

Report

	SRR18214264-contigs_abyss_fa
# contigs (≥ 0 bp)	1878
# contigs (≥ 1000 bp)	207
Total length (≥ 0 bp)	2140764
Total length (≥ 1000 bp)	1921577
# contigs	250
Largest contig	104390
Total length	1952587
Reference length	2191149
GC (%)	36.59
Reference GC (%)	37.07
N50	14825
NG50	13870
N90	3544
NG90	-
auN	23246.9
auNG	20715.9
L50	35
LG50	43
L90	132
LG90	-
# misassemblies	108
# misassembled contigs	58
Misassembled contigs length	1051816
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	12
# unaligned contigs	44 + 90 part
Unaligned length	430231
Genome fraction (%)	73.968
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1124.26
# indels per 100 kbp	79.61
Largest alignment	41271
Total aligned length	1509876
NA50	6803
NGA50	5135
NA90	-
NGA90	-
auNA	8334.7
auNGA	7427.3
LA50	81
LGA50	101
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

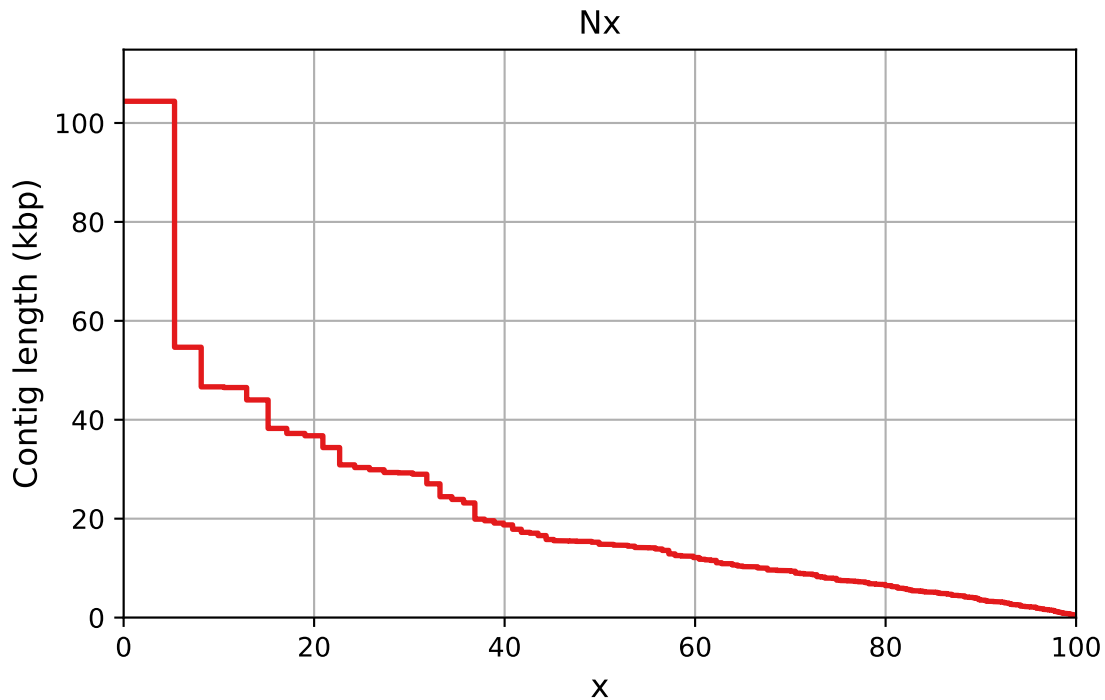
	SRR18214264-contigs_abyss_fa
# misassemblies	108
# contig misassemblies	108
# c. relocations	108
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	58
Misassembled contigs length	1051816
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	12
# mismatches	16975
# indels	1202
# indels (<= 5 bp)	936
# indels (> 5 bp)	266
Indels length	7838

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

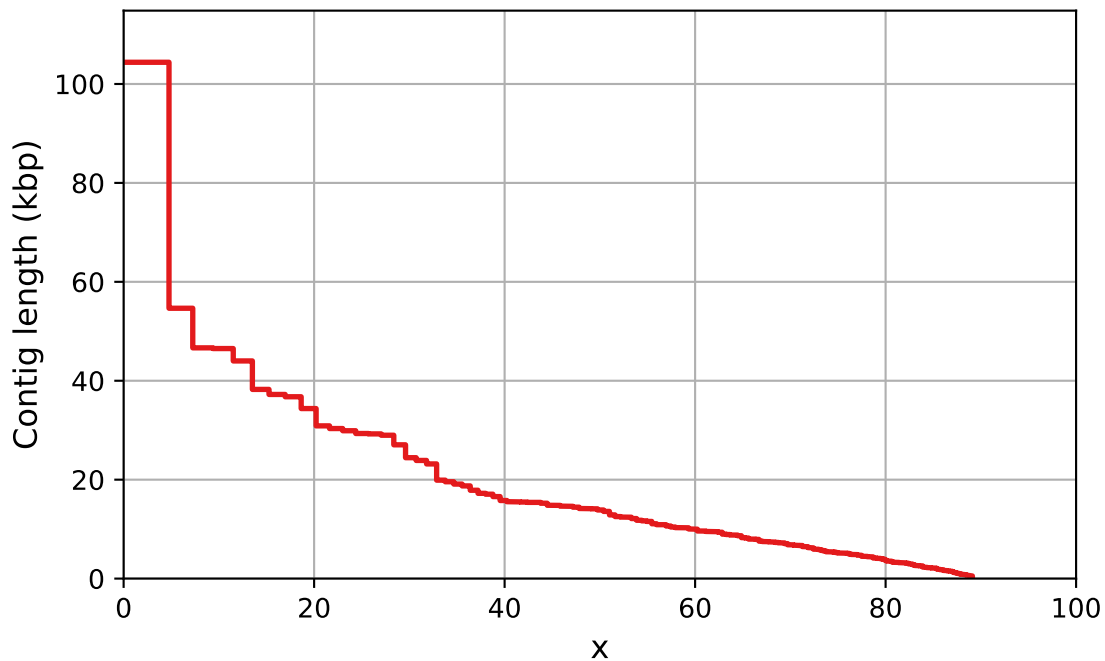
	SRR18214264-contigs_abyss_fa
# fully unaligned contigs	44
Fully unaligned length	81593
# partially unaligned contigs	90
Partially unaligned length	348638
# N's	0

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).



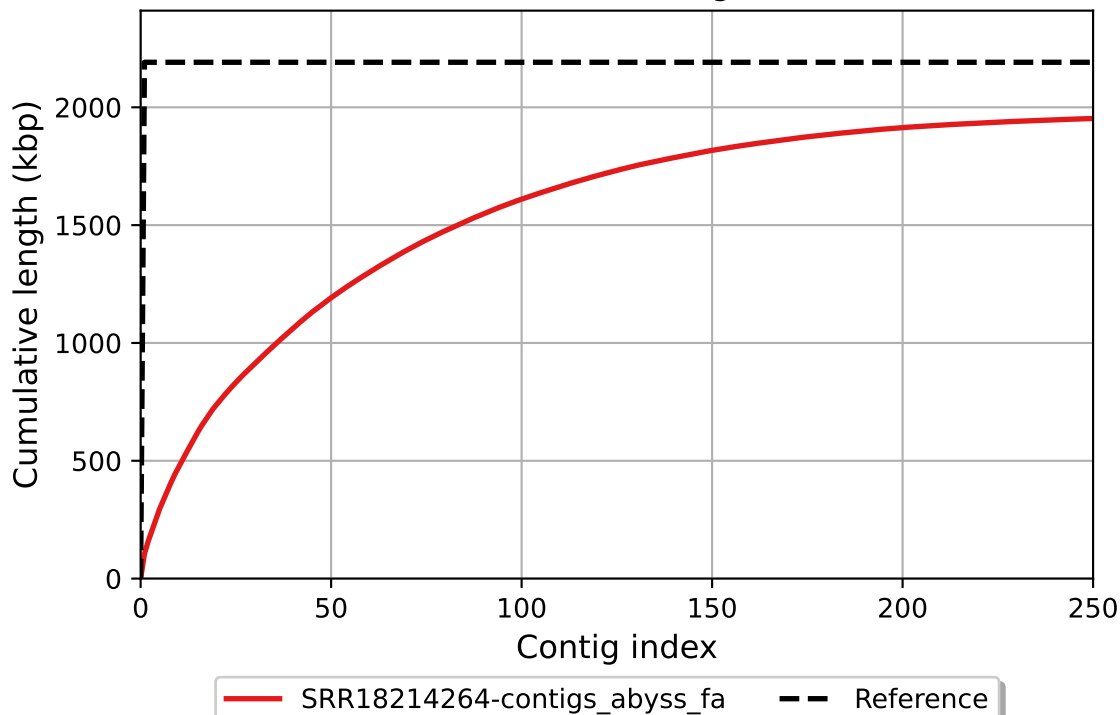
SRR18214264-contigs_abyss_fa

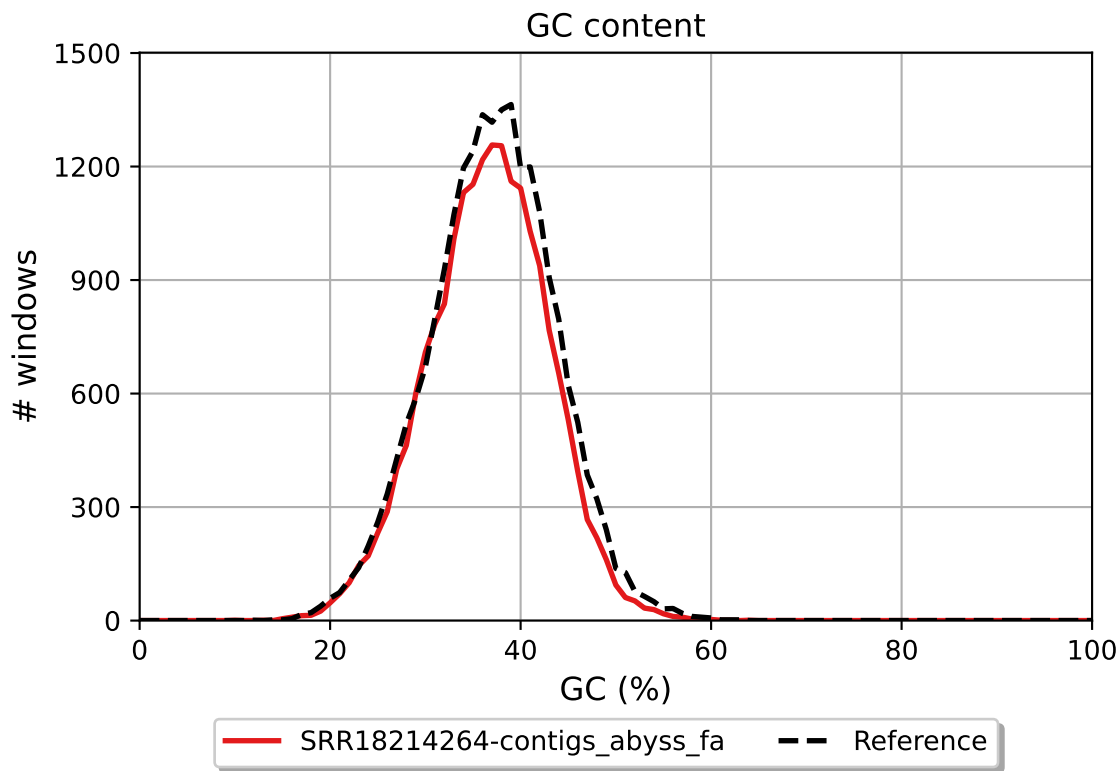
NGx



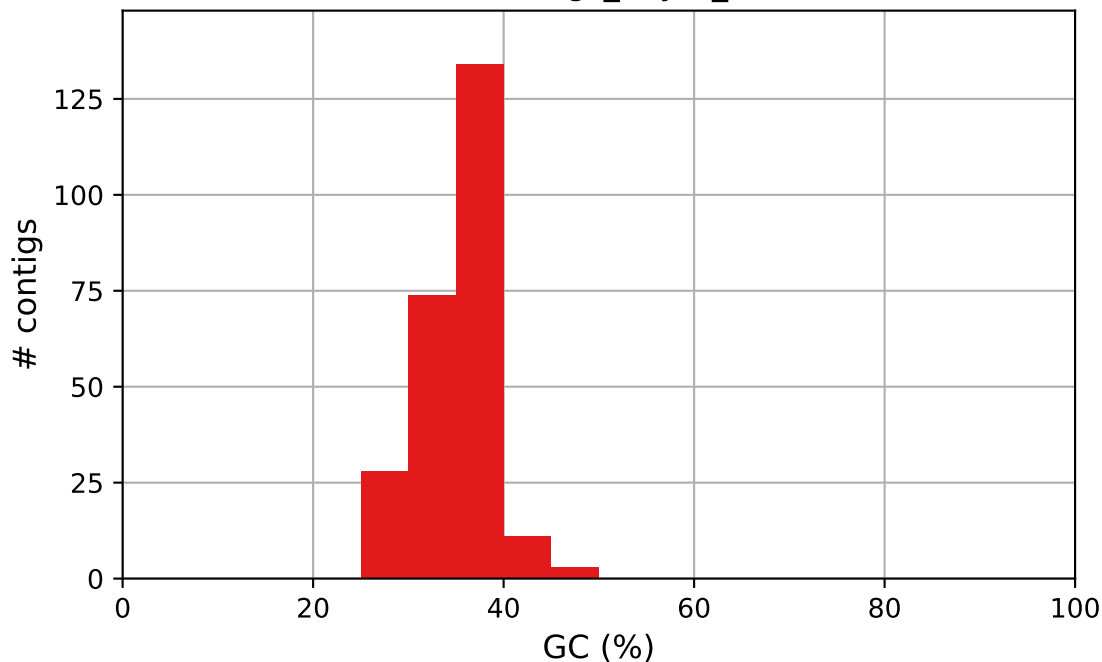
SRR18214264-contigs_abyss_fa

Cumulative length



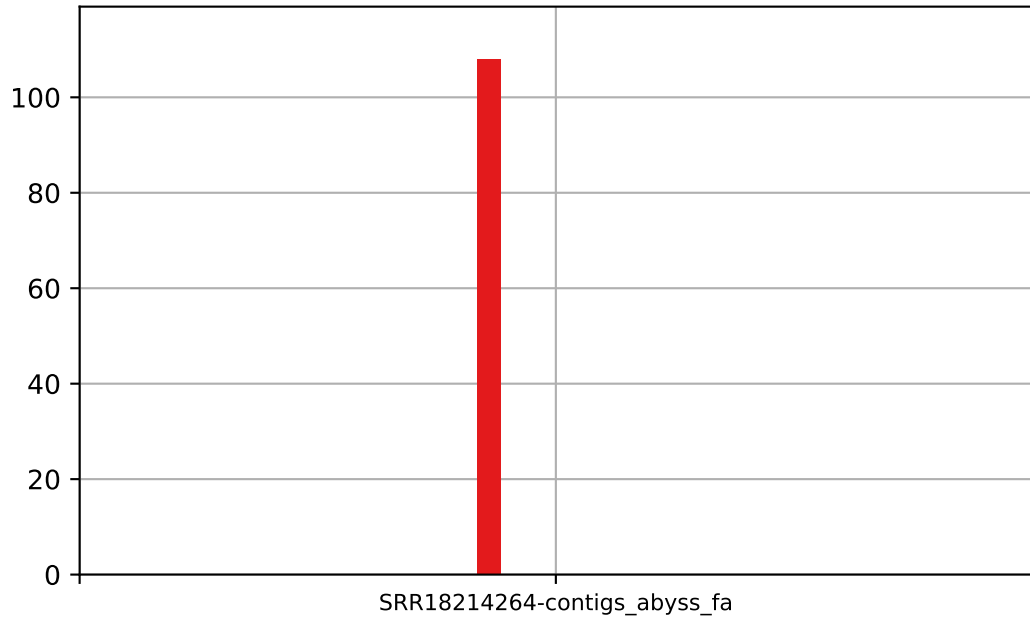


SRR18214264-contigs_abyss_fa GC content



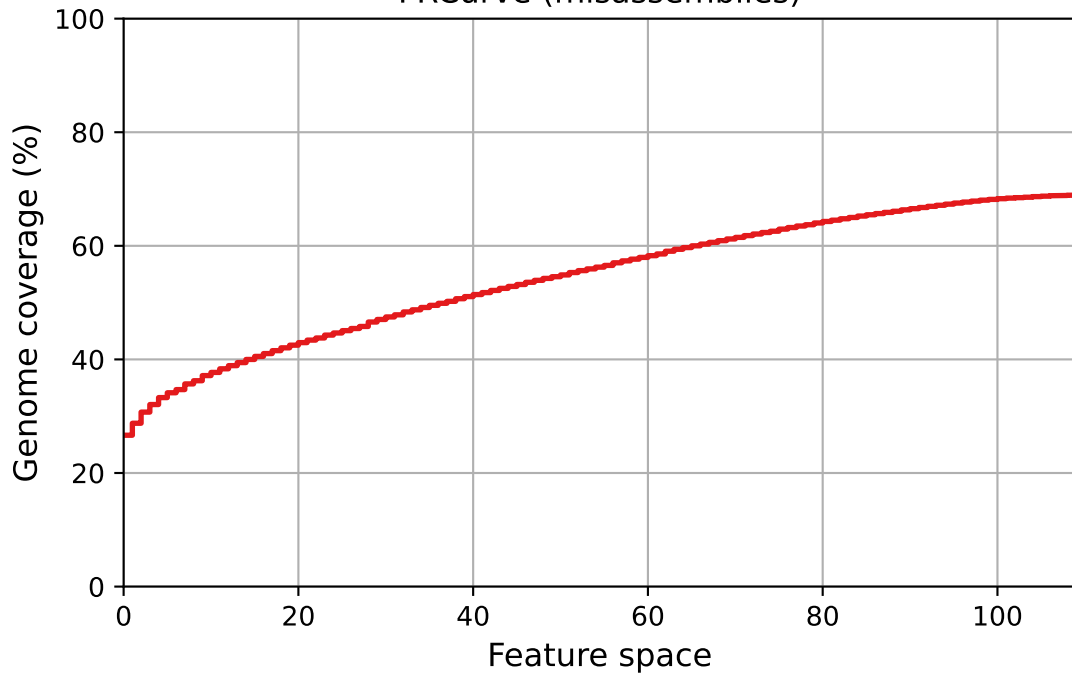
SRR18214264-contigs_abyss_fa

Misassemblies



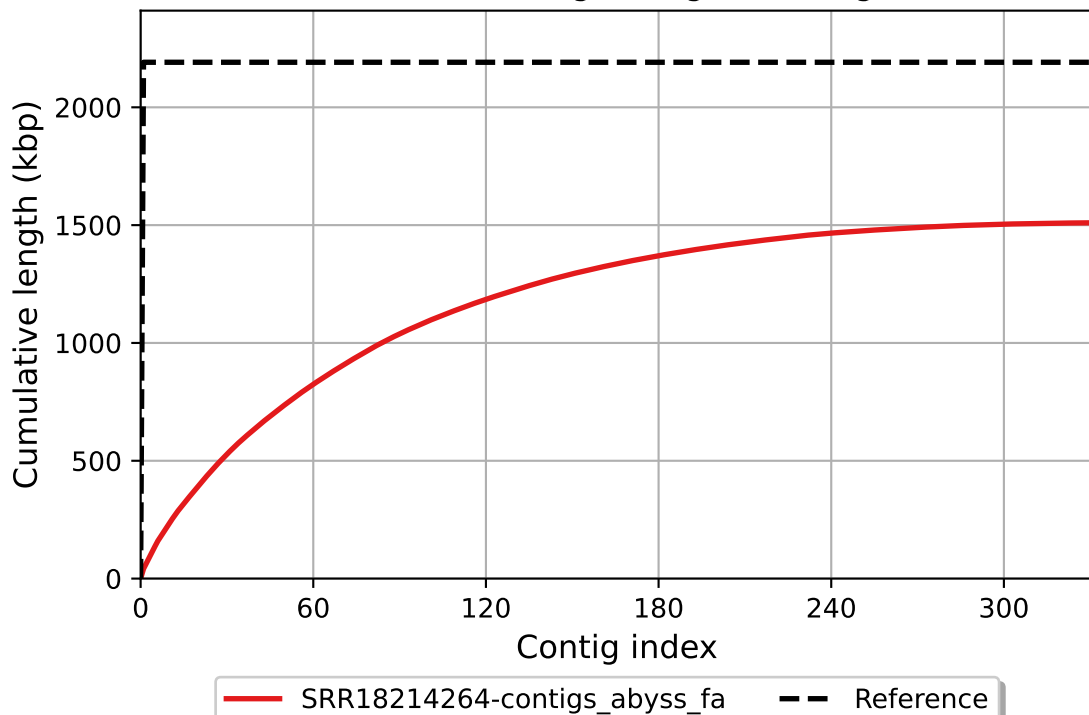
■ # relocations

FRCurve (misassemblies)

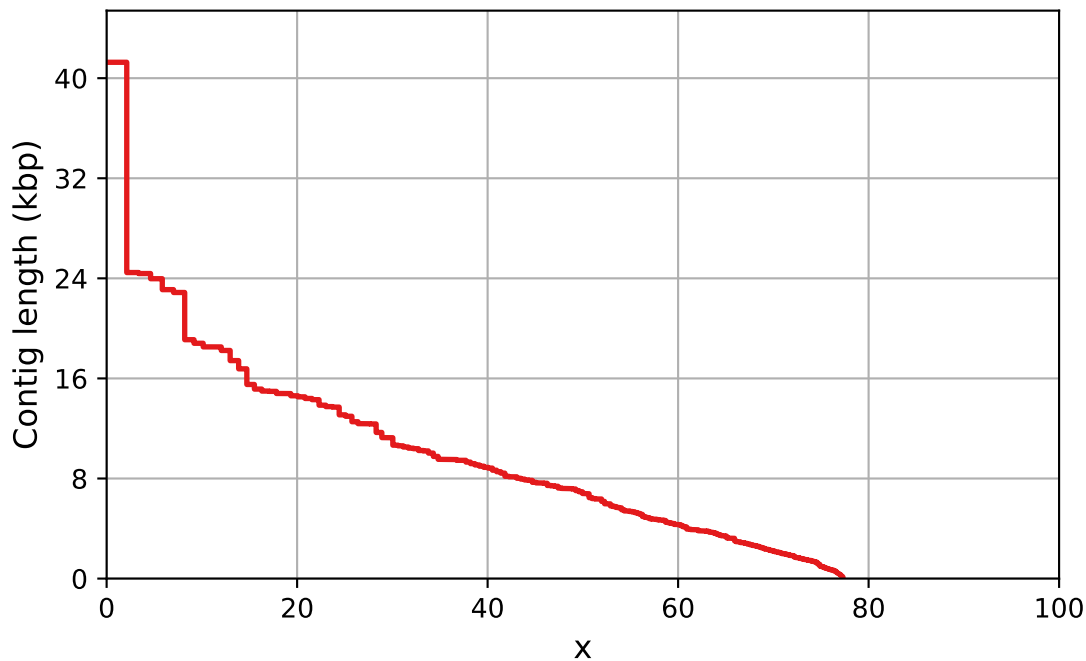


— SRR18214264-contigs_abyss_fa

Cumulative length (aligned contigs)

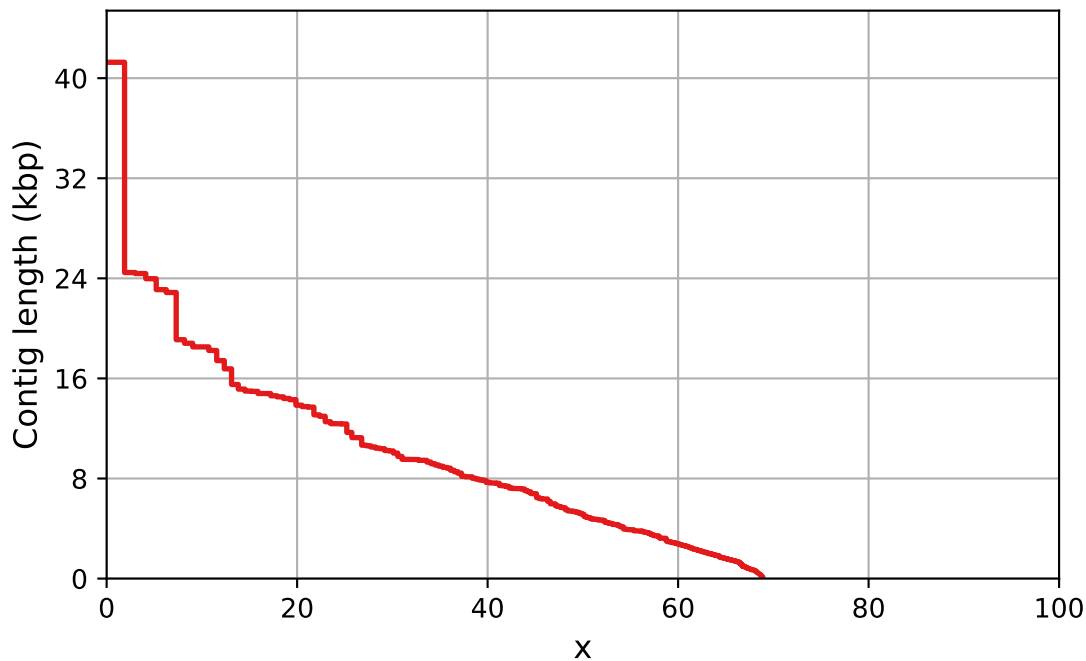


NAx



SRR18214264-contigs_abyss_fa

NGAx



— SRR18214264-contigs_abyss_fa