

Report

	assembly
# contigs (>= 1000 bp)	57
# contigs (>= 5000 bp)	56
# contigs (>= 10000 bp)	54
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	33
Total length (>= 1000 bp)	25401495
Total length (>= 5000 bp)	25397302
Total length (>= 10000 bp)	25384145
Total length (>= 25000 bp)	25098058
Total length (>= 50000 bp)	24904232
# contigs	57
Largest contig	5242943
Total length	25401495
Reference length	3234289
GC (%)	56.72
Reference GC (%)	46.73
N50	1163971
NG50	5242943
N90	235743
NG90	5242943
auN	2340297.0
auNG	18380250.4
L50	5
LG50	1
L90	19
LG90	1
# misassemblies	19
# misassembled contigs	10
Misassembled contigs length	447948
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	23
# unaligned contigs	5 + 50 part
Unaligned length	24827573
Genome fraction (%)	17.206
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7274.47
# indels per 100 kbp	1047.53
Largest alignment	164422
Total aligned length	573540
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	1338.1
auNGA	10509.5
LA50	-
LGA50	-
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

	assembly
# misassemblies	19
# contig misassemblies	19
# c. relocations	12
# c. translocations	7
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	447948
# possibly misassembled contigs	28
# possible misassemblies	82
# local misassemblies	31
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	23
# mismatches	41722
# indels	6008
# indels (<= 5 bp)	5922
# indels (> 5 bp)	86
Indels length	10018

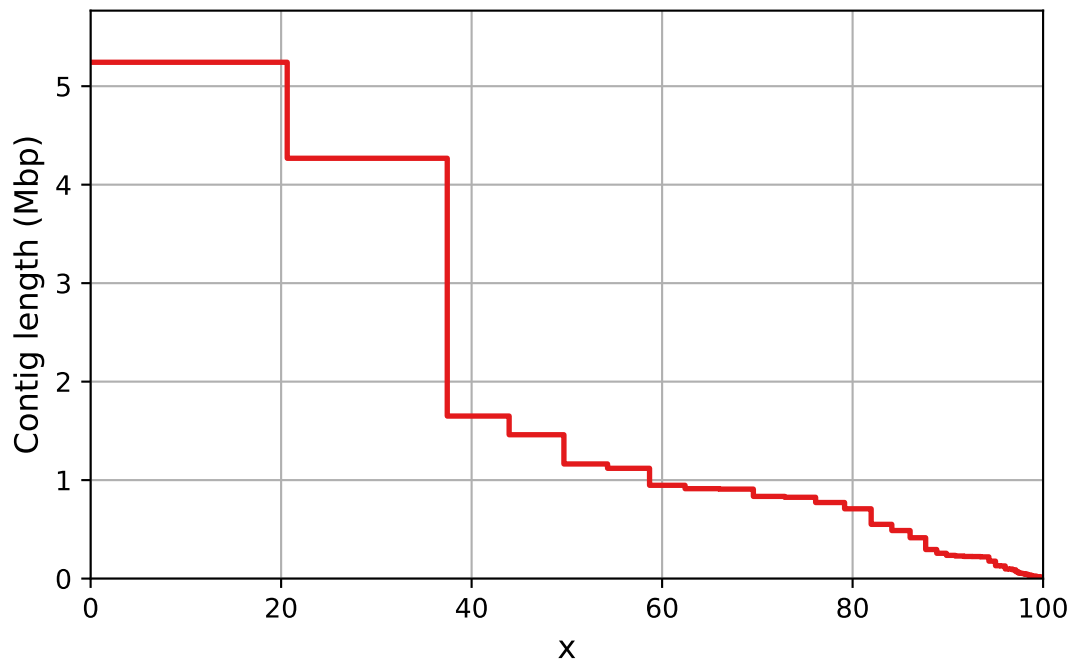
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	assembly
# fully unaligned contigs	5
Fully unaligned length	3624945
# partially unaligned contigs	50
Partially unaligned length	21202628
# N's	0

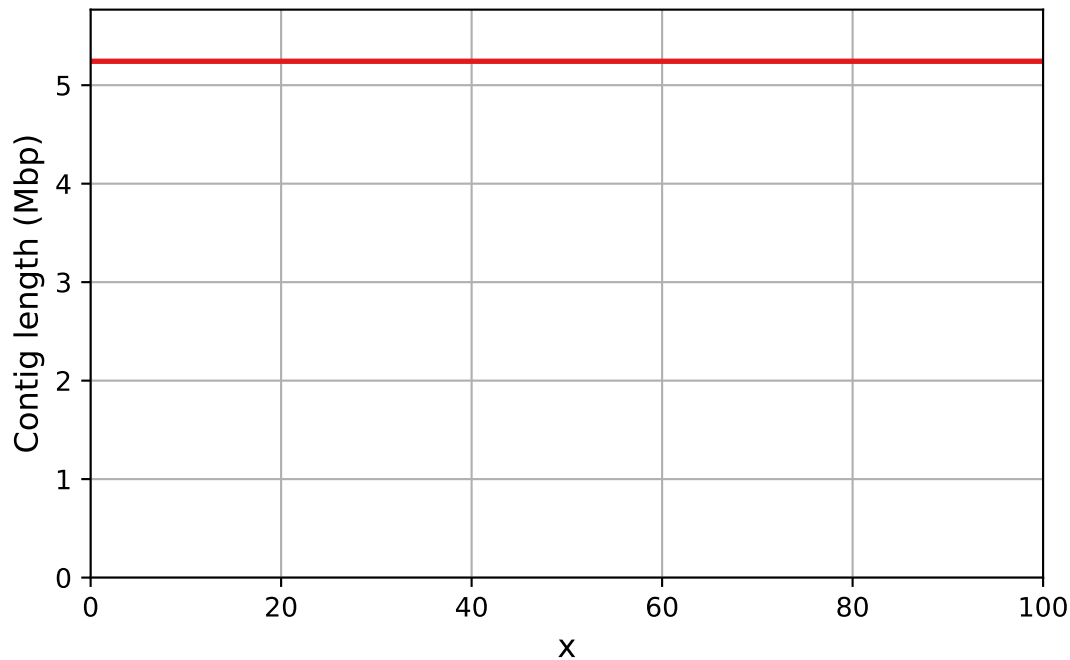
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



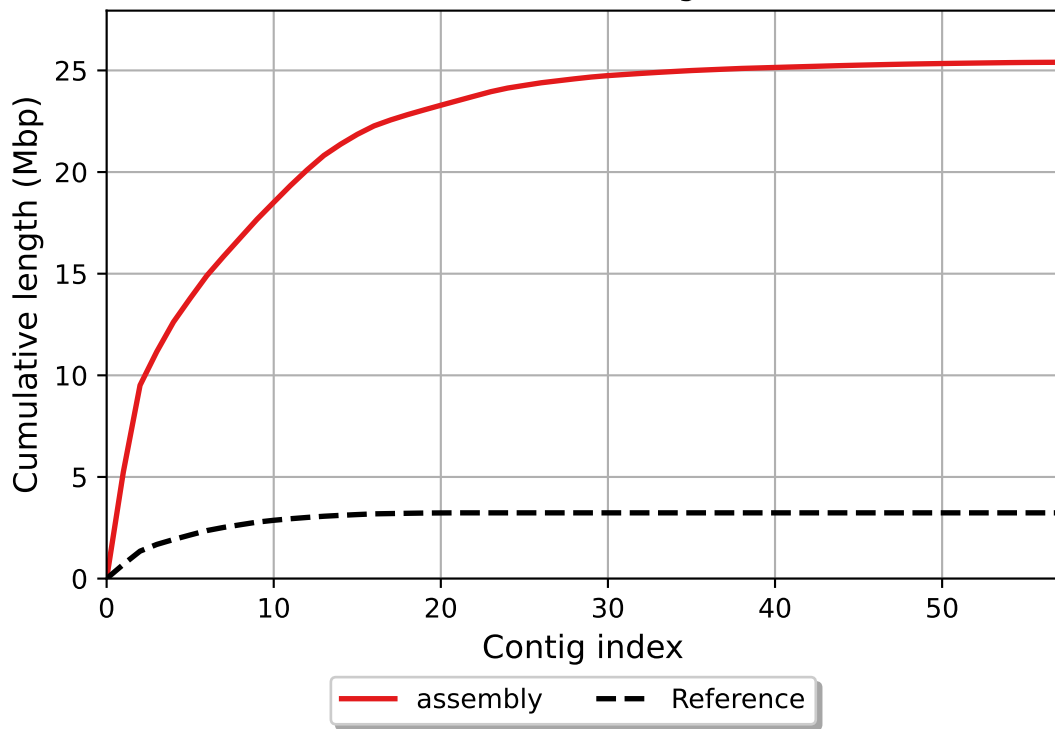
— assembly

NGx

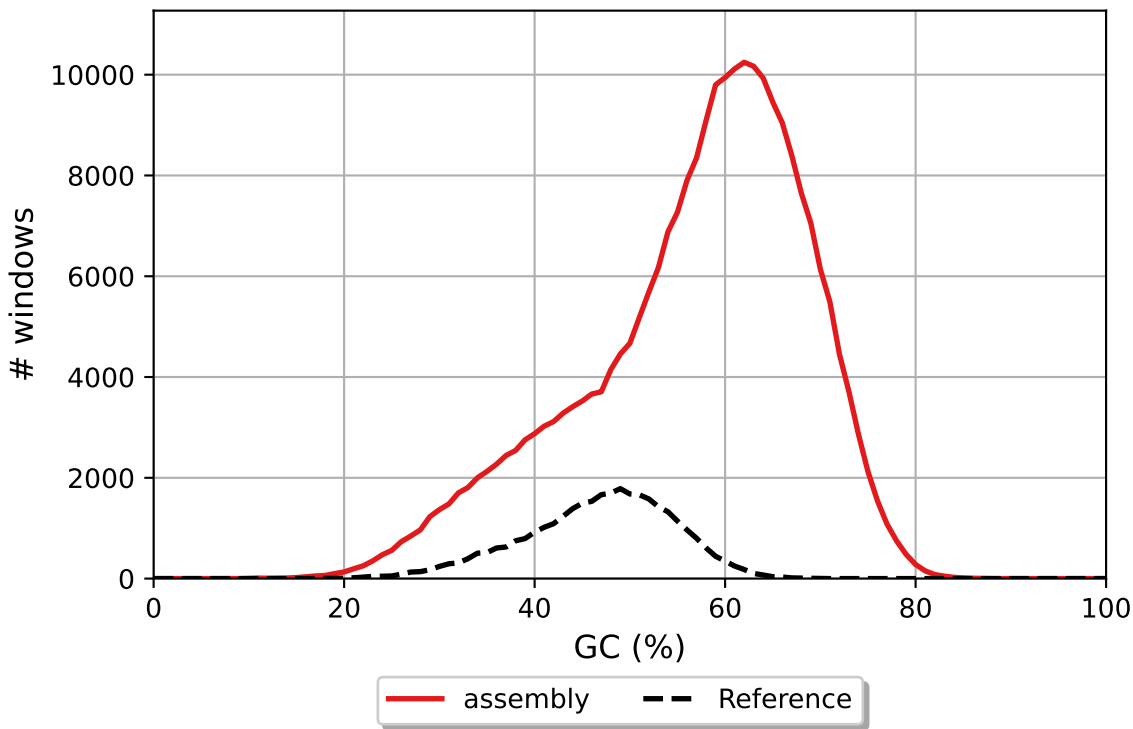


— assembly

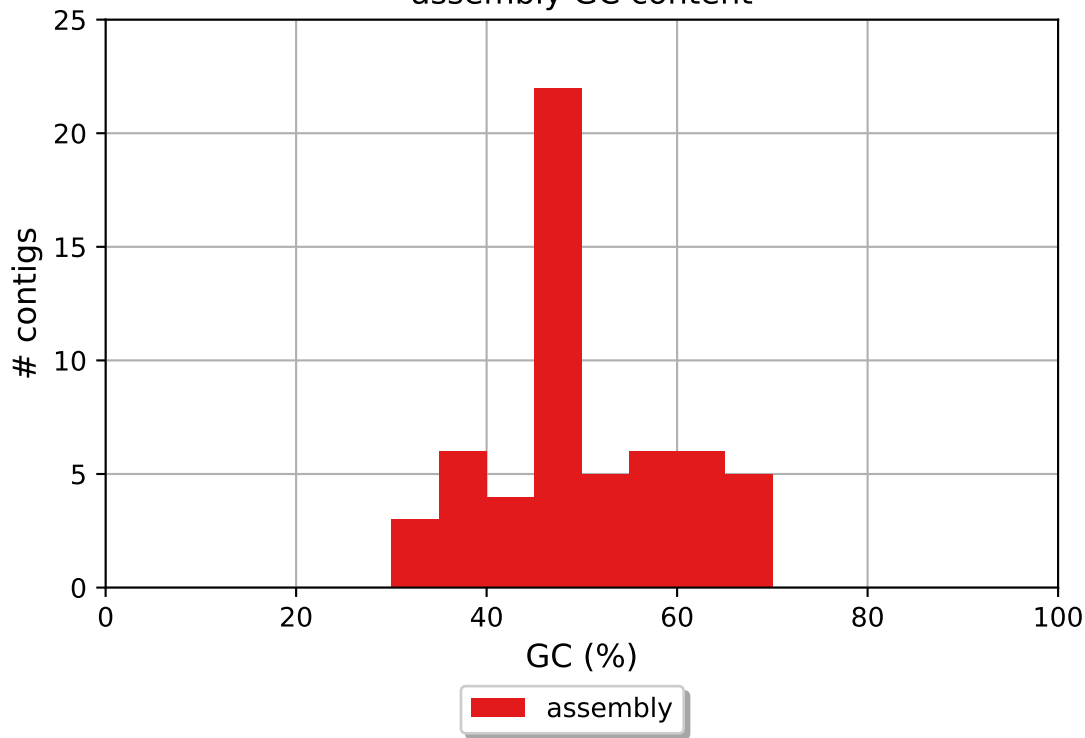
Cumulative length



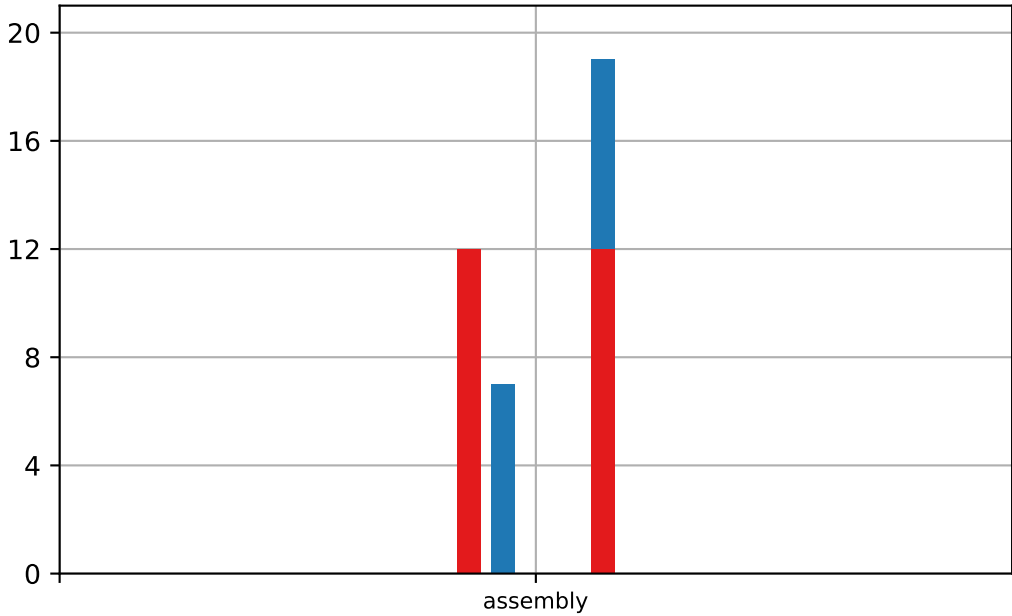
GC content



assembly GC content



Misassemblies

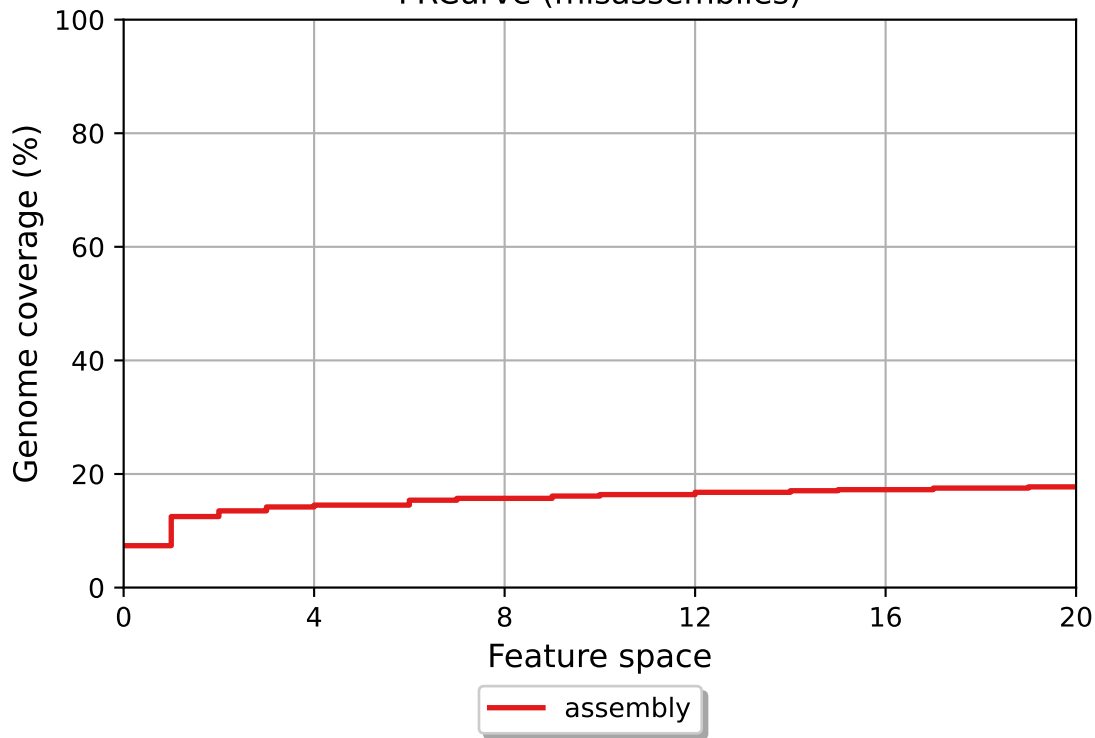


relocations

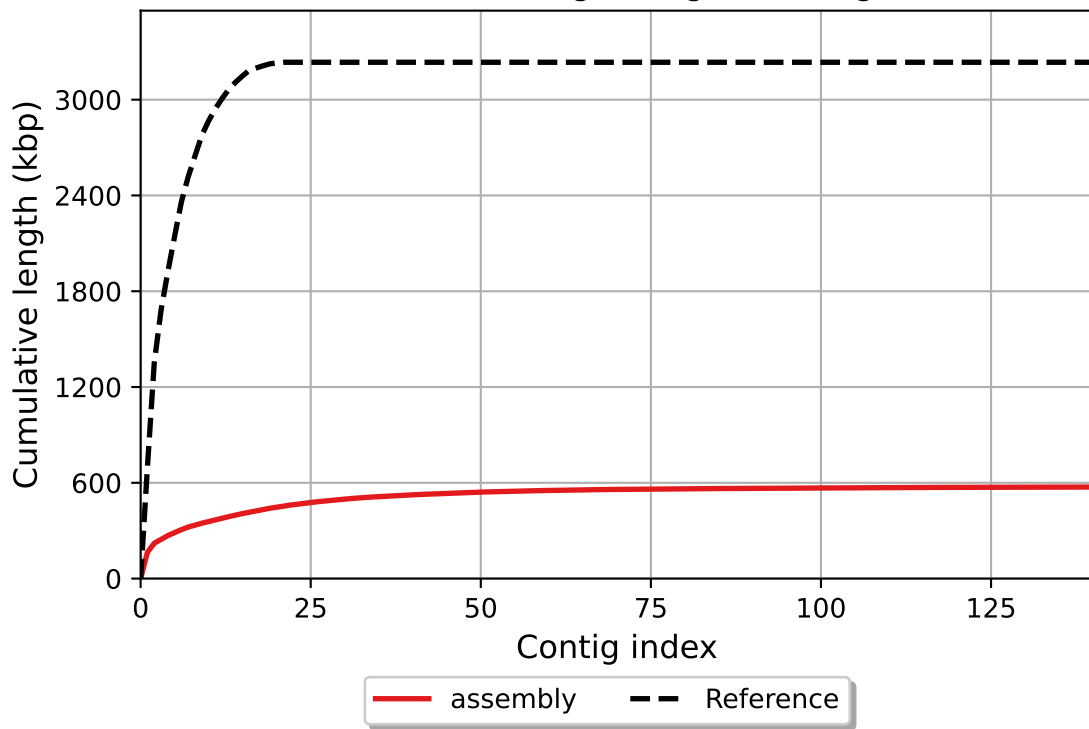


translocations

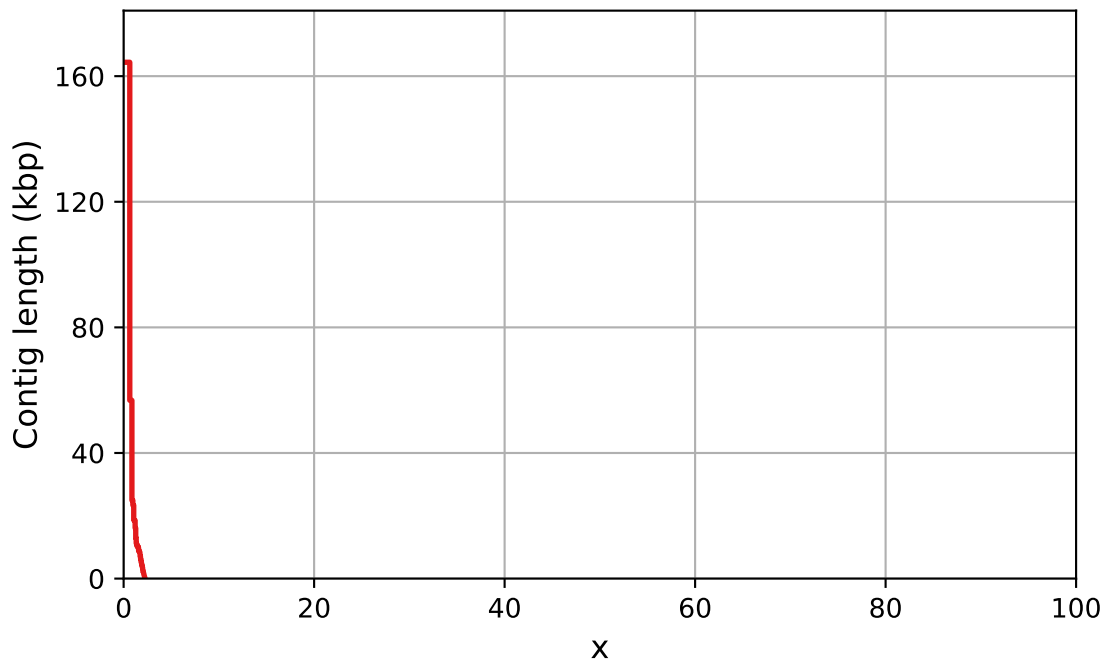
FRCurve (misassemblies)



Cumulative length (aligned contigs)

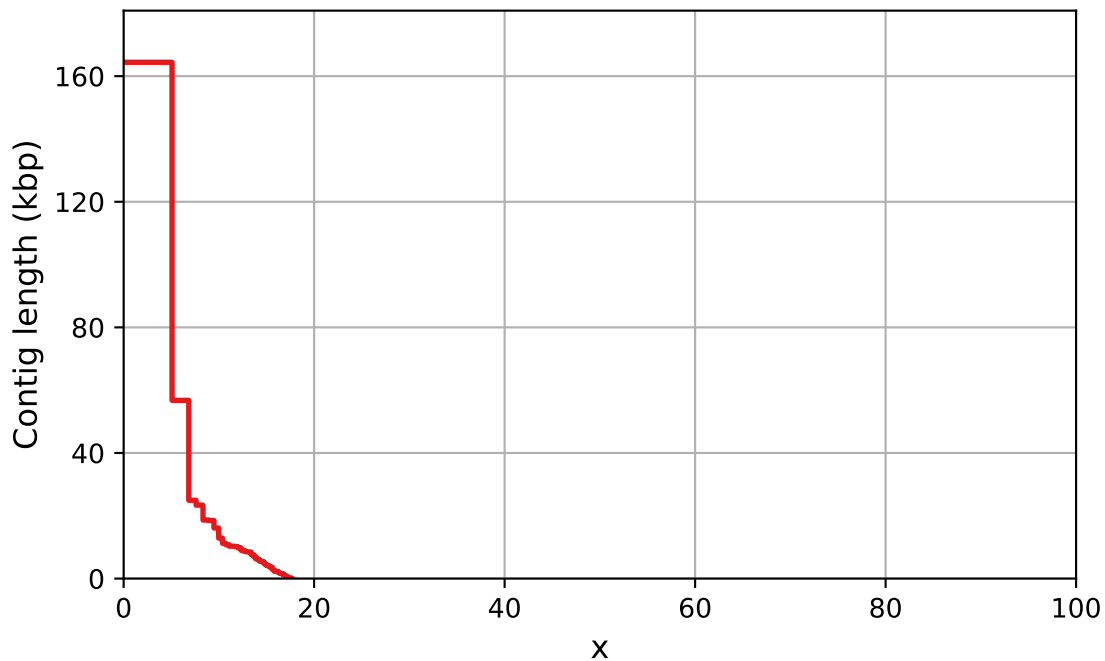


NAx



— assembly

NGAx



— assembly