

## Report

	final.contigs
# contigs ( $\geq 1000$ bp)	20
# contigs ( $\geq 5000$ bp)	2
# contigs ( $\geq 10000$ bp)	1
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	66580
Total length ( $\geq 5000$ bp)	22432
Total length ( $\geq 10000$ bp)	12904
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	36
Largest contig	12904
Total length	78036
Reference length	3261541
GC (%)	52.22
Reference GC (%)	56.74
N50	2776
N75	1736
L50	7
L75	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 28 part
Unaligned length	68458
Genome fraction (%)	0.169
Duplication ratio	1.735
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2790.36
# indels per 100 kbp	181.19
Largest alignment	1456
Total aligned length	6939
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

	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	2
# unaligned mis. contigs	0
# mismatches	154
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	10

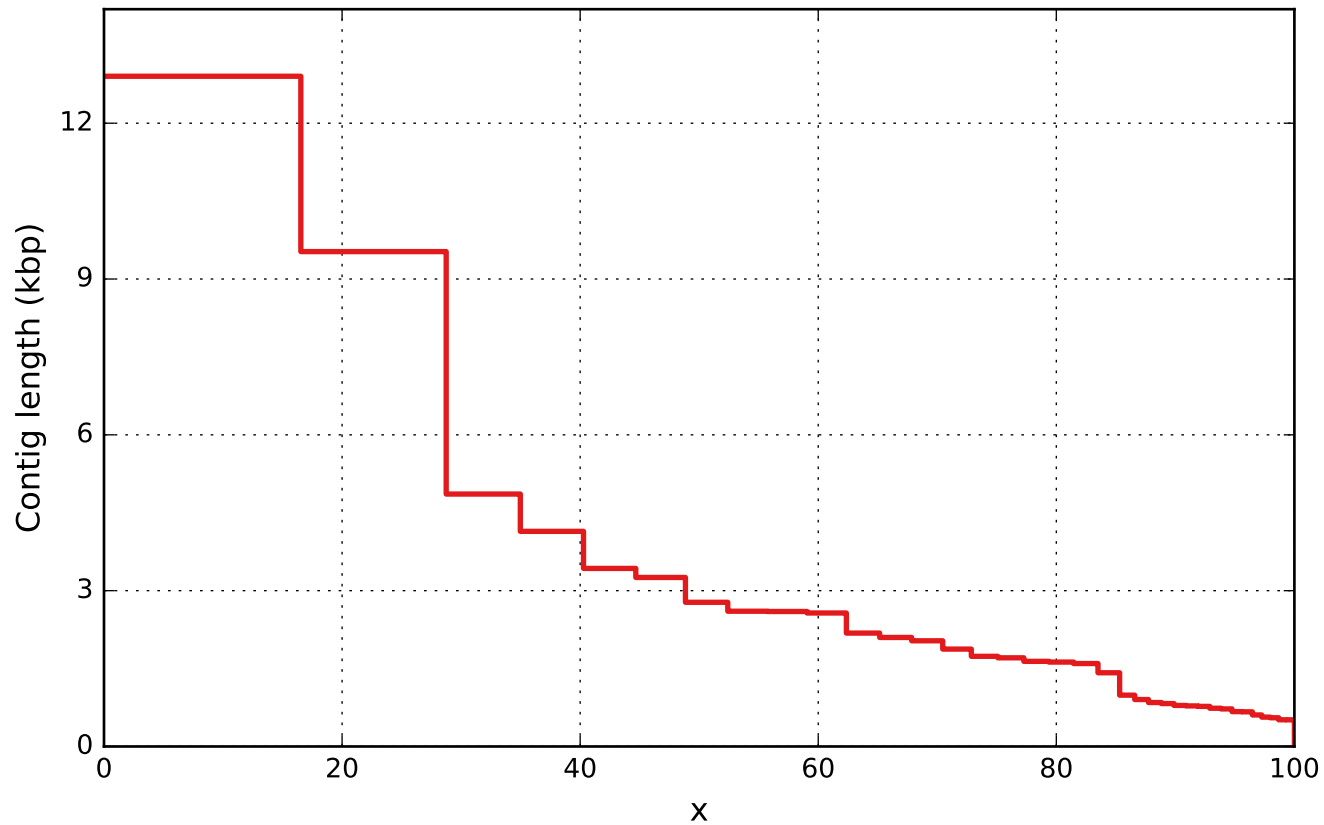
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	28
Partially unaligned length	68458
# N's	0

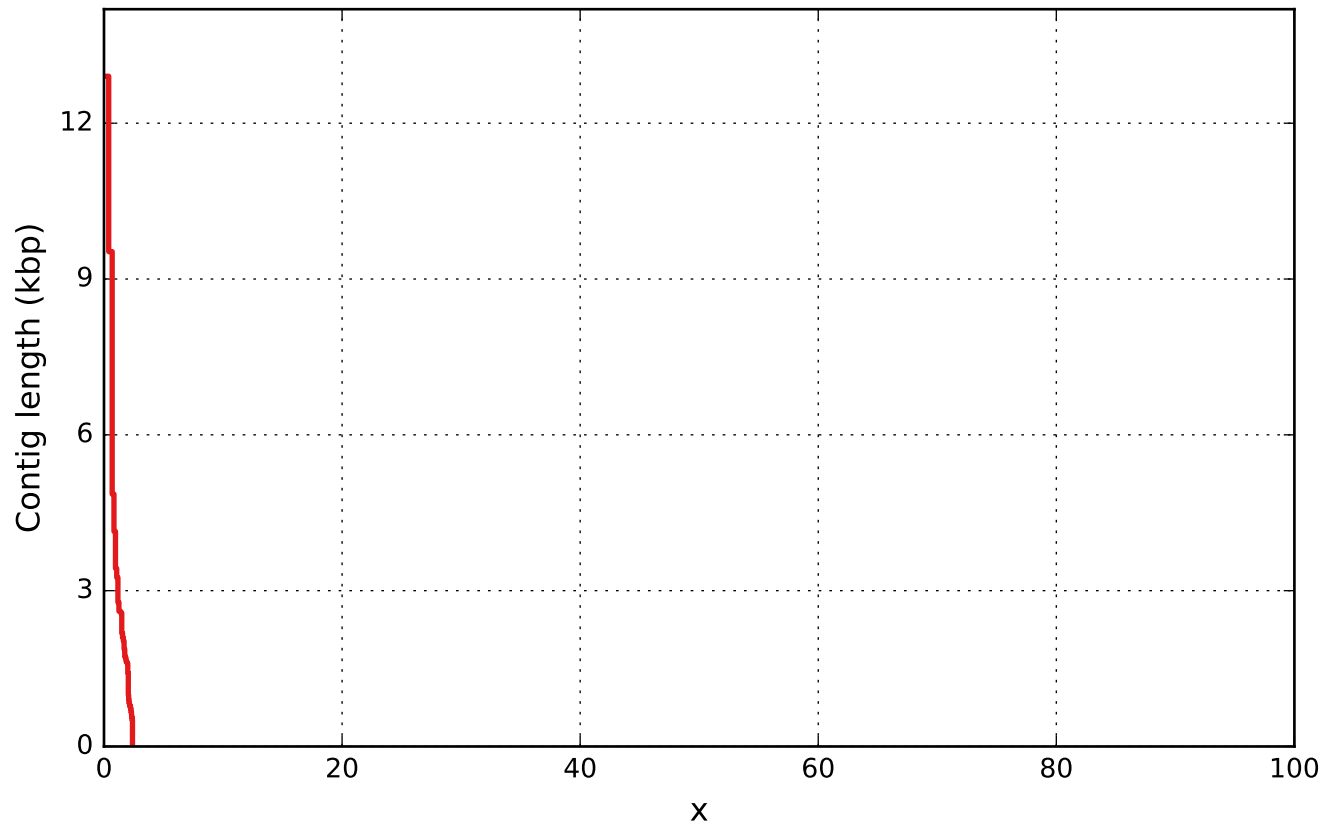
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

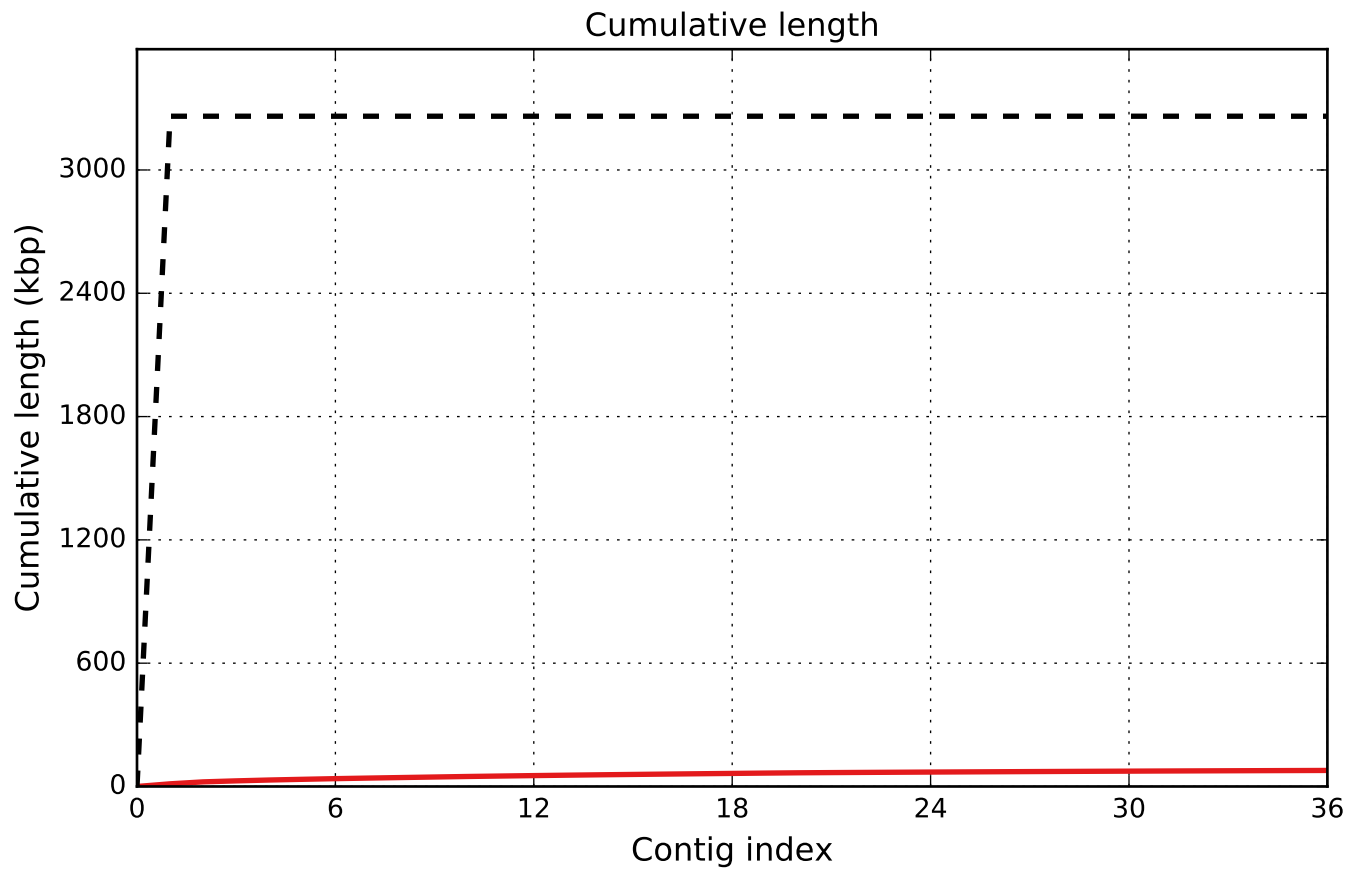


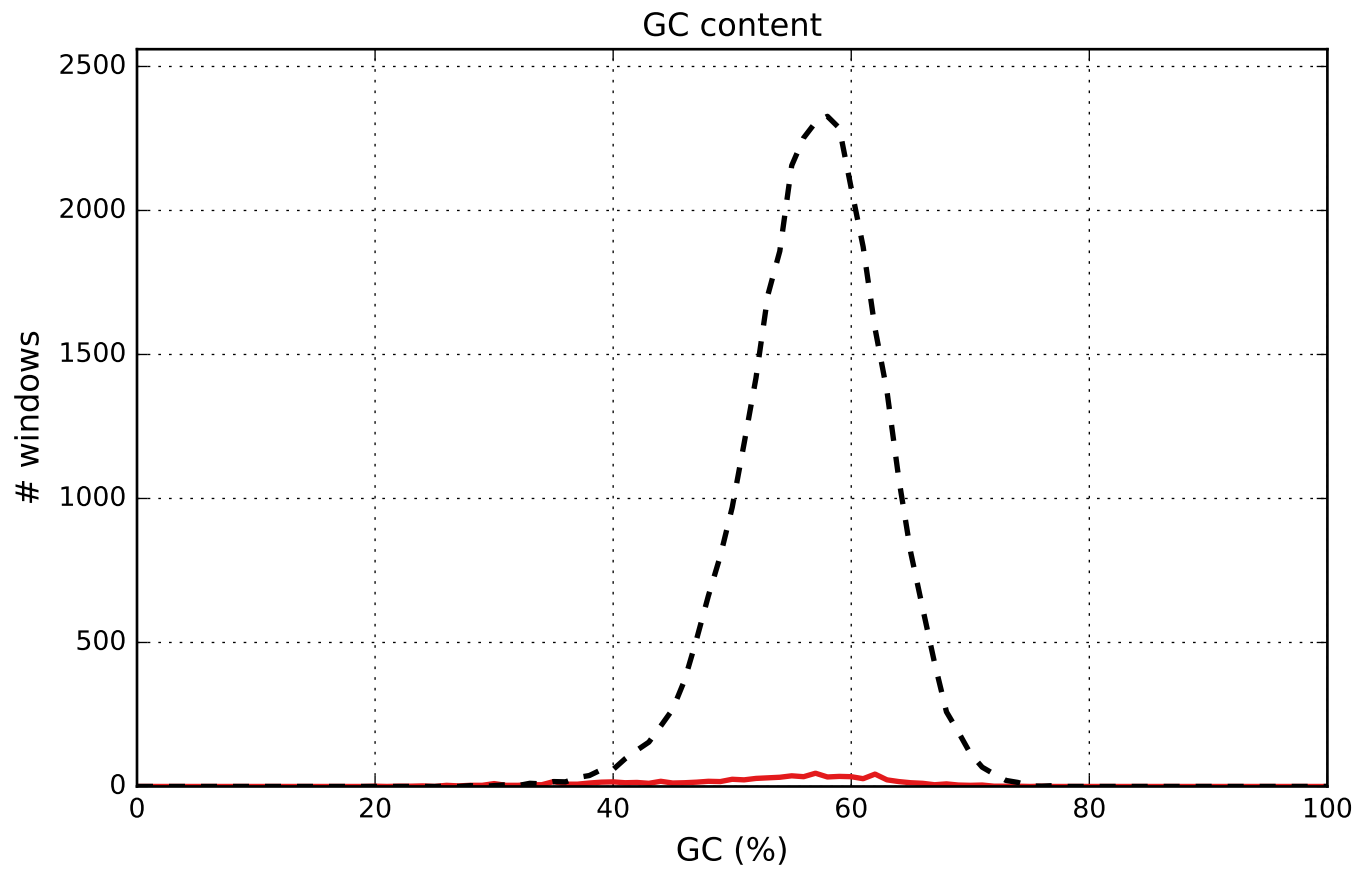
— final.contigs

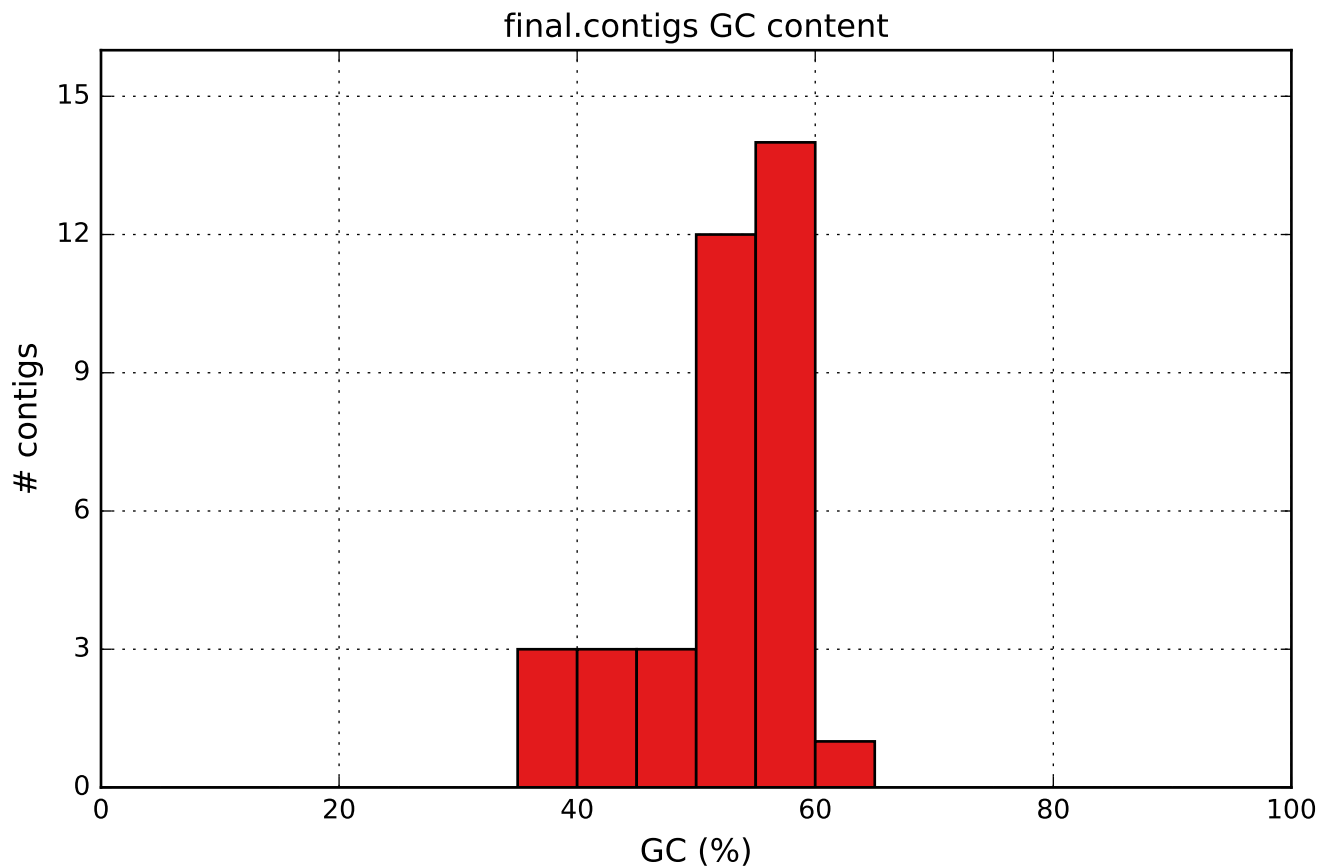
NGx



— final.contigs





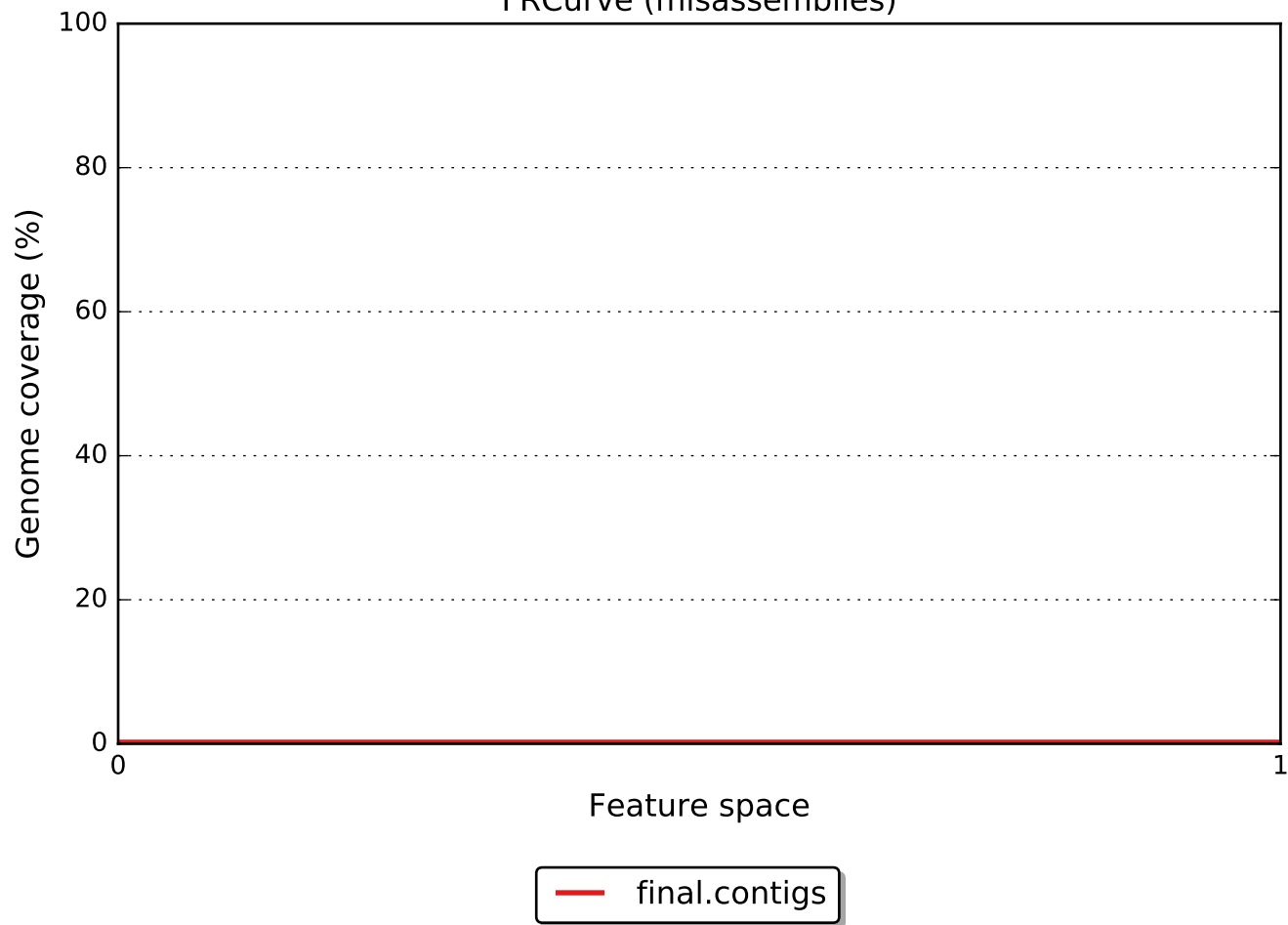


final.contigs

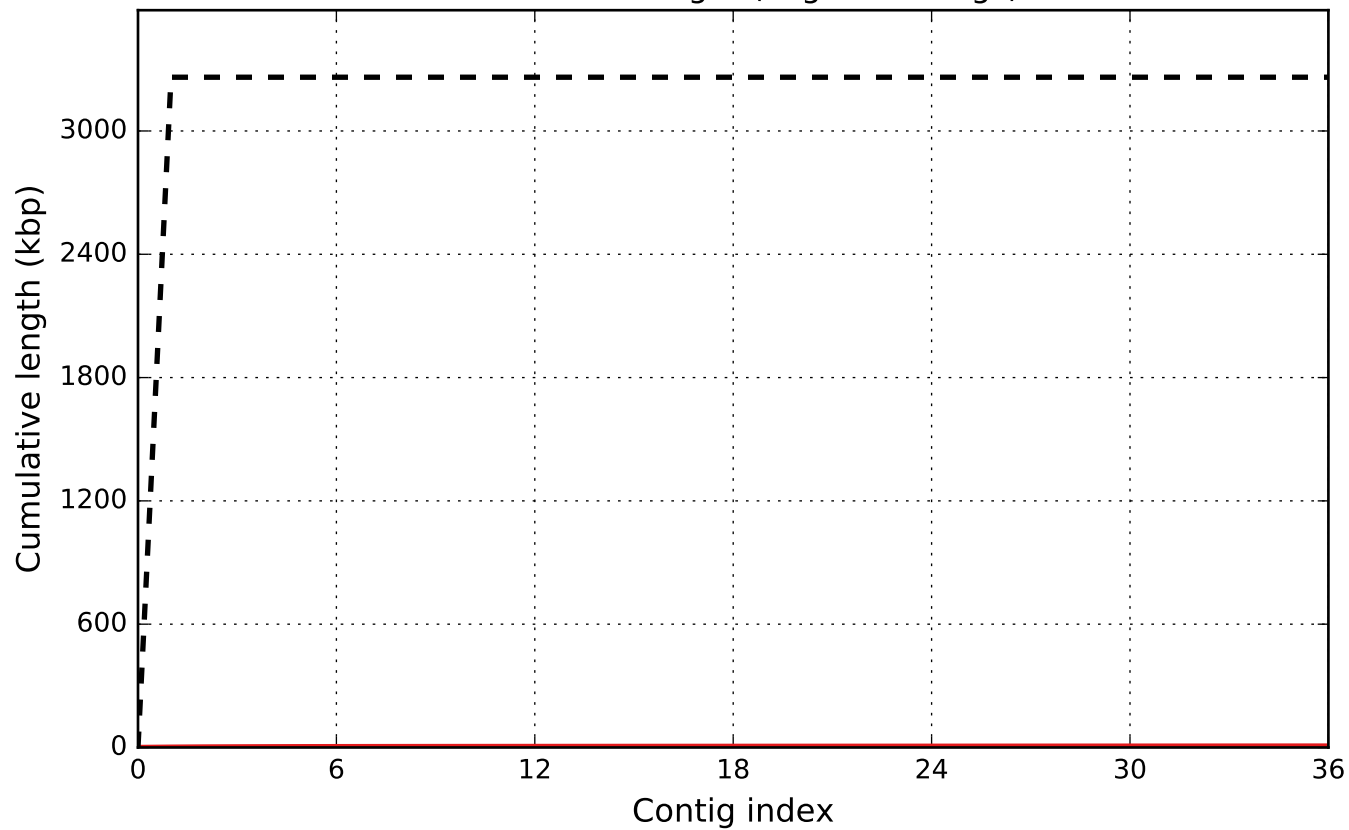


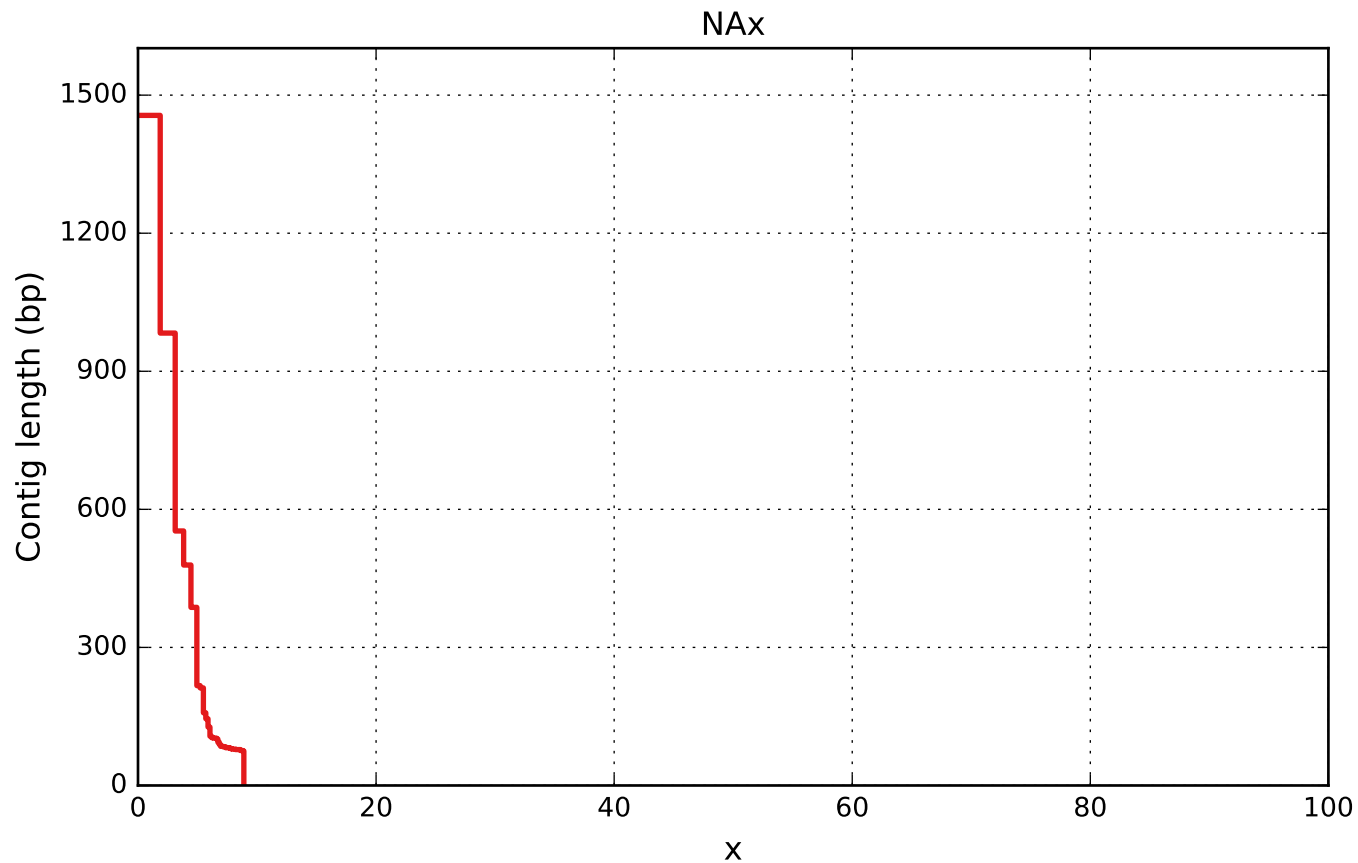


FRCurve (misassemblies)

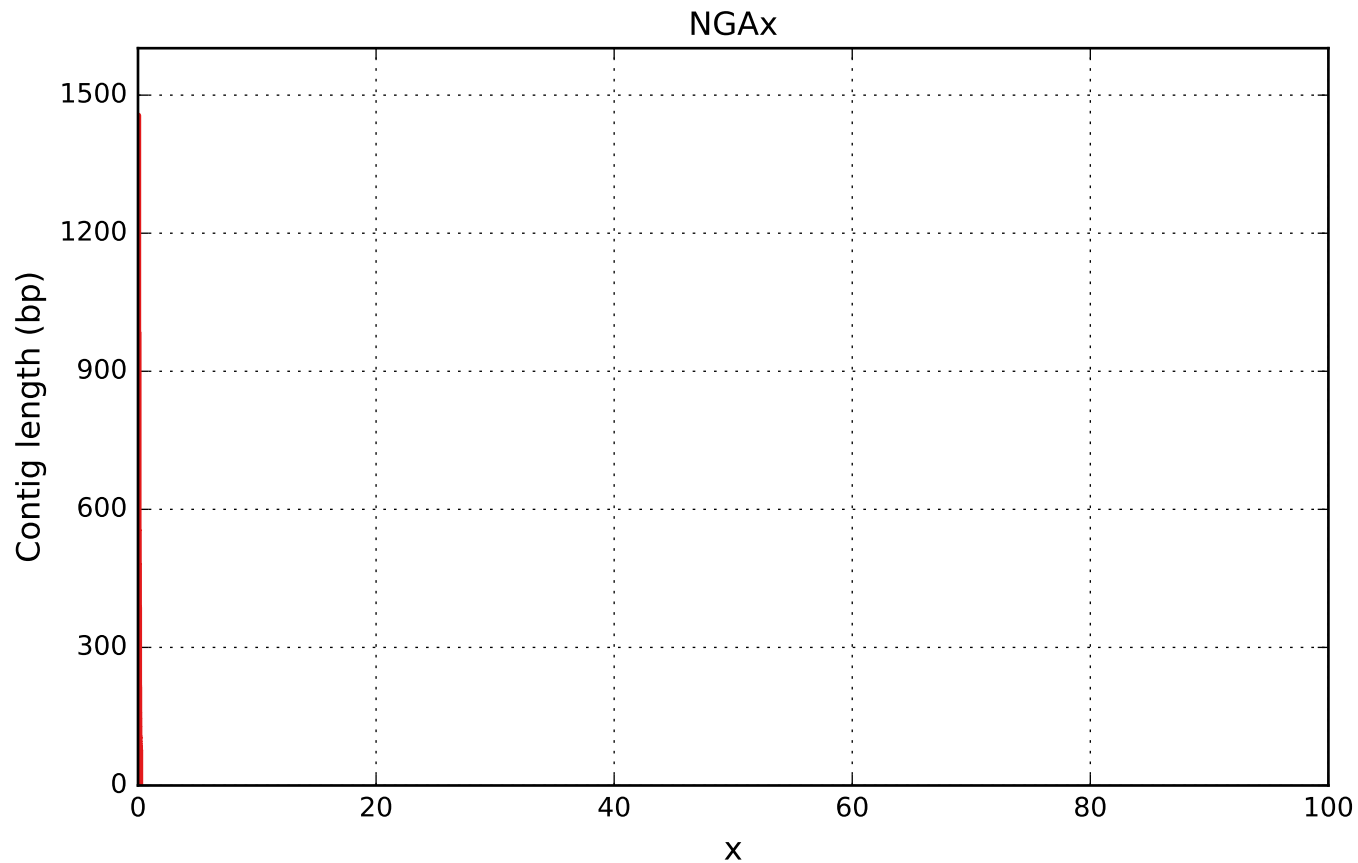


Cumulative length (aligned contigs)





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