

Report

	reads_contaminant_in
# contigs (>= 0 bp)	7380
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	2214000
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	7380
Largest contig	300
Total length	2214000
Reference length	48576
GC (%)	49.64
Reference GC (%)	49.87
N50	300
NG50	300
N75	300
NG75	300
L50	3690
LG50	81
L75	5535
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 (%)	99.212
Duplication ratio	45.940
# N's per 100 kbp	0.00
# mismatches per 100 kbp	41744.65
# indels per 100 kbp	0.00
Largest alignment	300
Total aligned length	2210561
NA50	300
NGA50	300
NA75	300
NGA75	300
LA50	3690
LGA50	81
LA75	5535
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

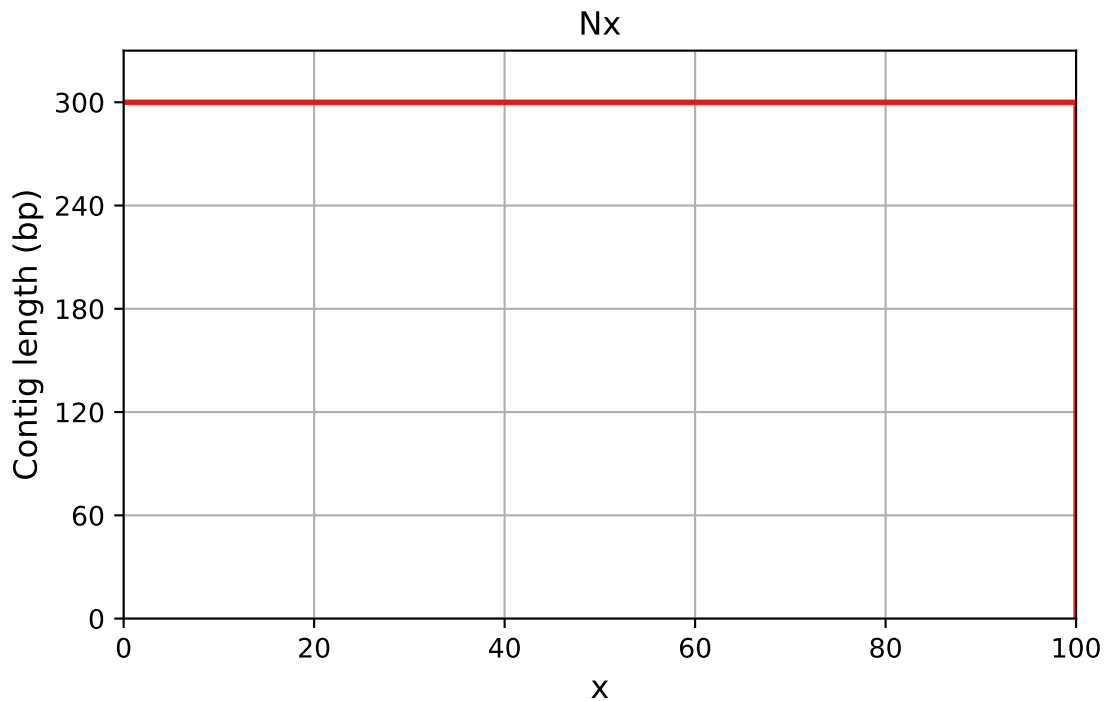
	reads_contaminant_in
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	20118
# 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

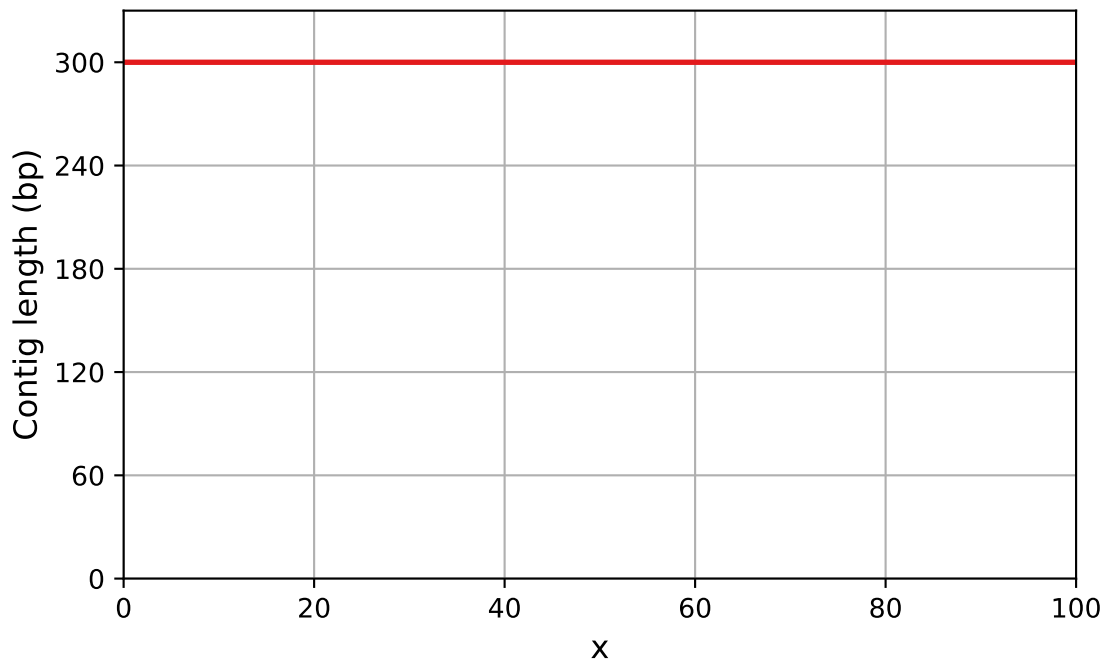
	reads_contaminant_in
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).



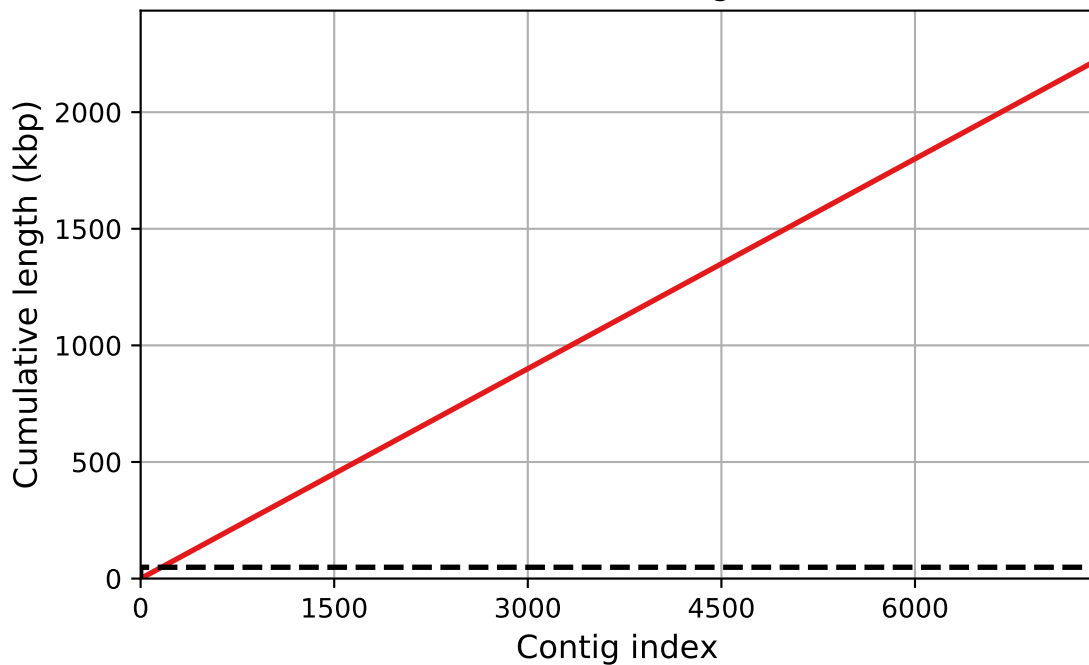
— reads_contaminant_in

NGx



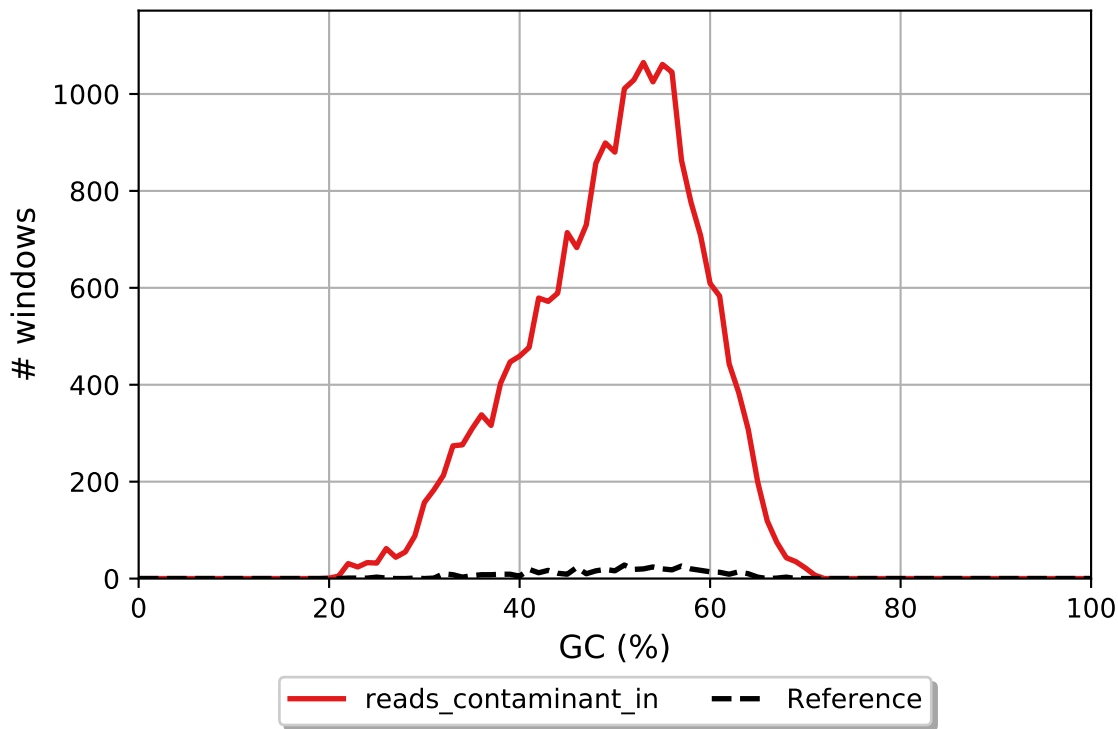
— reads_contaminant_in

Cumulative length

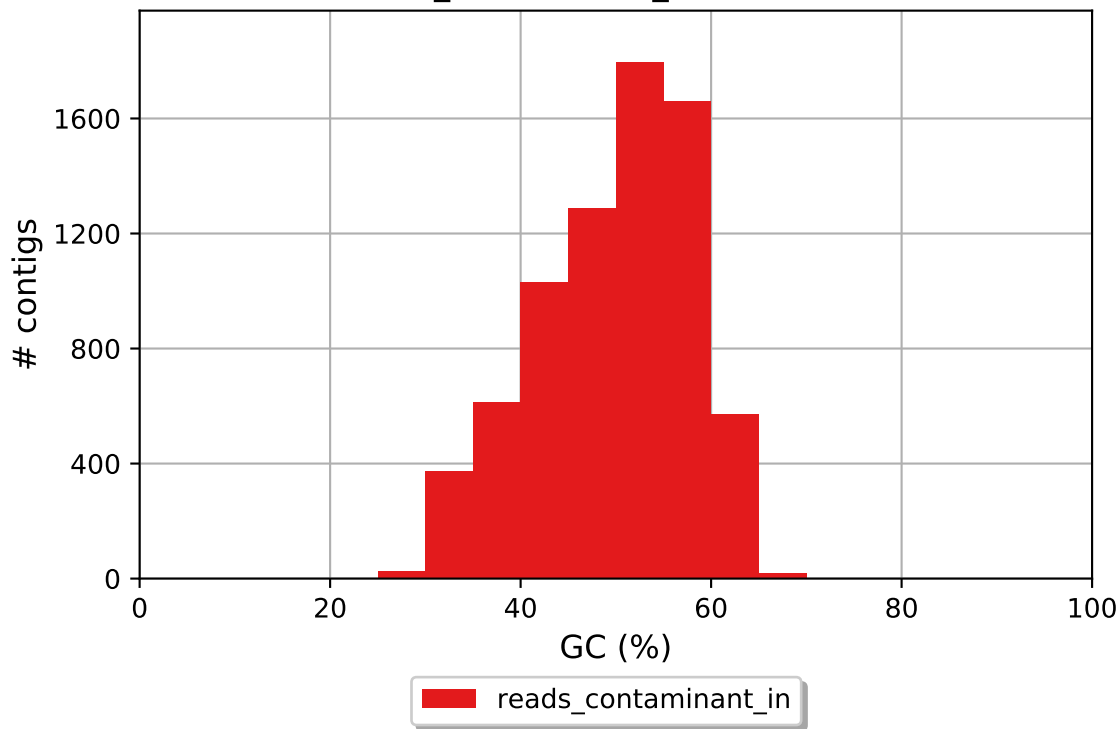


— reads_contaminant_in - - Reference

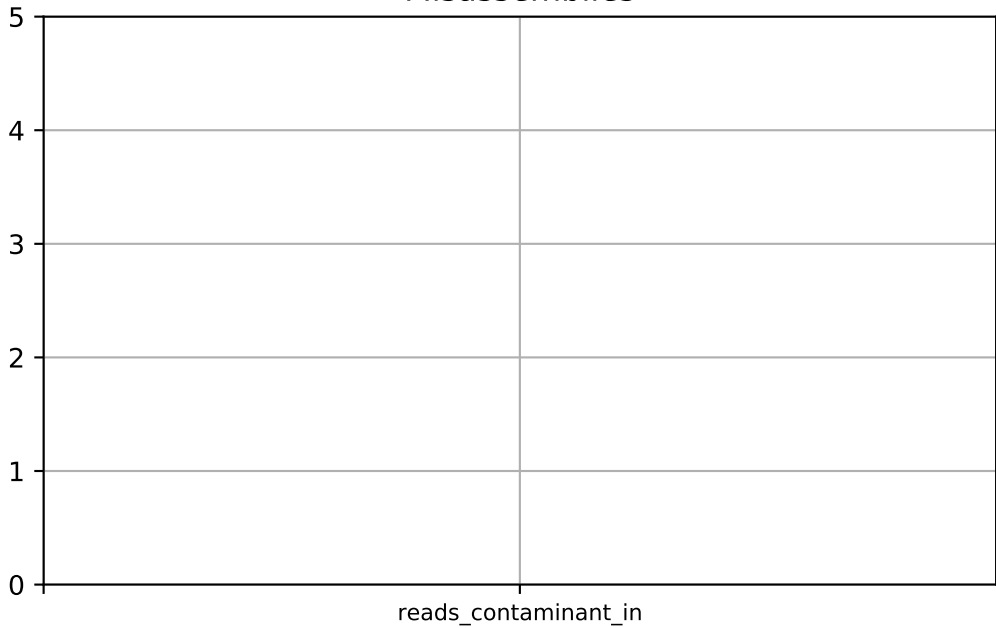
GC content



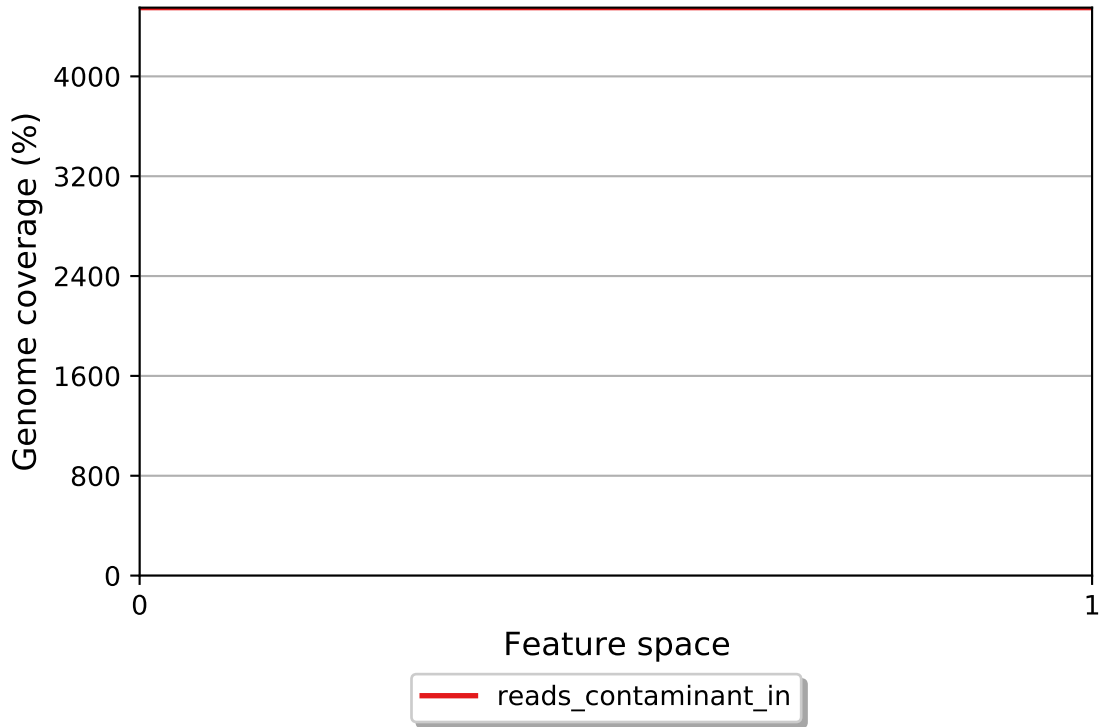
reads_contaminant_in GC content



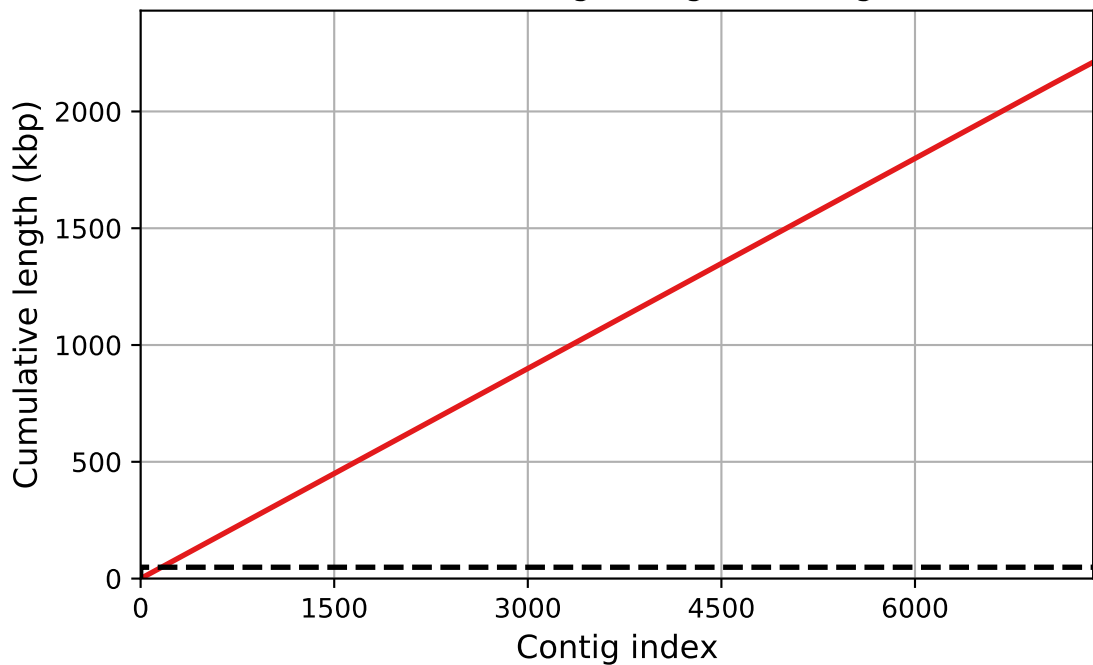
Misassemblies



FRCurve (misassemblies)

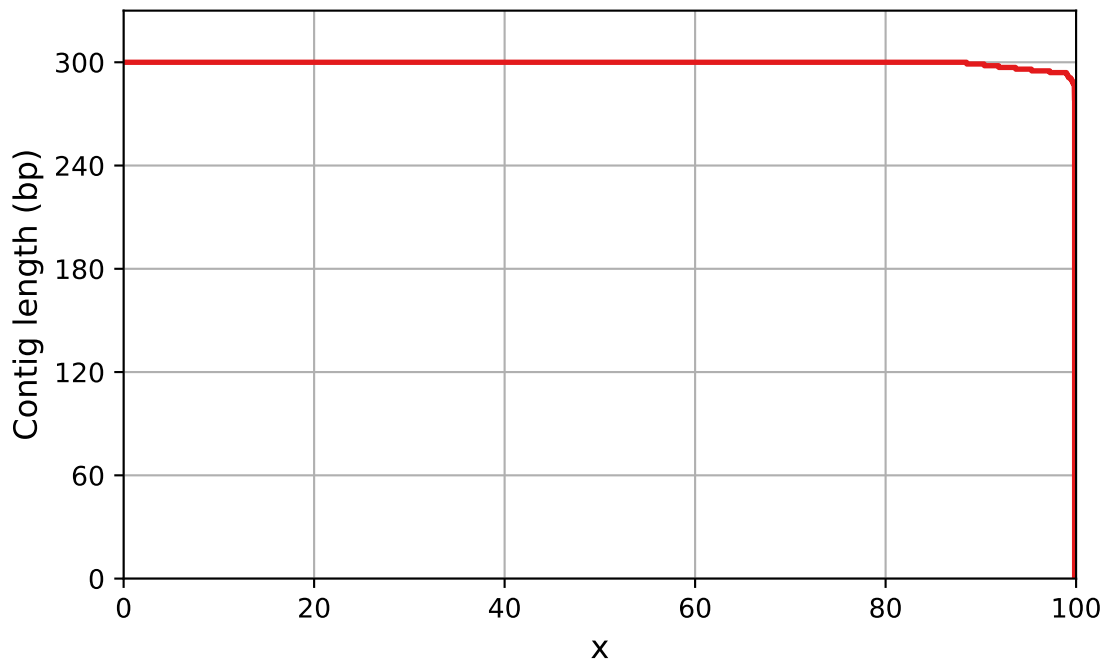


Cumulative length (aligned contigs)



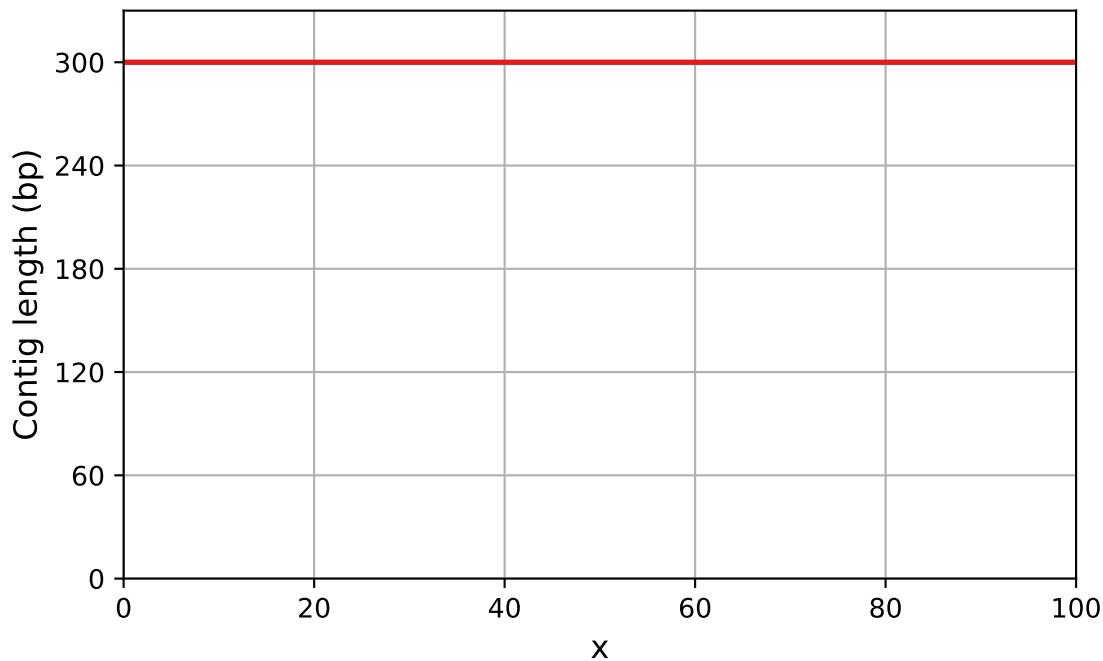
— reads_contaminant_in - - Reference

NAx



— reads_contaminant_in

NGAx



reads_contaminant_in