

Report

	contigs
# contigs (>= 0 bp)	175
# contigs (>= 1000 bp)	46
# contigs (>= 5000 bp)	36
# contigs (>= 10000 bp)	27
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	3101862
Total length (>= 1000 bp)	3075896
Total length (>= 5000 bp)	3047854
Total length (>= 10000 bp)	2985047
Total length (>= 25000 bp)	2867268
Total length (>= 50000 bp)	2724972
# contigs	53
Largest contig	458911
Total length	3080955
Reference length	2919198
GC (%)	37.64
Reference GC (%)	37.88
N50	162629
NG50	198407
N75	102479
NG75	125622
L50	6
LG50	5
L75	11
LG75	10
# misassemblies	169
# misassembled contigs	20
Misassembled contigs length	2682392
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# unaligned contigs	17 + 31 part
Unaligned length	550026
Genome fraction (%)	84.052
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	382.98
# indels per 100 kbp	14.47
Largest alignment	137660
Total aligned length	2529541
NA50	24242
NGA50	26511
NA75	5028
NGA75	9362
LA50	33
LGA50	29
LA75	88
LGA75	72

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

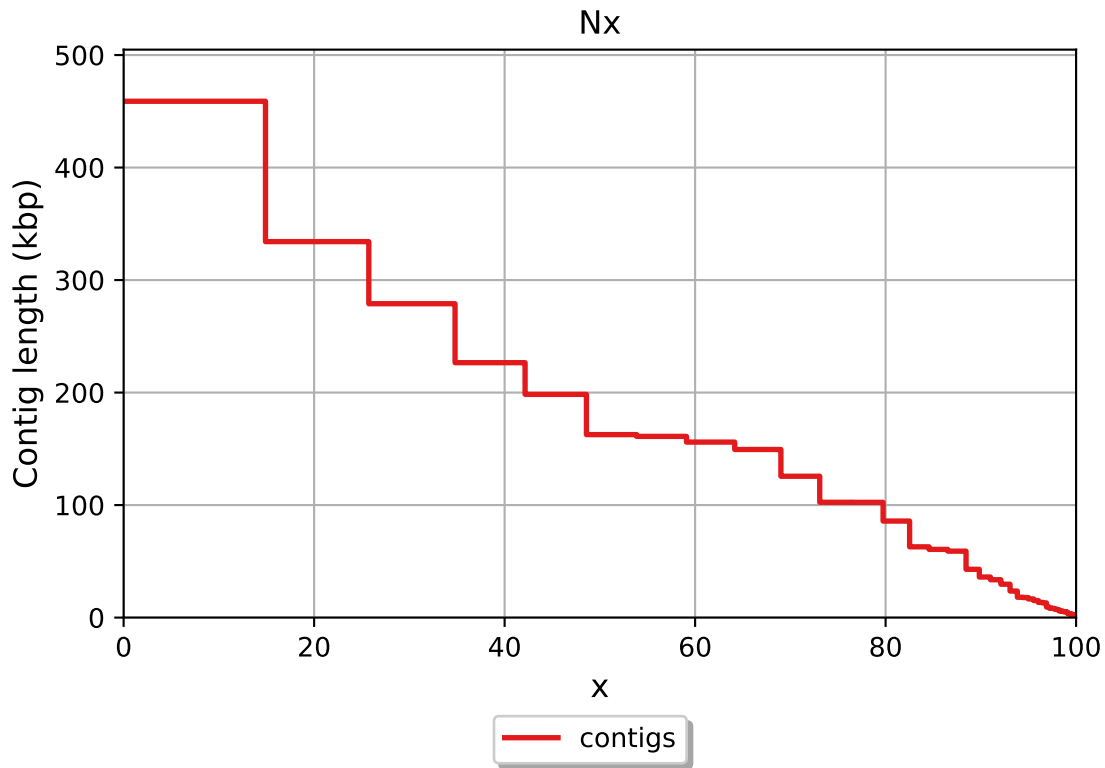
	contigs
# misassemblies	169
# contig misassemblies	169
# c. relocations	161
# c. translocations	5
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	20
Misassembled contigs length	2682392
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	8
# mismatches	9397
# indels	355
# indels (<= 5 bp)	320
# indels (> 5 bp)	35
Indels length	1371

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

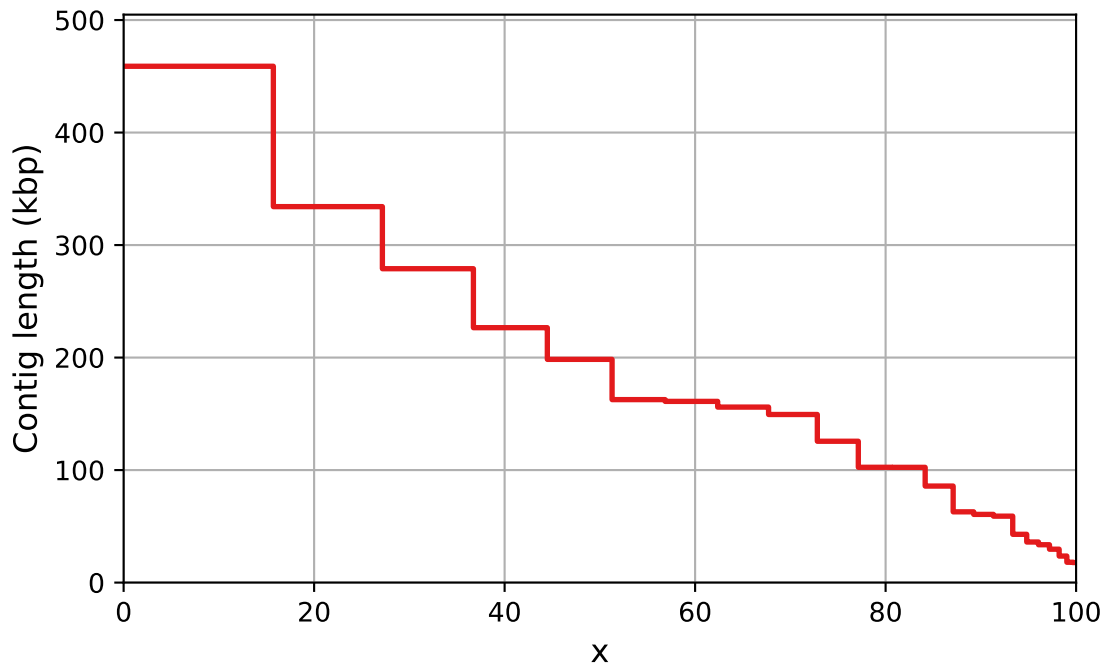
## Unaligned report

	contigs
# fully unaligned contigs	17
Fully unaligned length	48447
# partially unaligned contigs	31
Partially unaligned length	501579
# N's	0

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

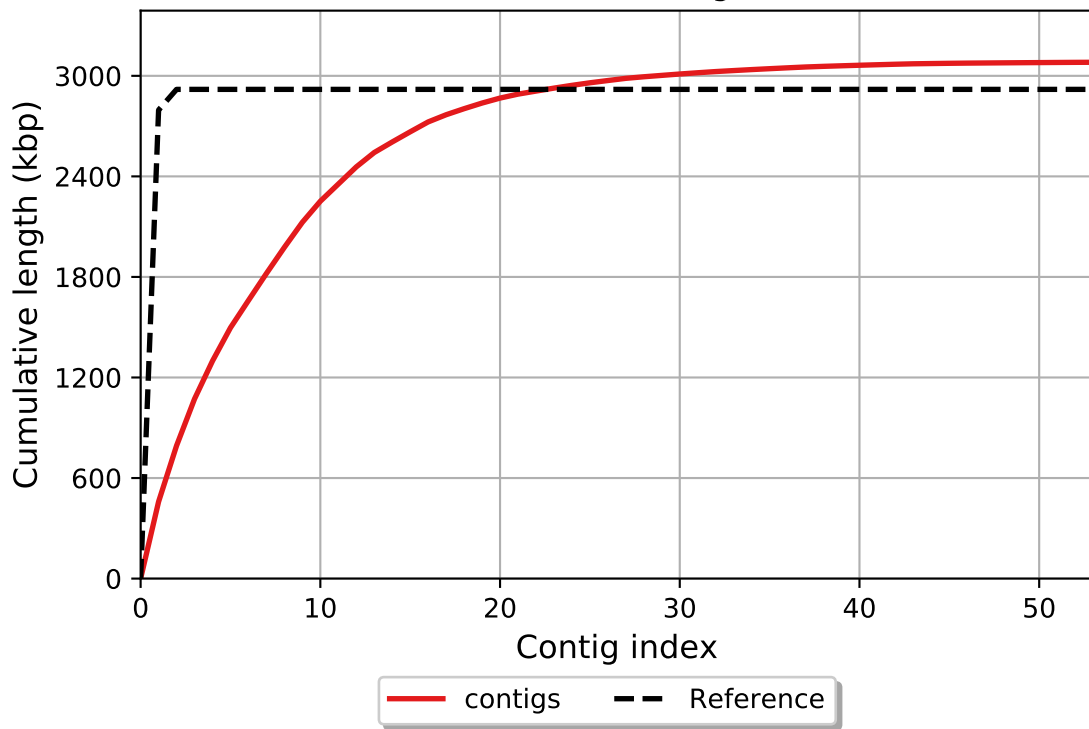


NGx

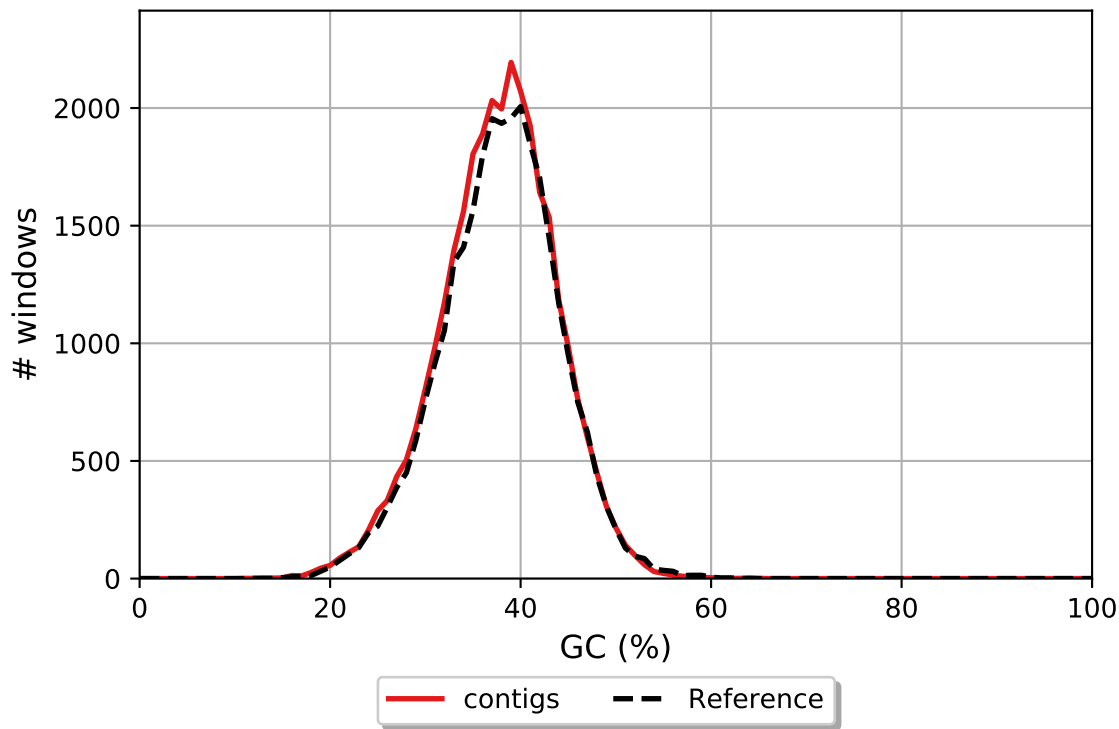


contigs

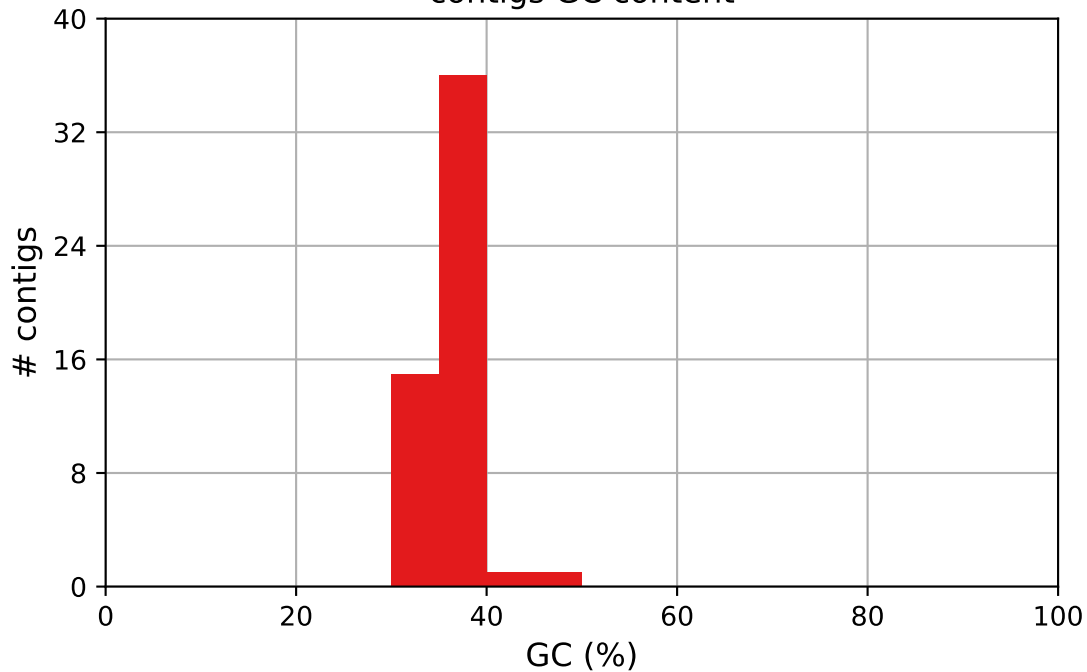
Cumulative length



# GC content



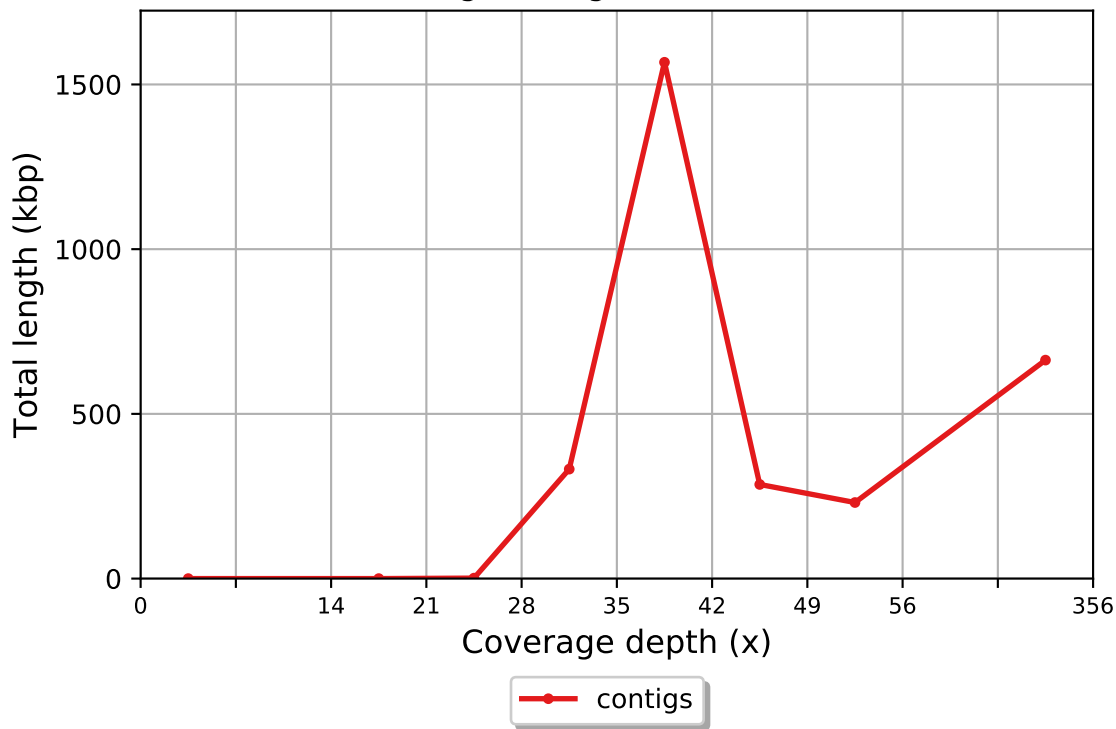
contigs GC content



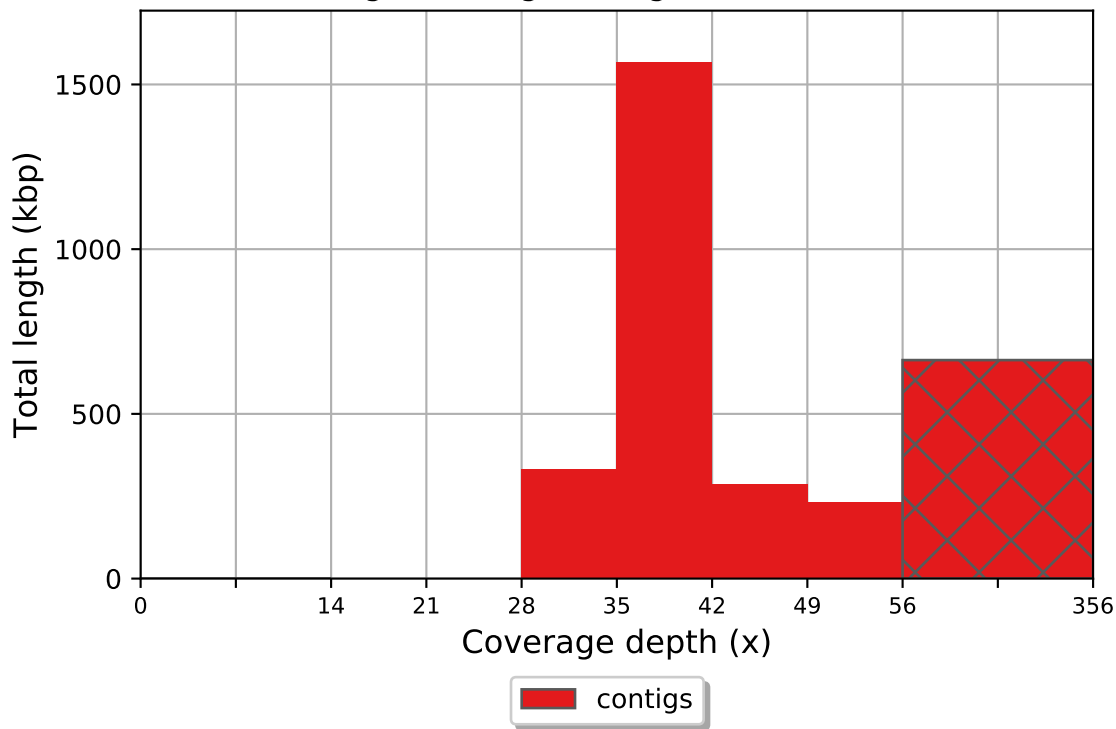
contigs



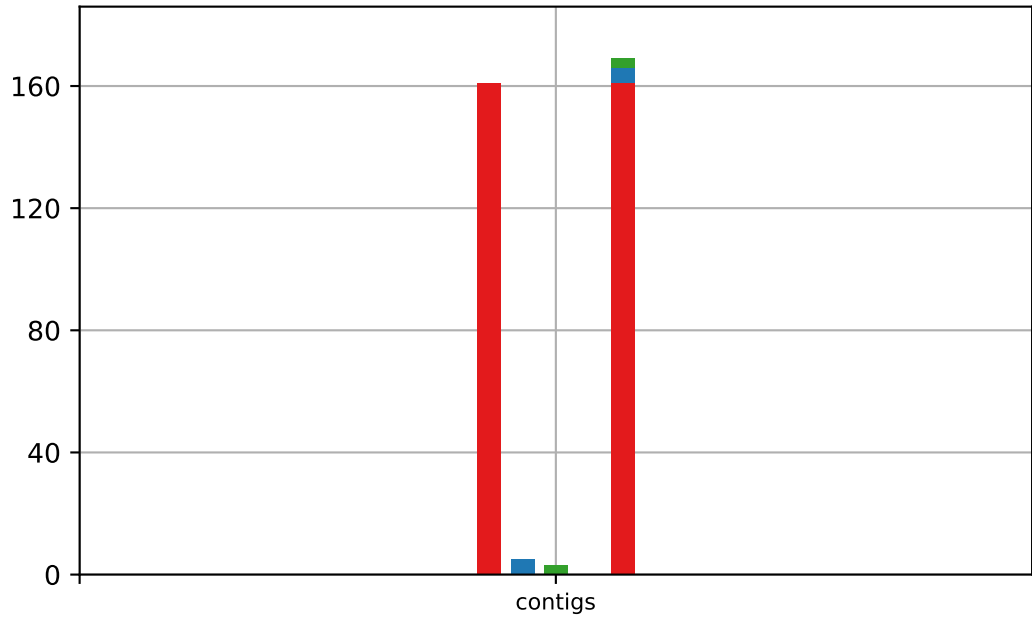
Coverage histogram (bin size: 7x)



contigs coverage histogram (bin size: 7x)



## Misassemblies



# relocations

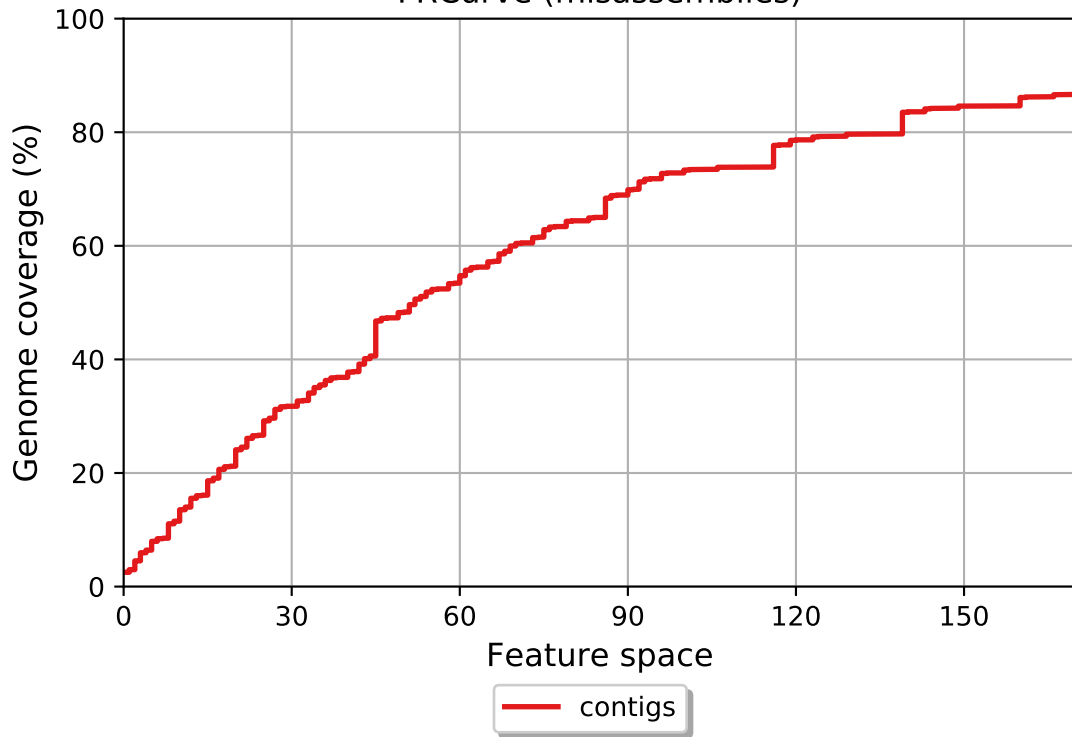


# translocations

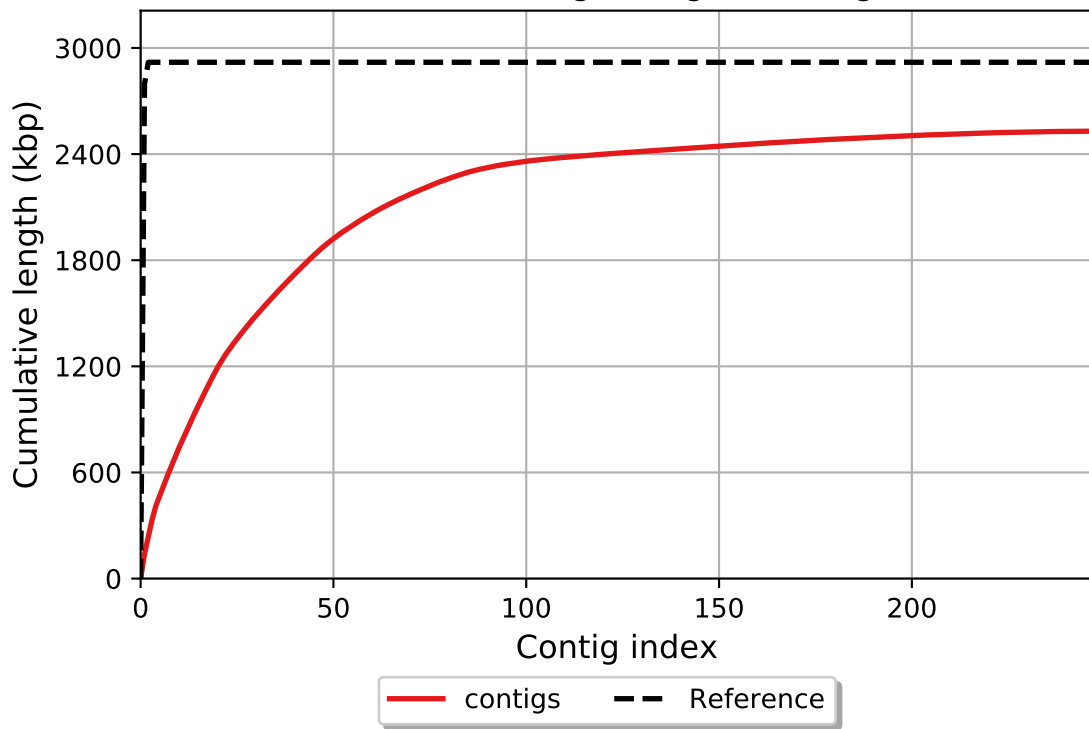


# inversions

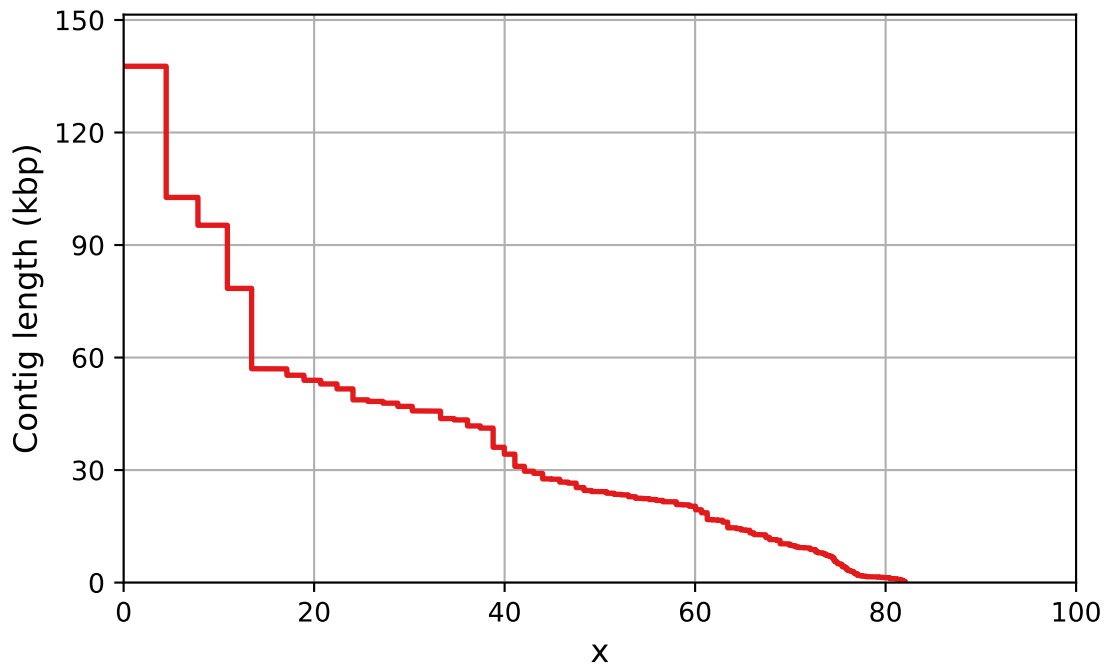
FRCurve (misassemblies)



Cumulative length (aligned contigs)

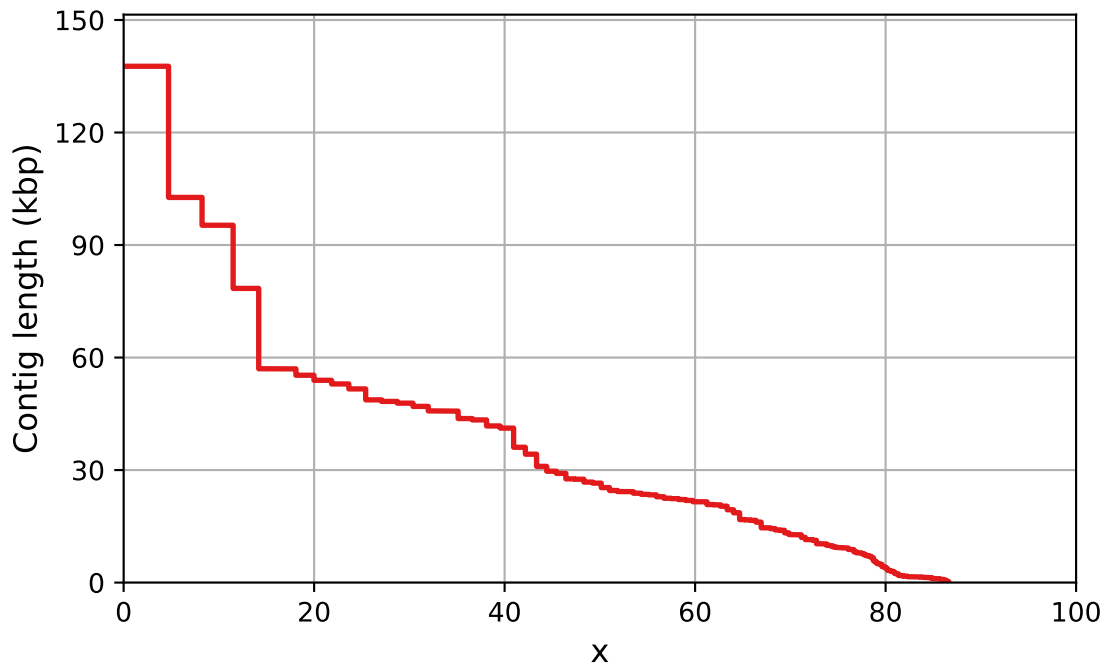


NAx



contigs

# NGAx



contigs