

Report

	out_11
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	24785
Total length (>= 1000 bp)	24785
Total length (>= 5000 bp)	24785
Total length (>= 10000 bp)	24785
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	24785
Total length	24785
Reference length	10624
GC (%)	44.22
Reference GC (%)	44.14
N50	24785
NG50	24785
N90	24785
NG90	24785
auN	24785.0
auNG	57821.6
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	23699
Genome fraction (%)	10.024
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	92.08
# indels per 100 kbp	644.57
Largest alignment	292
Total aligned length	1086
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	7.8
auNGA	18.2
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

	out_11
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	1
# indels	7
# indels (<= 5 bp)	7
# indels (> 5 bp)	0
Indels length	10

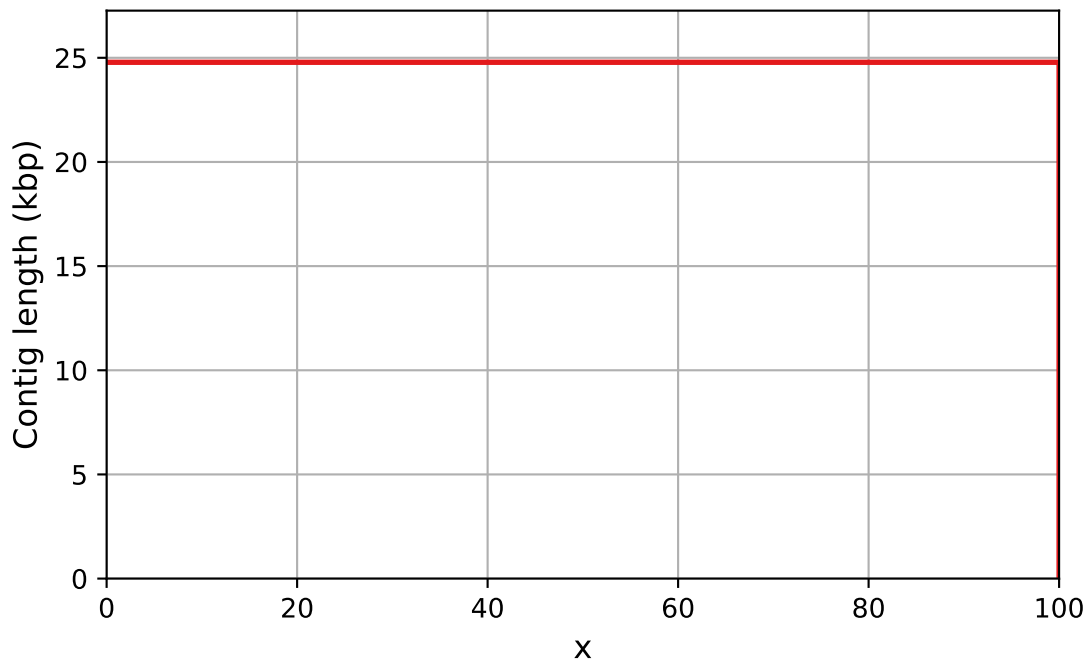
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	out_11
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	23699
# N's	0

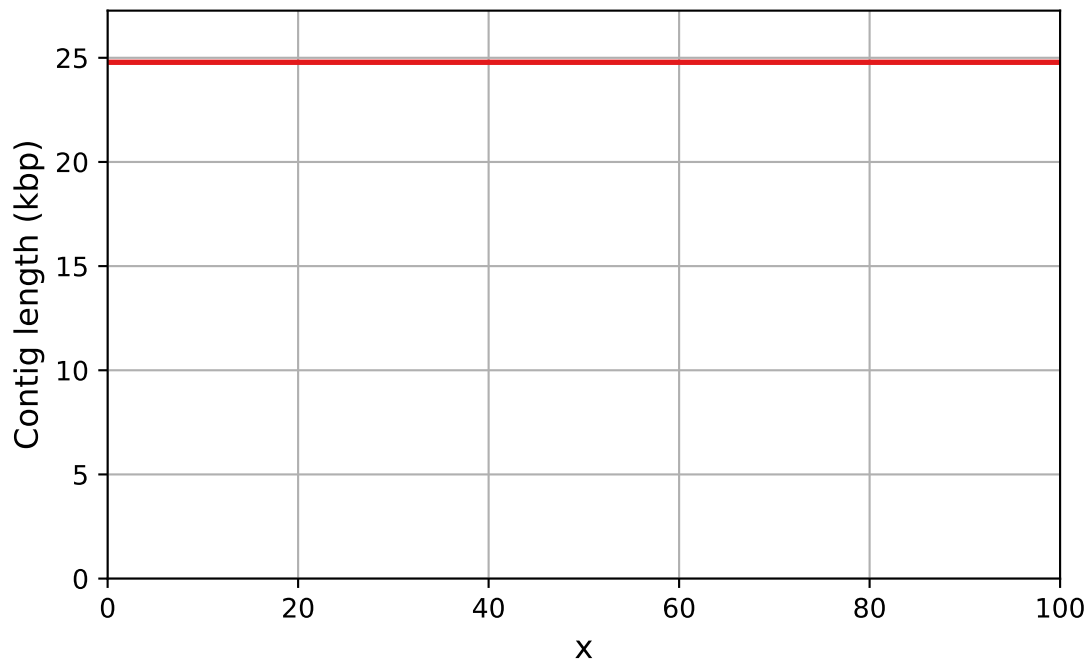
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



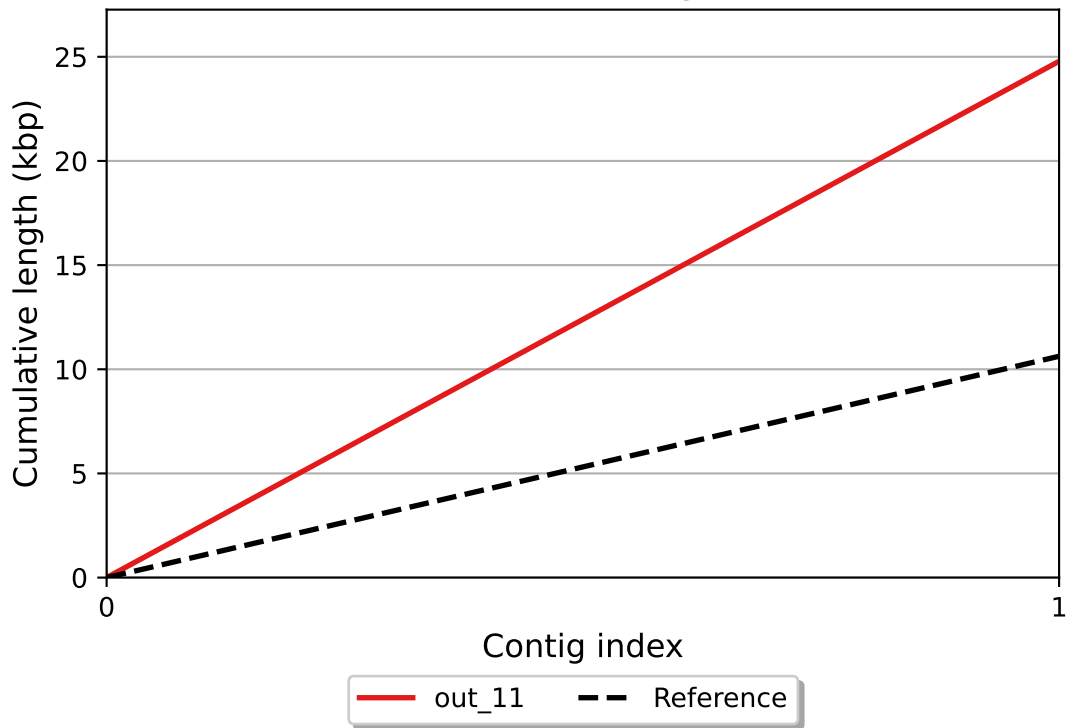
— out_11

NGx

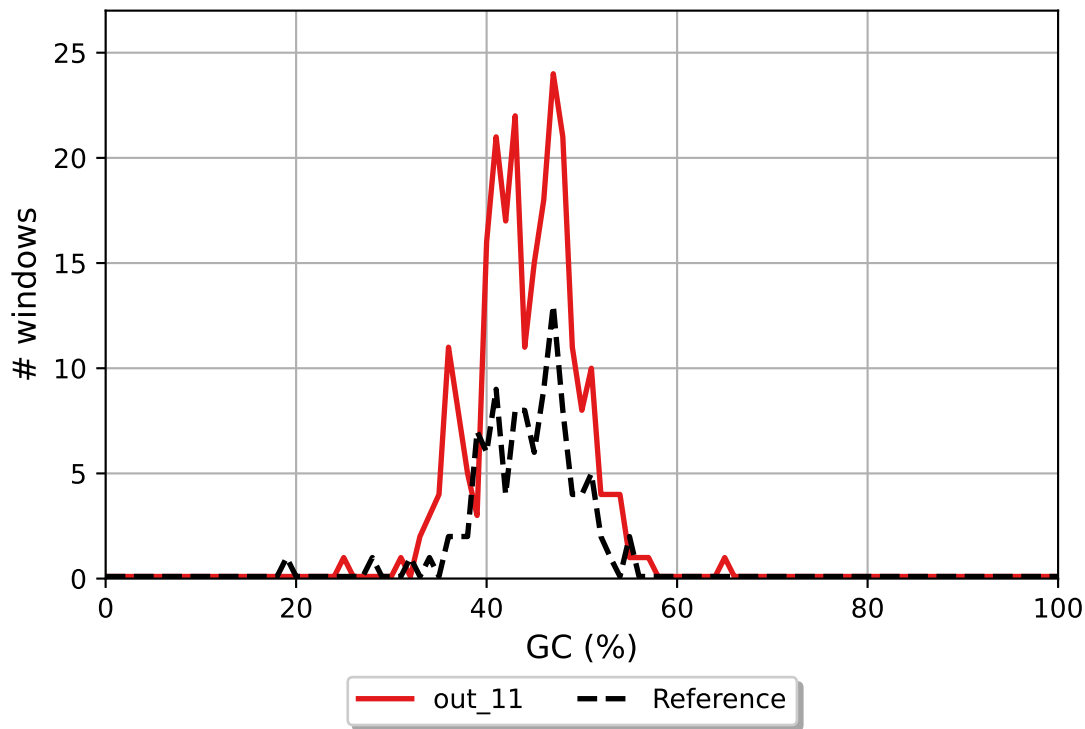


— out_11

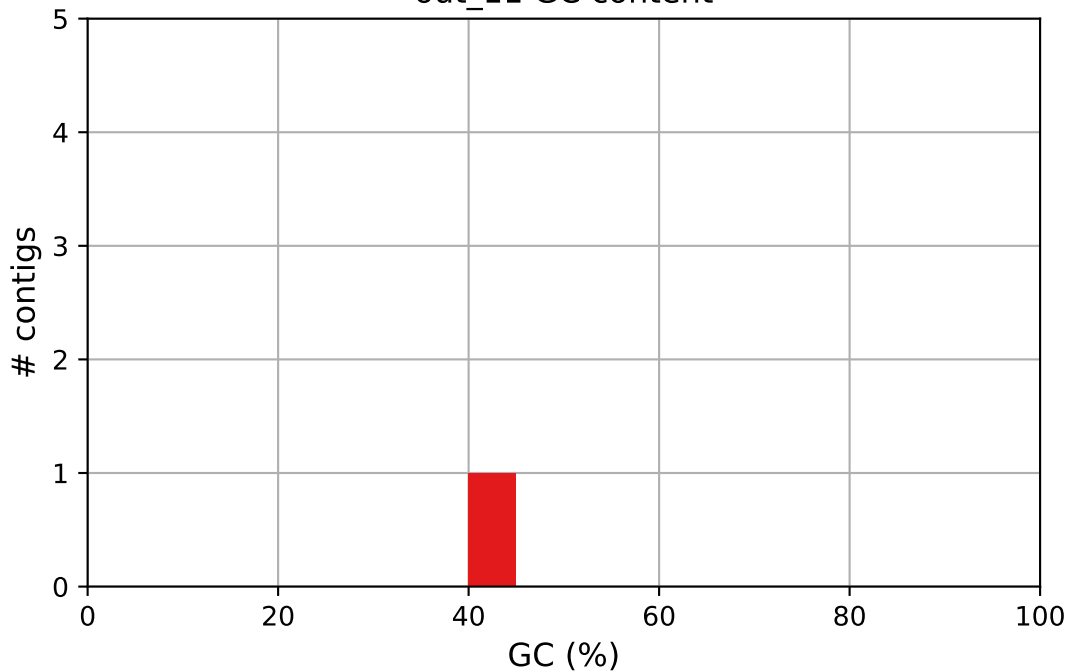
Cumulative length



GC content

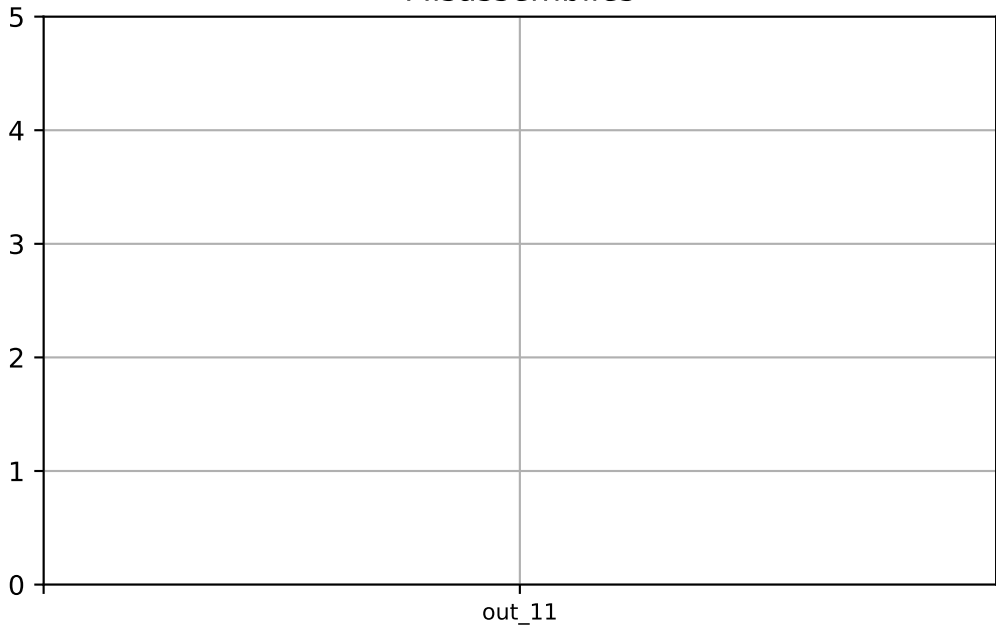


out_11 GC content

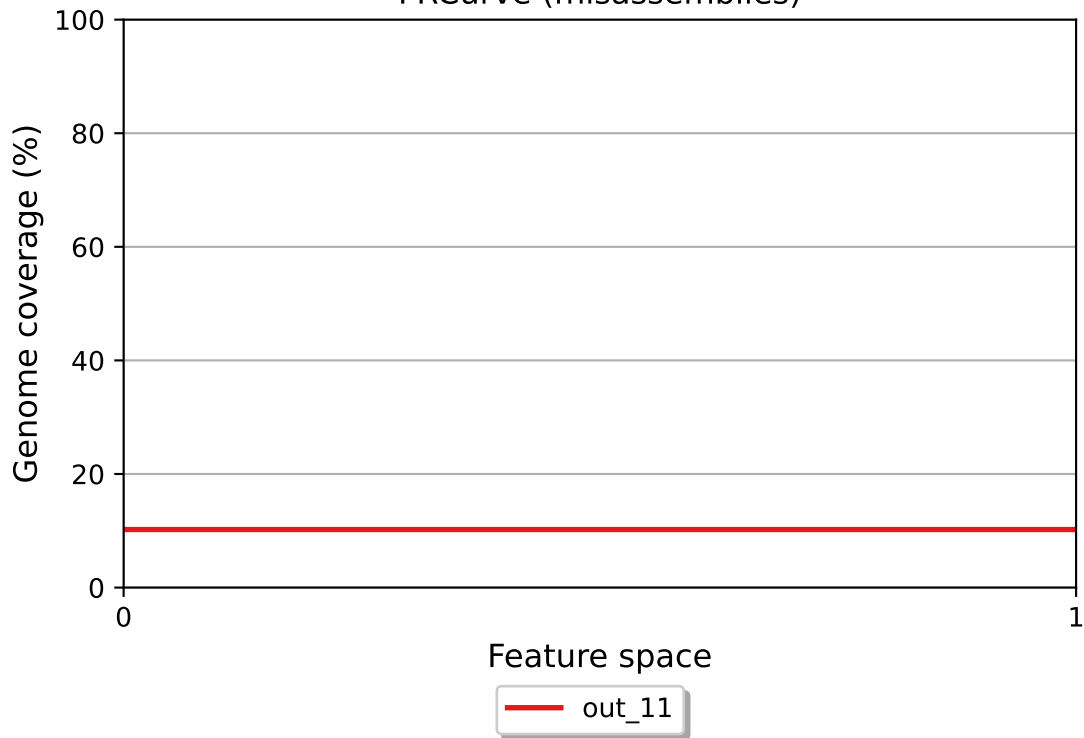


out_11

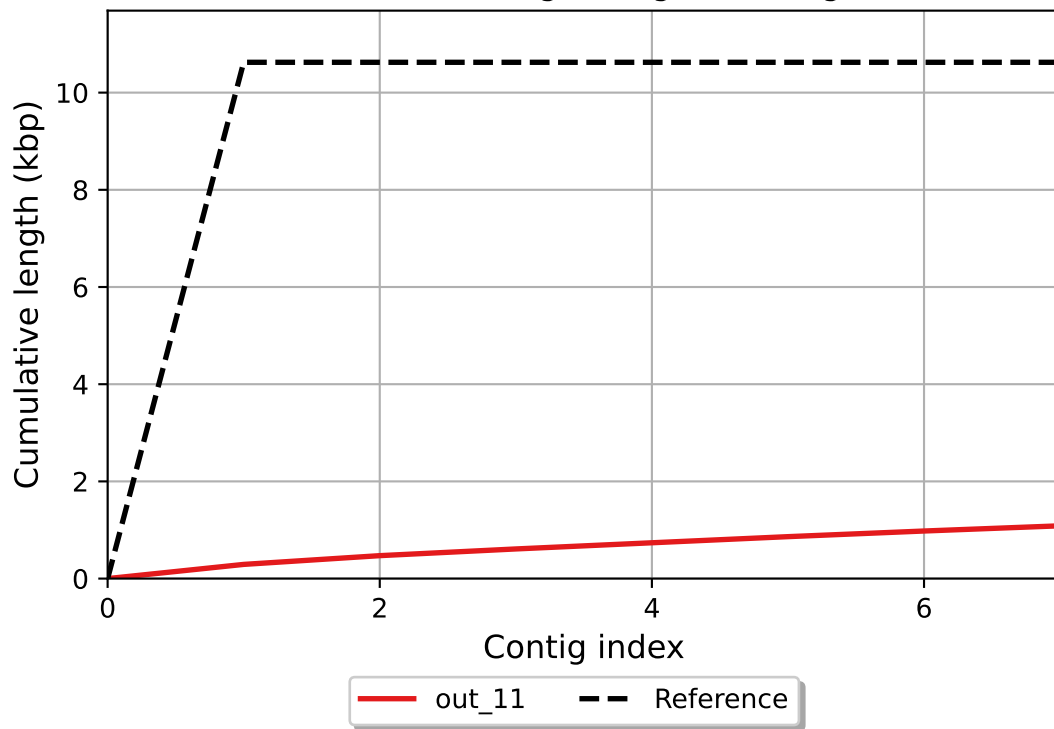
Misassemblies



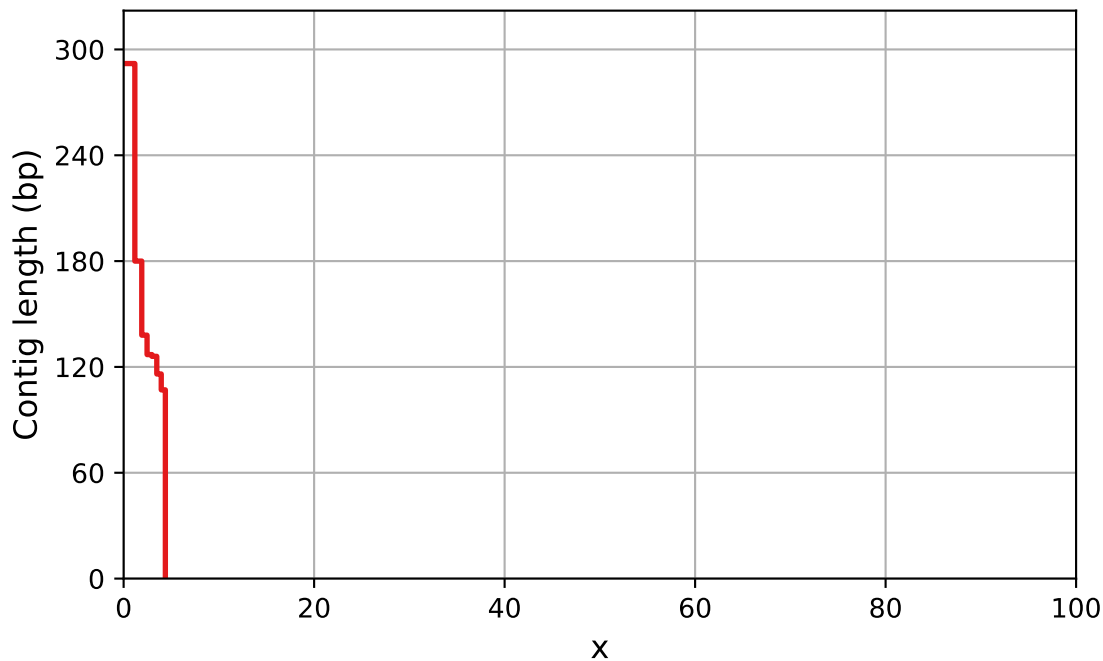
FRCurve (misassemblies)



Cumulative length (aligned contigs)

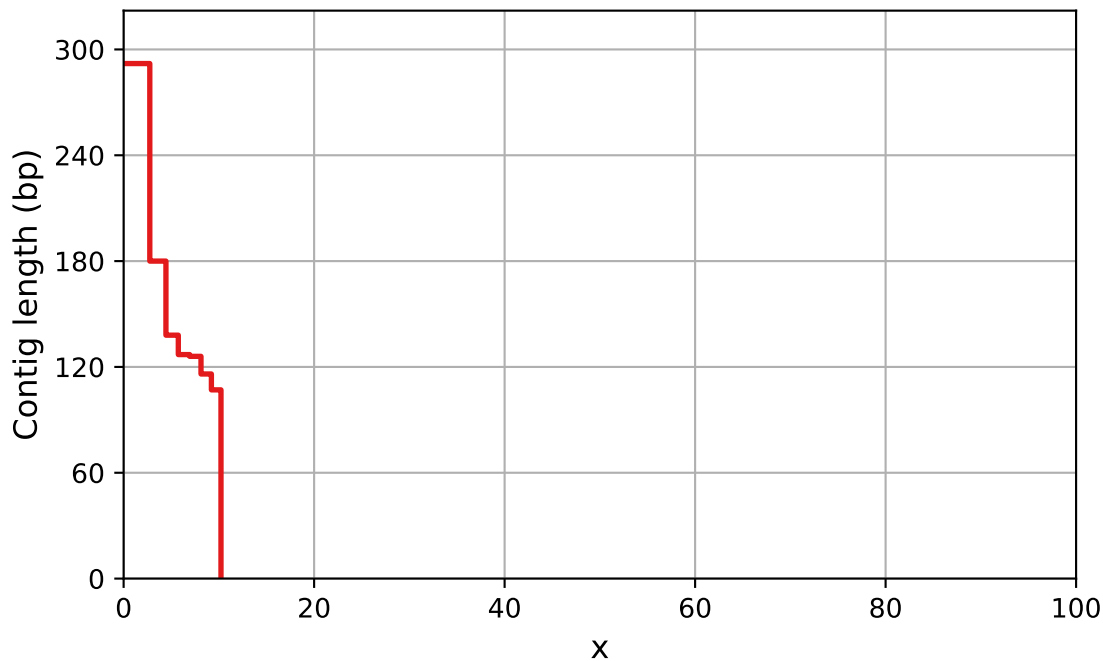


NAx



— out_11

NGAx



— out_11