

Report

	assembly
# contigs (>= 0 bp)	82
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	70
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	34
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	2616309
Total length (>= 1000 bp)	2613457
Total length (>= 5000 bp)	2593735
Total length (>= 10000 bp)	2548740
Total length (>= 25000 bp)	2072037
Total length (>= 50000 bp)	1433684
# contigs	82
Largest contig	152052
Total length	2616309
Reference length	2572027
GC (%)	32.75
Reference GC (%)	32.91
N50	63569
NG50	63569
N75	29925
NG75	32693
L50	14
LG50	14
L75	31
LG75	29
# misassemblies	76
# misassembled contigs	31
Misassembled contigs length	1776908
# local misassemblies	32
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	4 + 21 part
Unaligned length	344683
Genome fraction (%)	85.968
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	581.65
# indels per 100 kbp	181.81
Largest alignment	79608
Total aligned length	2267107
NA50	23959
NGA50	24244
NA75	12615
NGA75	13086
LA50	31
LGA50	30
LA75	70
LGA75	67

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

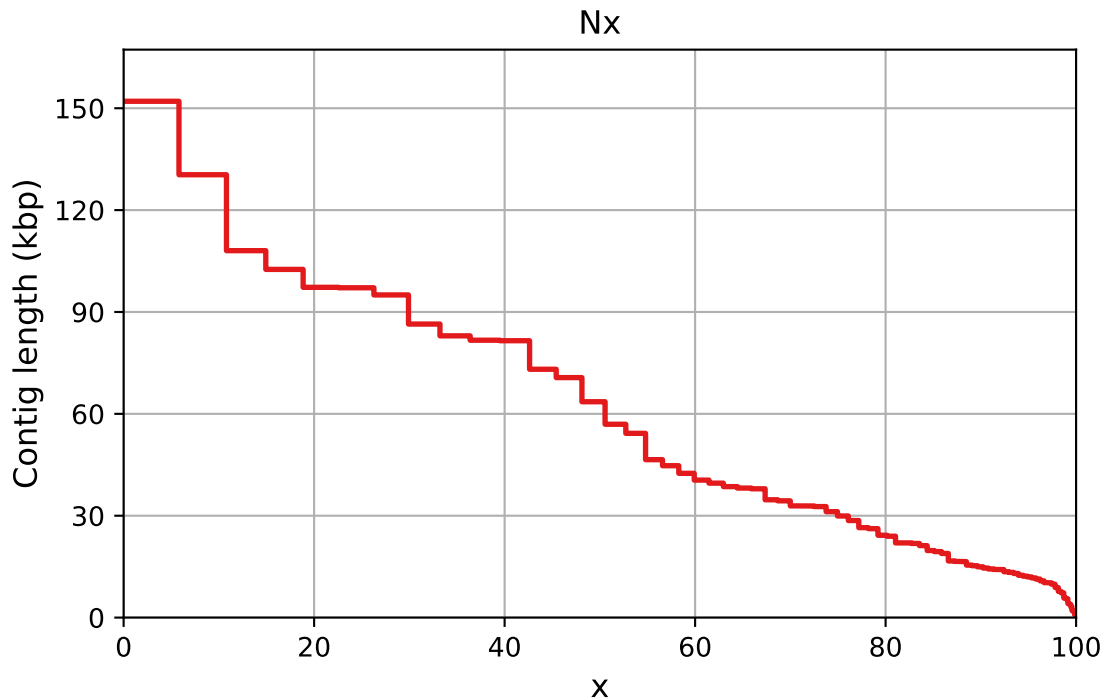
	assembly
# misassemblies	76
# contig misassemblies	76
# c. relocations	67
# c. translocations	9
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	31
Misassembled contigs length	1776908
# local misassemblies	32
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	12861
# indels	4020
# indels (<= 5 bp)	3974
# indels (> 5 bp)	46
Indels length	5666

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

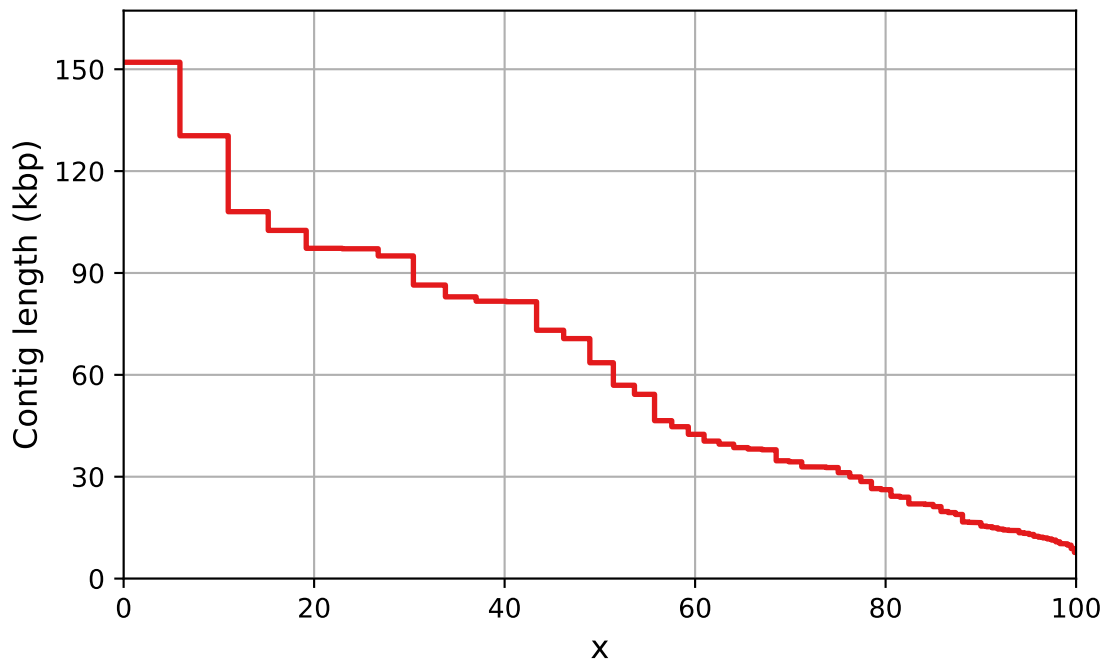
	assembly
# fully unaligned contigs	4
Fully unaligned length	16921
# partially unaligned contigs	21
Partially unaligned length	327762
# N's	0

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).



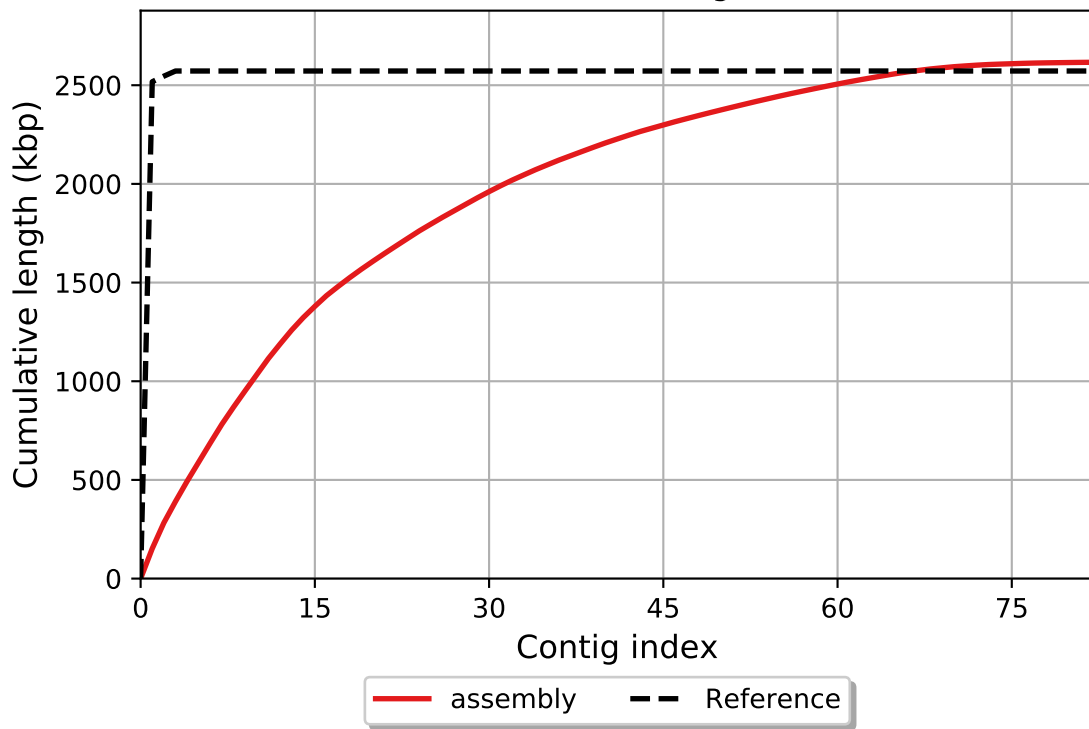
— assembly

NGx

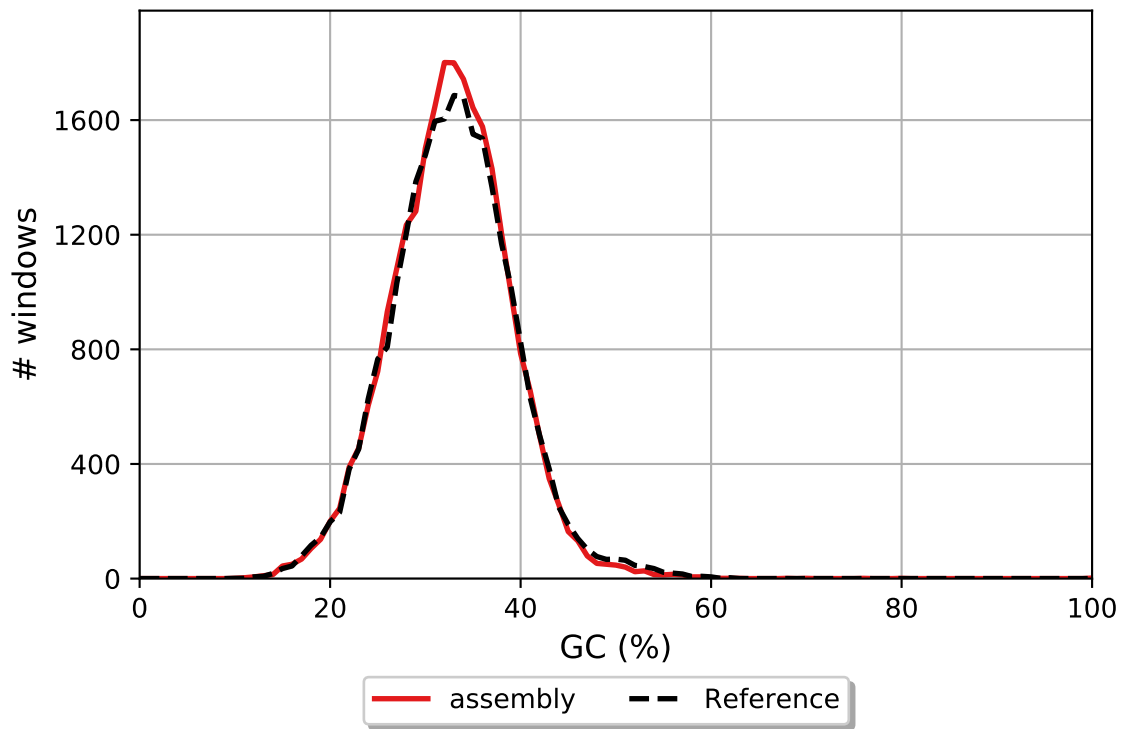


— assembly

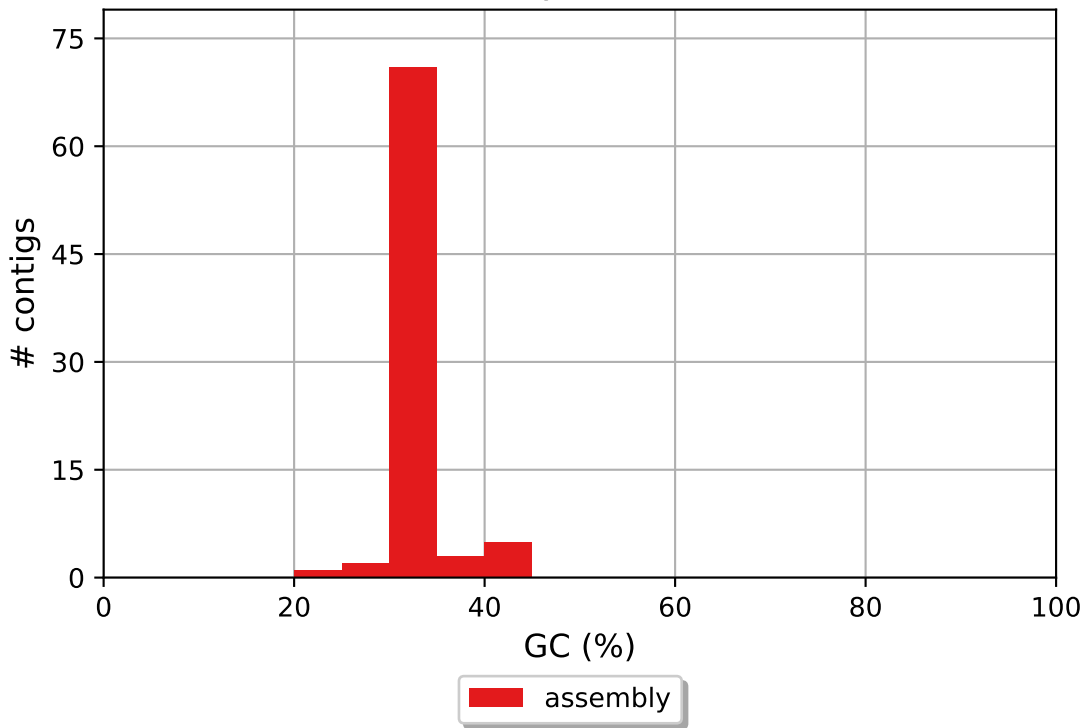
Cumulative length



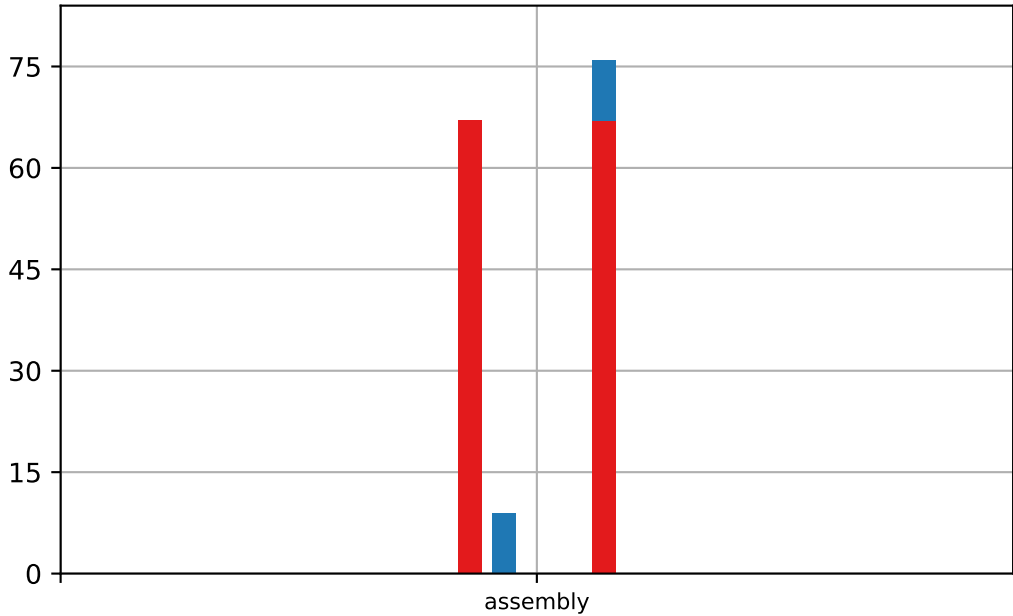
GC content



assembly GC content



Misassemblies

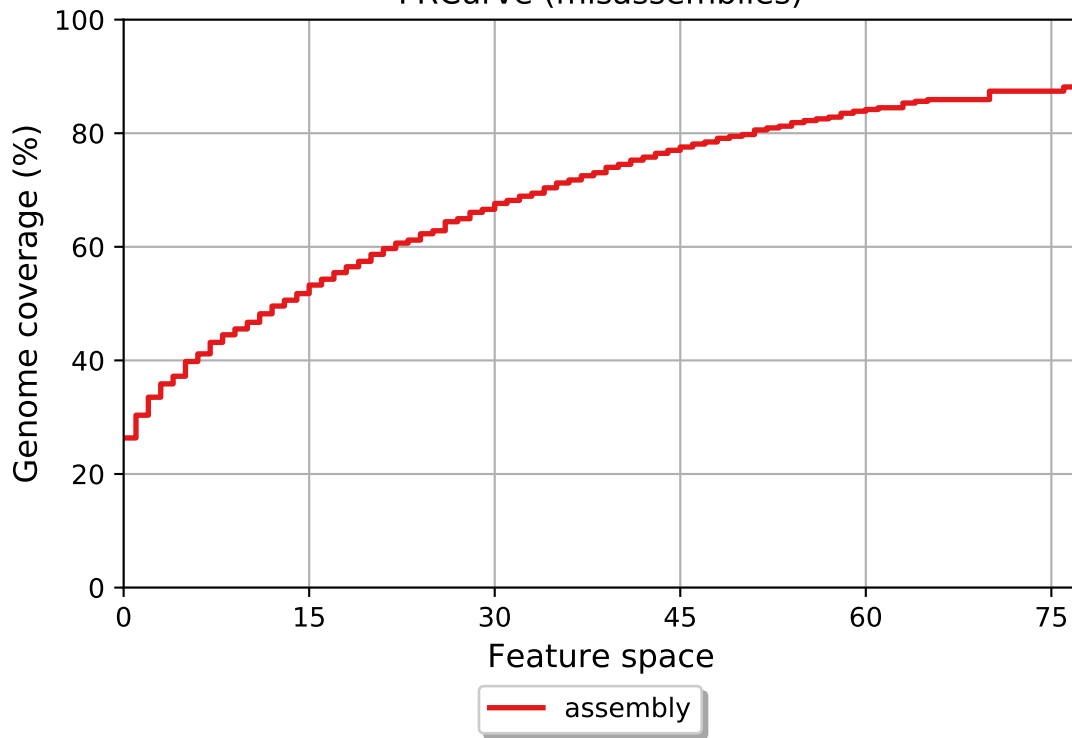


relocations

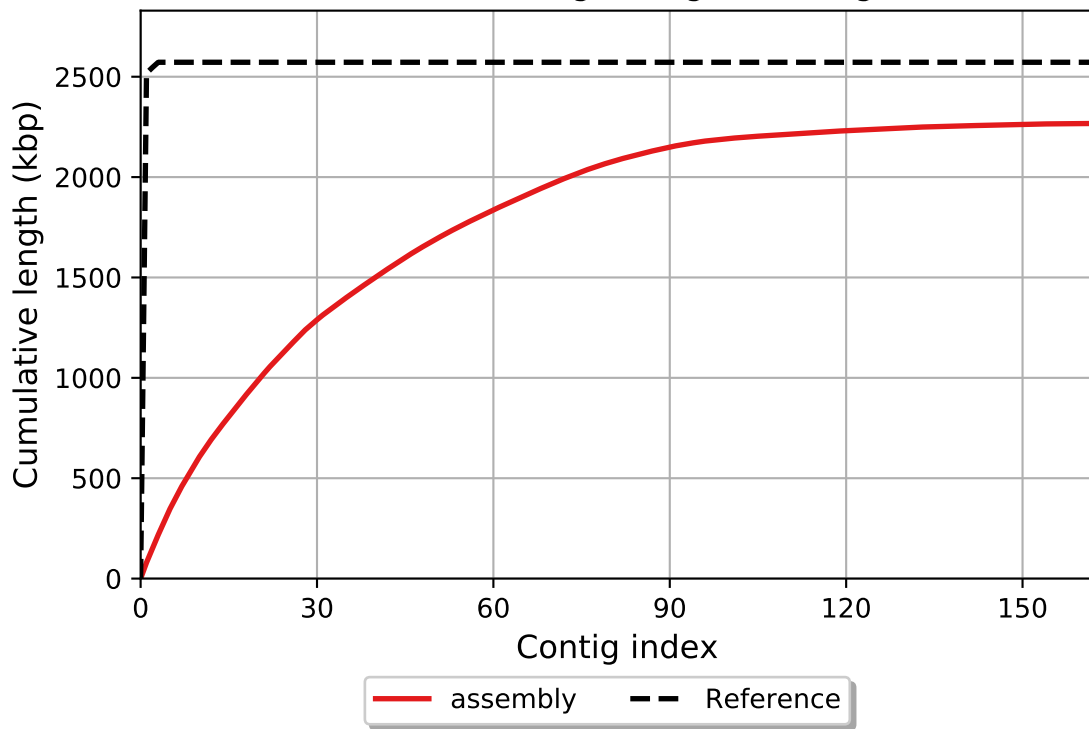


translocations

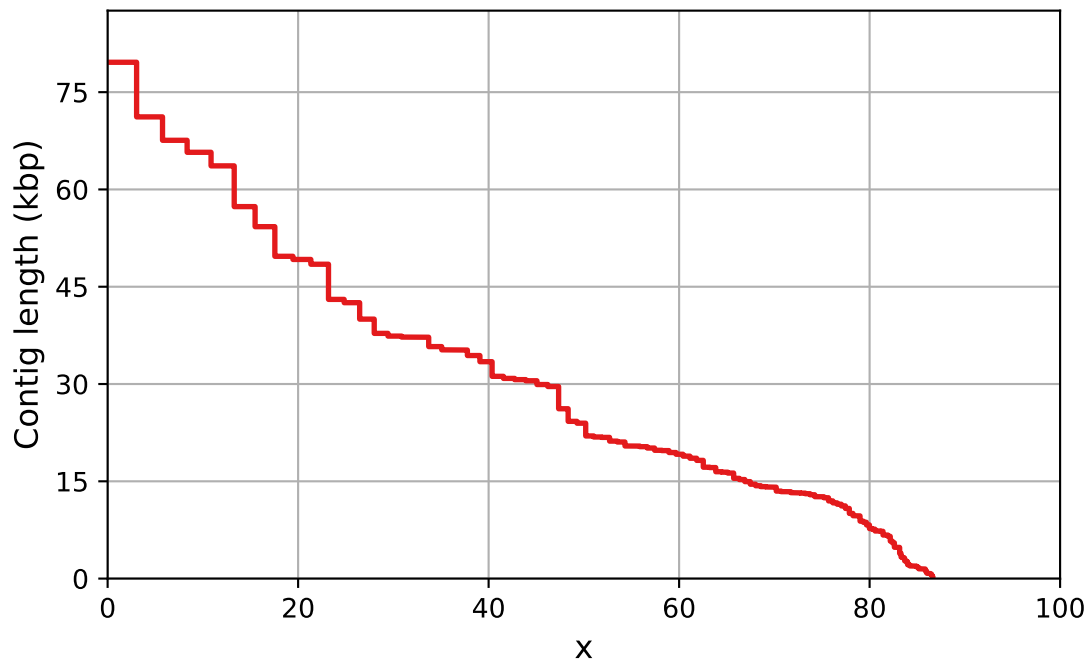
FRCurve (misassemblies)



Cumulative length (aligned contigs)

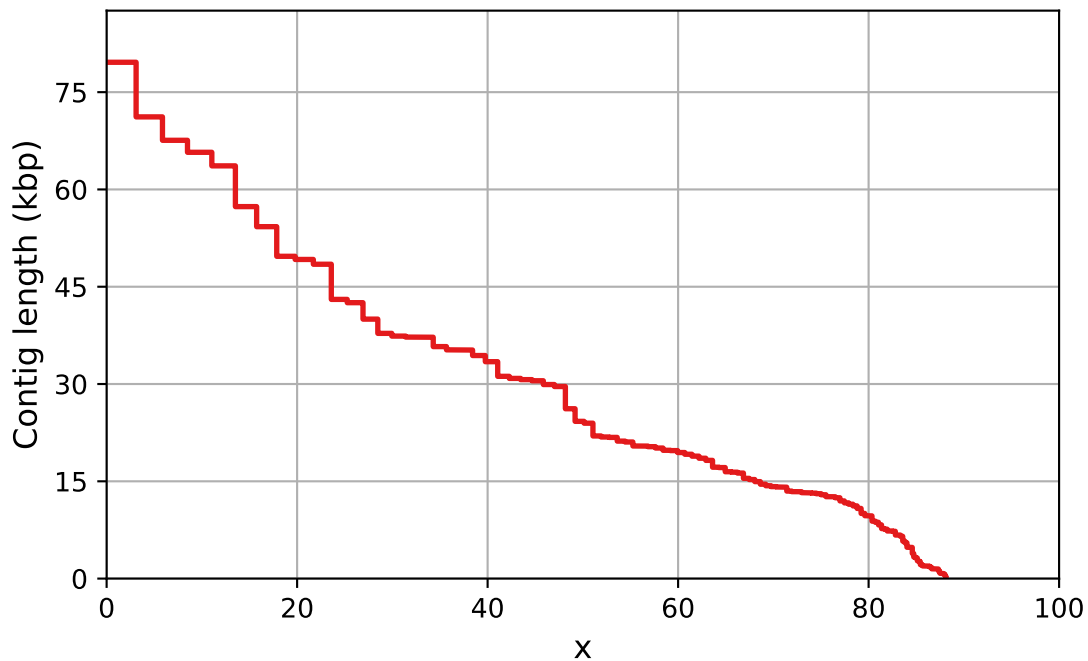


NAx



— assembly

NGAx



— assembly