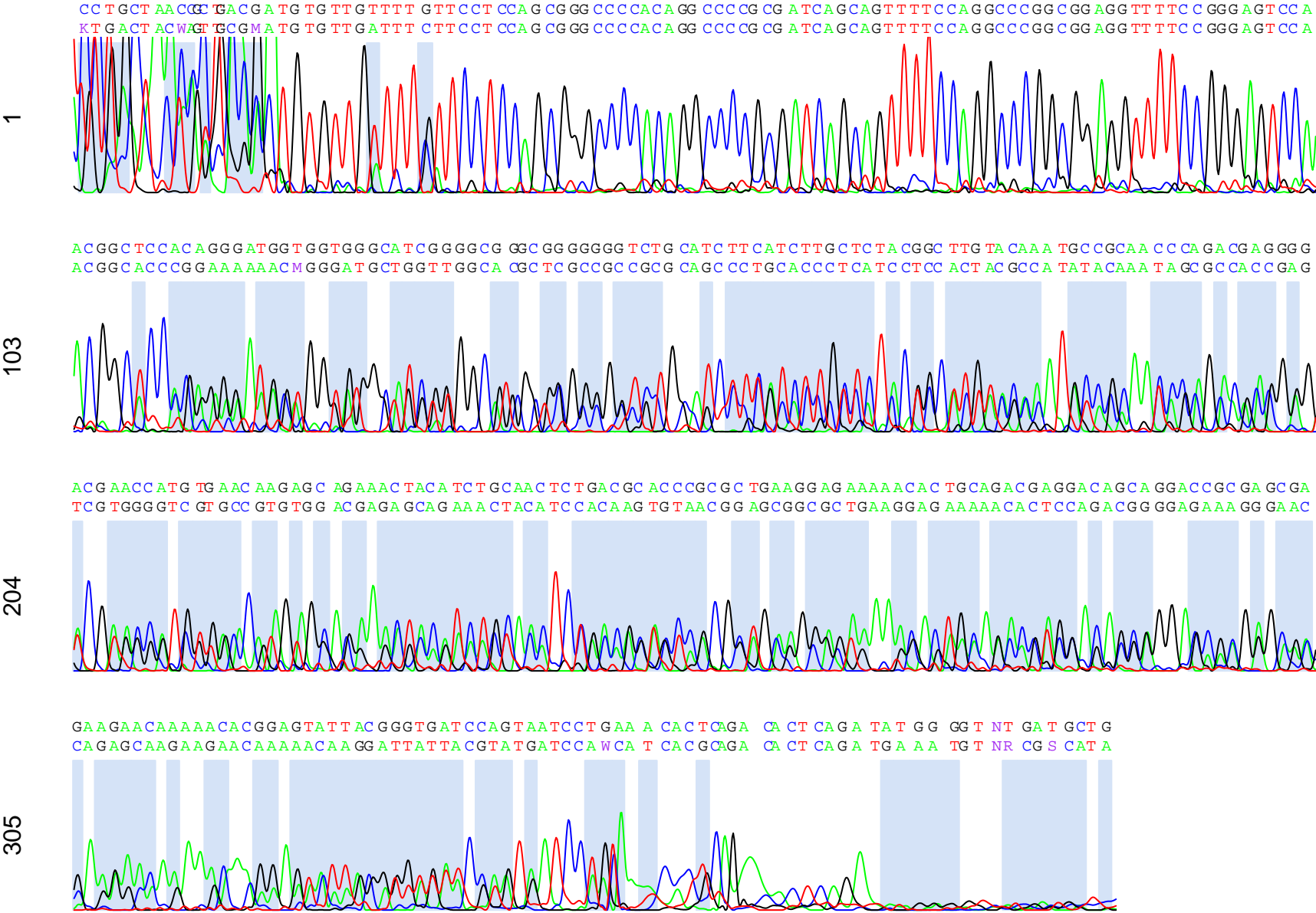


Chromatogram



## Alignment

Warning in setAllelePhase(data, refseq, trim5, trim3): Reference sequence does not encompass sequencing results.  
Ambiguous bases will be attributed to both alleles outside the region covered by the reference sequence.

Alt Allele	1	BYKRCTAMHMGYTGCGRATGTGTTGATTTCTTCCTCCAGCGGGCCCCACAGGCCCCGCGATCAGCAGTTTTCCAGGCCCG	80
Reference	31	BYKRCTAMHMGYTGACCATGTGTTGTTTGTTCCTCCAGCGGGCCCCACAGGCCCCGCGATCAGCAGTTTTCCAGGCCCG	110
Alt Allele	81	GCGGAGGTTTTCCGGGAGTCCAACGGCTCCCGGAAAAAACMGGGATGCTGGTGGGCA-CGCTGGCGGGCGCGCAGCTCTG	159
Reference	111	GCGGAGGTTTTCCGGGAGTCCAACGGCACC-----ACAGGGATGGTGGTGGGCATCG-TGGCGGGCGCGCGCTCTG	181
Alt Allele	160	CATCCTCATCCTGCTCTACGCCATGTACAAATACCGCCACCGAGACGAGGGGTCTGACCATGTGGACGAGAGCAGAACT	239
Reference	182	CATCCTCATCCTGCTCTACGCCATGTACAAATACCGCAACCGAGACGAGGGGTCTGACCATGTGGACGAGAGCAGAACT	261
Alt Allele	240	ACATCTGCAACTCTAACGGAGCGGCGCTGAAGGAGAAAAACACTGCAGACGA-----GGASMRMGRGMRMSARRMM	311
Reference	262	ACATCTGCAACTCCAACGGAGCCGCGCTGAAGGAGAAAAACACTGCAGACGACGACGCGGGASMRMGRGMRMSARRMM	341
Alt Allele	312	ARAARMACRRARWMWWSRKKKWWCSWRTRATCCWDMAWCACKCAGACACTCAGATWRRKGTNDSRBSMTR	384
Reference	342	ARAARMACRRARWMWWSRKKKWWCSWRTRATCCWDMAWCACKCAGACACTCAGATWRRKGTNDSRBSMTR	414

## Alternative allele

BYKRCTAMHMGYTGCGRATGTGTTGATTTCTTCCTCCAGCGGGCCCCACAGGCCCCGCGATCAGCAGTTTTCCAGGCCCGCGGAGGTTTTCCGGGAGTCCAACGGCTCCCGGAAAAAAC  
MGGGATGCTGGTGGGCACGCTGGCGGGCGCGCAGCTCTGCATCCTCATCCTGCTCTACGCCATGTACAAATACCGCCACCGAGACGAGGGGTCTGACCATGTGGACGAGAGCAGAACTA  
CATCTGCAACTCTAACGGAGCGGCGCTGAAGGAGAAAAACACTGCAGACGAGGASMRMGRGMRMSARRRMMARAARMACRRARWMWWSRKKKWWCSWRTRATCCWDMAWCACKCAGAC  
ACTCAGATWRRKGTNDSRBSMTR

## Reference sequence

GCTAGYAKCTRYAGYTRTSTATMWMWTVAWBYKRCTAMHMGYTGACCATGTGTTGTTTGTTCCTCCAGCGGGCCCCACAGGCCCCGCGATCAGCAGTTTTCCAGGCCCGCGGAGGTTT  
TCCGGGAGTCCAACGGCACACAGGGATGGTGGTGGGCATCGTGGCGGGCGCGGCGCTCTGCATCCTCATCCTGCTCTACGCCATGTACAAATACCGCAACCGAGACGAGGGGTCTGACC  
ATGTGGACGAGAGCAGAACTACATCTGCAACTCCAACGGAGCCGCGCTGAAGGAGAAAAACACTGCAGACGACGACGCGGGASMRMGRGMRMSARRRMMARAARMACRRARWMWWSR  
KKKWWCSWRTRATCCWDMAWCACKCAGACACTCAGATWRRKGTNDSRBSMTRYTMHTMHTACKHMDWCMGAAKMKAMGAA

## Alignment parameters

```
#####  
# Program: Biostrings (version 2.42.1), a Bioconductor package  
# Rundate: Fri Jul 23 07:45:25 2021  
#####  
#=====  
#  
# Aligned_sequences: 2  
# 1: Alt Allele  
# 2: Reference  
# Matrix: NA  
# Gap_penalty: 12.0  
# Extend_penalty: 2.0  
#  
# Length: 393  
# Identity:      362/393 (92.1%)  
# Similarity:    NA/393 (NA%)  
# Gaps:          18/393 (4.6%)  
# Score: 1250.908
```