

## Report

	combined.final.contigs
# contigs ( $\geq 1000$ bp)	13
# contigs ( $\geq 5000$ bp)	1
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	32359
Total length ( $\geq 5000$ bp)	7698
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	22
Largest contig	7698
Total length	38934
Reference length	4441664
GC (%)	49.95
Reference GC (%)	65.23
N50	2266
N75	1212
L50	5
L75	11
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 15 part
Unaligned length	32807
Genome fraction (%)	0.081
Duplication ratio	1.700
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1775.31
# indels per 100 kbp	55.48
Largest alignment	920
Total aligned length	3914
NGA50	-

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).

## Misassemblies report

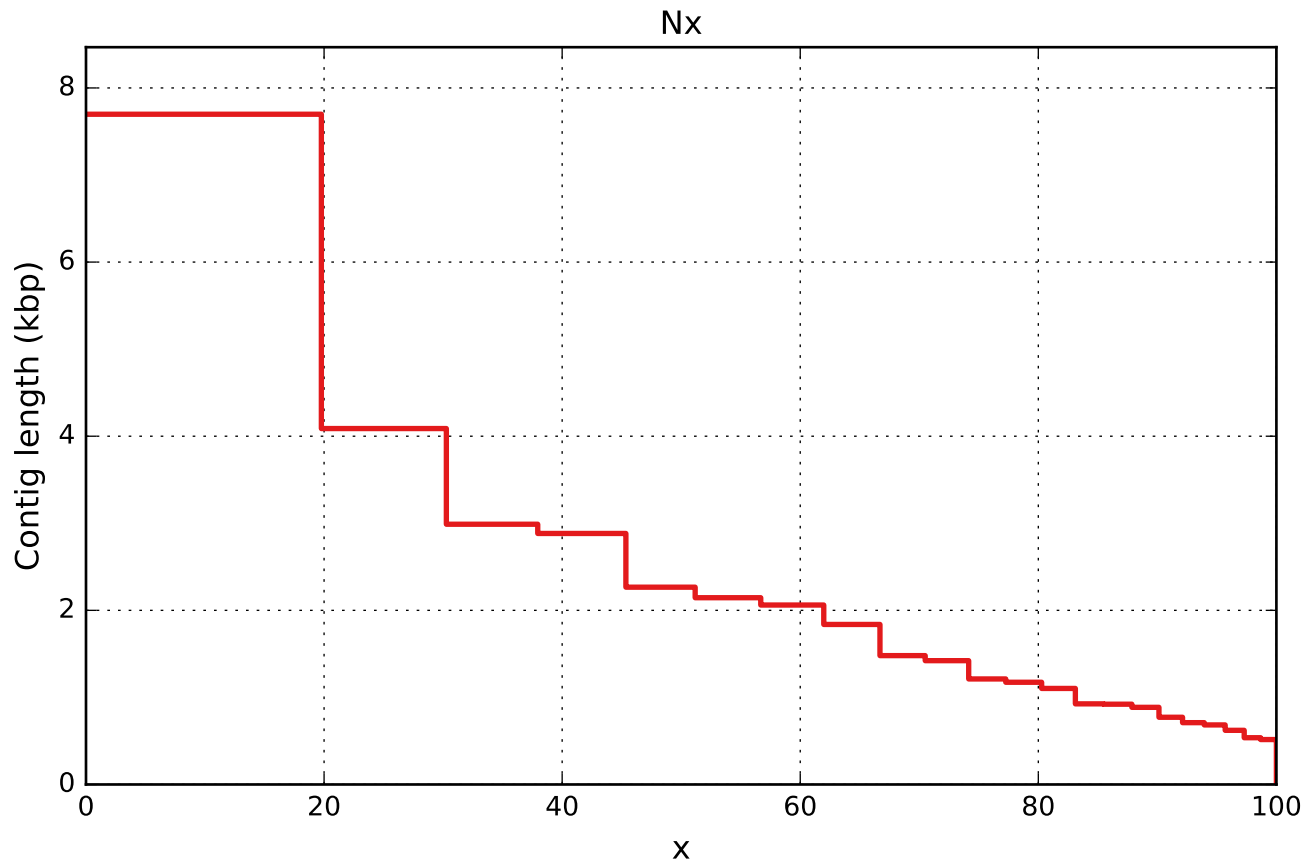
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	64
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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

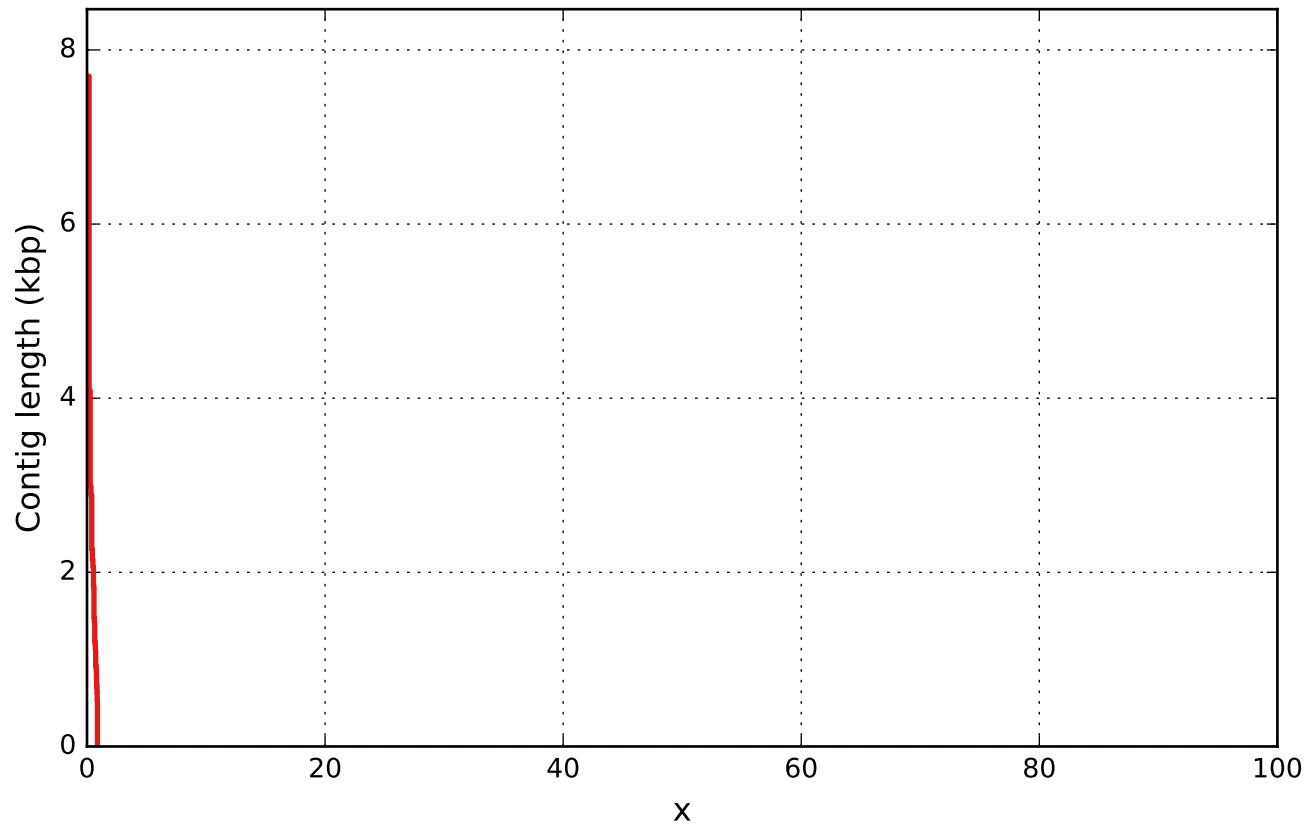
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	32807
# N's	0

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).

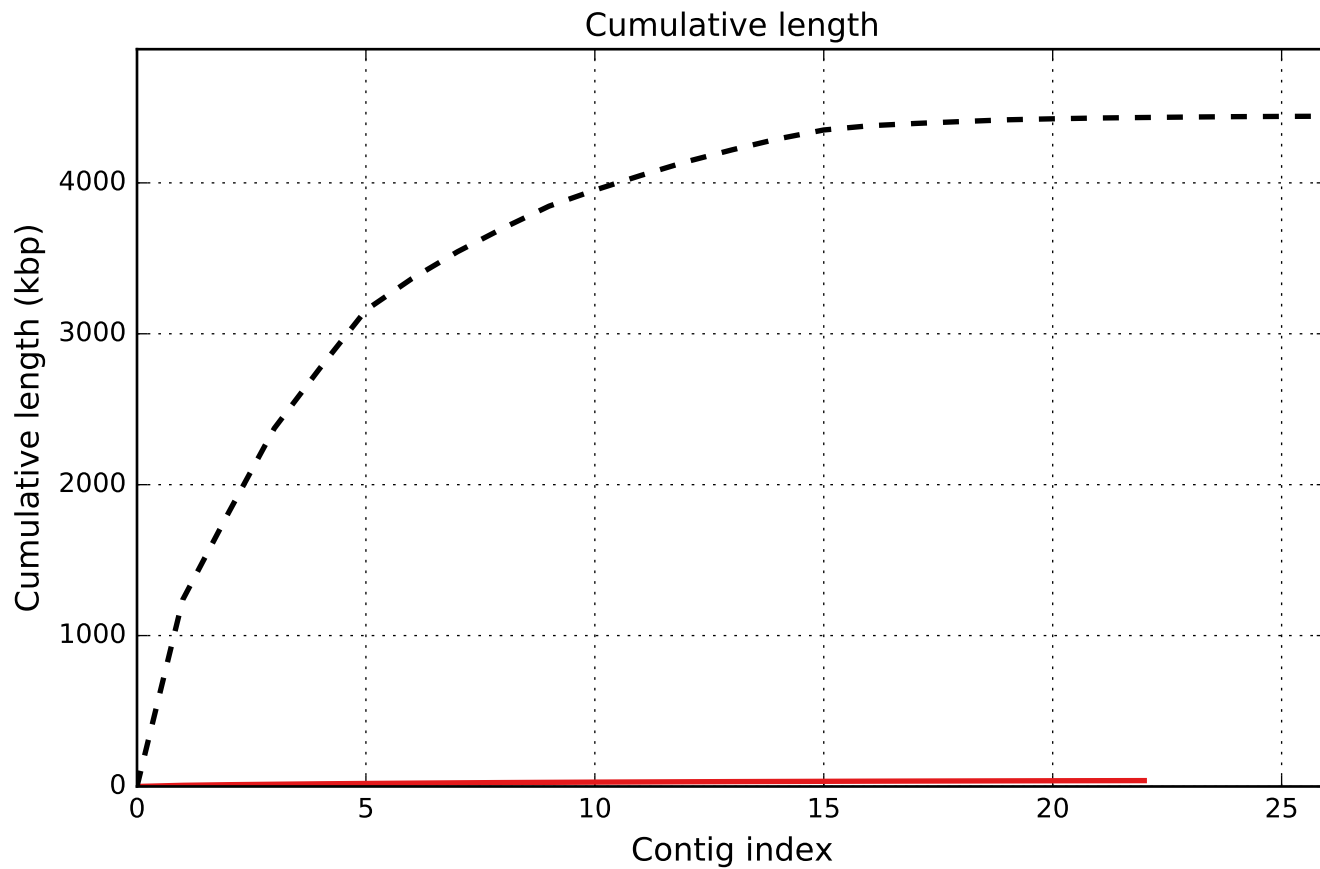


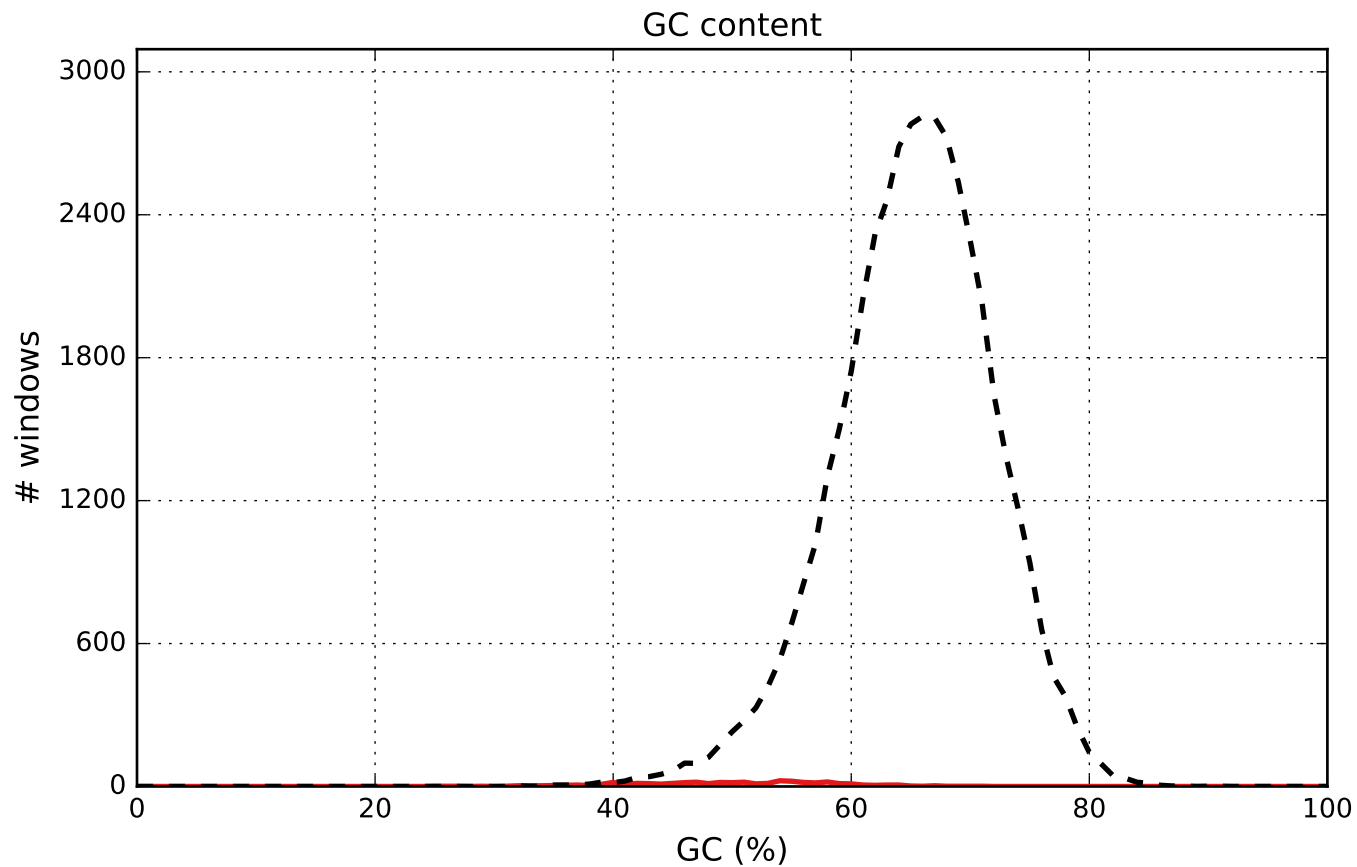
— combined.final.contigs

NGx



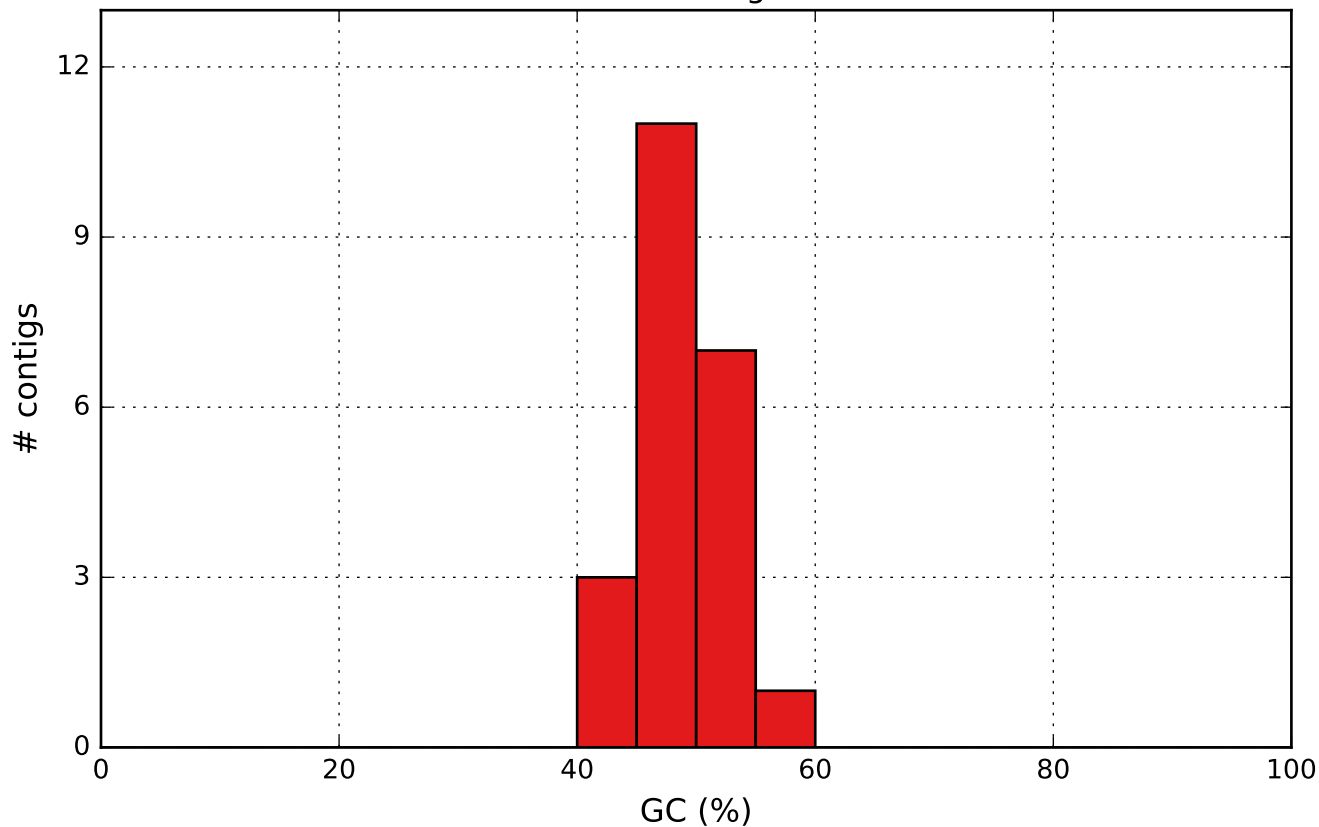
— combined.final.contigs






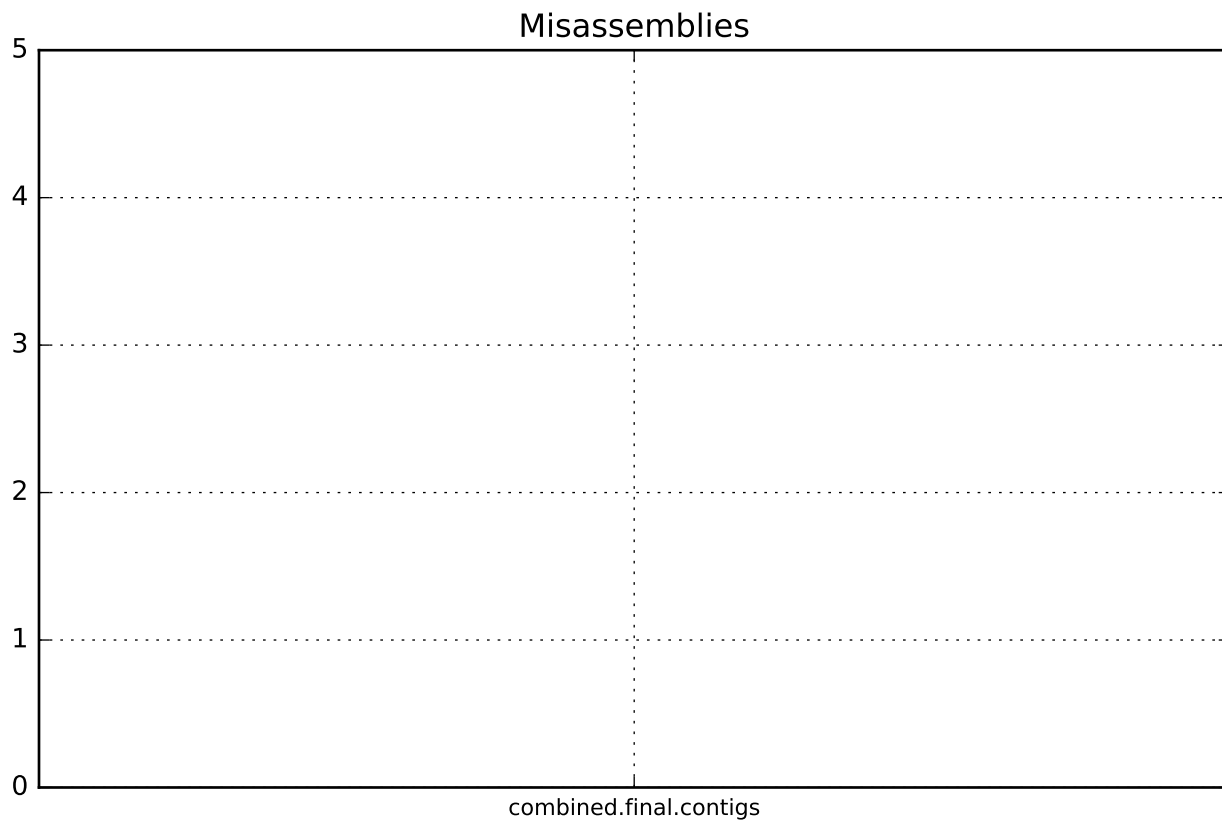
— combined.final.contigs      - - Reference

combined.final.contigs GC content

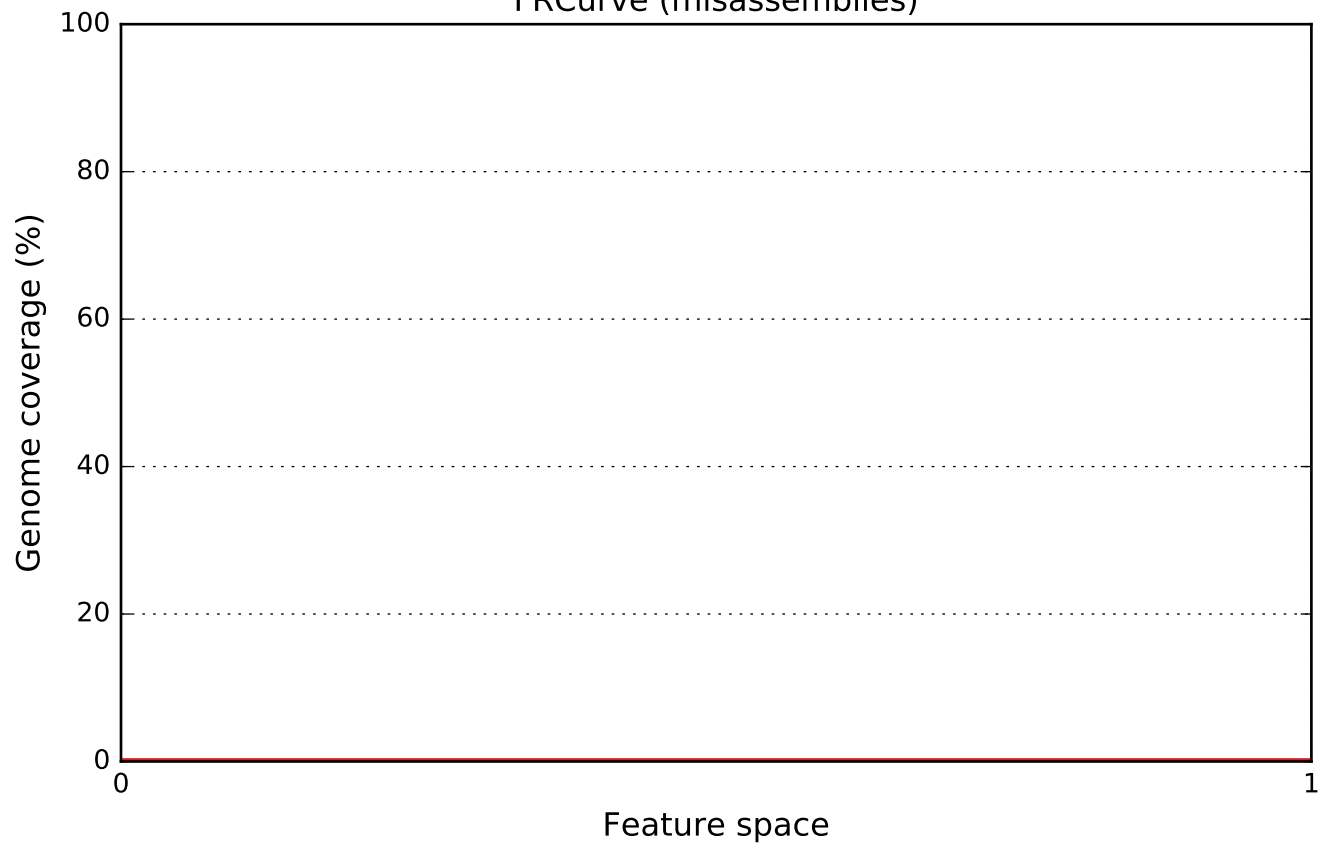


 combined.final.contigs



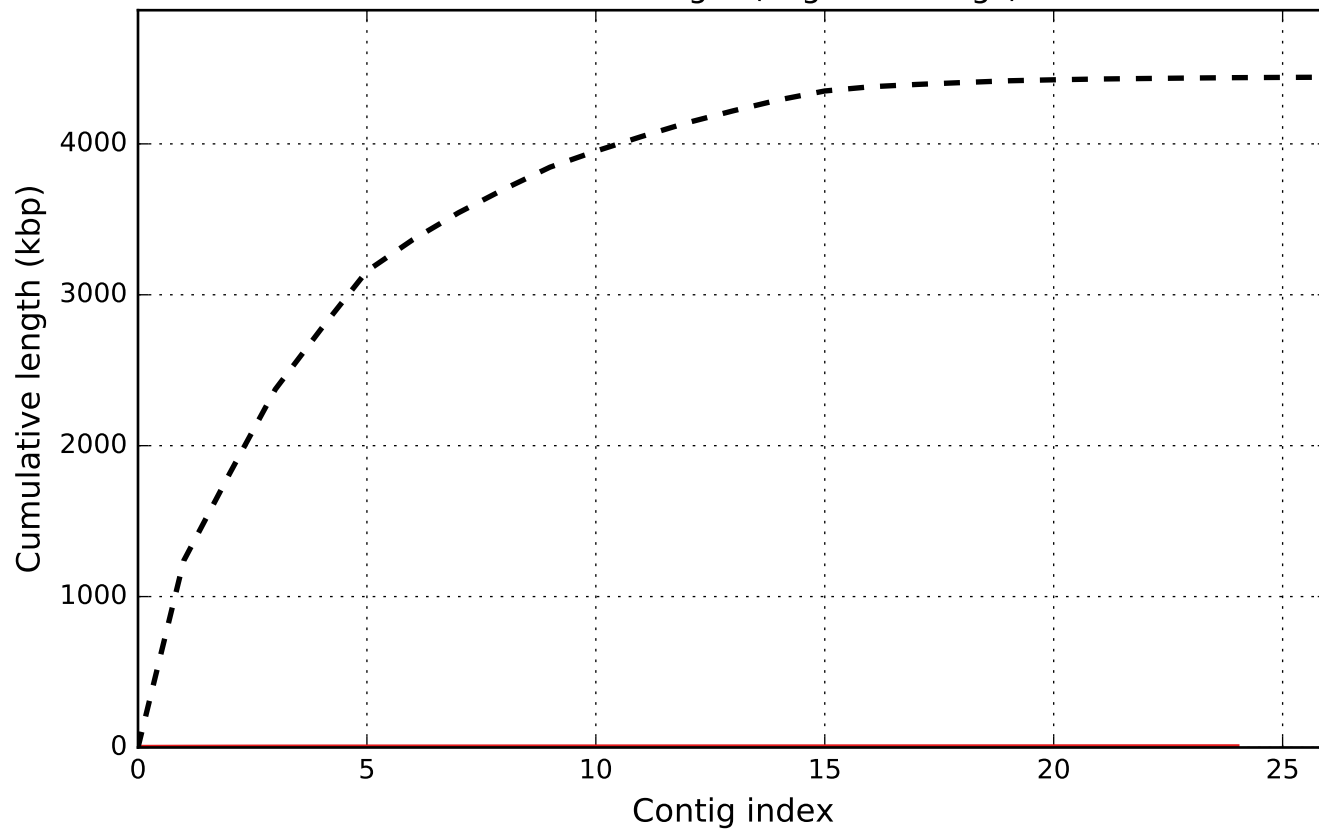


FRCurve (misassemblies)

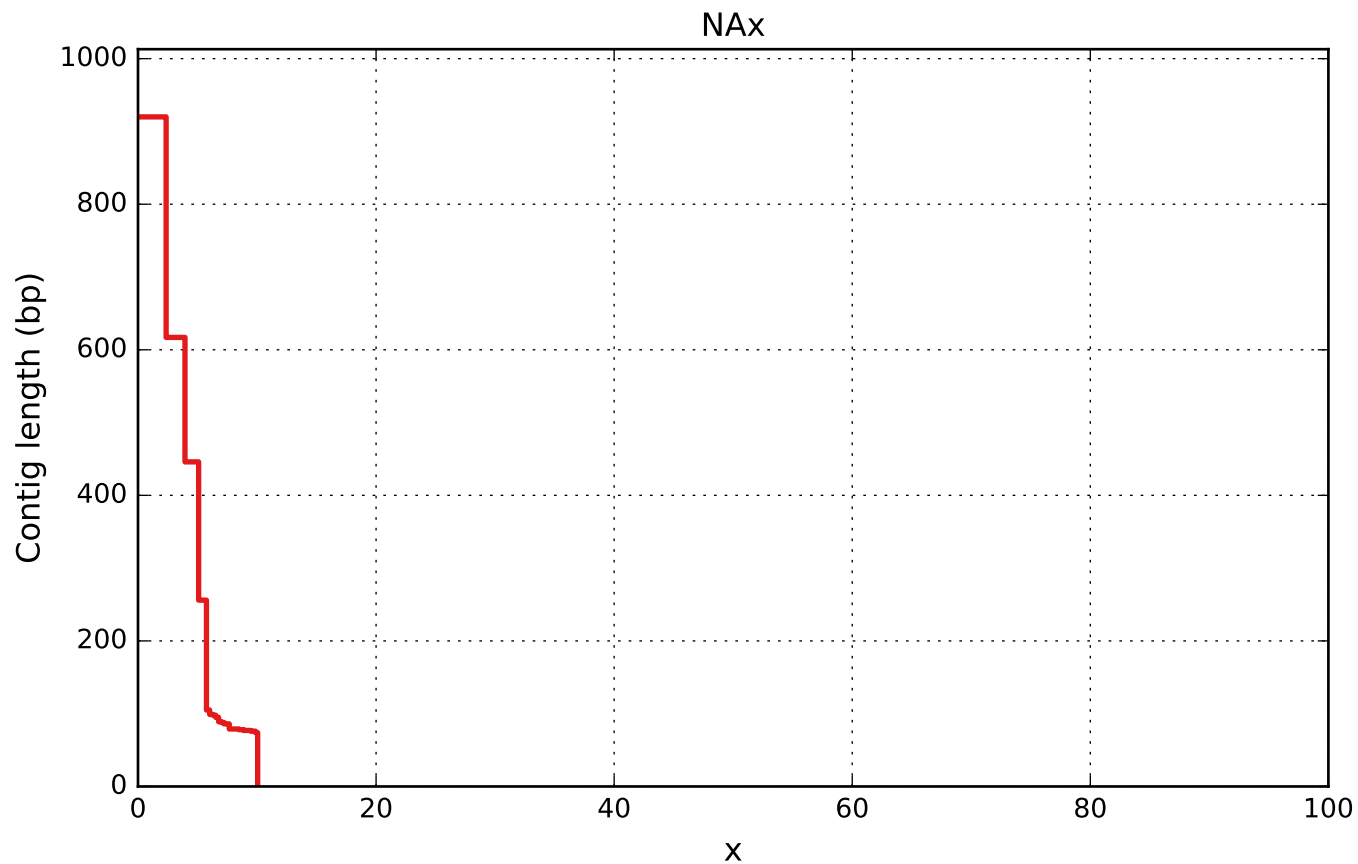


— combined.final.contigs

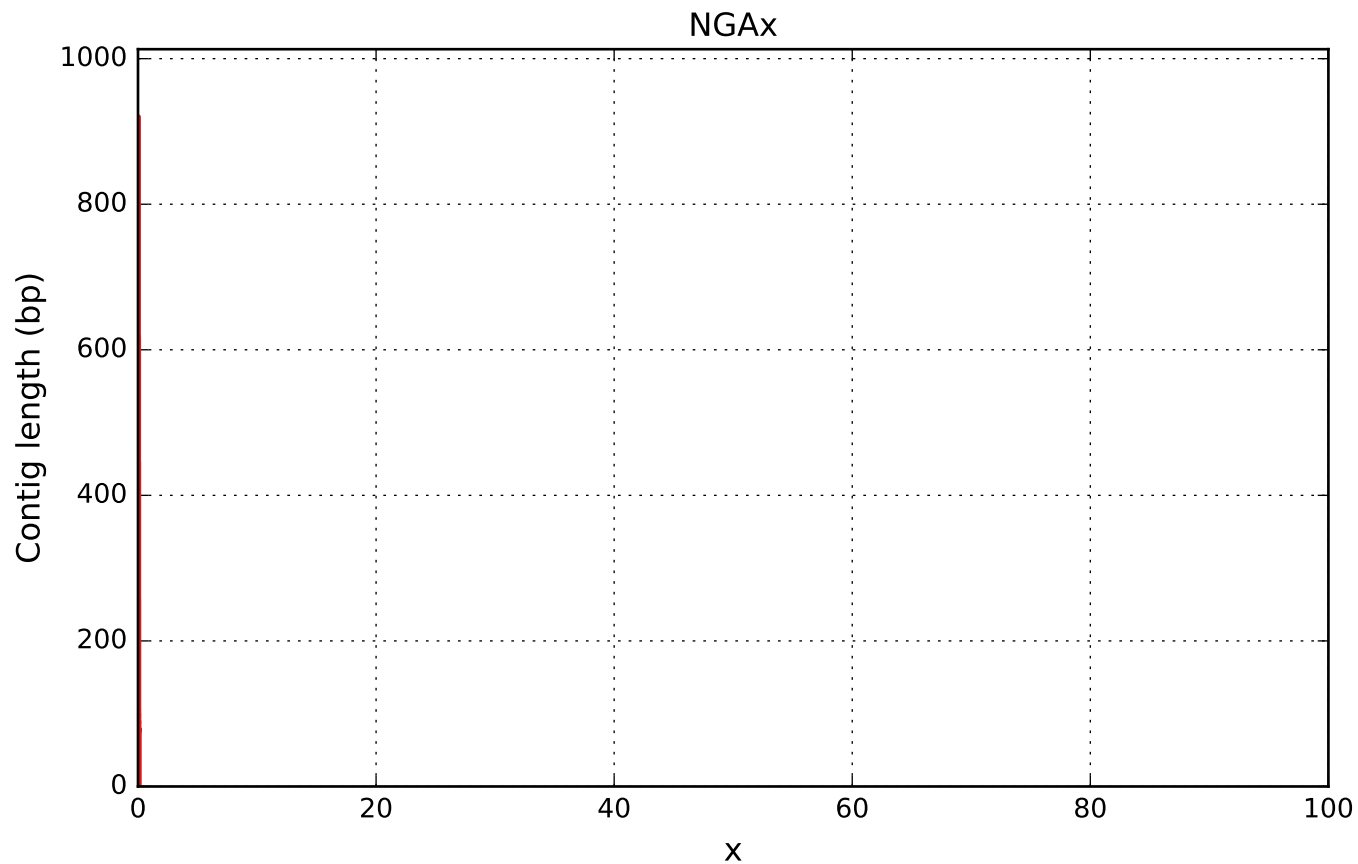
Cumulative length (aligned contigs)



— combined.final.contigs      - - Reference



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