

# Report

	Plate4BLANK1.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 (%)	39.90
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.	16
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	10.541
Duplication ratio	9.487
# N's per 100 kbp	88853.96
# mismatches per 100 kbp	126.90
# indels per 100 kbp	0.00
# genomic features	2 + 12 part
Largest alignment	3152
Total aligned length	3152
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

	Plate4BLANK1.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.	16
# unaligned mis. contigs	0
# mismatches	4
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

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

	Plate4BLANK1.consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	26570

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



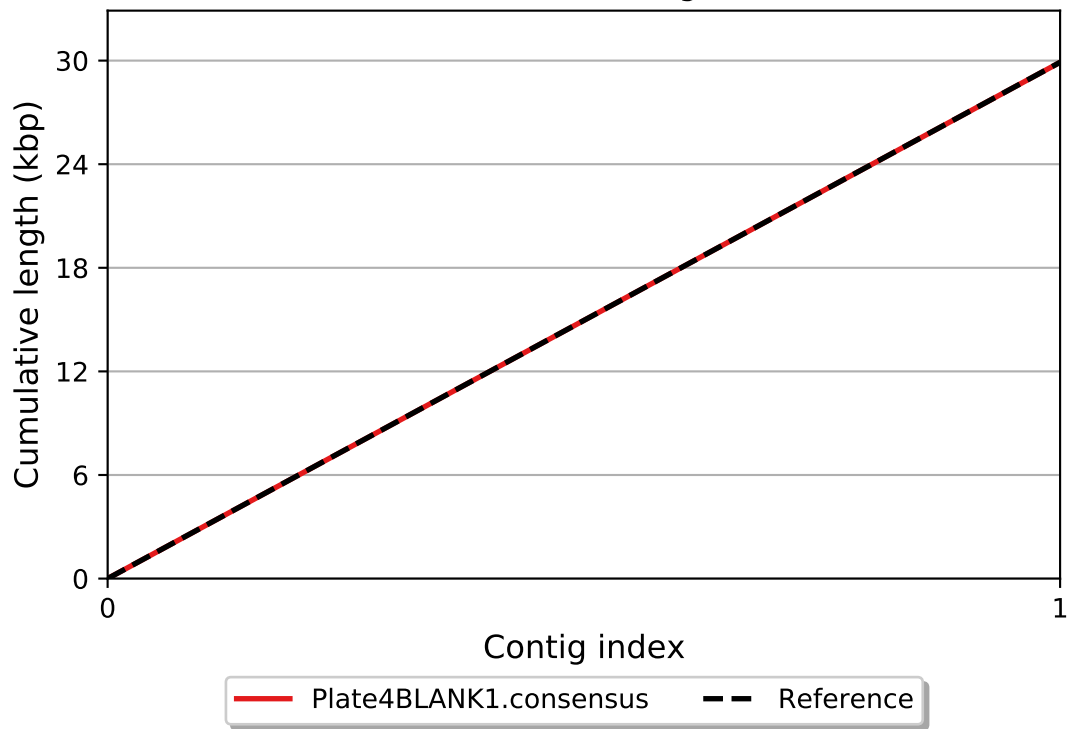
— Plate4BLANK1.consensus

NGx



— Plate4BLANK1.consensus

Cumulative length



## GC content

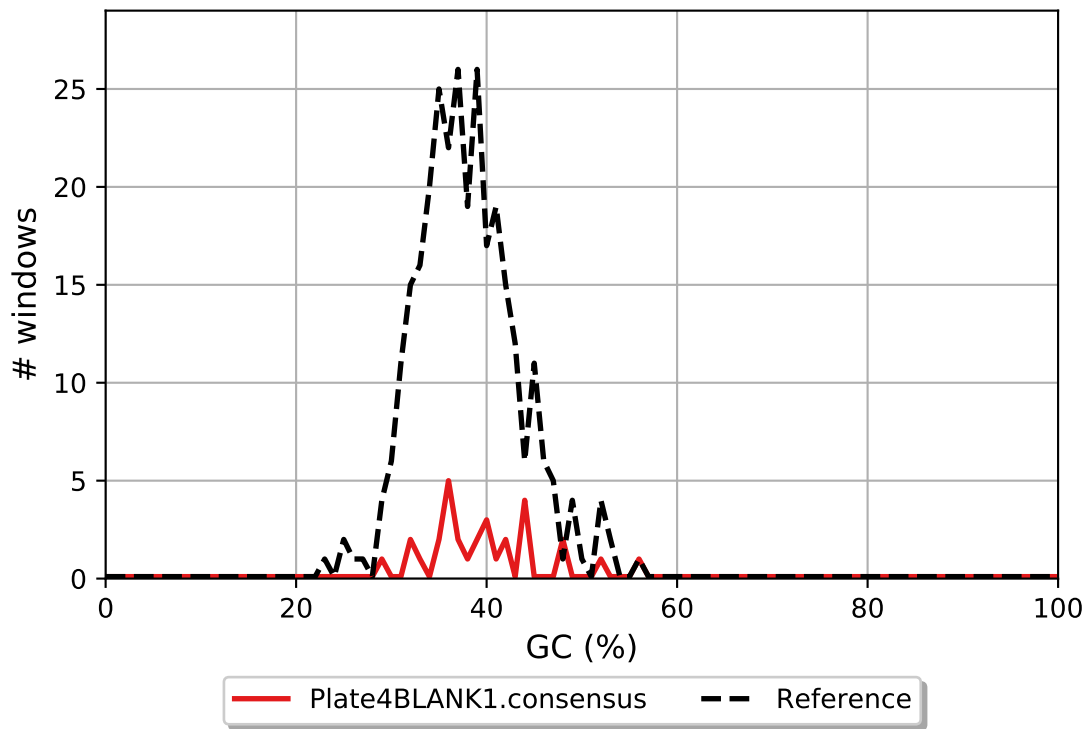


Plate4BLANK1.consensus GC content

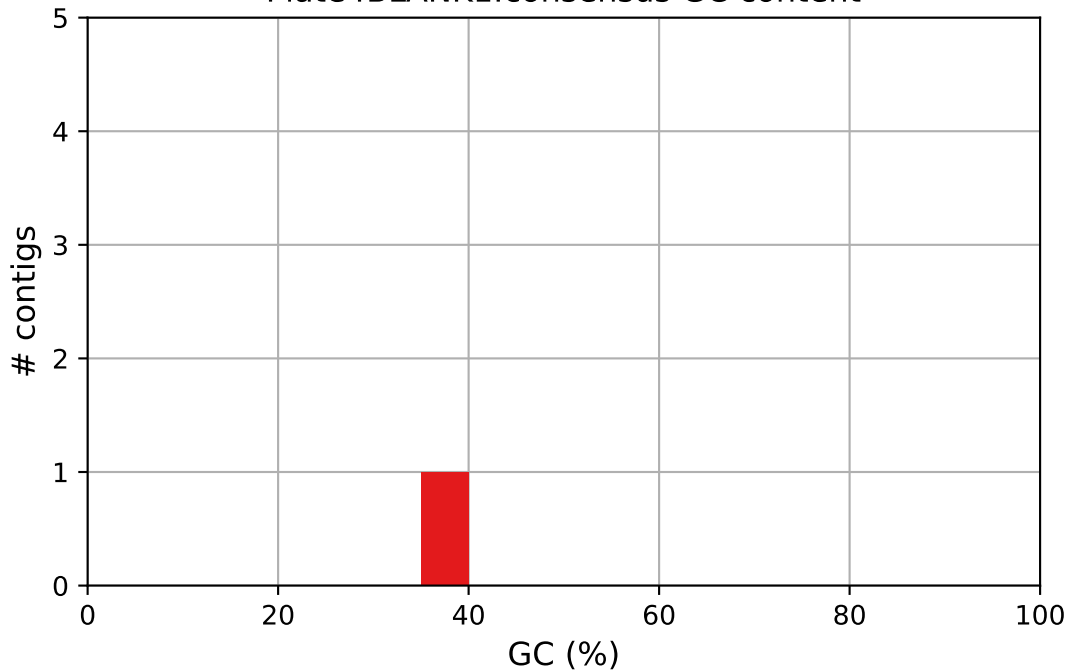
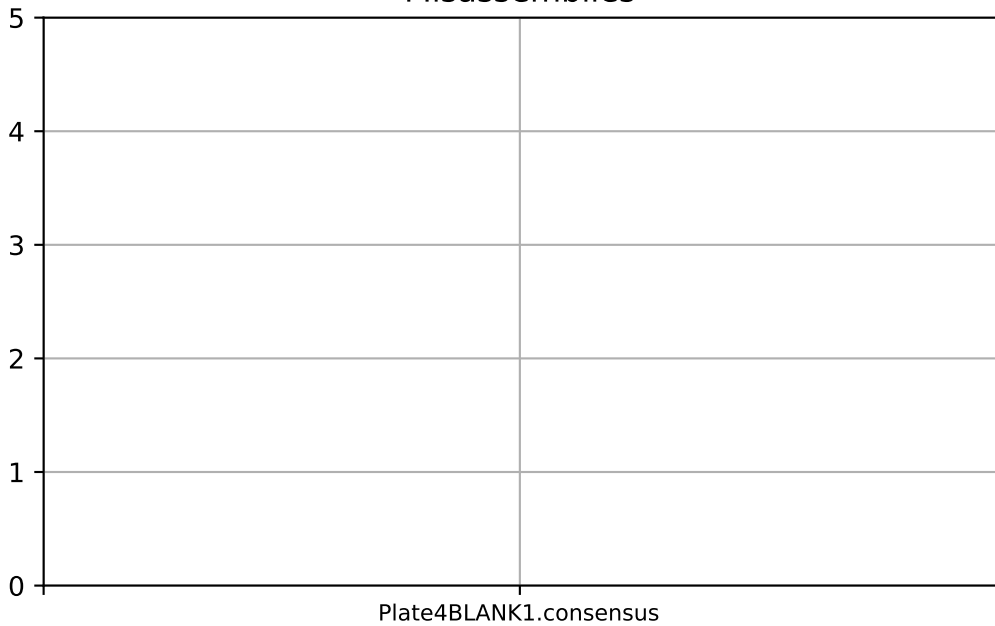


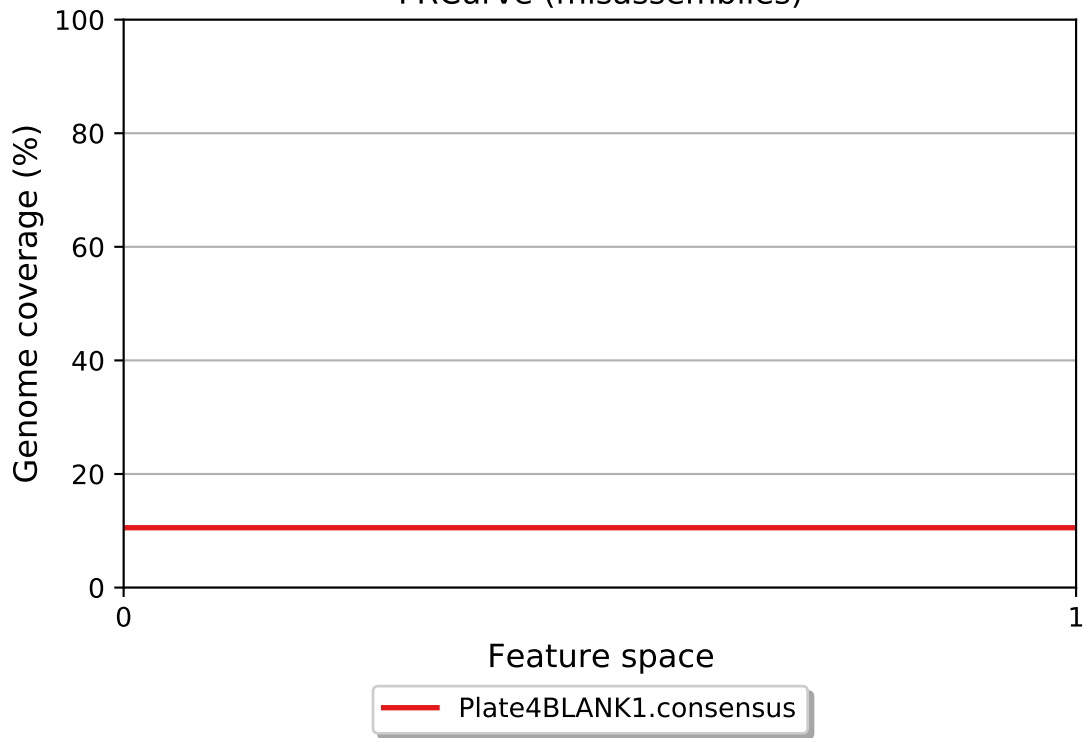
Plate4BLANK1.consensus



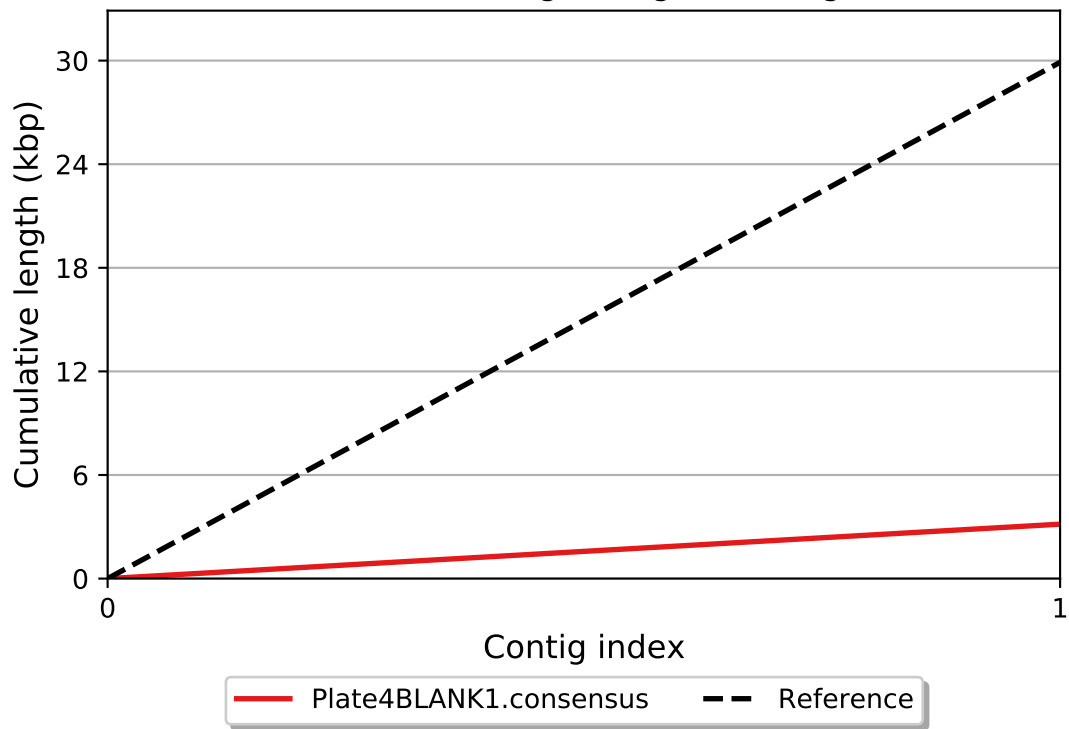
## Misassemblies



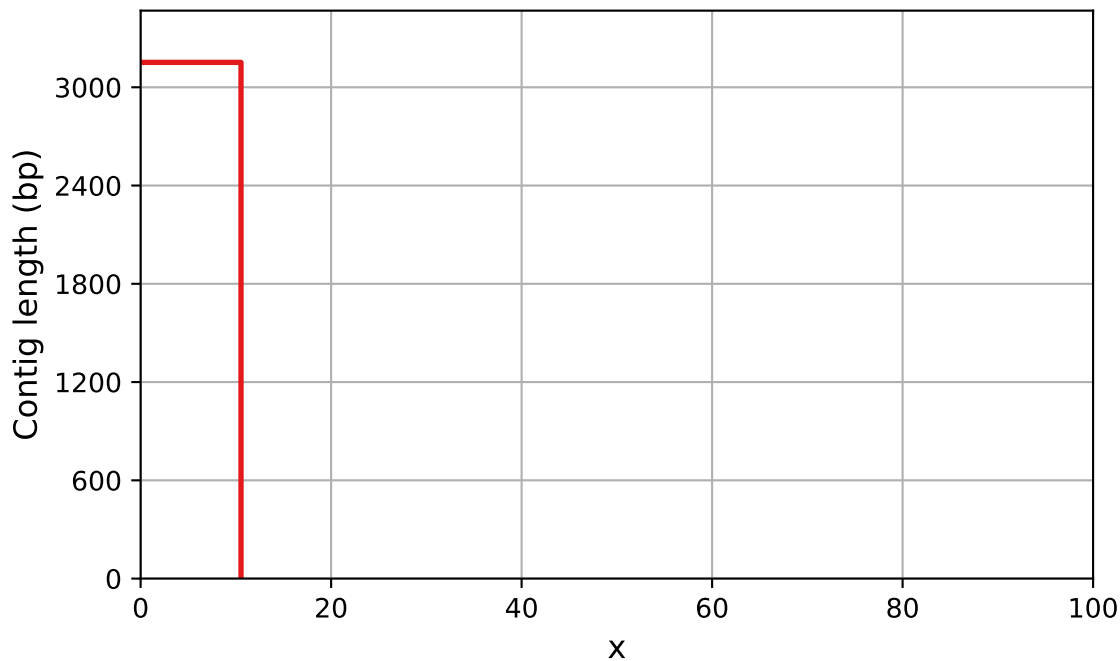
FRCurve (misassemblies)



Cumulative length (aligned contigs)

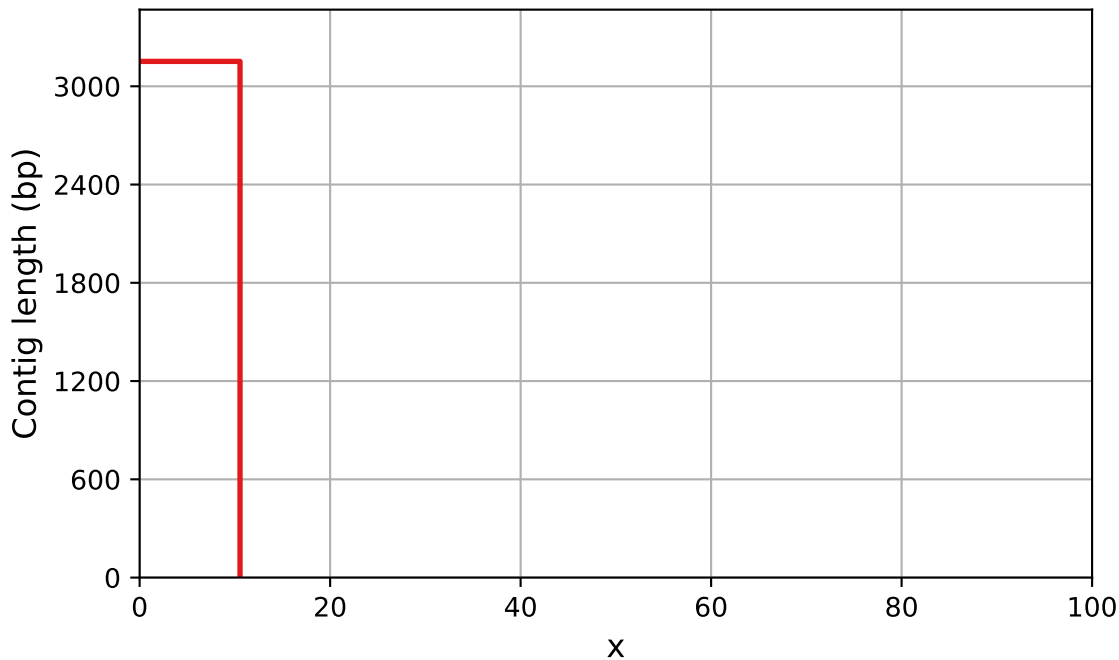


NAx

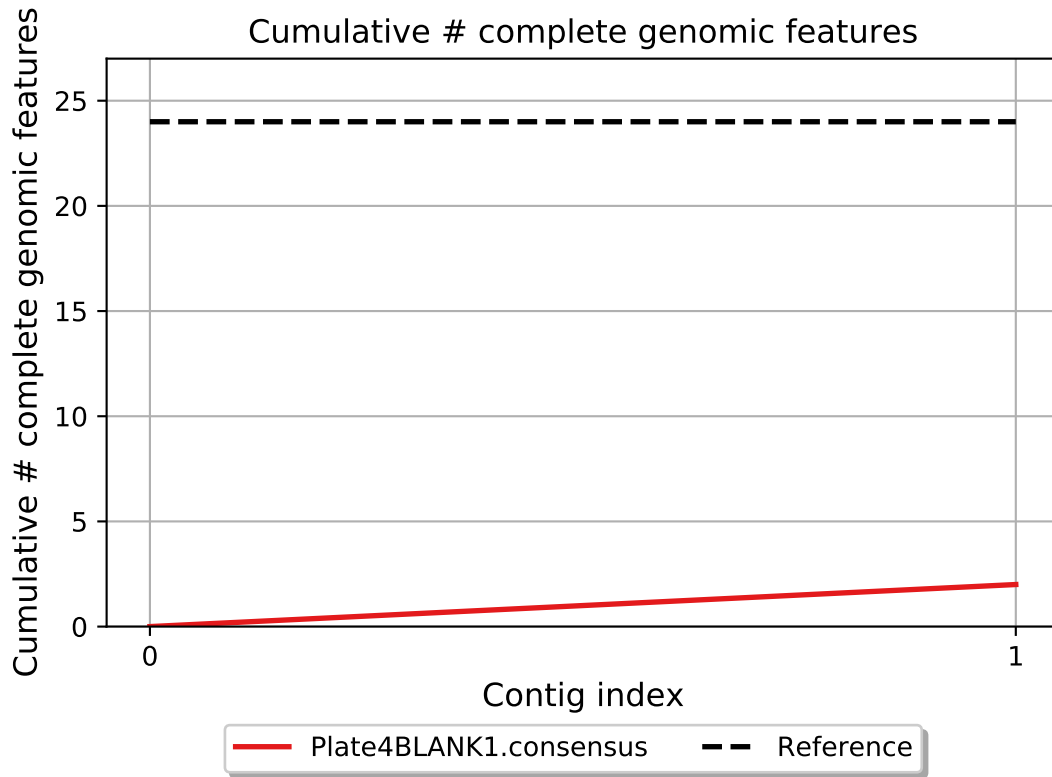


— Plate4BLANK1.consensus

## NGAx



— Plate4BLANK1.consensus



FRCurve (genomic features)



— Plate4BLANK1.consensus