

Report

	ERR204044-contigs_abyss_fa
# contigs (>= 0 bp)	837
# contigs (>= 1000 bp)	149
Total length (>= 0 bp)	2082004
Total length (>= 1000 bp)	1986950
# contigs	162
Largest contig	104390
Total length	1996676
Reference length	2191149
GC (%)	36.53
Reference GC (%)	37.07
N50	27525
NG50	23032
N90	5485
NG90	1681
auN	33109.9
auNG	30171.2
L50	23
LG50	27
L90	88
LG90	138
# misassemblies	126
# misassembled contigs	59
Misassembled contigs length	1378462
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	10
# unaligned contigs	19 + 79 part
Unaligned length	456703
Genome fraction (%)	75.099
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1130.20
# indels per 100 kbp	76.20
Largest alignment	51210
Total aligned length	1531593
NA50	7639
NGA50	6391
NA90	-
NGA90	-
auNA	10704.2
auNGA	9754.1
LA50	68
LGA50	81
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

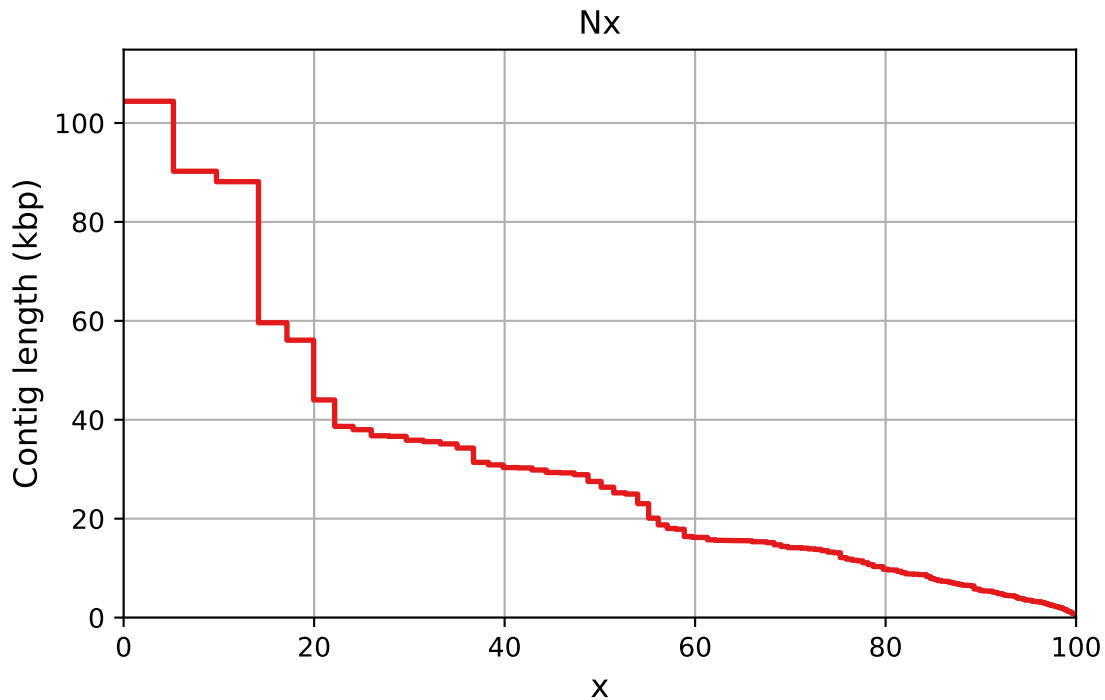
	ERR204044-contigs_abyss_fa
# misassemblies	126
# contig misassemblies	126
# c. relocations	126
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	59
Misassembled contigs length	1378462
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	10
# mismatches	17310
# indels	1167
# indels (<= 5 bp)	888
# indels (> 5 bp)	279
Indels length	8301

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

## Unaligned report

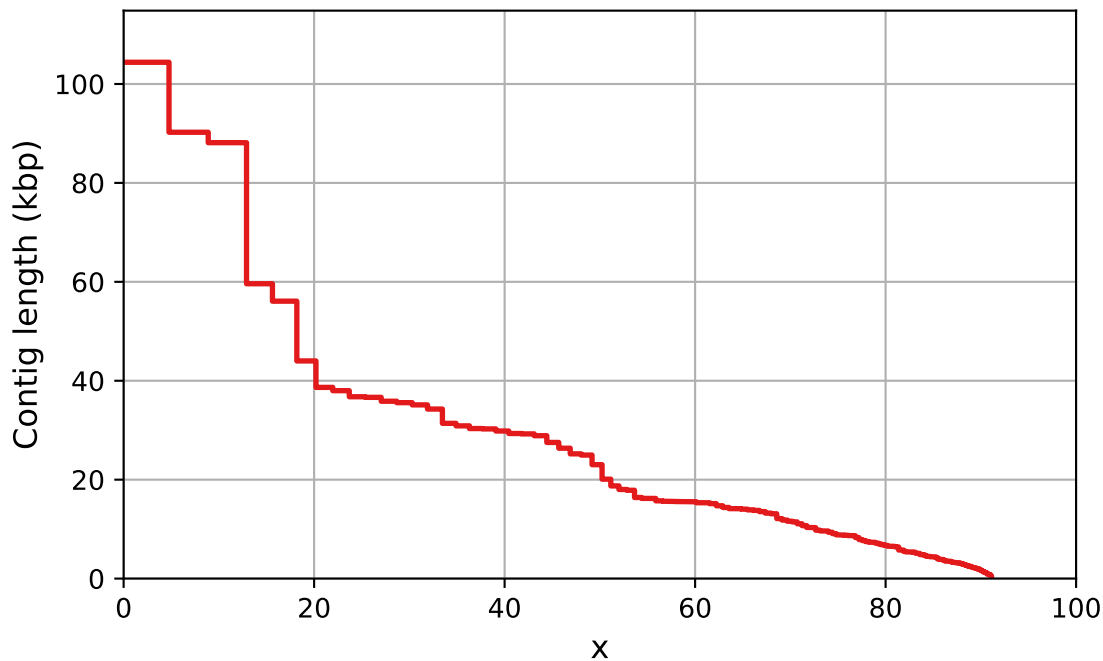
	ERR204044-contigs_abyss_fa
# fully unaligned contigs	19
Fully unaligned length	56346
# partially unaligned contigs	79
Partially unaligned length	400357
# N's	0

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



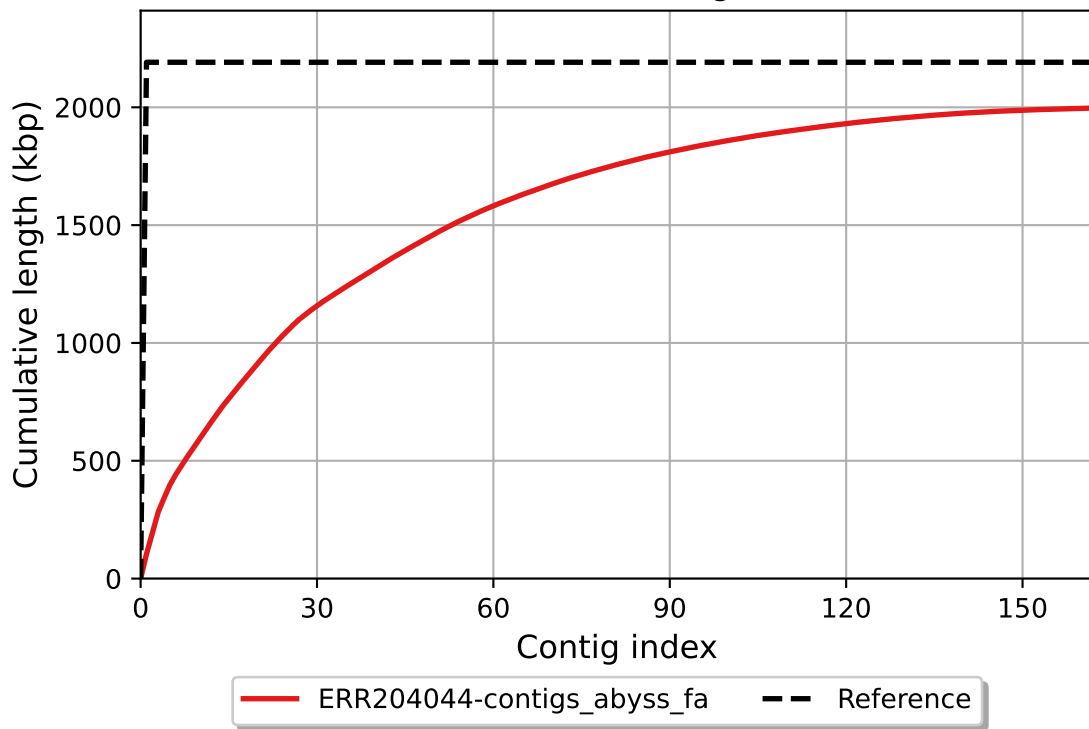
ERR204044-contigs\_abyss\_fa

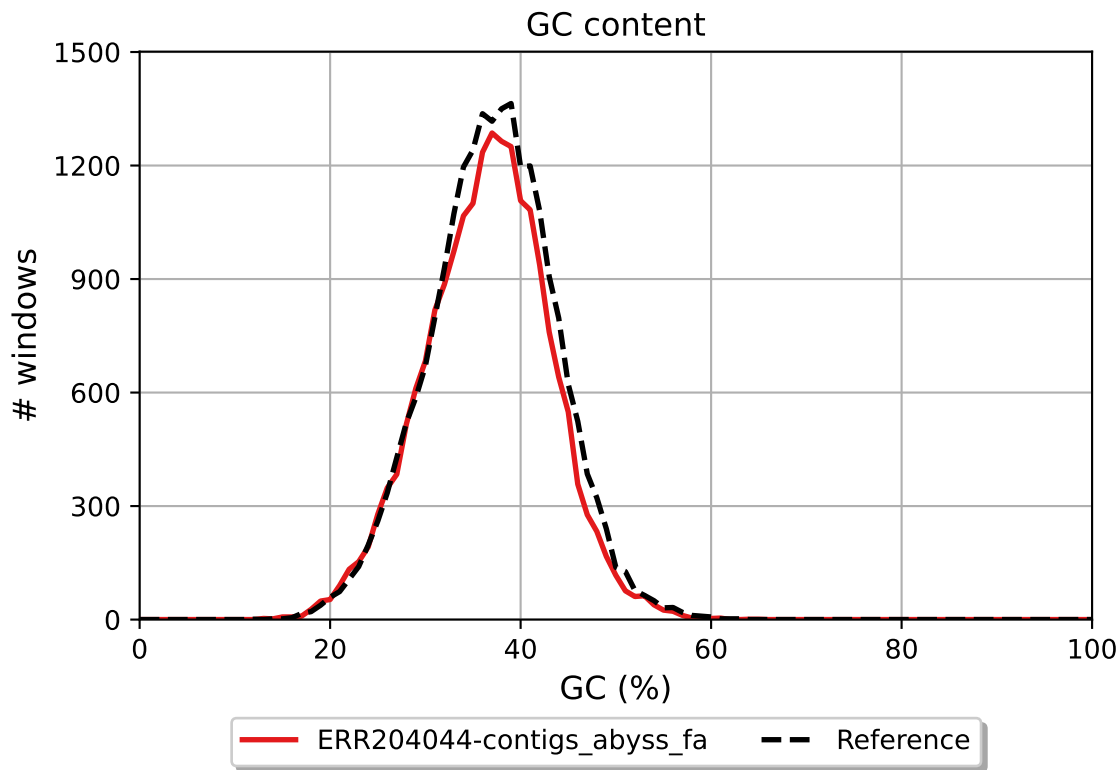
# NGx



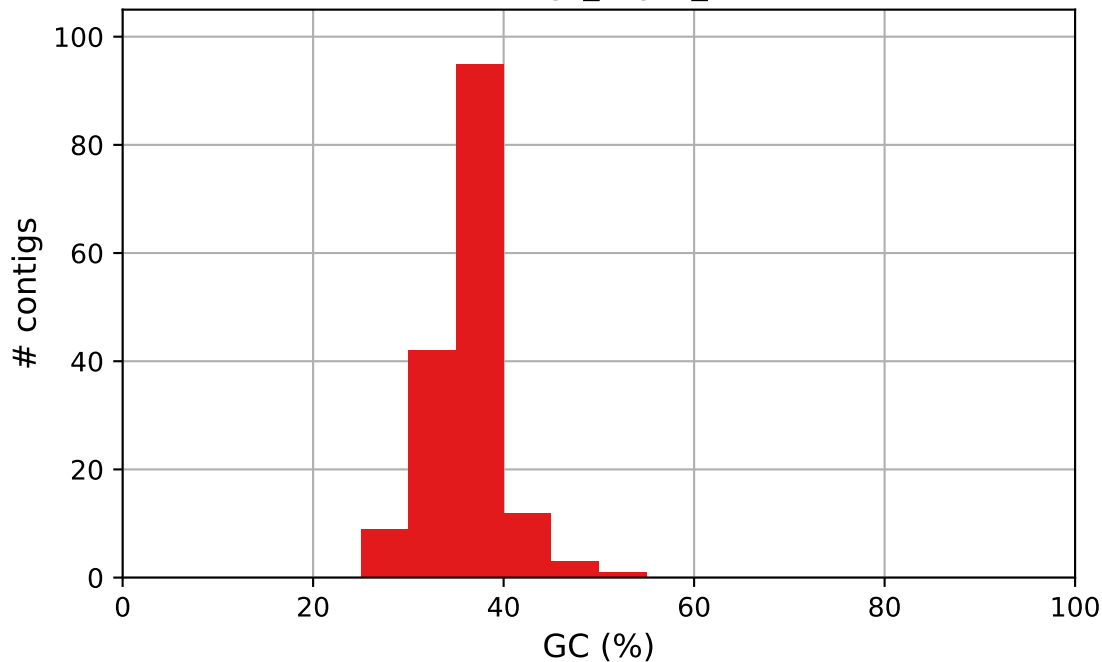
ERR204044-contigs\_abyss\_fa

Cumulative length





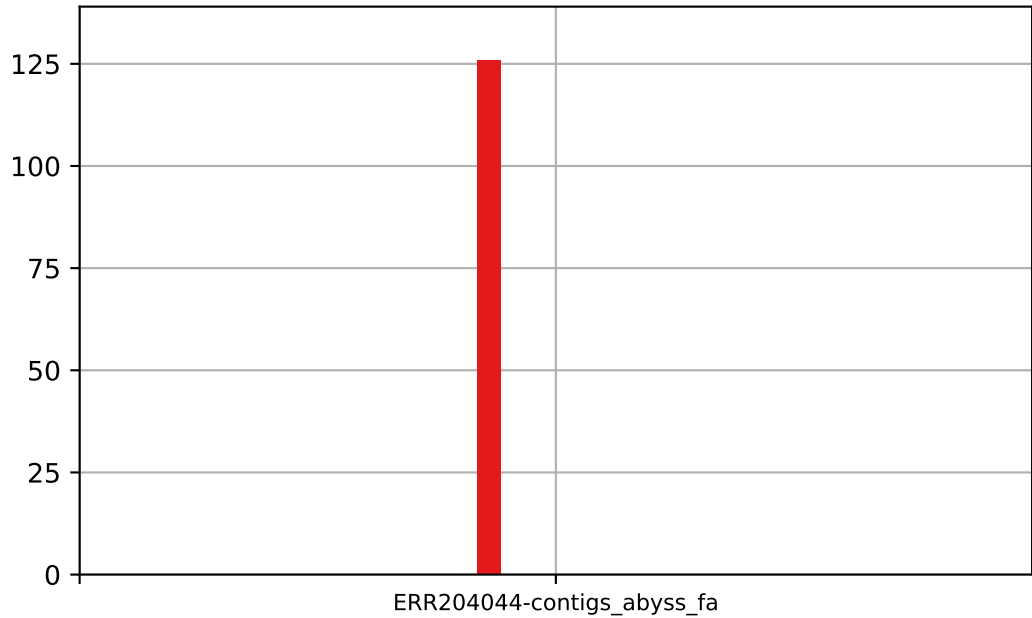
ERR204044-contigs\_abyss\_fa GC content



ERR204044-contigs\_abyss\_fa

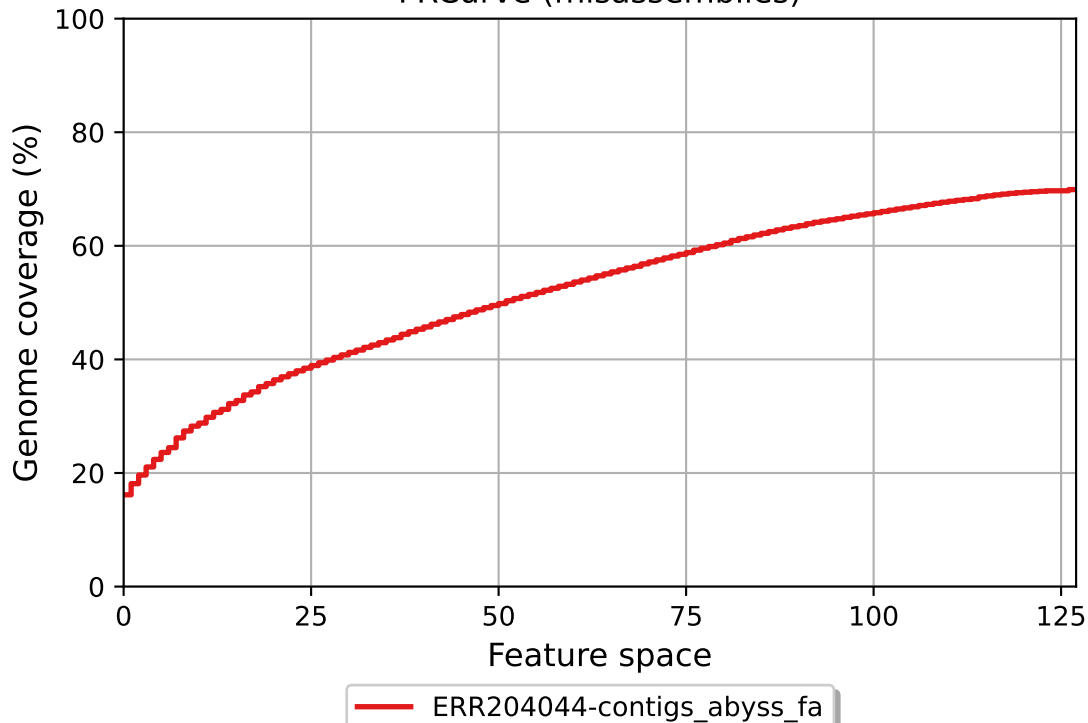


## Misassemblies

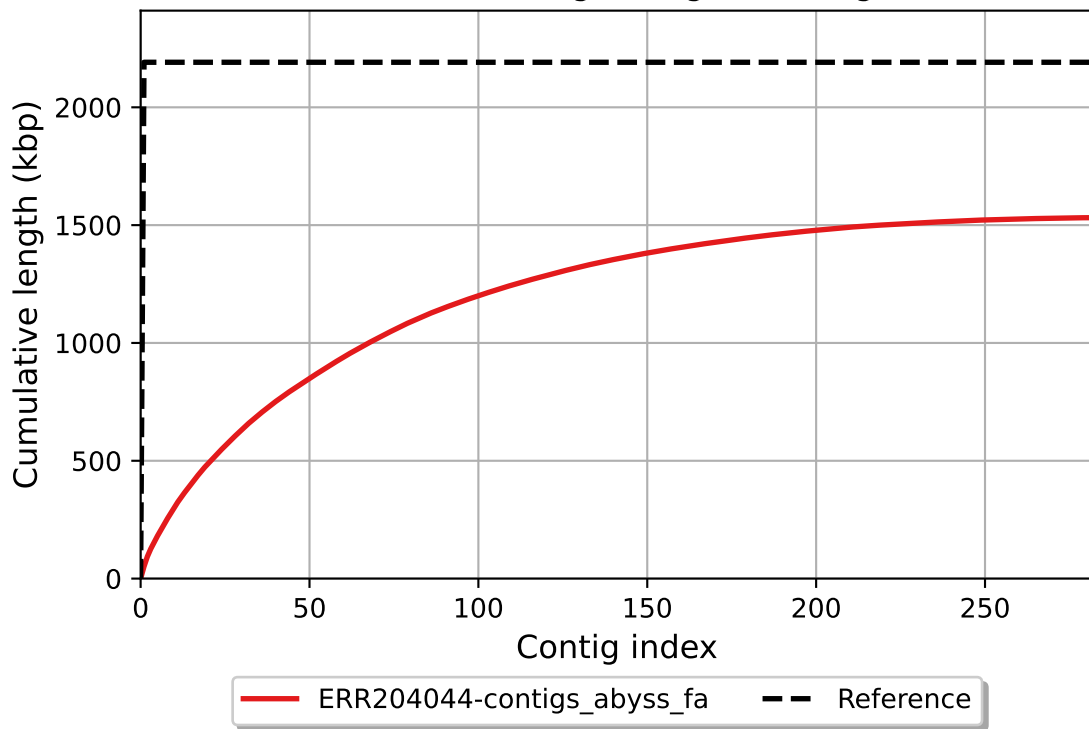


 # relocations

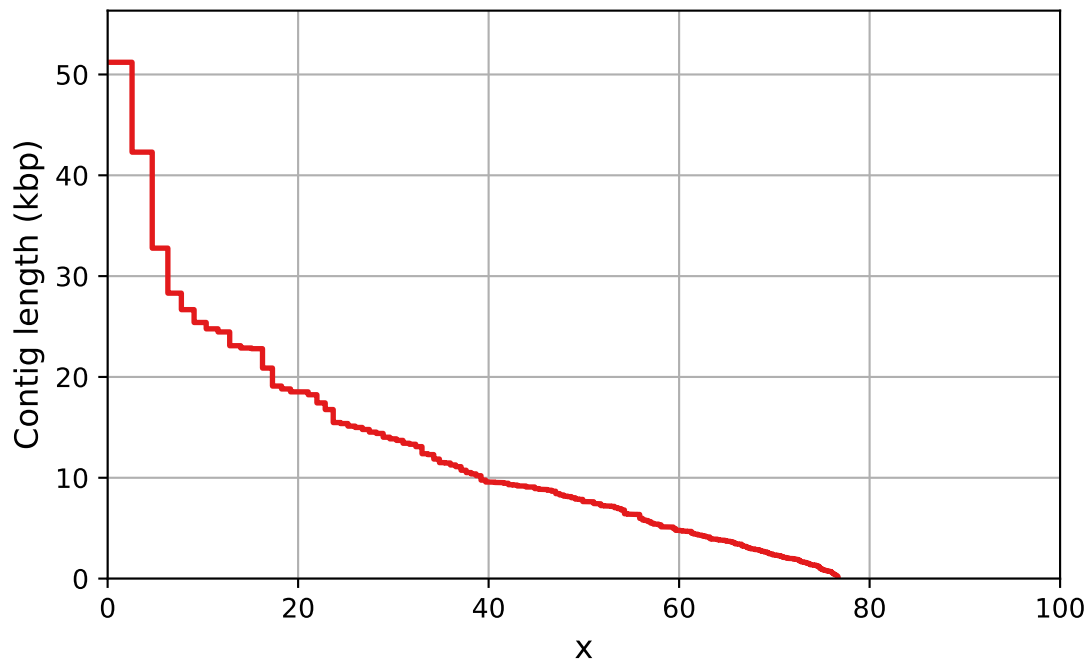
FRCurve (misassemblies)



Cumulative length (aligned contigs)

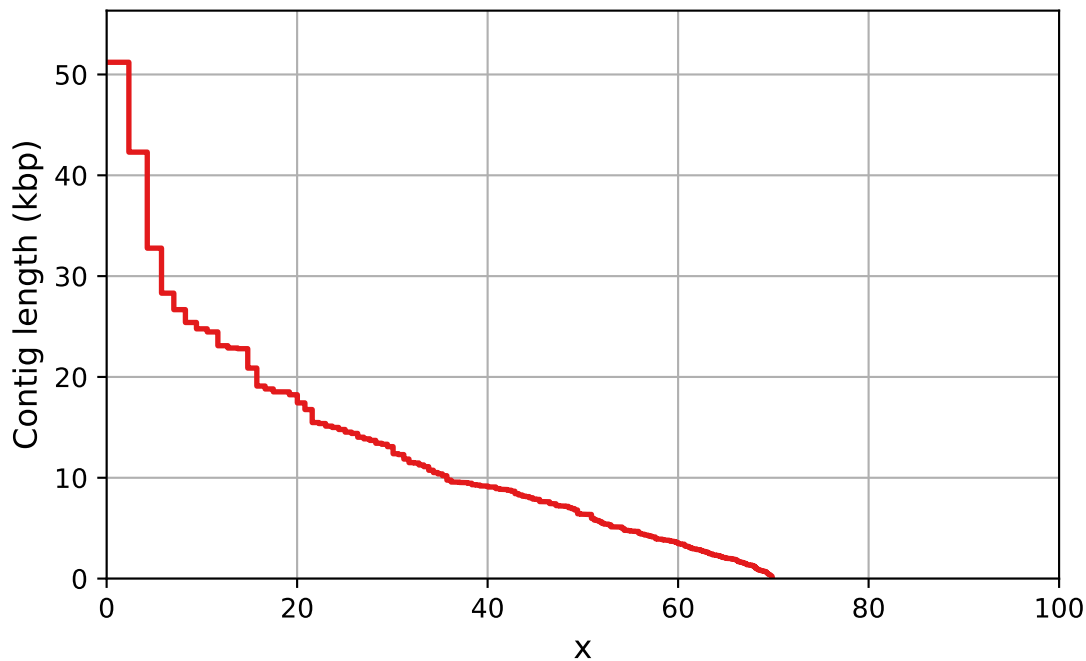


NAx



ERR204044-contigs\_abys\_f\_a

# NGAx



ERR204044-contigs\_abyss\_fa