

Report

	NODE_1_length_2765031_cov_46.3316
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2765031
Total length (>= 1000 bp)	2765031
Total length (>= 5000 bp)	2765031
Total length (>= 10000 bp)	2765031
Total length (>= 25000 bp)	2765031
Total length (>= 50000 bp)	2765031
# contigs	1
Largest contig	2765031
Total length	2765031
Reference length	2765010
GC (%)	38.11
Reference GC (%)	38.11
N50	2765031
NG50	2765031
N75	2765031
NG75	2765031
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2765031
# 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 (%)	99.978
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.60
# indels per 100 kbp	0.87
Largest alignment	1899903
Total aligned length	2758592
NA50	1899903
NGA50	1899903
NA75	858689
NGA75	858689
LA50	1
LGA50	1
LA75	2
LGA75	2

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

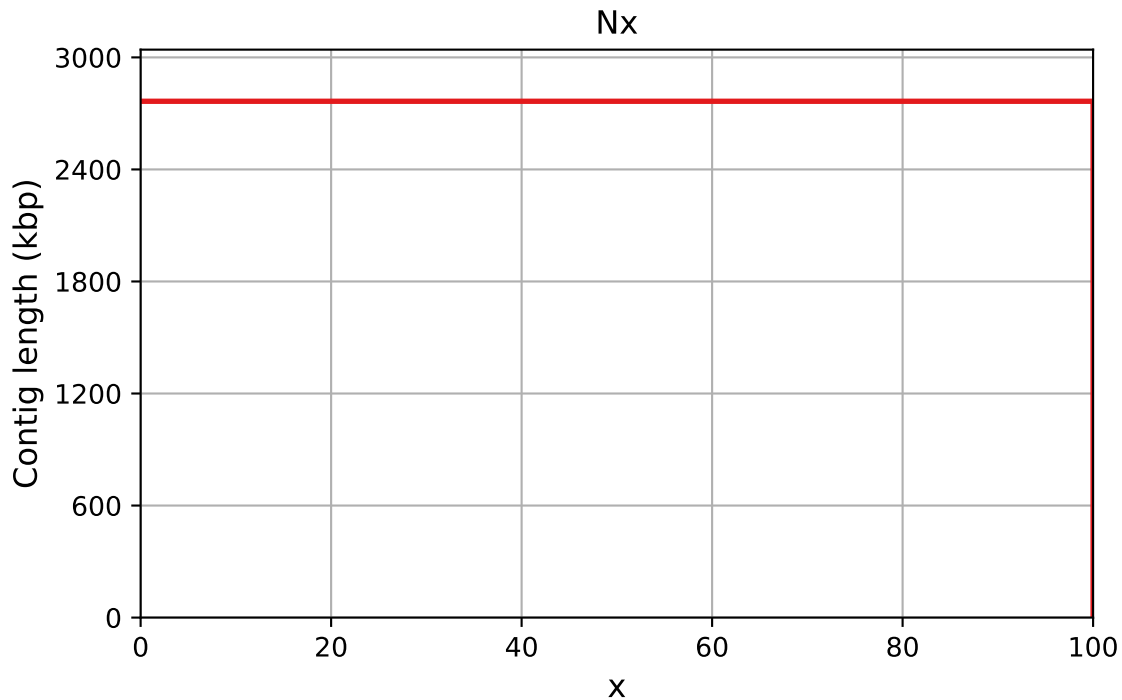
	NODE_1_length_2765031_cov_46.3316
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2765031
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	376
# indels	24
# indels (<= 5 bp)	22
# indels (> 5 bp)	2
Indels length	50

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

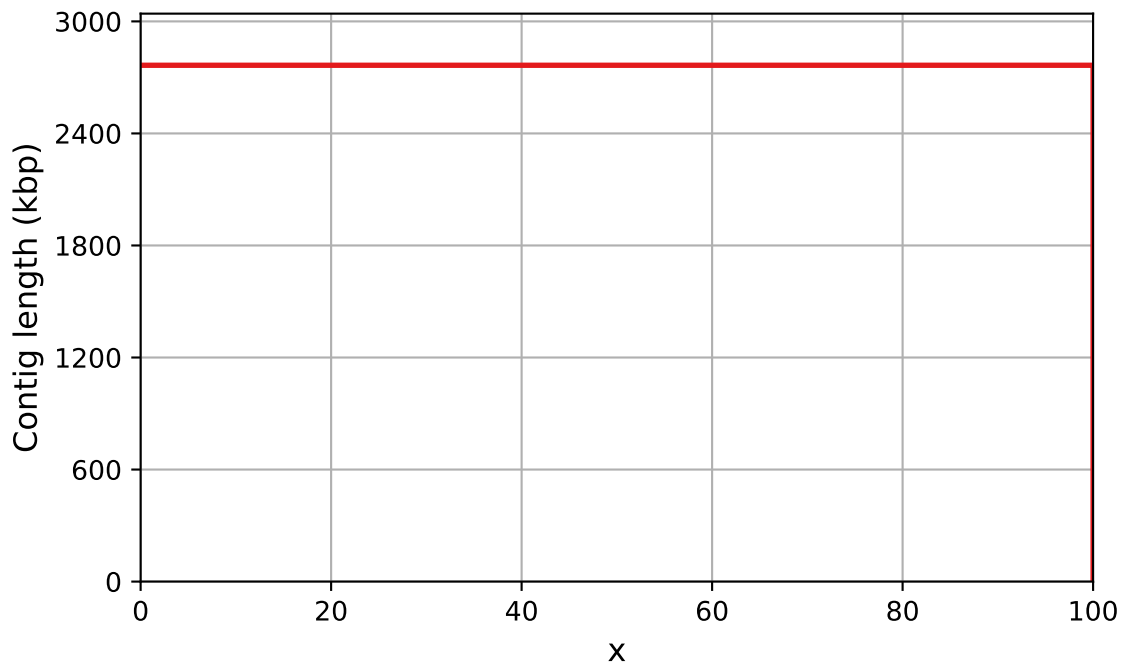
	NODE_1_length_2765031_cov_46.3316
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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

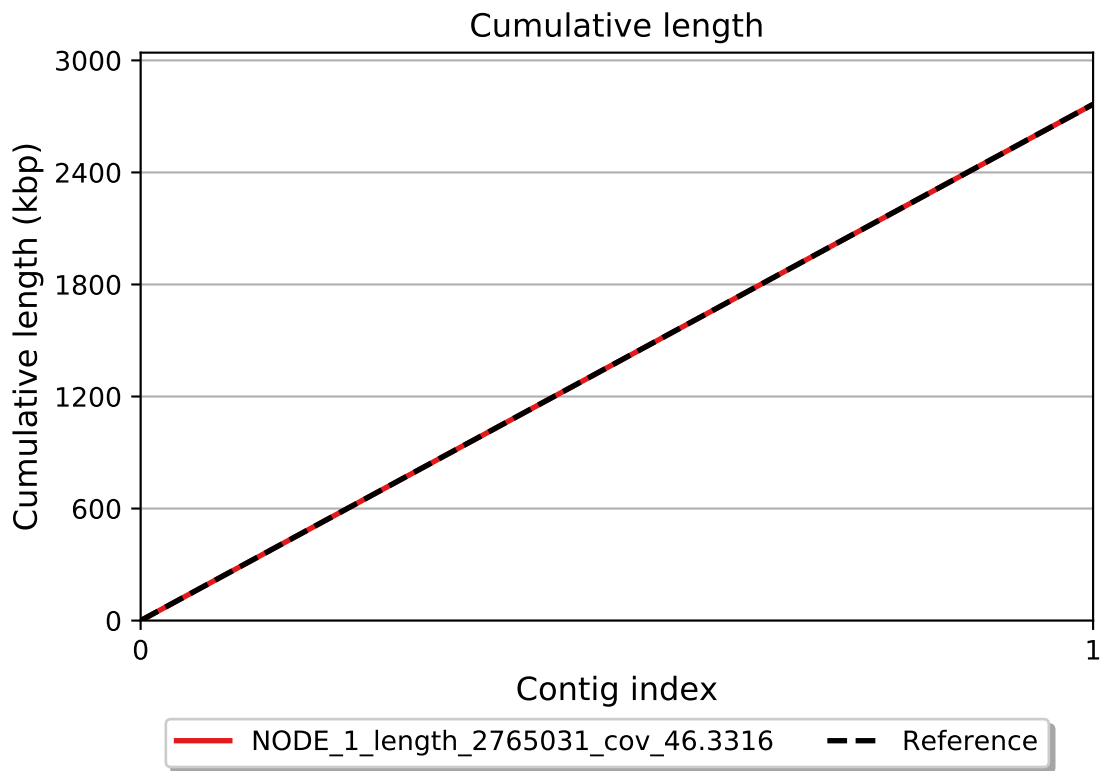


— NODE_1_length_2765031_cov_46.3316

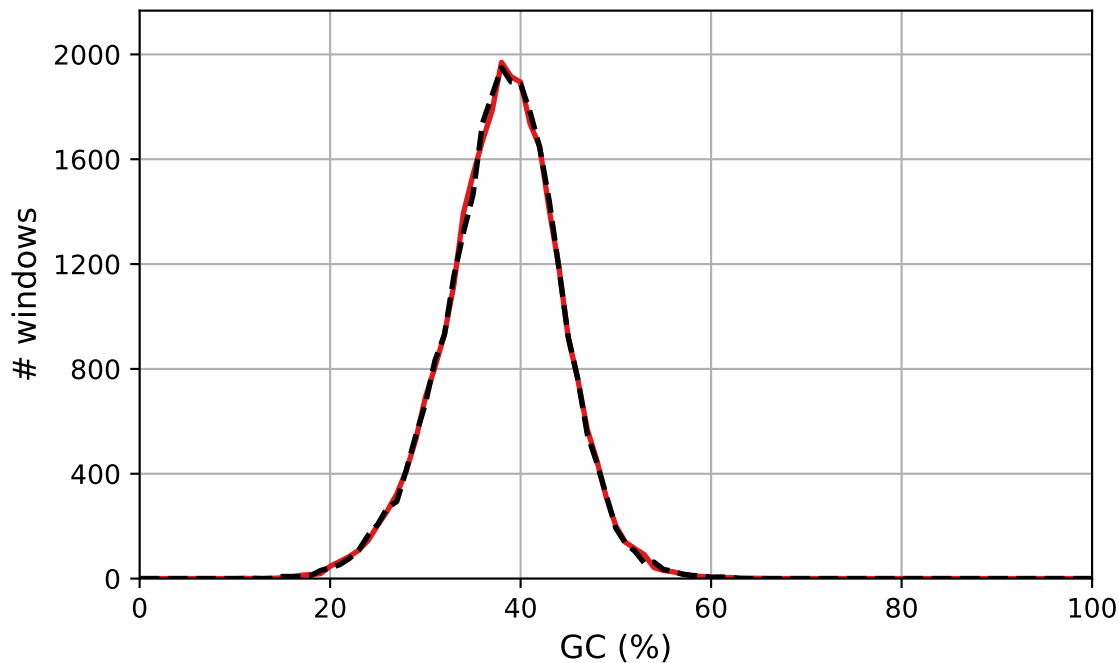
NGx



— NODE_1_length_2765031_cov_46.3316

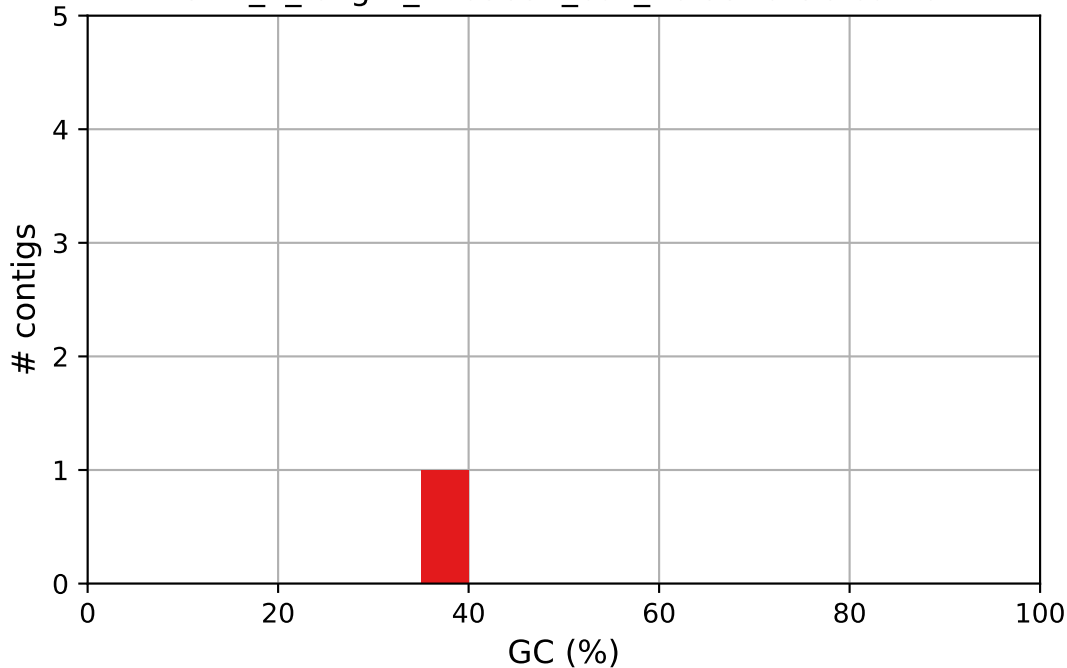


GC content



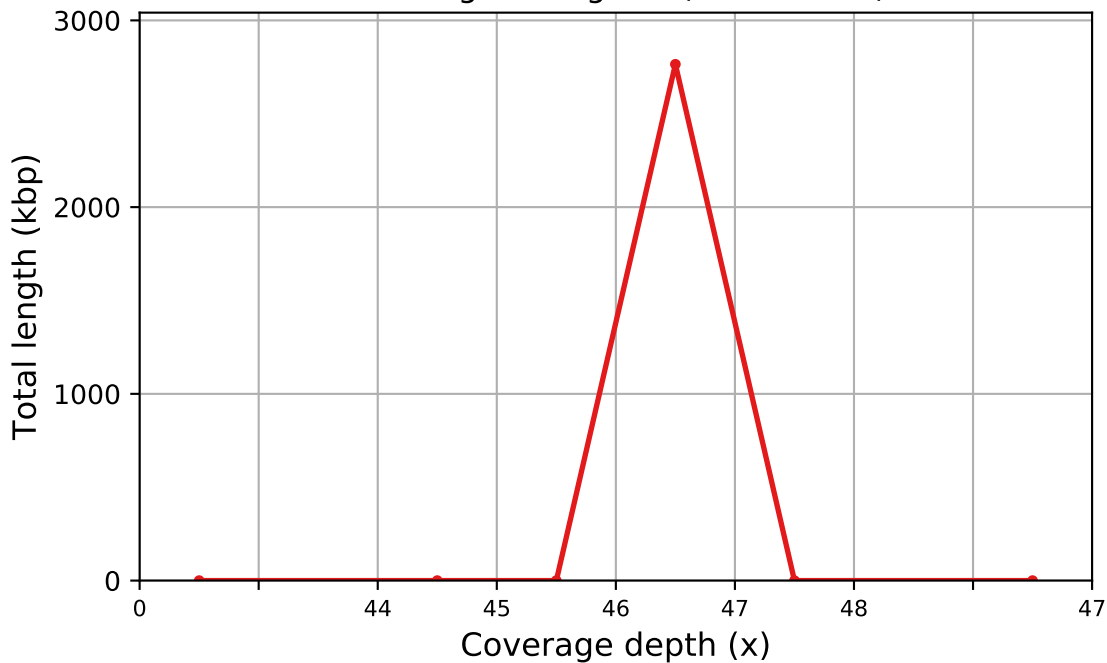
— NODE_1_length_2765031_cov_46.3316 - - Reference

NODE_1_length_2765031_cov_46.3316 GC content



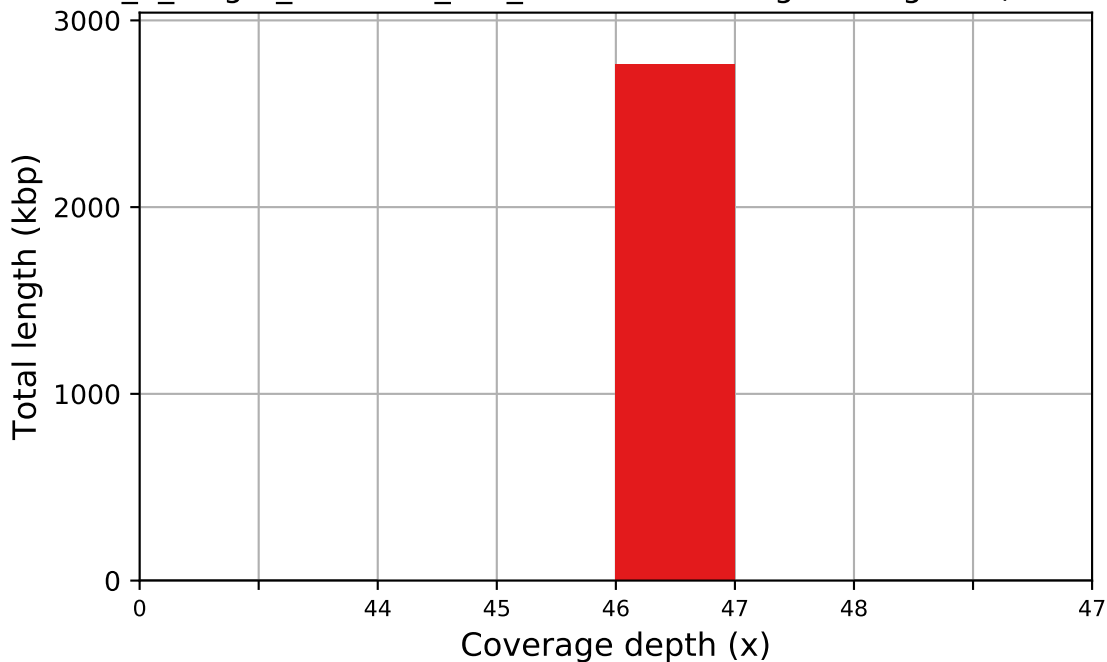
NODE_1_length_2765031_cov_46.3316

Coverage histogram (bin size: 1x)



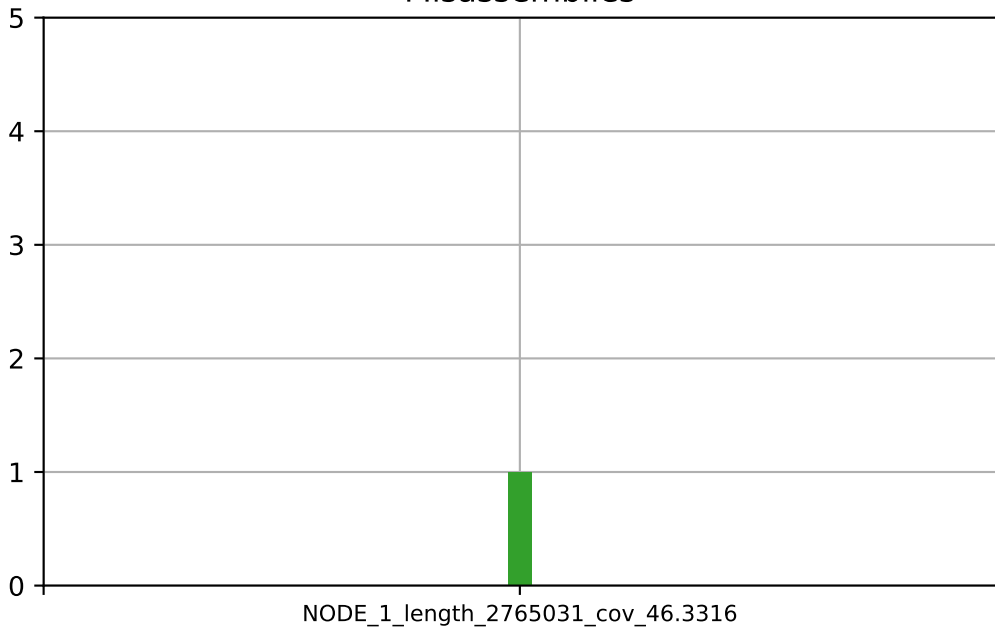
—●— NODE_1_length_2765031_cov_46.3316

NODE_1_length_2765031_cov_46.3316 coverage histogram (bin size: 1x)



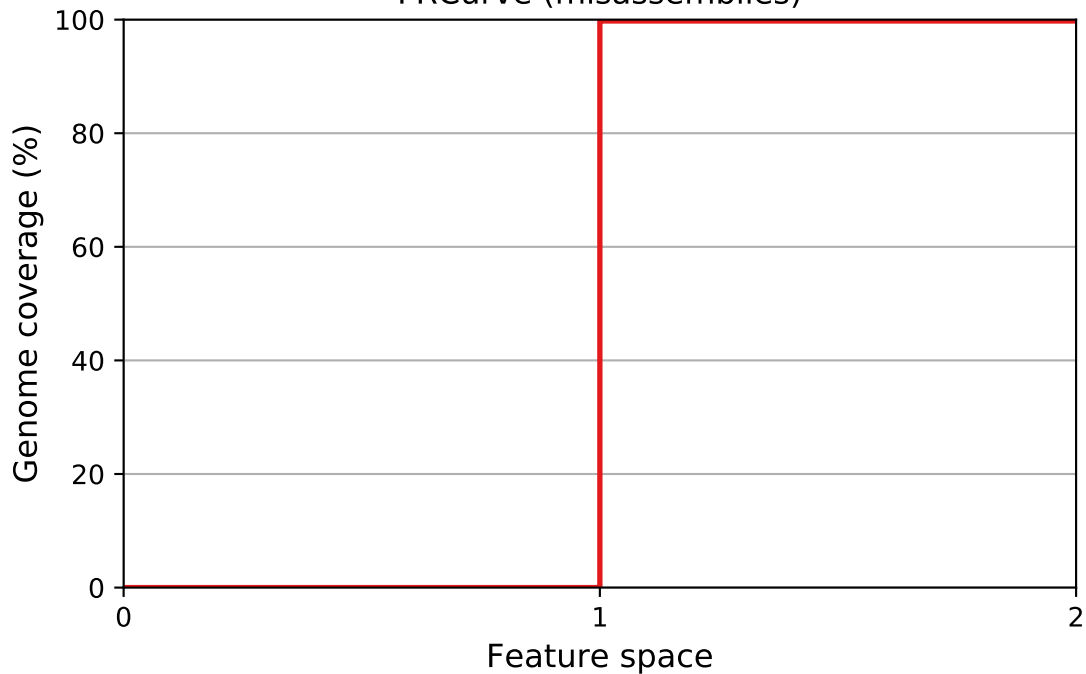
 NODE_1_length_2765031_cov_46.3316

Misassemblies



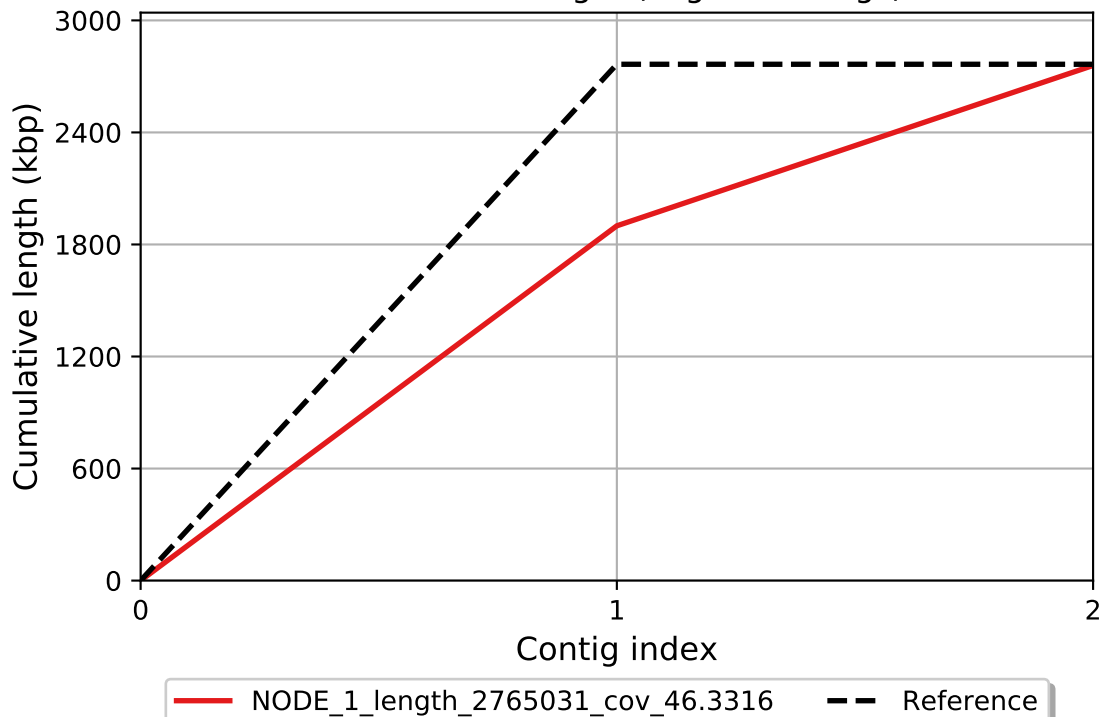
inversions

FRCurve (misassemblies)

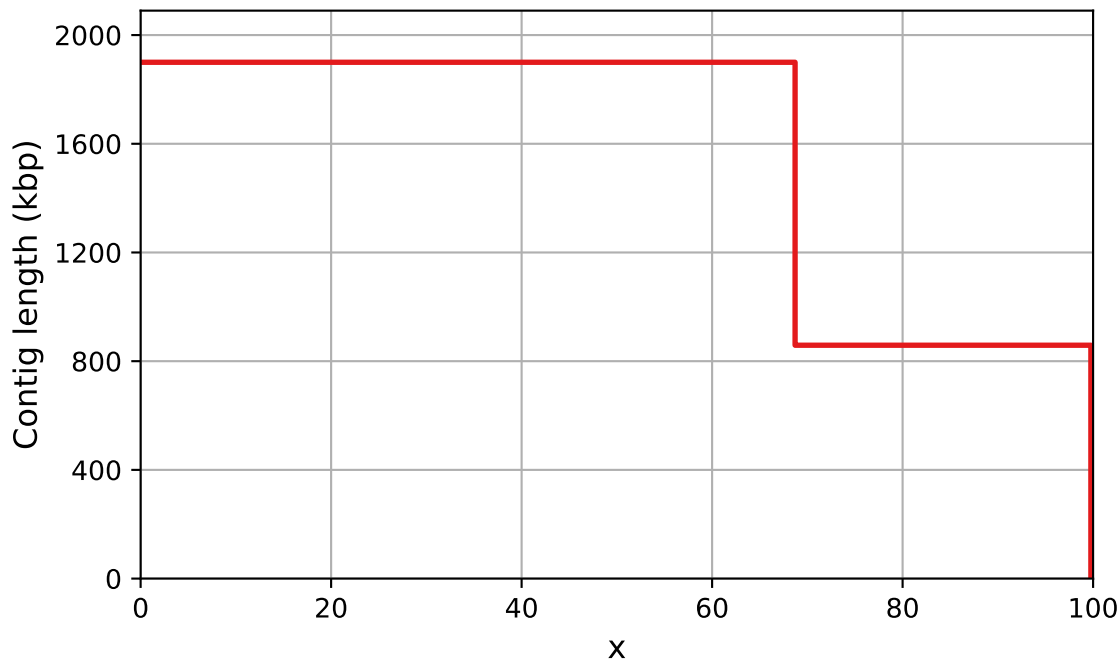


— NODE_1_length_2765031_cov_46.3316

Cumulative length (aligned contigs)

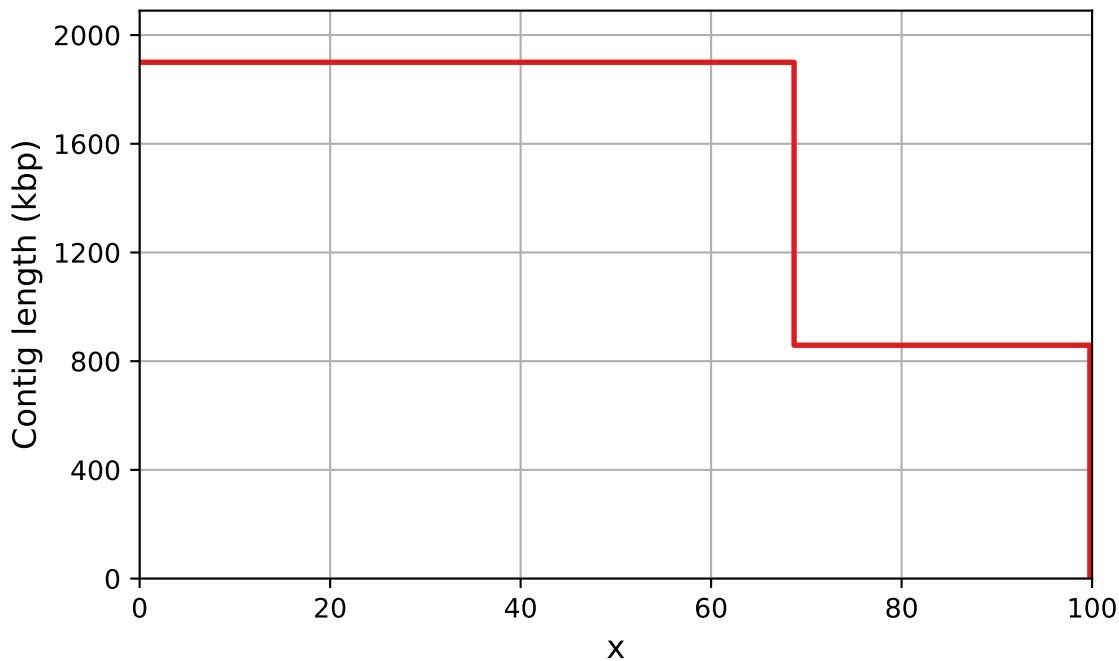


NAx



— NODE_1_length_2765031_cov_46.3316

NGAx



— NODE_1_length_2765031_cov_46.3316