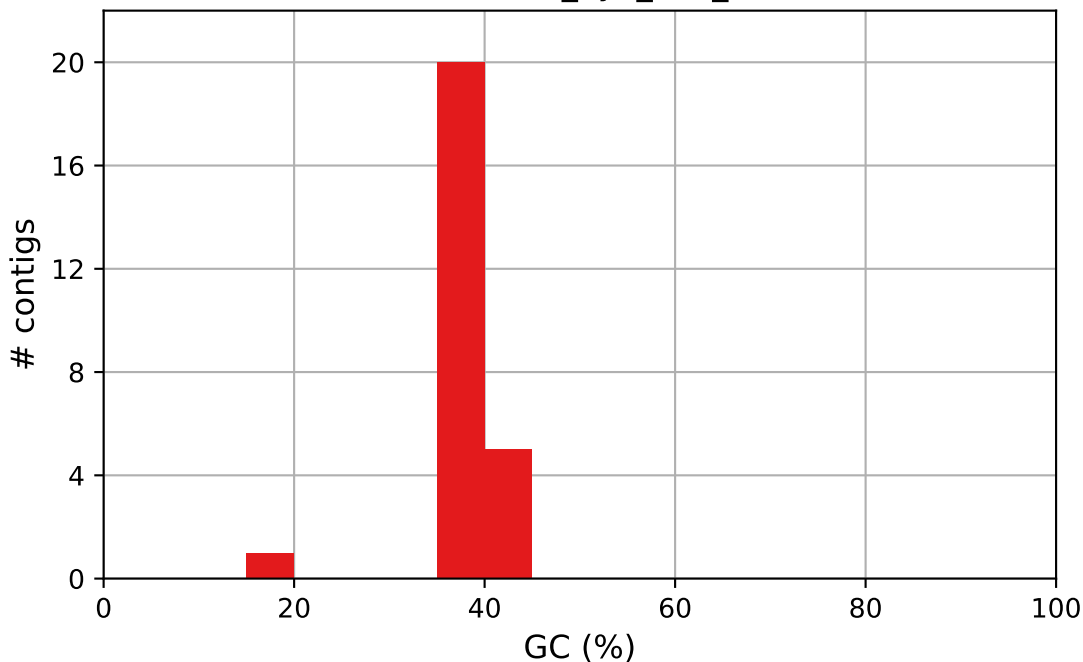


Scerevisiae-INSC1019_flye_30x_fa

Scerevisiae-INSC1019_hifiasm_30x_fa

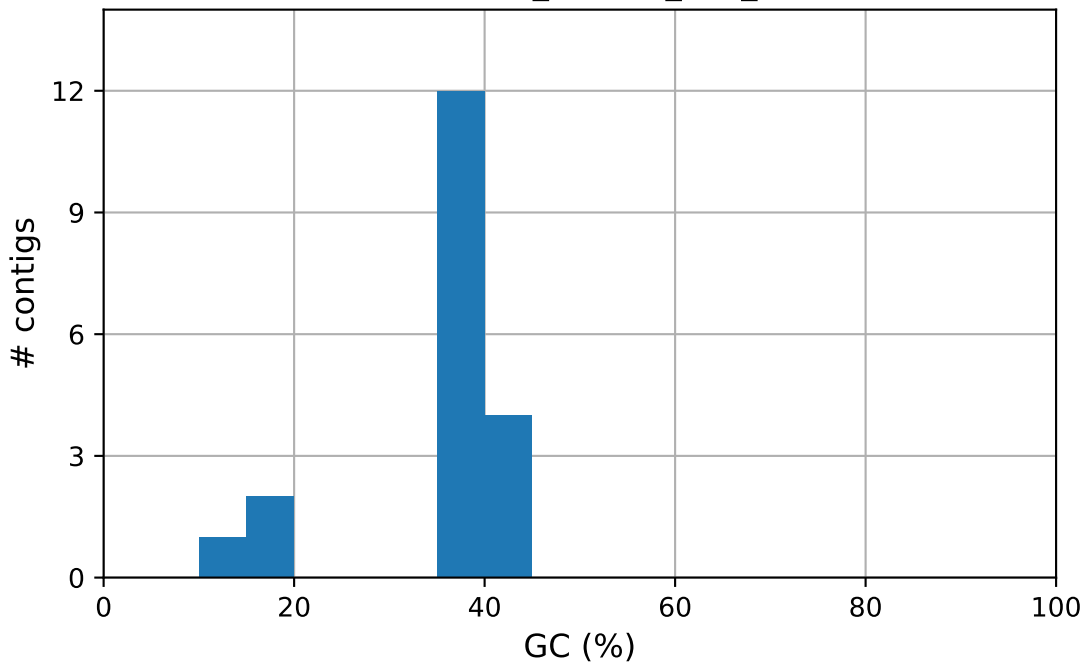
Re

Scerevisiae-INSC1019_flye_30x_fa GC content



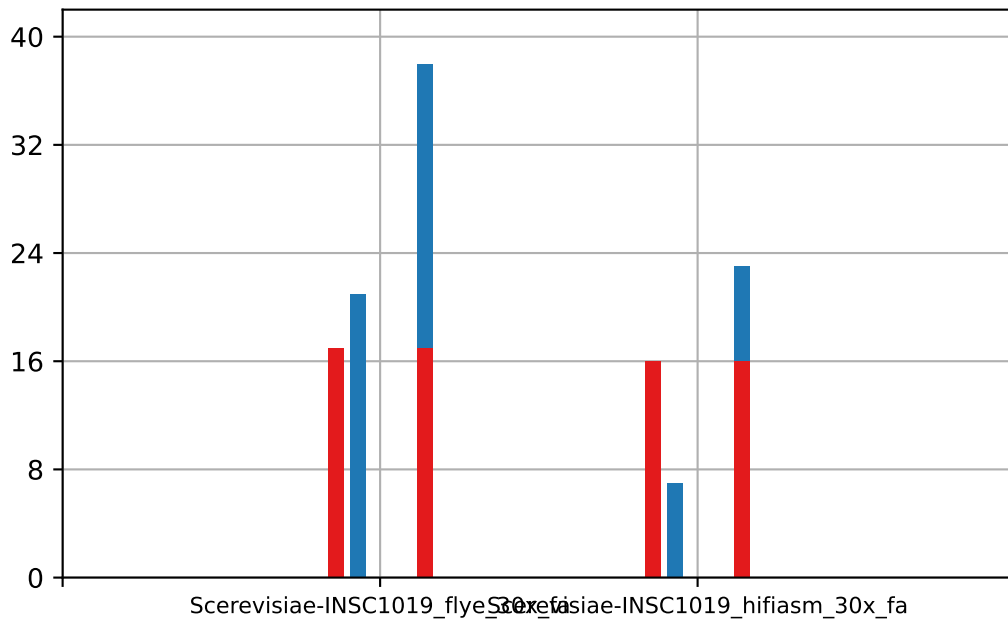
Scerevisiae-INSC1019_flye_30x_fa

Scerevisiae-INSC1019_hifiasm_30x_fa GC content



Scerevisiae-INSC1019_hifiasm_30x_fa

Misassemblies

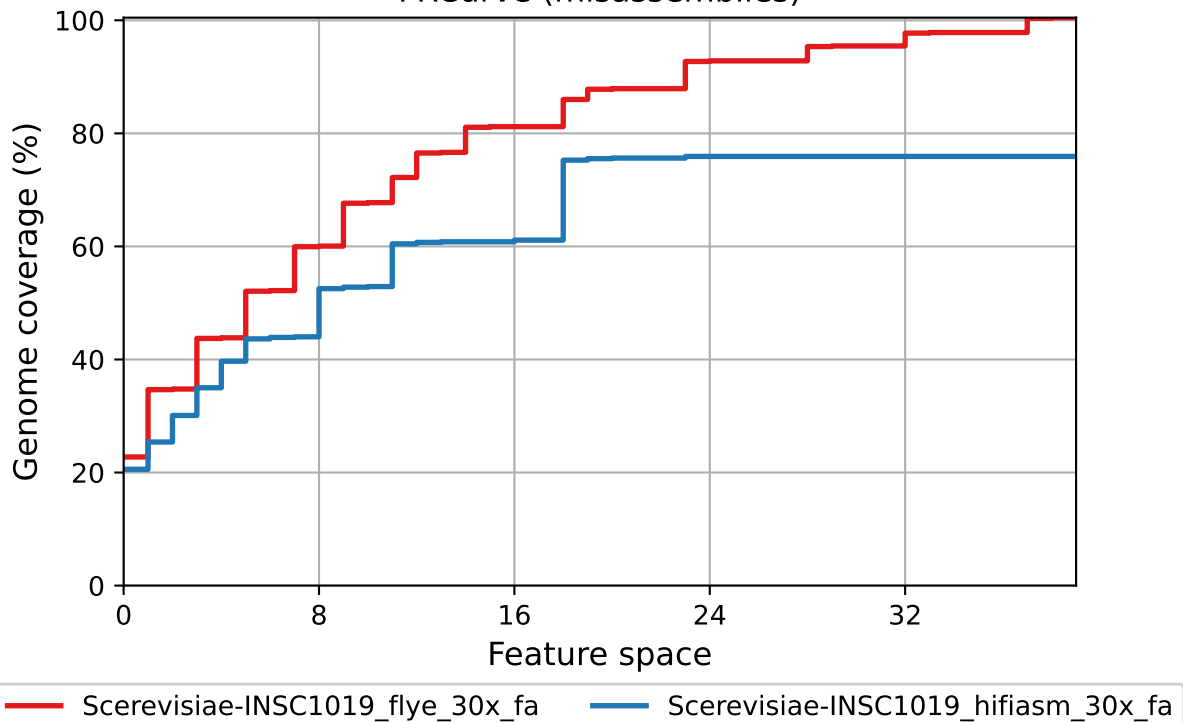


relocations

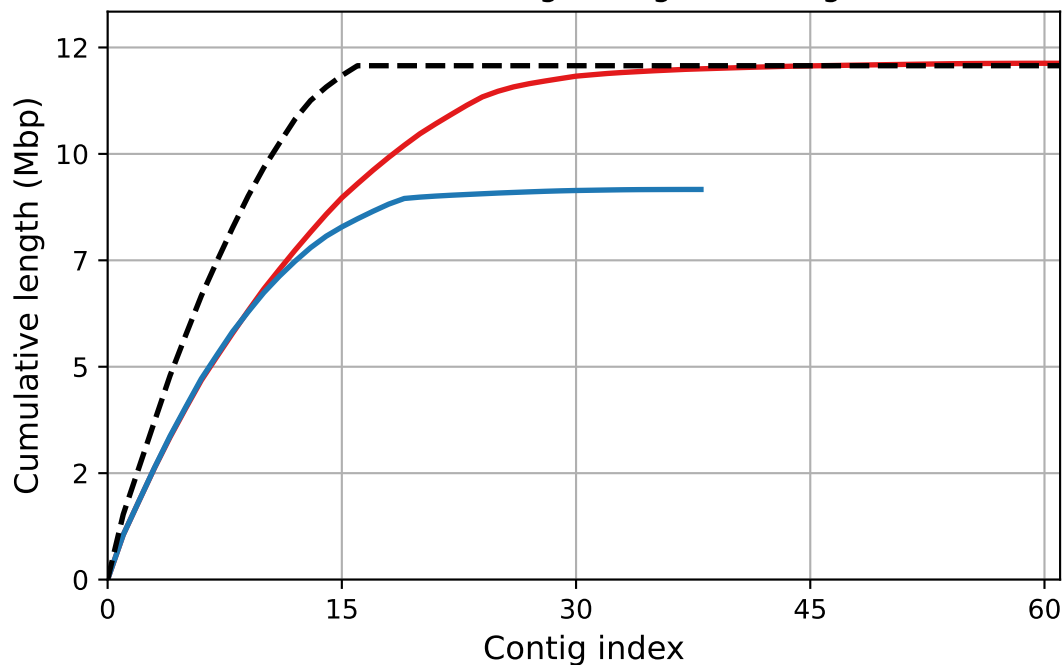


translocations

FRCurve (misassemblies)



Cumulative length (aligned contigs)

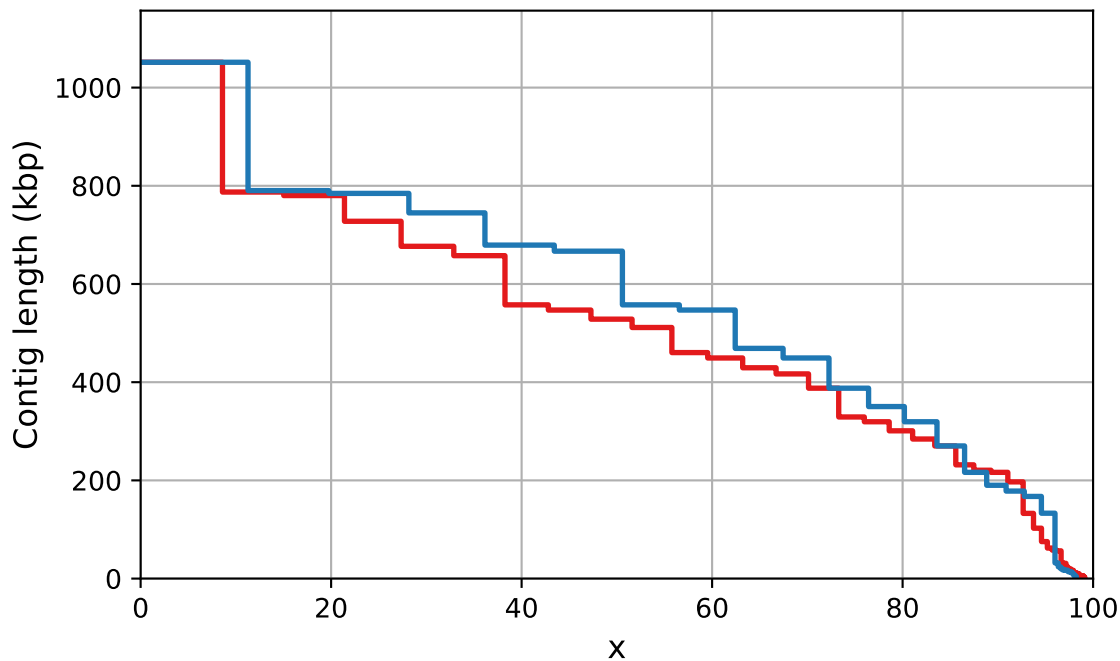


cerevisiae-INSC1019_flye_30x_fa

— Scerevisiae-INSC1019_hifiasm_30x_fa

- - Re

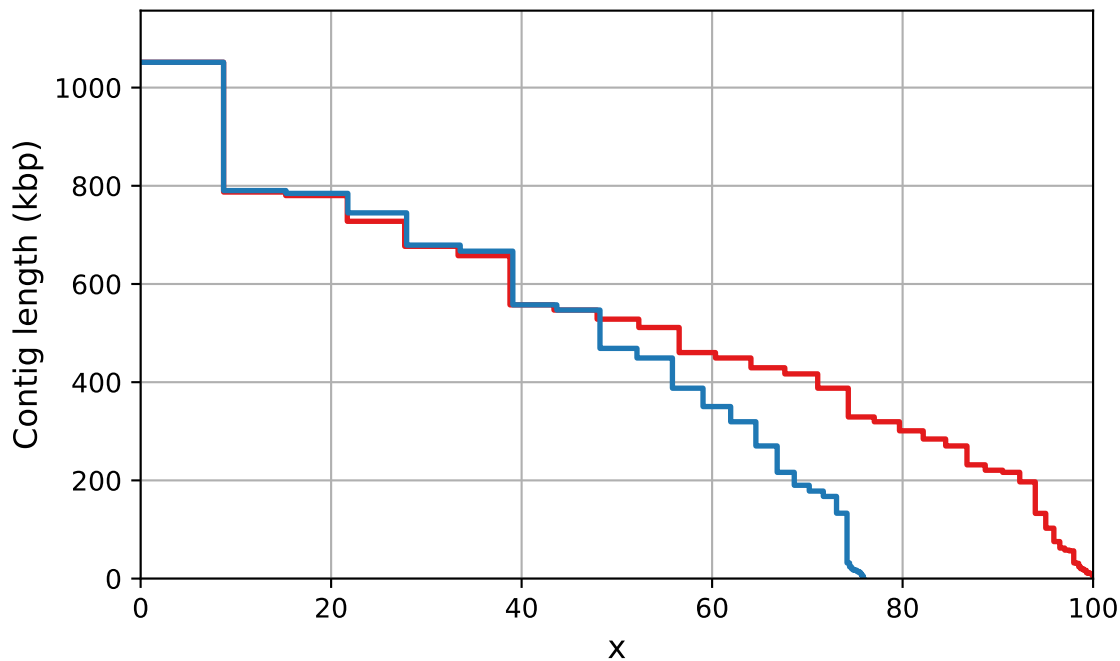
NAx



— Scerevisiae-INS1019_flye_30x_fa

— Scerevisiae-INS1019_hifiasm_30x_fa

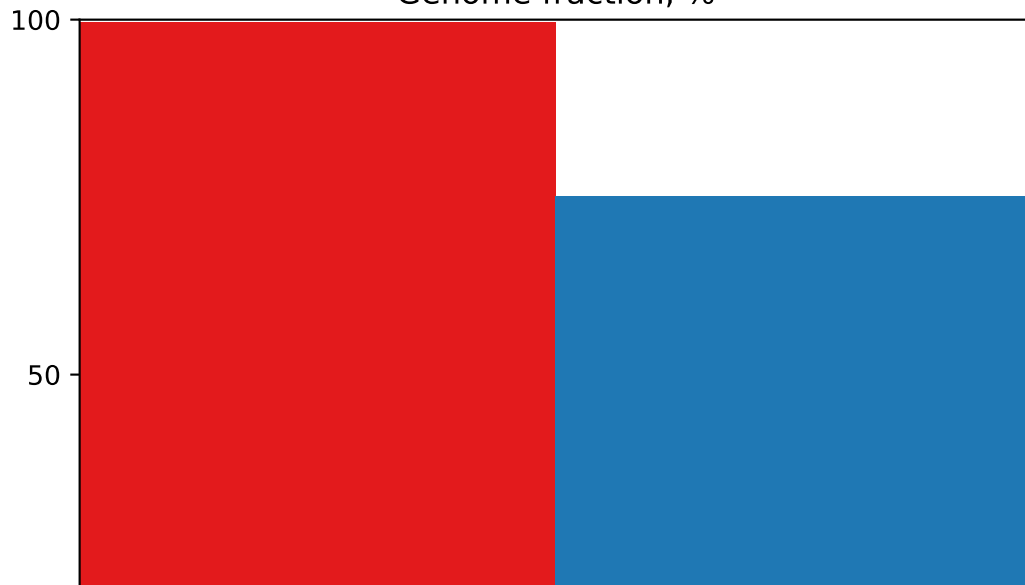
NGAx



— Scerevisiae-INS1019_flye_30x_fa

— Scerevisiae-INS1019_hifiasm_30x_fa

Genome fraction, %



■ Scerevisiae-INS1019_flye_30x_fa

■ Scerevisiae-INS1019_hifiasm_30x_fa