

Report

	CV29_contigs
# contigs (>= 0 bp)	31
# contigs (>= 1000 bp)	24
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	66226
Total length (>= 1000 bp)	60605
Total length (>= 5000 bp)	22178
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	31
Largest contig	7731
Total length	66226
Reference length	29903
GC (%)	45.10
Reference GC (%)	37.97
N50	3065
NG50	7534
N75	1433
NG75	4428
L50	7
LG50	2
L75	15
LG75	4
# 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	25 + 0 part
Unaligned length	33568
Genome fraction (%)	99.786
Duplication ratio	1.094
# N's per 100 kbp	0.00
# mismatches per 100 kbp	30.16
# indels per 100 kbp	0.00
# genomic features	49 + 10 part
Largest alignment	7598
Total aligned length	32041
NGA50	7459
NGA75	4321
LGA50	2
LGA75	4

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

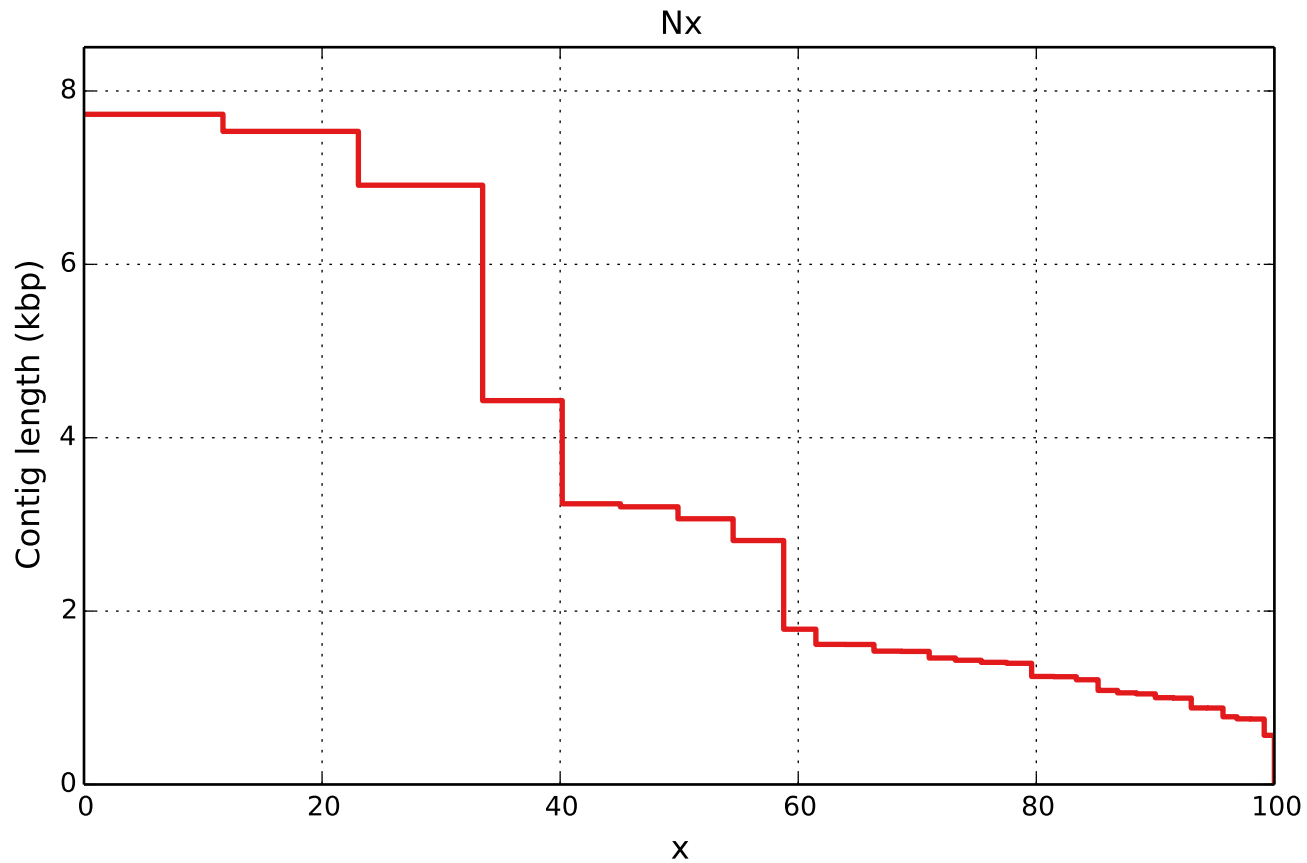
	CV29_contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	9
# 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).

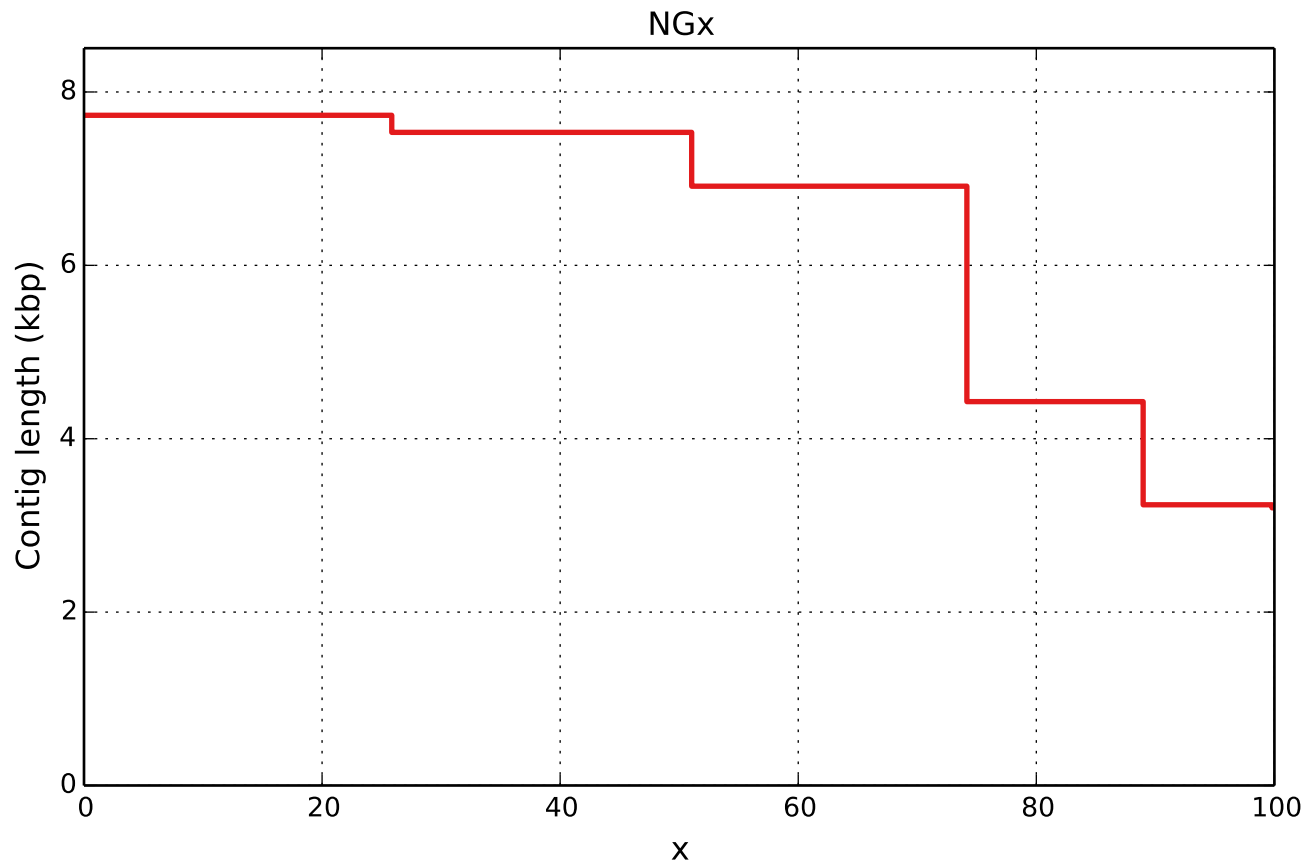
Unaligned report

	CV29_contigs
# fully unaligned contigs	25
Fully unaligned length	33568
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

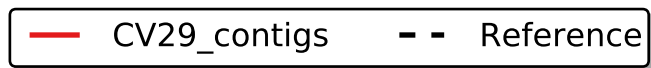
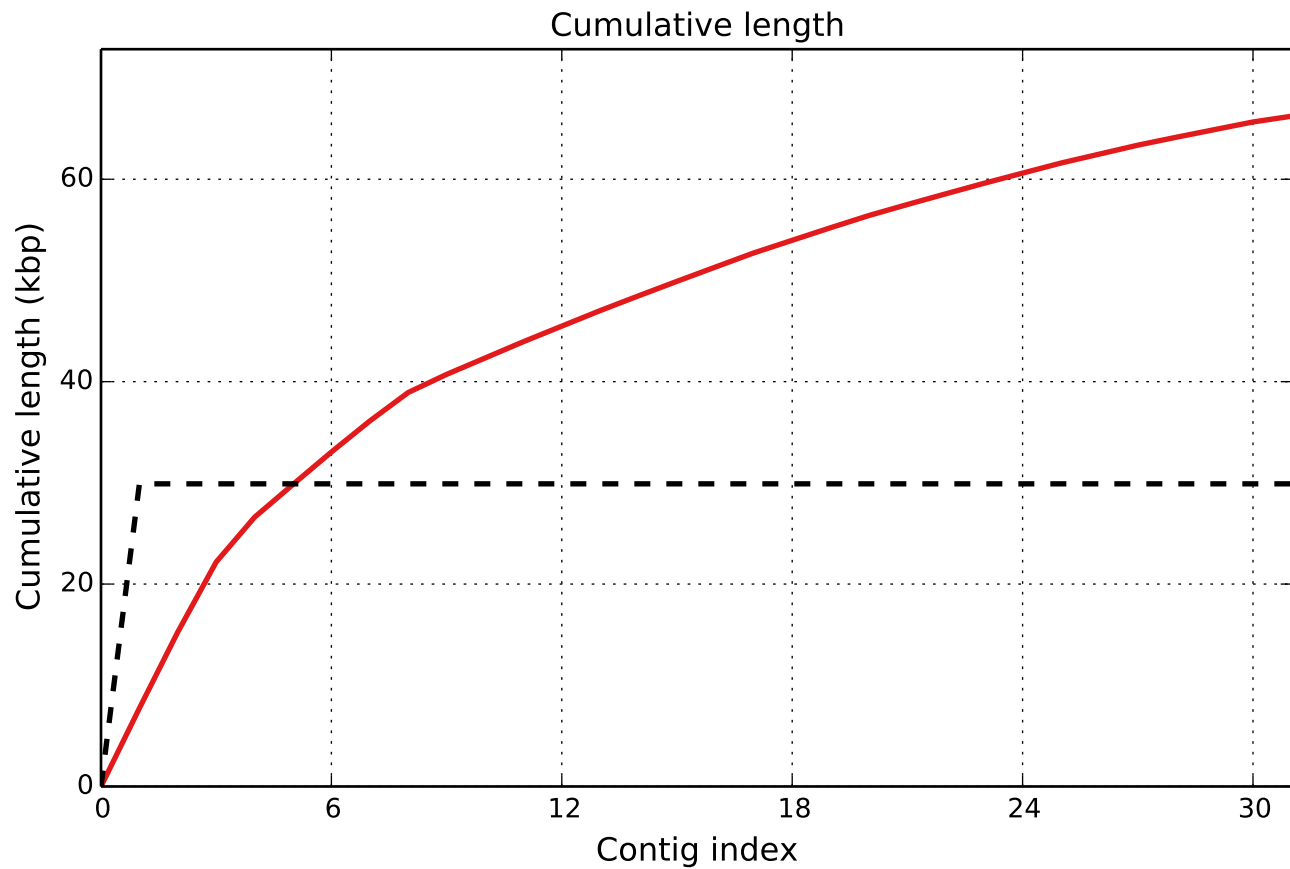
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

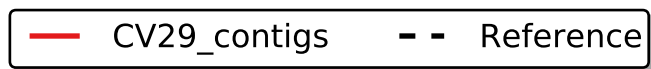
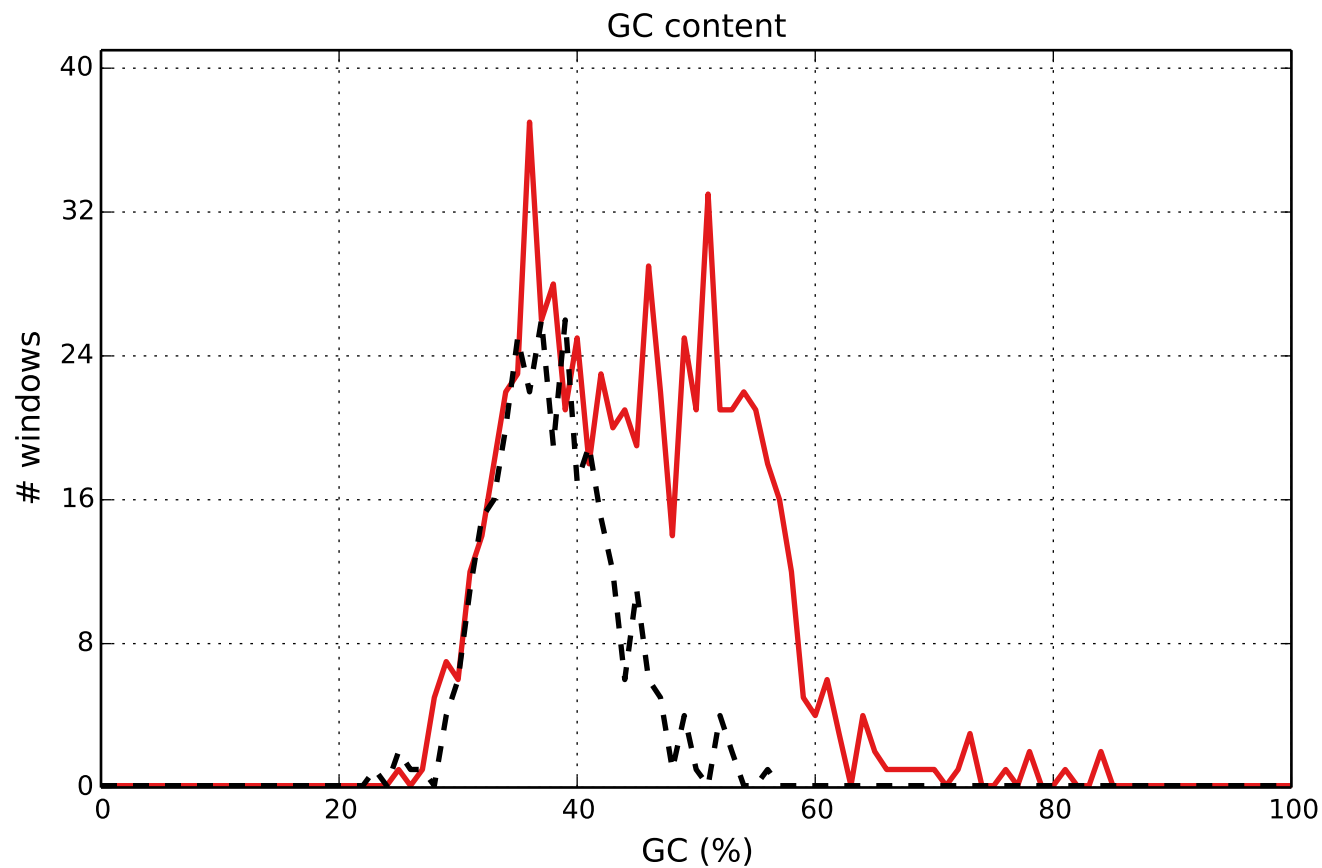


— CV29_contigs

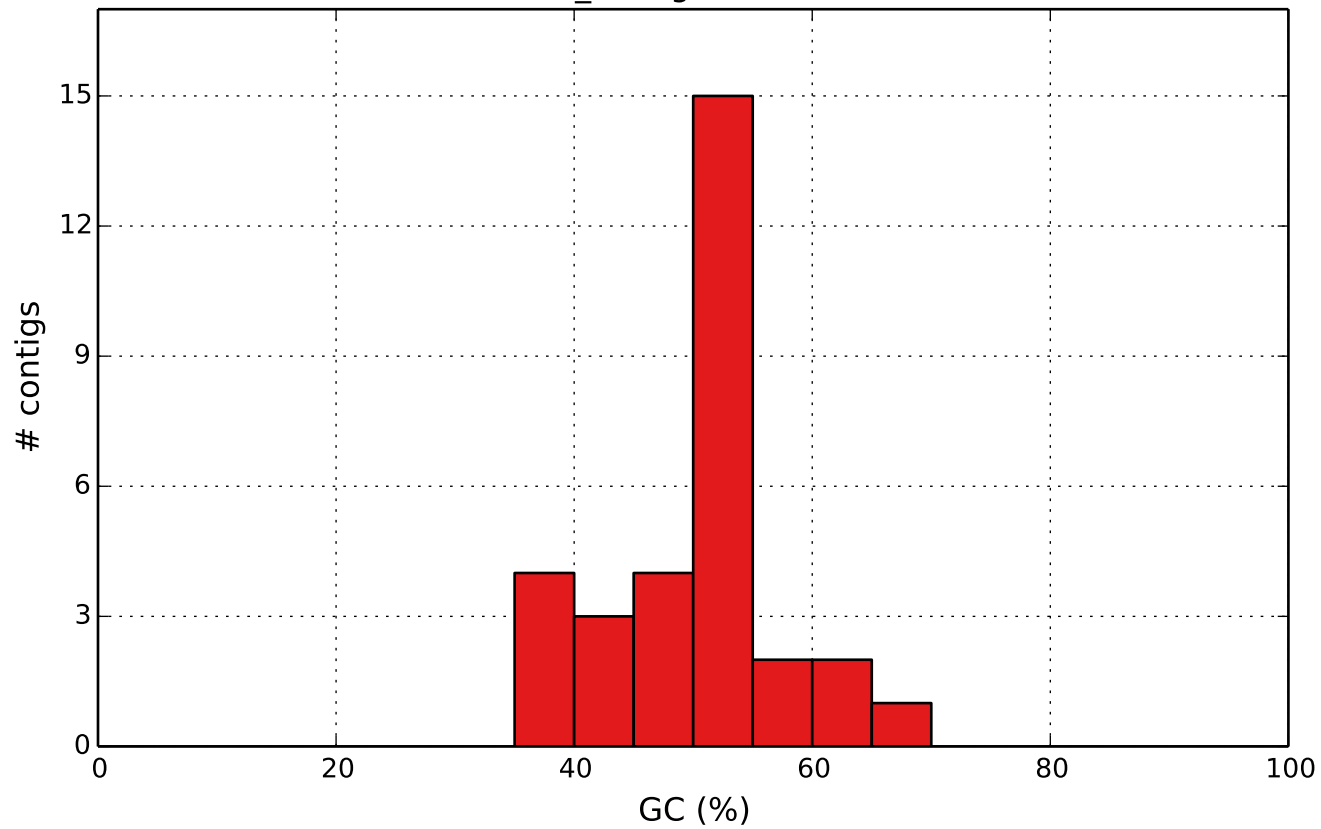


— CV29_contigs

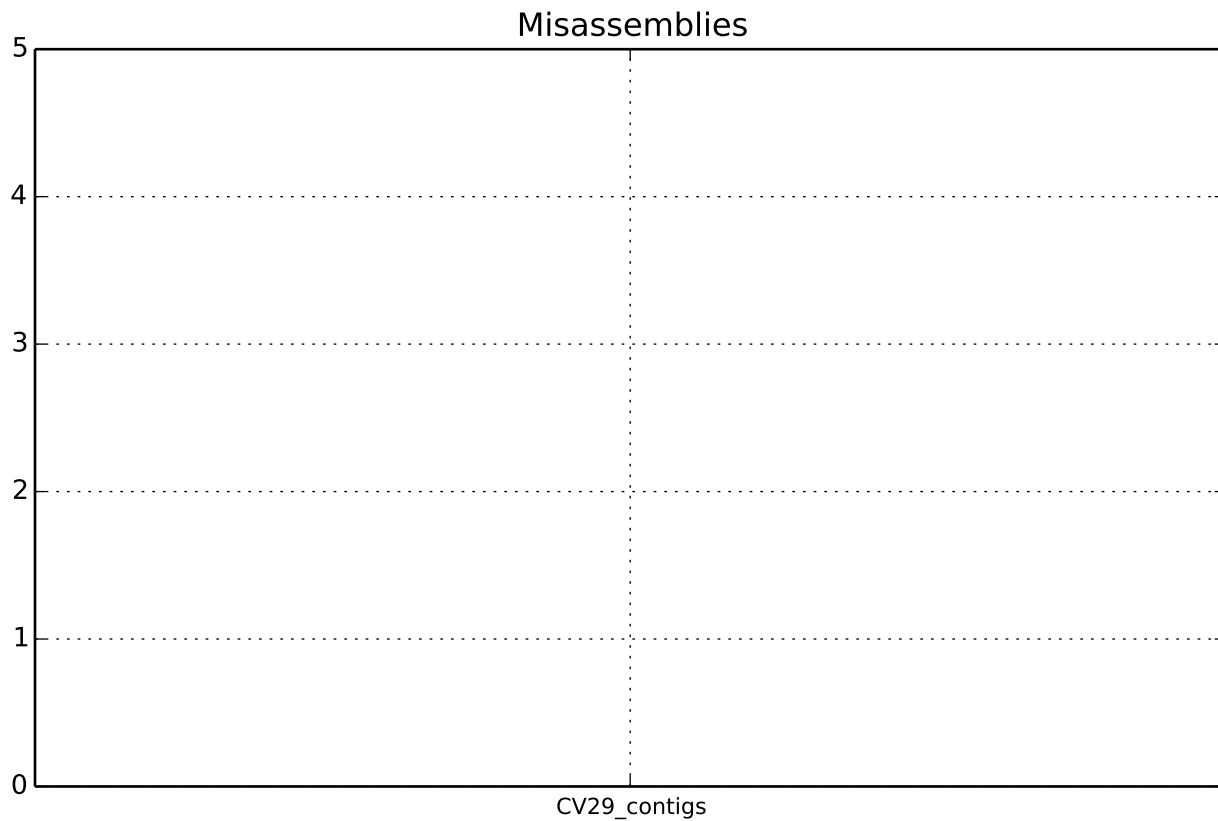




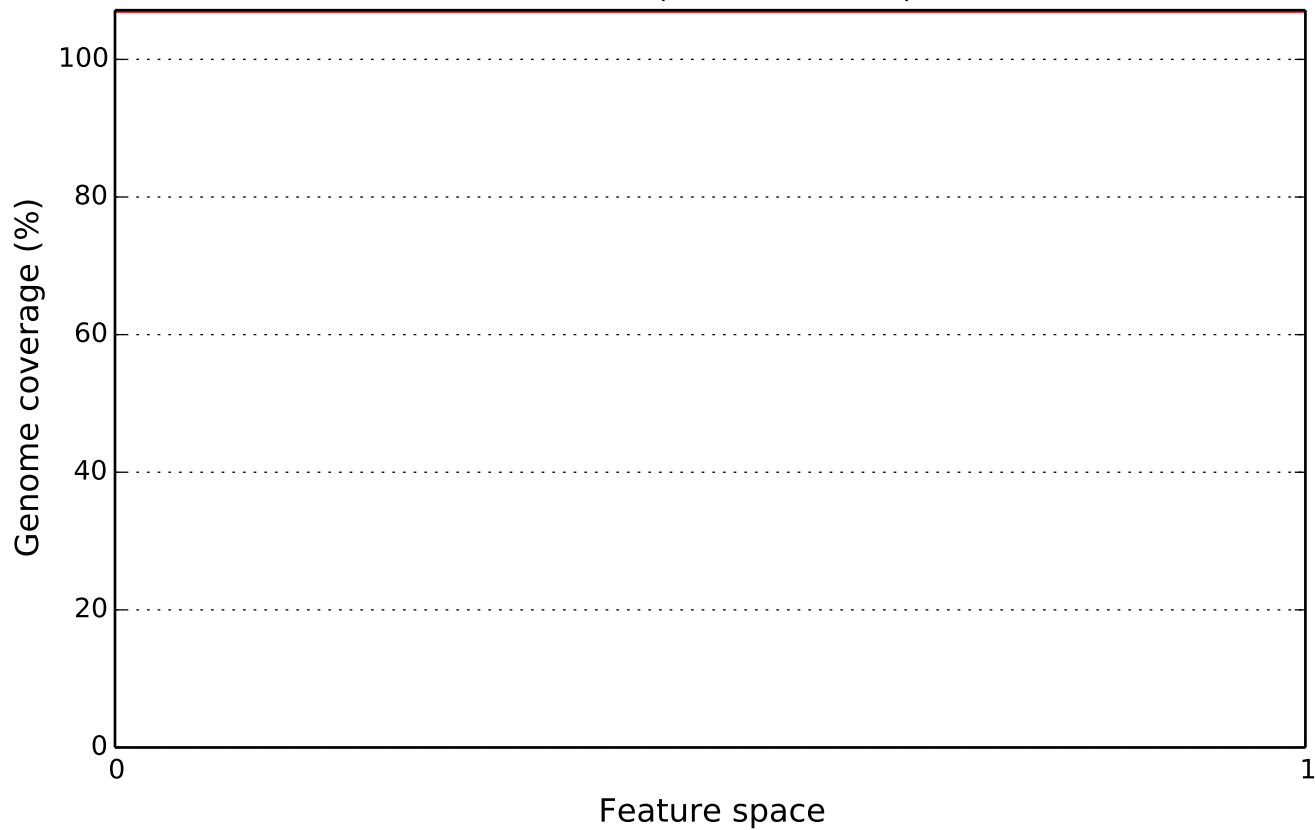
CV29_contigs GC content



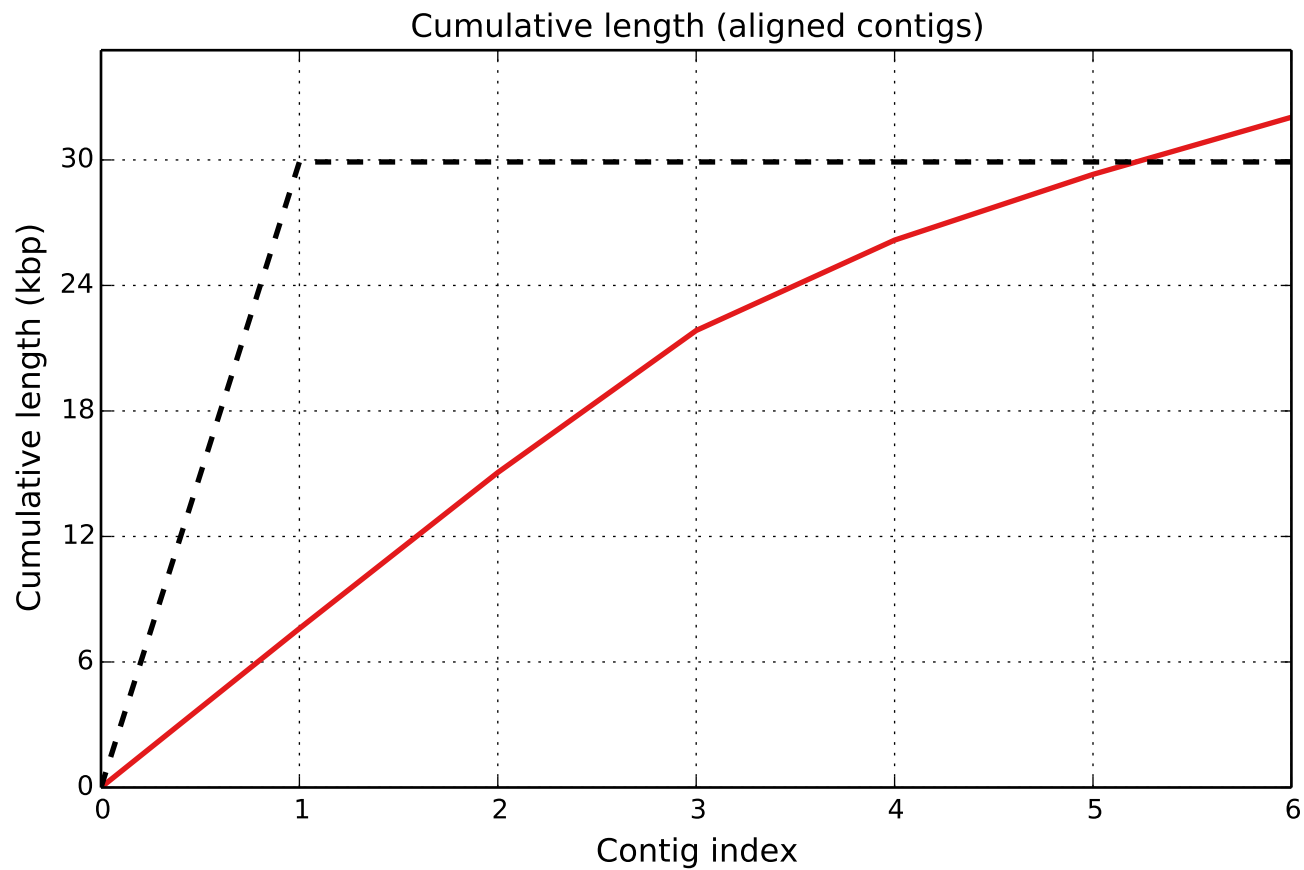
CV29_contigs



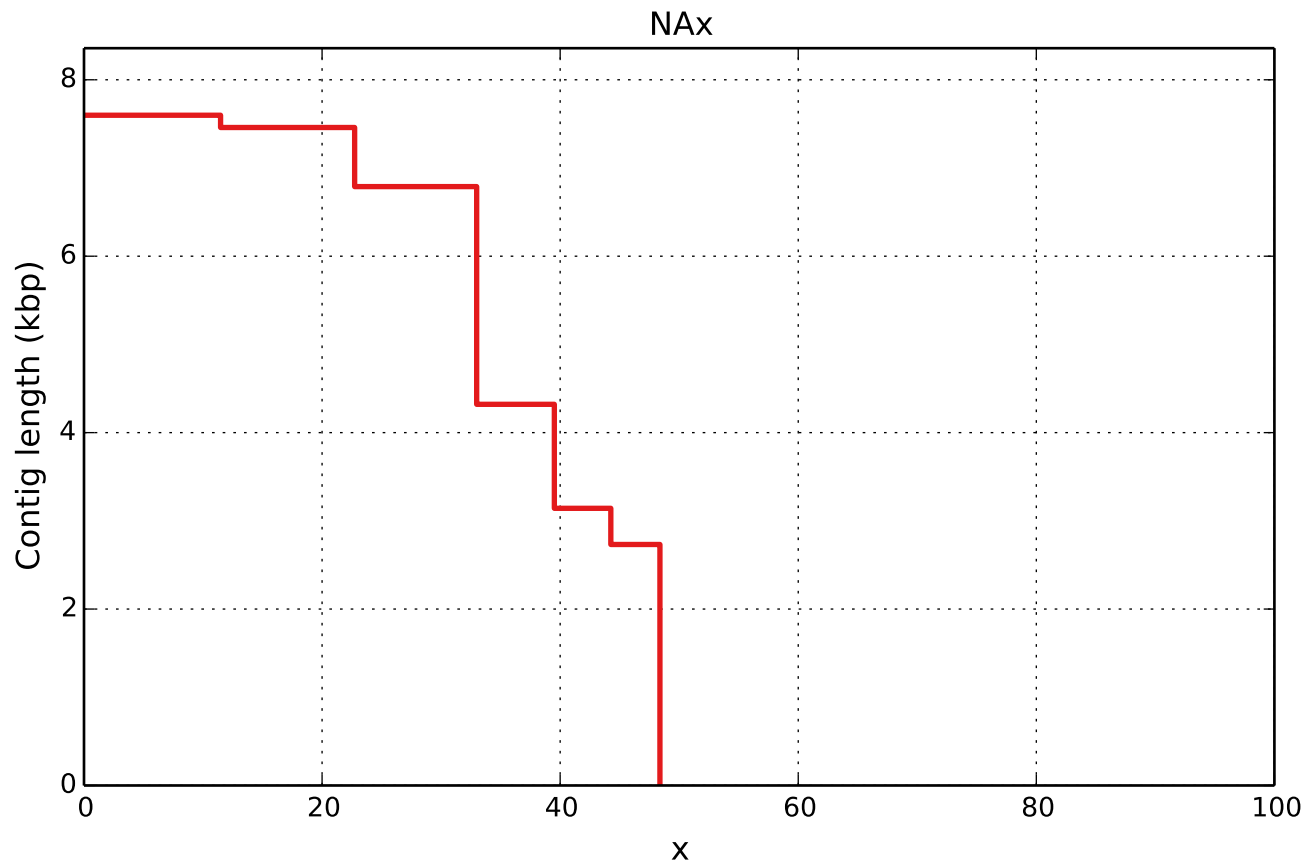
FRCurve (misassemblies)



CV29_contigs

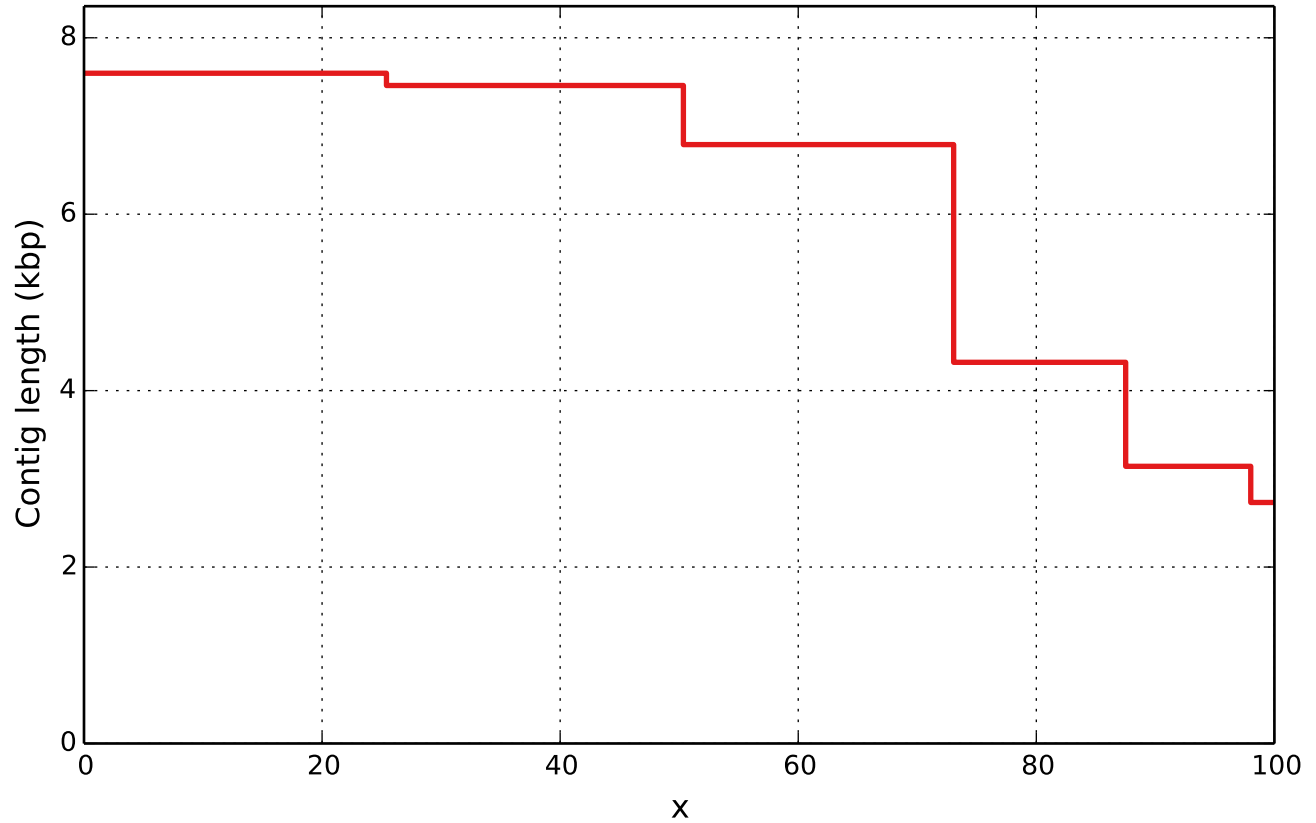


— CV29_contigs - - Reference



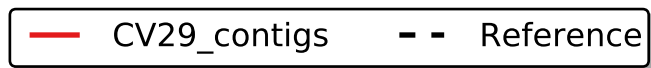
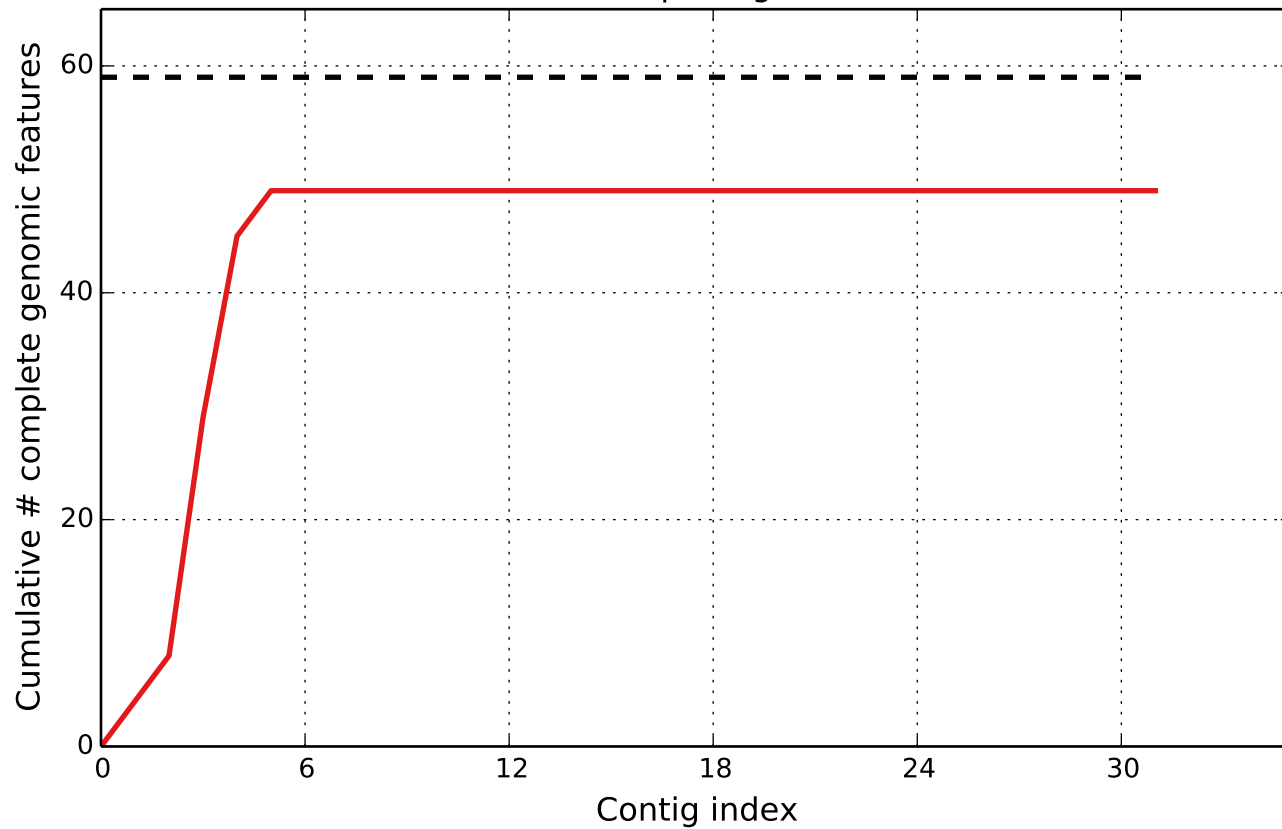
— CV29_contigs

NGAx

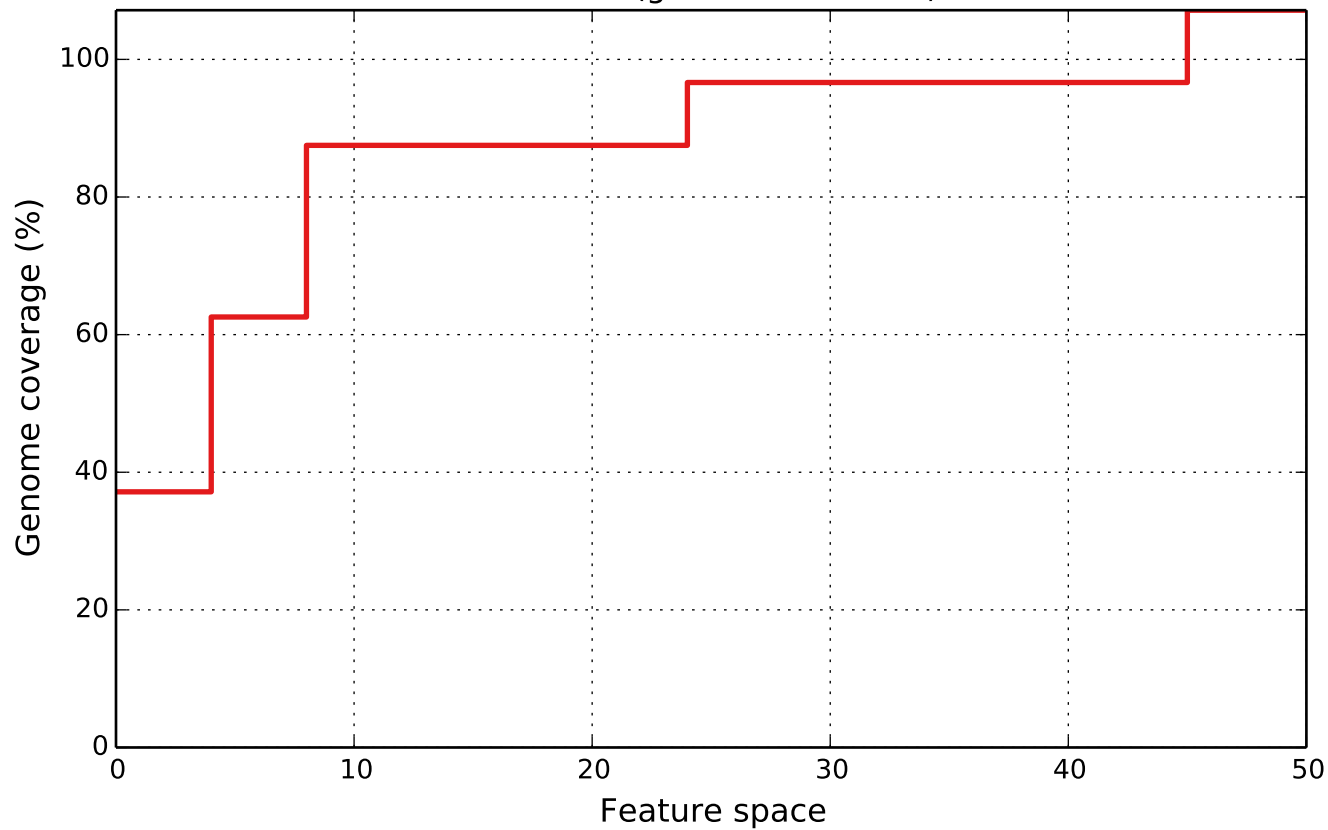


— CV29_contigs

Cumulative # complete genomic features



FRCurve (genomic features)



— CV29_contigs