

Report

	CV45_contigs
# contigs (>= 0 bp)	30
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	61636
Total length (>= 1000 bp)	53606
Total length (>= 5000 bp)	16248
Total length (>= 10000 bp)	16248
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	30
Largest contig	16248
Total length	61636
Reference length	29903
GC (%)	44.28
Reference GC (%)	37.97
N50	2603
NG50	16248
N75	1452
NG75	3419
L50	6
LG50	1
L75	14
LG75	3
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	24 + 0 part
Unaligned length	31092
Genome fraction (%)	98.291
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	37.43
# indels per 100 kbp	0.00
# genomic features	43 + 16 part
Largest alignment	16110
Total aligned length	30285
NGA50	16110
NGA75	3205
LGA50	1
LGA75	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

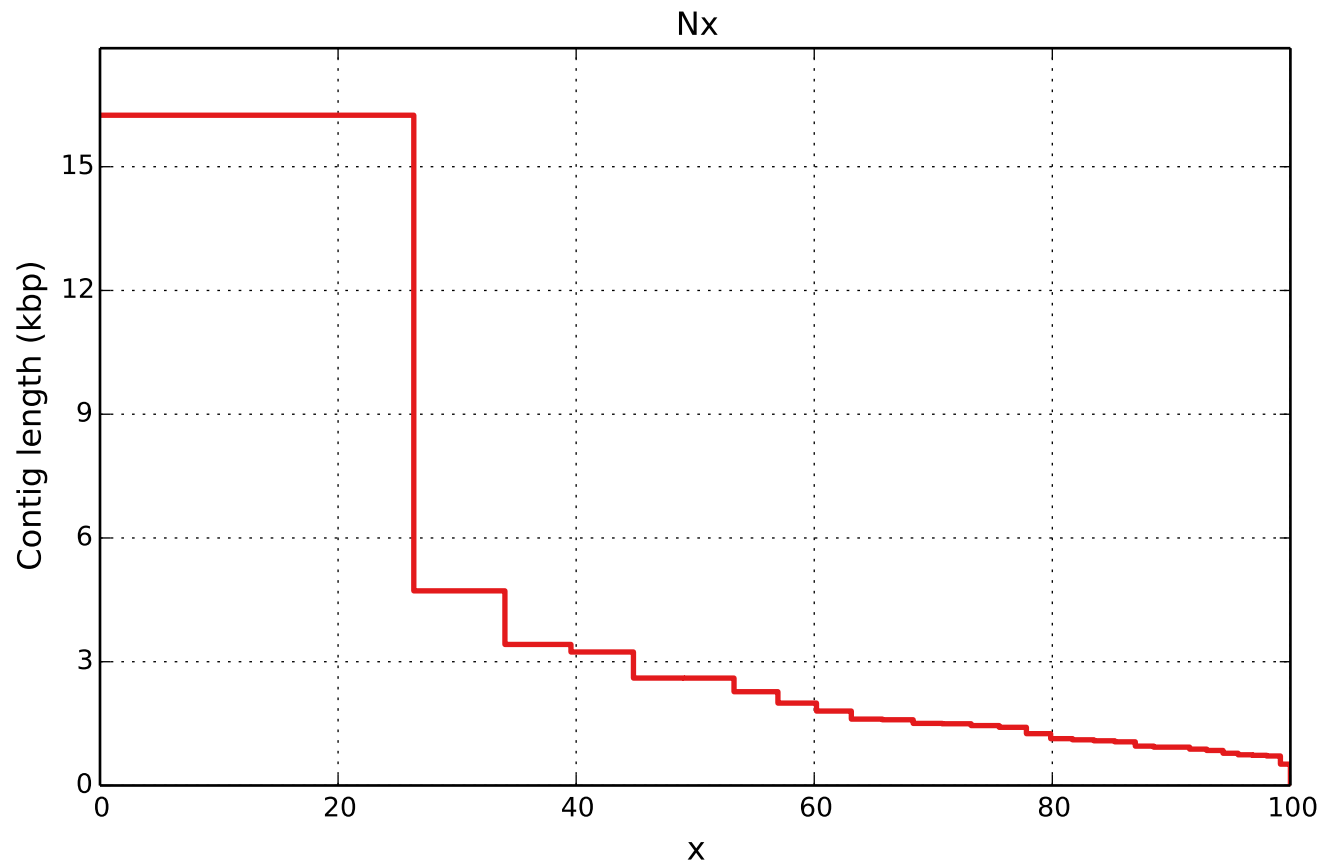
	CV45_contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	11
# 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).

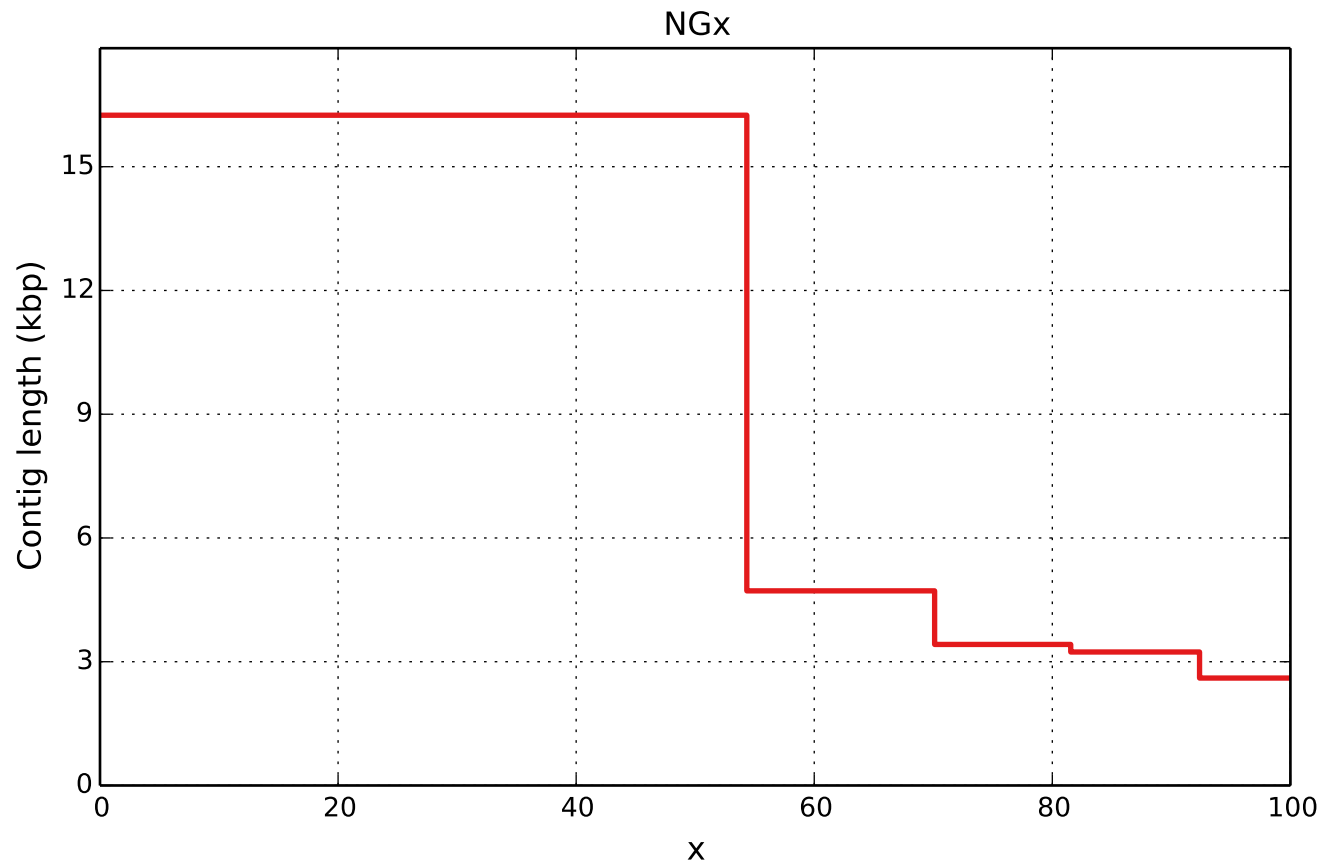
Unaligned report

	CV45_contigs
# fully unaligned contigs	24
Fully unaligned length	31092
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

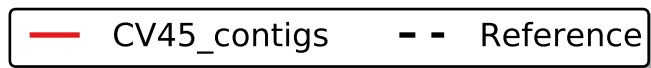
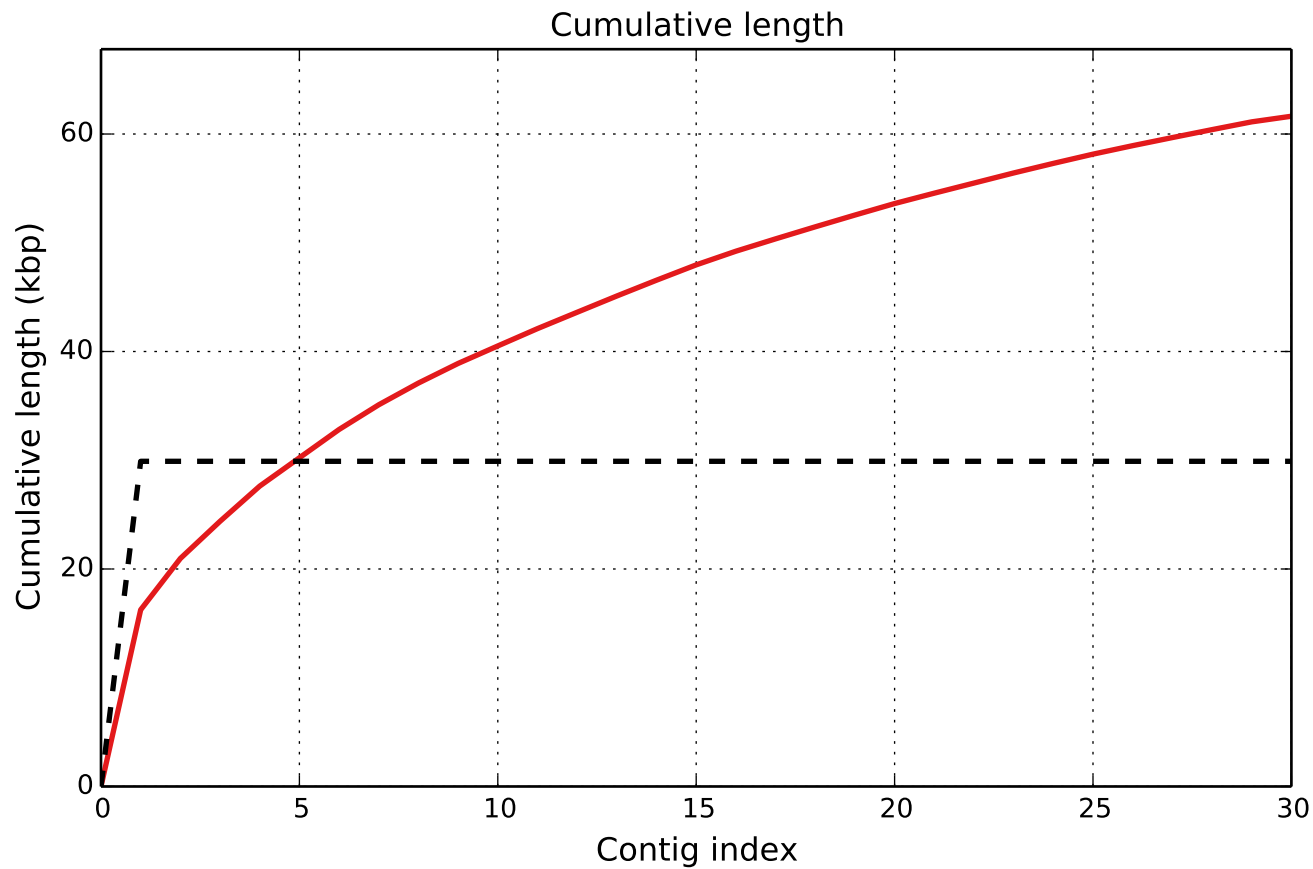
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

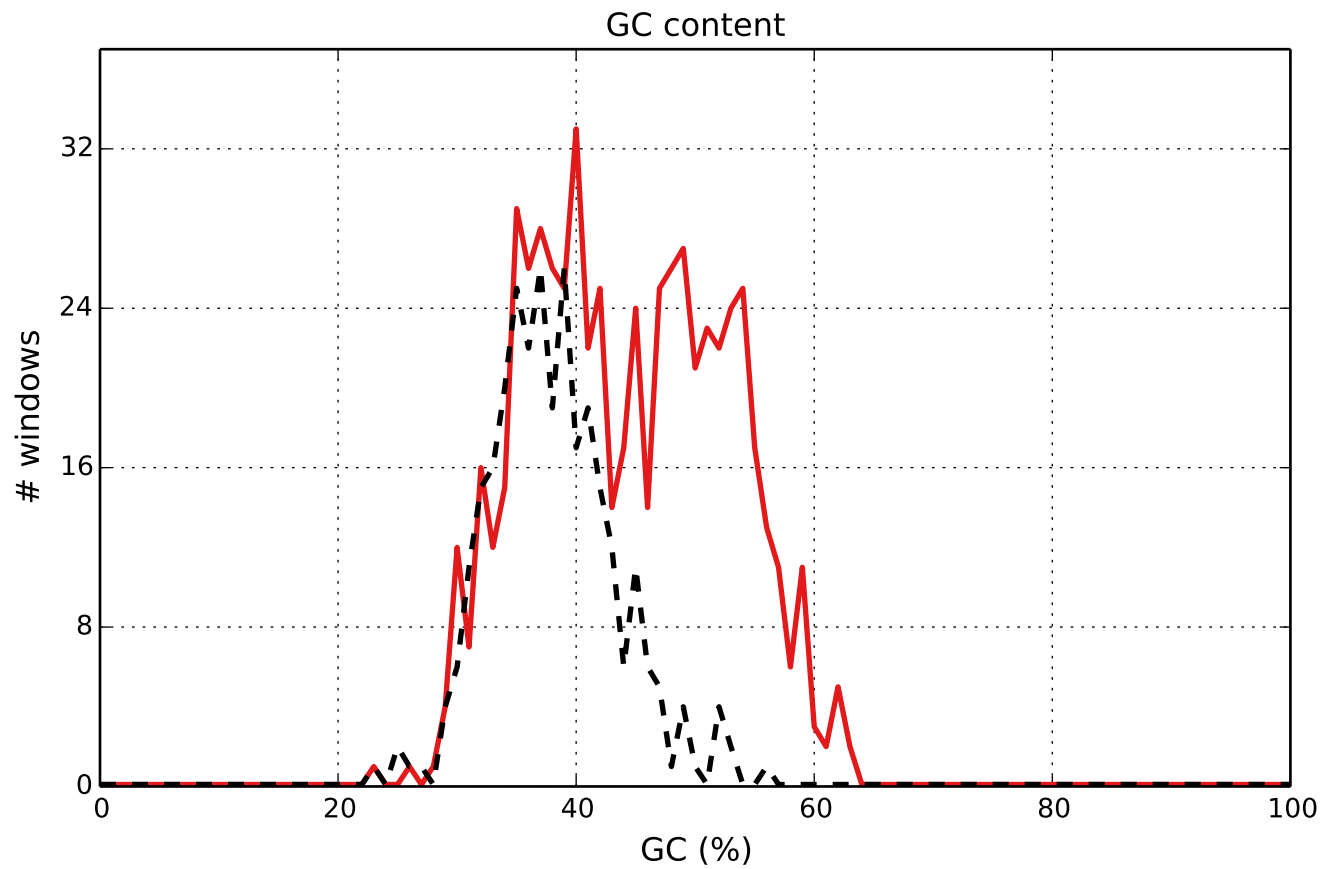


— CV45_contigs

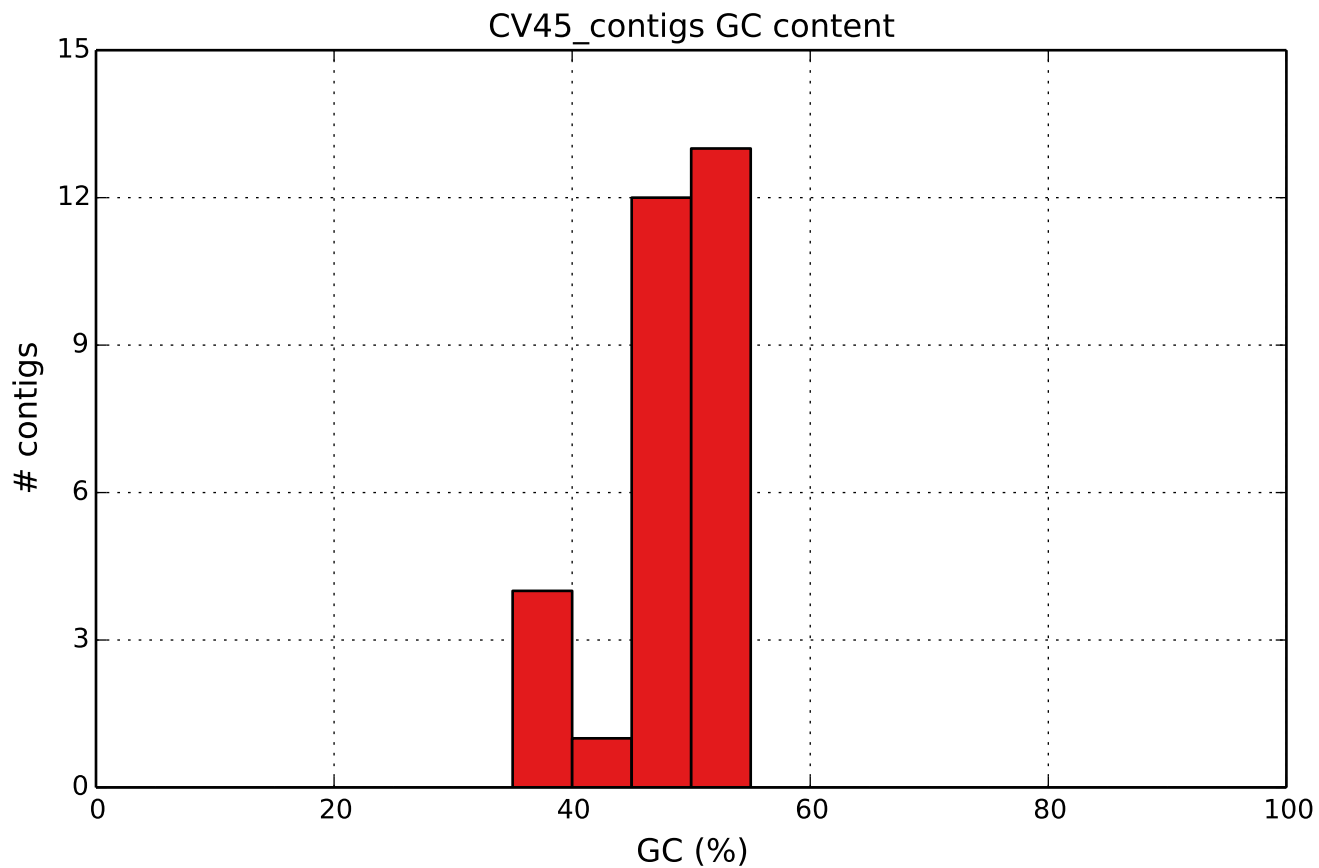


— CV45_contigs

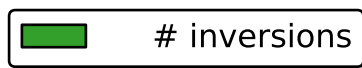
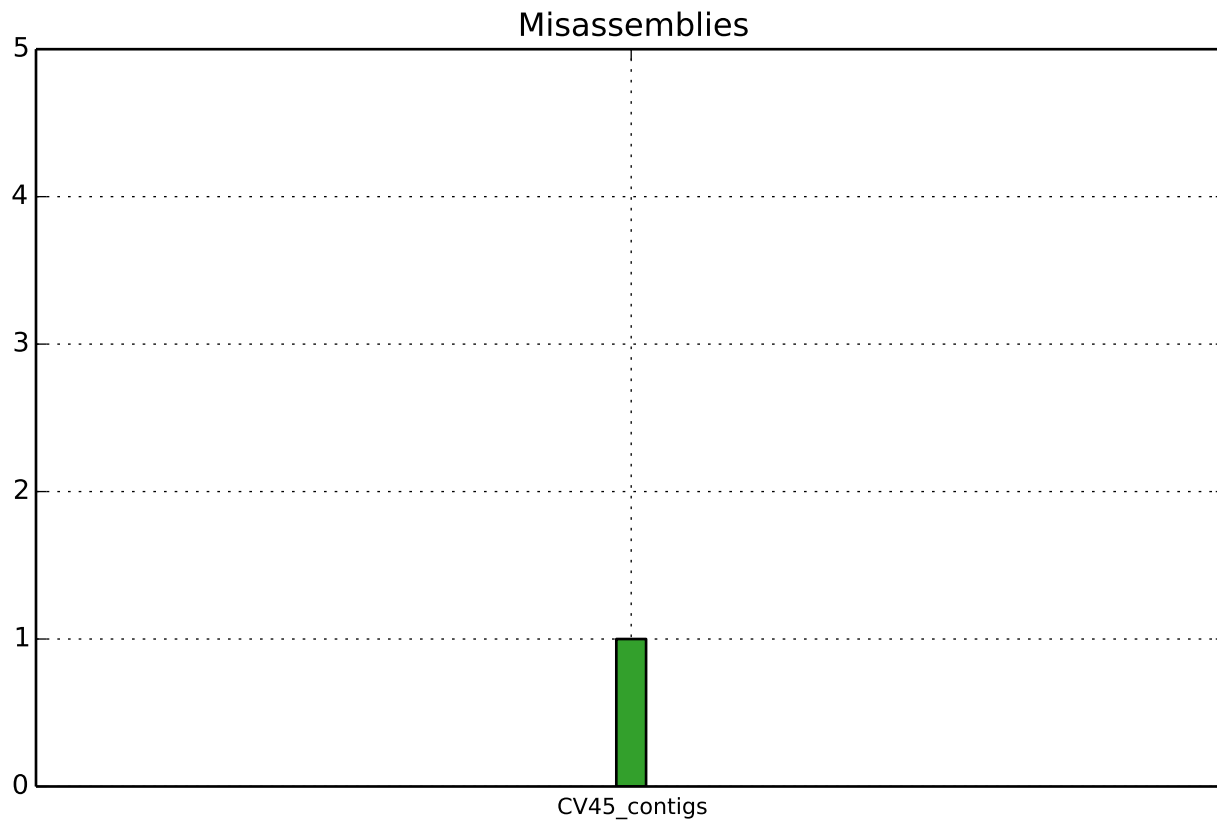




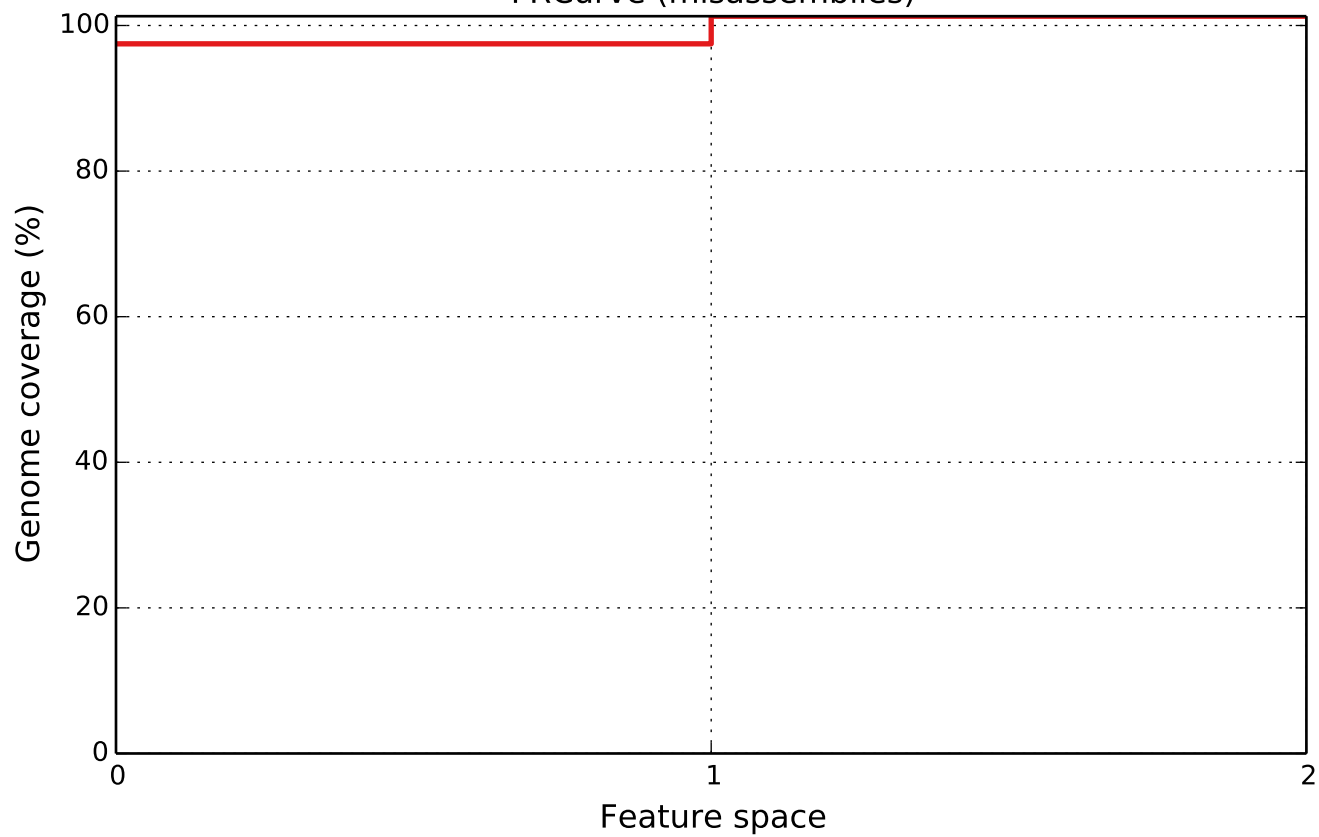
— CV45_contigs - - Reference



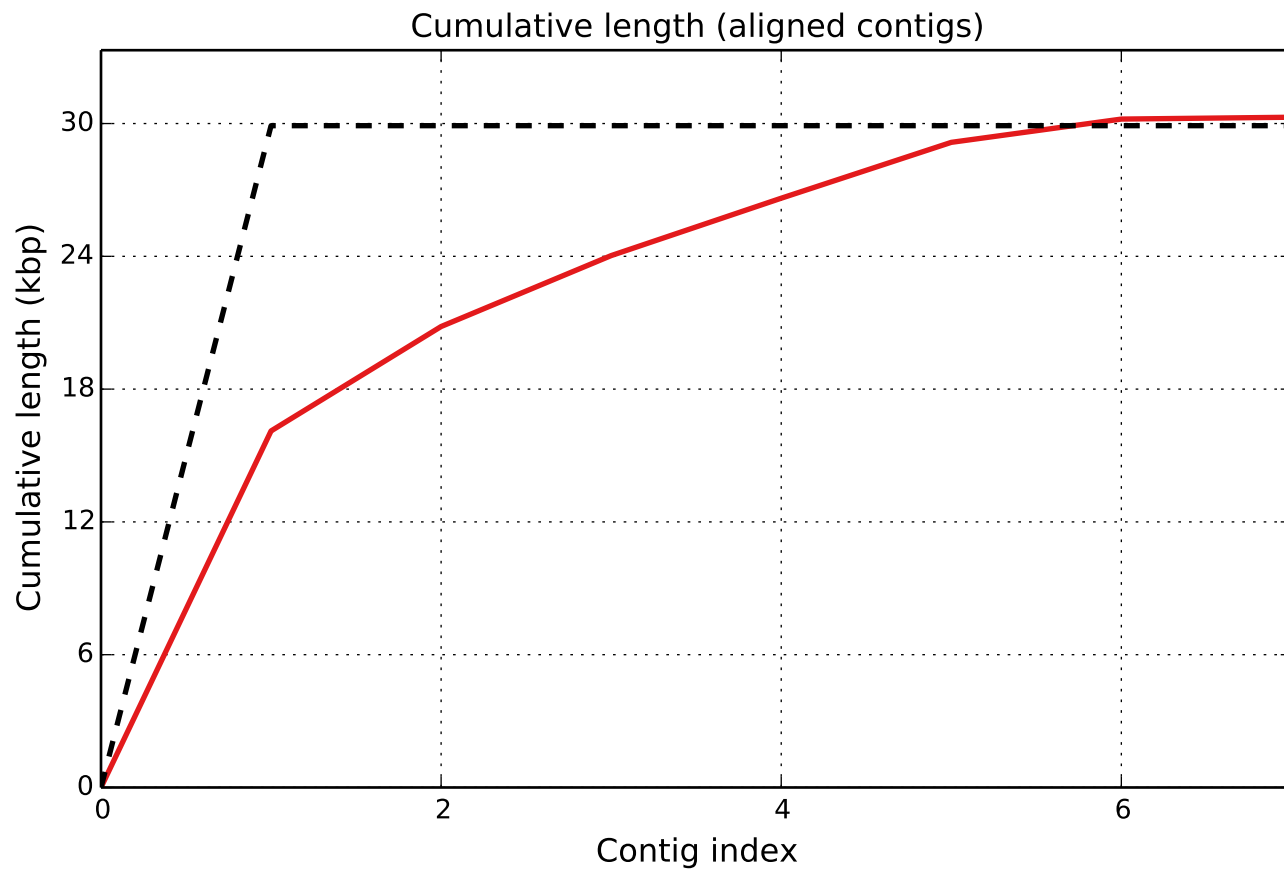
CV45_contigs



FRCurve (misassemblies)

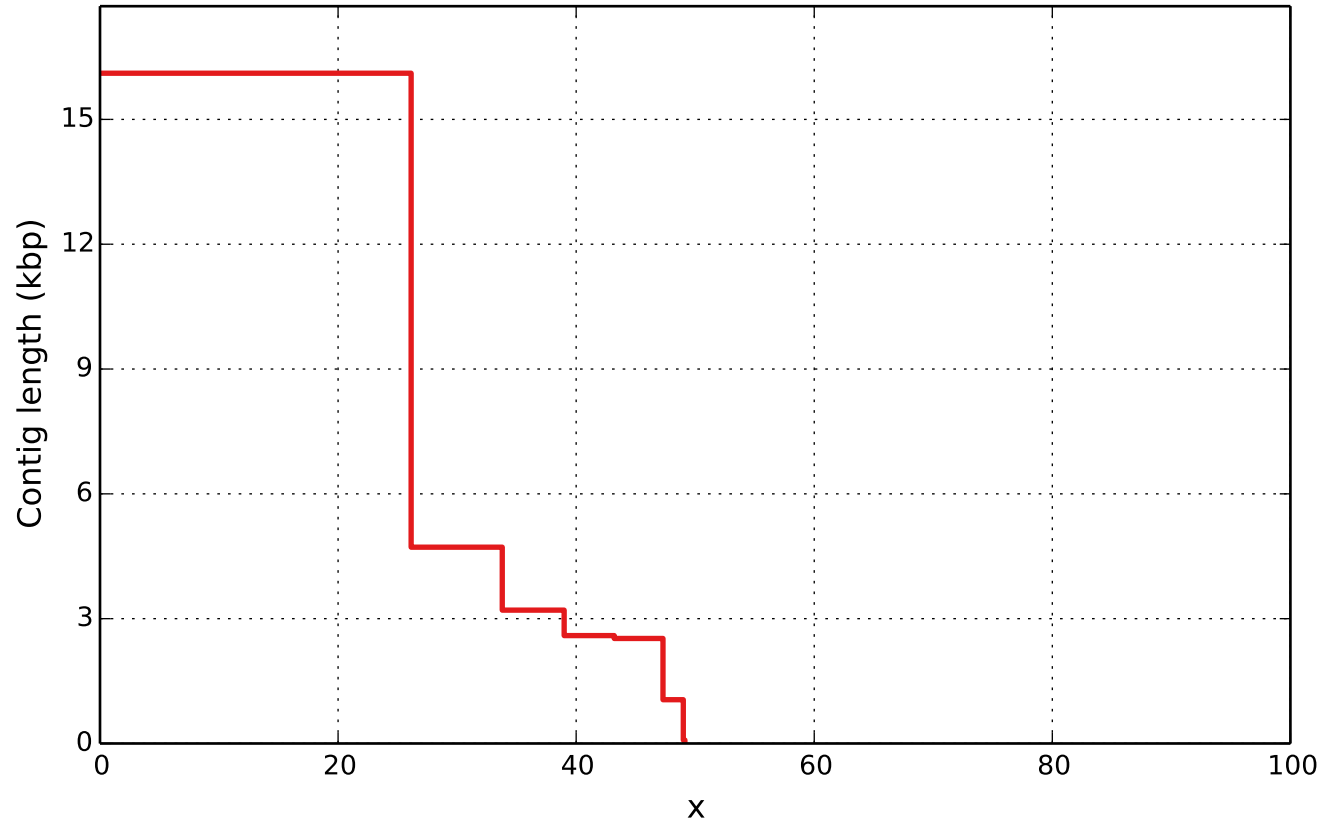


— CV45_contigs



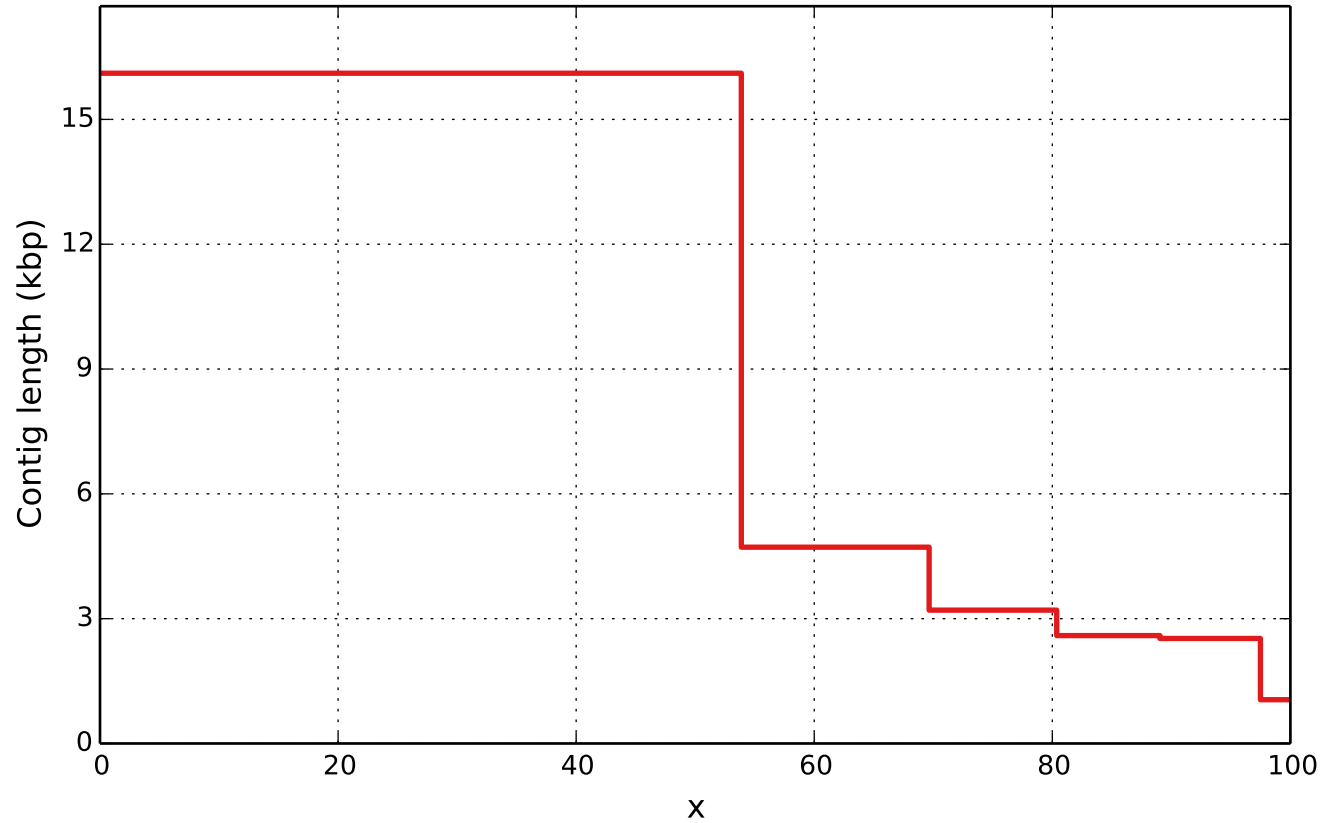
— CV45_contigs - - Reference

NAx



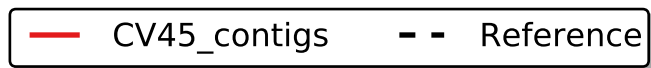
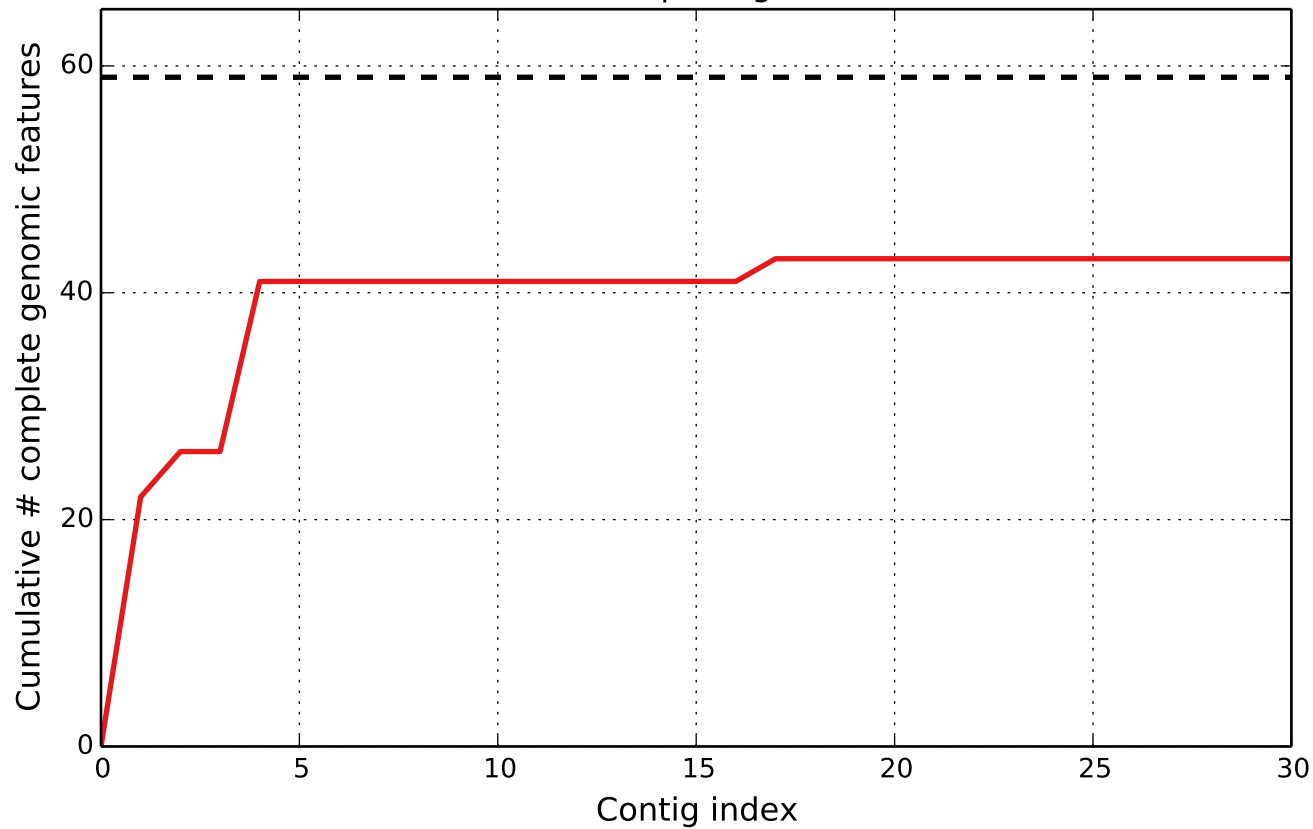
— CV45_contigs

NGAx

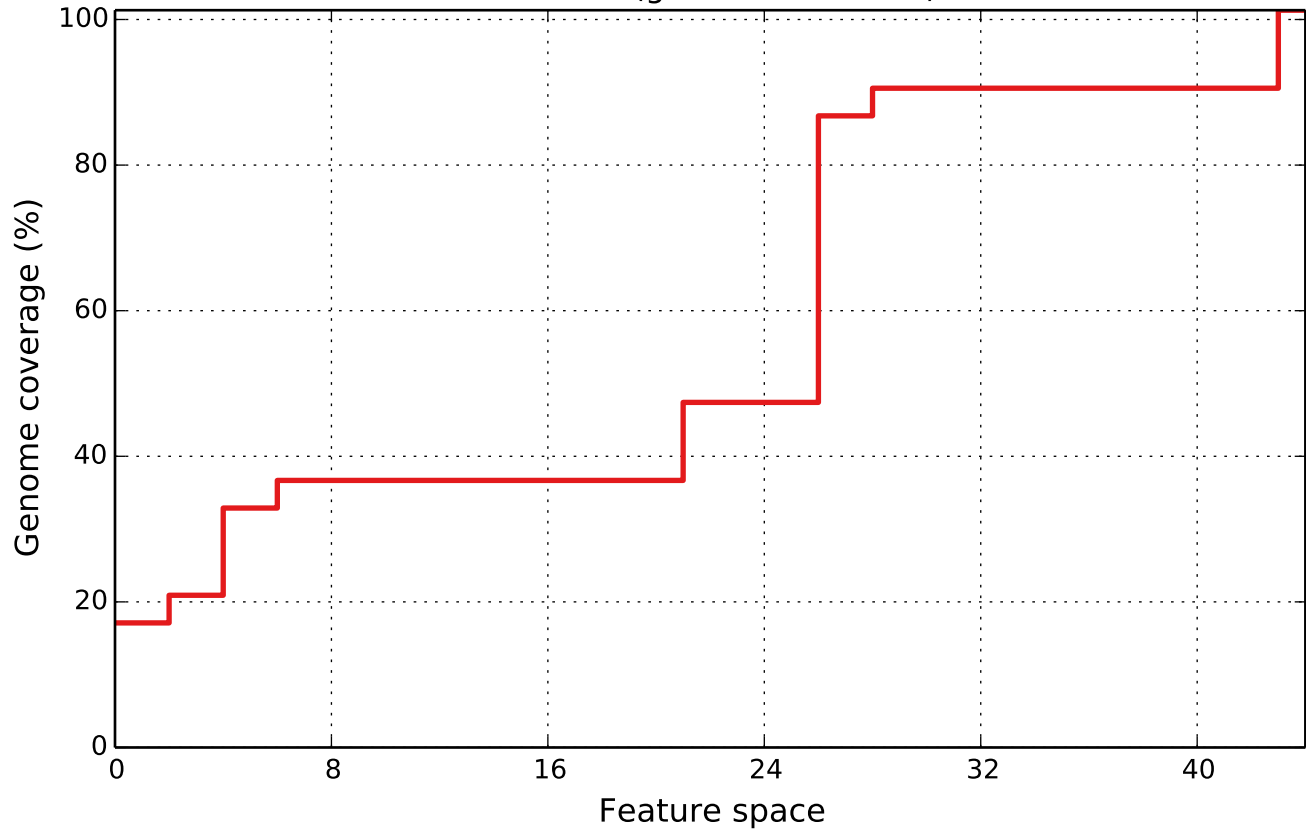


— CV45_contigs

Cumulative # complete genomic features



FRCurve (genomic features)



— CV45_contigs