

Report

	reads_sequencage1_in
# contigs (>= 0 bp)	736
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	220800
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	736
Largest contig	300
Total length	220800
Reference length	48576
GC (%)	51.22
Reference GC (%)	49.87
N50	300
NG50	300
N75	300
NG75	300
L50	368
LG50	81
L75	552
LG75	122
# 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	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.196
Duplication ratio	5.399
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8738.60
# indels per 100 kbp	0.00
Largest alignment	300
Total aligned length	220437
NA50	300
NGA50	300
NA75	300
NGA75	300
LA50	368
LGA50	81
LA75	552
LGA75	122

All statistics are based on contigs of size >= 1 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

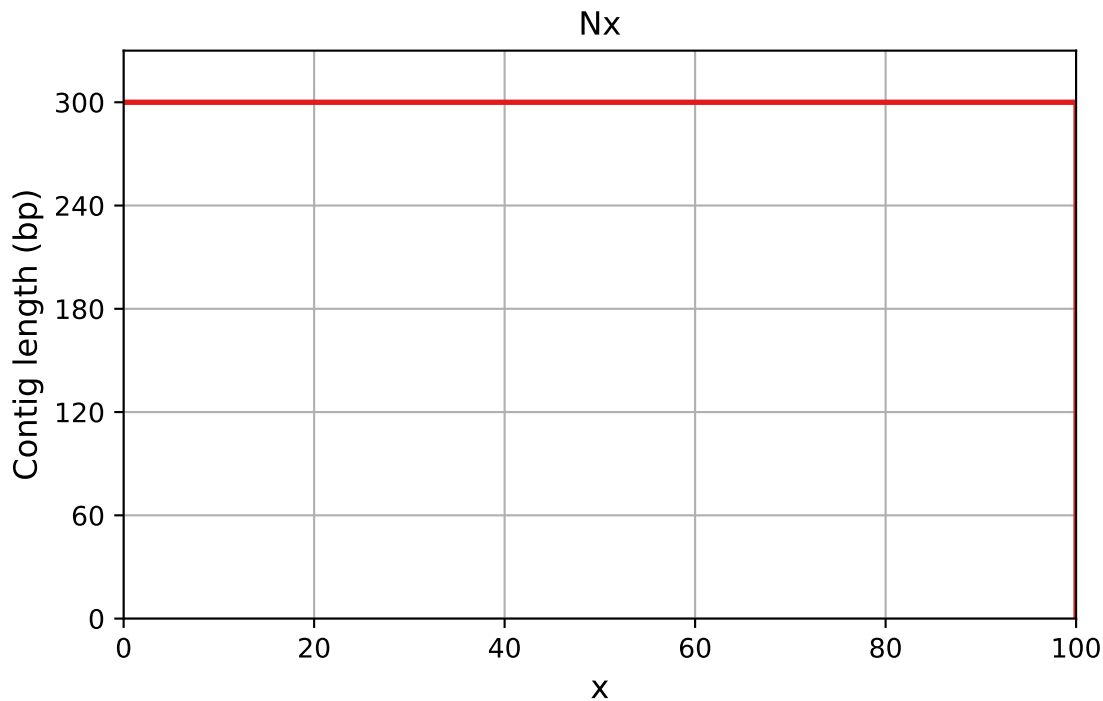
	reads_sequencage1_in
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3574
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size ≥ 1 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

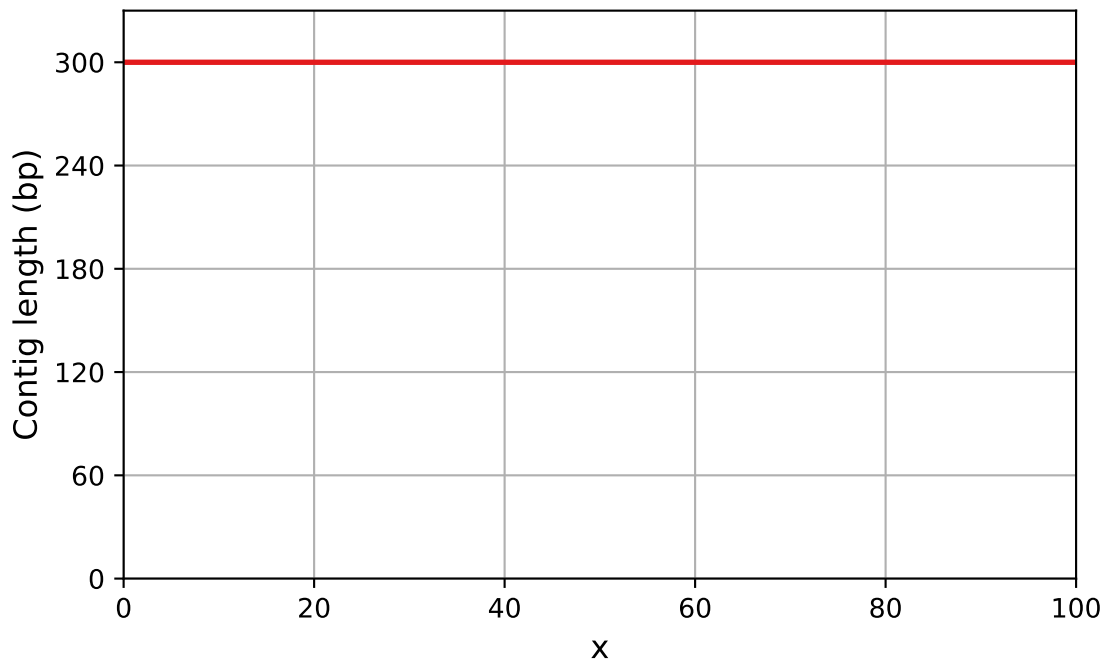
	reads_sequencage1_in
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size ≥ 1 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



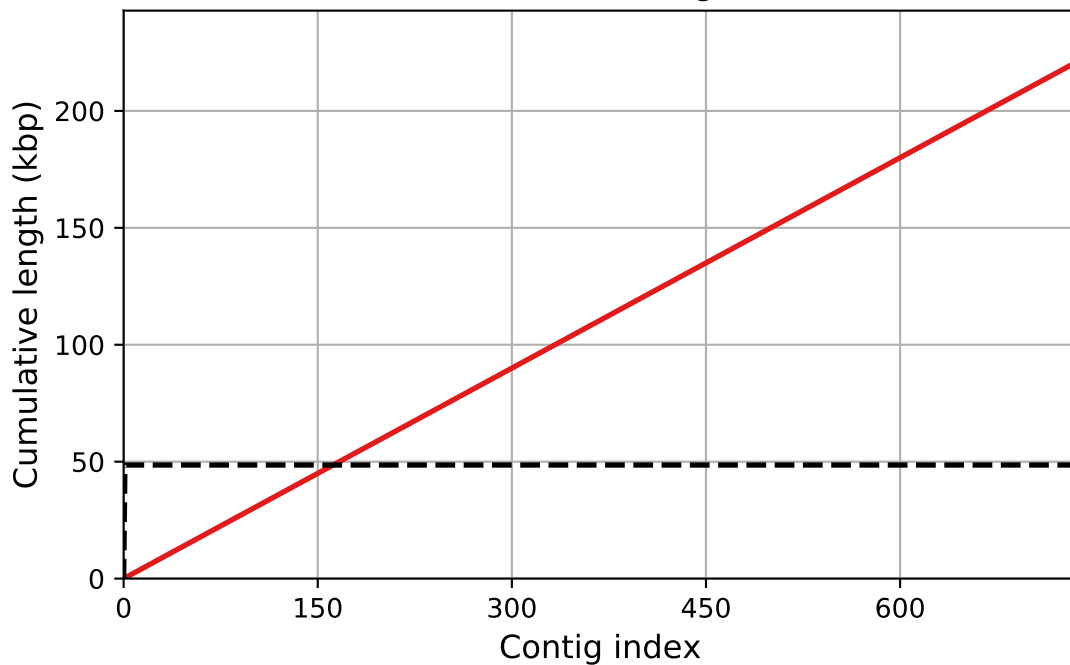
reads_sequencage1_in

NGx



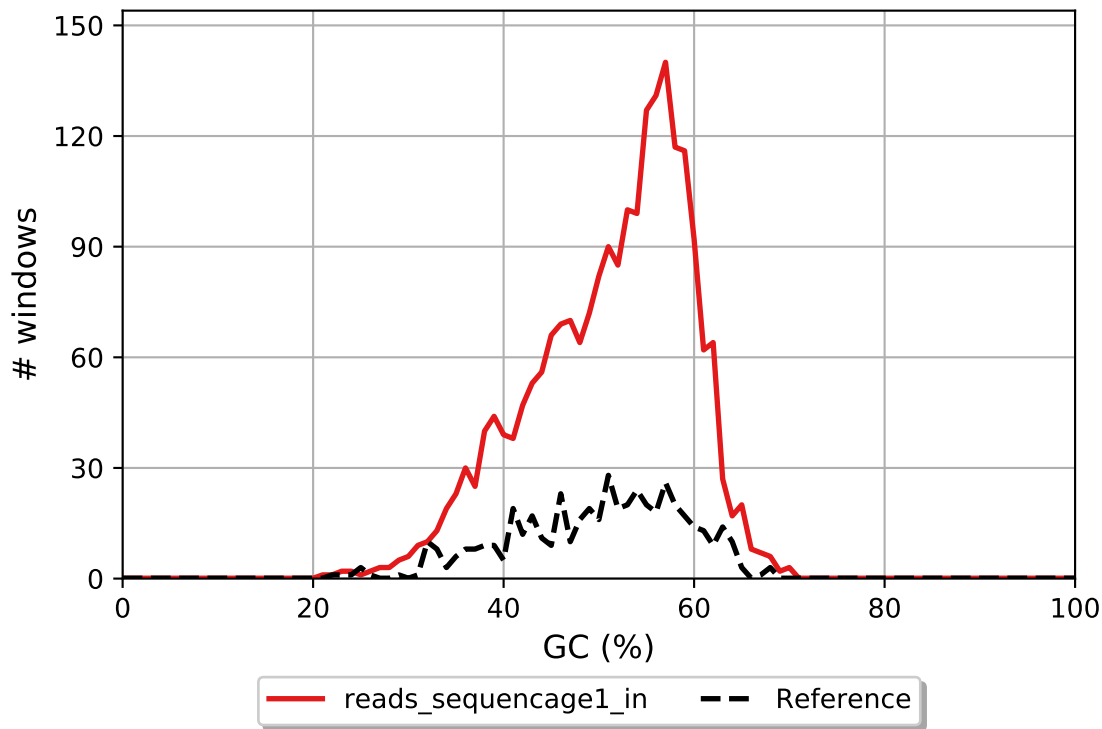
reads_sequencage1_in

Cumulative length

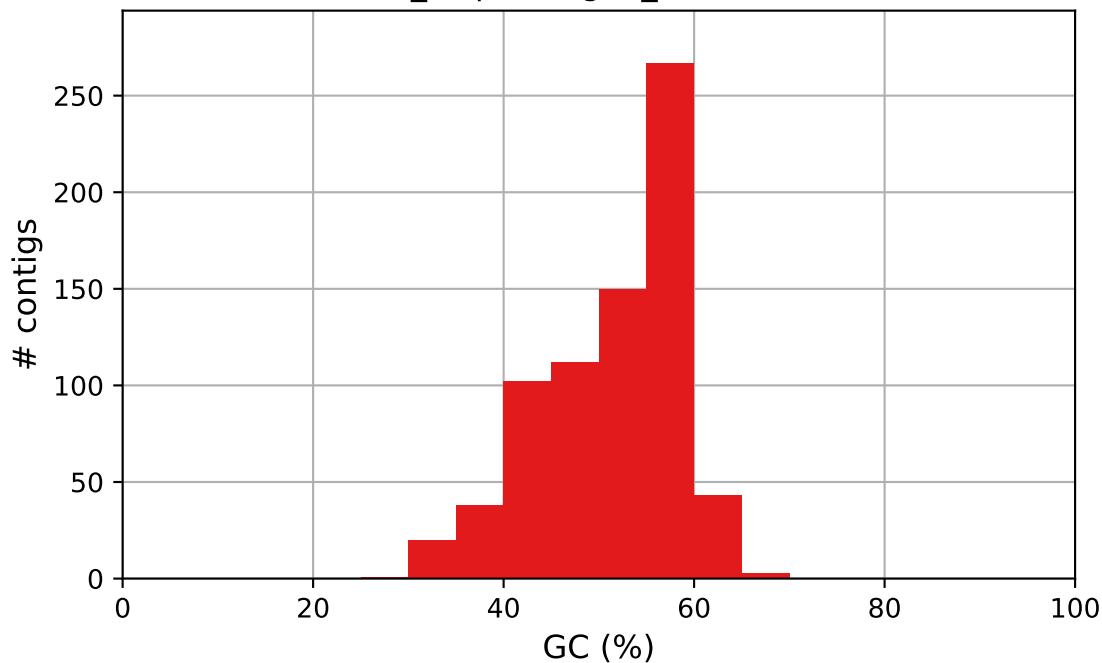


— reads_sequencage1_in - - Reference

GC content

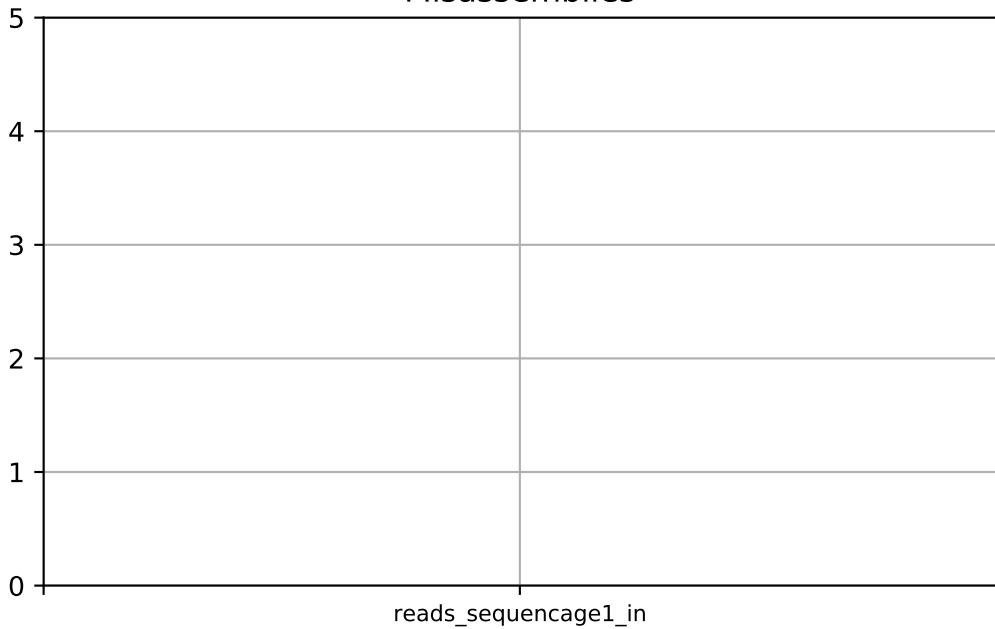


reads_sequencage1_in GC content

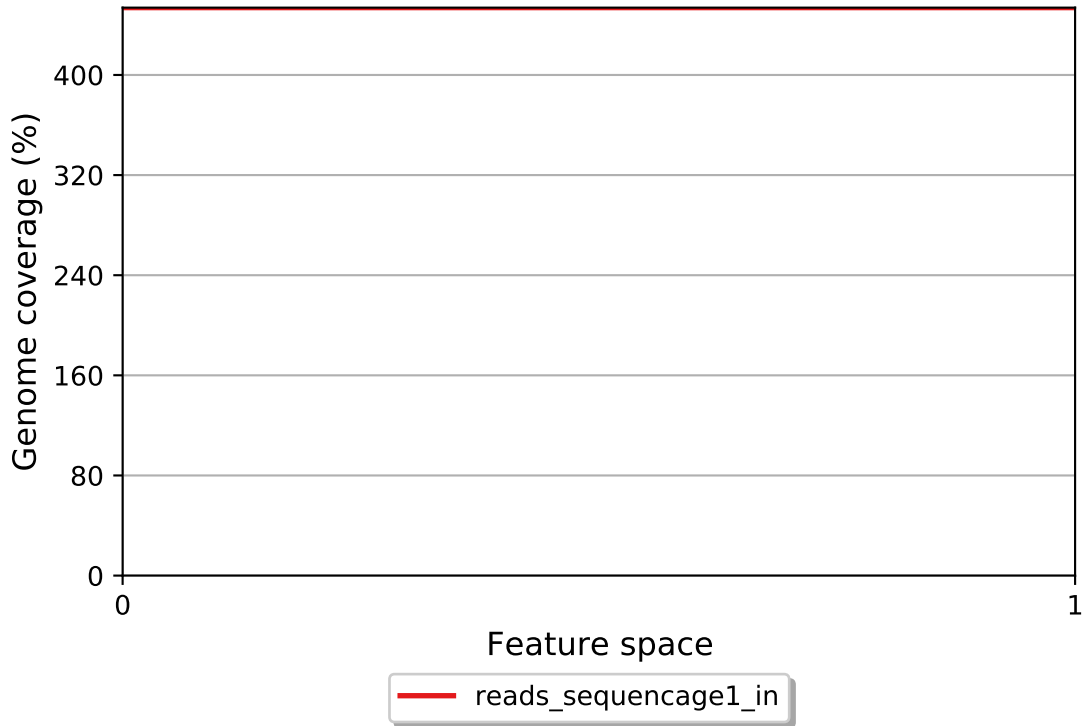


reads_sequencage1_in

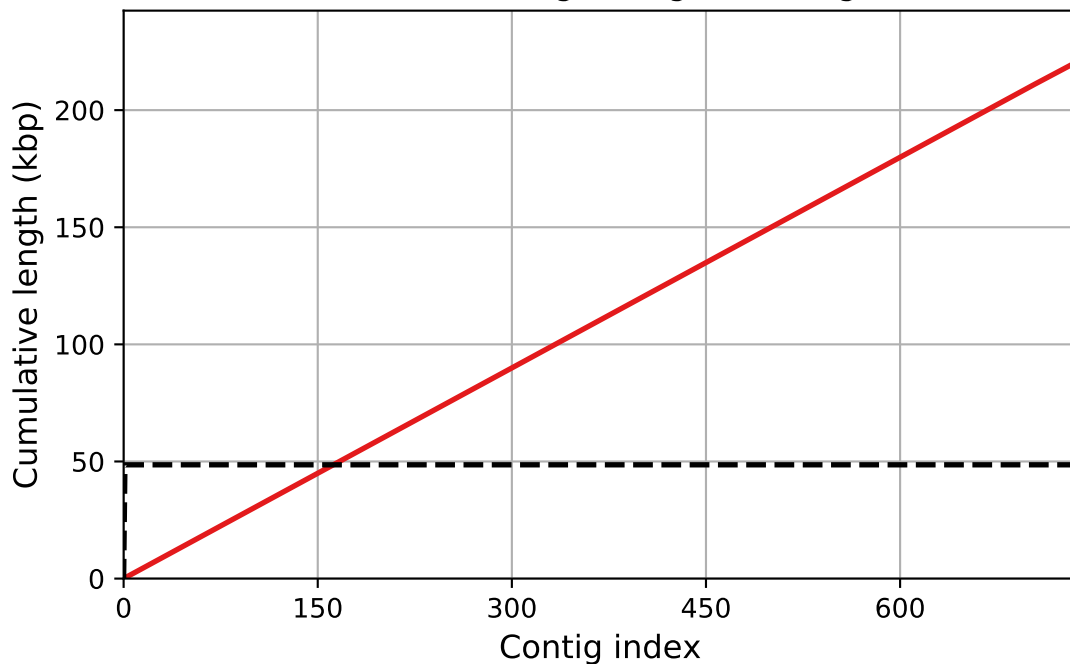
Misassemblies



FRCurve (misassemblies)

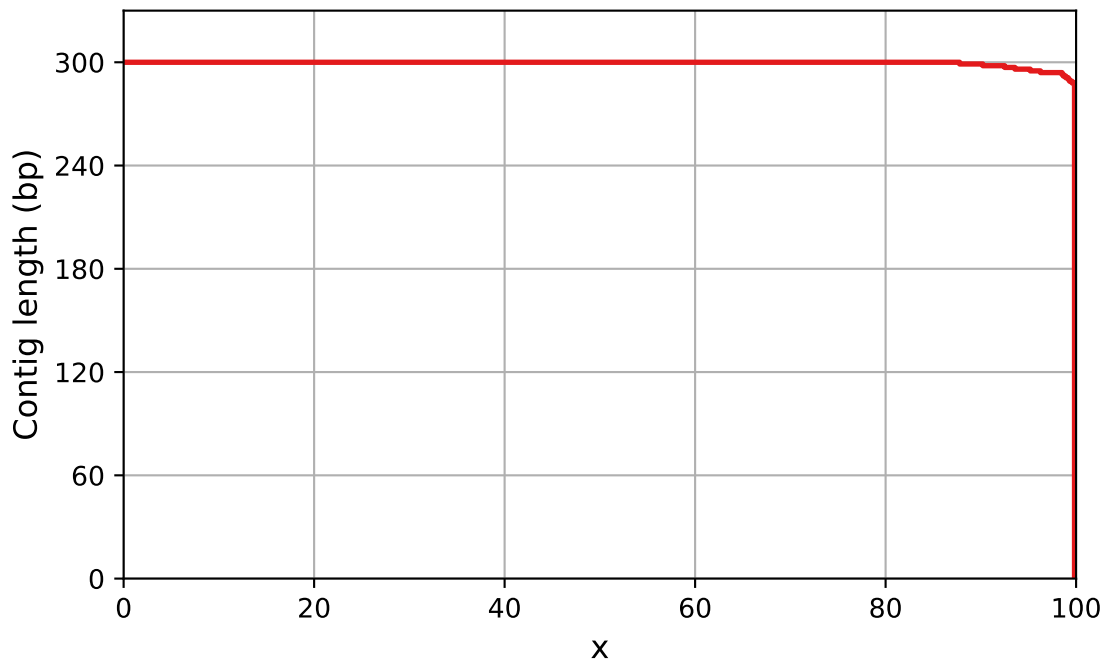


Cumulative length (aligned contigs)



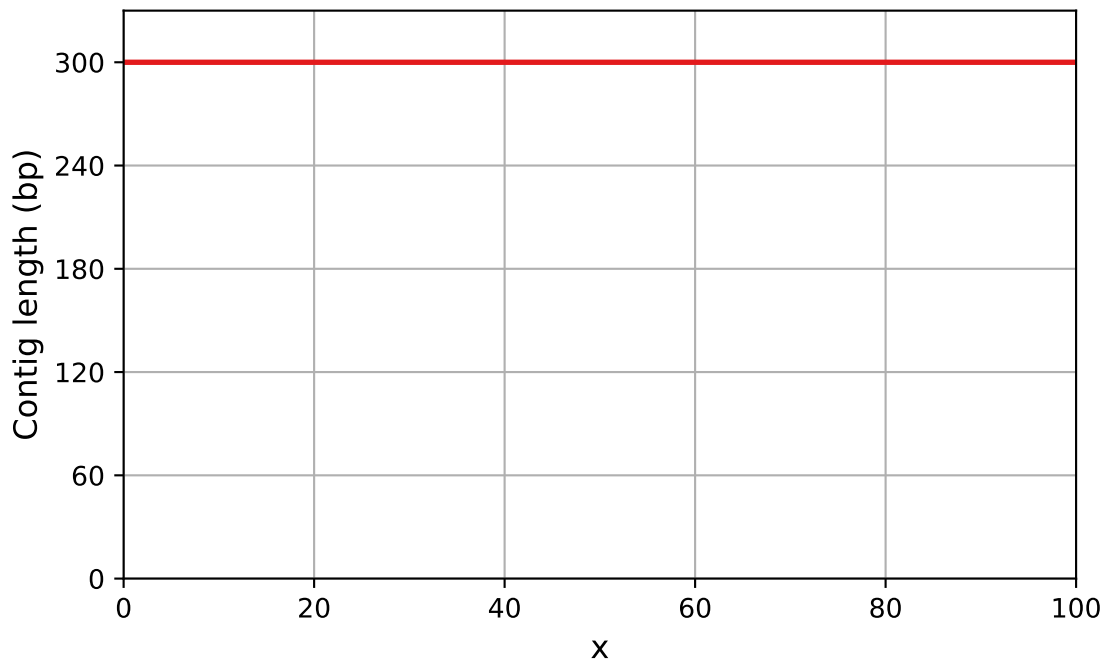
— reads_sequencage1_in - - Reference

NAx



reads_sequencage1_in

NGAx



reads_sequencage1_in