

Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	26227
Total length (>= 5000 bp)	9123
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	11
Largest contig	9123
Total length	28596
Reference length	4830181
GC (%)	61.05
Reference GC (%)	67.29
N50	3573
N75	2283
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	24590
Genome fraction (%)	0.044
Duplication ratio	1.867
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2749.30
# indels per 100 kbp	512.58
Largest alignment	977
Total aligned length	2293
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

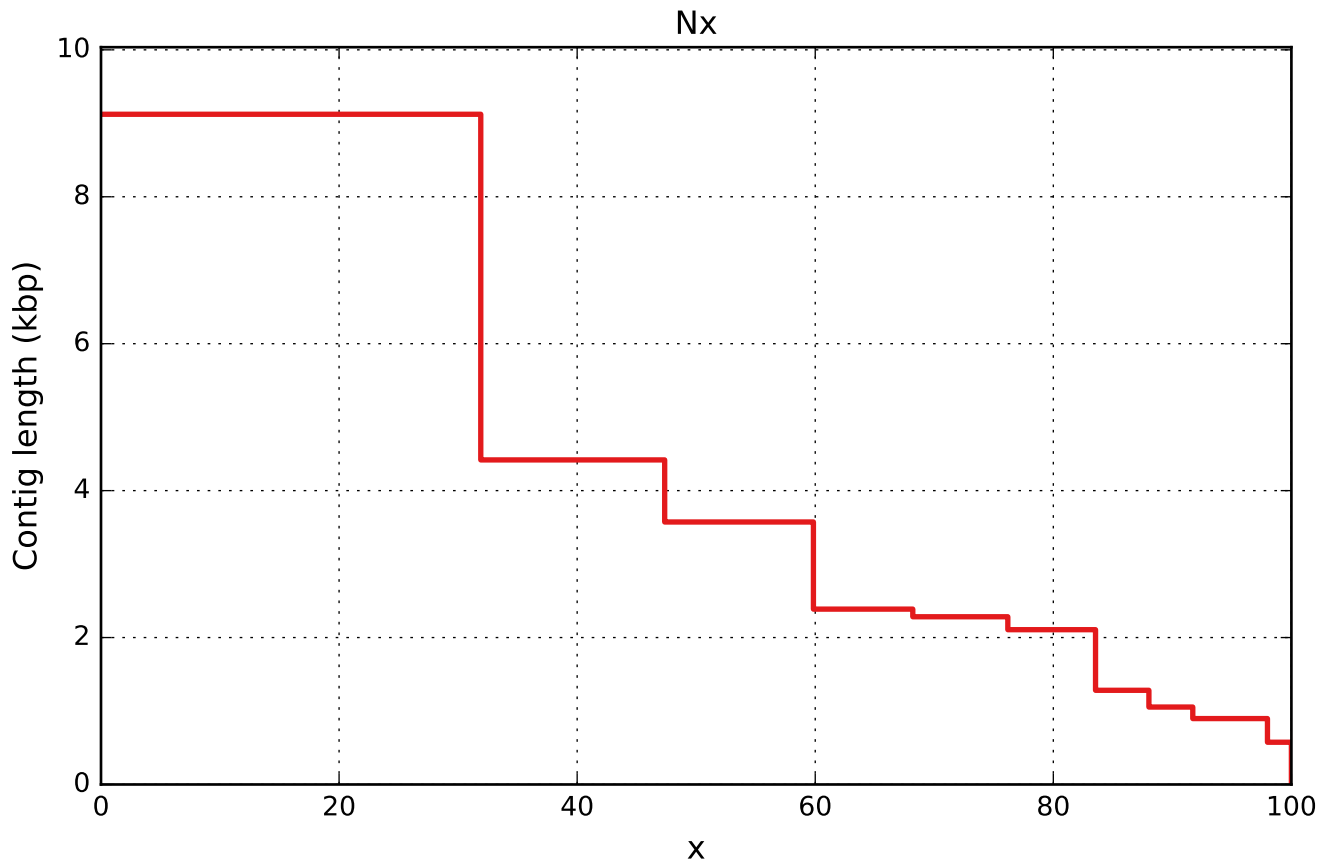
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	59
# indels	11
# indels (≤ 5 bp)	11
# indels (> 5 bp)	0
Indels length	14

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).

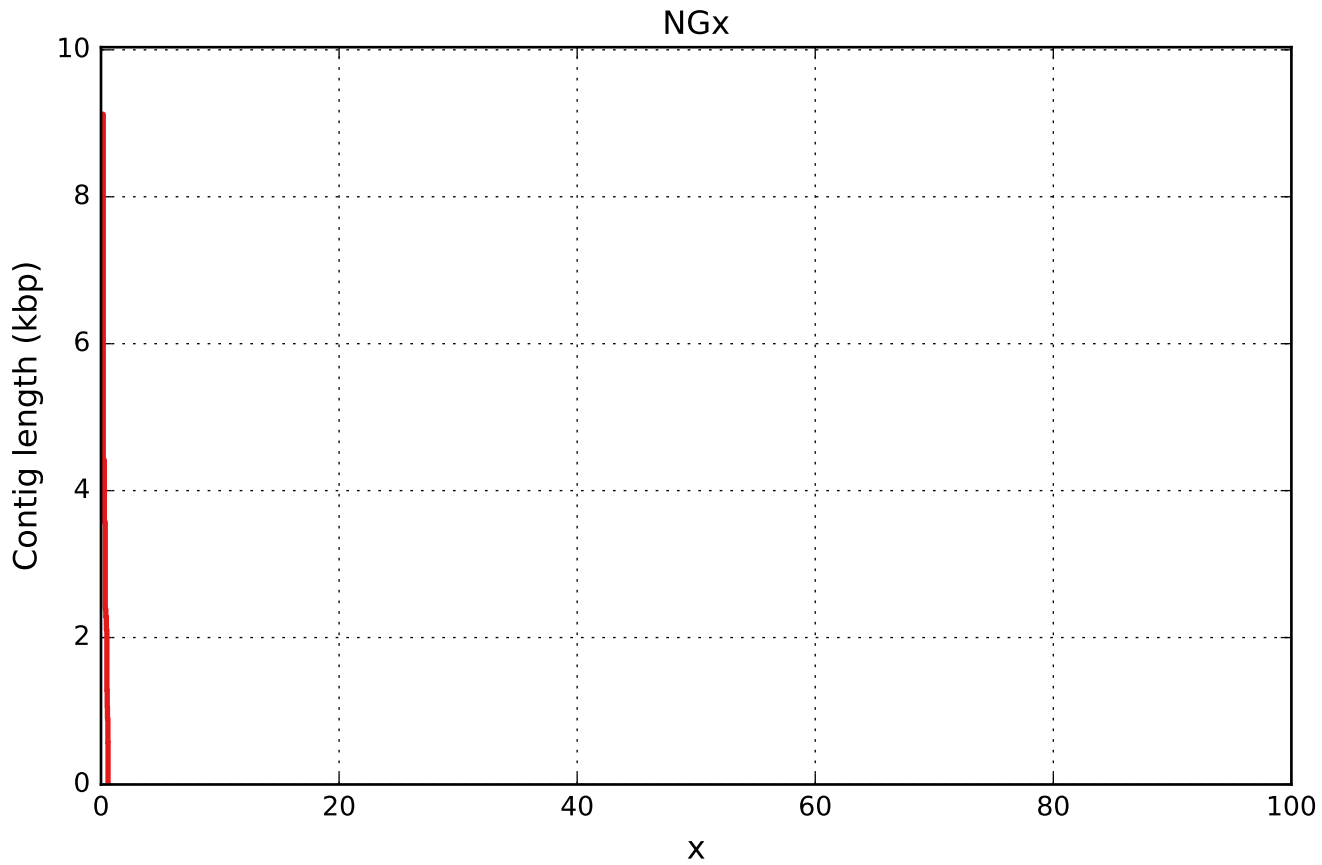
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	24590
# N's	0

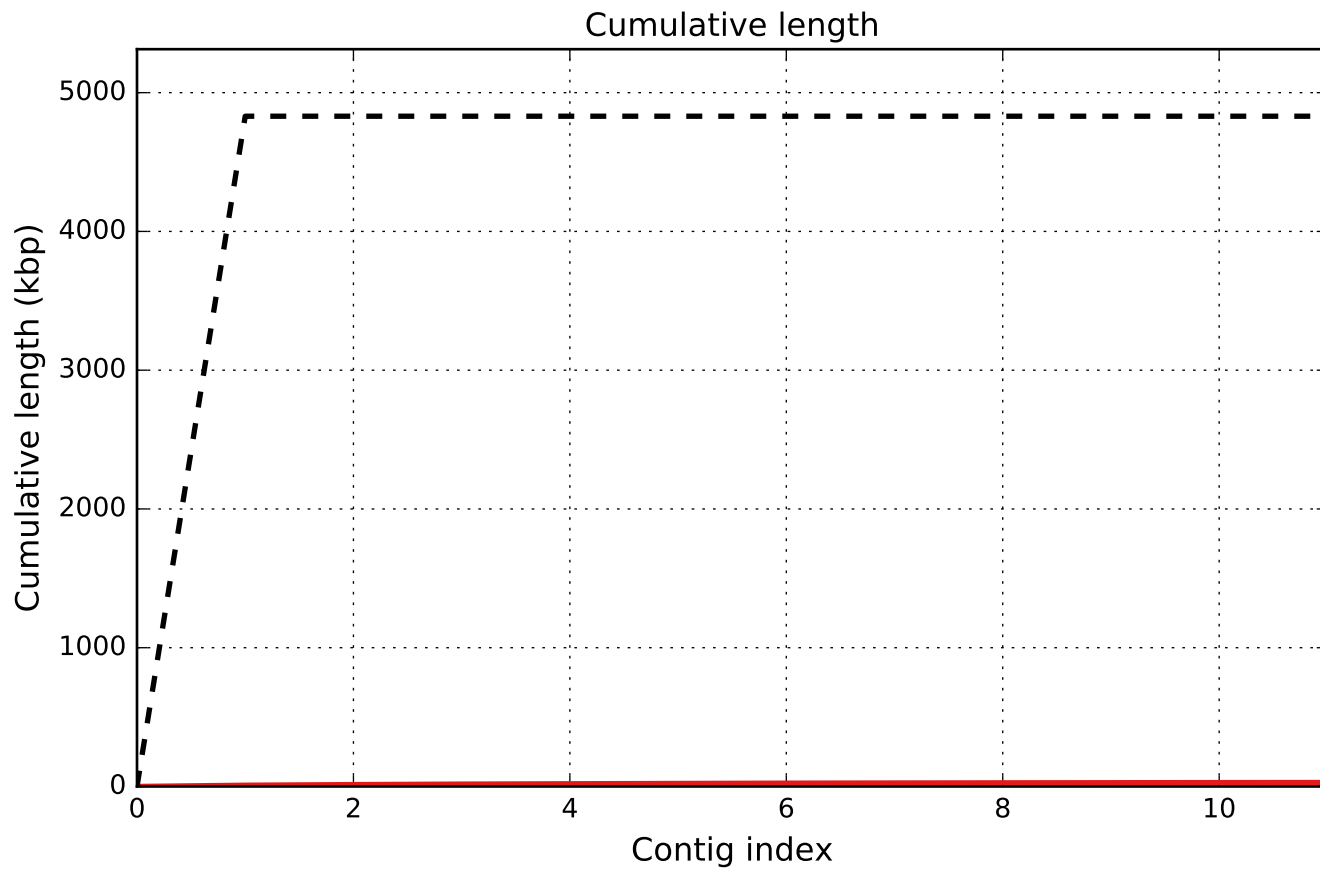
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

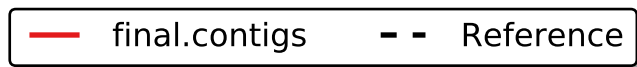
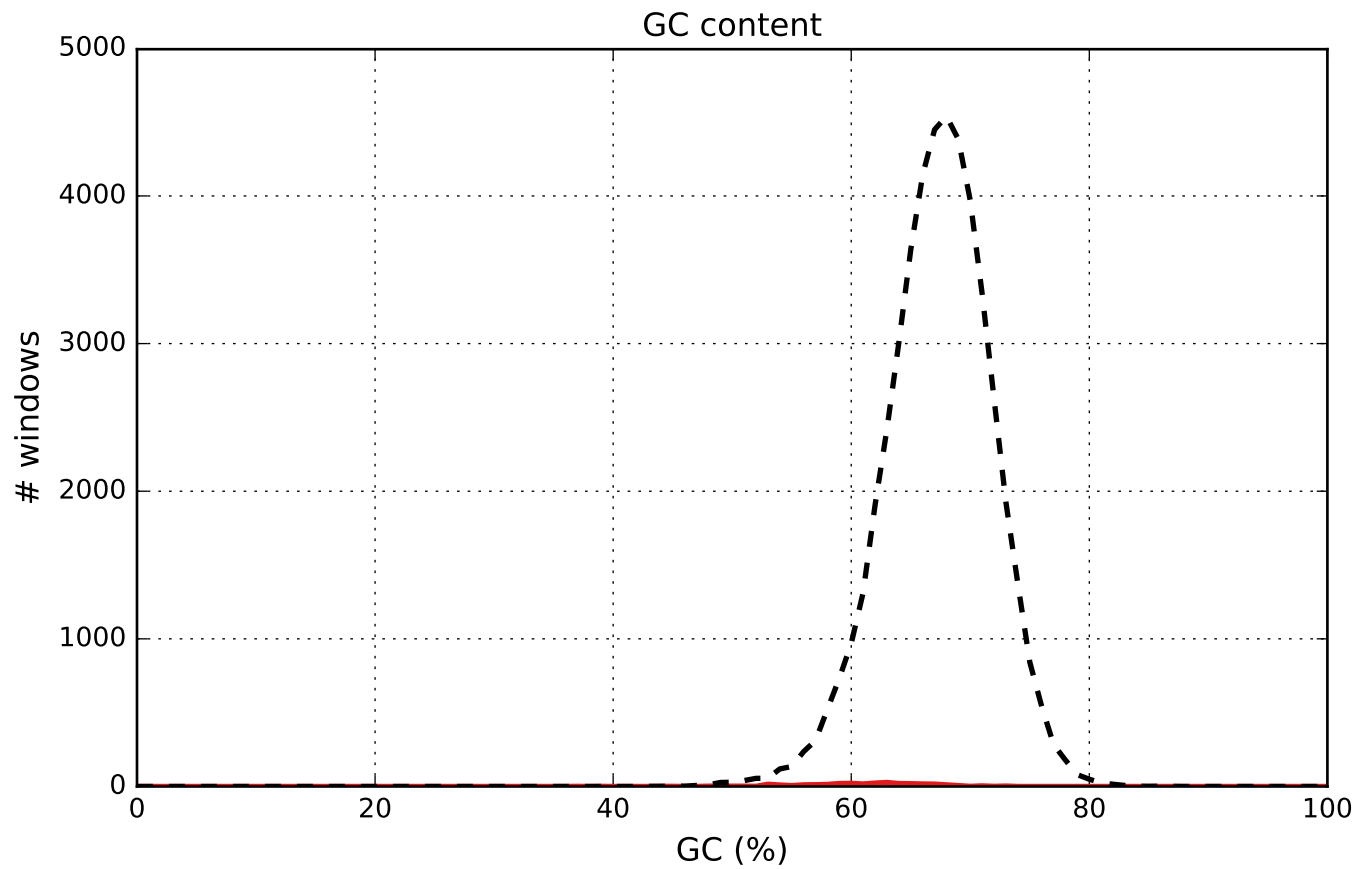


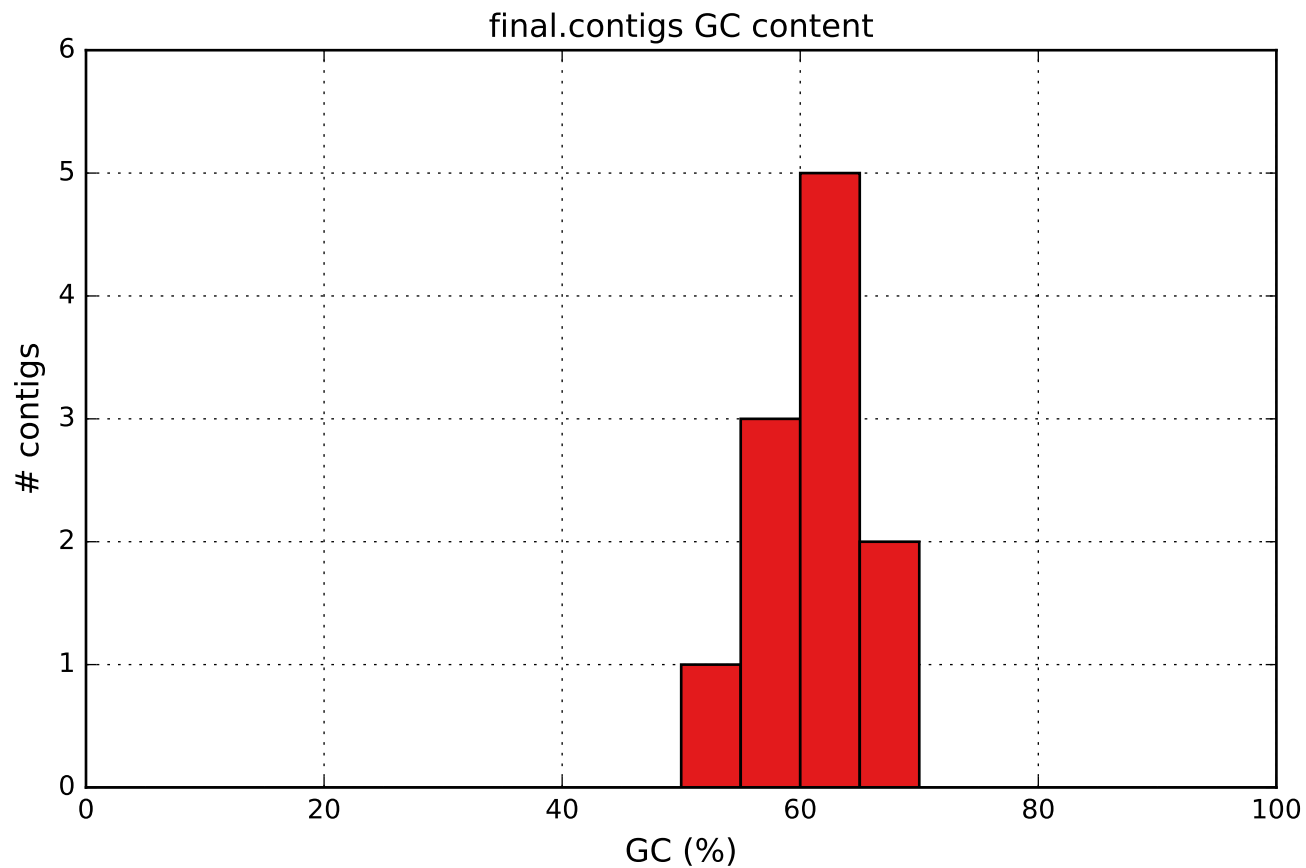
— final.contigs



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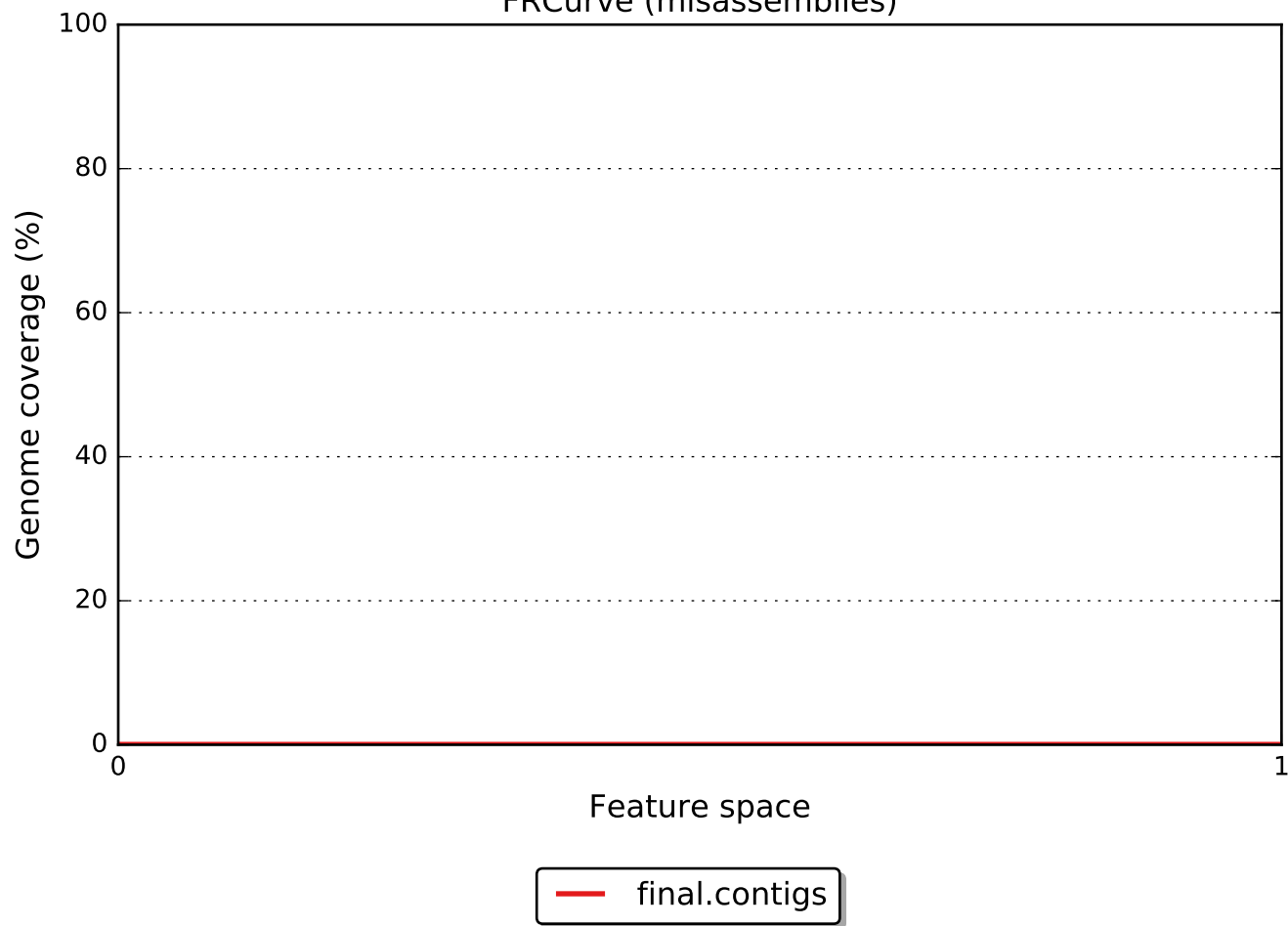




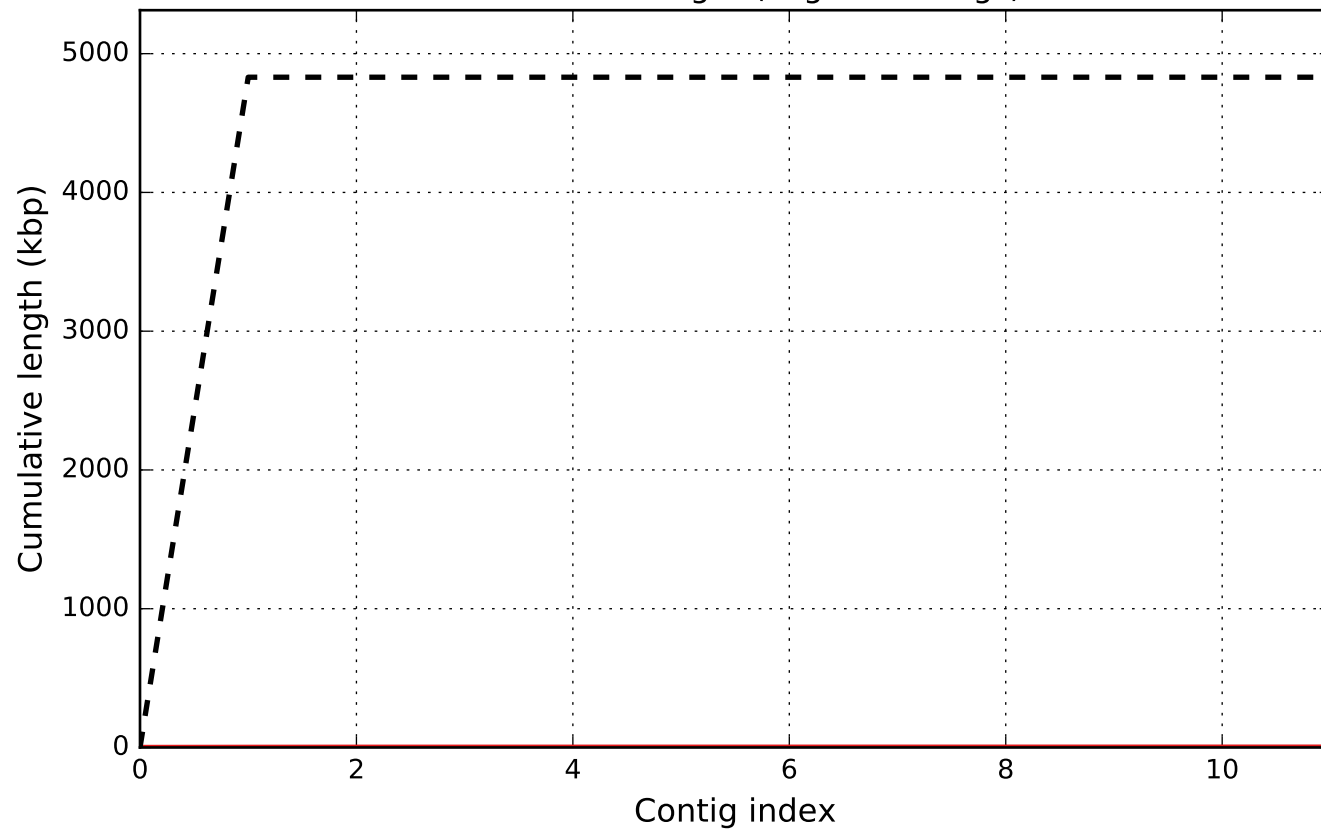
final.contigs



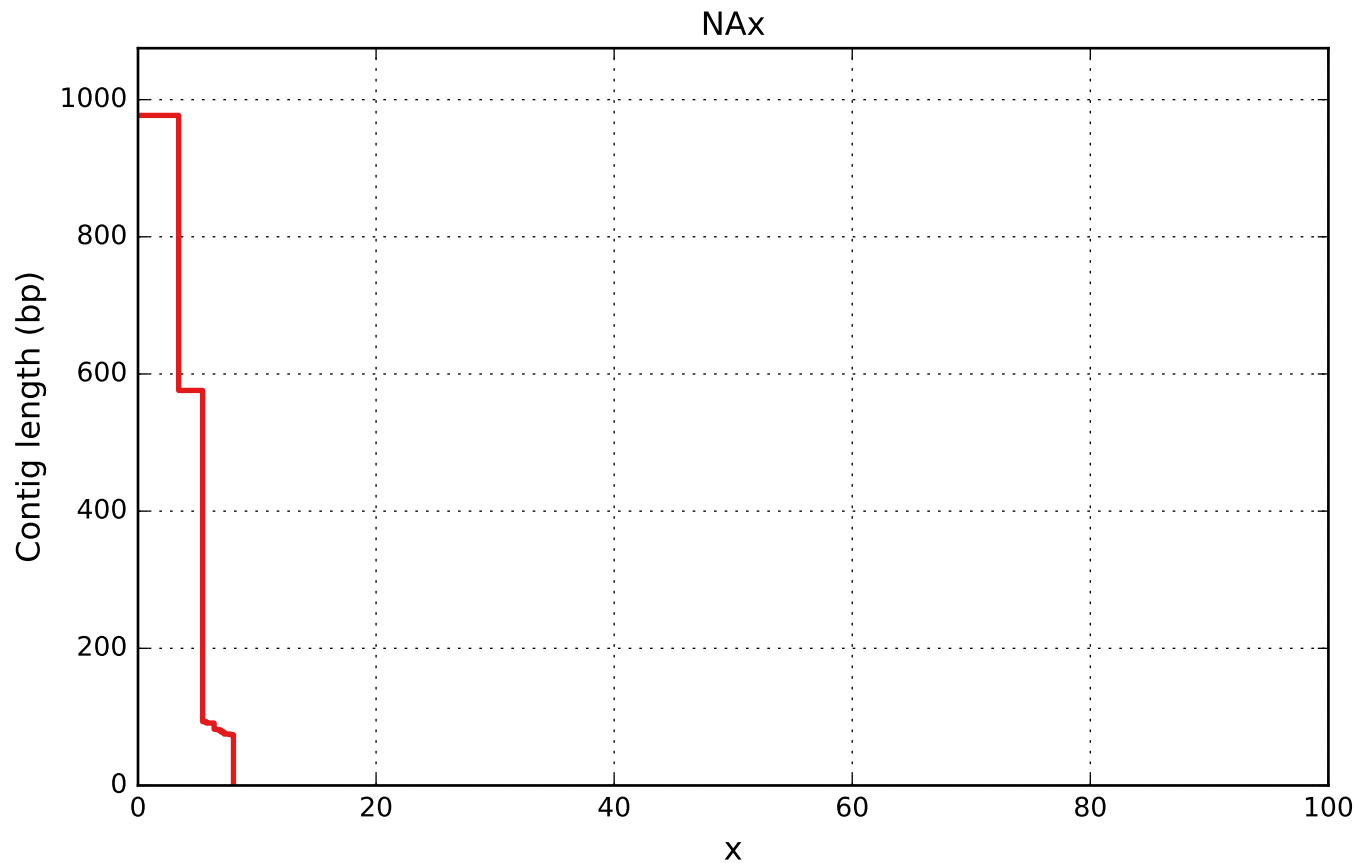
FRCurve (misassemblies)



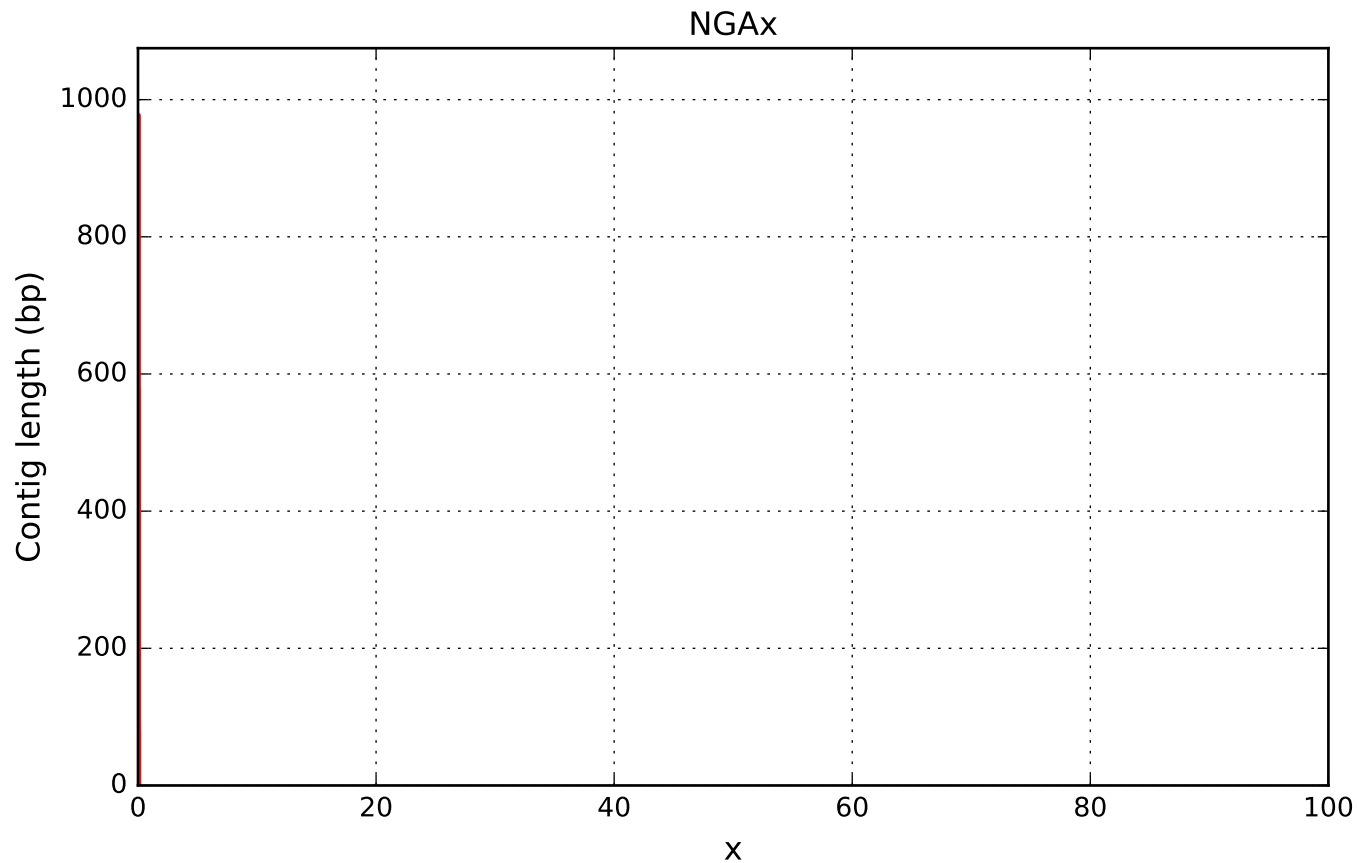
Cumulative length (aligned contigs)



— final.contigs - - Reference



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