

	Report	
	minia.contigs	ramilass_fuse.contigs
# contigs (>= 0 bp)	4	3
# contigs (>= 1000 bp)	1	1
# contigs (>= 5000 bp)	1	1
# contigs (>= 10000 bp)	0	1
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	10187	10301
Total length (>= 1000 bp)	9936	10094
Total length (>= 5000 bp)	9936	10094
Total length (>= 10000 bp)	0	10094
Total length (>= 25000 bp)	0	0
Total length (>= 50000 bp)	0	0
# contigs	1	1
Largest contig	9936	10094
Total length	9936	10094
Reference length	10624	10624
GC (%)	44.05	44.03
Reference GC (%)	44.14	44.14
N50	9936	10094
NG50	9936	10094
N90	9936	10094
NG90	9936	10094
auN	9936.0	10094.0
auNG	9292.6	9590.4
L50	1	1
LG50	1	1
L90	1	1
LG90	1	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 (%)	93.524	95.021
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	89.16
# indels per 100 kbp	0.00	9.91
Largest alignment	9936	10094
Total aligned length	9936	10094
NA50	9936	10094
NGA50	9936	10094
NA90	9936	10094
NGA90	9936	10094
auNA	9936.0	10094.0
auNGA	9292.6	9590.4
LA50	1	1
LGA50	1	1
LA90	1	1
LGA90	1	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

	minia.contigs	ramilass_fuse.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	0	9
# indels	0	1
# indels (<= 5 bp)	0	1
# indels (> 5 bp)	0	0
Indels length	0	1

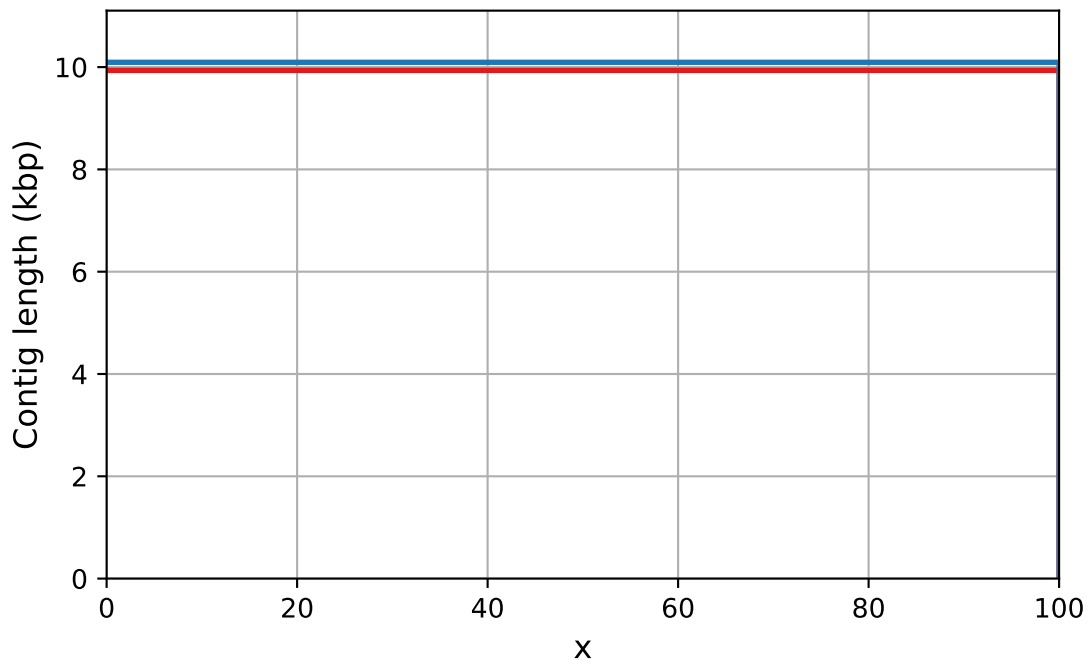
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	minia.contigs	ramilass_fuse.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

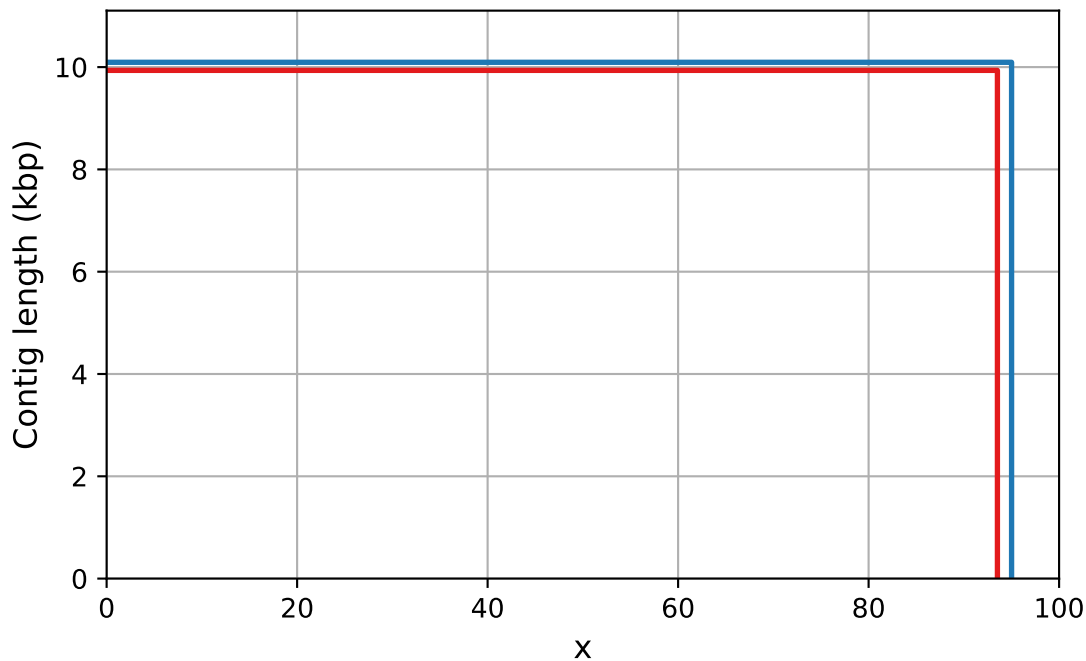
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



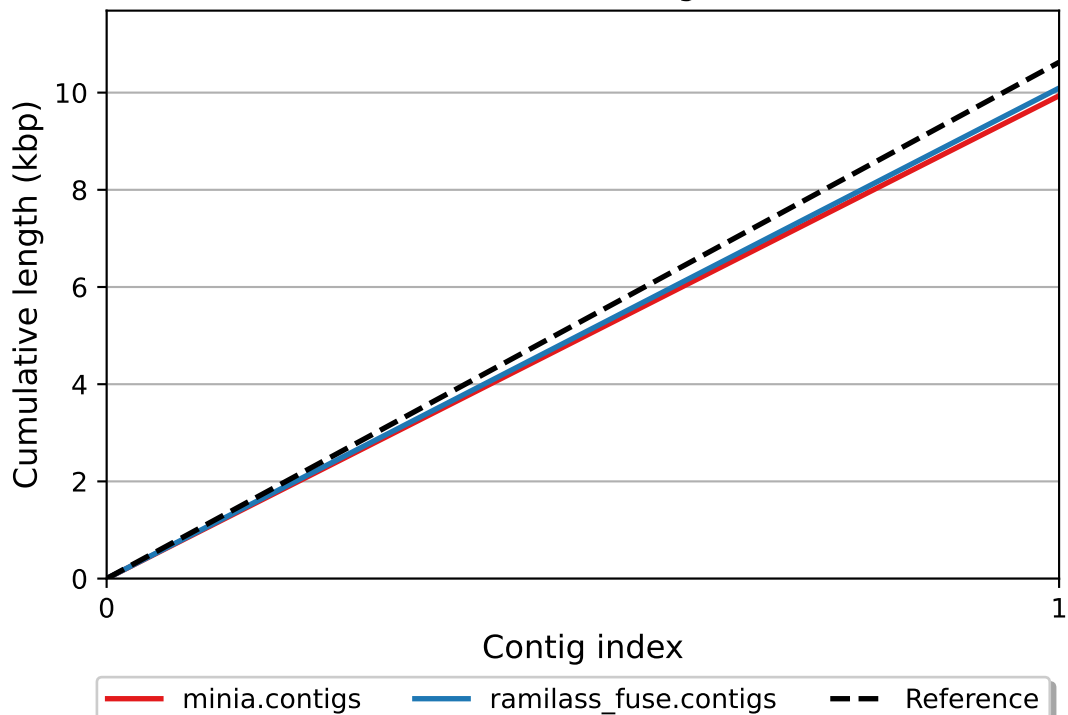
— minia.contigs — ramilass_fuse.contigs

NGx

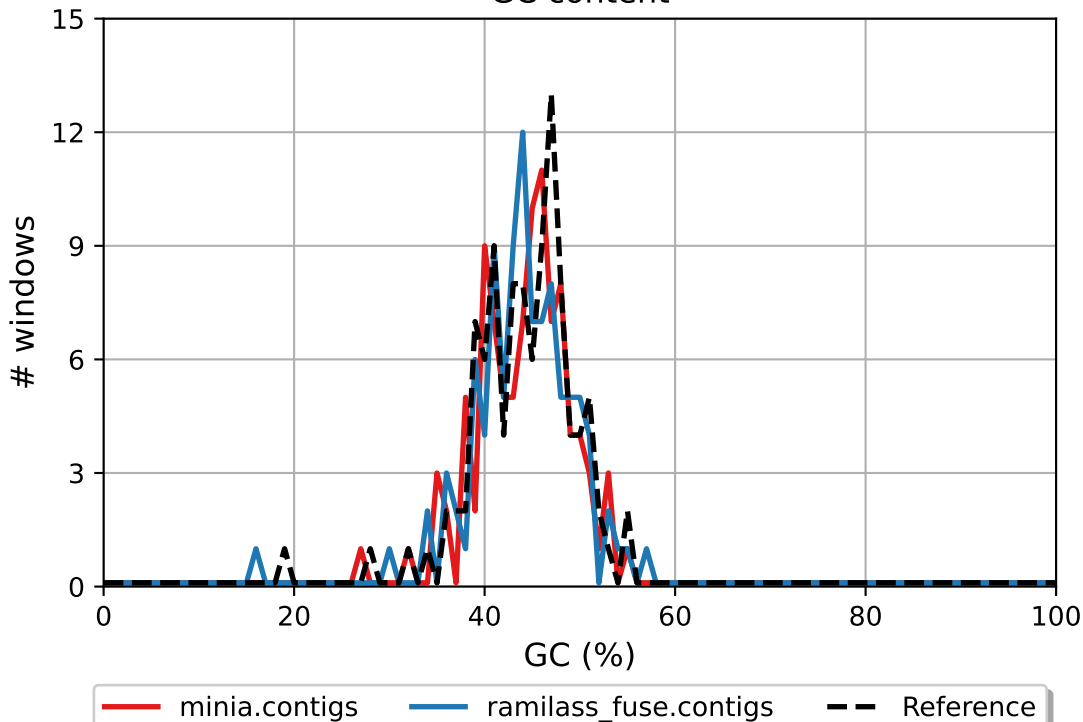


— minia.contigs — ramilass_fuse.contigs

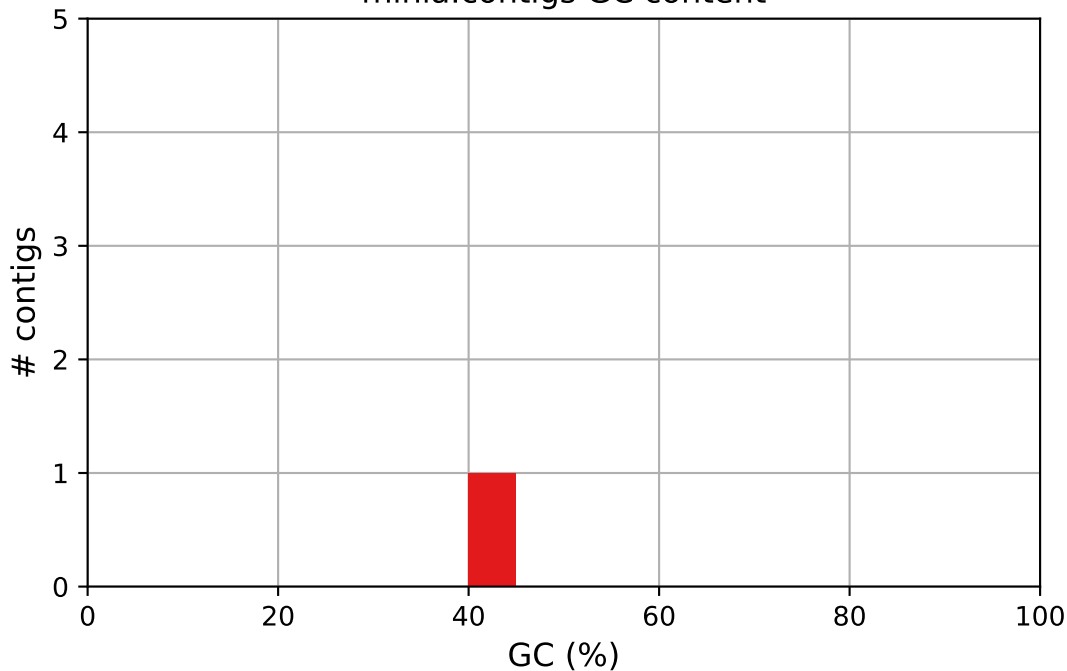
Cumulative length



GC content

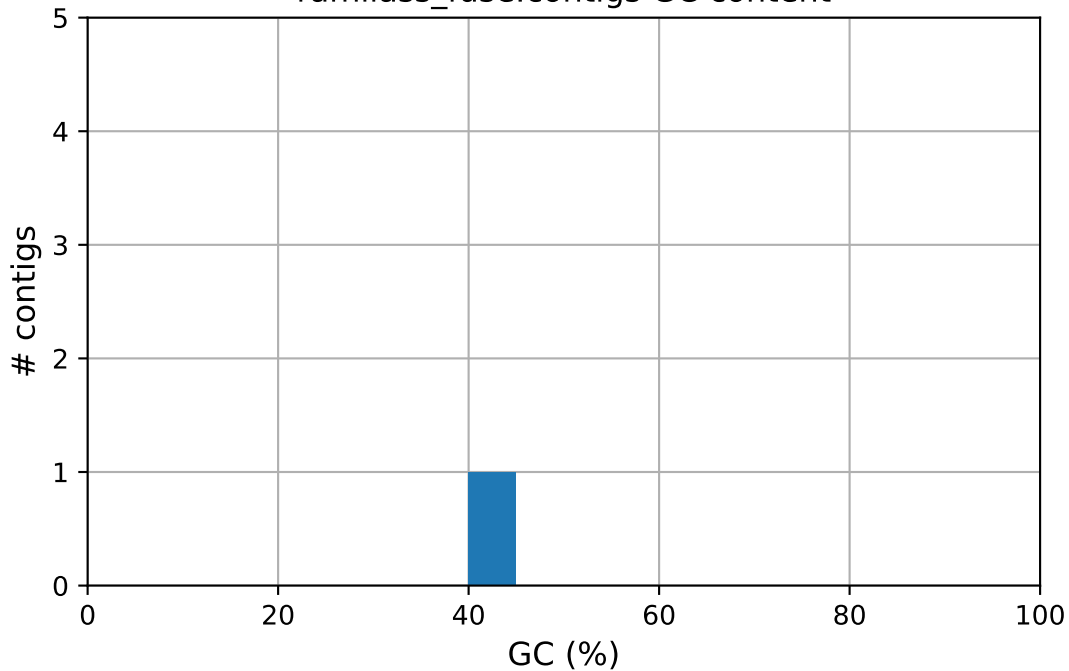


minia.contigs GC content



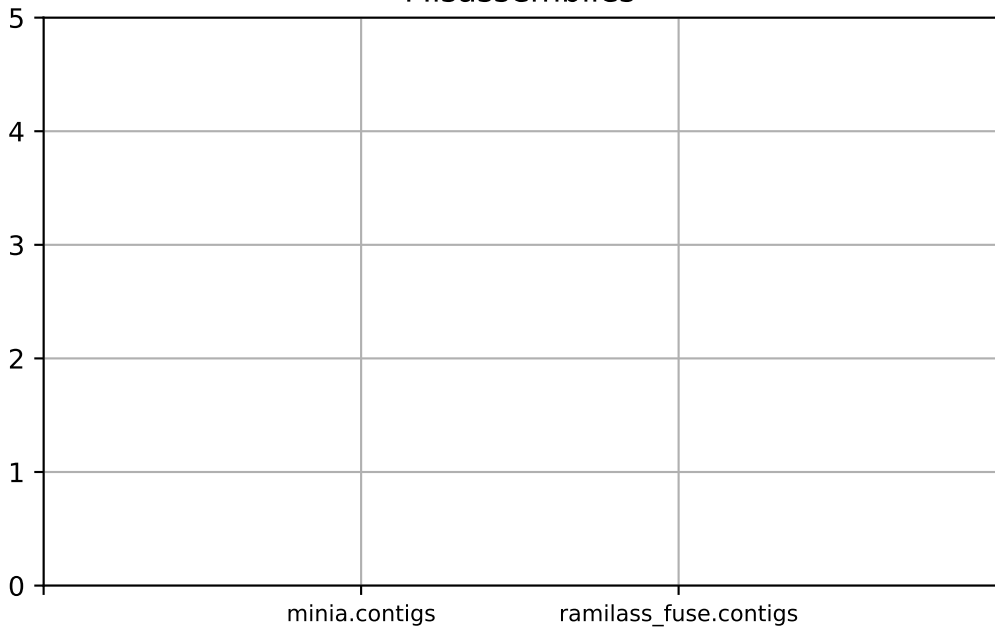
minia.contigs

ramilass_fuse.contigs GC content

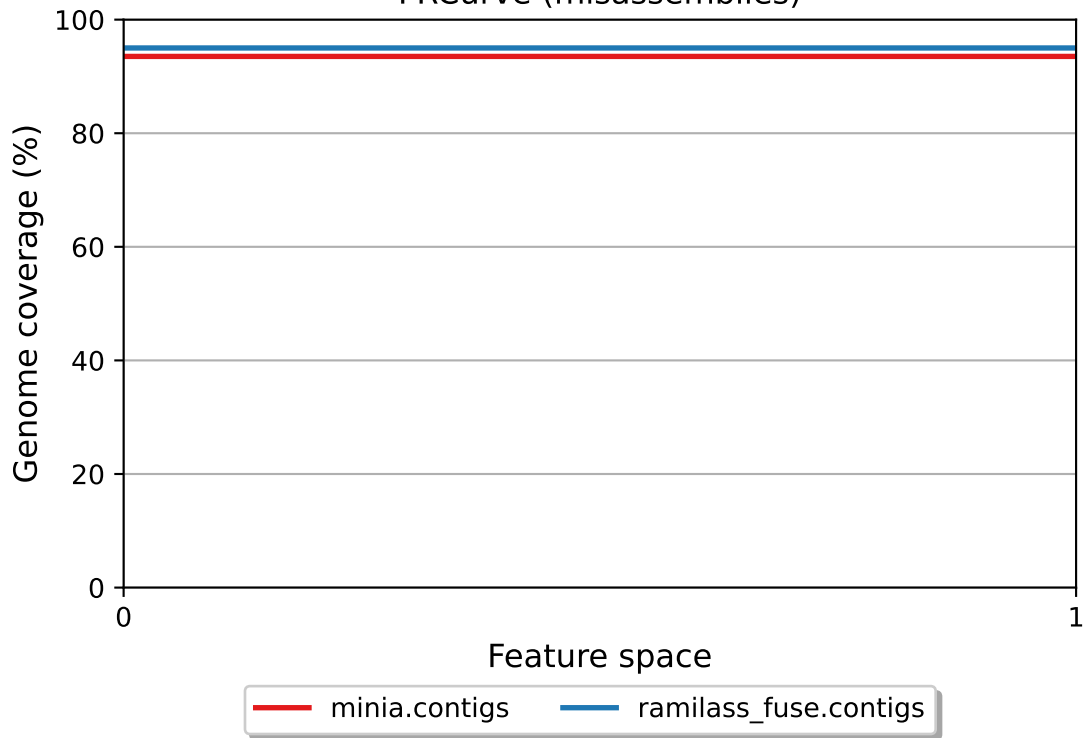


ramilass_fuse.contigs

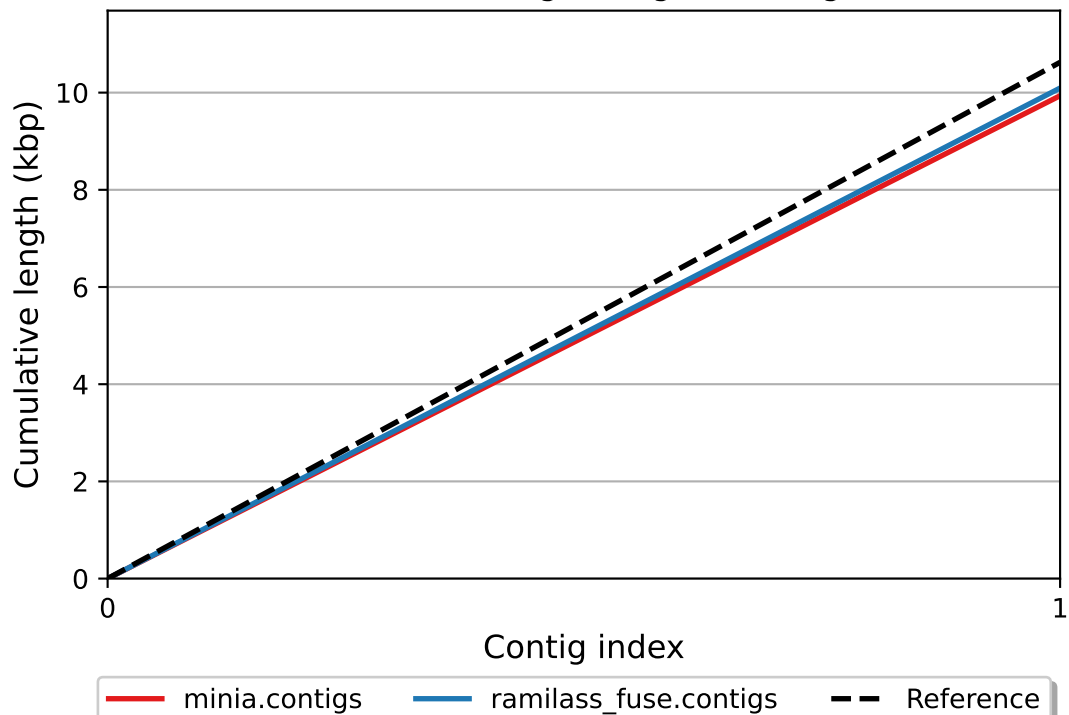
Misassemblies



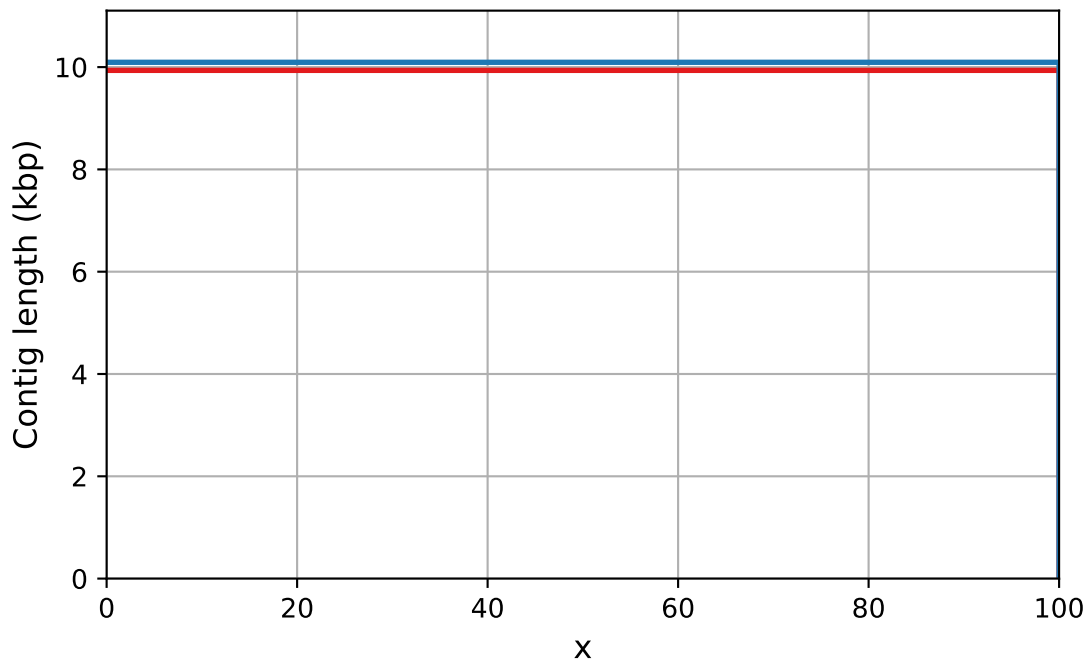
FRCurve (misassemblies)



Cumulative length (aligned contigs)

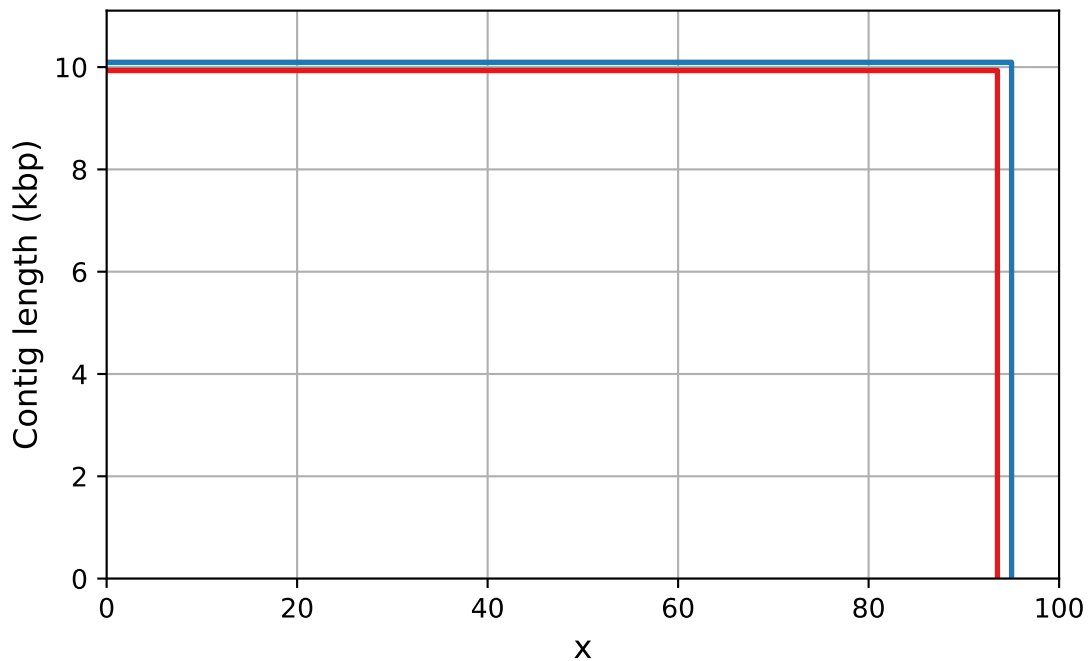


NAx



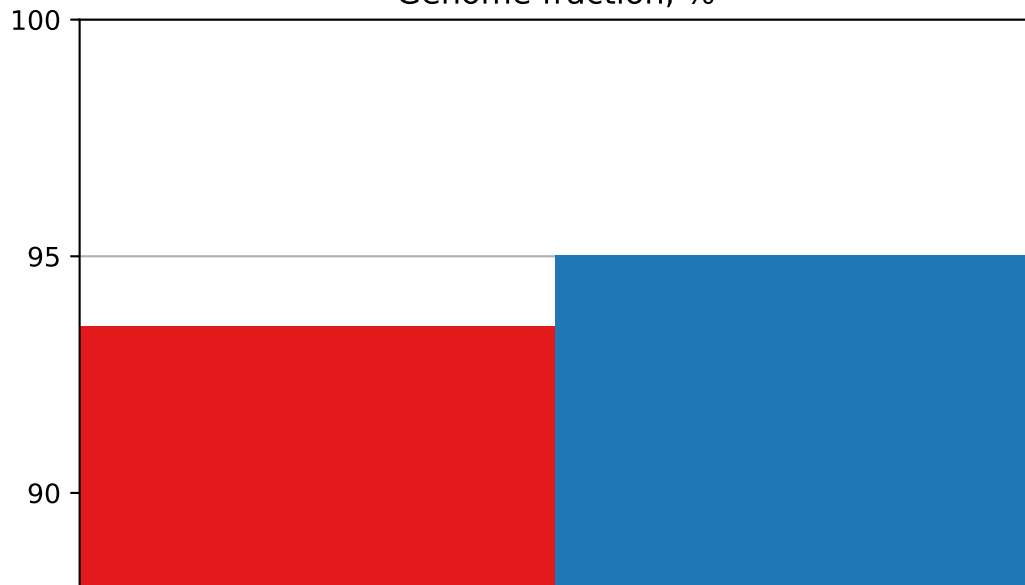
— minia.contigs — ramilass_fuse.contigs

NGAx



— minia.contigs — ramilass_fuse.contigs

Genome fraction, %



minia.contigs



ramilass_fuse.contigs