

Report

	final.contigs
# contigs (>= 1000 bp)	118
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	147772
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	854
Largest contig	2150
Total length	644137
Reference length	3551878
GC (%)	50.21
Reference GC (%)	50.65
N50	742
NG50	-
N90	545
NG90	-
auN	836.8
auNG	151.7
L50	324
LG50	-
L90	731
LG90	-
# misassemblies	8
# misassembled contigs	7
Misassembled contigs length	6746
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 35 part
Unaligned length	27453
Genome fraction (%)	16.211
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	961.47
# indels per 100 kbp	37.58
Largest alignment	2072
Total aligned length	580155
NA50	680
NGA50	-
NA90	94
NGA90	-
auNA	694.0
auNGA	125.9
LA50	360
LGA50	-
LA90	862
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

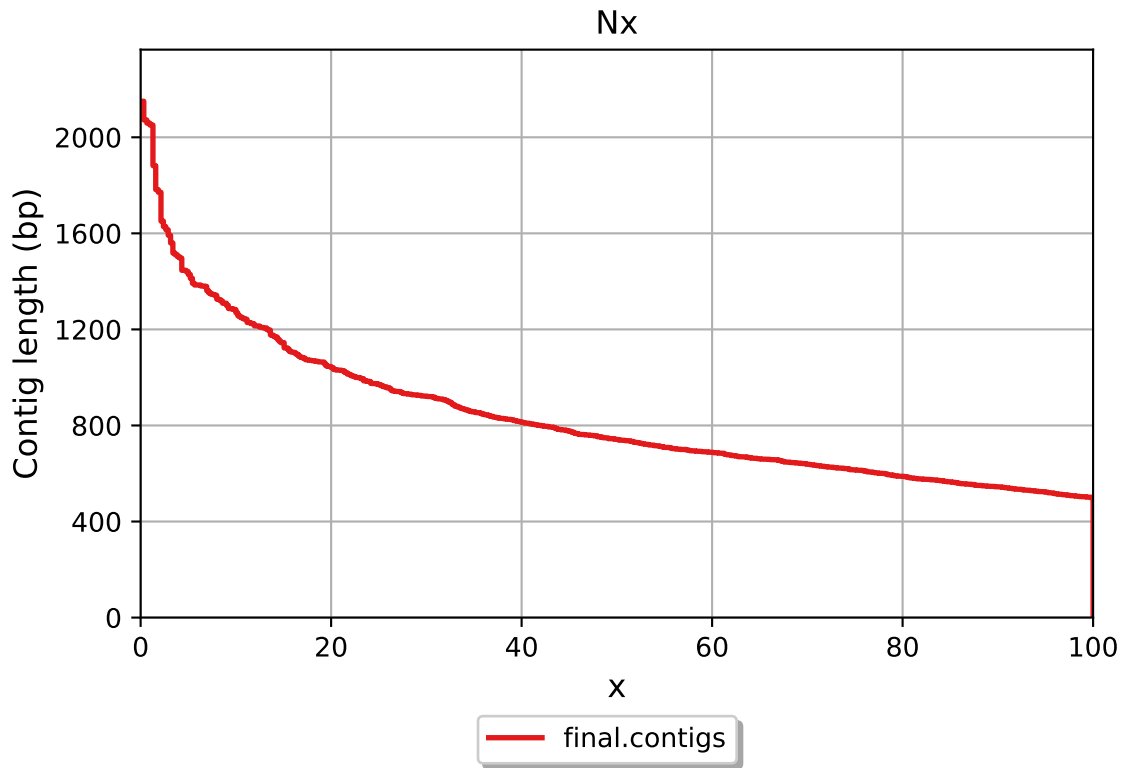
	final.contigs
# misassemblies	8
# contig misassemblies	8
# c. relocations	2
# c. translocations	6
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	6746
# possibly misassembled contigs	13
# possible misassemblies	13
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	5578
# indels	218
# indels (<= 5 bp)	203
# indels (> 5 bp)	15
Indels length	1158

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).

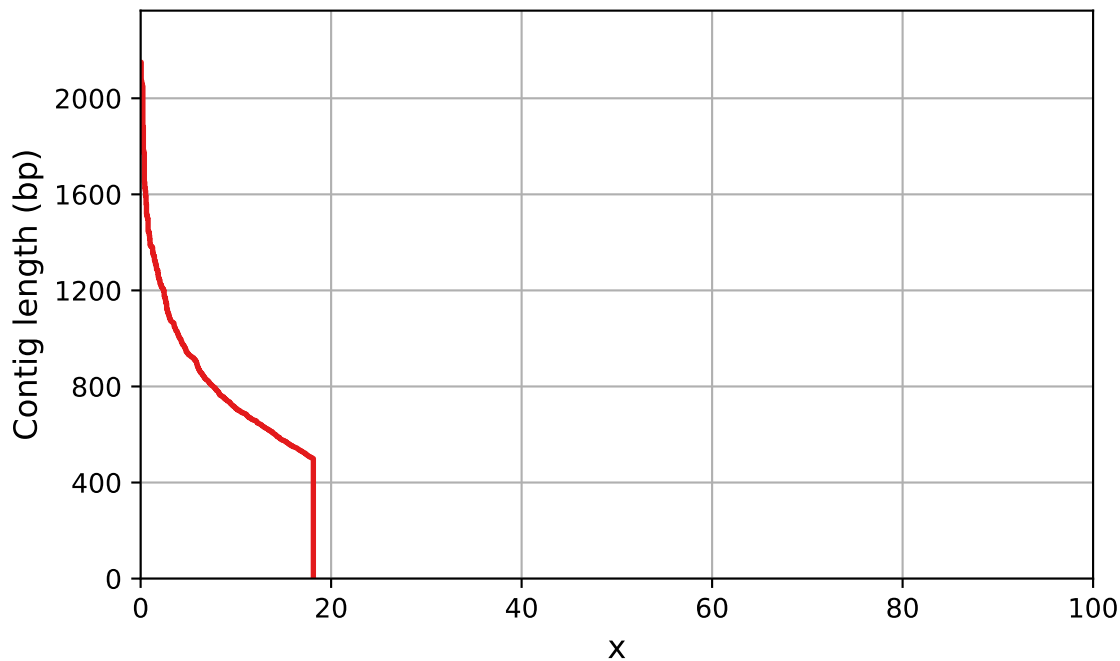
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	35
Partially unaligned length	27453
# N's	0

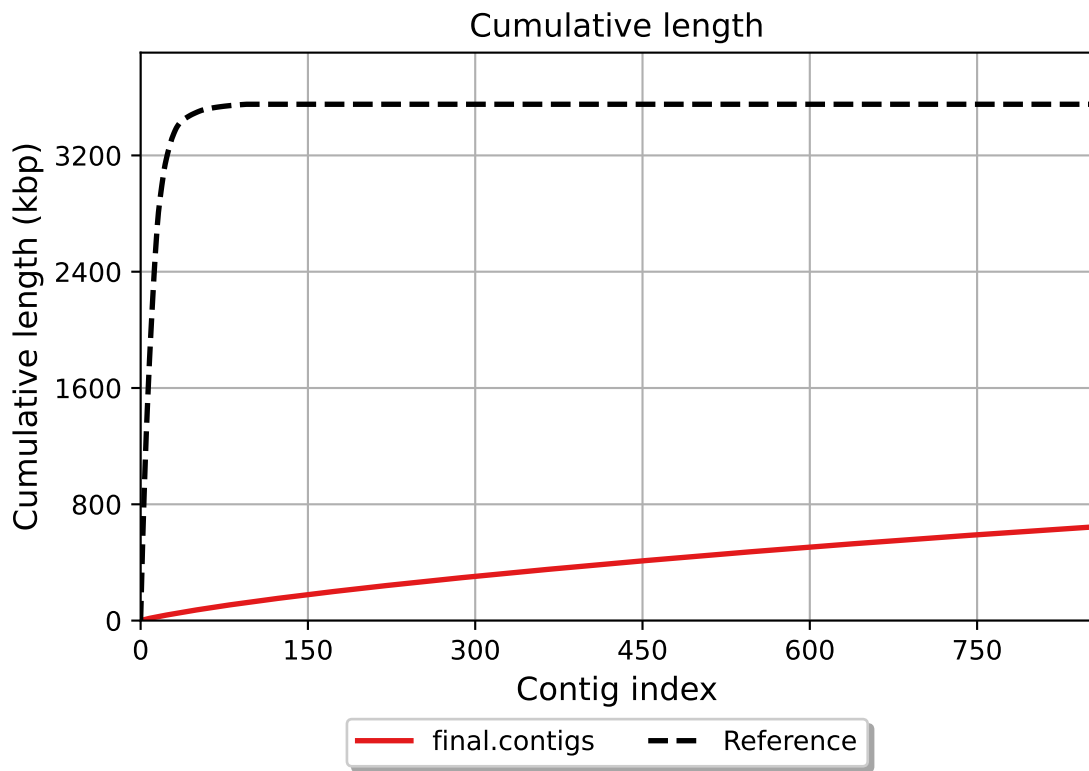
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

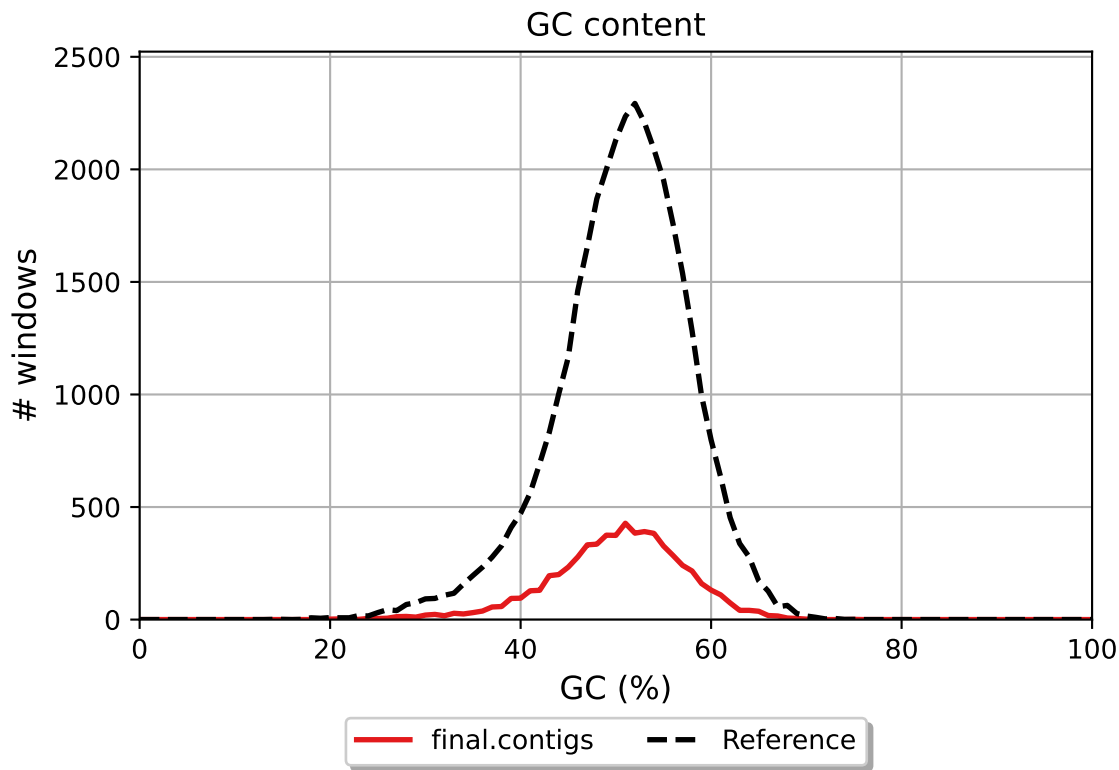


NGx

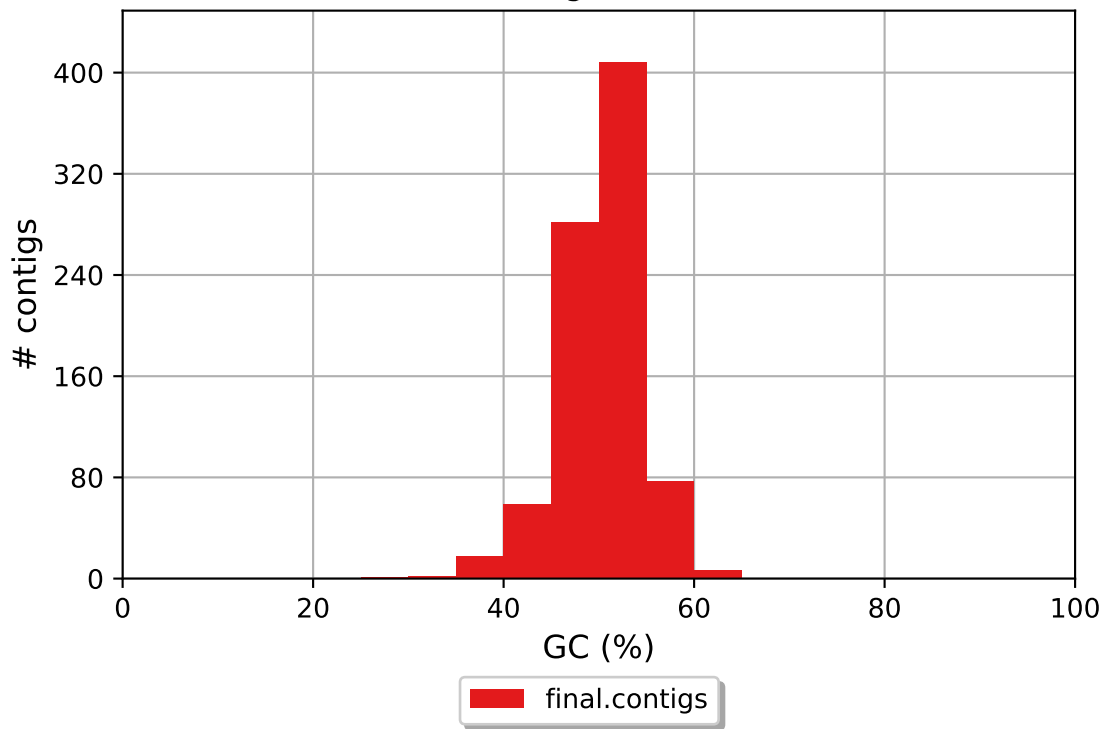


— final.contigs



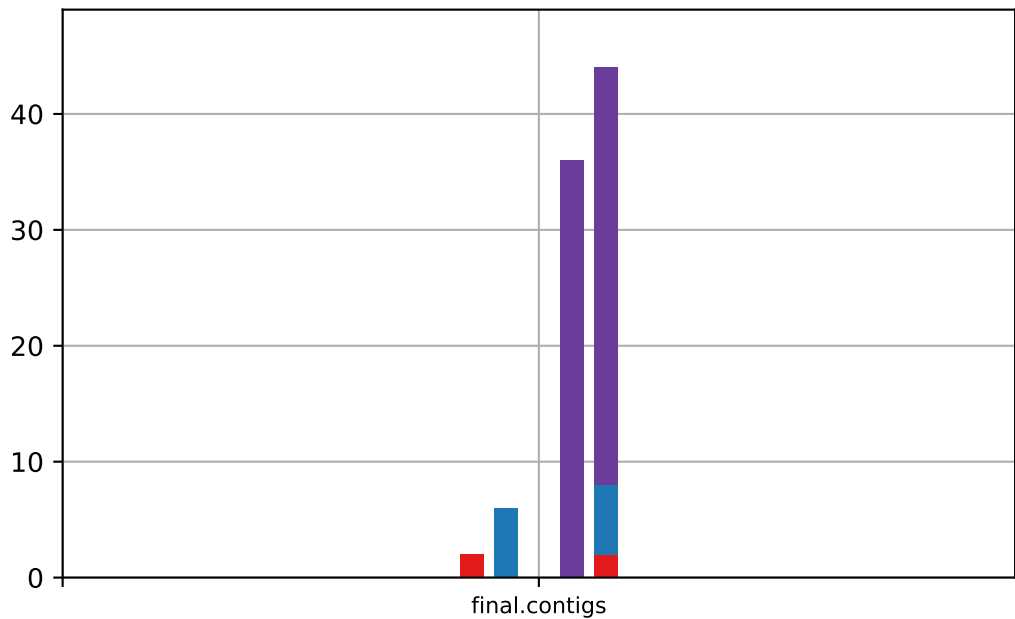


final.contigs GC content



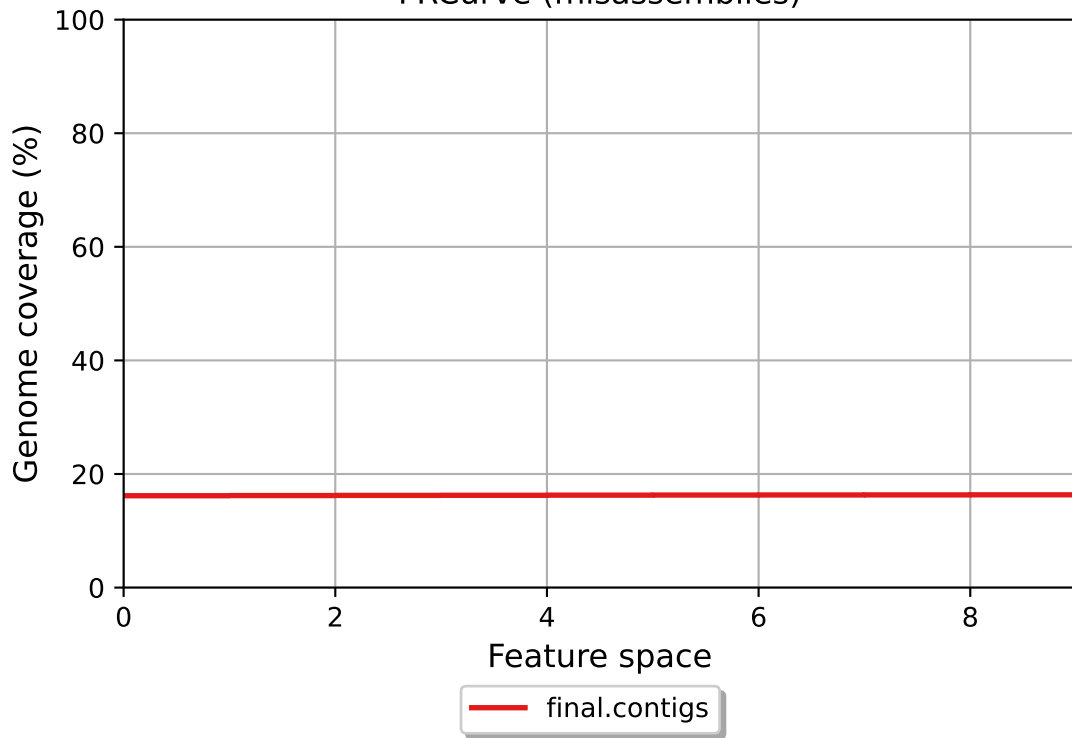


## Misassemblies

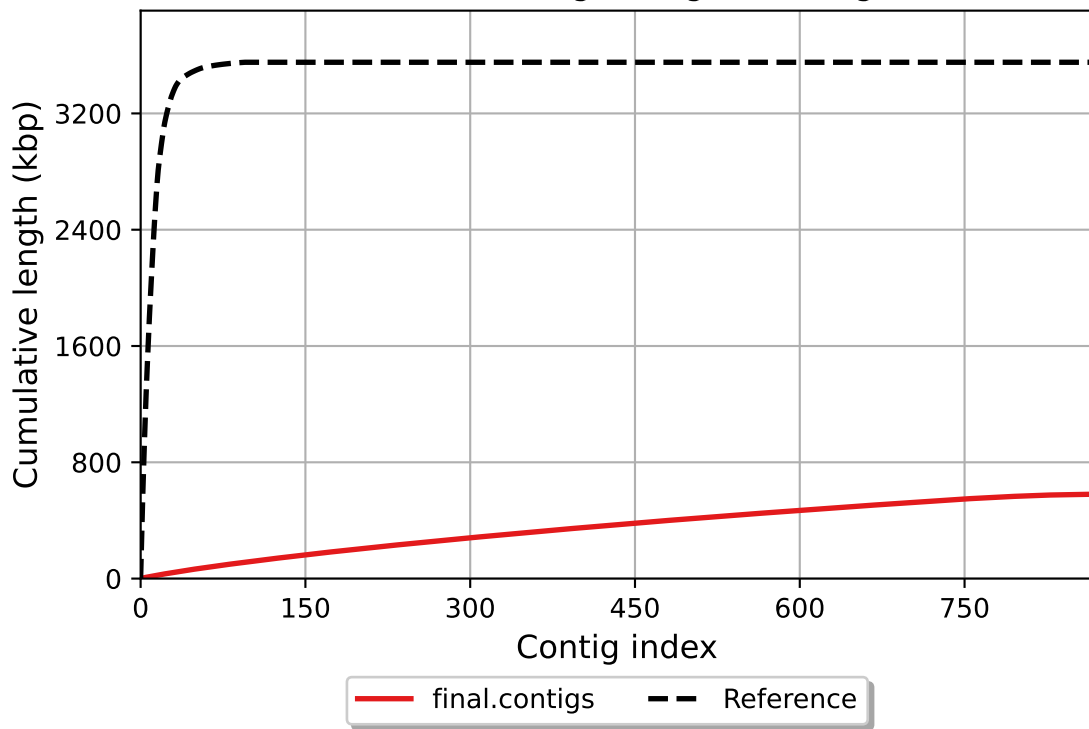


# relocations    # translocations    # interspecies translocations

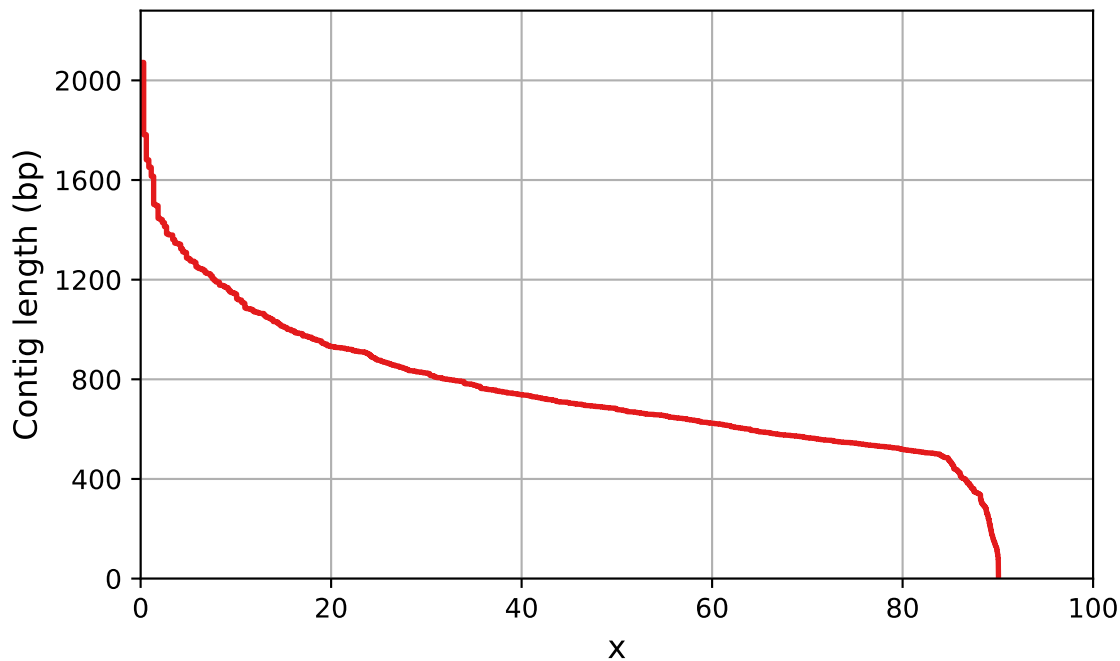
FRCurve (misassemblies)



Cumulative length (aligned contigs)

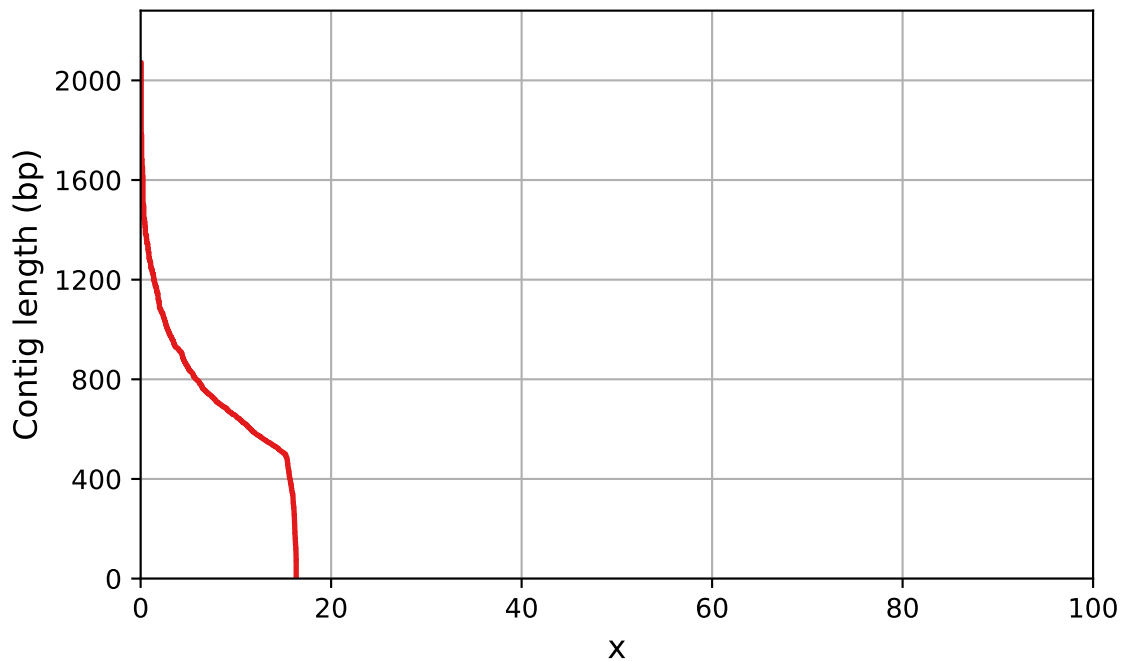


NAx



— final.contigs

# NGAx



— final.contigs