

Report

	NODE_3
# 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)	64343
Total length (>= 1000 bp)	64343
Total length (>= 5000 bp)	64343
Total length (>= 10000 bp)	64343
Total length (>= 25000 bp)	64343
Total length (>= 50000 bp)	64343
# contigs	1
Largest contig	64343
Total length	64343
Reference length	65558
GC (%)	31.96
Reference GC (%)	32.05
N50	64343
NG50	64343
N75	64343
NG75	64343
L50	1
LG50	1
L75	1
LG75	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	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.147
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.55
# indels per 100 kbp	0.00
Largest alignment	64343
Total aligned length	64343
NA50	64343
NGA50	64343
NA75	64343
NGA75	64343
LA50	1
LGA50	1
LA75	1
LGA75	1

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_3
# 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	1
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

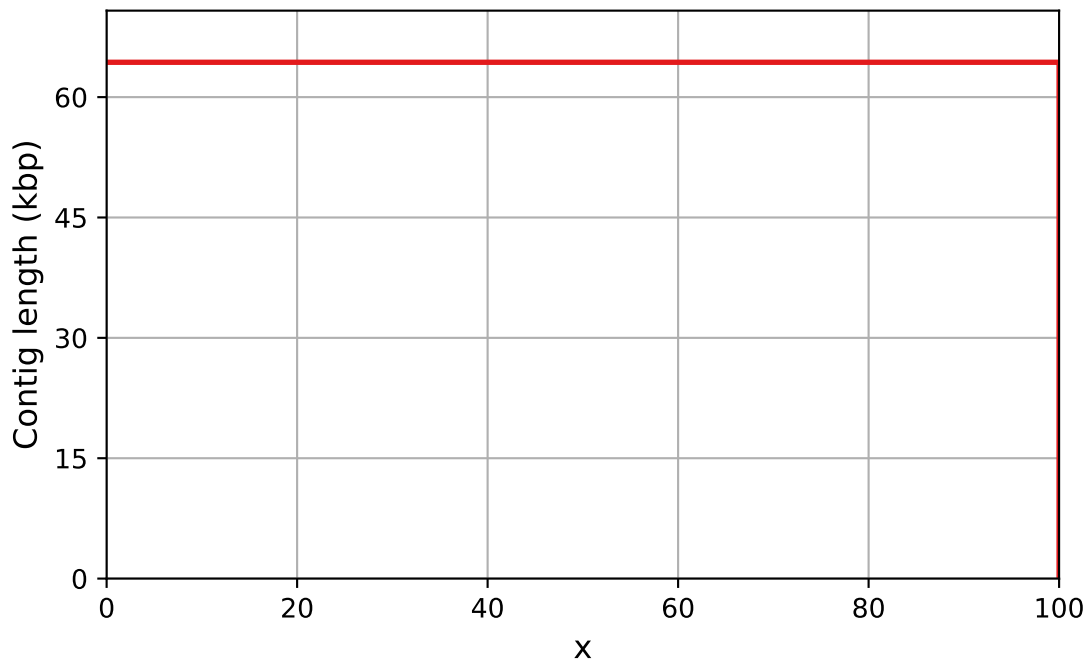
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	NODE_3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

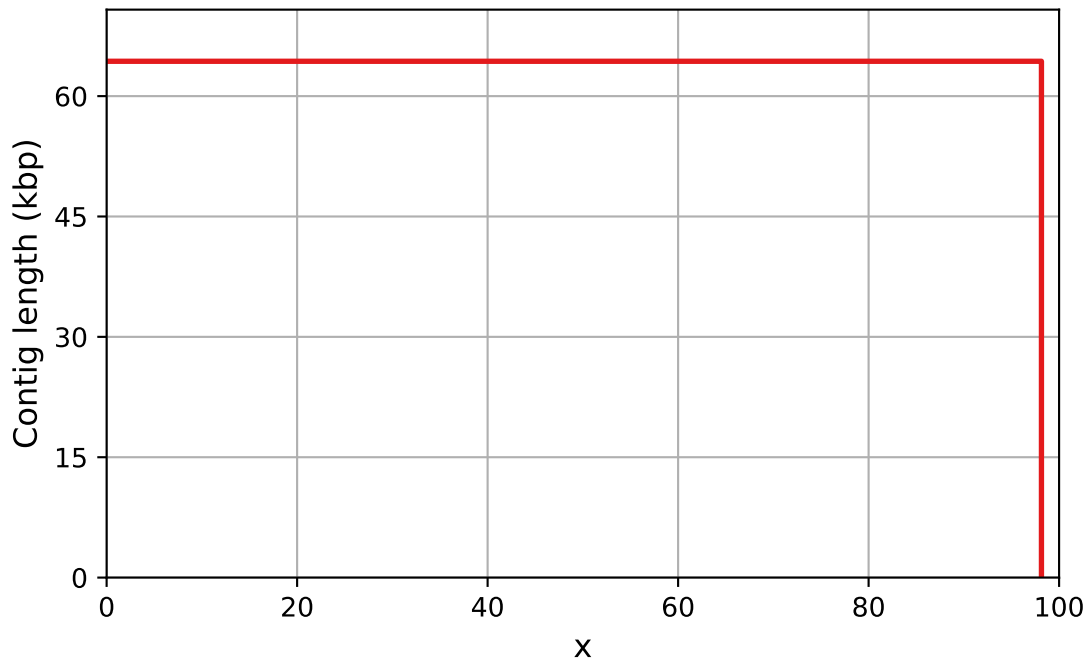
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



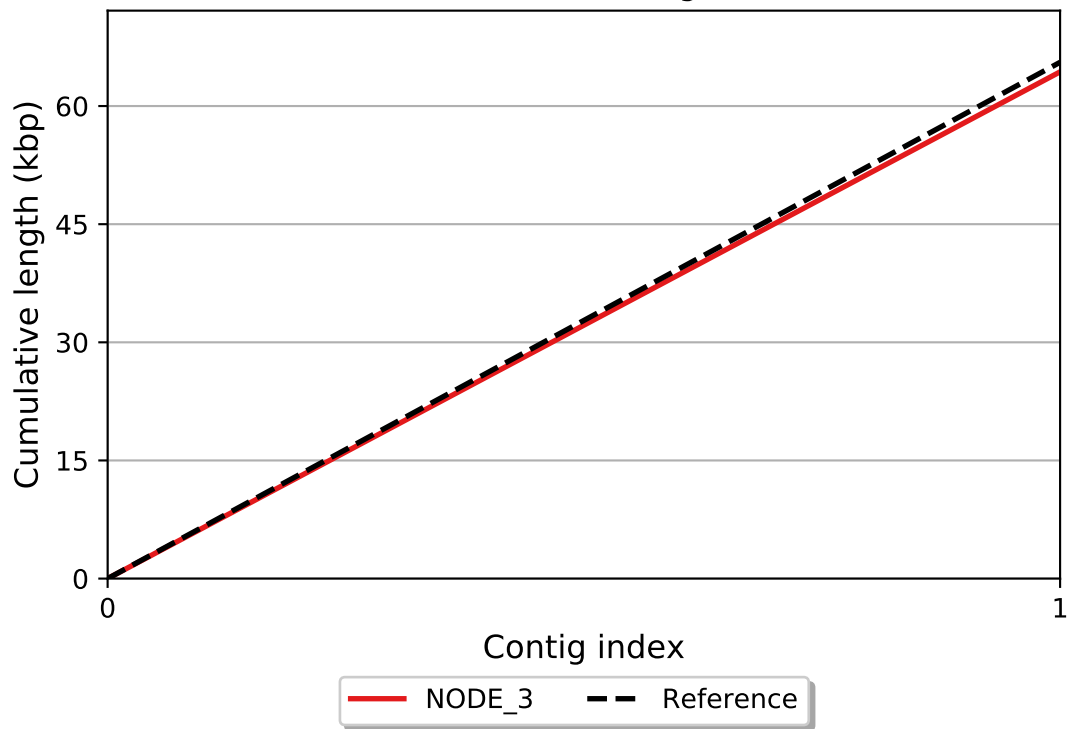
— NODE_3

NGx

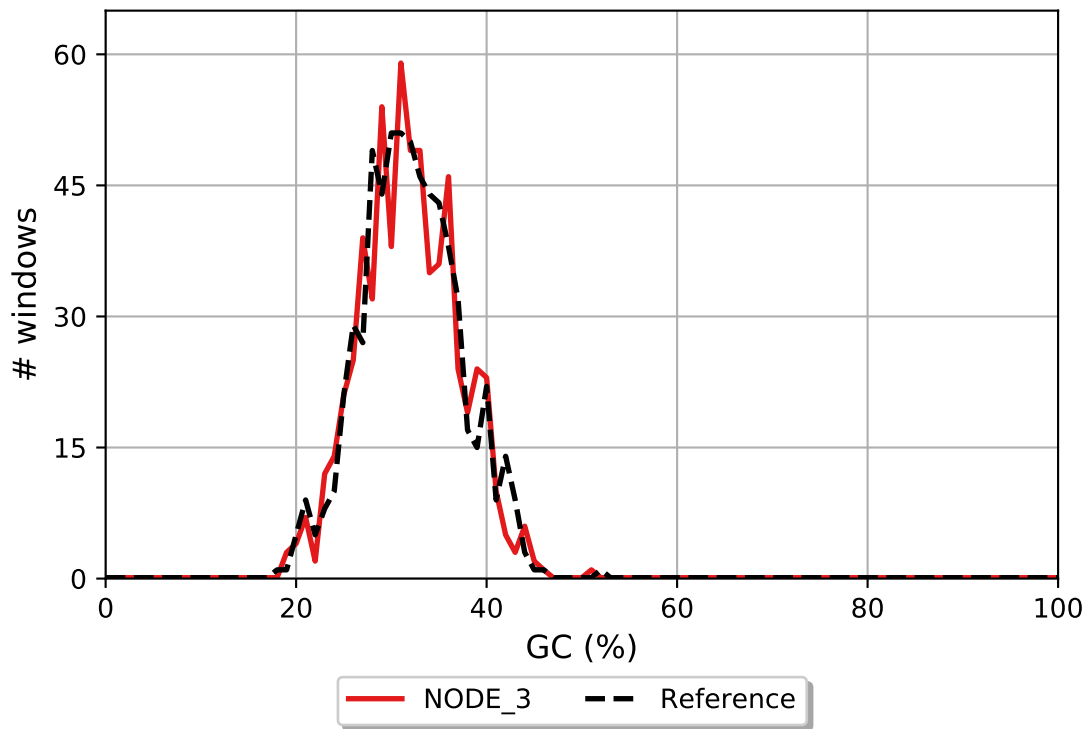


— NODE_3

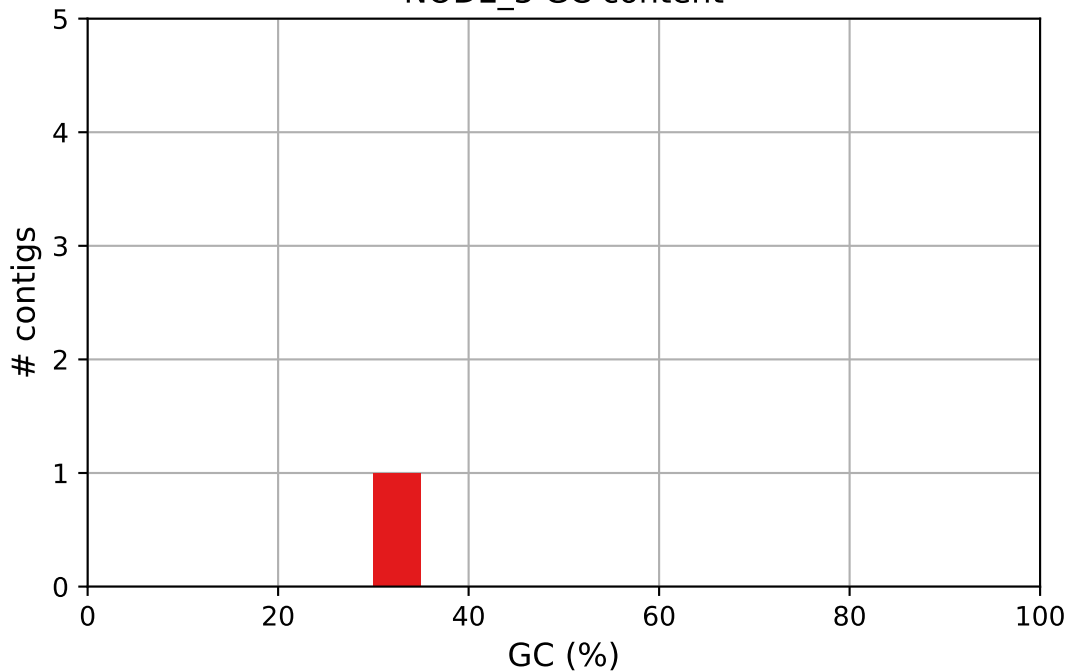
Cumulative length



GC content

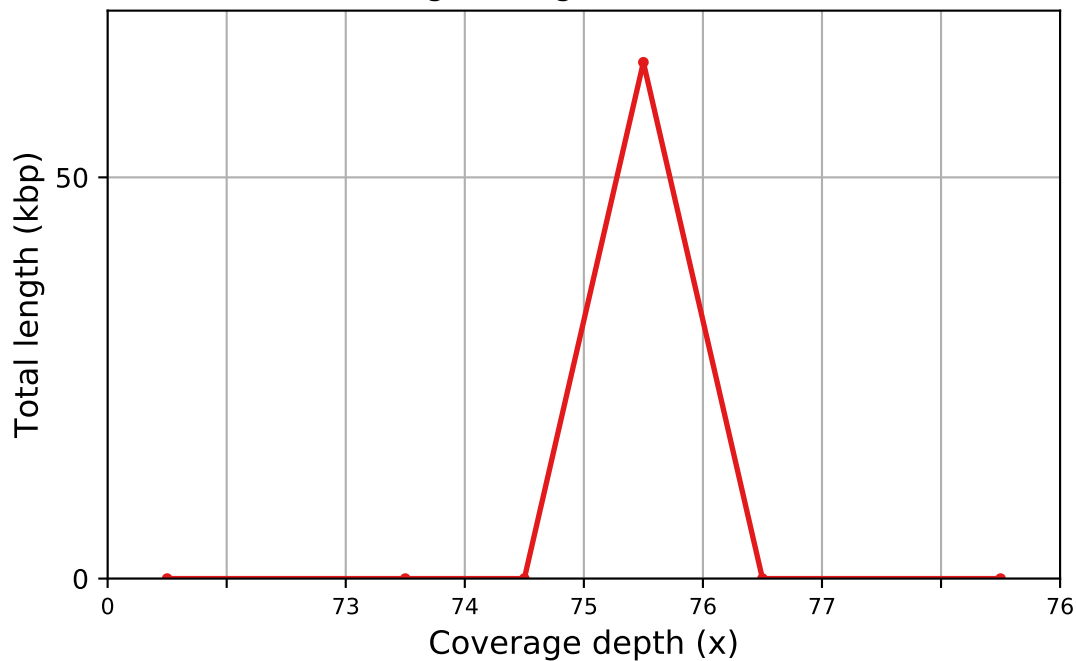


NODE_3 GC content



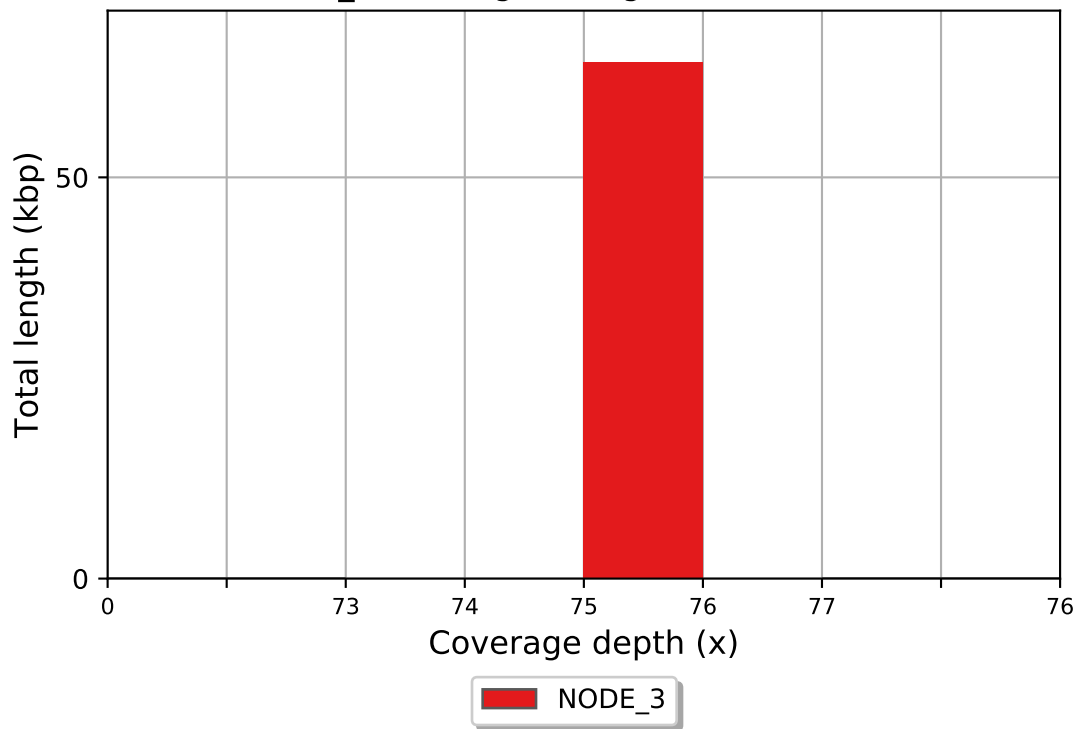
 NODE_3

Coverage histogram (bin size: 1x)

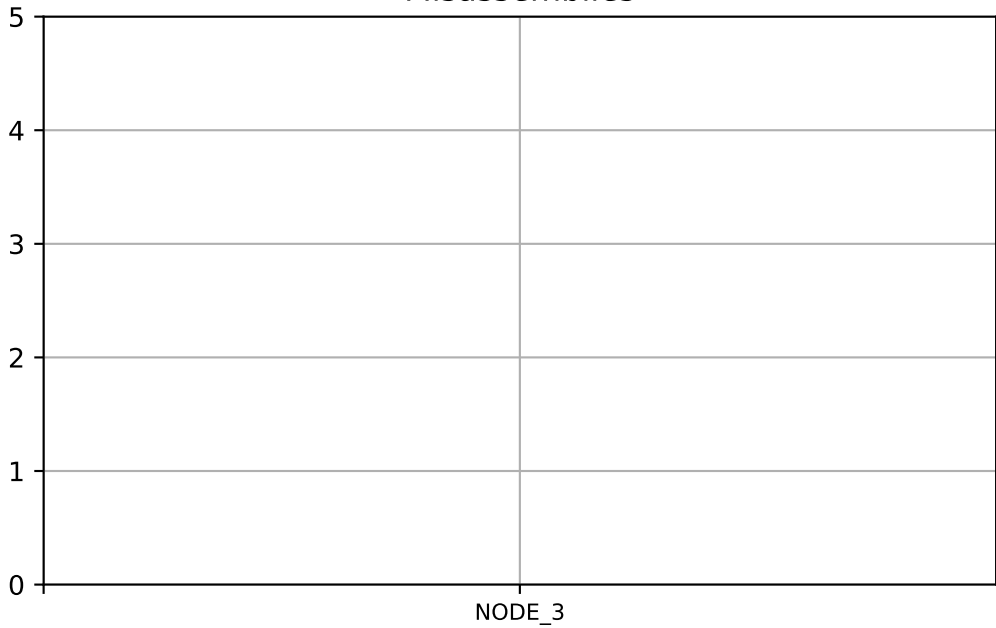


—●— NODE_3

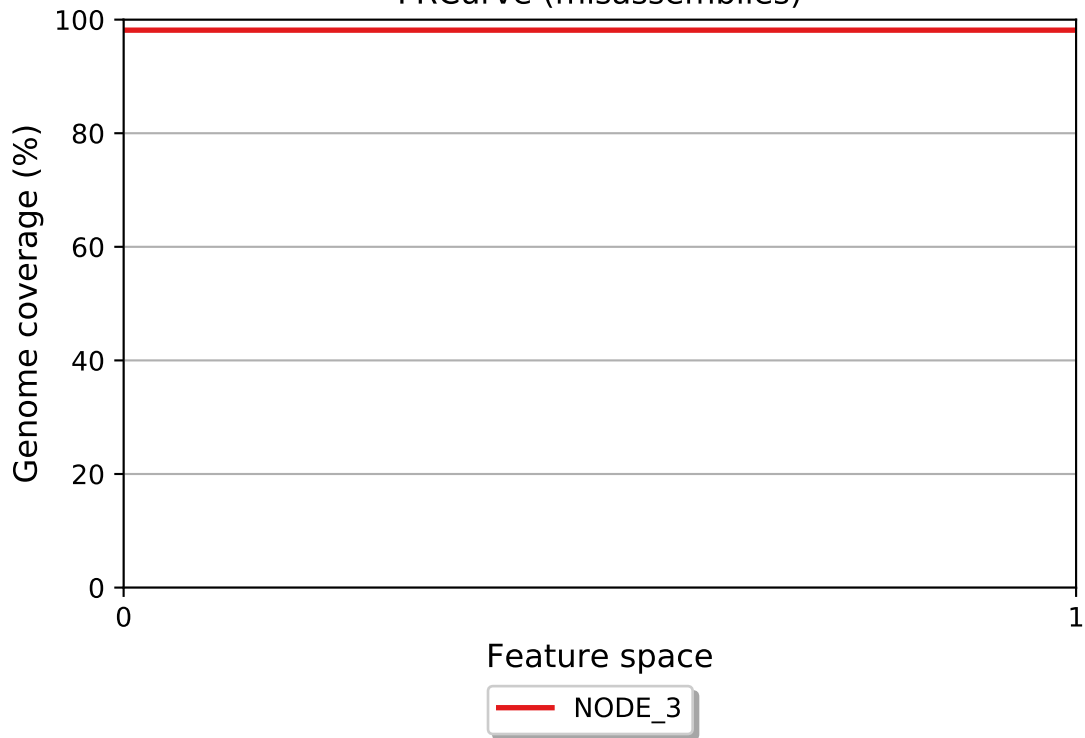
NODE_3 coverage histogram (bin size: 1x)



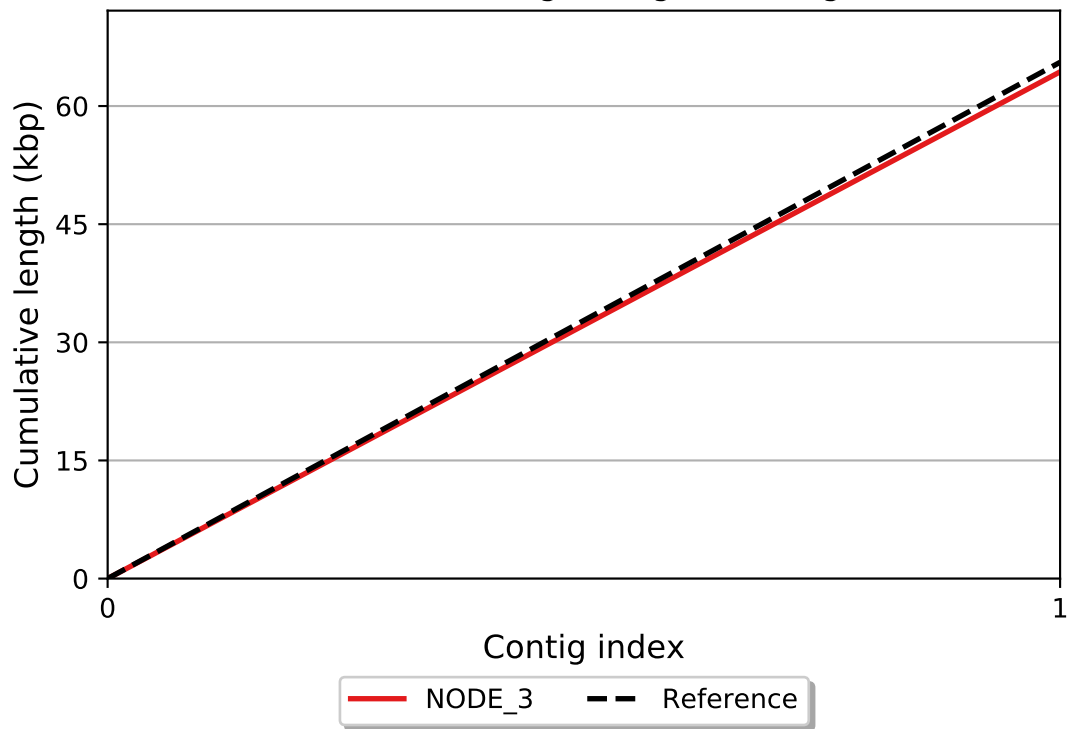
Misassemblies



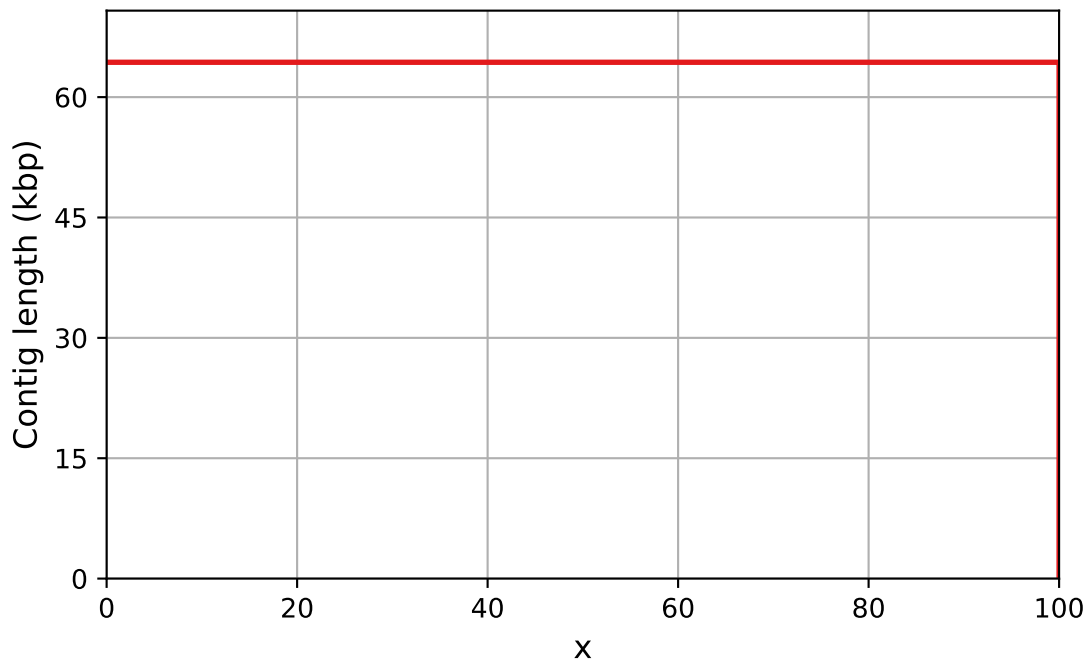
FRCurve (misassemblies)



Cumulative length (aligned contigs)

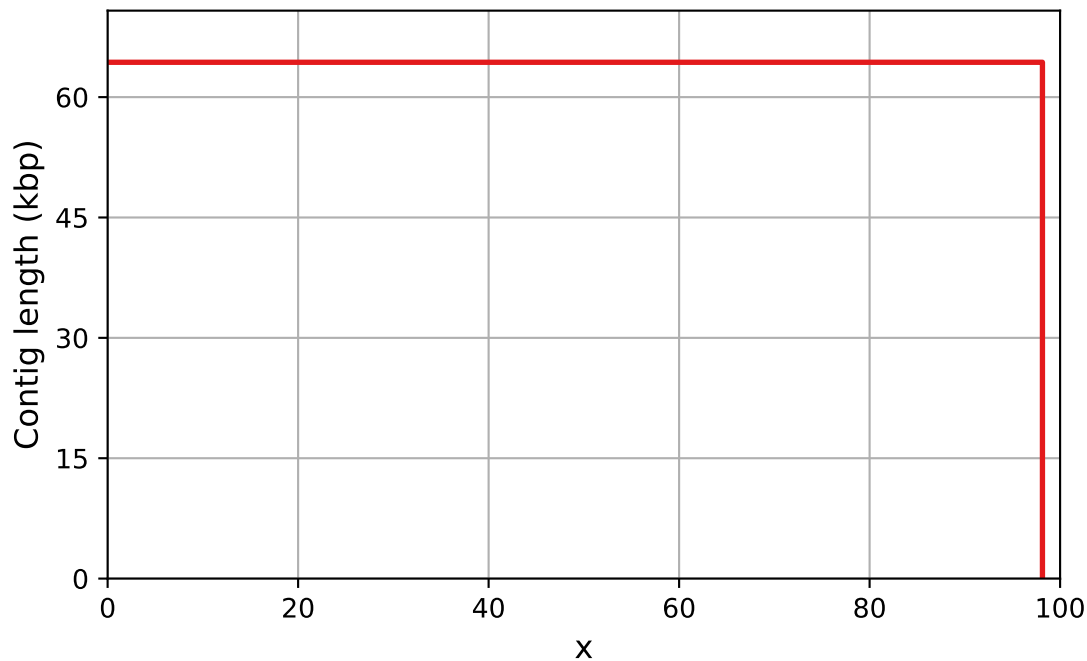


NAx



— NODE_3

NGAx



— NODE_3