

Report

	asm.contigs
# contigs (>= 0 bp)	96
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	96
# contigs (>= 10000 bp)	85
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	13150776
Total length (>= 1000 bp)	13150776
Total length (>= 5000 bp)	13150776
Total length (>= 10000 bp)	13047603
Total length (>= 25000 bp)	12111163
Total length (>= 50000 bp)	12083485
# contigs	96
Largest contig	1506339
Total length	13150776
Reference length	12157105
GC (%)	37.83
Reference GC (%)	38.15
N50	778969
NG50	808829
N90	274012
NG90	437058
auN	792651.6
auNG	857439.7
L50	7
LG50	6
L90	16
LG90	14
# misassemblies	108
# misassembled contigs	37
Misassembled contigs length	12398790
# local misassemblies	319
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	6 + 21 part
Unaligned length	186505
Genome fraction (%)	97.448
Duplication ratio	1.093
# N's per 100 kbp	0.00
# mismatches per 100 kbp	218.06
# indels per 100 kbp	32.18
# genomic features	26343 + 137 part
Largest alignment	843303
Total aligned length	12947107
NA50	247983
NGA50	284116
NA90	17455
NGA90	109892
auNA	345962.4
auNGA	374240.0
LA50	14
LGA50	12
LA90	59
LGA90	40

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

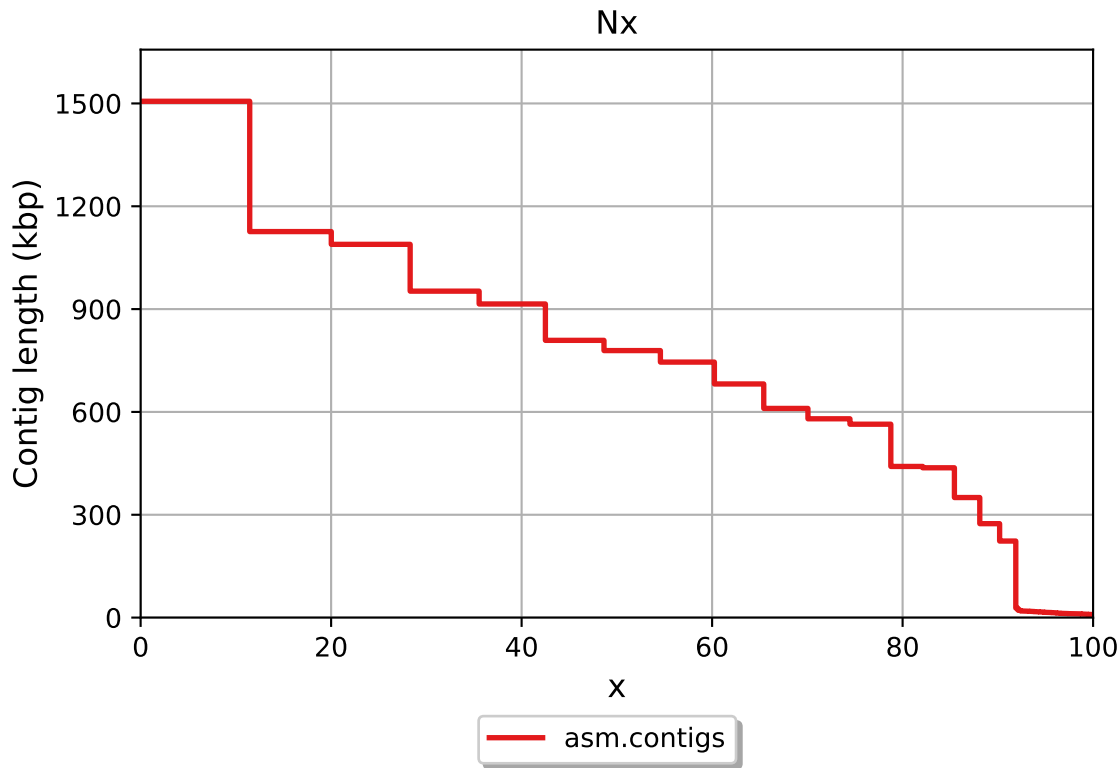
	asm.contigs
# misassemblies	108
# contig misassemblies	108
# c. relocations	46
# c. translocations	60
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	37
Misassembled contigs length	12398790
# local misassemblies	319
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	28232
# indels	4166
# indels (<= 5 bp)	3406
# indels (> 5 bp)	760
Indels length	23960

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).

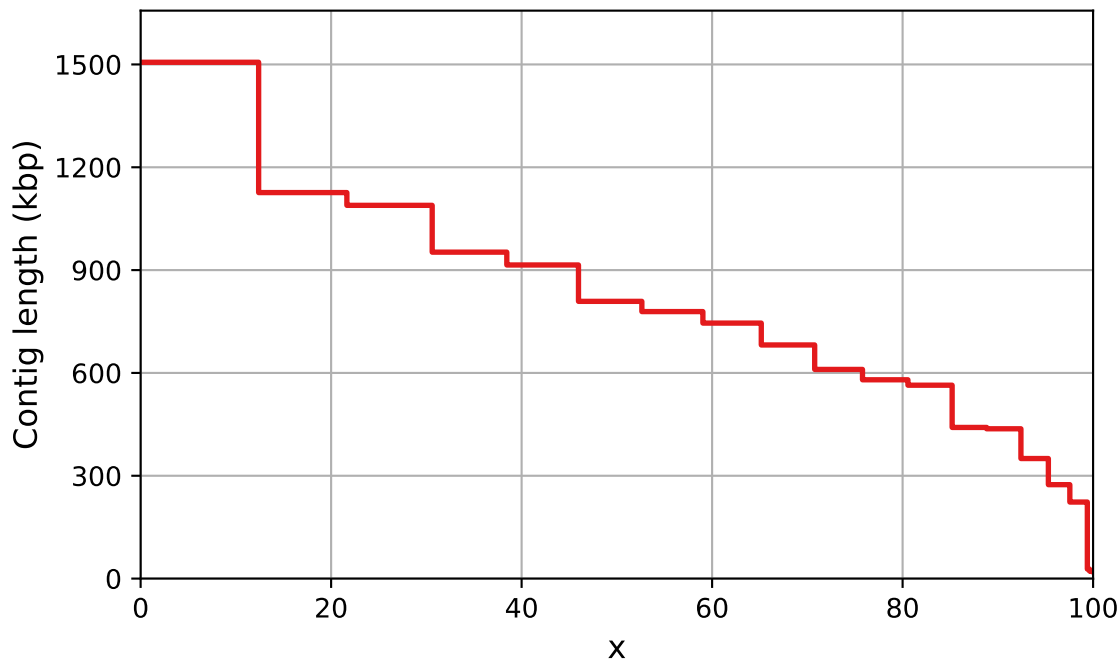
Unaligned report

	asm.contigs
# fully unaligned contigs	6
Fully unaligned length	73393
# partially unaligned contigs	21
Partially unaligned length	113112
# N's	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).

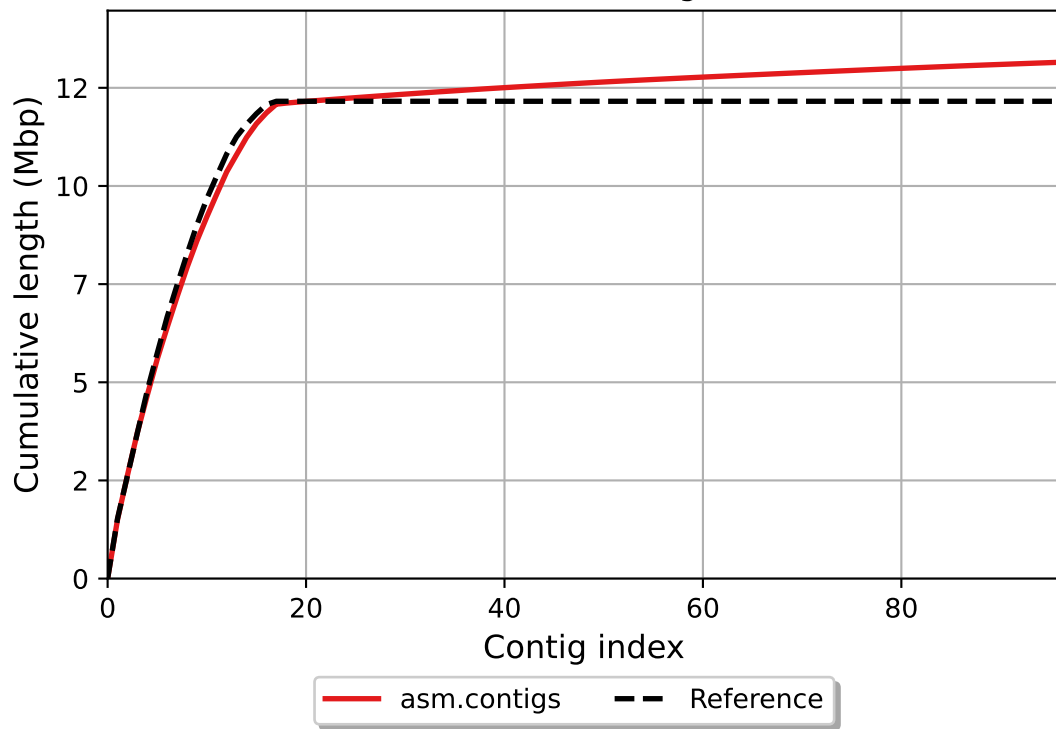


NGx

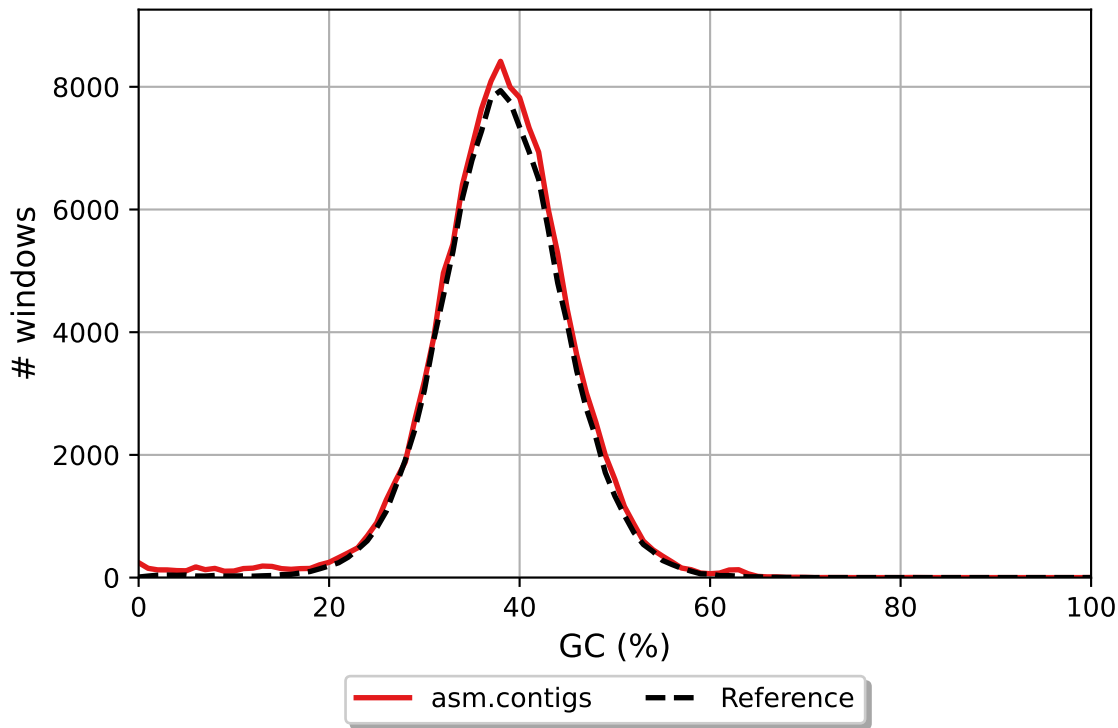


asm.contigs

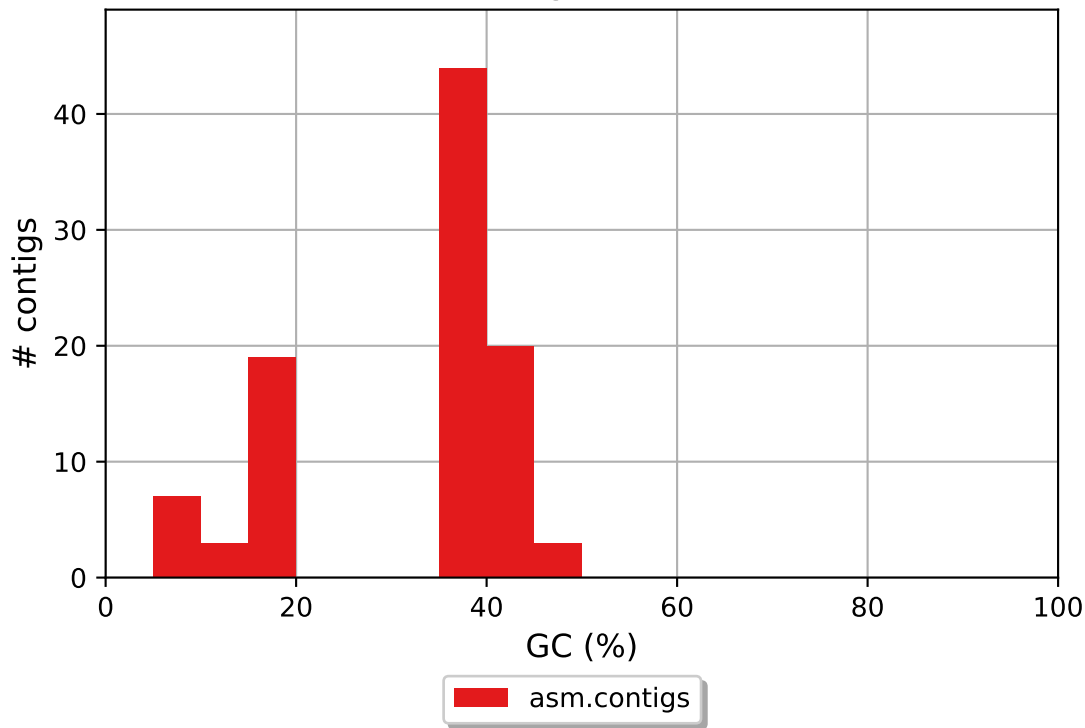
Cumulative length



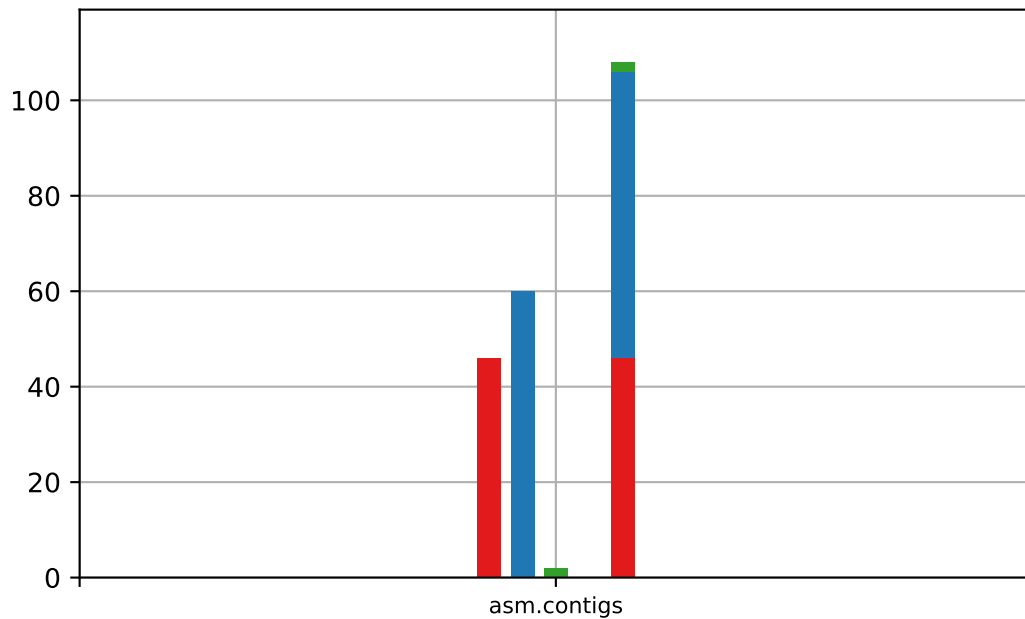
GC content



asm.contigs GC content



Misassemblies



relocations

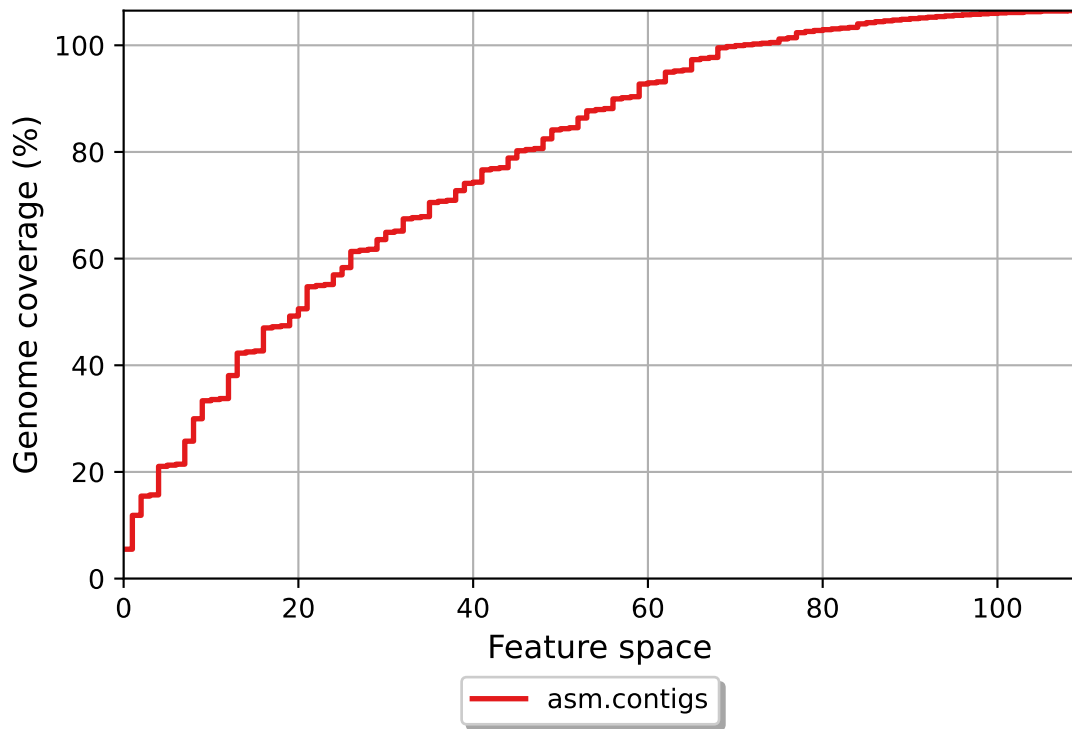


translocations

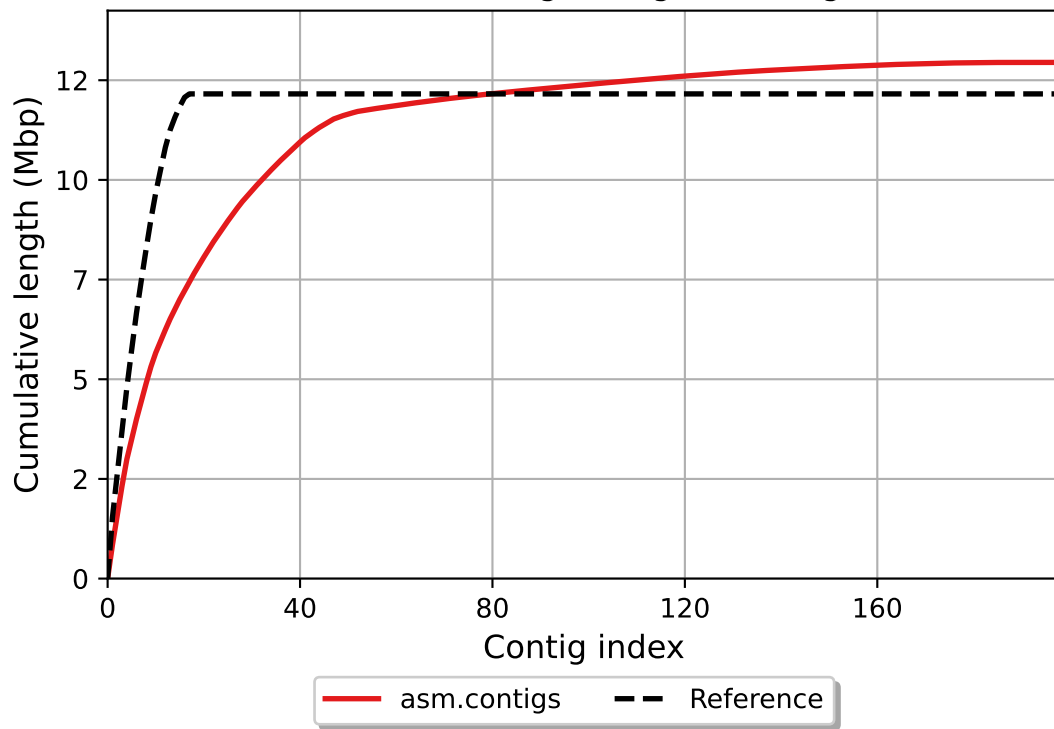


inversions

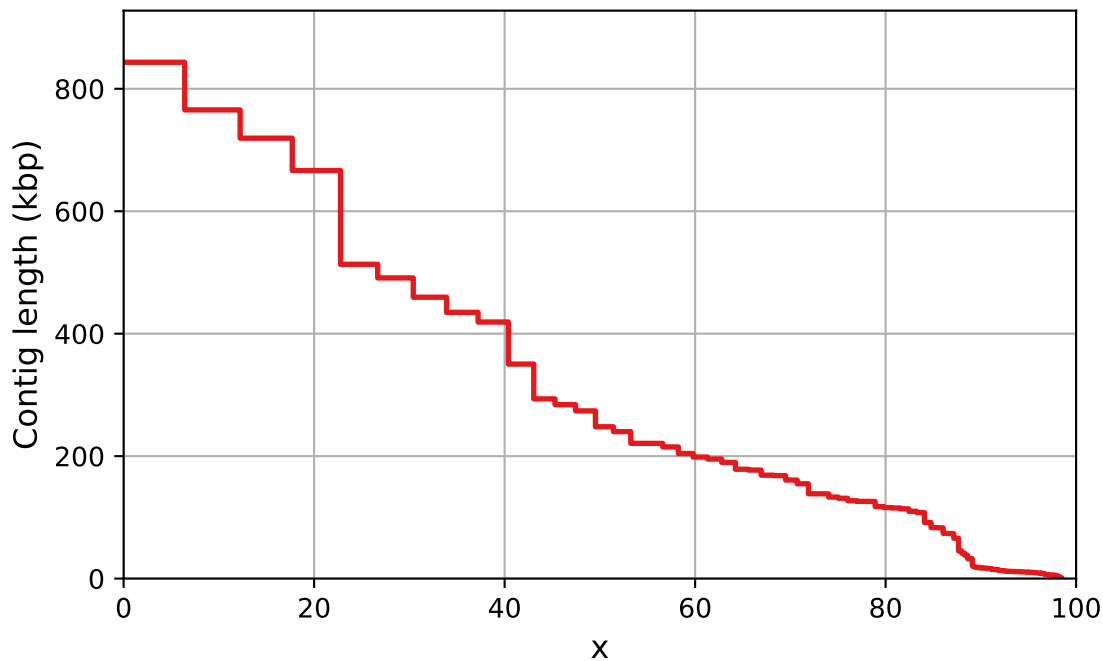
FRCurve (misassemblies)



Cumulative length (aligned contigs)

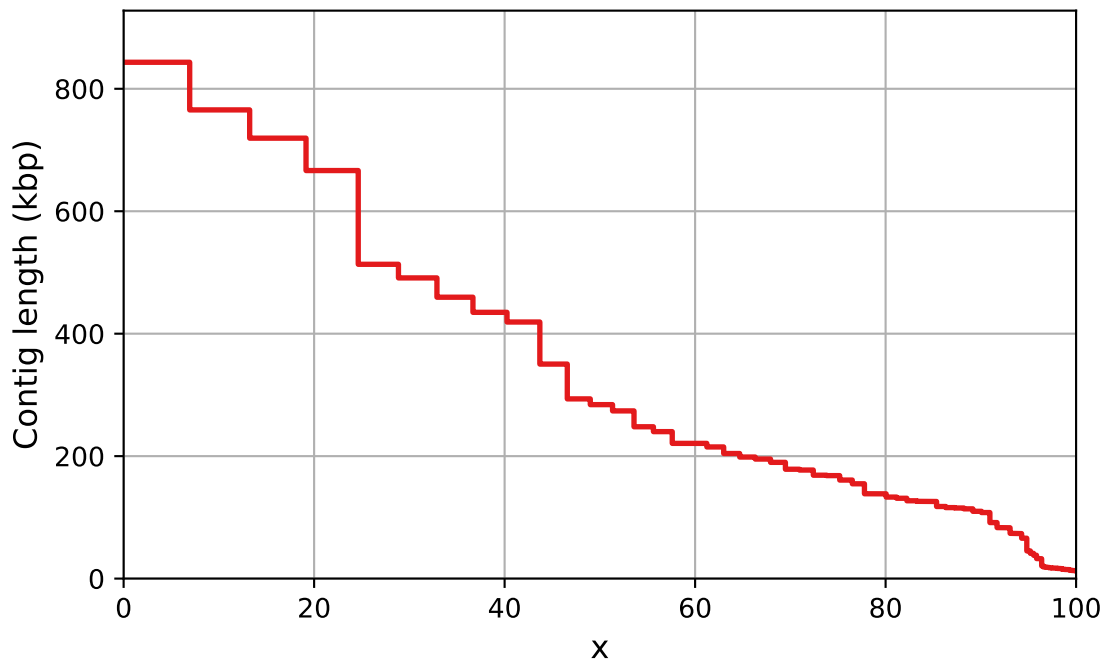


NAx



asm.contigs

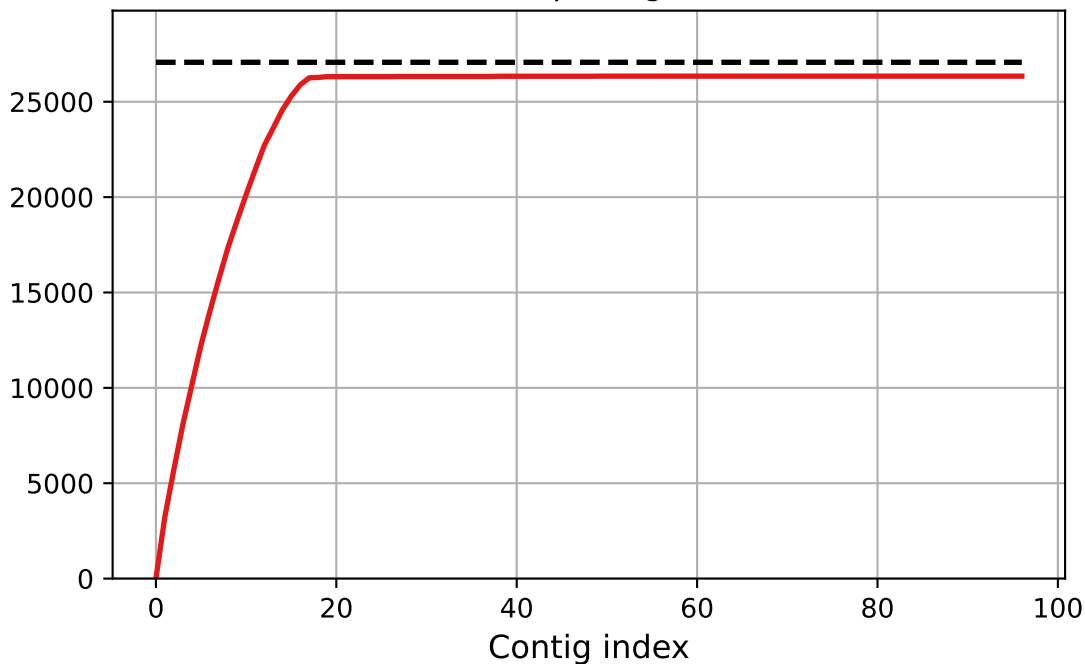
NGAx



asm.contigs

Cumulative # complete genomic features

Cumulative # complete genomic features



asm.contigs Reference

FRCurve (genomic features)

