

# Report

	CV18_contigs
# contigs (>= 0 bp)	42
# contigs (>= 1000 bp)	29
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	86685
Total length (>= 1000 bp)	76625
Total length (>= 5000 bp)	34976
Total length (>= 10000 bp)	29928
Total length (>= 25000 bp)	29928
Total length (>= 50000 bp)	0
# contigs	42
Largest contig	29928
Total length	86685
Reference length	29903
GC (%)	46.97
Reference GC (%)	37.97
N50	2294
NG50	29928
N75	1247
NG75	29928
L50	6
LG50	1
L75	19
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	41 + 0 part
Unaligned length	56757
Genome fraction (%)	99.776
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.52
# indels per 100 kbp	0.00
# genomic features	56 + 3 part
Largest alignment	29836
Total aligned length	29836
NGA50	29836
NGA75	29836
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

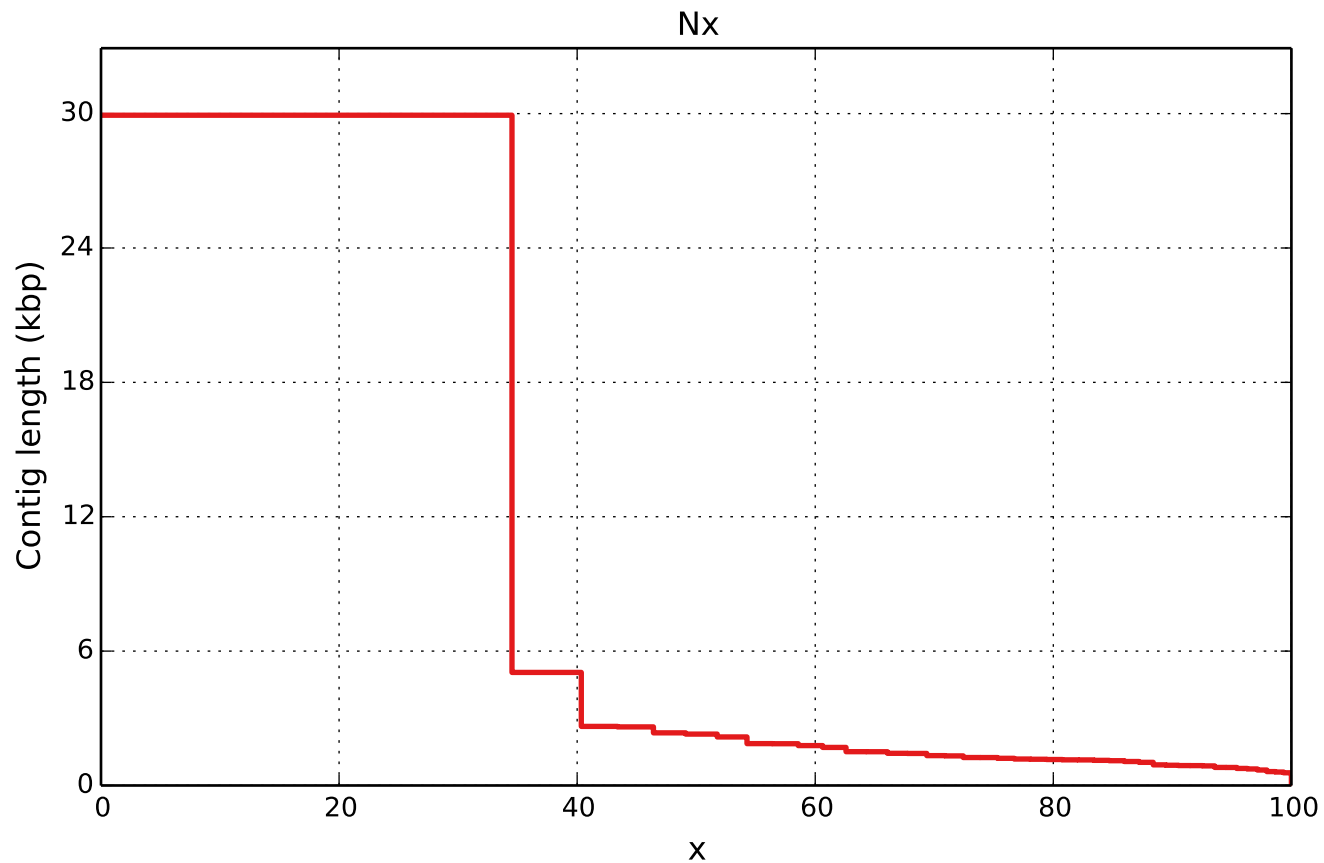
	CV18_contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	10
# 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).

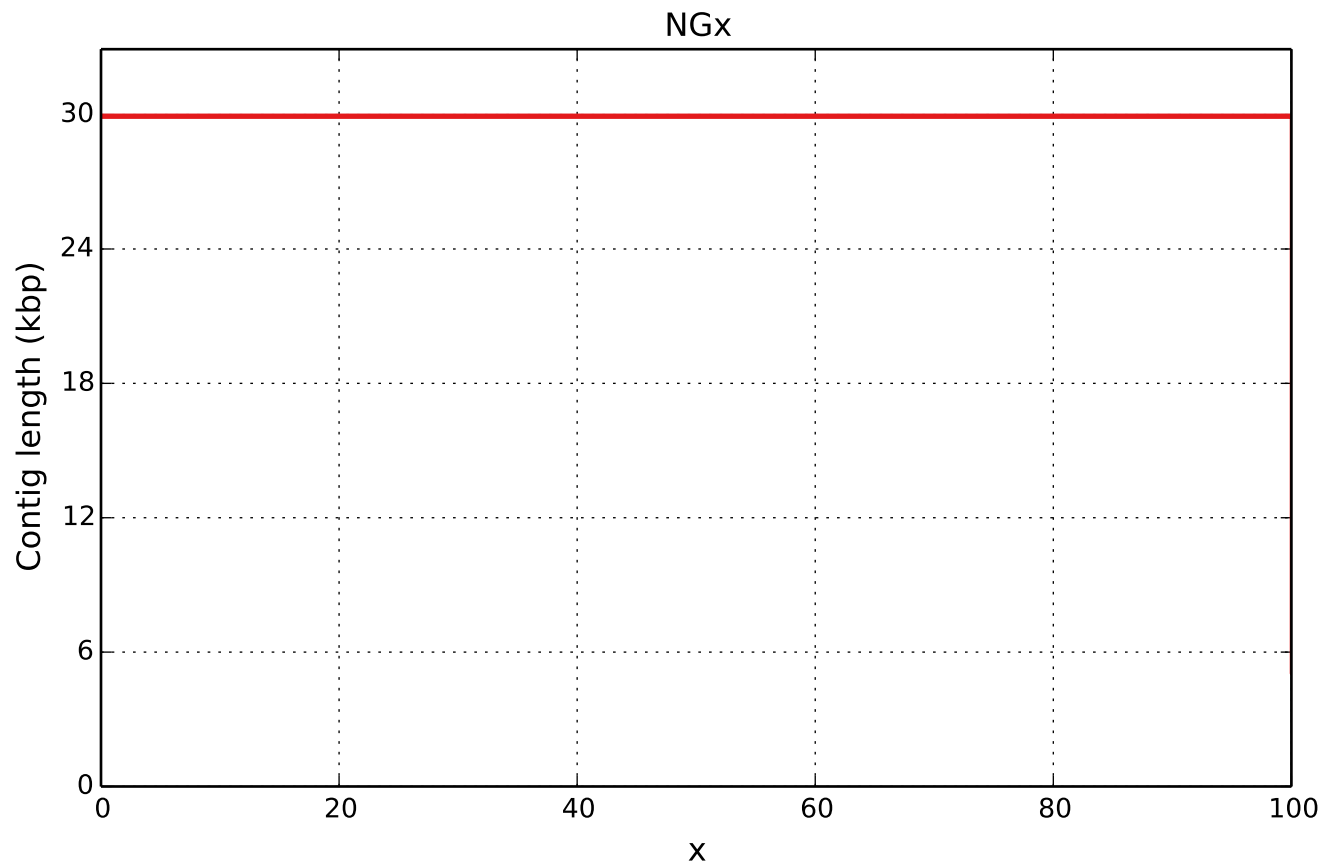
## Unaligned report

	CV18_contigs
# fully unaligned contigs	41
Fully unaligned length	56757
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

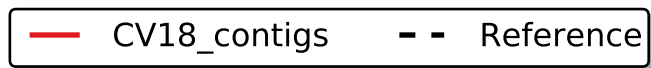
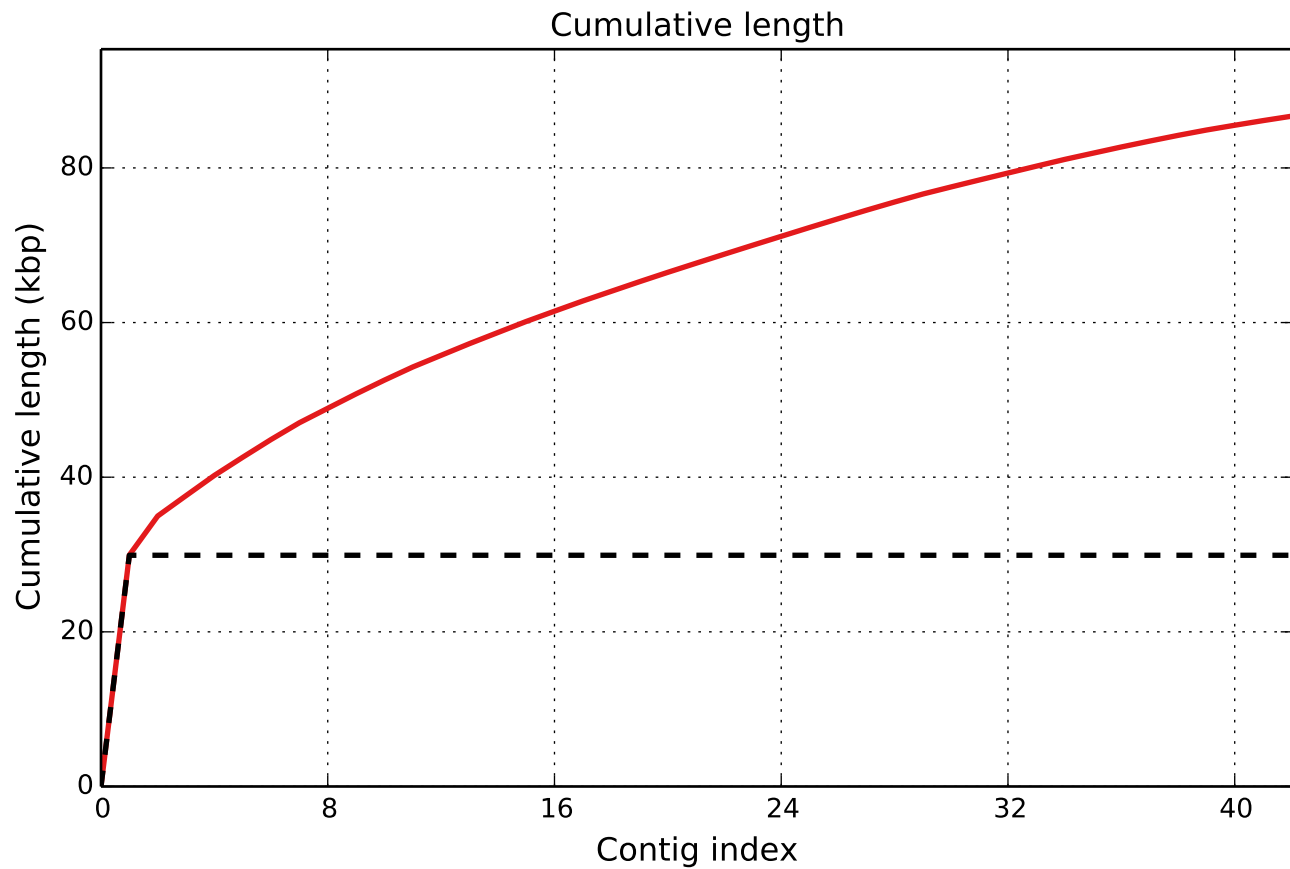
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

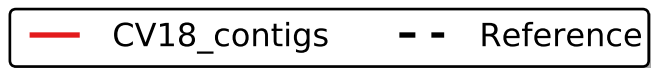
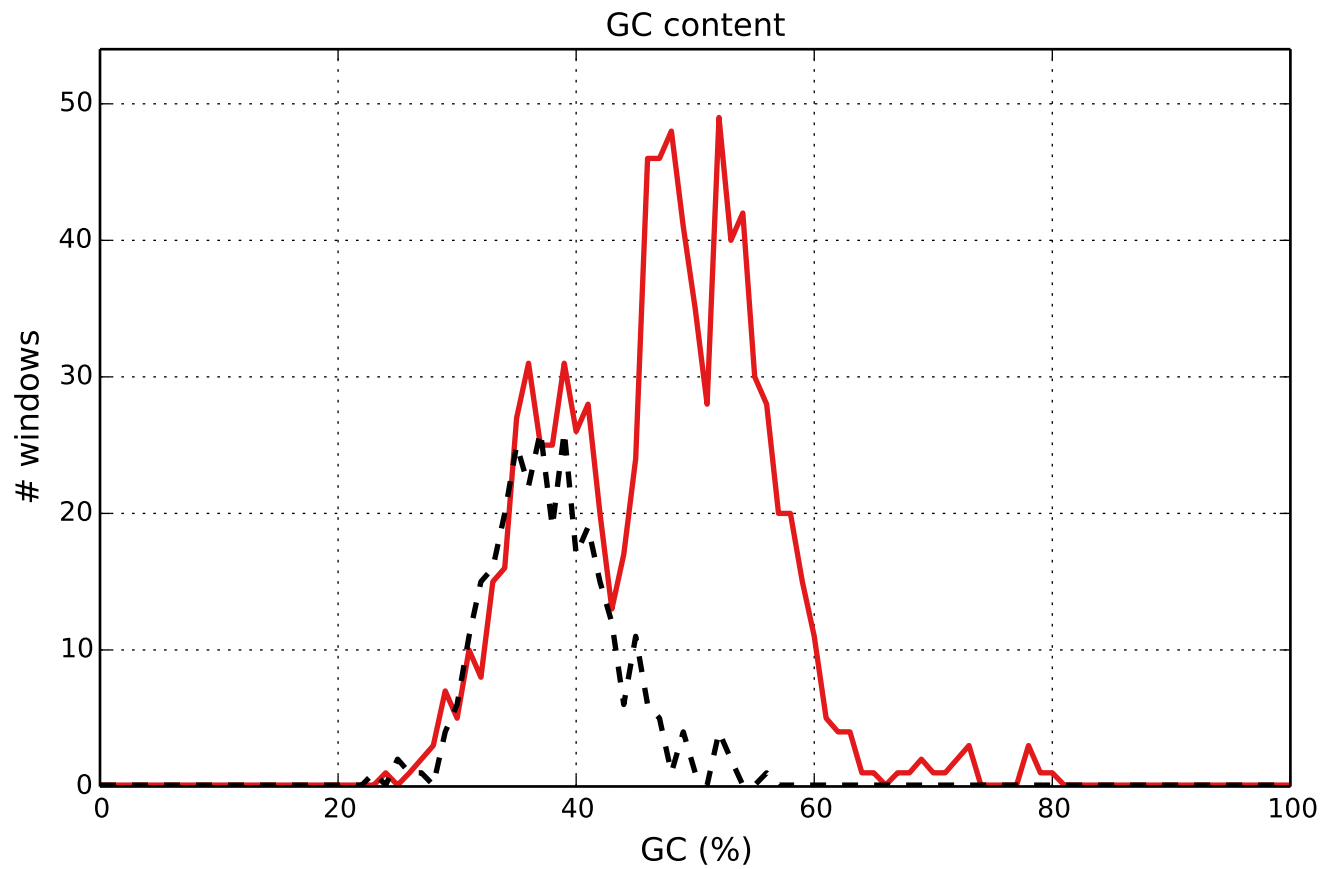


— CV18\_contigs

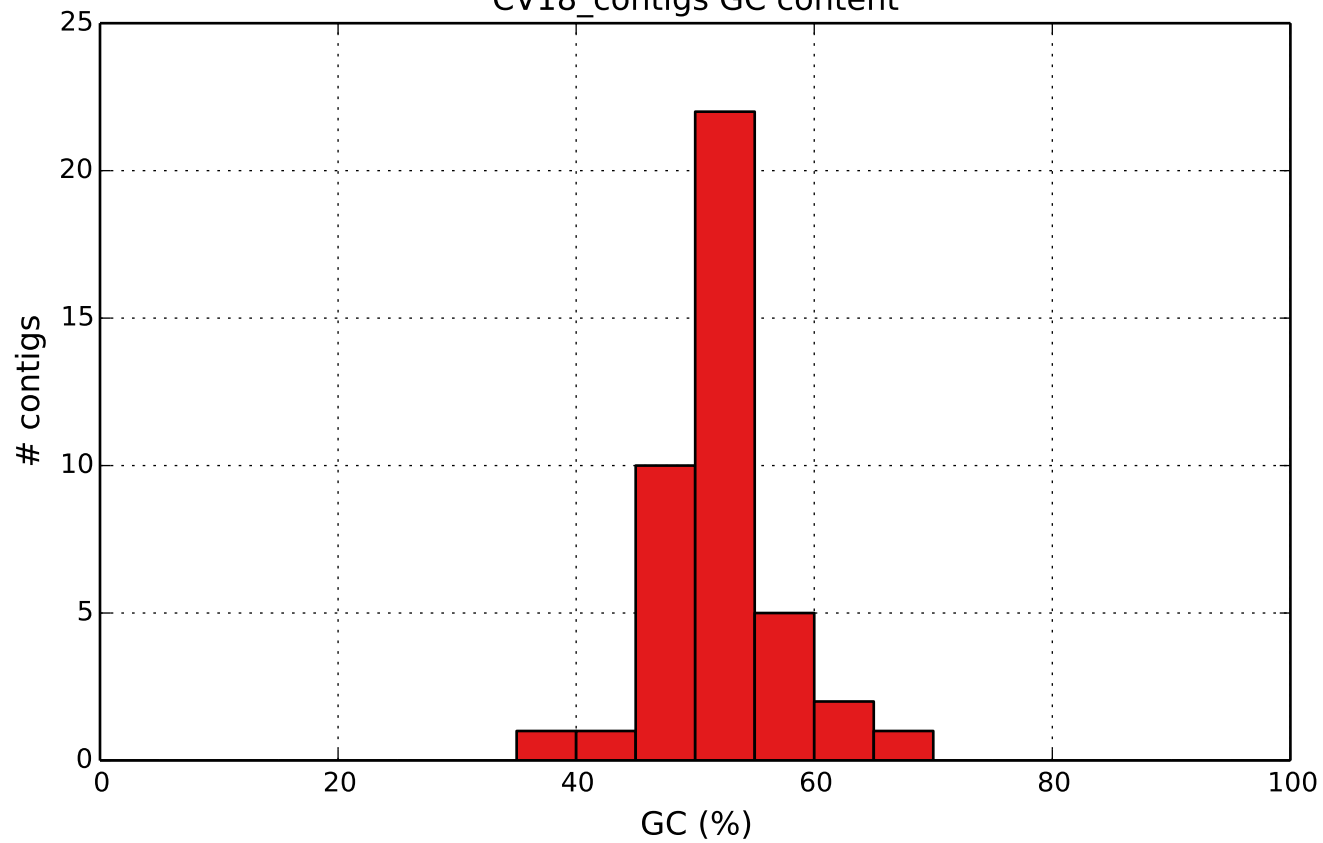


— CV18\_contigs



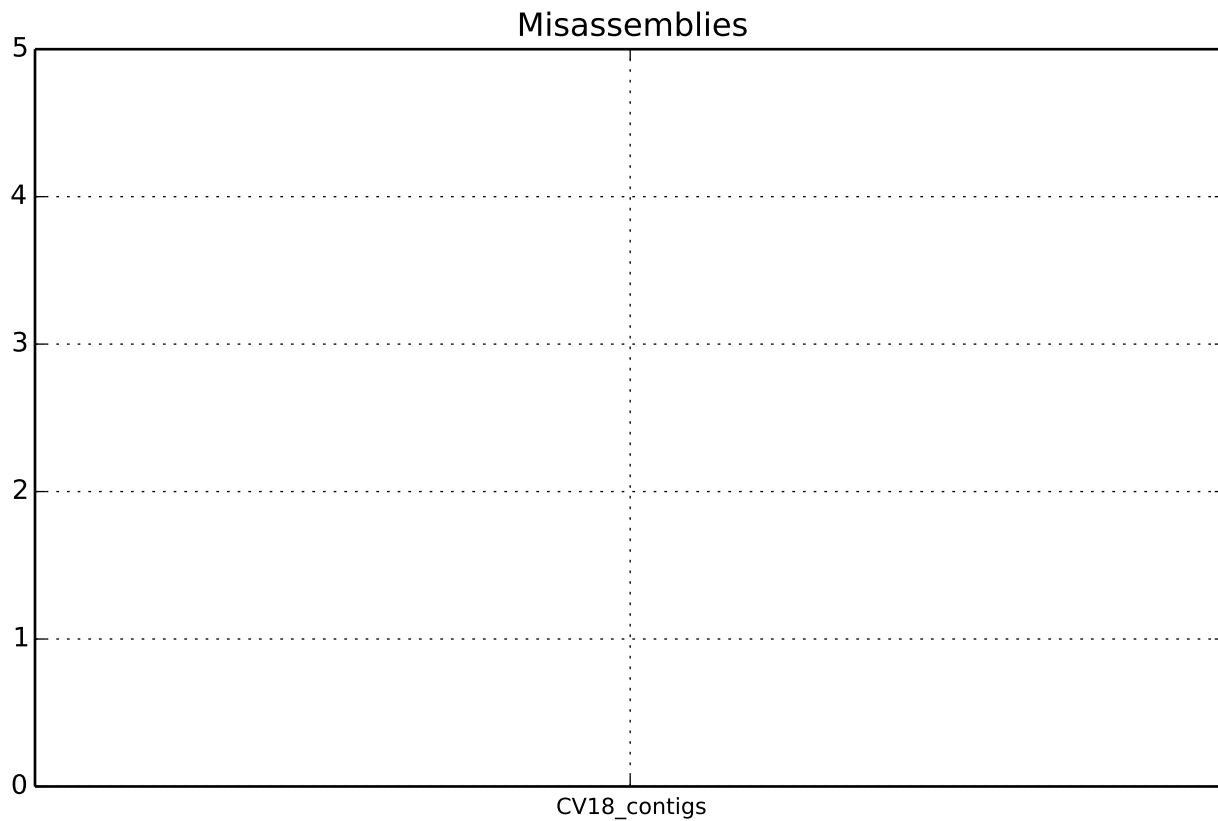


CV18\_contigs GC content

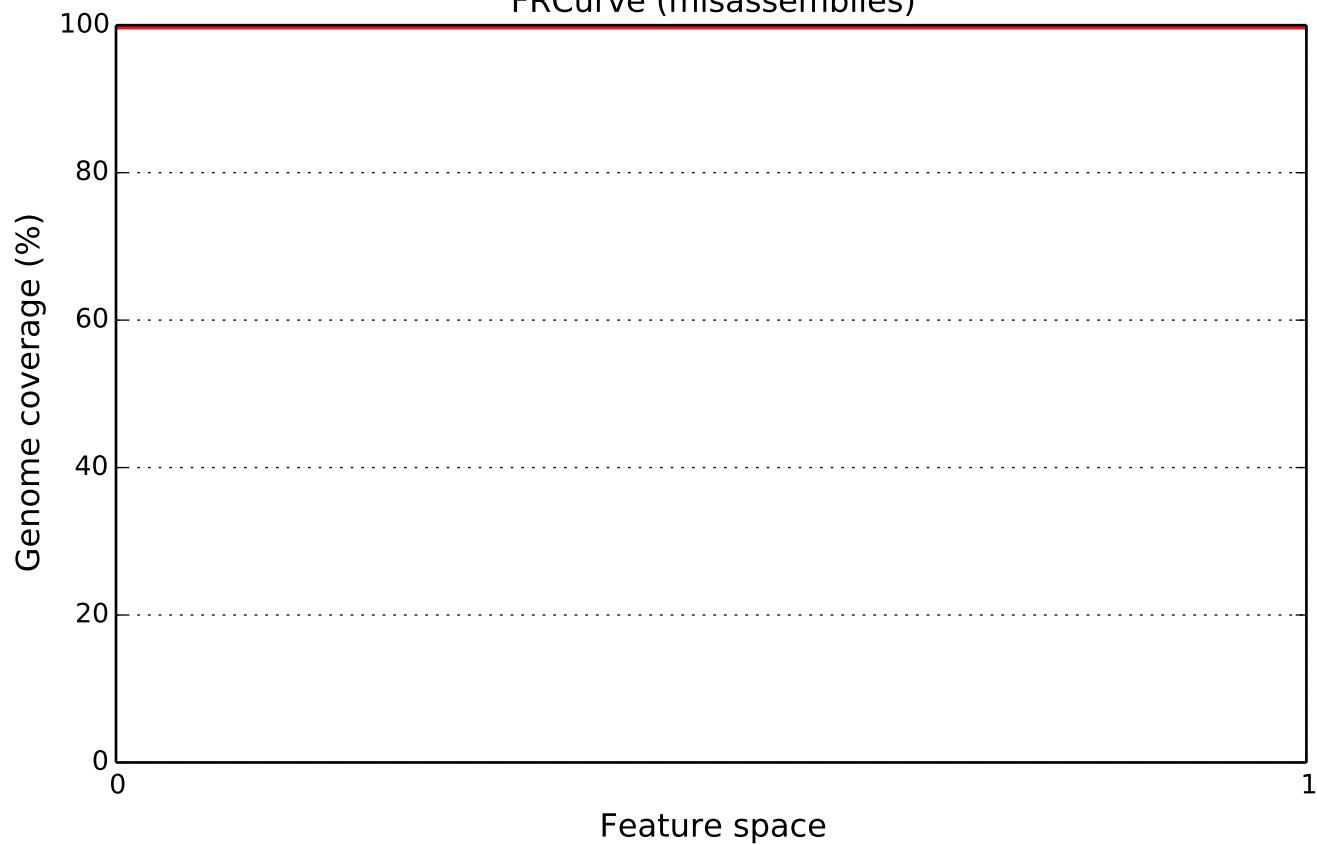


CV18\_contigs

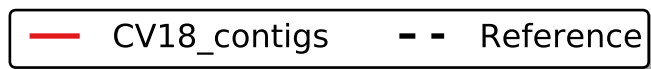
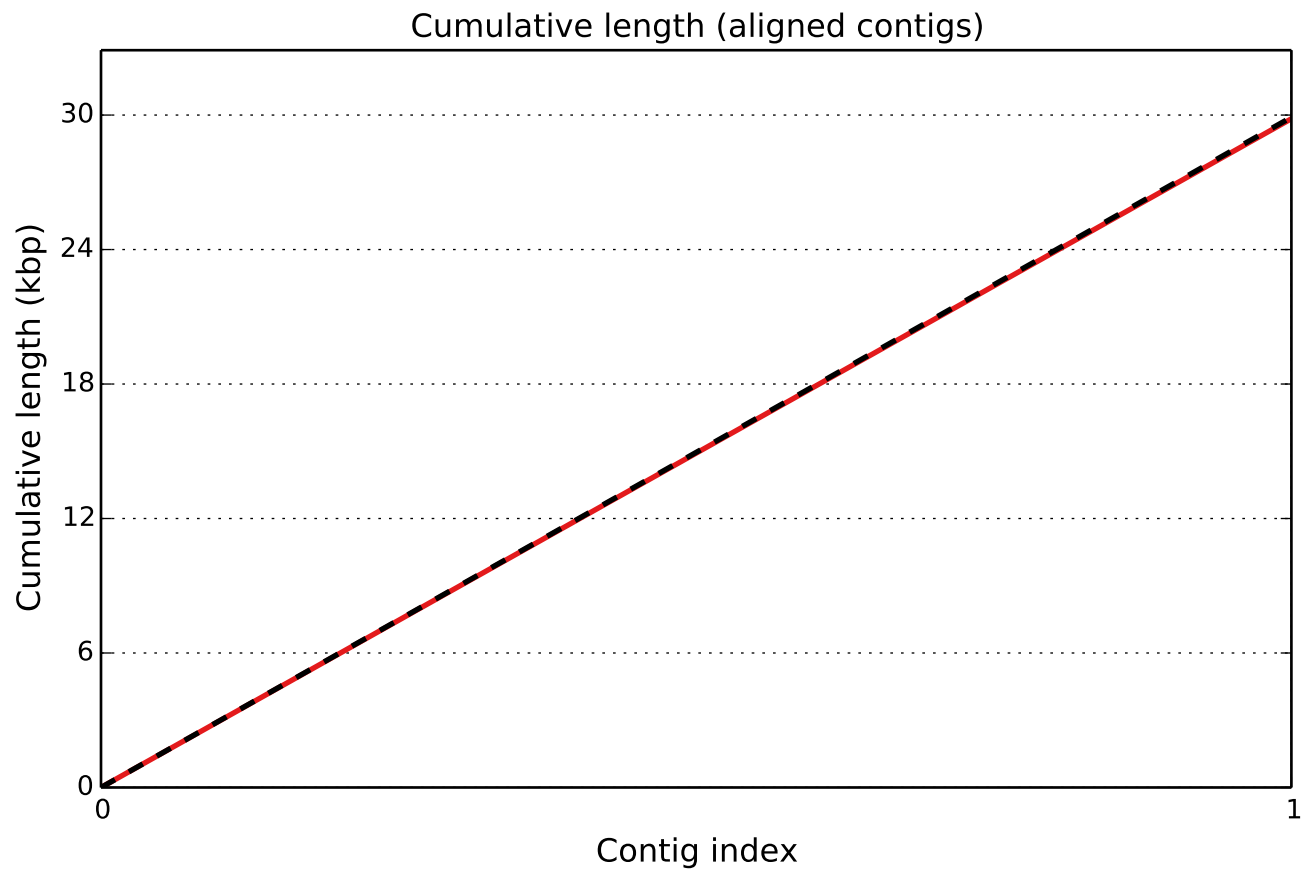


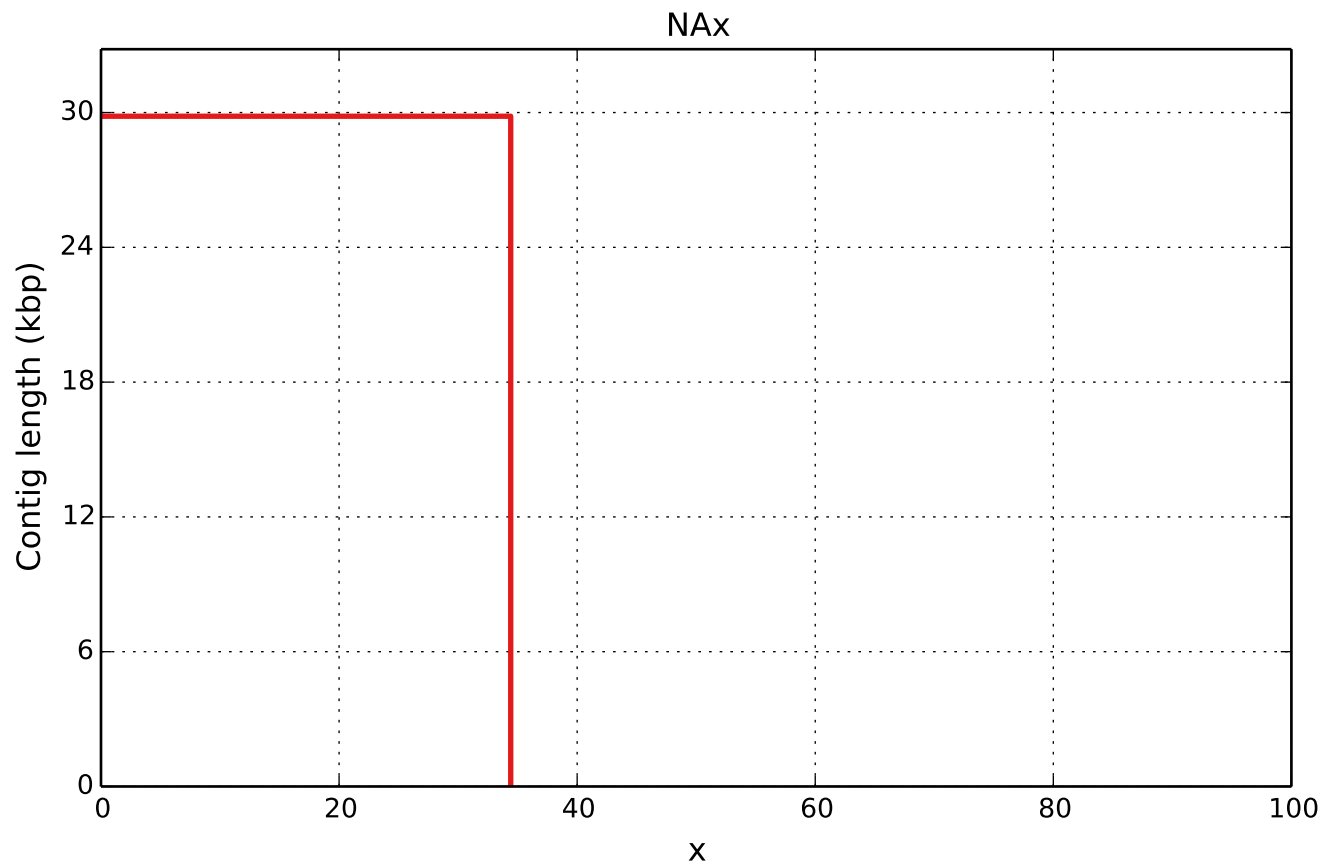


FRCurve (misassemblies)



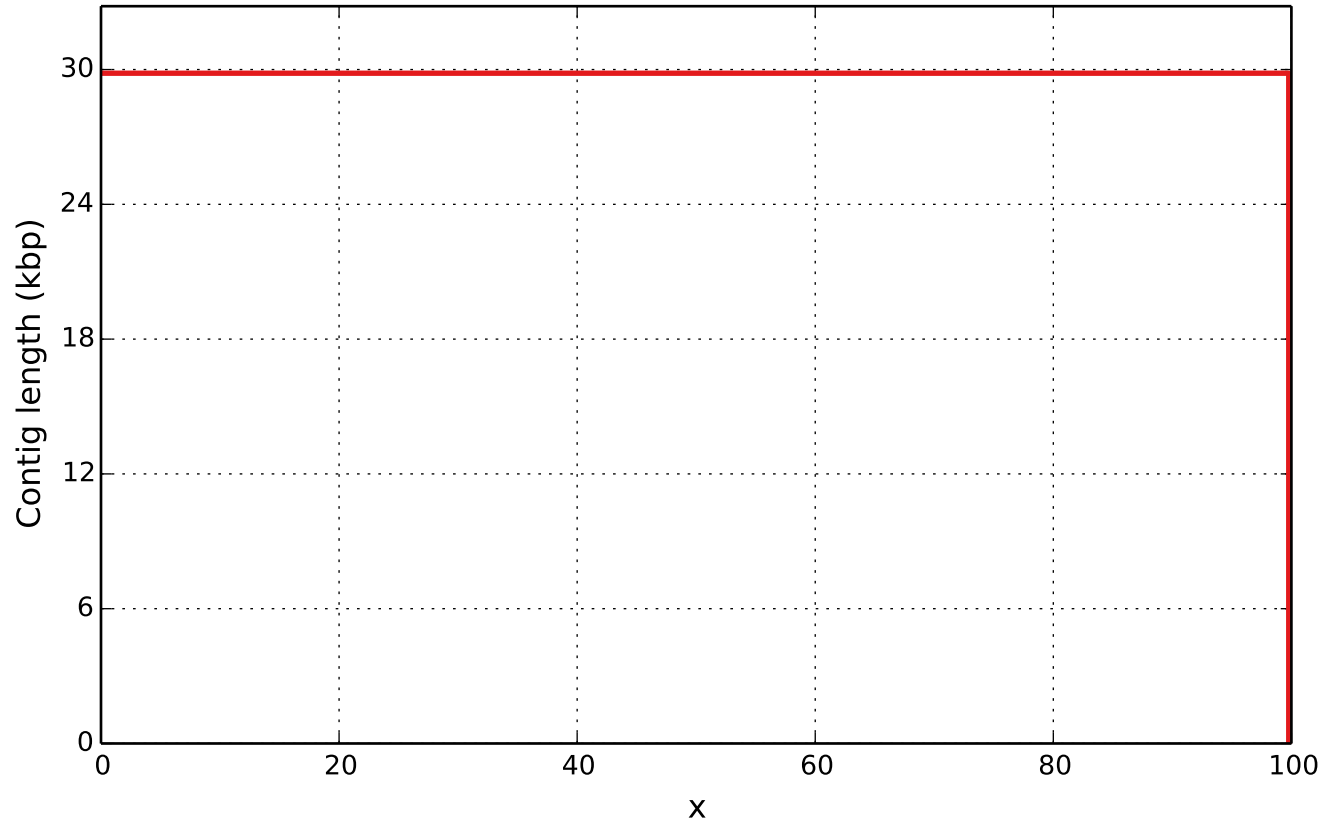
— CV18\_contigs





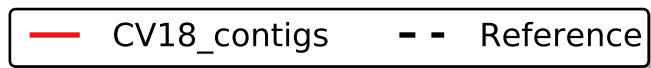
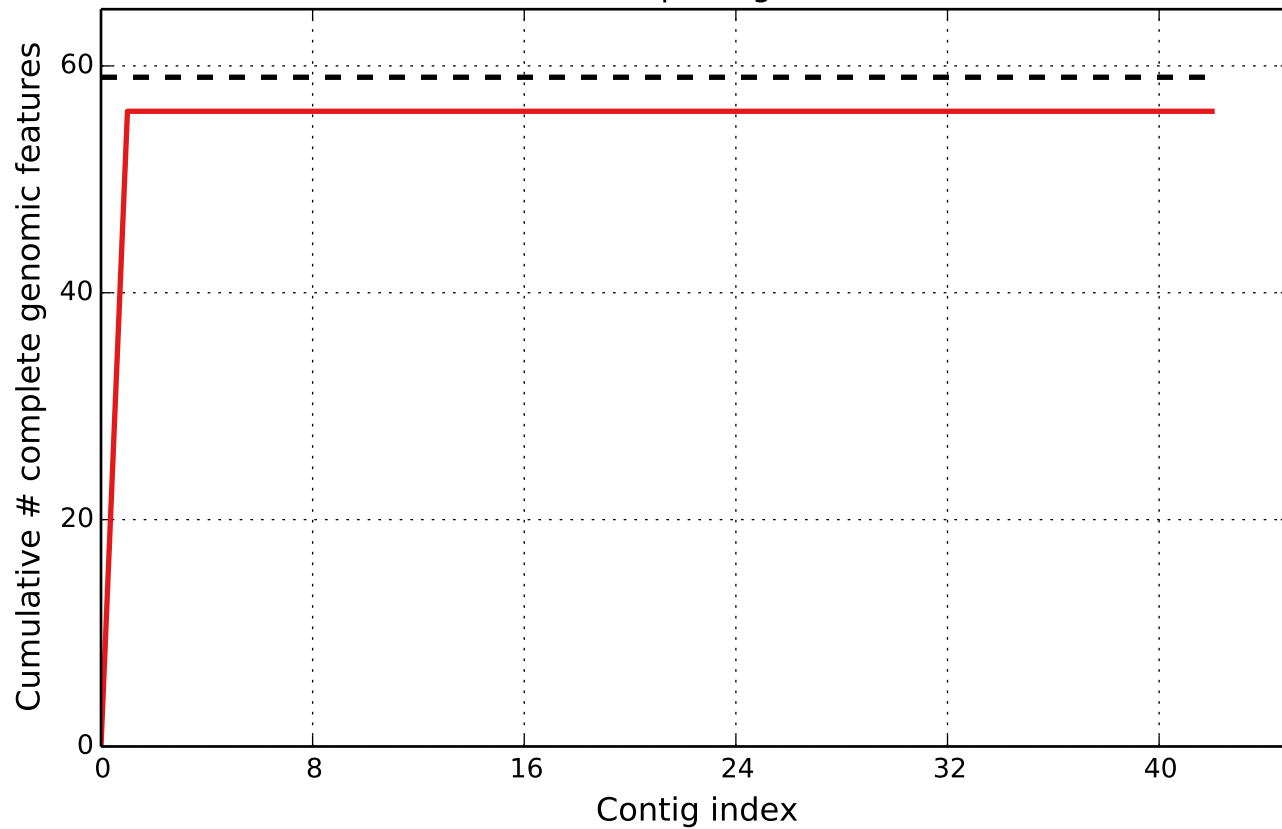
— CV18\_contigs

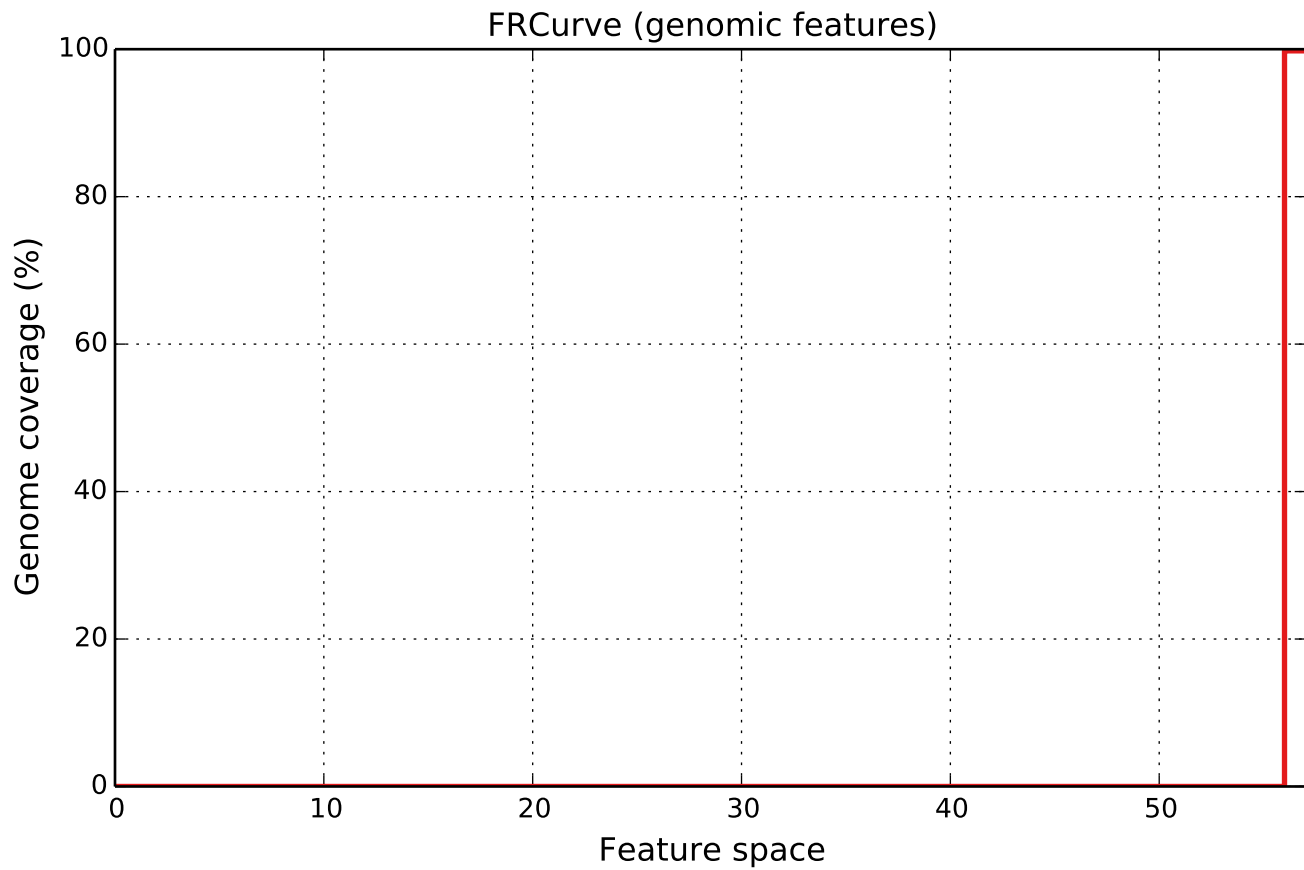
NGAx



— CV18\_contigs

Cumulative # complete genomic features





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