

# Report

	final.contigs
# contigs (>= 0 bp)	165198
# contigs (>= 1000 bp)	30750
# contigs (>= 5000 bp)	2595
# contigs (>= 10000 bp)	828
# contigs (>= 25000 bp)	158
# contigs (>= 50000 bp)	48
Total length (>= 0 bp)	149901860
Total length (>= 1000 bp)	81513165
Total length (>= 5000 bp)	29777202
Total length (>= 10000 bp)	17824104
Total length (>= 25000 bp)	8117721
Total length (>= 50000 bp)	4287431
# contigs	87802
Largest contig	266140
Total length	120124642
Reference length	143238253
N50	1705
N75	834
L50	13923
L75	40175
# misassemblies	18
# misassembled contigs	10
Misassembled contigs length	7253
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	71
# unaligned contigs	87432 + 218 part
Unaligned length	119986793
Genome fraction (%)	0.077
Duplication ratio	1.999
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5223.81
# indels per 100 kbp	104.86
Largest alignment	2016
Total aligned length	74570

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

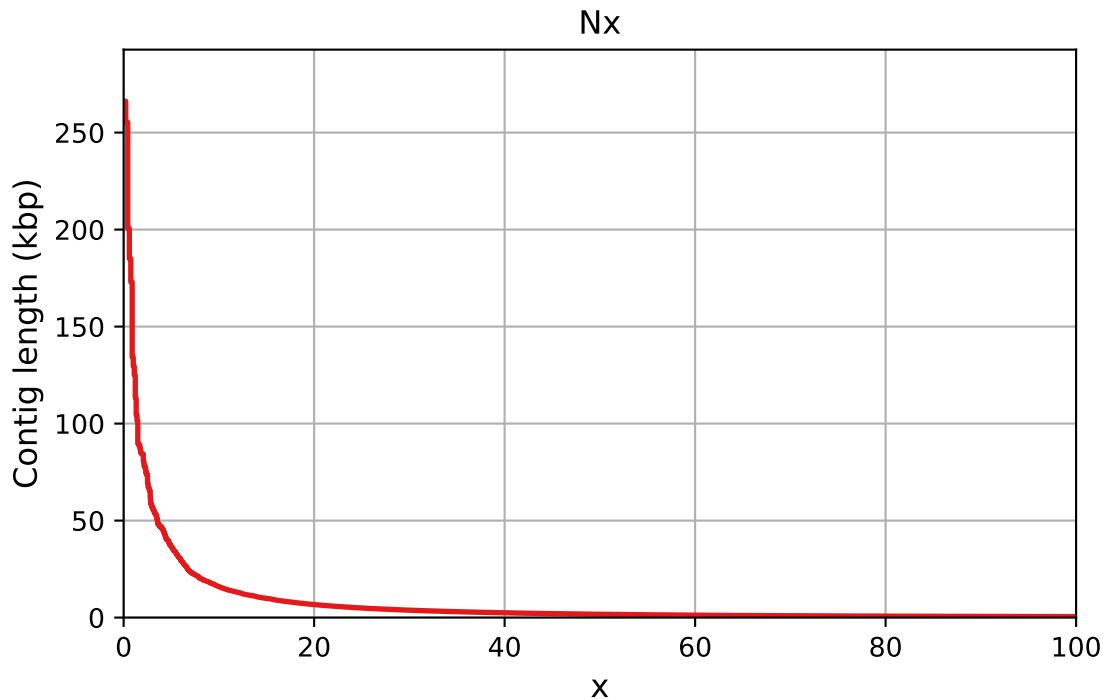
	final.contigs
# misassemblies	18
# contig misassemblies	18
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	18
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	10
Misassembled contigs length	7253
# possibly misassembled contigs	180
# possible misassemblies	240
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	71
# mismatches	5729
# indels	115
# indels (<= 5 bp)	114
# indels (> 5 bp)	1
Indels length	143

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

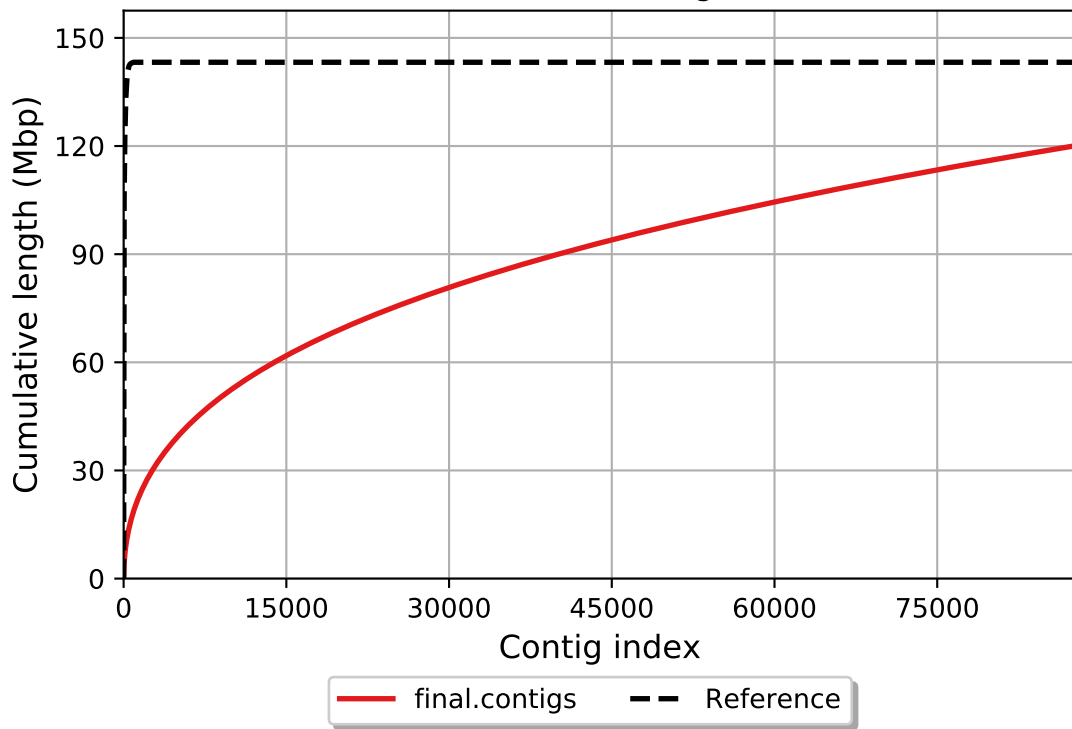
	final.contigs
# fully unaligned contigs	87432
Fully unaligned length	117544322
# partially unaligned contigs	218
Partially unaligned length	2442471
# N's	0

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).

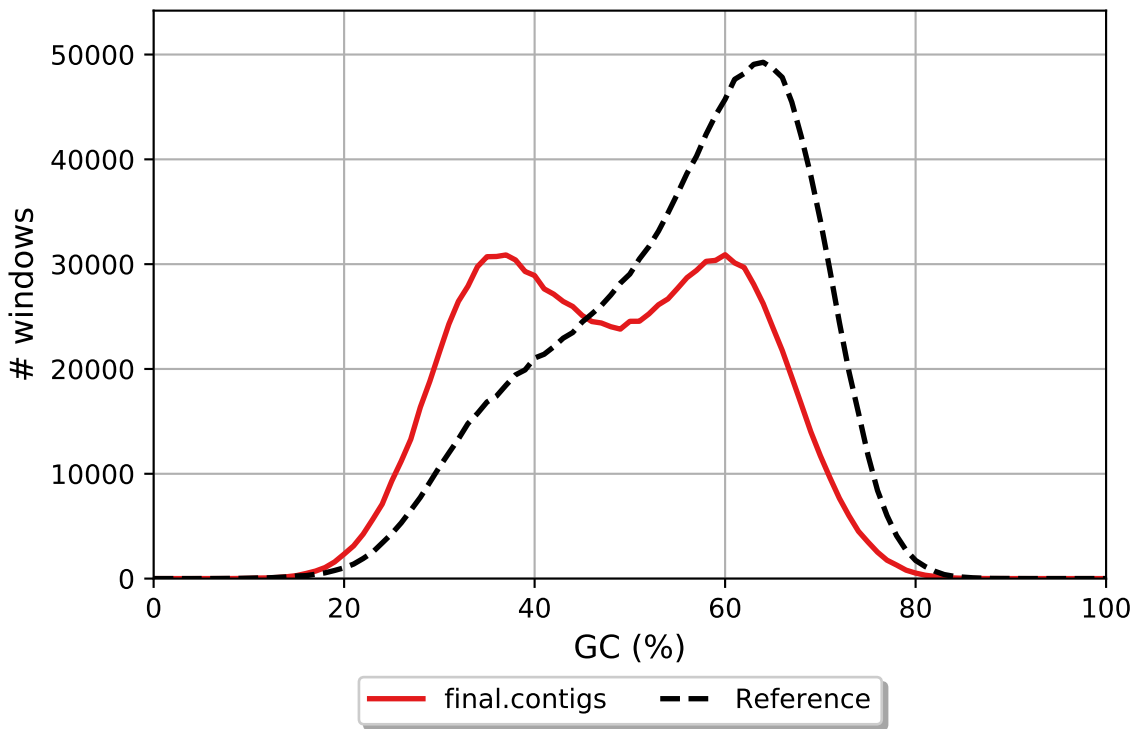


— final.contigs

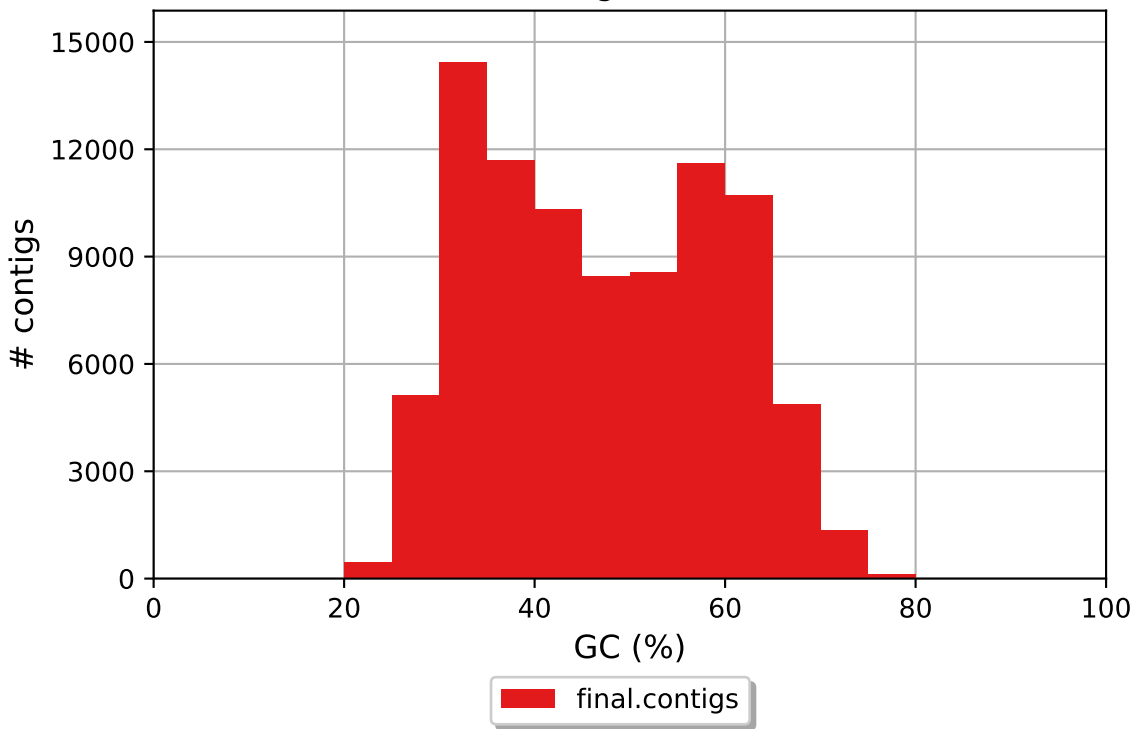
Cumulative length



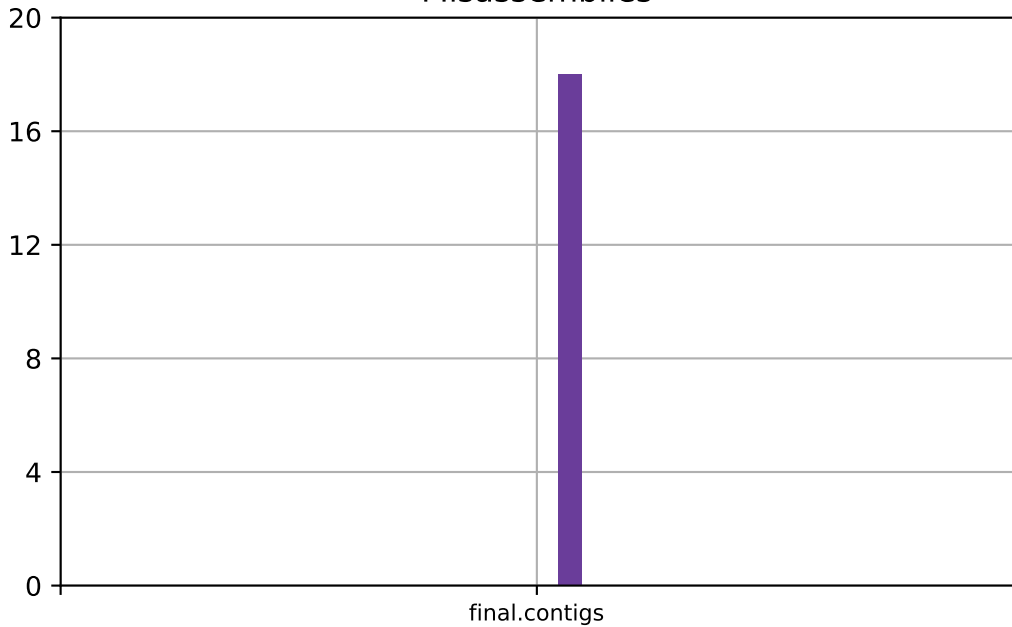
GC content



final.contigs GC content



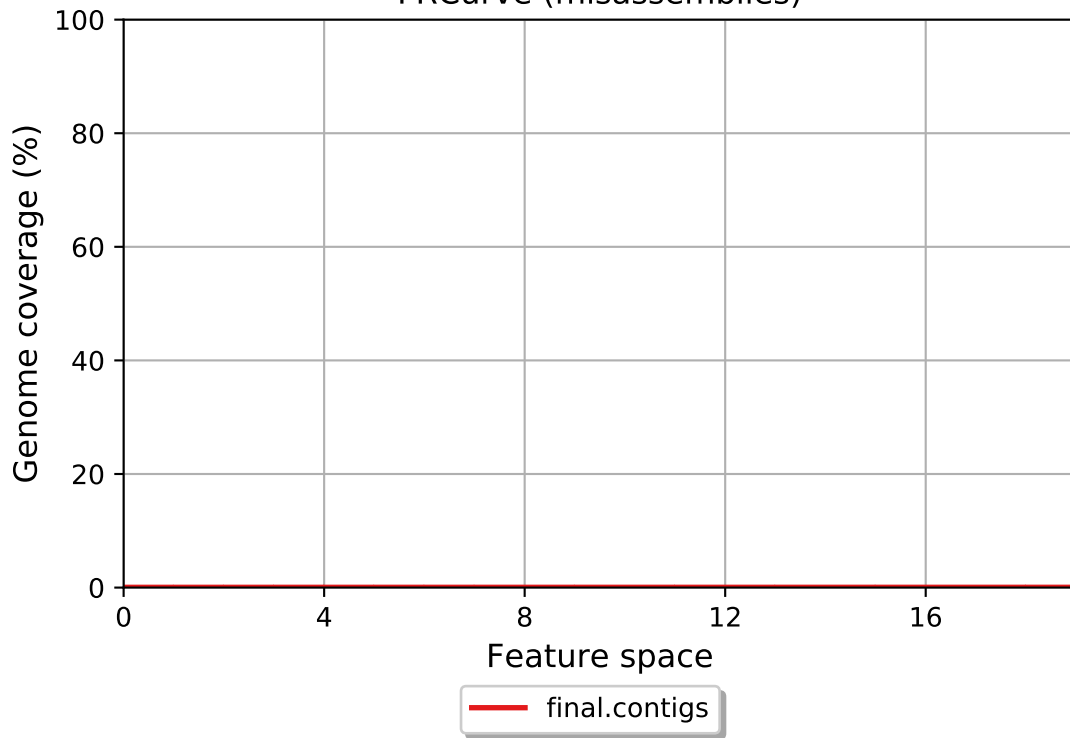
## Misassemblies



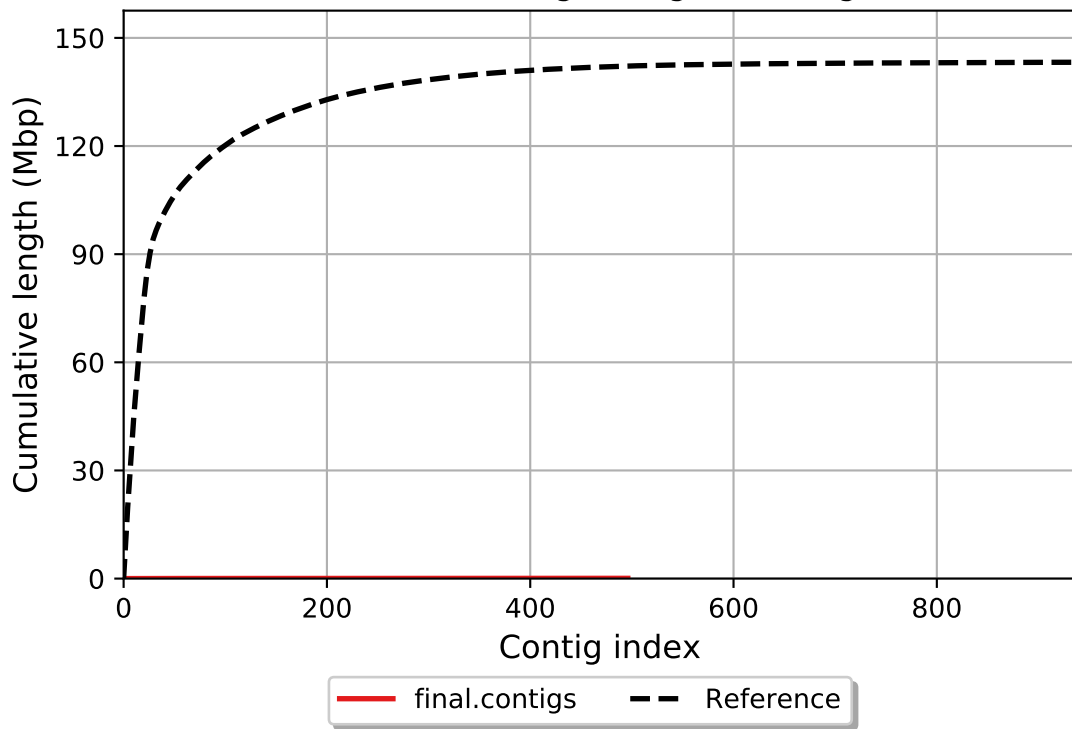
# interspecies translocations



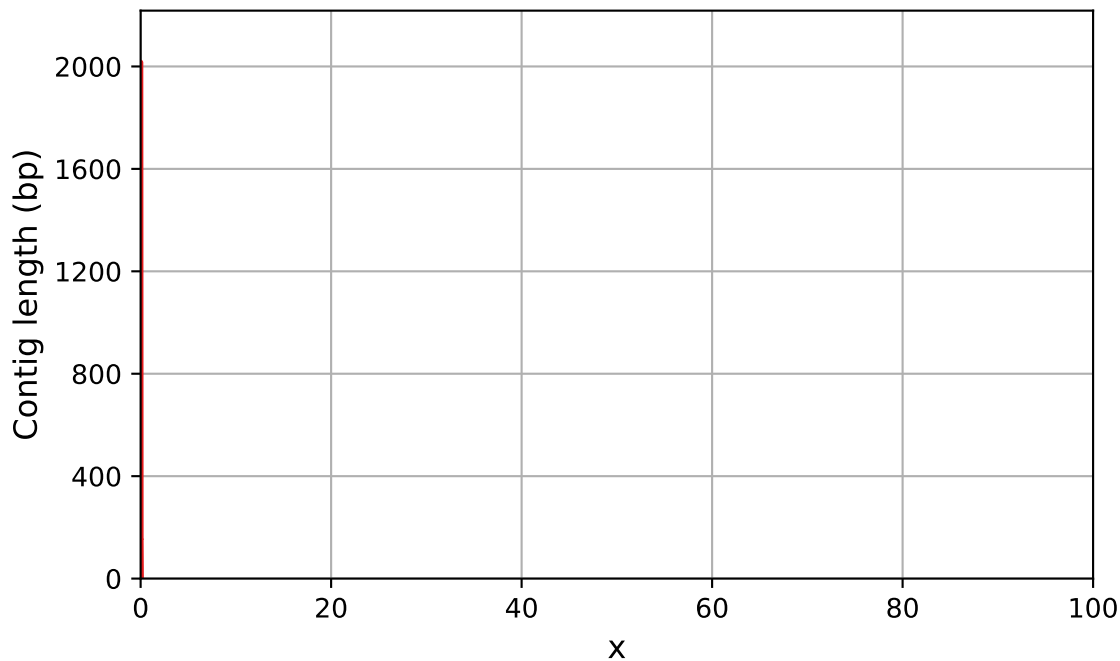
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs