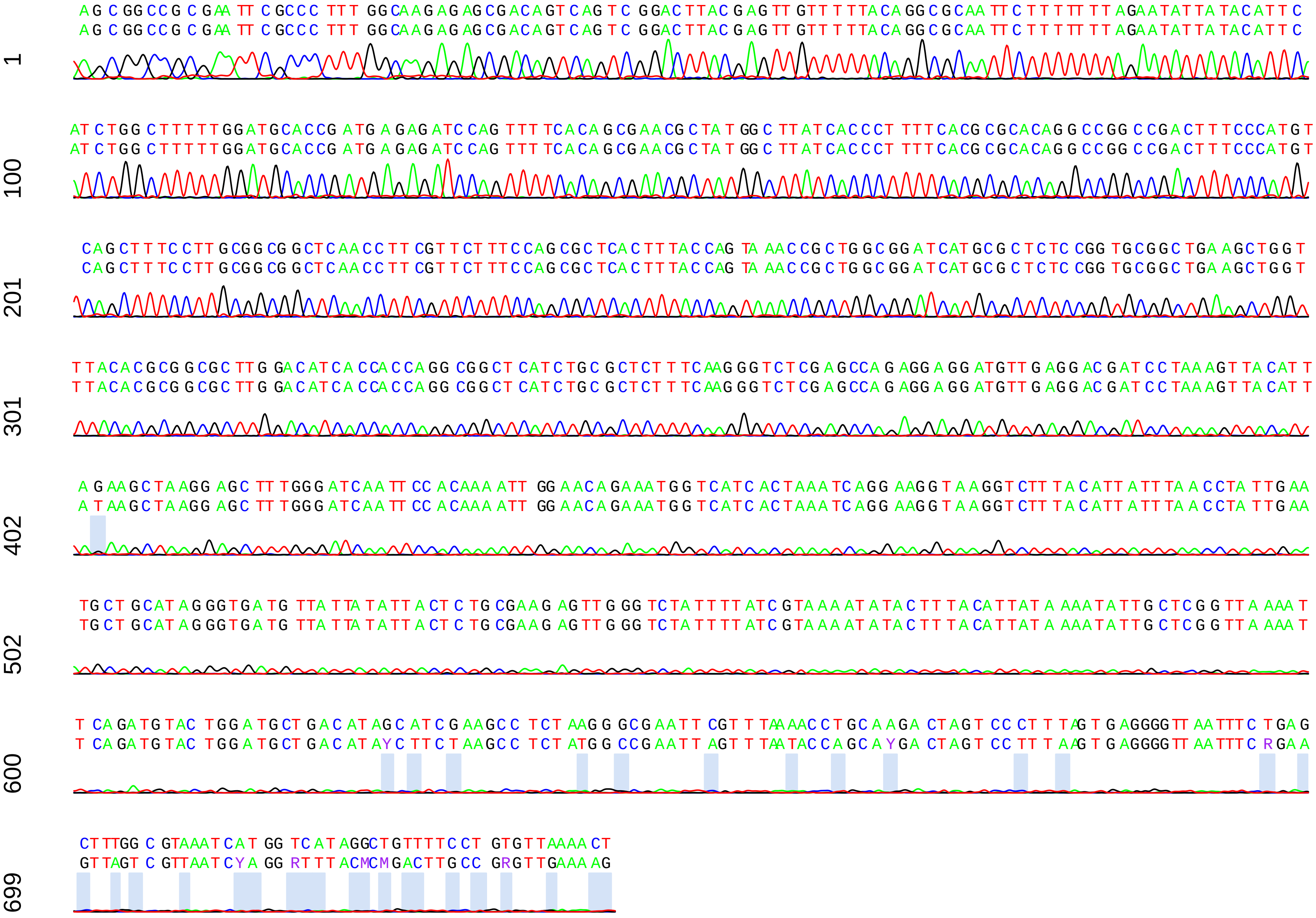
Tbx2a line B11

Supplemental Data **Developmental Dynamics**
Poly Peak Parser
Four examples: Tbx2a line B11, 3ost5 line F96, 3ost5 line M21, Left2 line 19



Tbx2a line B11

```
Warning:  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       122 ATGAGAGATCCAGTTTTCACAGCGAACGCTATGGCTTATCACCCTTTTCACGCGCACAGGCCGGCCGACTTTCCCATGTC    201
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Reference          1 ATGAGAGATCCAGTTTTCACAGCGAACGCTATGGCTTATCACCCTTTTCACGCGCACAGGCCGGCCGACTTTCCCATGTC     80

Alt Allele       202 AGCTTTCCTTGCGGCGGCTCAACCTTCGTTCTTTCCAGCGCTCACTTTACCA----------GTAAACCGCTGGCGGATC    271
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||          ||||||||||||||||||
Reference         81 AGCTTTCCTTGCGGCGGCTCAACCTTCGTTCTTTCCAGCGCTCACTTTACCACCGGGTCTCAGTAAACCGCTGGCGGATC    160

Alt Allele       272 ATGCGCTCTCCGGTGCGGCTGAAGCTGGTTTACACGCGGCGCTTGGACATCACCACCAGGCGGCTCATCTGCGCTCTTTC    351
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Reference        161 ATGCGCTCTCCGGTGCGGCTGAAGCTGGTTTACACGCGGCGCTTGGACATCACCACCAGGCGGCTCATCTGCGCTCTTTC    240

Alt Allele       352 AAGGGTCTCGAGCCAGAGGAGGATGTTGAGGACGATCCTAAAGTTACATTATAAGCTAAGGAGCTTTGGGATCAATTCCA    431
                     ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Reference        241 AAGGGTCTCGAGCCAGAGGAGGATGTTGAGGACGATCCTAAAGTTACATTAGAAGCTAAGGAGCTTTGGGATCAATTCCA    320

Alt Allele       432 CAAAATTGGAACAGAAATGGTCATCACTAAATCAGGAAGG    471
                     ||||||||||||||||||||||||||||||||||||||||
Reference        321 CAAAATTGGAACAGAAATGGTCATCACTAAATCAGGAAGG    360
```

Alternative allele

```
AGCGGCCGCGAATTCGCCCTTTGGCAAGAGAGCGACAGTCAGTCGGACTTACGAGTTGTTTTTACAGGCGCAATTCTTTTTTTAGAATATTATACATTCATCTGGCTTTTTGGATGCACC
GATGAGAGATCCAGTTTTCACAGCGAACGCTATGGCTTATCACCCTTTTCACGCGCACAGGCCGGCCGACTTTCCCATGTCAGCTTTCCTTGCGGCGGCTCAACCTTCGTTCTTTCCAGC
GCTCACTTTACCAGTAAACCGCTGGCGGATCATGCGCTCTCCGGTGCGGCTGAAGCTGGTTTACACGCGGCGCTTGGACATCACCACCAGGCGGCTCATCTGCGCTCTTTCAAGGGTCTC
GAGCCAGAGGAGGATGTTGAGGACGATCCTAAAGTTACATTATAAGCTAAGGAGCTTTGGGATCAATTCCACAAAATTGGAACAGAAATGGTCATCACTAAATCAGGAAGGTAAGGTCTT
TACATTATTTAACCTATTGAATGCTGCATAGGGTGATGTTATTATATTACTCTGCGAAGAGTTGGGTCTATTTTATCGTAAAATATACTTTACATTATAAAATATTGCTCGGTTAAAATT
CAGATGTACTGGATGCTGACATABCWTCKAAGCCTCTAWGGSCGAATTMGTTTAAWACCWGCAHGACTAGTCCYTTWAGTGAGGGGTTAATTTCDGARSTTWGKCGTWAATCHWGGDYWT
ASVCHGWYTTSCYGDGTTRAAAMK
```

Reference sequence

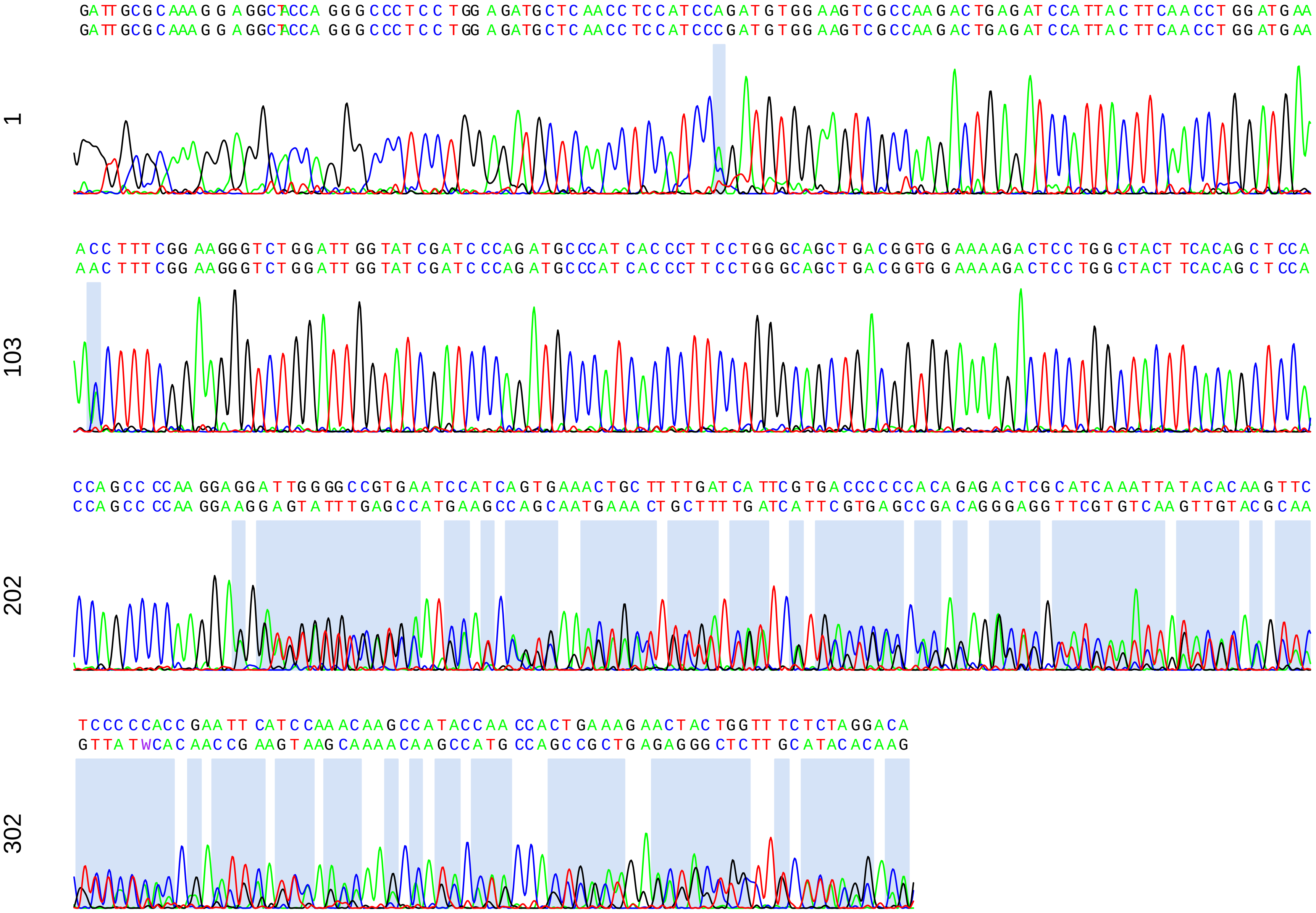
Tbx2a line B11

```
ATGAGAGATCCAGTTTTCACAGCGAACGCTATGGCTTATCACCCTTTTCACGCGCACAGGCCGGCCGACTTTCCCATGTCAGCTTTCCTTGCGGCGGCTCAACCTTCGTTCTTTCCAGCG
CTCACTTTACCACCGGGTCTCAGTAAACCGCTGGCGGATCATGCGCTCTCCGGTGCGGCTGAAGCTGGTTTACACGCGGCGCTTGGACATCACCACCAGGCGGCTCATCTGCGCTCTTTC
AAGGGTCTCGAGCCAGAGGAGGATGTTGAGGACGATCCTAAAGTTACATTAGAAGCTAAGGAGCTTTGGGATCAATTCCACAAAATTGGAACAGAAATGGTCATCACTAAATCAGGAAGG
```

Alignment parameters

```
########################################
# Program: Biostrings (version 2.26.3), a Bioconductor package
# Rundate: Thu May 22 20:25:16 2014
########################################
#=======================================
#
# Aligned_sequences: 2
# 1: Alt Allele
# 2: Reference
# Matrix: NA
# Gap_penalty: 12.0
# Extend_penalty: 2.0
#
# Length: 360
# Identity:     349/360 (96.9%)
# Similarity:    NA/360 (NA%)
# Gaps:          10/360 (2.8%)
# Score: 1286
```

3ost5 line F96



3ost5 line F96

Alignment

```
Alt Allele          4 TGCGCAAAGGAGGCTACCAGGGCCCTCCTGGAGATGCTCAACCTCCATCCCGATGTGGAAGTCGCCAAGACTGAGATCCA     83
                      |||||||||||||| ||||||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||||
Reference          96 TGCGCAAAGGAGGC-ACCAGGGCCCTCCTGGAGATGCTCAACCTCCATCCAGATGTGGAAGTCGCCAAGACCGAGATCCA    174

Alt Allele         84 TTACTTCAACCTGGATGAAACCTTTCGGAAGGGTCTGGATTGGTATCGATCCCAGATGCCCATCACCCTTCCTGGGCAGC    163
                      |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Reference         175 TTACTTCAACCTGGATGAAAACTTTCGGAAGGGTCTGGATTGGTATCGATCCCAGATGCCCATCACCCTTCCTGGGCAGC    254

Alt Allele        164 TGACGGTGGAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGAAGGAGGATTTGGGCCATGAATCCAGCAAT    243
                      |||| ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||||||| |
Reference         255 TGACAGTGGAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGA----GGATTTGGGCCATGAATCCAGCAGT    330

Alt Allele        244 GAAACTGCTTTTGATCATTCGTGACCCCACAGAGAGGCTCGTATCAAGTTATACGCAAGTTCTYCACAACCGAATTCAGC    323
                      |||||||||||||||||||||||||||| |||||||||||||||||  ||||||||||||||| ||||||||||||||||
Reference         331 GAAACTGCTTTTGATCATTCGTGACCCCGCAGAGAGGCTCGTATCAGATTATACGCAAGTTCTCCACAACCGAATTCAGC    410

Alt Allele        324 AAAACAAGCCATACCAGCCACTGAAAGAGCTGTTGCTTTCACAAG    368
                      ||||||||||||||||| ||||| |||||||| ||||||||||||
Reference         411 AAAACAAGCCATACCAGTCACTGGAAGAGCTGCTGCTTTCACAAG    455
```

Alternative allele

```
GATTGCGCAAAGGAGGCTACCAGGGCCCTCCTGGAGATGCTCAACCTCCATCCCGATGTGGAAGTCGCCAAGACTGAGATCCATTACTTCAACCTGGATGAAACCTTTCGGAAGGGTCTG
GATTGGTATCGATCCCAGATGCCCATCACCCTTCCTGGGCAGCTGACGGTGGAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGAAGGAGGATTTGGGCCATGAATCCAGC
AATGAAACTGCTTTTGATCATTCGTGACCCCACAGAGAGGCTCGTATCAAGTTATACGCAAGTTCTYCACAACCGAATTCAGCAAAACAAGCCATACCAGCCACTGAAAGAGCTGTTGCT
TTCACAAG
```

Reference sequence

```
ACAAGACACTTTGGACTTAGTGACTTCAGCGACACCTTCTGGACCTTCTAATGCTTCGACTTTGCAACGTCTCCCAGGGGCCATCATCATCGGGGTGCGCAAAGGAGGCACCAGGGCCCT
CCTGGAGATGCTCAACCTCCATCCAGATGTGGAAGTCGCCAAGACCGAGATCCATTACTTCAACCTGGATGAAAACTTTCGGAAGGGTCTGGATTGGTATCGATCCCAGATGCCCATCAC
CCTTCCTGGGCAGCTGACAGTGGAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGAGGATTTGGGCCATGAATCCAGCAGTGAAACTGCTTTTGATCATTCGTGACCCCGC
AGAGAGGCTCGTATCAGATTATACGCAAGTTCTCCACAACCGAATTCAGCAAAACAAGCCATACCAGTCACTGGAAGAGCTGCTGCTTTCACAAGGACACATCAACCCCAAATACAAGGC
CCTTCAGAGAAGTTTTTACTACCAGCACCTGGCCAGATGGTTGGAGCTTTTCCCCCGAGAGCAGATACACATTGTGGATGGAGAAGCACTGATTCGTAATCCATTCCCGGAGCTGCAGAA
AGCAGAGACTTTTTTGGAACTTCCGCCTCAGATAAAGCCGGACAACTTCTACTTTAATGTCACCAAGGGCTTTTATTGTATGCTGTCGGCAGGACATGACAAGTGCCTGGATGAGTCTAA
AGGAAGGCCACATGCTCCACTTAGCAATGAGGCTTTCCAGAAGCTTTGCCGCTACTTGCGAGTACCTAATCAAATCTTTTTCCGAATGGTGGGACAGAGGTTTG
```

3ost5 line F96

Alignment parameters

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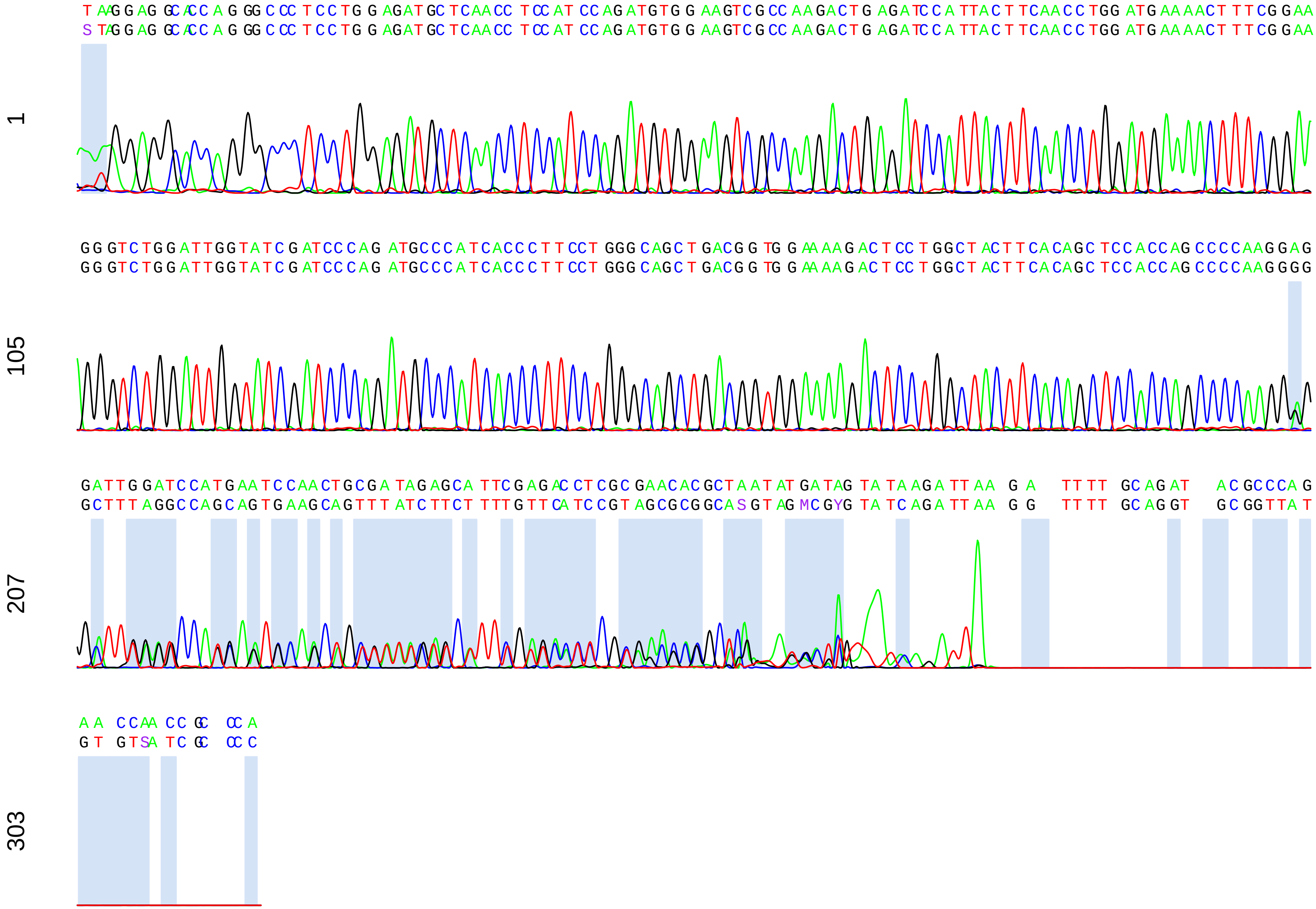
# Program: Biostrings (version 2.26.3), a Bioconductor package
# Rundate: Thu May 22 19:34:02 2014
########################################
#=======================================
#
# Aligned_sequences: 2
# 1: Alt Allele
# 2: Reference
# Matrix: NA
# Gap_penalty: 12.0
# Extend_penalty: 2.0
#
# Length: 365
# Identity:     348/365 (95.3%)
# Similarity:    NA/365 (NA%)
# Gaps:           5/365 (1.4%)
# Score: 699.8
```

3ost5 line M21



3ost5 line M21

Alignment

```
Alt Allele         3 AGGAGGCACCAGGGCCCTCCTGGAGATGCTCAACCTCCATCCAGATGTGGAAGTCGCCAAGACTGAGATCCATTACTTCA     82
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Reference        103 AGGAGGCACCAGGGCCCTCCTGGAGATGCTCAACCTCCATCCAGATGTGGAAGTCGCCAAGACCGAGATCCATTACTTCA    182

Alt Allele        83 ACCTGGATGAAAACTTTCGGAAGGGTCTGGATTGGTATCGATCCCAGATGCCCATCACCCTTCCTGGGCAGCTGACGGTG    162
                     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Reference        183 ACCTGGATGAAAACTTTCGGAAGGGTCTGGATTGGTATCGATCCCAGATGCCCATCACCCTTCCTGGGCAGCTGACAGTG    262

Alt Allele       163 GAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGGGGCTT--------GAATCCAGCAGTGAAACTGCTTTT    234
                     |||||||||||||||||||||||||||||||||||||||||| || ||        ||||||||||||||||||||||||
Reference        263 GAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGAGGATTTGGGCCATGAATCCAGCAGTGAAACTGCTTTT    342

Alt Allele       235 GATCATTCGTGACCCCGCAGAGAGGCTMGTATMAGWGTATA    275
                     ||||||||||||||||||||||||||| |||| ||  ||||
Reference        343 GATCATTCGTGACCCCGCAGAGAGGCTCGTATCAGATTATA    383
```

Alternative allele

```
BTAGGAGGCACCAGGGCCCTCCTGGAGATGCTCAACCTCCATCCAGATGTGGAAGTCGCCAAGACTGAGATCCATTACTTCAACCTGGATGAAAACTTTCGGAAGGGTCTGGATTGGTAT
CGATCCCAGATGCCCATCACCCTTCCTGGGCAGCTGACGGTGGAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGGGGCTTGAATCCAGCAGTGAAACTGCTTTTGATCAT
TCGTGACCCCGCAGAGAGGCTMGTATMAGWGTATAAGATTAAGRTTTTGCAGRTRCGSYTATGTSCRAYCGCCCA
```

Reference sequence

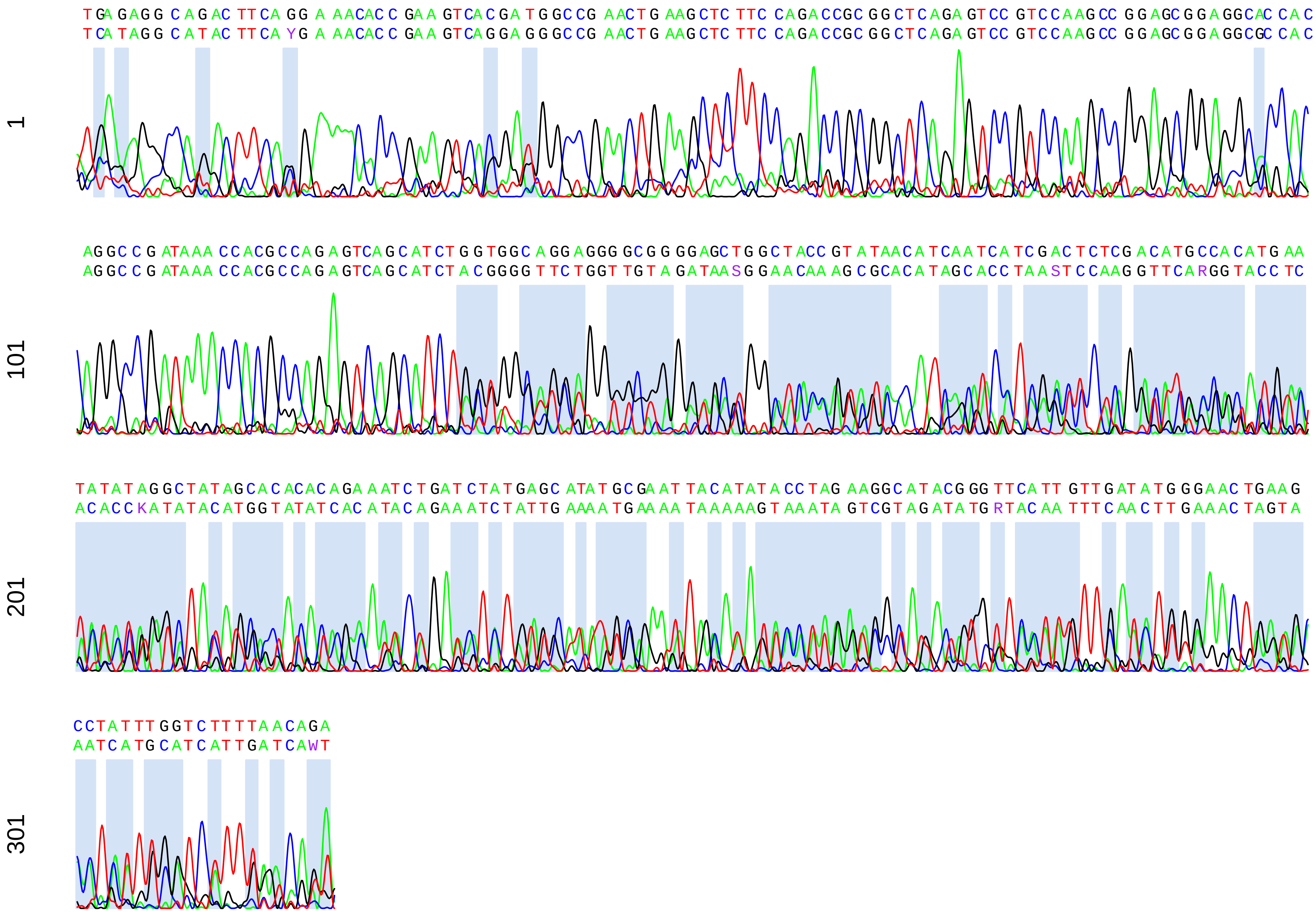
```
ACAAGACACTTTGGACTTAGTGACTTCAGCGACACCTTCTGGACCTTCTAATGCTTCGACTTTGCAACGTCTCCCAGGGGCCATCATCATCGGGGTGCGCAAAGGAGGCACCAGGGCCCT
CCTGGAGATGCTCAACCTCCATCCAGATGTGGAAGTCGCCAAGACCGAGATCCATTACTTCAACCTGGATGAAAACTTTCGGAAGGGTCTGGATTGGTATCGATCCCAGATGCCCATCAC
CCTTCCTGGGCAGCTGACAGTGGAAAAGACTCCTGGCTACTTCACAGCTCCACCAGCCCCAAGGAGGATTTGGGCCATGAATCCAGCAGTGAAACTGCTTTTGATCATTCGTGACCCCGC
AGAGAGGCTCGTATCAGATTATACGCAAGTTCTCCACAACCGAATTCAGCAAAACAAGCCATACCAGTCACTGGAAGAGCTGCTGCTTTCACAAGGACACATCAACCCCAAATACAAGGC
CCTTCAGAGAAGTTTTTACTACCAGCACCTGGCCAGATGGTTGGAGCTTTTCCCCCGAGAGCAGATACACATTGTGGATGGAGAAGCACTGATTCGTAATCCATTCCCGGAGCTGCAGAA
AGCAGAGACTTTTTTGGAACTTCCGCCTCAGATAAAGCCGGACAACTTCTACTTTAATGTCACCAAGGGCTTTTATTGTATGCTGTCGGCAGGACATGACAAGTGCCTGGATGAGTCTAA
AGGAAGGCCACATGCTCCACTTAGCAATGAGGCTTTCCAGAAGCTTTGCCGCTACTTGCGAGTACCTAATCAAATCTTTTTCCGAATGGTGGGACAGAGGTTTG
```

Alignment parameters

3ost5 line M21

```
########################################
# Program: Biostrings (version 2.26.3), a Bioconductor package
# Rundate: Thu May 22 19:35:32 2014
########################################
#=======================================
#
# Aligned_sequences: 2
# 1: Alt Allele
# 2: Reference
# Matrix: NA
# Gap_penalty: 12.0
# Extend_penalty: 2.0
#
# Length: 281
# Identity:     265/281 (94.3%)
# Similarity:    NA/281 (NA%)
# Gaps:           8/281 (2.8%)
# Score: 800.2
```

Left2 line 19



Left2 line 19

Alignment

```
Alt Allele         8 CAKACTTCAYGAAA-CACCGAAGTCAGGAGGGCCGAACTGAAGCTCTTCCAGACCGCGGCTCAGAGTCCGTCCAAGCCGG     86
                     || |||||| |||| ||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Reference         83 CAGACTTCAGGAAAACACCGAAGTCACGATGGCCGAACTGAAGCTCTTCCAGACCGCGGCTCAGAGTCCGTCCAAGCCGG    162

Alt Allele        87 AGCGGAGGCGCCACAGGCCGATAAACCACGCCAGAGTCAGCATCTGGGGGCATCTGGGTGGAGGTGCKGGAAAACGGCTC    166
                     ||||||||| |||||||||||||||||||||||||||||||||||        |||||||||||||| ||||||||||||
Reference        163 AGCGGAGGCACCACAGGCCGATAAACCACGCCAGAGTCAGCATCTA-------CTGGGTGGAGGTGCTGGAAAACGGCTC    235

Alt Allele       167 ACATAGAACATCASTCCTAGACTCASGGTATGACACAC    204
                       ||||||||||| ||||||||||| ||||||||||||
Reference        236 CAATAGAACATCACTCCTAGACTCACGGTATGACACAC    273
```

Alternative allele

```
TCATAGGCAKACTTCAYGAAACACCGAAGTCAGGAGGGCCGAACTGAAGCTCTTCCAGACCGCGGCTCAGAGTCCGTCCAAGCCGGAGCGGAGGCGCCACAGGCCGATAAACCACGCCAG
AGTCAGCATCTGGGGGCATCTGGGTGGAGGTGCKGGAAAACGGCTCACATAGAACATCASTCCTAGACTCASGGTATGACACACYKRKMTACAGSRYAYAYCGMAATCWGATCTMTRTGS
AWAWGSAAAWTACATAKAMMAWRRWSGYAKAYRKGDTMMWWKTTSAWMTKGRAACTRRWRMMTMWTKSRTCWTTKAWCADW
```

Reference sequence

```
AATGCTTATGTTTAACAGATATTACCGGAGAAATCAAGTACTCGGACACCACCCGTCAGCGTCTTGTGTTCGACATGGAGGCCAGACTTCAGGAAAACACCGAAGTCACGATGGCCGAAC
TGAAGCTCTTCCAGACCGCGGCTCAGAGTCCGTCCAAGCCGGAGCGGAGGCACCACAGGCCGATAAACCACGCCAGAGTCAGCATCTACTGGGTGGAGGTGCTGGAAAACGGCTCCAATA
GAACATCACTCCTAGACTCACGGTATGACACACCTATATAAATCTGATATATATGGAAATATATGCTAATTACATAGGCCTAGATGGCATACATGTT
```

Alignment parameters

```
########################################
# Program: Biostrings (version 2.26.3), a Bioconductor package
# Rundate: Thu May 22 20:10:05 2014
########################################
#=======================================
#
# Aligned_sequences: 2
```

Left2 line 19

```
# 1: Alt Allele
# 2: Reference
# Matrix: NA
# Gap_penalty: 12.0
# Extend_penalty: 2.0
#
# Length: 198
# Identity:     179/198 (90.4%)
# Similarity:    NA/198 (NA%)
# Gaps:           8/198 (4.0%)
# Score: 512
```