

Report

	draft_assembly
# contigs (>= 0 bp)	6
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	6
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4865333
Total length (>= 1000 bp)	4865333
Total length (>= 5000 bp)	4865333
Total length (>= 10000 bp)	4865333
Total length (>= 25000 bp)	4764783
Total length (>= 50000 bp)	4764783
# contigs	6
Largest contig	4764783
Total length	4865333
Reference length	4639675
GC (%)	50.64
Reference GC (%)	50.79
N50	4764783
NG50	4764783
N75	4764783
NG75	4764783
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	6
# unaligned contigs	0 + 6 part
Unaligned length	4733675
Genome fraction (%)	2.834
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1226.09
# indels per 100 kbp	3.80
Largest alignment	170
Total aligned length	131658
NGA50	-

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

	draft_assembly
# 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	6
# mismatches	1612
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	5

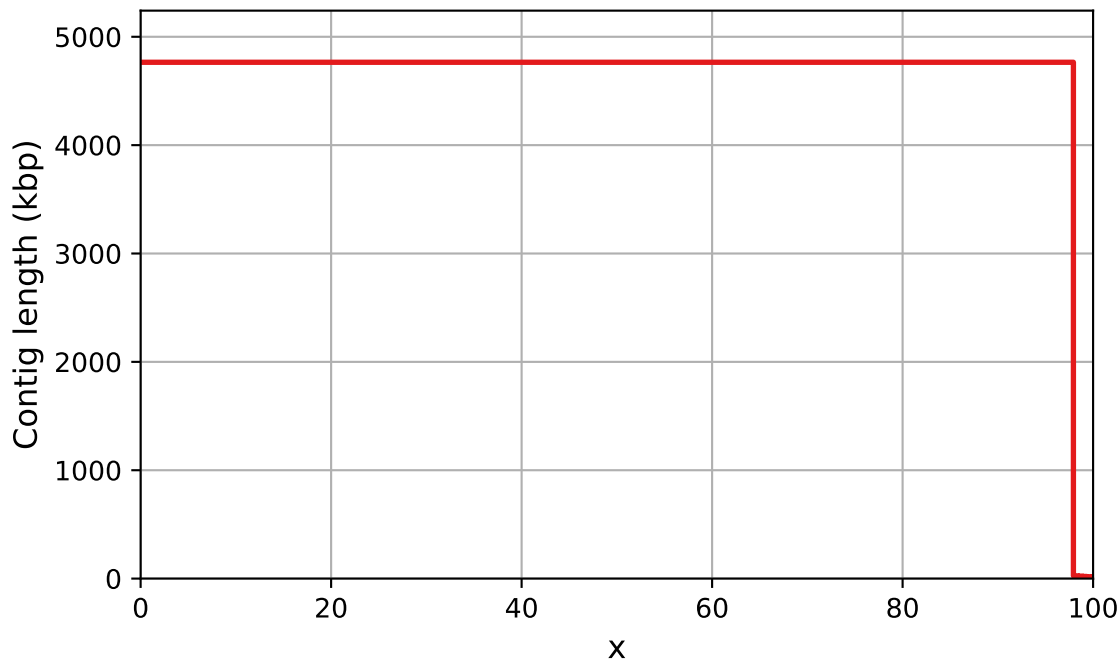
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	draft_assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	4733675
# N's	0

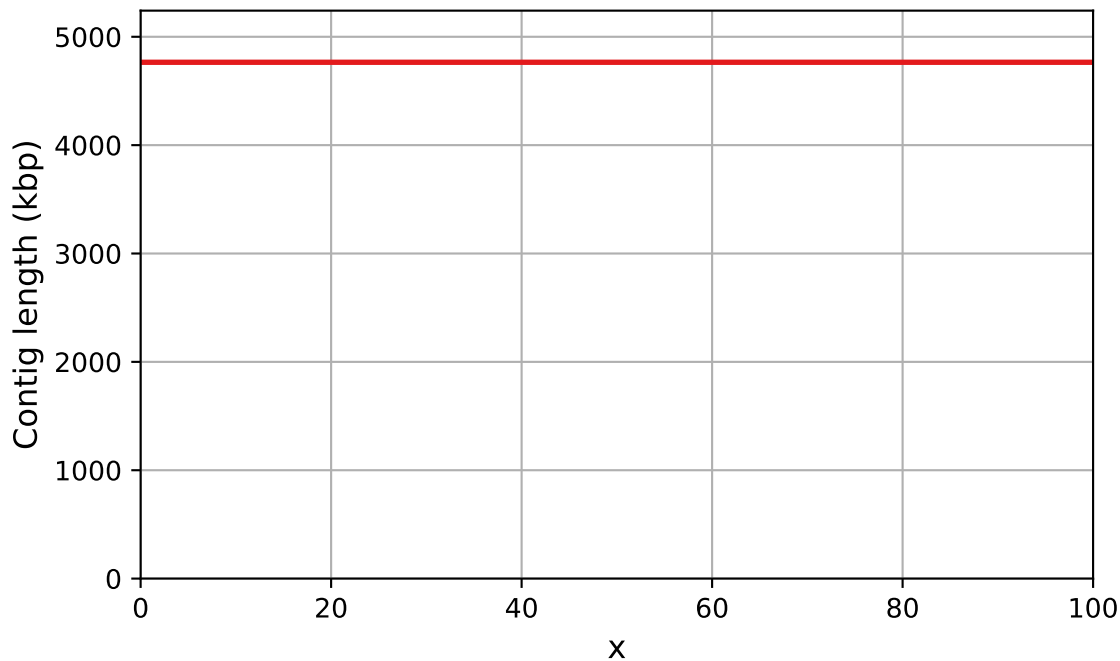
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

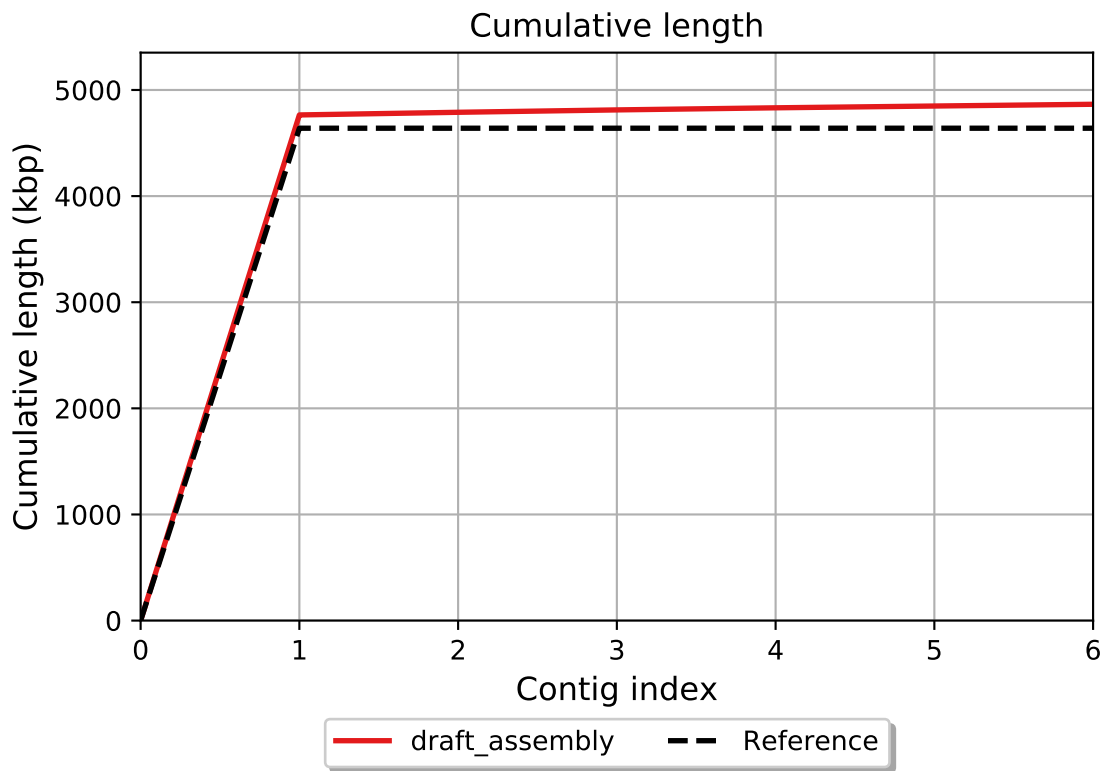


— draft_assembly

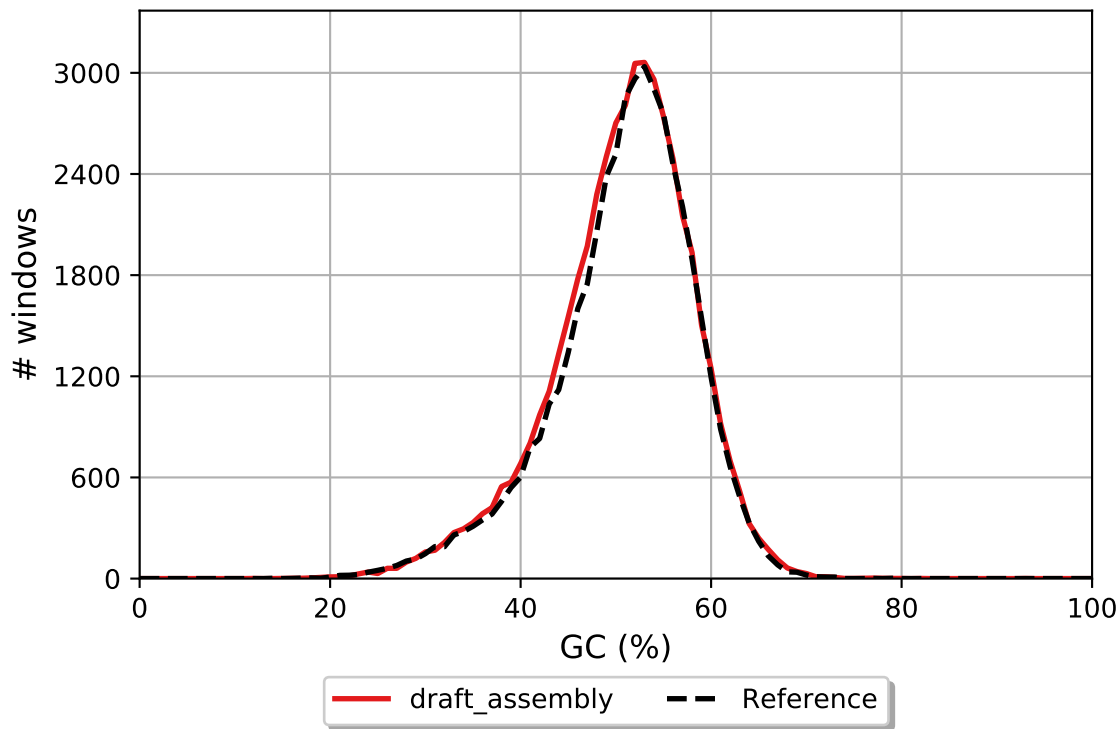
NGx



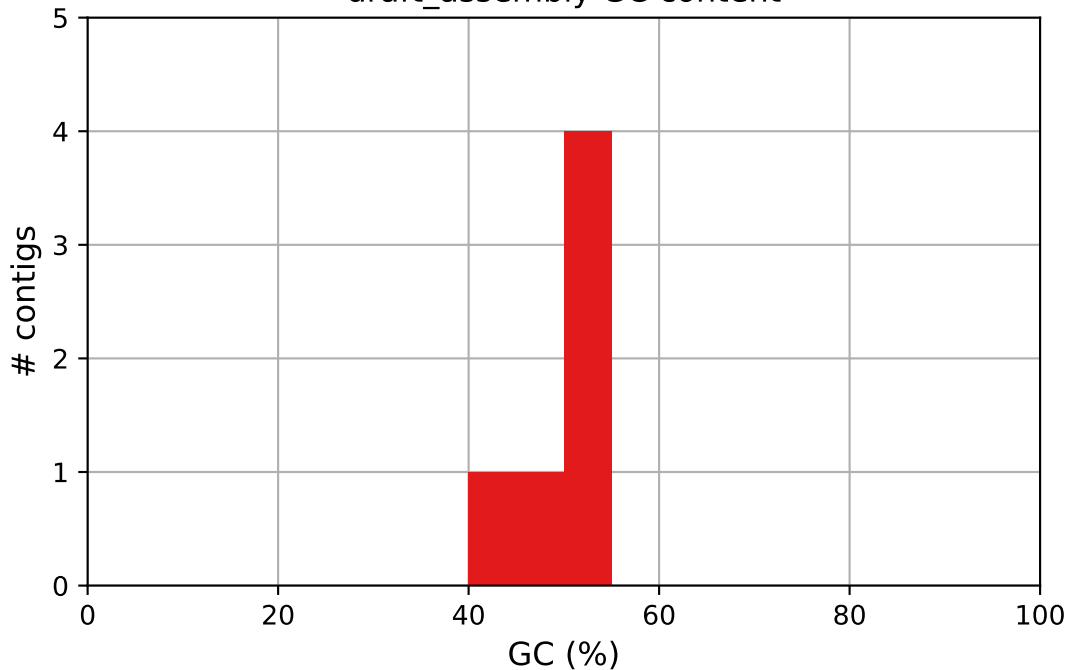
— draft_assembly



GC content

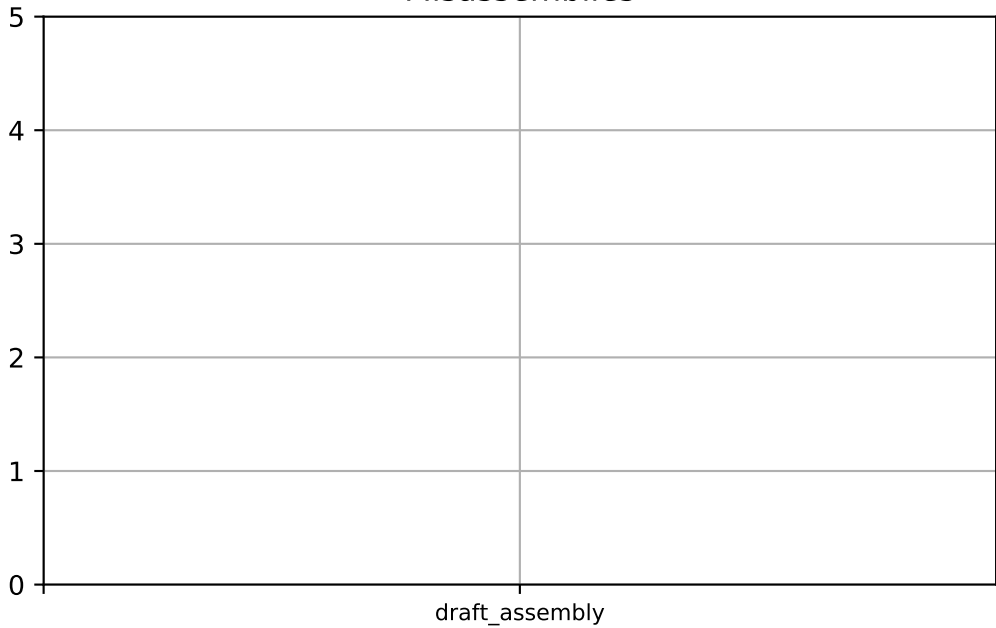


draft_assembly GC content

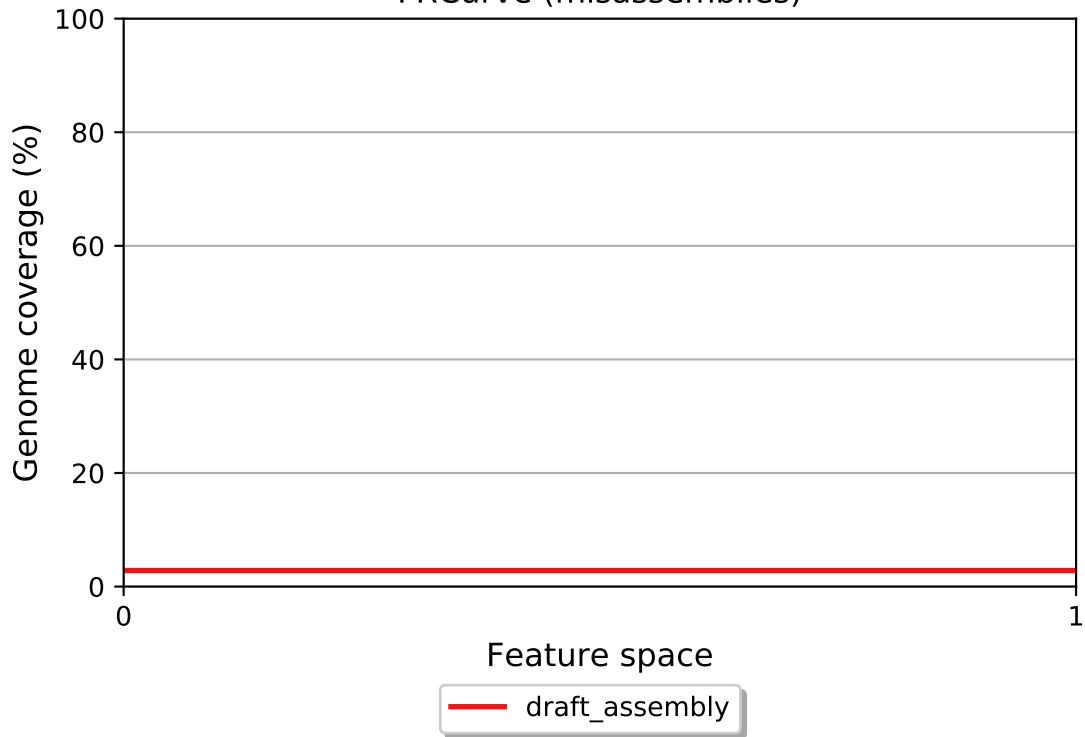


draft_assembly

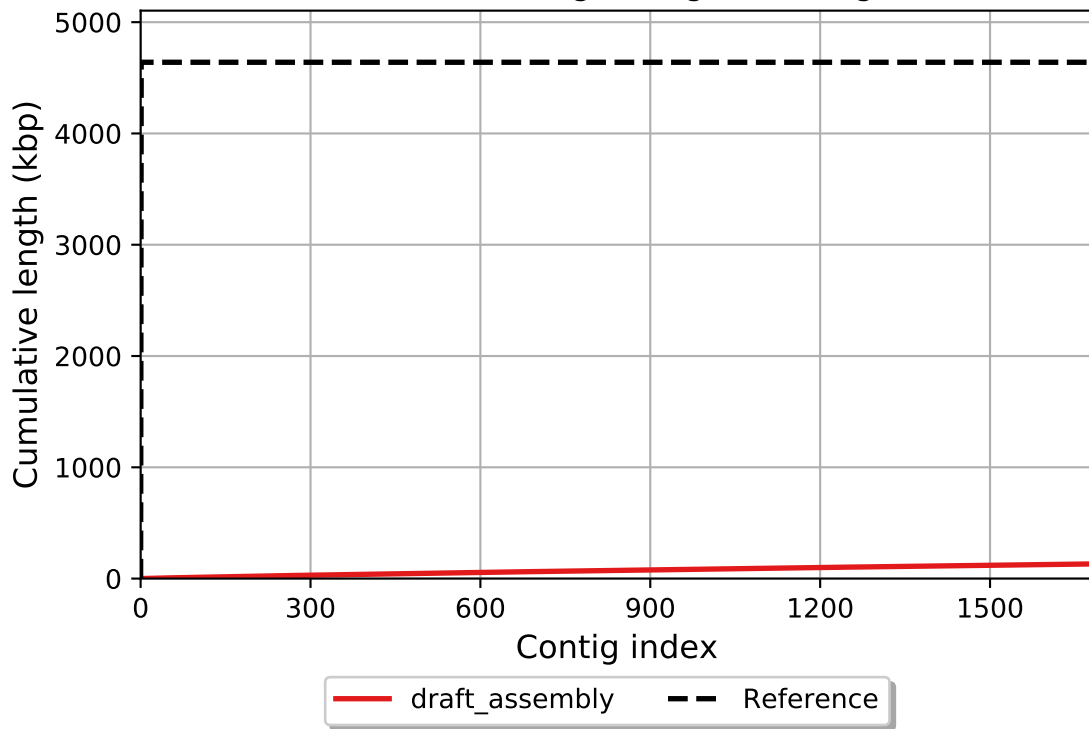
Misassemblies



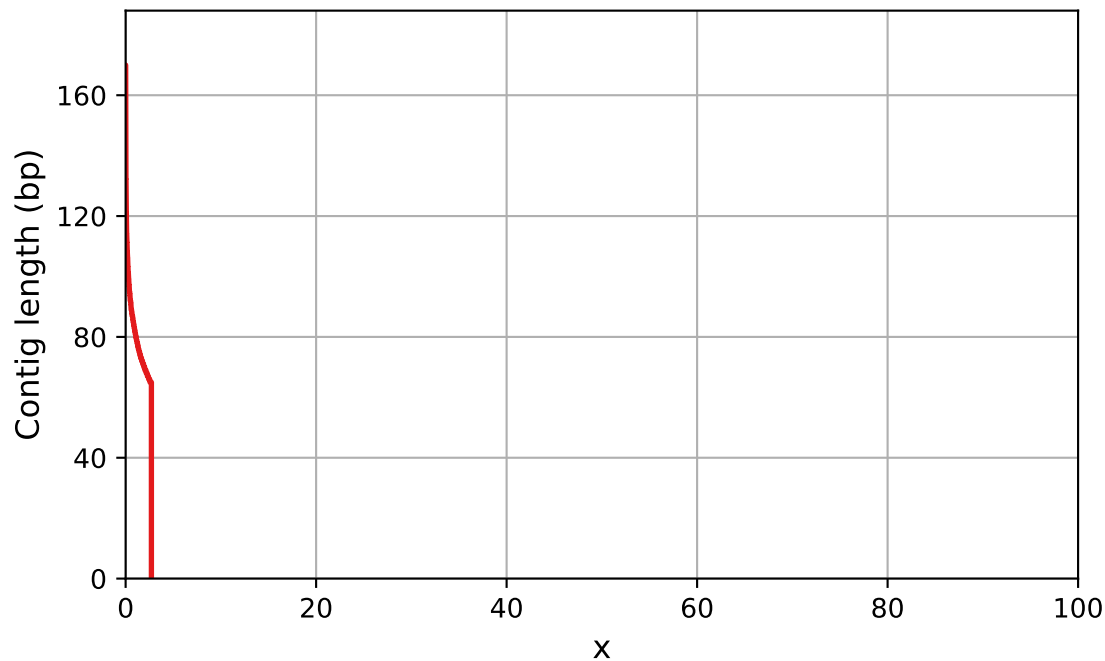
FRCurve (misassemblies)



Cumulative length (aligned contigs)

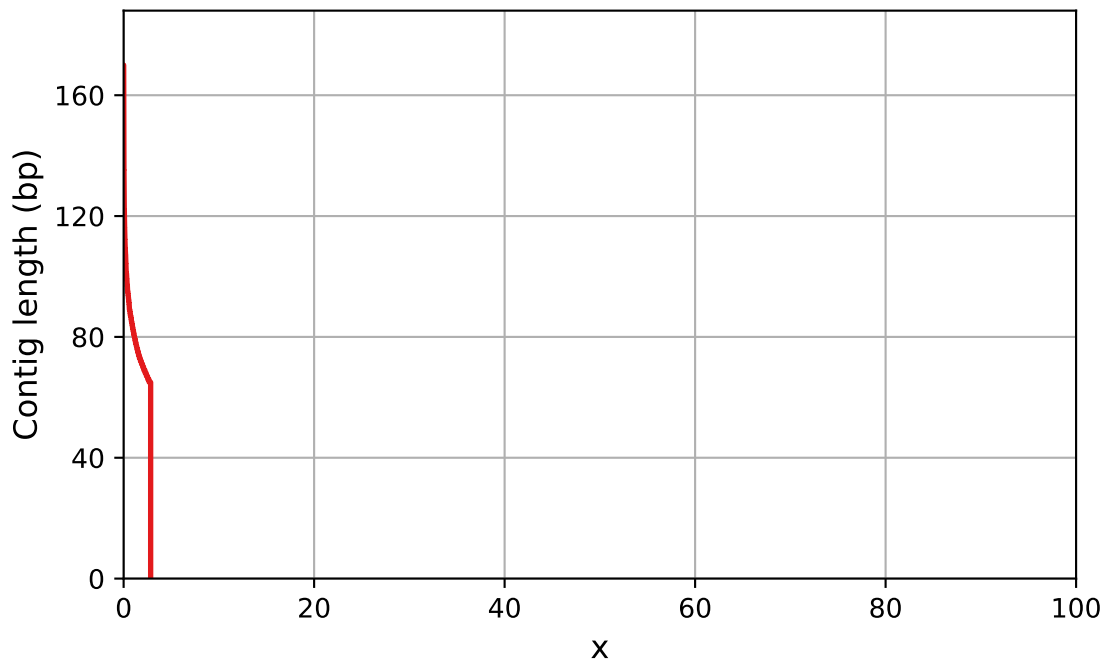


NAx



— draft_assembly

NGAx



— draft_assembly