

Report

	bin_23
# contigs (≥ 1000 bp)	1
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	5144
Total length (≥ 5000 bp)	5144
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1
Largest contig	5144
Total length	5144
Reference length	4282232
GC (%)	63.76
Reference GC (%)	66.99
N50	5144
N75	5144
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	5048
Genome fraction (%)	0.002
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2083.33
# indels per 100 kbp	0.00
Largest alignment	96
Total aligned length	96
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

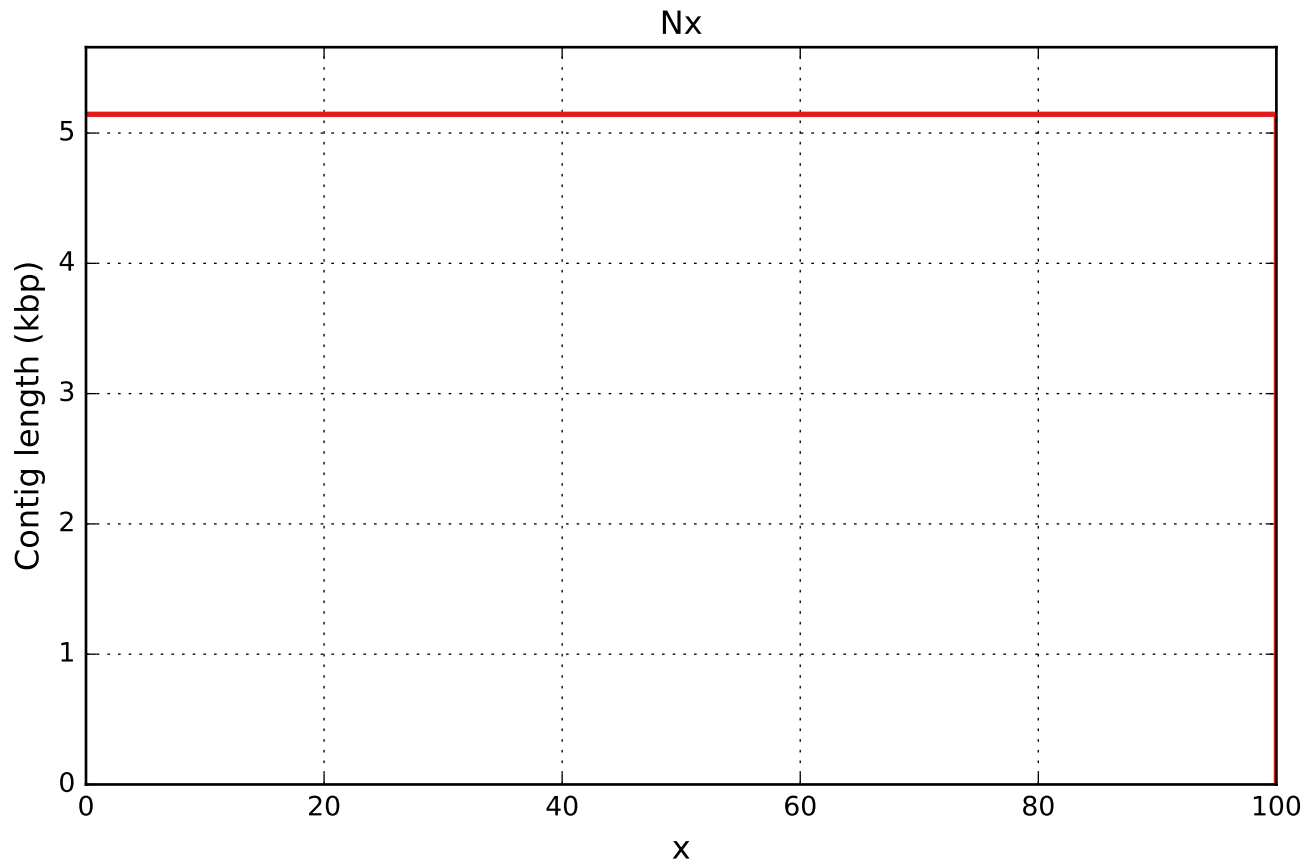
	bin_23
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	2
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

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).

Unaligned report

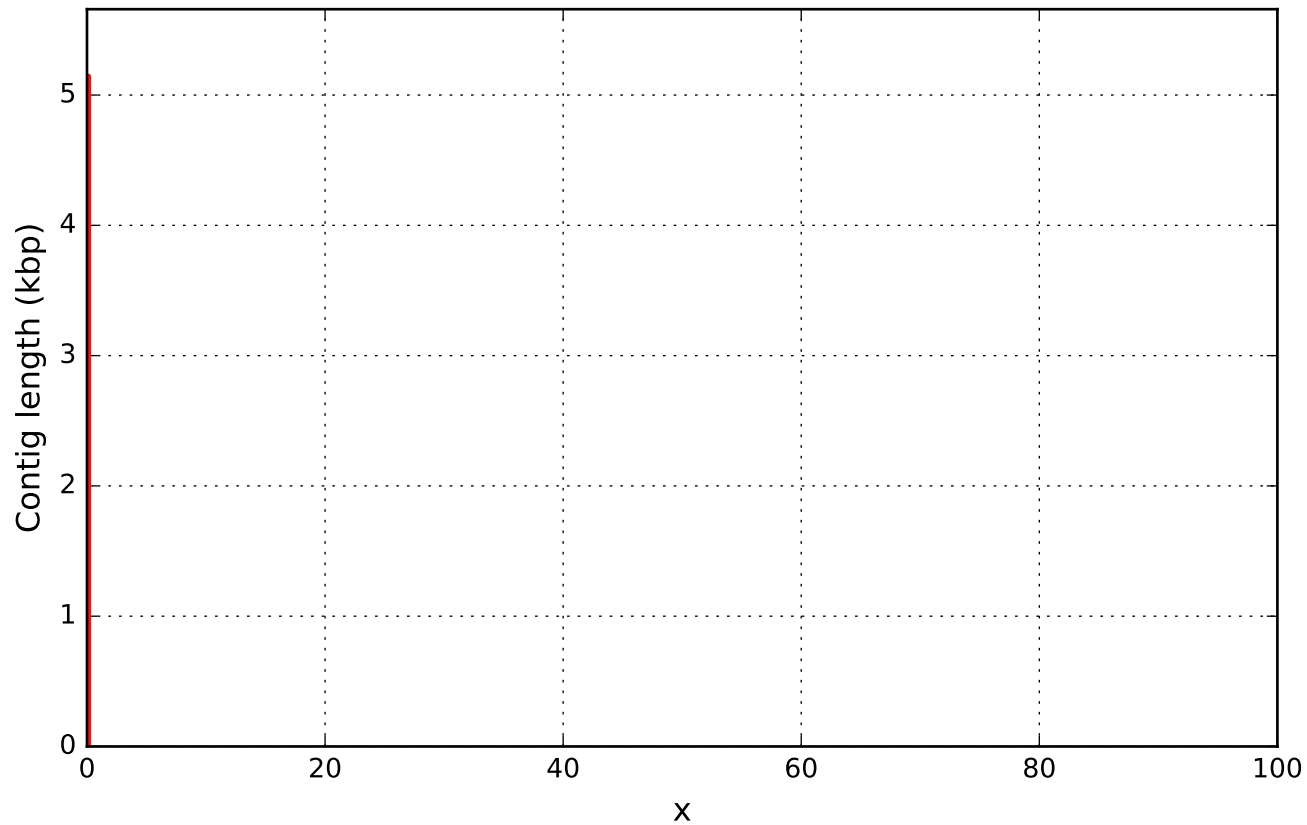
	bin_23
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	5048
# N's	0

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).

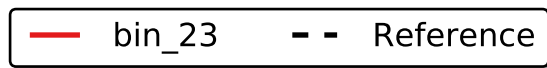
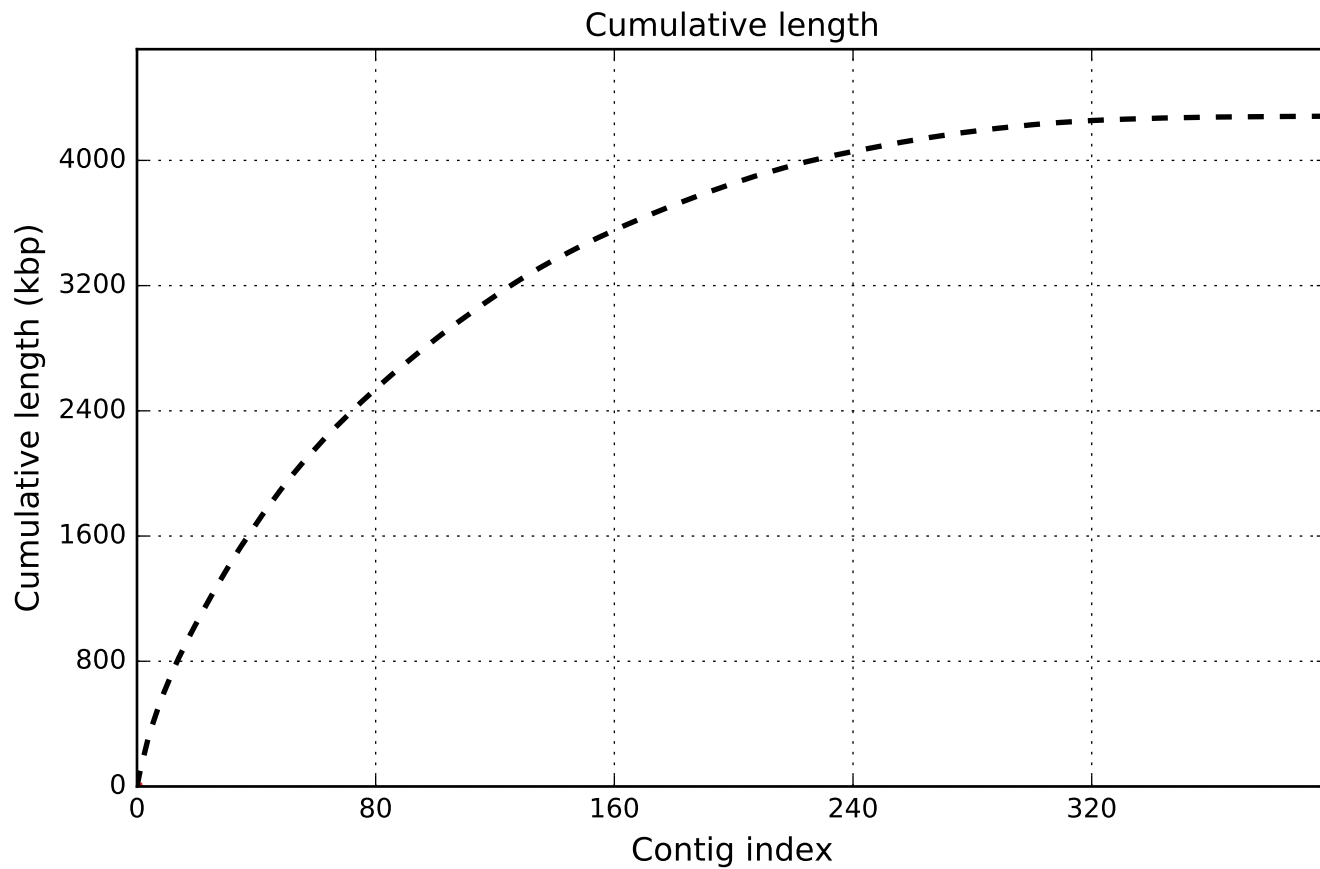


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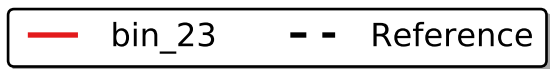
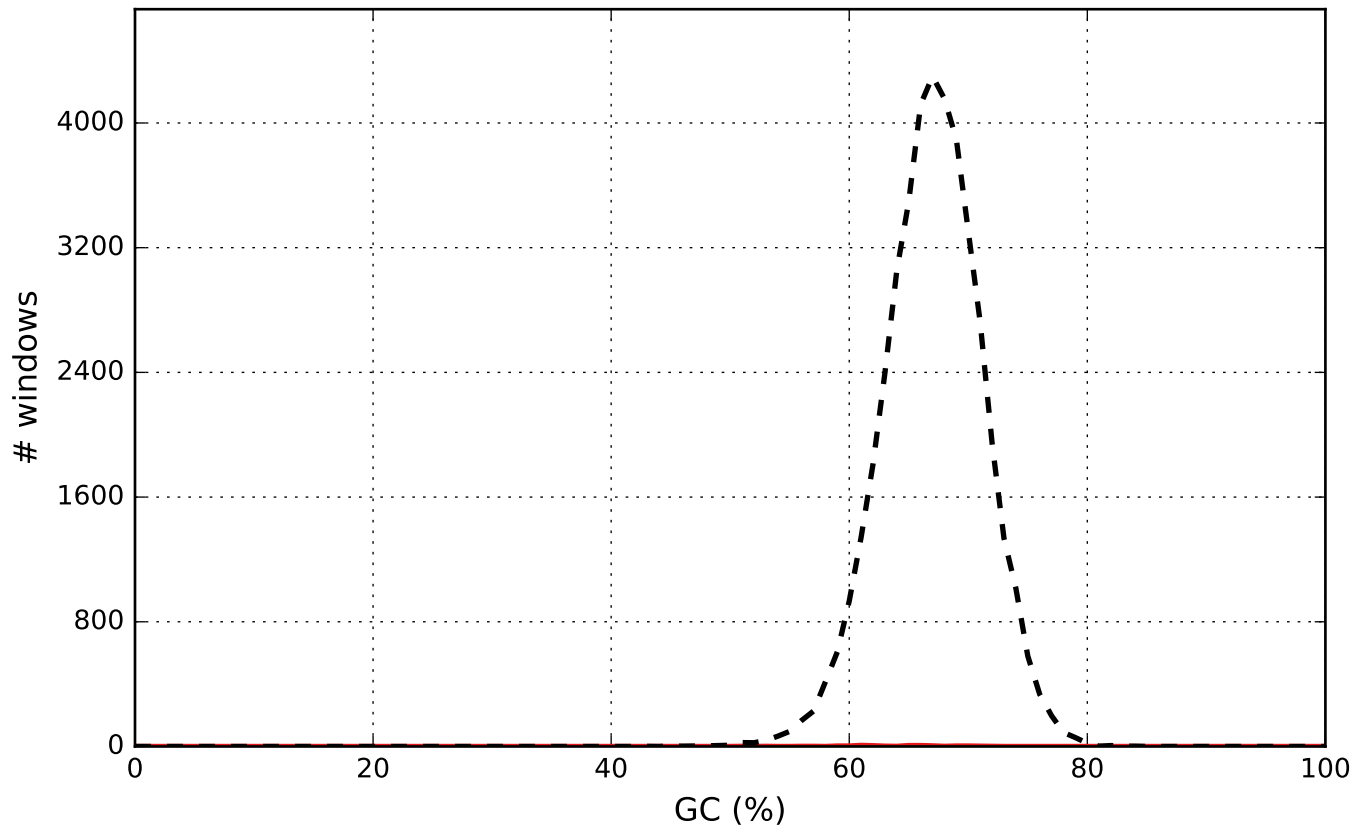
NGx

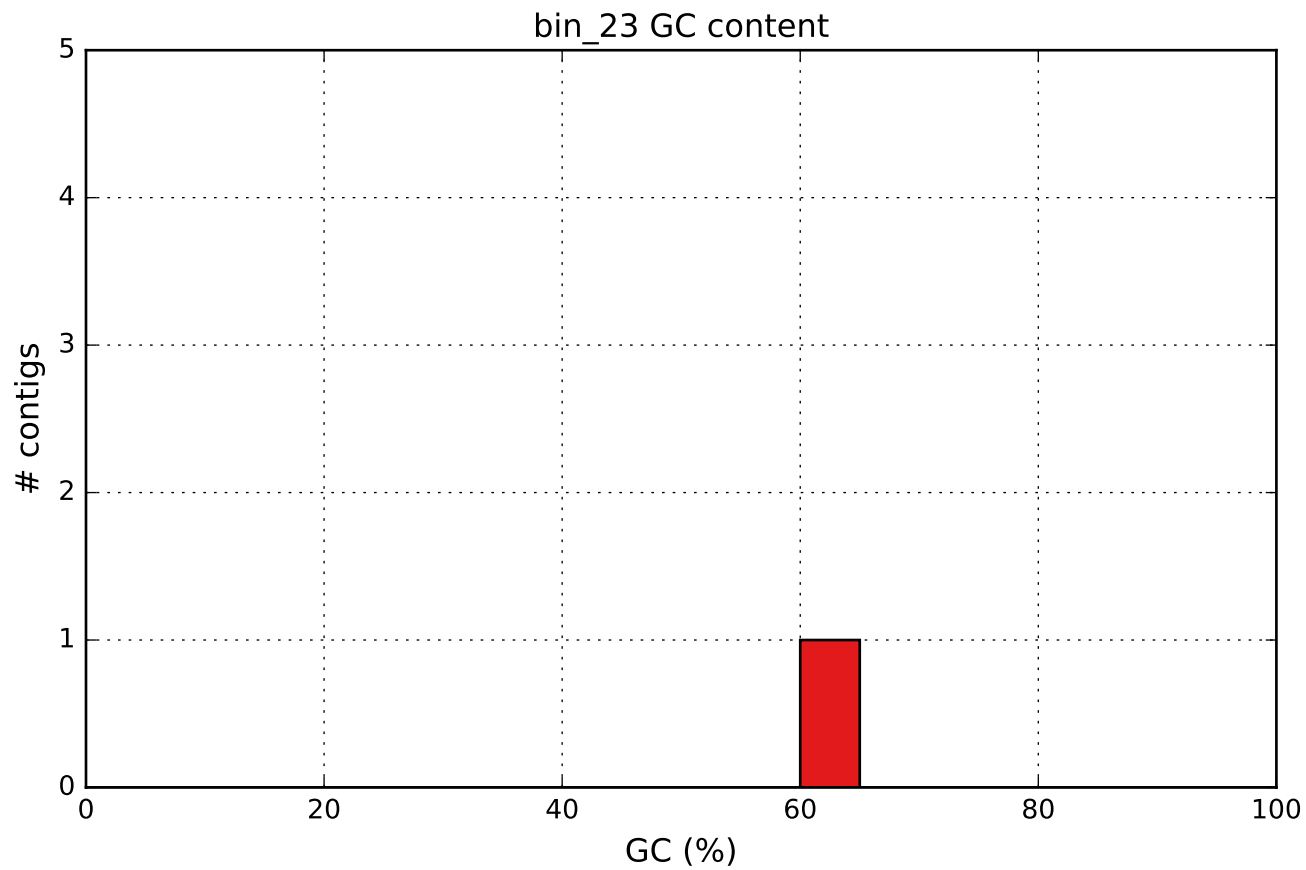


— bin_23



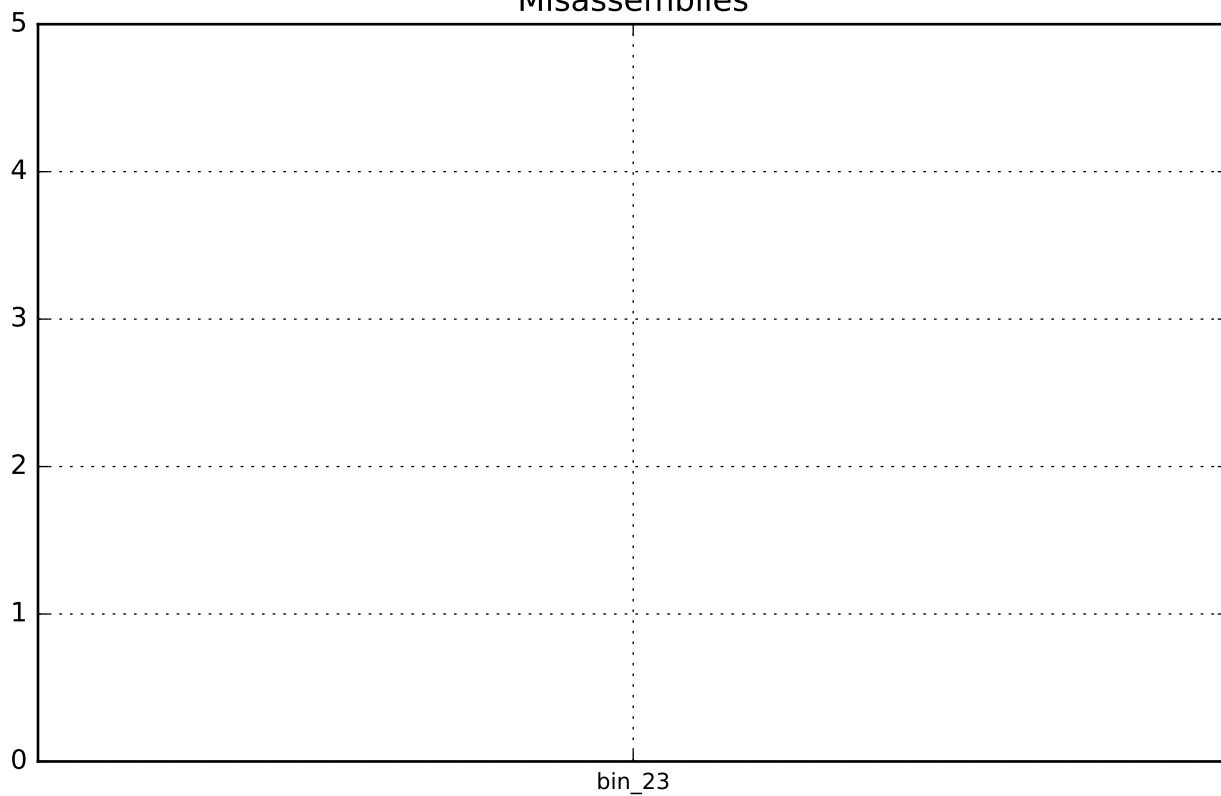
GC content



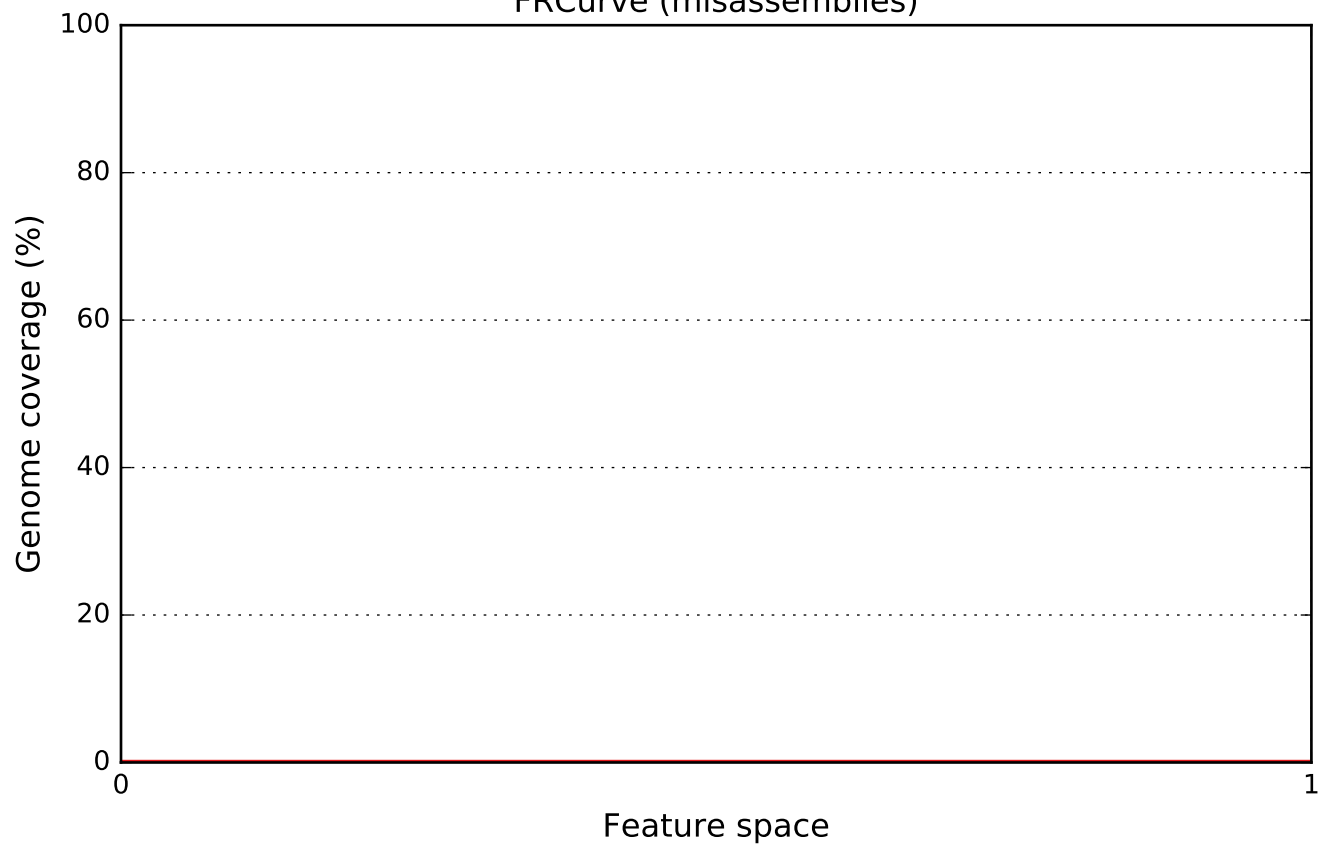


bin_23

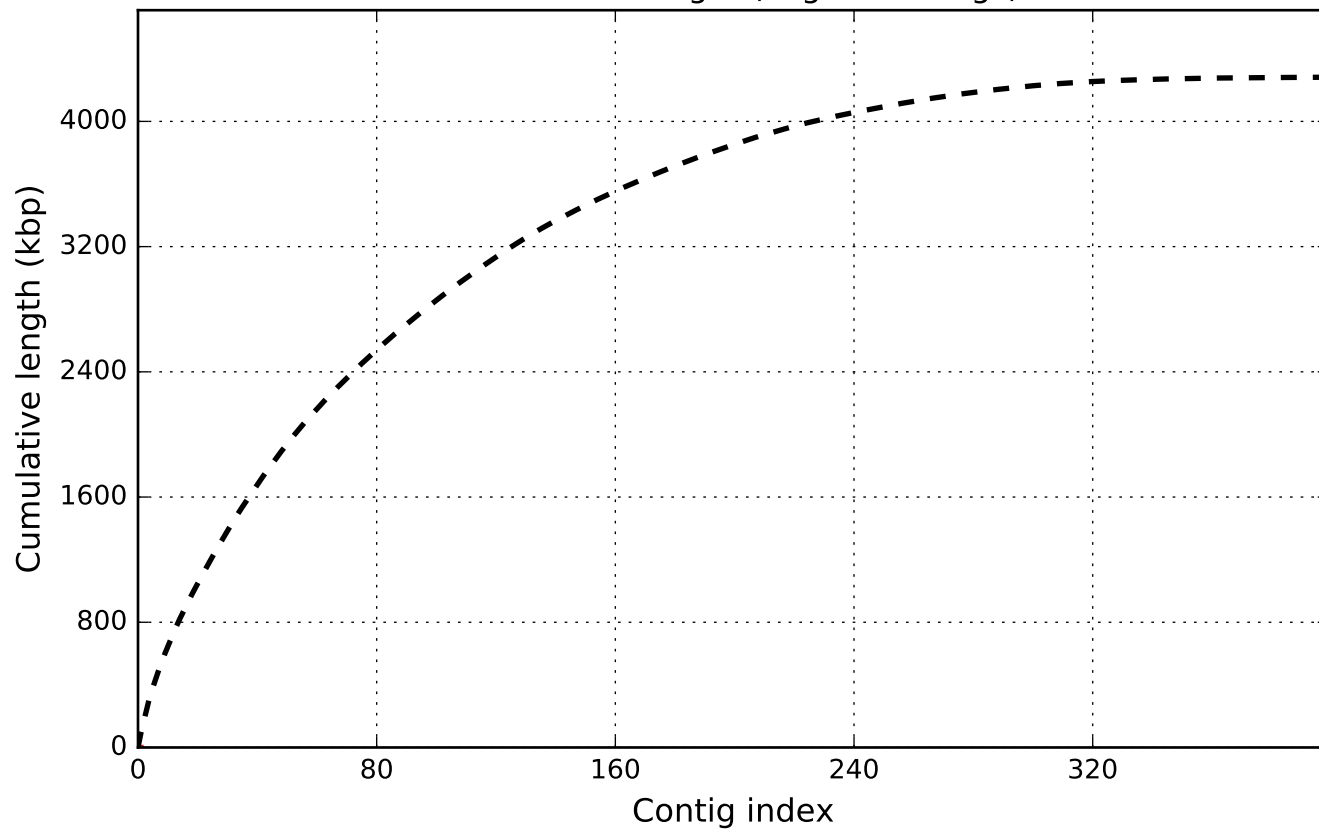
Misassemblies



FRCurve (misassemblies)

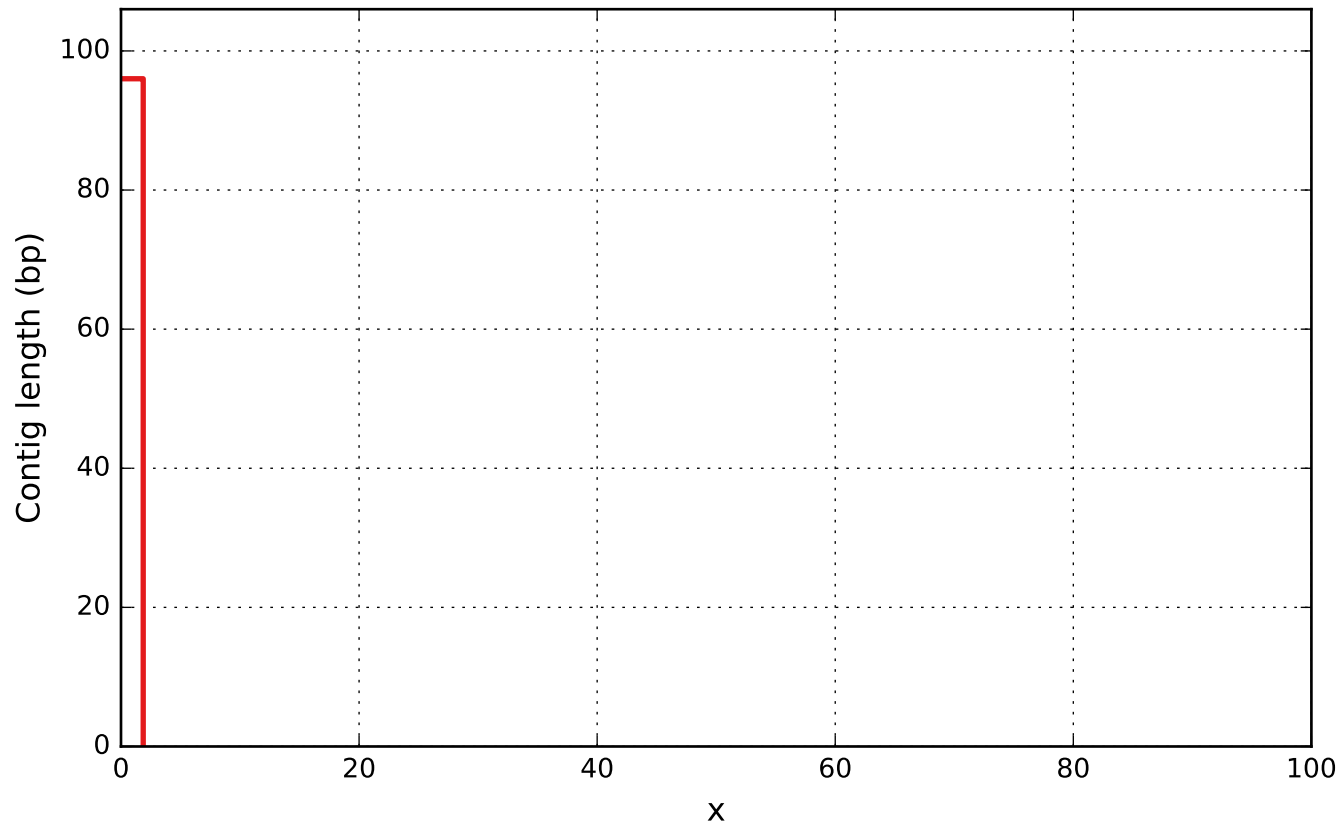


Cumulative length (aligned contigs)



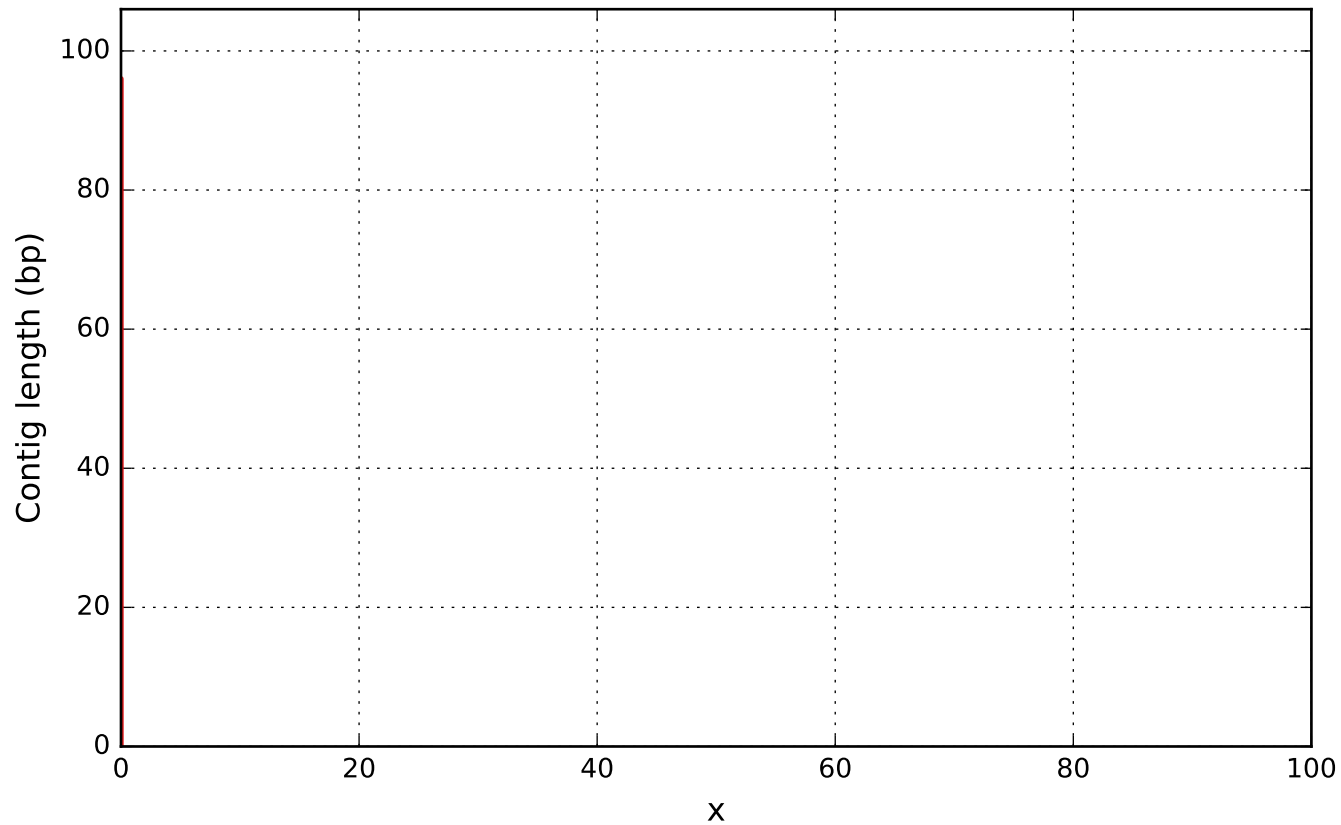
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NAx



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NGAx



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