

# Report

	CV29_spades_contigs
# contigs (>= 0 bp)	2165
# contigs (>= 1000 bp)	144
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	961507
Total length (>= 1000 bp)	283492
Total length (>= 5000 bp)	42733
Total length (>= 10000 bp)	42733
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	478
Largest contig	24904
Total length	511049
Reference length	29903
GC (%)	43.71
Reference GC (%)	37.97
N50	1136
NG50	24904
N75	716
NG75	24904
L50	118
LG50	1
L75	262
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	476 + 0 part
Unaligned length	481208
Genome fraction (%)	99.632
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.50
# indels per 100 kbp	0.00
# genomic features	54 + 5 part
Largest alignment	24904
Total aligned length	29793
NGA50	24904
NGA75	24904
LGA50	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

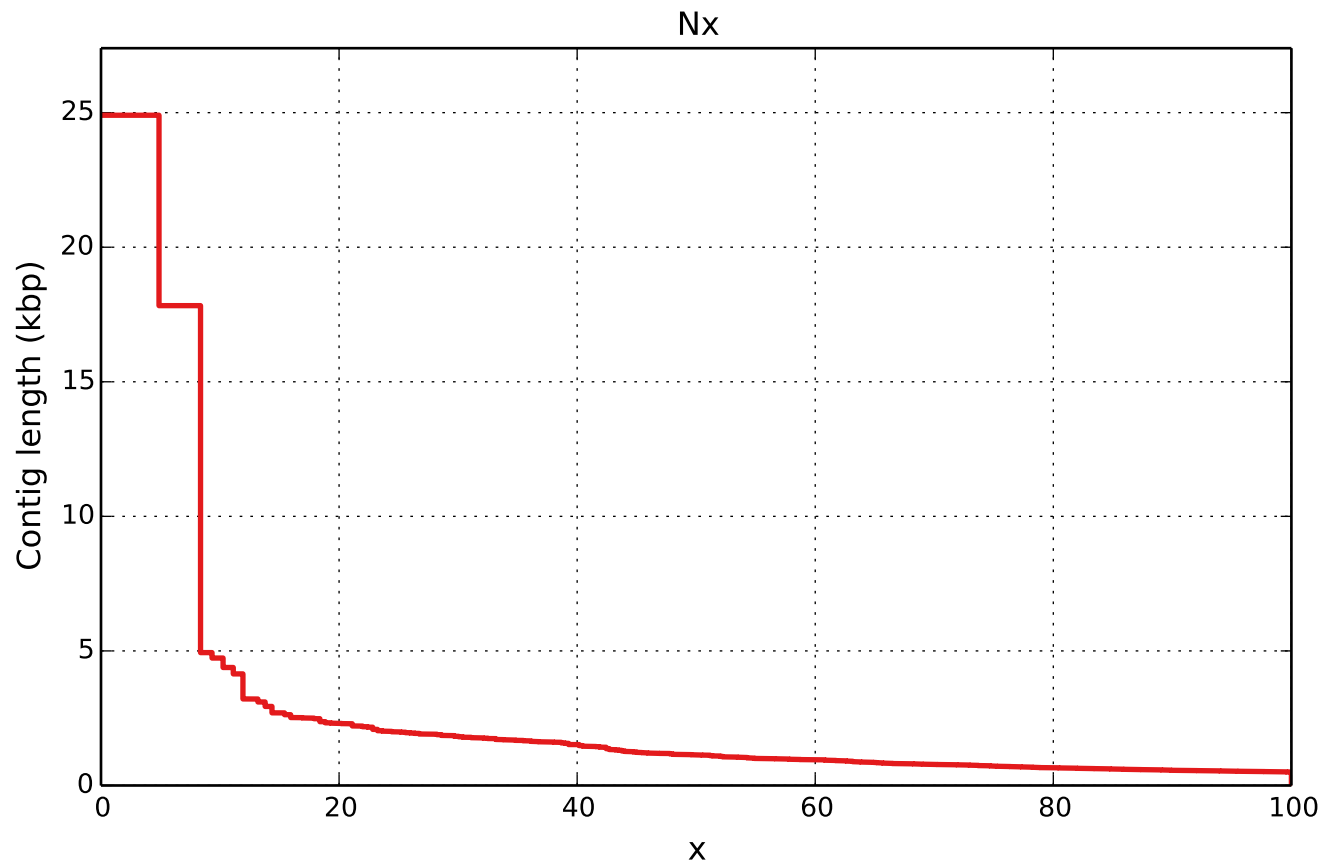
	CV29_spades_contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	7
# 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).

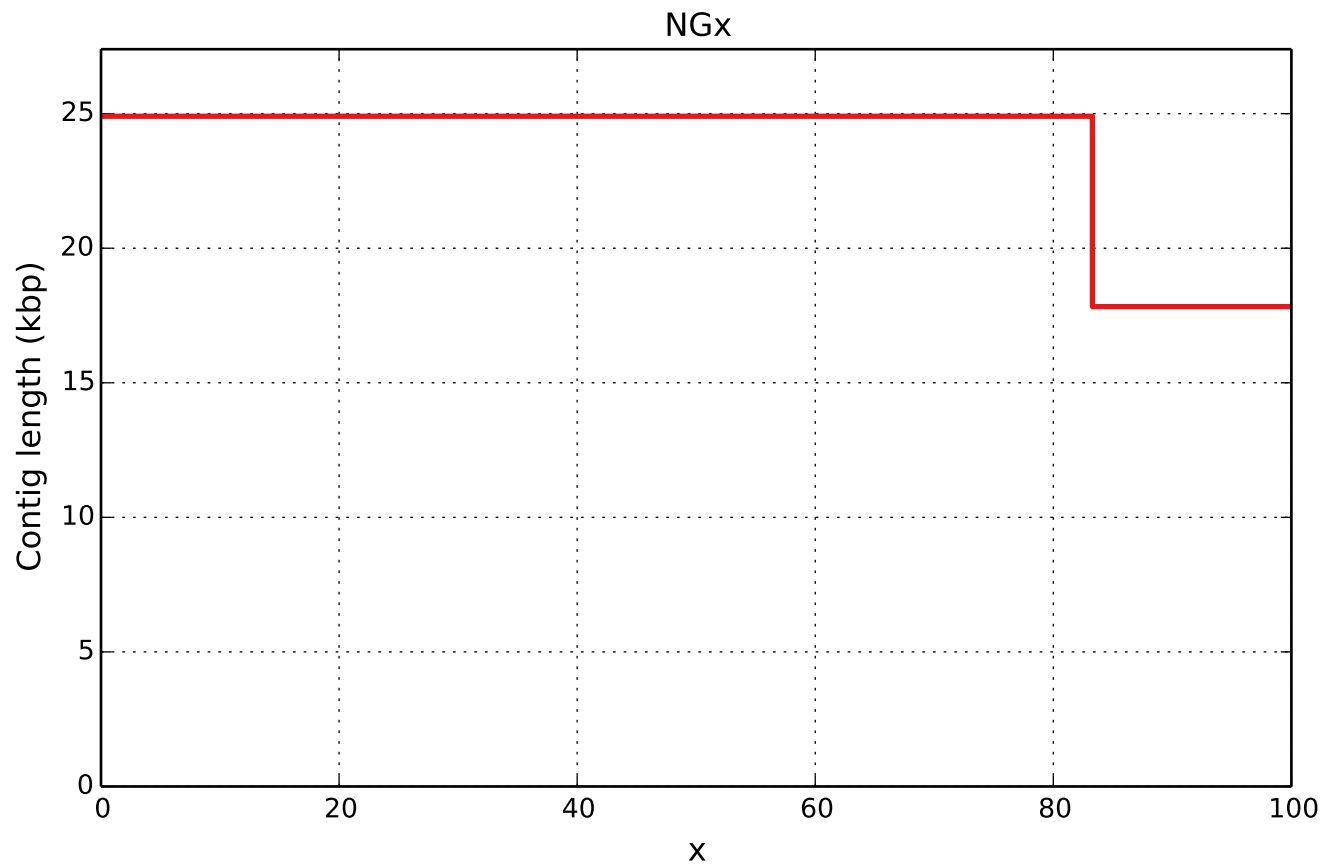
## Unaligned report

	CV29_spades_contigs
# fully unaligned contigs	476
Fully unaligned length	481208
# 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).

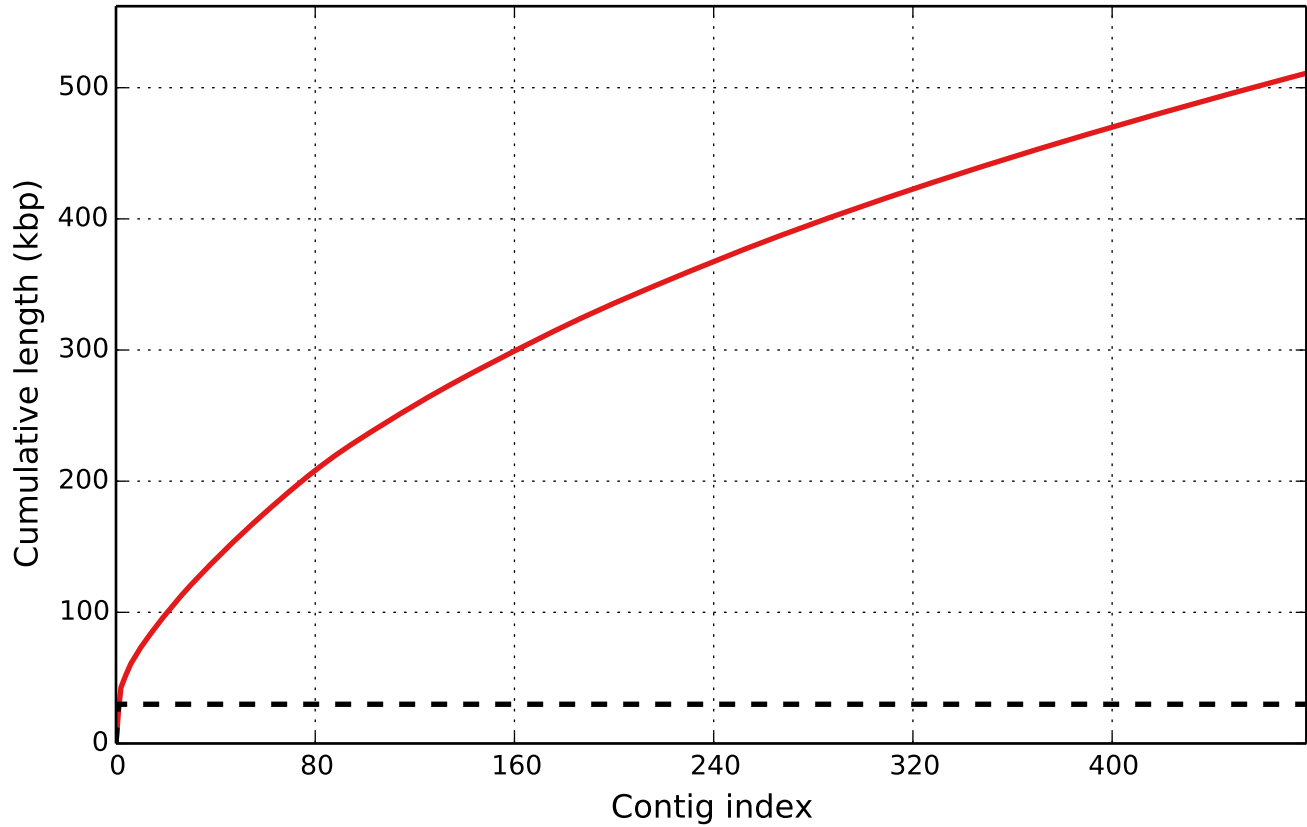


— CV29\_spades\_contigs



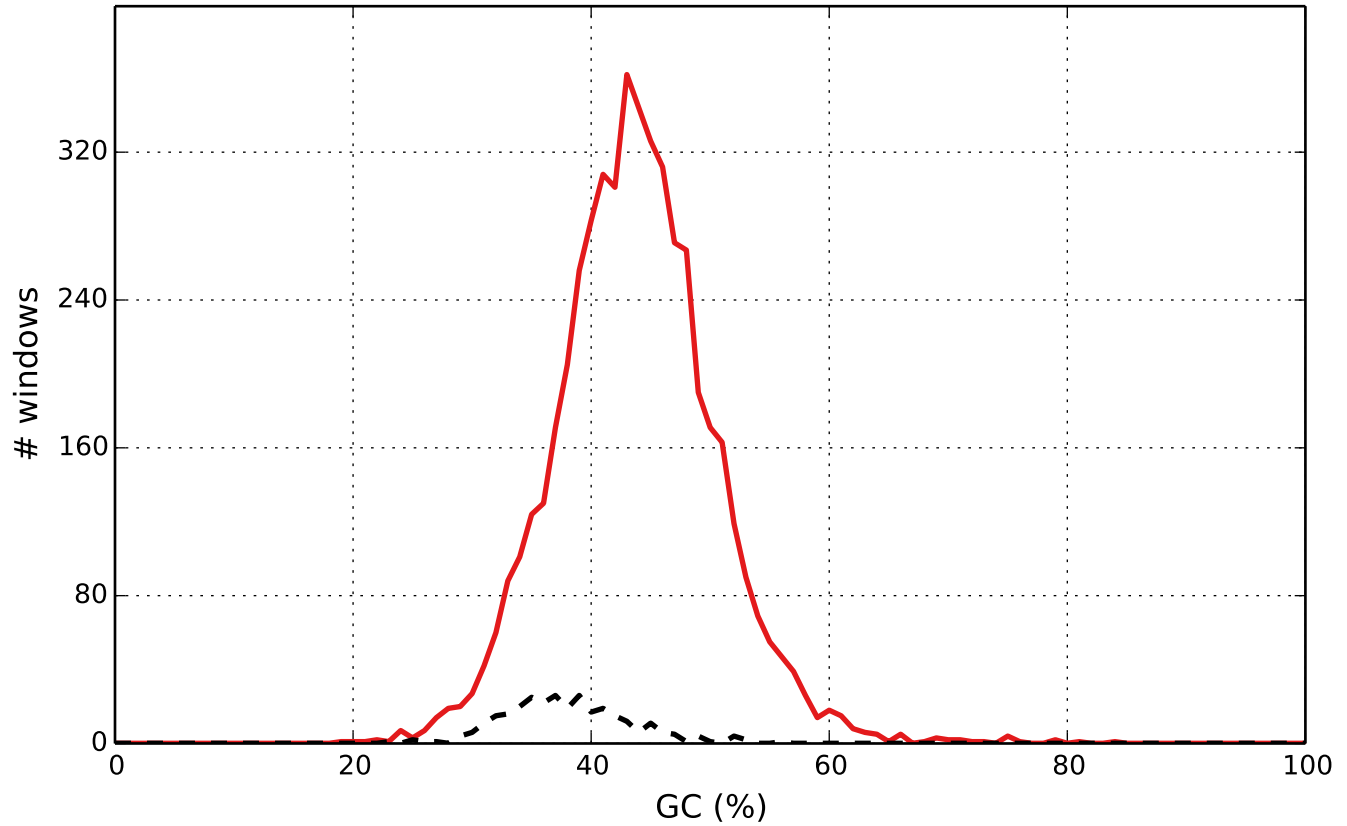
— CV29\_spades\_contigs

Cumulative length



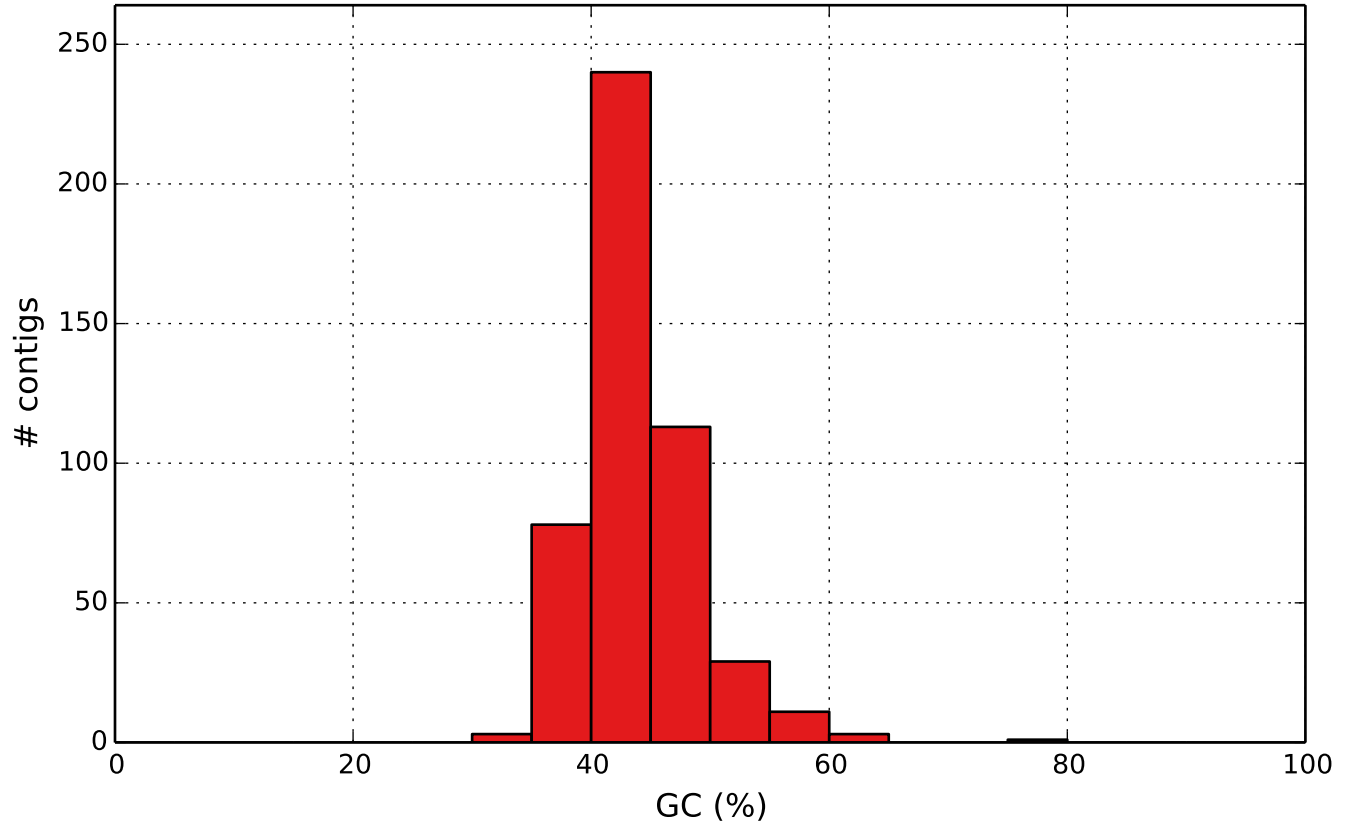
— CV29\_spades\_contigs    - - Reference

# GC content



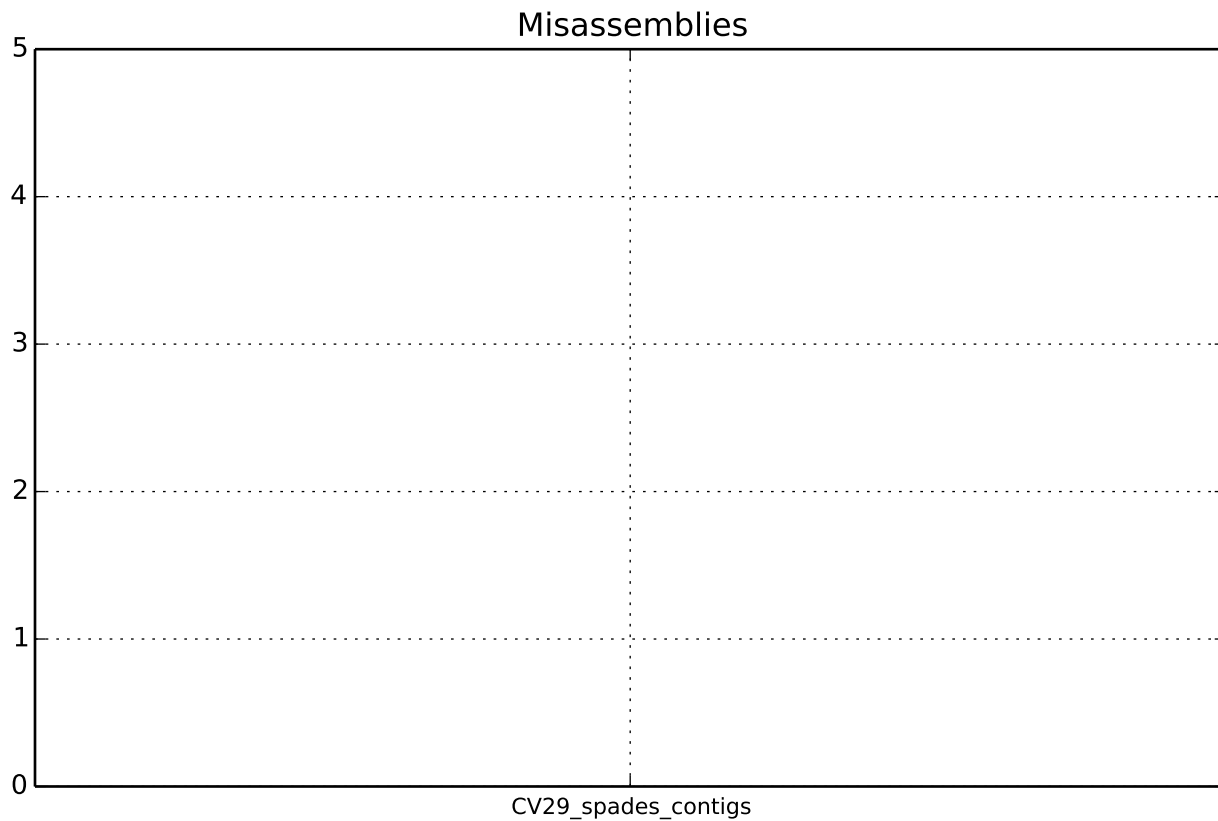
— CV29\_spades\_contigs    - - Reference

CV29\_spades\_contigs GC content

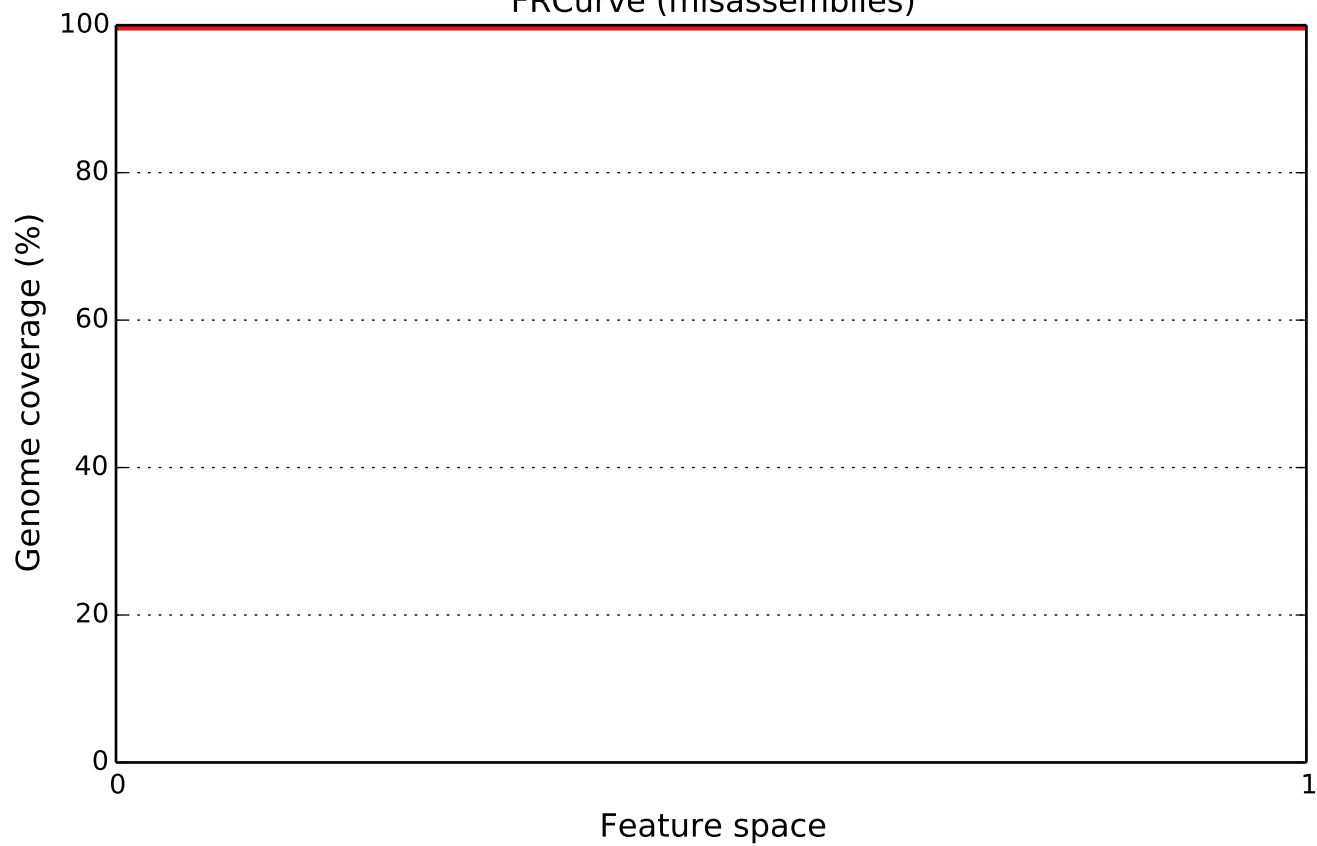


CV29\_spades\_contigs

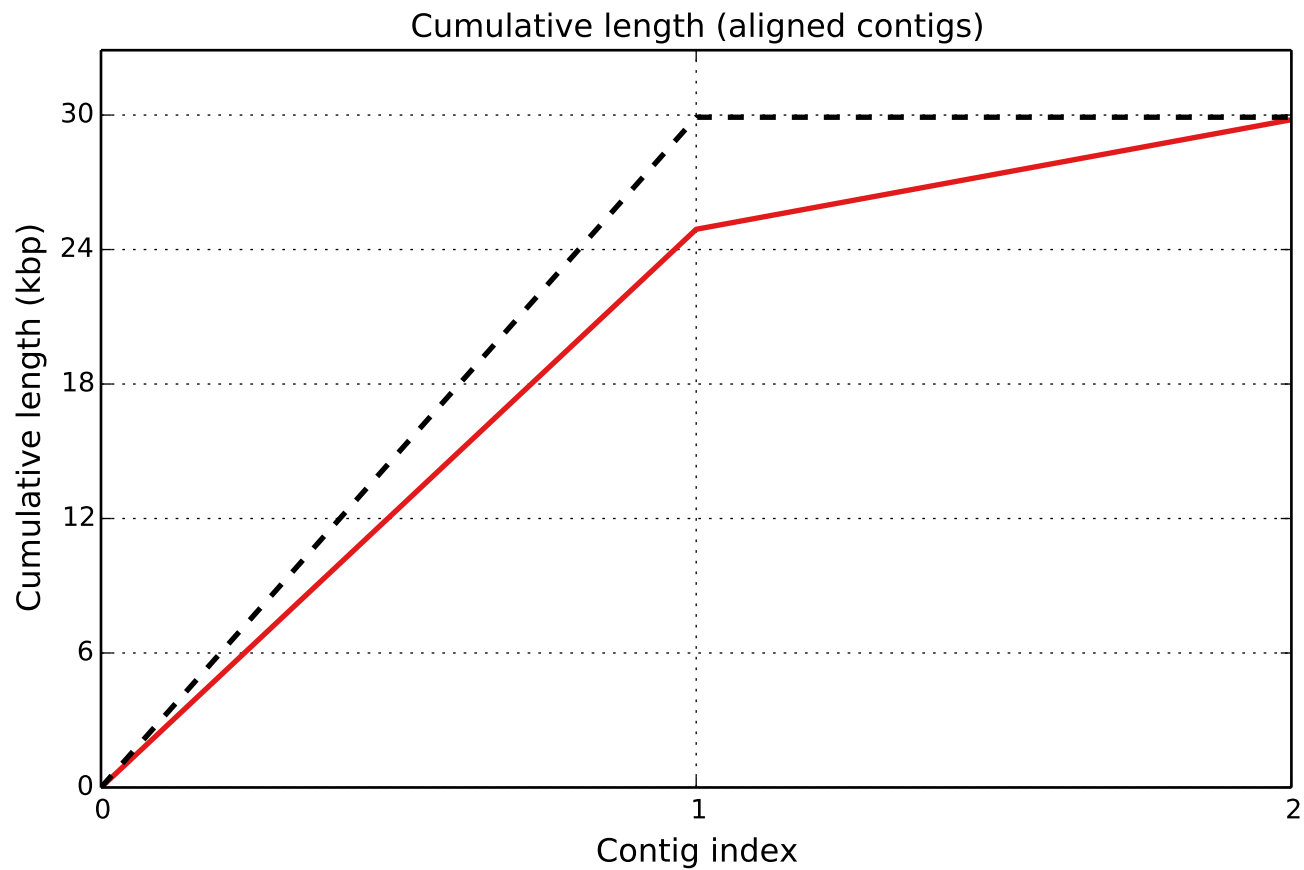


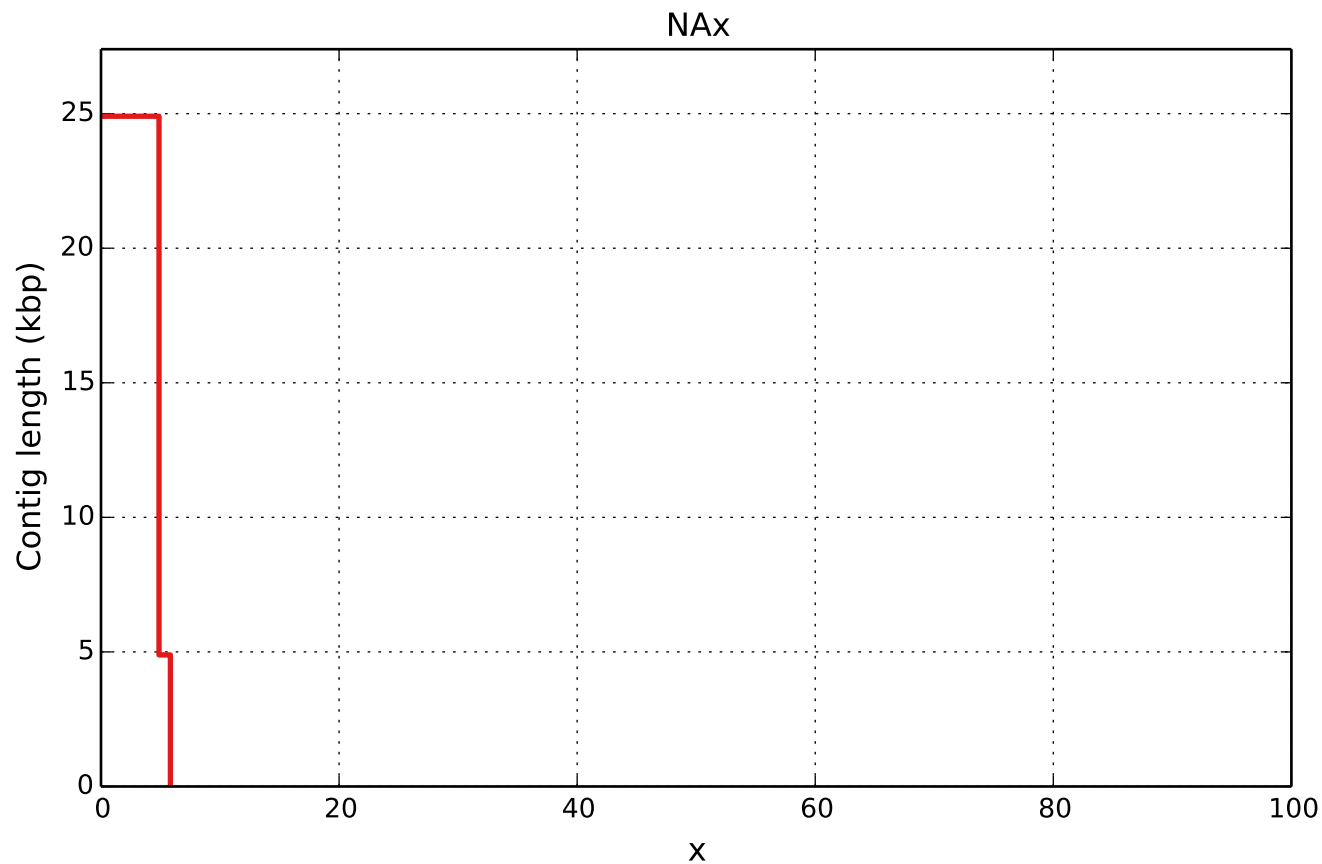


FRCurve (misassemblies)



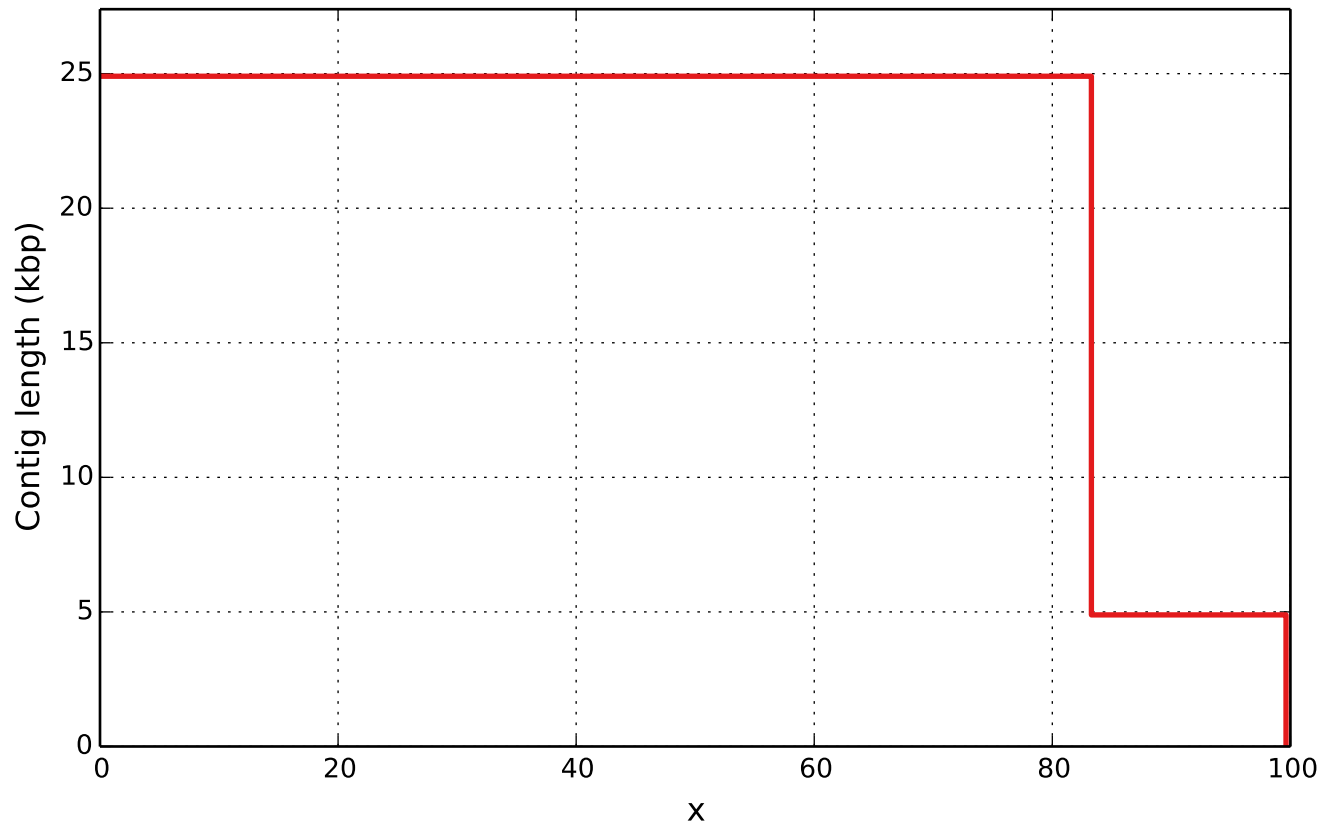
— CV29\_spades\_contigs



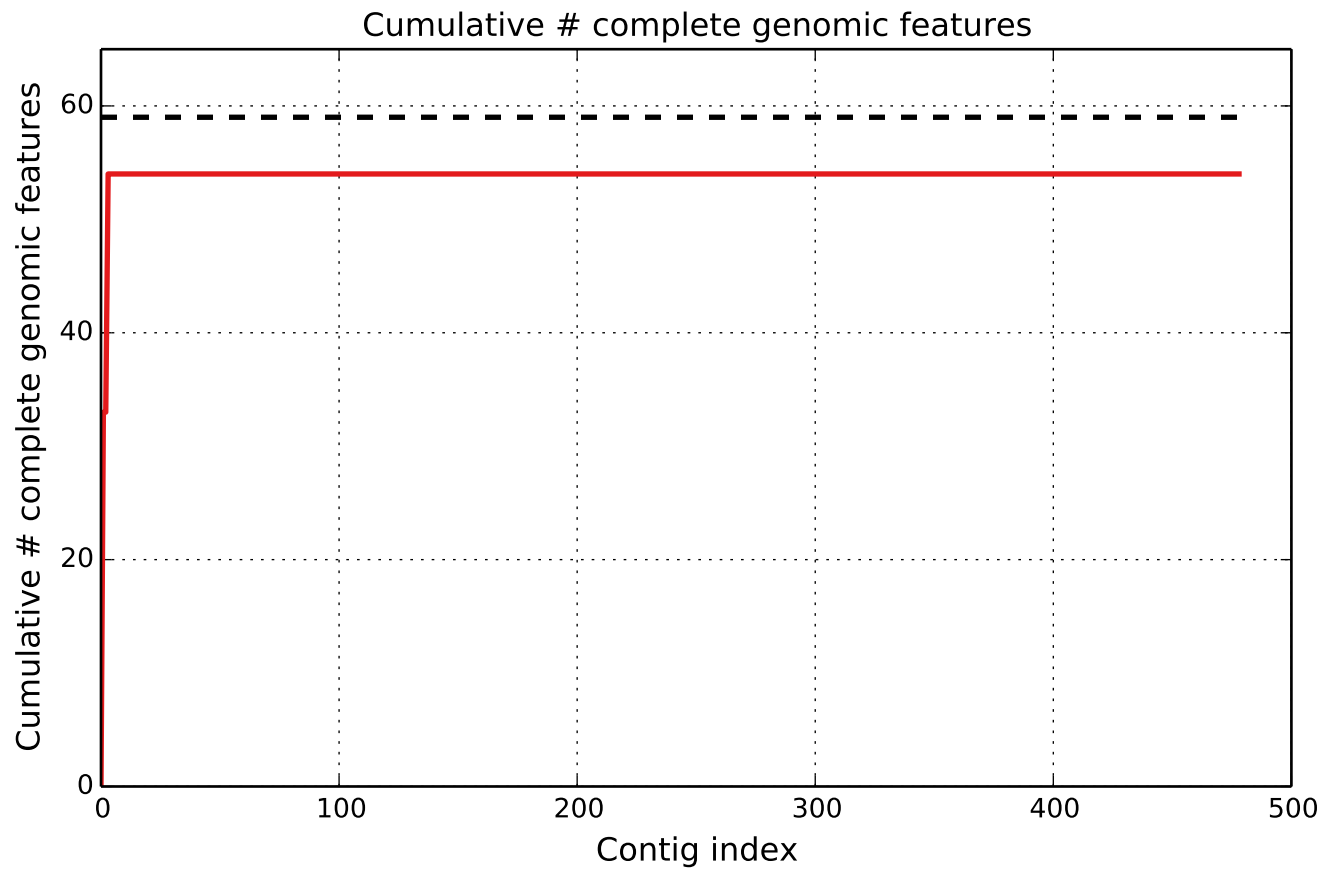


— CV29\_spades\_contigs

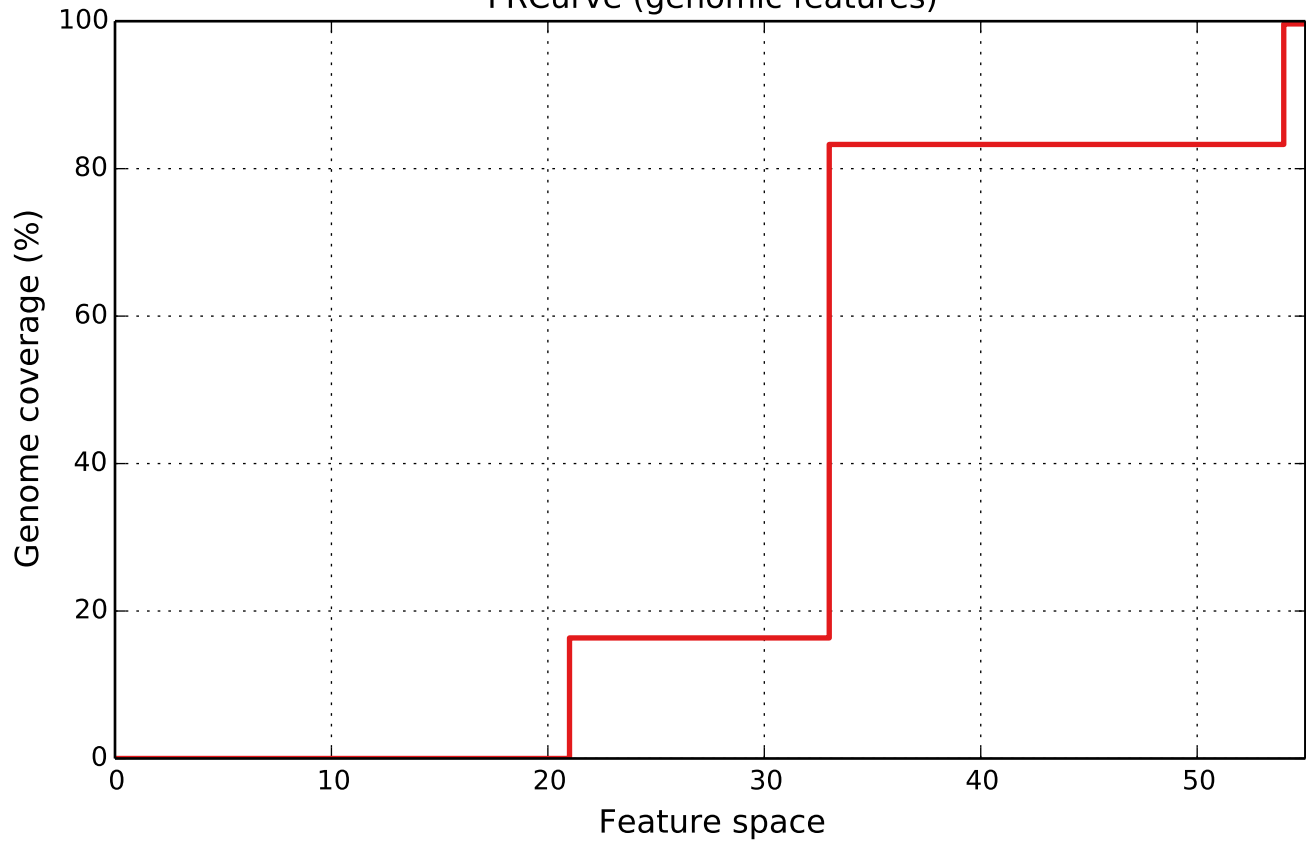
NGAx



— CV29\_spades\_contigs



FRCurve (genomic features)



— CV29\_spades\_contigs