

# Report

	33_380.30
# contigs (>= 1000 bp)	34
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	302316
Total length (>= 5000 bp)	264045
Total length (>= 10000 bp)	208225
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	39
Largest contig	19255
Total length	306475
Reference length	29903
GC (%)	38.00
Reference GC (%)	37.97
N50	13909
NG50	19255
N75	8272
NG75	19255
L50	9
LG50	1
L75	16
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.214
Duplication ratio	10.435
# N's per 100 kbp	0.00
# mismatches per 100 kbp	173.65
# indels per 100 kbp	71.50
Largest alignment	19255
Total aligned length	306445
NA50	13908
NGA50	19255
NA75	8271
NGA75	19254
LA50	9
LGA50	1
LA75	16
LGA75	2

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

	33_380.30
# 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	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	51
# indels	21
# indels (<= 5 bp)	21
# indels (> 5 bp)	0
Indels length	21

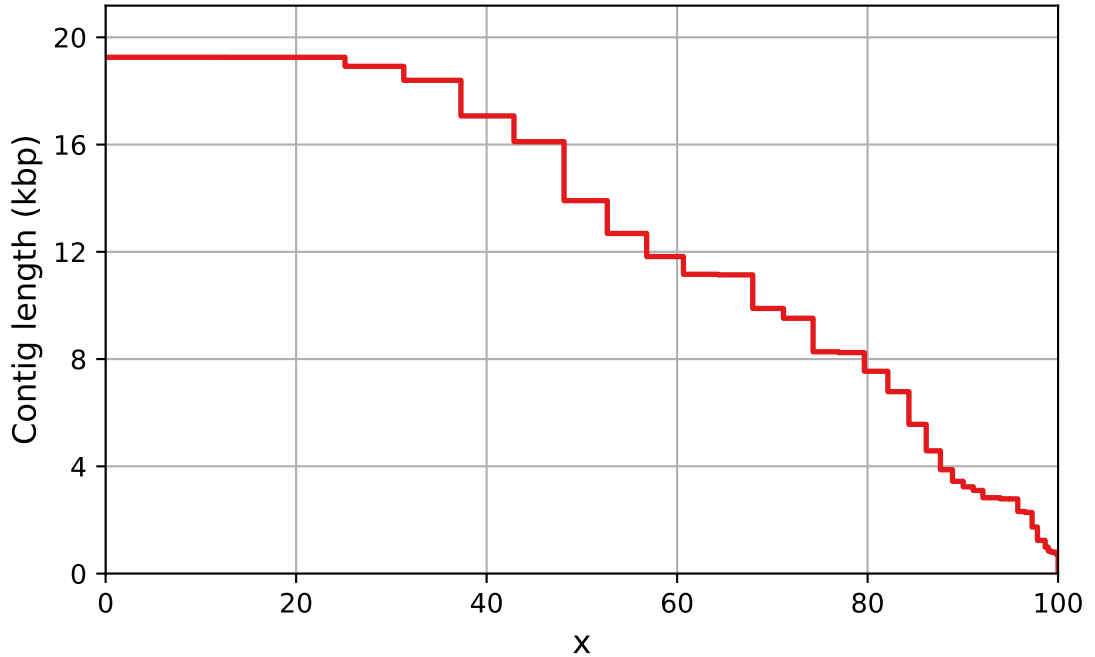
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	33_380.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

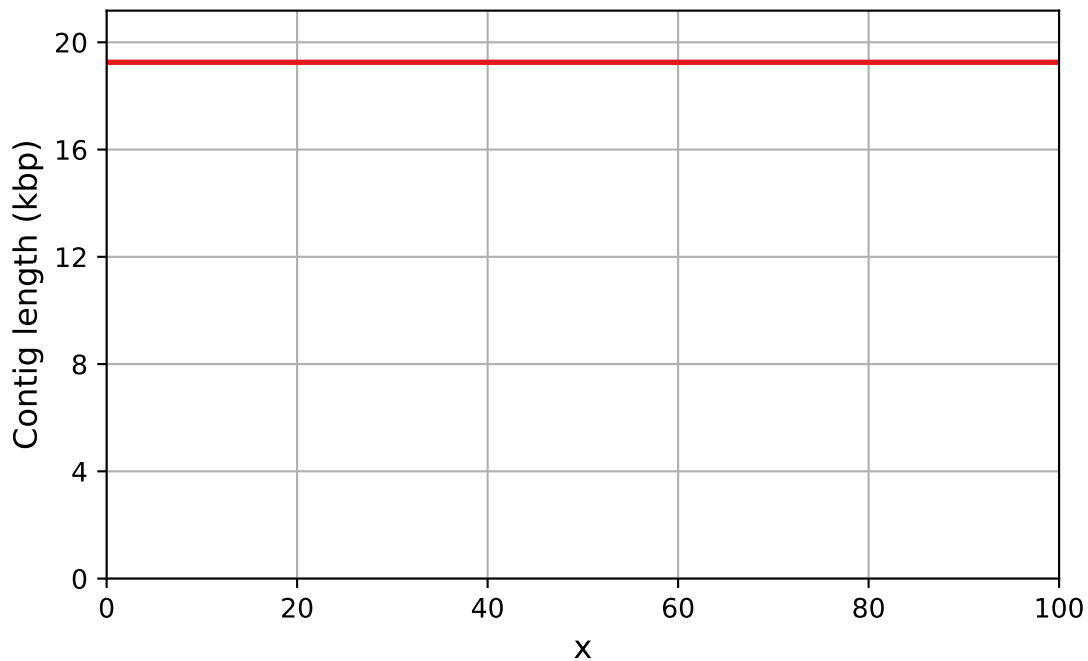
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



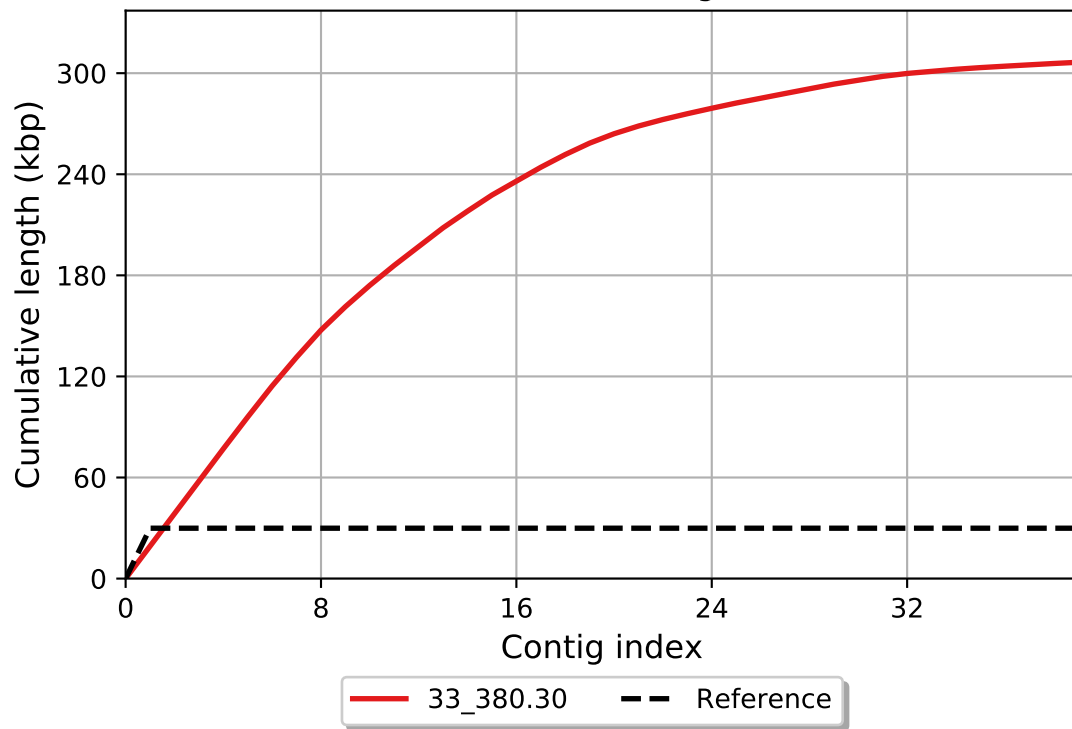
33\_380.30

NGx

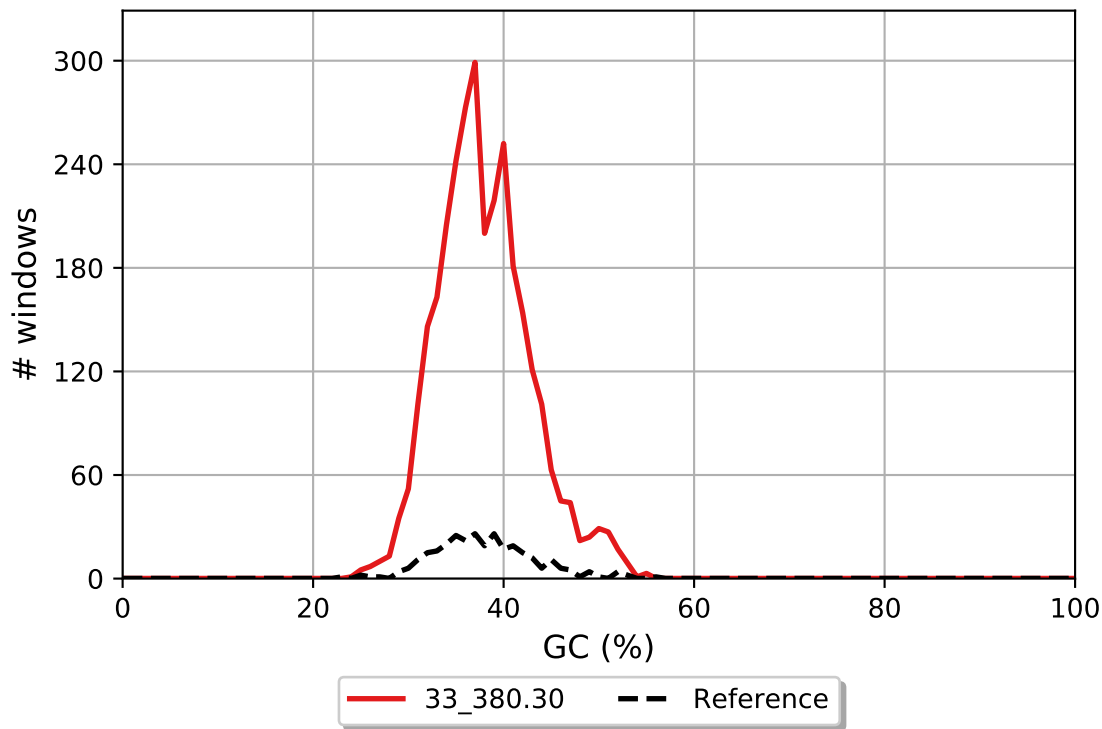


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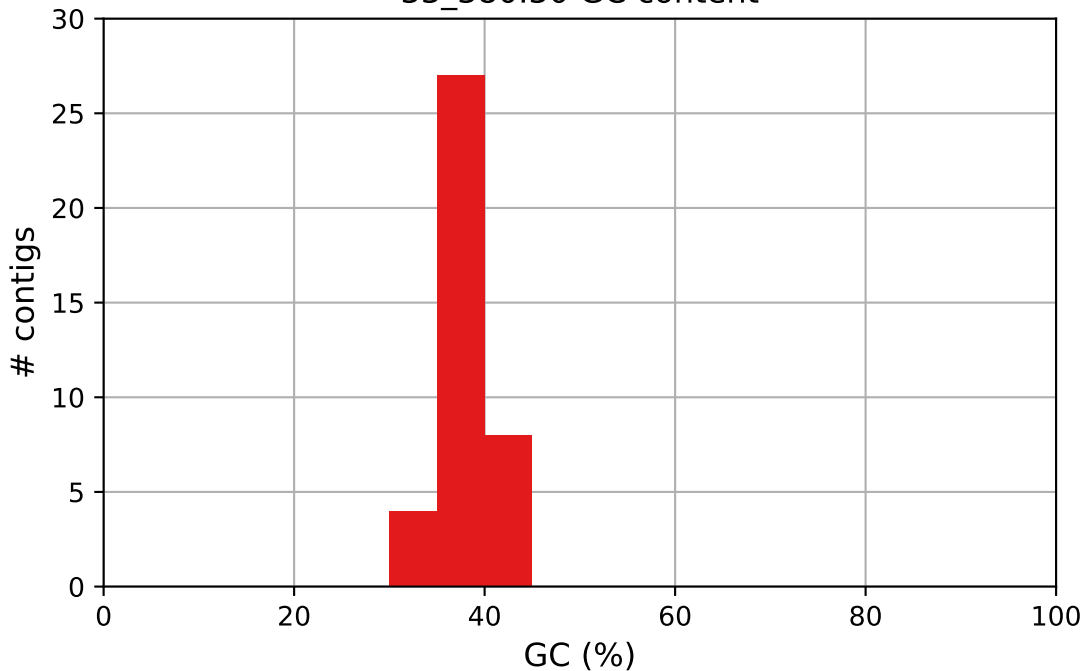
Cumulative length



## GC content



33\_380.30 GC content



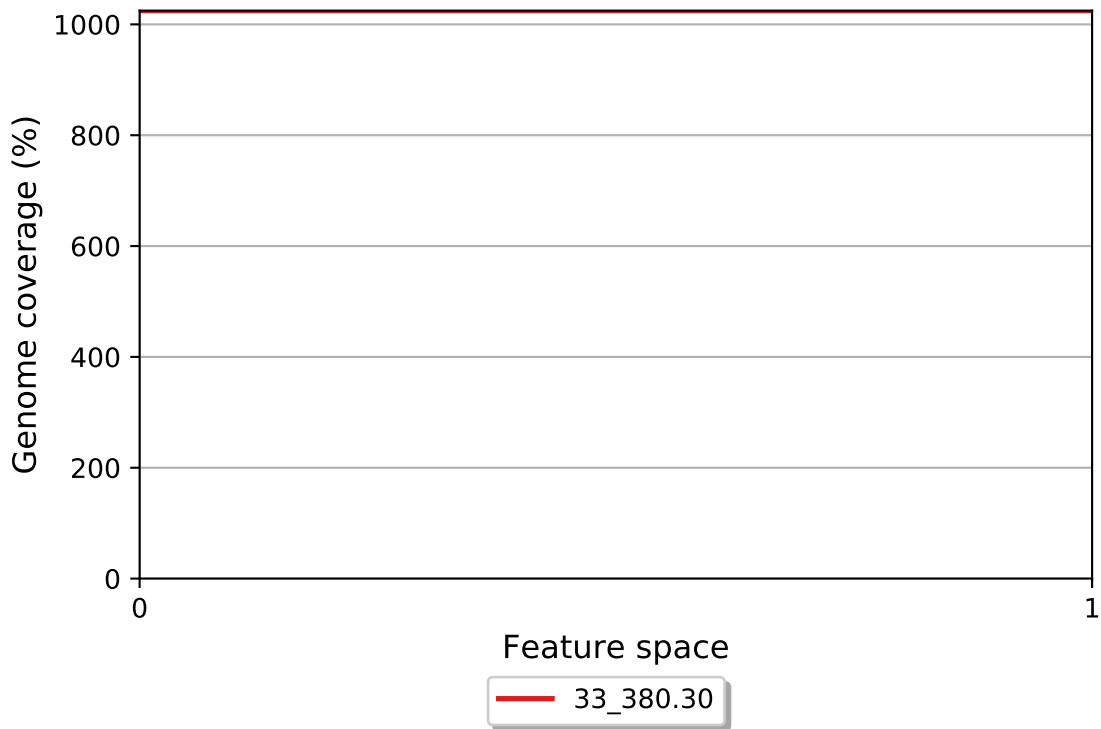
33\_380.30



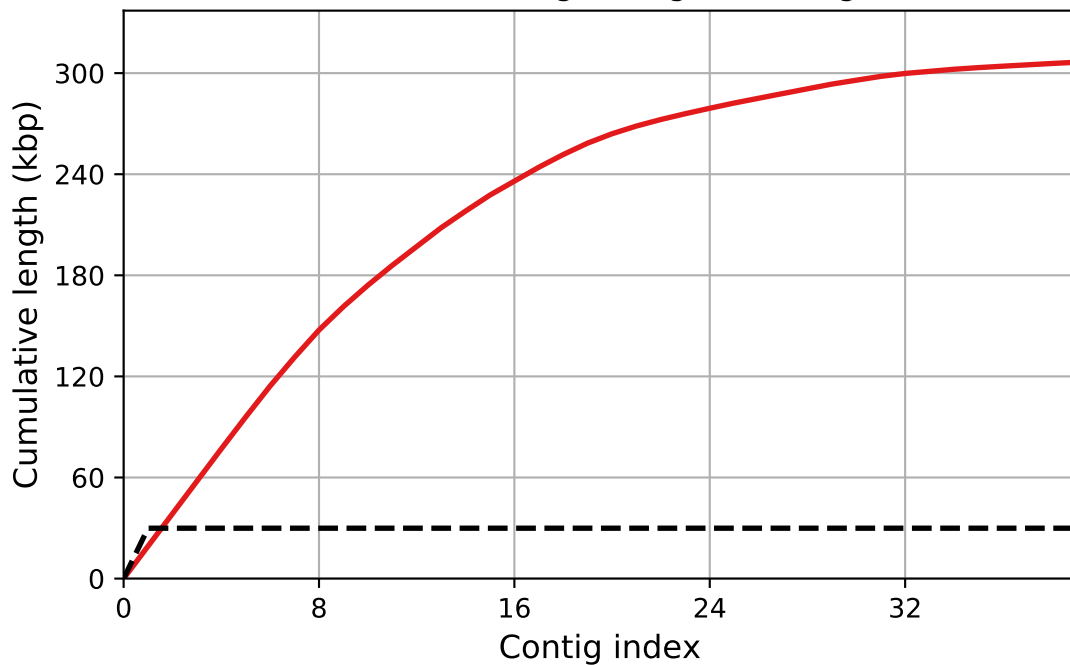
## Misassemblies



FRCurve (misassemblies)

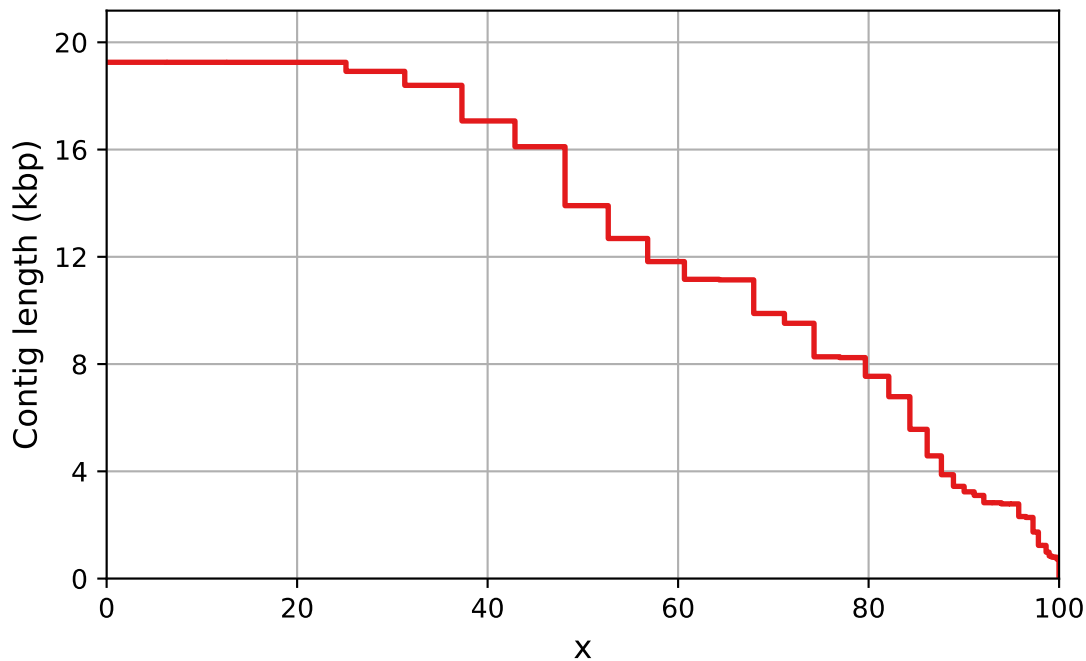


Cumulative length (aligned contigs)



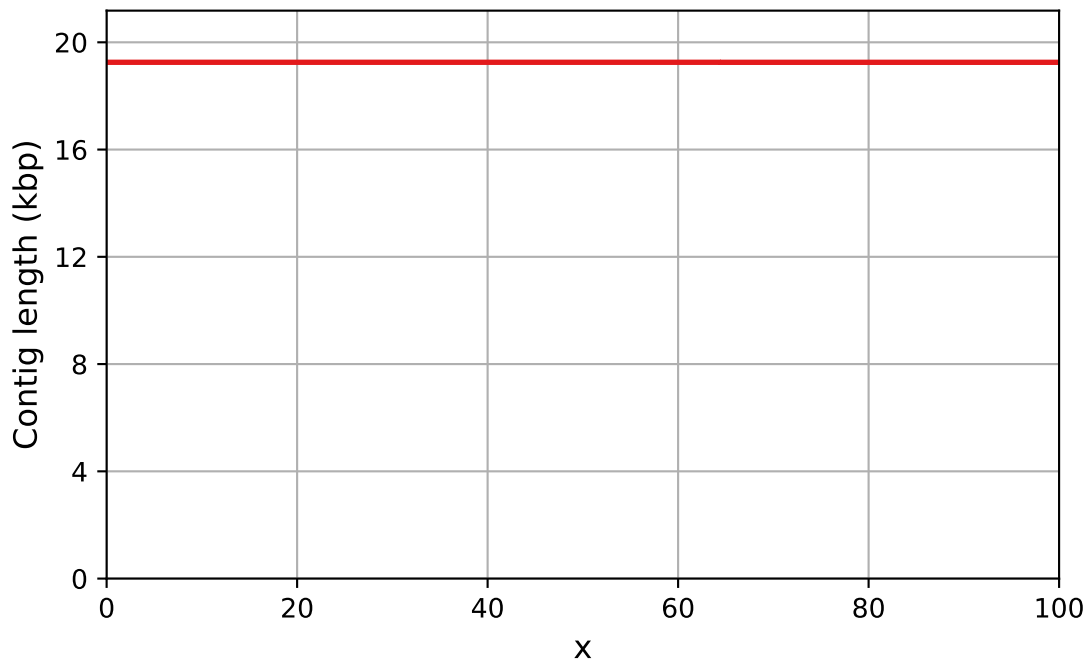
— 33\_380.30    - - - Reference

NAx



33\_380.30

NGAx



33\_380.30