

## Report

	contigs_SRR18214264_spades_fasta
# contigs (>= 0 bp)	447
# contigs (>= 1000 bp)	142
Total length (>= 0 bp)	2036064
Total length (>= 1000 bp)	1979187
# contigs	159
Largest contig	103582
Total length	1991331
Reference length	2191149
GC (%)	36.49
Reference GC (%)	37.07
N50	30018
NG50	28208
N90	6193
NG90	1196
auN	34631.5
auNG	31473.3
L50	22
LG50	26
L90	80
LG90	136
# misassemblies	127
# misassembled contigs	55
Misassembled contigs length	1350869
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	12
# unaligned contigs	6 + 85 part
Unaligned length	446120
Genome fraction (%)	77.829
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1170.59
# indels per 100 kbp	80.16
Largest alignment	51210
Total aligned length	1534348
NA50	7882
NGA50	6431
NA90	-
NGA90	-
auNA	10739.0
auNGA	9759.6
LA50	67
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

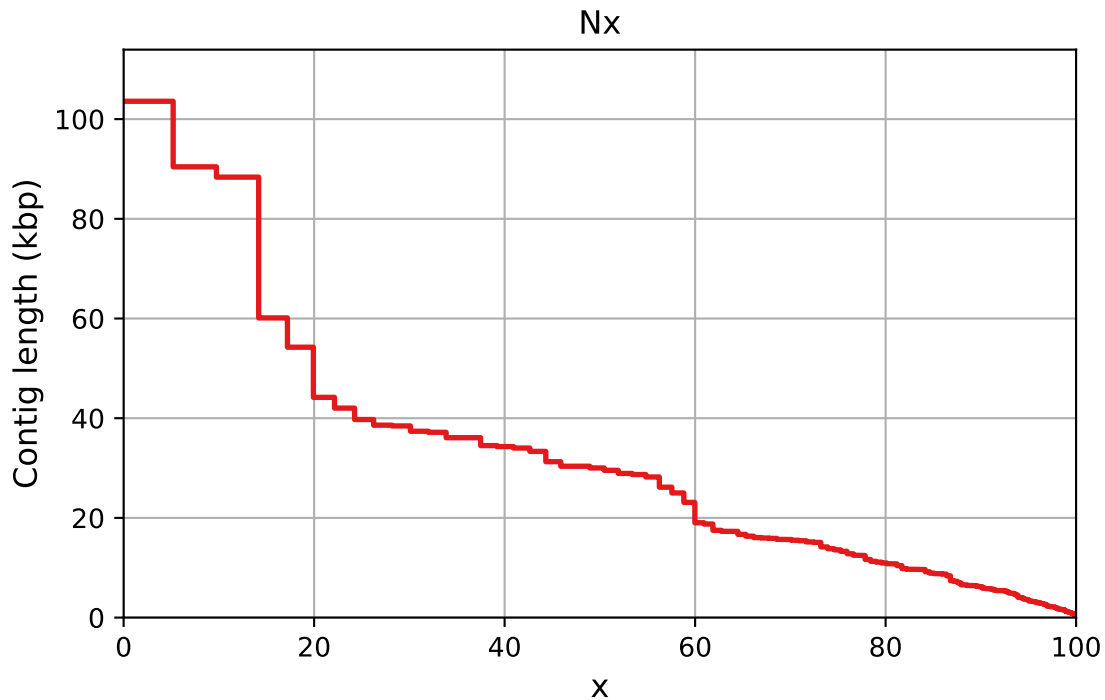
	contigs_SRR18214264_spades_fasta
# misassemblies	127
# contig misassemblies	127
# c. relocations	127
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	55
Misassembled contigs length	1350869
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	12
# mismatches	17961
# indels	1230
# indels (<= 5 bp)	945
# indels (> 5 bp)	285
Indels length	8277

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

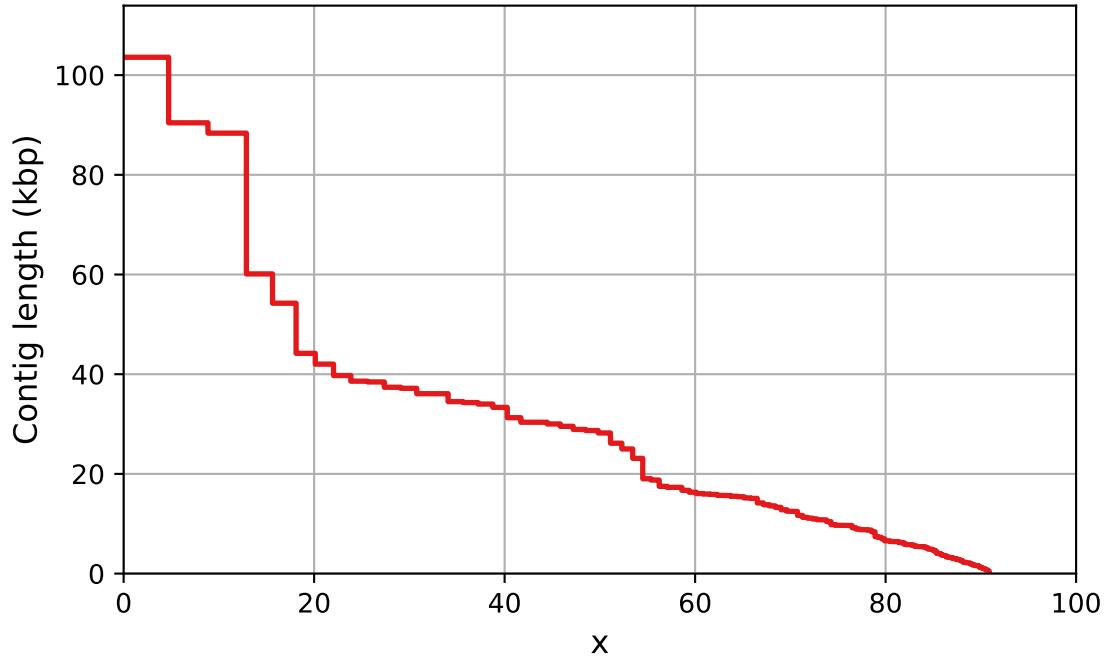
	contigs_SRR18214264_spades_fasta
# fully unaligned contigs	6
Fully unaligned length	5389
# partially unaligned contigs	85
Partially unaligned length	440731
# N's	0

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).



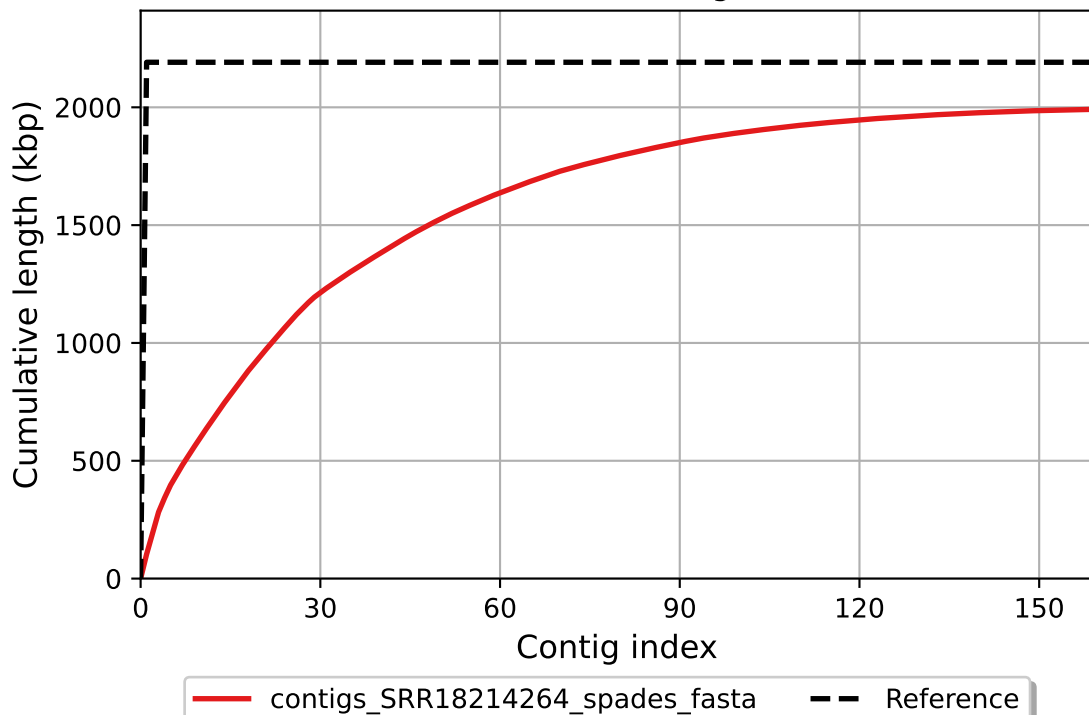
— contigs\_SRR18214264\_spades\_fasta

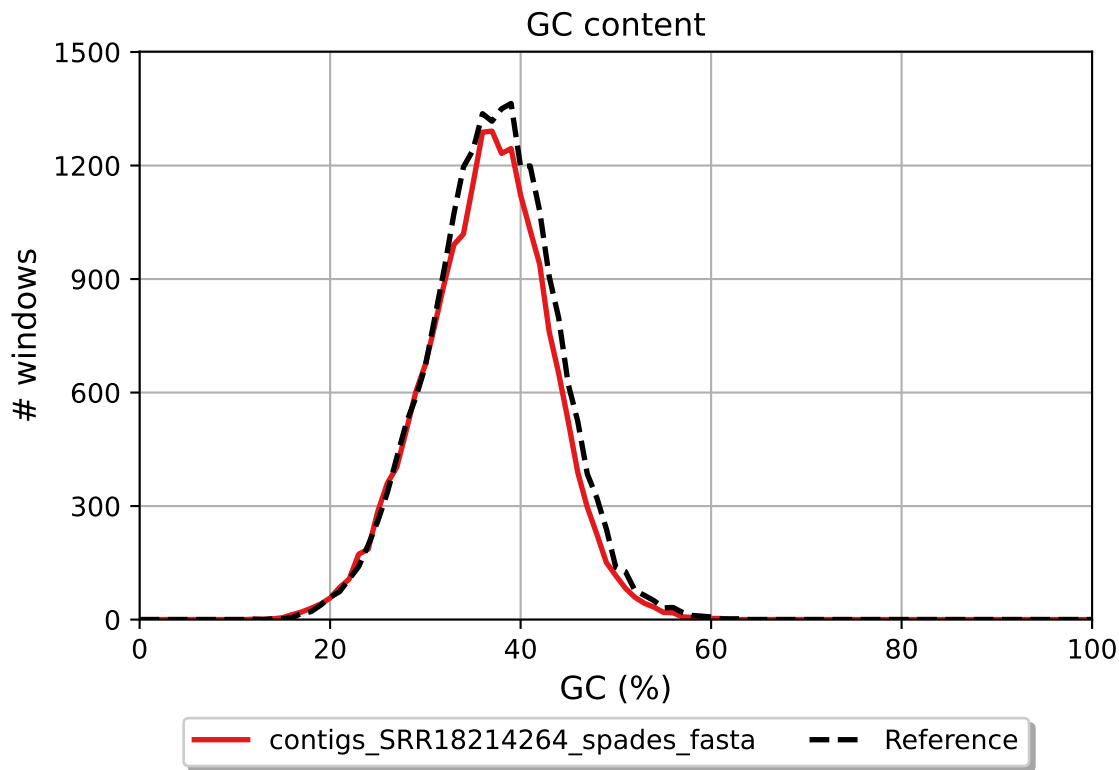
# NGx



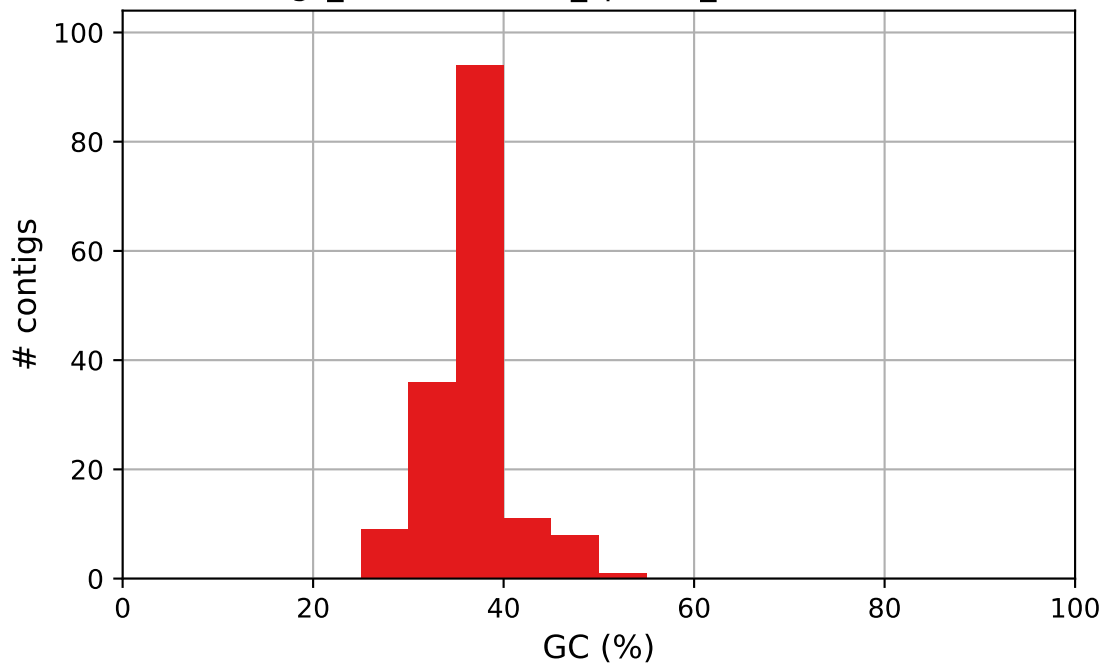
— contigs\_SRR18214264\_spades\_fasta

Cumulative length





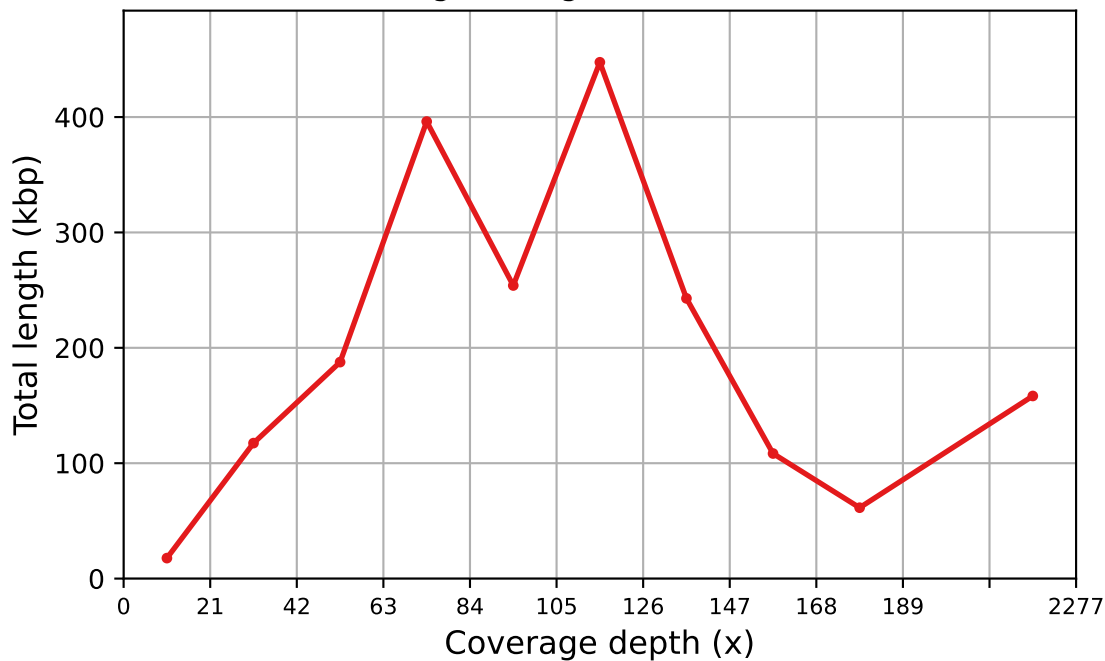
contigs\_SRR18214264\_spades\_fasta GC content



contigs\_SRR18214264\_spades\_fasta

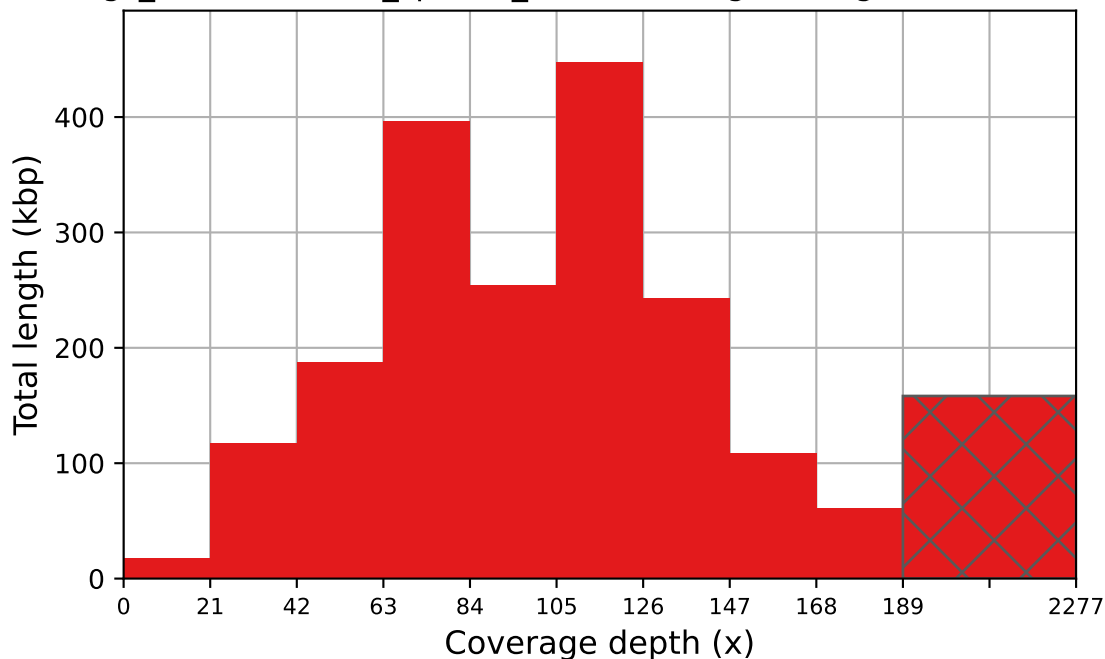


Coverage histogram (bin size: 21x)



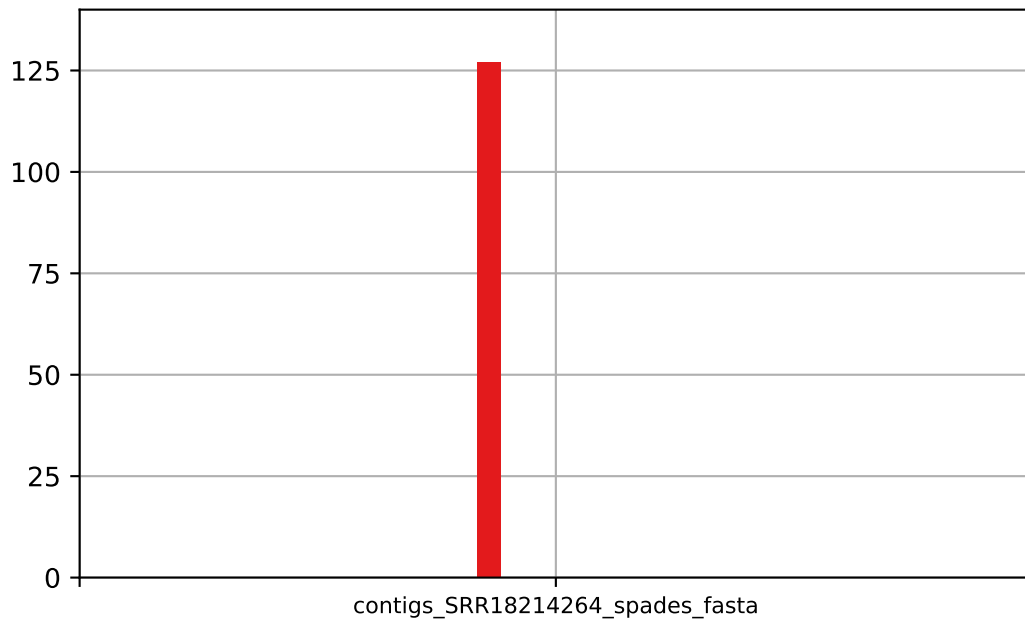
contigs\_SRR18214264\_spades\_fasta

contigs\_SRR18214264\_spades\_fasta coverage histogram (bin size: 21x)



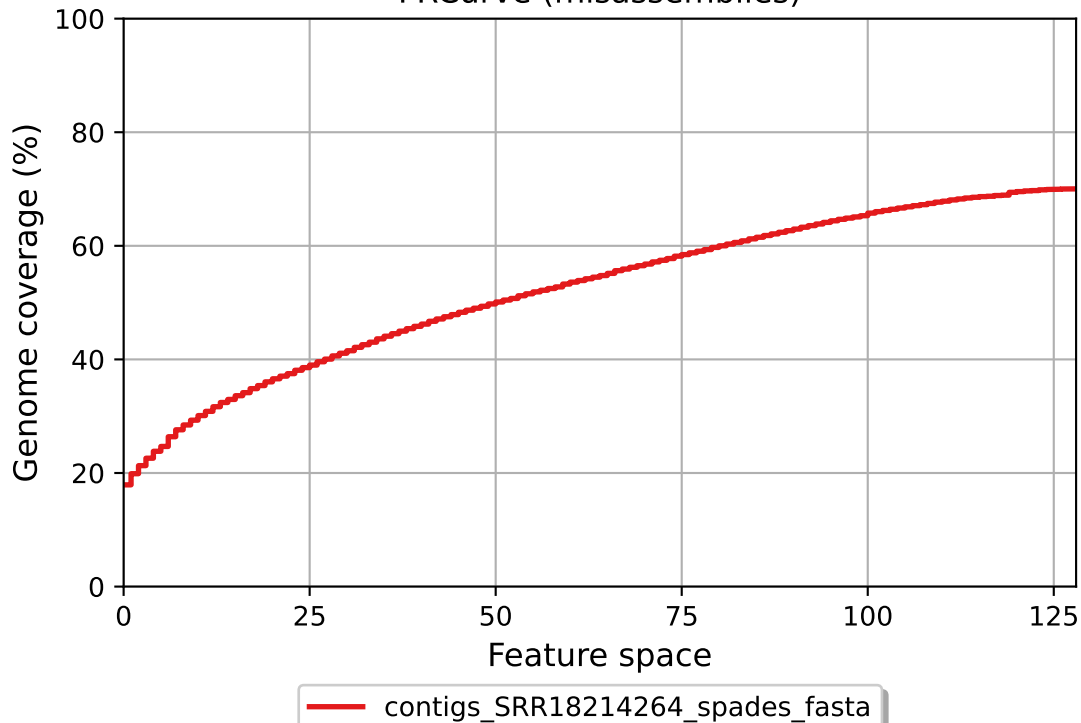
contigs\_SRR18214264\_spades\_fasta

## Misassemblies

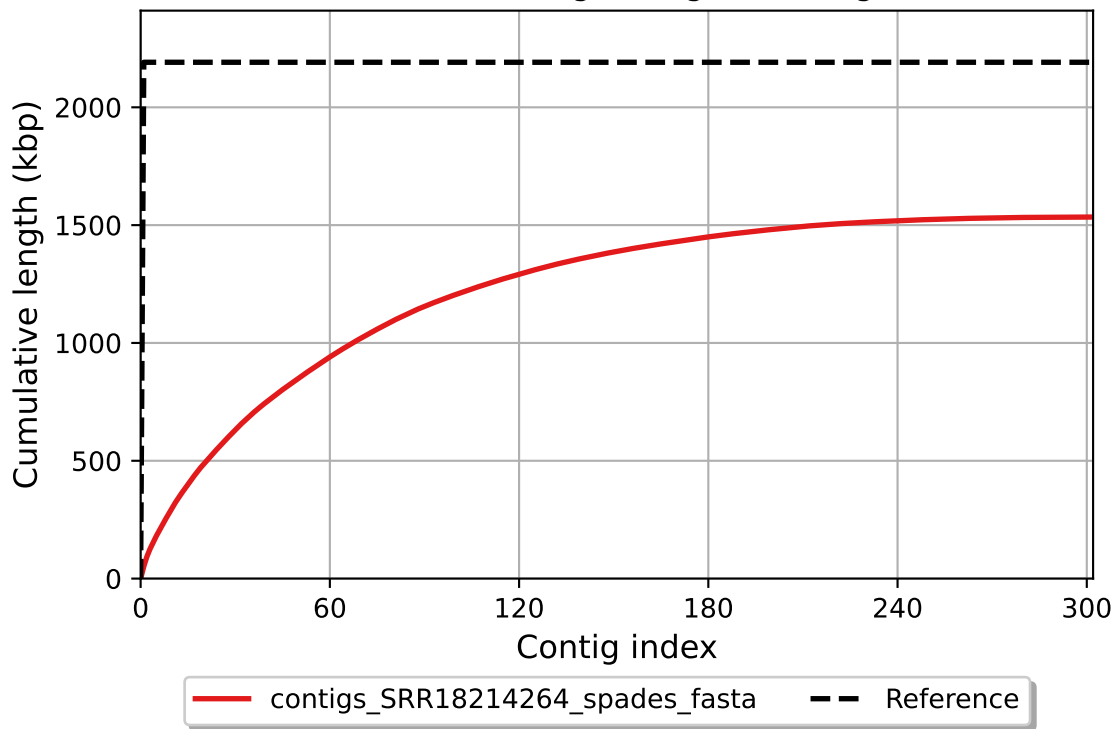


 # relocations

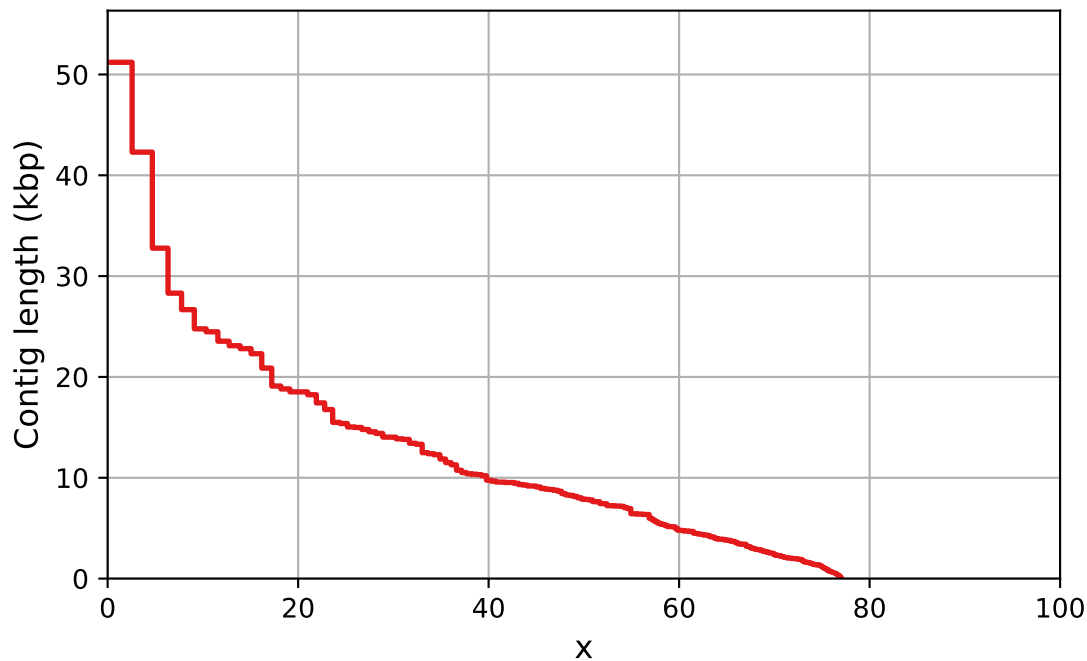
FRCurve (misassemblies)



Cumulative length (aligned contigs)

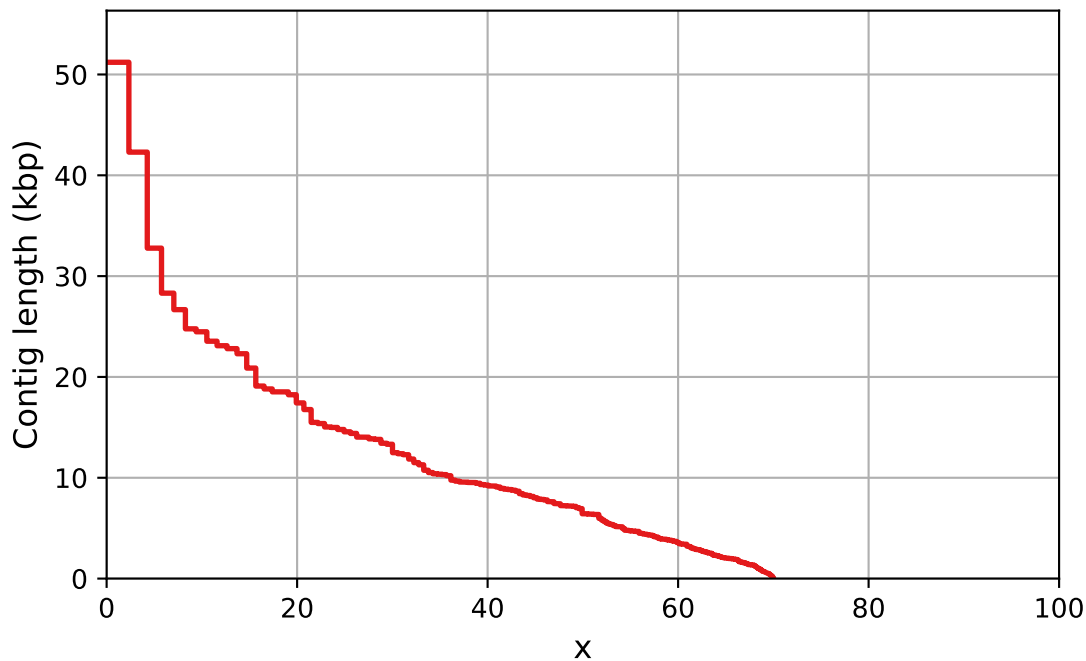


NAx



— contigs\_SRR18214264\_spades\_fasta

## NGAx



— contigs\_SRR18214264\_spades\_fasta