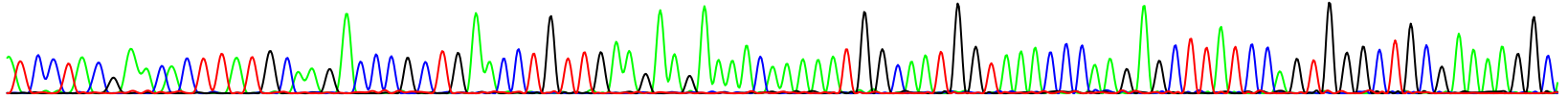


# Chromatogram

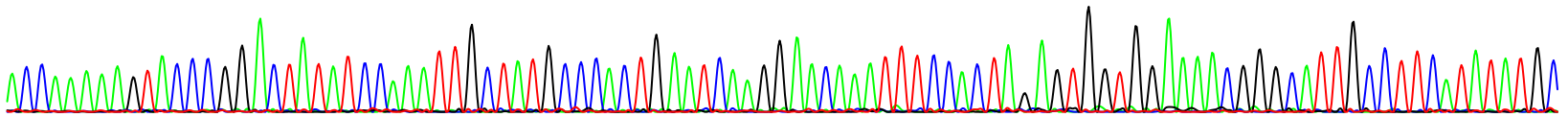
T C CTAC GAA CACTT A TGCAAGACCC G CTGAACCTGT TGAAAGAA GAAAACAA AAATG GCAATGG TA AAC CC AA GA GCTTAT CCA GTGG GCTG C G AAAA GGC  
T C CTAC GAA CACTT A TGCAAGACCC G CTGAACCTGT TGAAAGAA GAAAACAA AAATG GCAATGG TA AAC CC AA GA GCTTAT CCA GTGG GCTG C G AAAA GGC

1



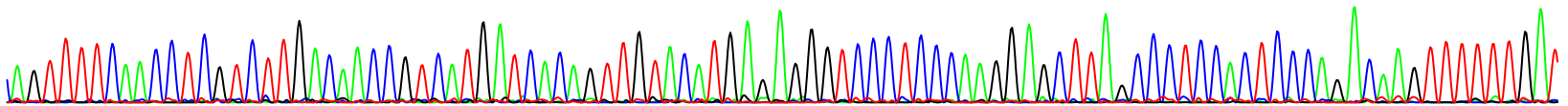
ACCAAAAAGTACCCG GACTATA TCCAAAT TGCTATGCCACTG AATCAA GGAACAAAT TTCCACTAGA GTGGTG GAAAACGGG CAT TGCCTTCATATAT GC  
ACCAAAAAGTACCCG GACTATA TCCAAAT TGCTATGCCACTG AATCAA GGAACAAAT TTCCACTAGA GTGGTG GAAAACGGG CAT TGCCTTCATATAT GC

101



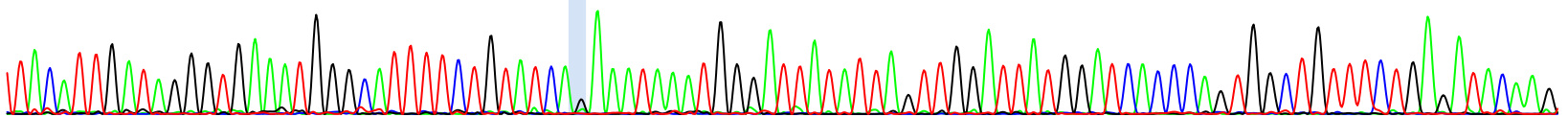
AGT TTT CAA CC TCG TCTTG ACAAC CGT CATG ATCACA GTTG TACA TGA GAGGG TCCCTCCCAAGG AGCTTA GCCCTCCACTCCAG ACAAGT TTT TTGAT  
AGT TTT CAA CC TCG TCTTG ACAAC CGT CATG ATCACA GTTG TACA TGA GAGGG TCCCTCCCAAGG AGCTTA GCCCTCCACTCCAG ACAAGT TTT TTGAT

202



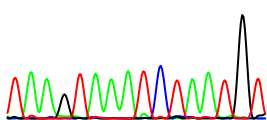
TACATT GA TAGG GTGAA ATG GGCATTTTC TGTATCAGA AATAAAT GGG ATTATAT TAGT TGGATTATG GATCA CCCAG TG GCTG TTTC T GAG ATACA AG  
TACATT GA TAGG GTGAA ATG GGCATTTTC TGTATCAGA AATAAAT GGG ATTATAT TAGT TGGATTATG GATCA CCCAG TG GCTG TTTC T GAG ATACA AG

302



T AAGTA AATC TAA TGT  
T AAGTA AATC TAA TGT

401



## Alignment

Alt Allele	1	TCCTACGAACACTTATGCAAGACCCGCTGAACCTGTTGAAGAAGAAAACAAAAATGGCAATGGTAAACCCAAGAGCTTAT	80
Reference	31	TCCTACGAACACTTATGCAAGACCCGCTGAACCTGTTGAAGAAGAAAACAAAAATGGCAATGGTAAACCCAAGAGCTTAT	110
Alt Allele	81	CCAGTGGGCTGCGAAAAGGCACAAAAAGTACCCGGACTATATCCAAATTGCTATGCCCACTGAATCAAGGAACAAATTT	160
Reference	111	CCAGTGGGCTGCGAAAAGGCACAAAAAGTACCCGGACTATATCCAAATTGCTATGCCCACTGAATCAAGGAACAAATTT	190
Alt Allele	161	CCACTAGAGTGGTGGAAAACGGGCATTGCCTTCATATATGCAGTTTTCAACCTCGTCTTGACAACCGTCATGATCACAGT	240
Reference	191	CCACTAGAGTGGTGGAAAACGGGCATTGCCTTCATATATGCAGTTTTCAACCTCGTCTTGACAACCGTCATGATCACAGT	270
Alt Allele	241	TGTACATGAGAGGGTCCCTCCCAAGGAGCTTAGCCCTCCACTCCCAGACAAGTTTTTTGATTACATTGATAGGGTGAAAT	320
Reference	271	TGTACATGAGAGGGTCCCTCCCAAGGAGCTTAGCCCTCCACTCCCAGACAAGTTTTTTGATTACATTGATAGGGTGAAAT	350
Alt Allele	321	GGGCATTTTCTGTATCAAAAATAAATGGGATTATATTAGTTGGATTATGGATCACCCAGTGGCTGTTTCTGAGATAACAAG	400
Reference	351	GGGCATTTTCTGTATCAGAAAATAAATGGGATTATATTAGTTGGATTATGGATCACCCAGTGGCTGTTTCTGAGATAACAAG	430
Alt Allele	401	TAAGTAAATCTAATGT	416
Reference	431	TAAGTAAATCTAATGT	446

## Alternative allele

TCCTACGAACACTTATGCAAGACCCGCTGAACCTGTTGAAGAAGAAAACAAAAATGGCAATGGTAAACCCAAGAGCTTATCCAGTGGGCTGCGAAAAGGCACAAAAAGTACCCGGACTATATCCAAATTGCTATGCCCACTGAATCAAGGAACAAATTTCCACTAGAGTGGTGGAAAACGGGCATTGCCTTCATATATGCAGTTTTCAACCTCGTCTTGACAACCGTCATGATCACAGT  
TGTACATGAGAGGGTCCCTCCCAAGGAGCTTAGCCCTCCACTCCCAGACAAGTTTTTTGATTACATTGATAGGGTGAAATGGGCATTTTCTGTATCAAAAATAAATGGGATTATATTAGTTGGATTATGGATCACCCAGTGGCTGTTTCTGAGATAACAAGTAAATCTAATGT

## Reference sequence

AAKGACCTTTTGTGCAAAATCAACCCAGTATCCTACGAACACTTATGCAAGACCCGCTGAACCTGTTGAAGAAGAAAACAAAAATGGCAATGGTAAACCCAAGAGCTTATCCAGTGGGCTGCGAAAAGGCACAAAAAGTACCCGGACTATATCCAAATTGCTATGCCCACTGAATCAAGGAACAAATTTCCACTAGAGTGGTGGAAAACGGGCATTGCCTTCATATATGCAGTTTTCAA

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CCTCGTCTTGACAACCGTCATGATCACAGTTGTACATGAGAGGGTCCCTCCCAAGGAGCTTAGCCCTCCACTCCCAGACAAGTTTTTTGATTACATTGATAGGGTGAAATGGGCATTTTC
TGTATCAGAAATAAATGGGATTATATTAGTTGGATTATGGATCACCAGTGGCTGTTTCTGAGATAACAAGTAAATCTAATGTTTTGAGGATTTGTCATGGGTTTGTAAWAA
```

## Alignment parameters

```
#####
# Program: Biostrings (version 2.42.1), a Bioconductor package
# Rundate: Fri May 17 08:17:40 2019
#####
#=====
#
# Aligned_sequences: 2
# 1: Alt Allele
# 2: Reference
# Matrix: NA
# Gap_penalty: 12.0
# Extend_penalty: 2.0
#
# Length: 416
# Identity:      415/416 (99.8%)
# Similarity:    NA/416 (NA%)
# Gaps:          0/416 (0.0%)
# Score: 1059.134
```