

# Report

	final.contigs
# contigs (>= 0 bp)	346474
# contigs (>= 1000 bp)	61509
# contigs (>= 5000 bp)	3941
# contigs (>= 10000 bp)	1100
# contigs (>= 25000 bp)	204
# contigs (>= 50000 bp)	55
Total length (>= 0 bp)	291644575
Total length (>= 1000 bp)	143821520
Total length (>= 5000 bp)	41599652
Total length (>= 10000 bp)	22518783
Total length (>= 25000 bp)	9767207
Total length (>= 50000 bp)	4757023
# contigs	190395
Largest contig	266140
Total length	231304240
Reference length	2627046
N50	1358
N75	764
L50	37129
L75	95711
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	986
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	189871 + 20 part
Unaligned length	230948363
Genome fraction (%)	13.367
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2865.94
# indels per 100 kbp	27.34
Largest alignment	4519
Total aligned length	349658

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	1
Misassembled contigs length	986
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	10064
# indels	96
# indels (<= 5 bp)	94
# indels (> 5 bp)	2
Indels length	141

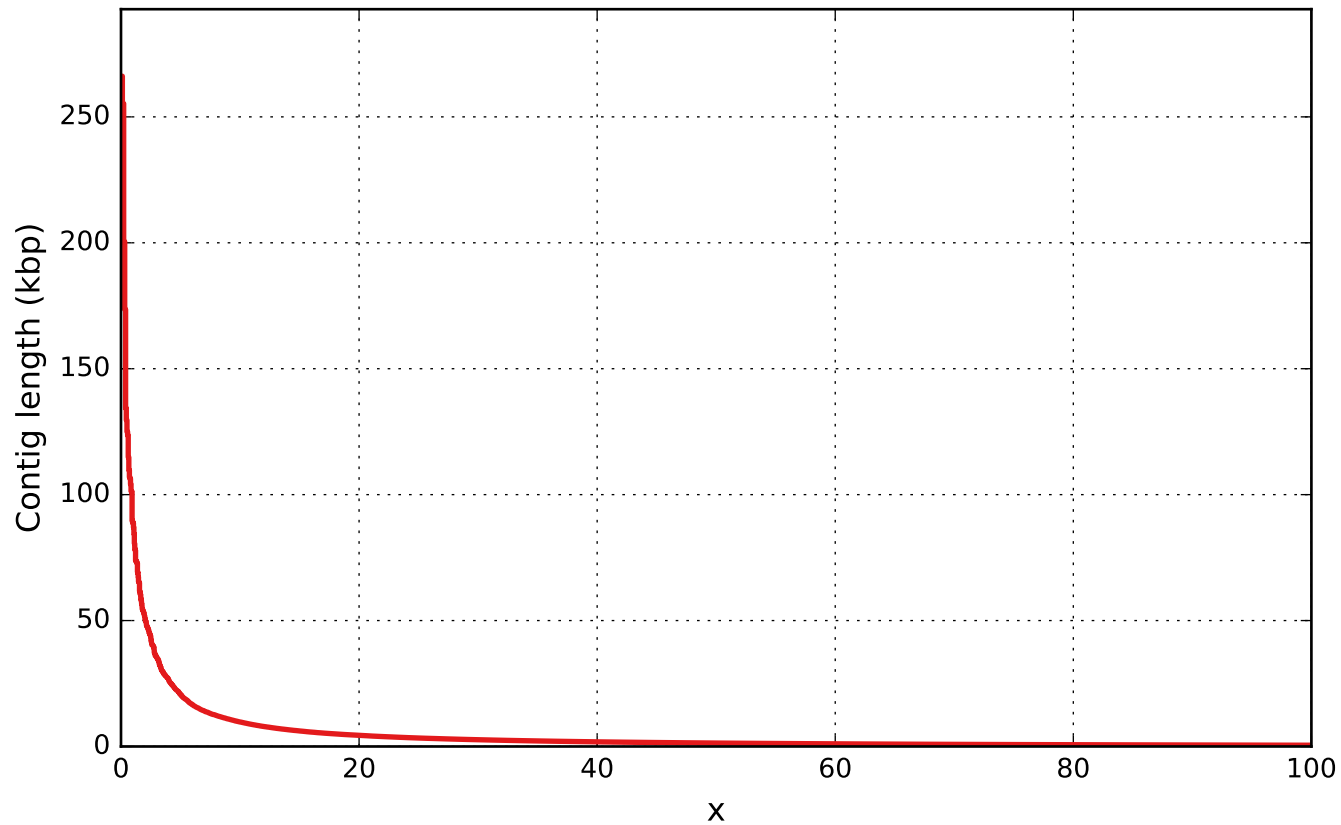
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	189871
Fully unaligned length	230901004
# partially unaligned contigs	20
Partially unaligned length	47359
# N's	0

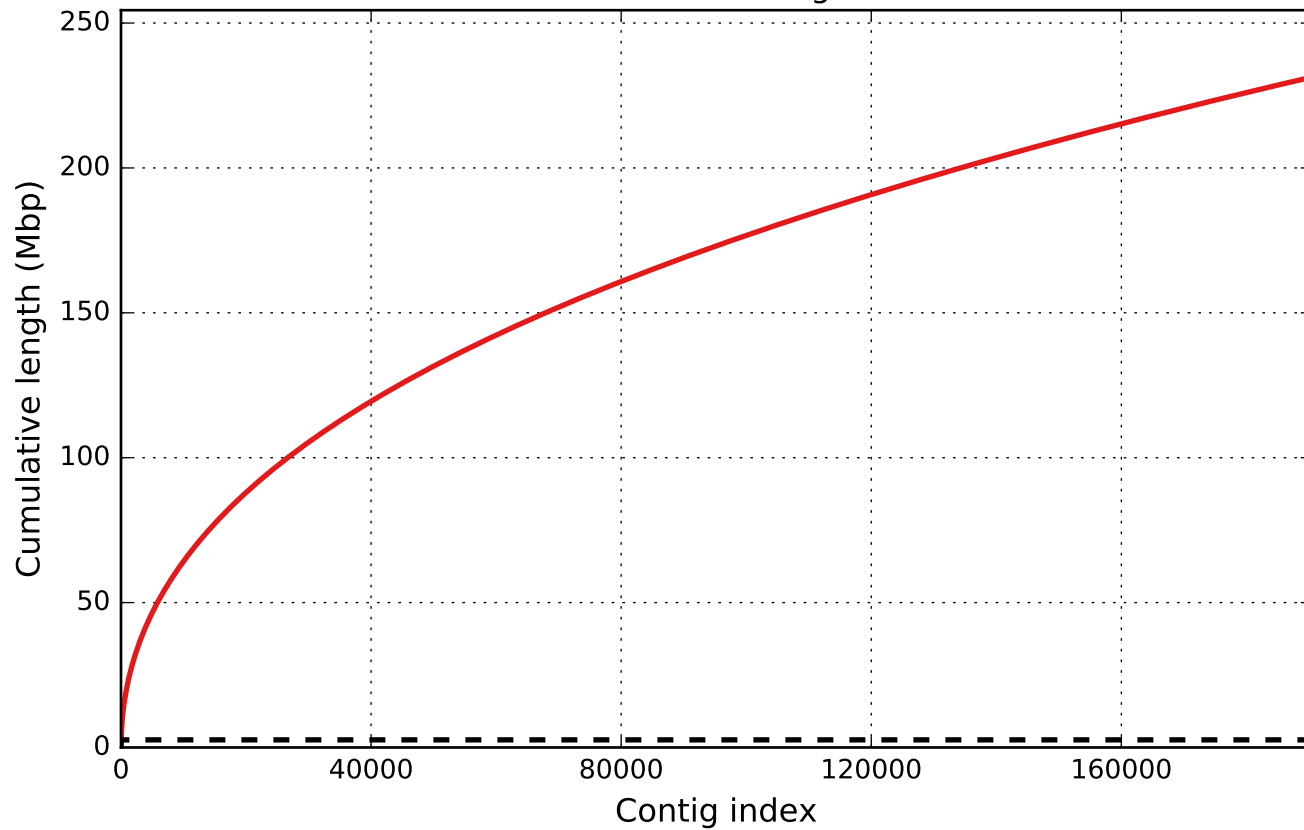
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

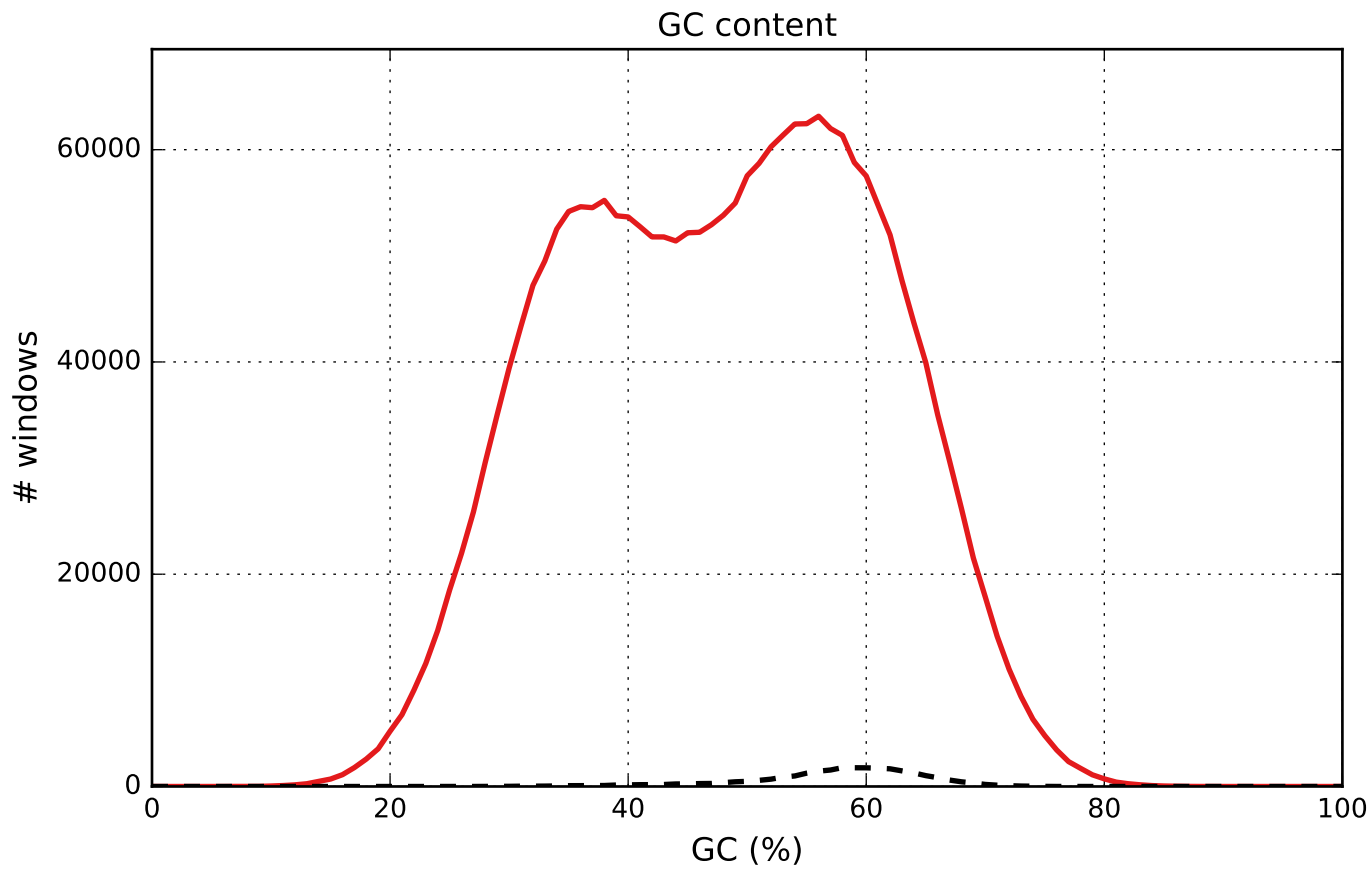


— final.contigs

Cumulative length

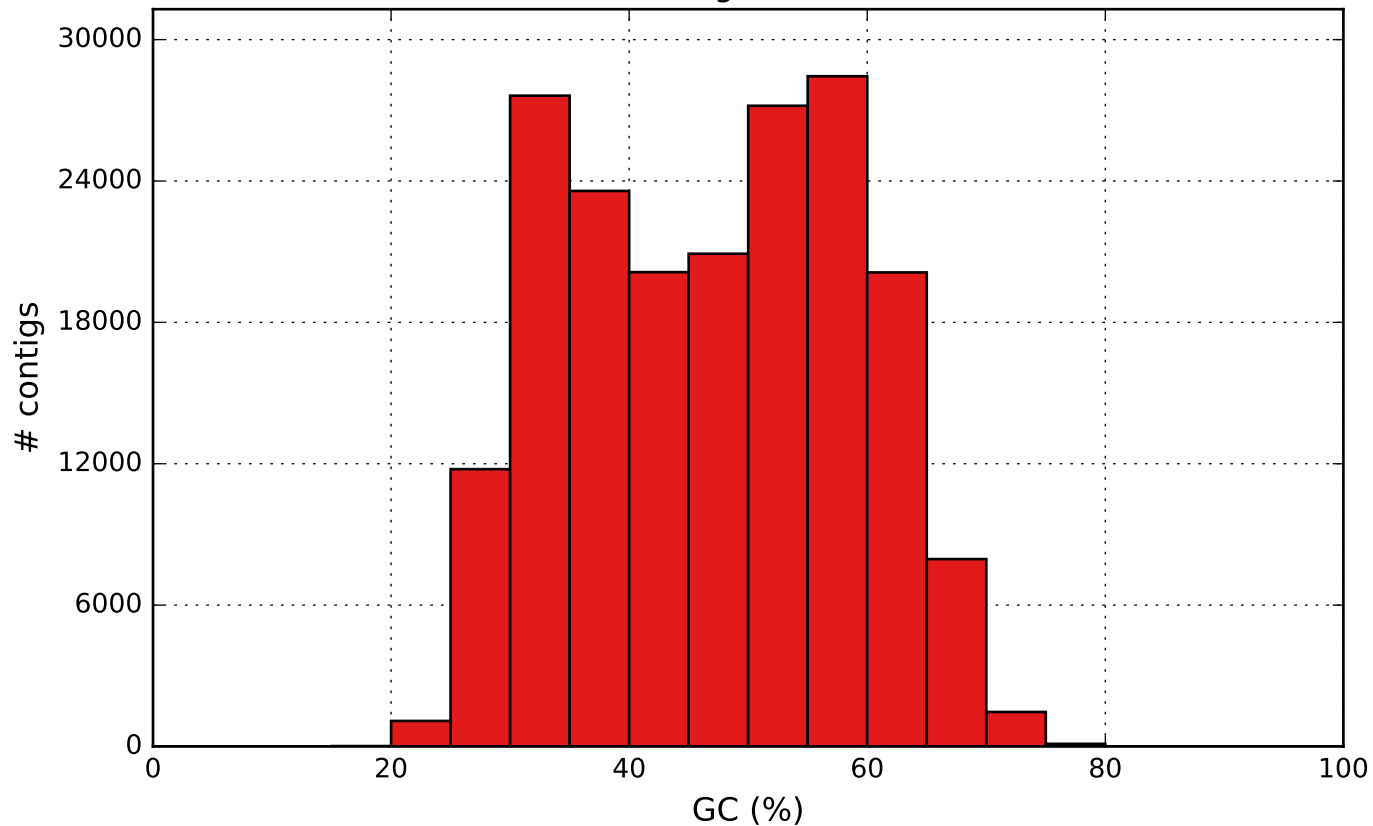


— final.contigs    - - Reference

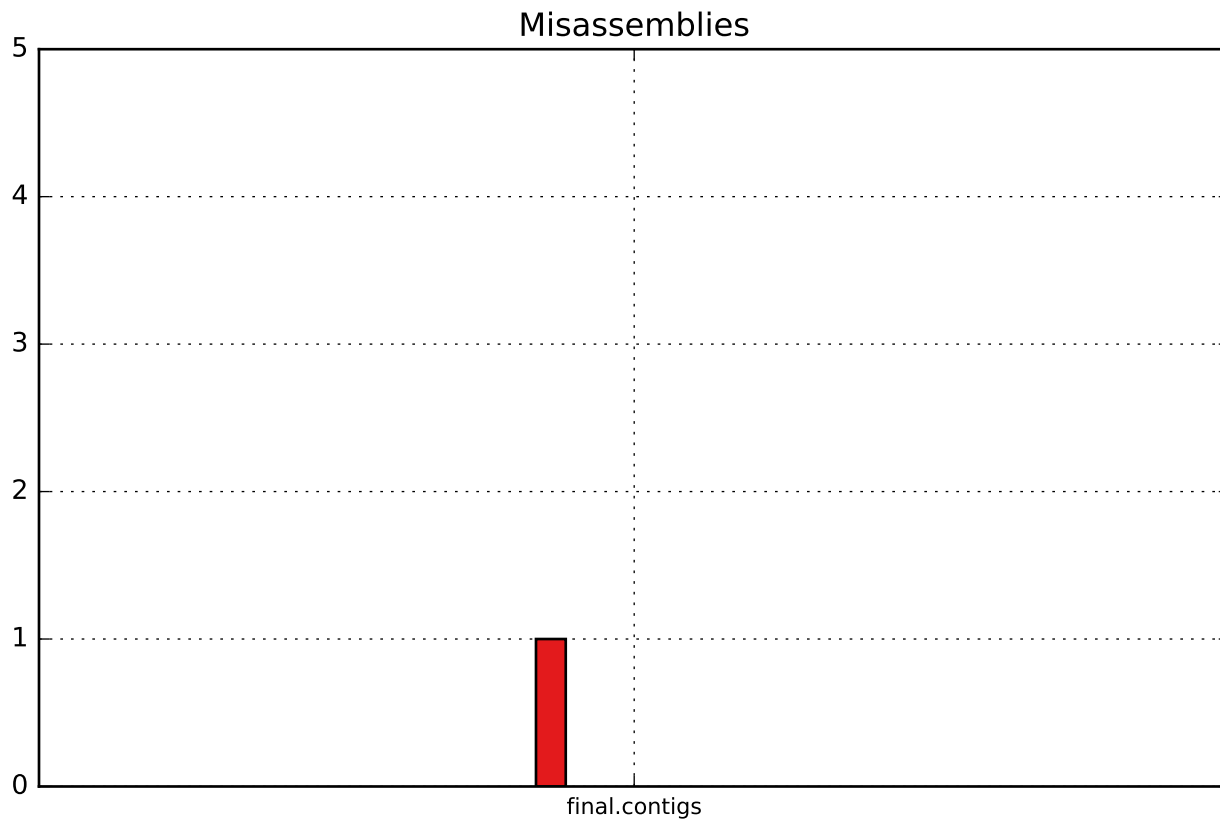


— final.contigs    - - Reference

final.contigs GC content

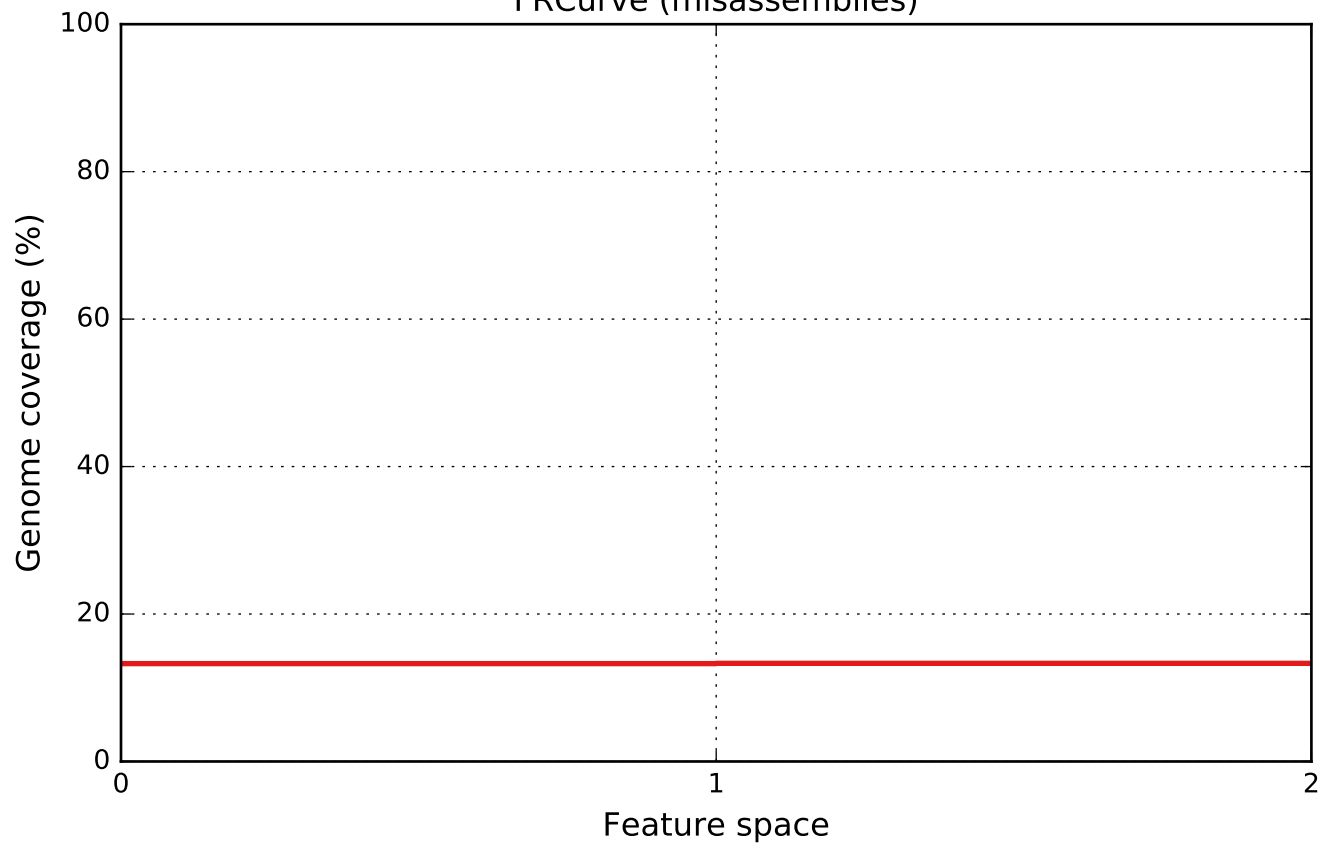


final.contigs



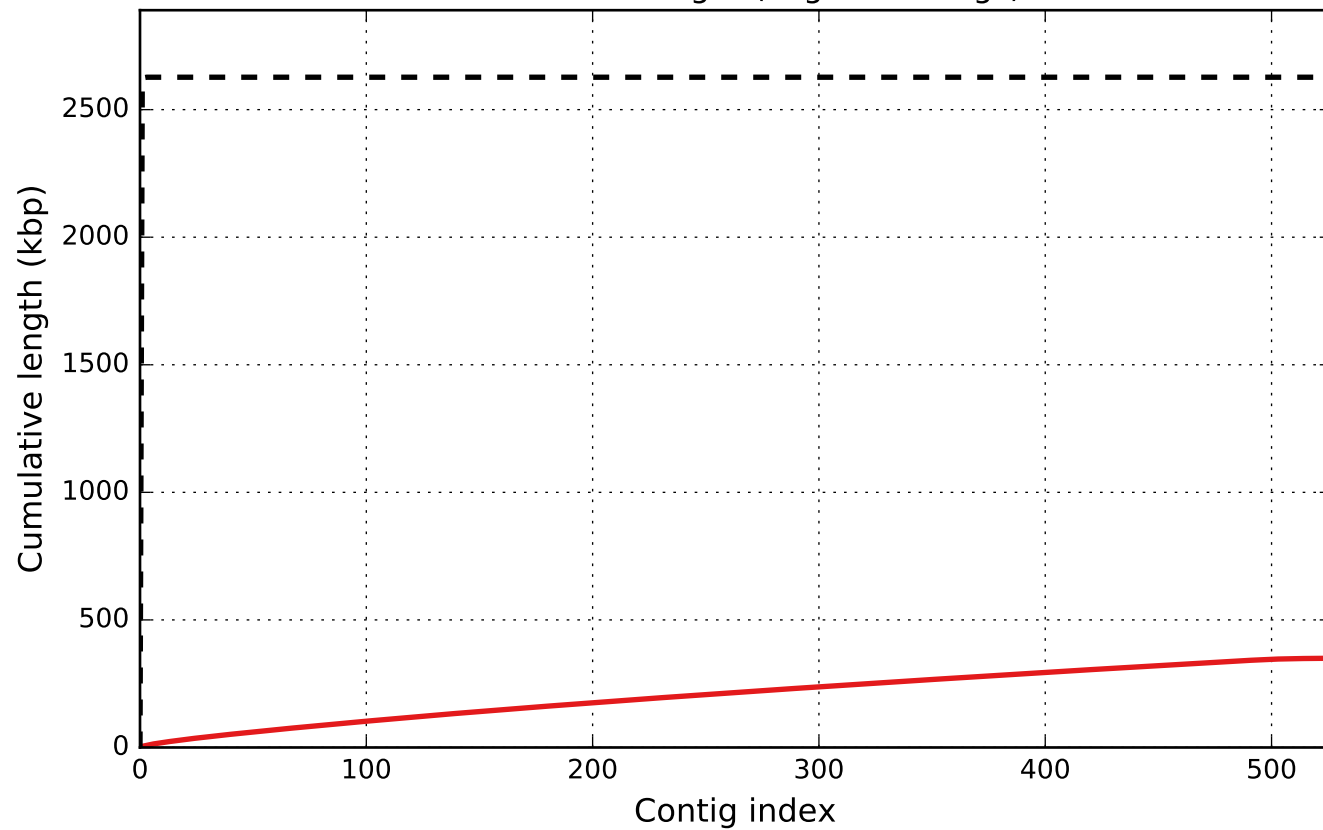


FRCurve (misassemblies)

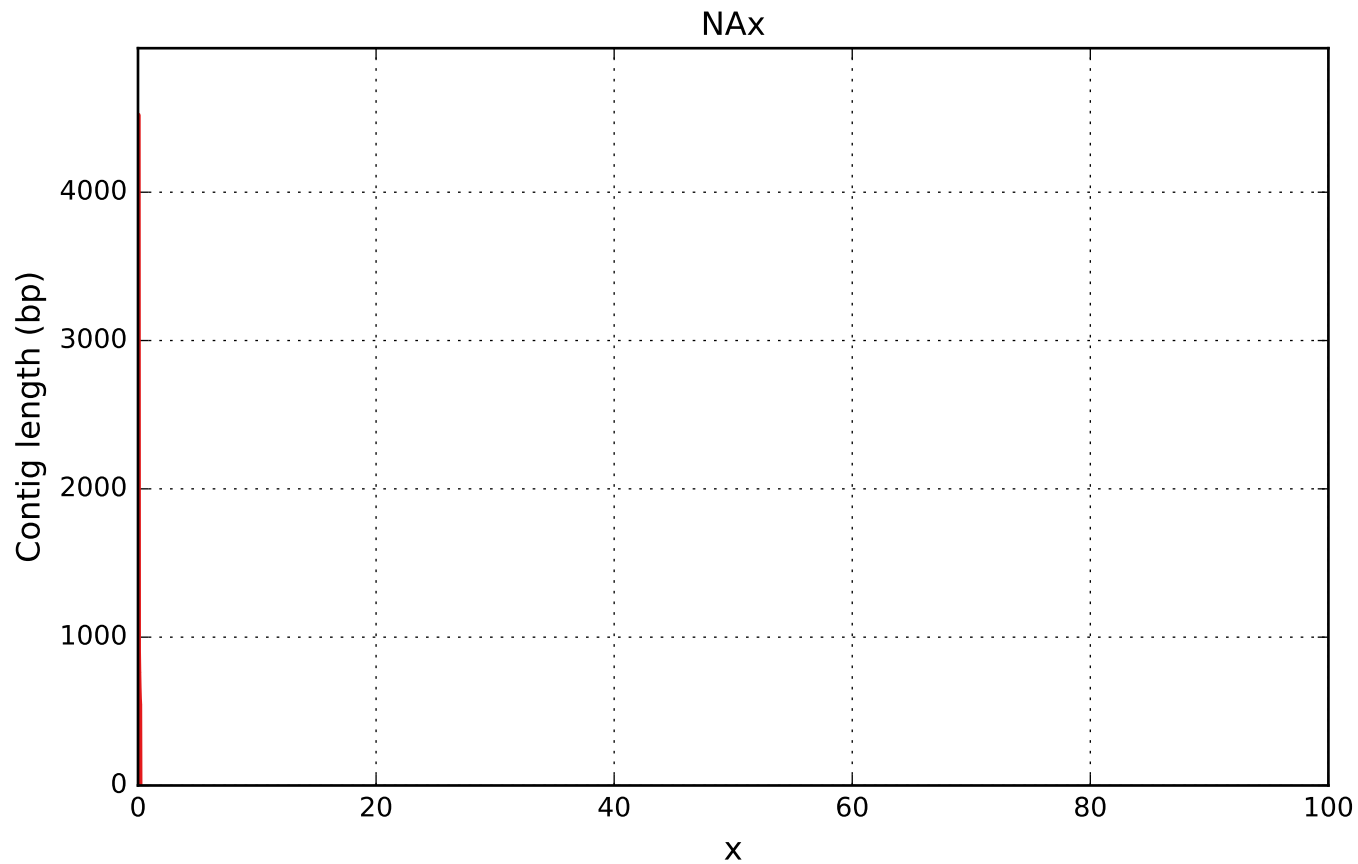


— final.contigs

Cumulative length (aligned contigs)



— final.contigs    - - Reference



— final.contigs