

Report

	Plate4BLANK3.consensus
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29903
Total length (>= 1000 bp)	29903
Total length (>= 5000 bp)	29903
Total length (>= 10000 bp)	29903
Total length (>= 25000 bp)	29903
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29903
Total length	29903
Reference length	29903
GC (%)	38.16
Reference GC (%)	37.97
N50	29903
NG50	29903
N75	29903
NG75	29903
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	30
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	26.422
Duplication ratio	3.785
# N's per 100 kbp	72698.39
# mismatches per 100 kbp	37.97
# indels per 100 kbp	0.00
# genomic features	4 + 16 part
Largest alignment	7901
Total aligned length	7901
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

	Plate4BLANK3.consensus
# 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.	30
# 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

	Plate4BLANK3.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	21739

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



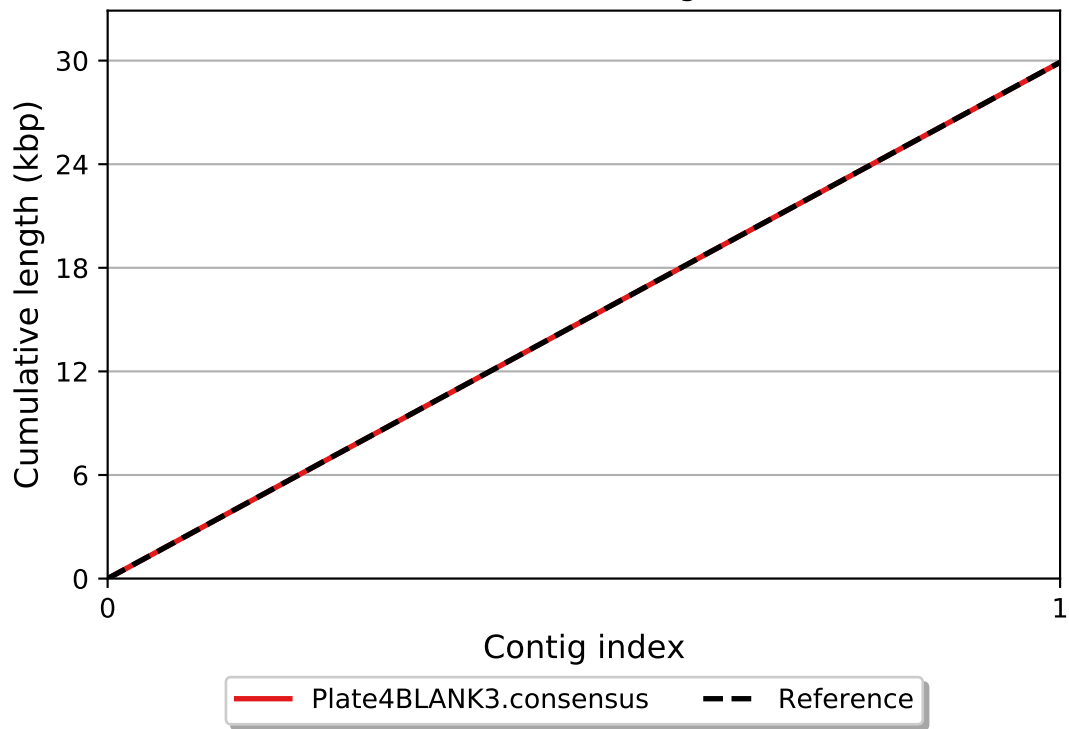
— Plate4BLANK3.consensus

NGx



— Plate4BLANK3.consensus

Cumulative length



GC content

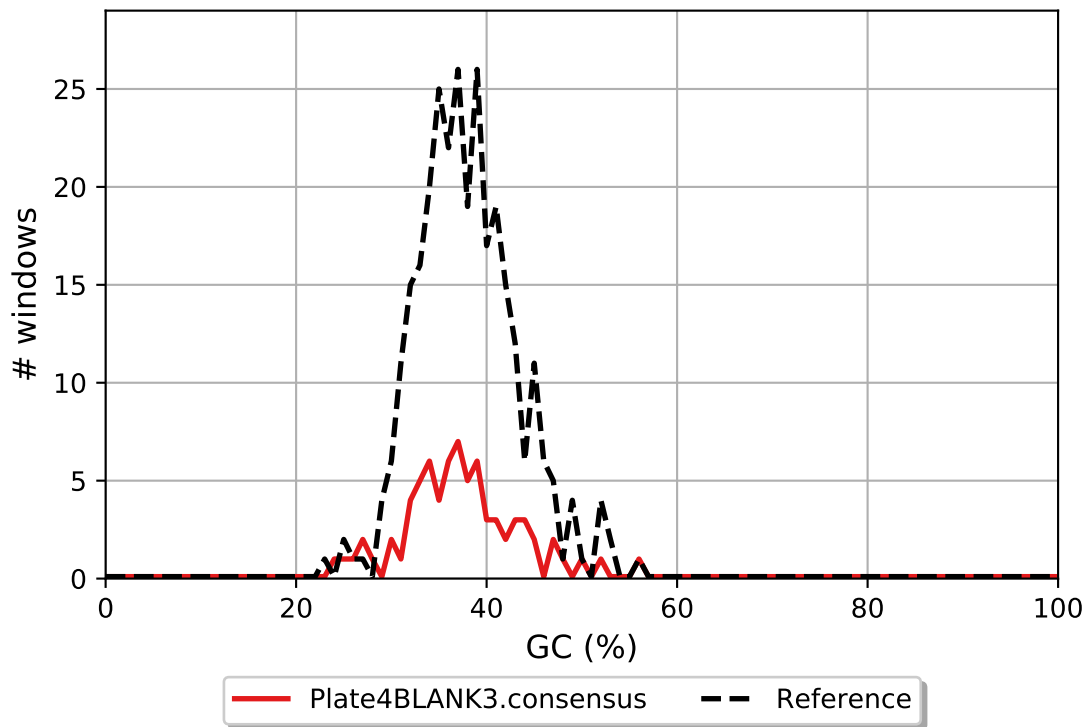


Plate4BLANK3.consensus GC content

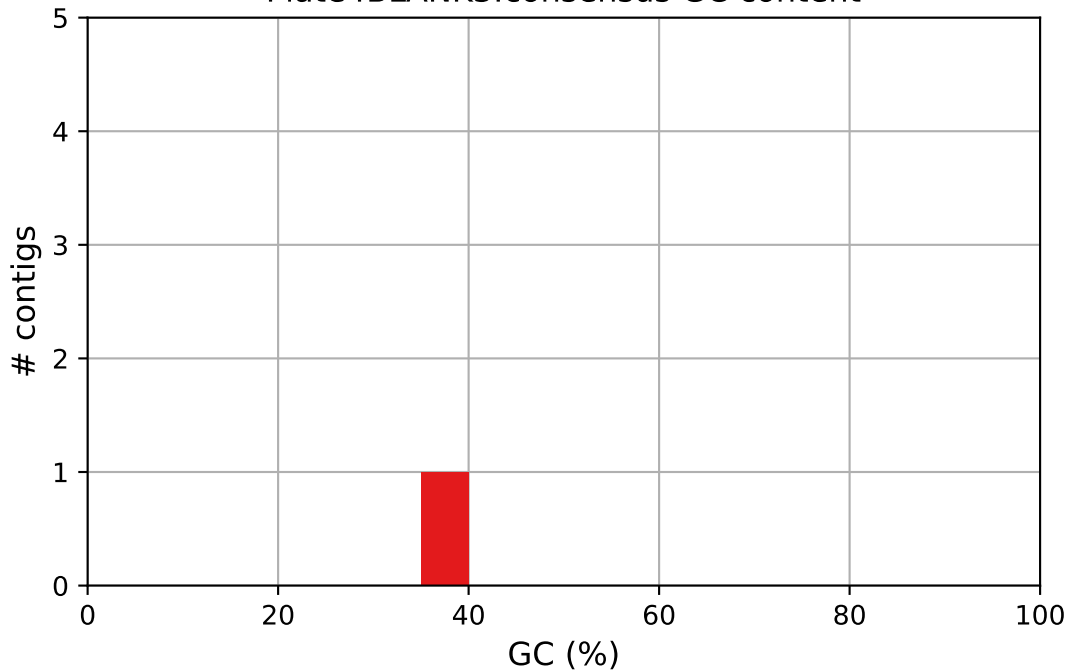
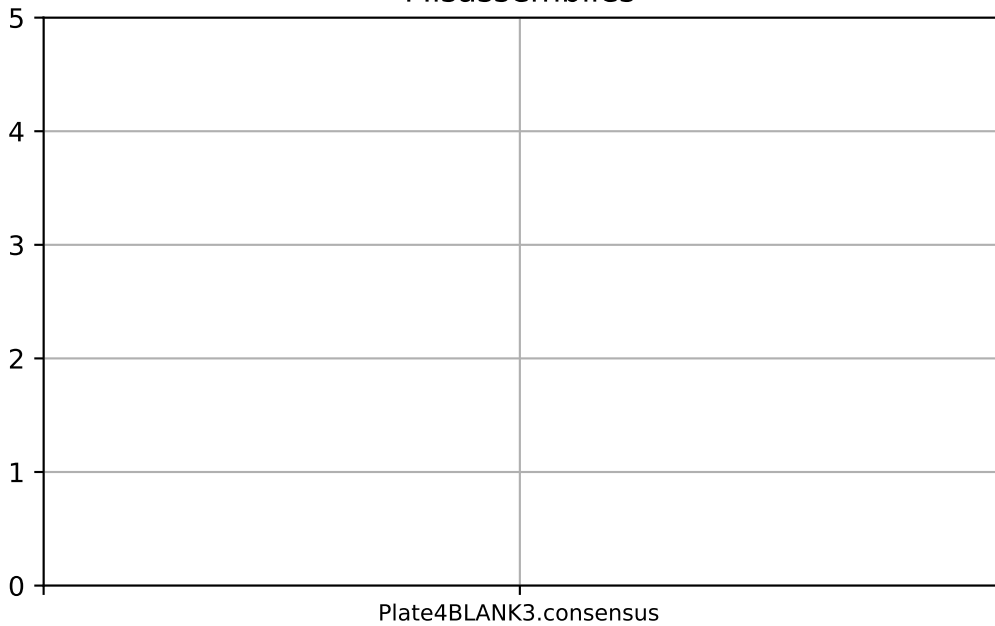
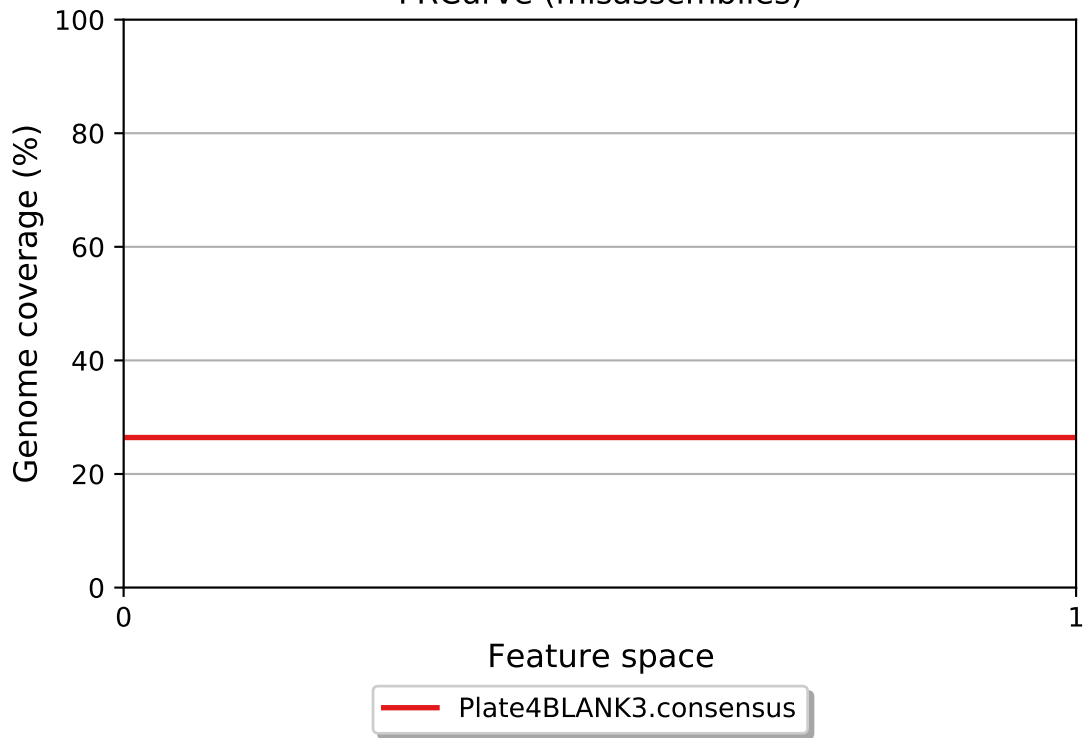


Plate4BLANK3.consensus

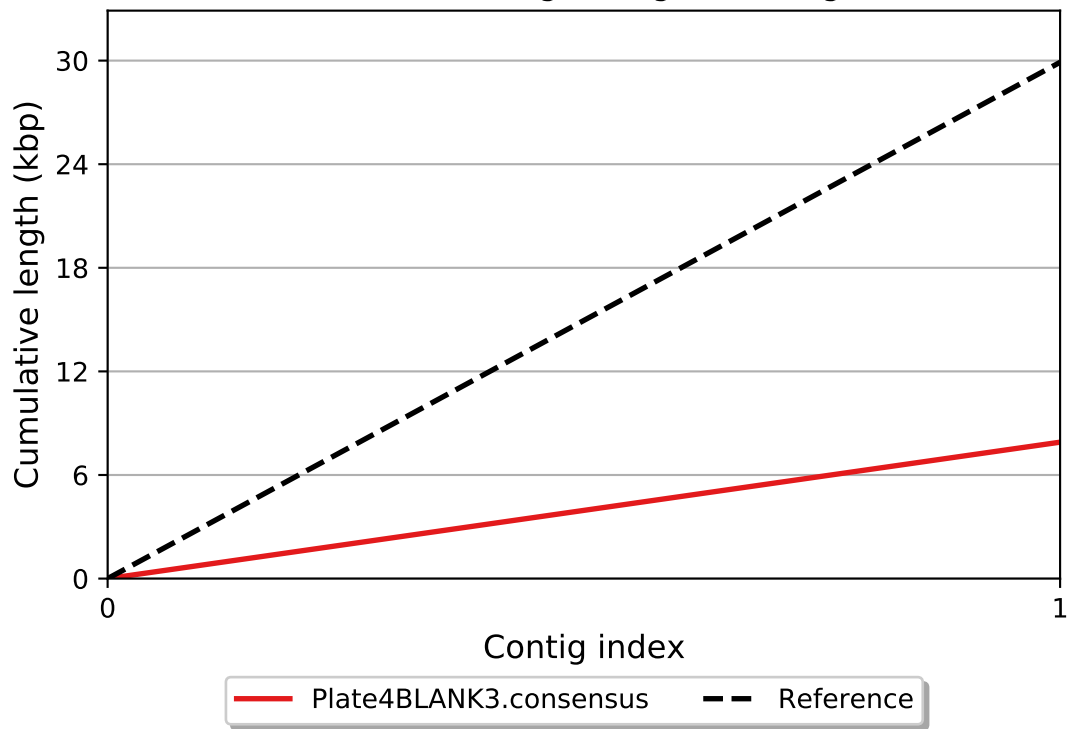
Misassemblies



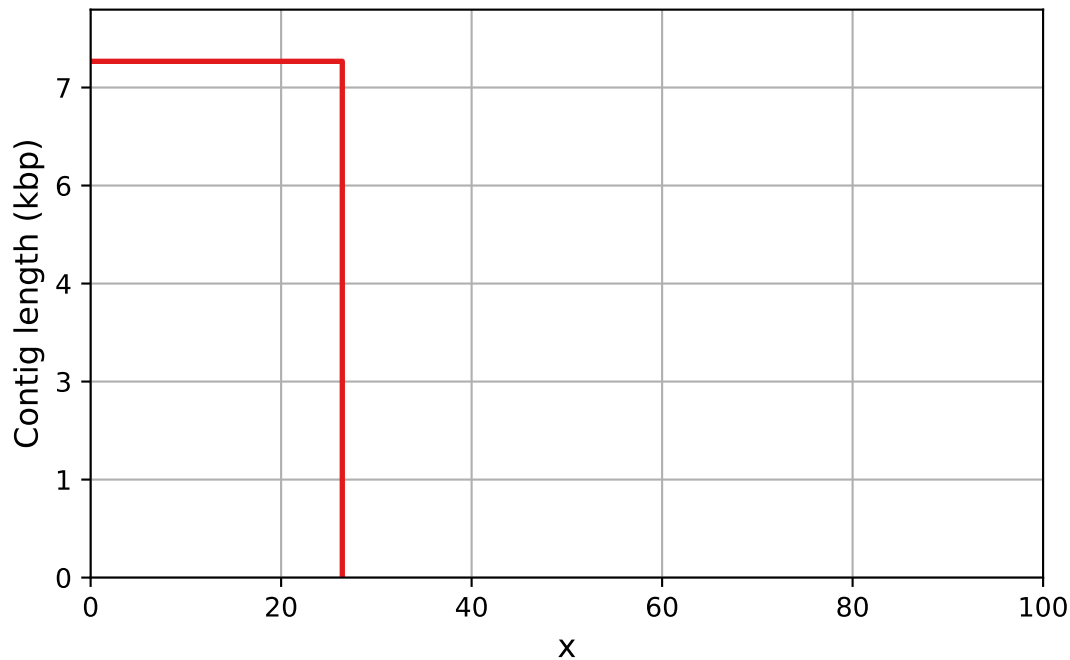
FRCurve (misassemblies)



Cumulative length (aligned contigs)

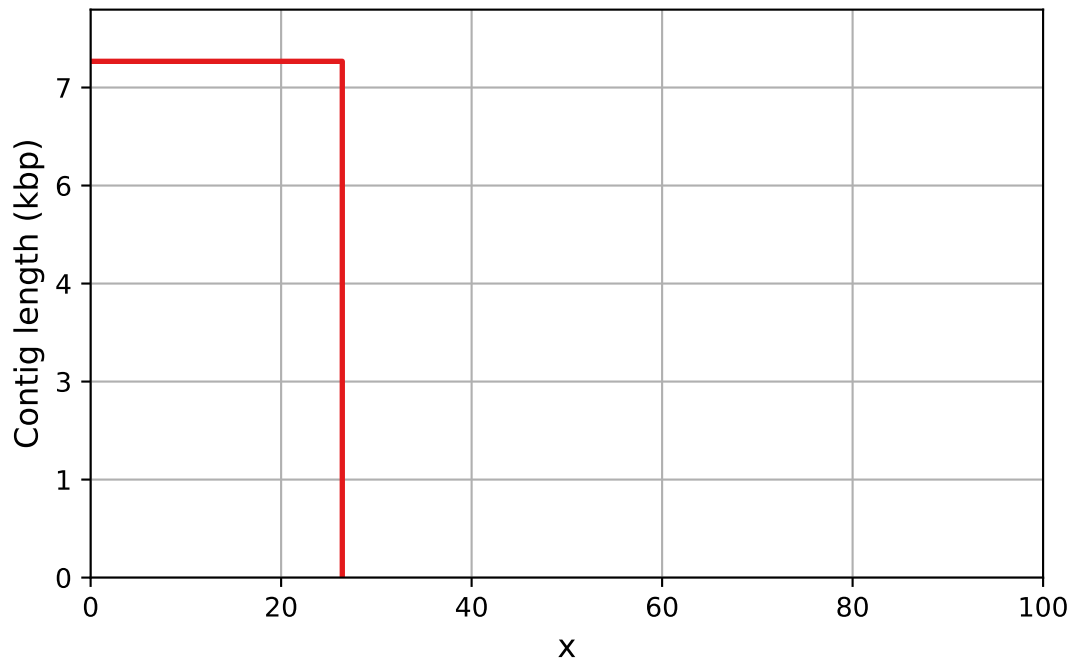


NAx

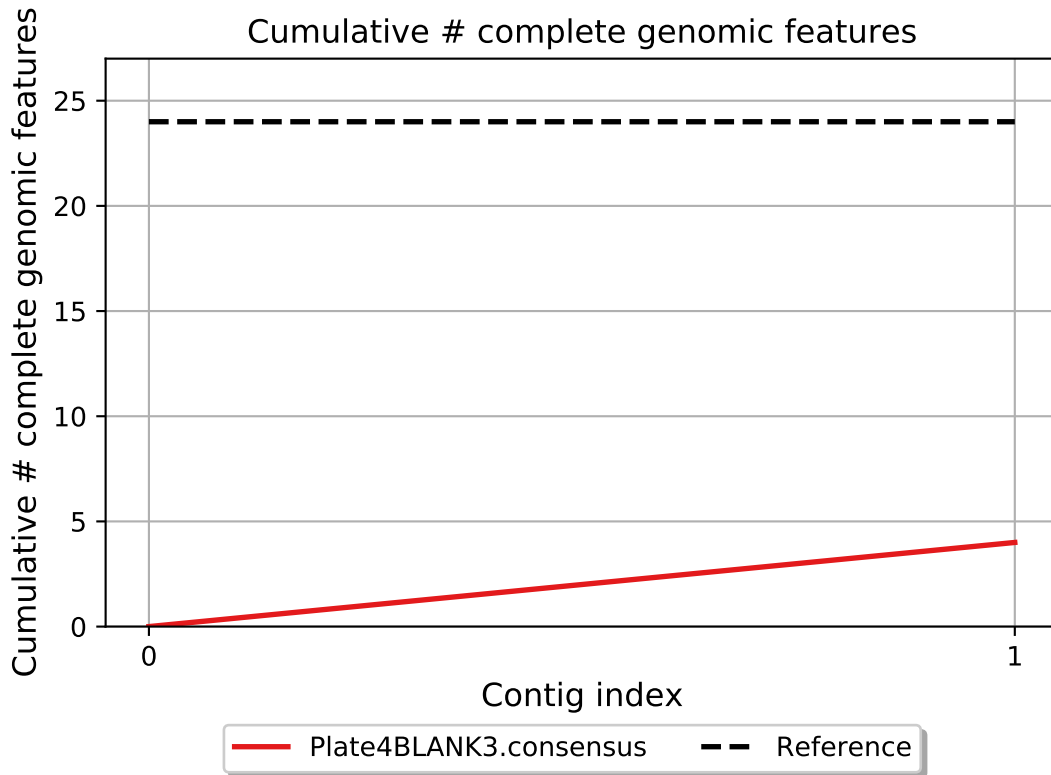


— Plate4BLANK3.consensus

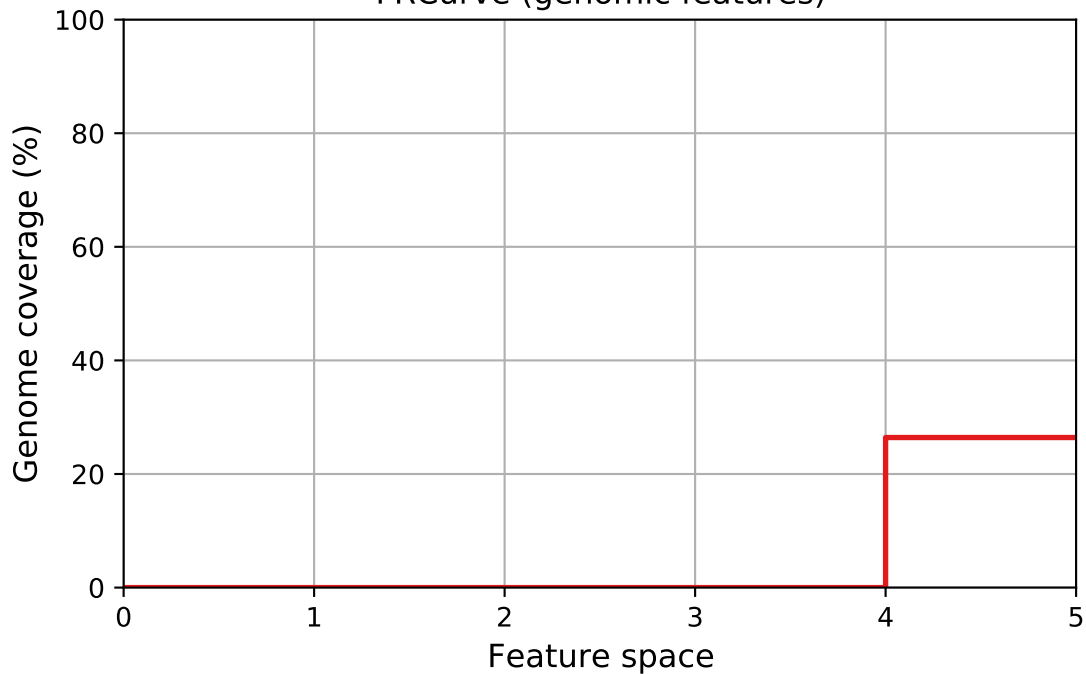
NGAx



— Plate4BLANK3.consensus



FRCurve (genomic features)



— Plate4BLANK3.consensus