

Report

soy_zarir_benson_apr2022.asm.p_ctg	
# contigs (>= 0 bp)	850
# contigs (>= 1000 bp)	850
# contigs (>= 5000 bp)	850
# contigs (>= 10000 bp)	849
# contigs (>= 25000 bp)	814
# contigs (>= 50000 bp)	192
Total length (>= 0 bp)	1050801700
Total length (>= 1000 bp)	1050801700
Total length (>= 5000 bp)	1050801700
Total length (>= 10000 bp)	1050795859
Total length (>= 25000 bp)	1050003127
Total length (>= 50000 bp)	1027312906
# contigs	850
Largest contig	55602273
Total length	1050801700
Reference length	978491270
GC (%)	35.15
Reference GC (%)	34.76
N50	29726422
NG50	32634045
N90	9730069
NG90	14011717
L50	13
LG50	12
L90	36
LG90	30
# misassemblies	30070
# misassembled contigs	492
Misassembled contigs length	1035342021
# local misassemblies	14772
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	263
# unaligned contigs	1 + 745 part
Unaligned length	63649031
Genome fraction (%)	96.877
Duplication ratio	1.060
# N's per 100 kbp	0.00
# mismatches per 100 kbp	240.27
# indels per 100 kbp	45.07
Largest alignment	2226700
Total aligned length	980680756
NA50	246334
NGA50	273181
NA90	6523
NGA90	31728
LA50	1085
LGA50	945
LA90	9193
LGA90	4669

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

	soy_zarir_benson_apr2022.asm.p_ctg
# misassemblies	30070
# contig misassemblies	30070
# c. relocations	10638
# c. translocations	19372
# c. inversions	60
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	492
Misassembled contigs length	1035342021
# local misassemblies	14772
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	263
# mismatches	2356252
# indels	441982
# indels (<= 5 bp)	355856
# indels (> 5 bp)	86126
Indels length	2569608

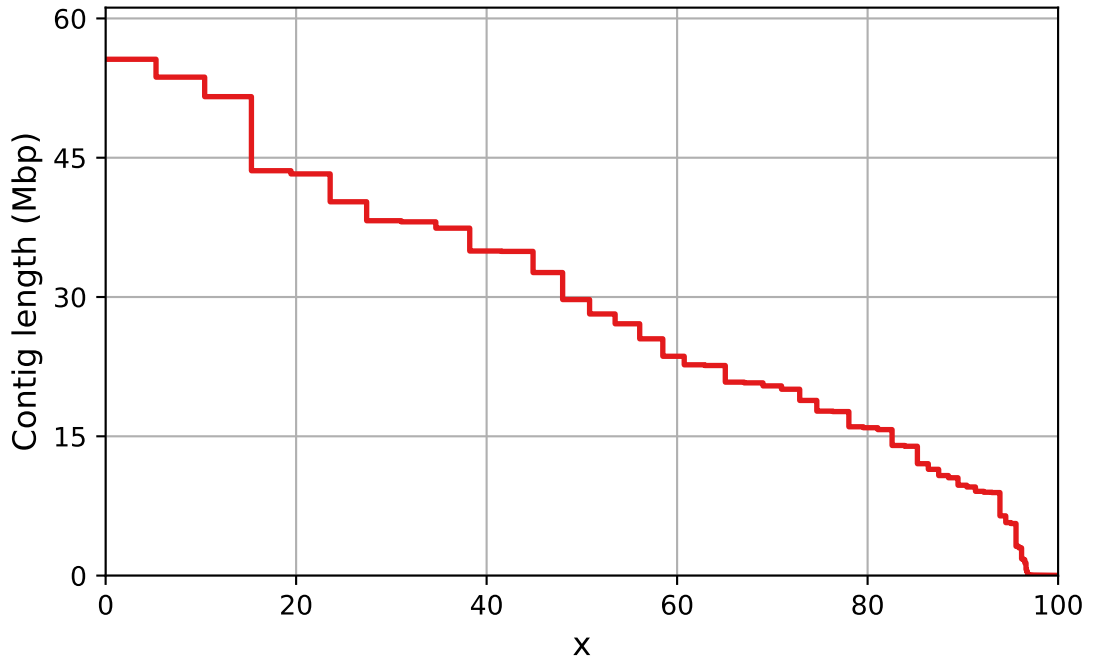
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	soy_zarir_benson_apr2022.asm.p_ctg
# fully unaligned contigs	1
Fully unaligned length	5841
# partially unaligned contigs	745
Partially unaligned length	63643190
# N's	0

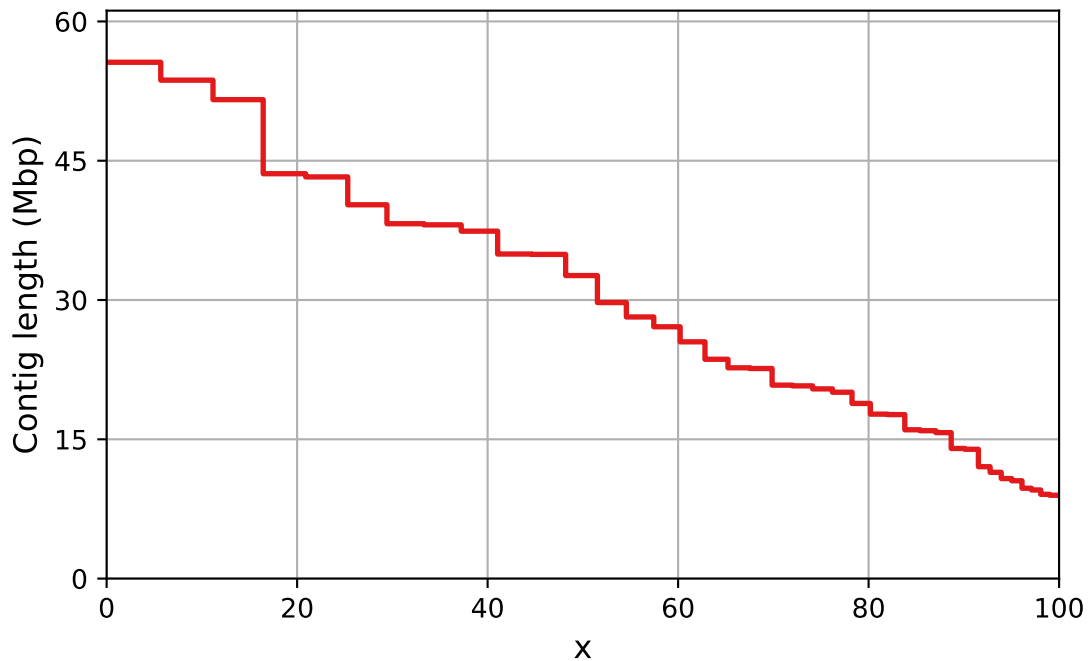
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



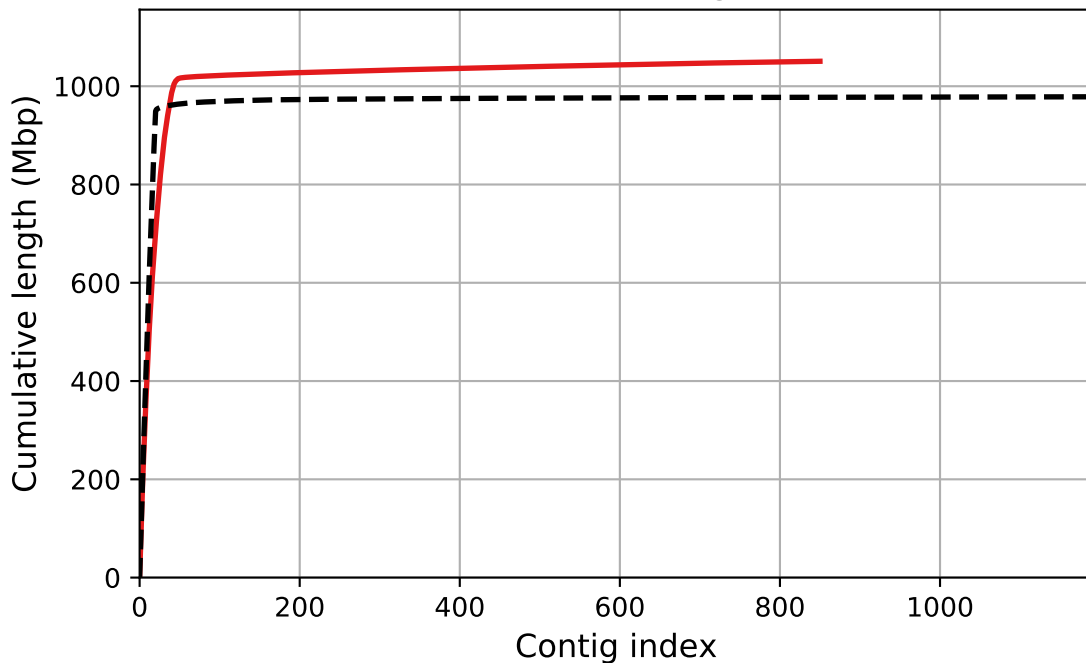
soy_zarir_benson_apr2022.asm.p_ctg

NGx



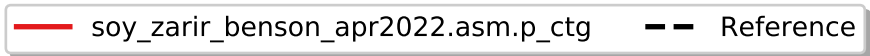
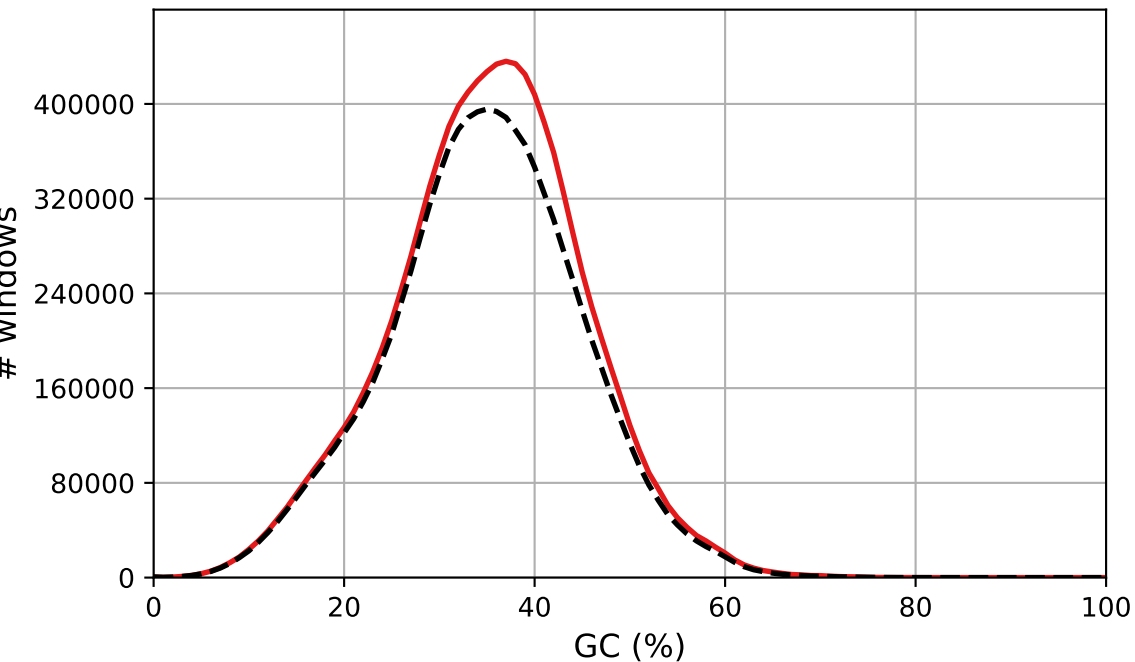
soy_zarir_benson_apr2022.asm.p_ctg

Cumulative length

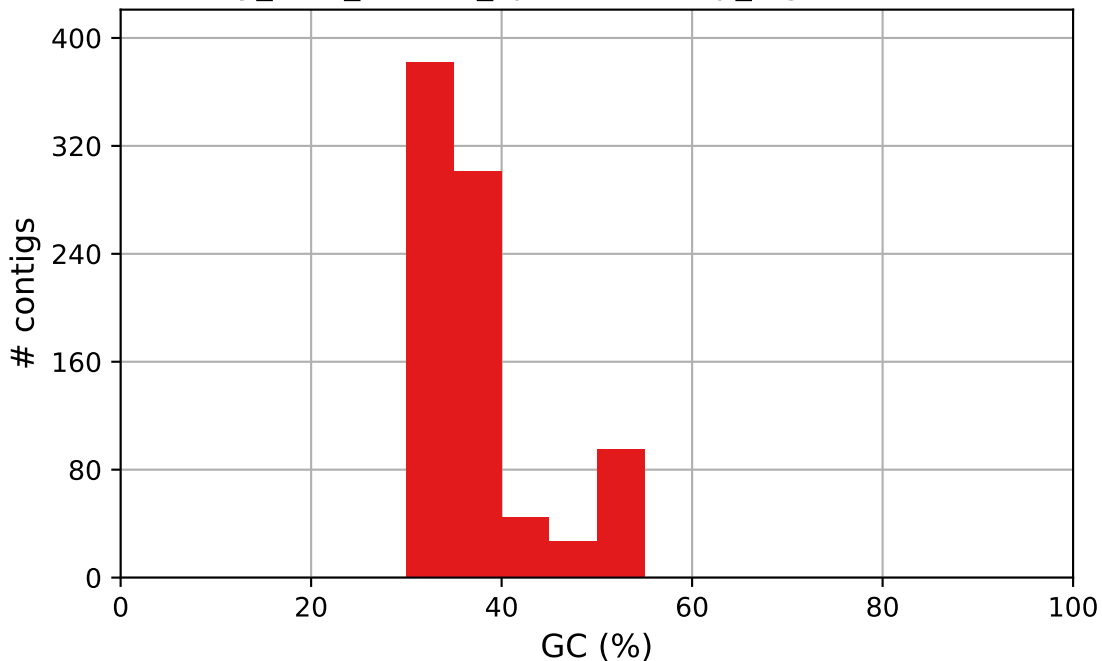


— soy_zarir_benson_apr2022.asm.p_ctg - - Reference

GC content

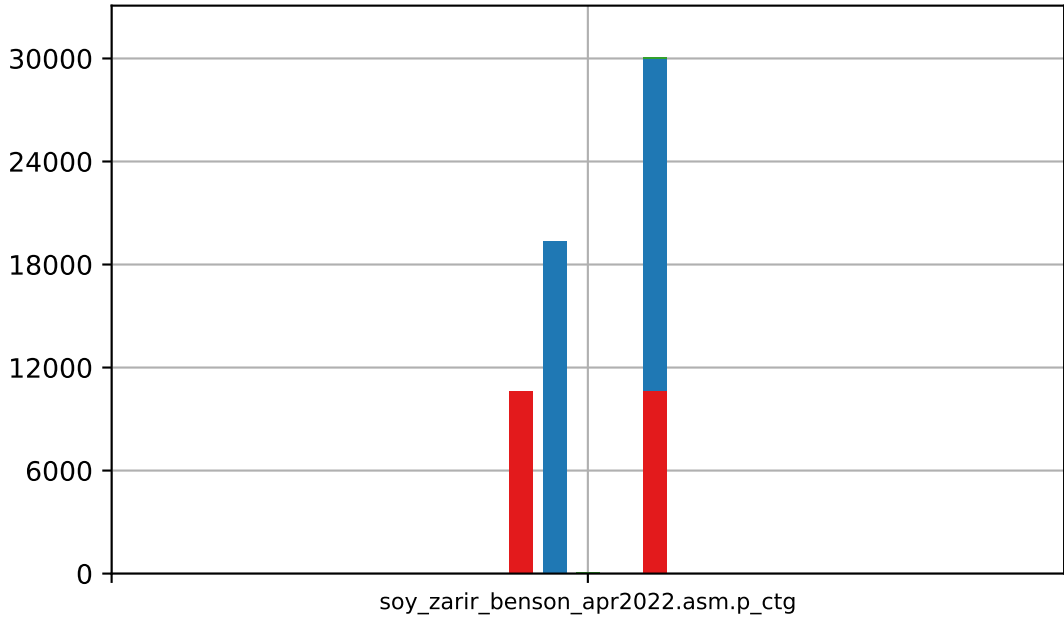


soy_zarir_benson_apr2022.asm.p_ctg GC content



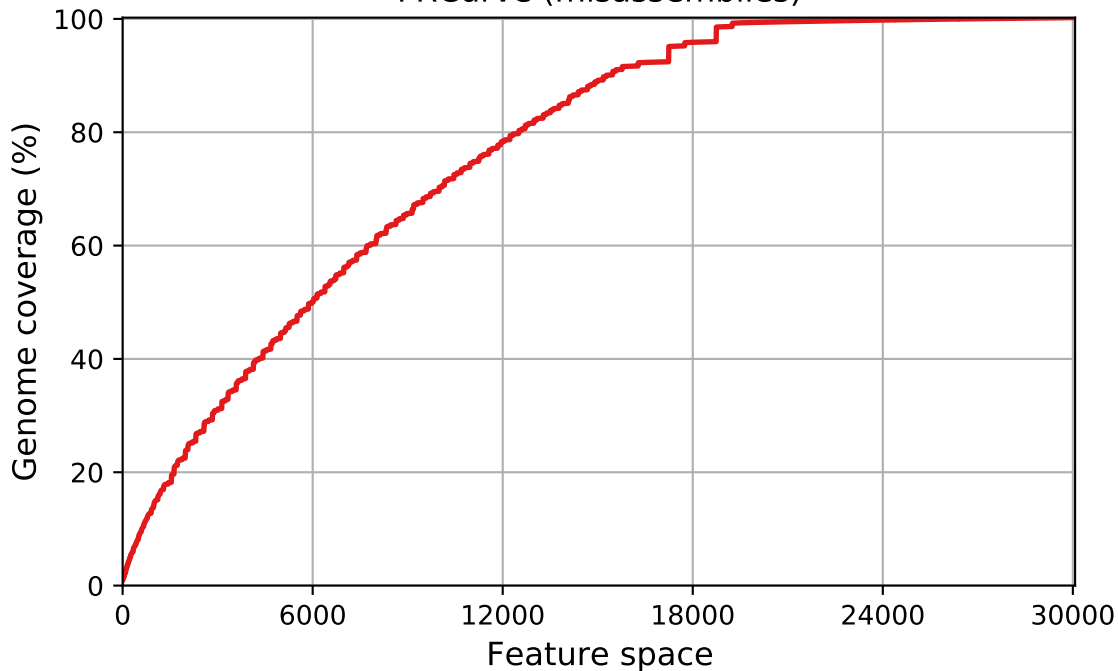
soy_zarir_benson_apr2022.asm.p_ctg

Misassemblies



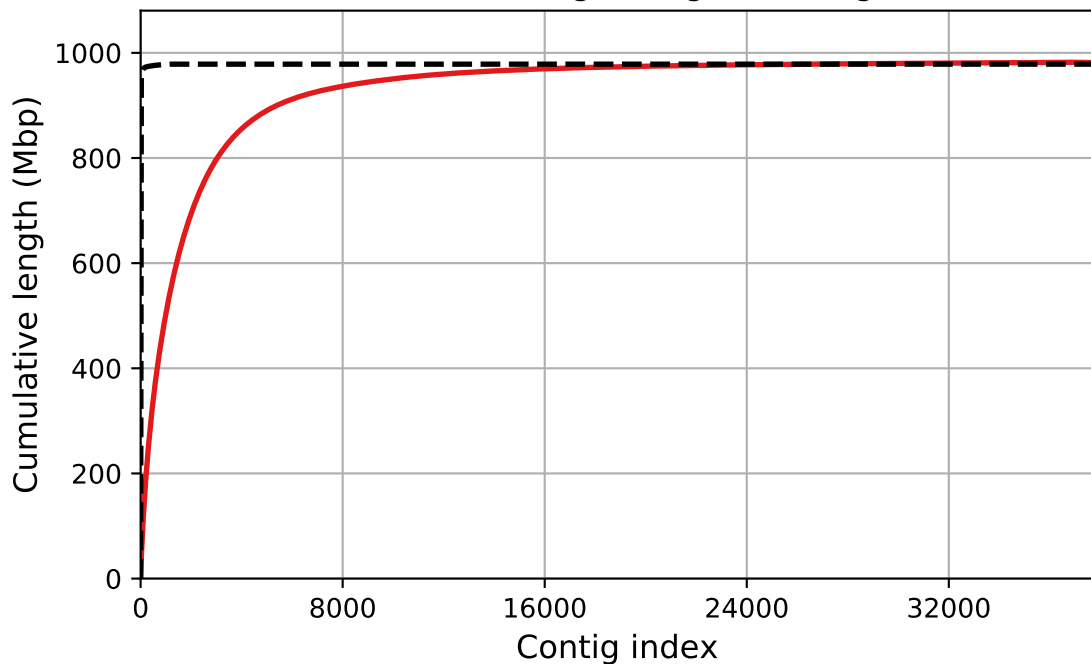
■ # relocations ■ # translocations ■ # inversions

FRCurve (misassemblies)



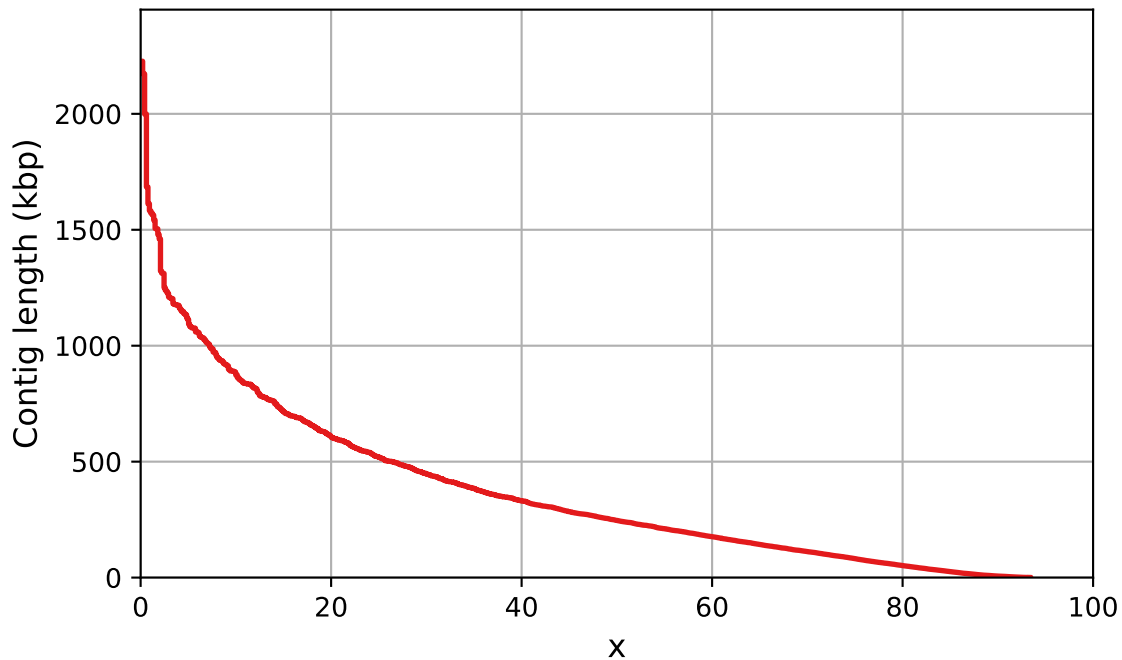
soy_zarir_benson_apr2022.asm.p_ctg

Cumulative length (aligned contigs)



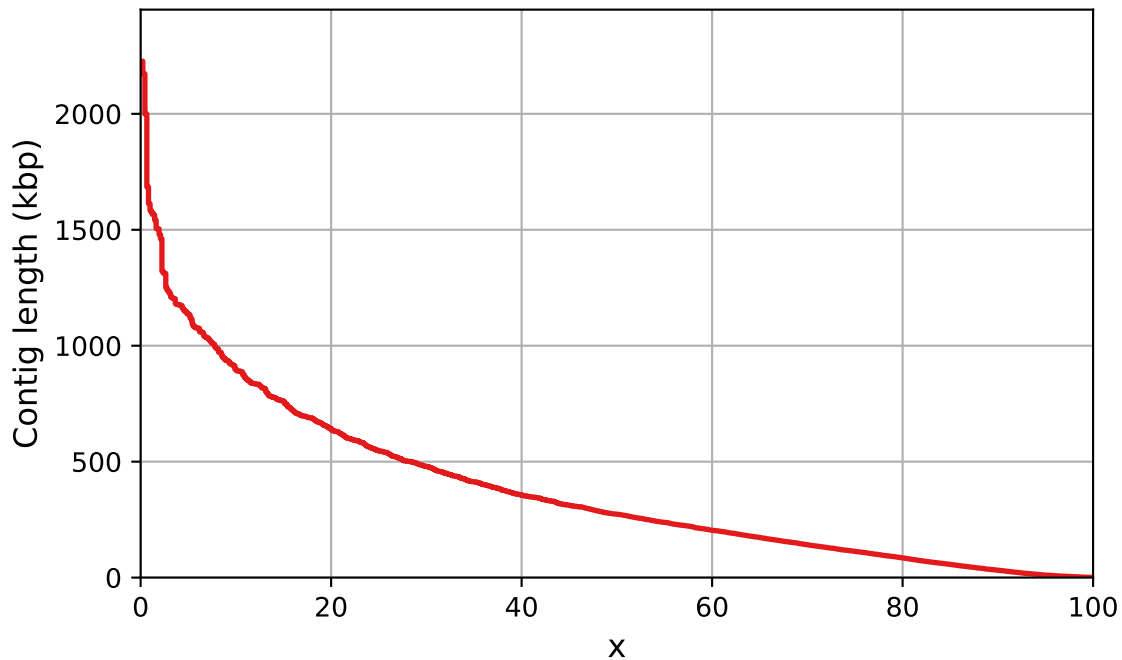
soy_zarir_benson_apr2022.asm.p_ctg Reference

NAx



soy_zarir_benson_apr2022.asm.p_ctg

NGAx



soy_zarir_benson_apr2022.asm.p_ctg