

# Report

	ERR1795073.contigs
# contigs (>= 0 bp)	557
# contigs (>= 1000 bp)	150
# contigs (>= 5000 bp)	86
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	33
Total length (>= 0 bp)	5881752
Total length (>= 1000 bp)	5730301
Total length (>= 5000 bp)	5571890
Total length (>= 10000 bp)	5432736
Total length (>= 25000 bp)	5053531
Total length (>= 50000 bp)	4661625
# contigs	187
Largest contig	329050
Total length	5755059
Reference length	5781501
GC (%)	57.04
Reference GC (%)	56.97
N50	134791
NG50	134791
N75	84908
NG75	84908
L50	15
LG50	15
L75	28
LG75	28
# misassemblies	34
# misassembled contigs	27
Misassembled contigs length	2050270
# local misassemblies	35
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	9
# unaligned contigs	41 + 45 part
Unaligned length	463150
Genome fraction (%)	91.106
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	191.90
# indels per 100 kbp	5.47
Largest alignment	319821
Total aligned length	5285132
NA50	116791
NGA50	116791
NA75	45242
NGA75	42239
LA50	17
LGA50	17
LA75	36
LGA75	37

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

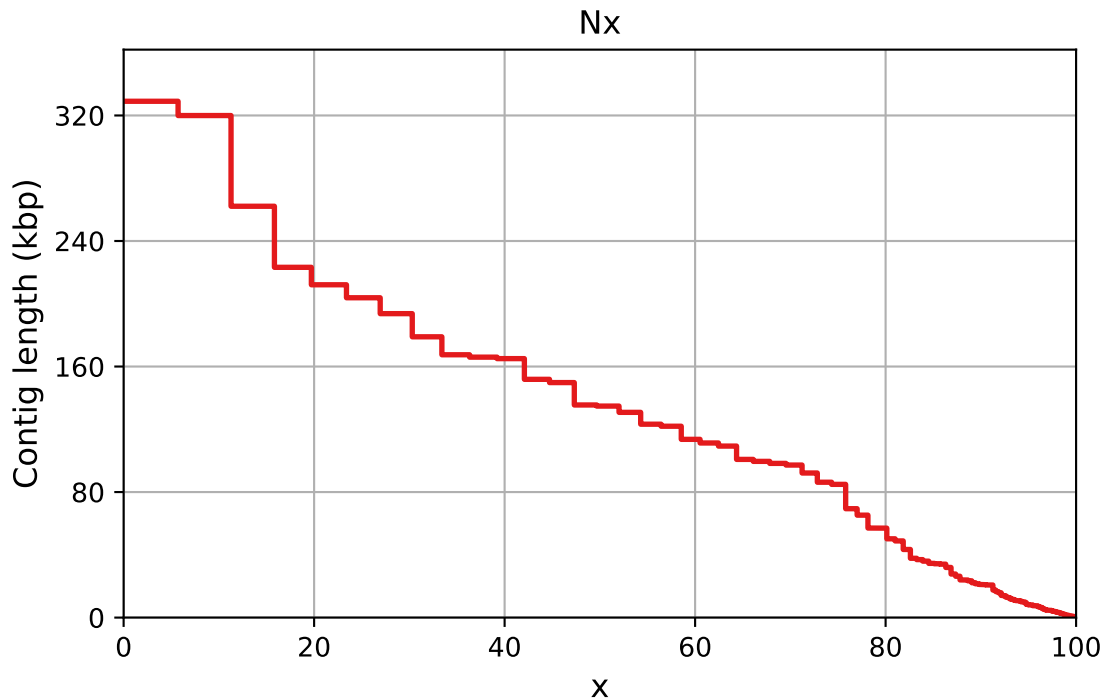
	ERR1795073.contigs
# misassemblies	34
# contig misassemblies	34
# c. relocations	30
# c. translocations	3
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	27
Misassembled contigs length	2050270
# local misassemblies	35
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	9
# mismatches	10108
# indels	288
# indels (<= 5 bp)	248
# indels (> 5 bp)	40
Indels length	1131

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

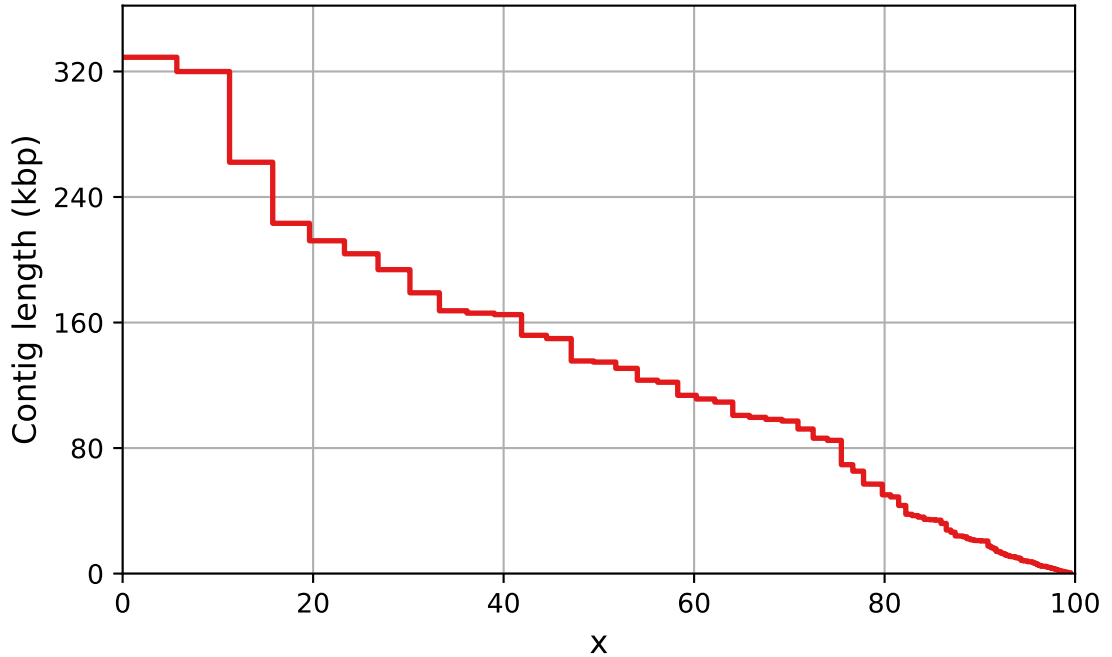
	ERR1795073.contigs
# fully unaligned contigs	41
Fully unaligned length	105919
# partially unaligned contigs	45
Partially unaligned length	357231
# N's	0

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).



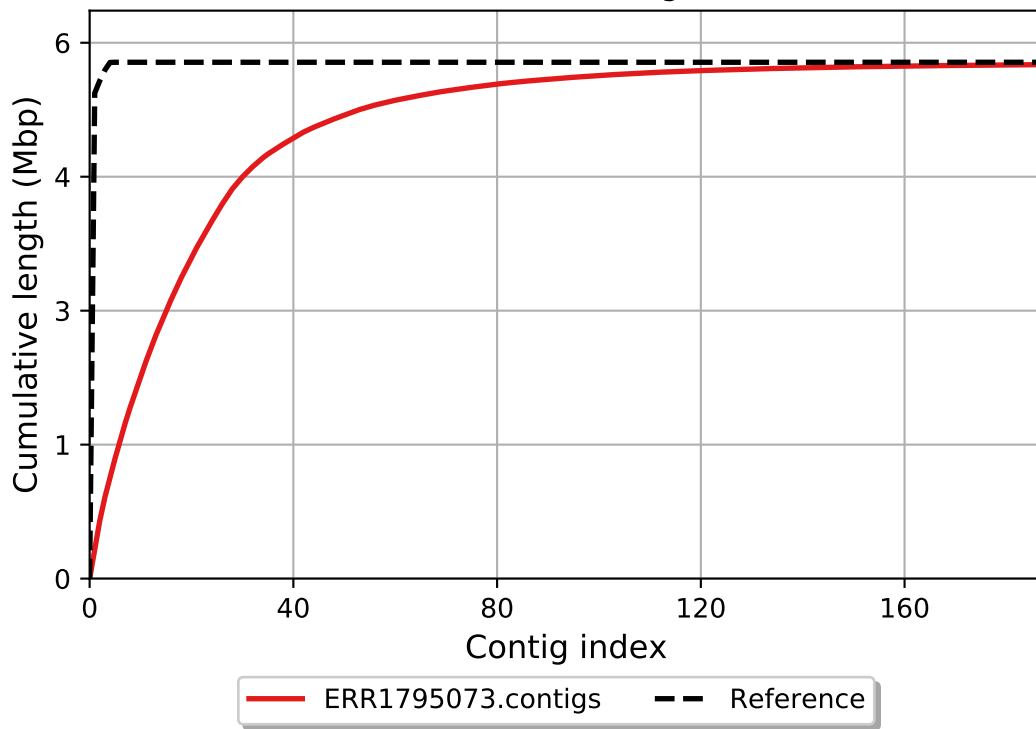
ERR1795073.contigs

# NGx

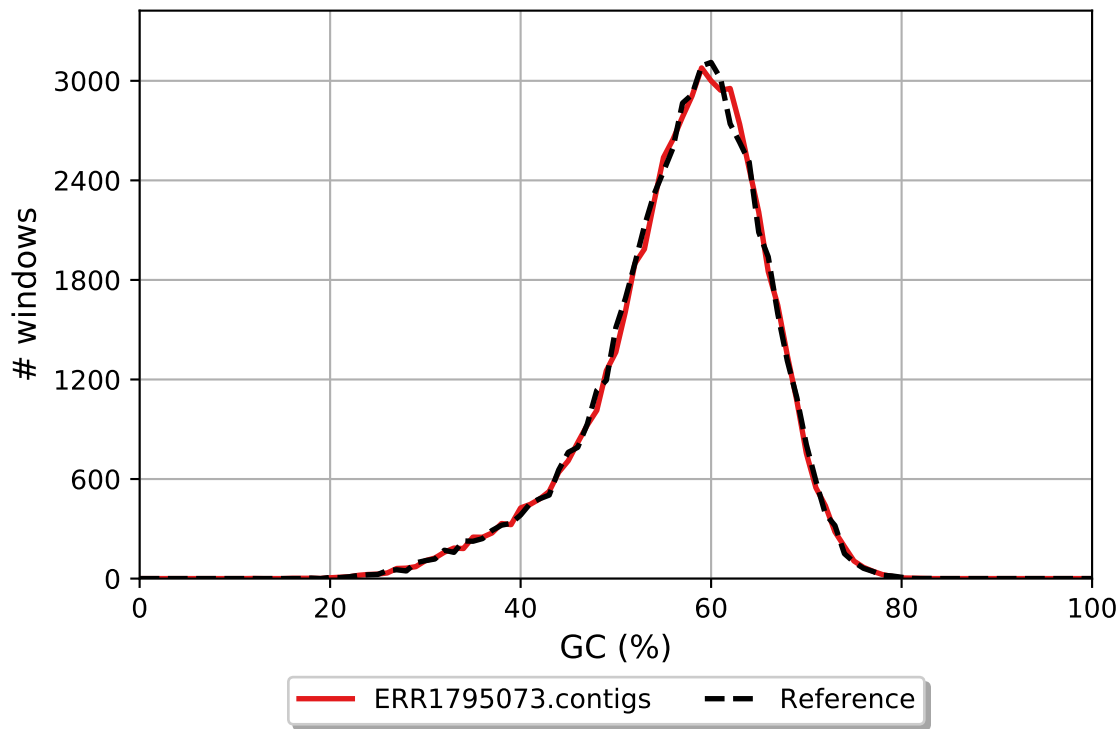


ERR1795073.contigs

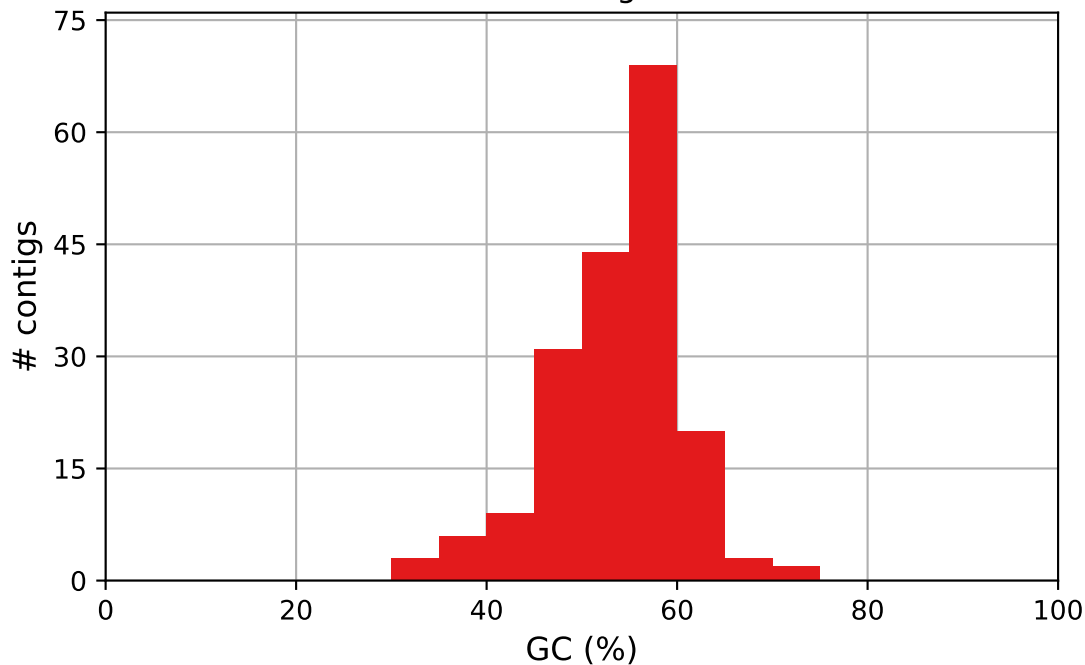
Cumulative length



# GC content



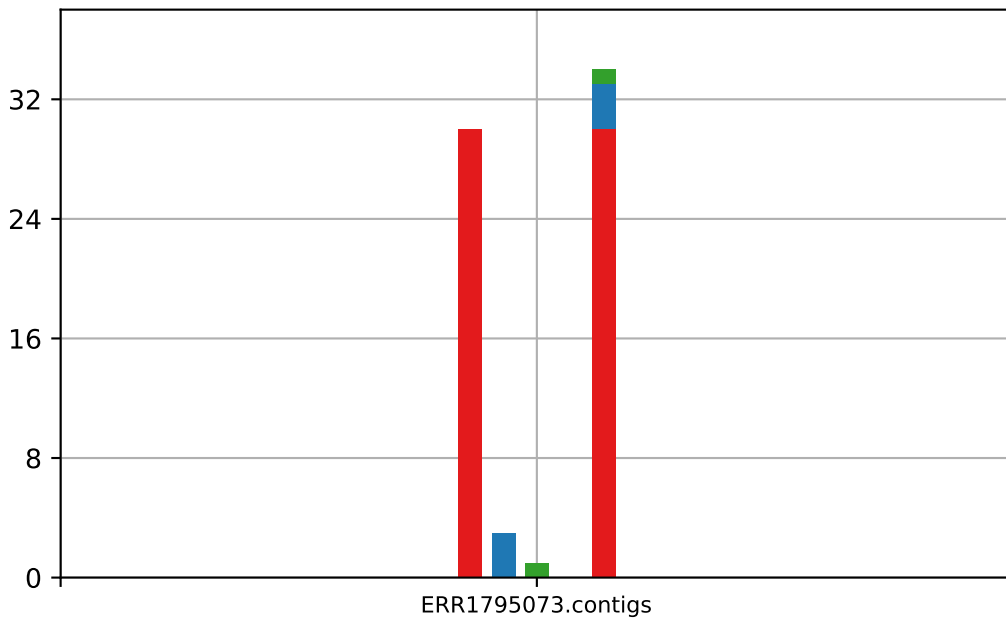
ERR1795073.contigs GC content



ERR1795073.contigs



## Misassemblies



# relocations

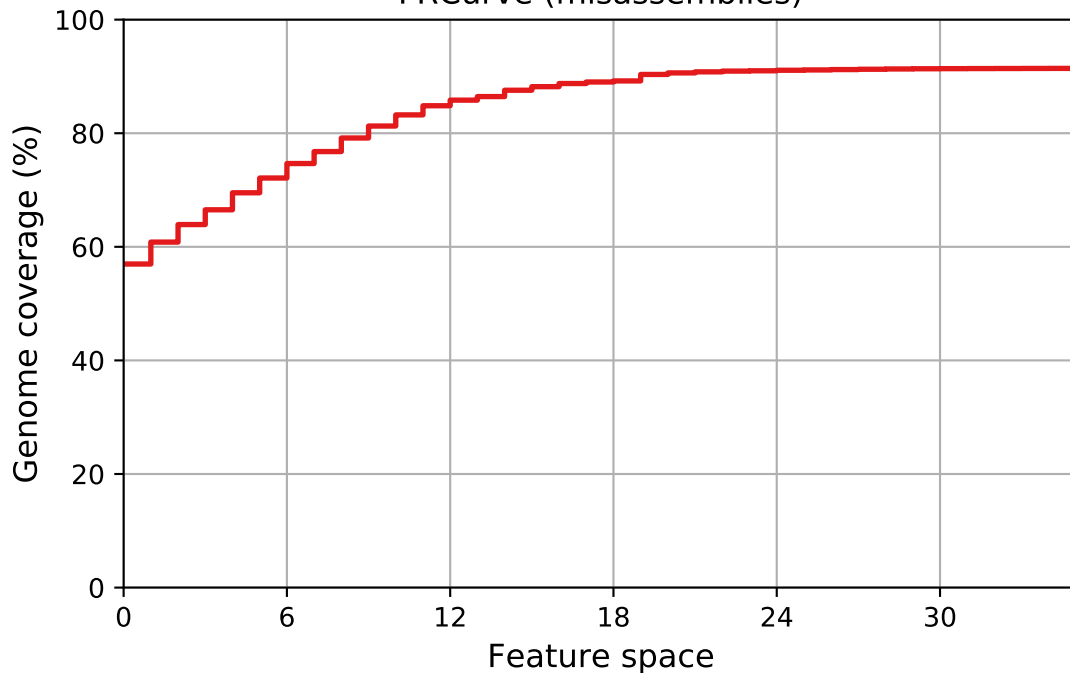


# translocations



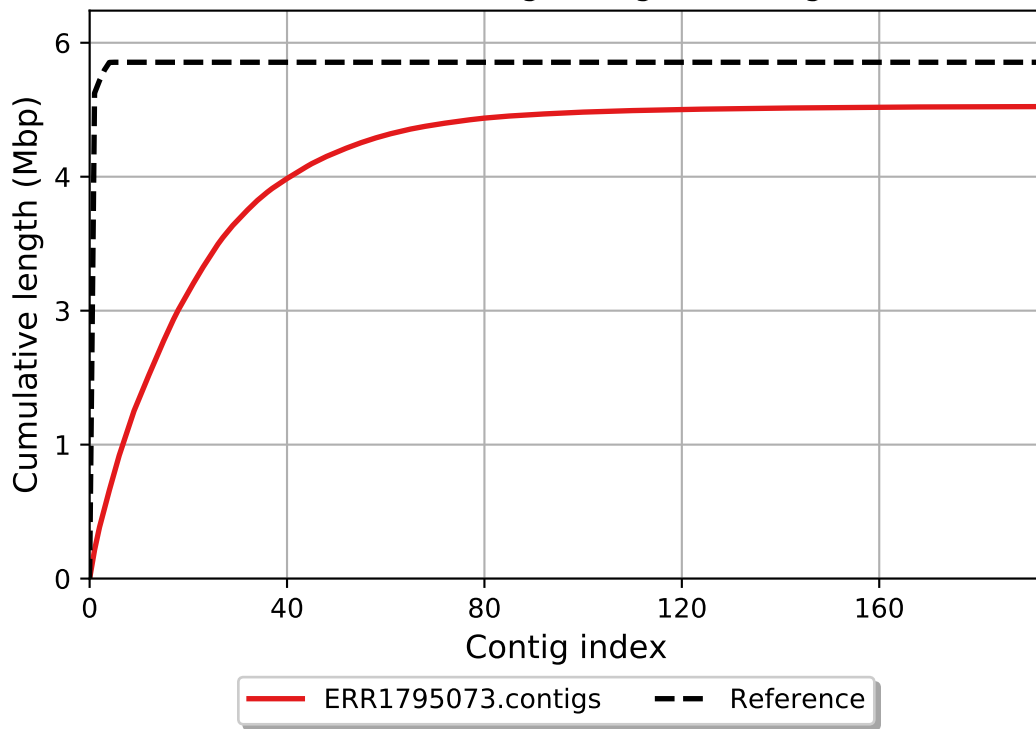
# inversions

FRCurve (misassemblies)

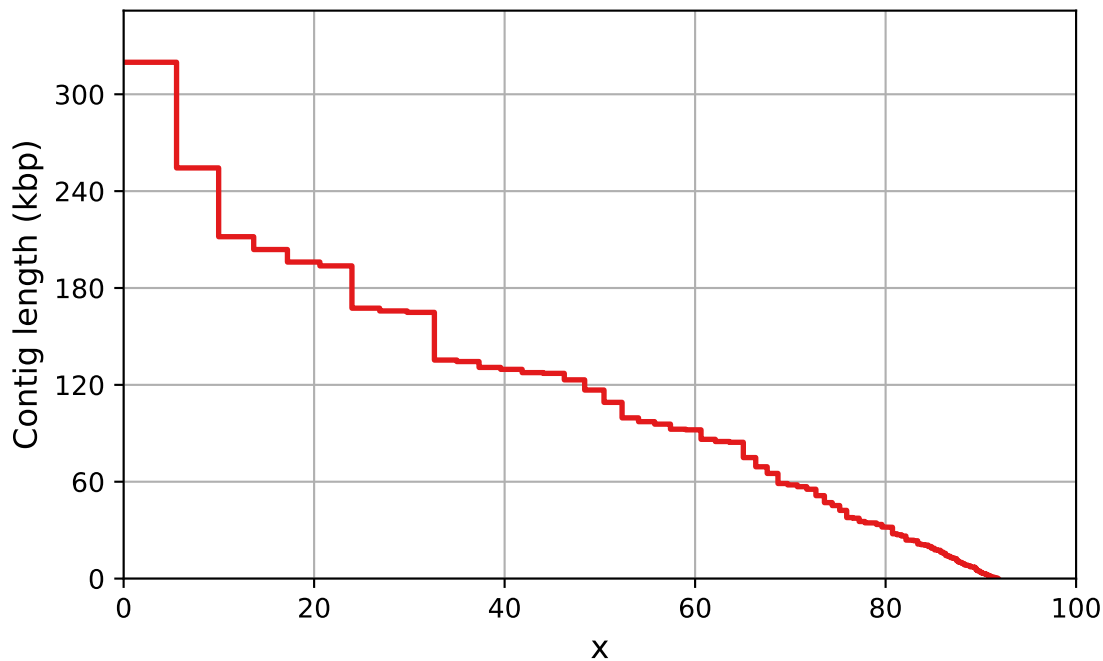


ERR1795073.contigs

Cumulative length (aligned contigs)

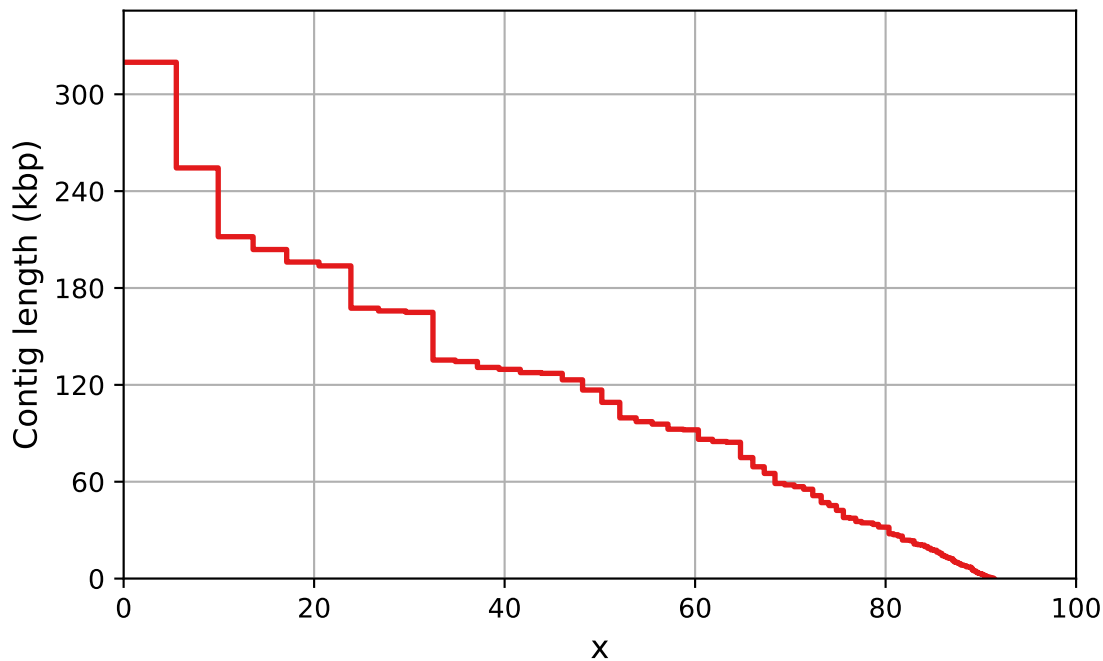


NAx



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# NGAx



ERR1795073.contigs