

## Report

	reNameResult
# contigs (>= 0 bp)	37
# contigs (>= 1000 bp)	37
# contigs (>= 5000 bp)	37
# contigs (>= 10000 bp)	37
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	12325448
Total length (>= 1000 bp)	12325448
Total length (>= 5000 bp)	12325448
Total length (>= 10000 bp)	12325448
Total length (>= 25000 bp)	12233243
Total length (>= 50000 bp)	12018991
# contigs	37
Largest contig	1076233
Total length	12325448
Reference length	12157105
GC (%)	38.22
Reference GC (%)	38.15
N50	678403
NG50	678403
N75	432839
NG75	432839
L50	8
LG50	8
L75	14
LG75	14
# misassemblies	79
# misassembled contigs	30
Misassembled contigs length	10380502
# local misassemblies	25
# unaligned mis. contigs	0
# unaligned contigs	1 + 11 part
Unaligned length	62721
Genome fraction (%)	98.221
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	80.67
# indels per 100 kbp	59.62
Largest alignment	1076081
Total aligned length	12257442
NA50	374994
NGA50	374994
NA75	198911
NGA75	198911
LA50	11
LGA50	11
LA75	22
LGA75	22

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

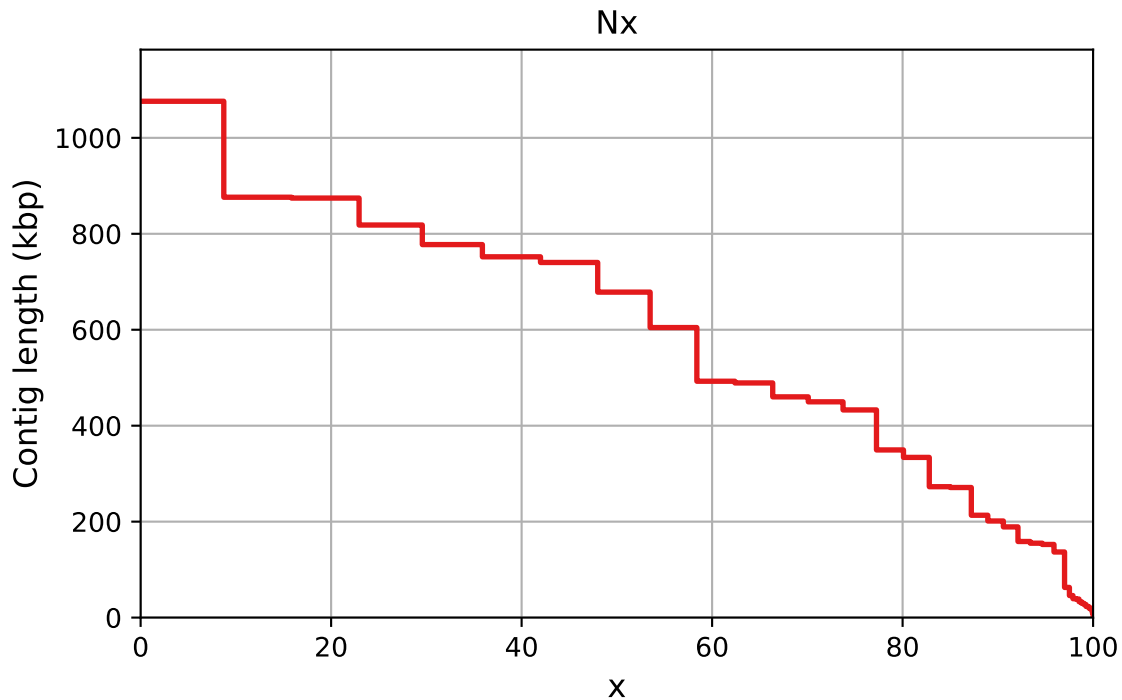
	reNameResult
# misassemblies	79
# relocations	33
# translocations	46
# inversions	0
# misassembled contigs	30
Misassembled contigs length	10380502
# local misassemblies	25
# unaligned mis. contigs	0
# mismatches	9633
# indels	7119
# indels ( $\leq 5$ bp)	6969
# indels ( $> 5$ bp)	150
Indels length	10252

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

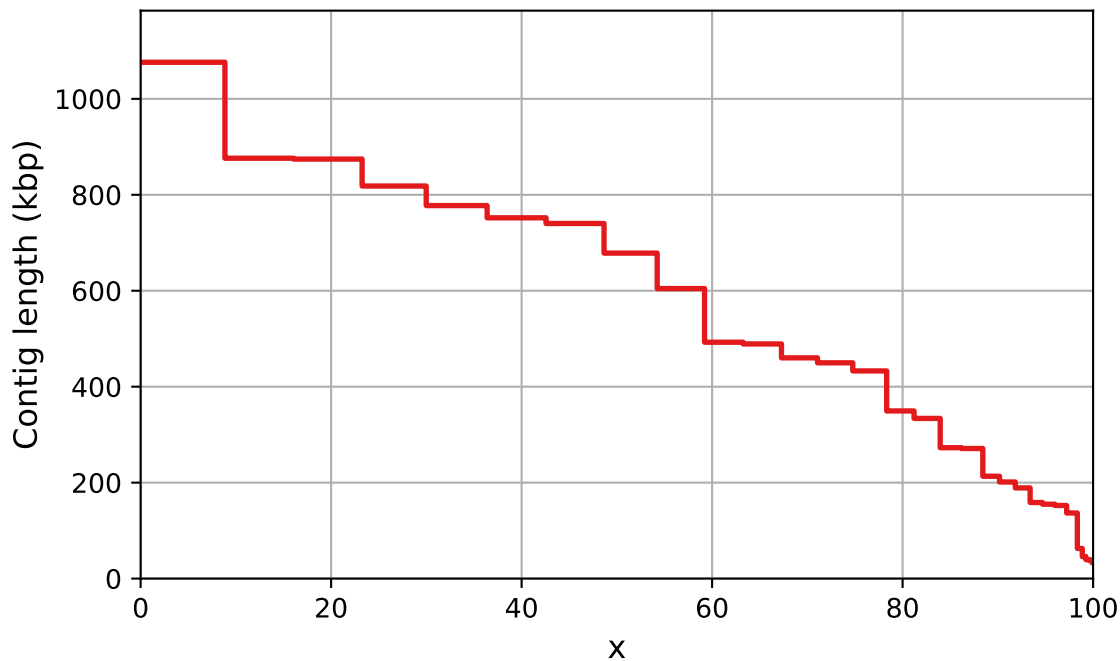
	reNameResult
# fully unaligned contigs	1
Fully unaligned length	18754
# partially unaligned contigs	11
Partially unaligned length	43967
# N's	0

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).



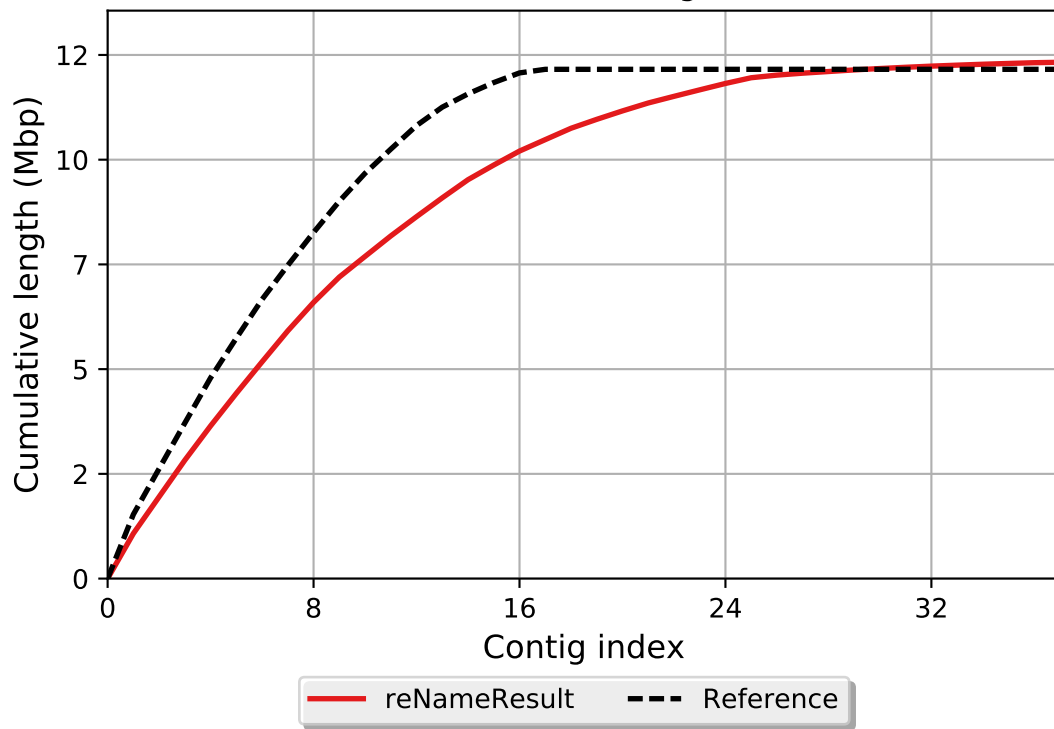
reNameResult

## NGx

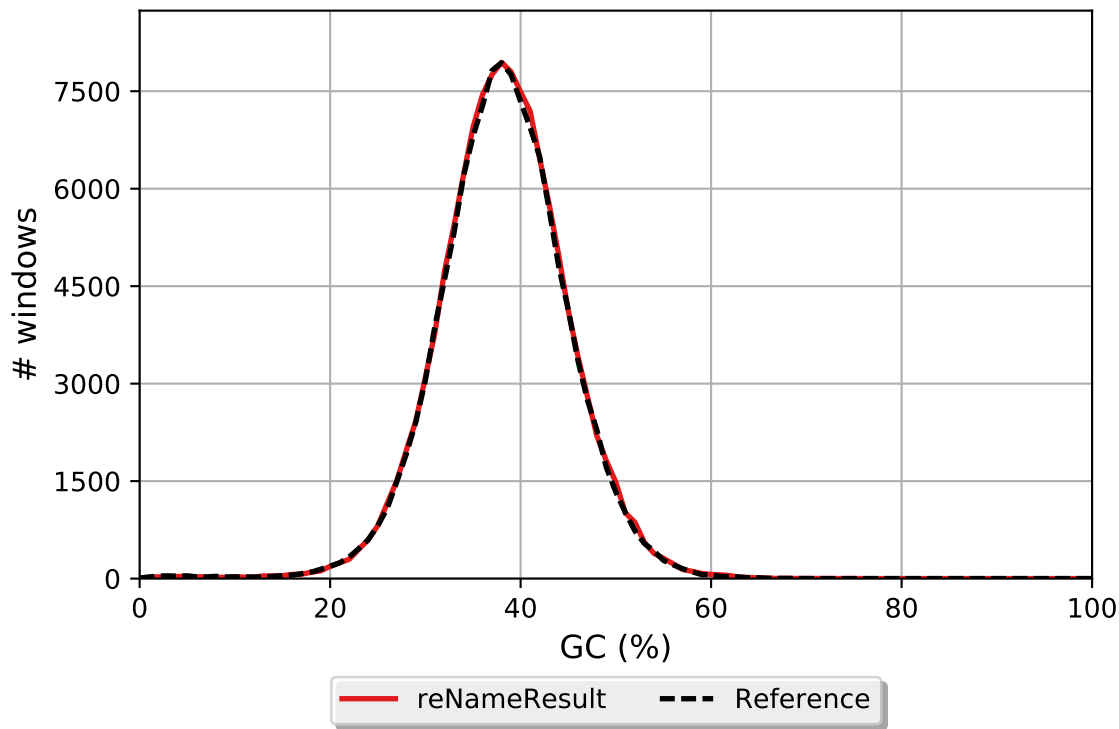


reNameResult

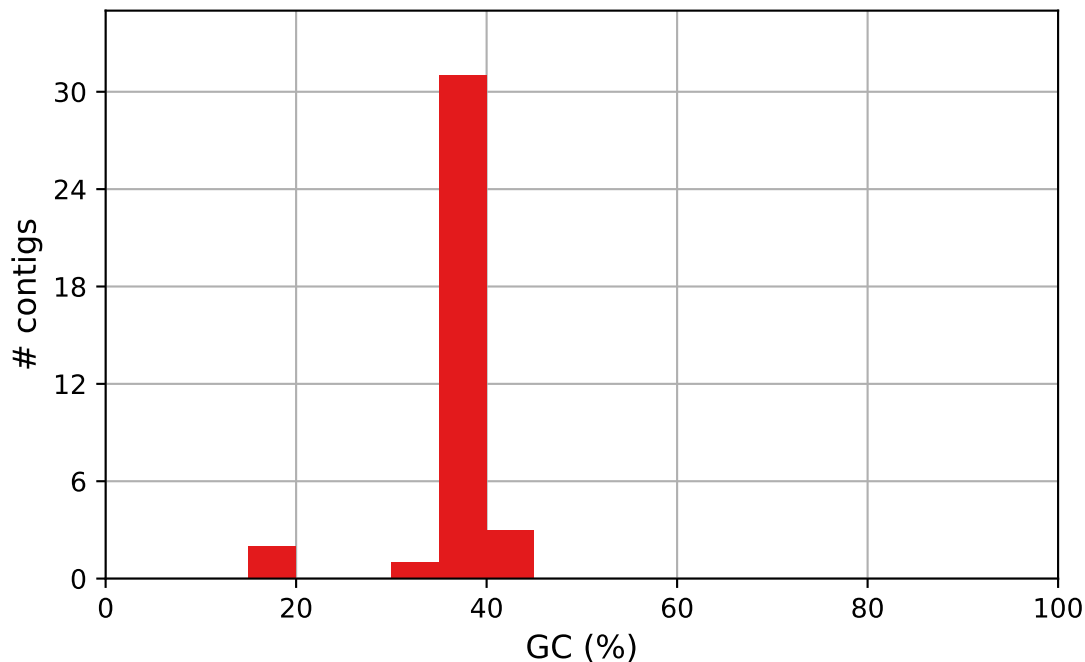
Cumulative length



## GC content



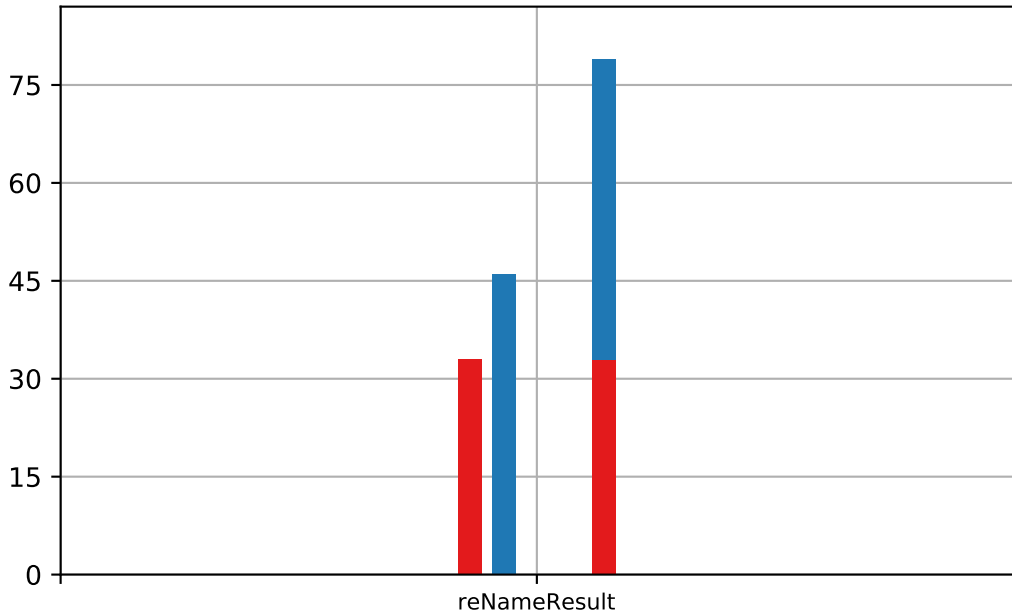
reNameResult GC content



reNameResult



## Misassemblies

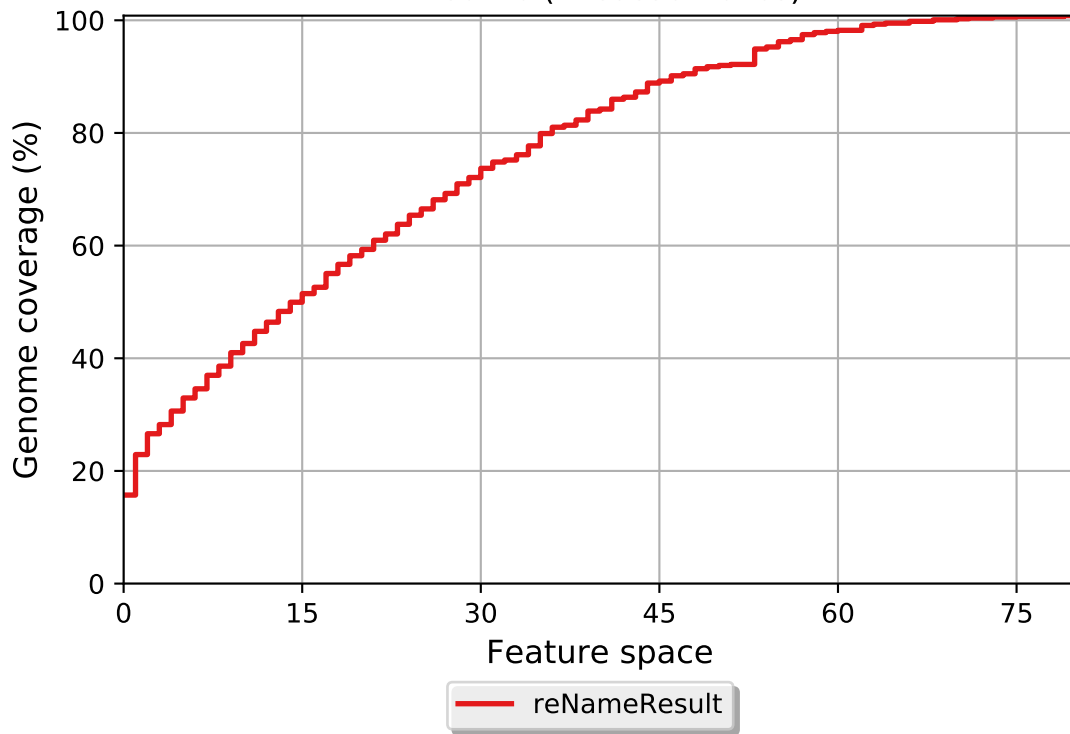


# relocations

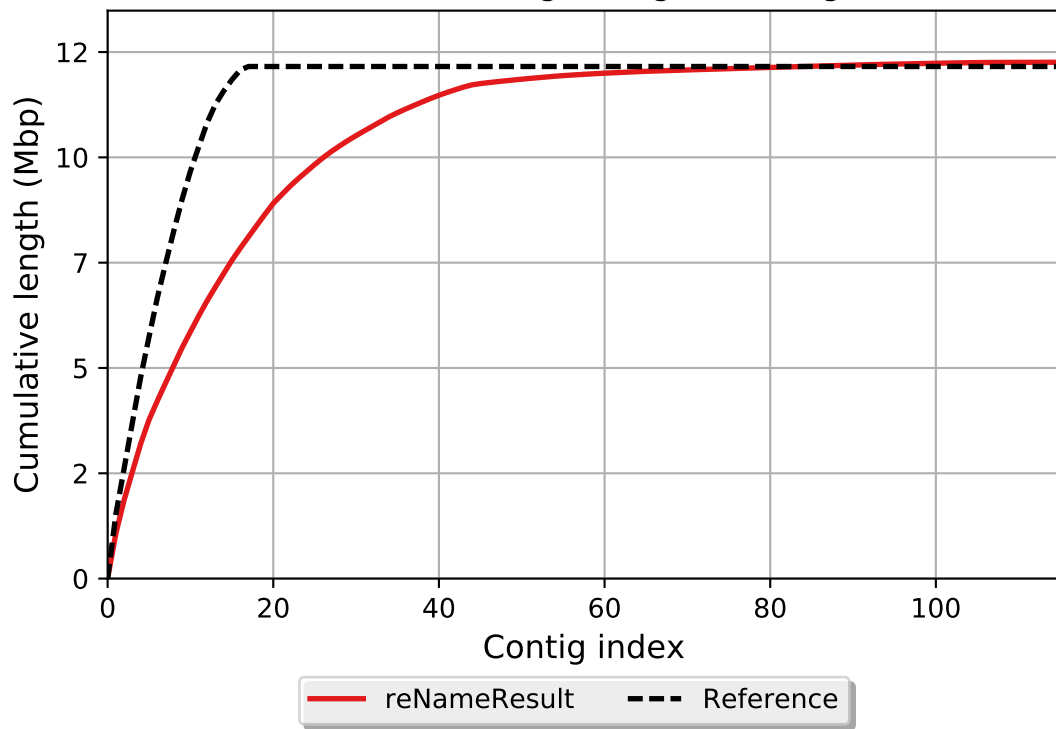


# translocations

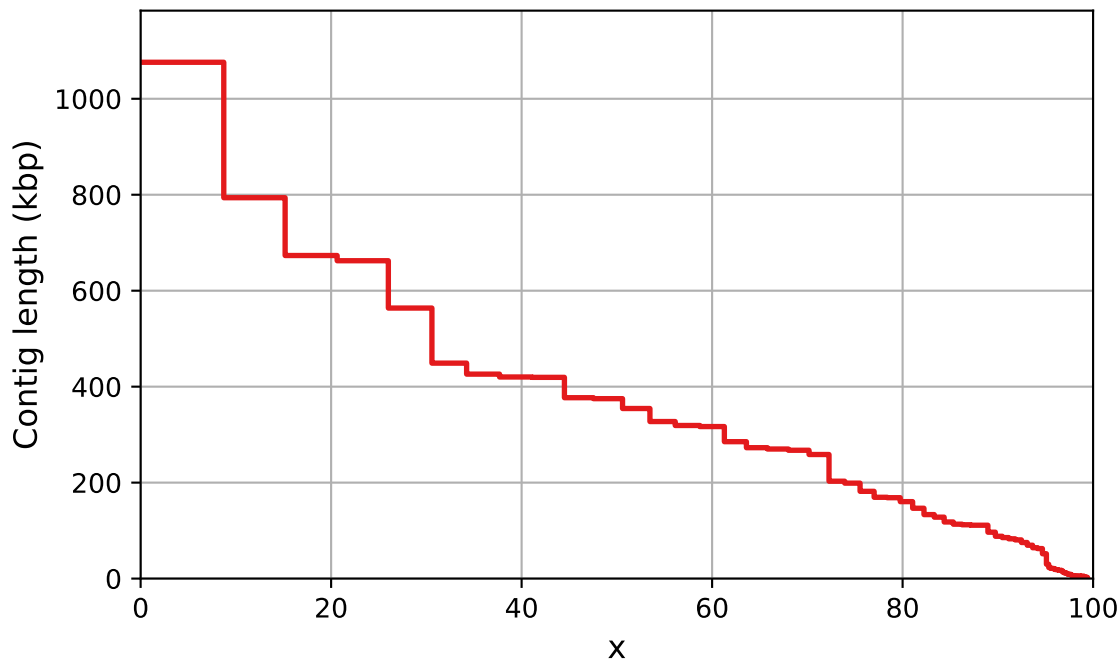
FRCurve (misassemblies)



Cumulative length (aligned contigs)

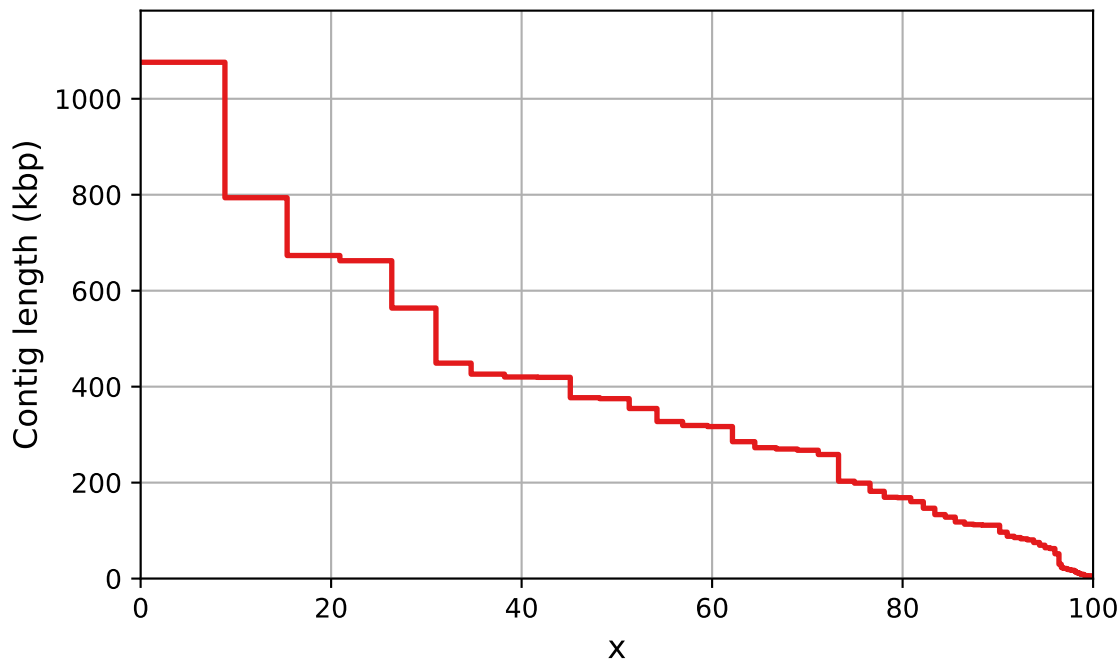


NAx



reNameResult

## NGAx



reNameResult