

Report

	OLC_Result	minia.contigs
# contigs (>= 0 bp)	101	4
# contigs (>= 1000 bp)	5	1
# contigs (>= 5000 bp)	0	1
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	45443	10187
Total length (>= 1000 bp)	7284	9936
Total length (>= 5000 bp)	0	9936
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	30	1
Largest contig	2233	9936
Total length	24835	9936
Reference length	10624	10624
GC (%)	44.47	44.05
Reference GC (%)	44.14	44.14
N50	818	9936
NG50	1101	9936
N90	578	9936
NG90	934	9936
auN	985.2	9936.0
auNG	2303.1	9292.6
L50	11	1
LG50	4	1
L90	26	1
LG90	8	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.296	93.524
Duplication ratio	2.374	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	302.48	0.00
# indels per 100 kbp	4.03	0.00
Largest alignment	2233	9936
Total aligned length	24795	9936
NA50	818	9936
NGA50	1098	9936
NA90	578	9936
NGA90	925	9936
auNA	982.7	9936.0
auNGA	2297.3	9292.6
LA50	11	1
LGA50	4	1
LA90	26	1
LGA90	8	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

	OLC_Result	minia.contigs
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	75	0
# indels	1	0
# indels (<= 5 bp)	1	0
# indels (> 5 bp)	0	0
Indels length	1	0

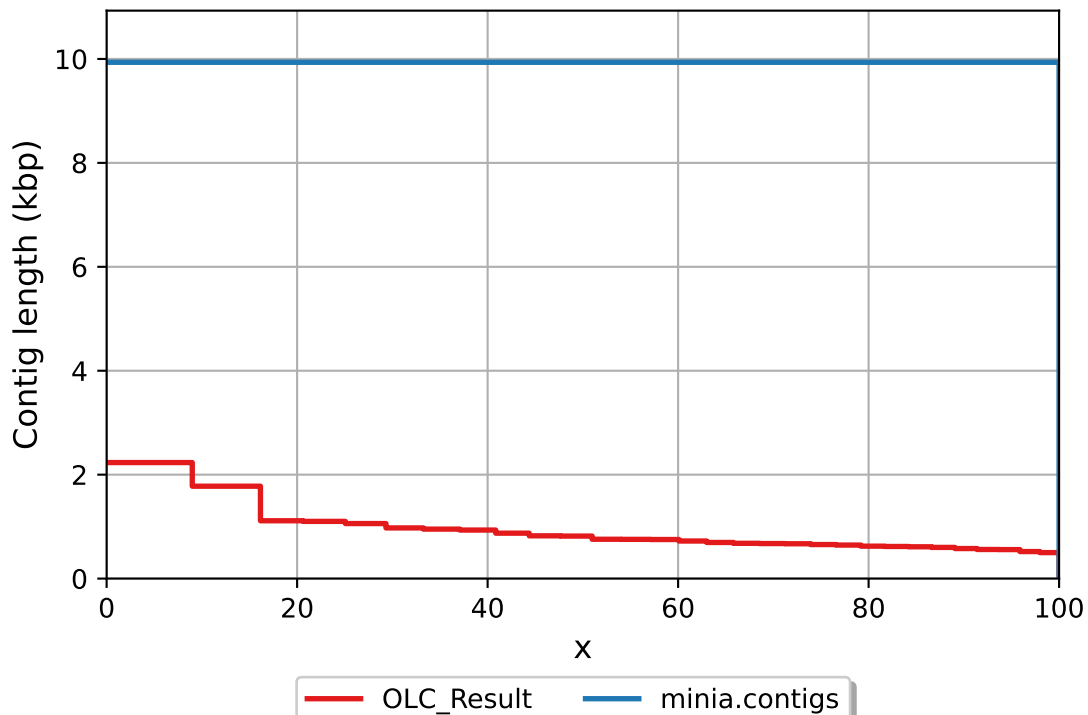
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

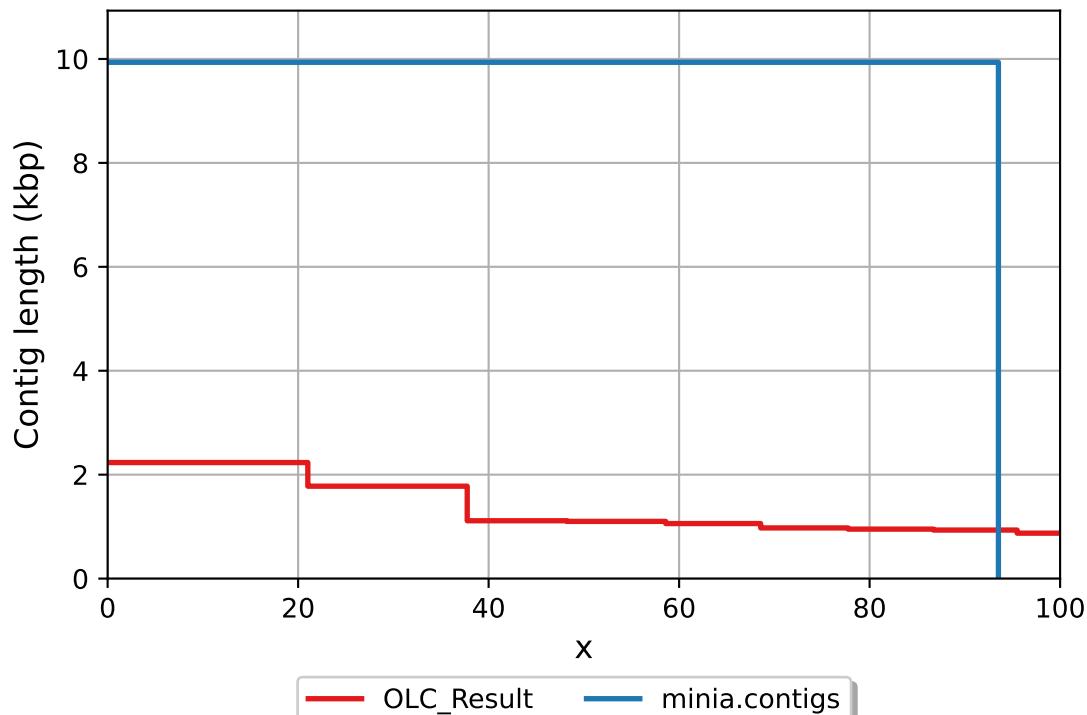
	OLC_Result	minia.contigs
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

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).

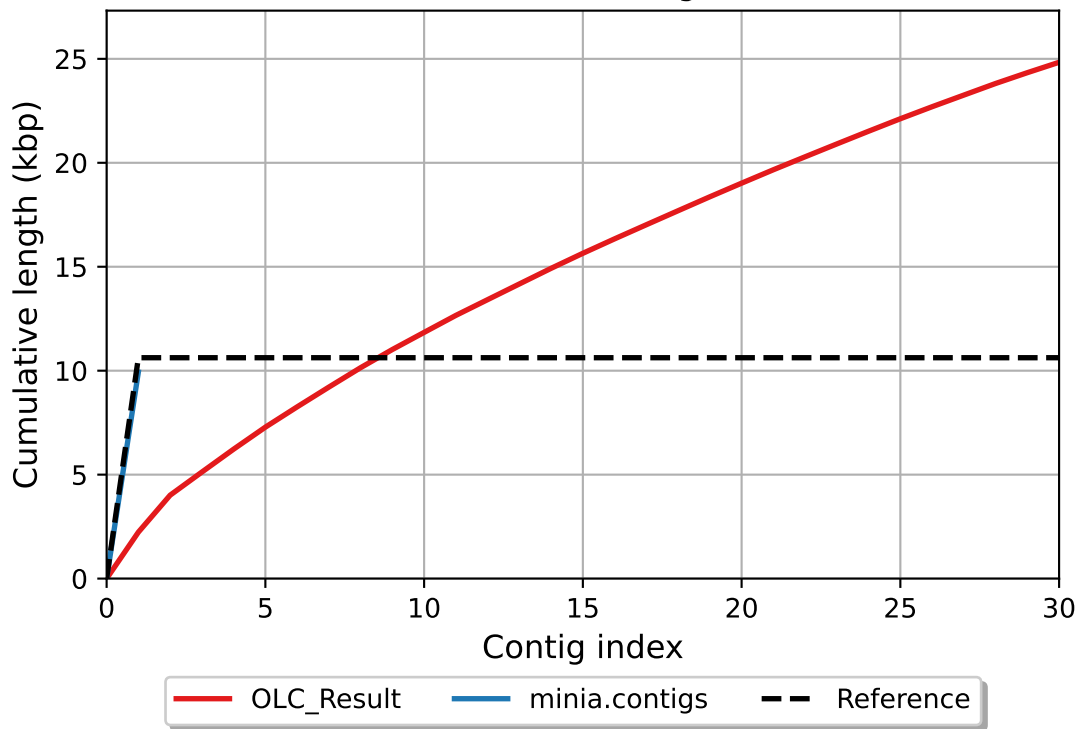
Nx



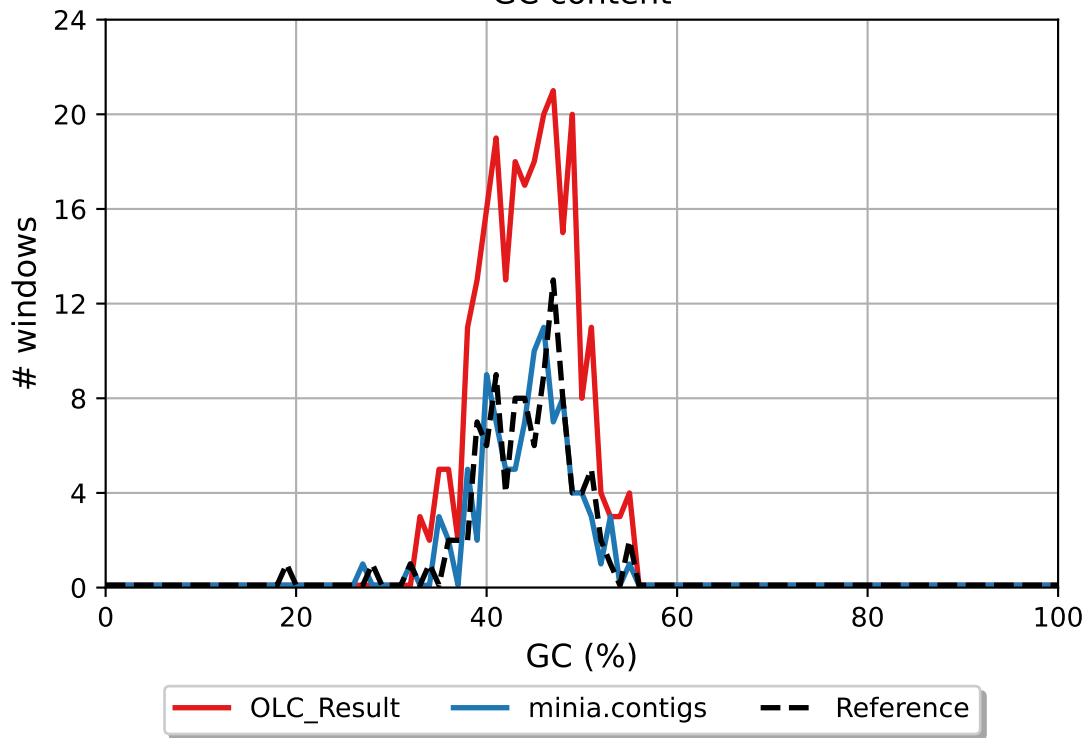
NGx



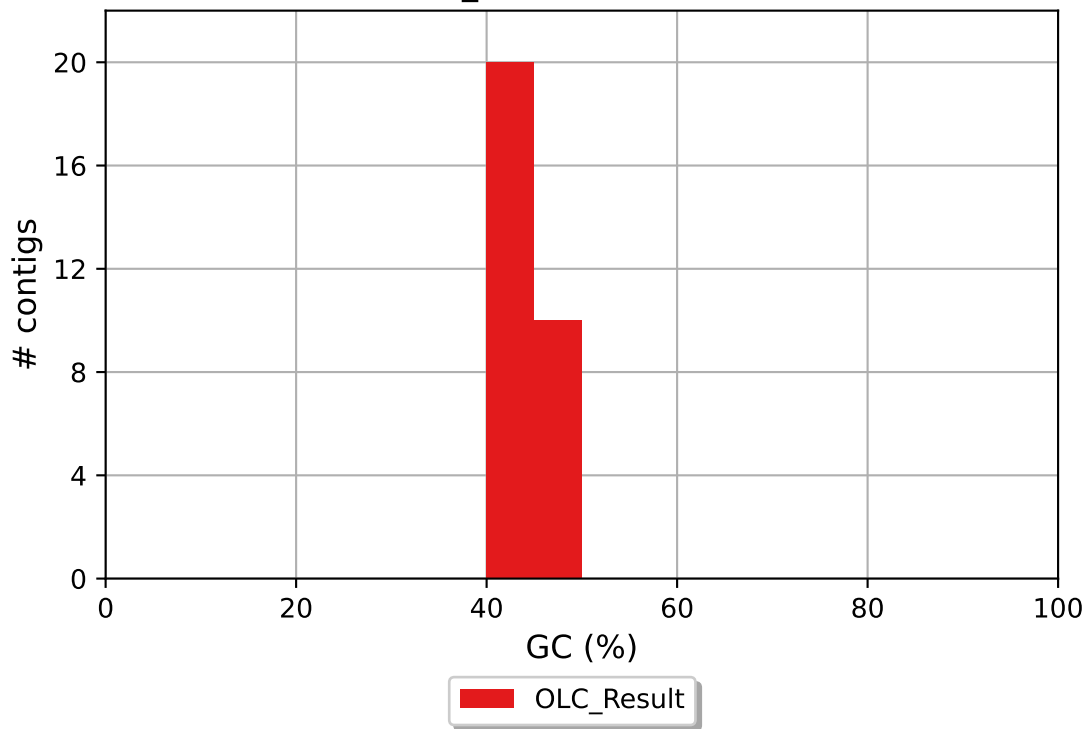
Cumulative length



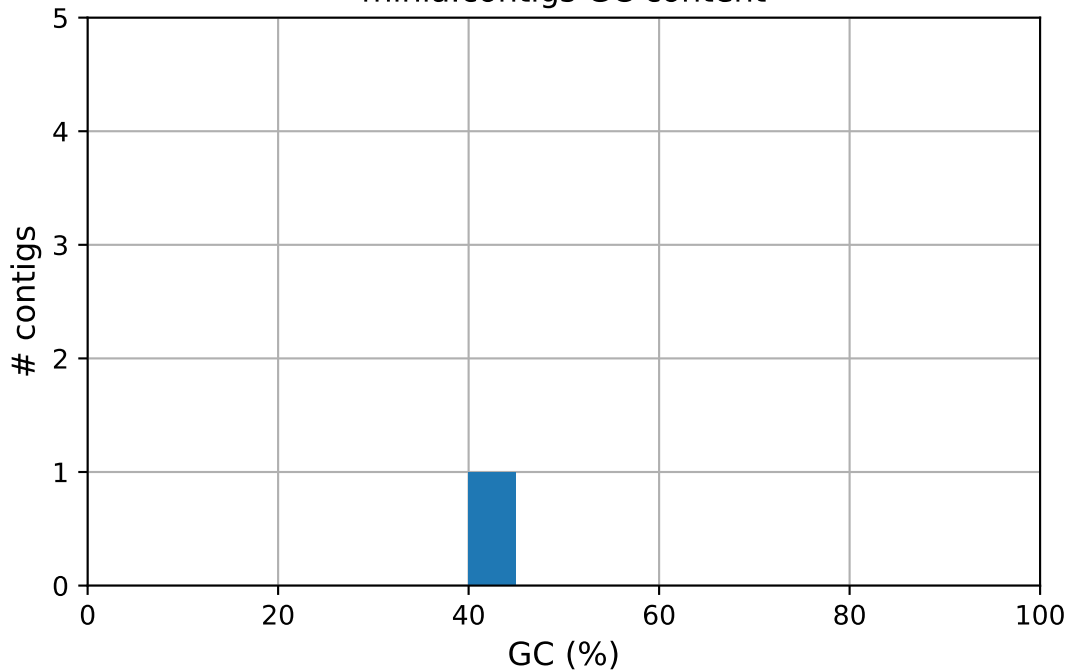
GC content



OLC_Result GC content



minia.contigs GC content

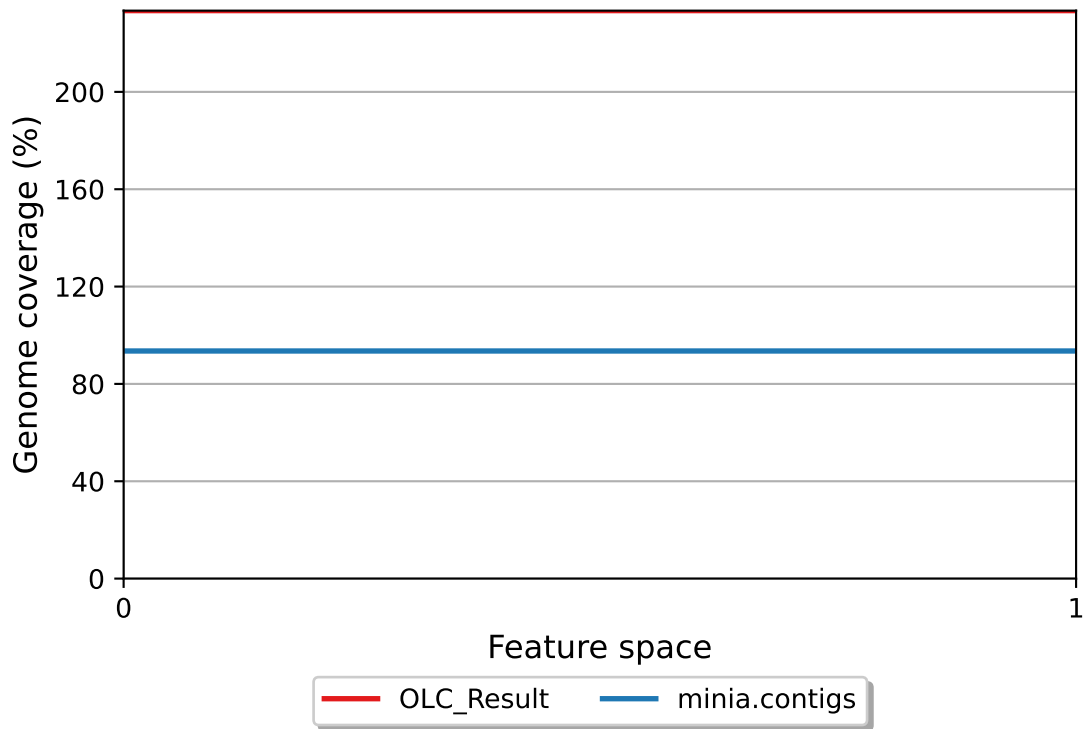


minia.contigs

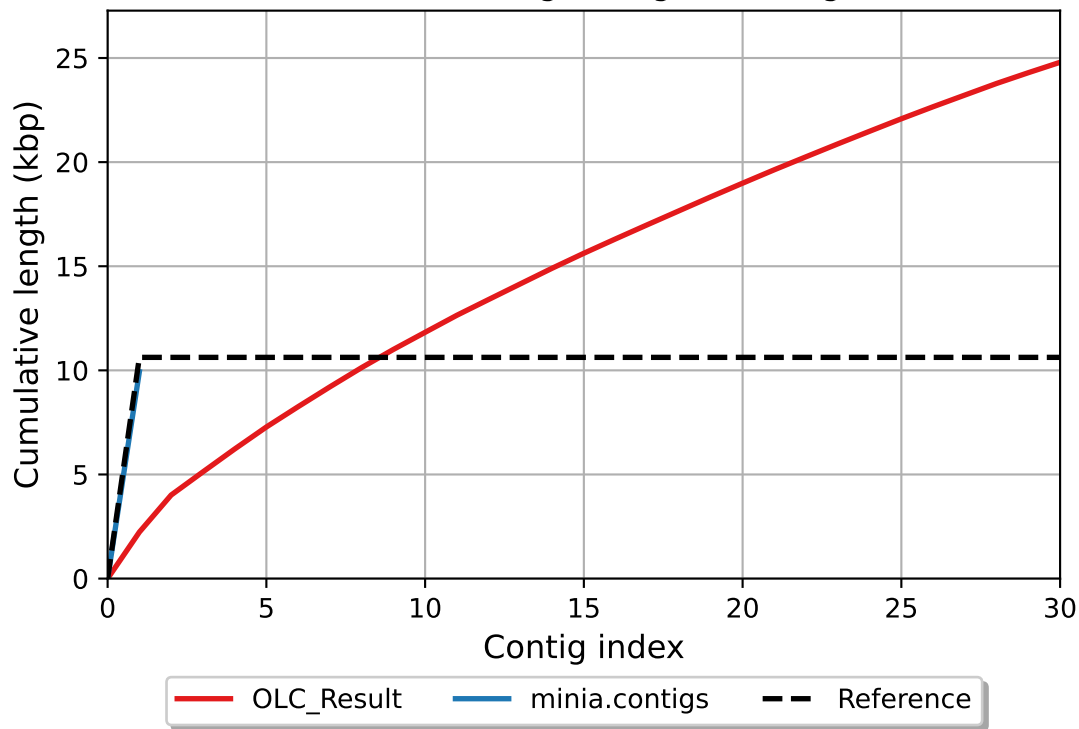
Misassemblies



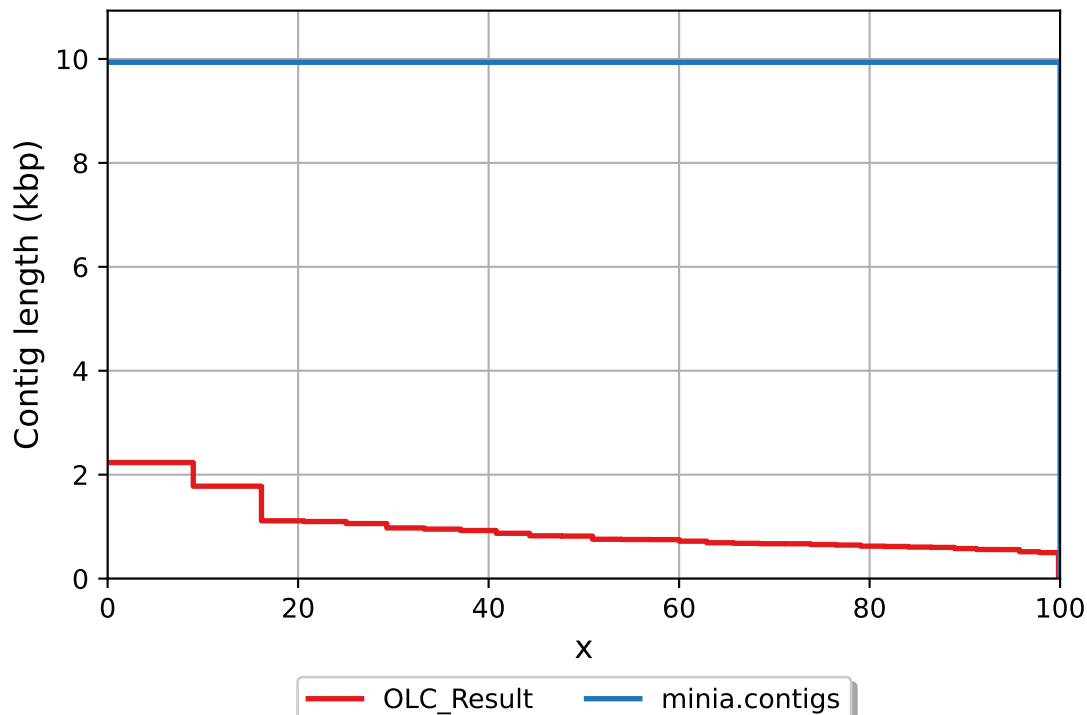
FRCurve (misassemblies)



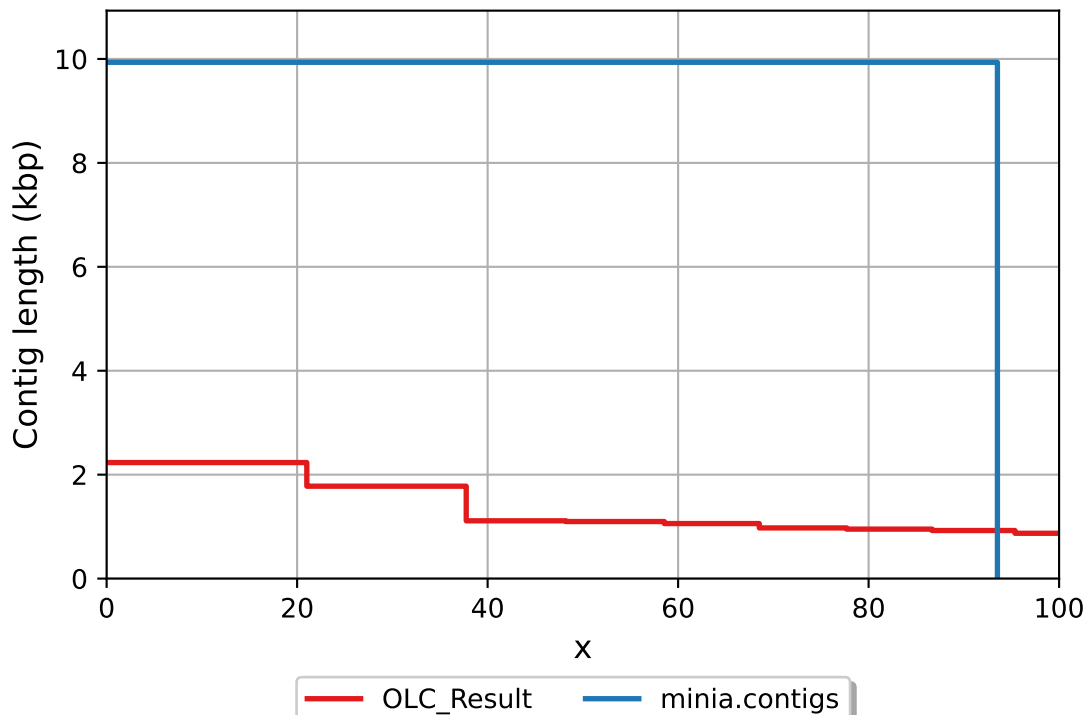
Cumulative length (aligned contigs)



NAx



NGAx



Genome fraction, %

