

# Report

	9Btwo_filtered
# contigs (>= 0 bp)	128
# contigs (>= 1000 bp)	46
# contigs (>= 5000 bp)	39
# contigs (>= 10000 bp)	38
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	5874982
Total length (>= 1000 bp)	5844066
Total length (>= 5000 bp)	5832282
Total length (>= 10000 bp)	5826052
Total length (>= 25000 bp)	5783778
Total length (>= 50000 bp)	5466390
# contigs	54
Largest contig	566821
Total length	5850128
Reference length	5682322
GC (%)	56.90
Reference GC (%)	57.12
N50	247549
NG50	272670
N75	121110
NG75	153665
L50	8
LG50	7
L75	15
LG75	14
# misassemblies	54
# misassembled contigs	14
Misassembled contigs length	2572600
# local misassemblies	134
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	16
# unaligned contigs	4 + 39 part
Unaligned length	2818773
Genome fraction (%)	53.271
Duplication ratio	1.001
# N's per 100 kbp	5.20
# mismatches per 100 kbp	3979.72
# indels per 100 kbp	44.47
# genomic features	2823 + 253 part
Largest alignment	146117
Total aligned length	3029666
NA50	1514
NGA50	2235
LA50	243
LGA50	197

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

	9Btwo_filtered
# misassemblies	54
# contig misassemblies	53
# c. relocations	53
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	1
# s. relocations	1
# s. translocations	0
# s. inversions	0
# misassembled contigs	14
Misassembled contigs length	2572600
# local misassemblies	134
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	16
# mismatches	120468
# indels	1346
# indels (<= 5 bp)	1255
# indels (> 5 bp)	91
Indels length	3655

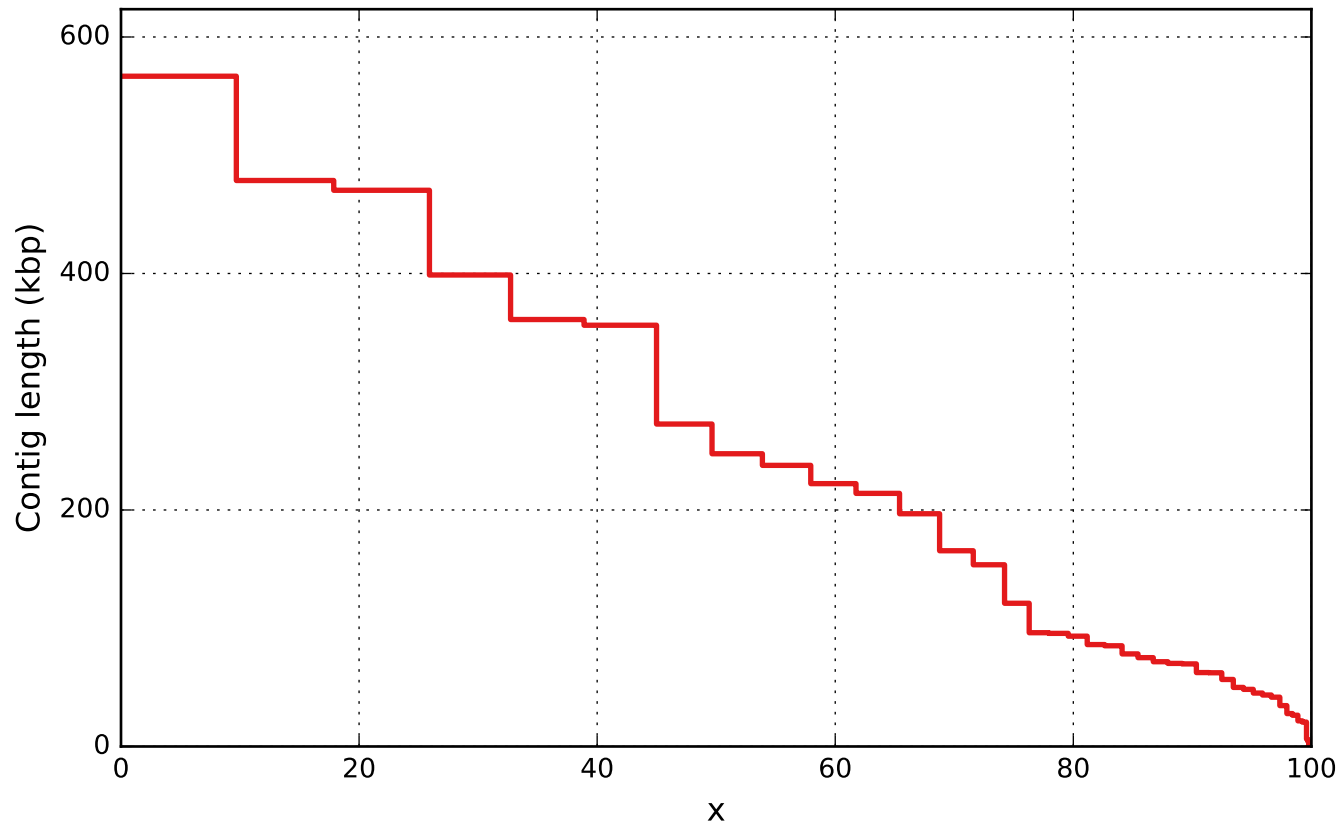
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	9Btwo_filtered
# fully unaligned contigs	4
Fully unaligned length	74800
# partially unaligned contigs	39
Partially unaligned length	2743973
# N's	304

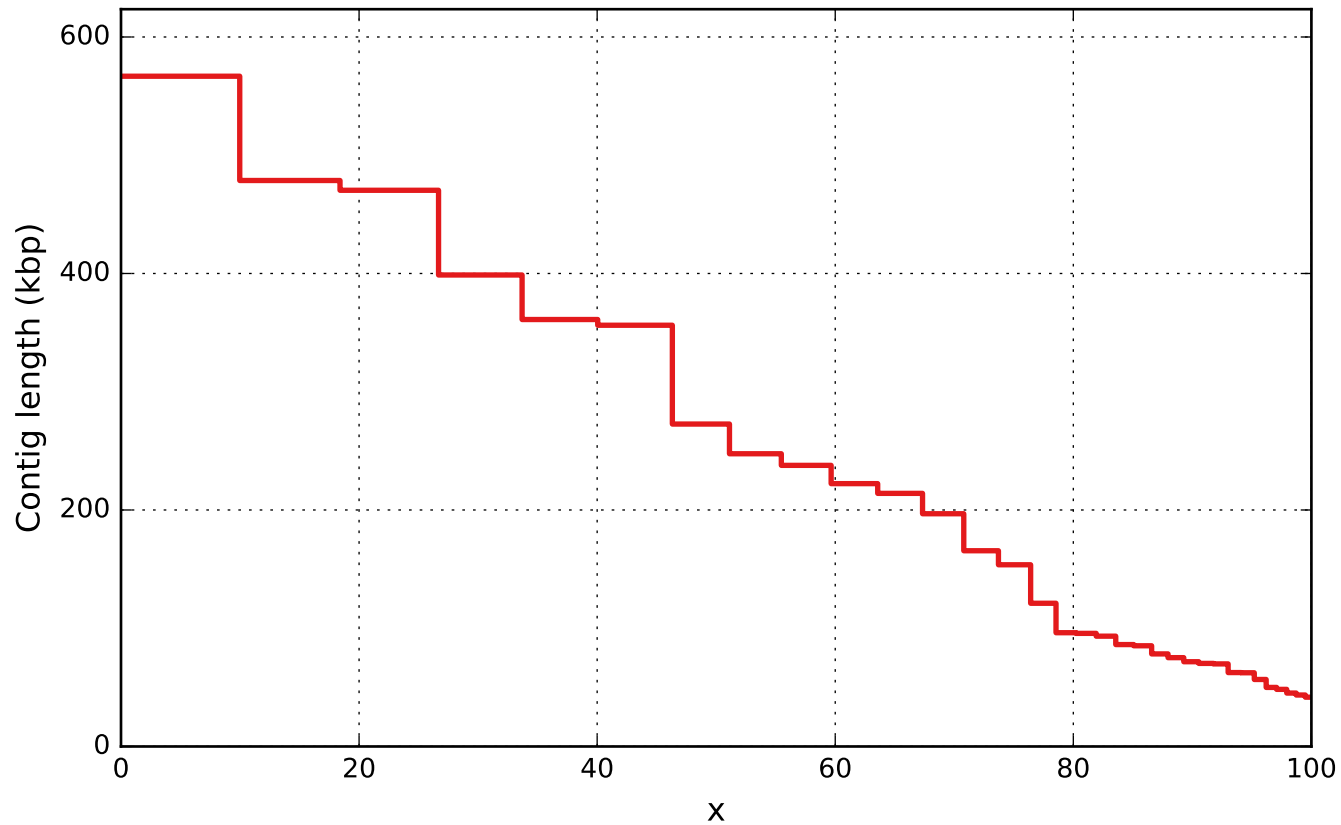
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

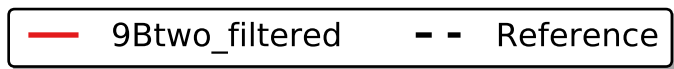
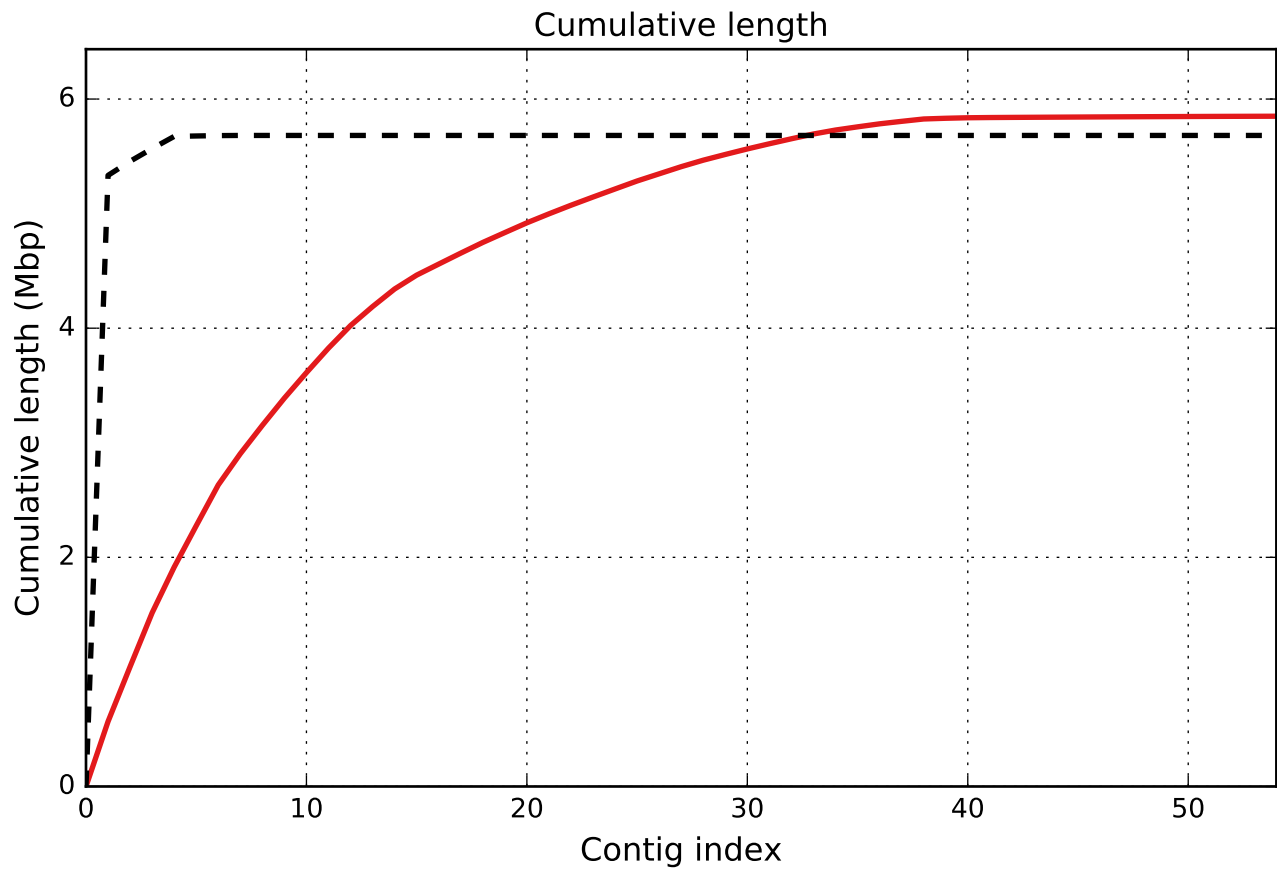


9Btwo\_filtered

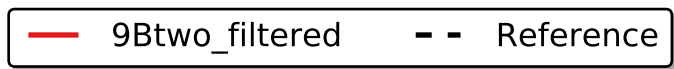
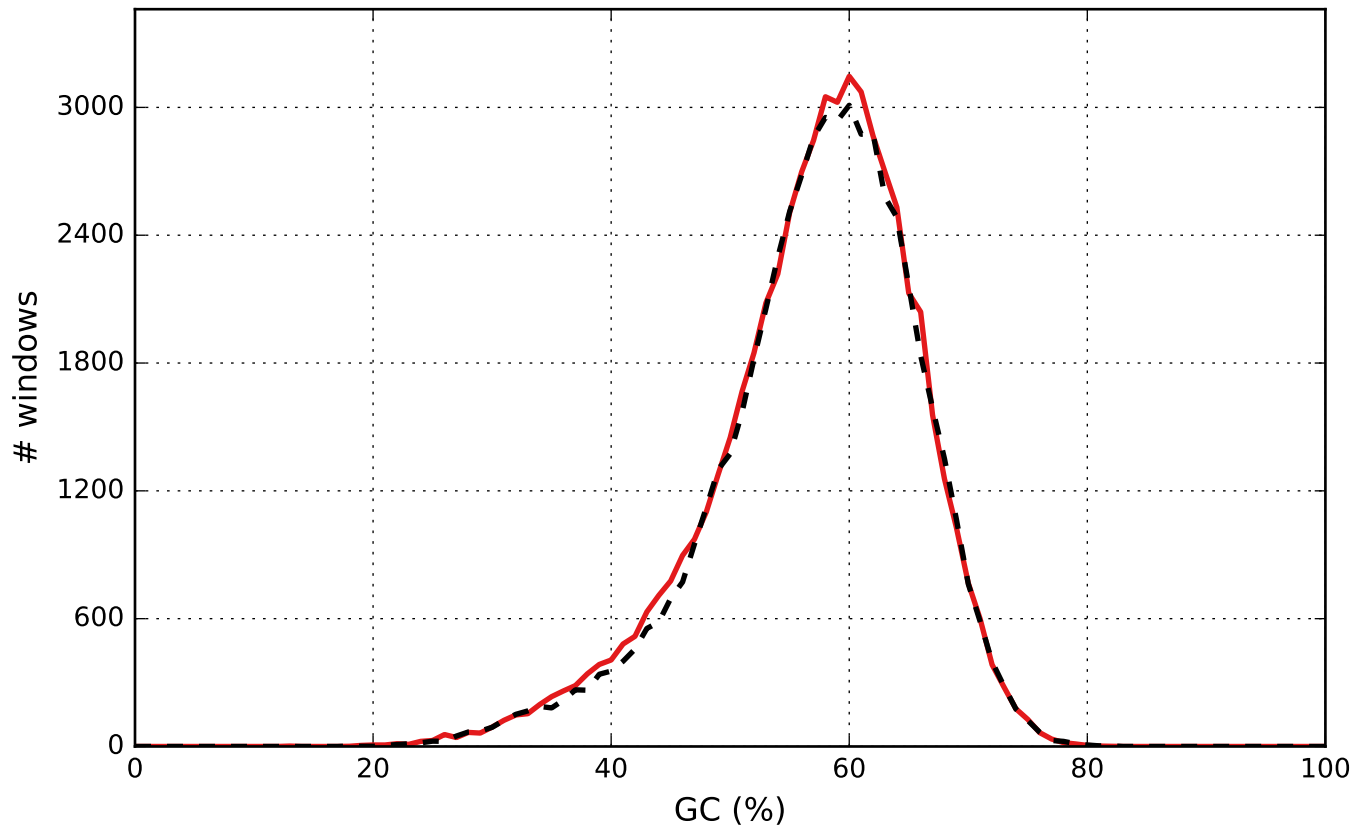
NGx



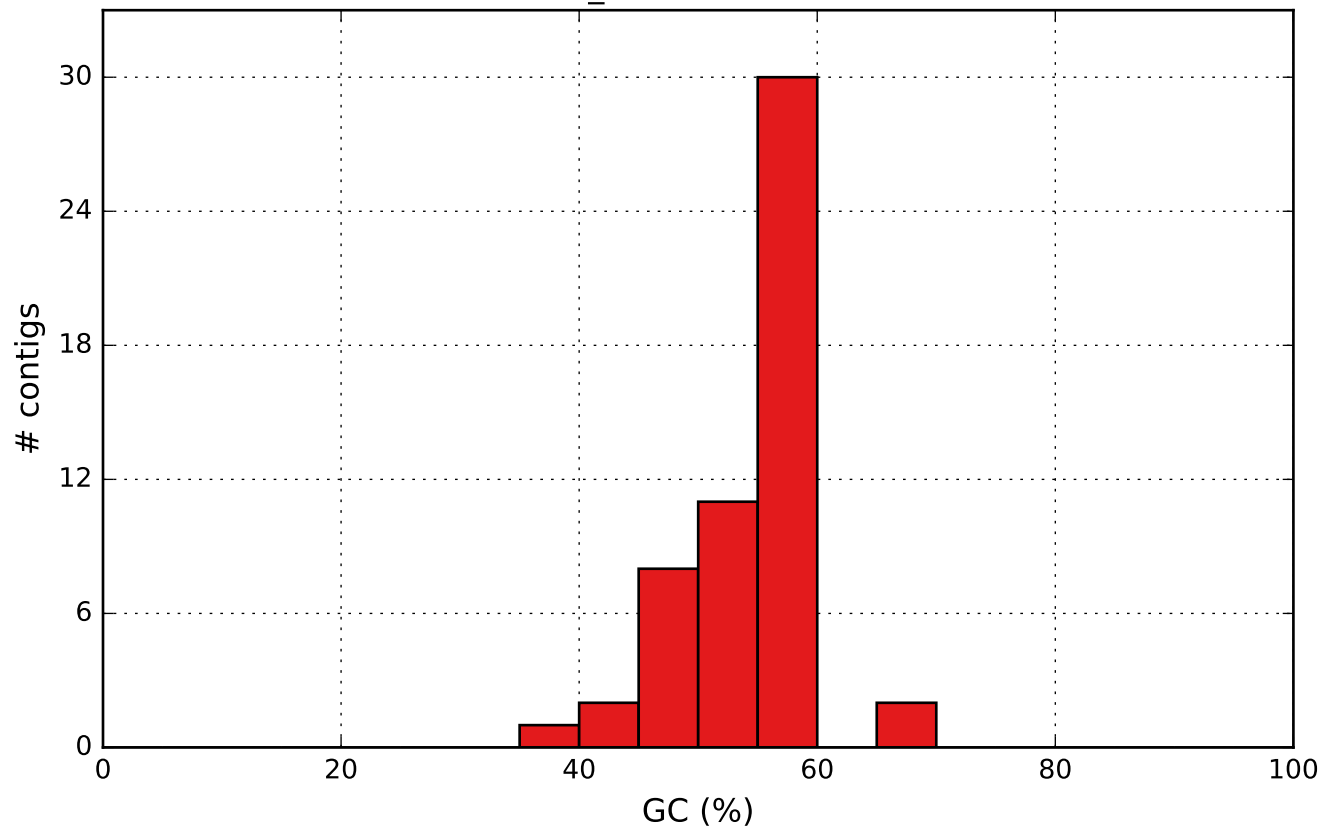
9Btwo\_filtered



GC content



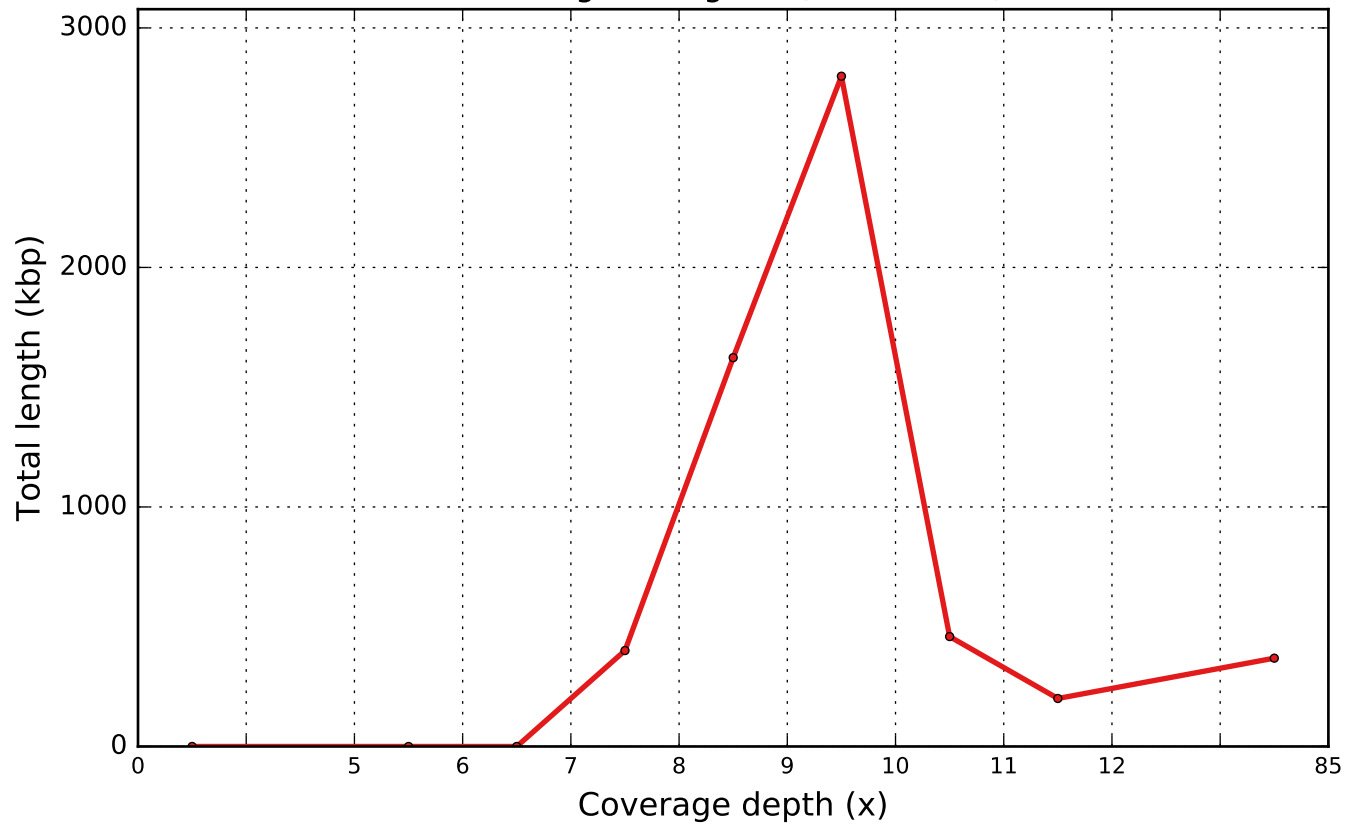
9Btwo\_filtered GC content



9Btwo\_filtered

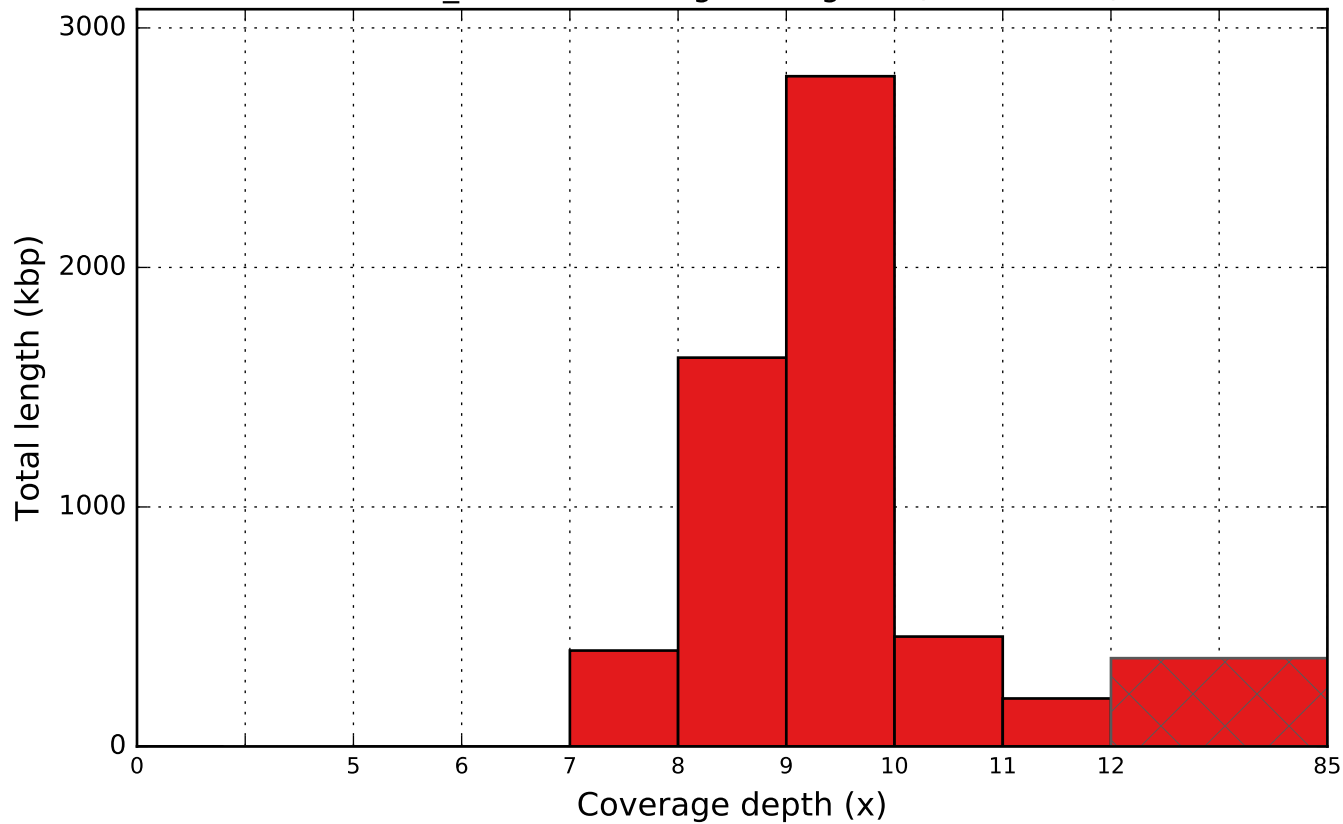


Coverage histogram (bin size: 1x)

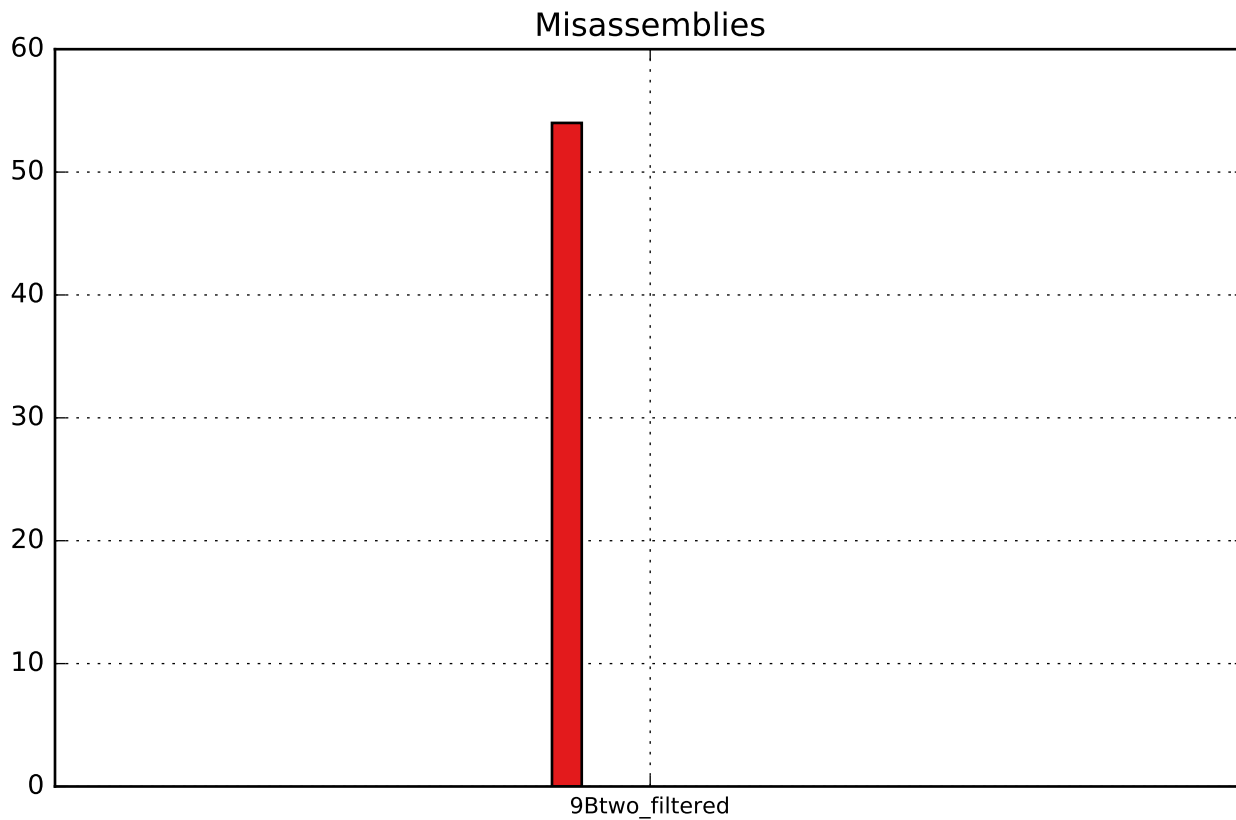


9Btwo\_filtered

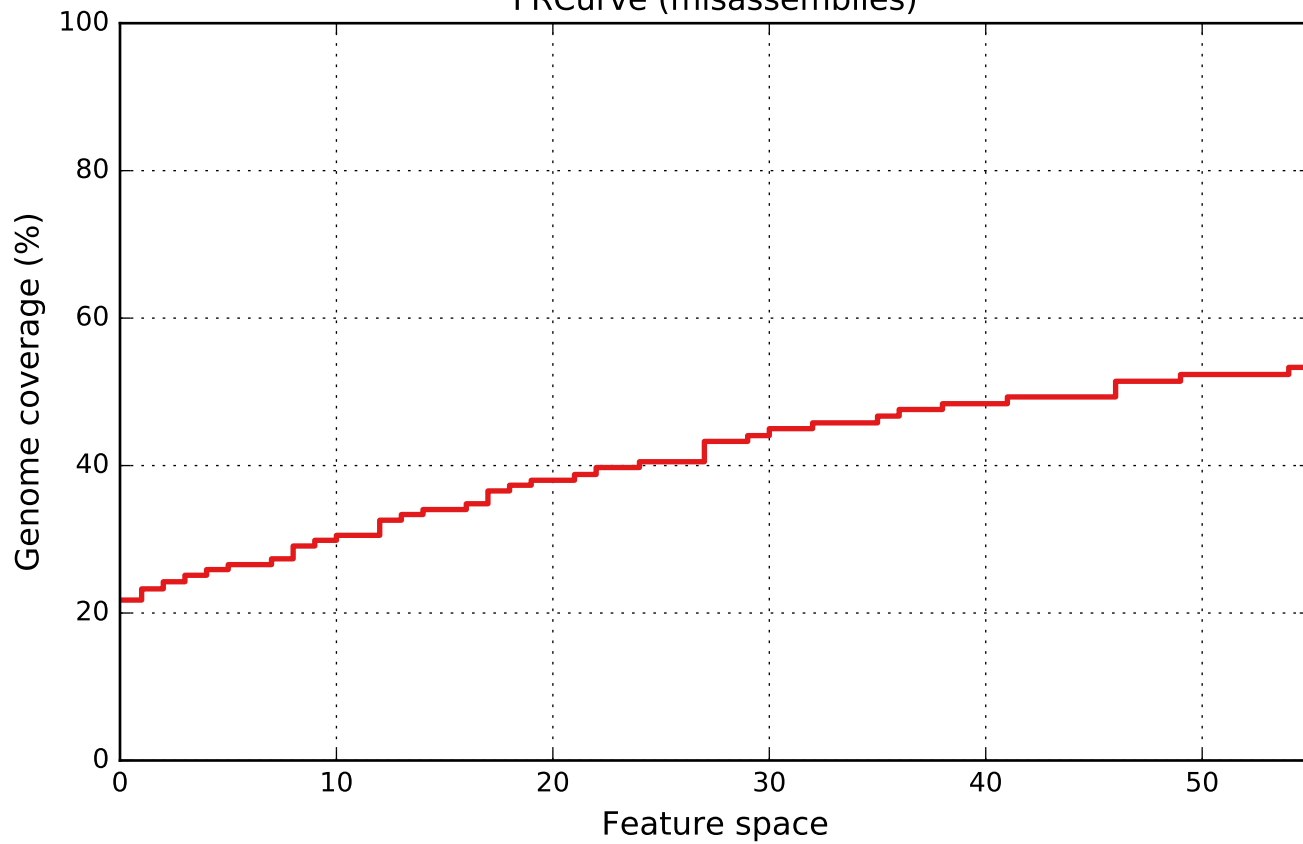
9Btwo\_filtered coverage histogram (bin size: 1x)



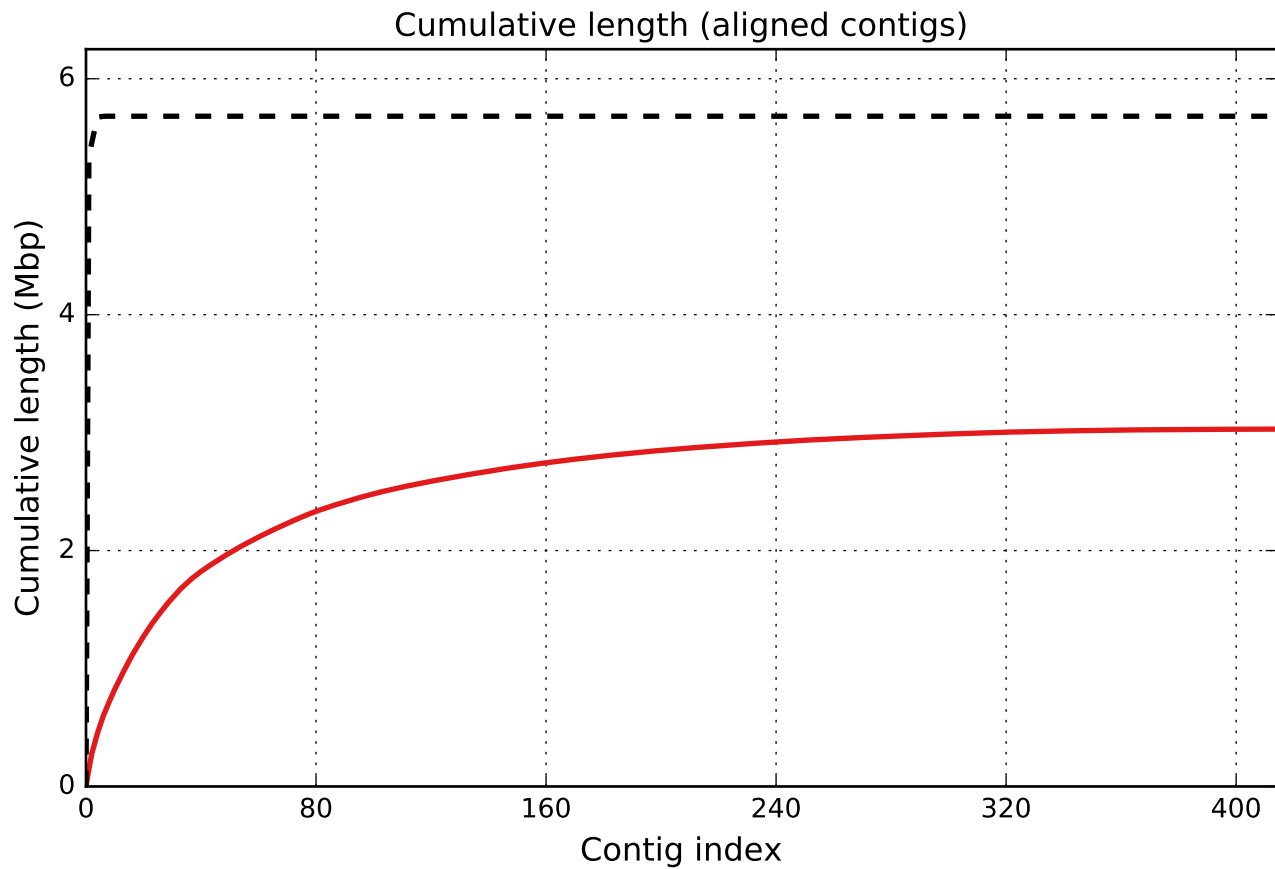
9Btwo\_filtered



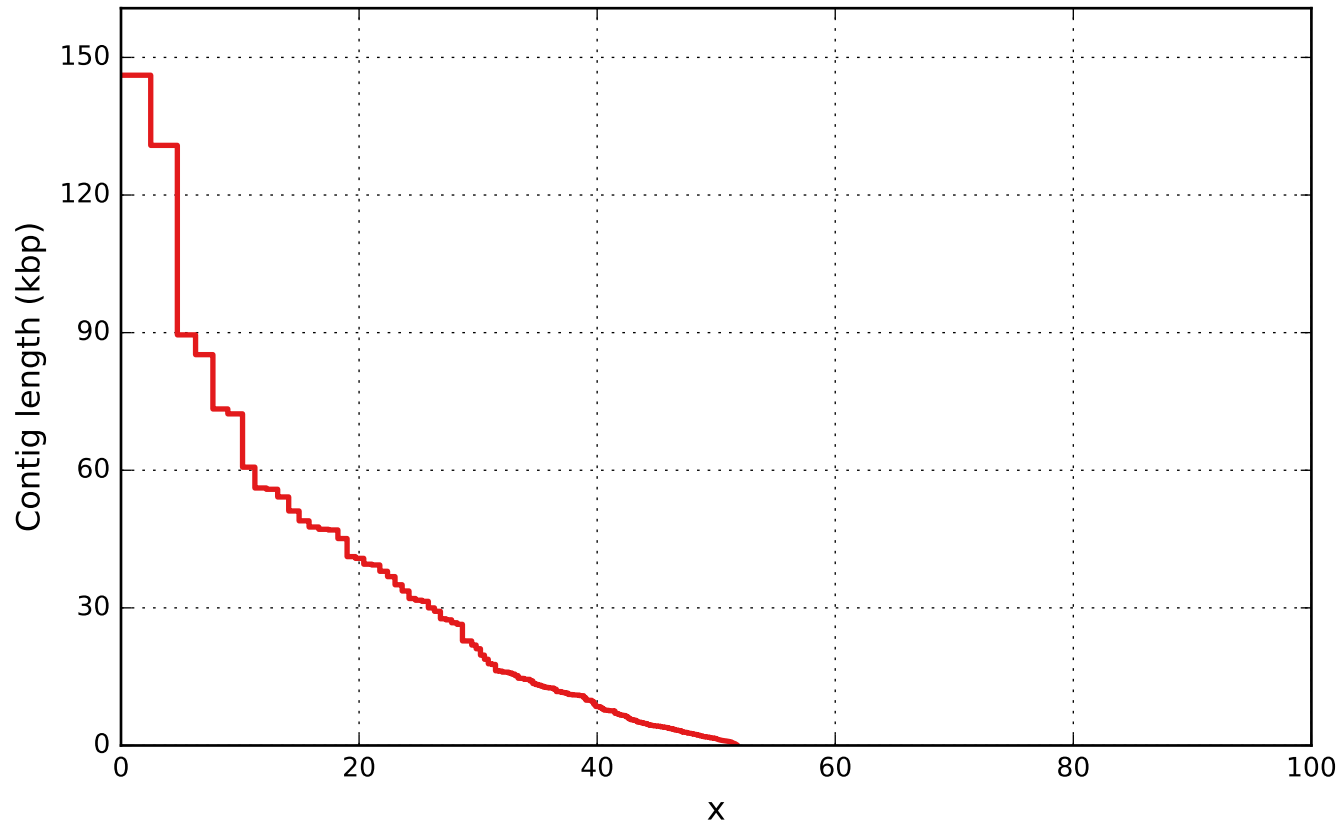
FRCurve (misassemblies)



— 9Btwo\_filtered

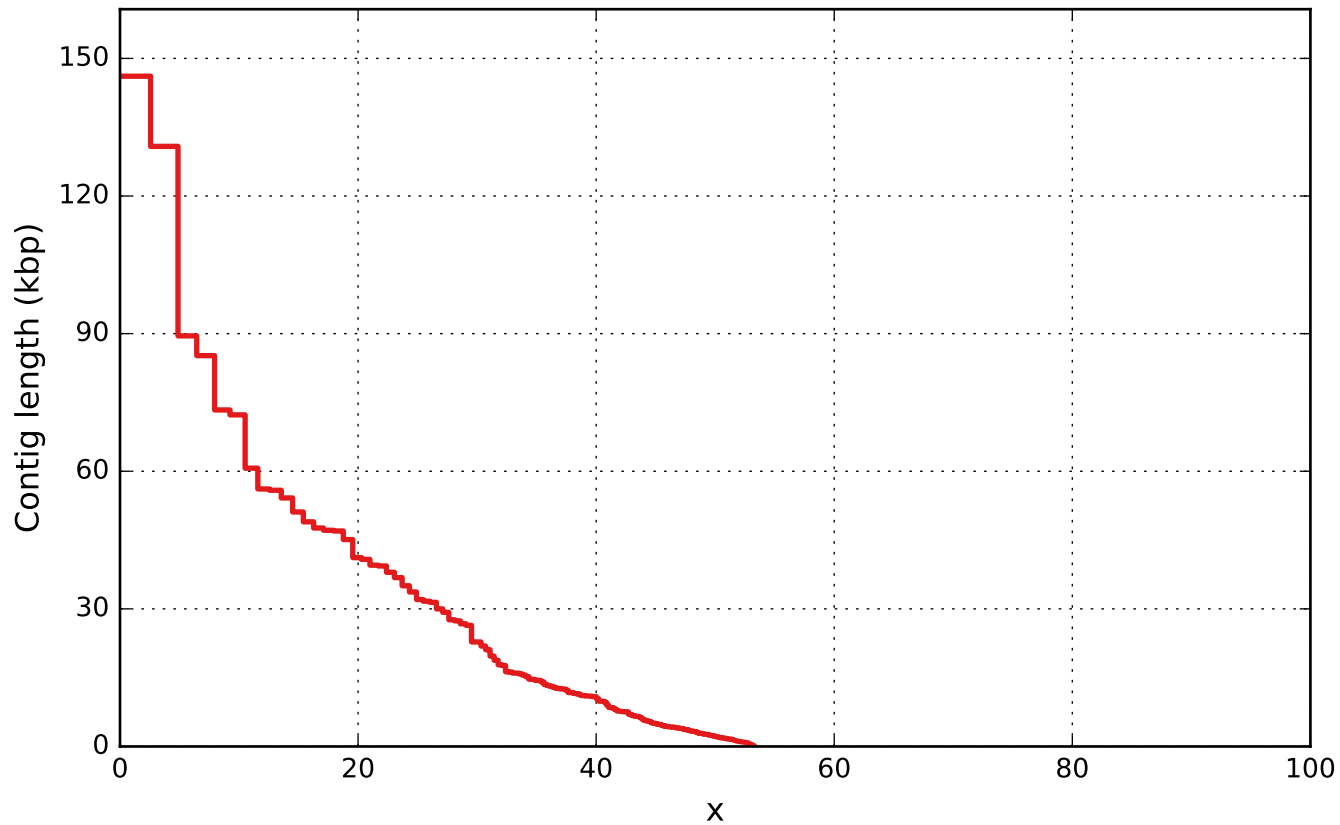


NAx



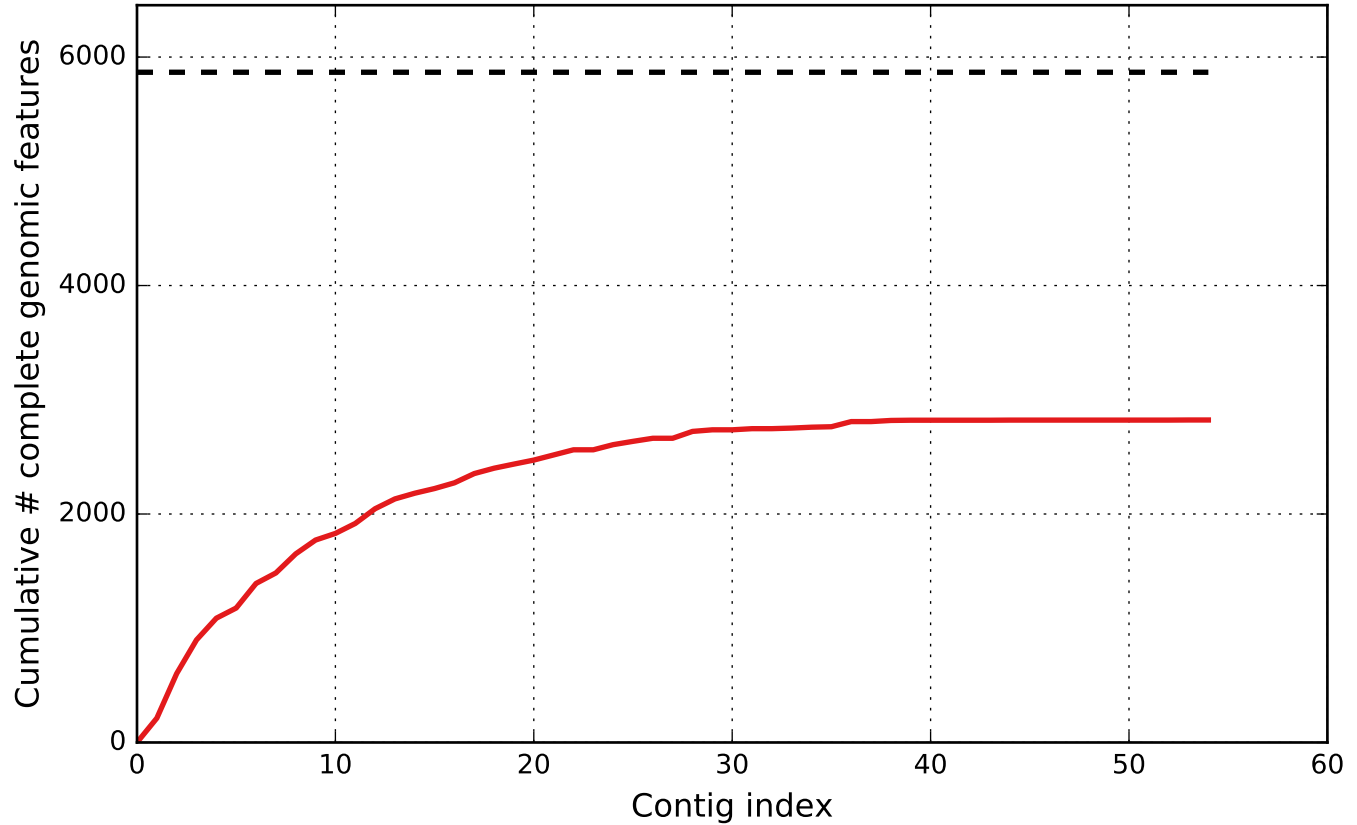
— 9Btwo\_filtered

NGAx



— 9Btwo\_filtered

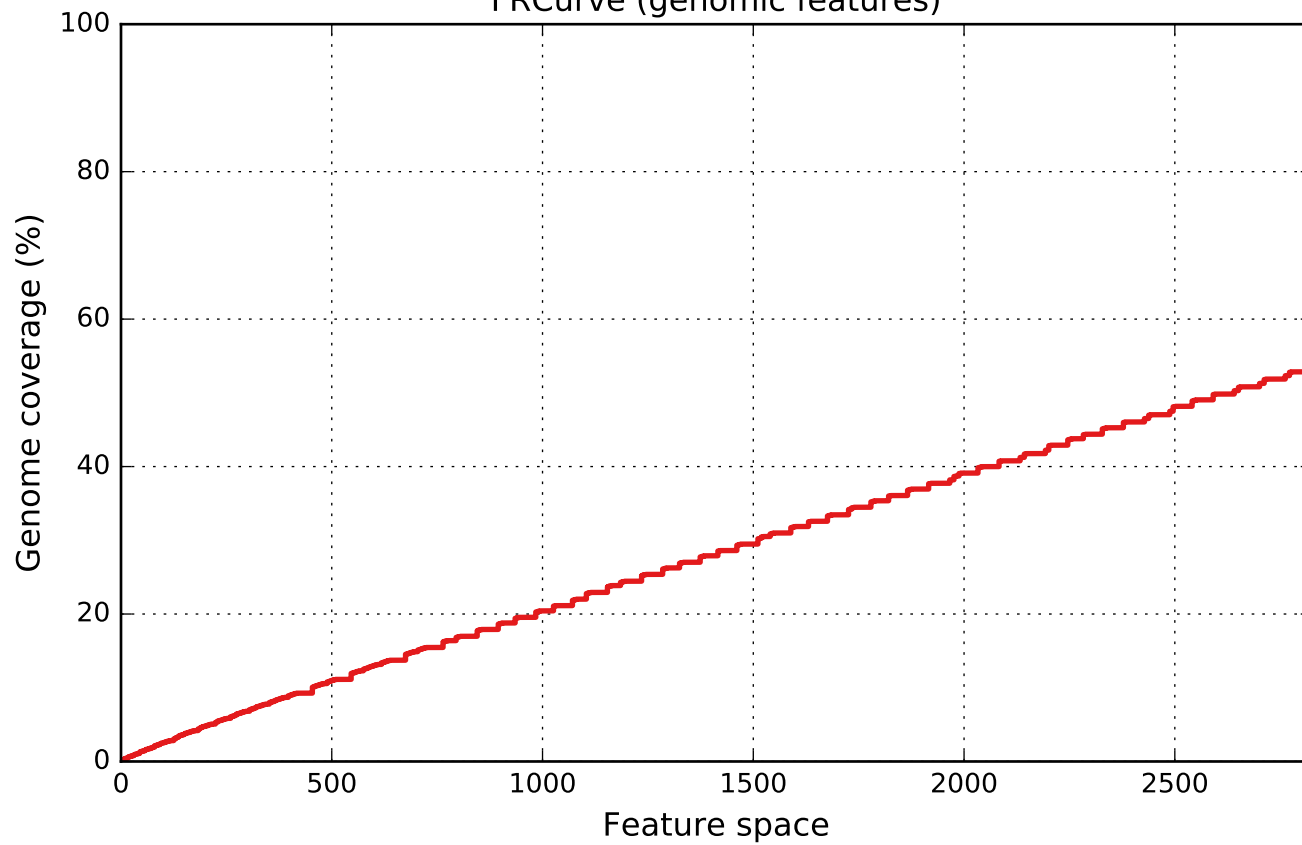
Cumulative # complete genomic features



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FRCurve (genomic features)



— 9Btwo\_filtered