

Report

	contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	9737
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	26
Largest contig	2009
Total length	22633
Reference length	2664814
GC (%)	37.21
Reference GC (%)	36.58
N50	849
NG50	-
N90	576
NG90	-
auN	1025.9
auNG	8.7
L50	9
LG50	-
L90	22
LG90	-
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	2858
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	568
Genome fraction (%)	0.825
Duplication ratio	0.988
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2233.27
# indels per 100 kbp	82.88
Largest alignment	1644
Total aligned length	21717
NA50	746
NGA50	-
NA90	475
NGA90	-
auNA	852.4
auNGA	7.2
LA50	11
LGA50	-
LA90	26
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

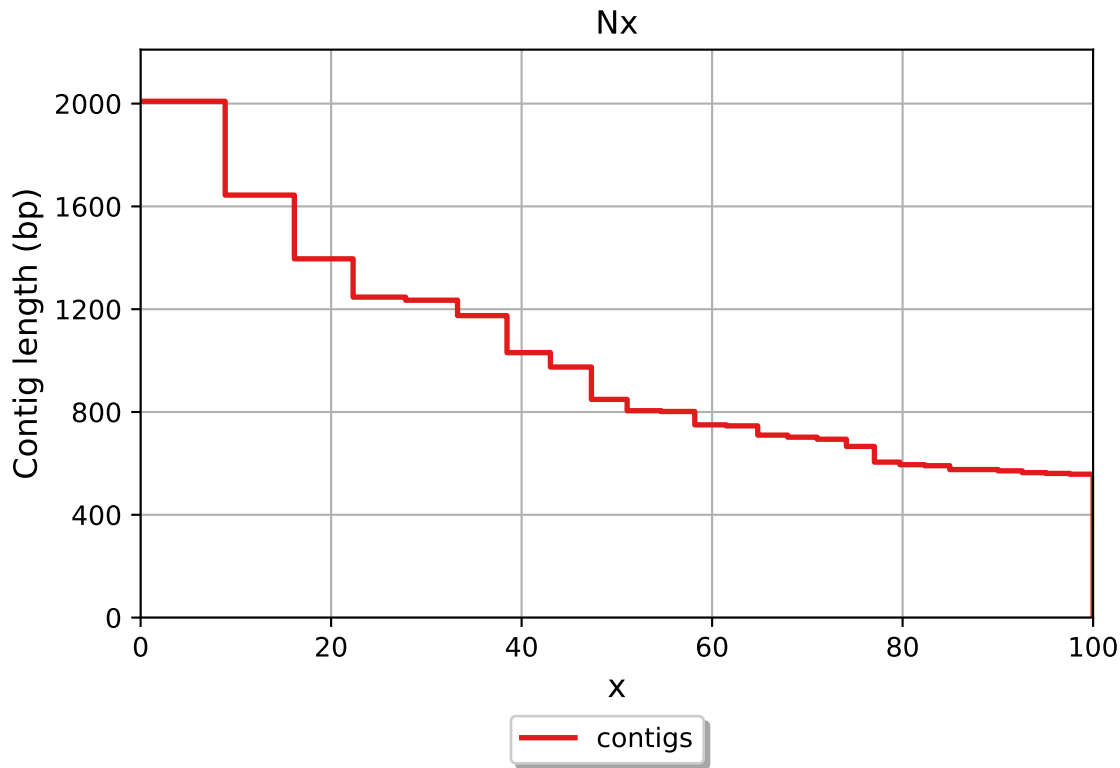
	contigs
# misassemblies	3
# contig misassemblies	3
# c. relocations	0
# c. translocations	3
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	2858
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	485
# indels	18
# indels (≤ 5 bp)	15
# indels (> 5 bp)	3
Indels length	134

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).

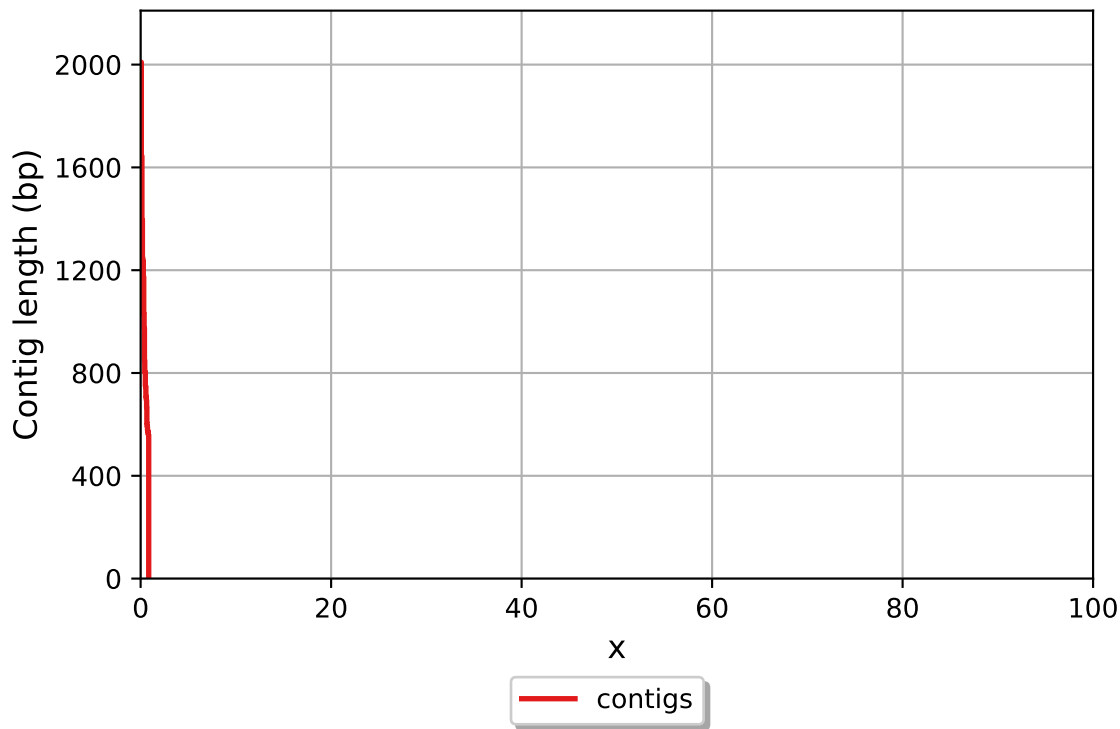
Unaligned report

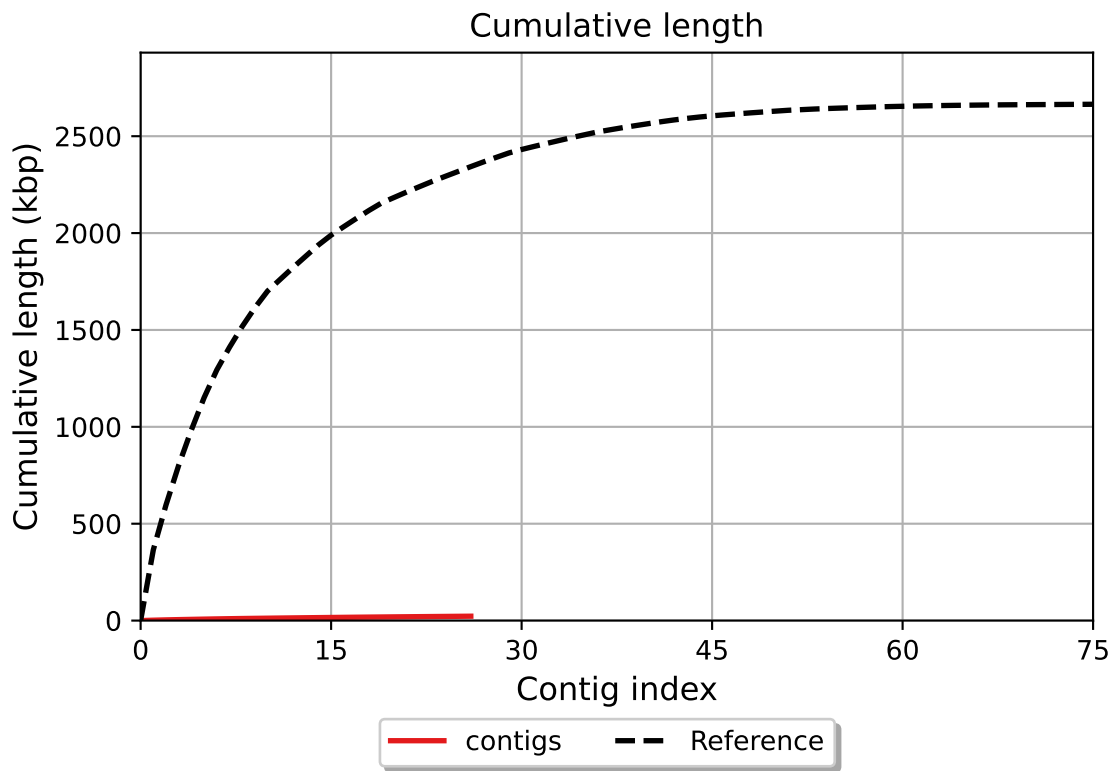
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	568
# N's	0

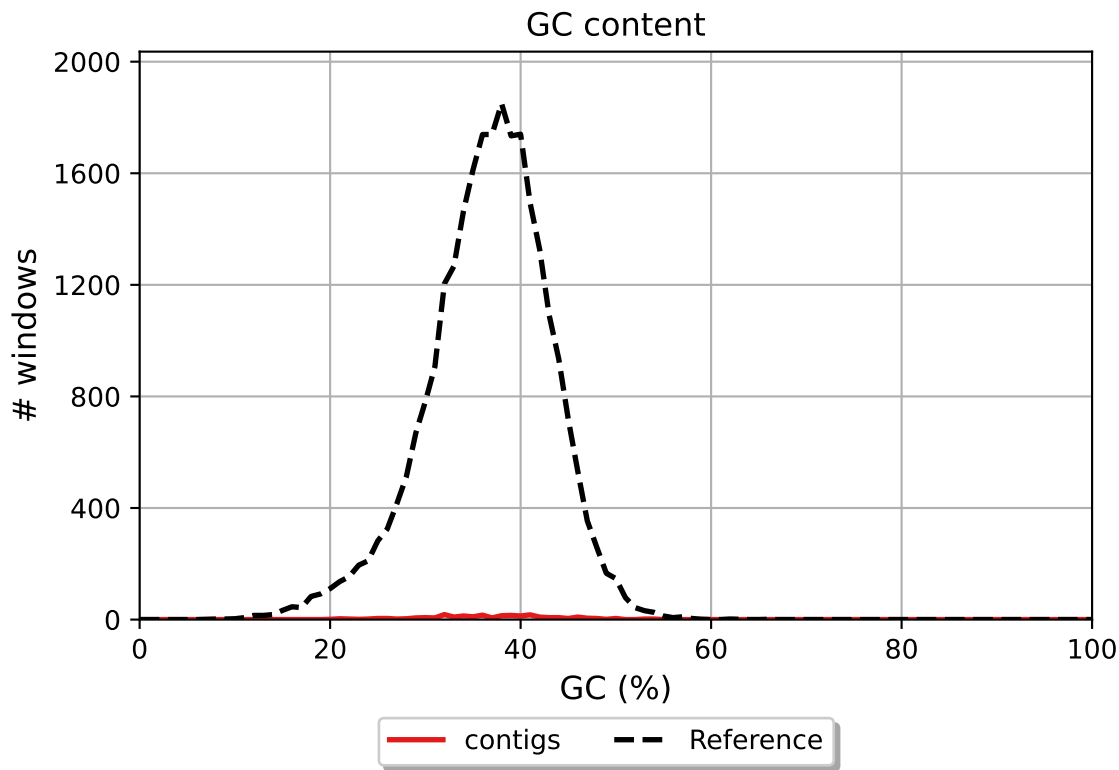
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



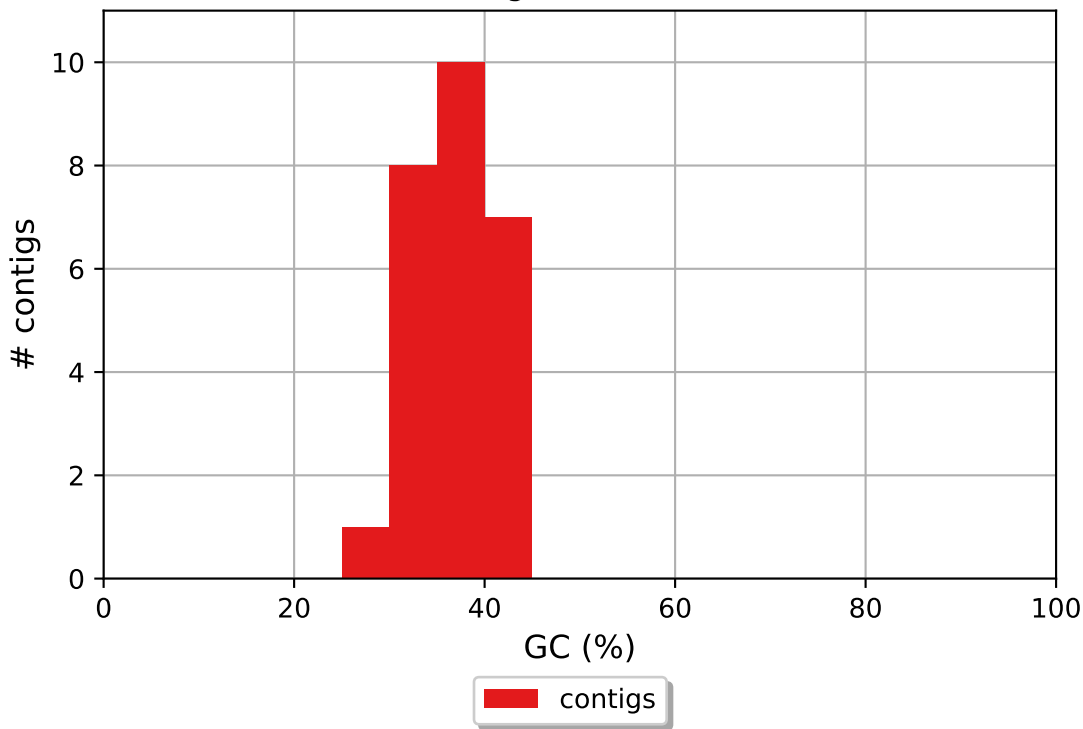
NGx



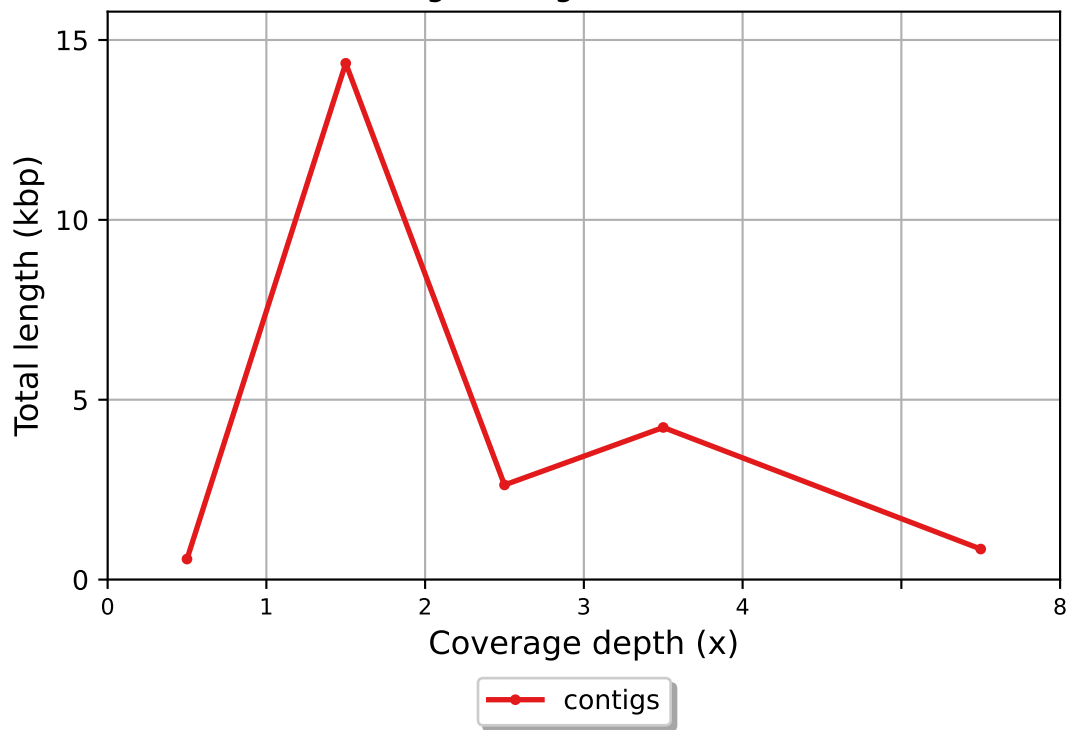




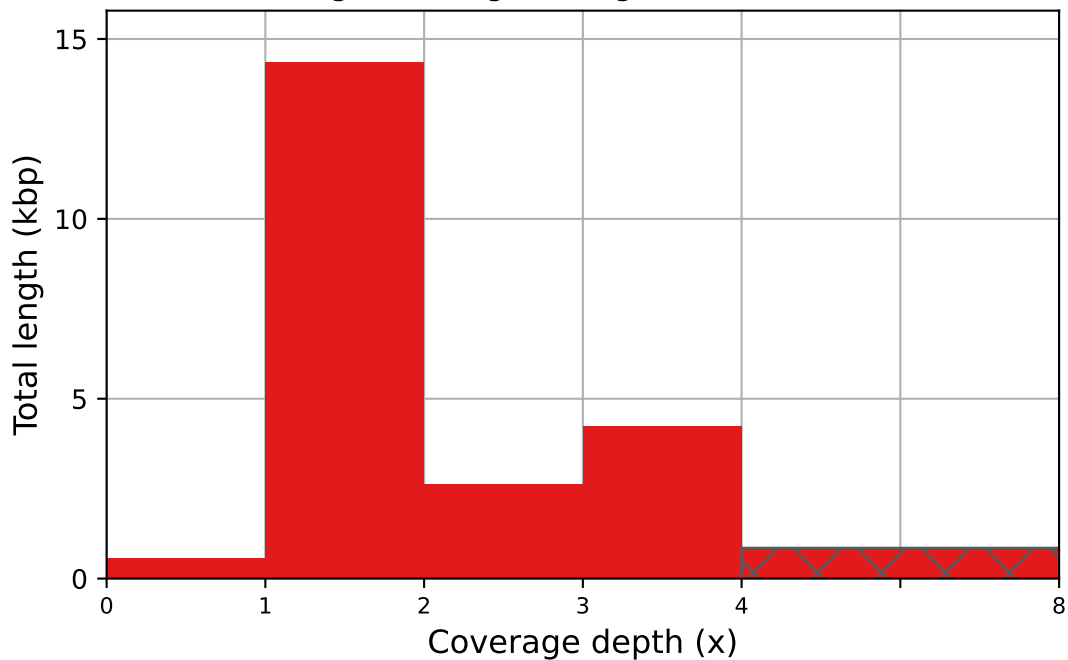
contigs GC content



Coverage histogram (bin size: 1x)

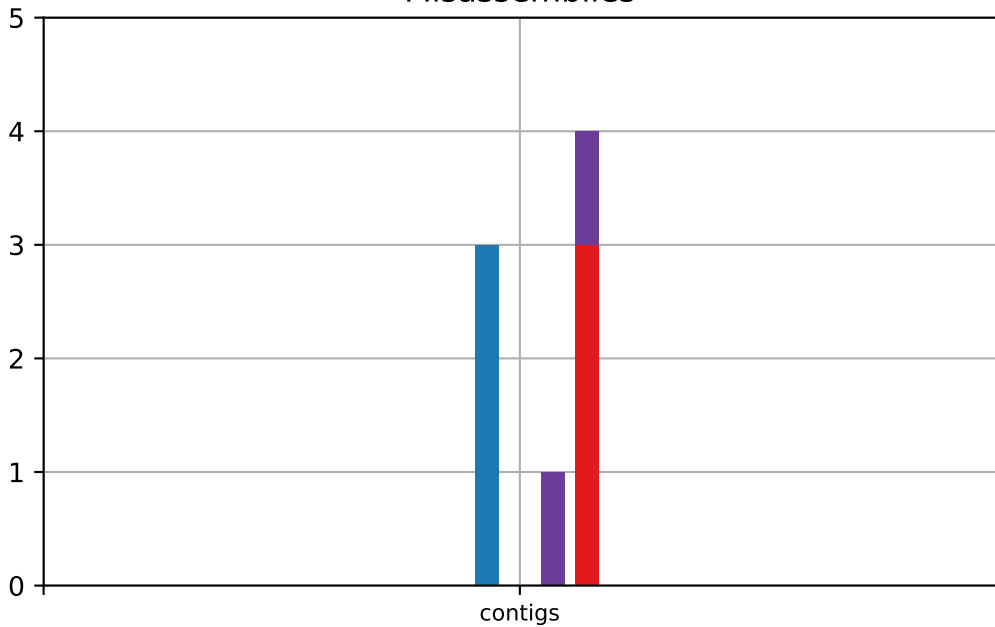


contigs coverage histogram (bin size: 1x)



contigs

Misassemblies

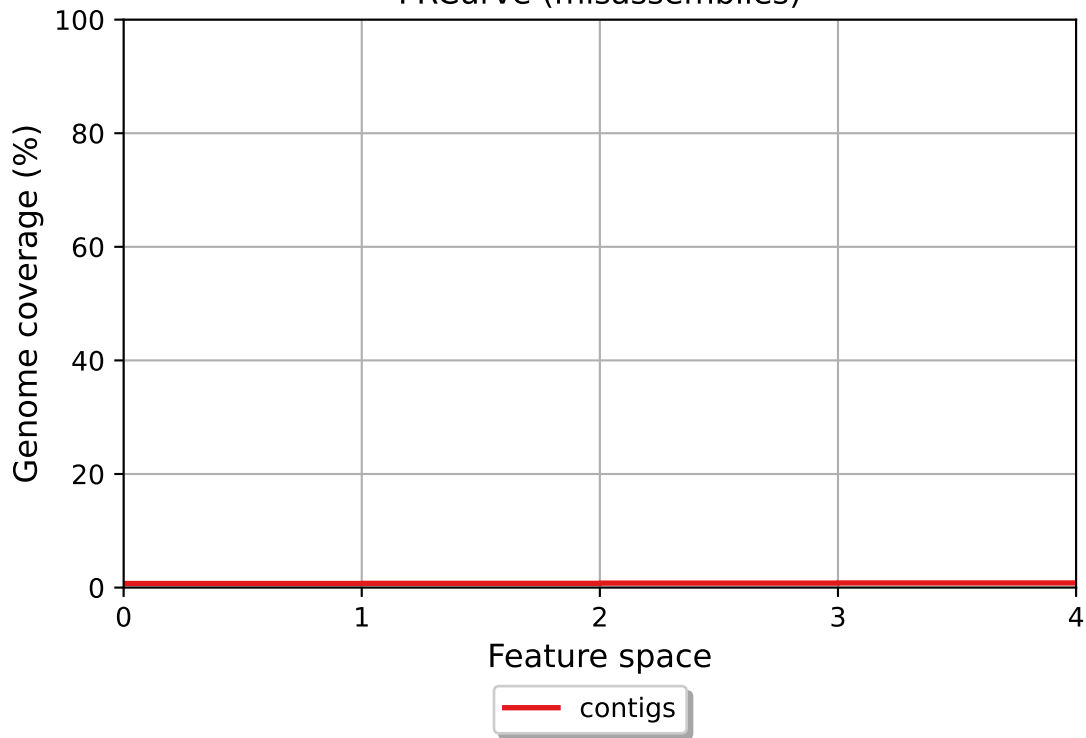


translocations

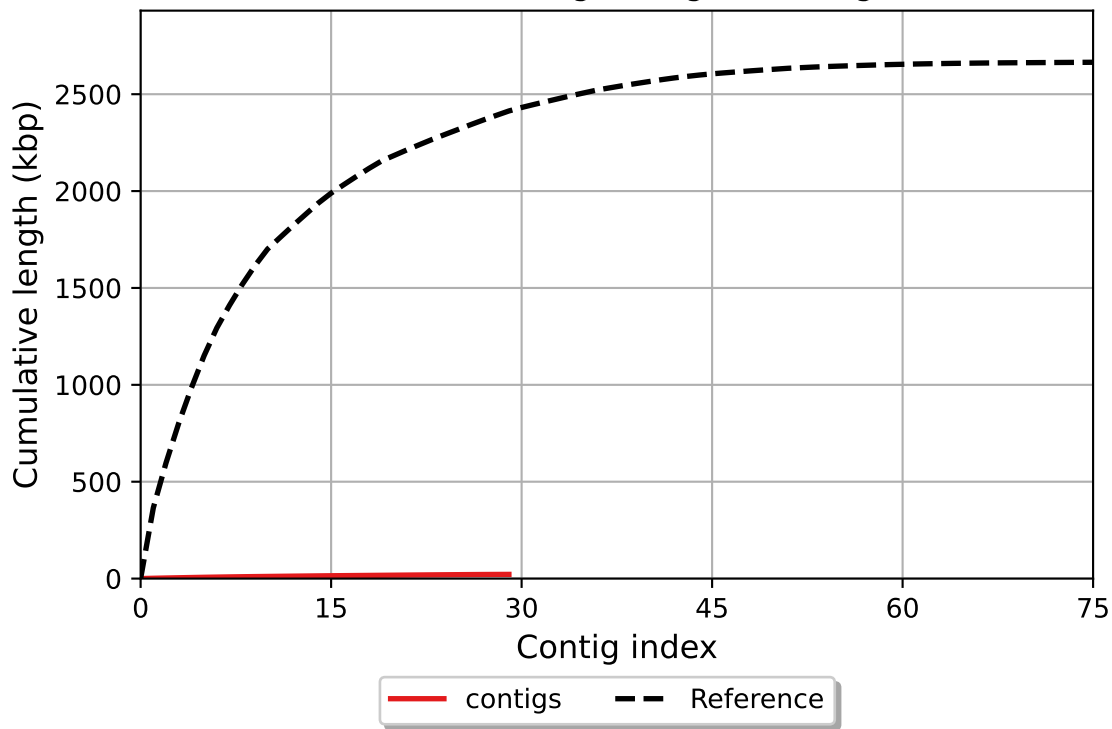


interspecies translocations

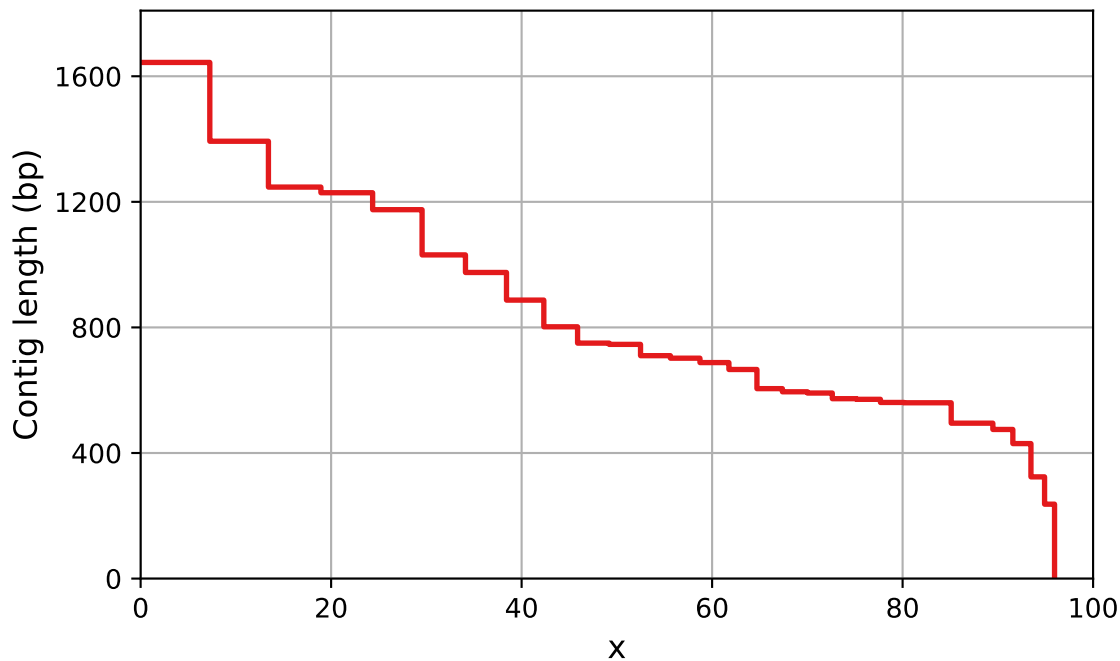
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



contigs

NGAx

