

Report

	CV145_contigs
# contigs (>= 0 bp)	28
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	51614
Total length (>= 1000 bp)	44724
Total length (>= 5000 bp)	6807
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	28
Largest contig	6807
Total length	51614
Reference length	29903
GC (%)	45.65
Reference GC (%)	37.97
N50	2049
NG50	4214
N75	1213
NG75	2413
L50	7
LG50	3
L75	15
LG75	6
# 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	22 + 0 part
Unaligned length	29418
Genome fraction (%)	73.093
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	64.05
# indels per 100 kbp	0.00
# genomic features	29 + 17 part
Largest alignment	6734
Total aligned length	21984
NGA50	4214
LGA50	3

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

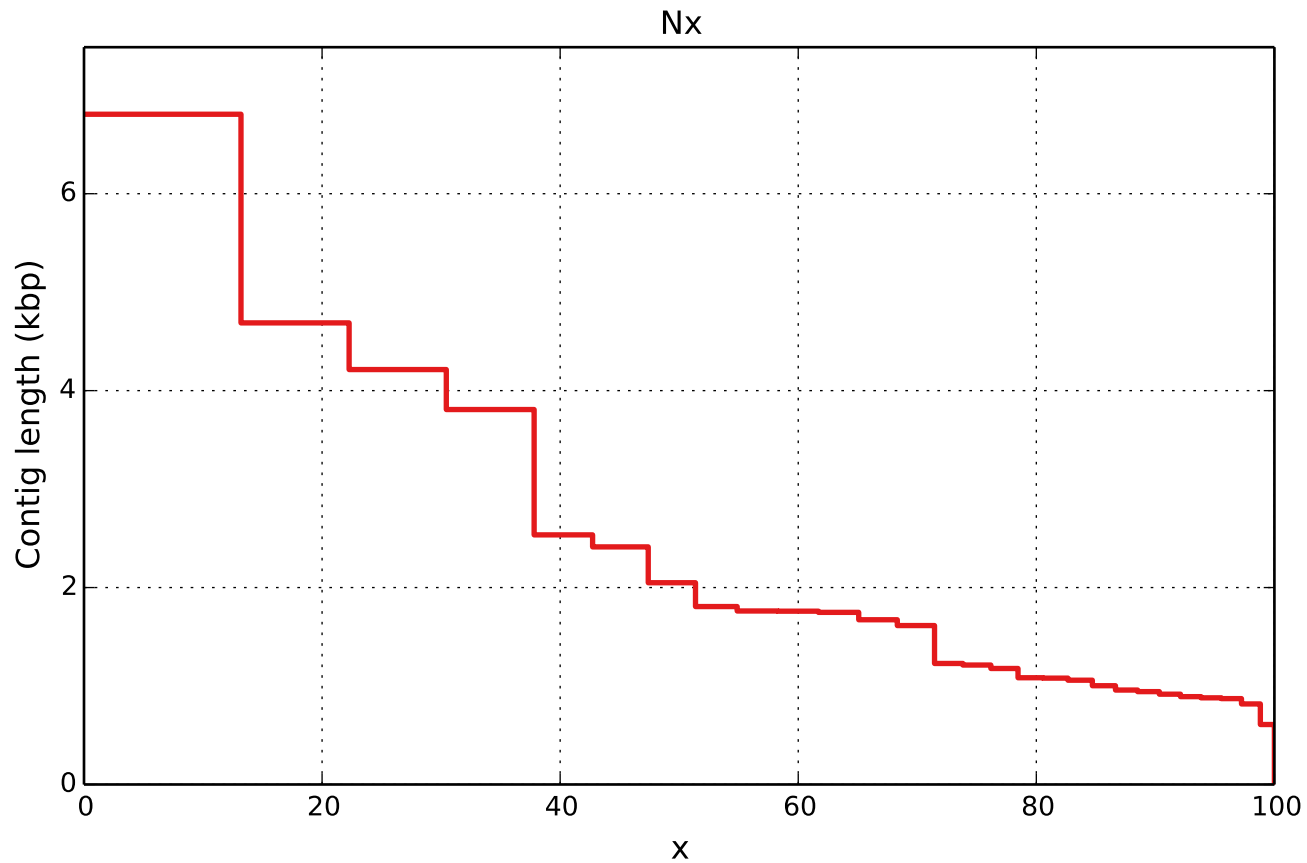
	CV145_contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	14
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

Unaligned report

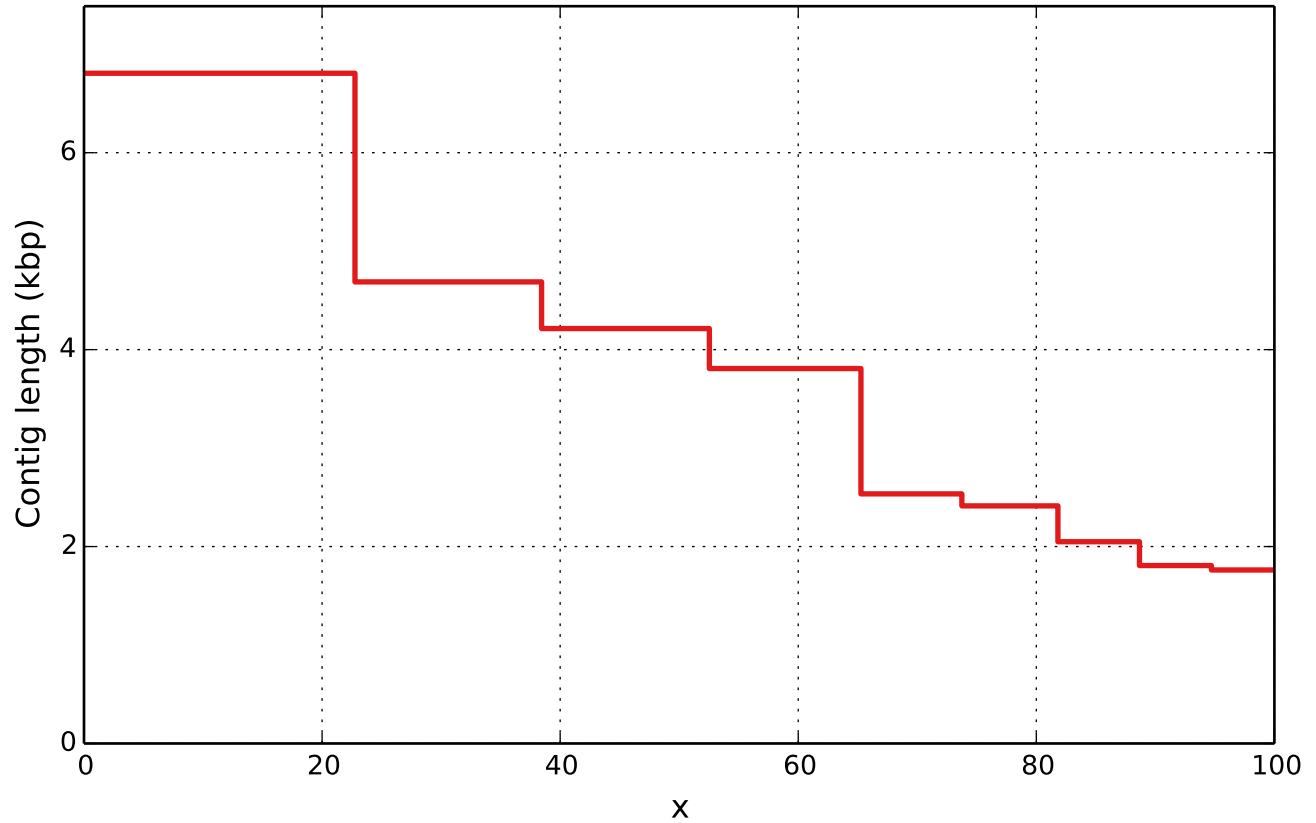
	CV145_contigs
# fully unaligned contigs	22
Fully unaligned length	29418
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

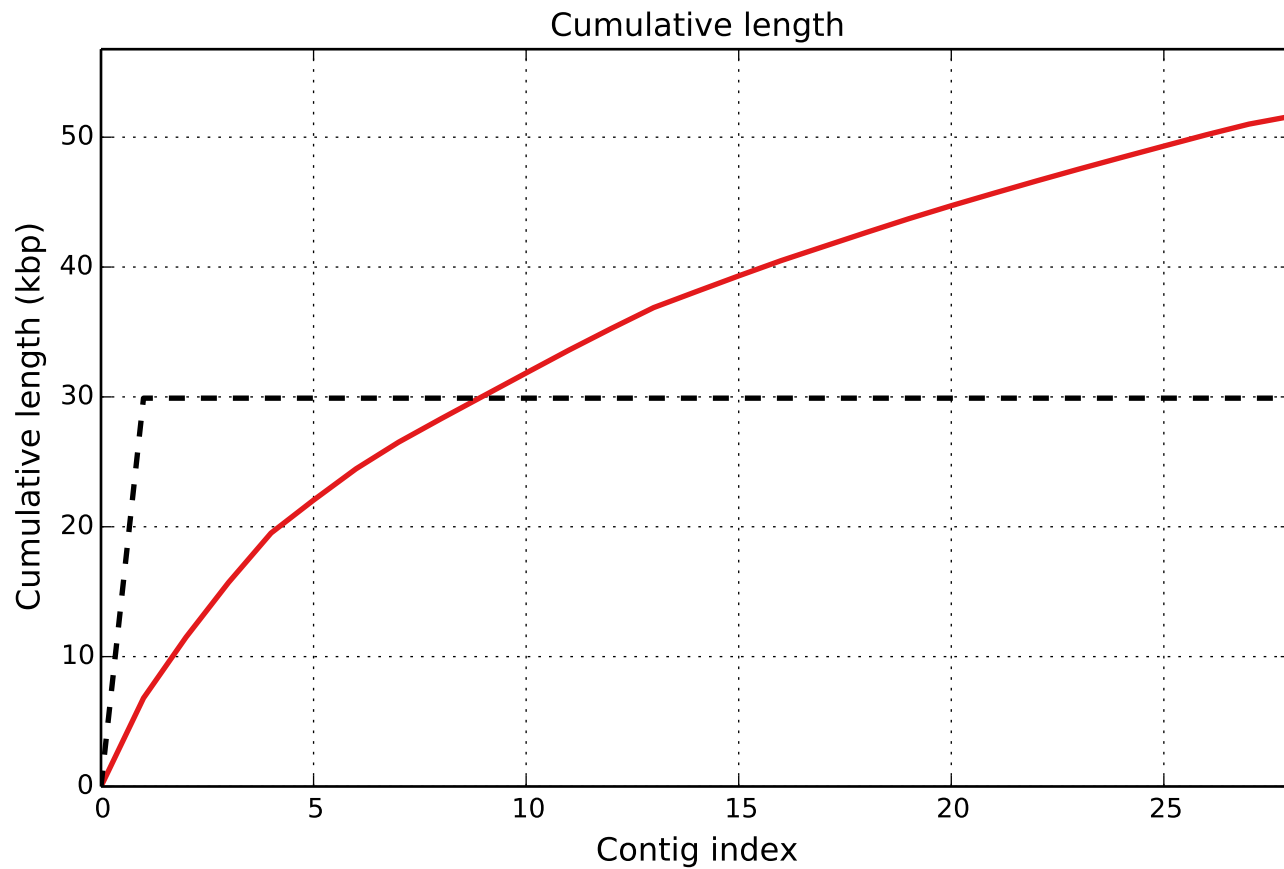


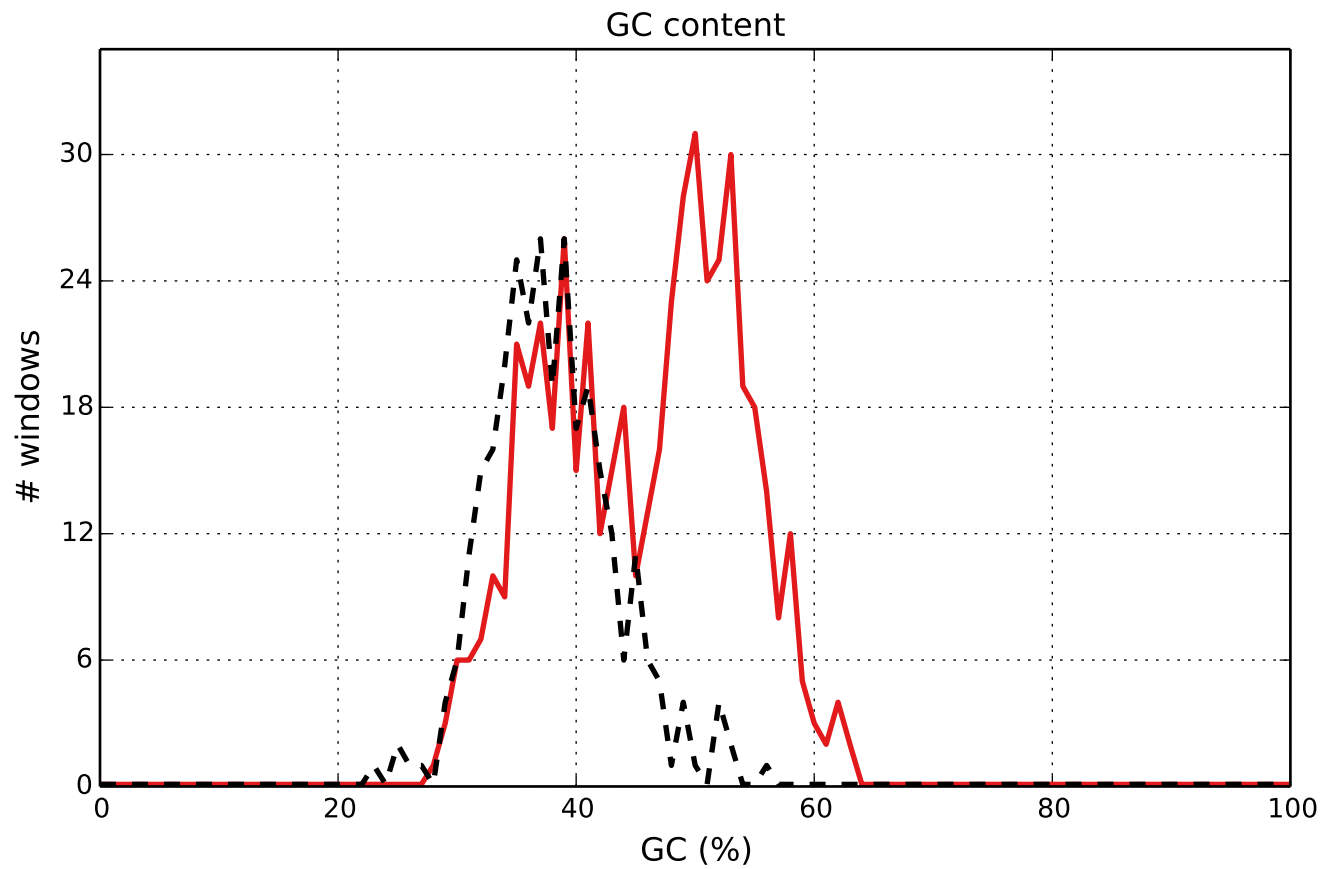
— CV145_contigs

NGx

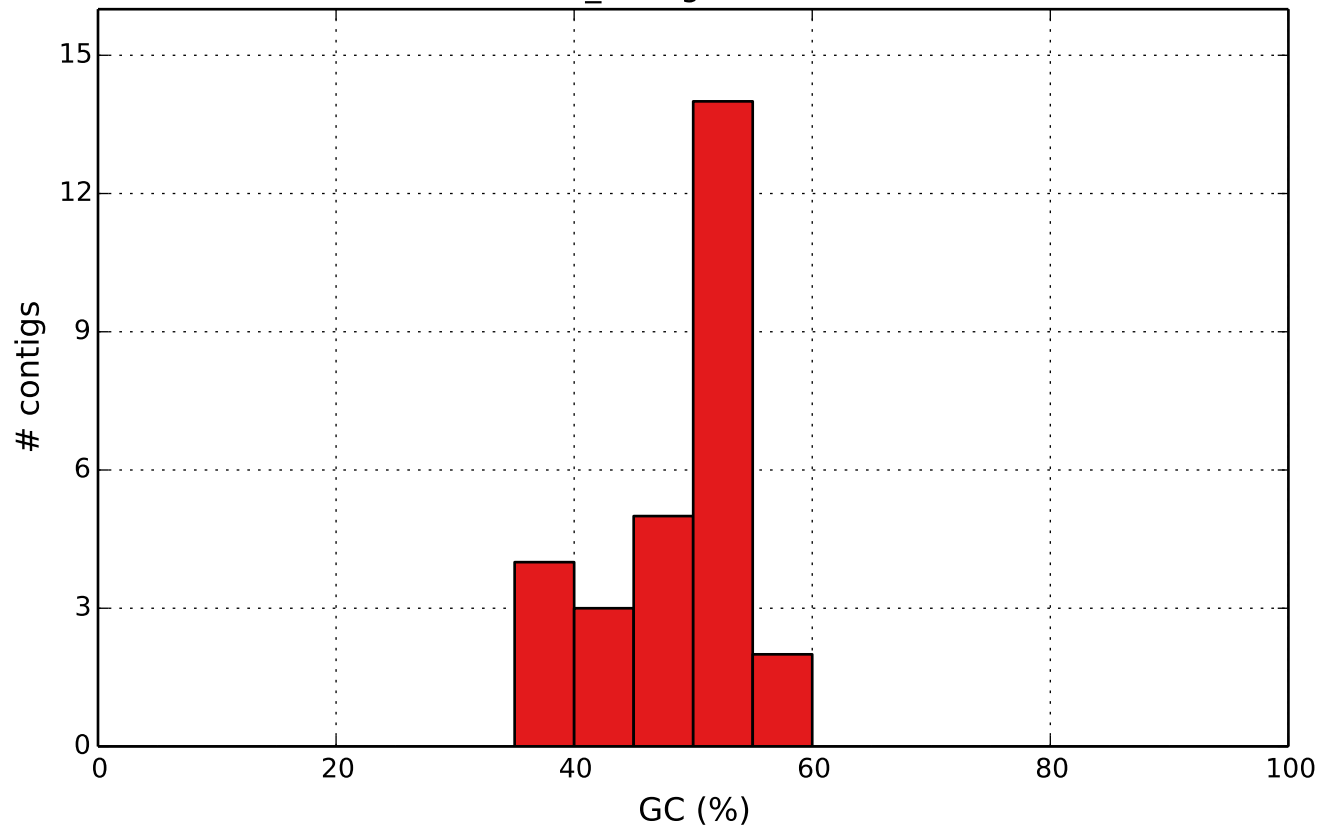


— CV145_contigs

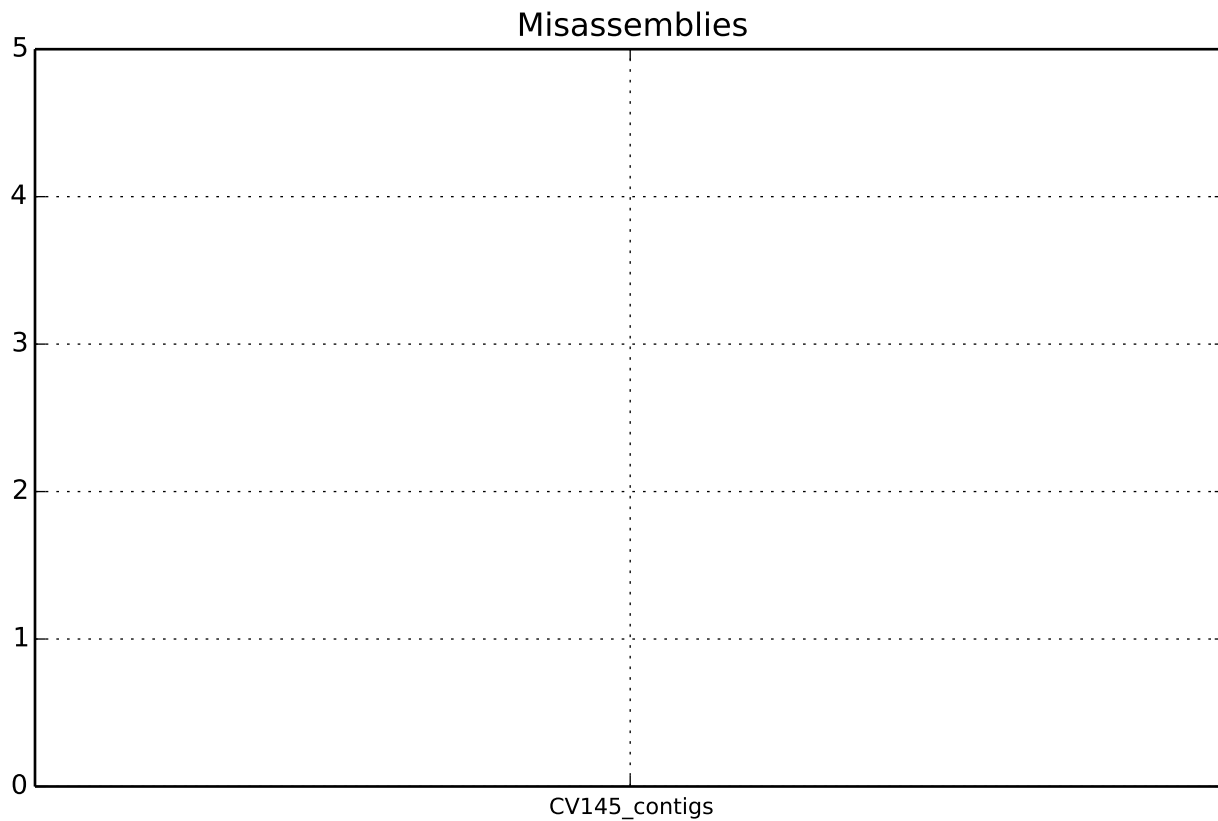




CV145_contigs GC content



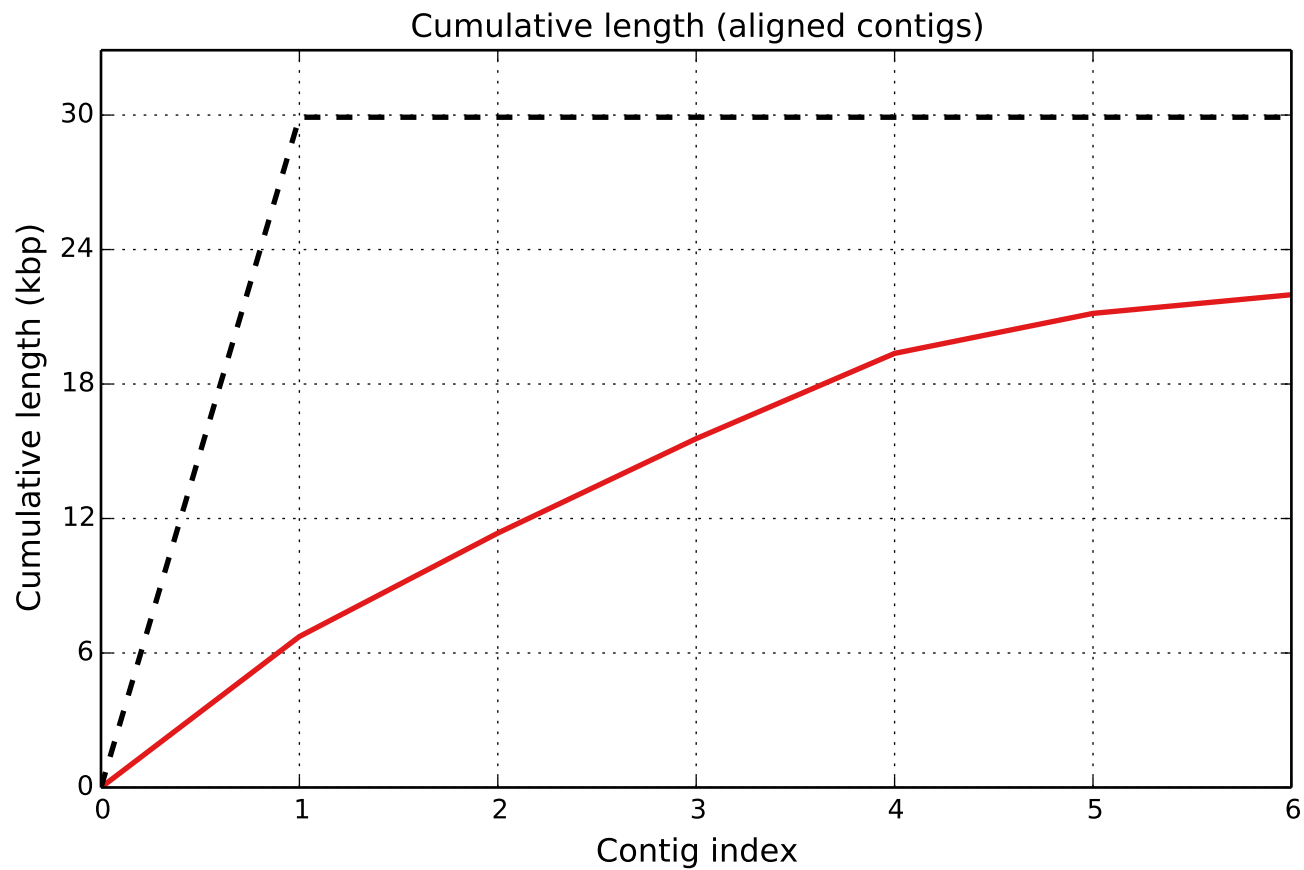
CV145_contigs

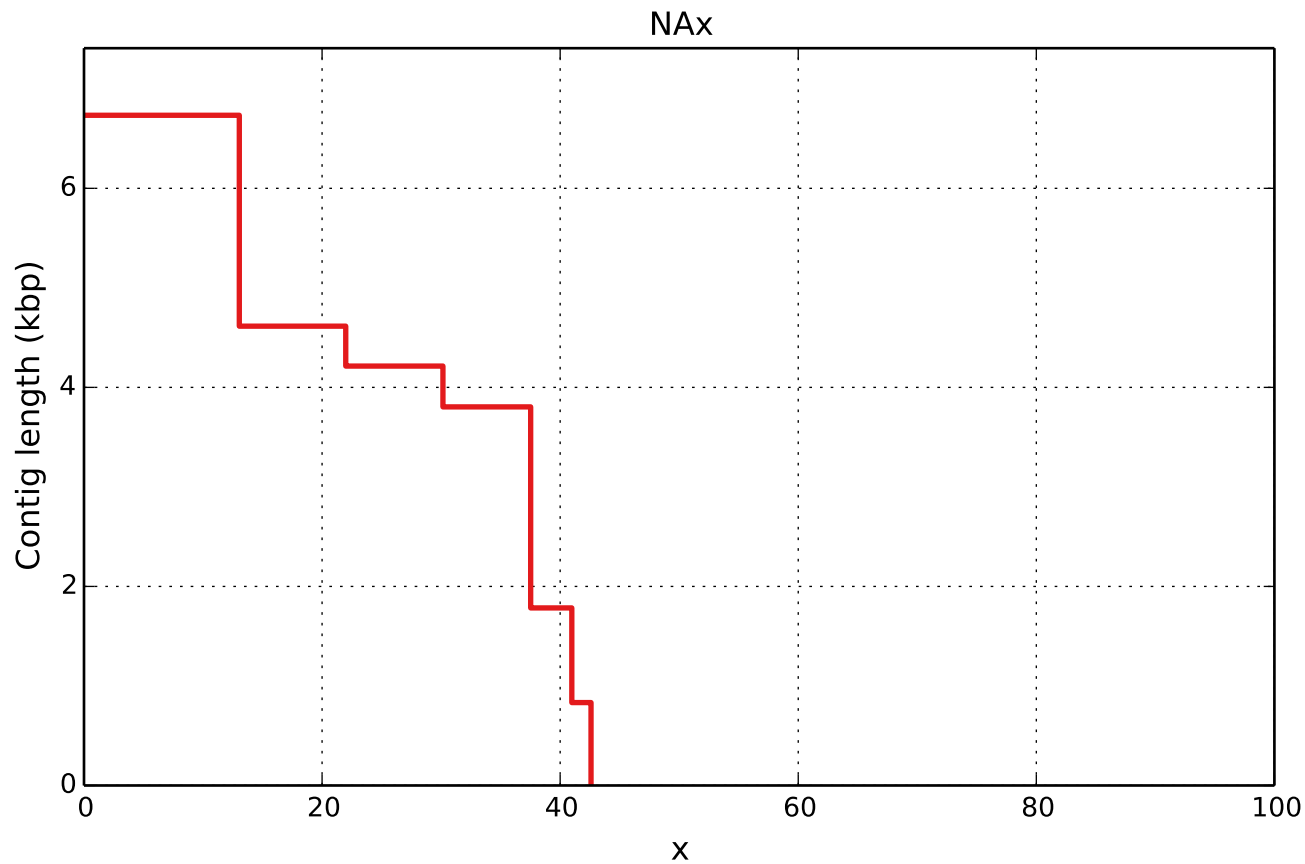


FRCurve (misassemblies)



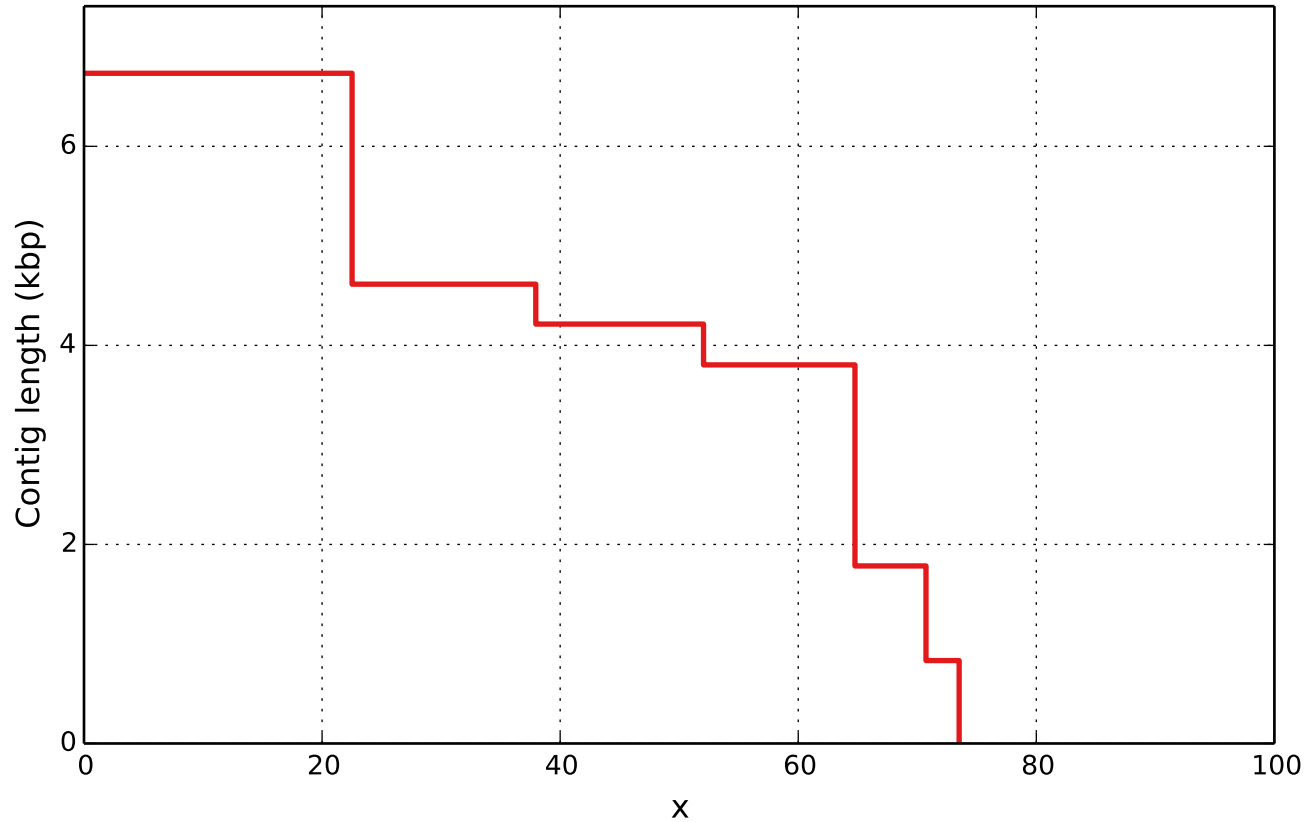
— CV145_contigs





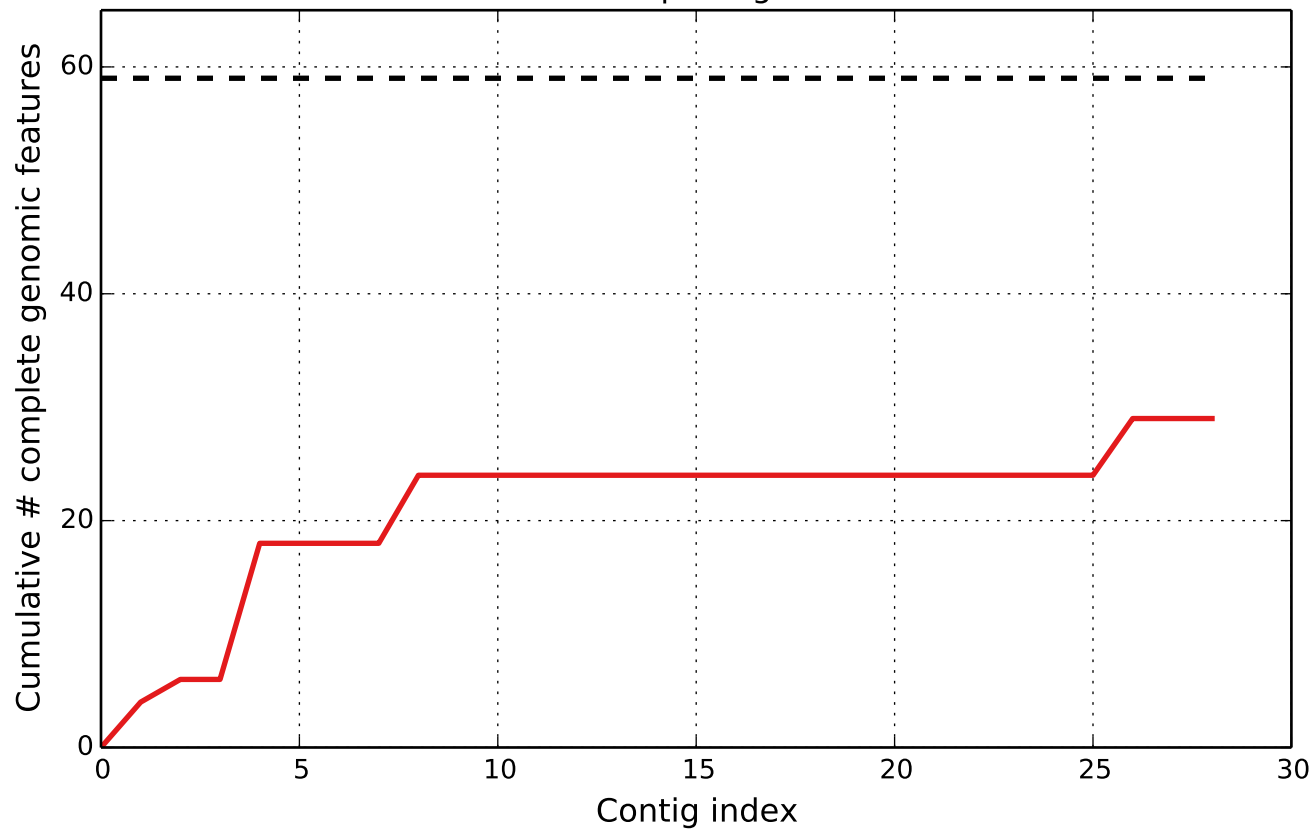
— CV145_contigs

NGAx

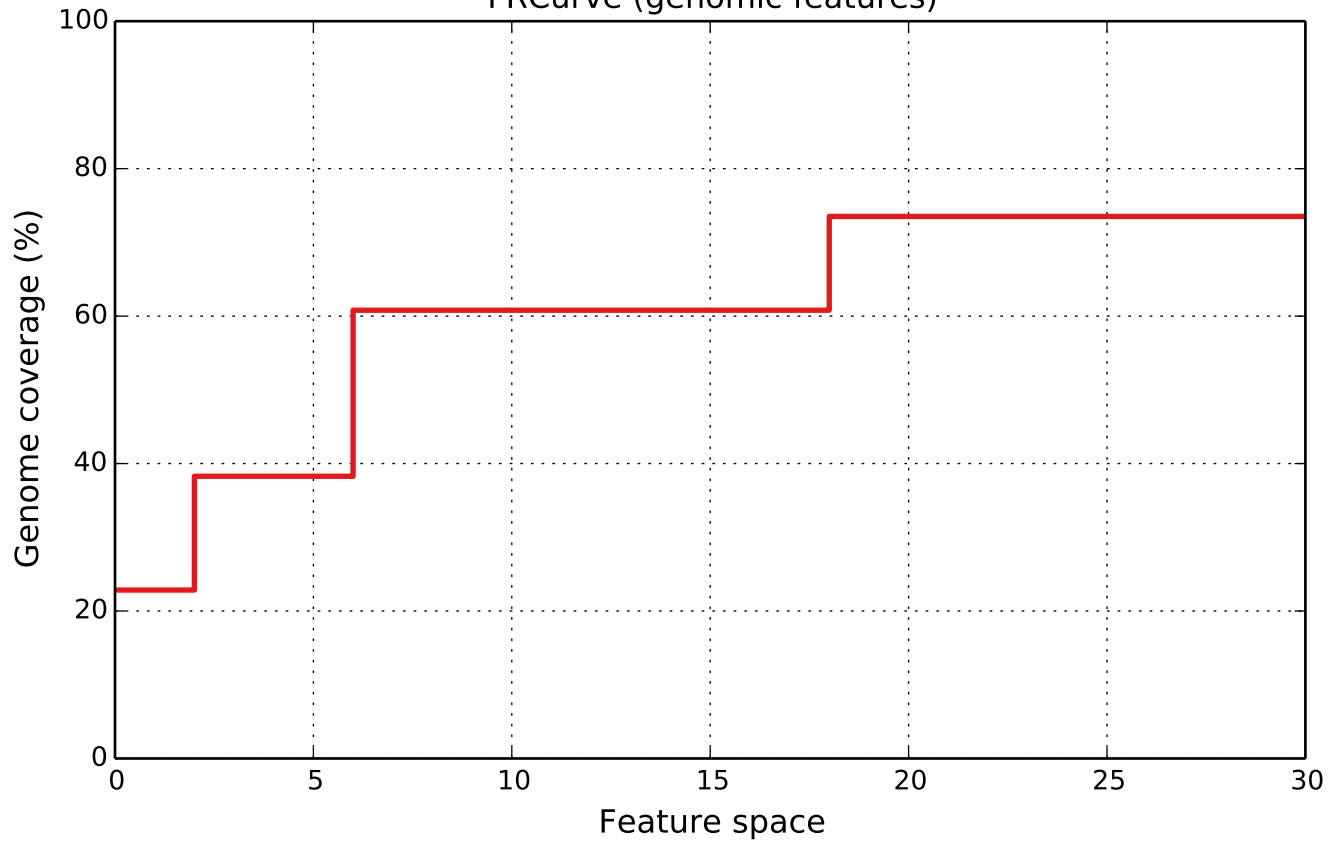


— CV145_contigs

Cumulative # complete genomic features



FRCurve (genomic features)



— CV145_contigs