

Report

APPLdM_assembly.merfin_racon2	
# contigs (>= 0 bp)	235
# contigs (>= 1000 bp)	235
# contigs (>= 5000 bp)	235
# contigs (>= 10000 bp)	235
# contigs (>= 25000 bp)	206
# contigs (>= 50000 bp)	159
Total length (>= 0 bp)	173214323
Total length (>= 1000 bp)	173214323
Total length (>= 5000 bp)	173214323
Total length (>= 10000 bp)	173214323
Total length (>= 25000 bp)	172635514
Total length (>= 50000 bp)	170906464
# contigs	235
Largest contig	28232861
Total length	173214323
Reference length	143726002
GC (%)	41.27
Reference GC (%)	42.01
N50	15830123
NG50	15830123
N90	416558
NG90	1680734
auN	13396934.8
auNG	16145589.2
L50	4
LG50	4
L90	46
LG90	14
# misassemblies	9492
# misassembled contigs	125
Misassembled contigs length	165916140
# local misassemblies	2278
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	42
# unaligned contigs	29 + 167 part
Unaligned length	10280806
Genome fraction (%)	93.466
Duplication ratio	1.214
# N's per 100 kbp	3.10
# mismatches per 100 kbp	569.84
# indels per 100 kbp	125.60
Largest alignment	606777
Total aligned length	161752283
NA50	83703
NGA50	105961
NA90	2705
NGA90	19362
auNA	120763.5
auNGA	145540.6
LA50	523
LGA50	366
LA90	5514
LGA90	1509

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

	APPLdM_assembly.merfin_racon2
# misassemblies	9492
# contig misassemblies	9492
# c. relocations	3538
# c. translocations	5906
# c. inversions	48
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	125
Misassembled contigs length	165916140
# local misassemblies	2278
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	42
# mismatches	921734
# indels	203158
# indels (<= 5 bp)	150938
# indels (> 5 bp)	52220
Indels length	1386890

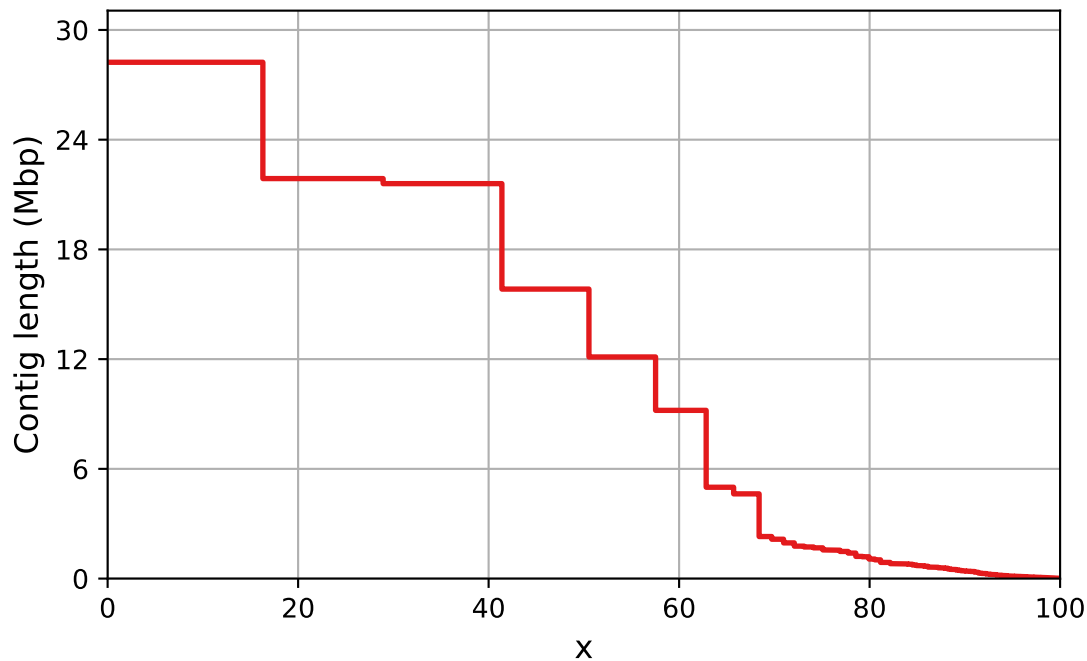
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	APPLdM_assembly.merfin_racon2
# fully unaligned contigs	29
Fully unaligned length	1198849
# partially unaligned contigs	167
Partially unaligned length	9081957
# N's	5377

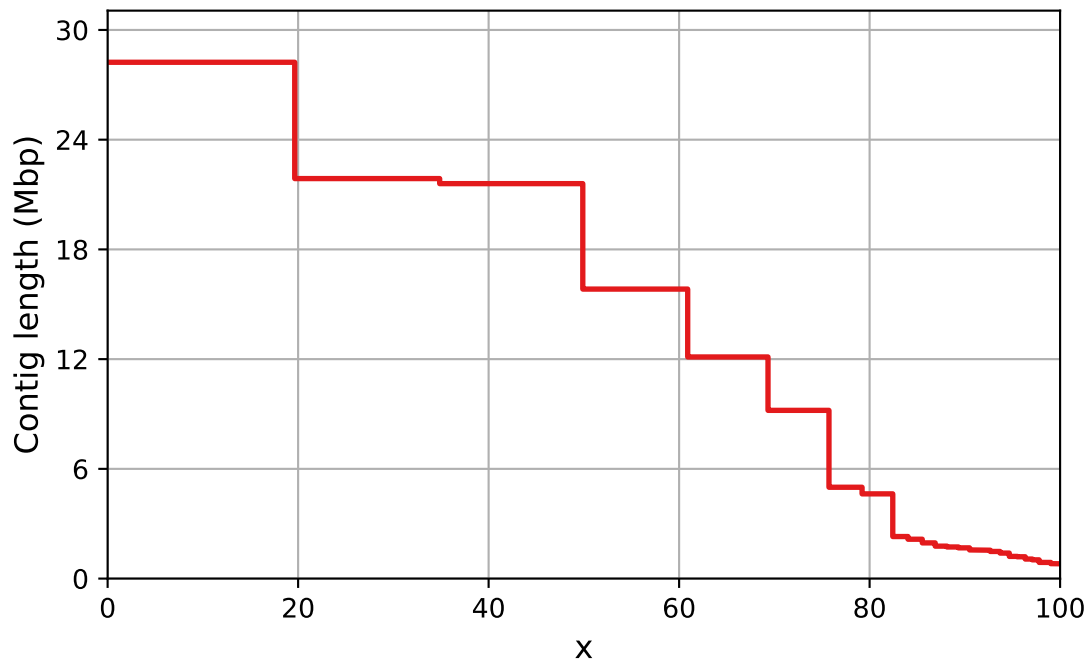
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

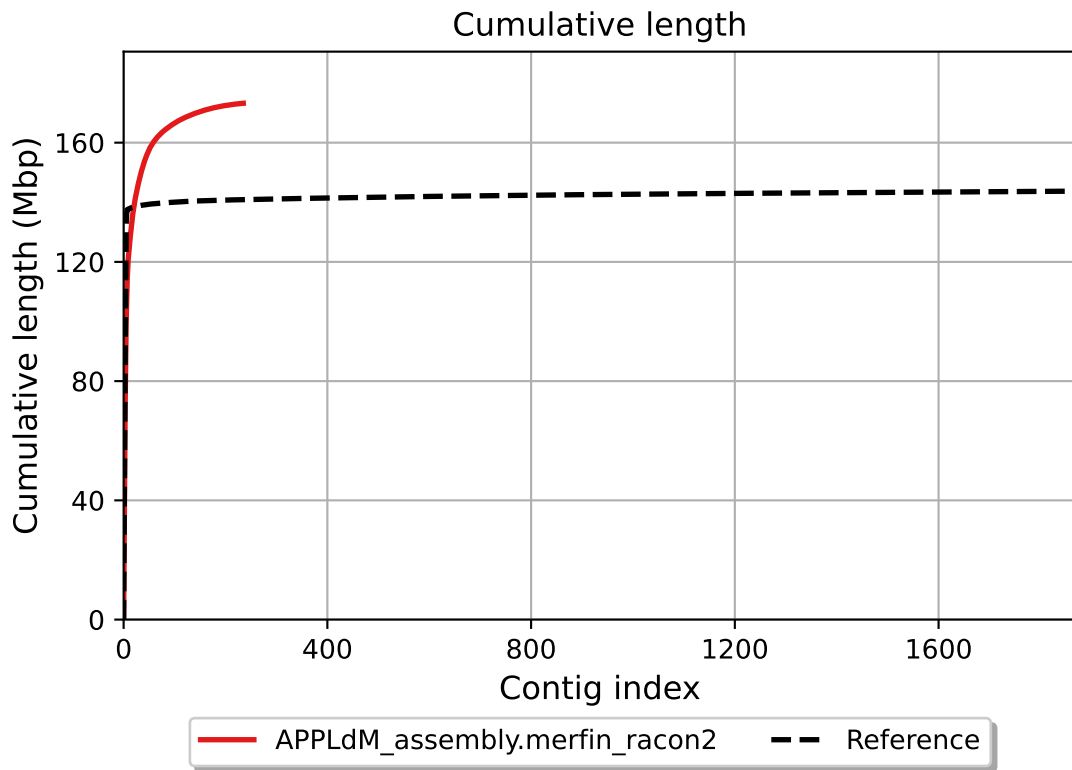


APPLdM_assembly.merfin_racon2

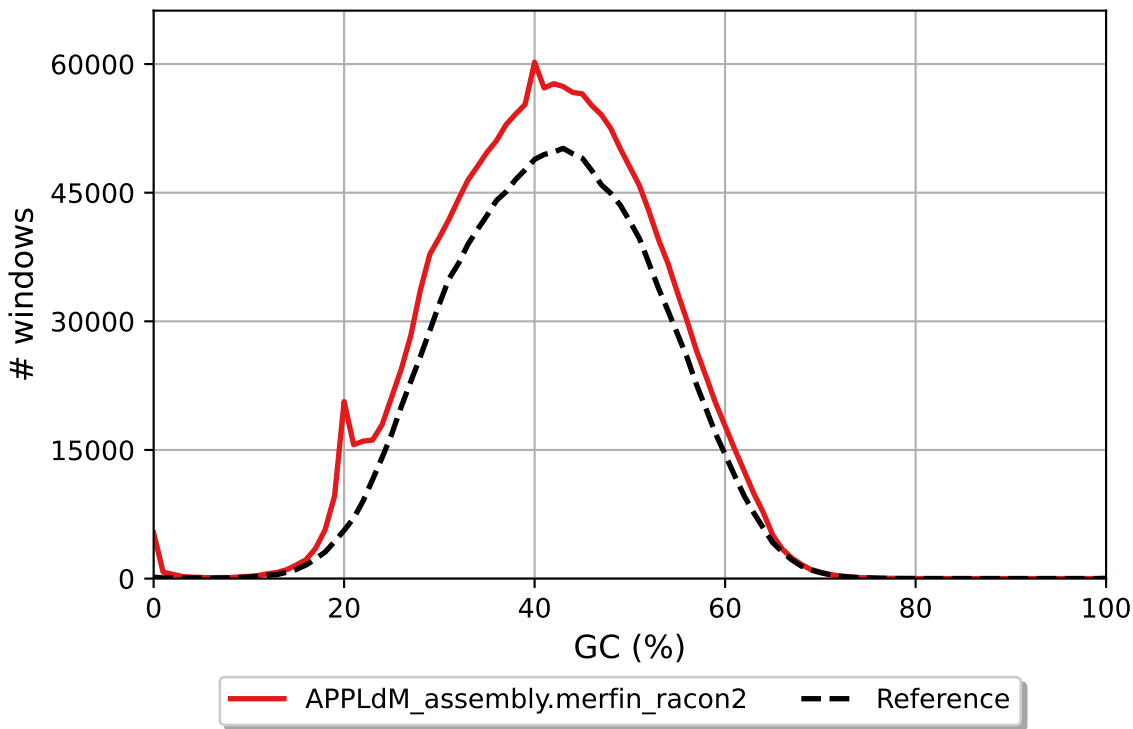
NGx



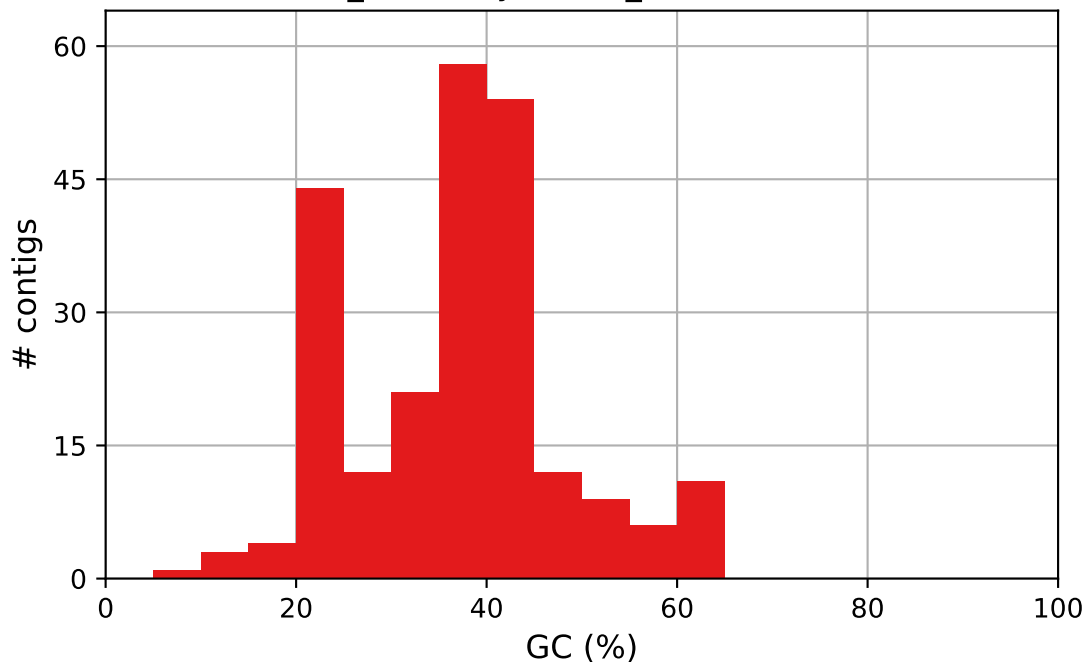
— APPLdM_assembly.merfin_racon2



GC content

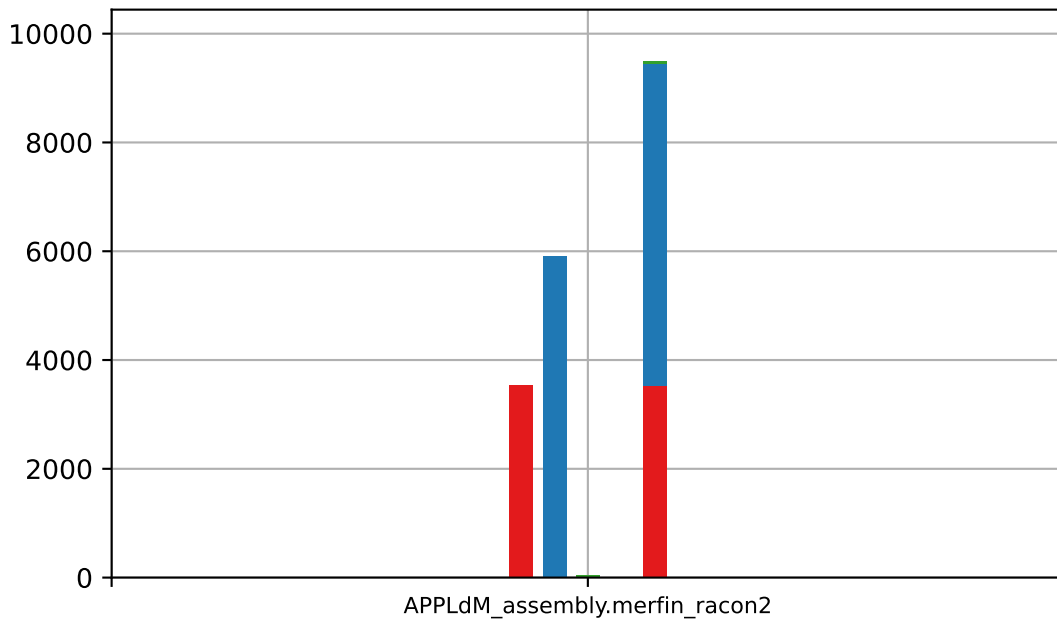


APPLdM_assembly.merfin_racon2 GC content



APPLdM_assembly.merfin_racon2

Misassemblies



relocations

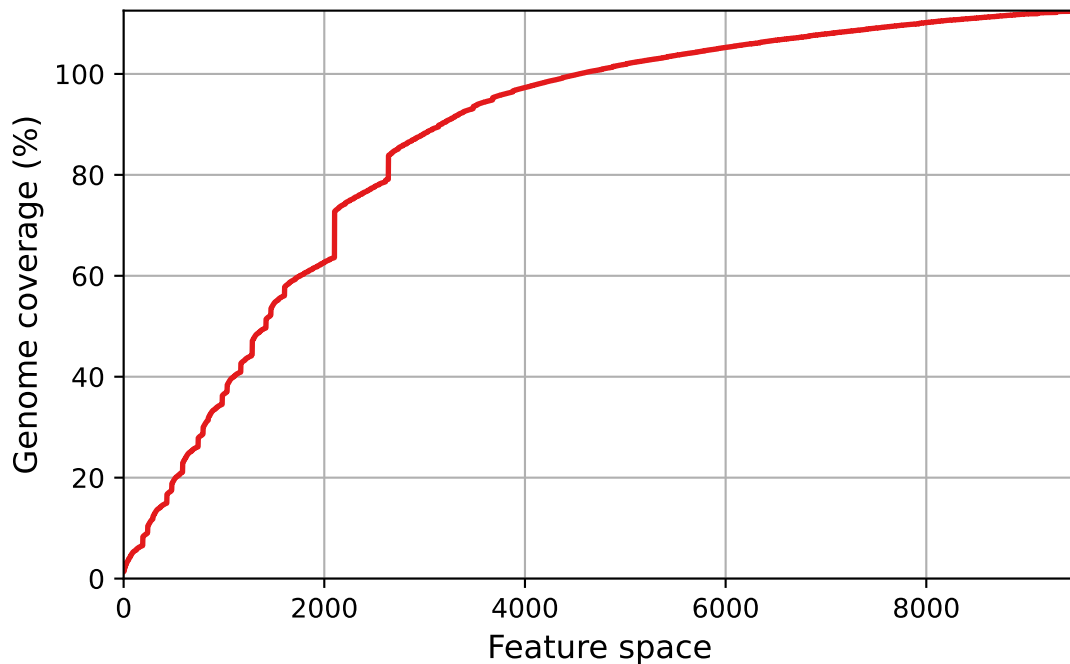


translocations



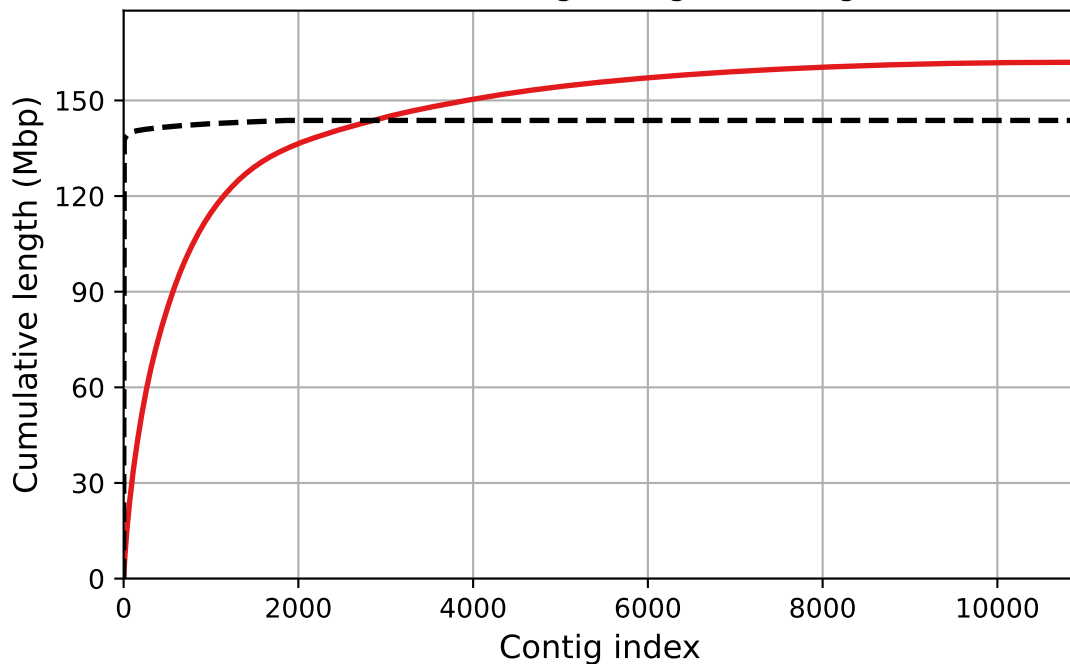
inversions

FRCurve (misassemblies)



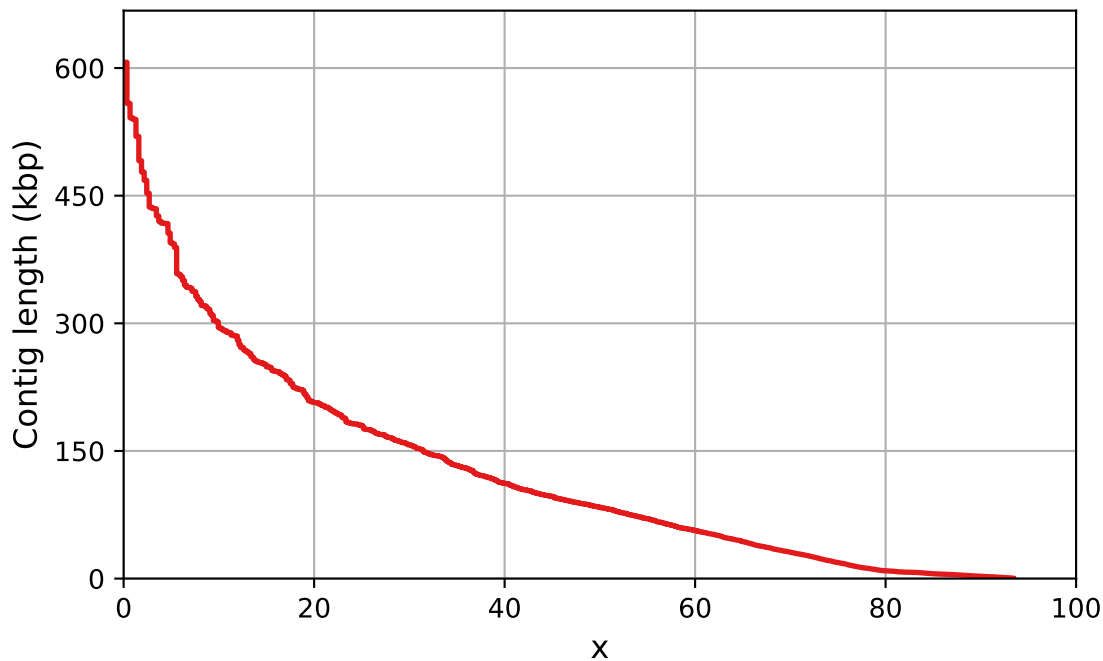
— APPLdM_assembly.merfin_racon2

Cumulative length (aligned contigs)



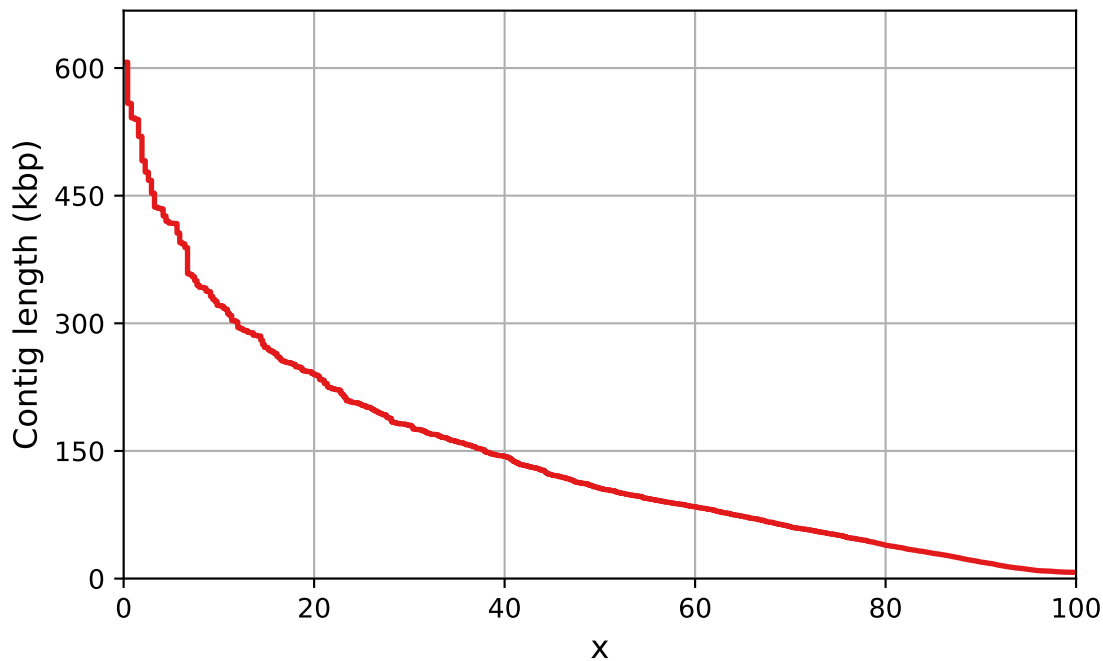
— APPLdM_assembly.merfin_racon2 - - Reference

NAx



— APPLdM_assembly.merfin_racon2

NGAx



— APPLdM_assembly.merfin_racon2