

Report

	genome_assembly.contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	2623952
Total length (>= 1000 bp)	2623952
Total length (>= 5000 bp)	2623952
Total length (>= 10000 bp)	2623952
Total length (>= 25000 bp)	2623952
Total length (>= 50000 bp)	2623952
# contigs	2
Largest contig	2568209
Total length	2623952
Reference length	2610531
GC (%)	54.12
Reference GC (%)	54.14
N50	2568209
NG50	2568209
N75	2568209
NG75	2568209
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2568209
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	55743
Genome fraction (%)	97.566
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	7.11
Largest alignment	2193723
Total aligned length	2568209
NA50	2193723
NGA50	2193723
NA75	2193723
NGA75	2193723
LA50	1
LGA50	1
LA75	1
LGA75	1

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

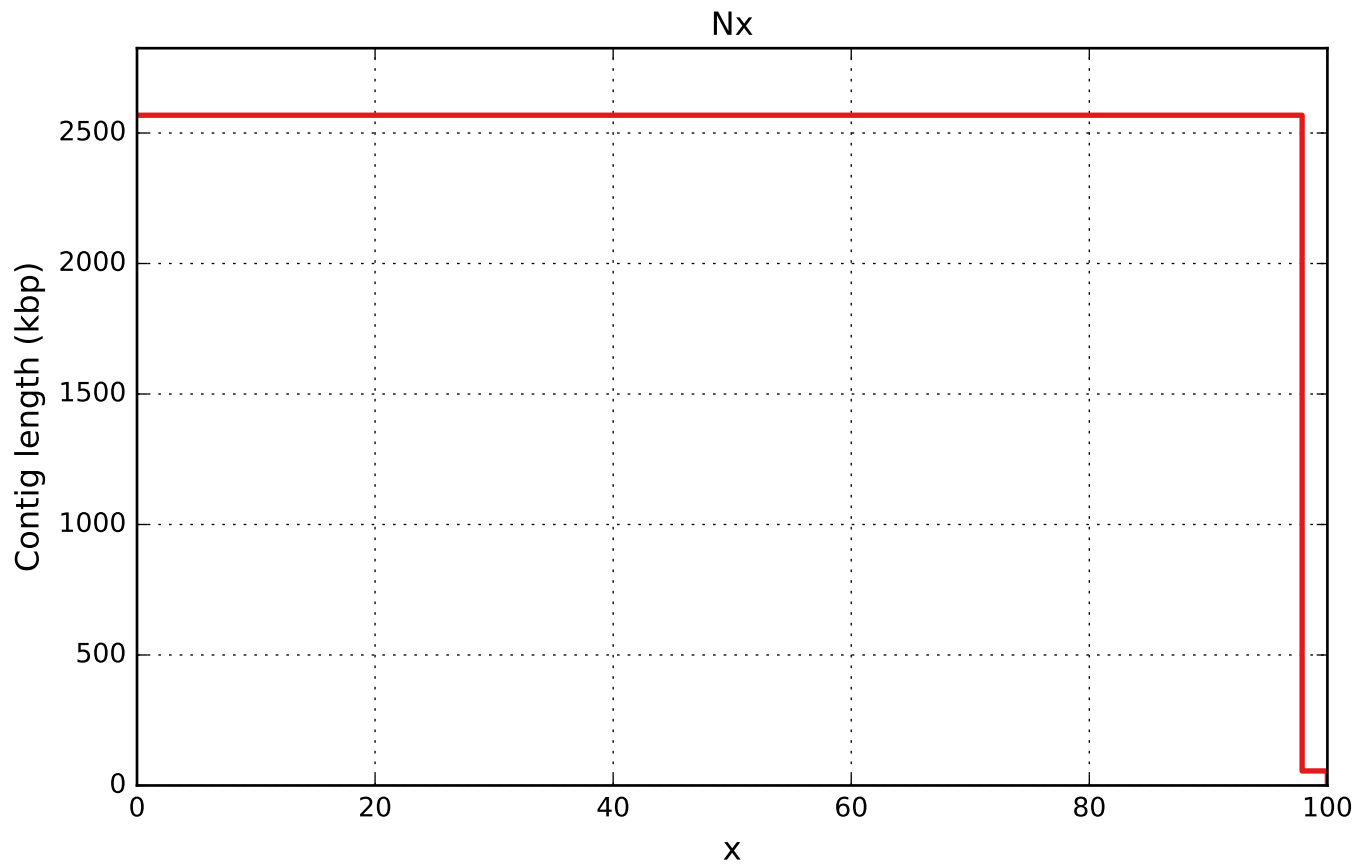
	genome_assembly.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2568209
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	181
# indels (<= 5 bp)	181
# indels (> 5 bp)	0
Indels length	181

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).

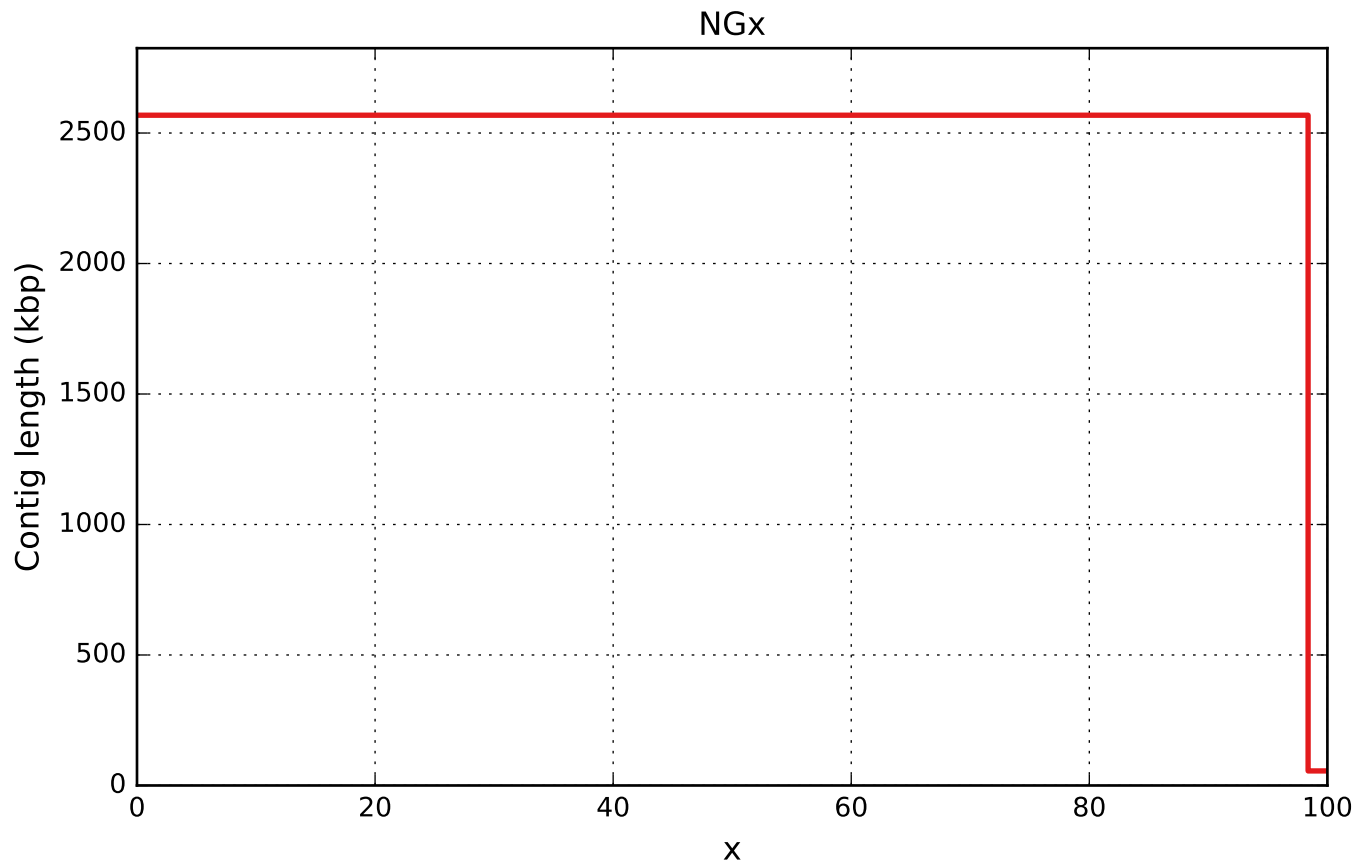
## Unaligned report

	genome_assembly.contigs
# fully unaligned contigs	1
Fully unaligned length	55743
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

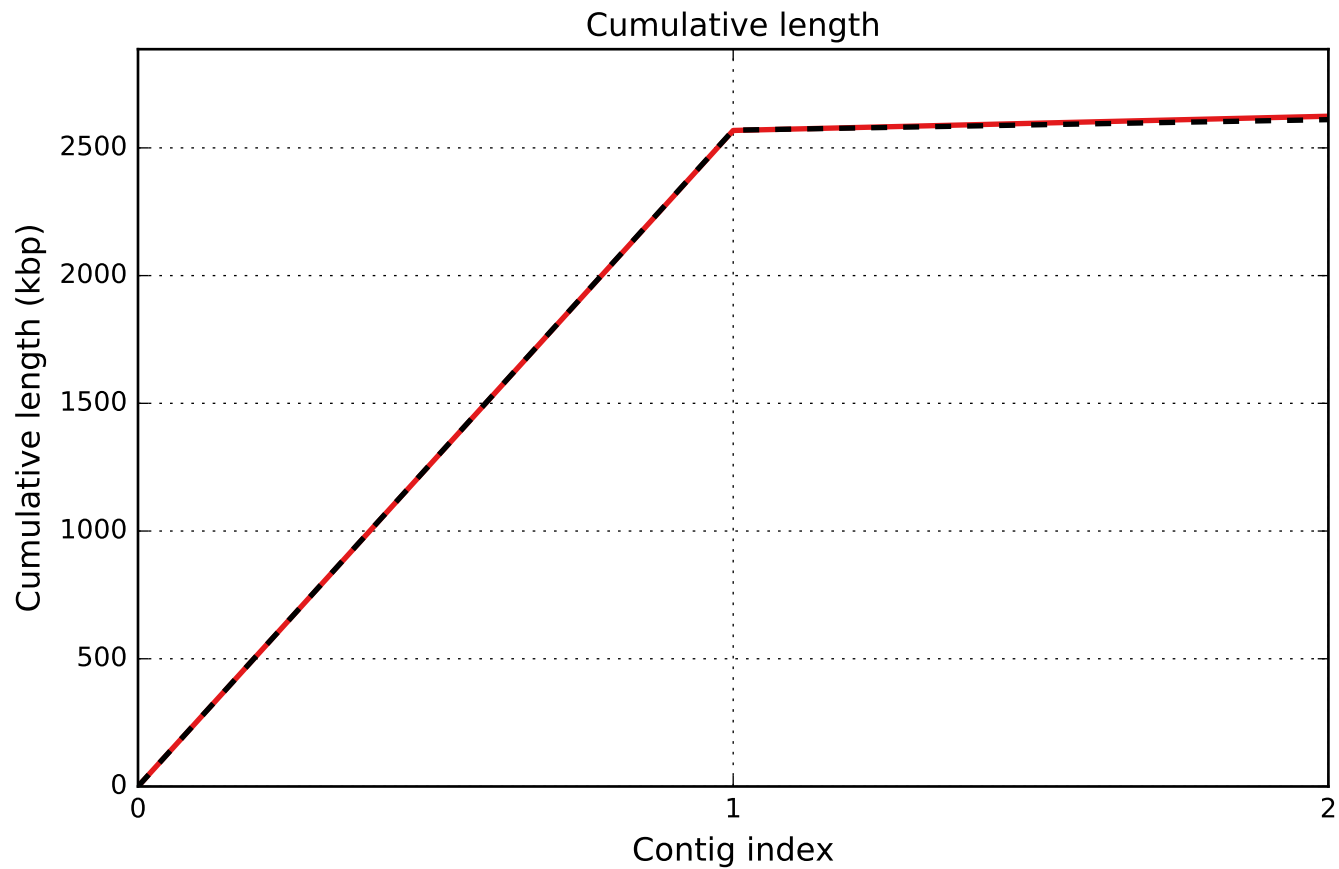
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



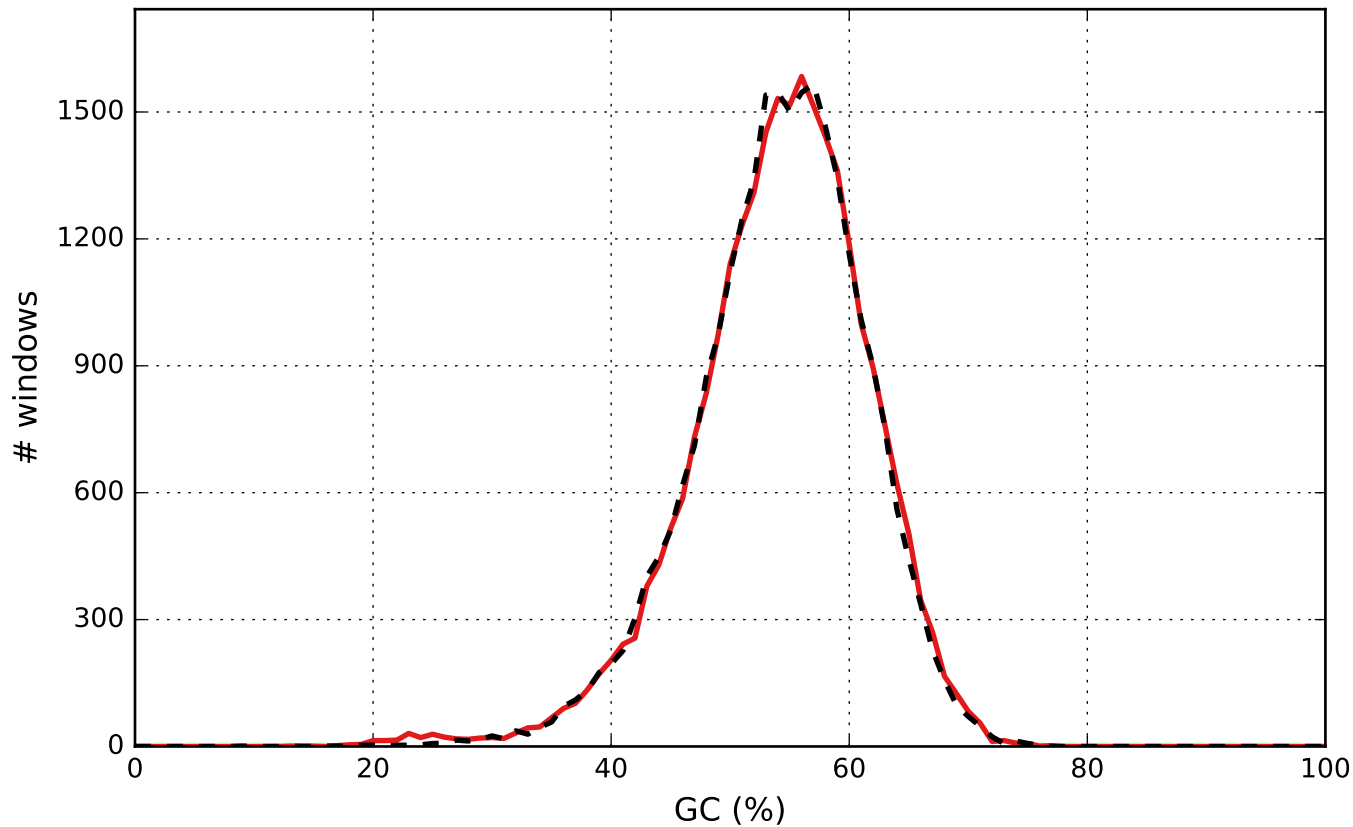
— genome\_assembly.contigs



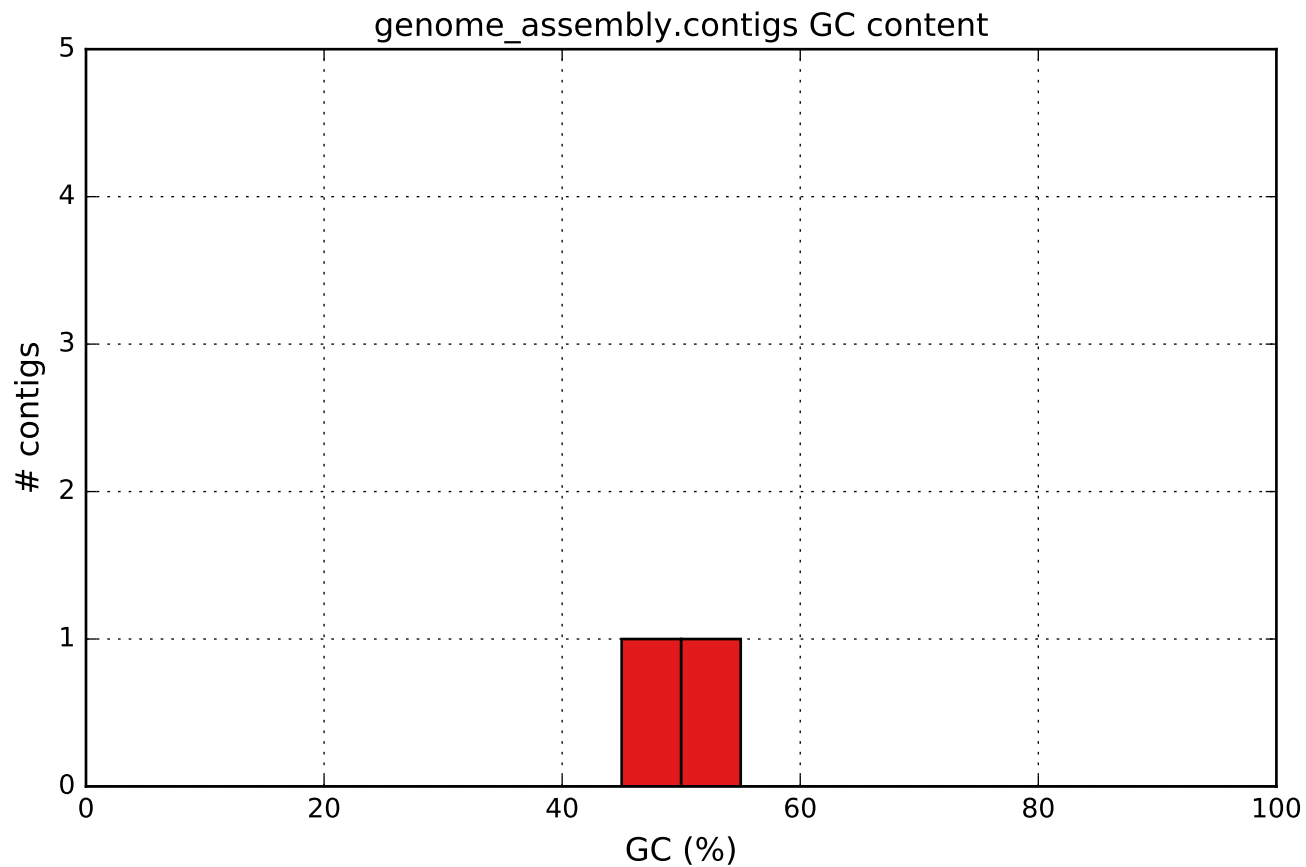
— genome\_assembly.contigs



# GC content

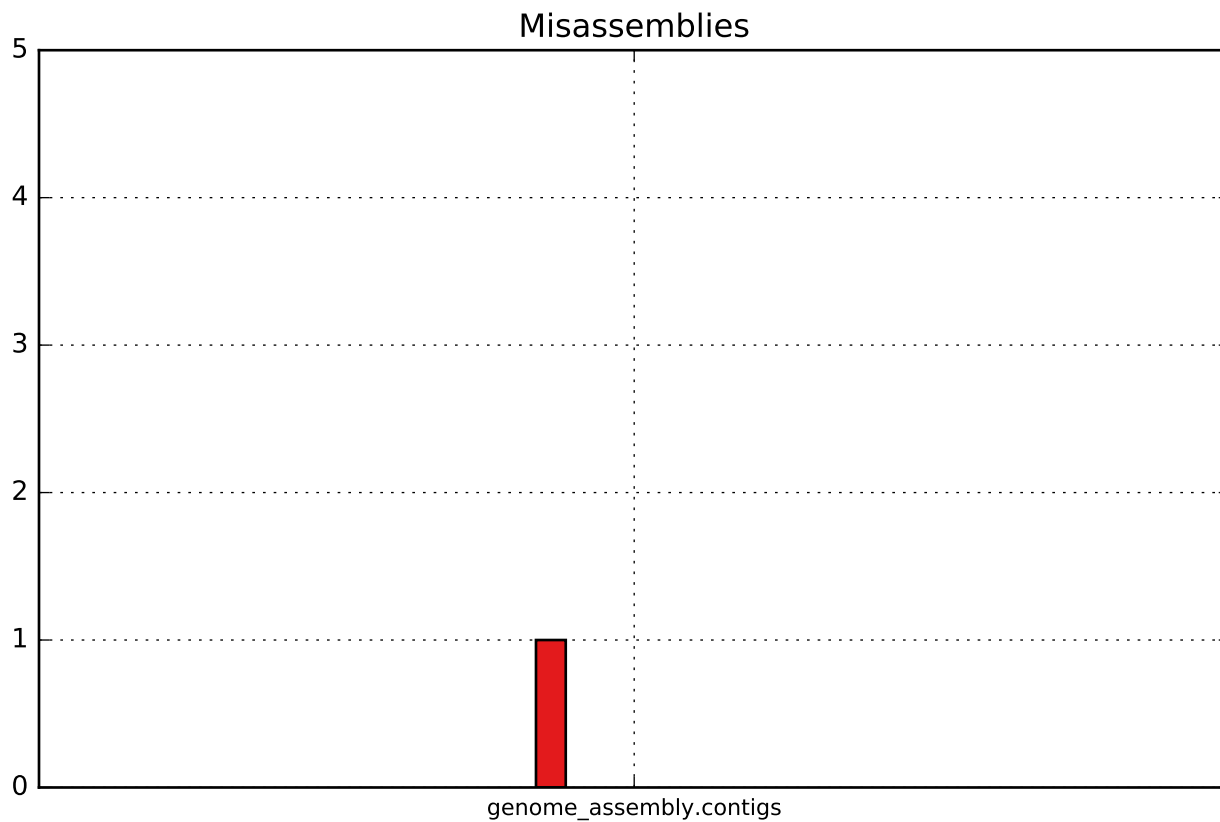


— genome\_assembly.contigs    - - Reference

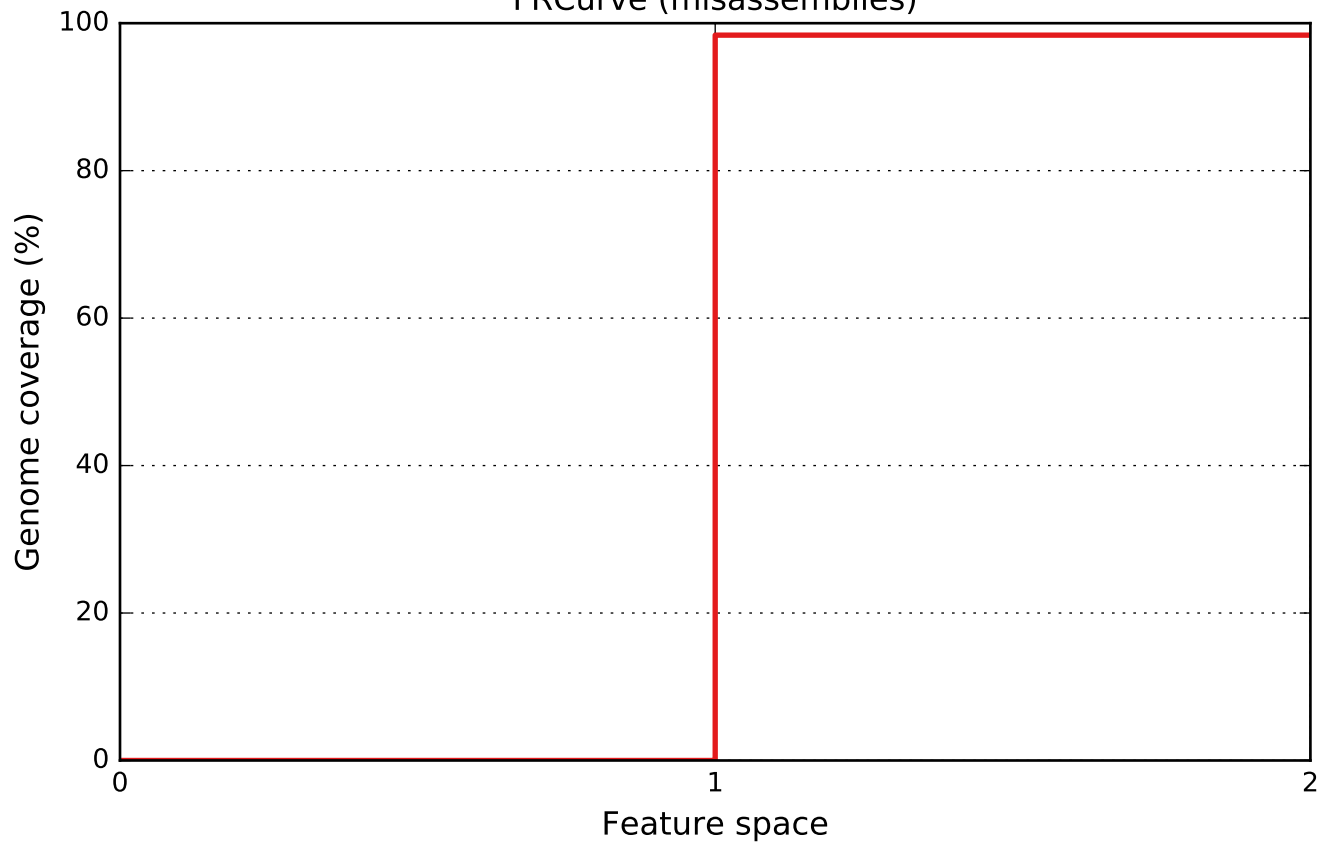


genome\_assembly.contigs



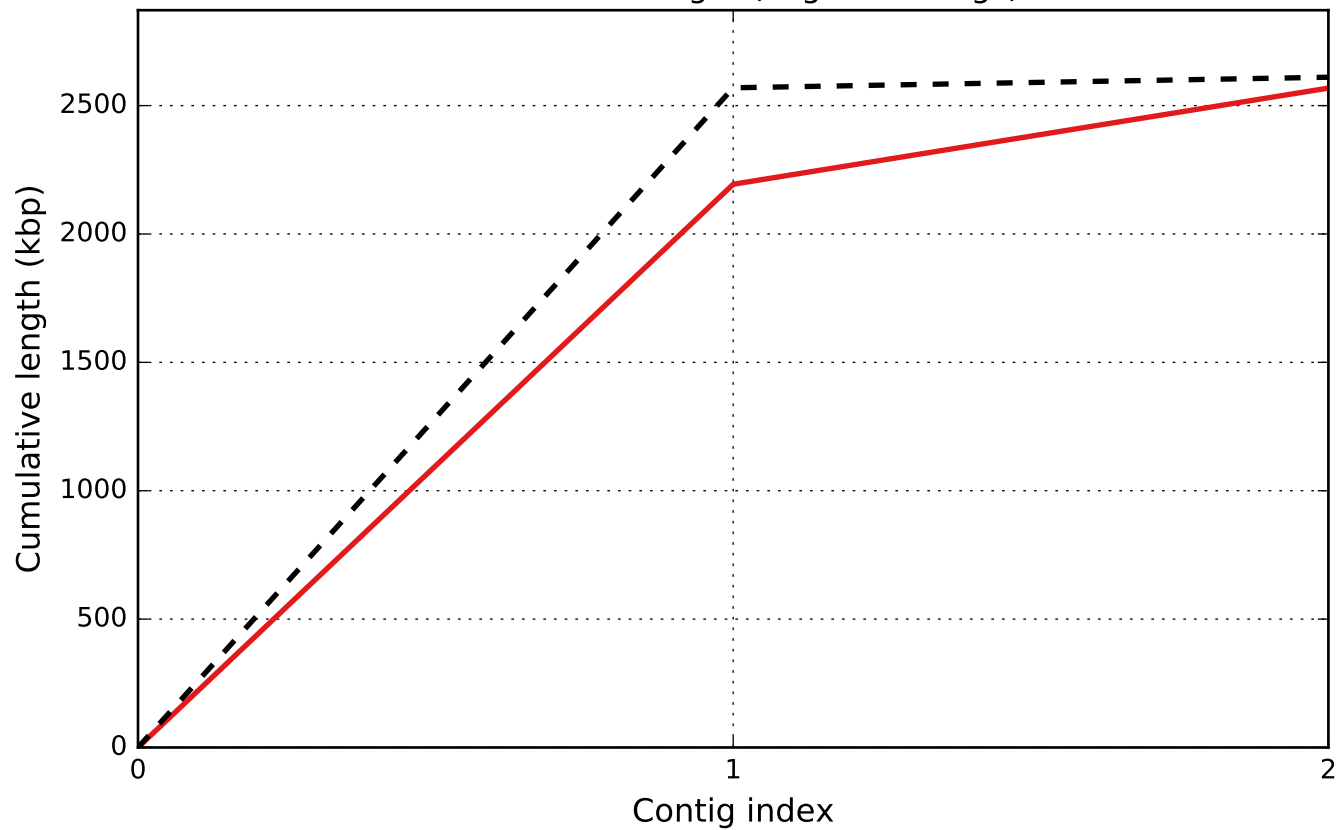


FRCurve (misassemblies)

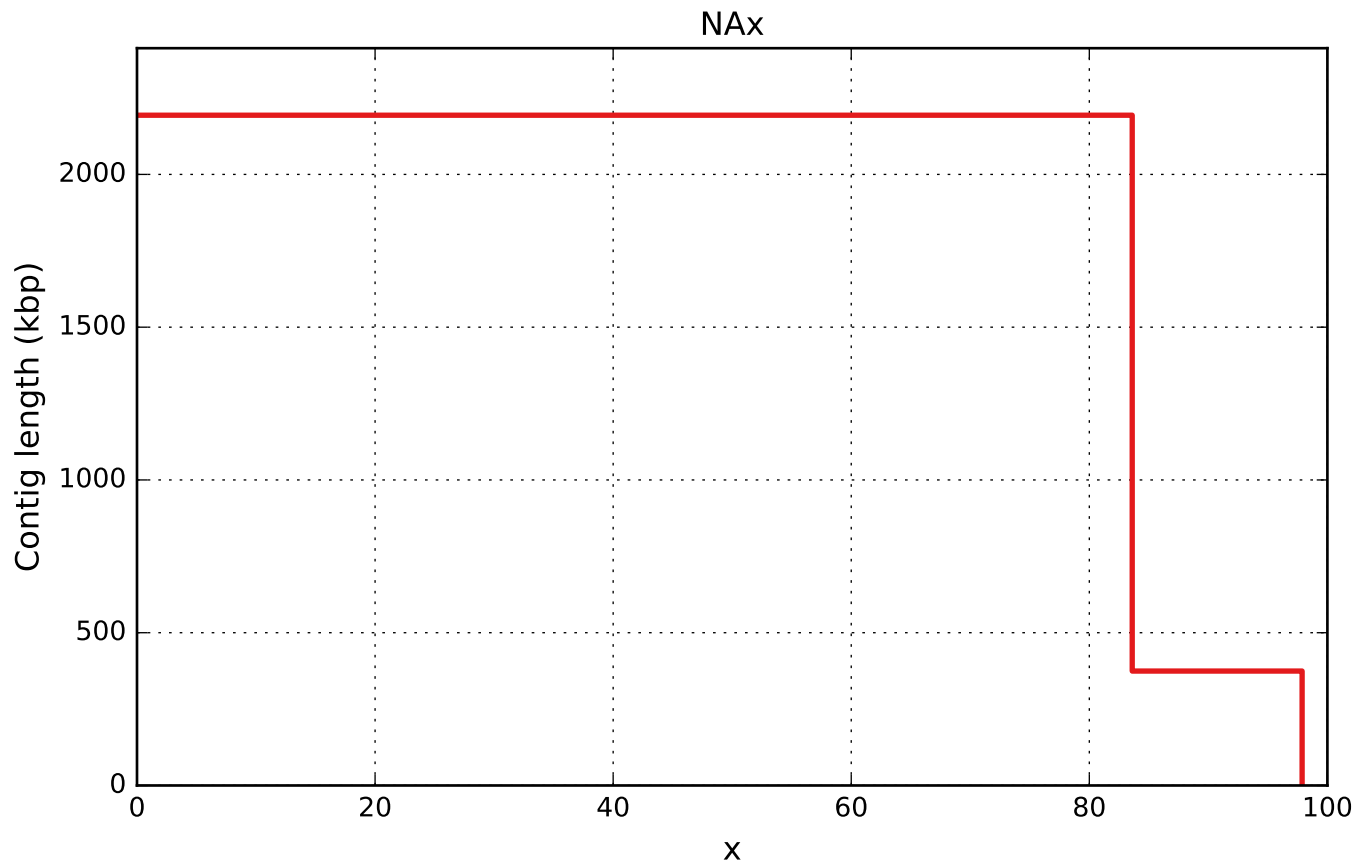


— genome\_assembly.contigs

Cumulative length (aligned contigs)

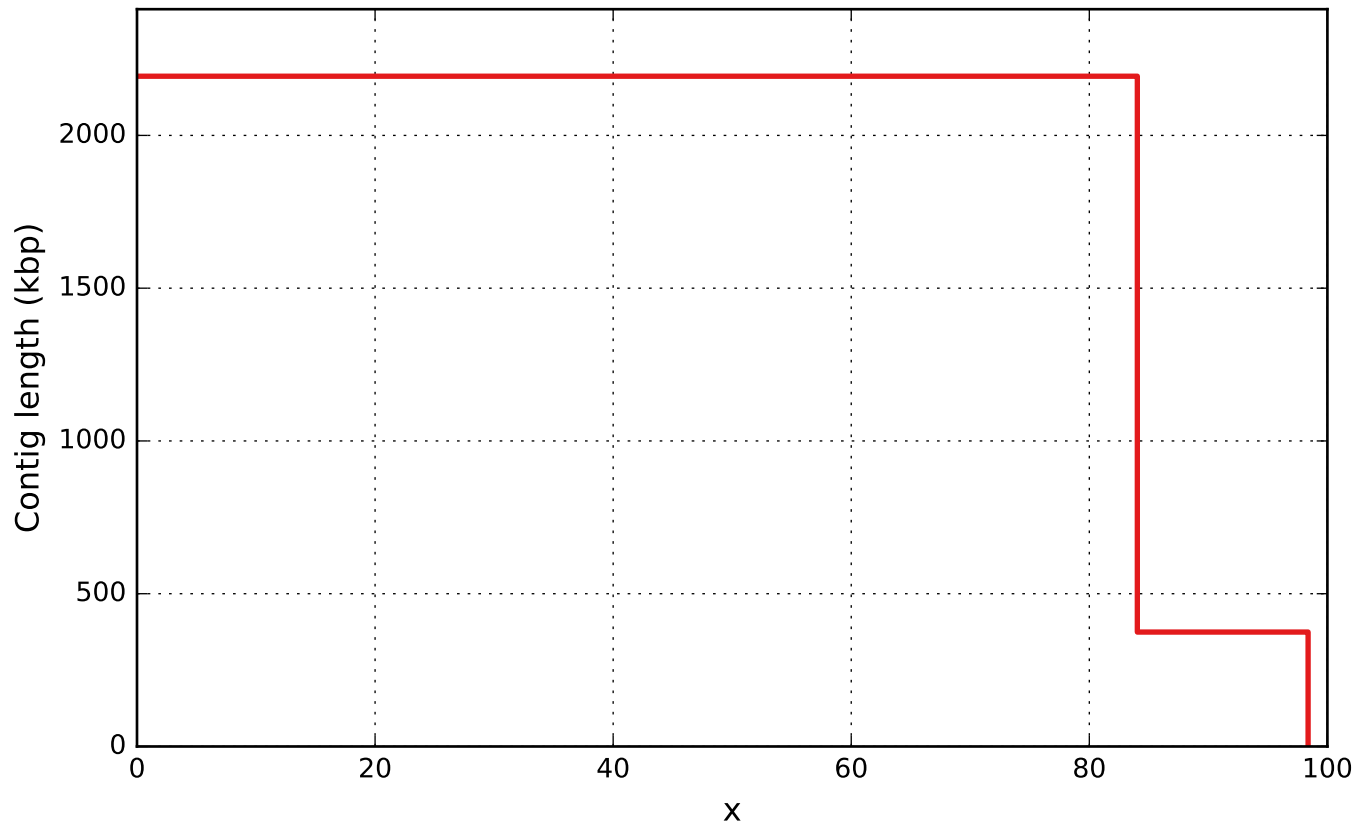


— genome\_assembly.contigs    - - Reference



— genome\_assembly.contigs

NGAx



— genome\_assembly.contigs