

Report

	CV18_velvet_contigs
# contigs (>= 0 bp)	883
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	233772
Total length (>= 1000 bp)	9484
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	68
Largest contig	1858
Total length	50125
Reference length	29903
GC (%)	47.82
Reference GC (%)	37.97
N50	728
NG50	922
N75	605
NG75	799
L50	27
LG50	14
L75	45
LG75	23
# 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	60 + 0 part
Unaligned length	44197
Genome fraction (%)	19.326
Duplication ratio	1.026
# N's per 100 kbp	297.26
# mismatches per 100 kbp	51.91
# indels per 100 kbp	0.00
# genomic features	0 + 18 part
Largest alignment	1140
Total aligned length	5779
NGA50	-

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_velvet_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	3
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

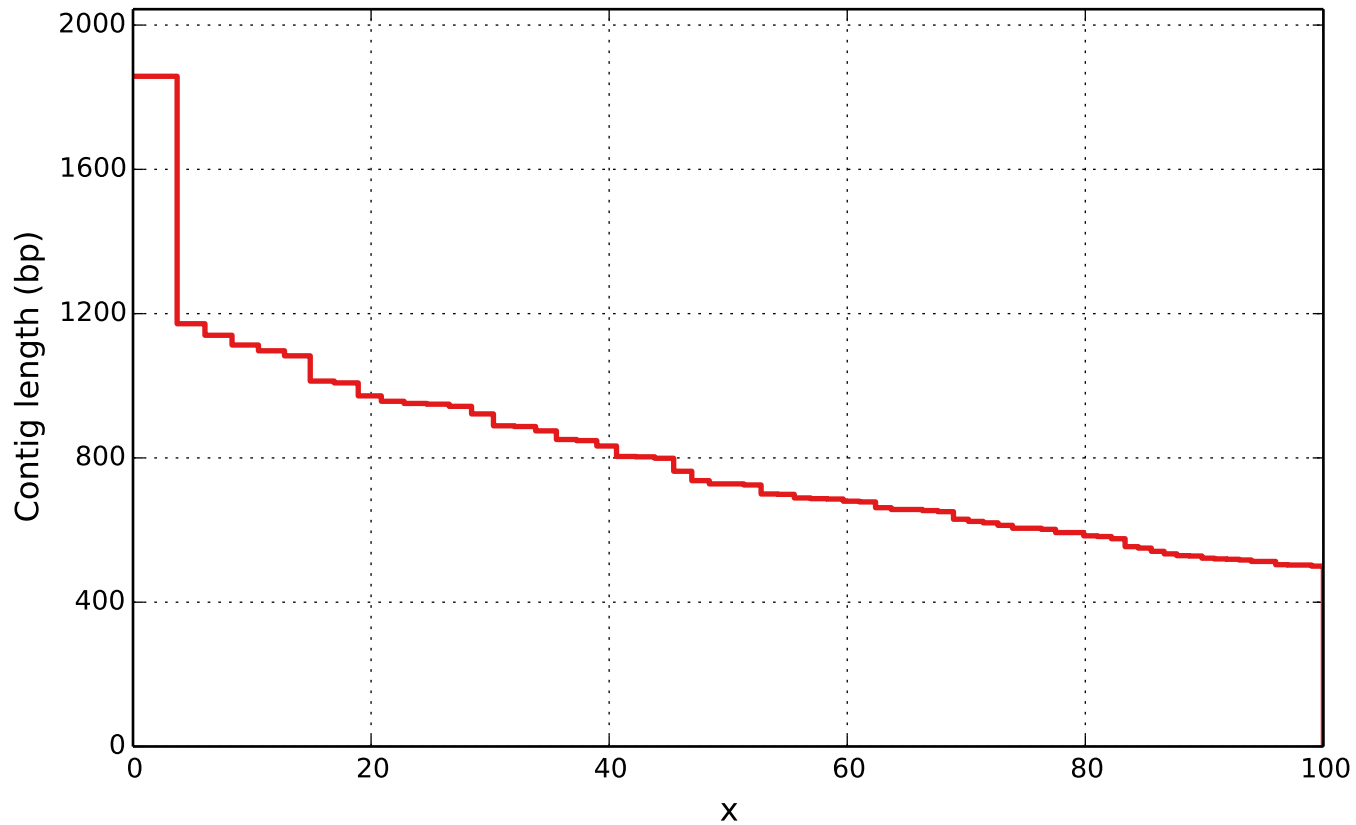
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	CV18_velvet_contigs
# fully unaligned contigs	60
Fully unaligned length	44197
# partially unaligned contigs	0
Partially unaligned length	0
# N's	149

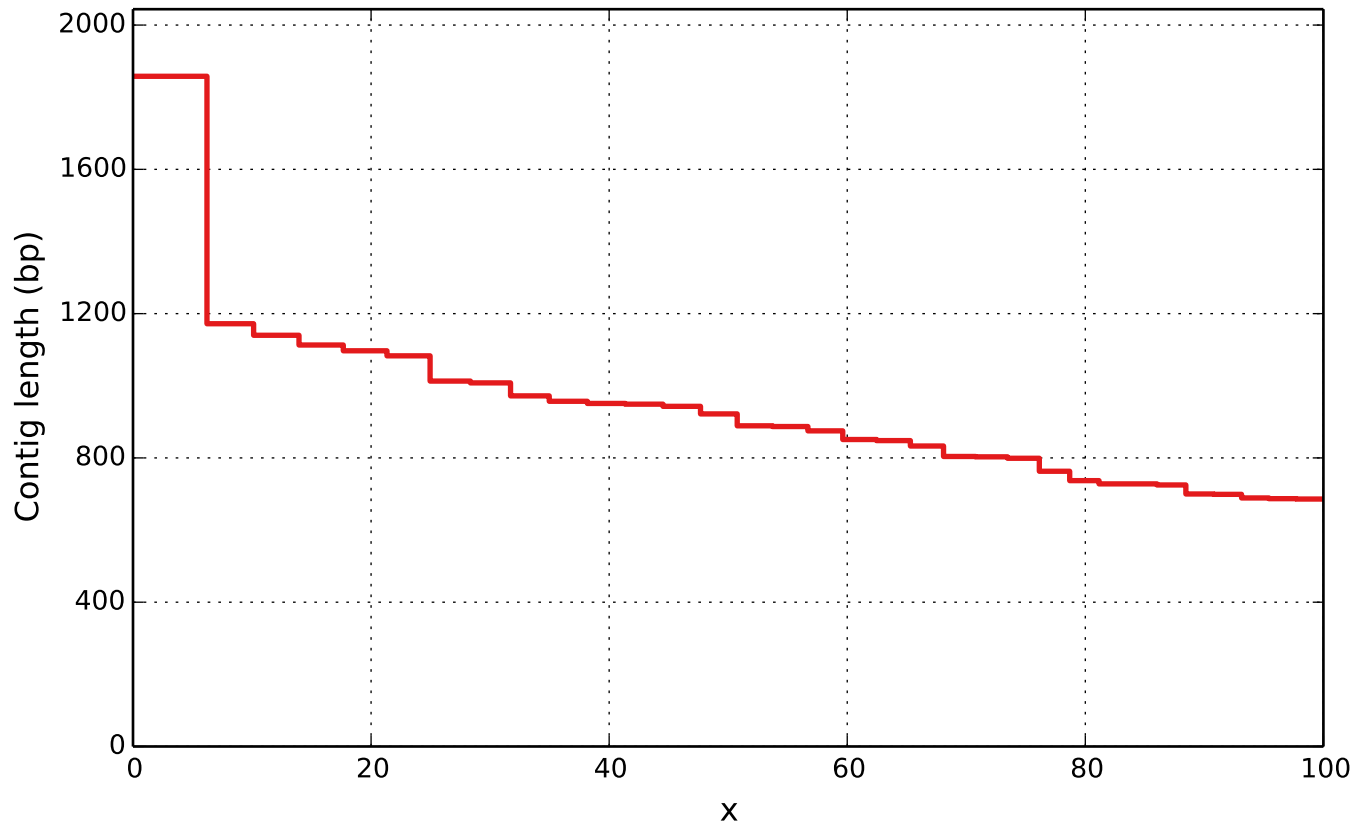
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

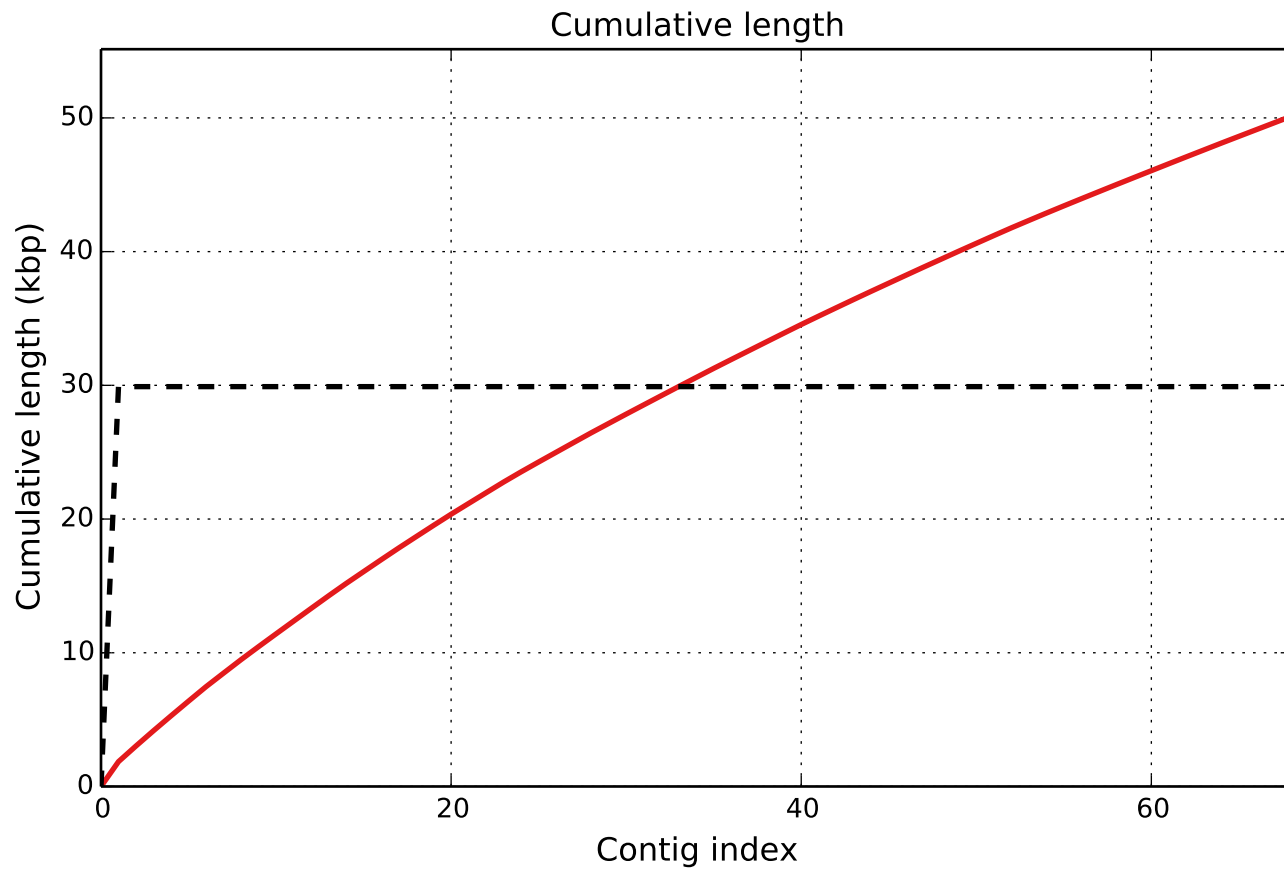


CV18_velvet_contigs

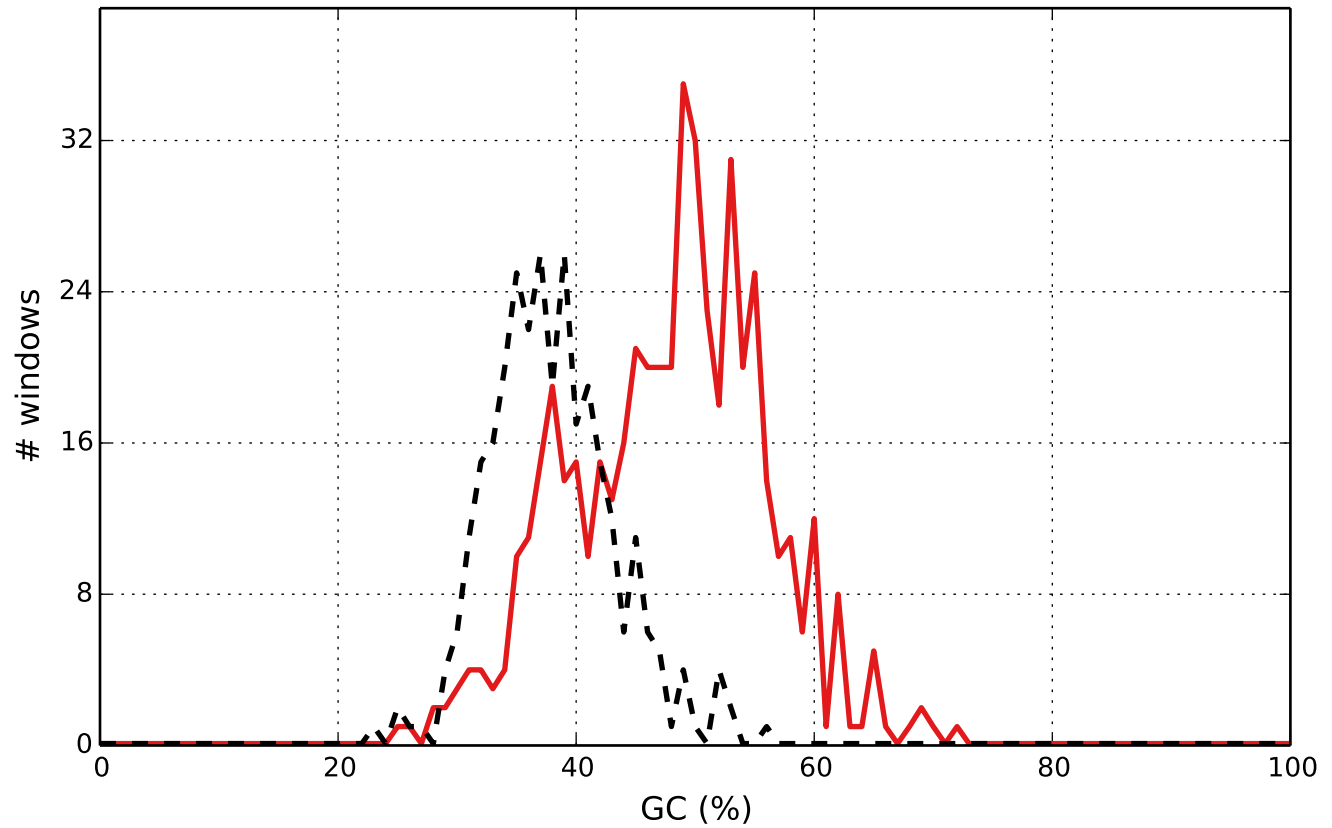
NGx

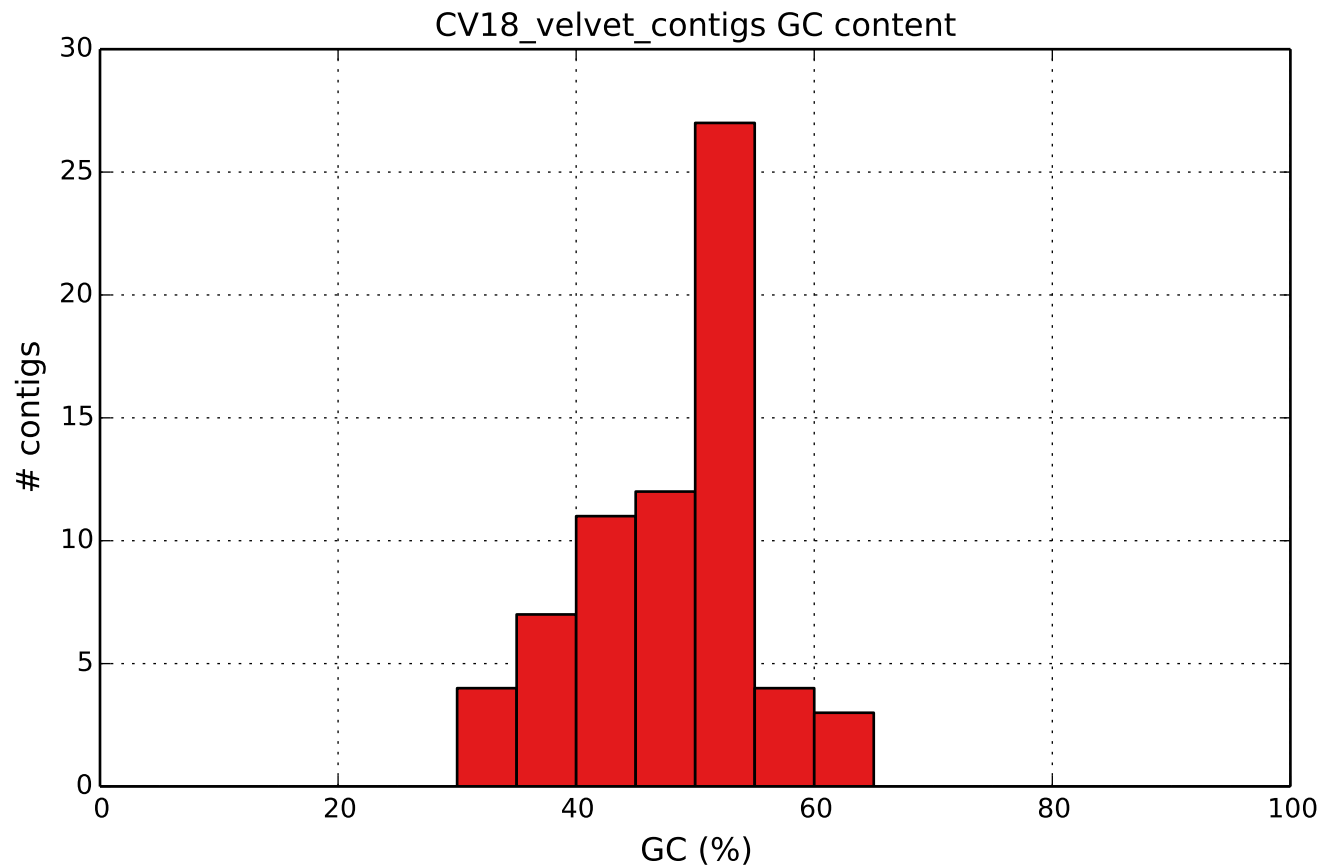


CV18_velvet_contigs

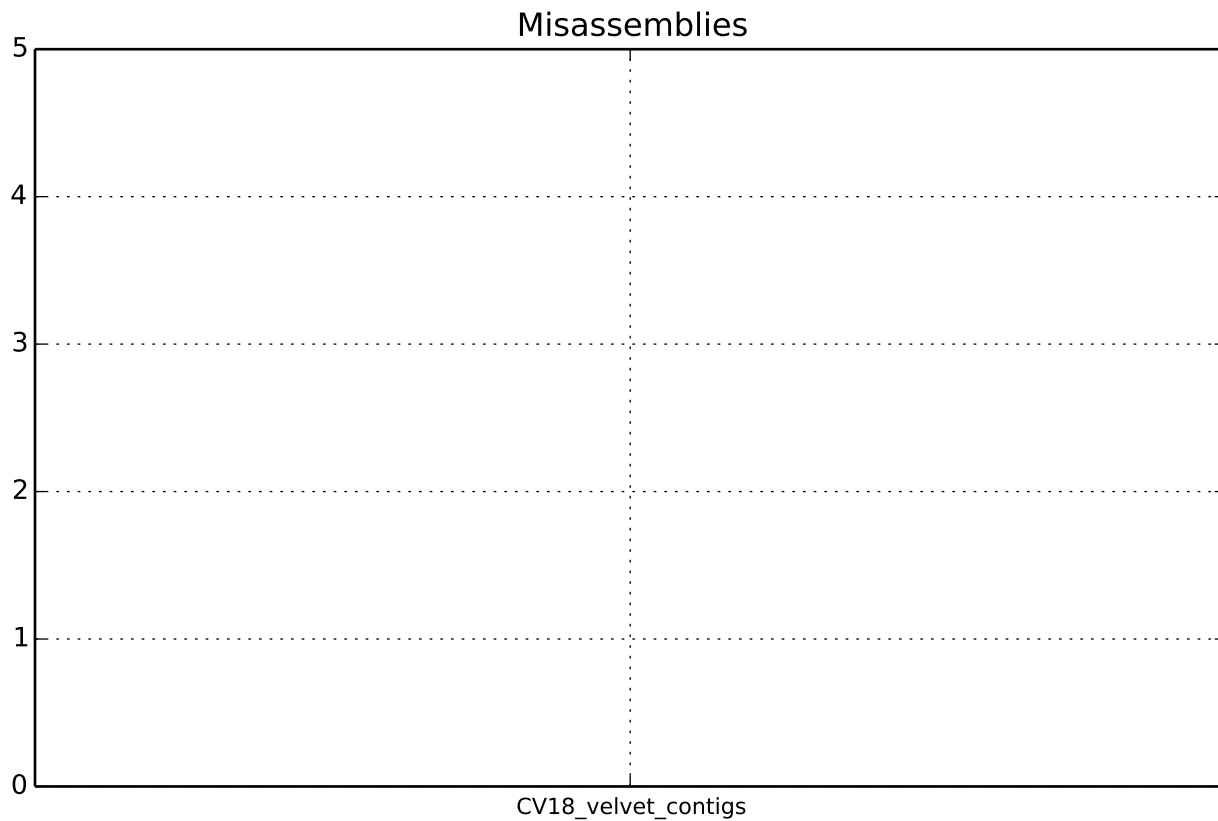


GC content





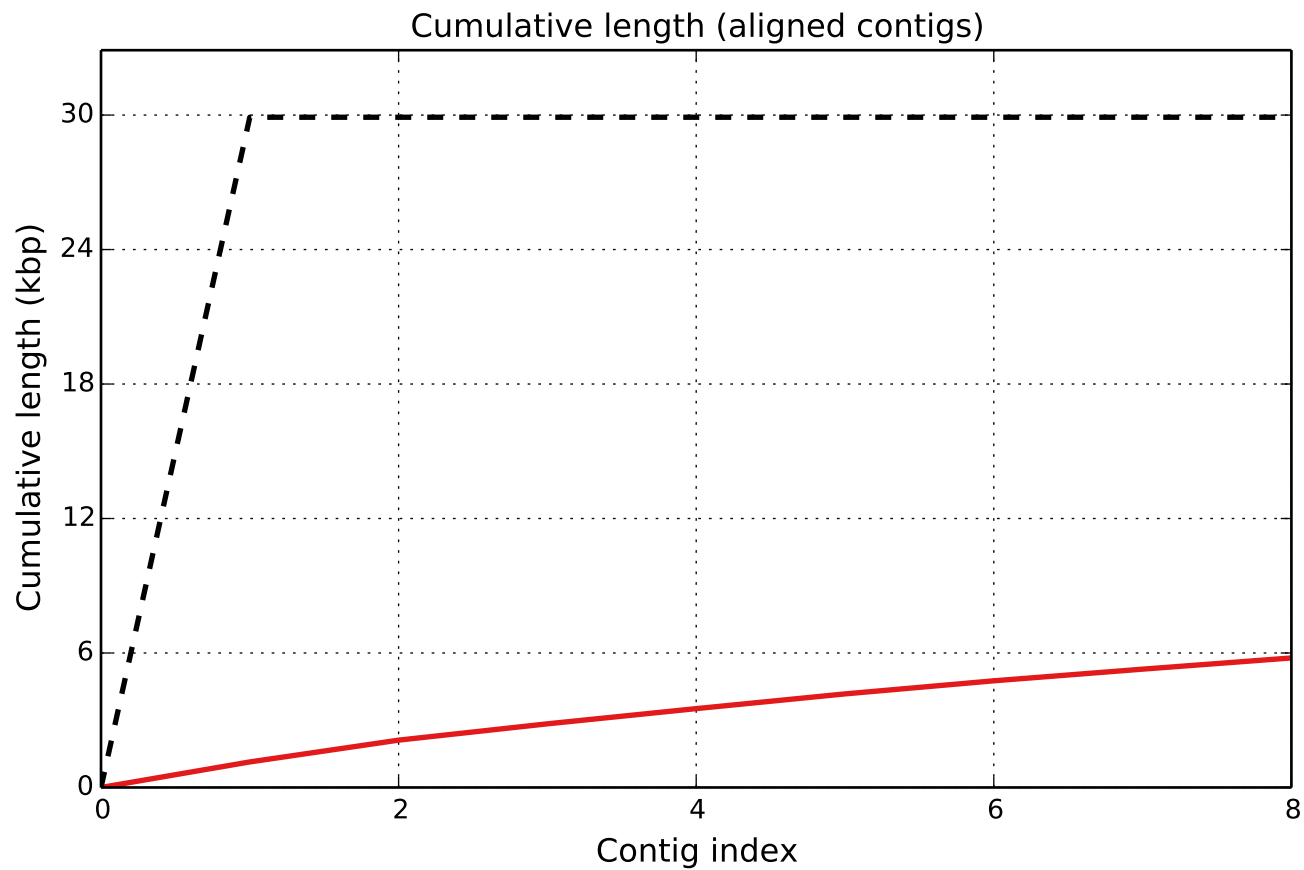
CV18_velvet_contigs



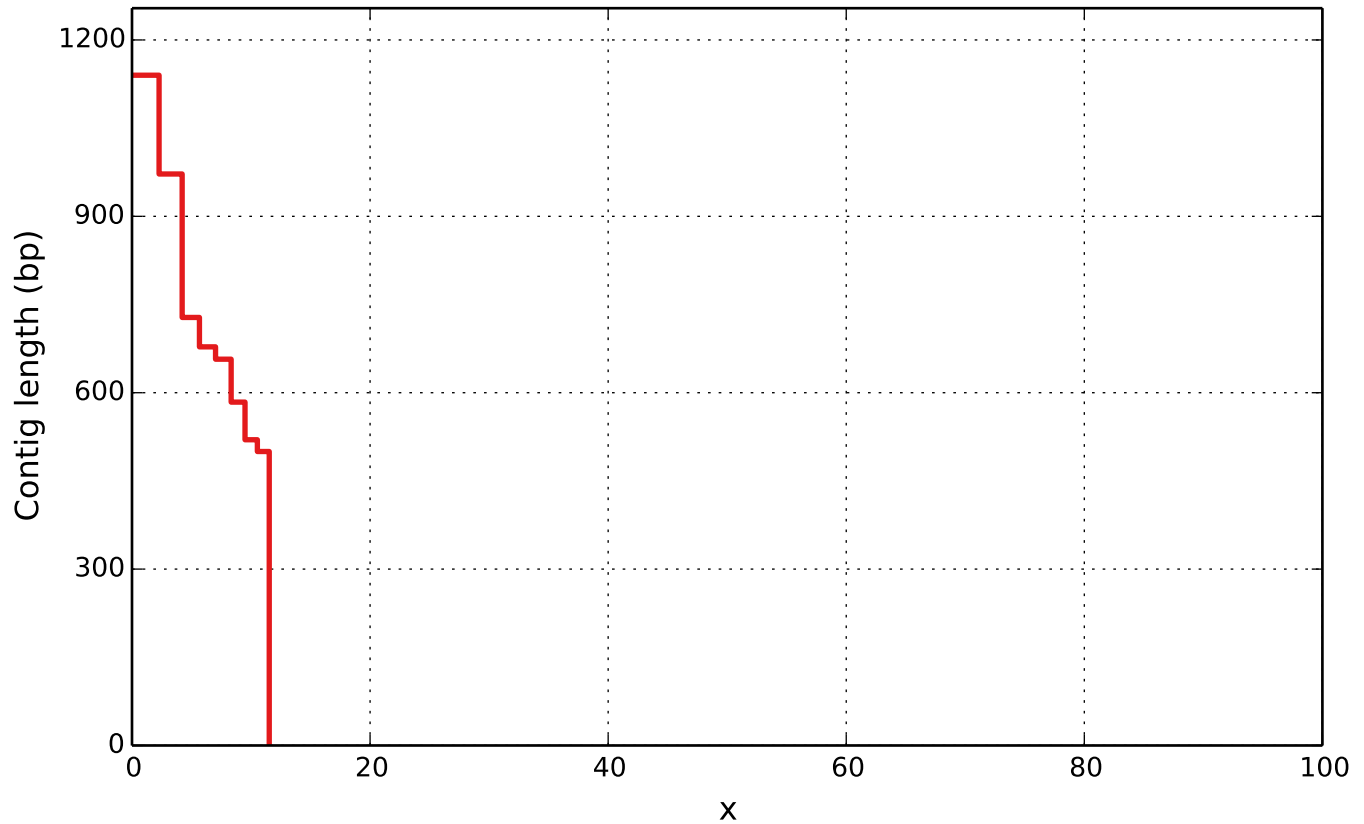
FRCurve (misassemblies)



— CV18_velvet_contigs

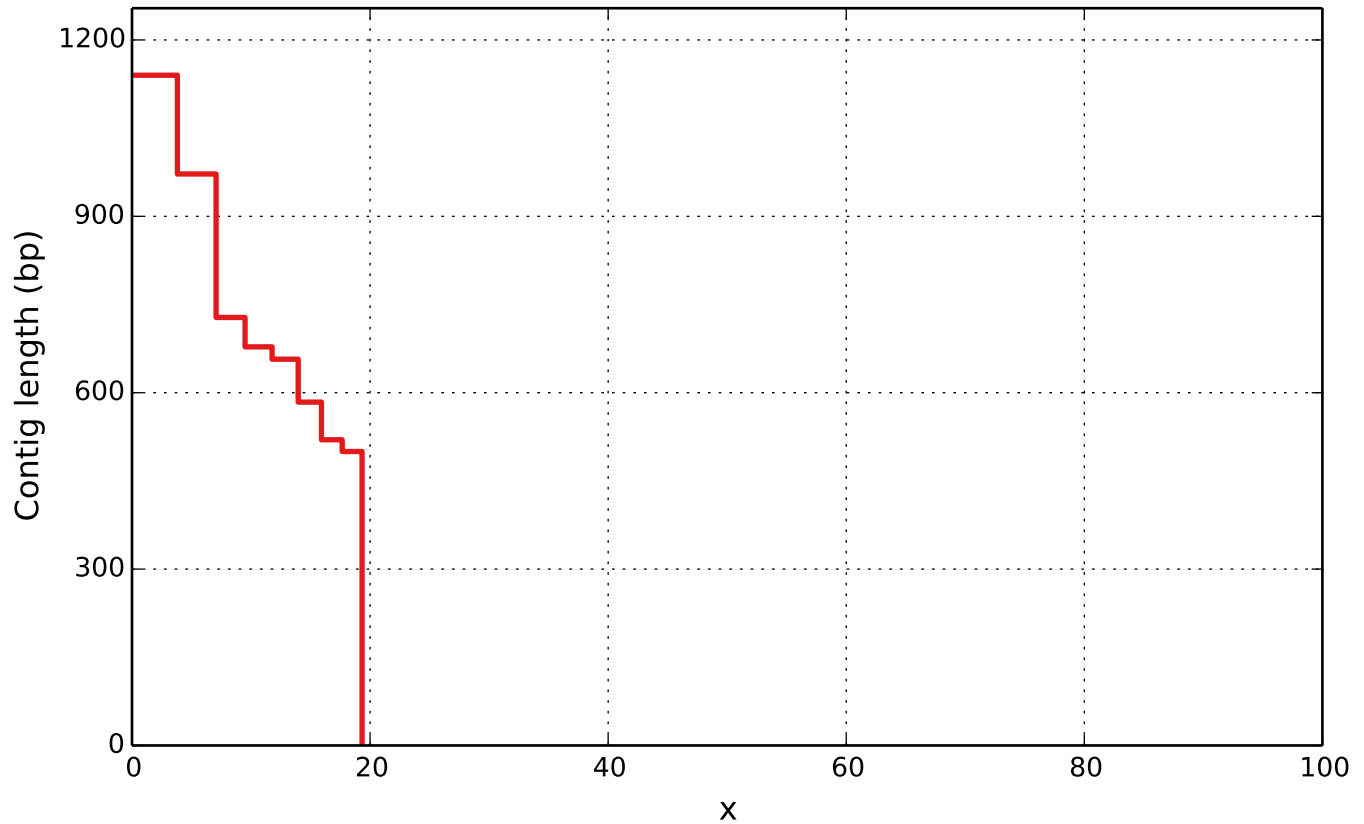


NAx

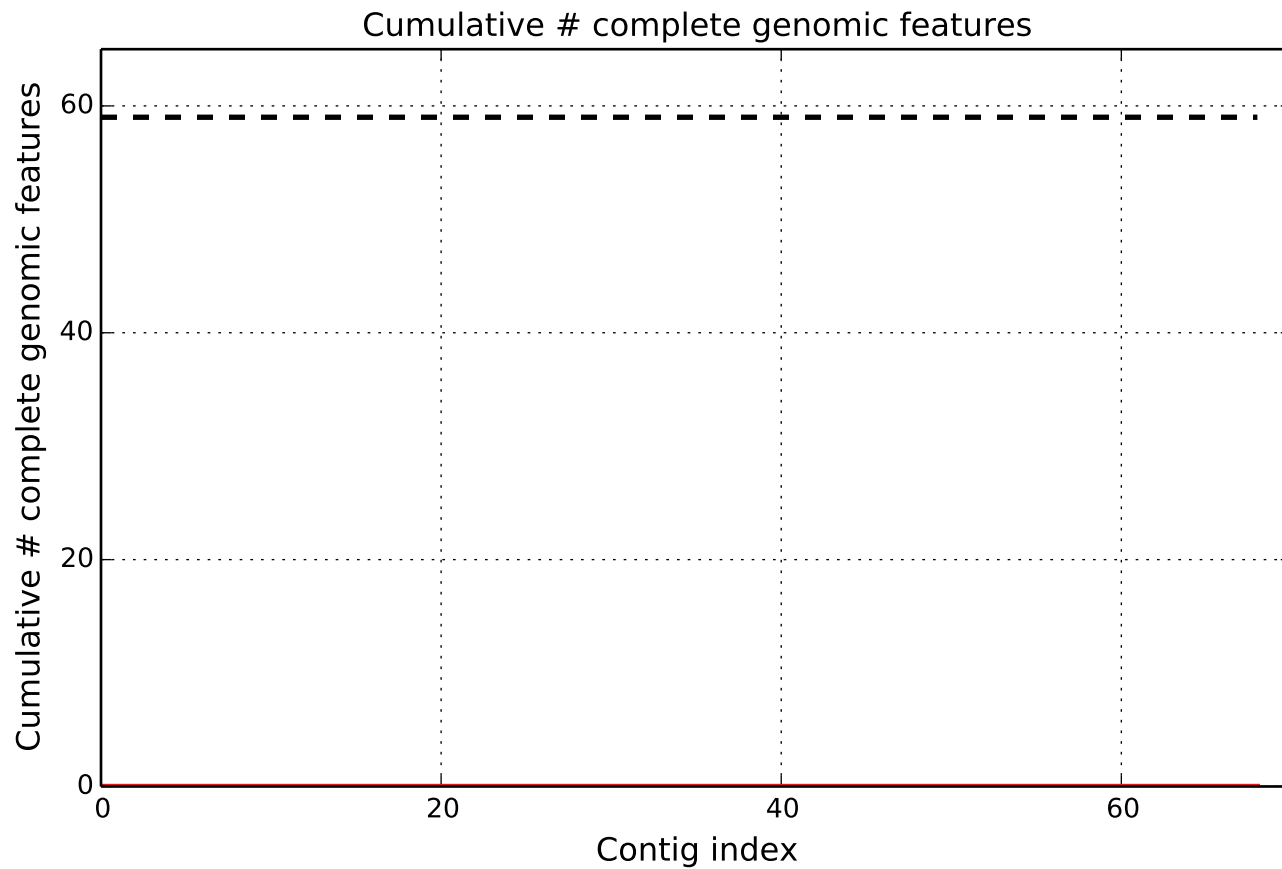


— CV18_velvet_contigs

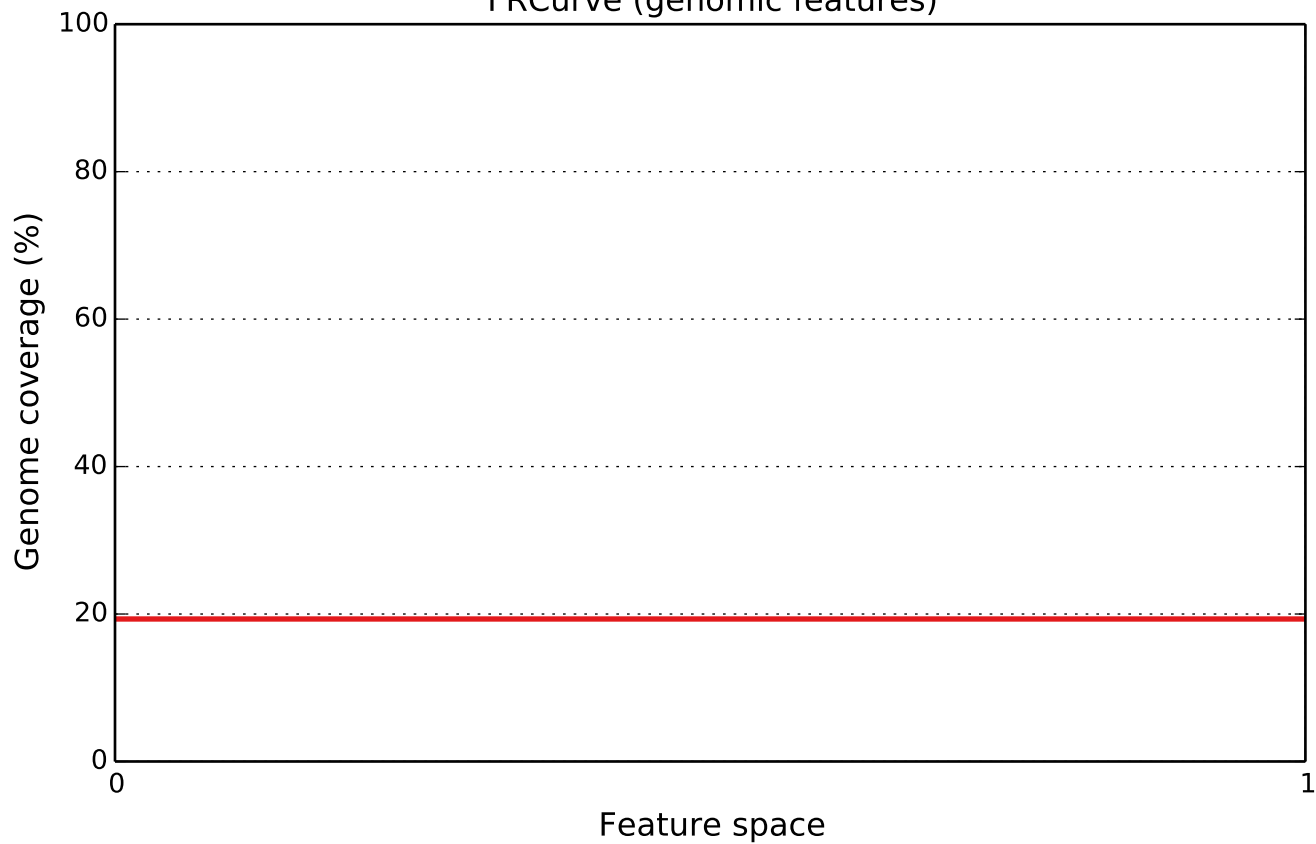
NGAx



CV18_velvet_contigs



FRCurve (genomic features)



CV18_velvet_contigs