

Report

	OLC_Result	minia.contigs
# contigs (>= 0 bp)	9	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)	10822	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	9	1
Largest contig	2233	9936
Total length	10822	9936
Reference length	10624	10624
GC (%)	44.55	44.05
Reference GC (%)	44.14	44.14
N50	1101	9936
NG50	1101	9936
N90	874	9936
NG90	874	9936
auN	1374.7	9936.0
auNG	1400.3	9292.6
L50	4	1
LG50	4	1
L90	8	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 (%)	80.055	93.524
Duplication ratio	1.270	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	166.64	0.00
# indels per 100 kbp	0.00	0.00
Largest alignment	2233	9936
Total aligned length	10802	9936
NA50	1098	9936
NGA50	1098	9936
NA90	872	9936
NGA90	872	9936
auNA	1371.3	9936.0
auNGA	1396.9	9292.6
LA50	4	1
LGA50	4	1
LA90	8	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	18	0
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

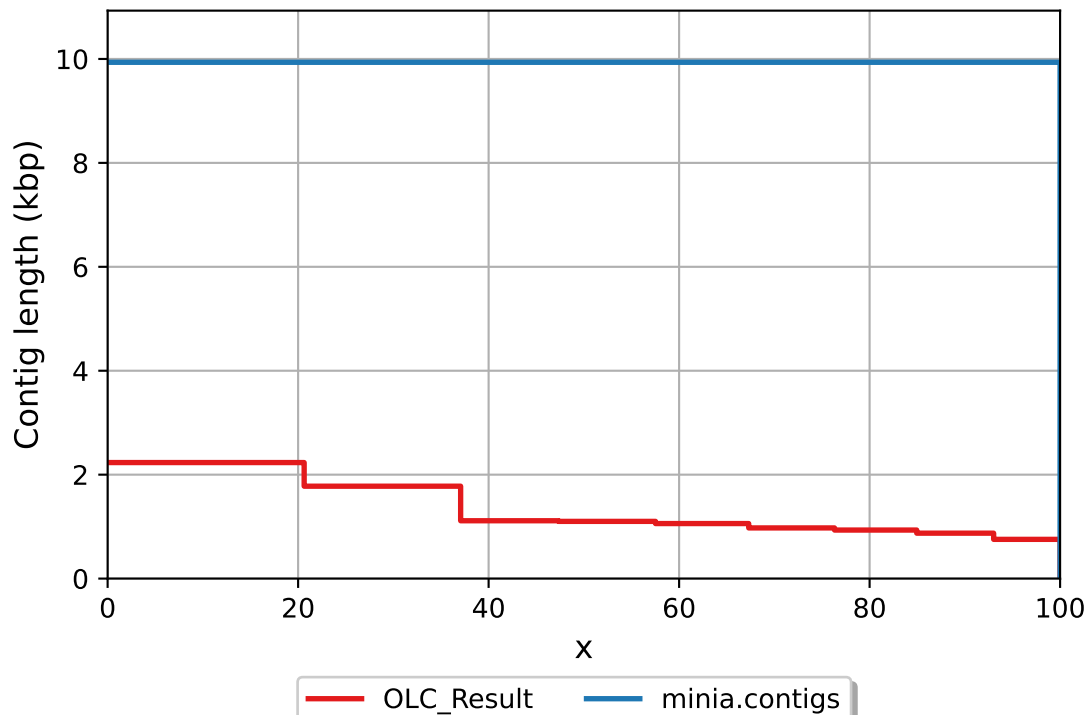
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

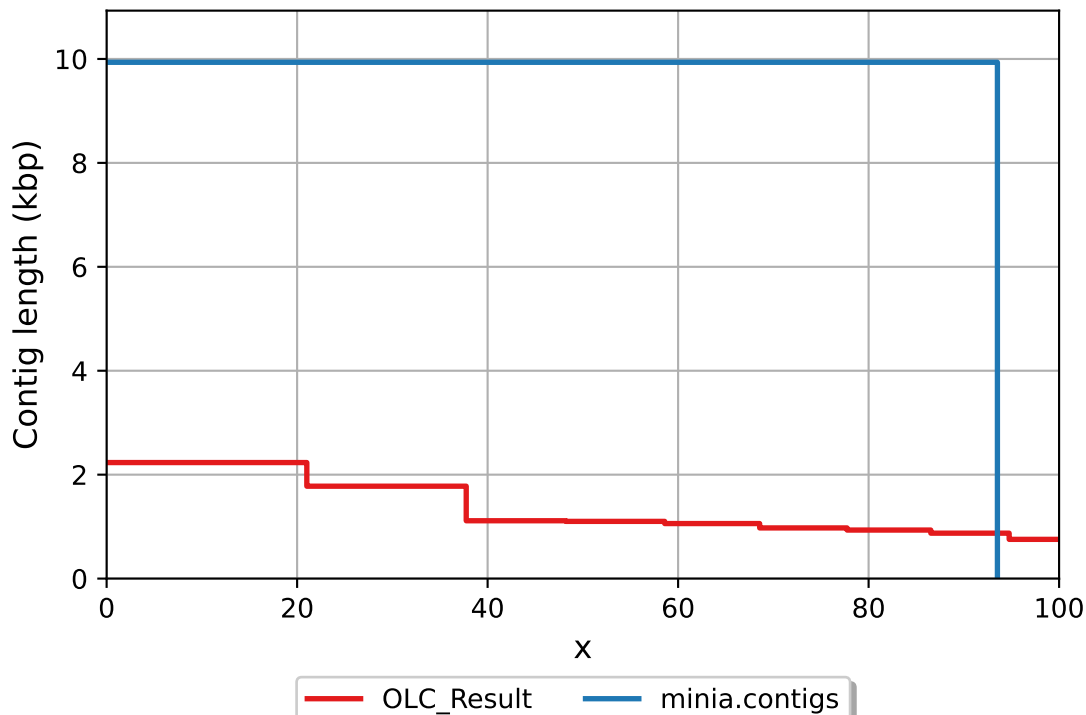
	OLC_Result	minia.contigs
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

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).

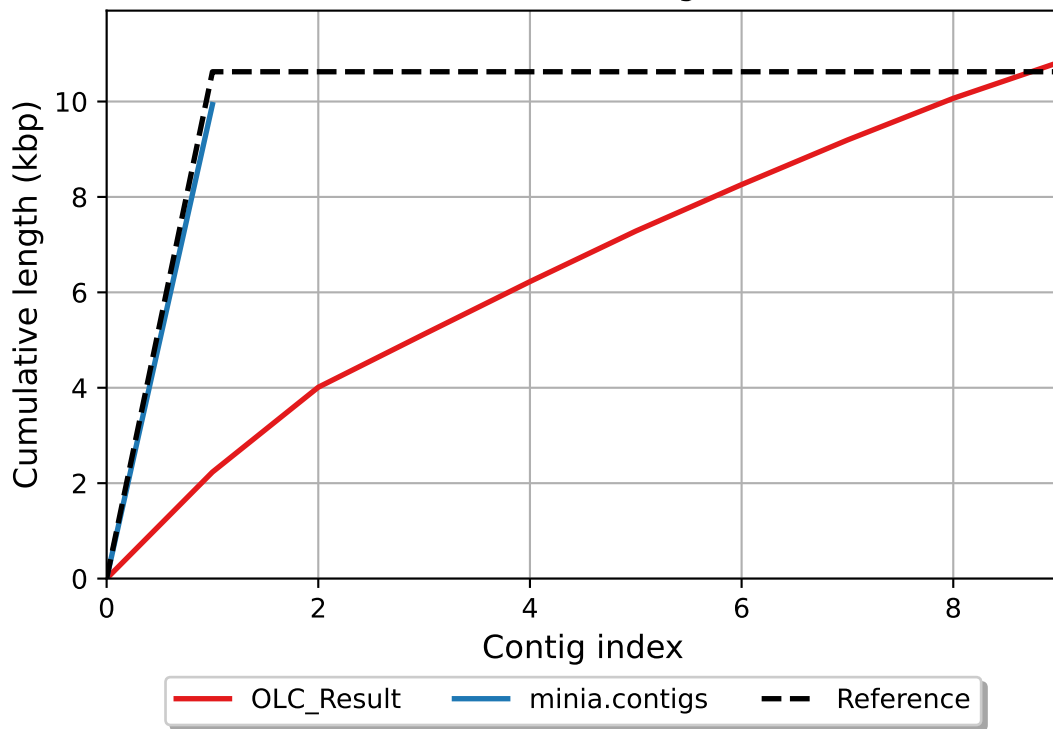
Nx



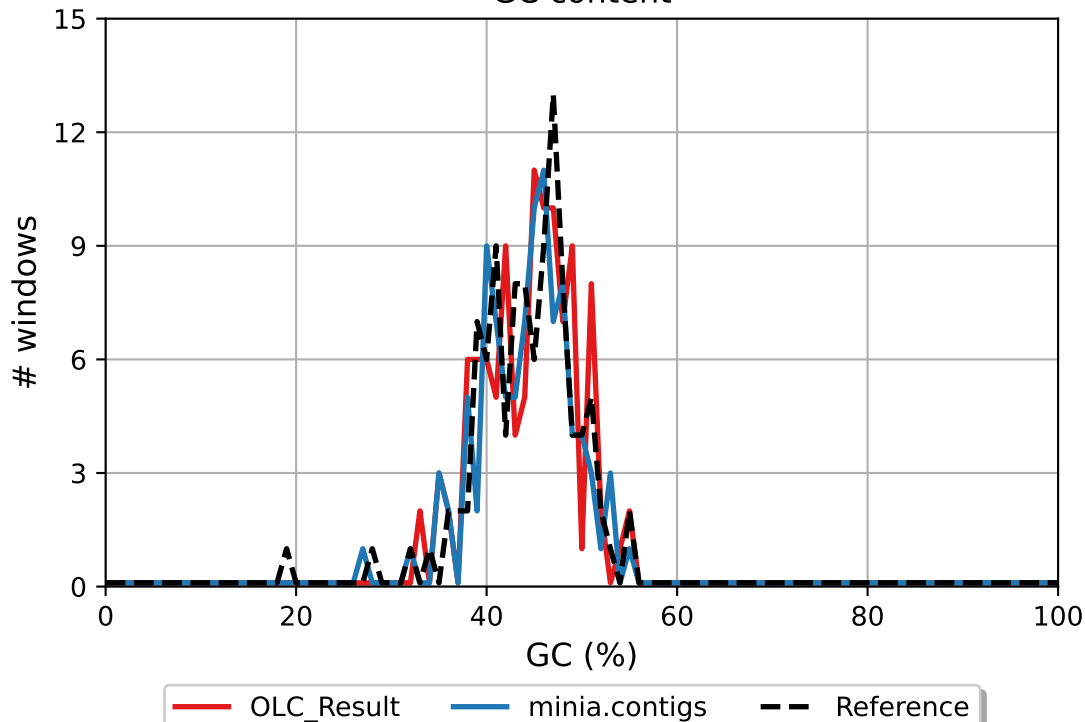
NGx



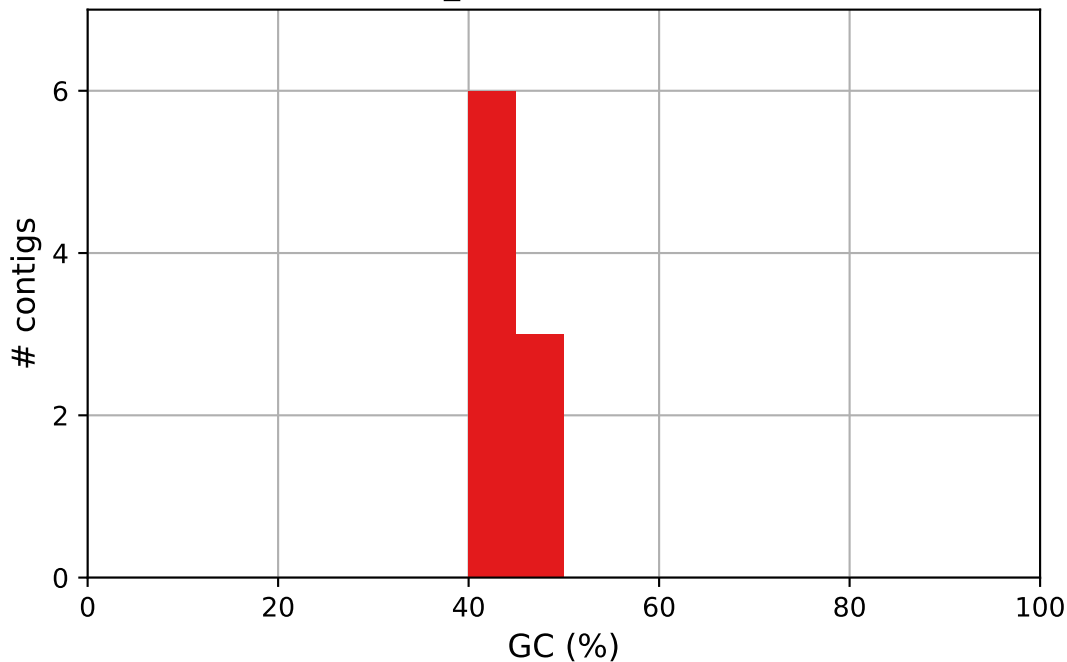
Cumulative length



GC content

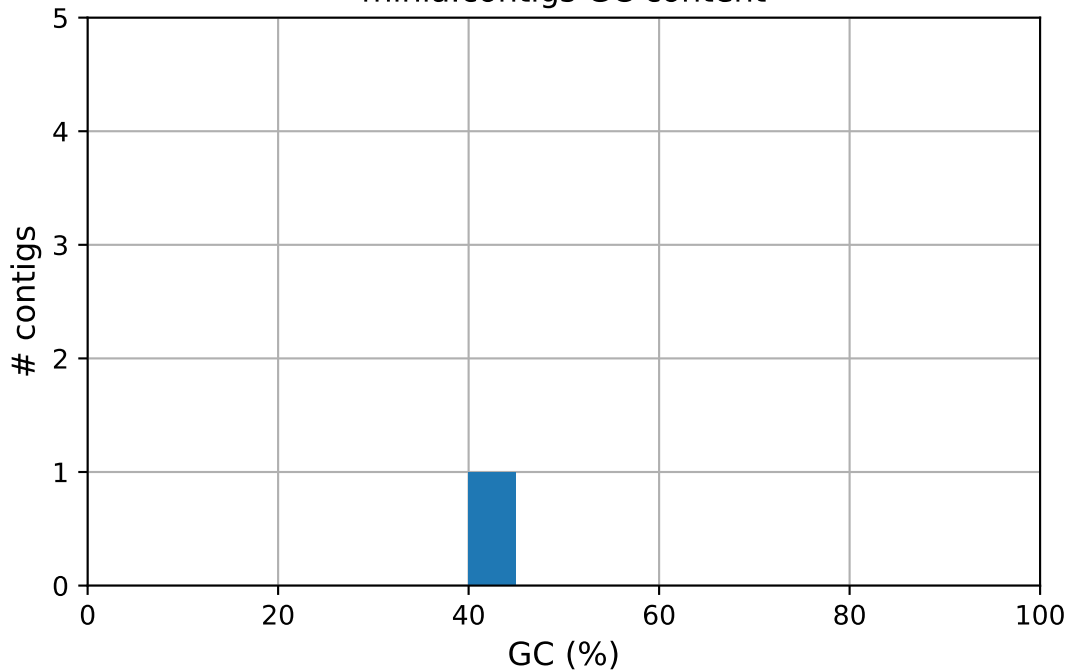


OLC_Result GC content



OLC_Result

minia.contigs GC content

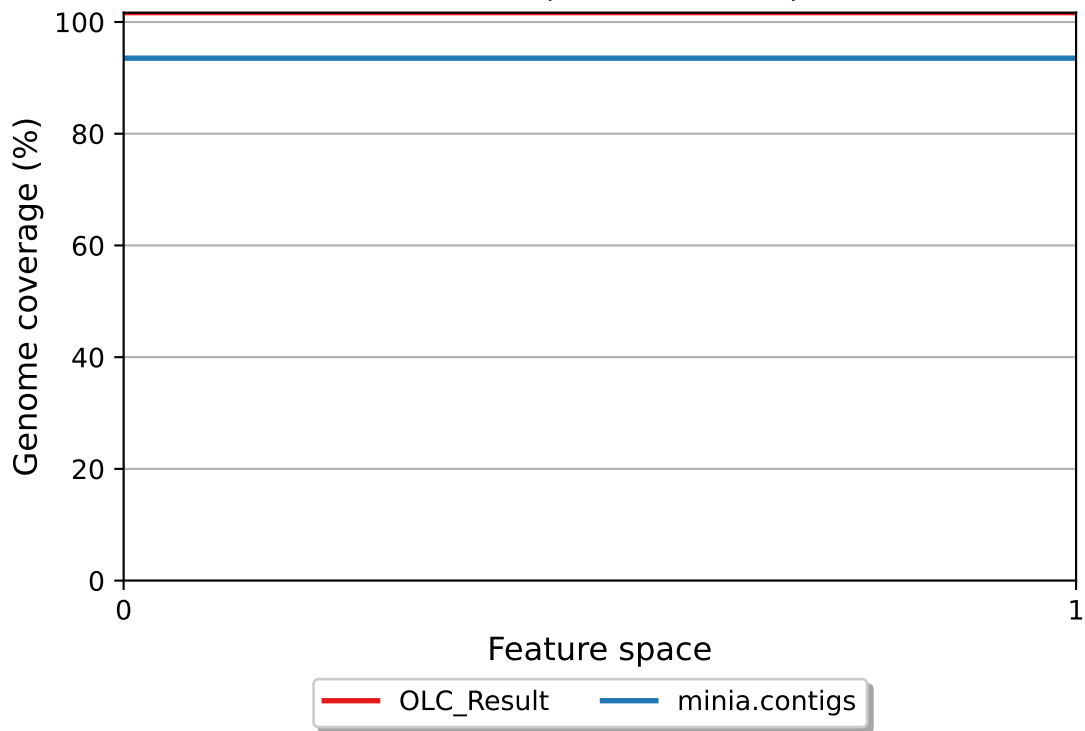


minia.contigs

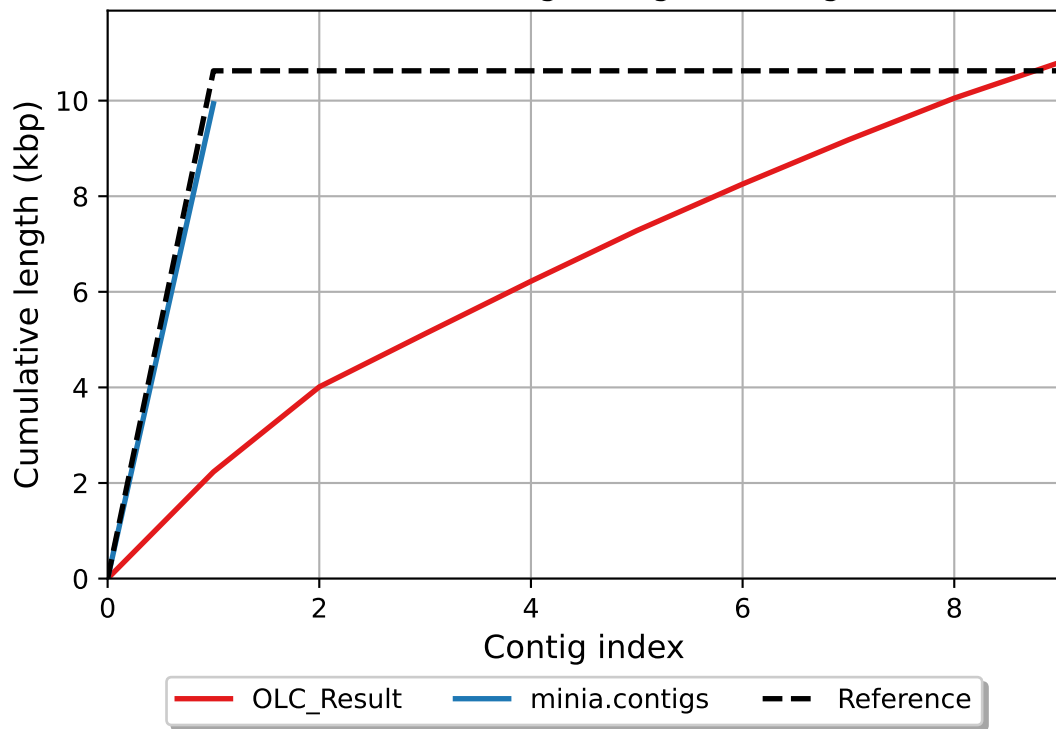
Misassemblies



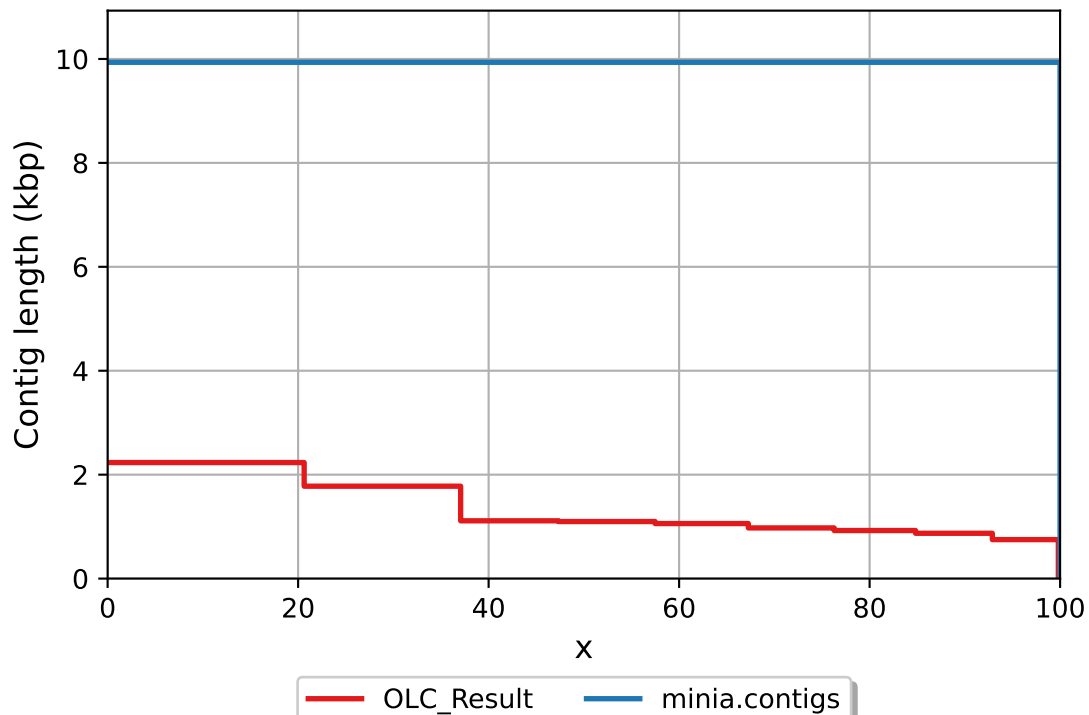
FRCurve (misassemblies)



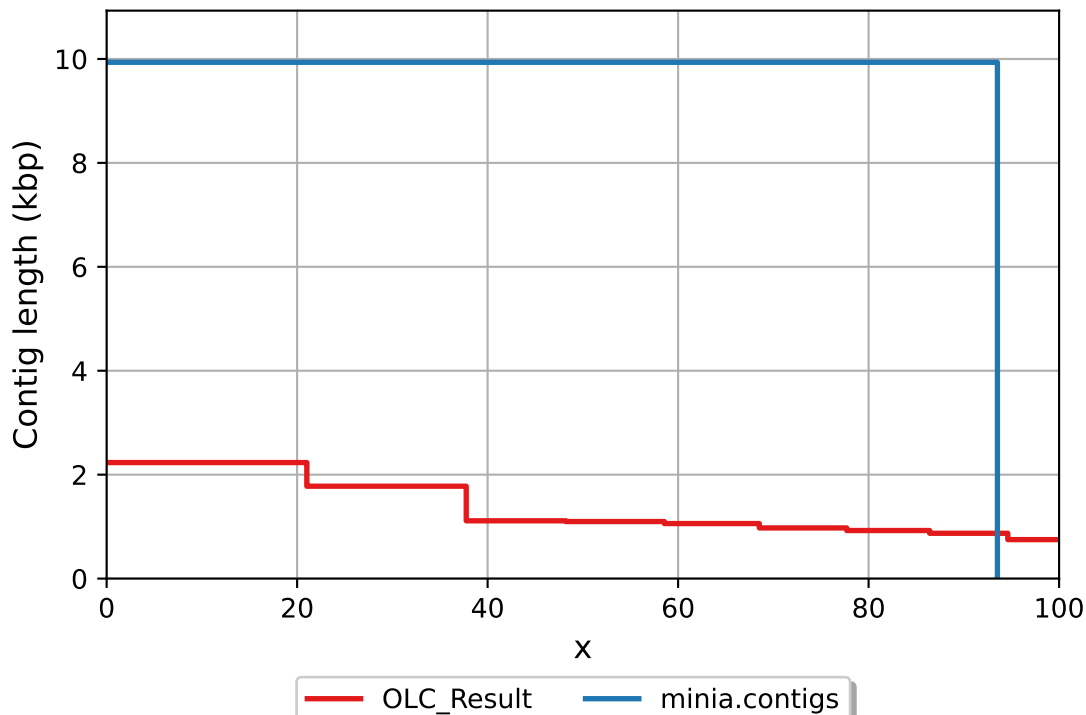
Cumulative length (aligned contigs)



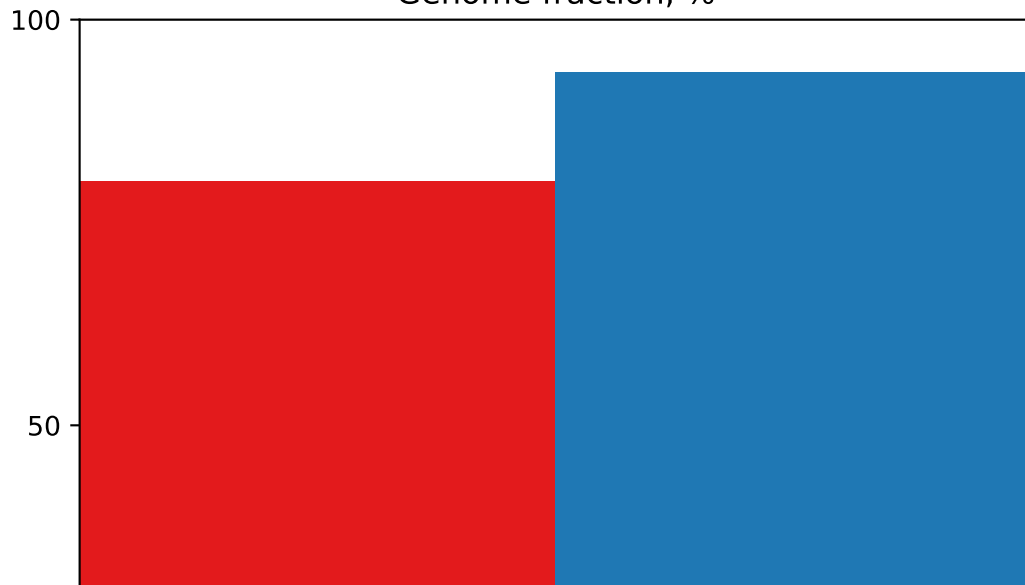
NAx



NGAx



Genome fraction, %



OLC_Result minia.contigs