

Report

	contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	12979
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	26
Largest contig	3139
Total length	25026
Reference length	2664173
GC (%)	36.36
Reference GC (%)	36.60
N50	1031
NG50	-
N90	576
NG90	-
auN	1309.7
auNG	12.3
L50	8
LG50	-
L90	22
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	4974
Genome fraction (%)	0.747
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2260.54
# indels per 100 kbp	95.23
Largest alignment	1644
Total aligned length	19951
NA50	688
NGA50	-
NA90	-
NGA90	-
auNA	716.8
auNGA	6.7
LA50	13
LGA50	-
LA90	-
LGA90	-

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

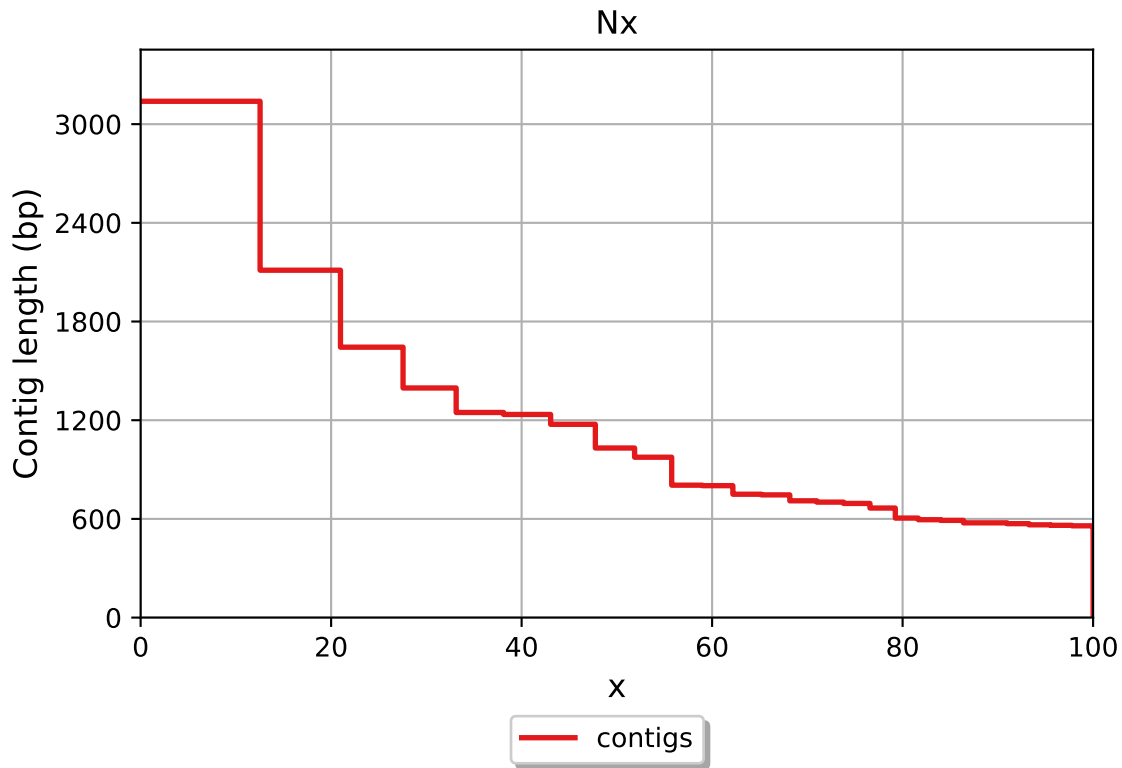
	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	451
# indels	19
# indels (<= 5 bp)	16
# indels (> 5 bp)	3
Indels length	135

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).

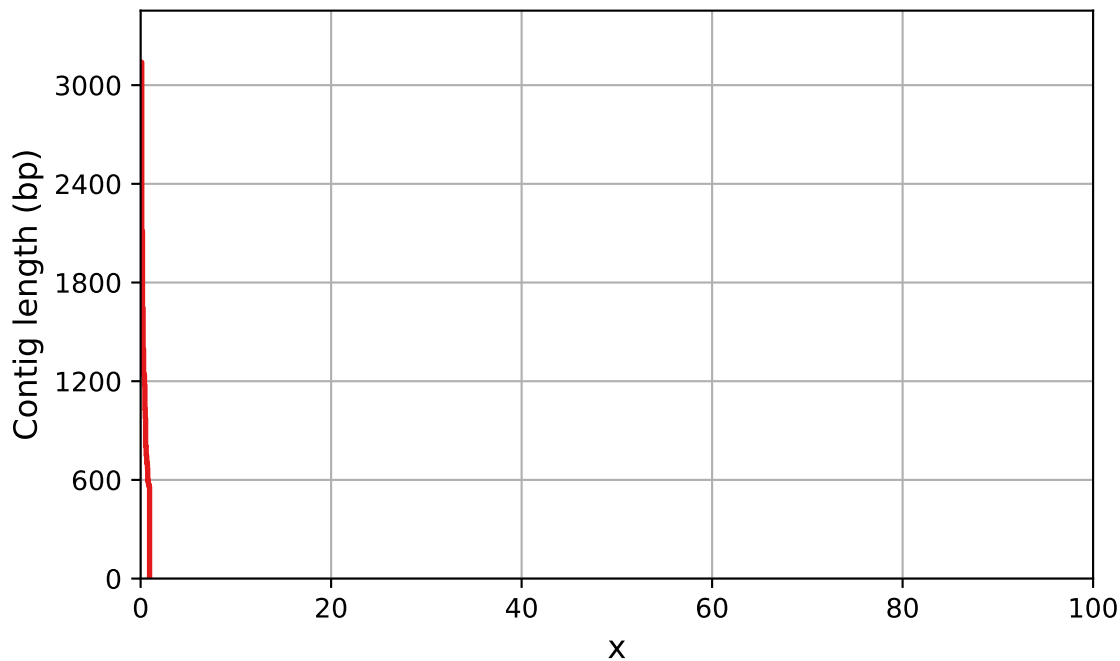
## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	4974
# N's	0

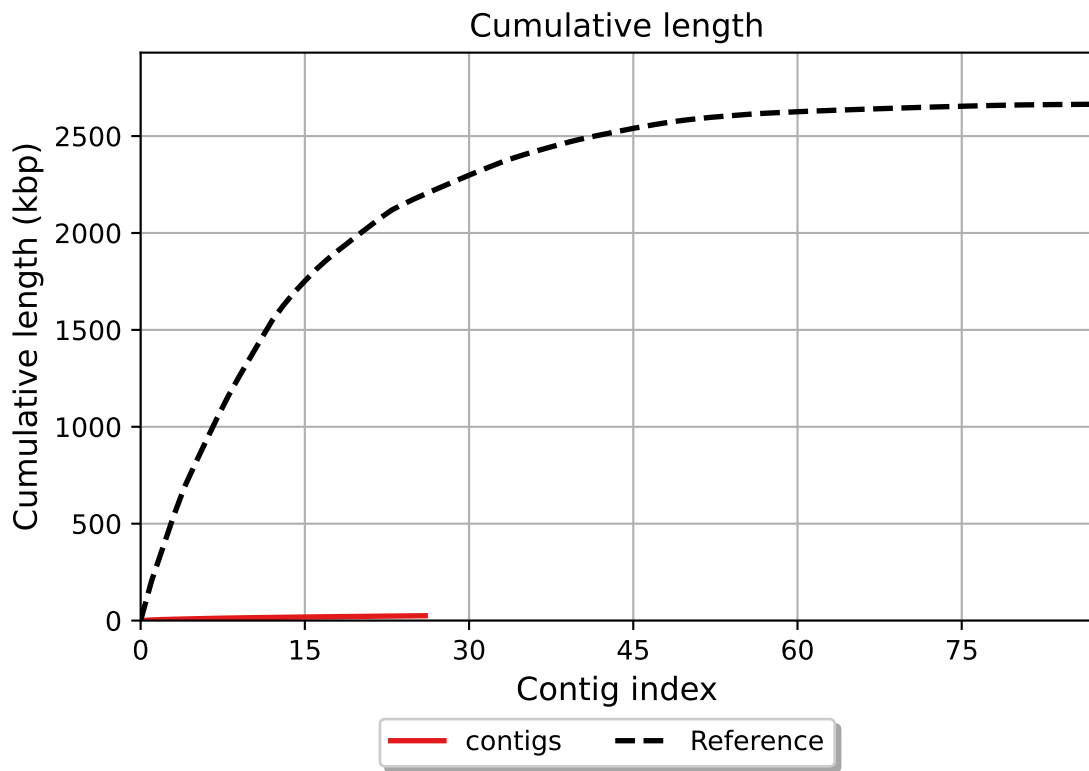
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

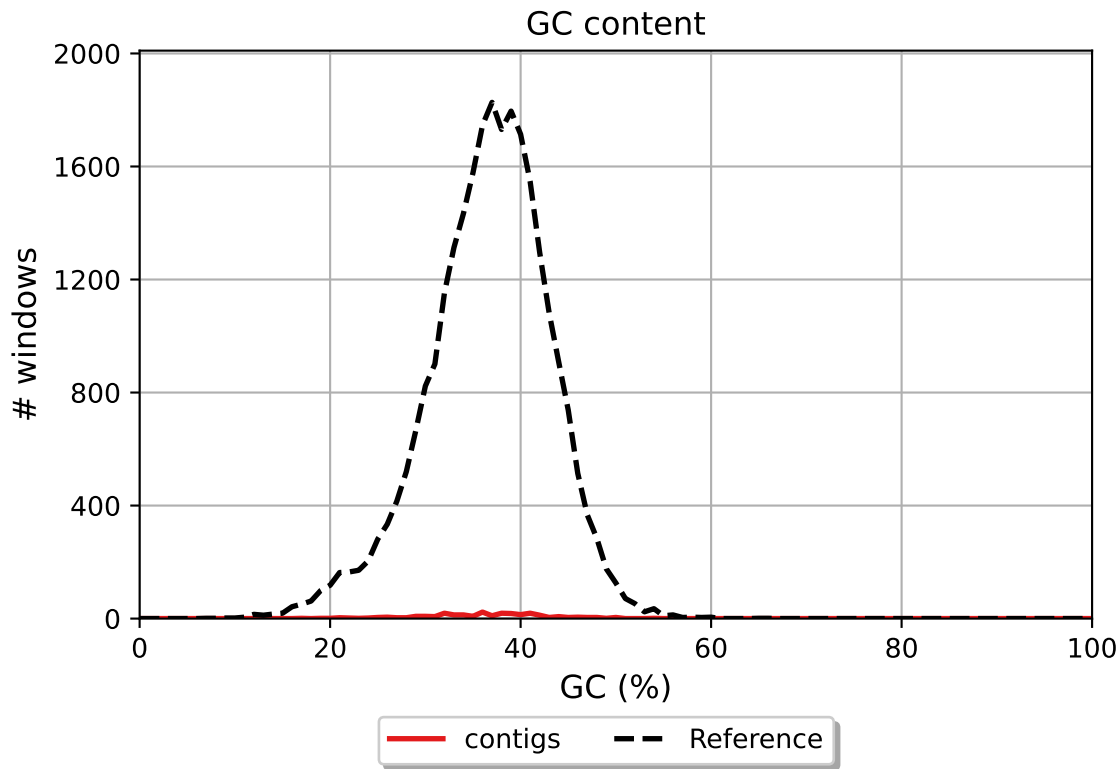


# NGx

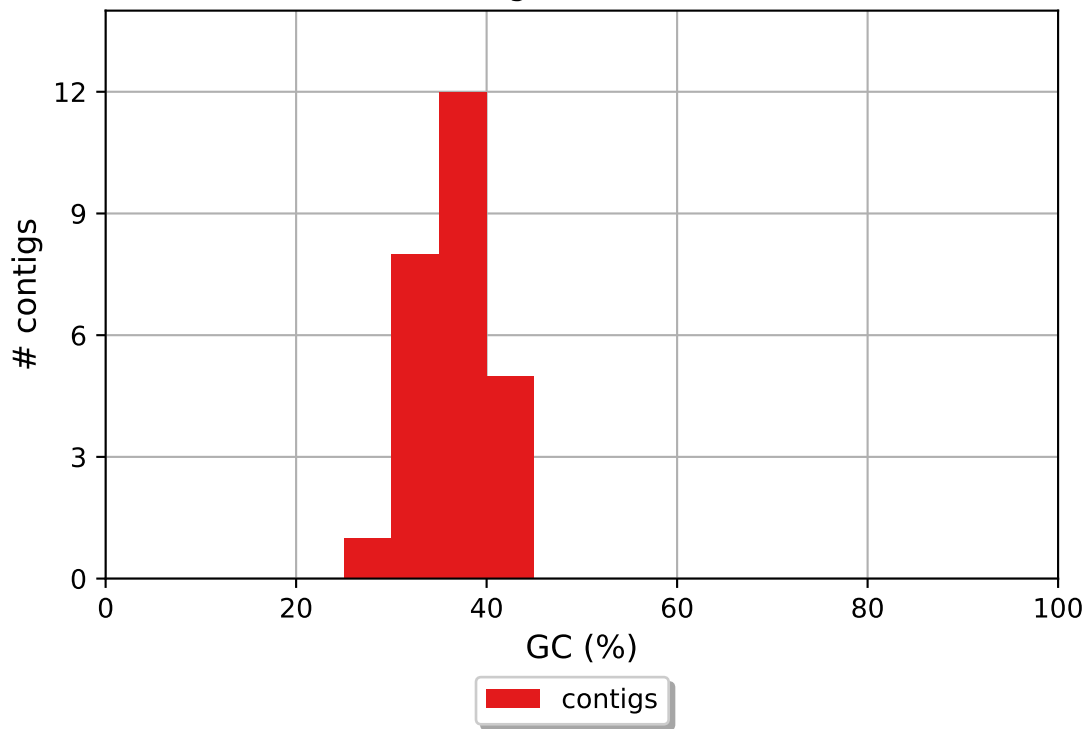


— contigs



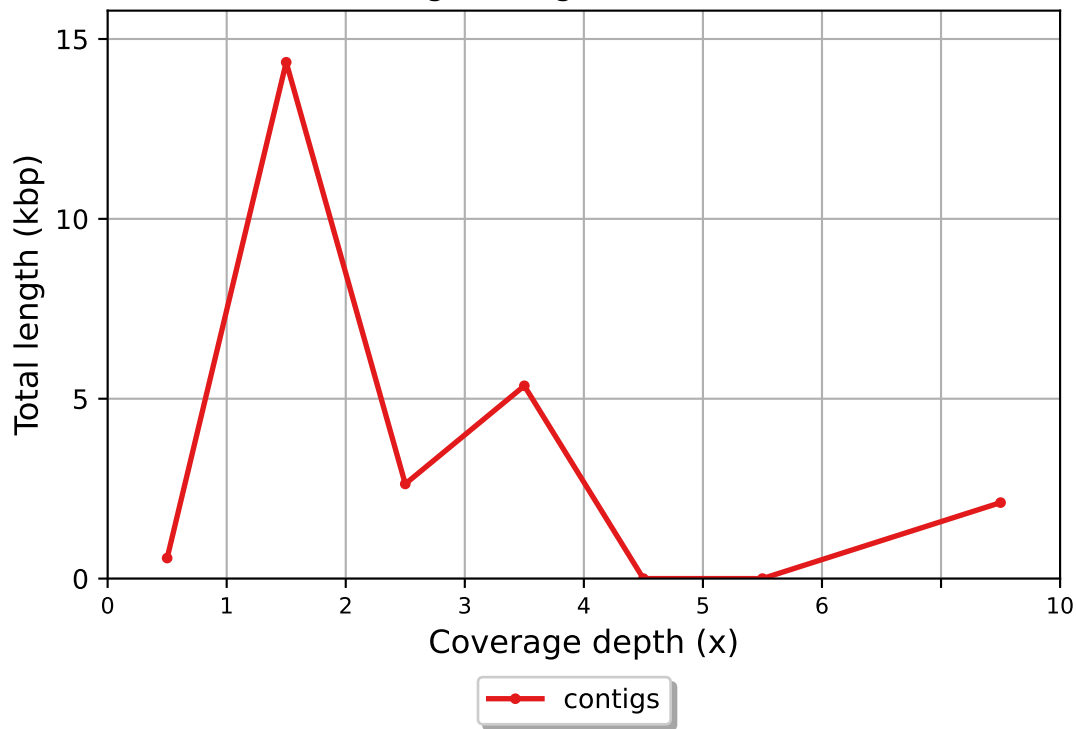


contigs GC content

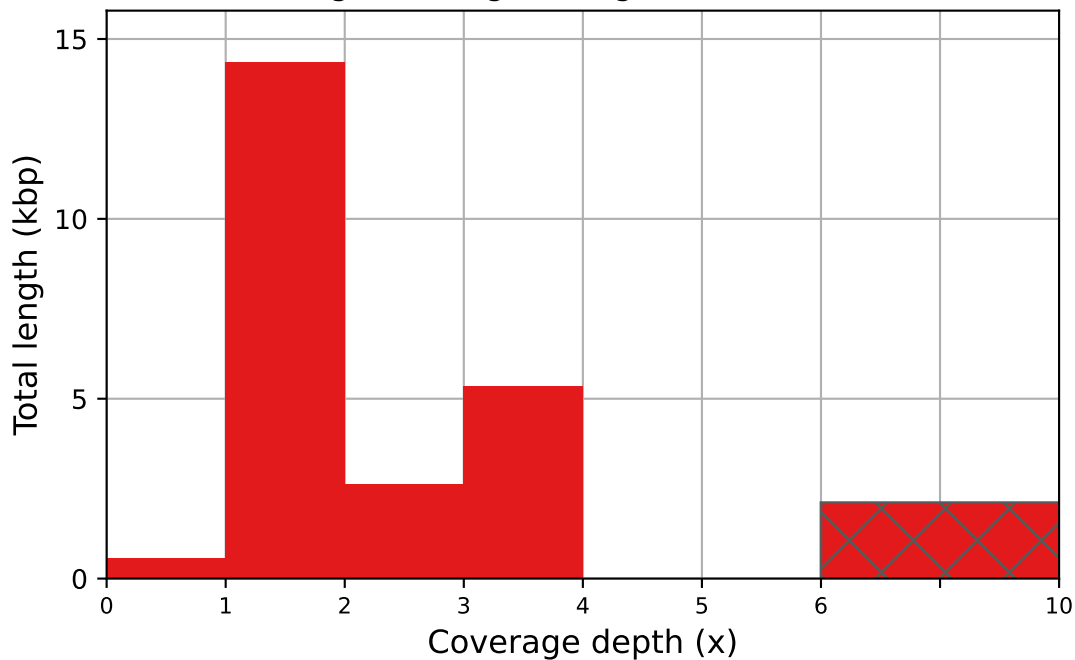




Coverage histogram (bin size: 1x)

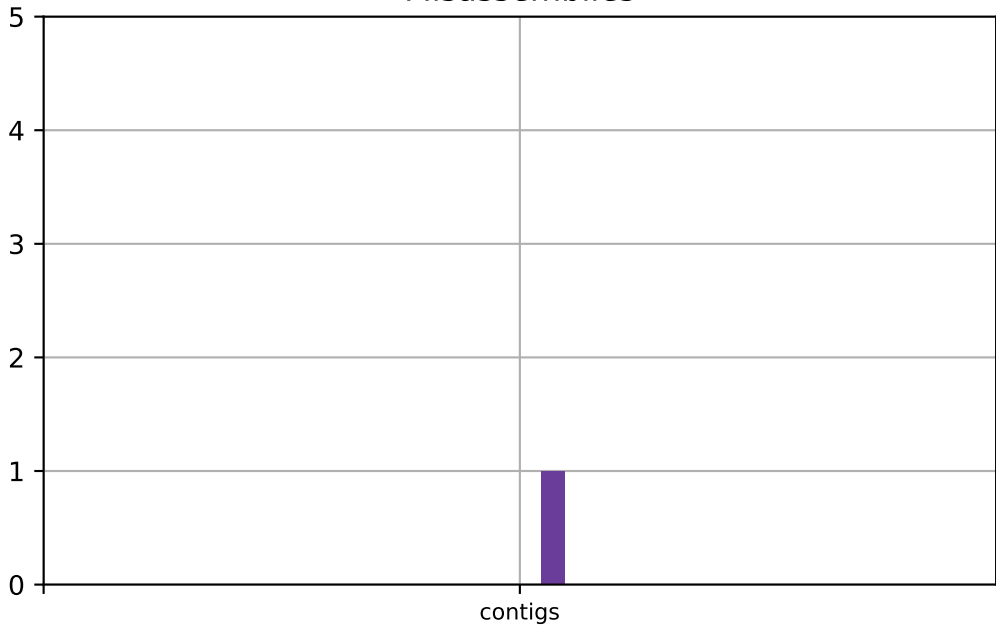


contigs coverage histogram (bin size: 1x)



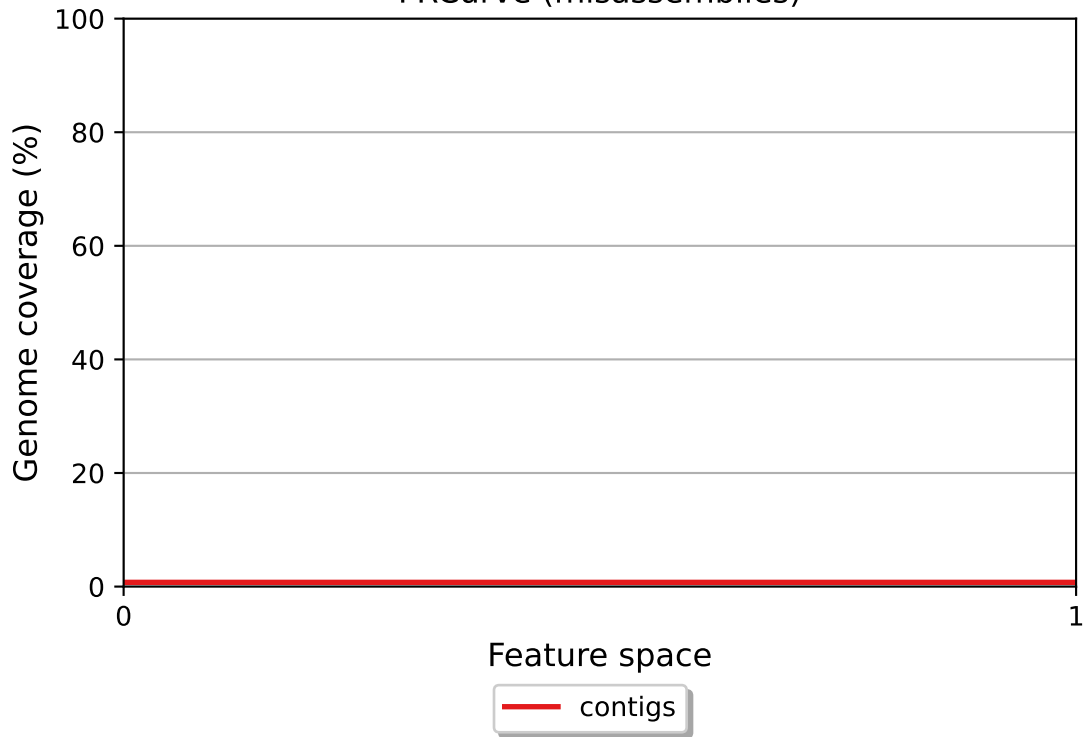
contigs

## Misassemblies

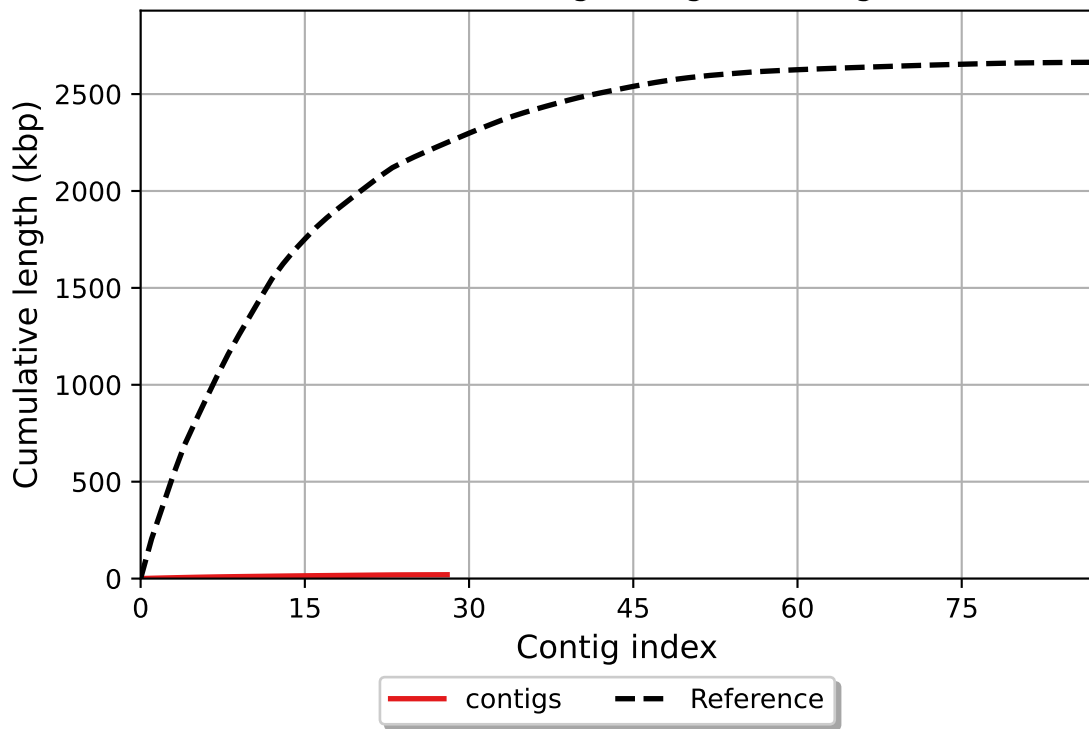


# interspecies translocations

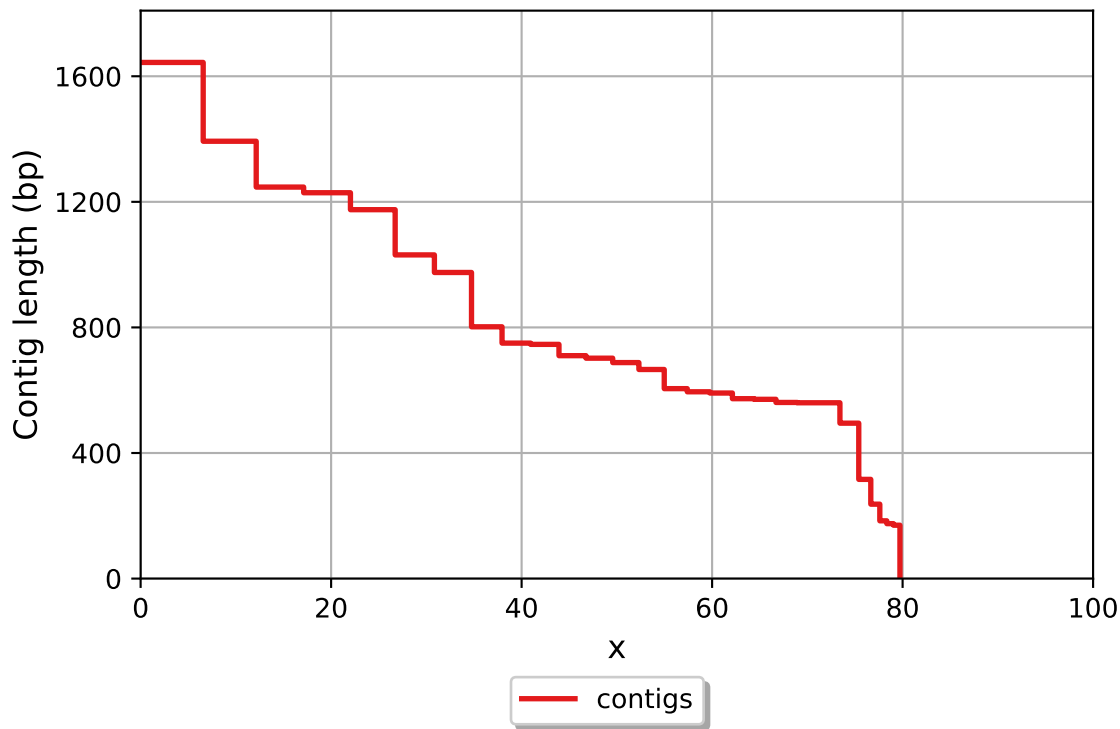
FRCurve (misassemblies)



Cumulative length (aligned contigs)



# NAx



# NGAx

