

## Report

	contigs
# contigs (>= 0 bp)	2727
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	87505
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	417
Largest contig	201
Total length	20515
Reference length	64302
GC (%)	38.41
Reference GC (%)	37.76
N50	46
N75	37
L50	138
L75	262
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	358 + 0 part
Unaligned length	14693
Genome fraction (%)	8.990
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	51.89
# indels per 100 kbp	17.30
Largest alignment	196
Total aligned length	5783
NGA50	-

All statistics are based on contigs of size >= 30 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

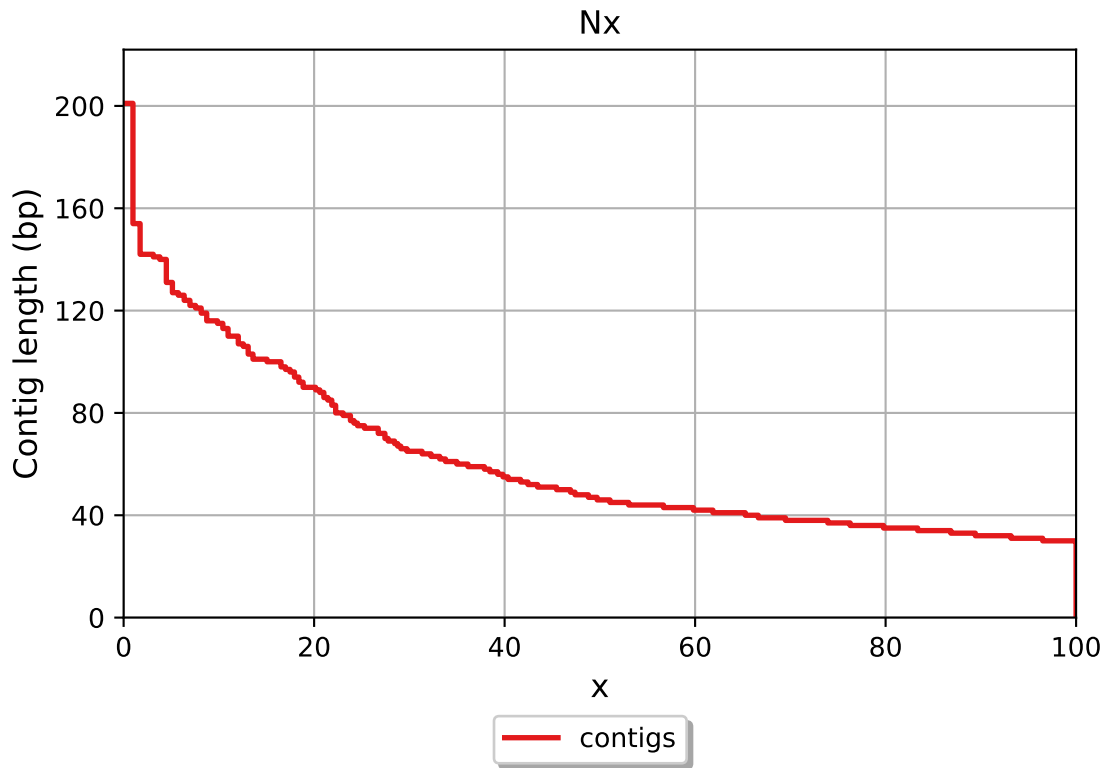
	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3
# indels	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	6

All statistics are based on contigs of size  $\geq 30$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

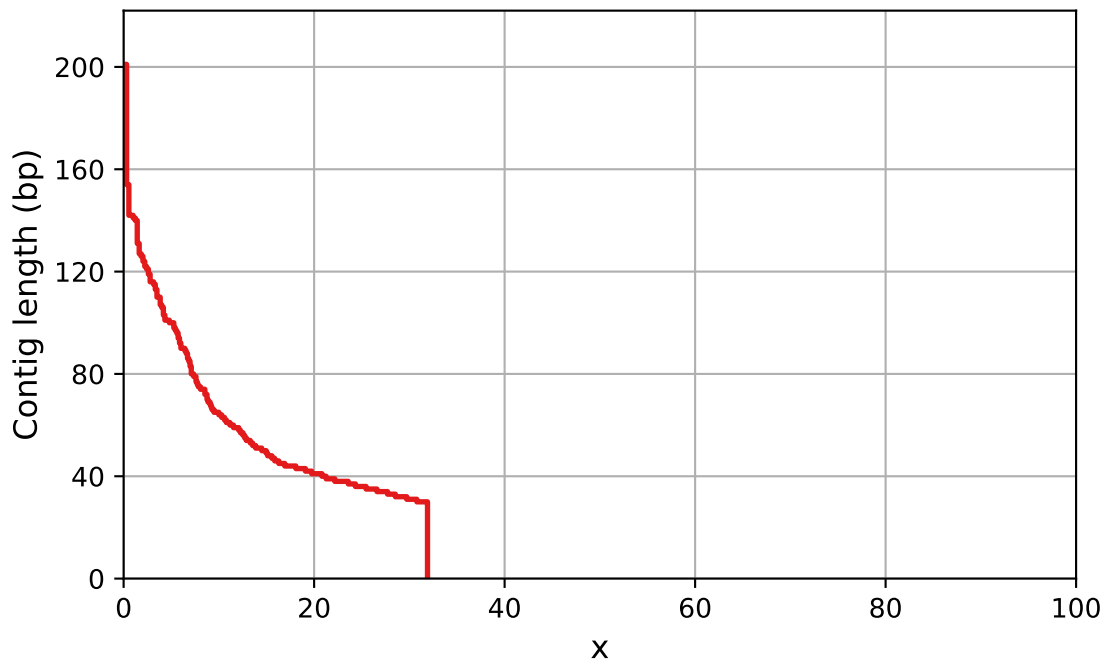
## Unaligned report

	contigs
# fully unaligned contigs	358
Fully unaligned length	14693
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size  $\geq 30$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

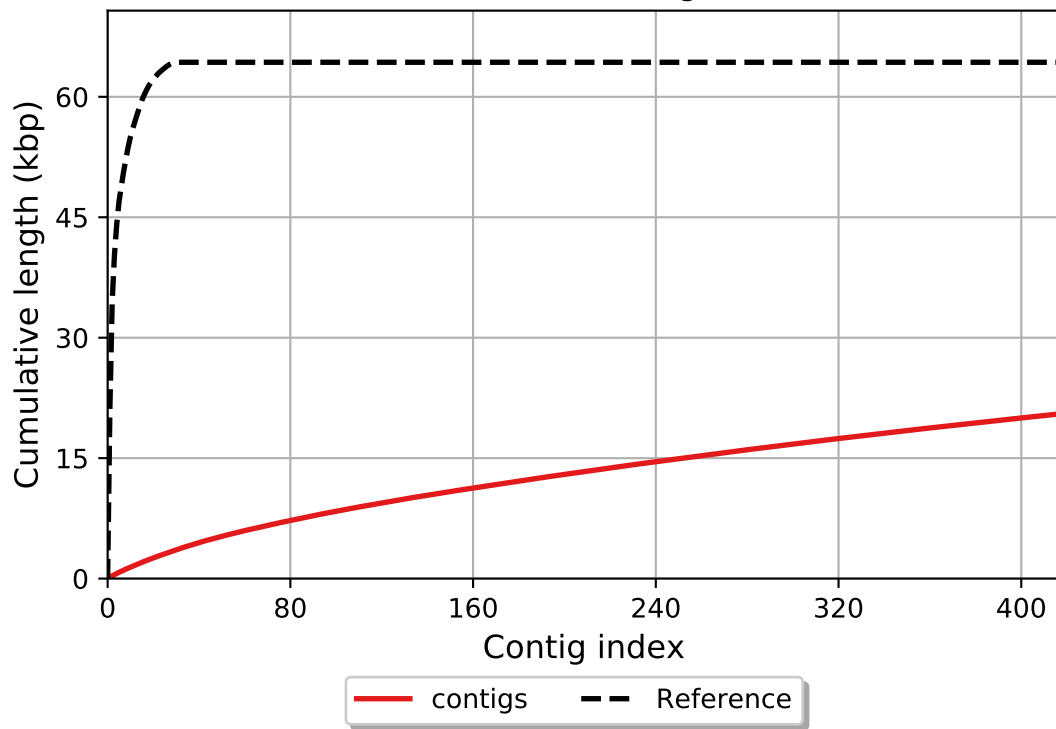


# NGx

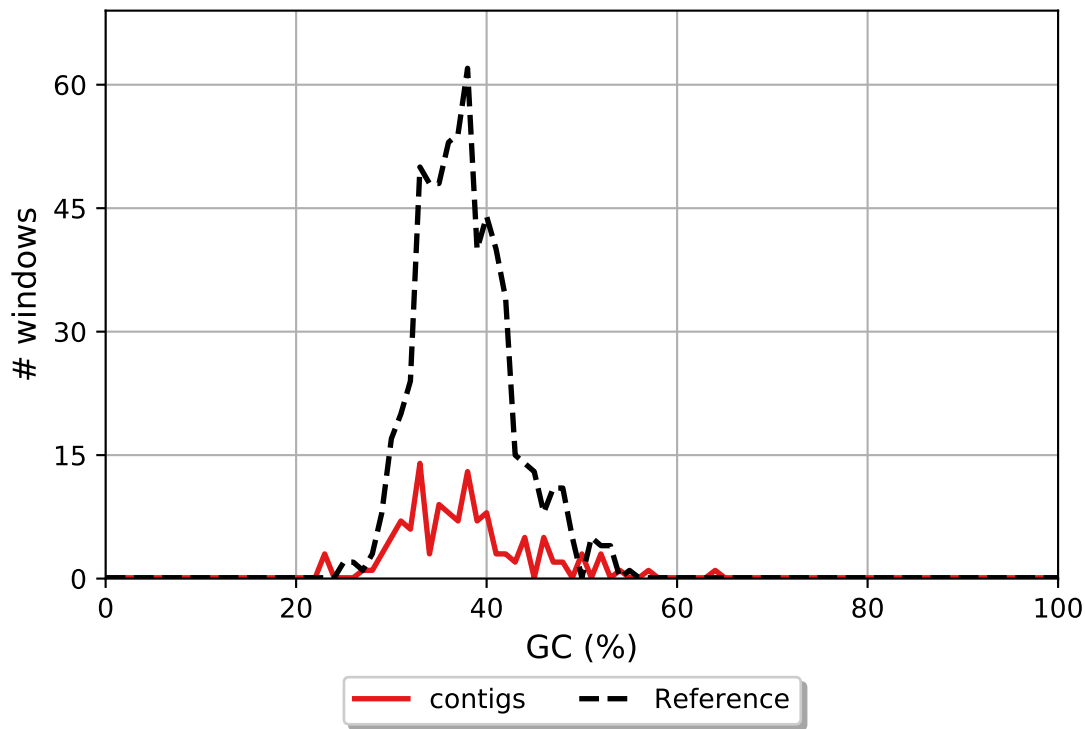


— contigs

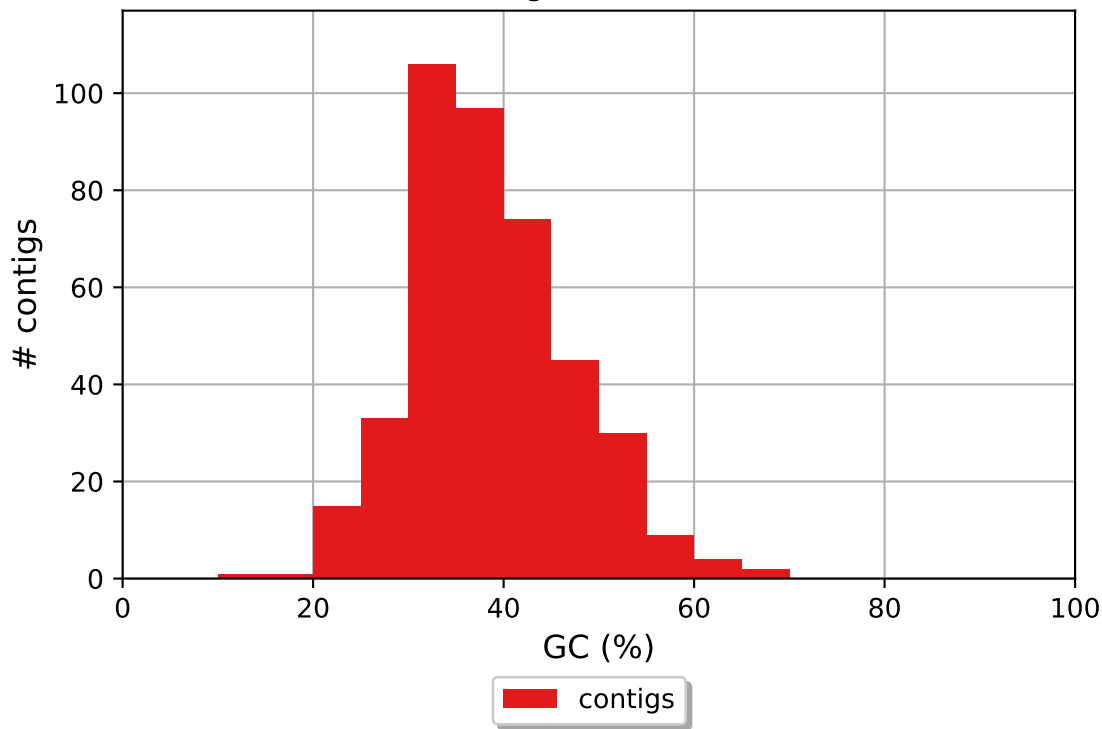
Cumulative length



# GC content

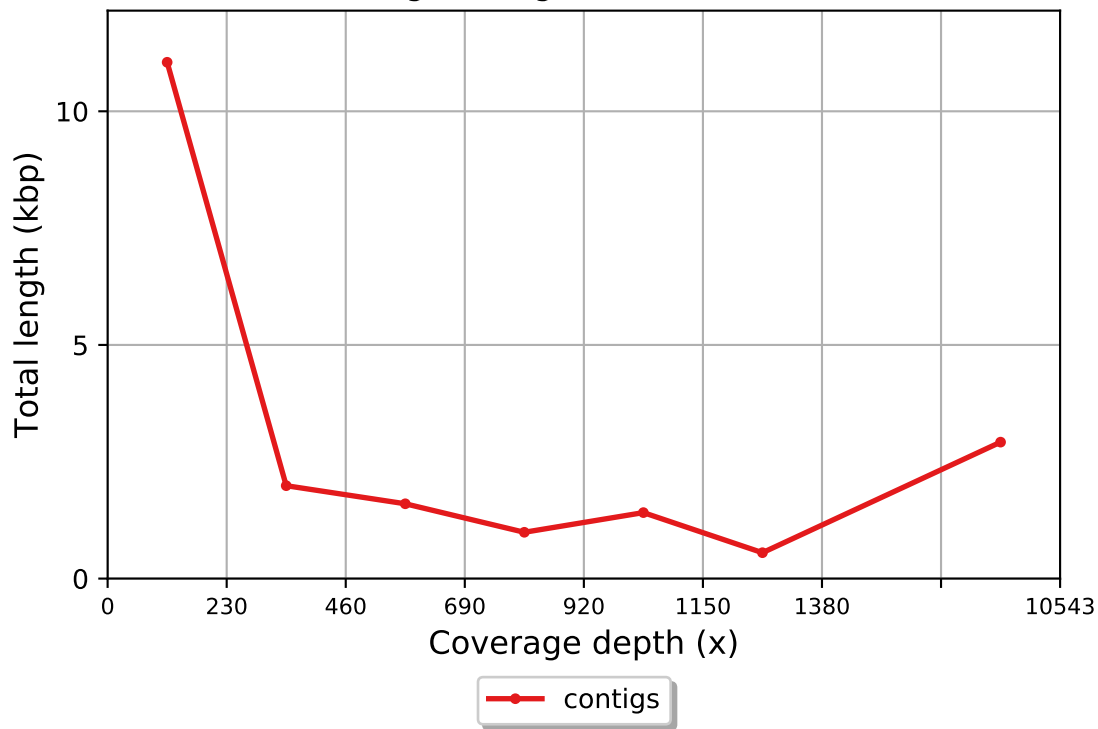


contigs GC content

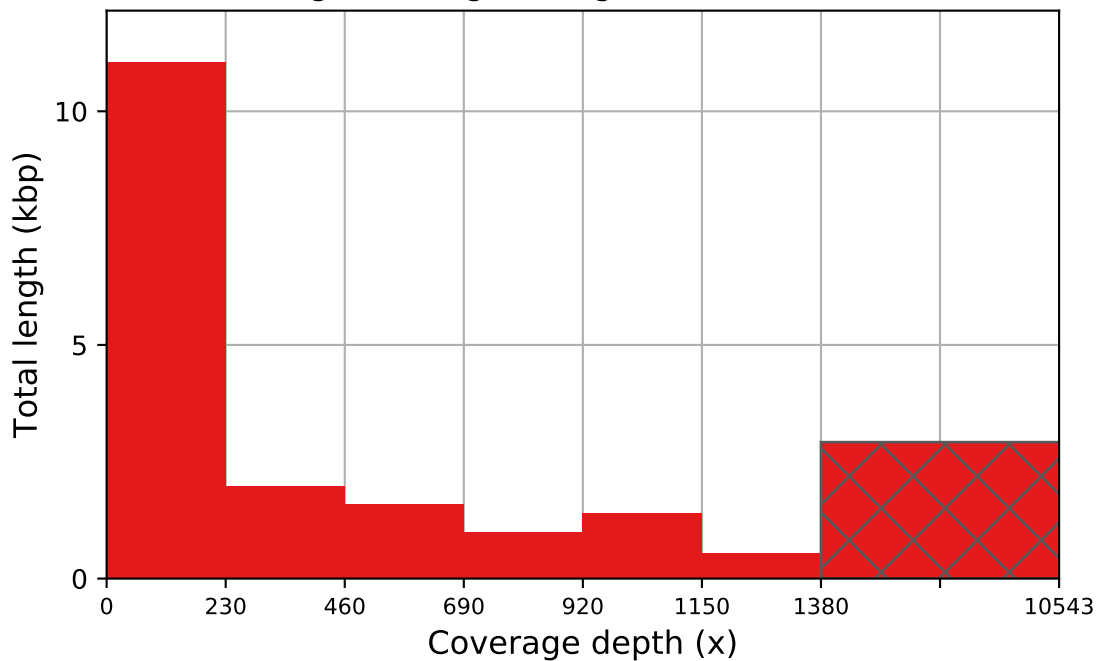




Coverage histogram (bin size: 230x)

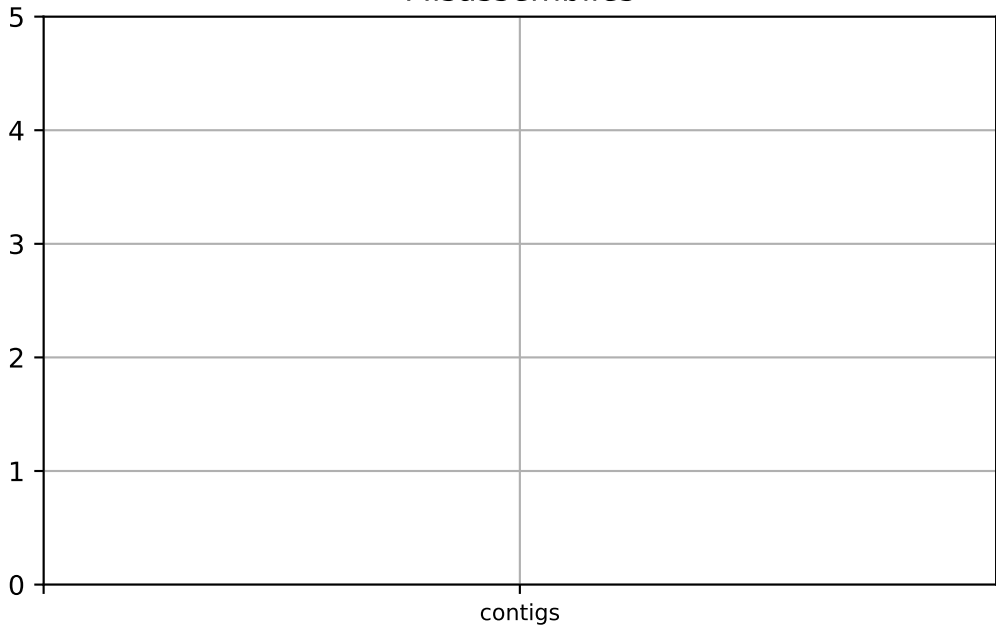


contigs coverage histogram (bin size: 230x)

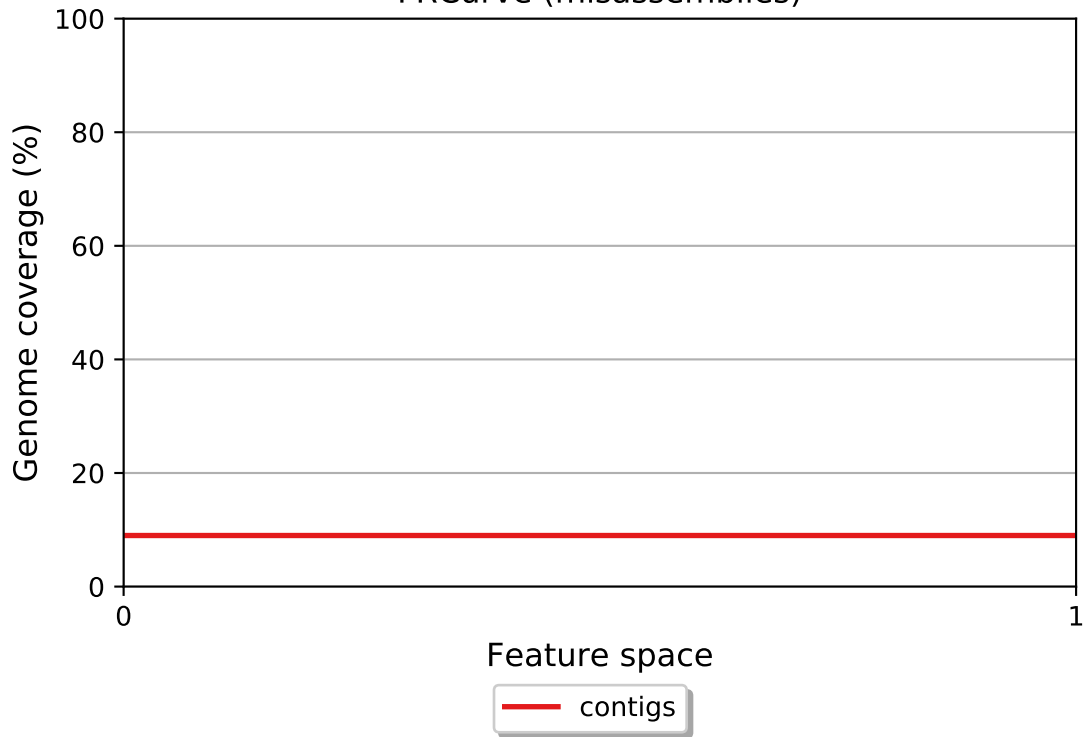


contigs

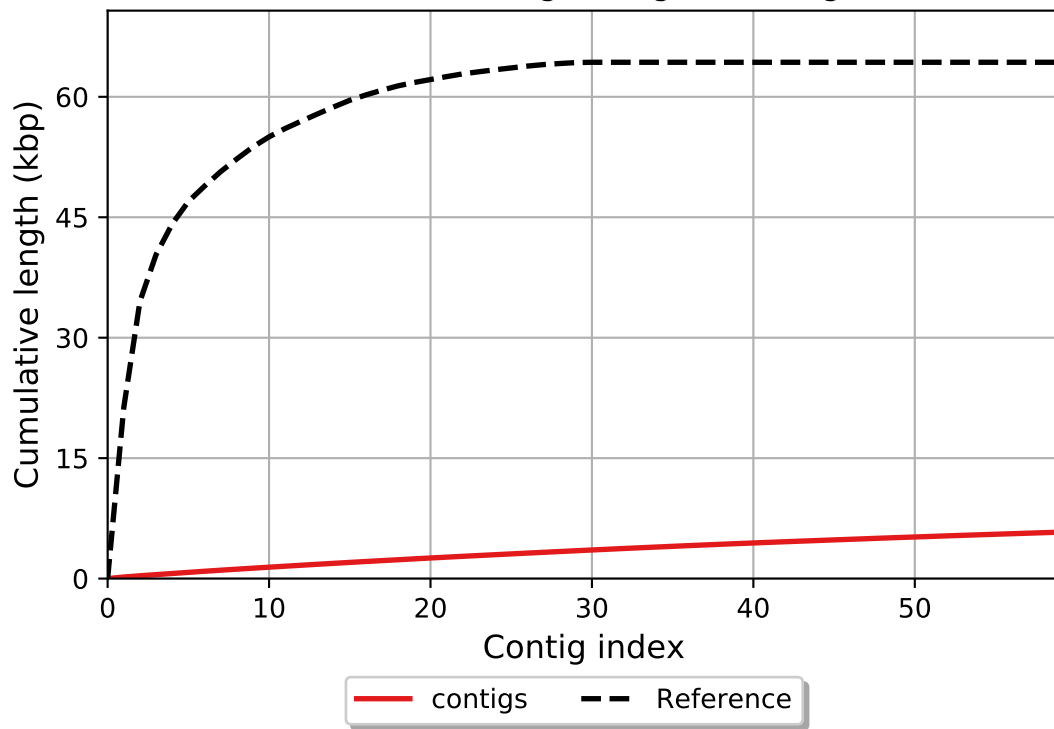
## Misassemblies



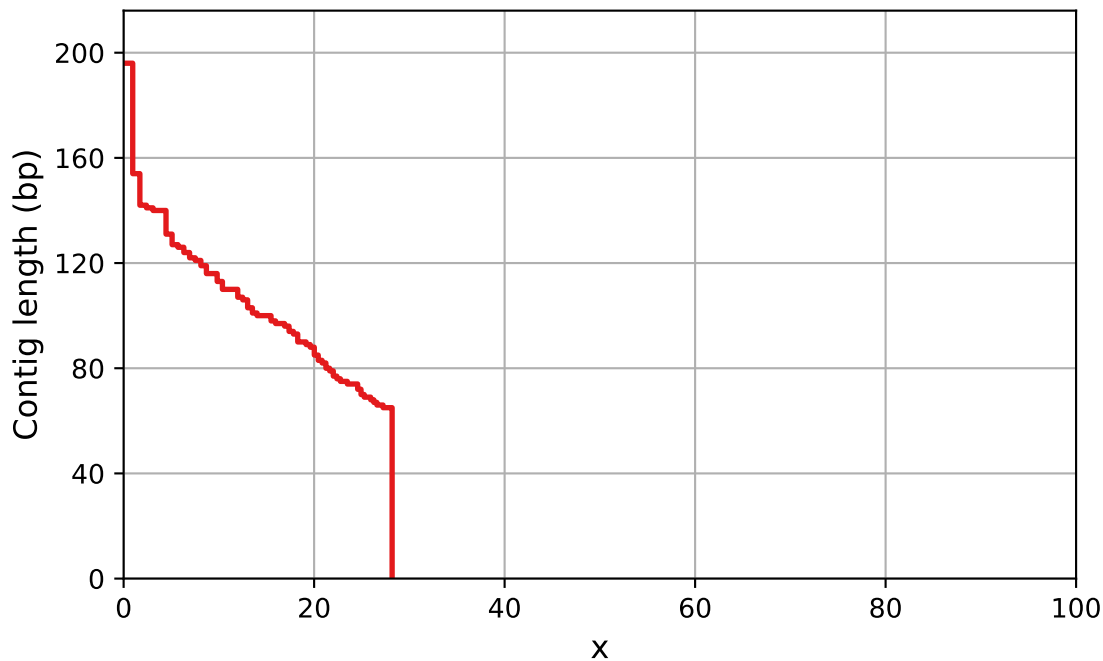
FRCurve (misassemblies)



Cumulative length (aligned contigs)

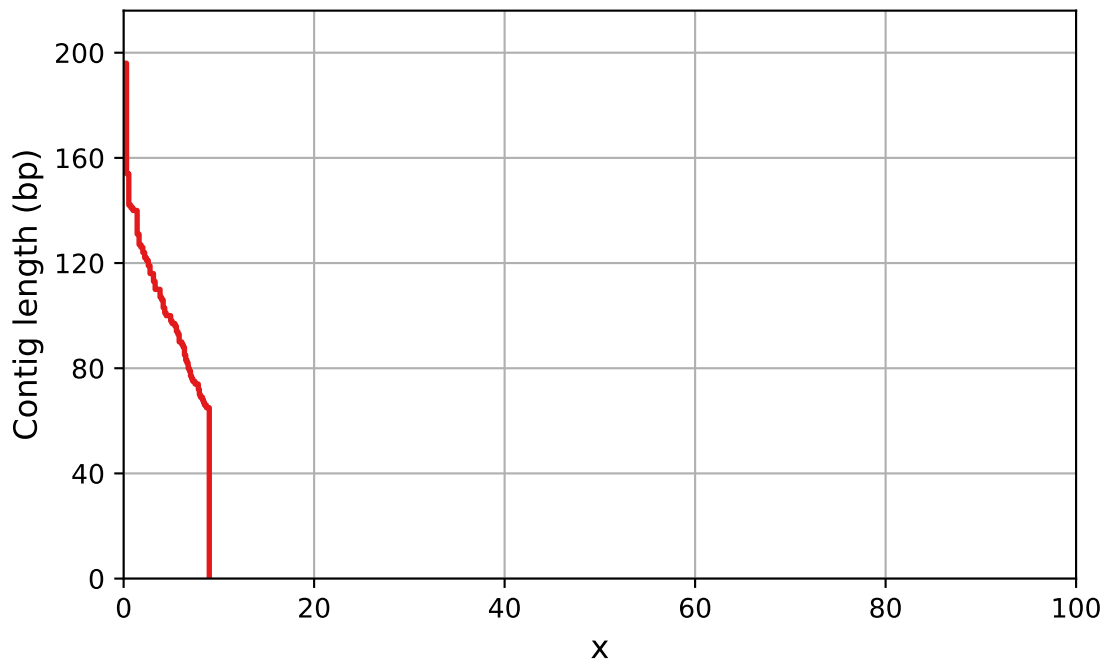


NAx



contigs

# NGAx



— contigs