

## Report

	bin_7
# contigs ( $\geq$ 1000 bp)	2
# contigs ( $\geq$ 5000 bp)	2
# contigs ( $\geq$ 10000 bp)	2
# contigs ( $\geq$ 25000 bp)	0
# contigs ( $\geq$ 50000 bp)	0
Total length ( $\geq$ 1000 bp)	29461
Total length ( $\geq$ 5000 bp)	29461
Total length ( $\geq$ 10000 bp)	29461
Total length ( $\geq$ 25000 bp)	0
Total length ( $\geq$ 50000 bp)	0
# contigs	2
Largest contig	16895
Total length	29461
Reference length	3633537
GC (%)	32.38
Reference GC (%)	32.71
N50	16895
N75	12566
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	29310
Genome fraction (%)	0.004
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	76
Total aligned length	151
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

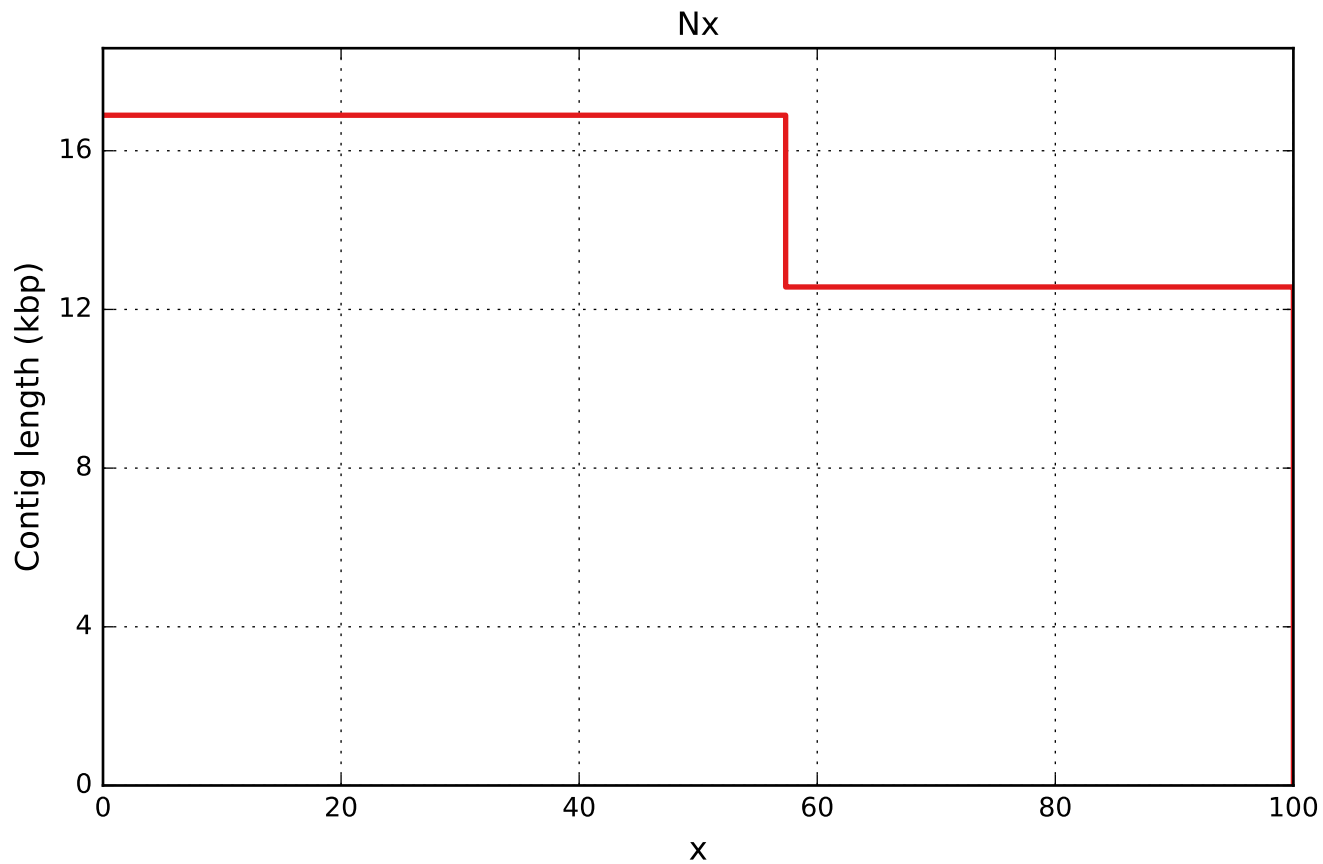
	bin_7
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

## Unaligned report

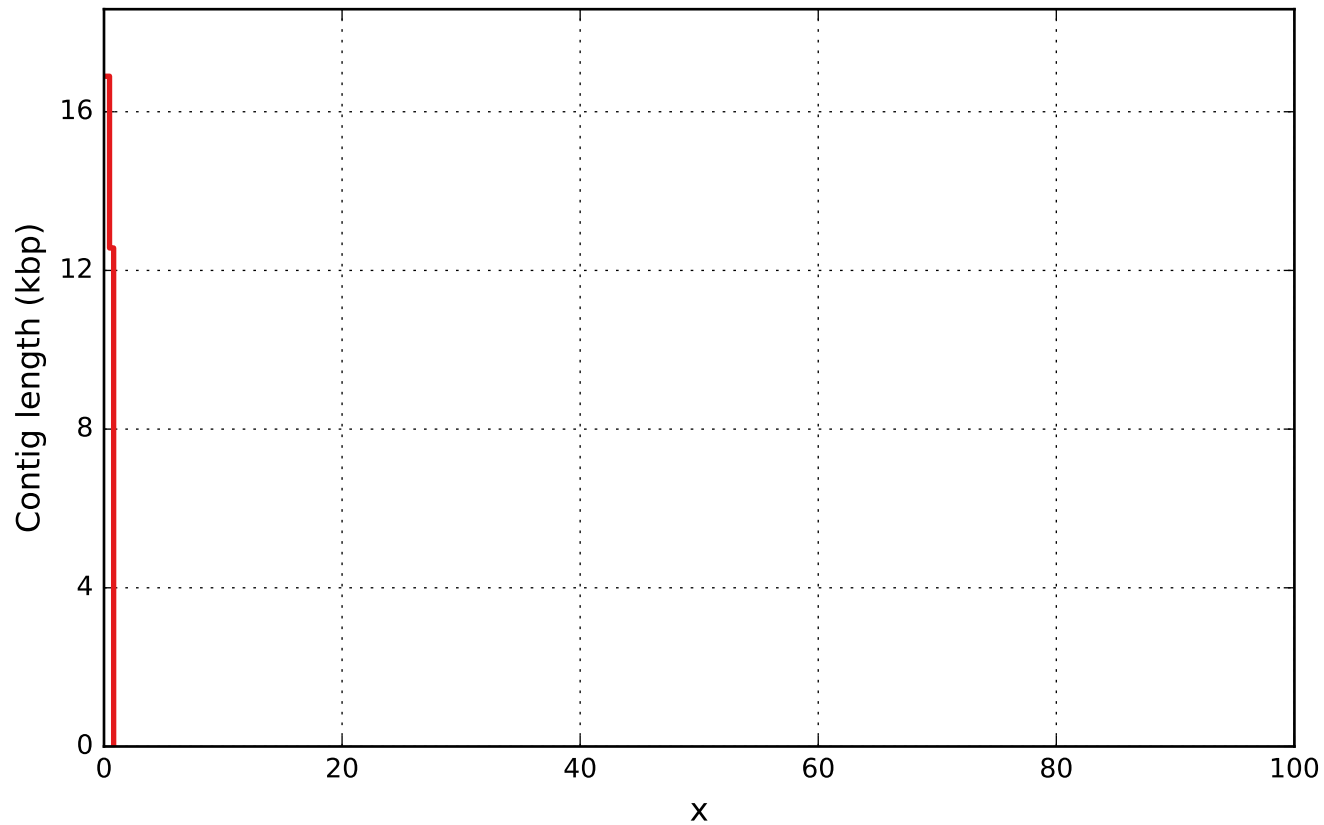
	bin_7
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	29310
# N's	0

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).

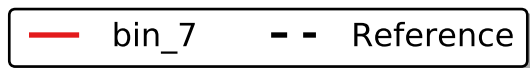
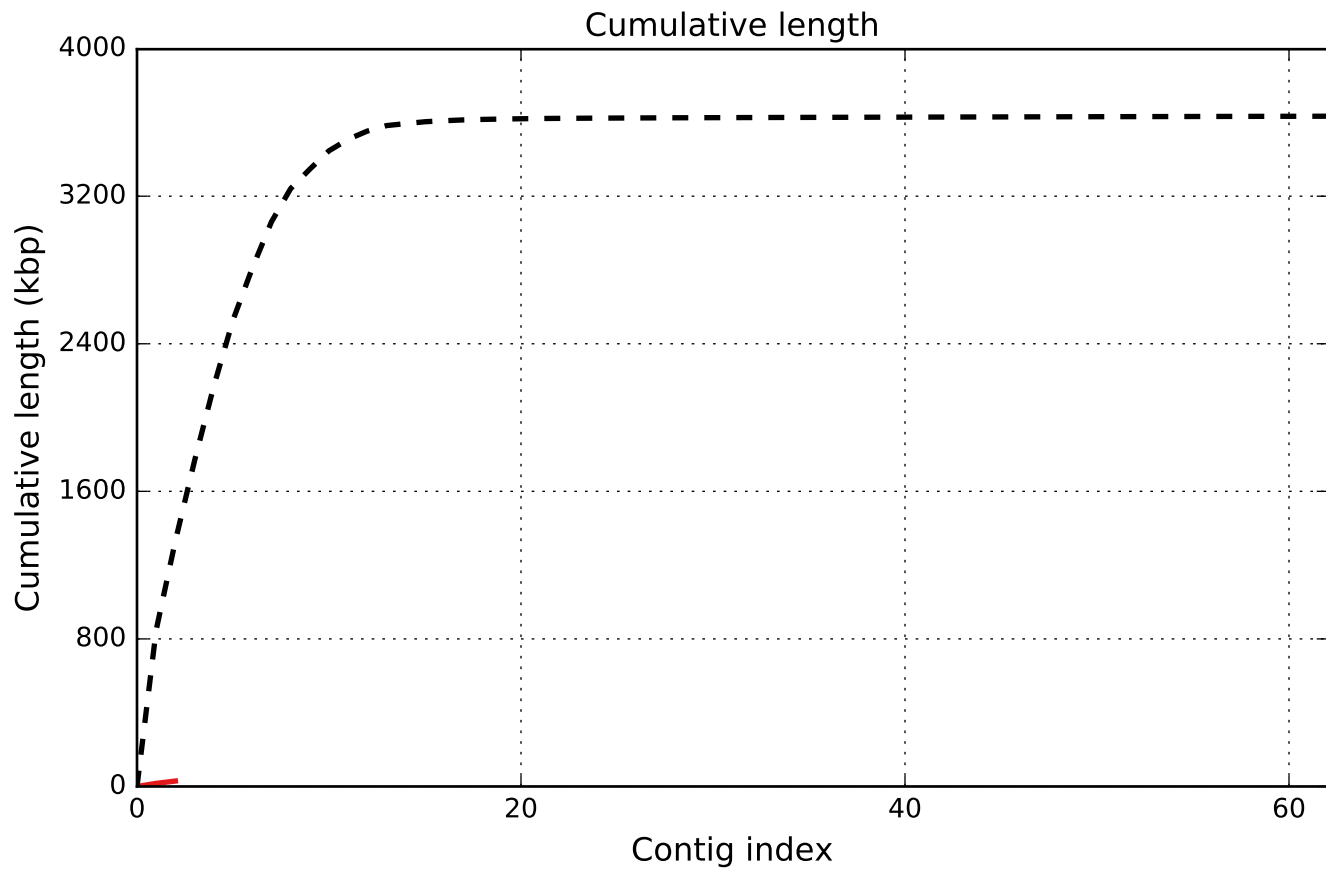


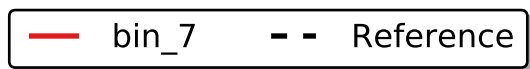
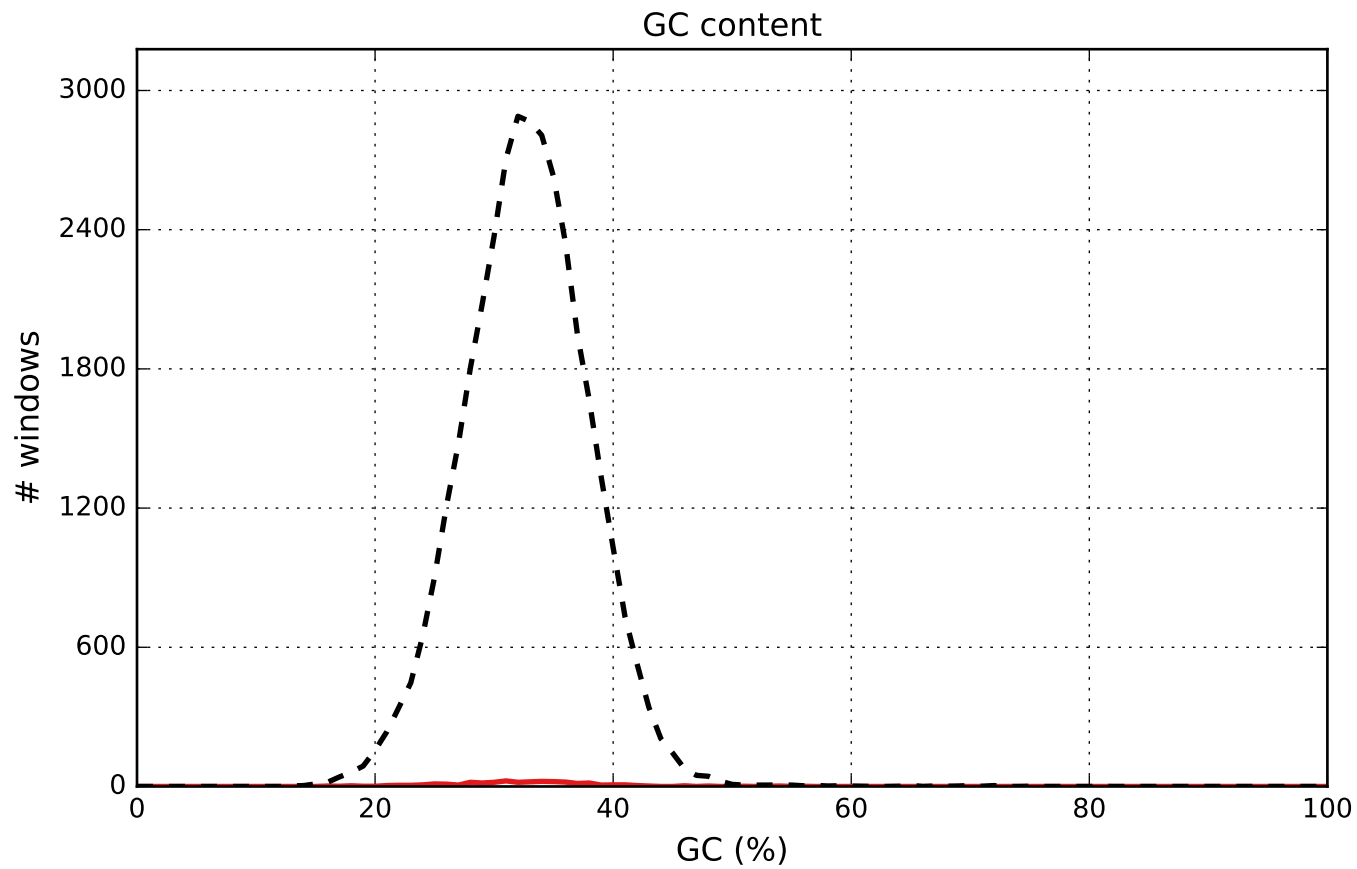
— bin\_7

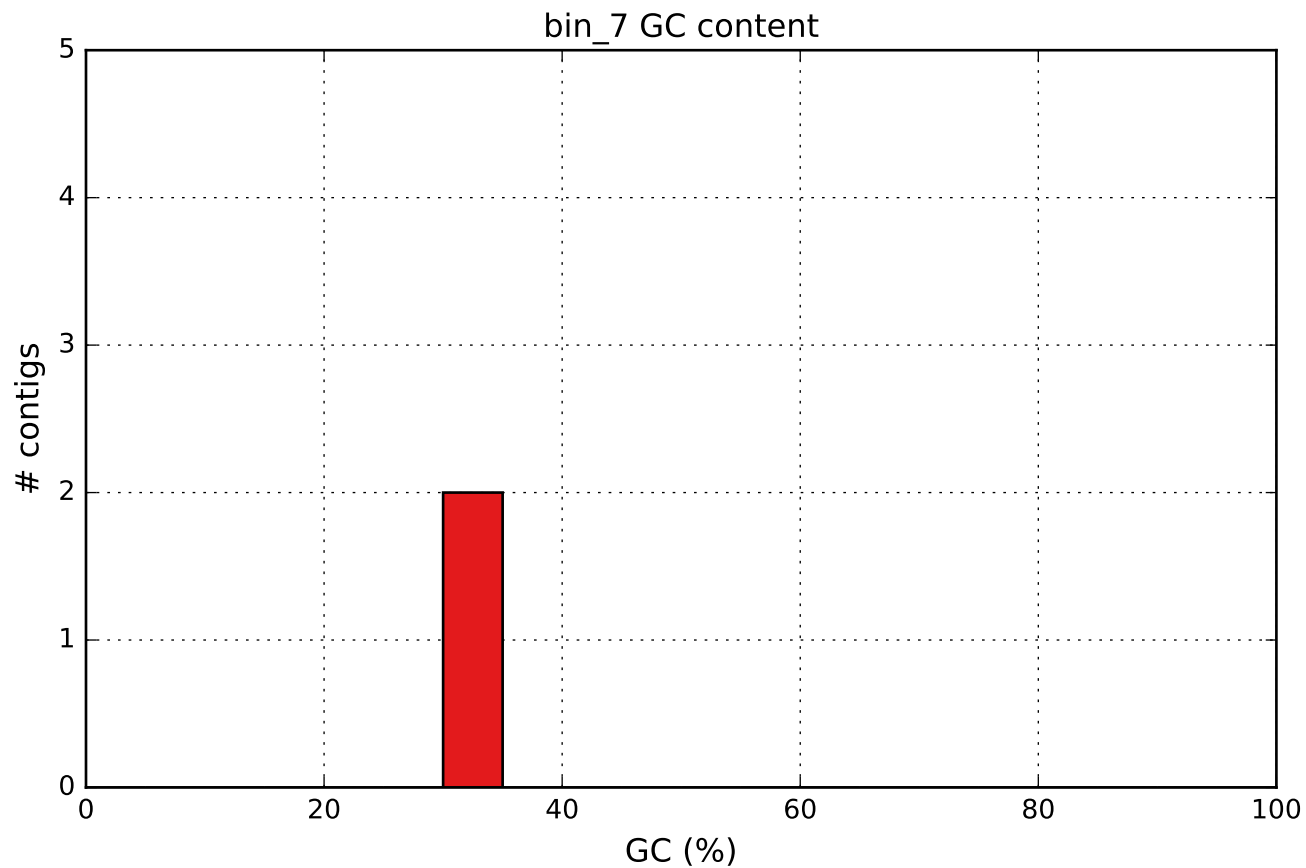
NGx



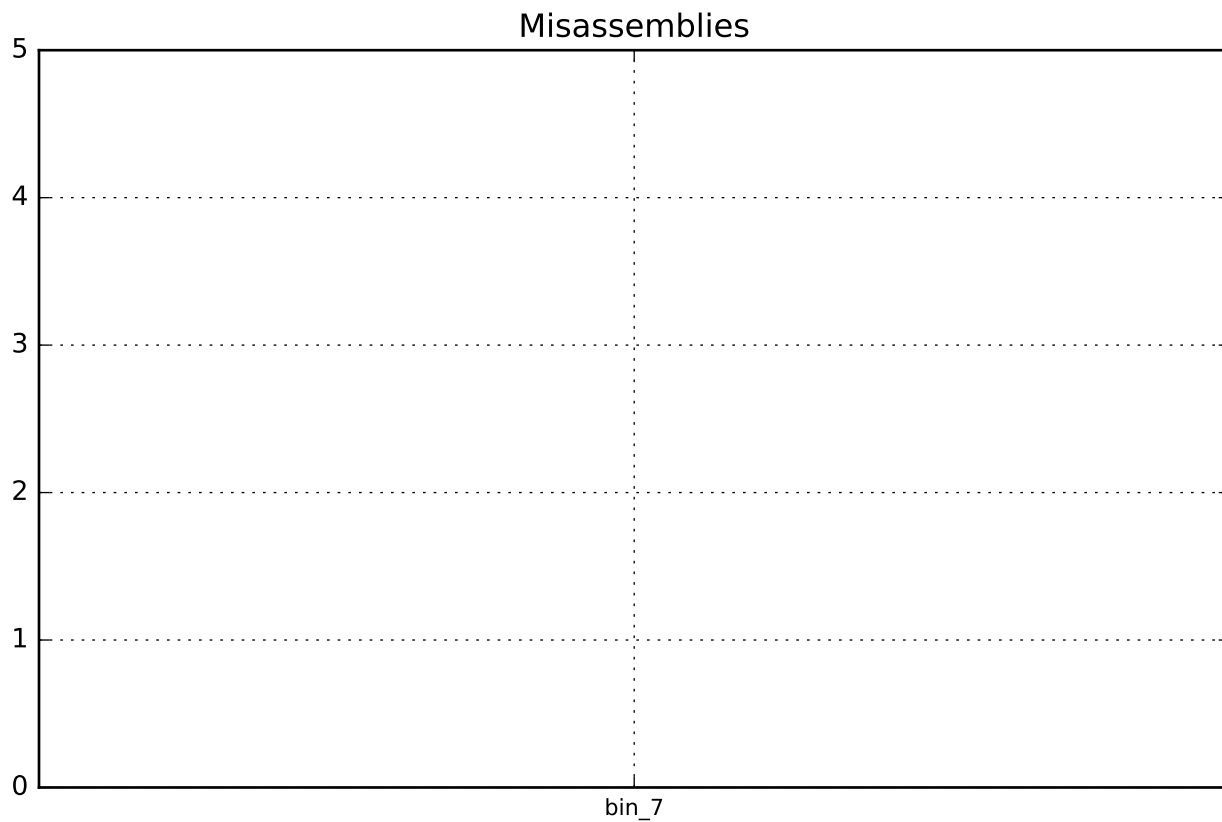
— bin\_7



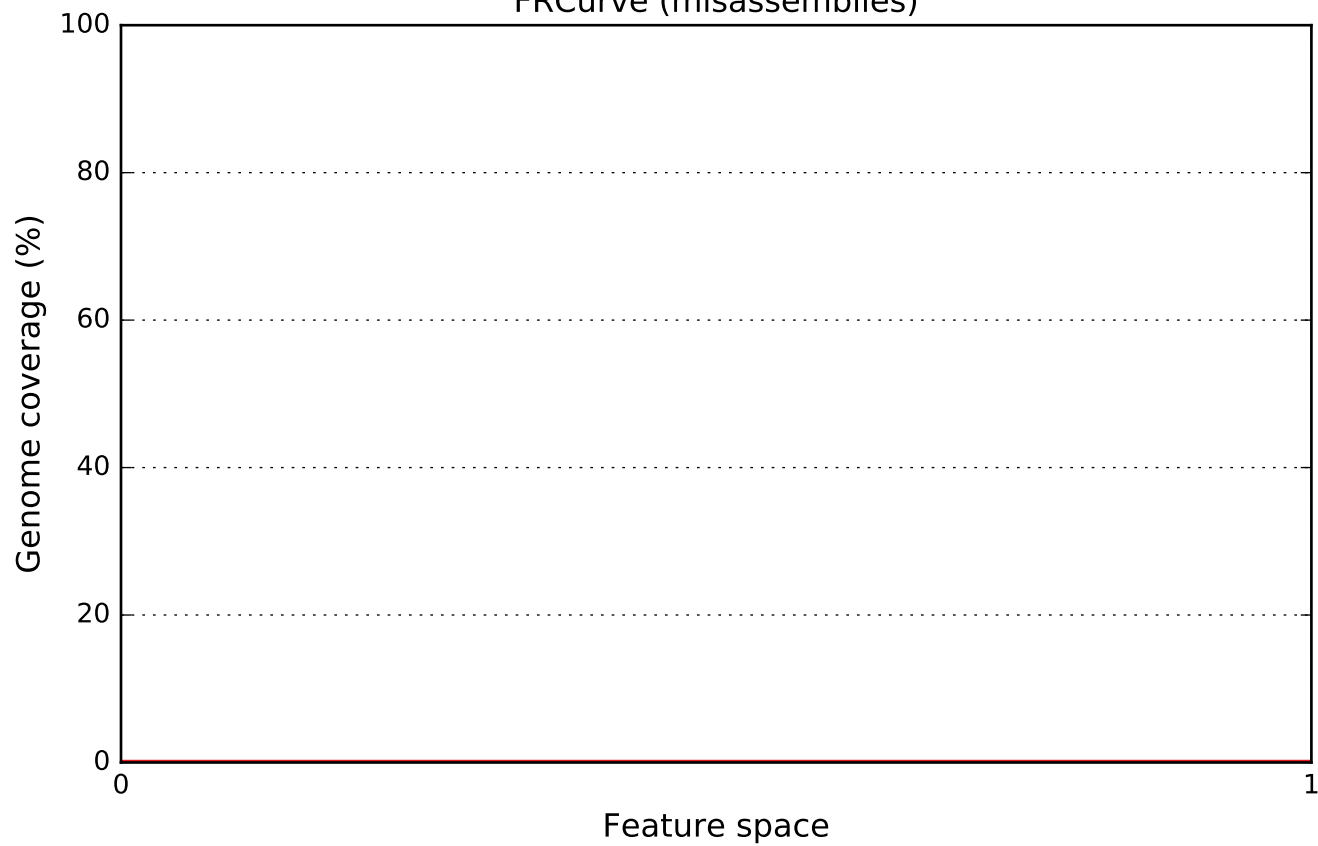






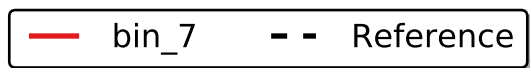
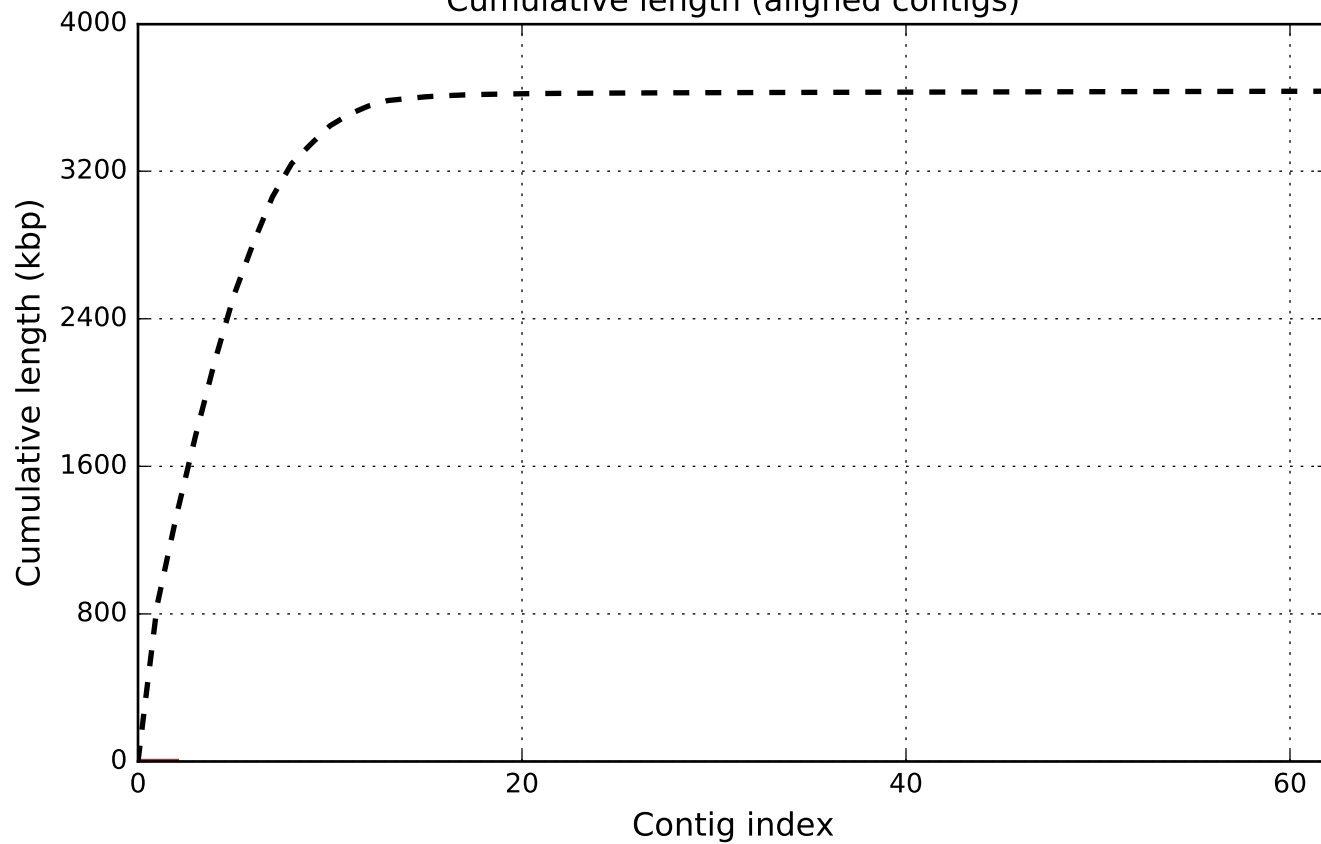


FRCurve (misassemblies)

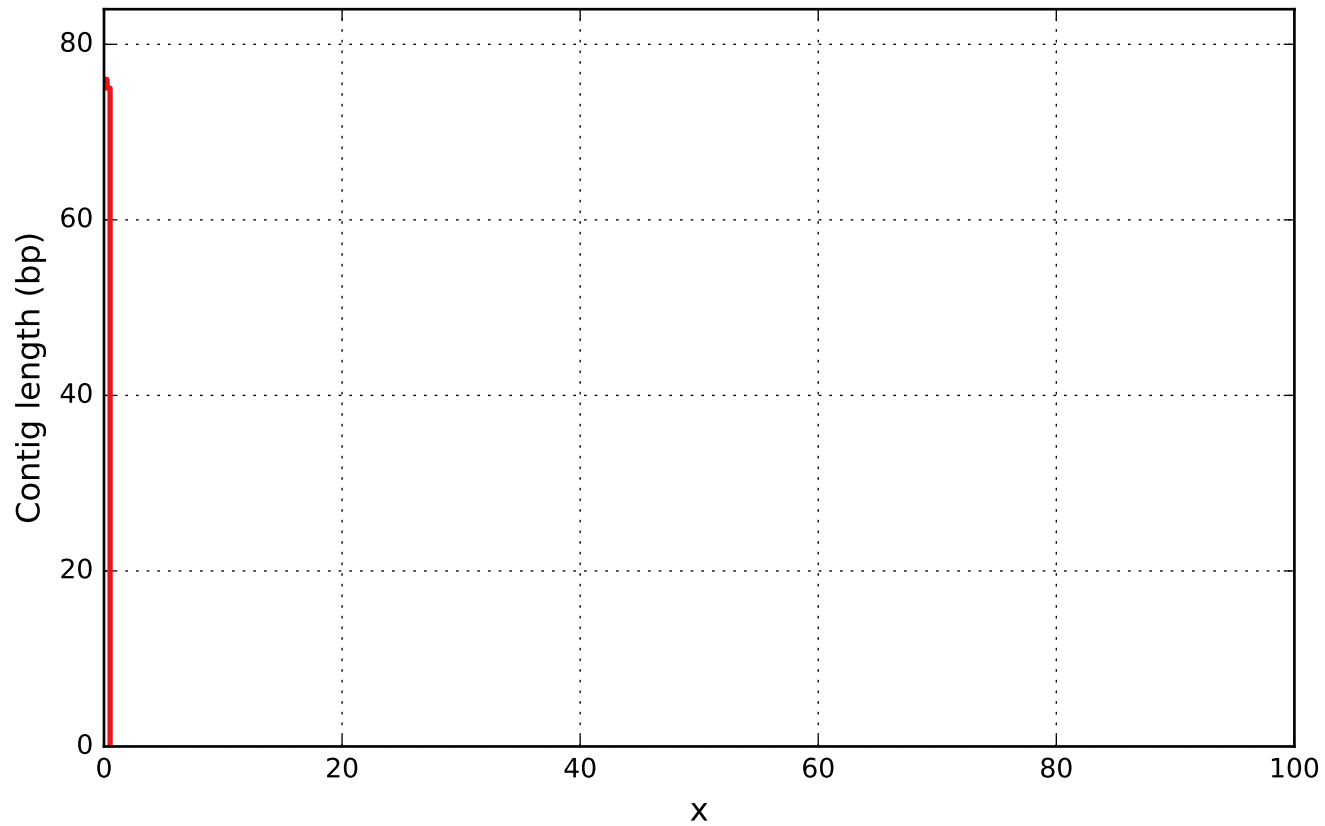


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Cumulative length (aligned contigs)

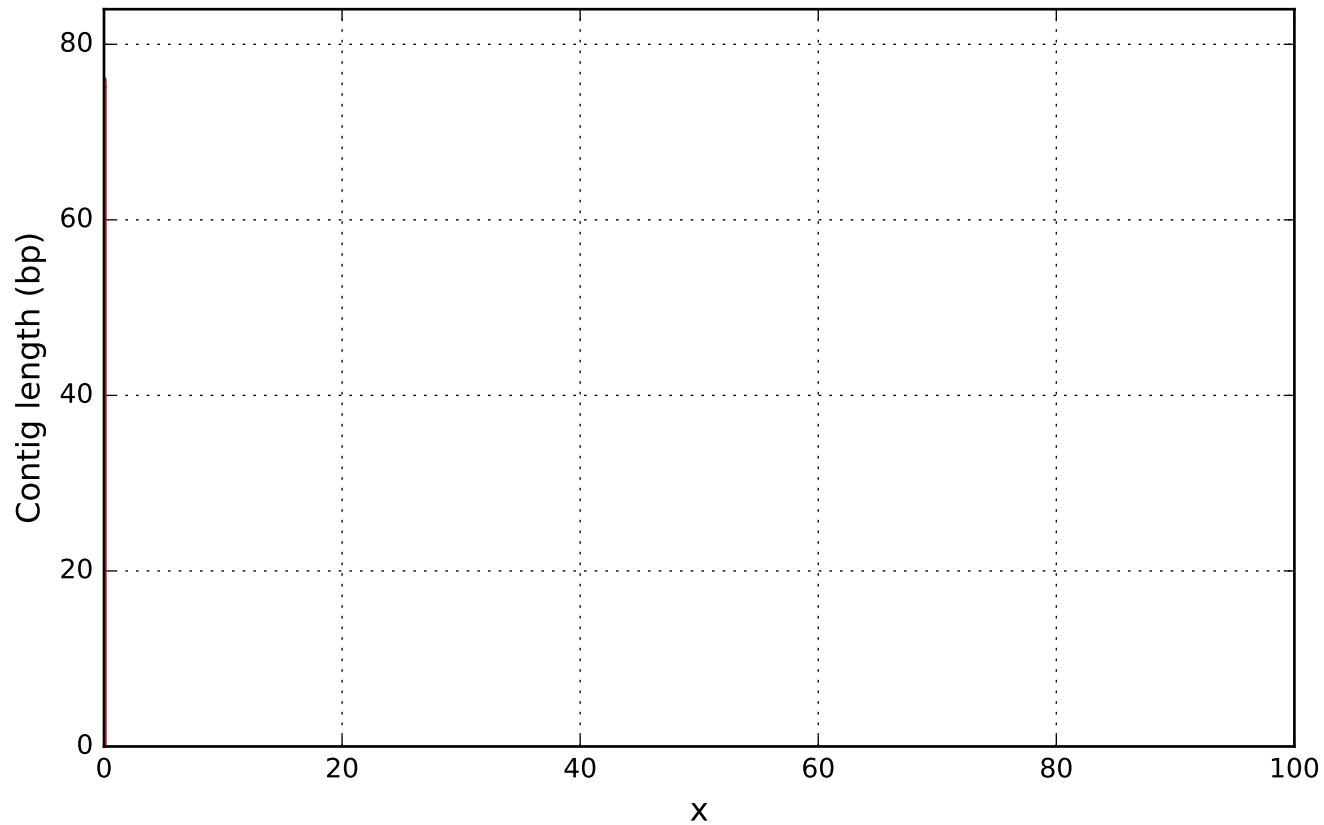


NAx



— bin\_7

NGAx



bin\_7