

Report

	CV18_spades_contigs
# contigs (>= 0 bp)	1198
# contigs (>= 1000 bp)	190
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	614425
Total length (>= 1000 bp)	353433
Total length (>= 5000 bp)	44723
Total length (>= 10000 bp)	22141
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	384
Largest contig	22141
Total length	493639
Reference length	29903
GC (%)	50.68
Reference GC (%)	37.97
N50	1435
NG50	22141
N75	940
NG75	9089
L50	101
LG50	1
L75	208
LG75	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9089
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	381 + 0 part
Unaligned length	454716
Genome fraction (%)	99.652
Duplication ratio	1.306
# N's per 100 kbp	0.00
# mismatches per 100 kbp	60.40
# indels per 100 kbp	3.36
# genomic features	54 + 5 part
Largest alignment	22069
Total aligned length	38746
NGA50	22069
NGA75	7689
LGA50	1
LGA75	2

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

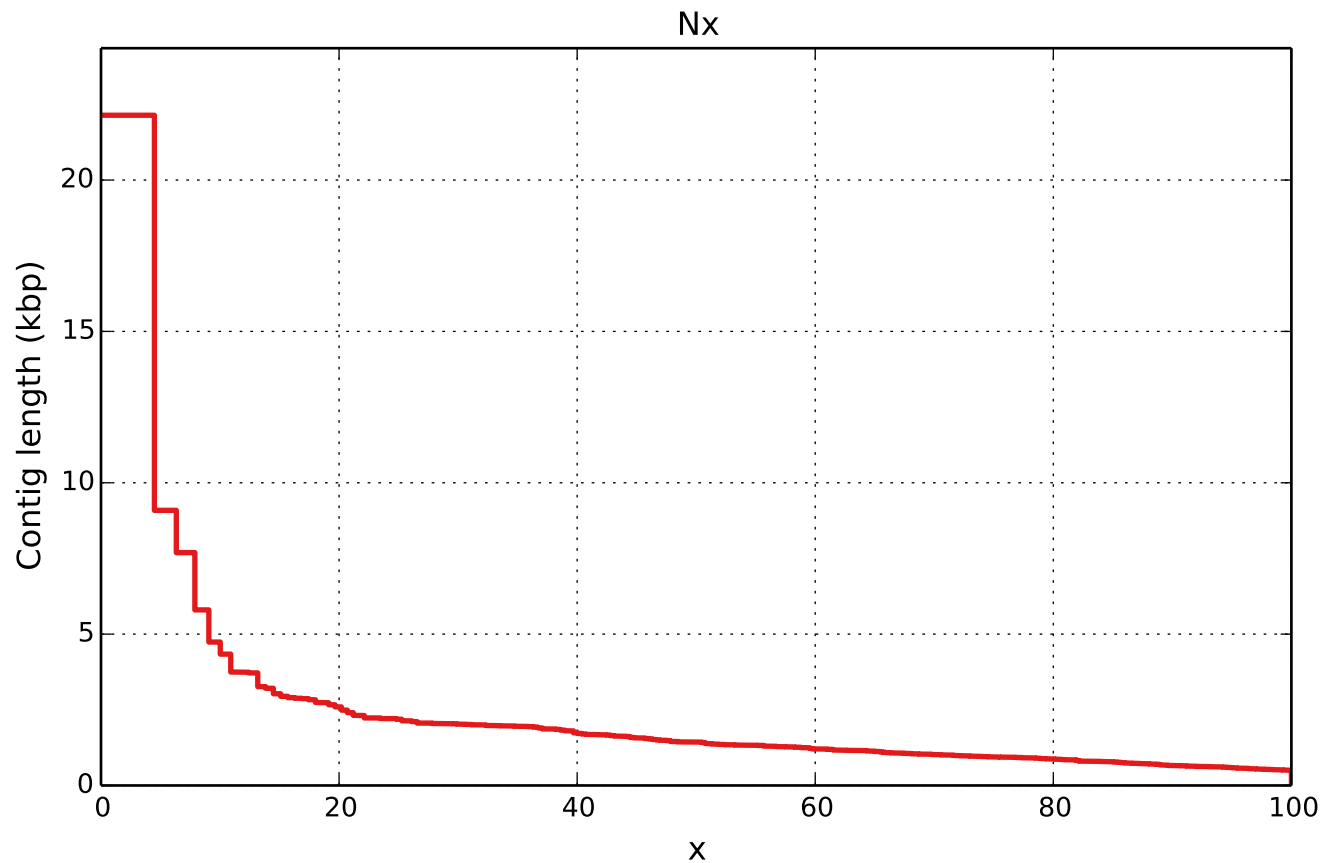
	CV18_spades_contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	9089
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	18
# indels	1
# indels (<= 5 bp)	0
# indels (> 5 bp)	1
Indels length	41

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).

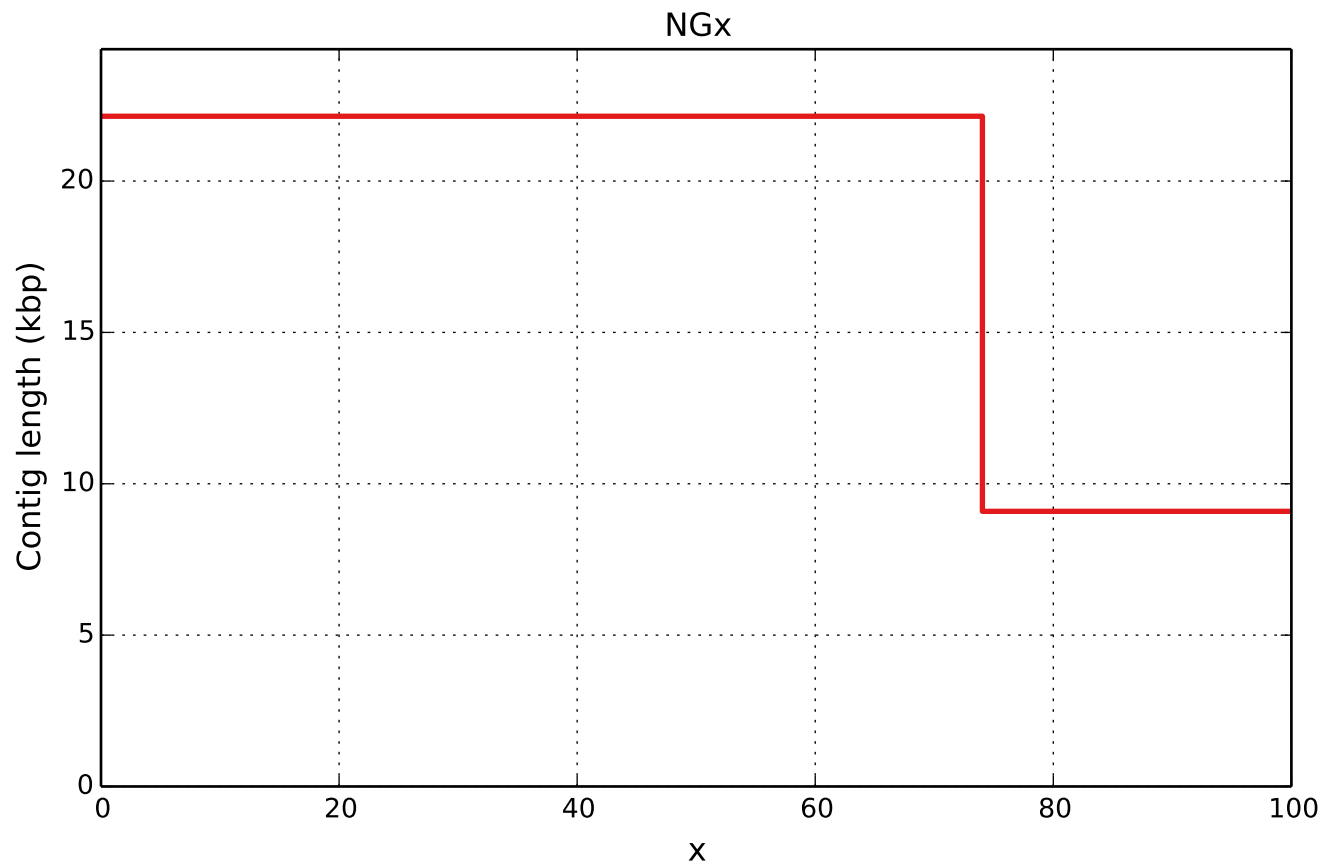
Unaligned report

	CV18_spades_contigs
# fully unaligned contigs	381
Fully unaligned length	454716
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

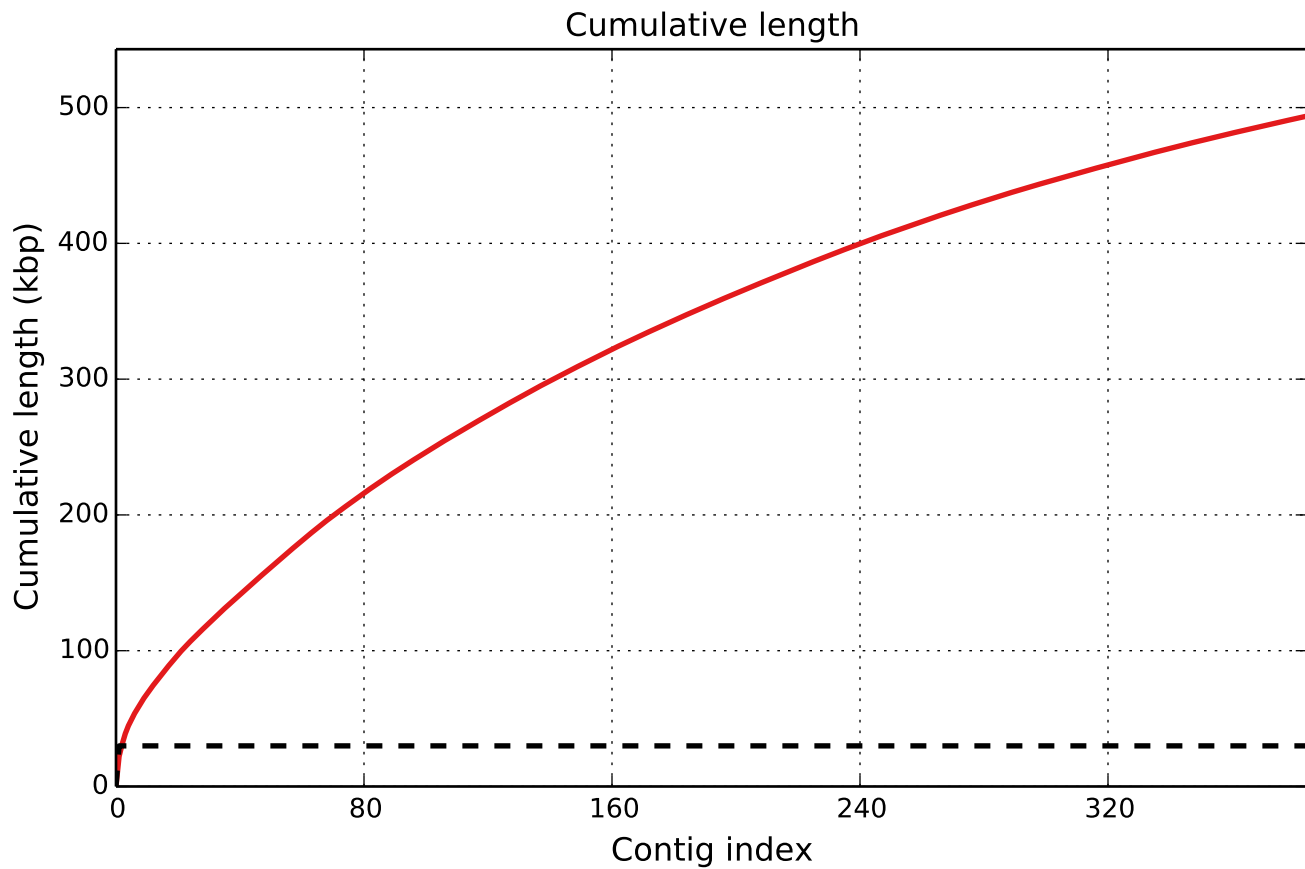
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



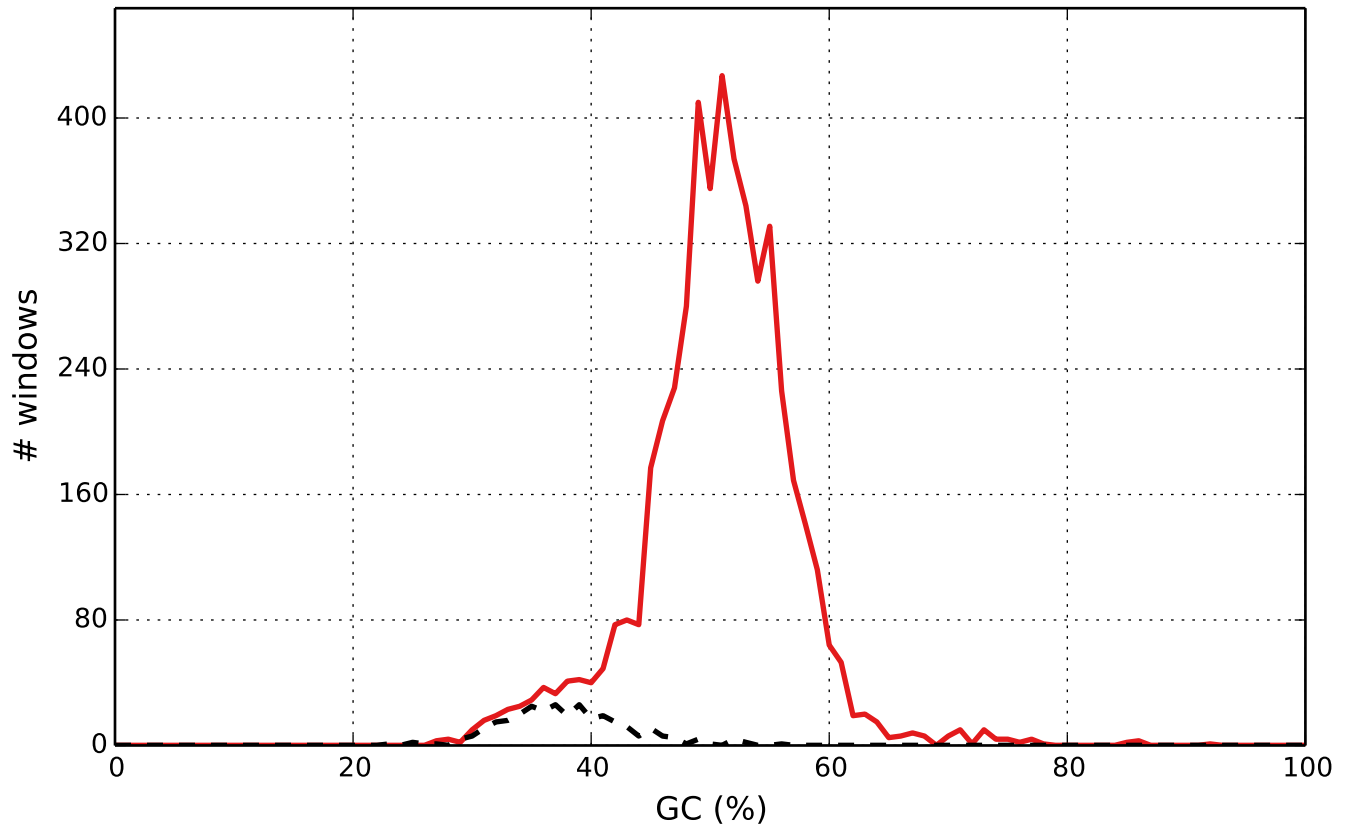
— CV18_spades_contigs



— CV18_spades_contigs

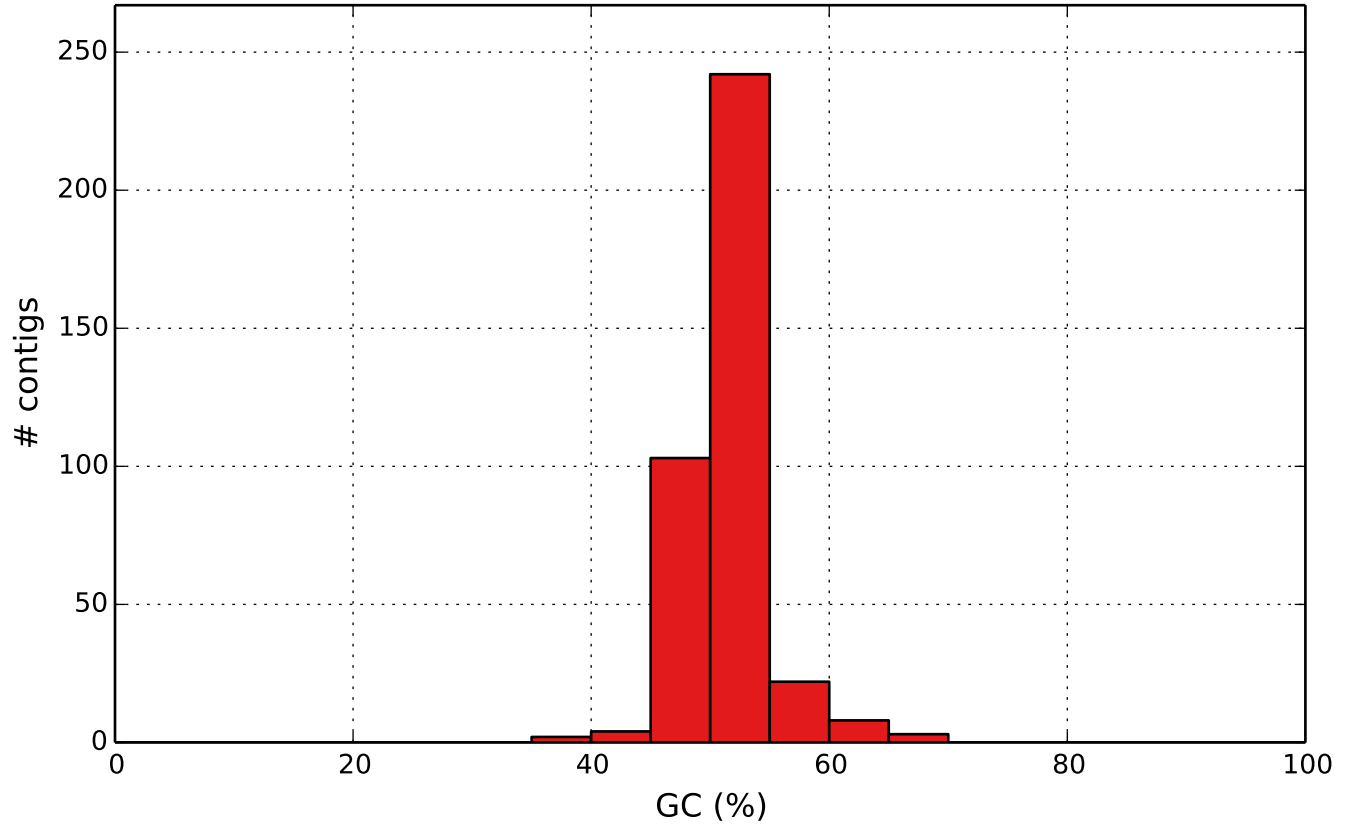


GC content

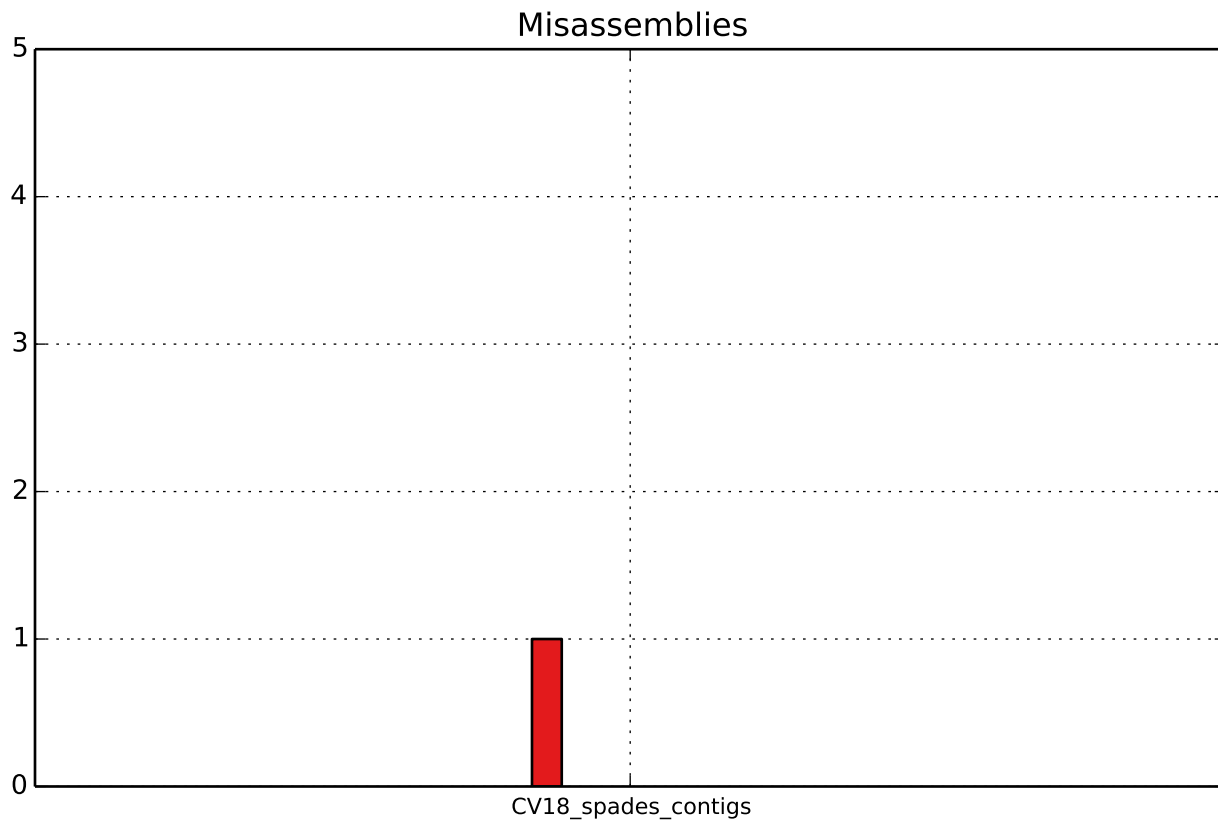


— CV18_spades_contigs - - Reference

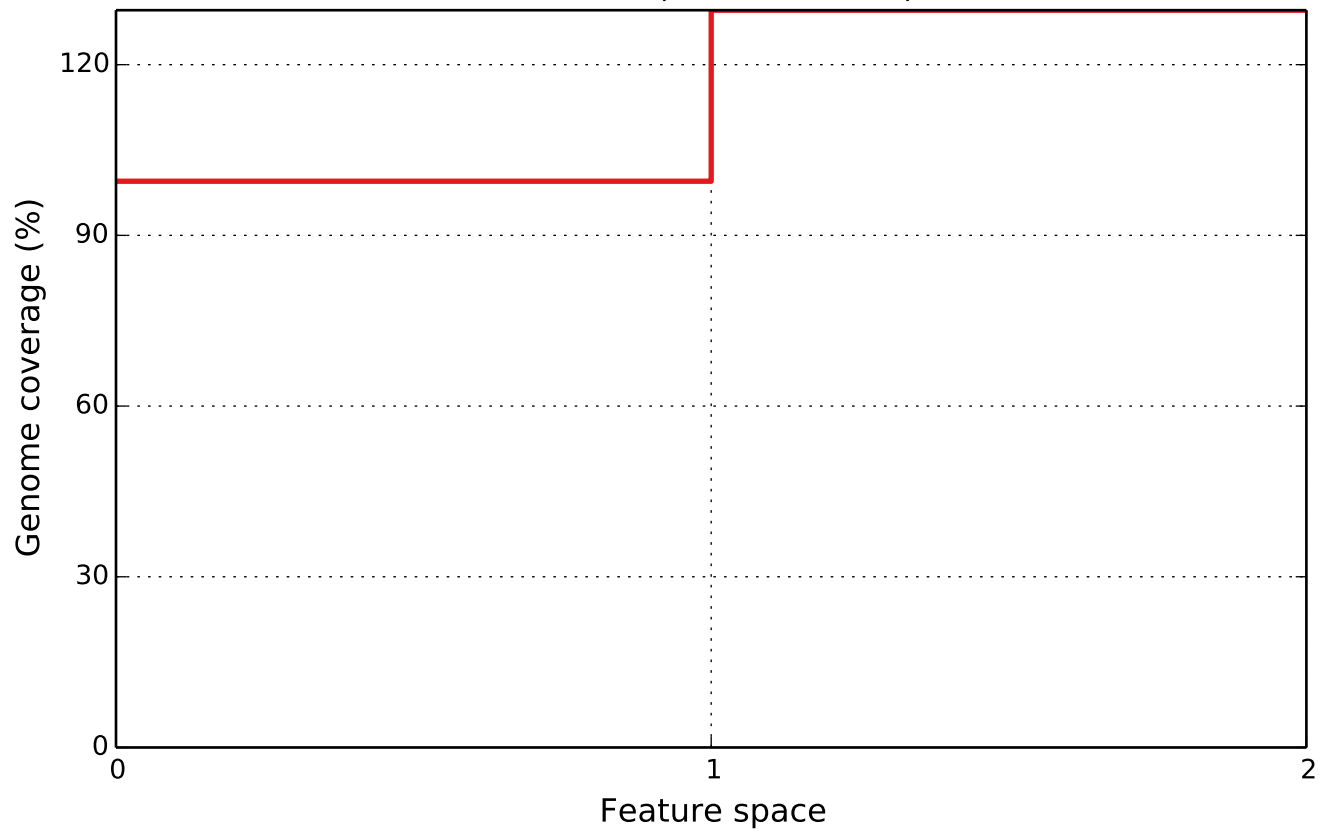
CV18_spades_contigs GC content



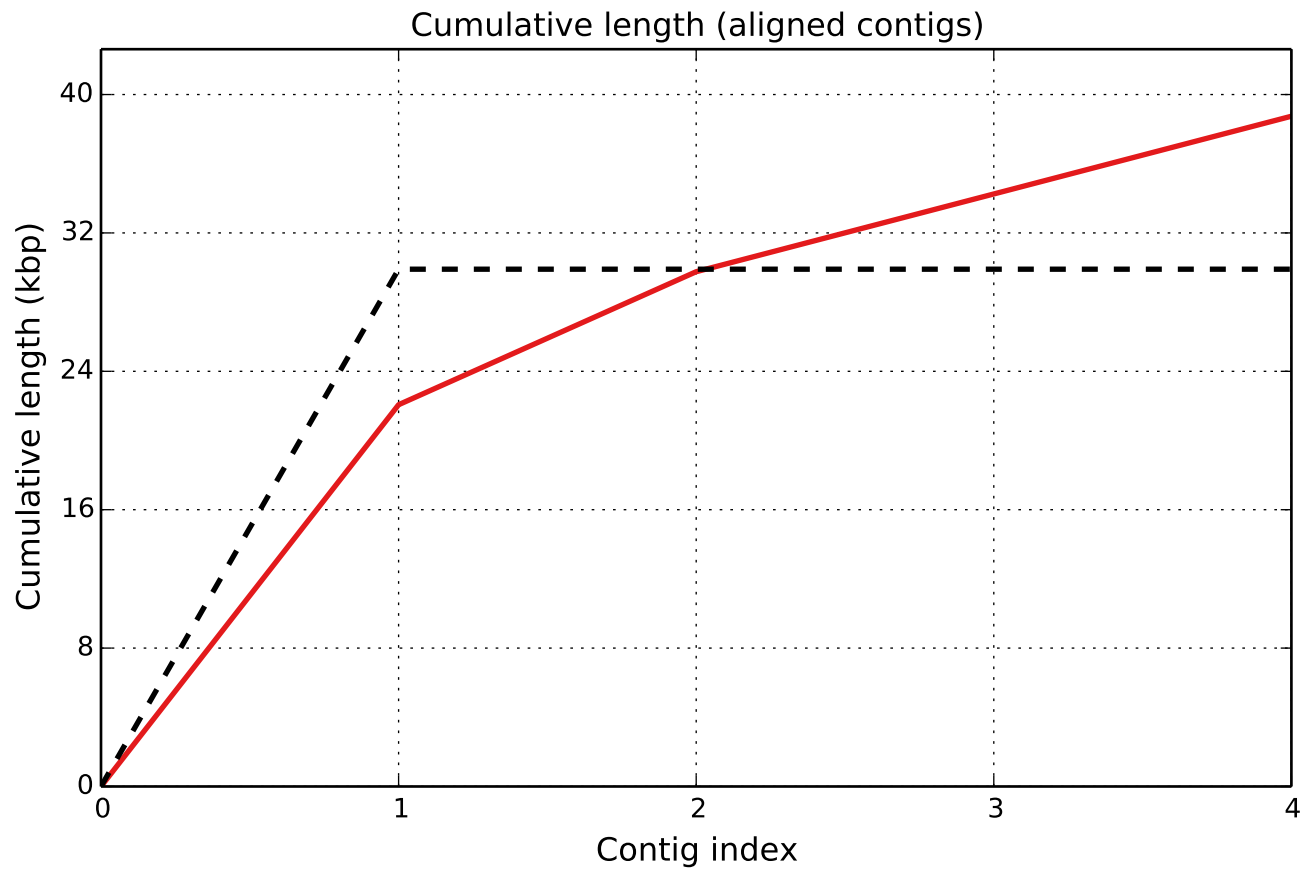
CV18_spades_contigs

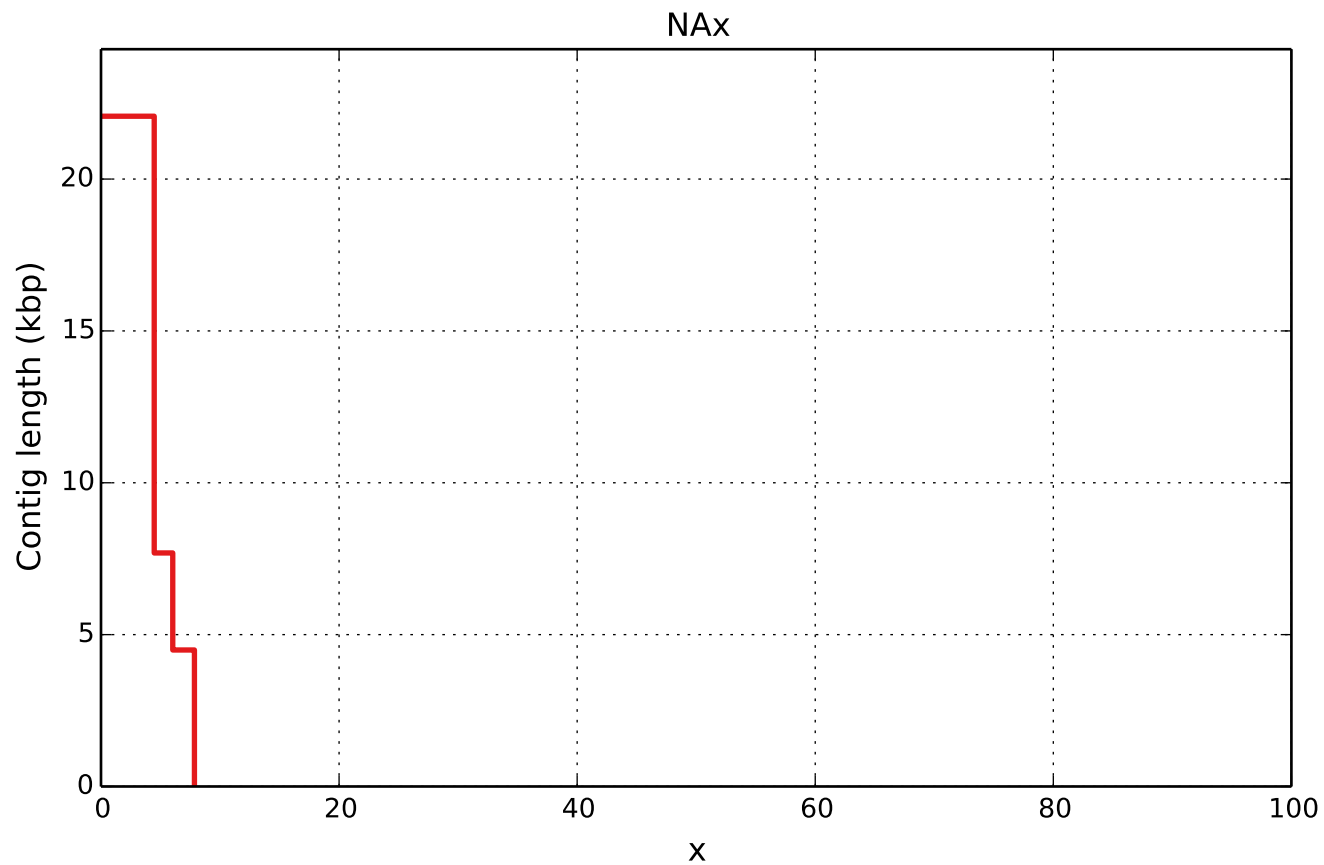


FRCurve (misassemblies)

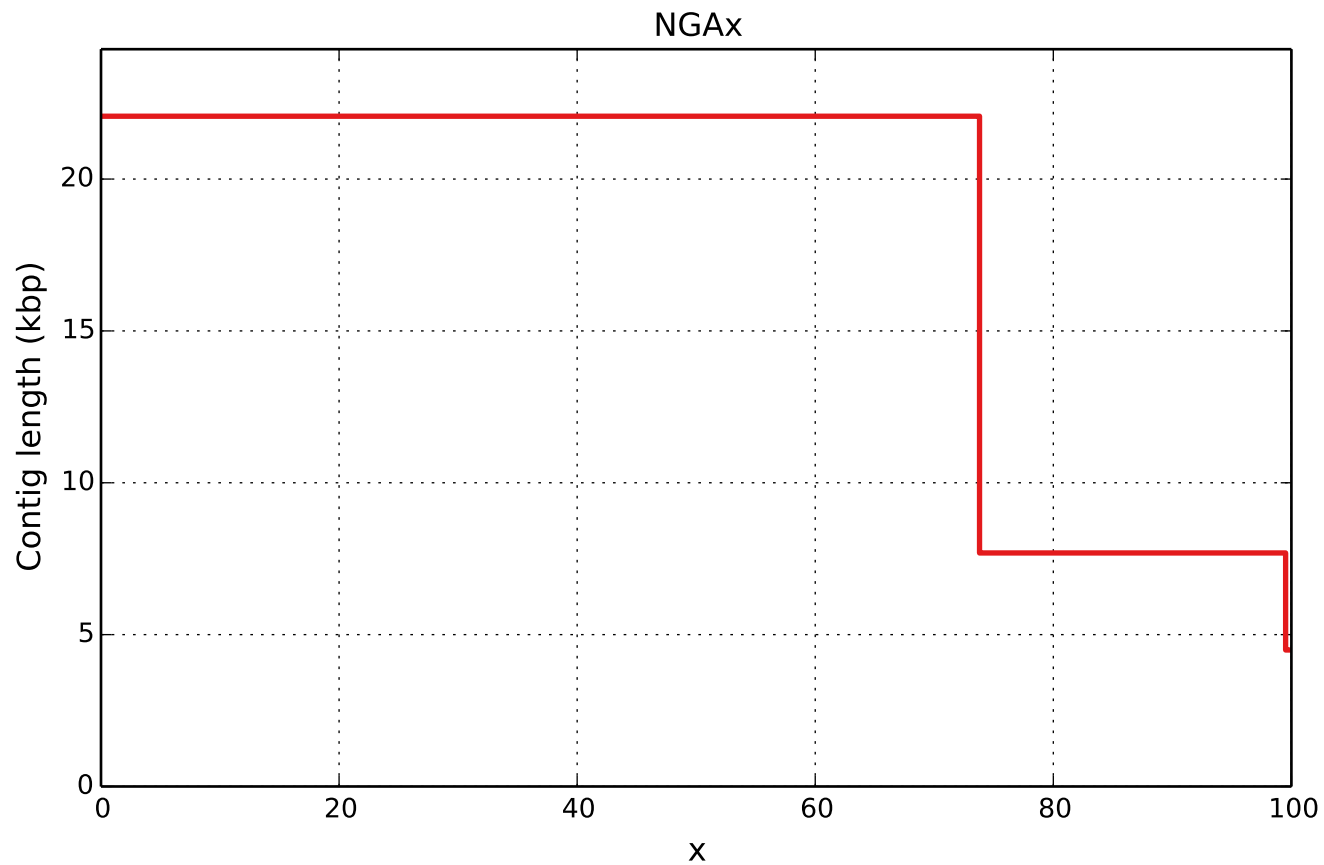


— CV18_spades_contigs

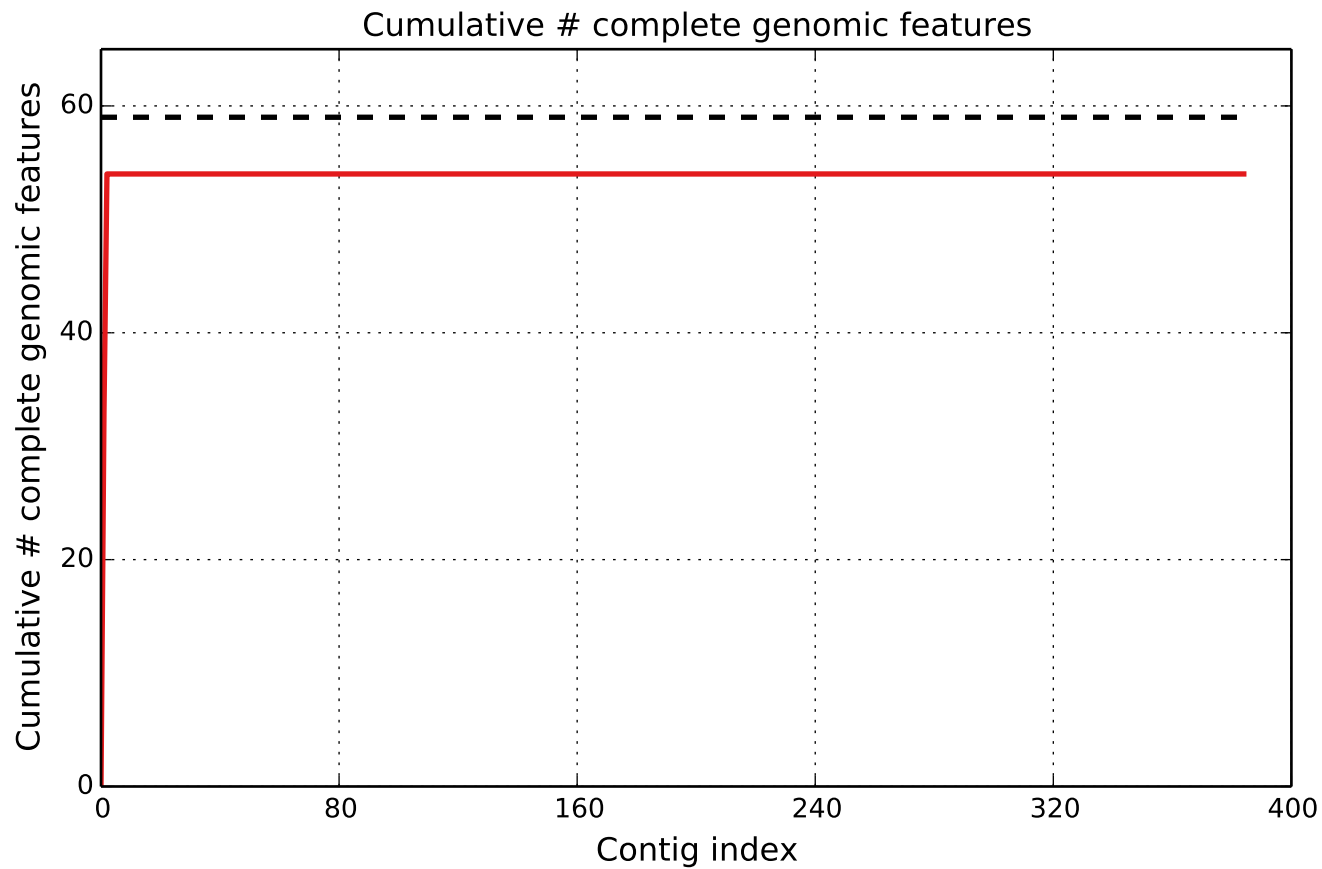




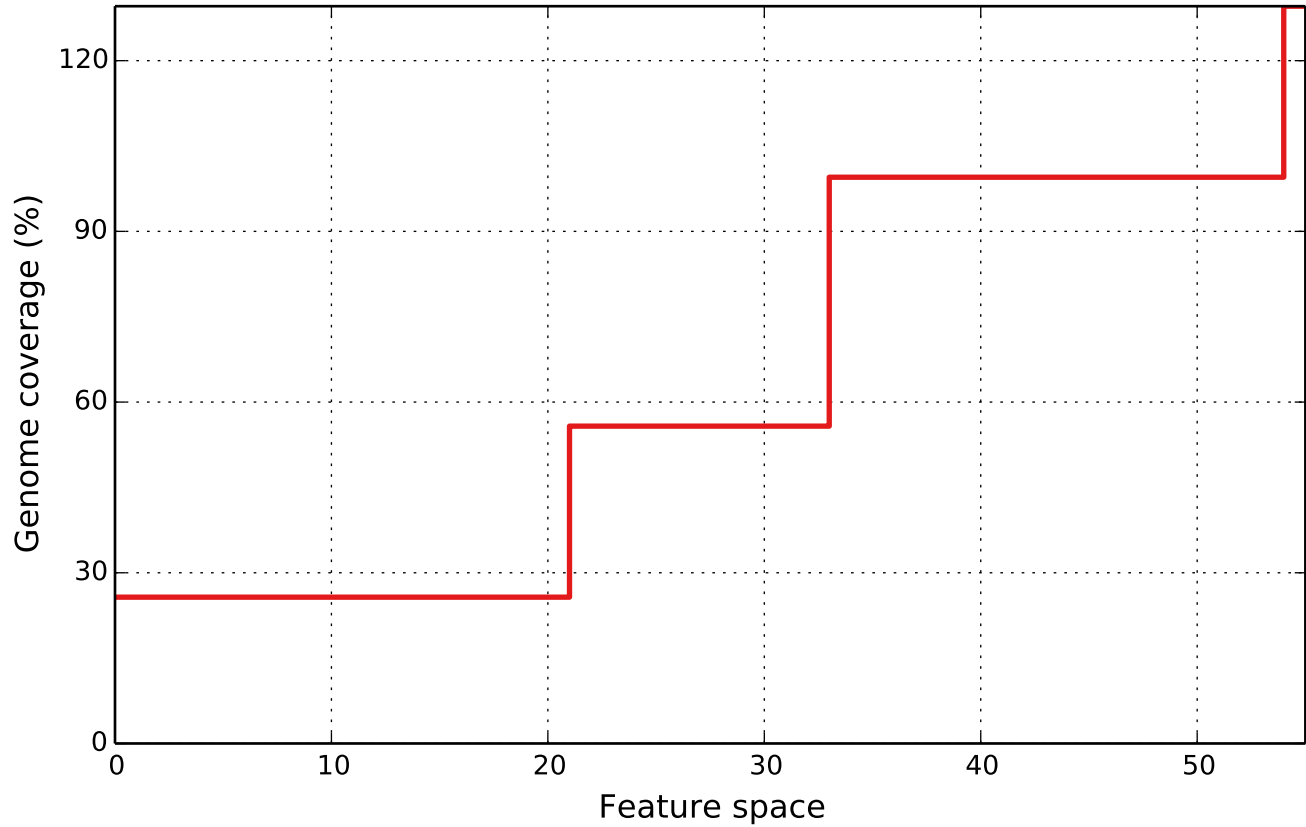
— CV18_spades_contigs



— CV18_spades_contigs



FRCurve (genomic features)



— CV18_spades_contigs