

# Report

	final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	5313
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	1809
Total length	10868
Reference length	3098747
GC (%)	50.45
Reference GC (%)	49.73
N50	791
N75	712
L50	5
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	4458
Genome fraction (%)	0.092
Duplication ratio	2.260
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3102.96
# indels per 100 kbp	282.09
Largest alignment	1467
Total aligned length	3334
NGA50	-

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

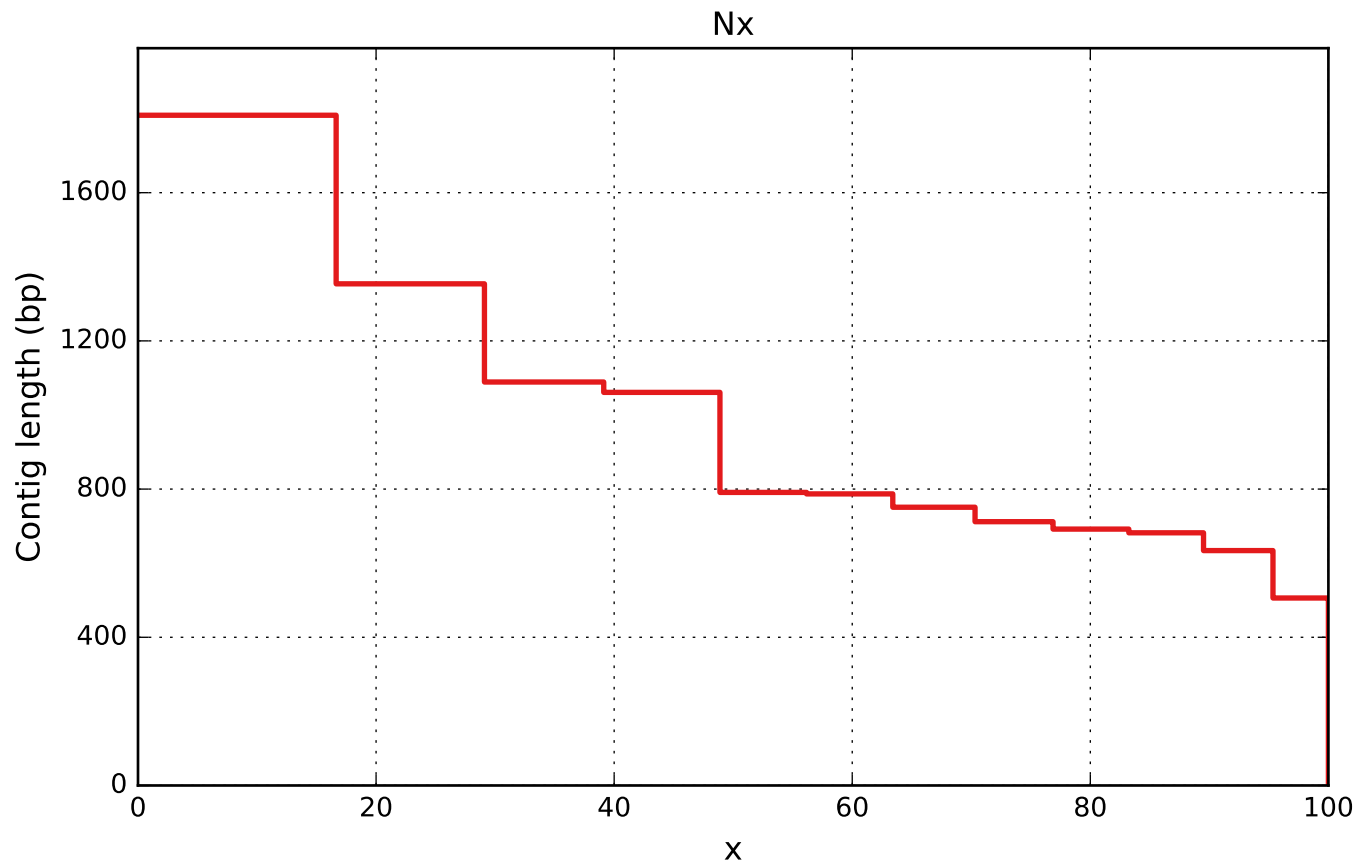
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	88
# indels	8
# indels ( $\leq 5$ bp)	8
# indels ( $> 5$ bp)	0
Indels length	8

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).

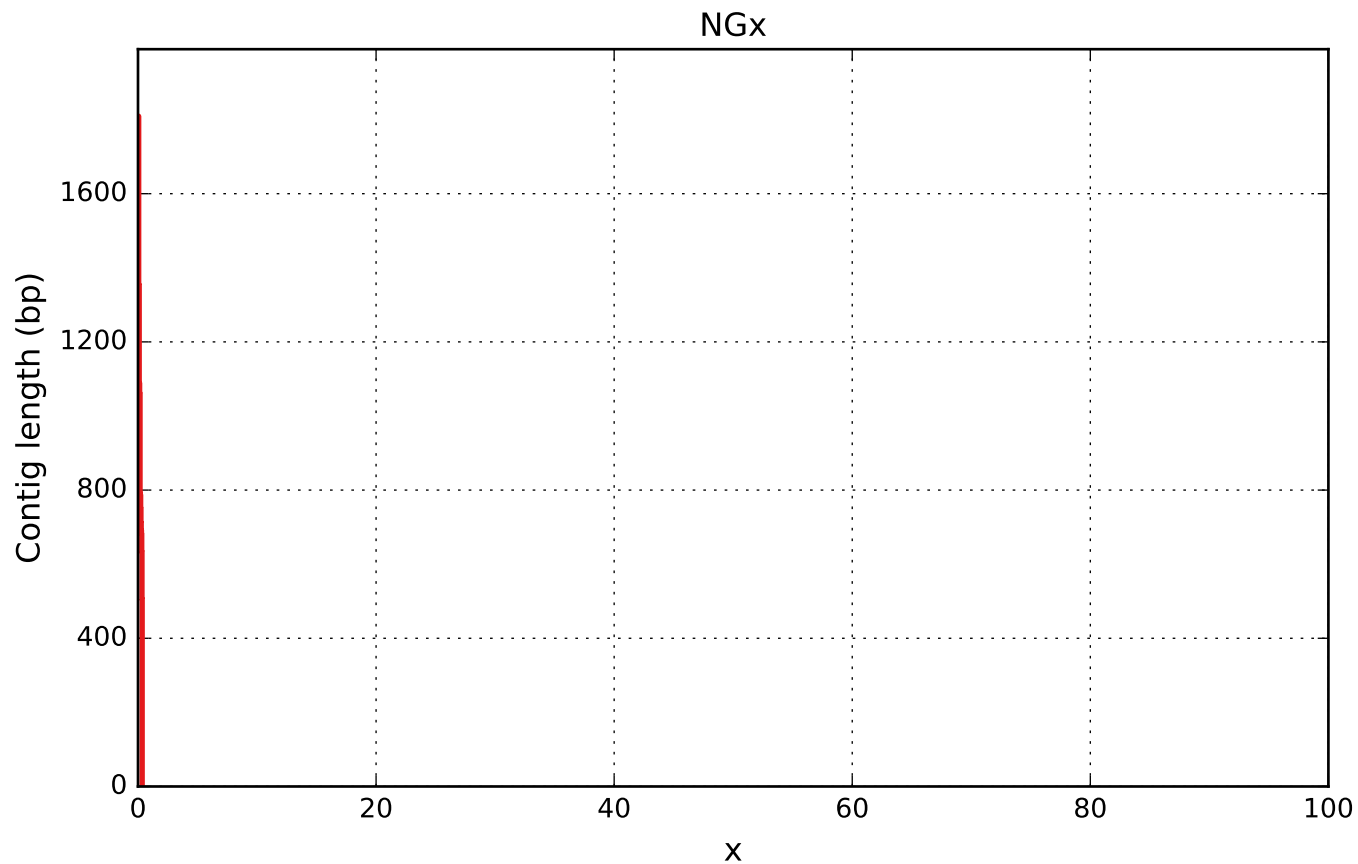
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	4458
# N's	0

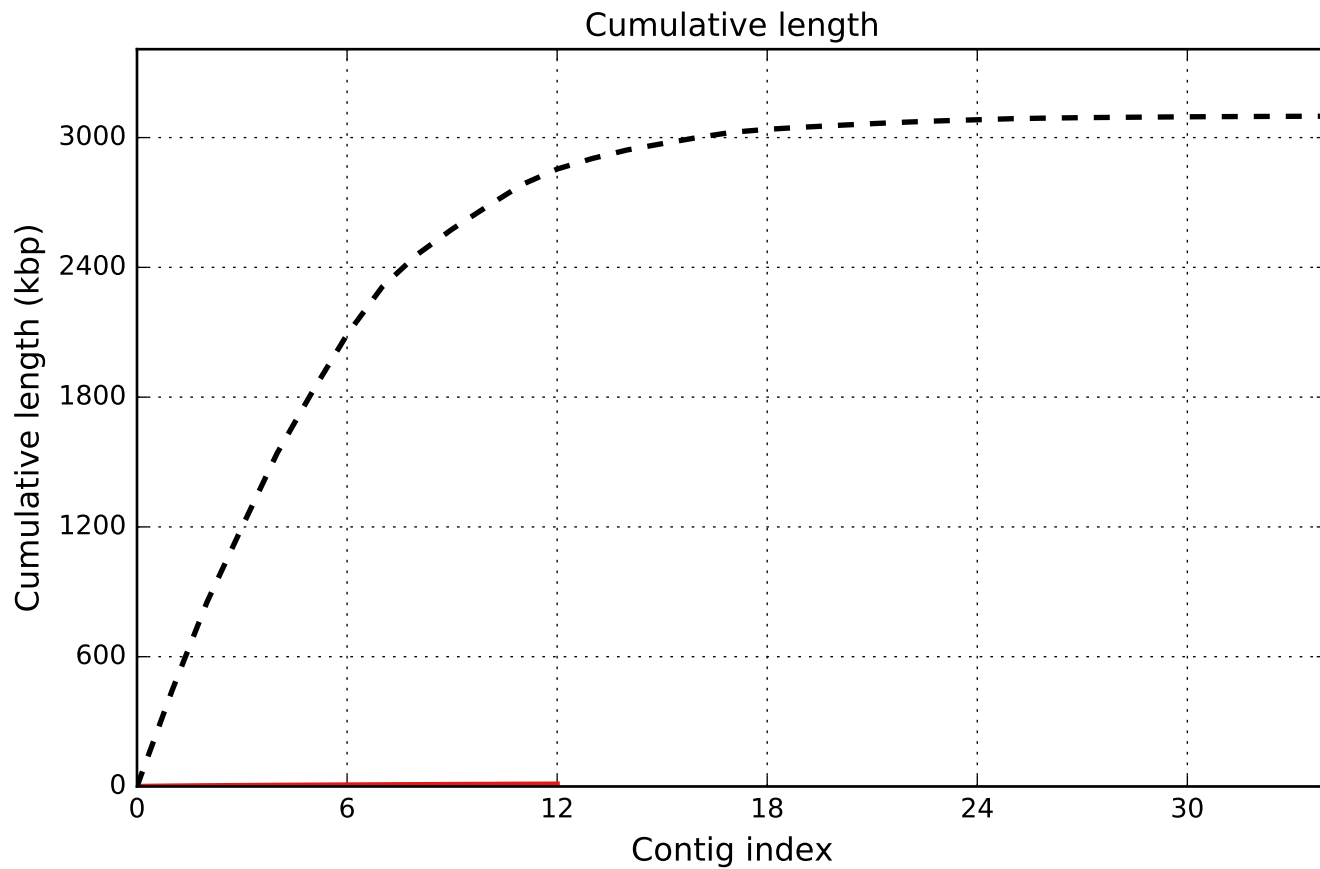
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



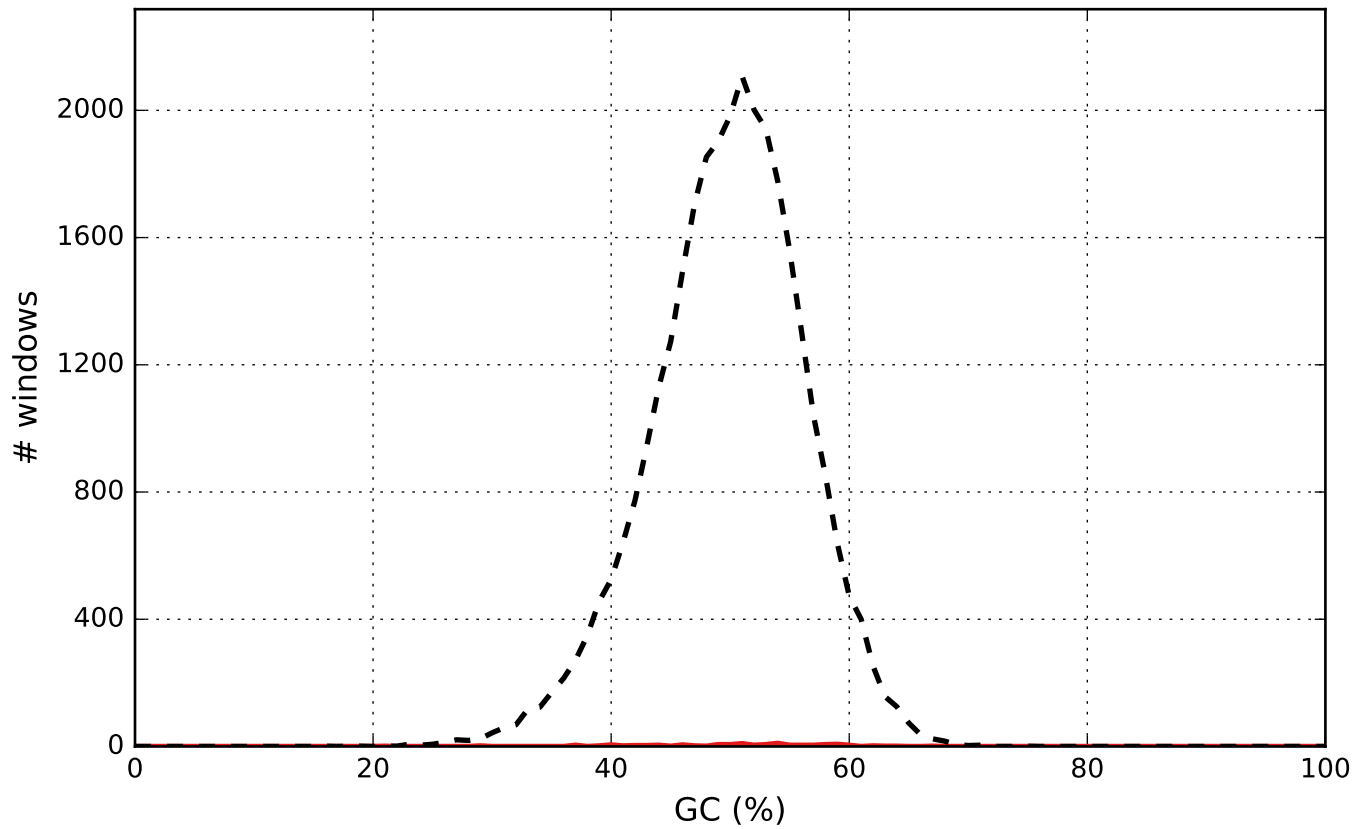
— final.contigs



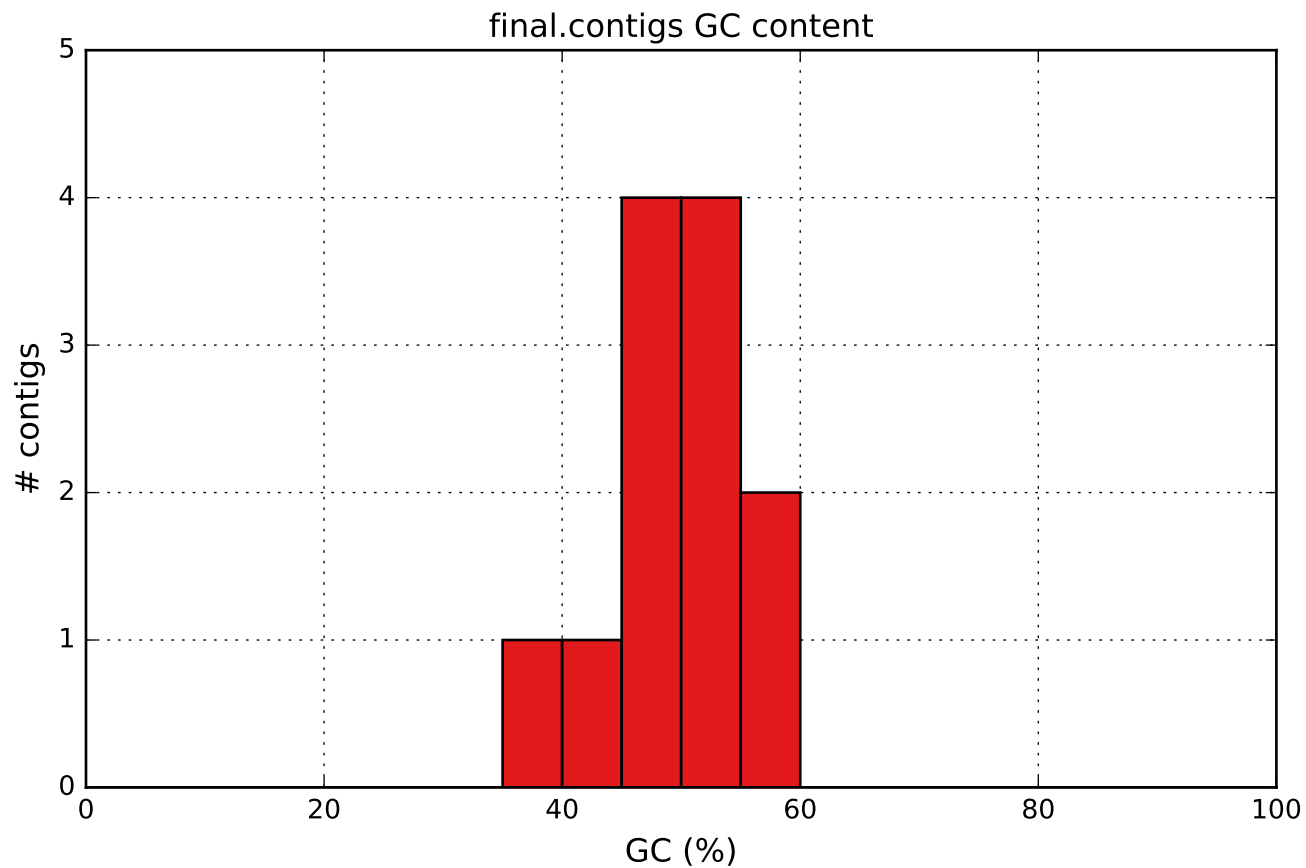
— final.contigs



GC content



— final.contigs    - - Reference

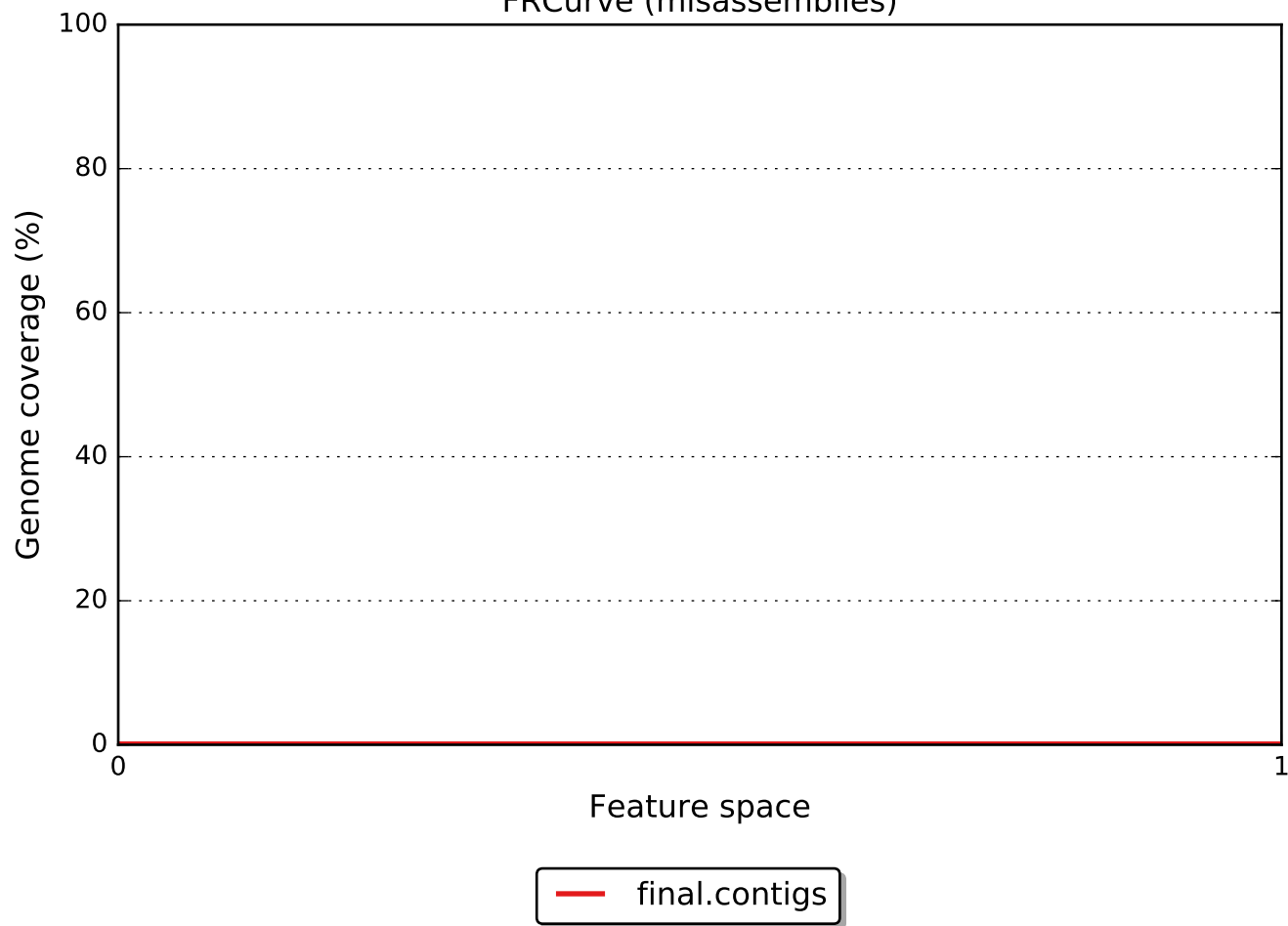


final.contigs

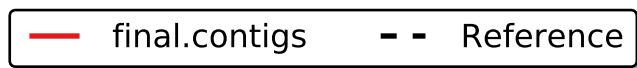
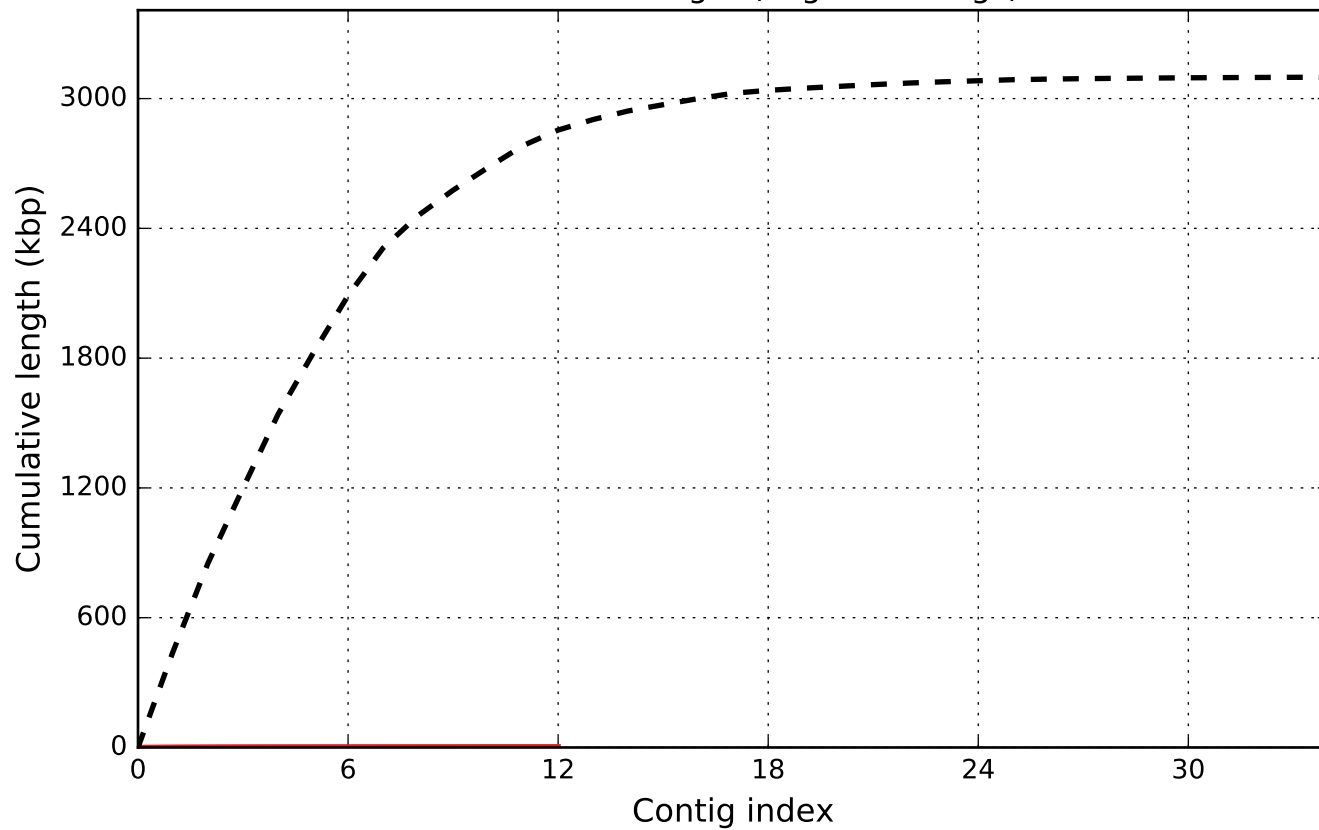


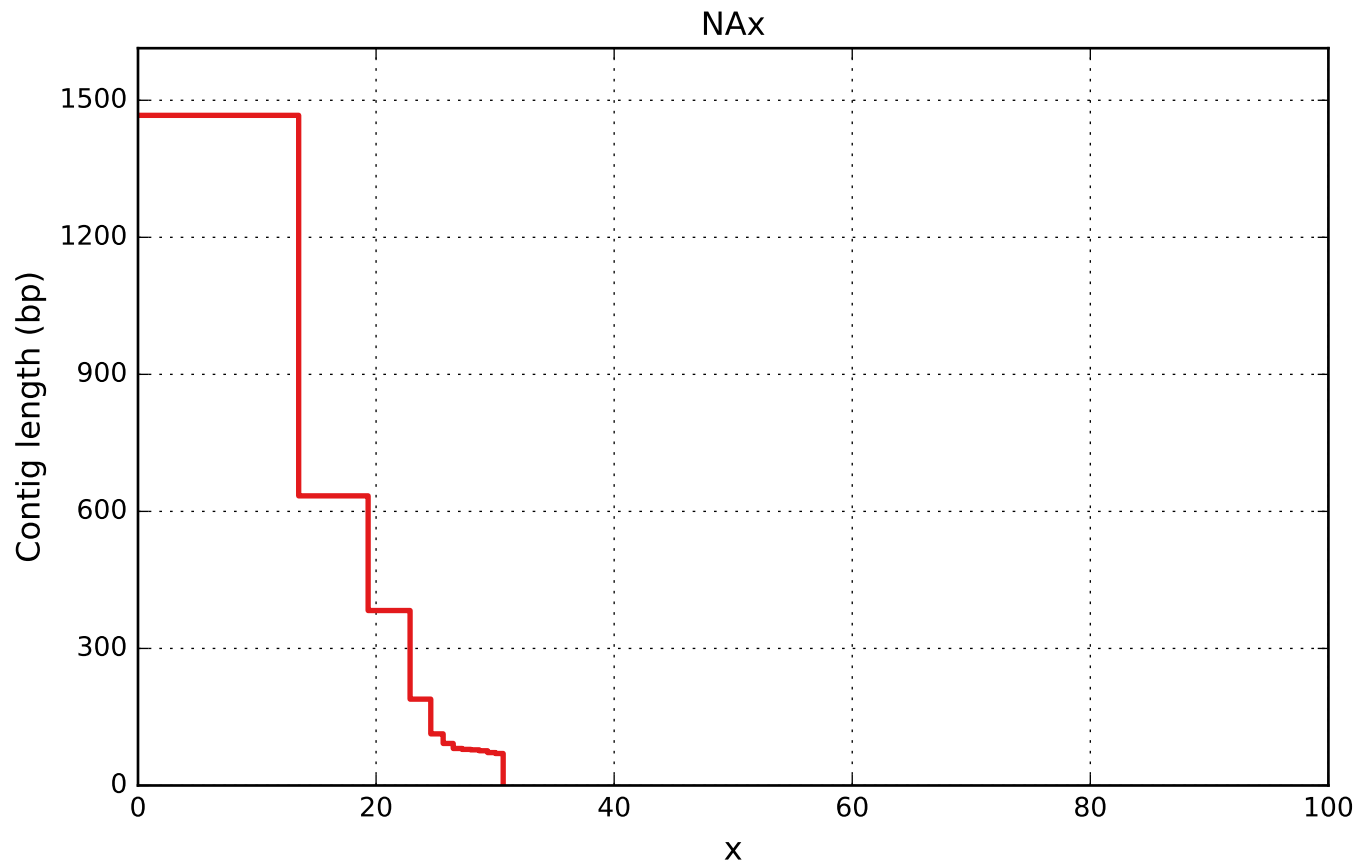


FRCurve (misassemblies)

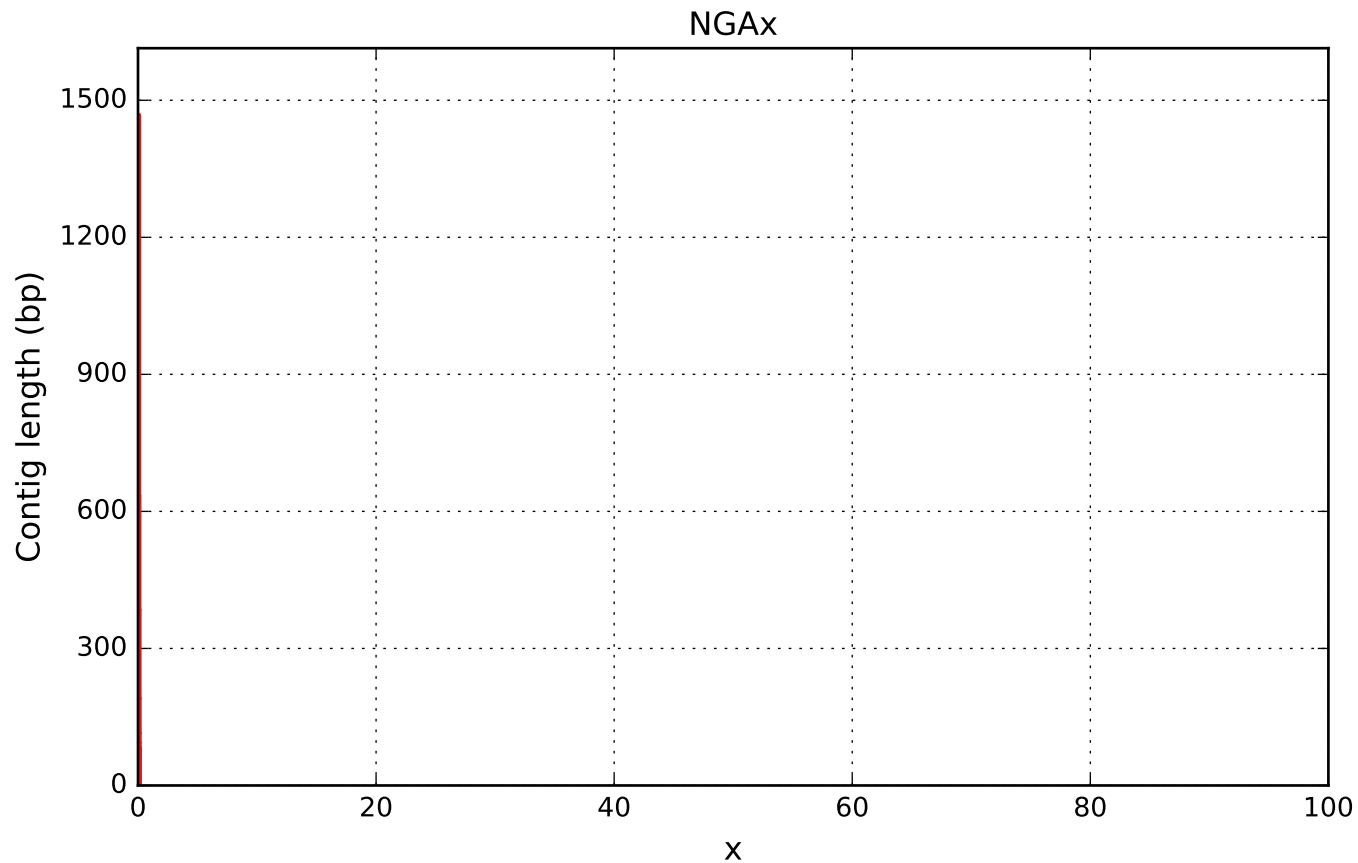


Cumulative length (aligned contigs)





— final.contigs



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