

Report

	assembly_read_sequence1
# contigs (>= 0 bp)	490
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	106624
Total length (>= 1000 bp)	26329
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	490
Largest contig	3735
Total length	106624
Reference length	48576
GC (%)	50.33
Reference GC (%)	49.87
N50	299
NG50	1209
N75	153
NG75	300
L50	89
LG50	12
L75	212
LG75	33
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	45
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	9
# unaligned contigs	78 + 2 part
Unaligned length	8634
Genome fraction (%)	76.573
Duplication ratio	2.634
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4801.59
# indels per 100 kbp	115.60
Largest alignment	1747
Total aligned length	86100
NA50	181
NGA50	300
NA75	99
NGA75	269
LA50	172
LGA50	55
LA75	385
LGA75	96

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

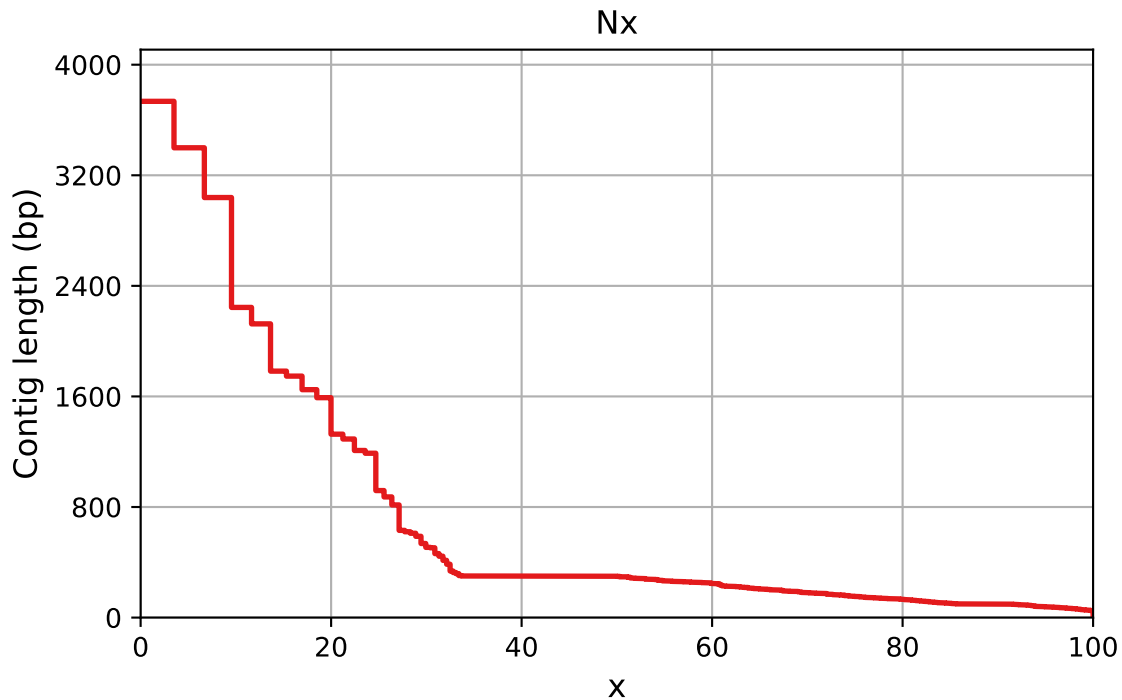
	assembly_read_sequence1
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	45
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	9
# mismatches	1786
# indels	43
# indels (<= 5 bp)	20
# indels (> 5 bp)	23
Indels length	913

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

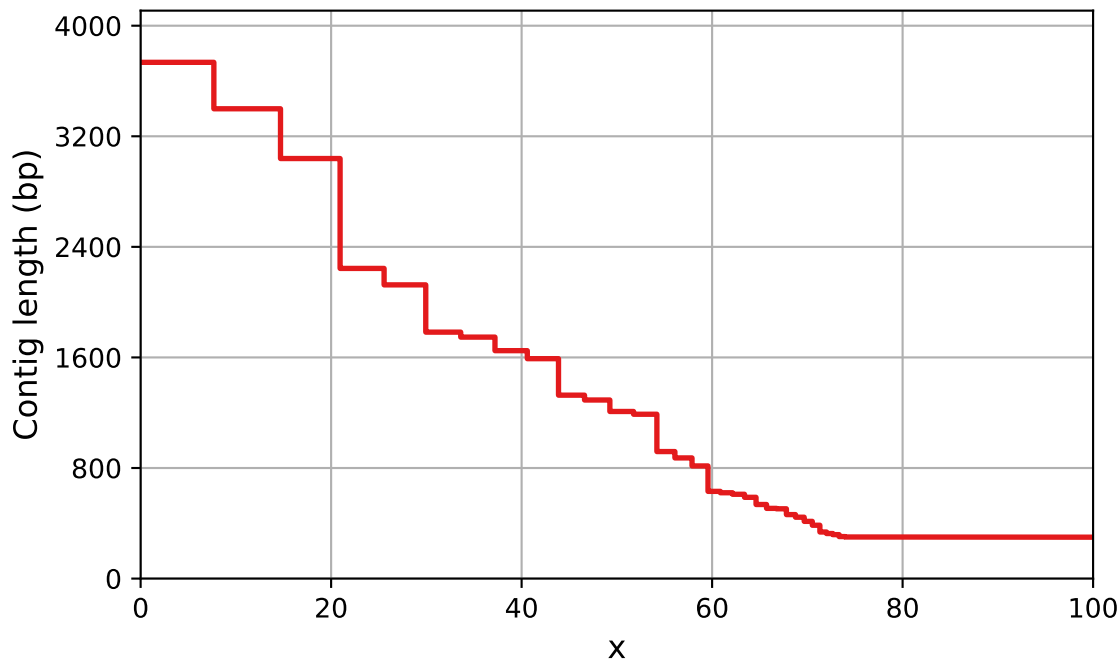
	assembly_read_sequence1
# fully unaligned contigs	78
Fully unaligned length	5251
# partially unaligned contigs	2
Partially unaligned length	3383
# N's	0

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).



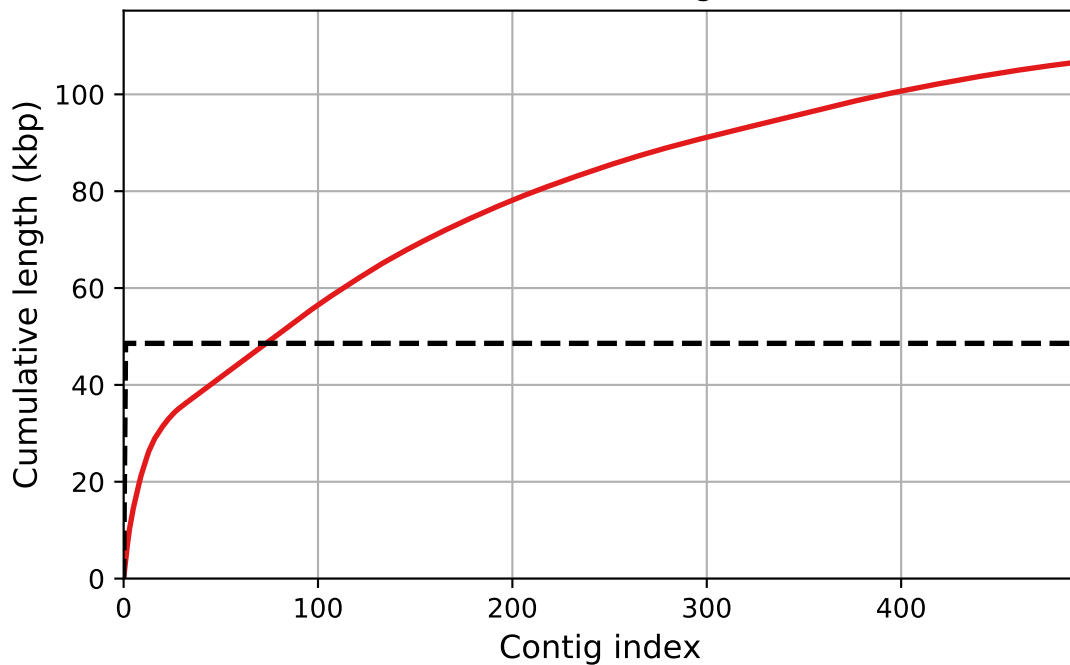
— assembly_read_sequence1

NGx



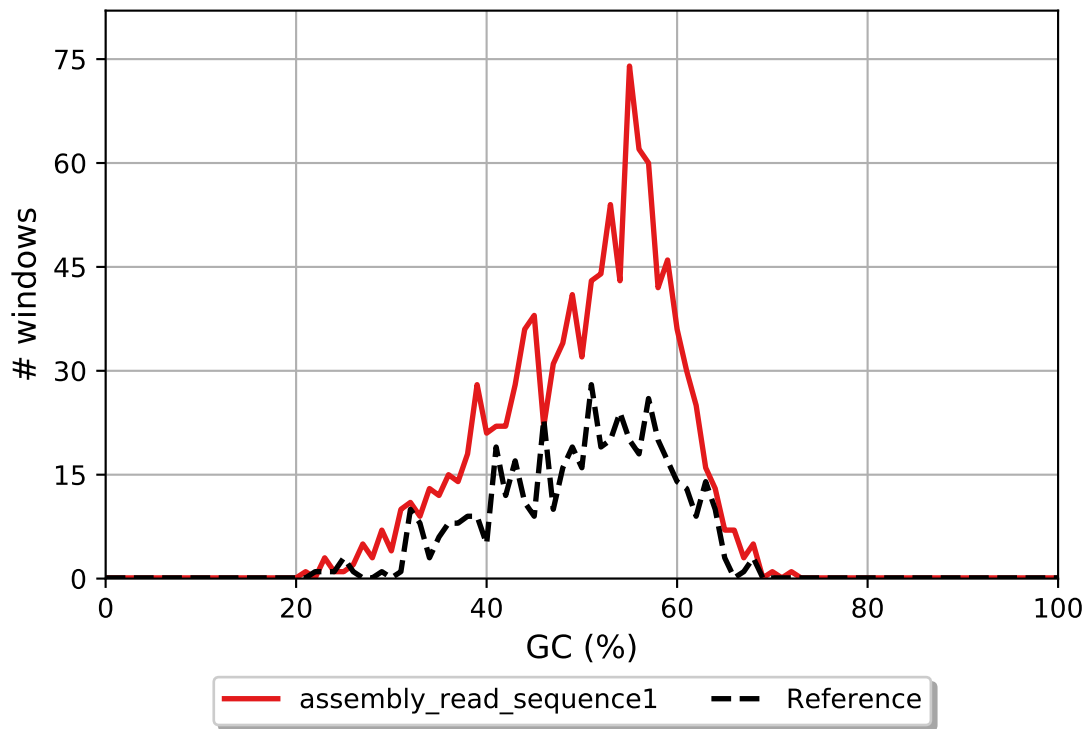
— assembly_read_sequence1

Cumulative length

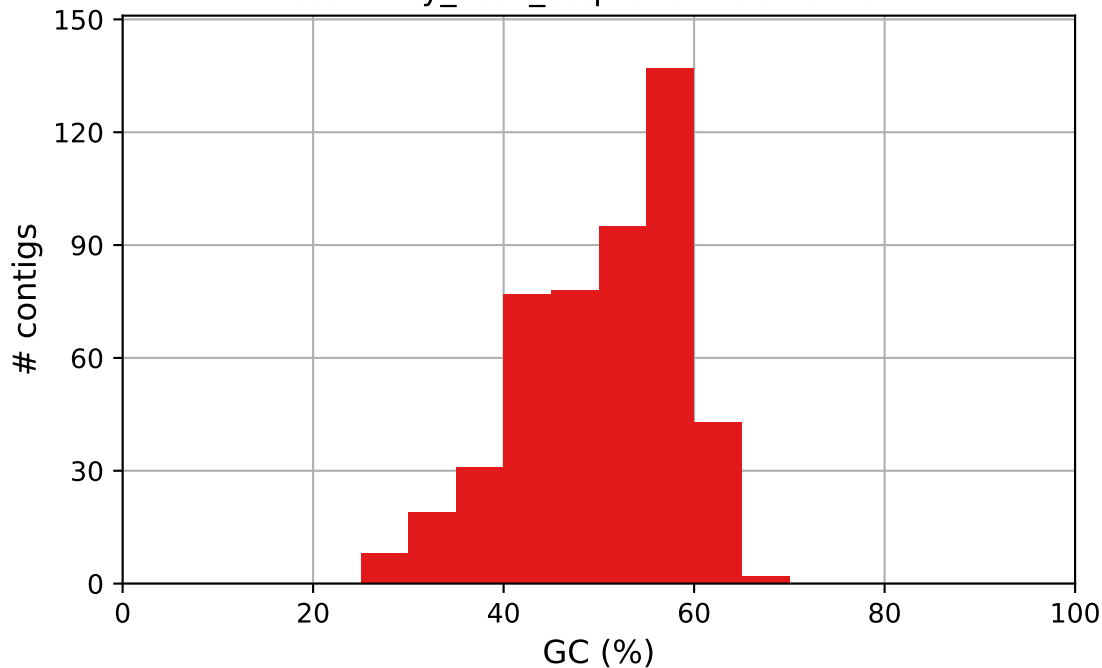


— assembly_read_sequence1 - - Reference

GC content

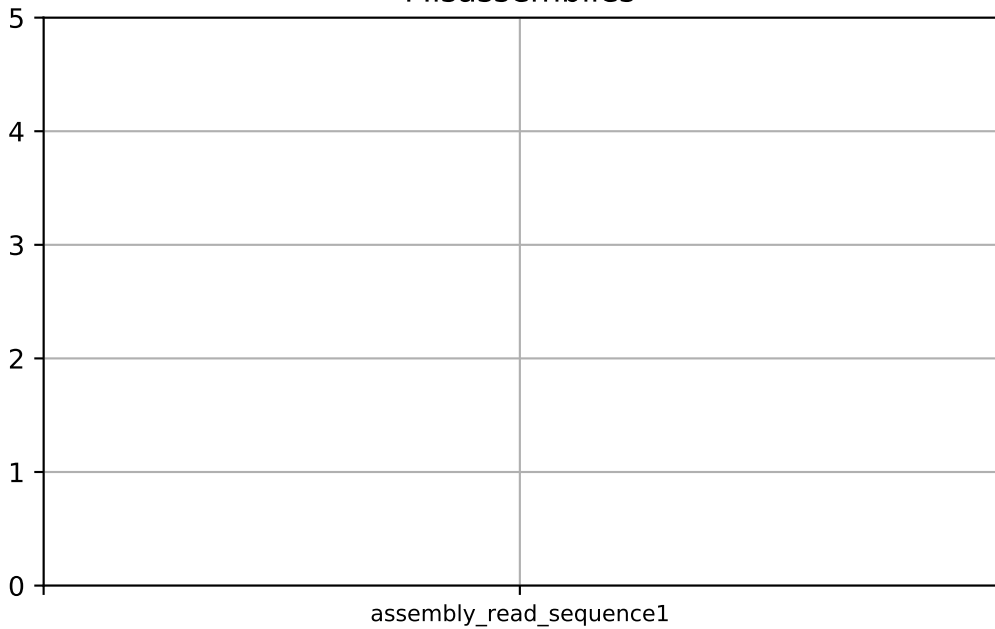


assembly_read_sequence1 GC content

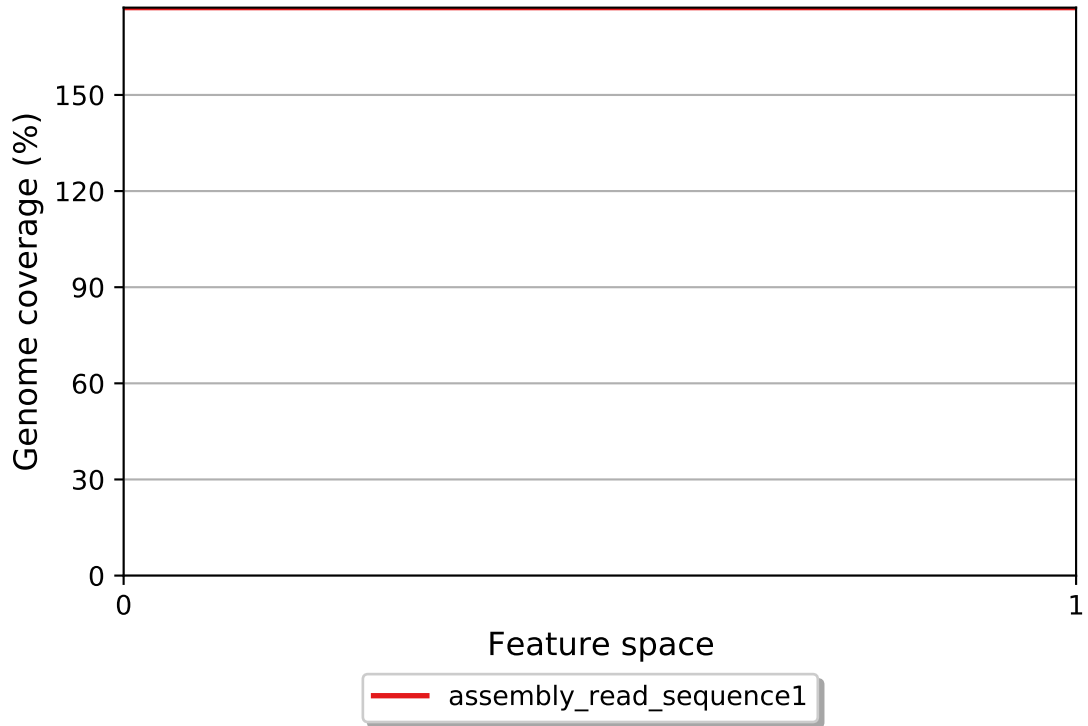


assembly_read_sequence1

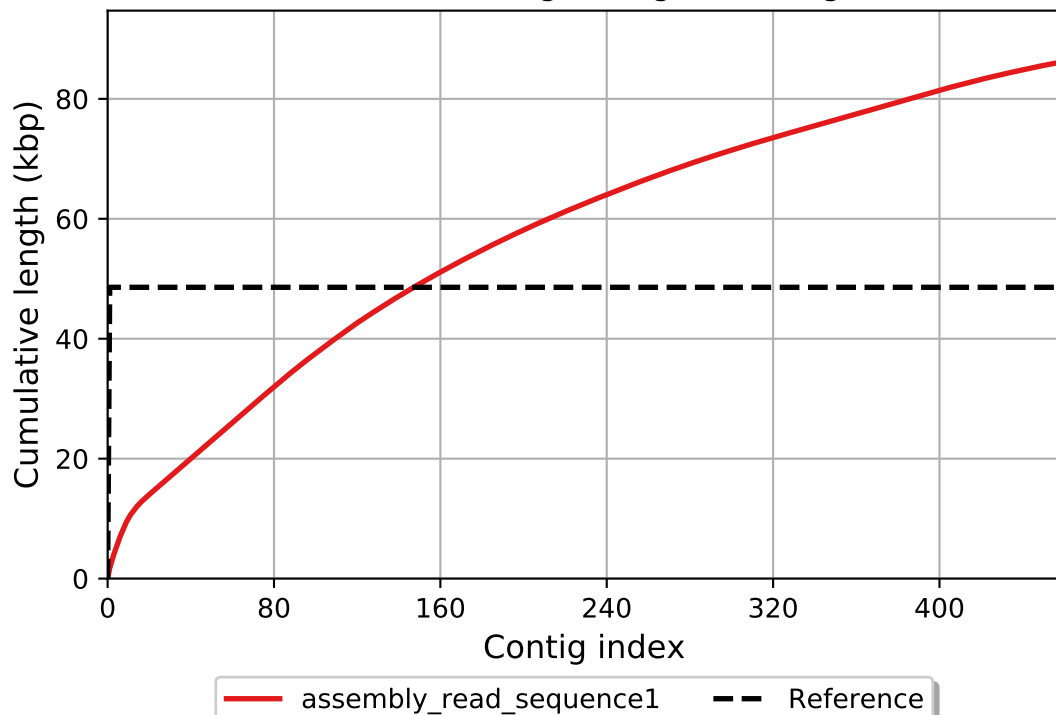
Misassemblies



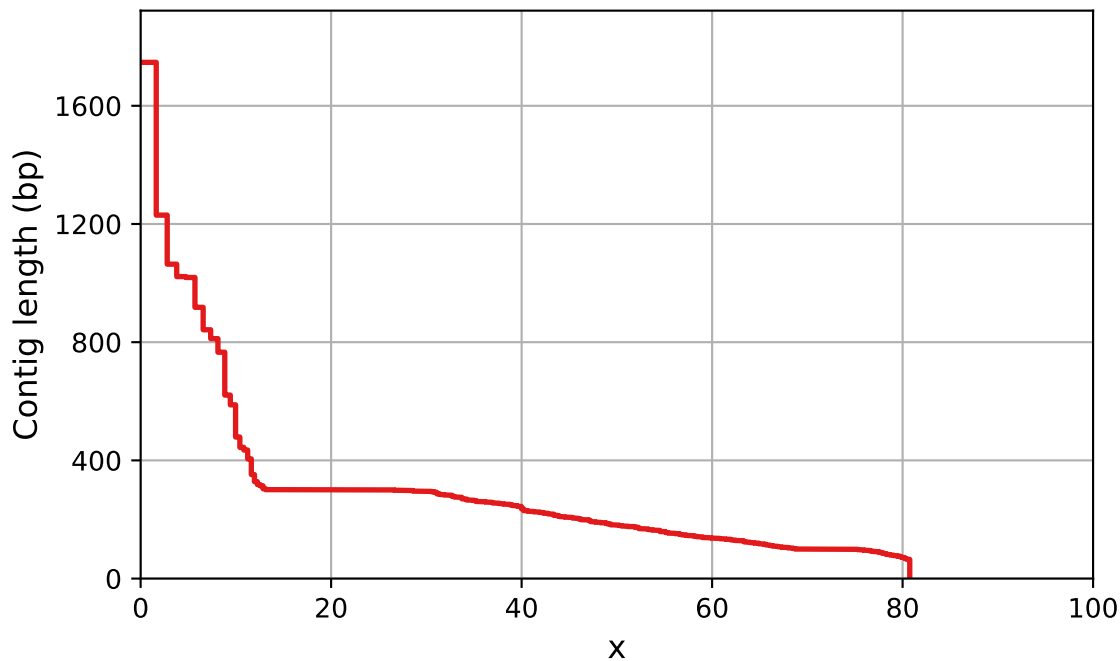
FRCurve (misassemblies)



Cumulative length (aligned contigs)

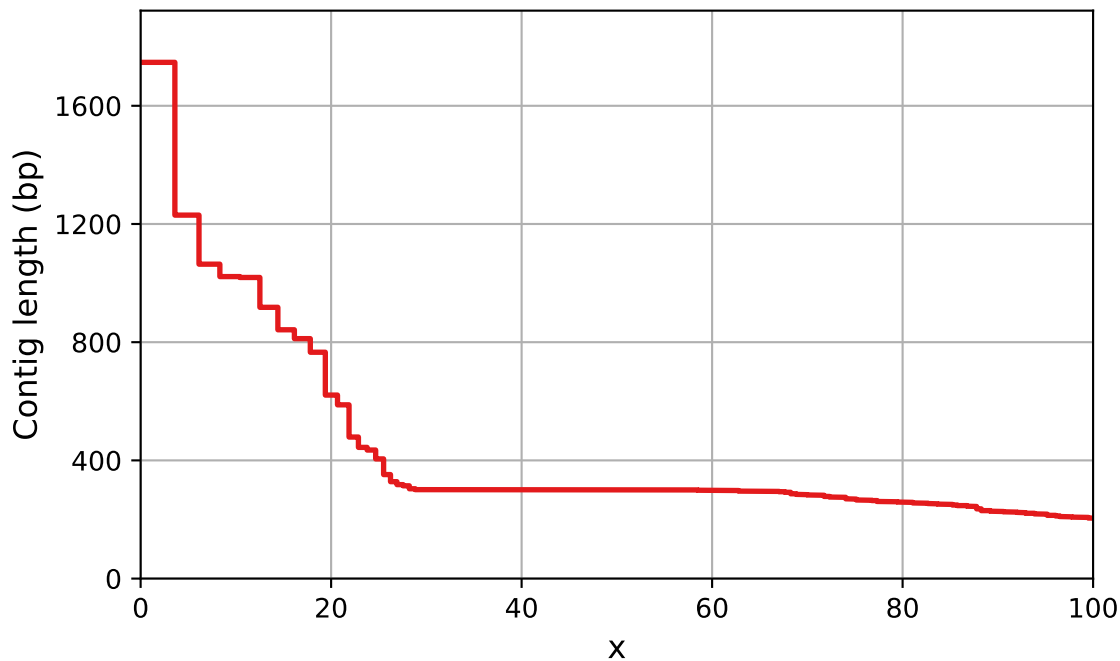


NAx



— assembly_read_sequence1

NGAx



— assembly_read_sequence1