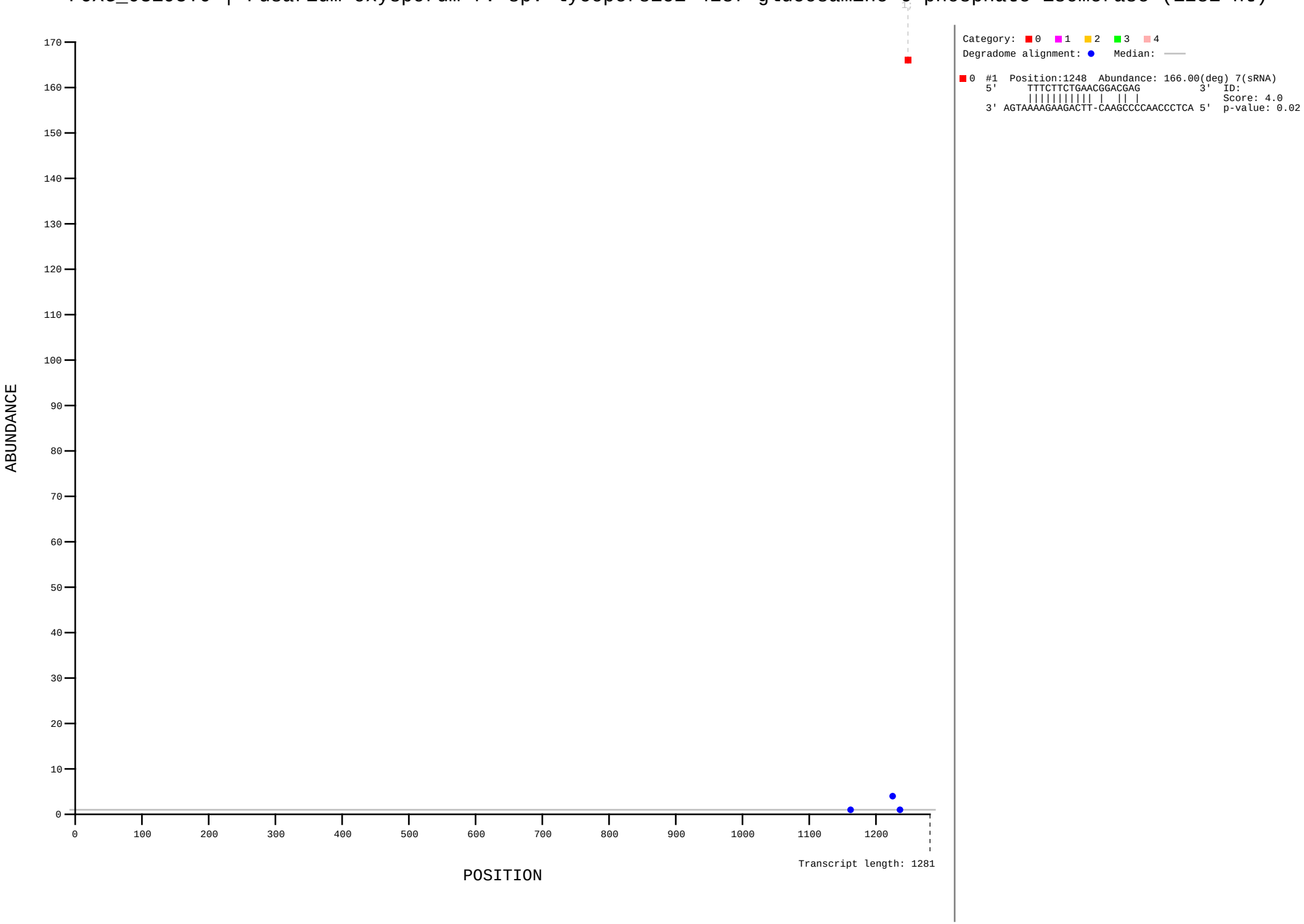
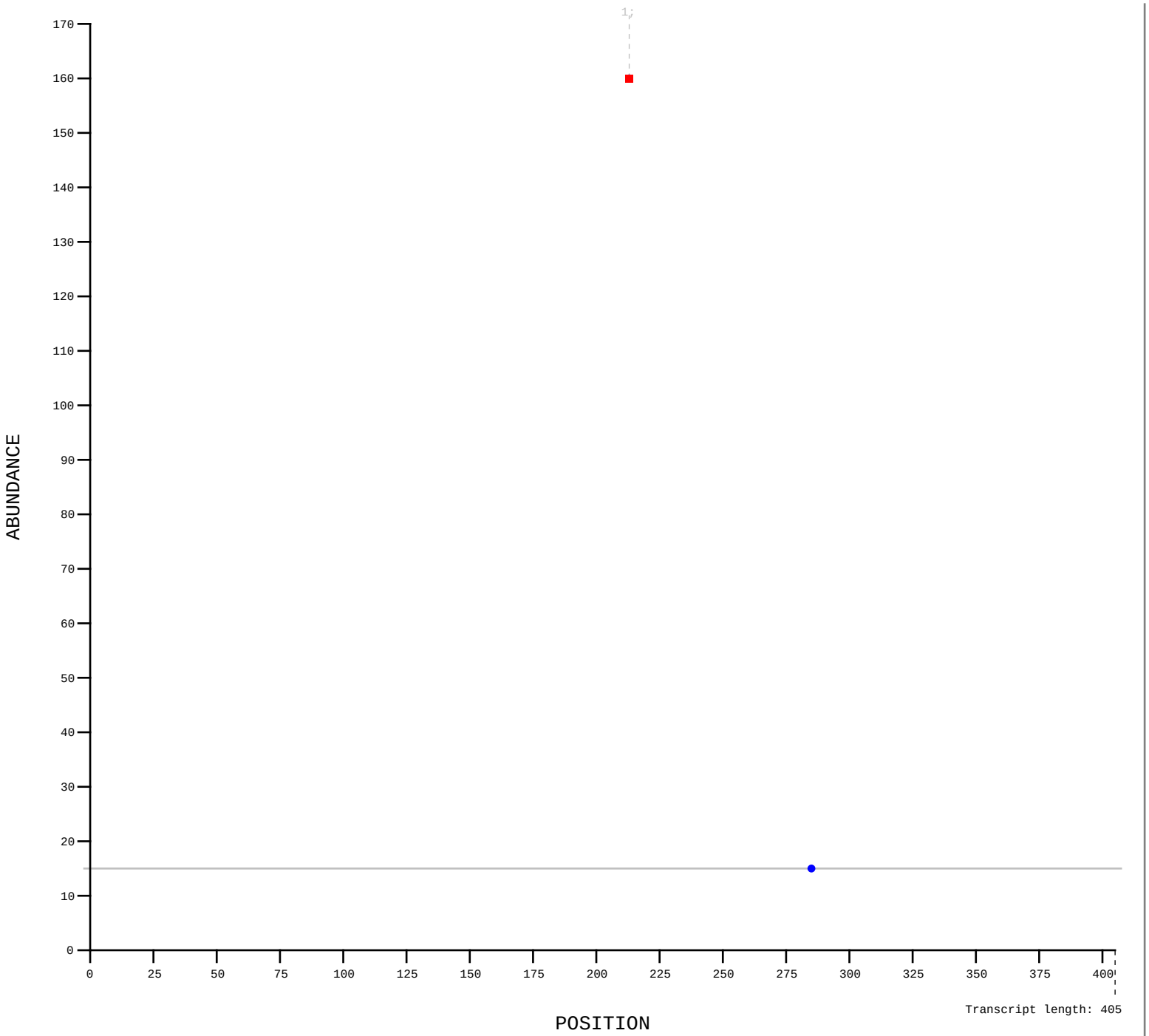
FOXG_03195T0 | Fusarium oxysporum f. sp. lycopersici 4287 glucosamine-6-phosphate isomerase (1281 nt)



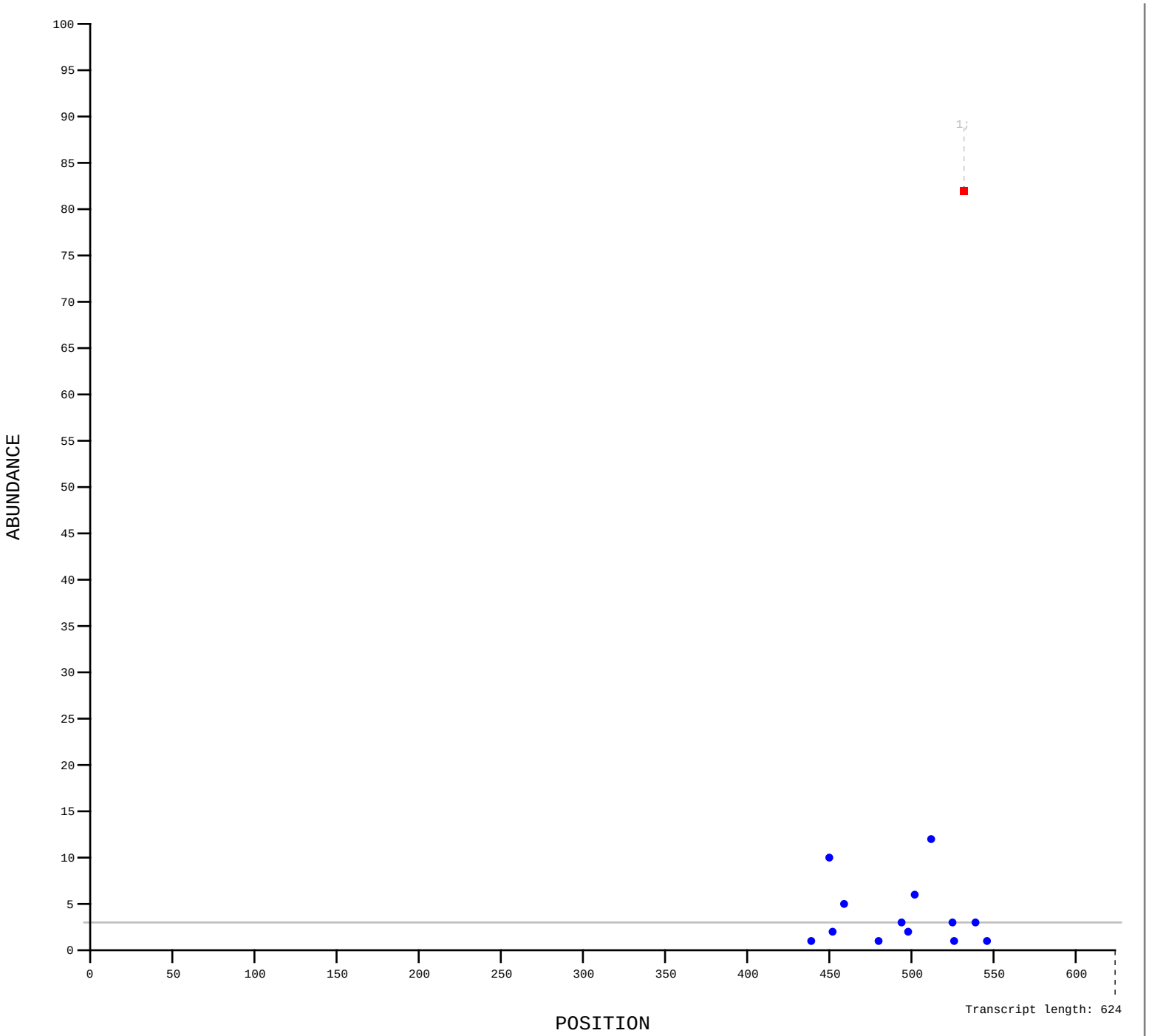
FOXG_10349T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (405 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:213 Abundance: 160.00(deg) 5(sRNA)
5' TCTAAAAGCGAGATTGTGGA 3' ID:
|| ||| ||||||o| ||| Score: 3.5
3' CTCGAG-TTTCCGCTCTAGCCCCTGCAGCAGC 5' p-value: 0.0

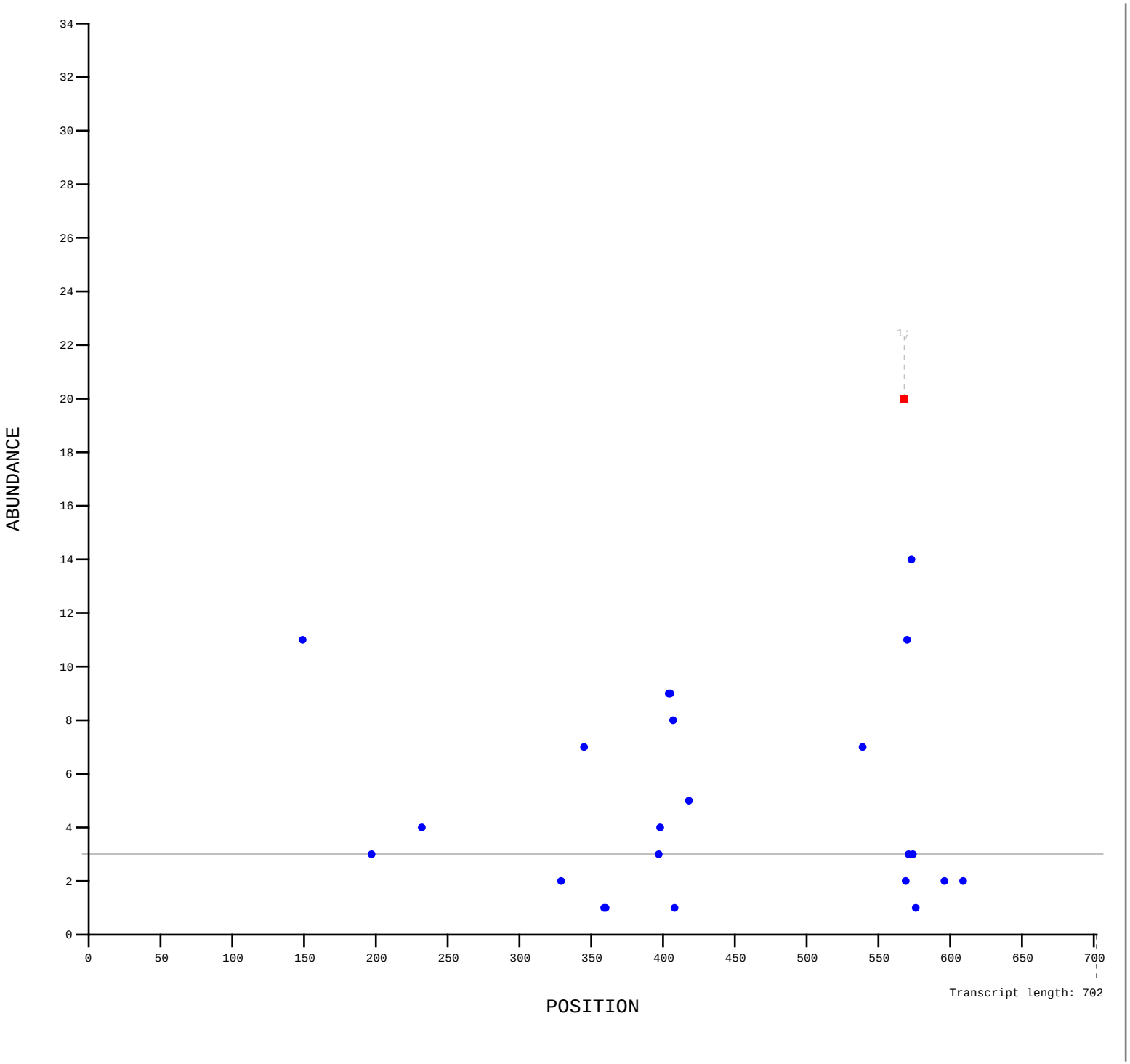
FOXG_08089T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (624 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:532  Abundance: 82.00(deg) 5(sRNA)
    5'     CATAACCCGGAGGTCGCACG         3'  ID:
            |||| || |||||||| | |            Score: 4.0
    3' AGGAGTATAGGTCCTCCAGCCTACGGAGCTGG 5'  p-value: 0.0
```

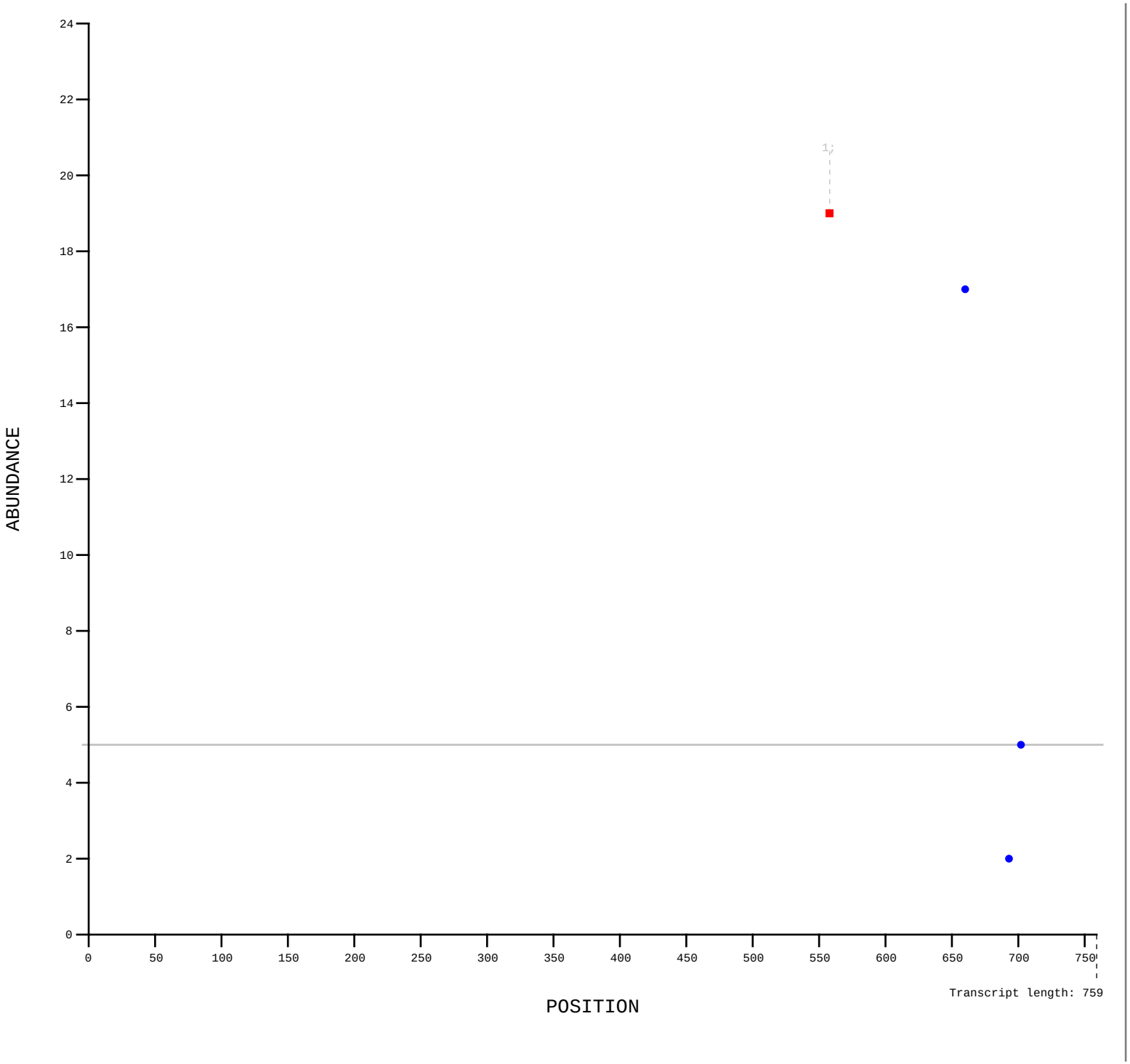
FOXG_05954T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (702 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:568 Abundance: 20.00(deg) 9(sRNA)
5' TAGCAGTGTTATGAGTACA 3' ID:
|| |||||||o|||o|| Score: 4.0
3' GACGTTC-TCACAATGCTCGTGCGAAGTACCG 5' p-value: 0.01

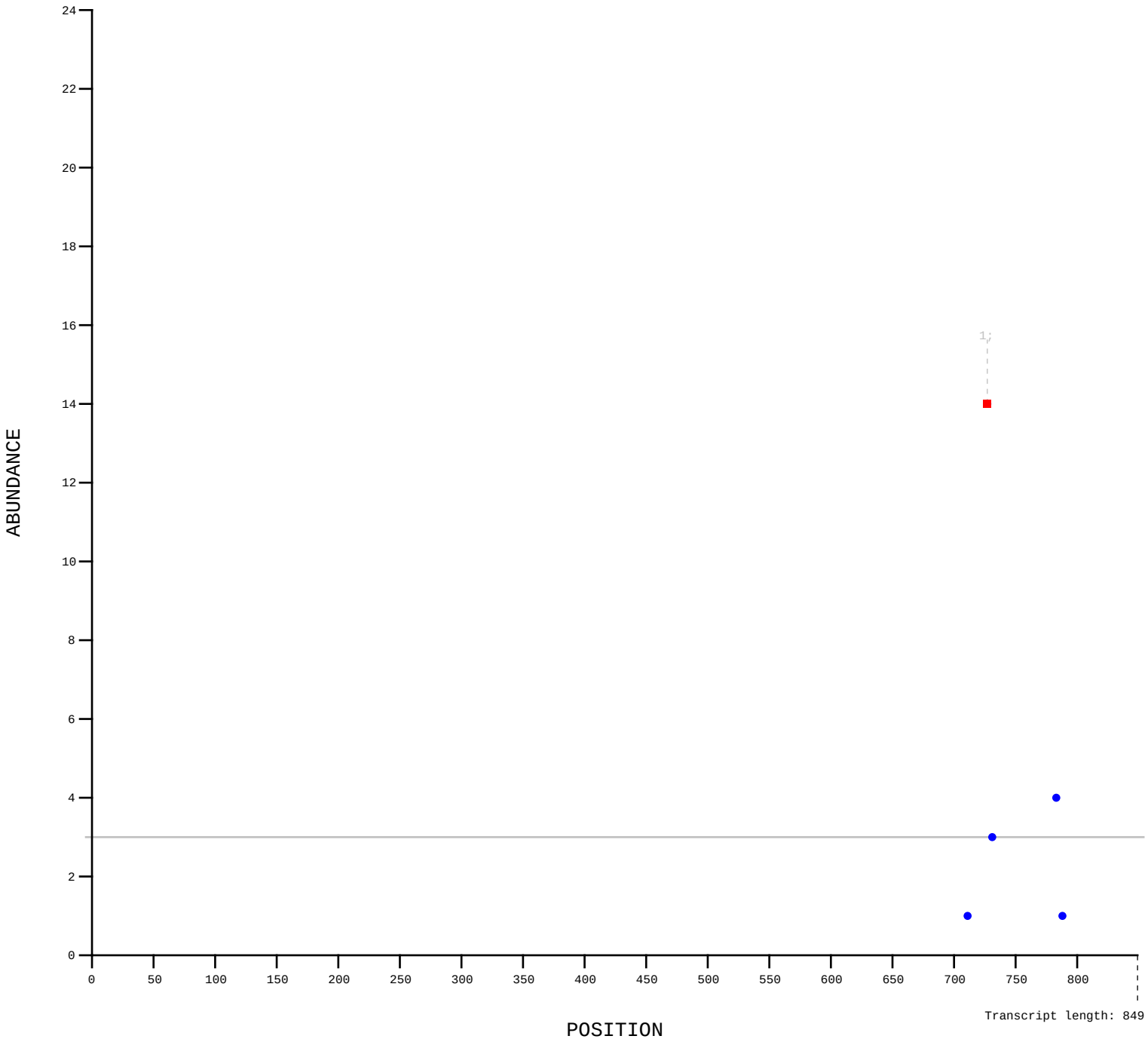
FOXG_10323T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (759 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:558  Abundance: 19.00(deg) 12(sRNA)
    5'      TTCGATTCCCAGATTACGCA          3'  ID:
            | |o|| ||||||o| |||               Score: 4.0
    3' GTACATGTTATGGGTCTAGTACGTCAAAAACG 5'  p-value: 0.0
```

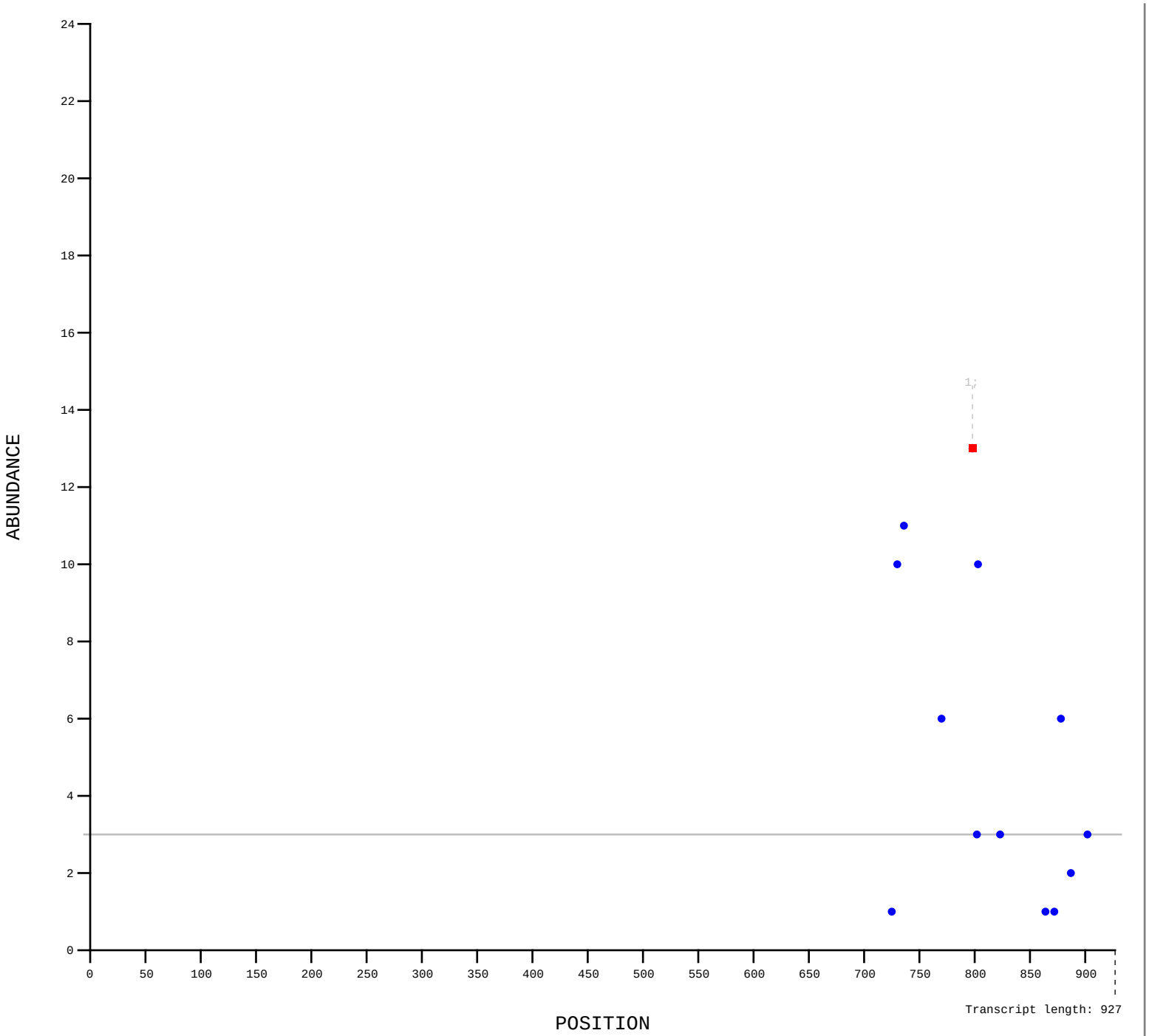
FOXG_00784T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (849 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:727  Abundance: 14.00(deg) 138(sRNA)
    5'     CGGGCTTGAGAAATACAGC          3'  ID:
           |o|||||||| |o | ||               Score: 4.0
    3' CTAGGTCCGAACTCTCTGAG-CGATAGCTTCG 5'  p-value: 0.0
```

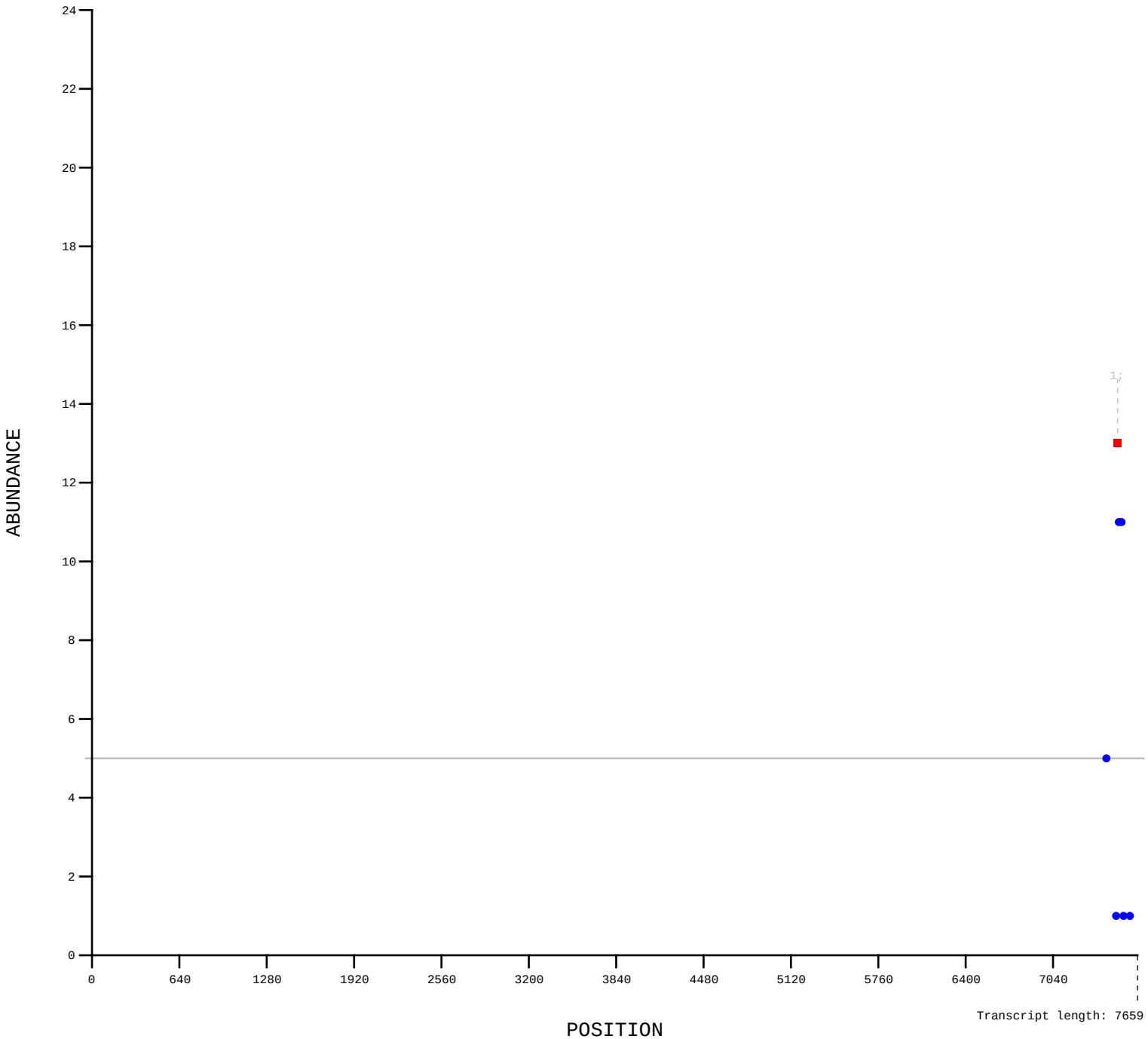
FOXG_06358T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (927 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:798 Abundance: 13.00(deg) 11(sRNA)
5' TAGGAACTCATTTTCAGGAG 3' ID:
o|||||| ||||o||o || Score: 3.5
3' TGCGGTCCTTGAATAAAGGTTGTCTGCGGCTG 5' p-value: 0.0

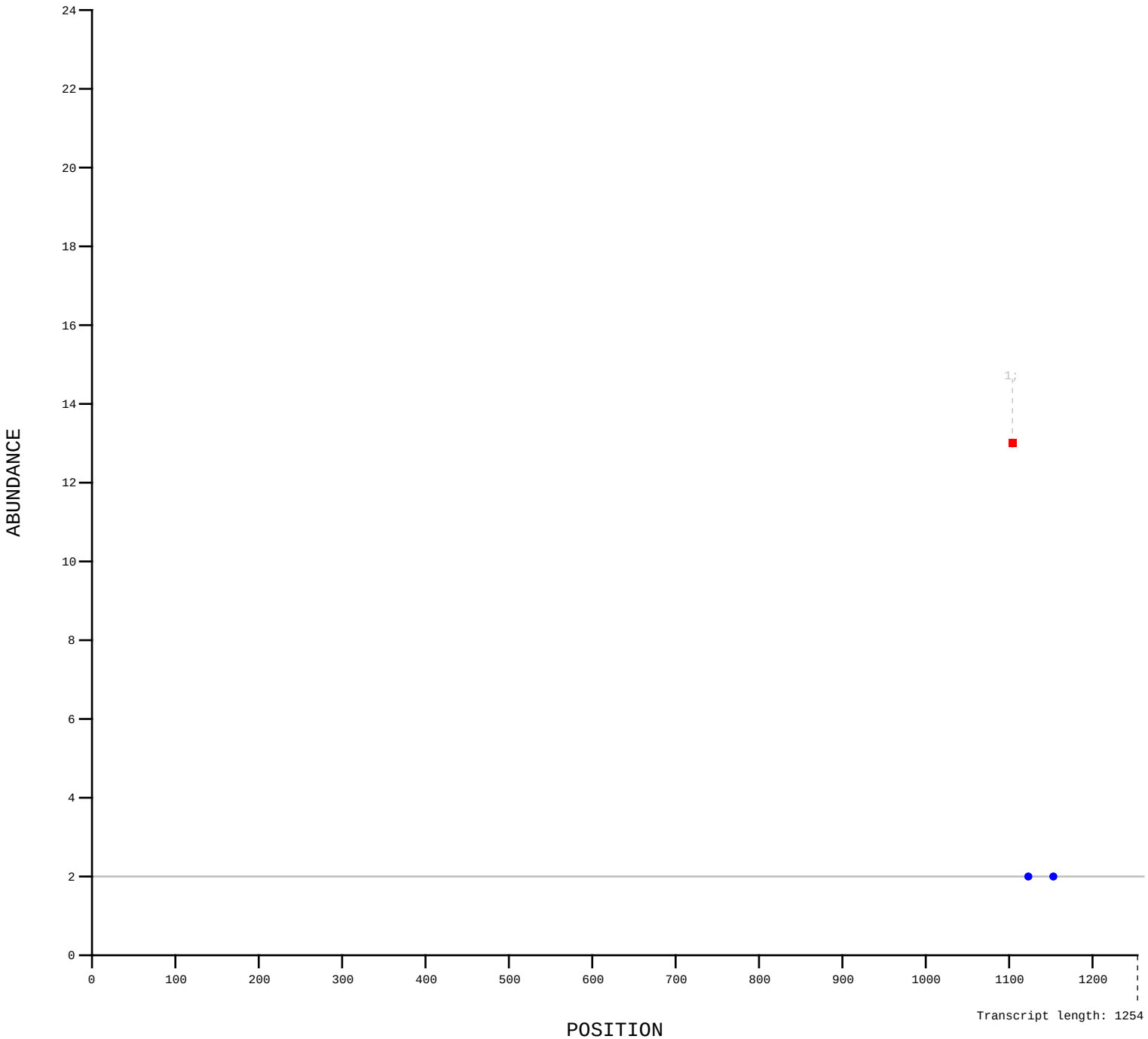
FOXG_02741T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (7659 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:7513  Abundance: 13.00(deg) 10(sRNA)
    5'     TAAACTGCCAATTTCTGA-CT         3'   ID:
           ||||| |||||||o|| | ||              Score: 3.5
    3' AGAGATTTGTCGGTTAAGGAGTTGAGTTGGCG 5'   p-value: 0.0
```

FOXG_02954T0 | Fusarium oxysporum f. sp. lycopersici 4287 3-ketoacyl-CoA thiolase B (1254 nt)

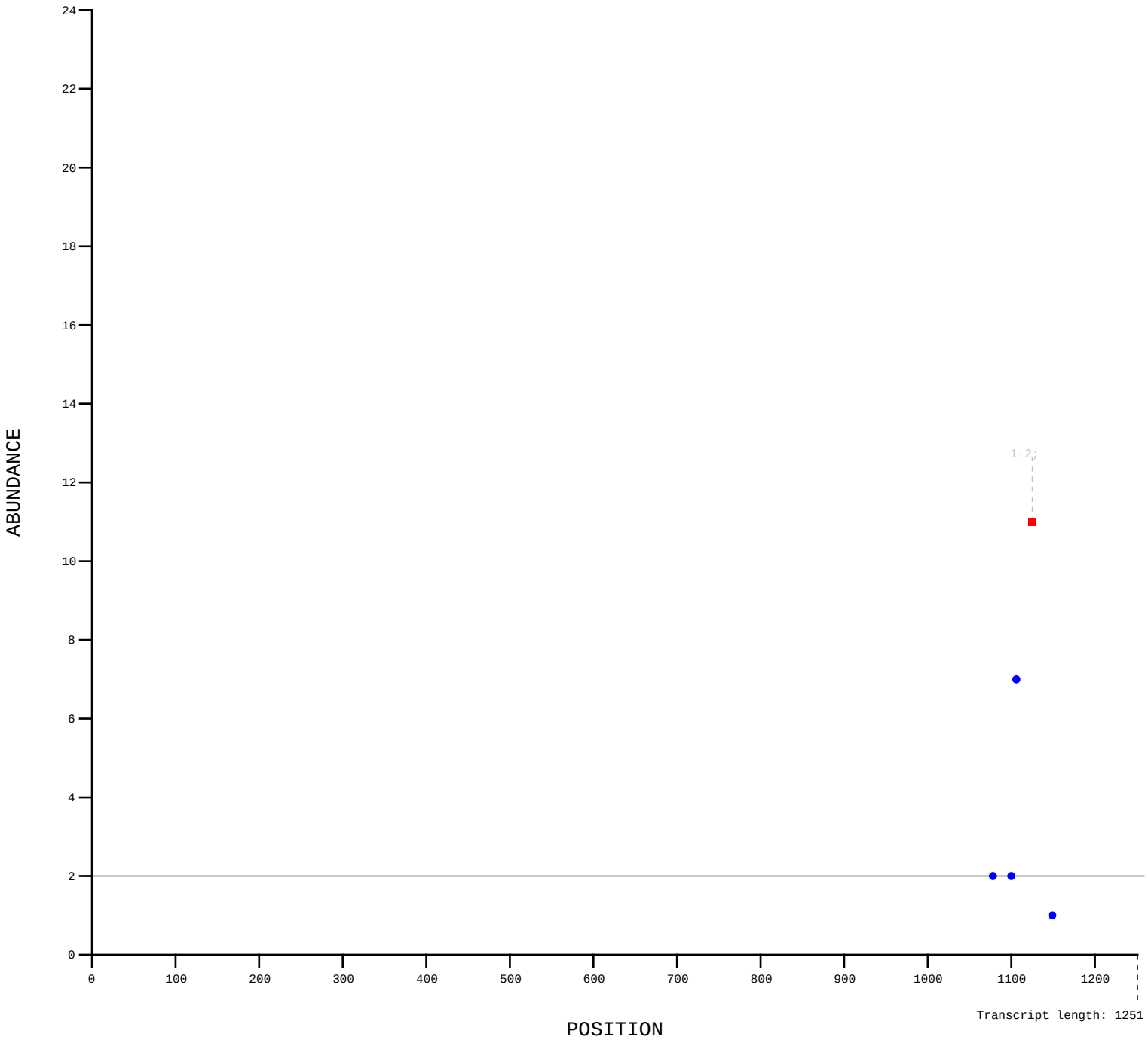


Category: 0 1 2 3 4

Degradome alignment: Median:

0 #1 Position:1104 Abundance: 13.00(deg) 6(sRNA)
5' AAGCGCGACAGCGCTTCGG 3' ID:
|||||o| |||||o|| | Score: 4.0
3' CAGGGTCGCGTTATCGCGGAGGCAGTCCCAAC 5' p-value: 0.0

FOXG_12677T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1251 nt)

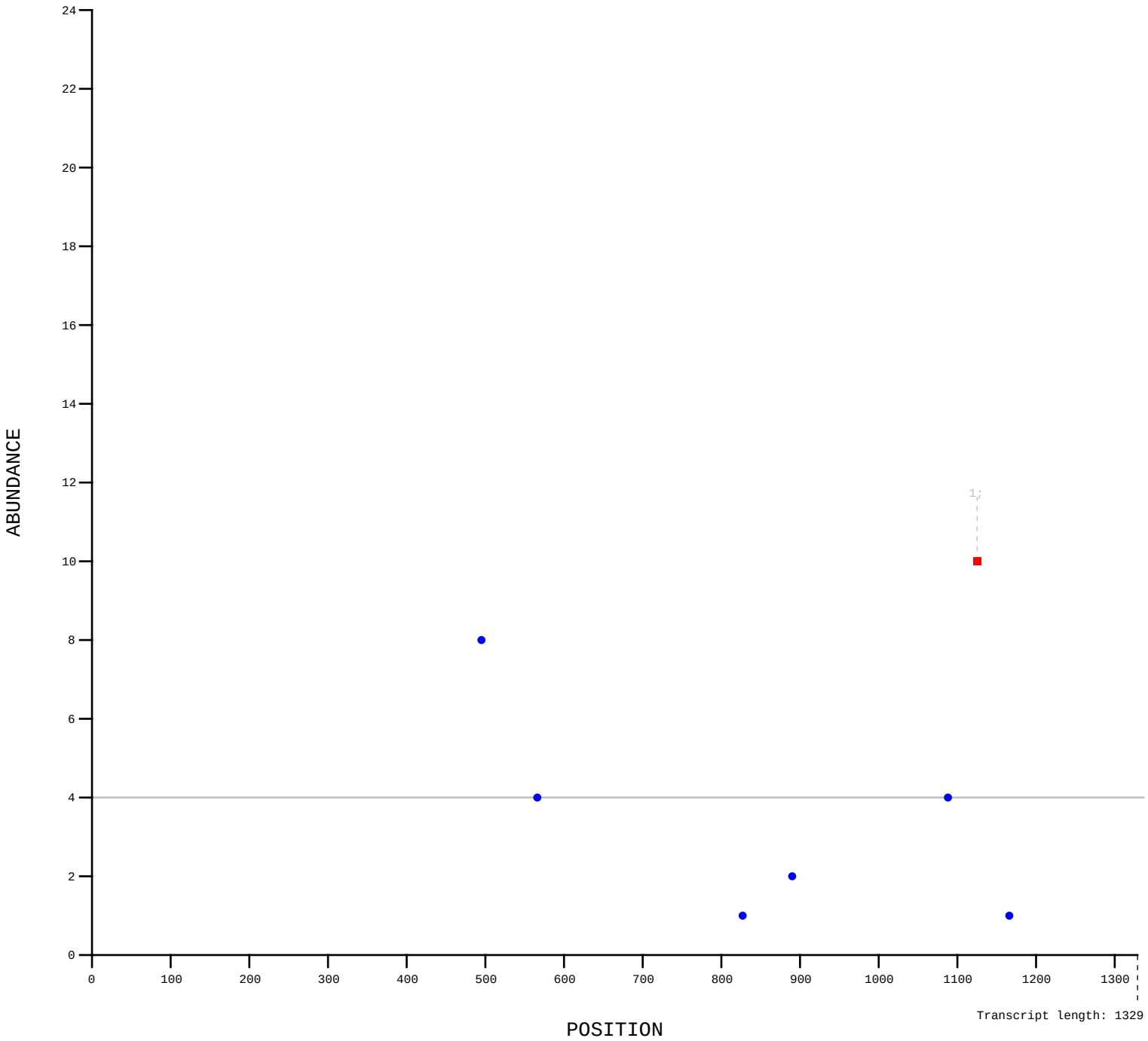


Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1125 Abundance: 11.00(deg) 9(sRNA)
5' TTTTTCTCCTTTGAAGGCA 3' ID:
||||||| |||oo| | || Score: 4.0
3' GACCAAAAAGA-GAAGTTACGGTTATCGTCGC 5' p-value: 0.05

0 #2 Position:1125 Abundance: 11.00(deg) 6(sRNA)
5' TTTTTCTCCTTTGAAGGCAA 3' ID:
||||||| |||oo| | ||| Score: 4.0
3' GACCAAAAAGA-GAAGTTACGGTTATCGTCGC 5' p-value: 0.01

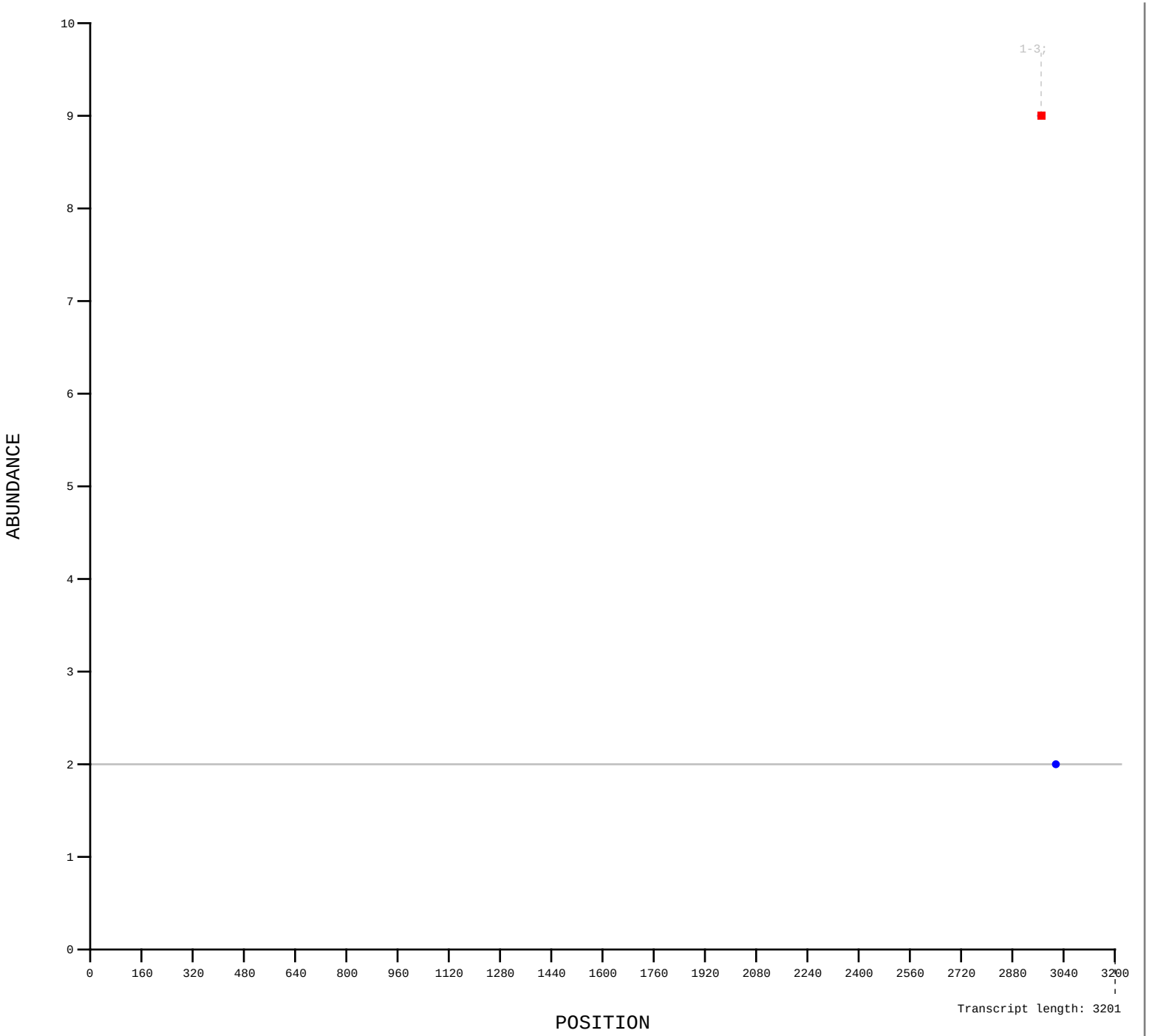
FOXG_03515T0 | Fusarium oxysporum f. sp. lycopersici 4287 elongation factor 1-alpha (1329 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1125 Abundance: 10.00(deg) 14(sRNA)
5' ACCAGACTCGACGGAACTC 3' ID:
||||||| || | |||| Score: 4.0
3' TCAGTGGTCTGAACTAC-TTGAACCCCCGCCG 5' p-value: 0.0

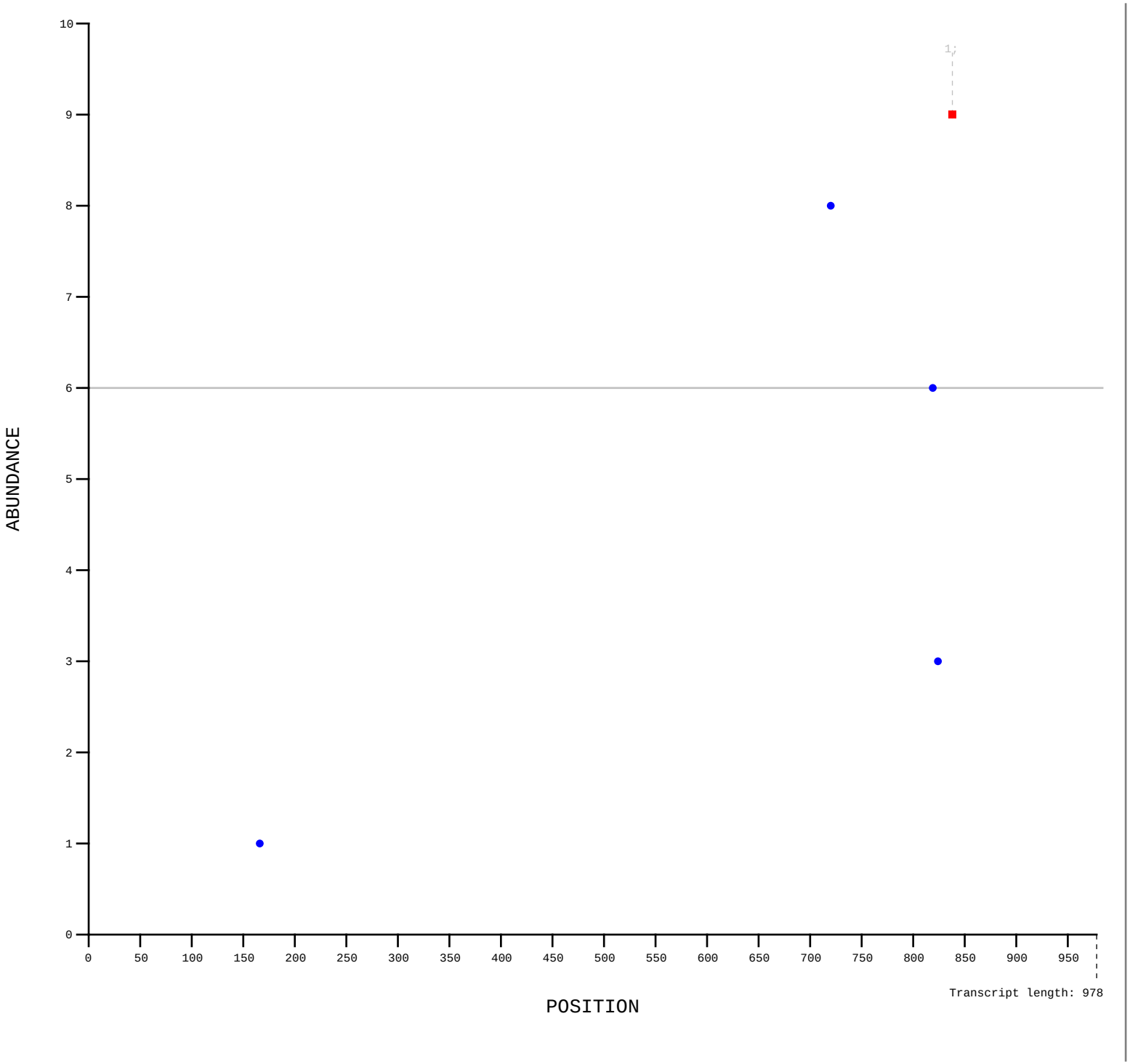
FOXG_01064T0 | Fusarium oxysporum f. sp. lycopersici 4287 N-acetyltransferase 10 (3201 nt)



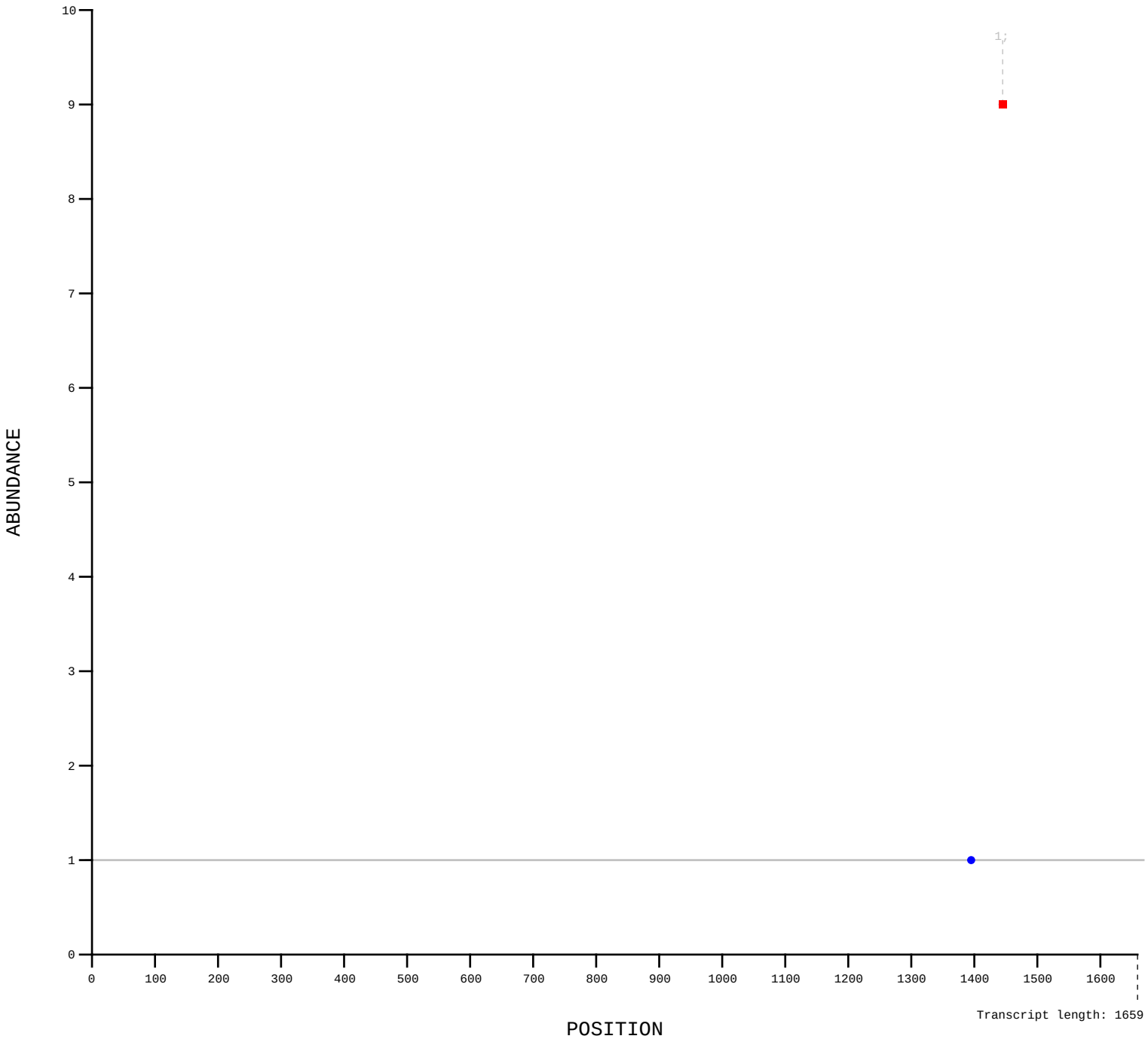
Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:2970  Abundance: 9.00(deg) 29(sRNA)
    5'    AAGAAT-AATGAGCTCTCCTTA        3'  ID:
           |||| | |||||||||| ||             Score: 4.0
    3' CGTTTCTCAGTTACTCGAGAGAAACGAAGAAG 5'  p-value: 0.0

0  #2  Position:2970  Abundance: 9.00(deg) 6(sRNA)
    5'    AAGAAT-AATGAGCTCTCCTT         3'  ID:
           |||| | |||||||||| ||             Score: 3.0
    3' CGTTTCTCAGTTACTCGAGAGAAACGAAGAAG 5'  p-value: 0.0

0  #3  Position:2970  Abundance: 9.00(deg) 5(sRNA)
    5'    AAGAAT-AATGAGCTCTCCT          3'  ID:
           |||| | |||||||||| |              Score: 3.0
    3' CGTTTCTCAGTTACTCGAGAGAAACGAAGAAG 5'  p-value: 0.0
```

FOXG_12121T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (978 nt)



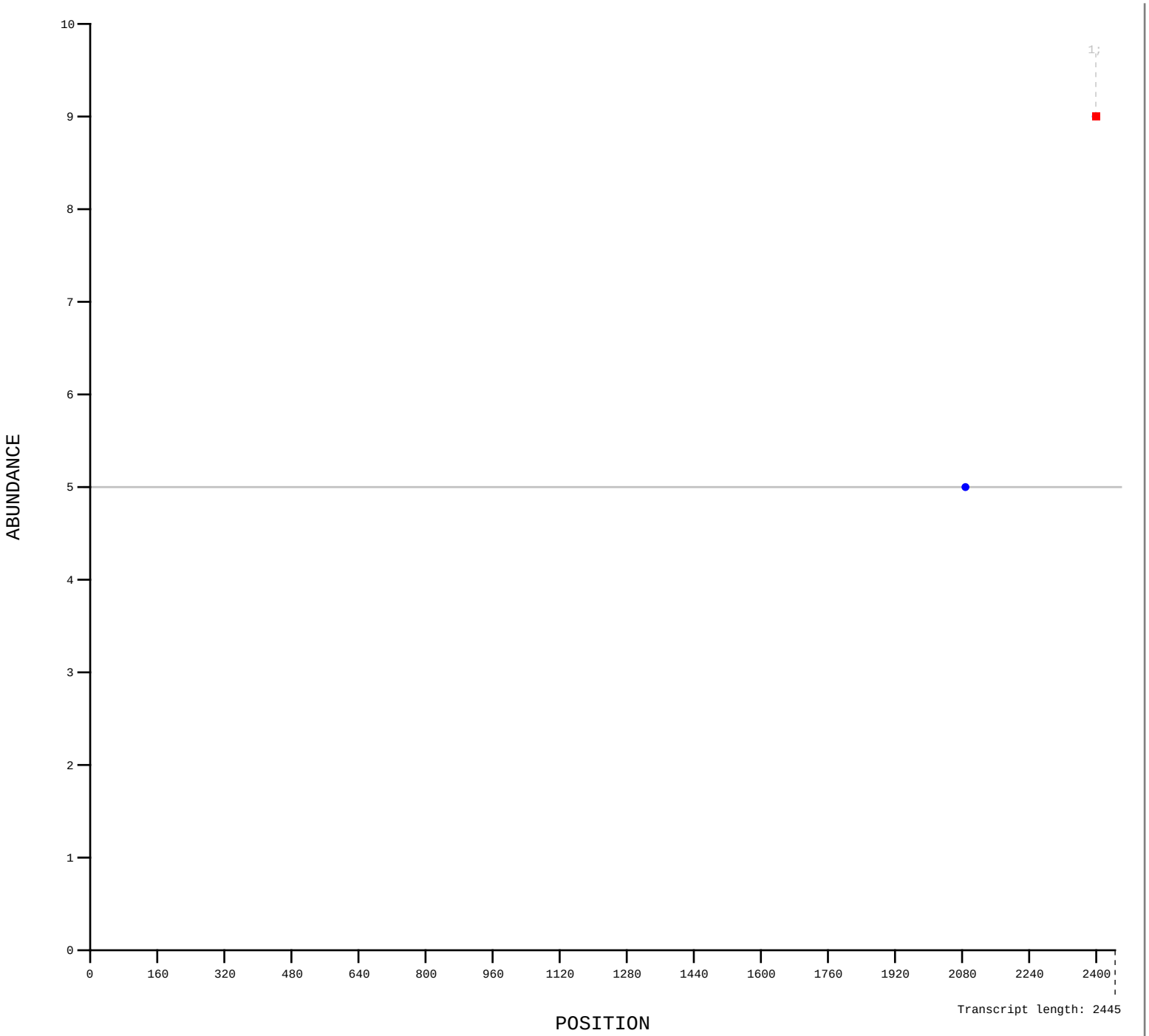
FOXG_13830T0 | Fusarium oxysporum f. sp. lycopersici 4287 small nucleolar ribonucleoprotein com (truncated)



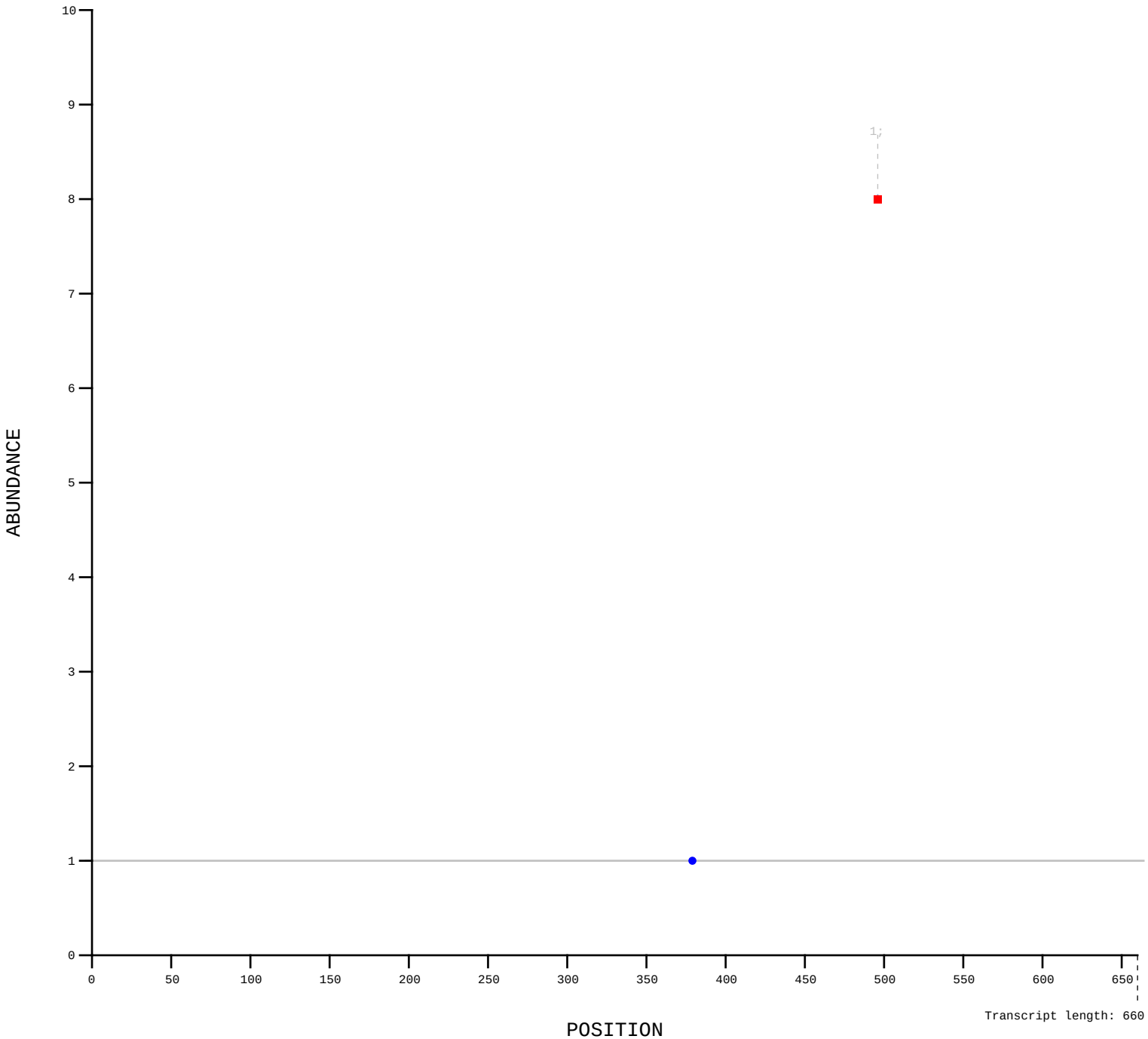
Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1445 Abundance: 9.00(deg) 12(sRNA)
5' ACGATGTCTGTAGGCGGTG 3' ID:
||||||||| ||| | | Score: 4.0
3' GAGCCGCTACAGACA-CCGACCCCACAGCTCT 5' p-value: 0.03

FOXG_08406T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2445 nt) Note(s): (truncated)



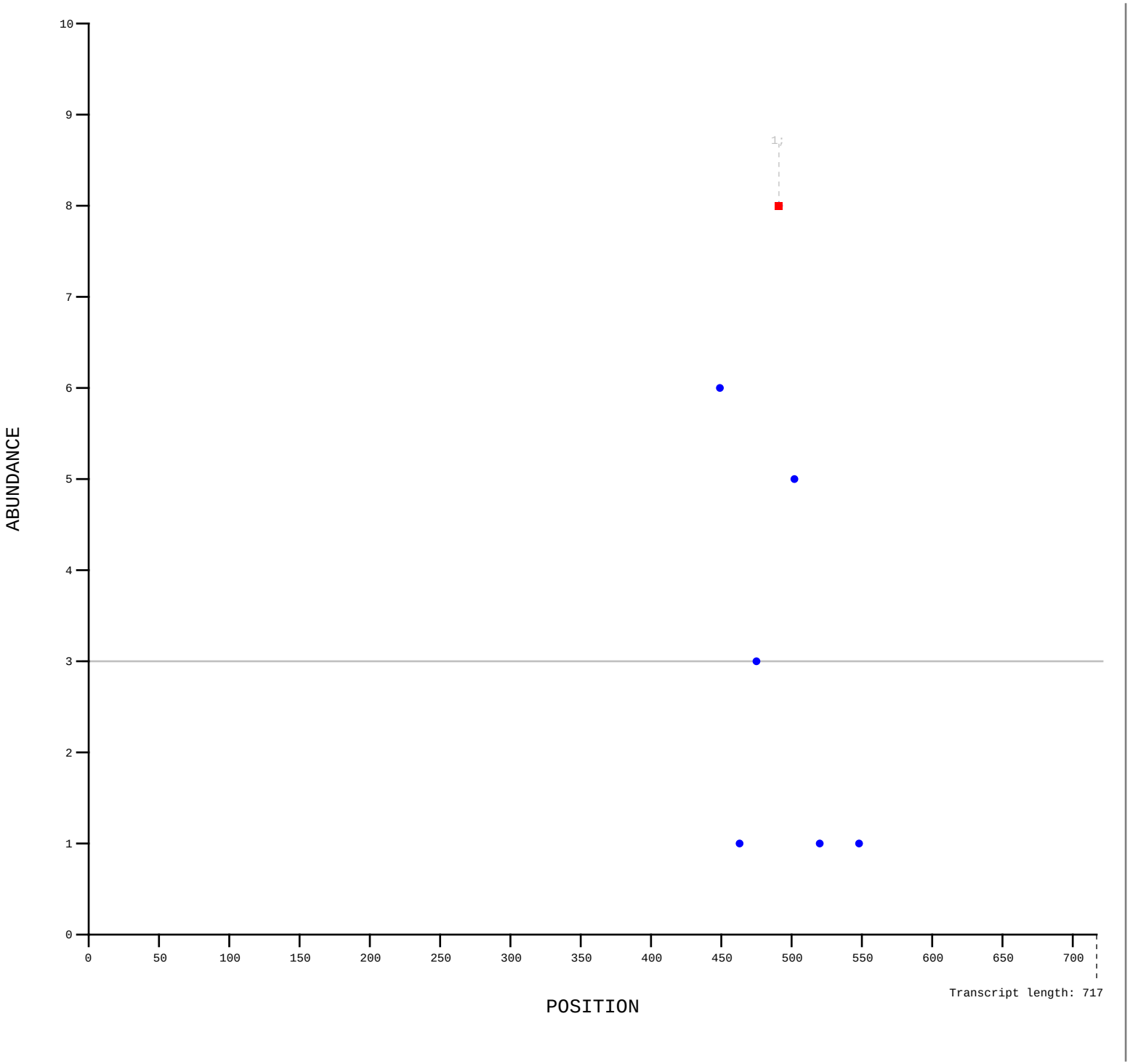
FOXG_13036T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (660 nt)



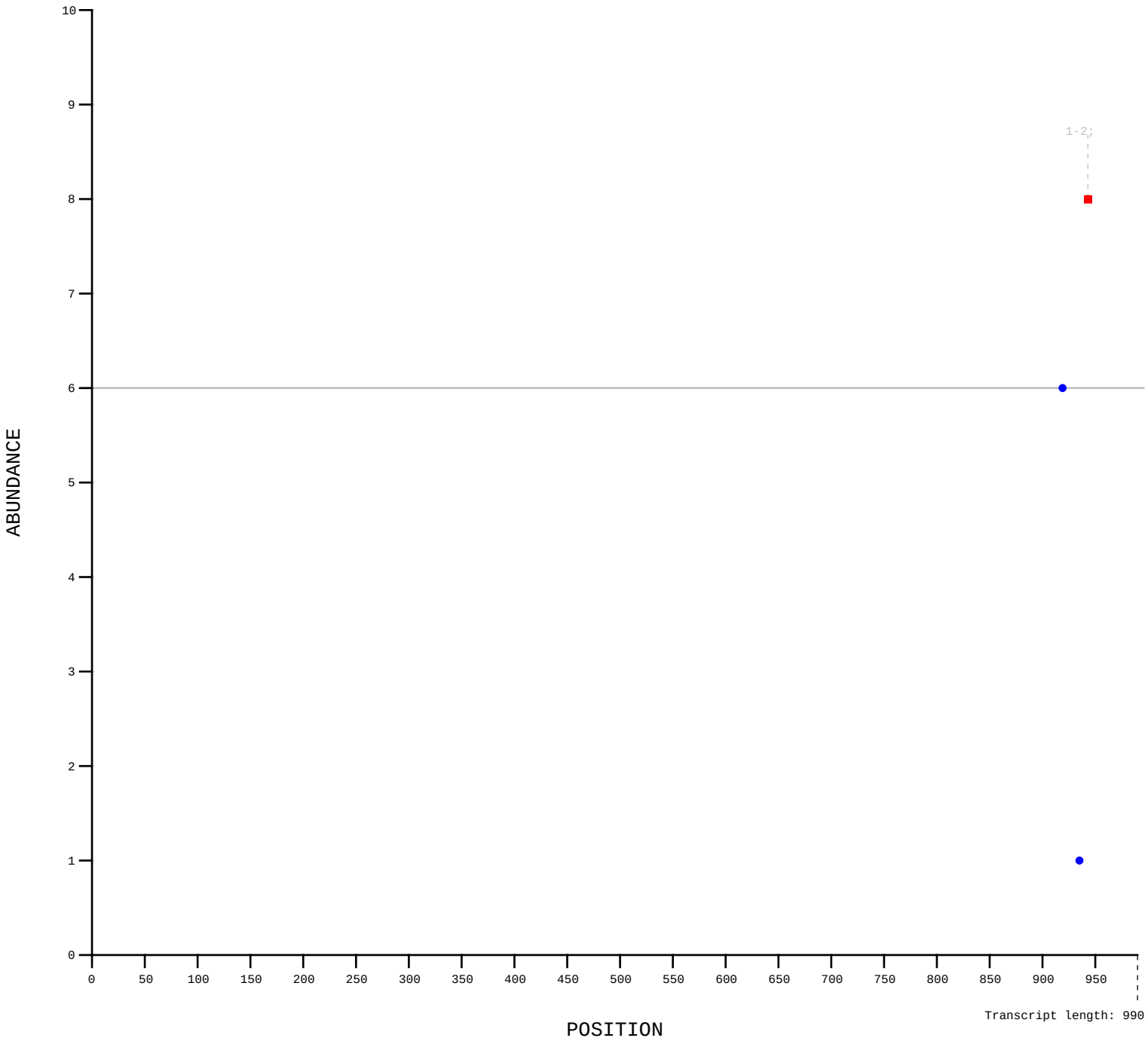
Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:496 Abundance: 8.00(deg) 45(sRNA)
5' CGATTCCCCTCGGTCGCAA 3' ID:
| |||||| ||||| |||| Score: 3.0
3' AGAAGGTAAGGGAAGCCAACGTTCAGTACGTG 5' p-value: 0.0

FOXG_00061T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (717 nt)



FOXG_05558T0 | Fusarium oxysporum f. sp. lycopersici 4287 oligosaccharyl transferase subunit gamma (990 nt)

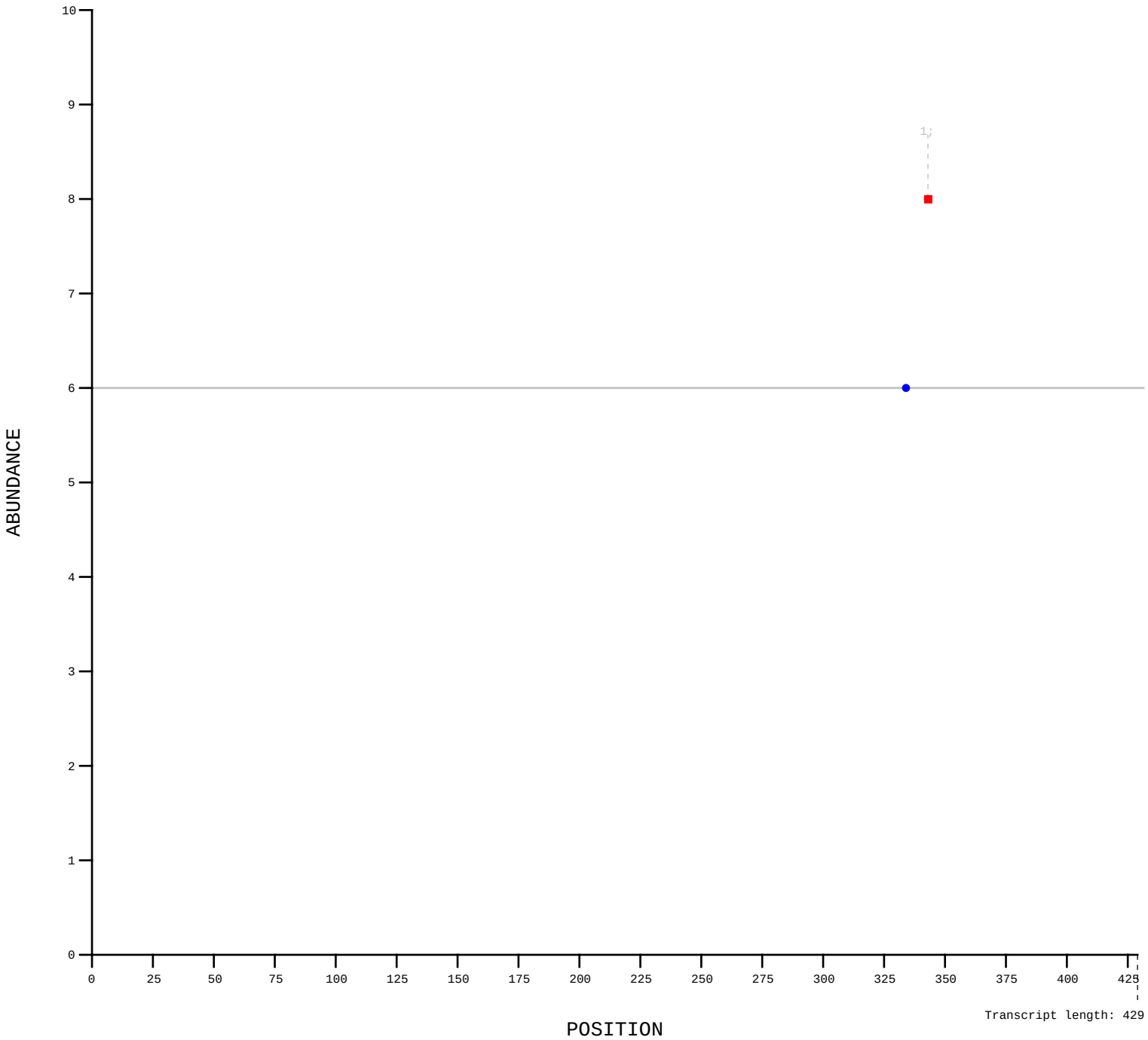


Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:943 Abundance: 8.00(deg) 27(sRNA)
5' TTAGATATCGGAGGACGAT 3' ID:
o| |||| ||||o|||| | Score: 4.0
3' CCAAGAACTAT-GCCTTCTGCGAGTCGTCTTT 5' p-value: 0.03

0 #2 Position:943 Abundance: 8.00(deg) 5(sRNA)
5' TTAGATATCGGAGGACGGT 3' ID:
o| |||| ||||o|||| | Score: 4.0
3' CCAAGAACTAT-GCCTTCTGCGAGTCGTCTTT 5' p-value: 0.01

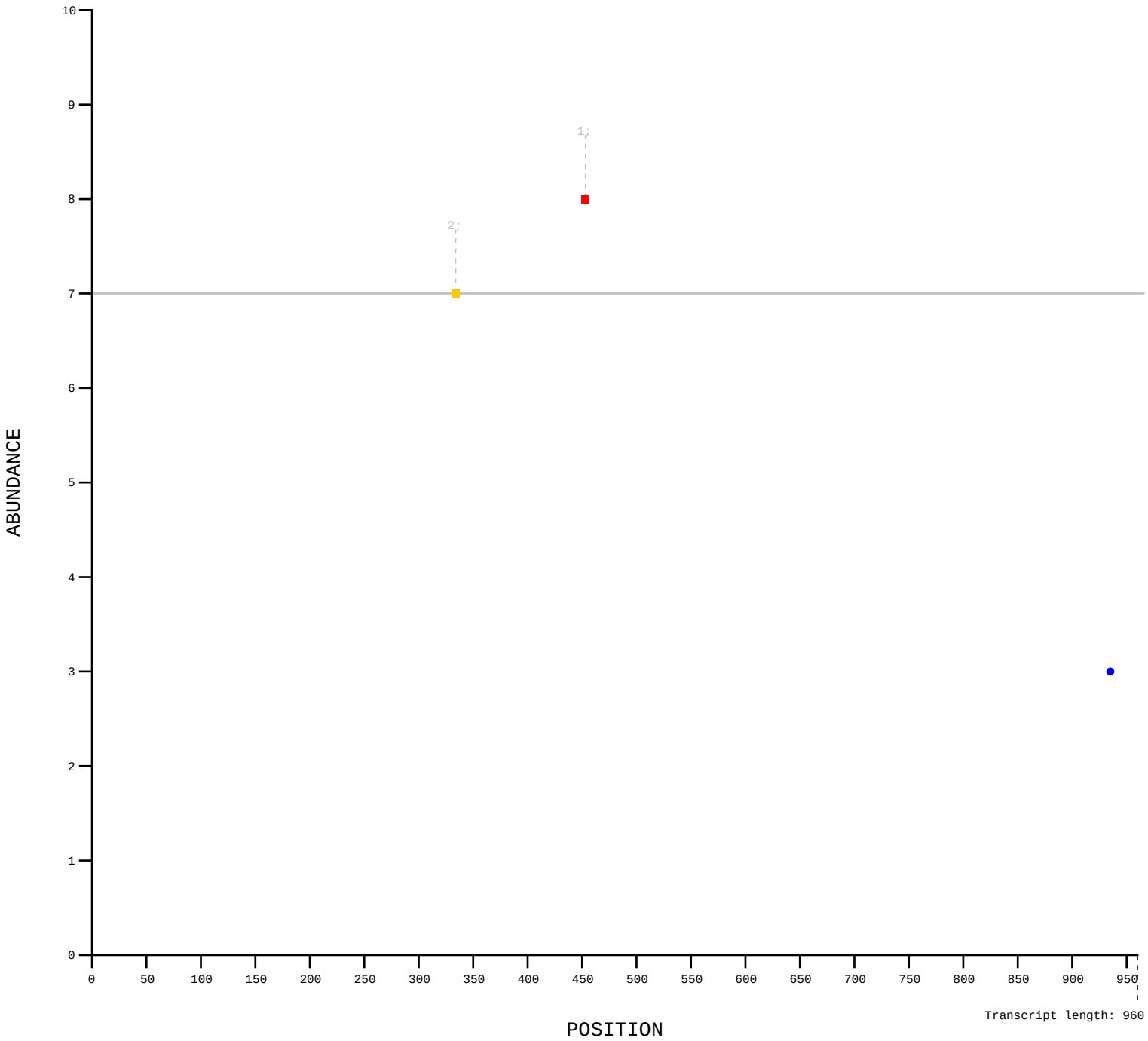
FOXG_07714T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (429 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:343 Abundance: 8.00(deg) 16(sRNA)
5' TGACTGTGTCGGTTAGATGC 3' ID:
o||||||o||o |||||o Score: 4.0
3' CCTAGCTGACACGGCTTATCTATAACACAGAA 5' p-value: 0.0

FOXG_05275T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (960 nt)

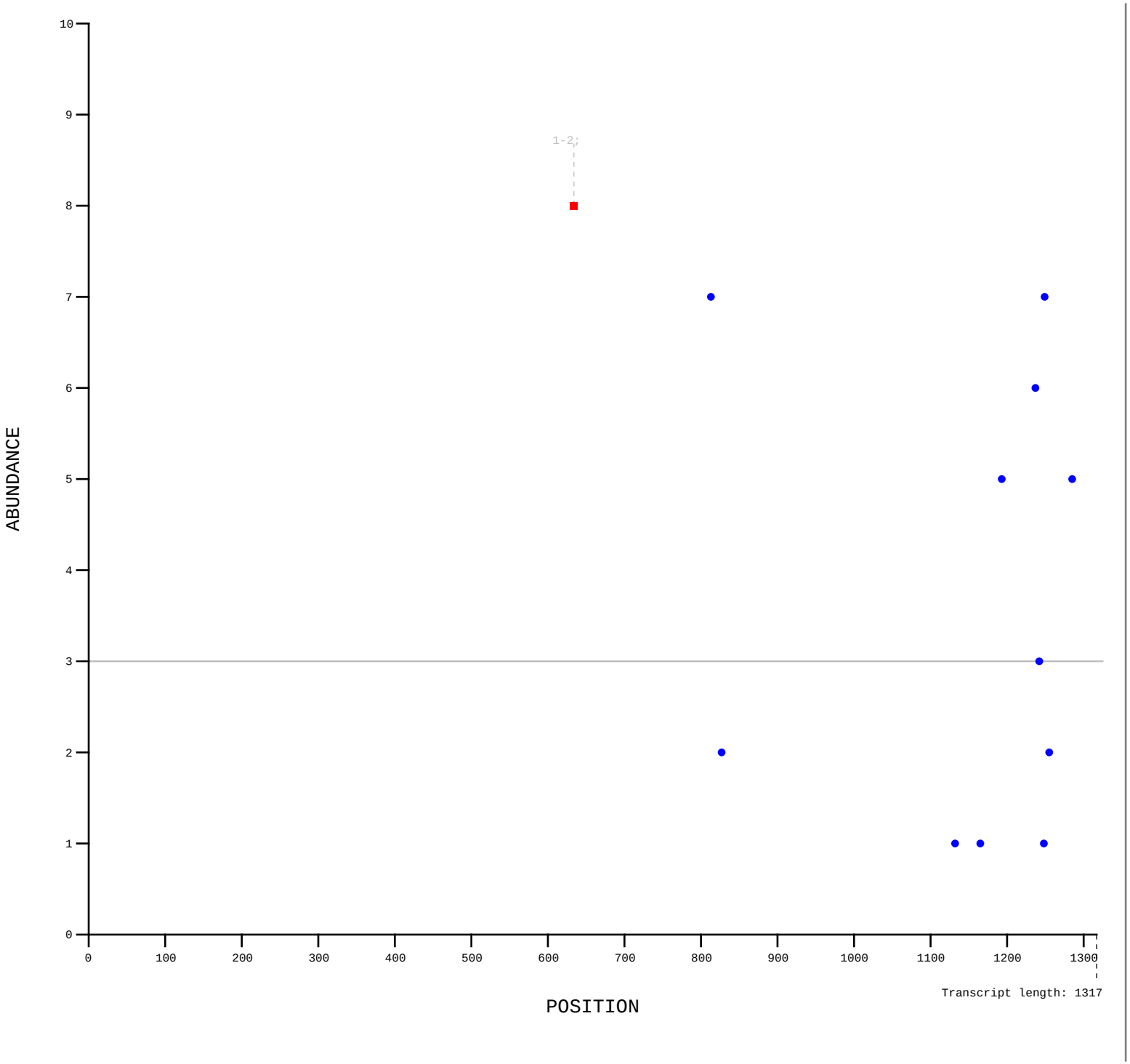


Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:453 Abundance: 8.00(deg) 10(sRNA)
5' CGCAGAAGGTCCCGAGTTC 3' ID:
||| ||||o|| ||| |o| Score: 4.0
3' CCTAGCG-CTTCTAGCGCTGAGGAACAGGAAC 5' p-value: 0.01

2 #2 Position:334 Abundance: 7.00(deg) 5(sRNA)
5' AAATTTGGAAAGATAAAGG 3' ID:
| |o|||| ||||| |||o Score: 4.0
3' TCCTTCTGAACC-TTCTACTTCTCGCCACCCT 5' p-value: 0.0

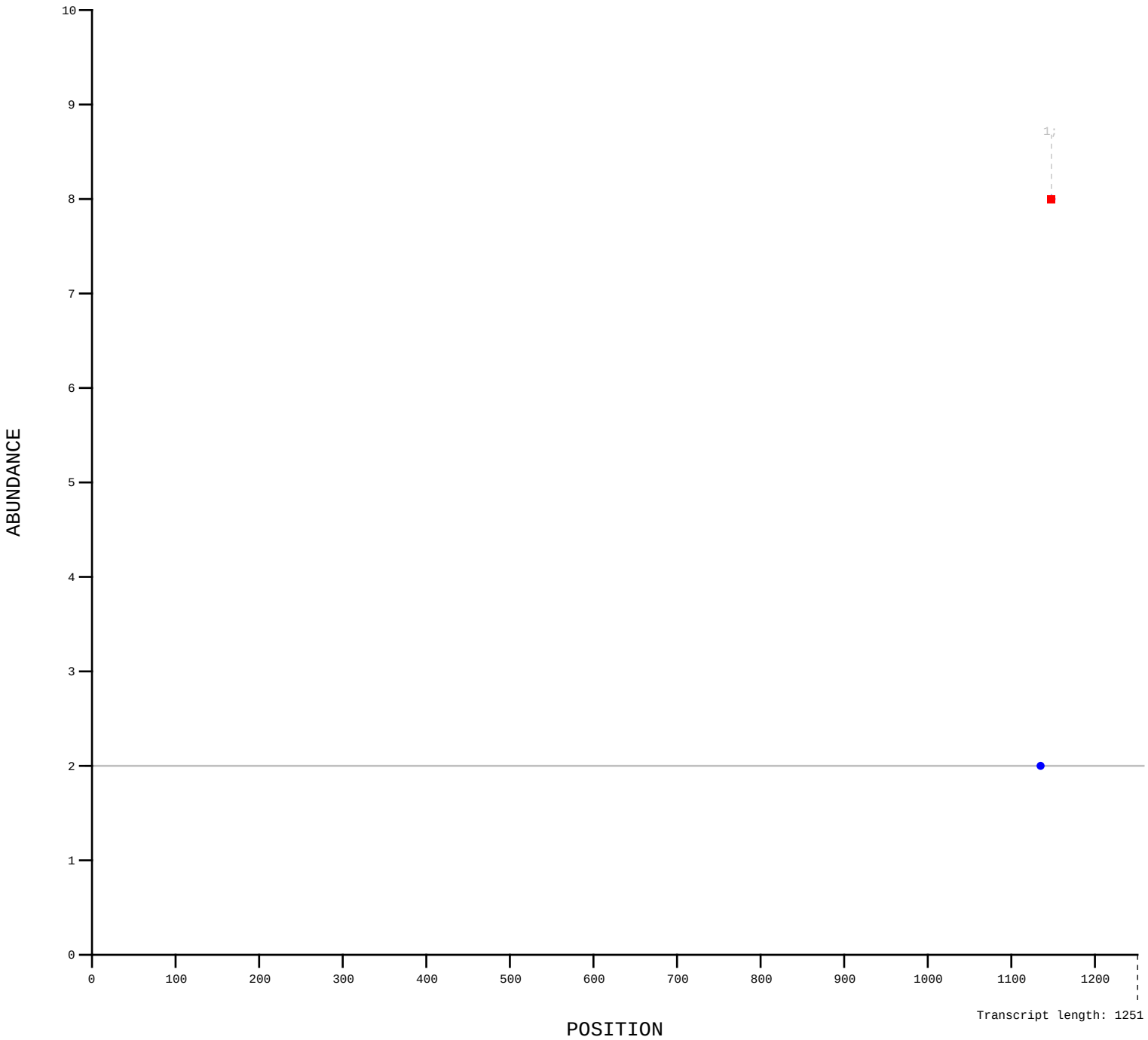
FOXG_00035T0 | Fusarium oxysporum f. sp. lycopersici 4287 enolase (1317 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:634  Abundance: 8.00(deg) 10(sRNA)
    5'     CATCACCACCCT-ATGACGGAC        3'  ID:
           || ||||||||| || || |||            Score: 4.0
    3' CCTCGTTGTGGTGGGAGTAGTGGCTGCAACGG 5'  p-value: 0.0

0  #2  Position:634  Abundance: 8.00(deg) 6(sRNA)
    5'     CATCACCACCCT-ATGACGGA         3'  ID:
           || ||||||||| || || ||             Score: 4.0
    3' CCTCGTTGTGGTGGGAGTAGTGGCTGCAACGG 5'  p-value: 0.0
```

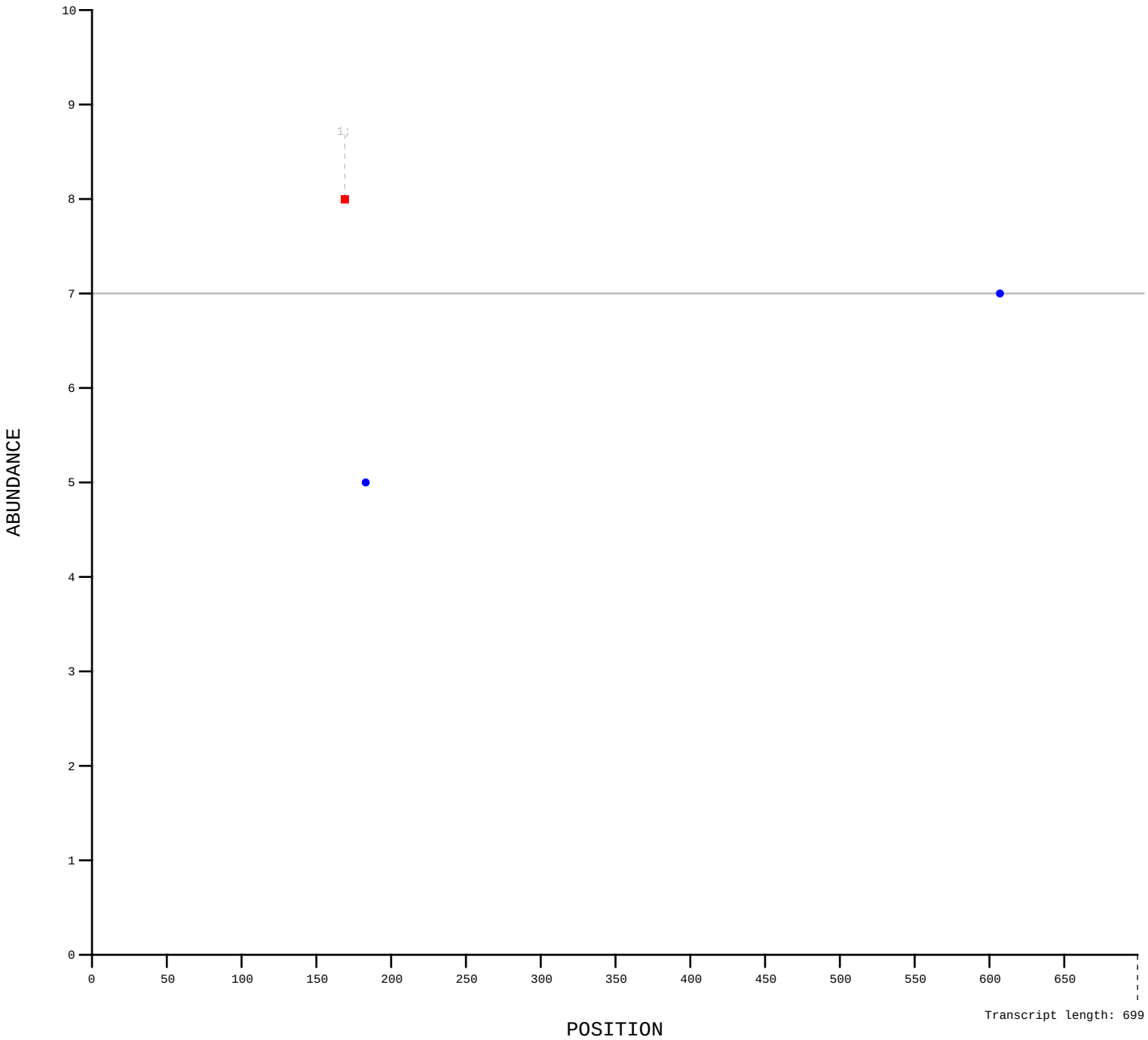
FOXG_11167T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1251 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1148 Abundance: 8.00(deg) 9(sRNA)
5' TTATAGTCGTTGAACGTCT 3' ID:
|||| ||| |||| | ||| Score: 4.0
3' TCAGAATAGCAGGAACTAGAAGACTACACAAA 5' p-value: 0.03

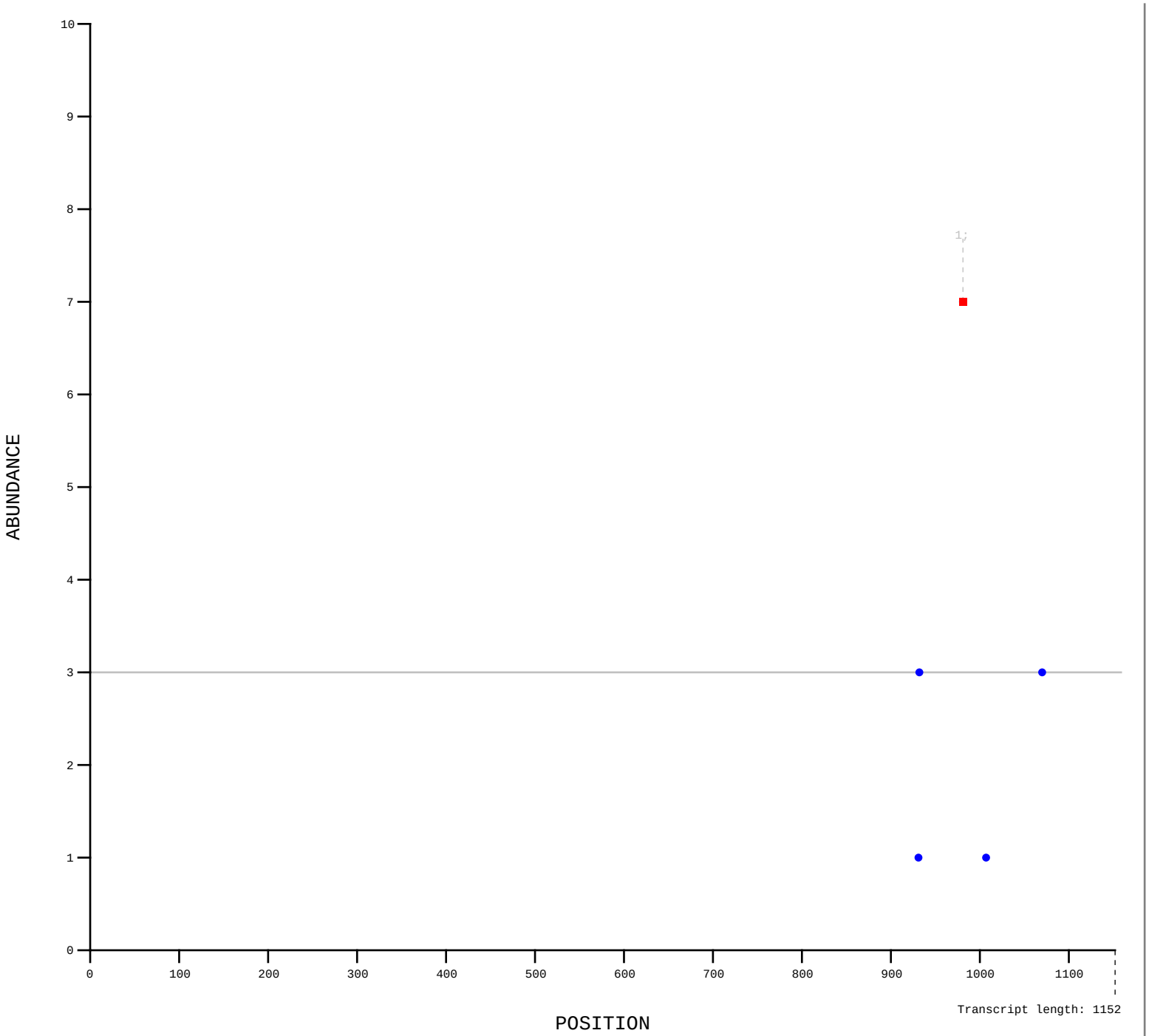
FOXG_00291T0 | Fusarium oxysporum f. sp. lycopersici 4287 bromodomain associated protein (699 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:169 Abundance: 8.00(deg) 5(sRNA)
5' TTGGTTATGGCATCTCGTT 3' ID:
|||o|||| ||||| |o| Score: 4.0
3' GCGGAACTAATA-CGTAGCGTACGACCCGTCA 5' p-value: 0.01

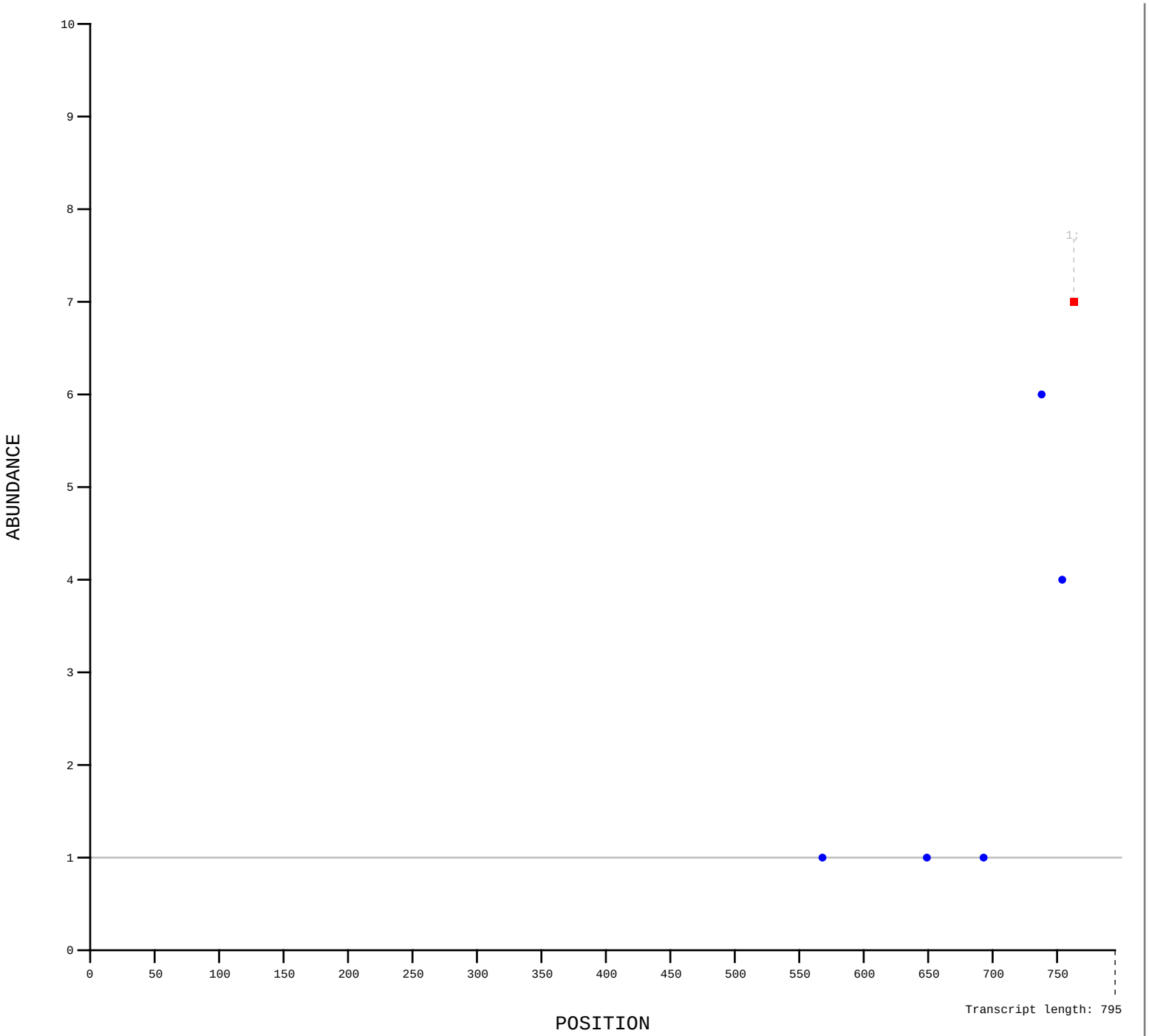
FOXG_07910T0 | Fusarium oxysporum f. sp. lycopersici 4287 inositolphosphorylceramide-B C-26 hydroxylase (1152 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:981 Abundance: 7.00(deg) 23(sRNA)
5' TAATGTTGTGAAACTGTGG 3' ID:
||||| ||||| | o||o| Score: 4.0
3' CTTCATTAC-ACACTCTAGCATCGTCTGCATA 5' p-value: 0.01

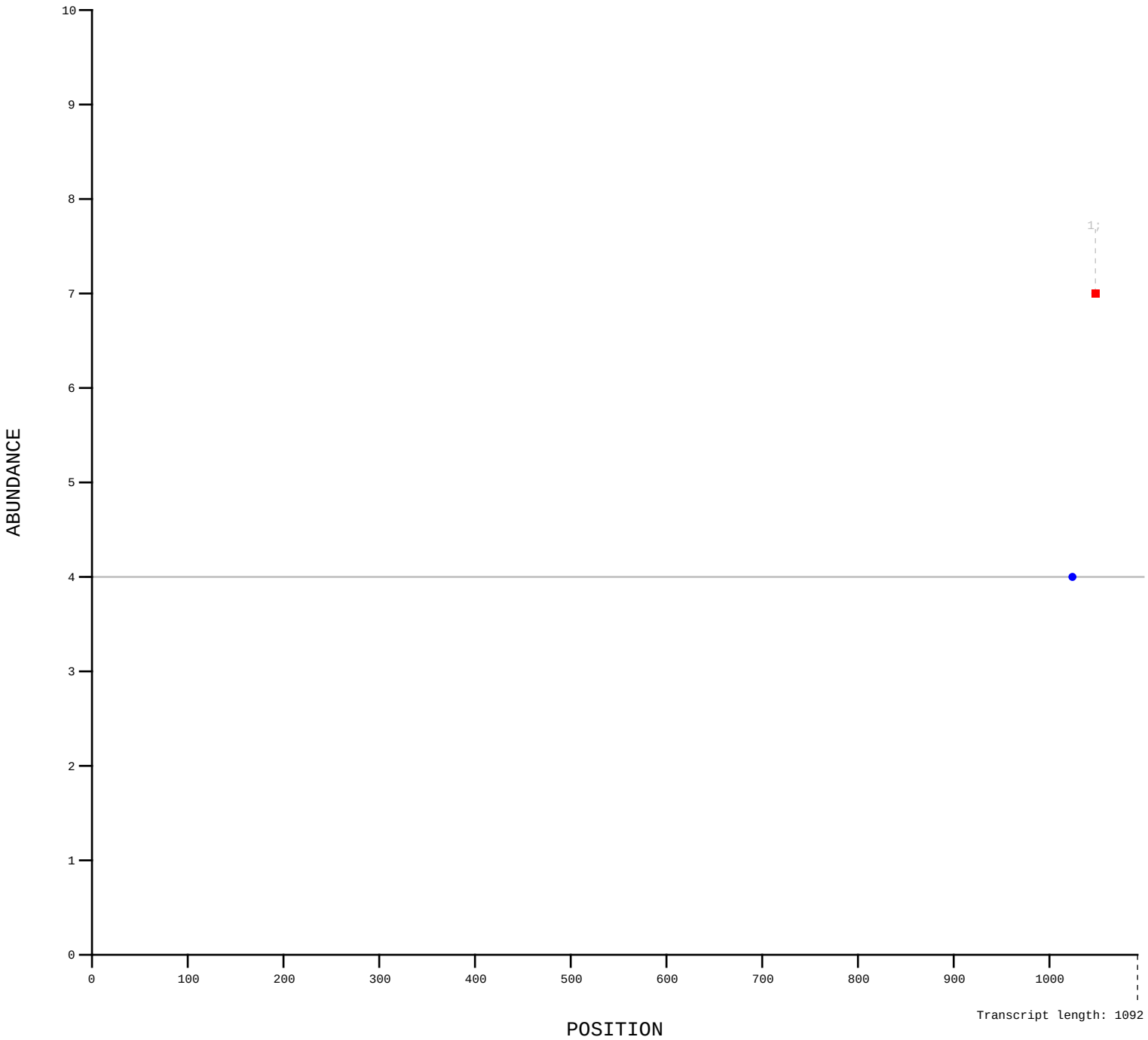
FOXG_04260T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (795 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:763 Abundance: 7.00(deg) 6(sRNA)
5' CGGCACCTCAGAACCAGAA 3' ID:
|| || |o|||||||o | Score: 4.0
3' TATAGCGGTCGGGTCTTGGTTATATTACACCG 5' p-value: 0.03

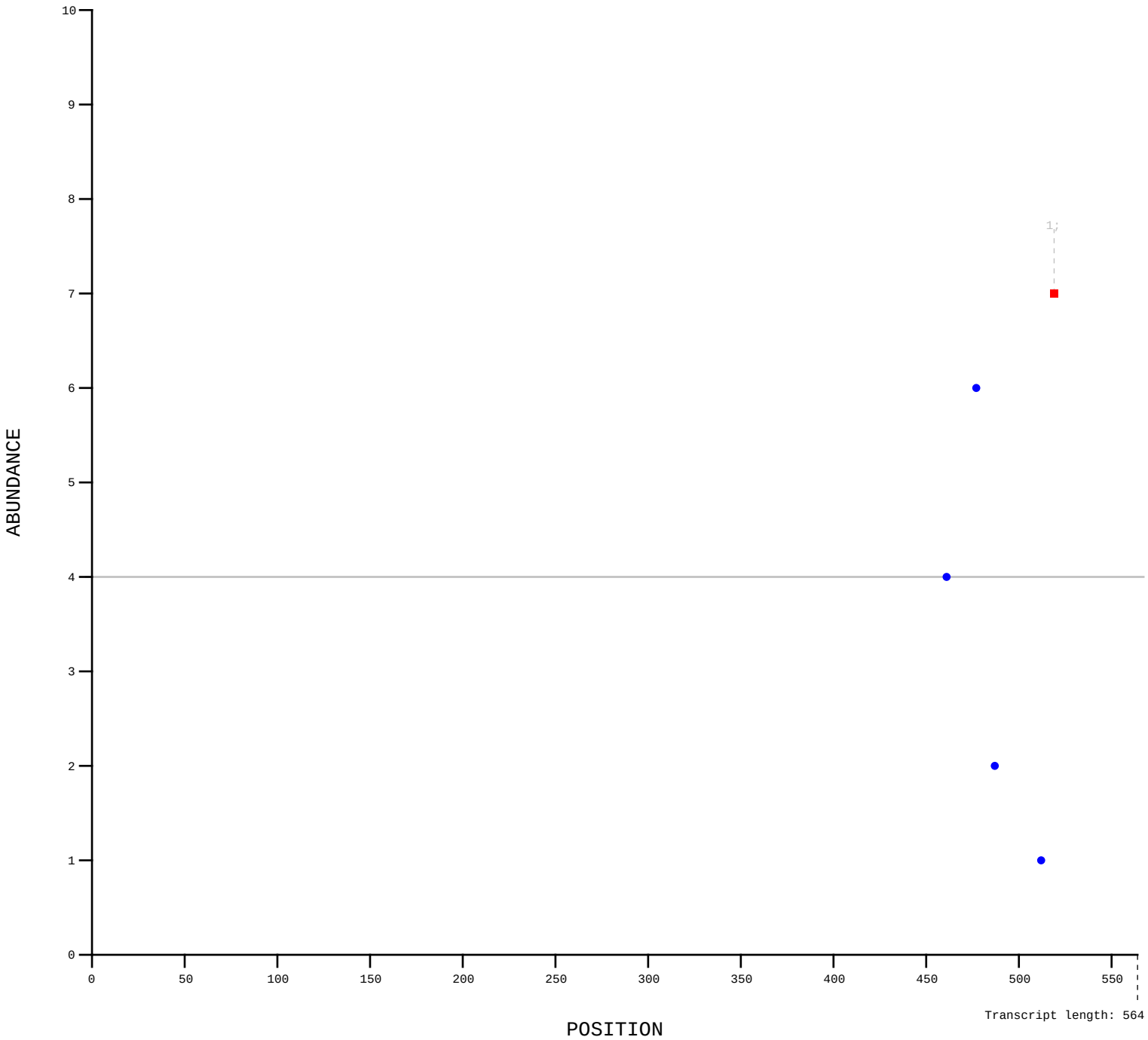
FOXG_05979T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1092 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1048 Abundance: 7.00(deg) 5(sRNA)
5' TAGCTTTGACCTG-GACGAC 3' ID:
o ||o||||||| | |||| Score: 4.0
3' AGCAGCCGGAACTGGACTCAGCTGCTACATAG 5' p-value: 0.0

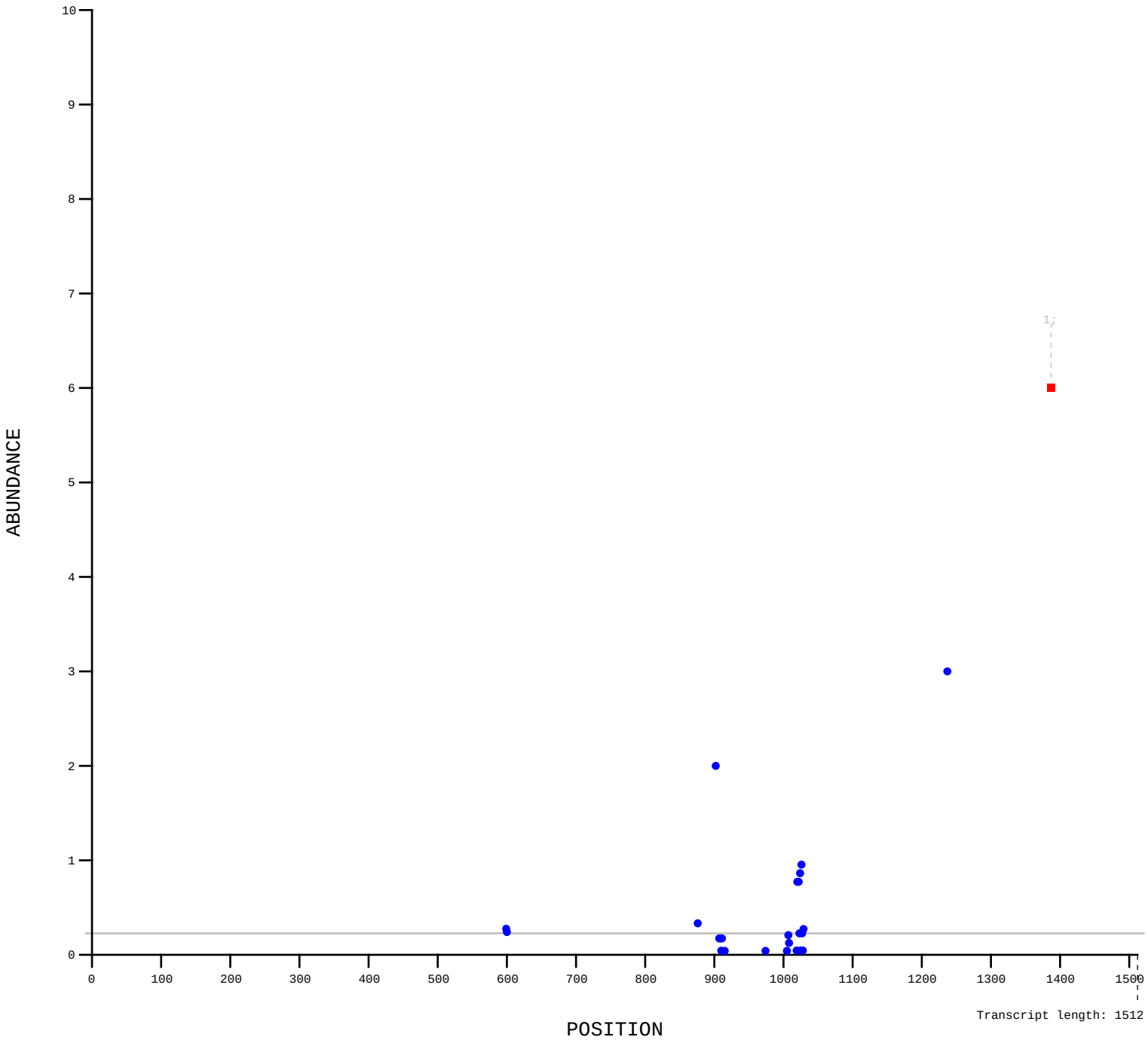
FOXG_01973T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (564 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:519 Abundance: 7.00(deg) 5(sRNA)
5' TCTGGCTGTGACGATGGCT 3' ID:
o| | ||||||||| |||o Score: 4.0
3' CCAAGGCCGGACACTGCT-CCGGCAACTTCCT 5' p-value: 0.02

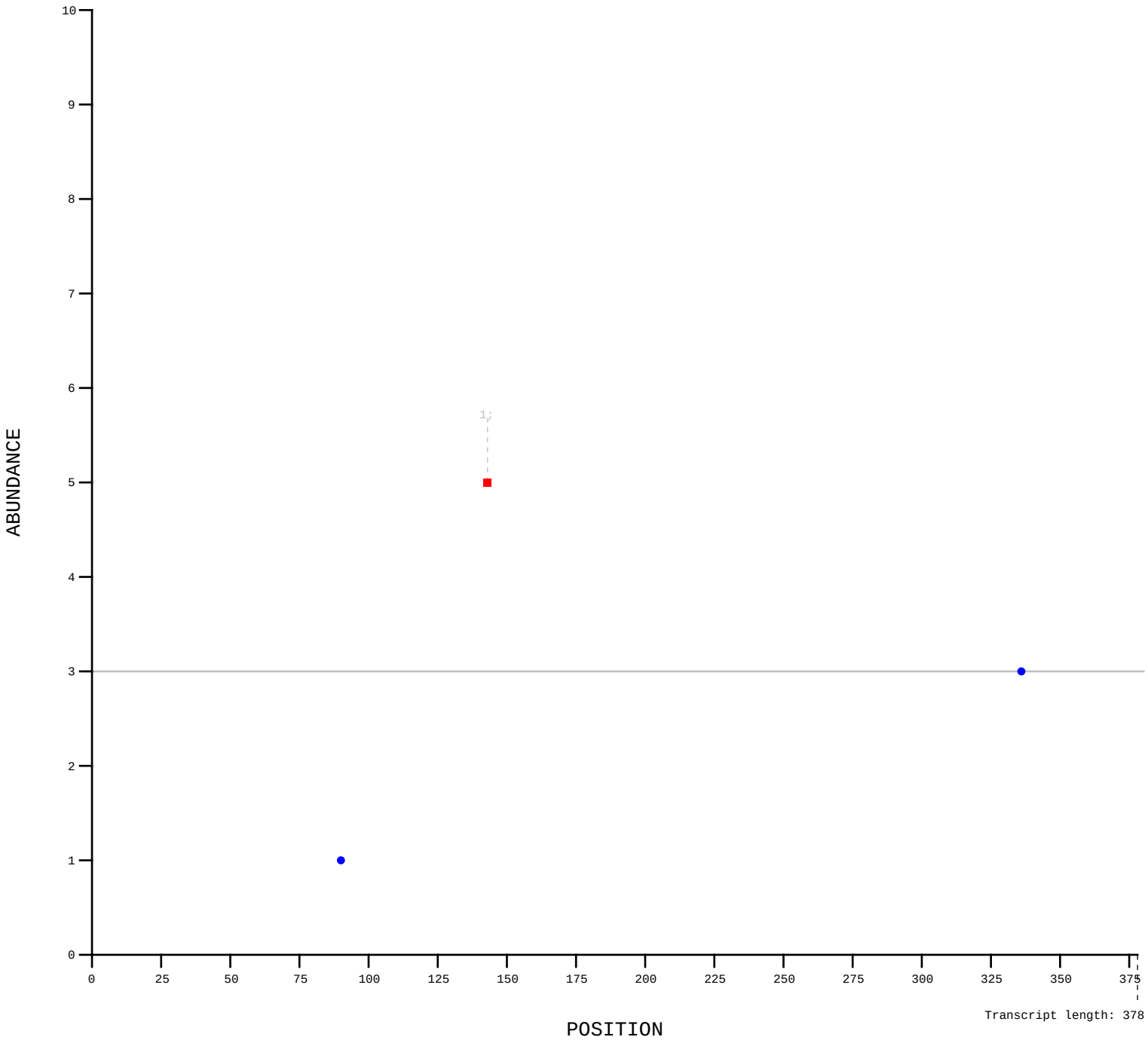
FOXG_09996T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1512 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1387 Abundance: 6.00(deg) 10(sRNA)
5' TTAAATCATCAGACATAGA 3' ID:
oo||||||||||| || | Score: 4.0
3' CGGGGGTTTAGTAGTCTAGATGTTTATCGGAG 5' p-value: 0.0

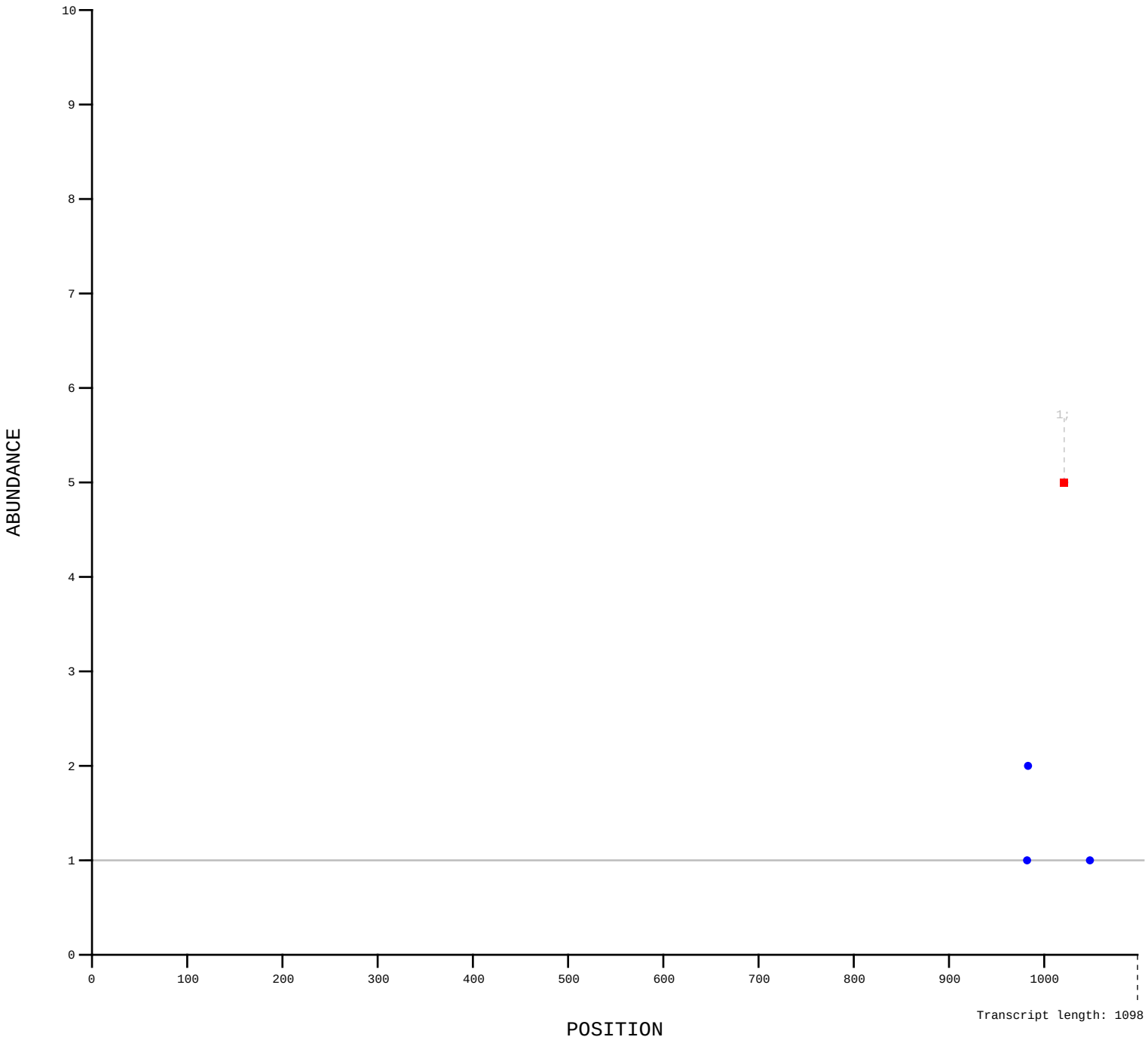
FOXG_07599T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (378 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:143 Abundance: 5.00(deg) 32(sRNA)
5' TGAAGCTCTGAAGGAAGGA 3' ID:
||||||| ||| ||||o Score: 3.5
3' CCCCACTTCGA-ACTCCCTTCTCGACAAGAAG 5' p-value: 0.0

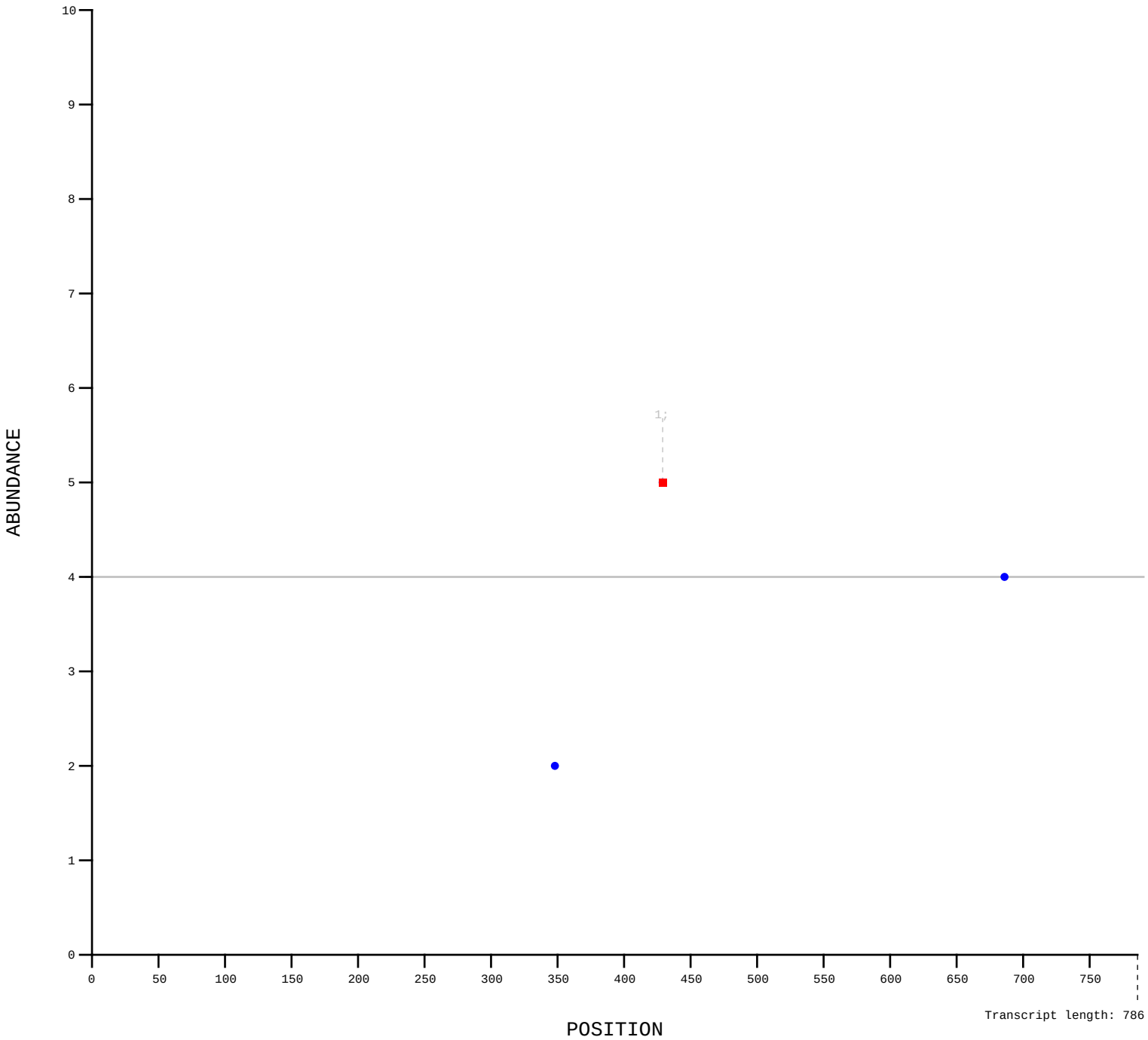
FOXG_17419T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1098 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:1021 Abundance: 5.00(deg) 10(sRNA)
5' TAGGATTAAGATTAGCCGC 3' ID:
||||| ||||| ||| || Score: 4.0
3' CGGTATCCT-ATTCTTATCATCGGTCCTCCTC 5' p-value: 0.0

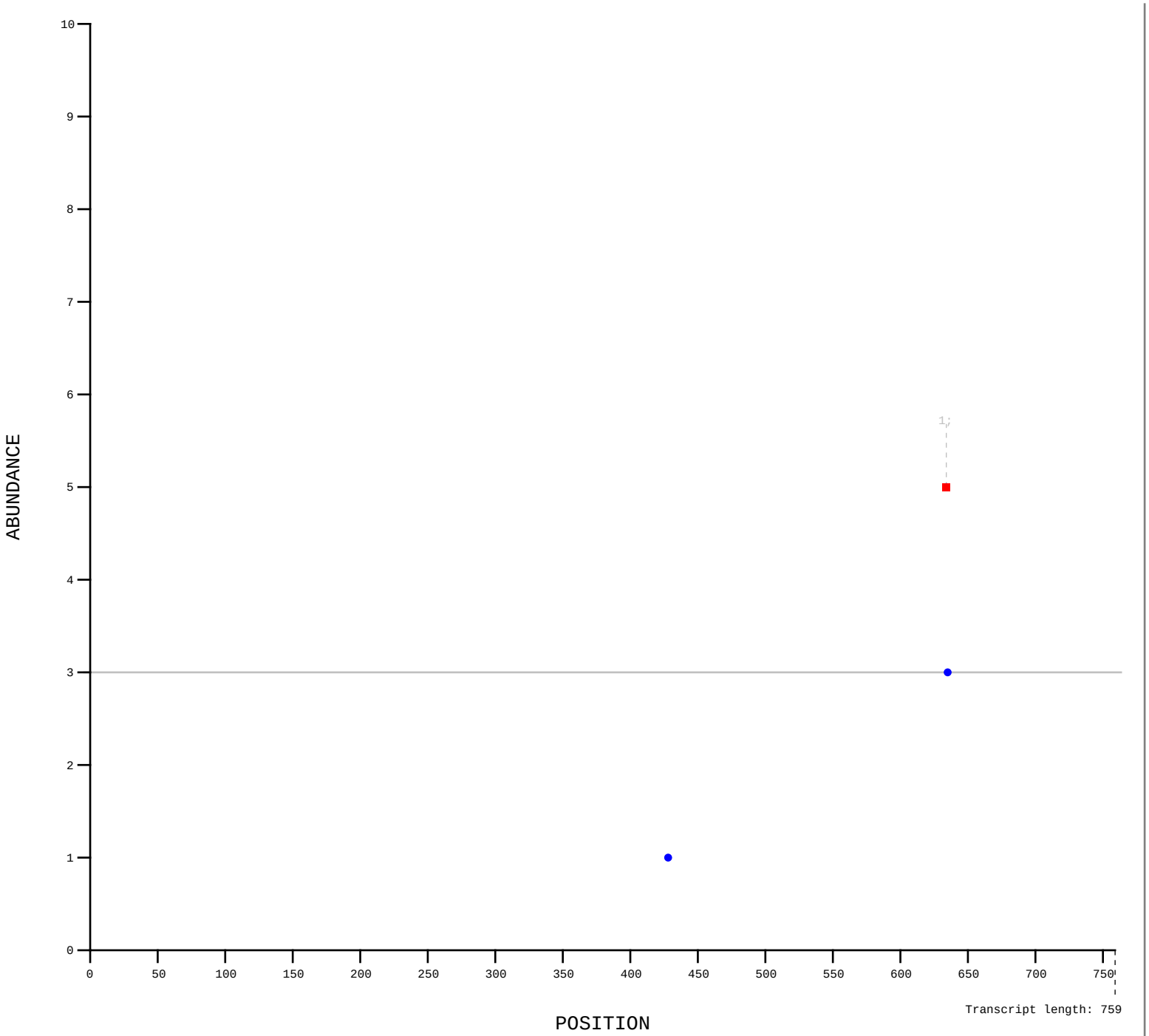
FOXG_00189T0 | Fusarium oxysporum f. sp. lycopersici 4287 20S proteasome subunit (786 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:429 Abundance: 5.00(deg) 8(sRNA)
5' GTCGACAAGGAGATAGGCT 3' ID:
o |o||||||||| || | Score: 4.0
3' CCGGTCGTTGTTCCTCTA-CCAAGGTGTCTCC 5' p-value: 0.02

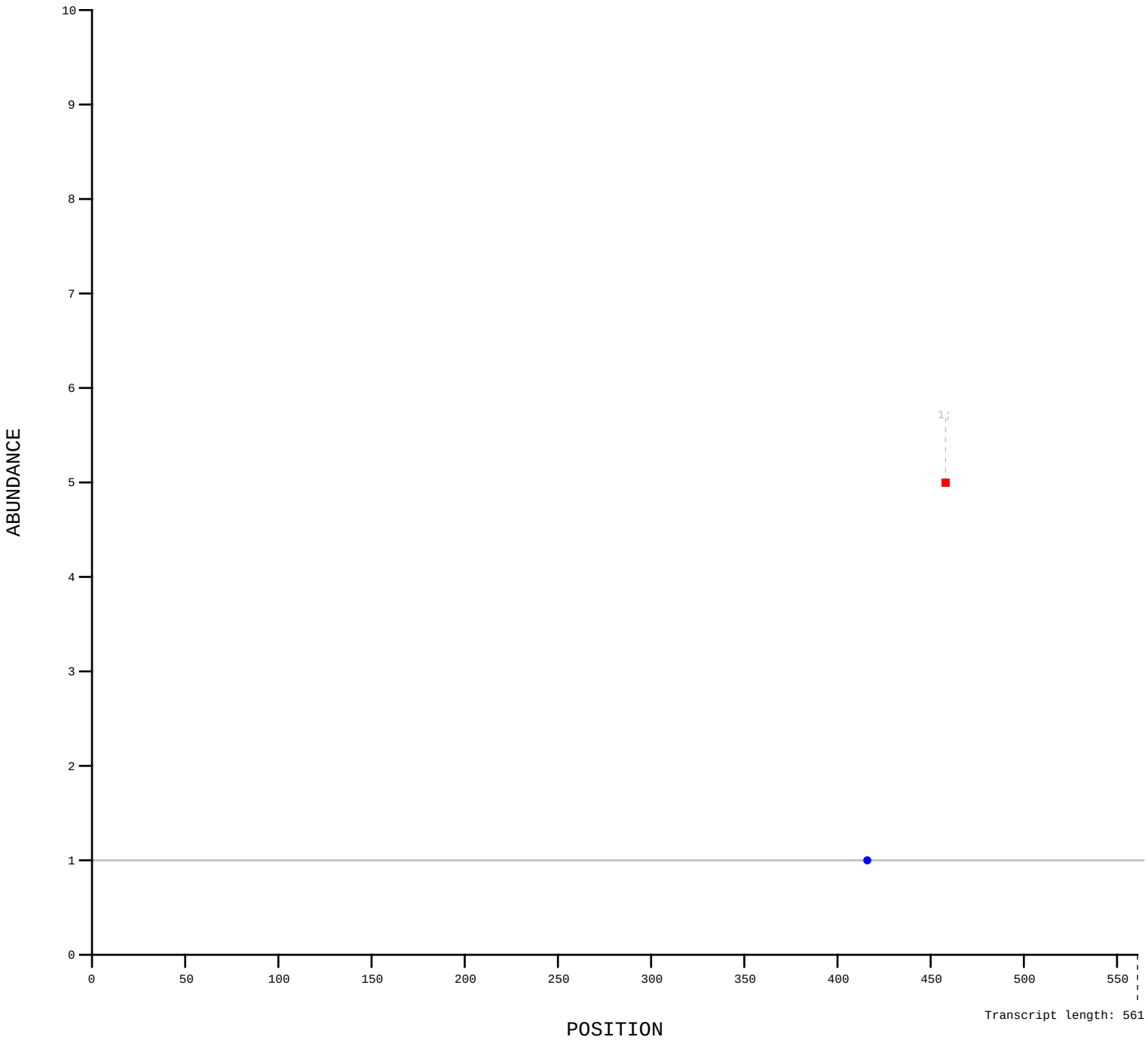
FOXG_07809T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (759 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:634 Abundance: 5.00(deg) 8(sRNA)
5' CTTTATGATGA-CGTCGCGG 3' ID:
||o| |||||| | ||o||| Score: 4.0
3' GGAGGAGAAACTACTCGGAGTGCCACTGCGGA 5' p-value: 0.02

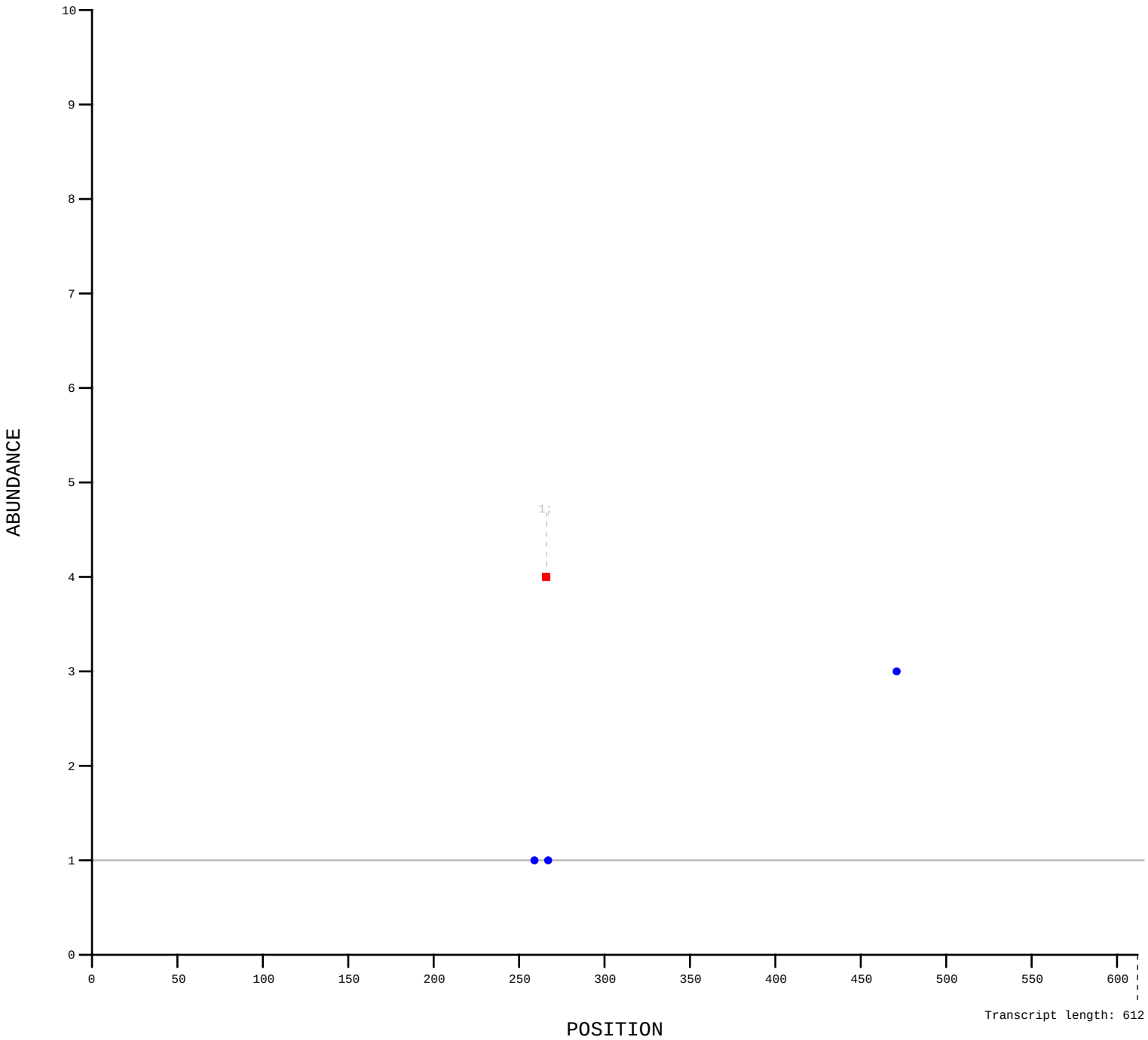
FOXG_03524T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (561 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:458  Abundance: 5.00(deg) 5(sRNA)
    5'     GCTAAAGCTAGGATTAGAA          3'  ID:
           ||o||||| ||||o | |               Score: 4.0
    3' TTCGCGGTTTCGCTCCTAGACGTCAAAAGAGG 5'  p-value: 0.0
```

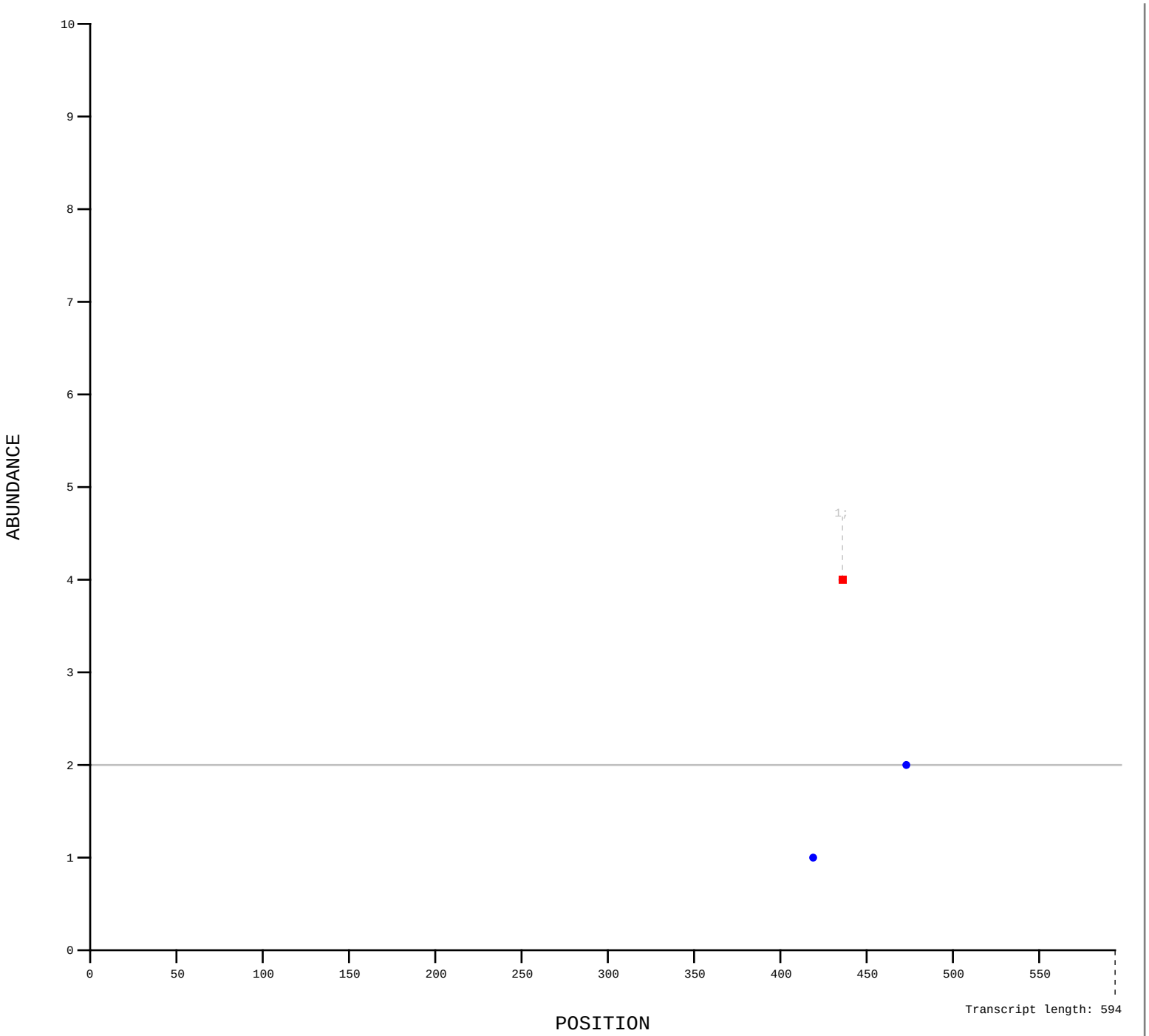
FOXG_06092T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (612 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:266 Abundance: 4.00(deg) 8(sRNA)
5' TTGAGTGGGAGGGTTAGAGA 3' ID:
| ||o||| |||||o|| || Score: 4.0
3' ATGCATCTTACCATCCCAGTCCCTCATAAGTC 5' p-value: 0.04

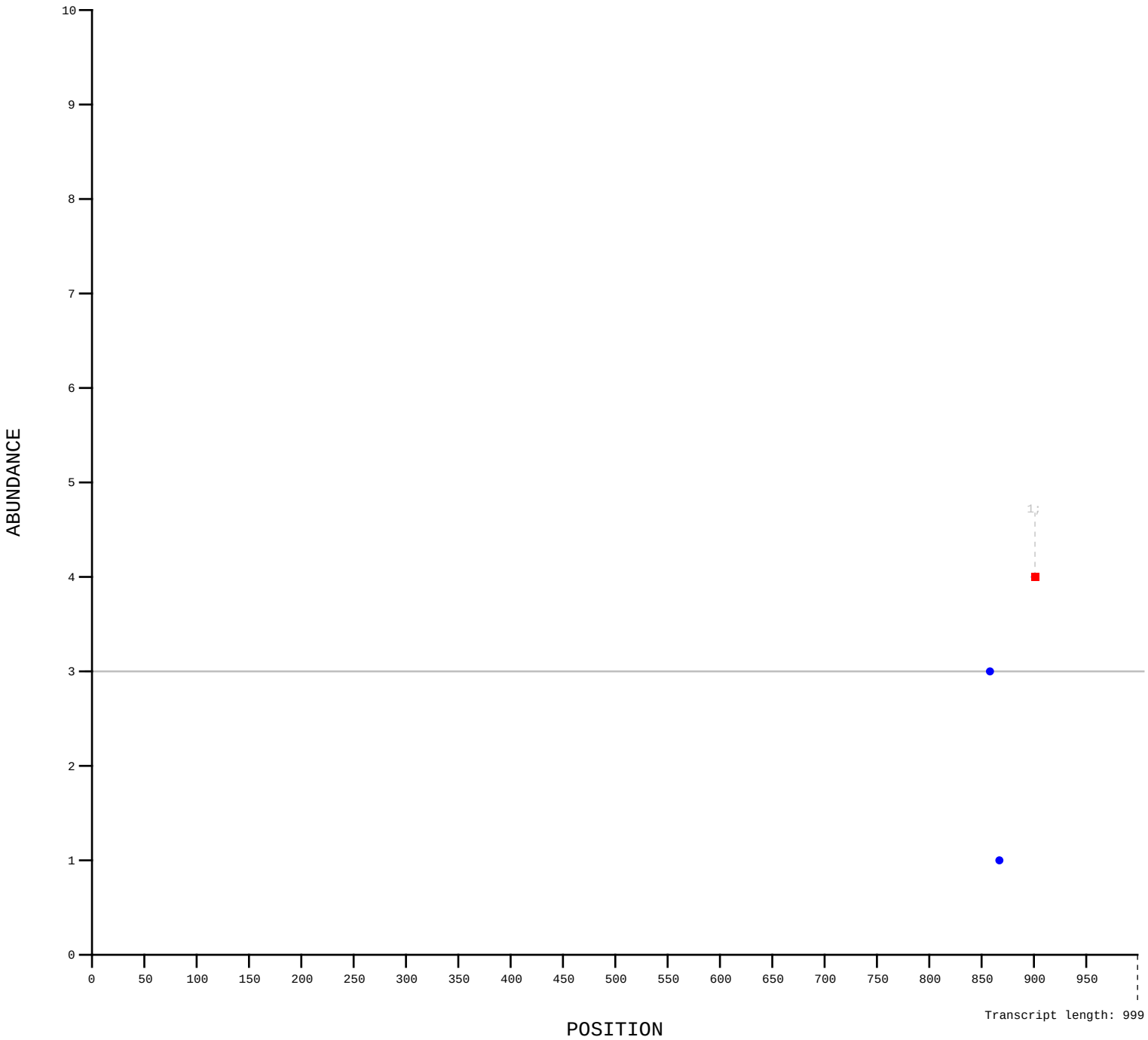
FOXG_03365T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (594 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:436  Abundance: 4.00(deg) 5(sRNA)
    5'    TGAGT-TTGGTGATGGCTCTG          3'  ID:
           ||||| |||||| ||| o|o|             Score: 4.0
    3' GGCACTCAGAACCACCACCAGGGCAACGGCCC 5'  p-value: 0.03
```

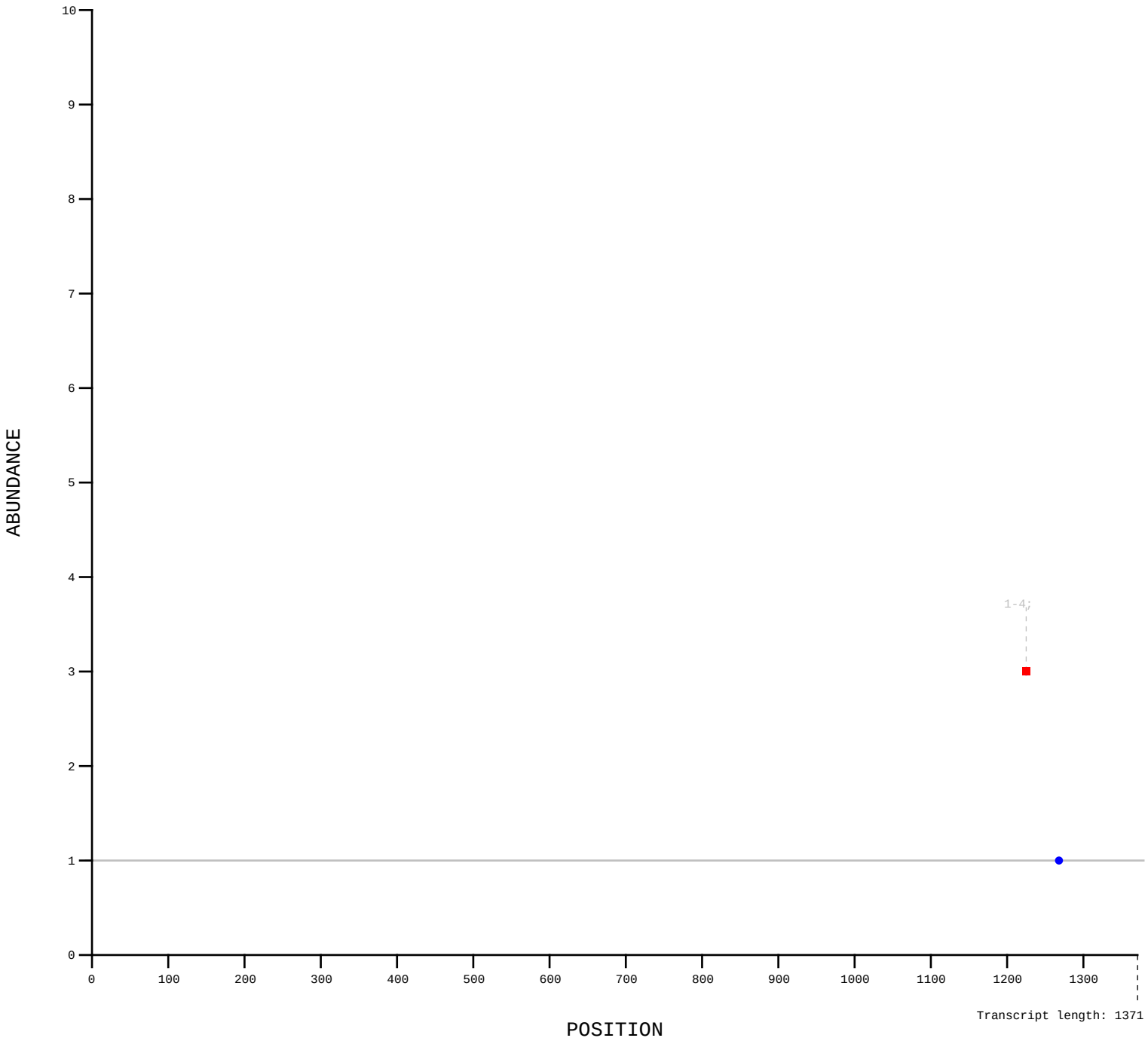
FOXG_15827T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (999 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:901 Abundance: 4.00(deg) 5(sRNA)
5' TGAGAATAGTGAACTTATT 3' ID:
|||o||o||||| |o| || Score: 3.5
3' CGCTACTTTTGTCACT-GGAGAAGGAAGCTGG 5' p-value: 0.01

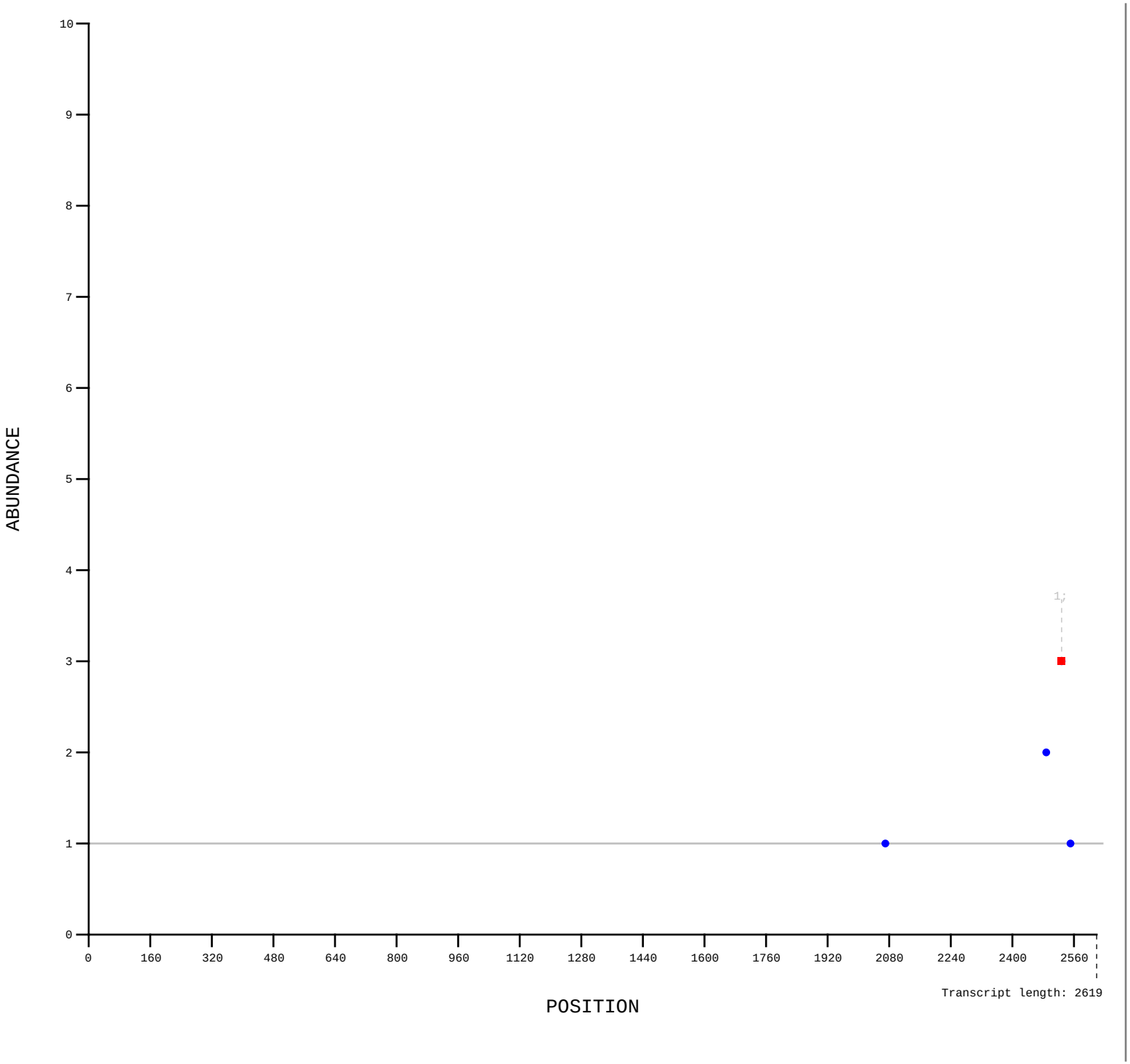
FOXG_04985T0 | Fusarium oxysporum f. sp. lycopersici 4287 golgi integral membrane protein Cln3 (1371 nt) (truncated)



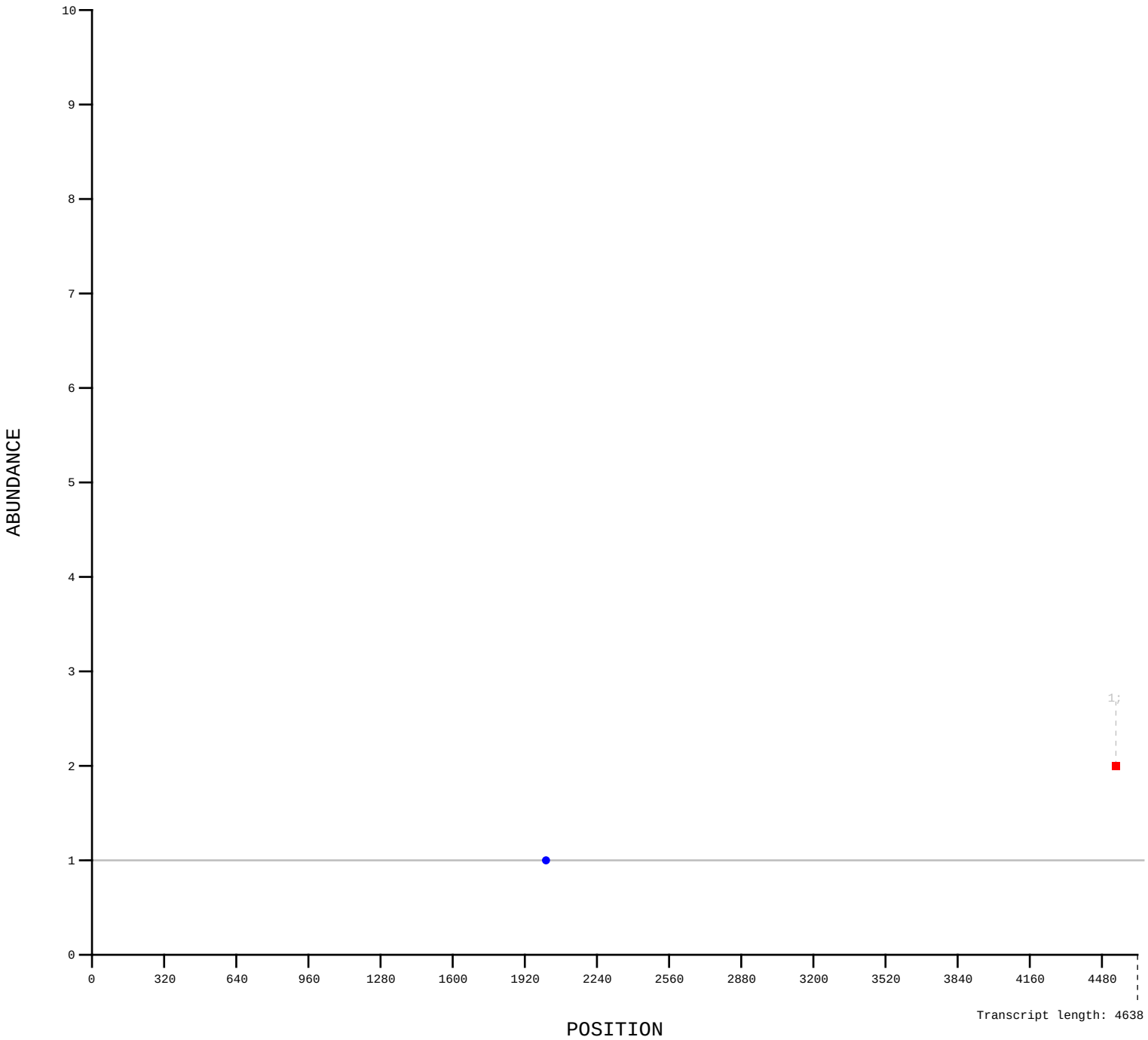
Category: 0 1 2 3 4
Degradome alignment: Median:

```
0  #1  Position:1225  Abundance: 3.00(deg) 49(sRNA)
   5'     CAGGACTGAATGCTTTATCGT        3'  ID:
          ||o||||o||| ||o|||| |            Score: 3.5
   3' CGAGGTTCTGATTTAAGAGATAGGAGCCCACC 5'  p-value: 0.0

0  #2  Position:1225  Abundance: 3.00(deg) 32(sRNA)
   5'     TGAGATTAAATTCTGTACC          3'  ID:
          oo|||o||||||| || |               Score: 3.5
   3' CGAGGTTCTGATTTAAGAGATAGGAGCCCACC 5'  p-value: 0.01

0  #3  Position:1225  Abundance: 3.00(deg) 22(sRNA)
   5'     CAGGACTGAATGCTTTATC          3'  ID:
          ||o||||o||| ||o||||              Score: 2.5
   3' CGAGGTTCTGATTTAAGAGATAGGAGCCCACC 5'  p-value: 0.0

0  #4  Position:1225  Abundance: 3.00(deg) 5(sRNA)
   5'     CAGGACTGAATGCTTTATCG         3'  ID:
          ||o||||o||| ||o||||              Score: 3.5
   3' CGAGGTTCTGATTTAAGAGATAGGAGCCCACC 5'  p-value: 0.0
```

FOXG_10289T0 | Fusarium oxysporum f. sp. lycopersici 4287 vacuolar protein sorting-associated protein 35 (2619 nt)



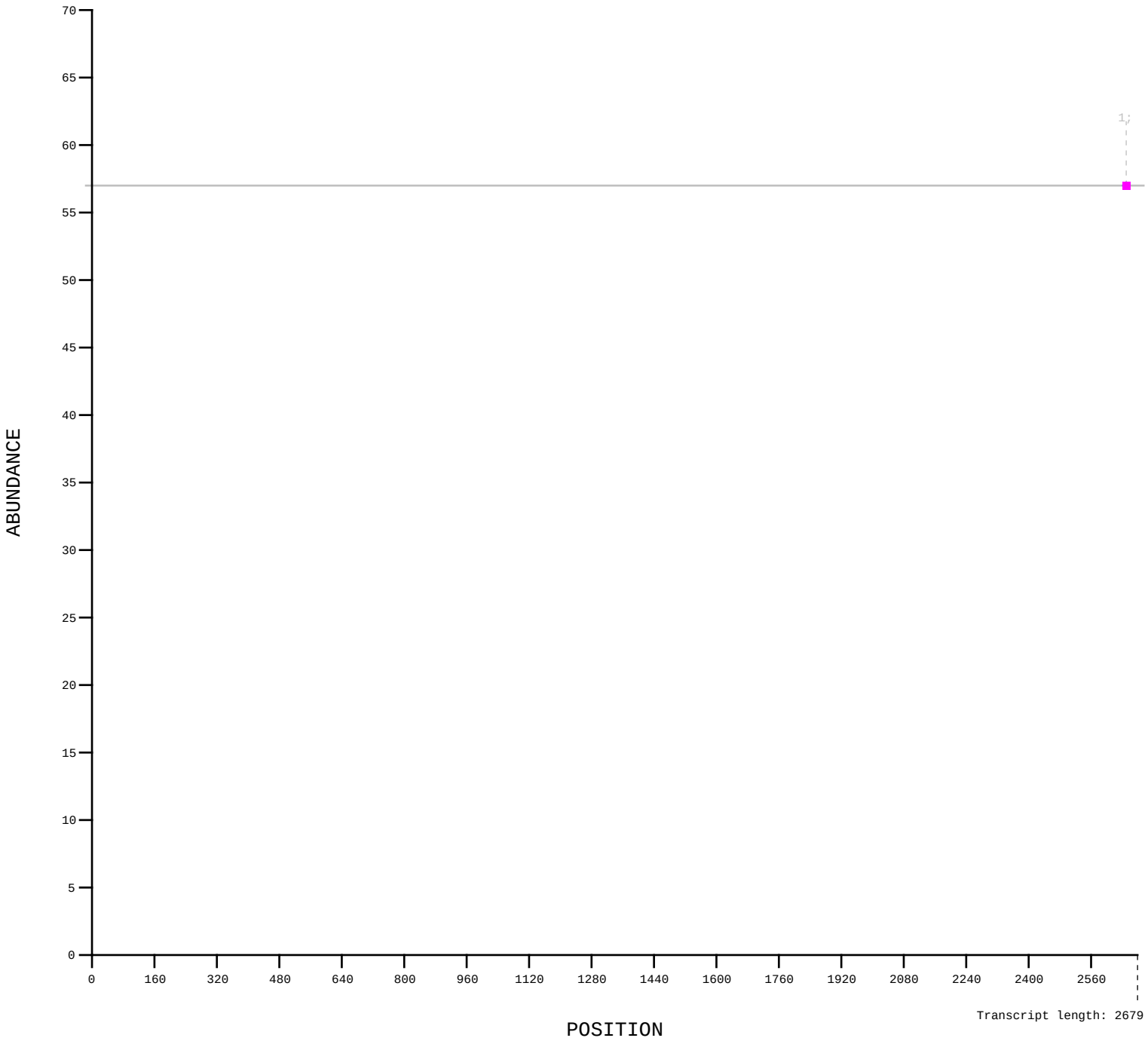
FOXG_01612T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (4638 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

0 #1 Position:4542 Abundance: 2.00(deg) 5(sRNA)
5' TAAAGCTCGCAGACTCTTCG 3' ID:
o|| || |||||||o||| | Score: 4.0
3' GGTGGTTACG-GCGTCTGGGAACCGCATAAGC 5' p-value: 0.0

FOXG_09230T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2679 nt)



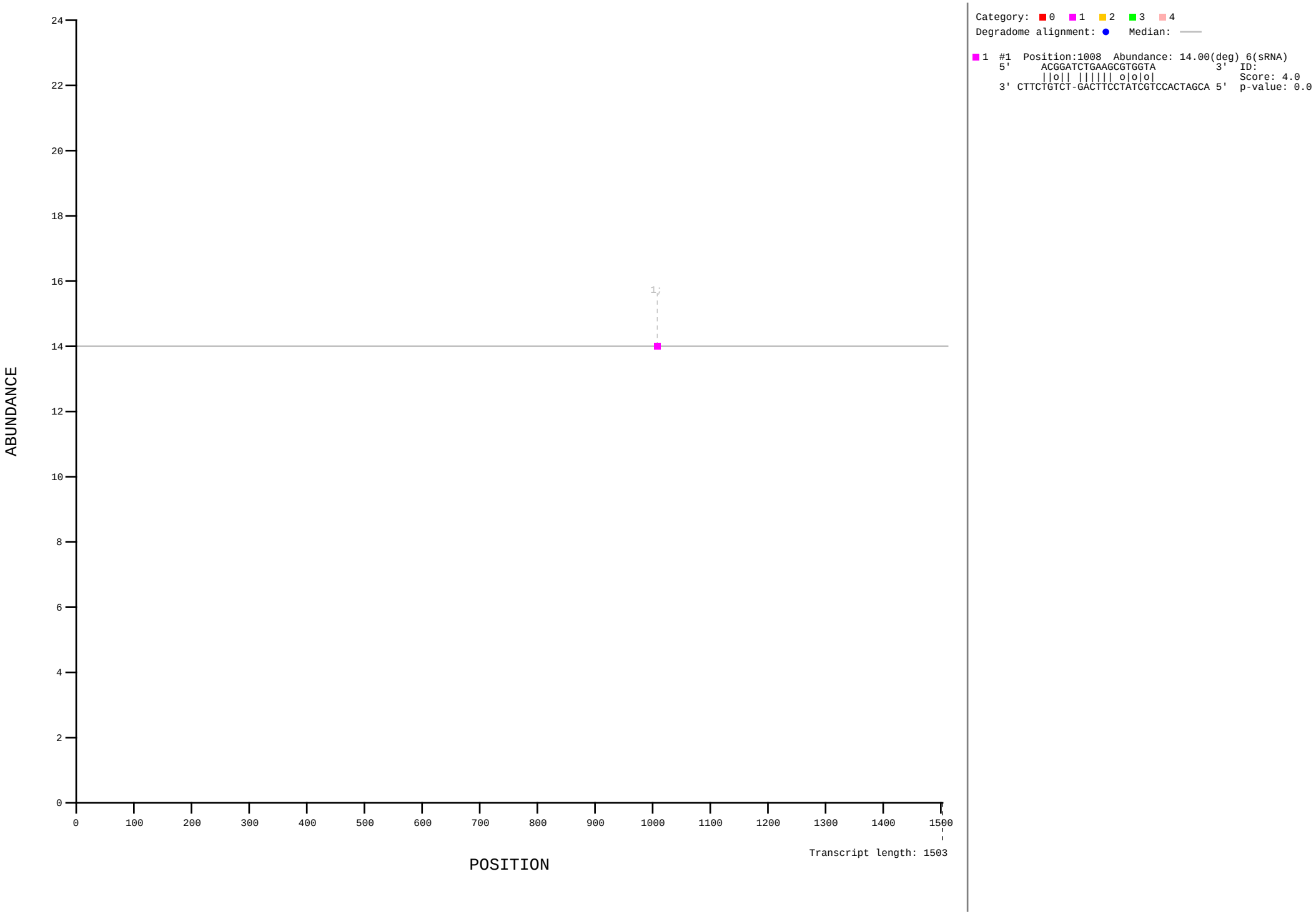
Category: 0 1 2 3 4

Degradome alignment: Median:

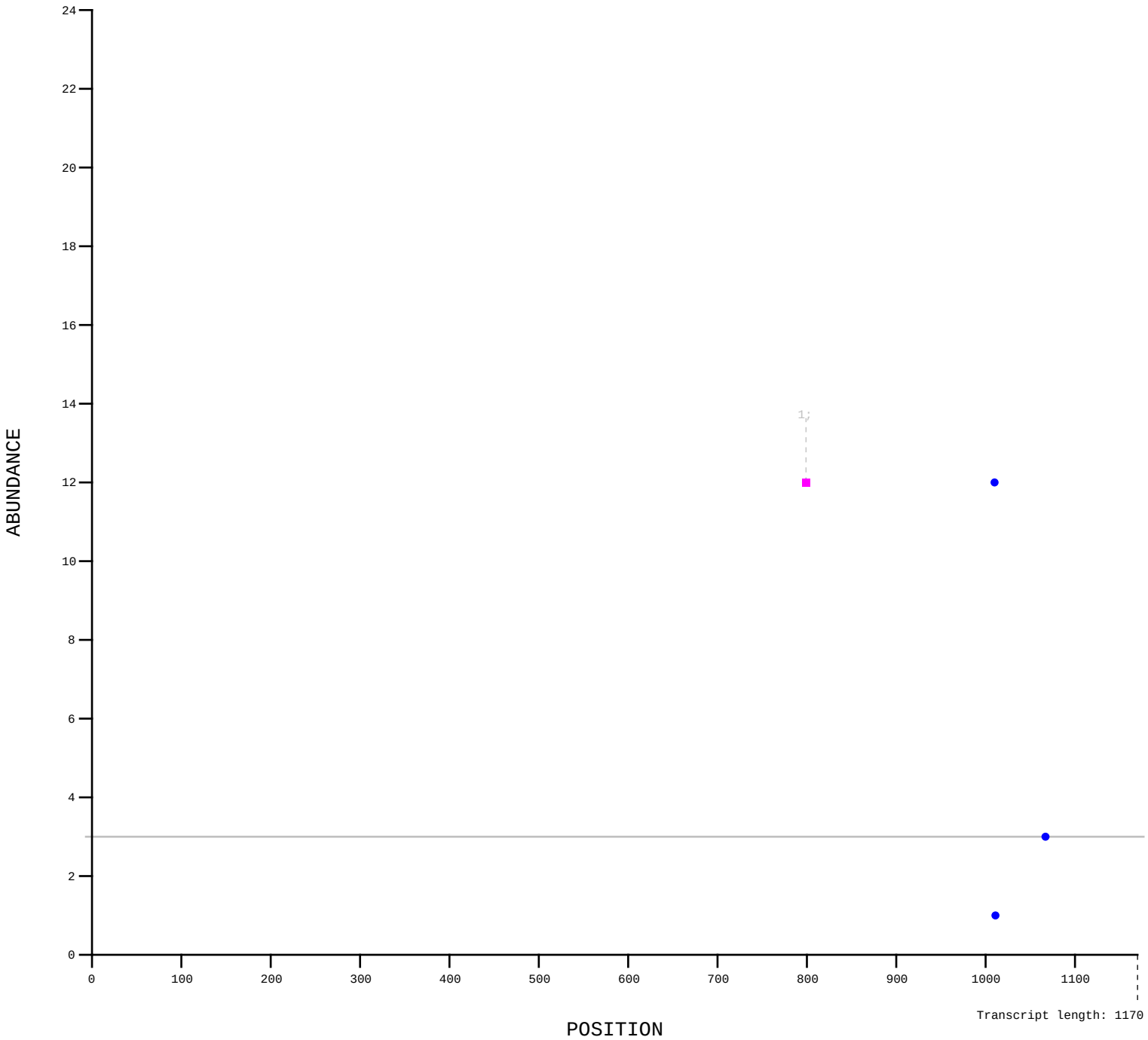
1 #1 Position:2650 Abundance: 57.00(deg) 8(sRNA)

```
5'    CTCCAG-TAGGAGATCTGGC          3'  ID:
       |||||| |||||| ||  ||              Score: 4.0
3' AGCGAGGTCTATCCTCCAGCACGAGGGAGTCA 5'  p-value: 0.03
```

FOXG_05210T0 | Fusarium oxysporum f. sp. lycopersici 4287 tyrosine decarboxylase (1503 nt)



FOXG_09184T0 | Fusarium oxysporum f. sp. lycopersici 4287 Arc1p protein (1170 nt)



Category: 0 1 2 3 4

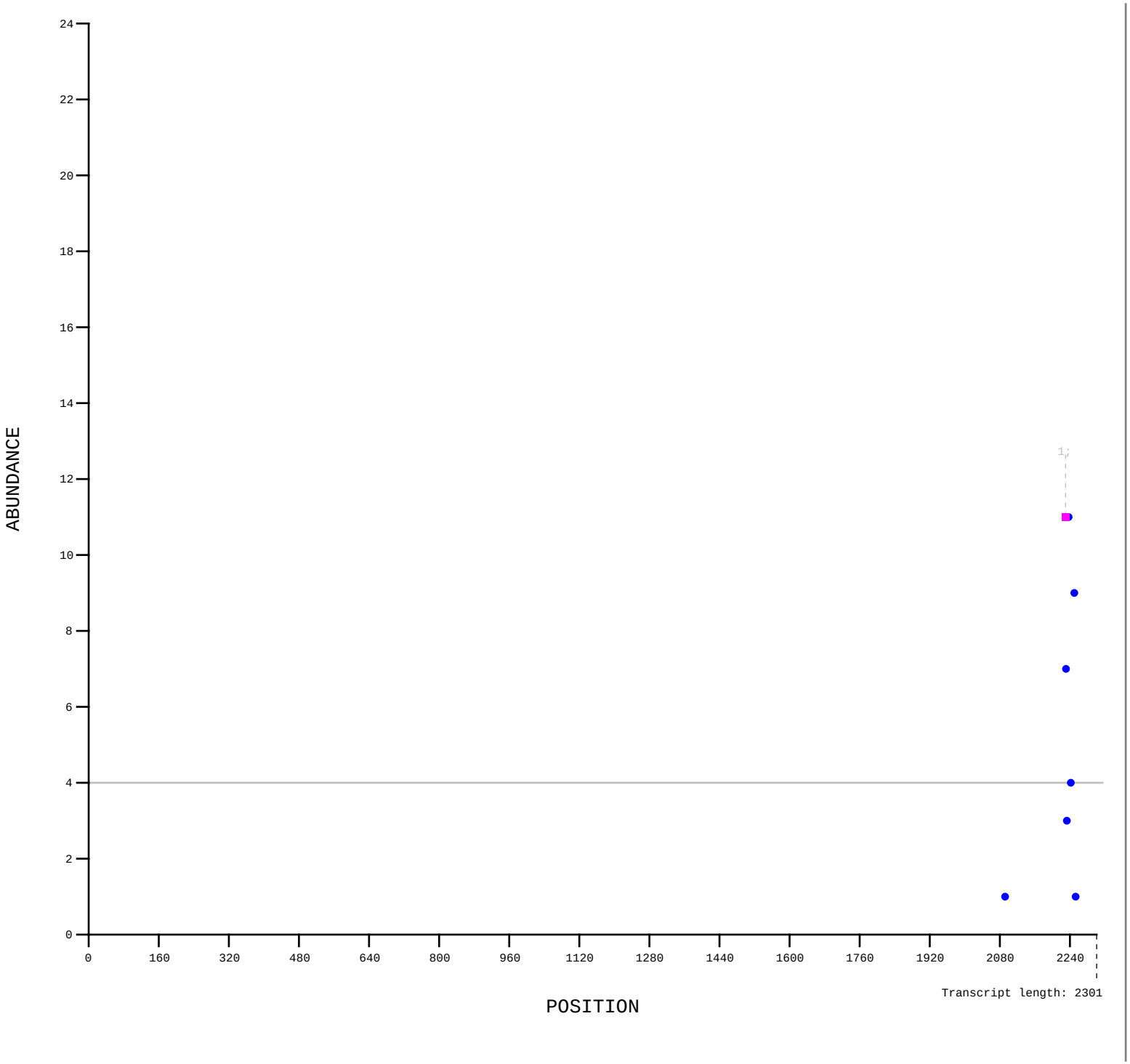
Degradome alignment: Median:

1 #1 Position:799 Abundance: 12.00(deg) 28(sRNA)

```
5'     TGGGGTAGCAGAACGTTGA          3'
        ||o||| ||||| || o||
3' CCGAACTCCAACGTCT-GCTGCTGCTGAAACG 5'
```

ID:
Score: 4.0
p-value: 0.0

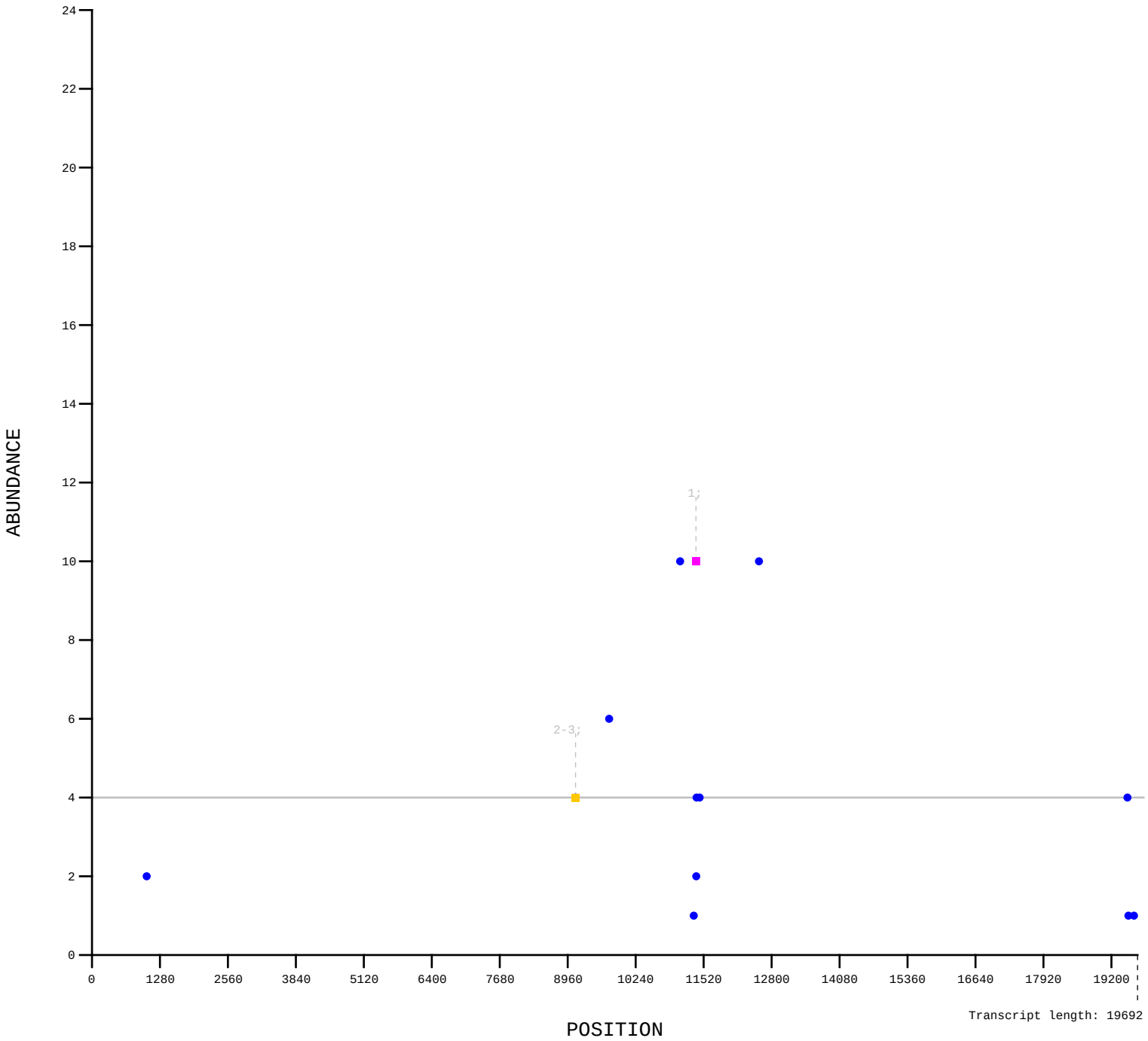
FOXG_11178T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2301 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:2230 Abundance: 11.00(deg) 7(sRNA)
5' AGATTGTCCCATGTCCCAT 3' ID:
|o||o|| |||||||| | Score: 4.0
3' CTGTTTTAGCA-GGTACAGGAGAAAGGTACGC 5' p-value: 0.0

FOXG_00340T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (19692 nt) Note(s): (truncated)



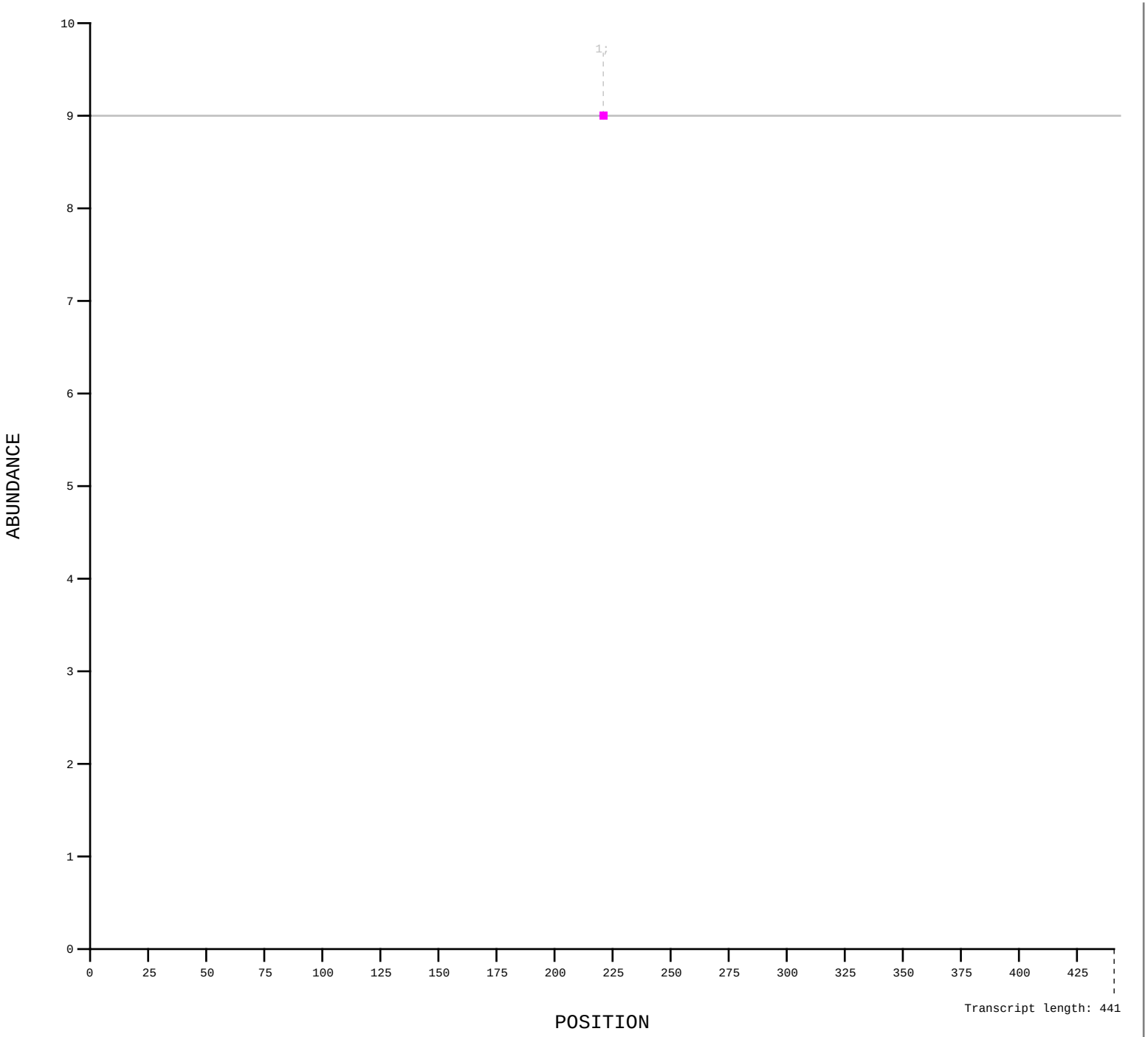
Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:11375 Abundance: 10.00(deg) 9(sRNA)
5' TTCTCTTCGGAGGCGTCTG 3' ID:
o|||||o|||| ||o| Score: 3.5
3' ACCATGGAGAAGTCTCCG-AGGCCAAAGGAAC 5' p-value: 0.0

2 #2 Position:9108 Abundance: 4.00(deg) 8(sRNA)
5' CTCCAGTAGGAGATCTGGC 3' ID:
|o||| ||||||||| | | Score: 3.5
3' GCCCGGGGTAATCCTCTAGCCAGACGCTCGCA 5' p-value: 0.01

2 #3 Position:9108 Abundance: 4.00(deg) 6(sRNA)
5' CTCCAGTAGGAGATTTGGC 3' ID:
|o||| |||||||o | | Score: 4.0
3' GCCCGGGGTAATCCTCTAGCCAGACGCTCGCA 5' p-value: 0.01

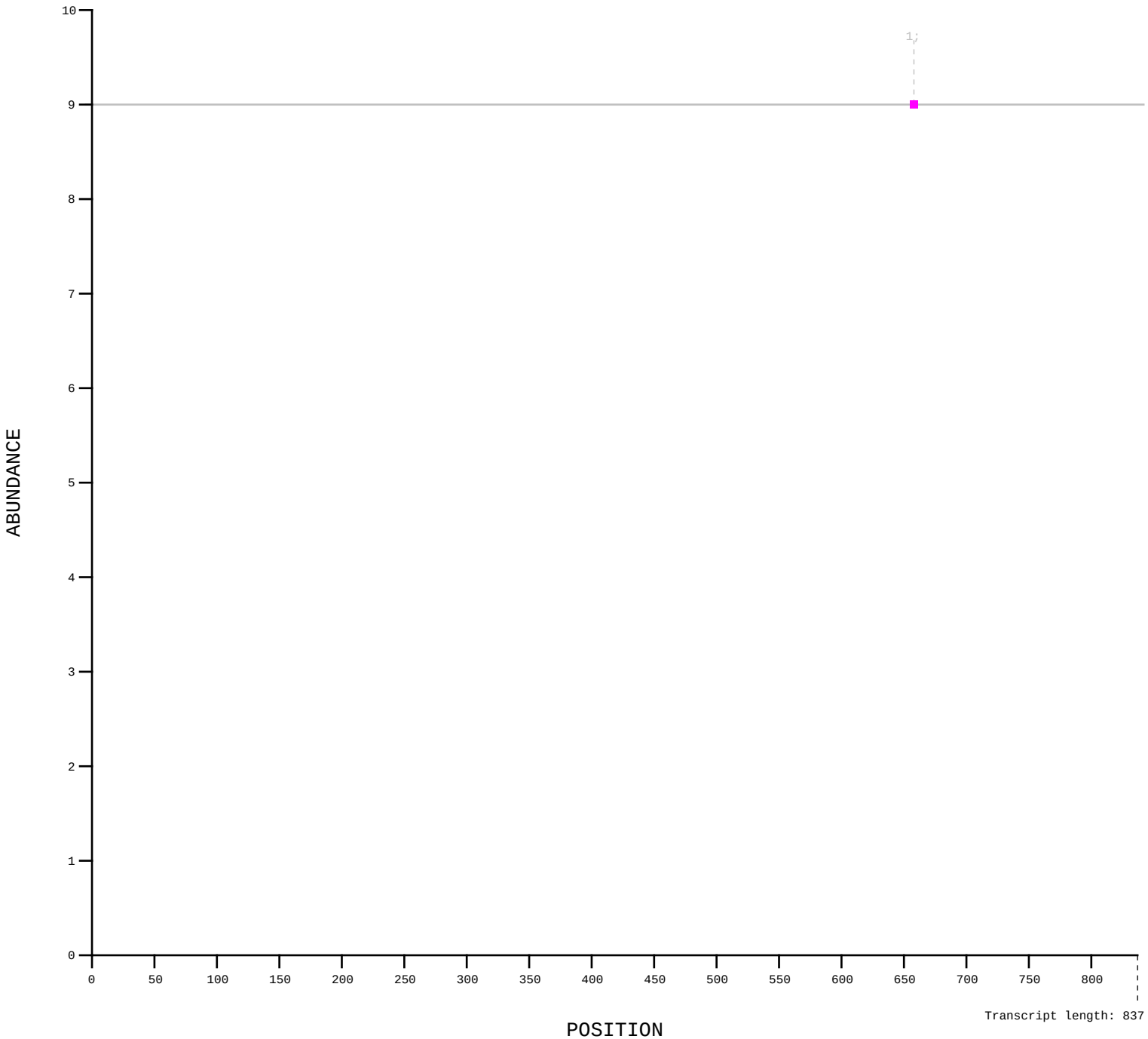
FOXG_07584T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (441 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:221 Abundance: 9.00(deg) 11(sRNA)
5' AGCACGACGTAGAACGACGC 3' ID:
|||| || ||||| || ||| Score: 4.0
3' CCCCTCGTACTACATCT-GCGGCGGACGCTAA 5' p-value: 0.0

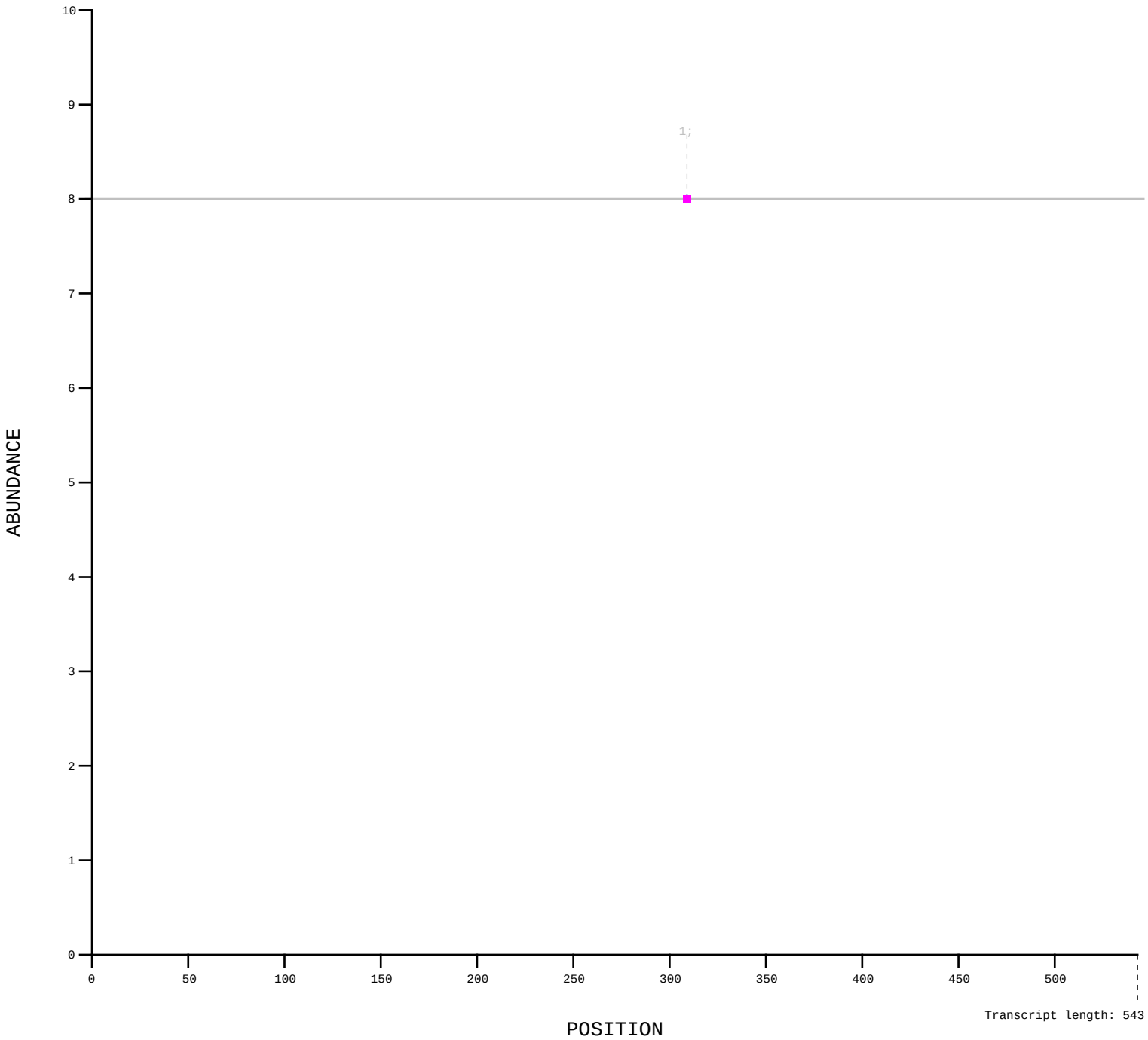
FOXG_11413T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (837 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:658 Abundance: 9.00(deg) 5(sRNA)
5' CTGATACTCATACTTTTCTTG 3' ID:
||||| |o||| |||| |||| Score: 3.5
3' TACCGACTAGGGGTACGAAA-GAACAGGAGGC 5' p-value: 0.0

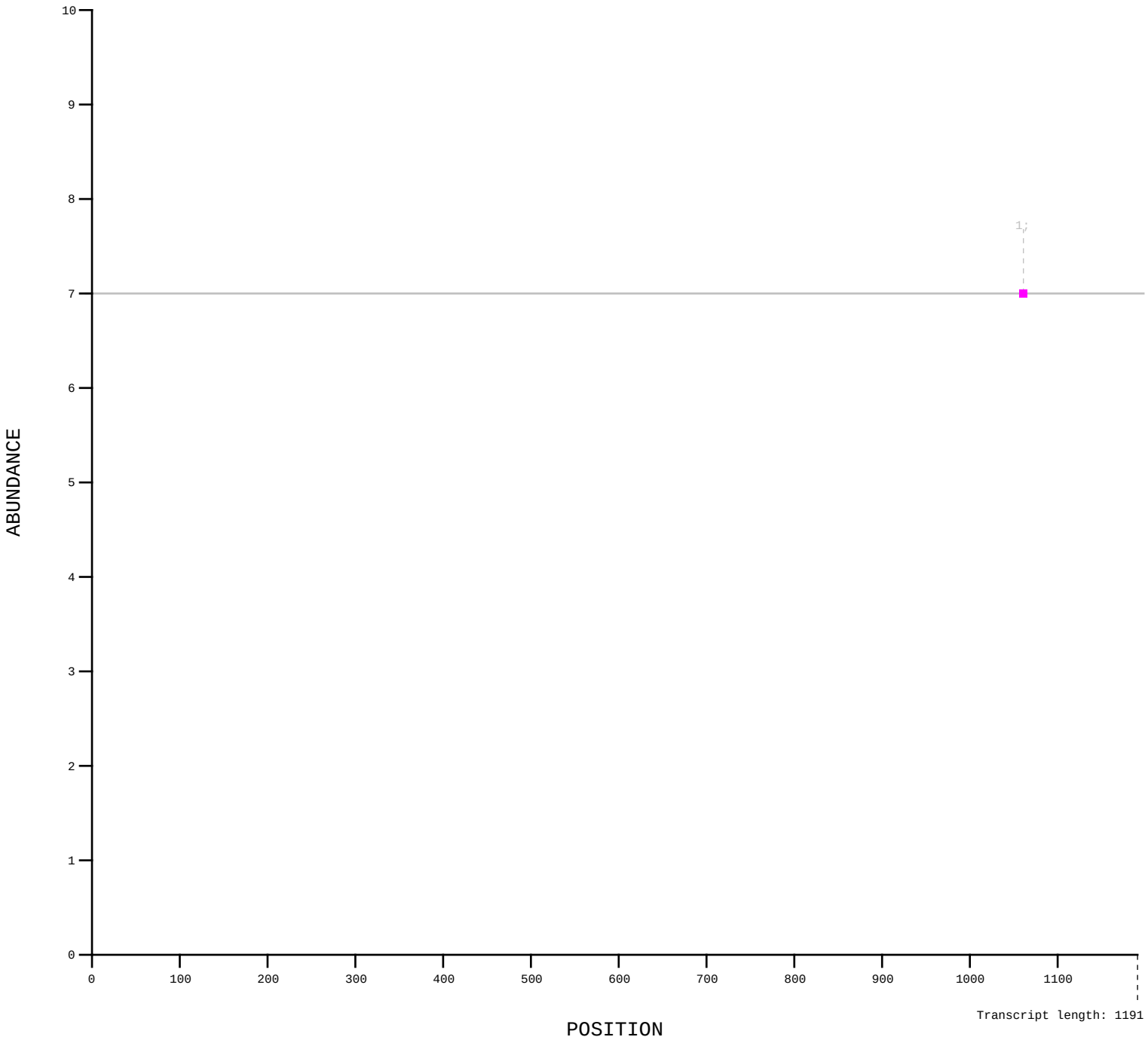
FOXG_13120T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (543 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:309 Abundance: 8.00(deg) 35(sRNA)
5' CGATTCCCTGT-ACCGGAGA 3' ID:
||||o|| ||| ||||||o| Score: 3.0
3' AGTCGCTAGGGAACACTGGCCTTTATGGACGG 5' p-value: 0.0

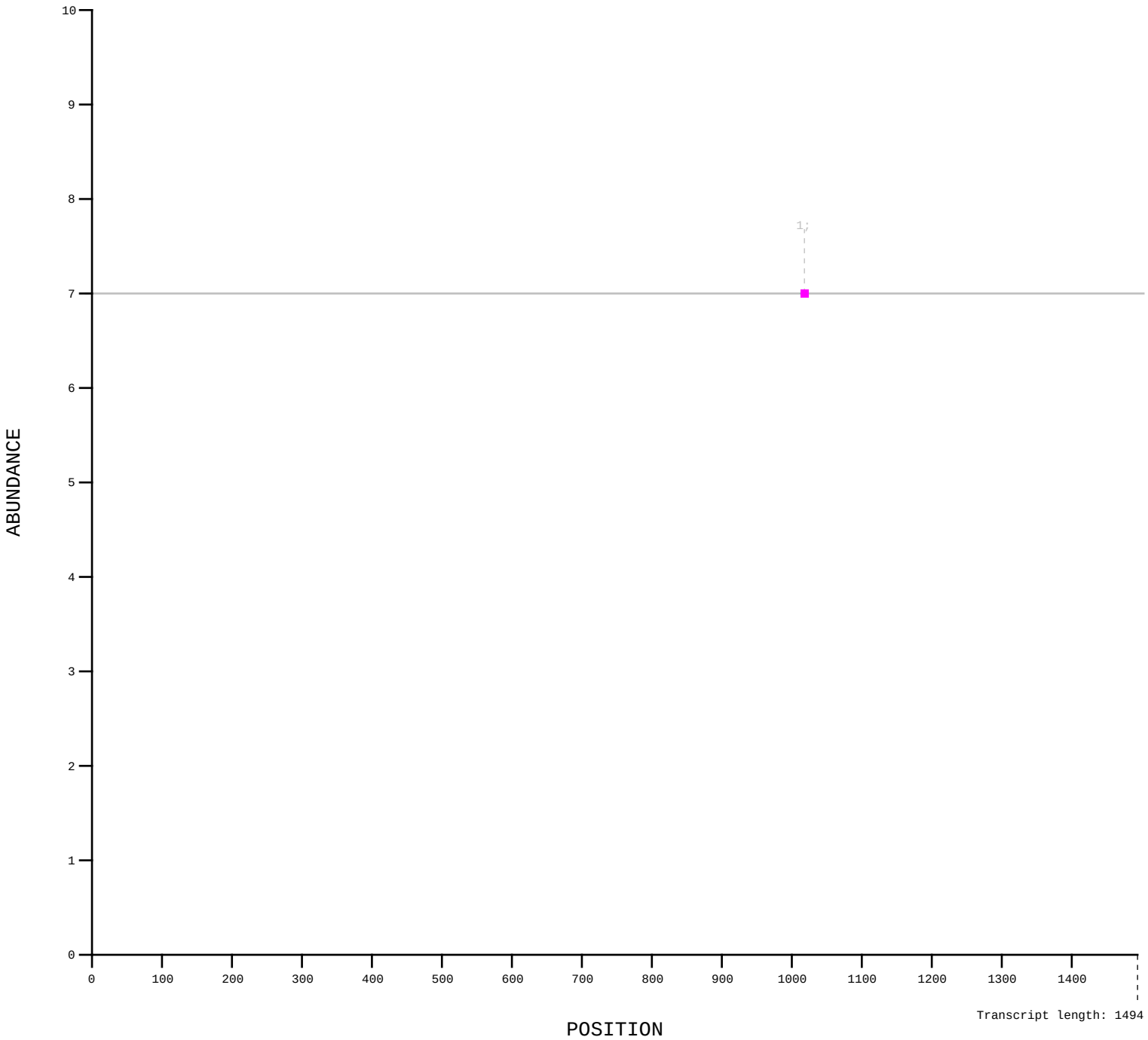
FOXG_11704T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1191 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:1061 Abundance: 7.00(deg) 14(sRNA)
5' TCCACGATTTTCTTATGAA 3' ID:
|| ||||o|||o| || Score: 4.0
3' TAGAAGTTGCTAGAAGAGTTGTTGTATGAGGG 5' p-value: 0.02

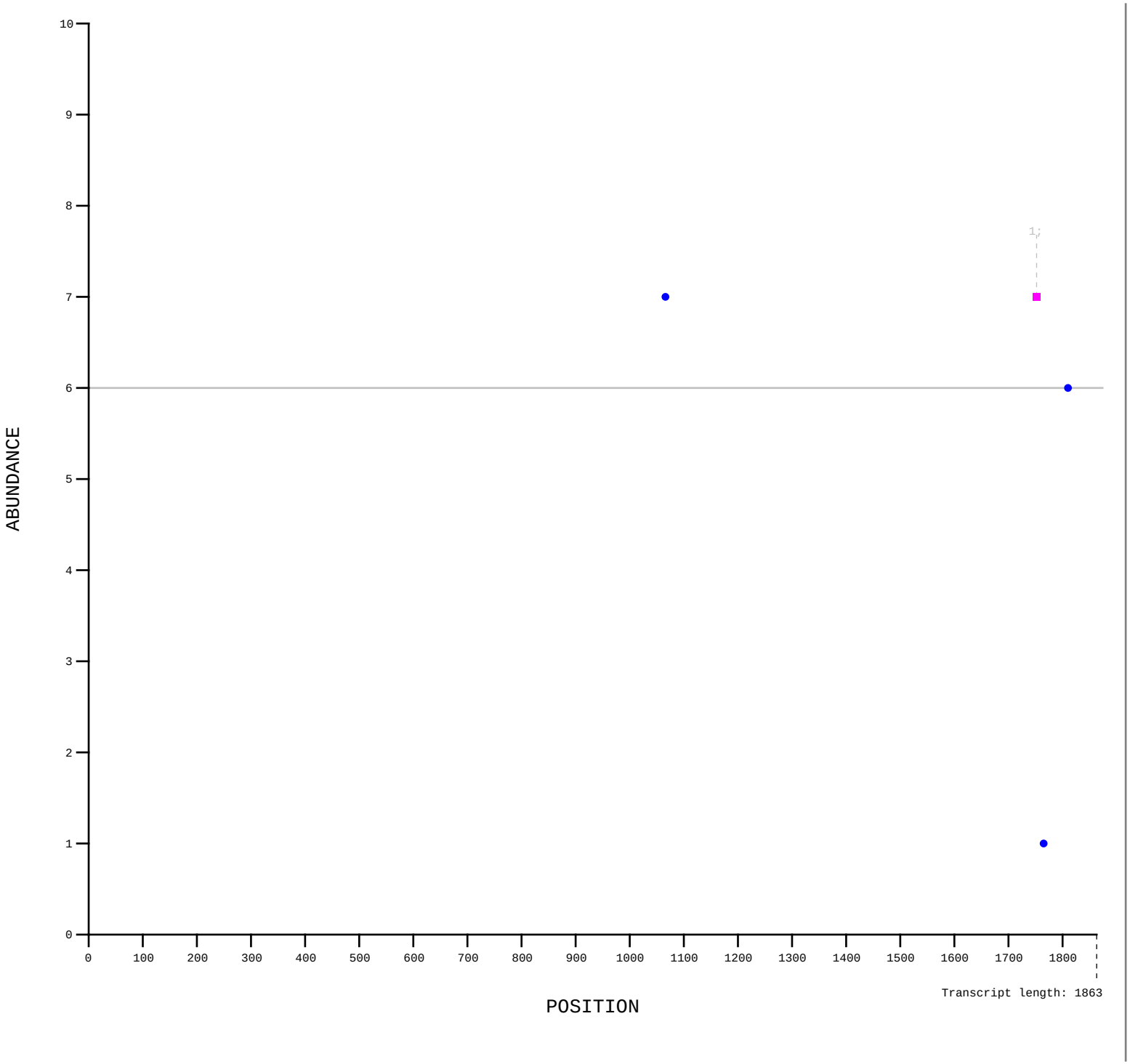
FOXG_02353T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1494 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:1018 Abundance: 7.00(deg) 14(sRNA)
5' TACTGTGAACAGCTAG-AGG 3' ID:
o||||||||||| | | ||| Score: 3.5
3' TGGTGTGACACTTGTCTAGCCTCCCGCAGCTC 5' p-value: 0.0

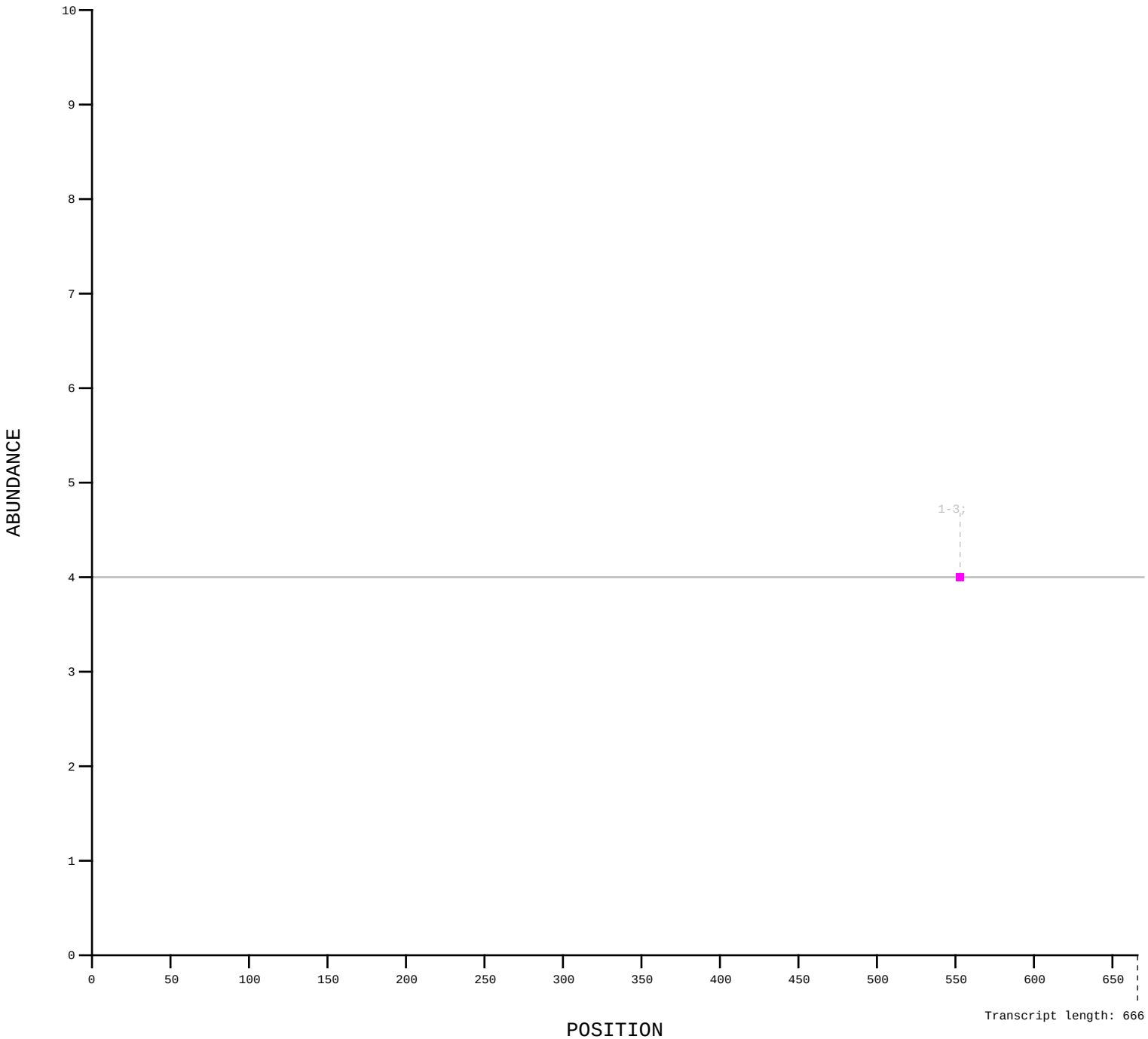
FOXG_05497T0 | Fusarium oxysporum f. sp. lycopersici 4287 mitochondrial precursor proteins import receptor (1863 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:1752 Abundance: 7.00(deg) 5(sRNA)
5' TTCAGCATGTGACGAGTGG 3' ID:
o||||||o|||o|| | Score: 3.5
3' AACGGAGTCGTATACTGTTCCGCAACTGTTAG 5' p-value: 0.0

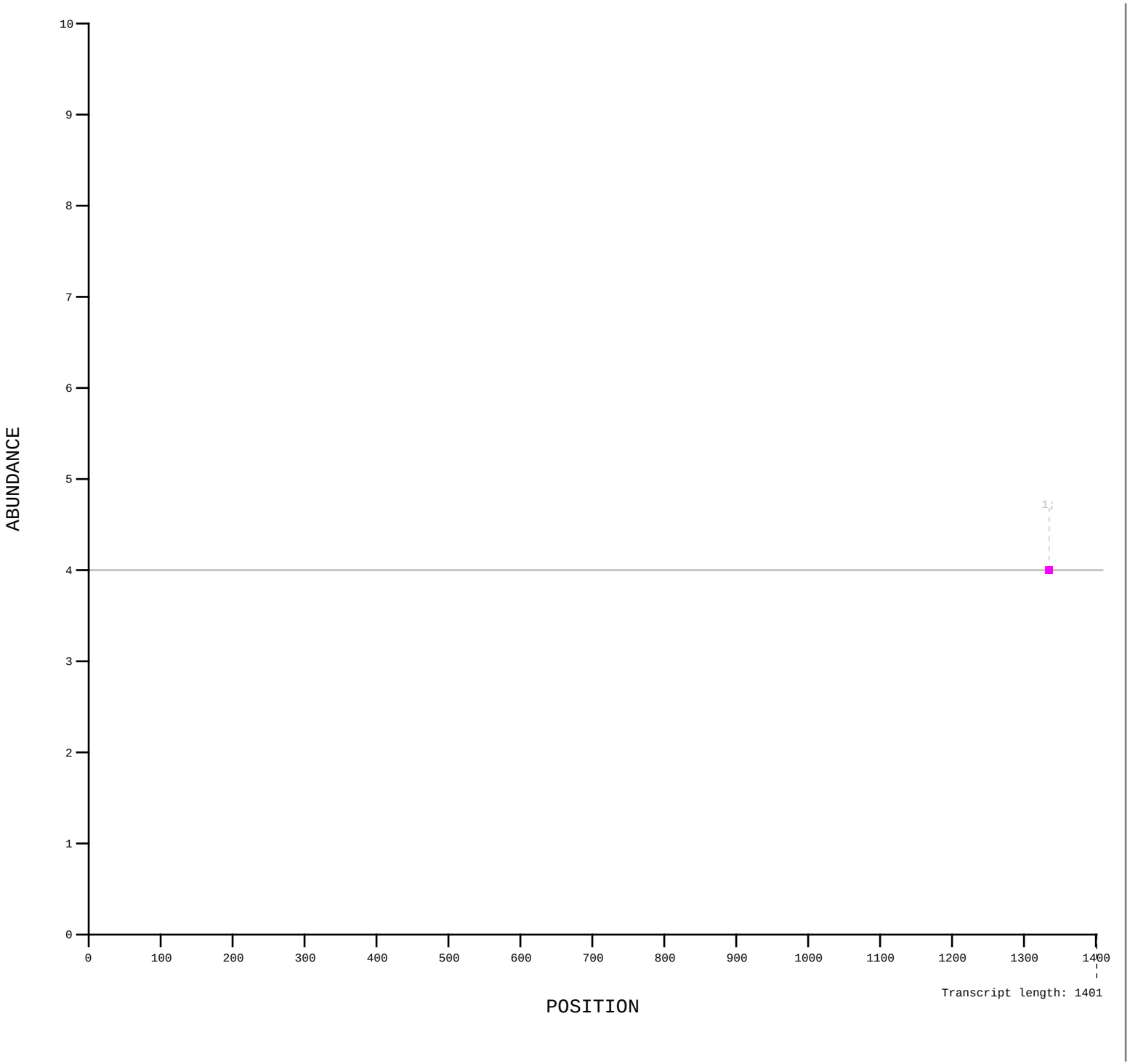
FOXG_01130T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (666 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
1  #1  Position:553  Abundance: 4.00(deg) 322(sRNA)
    5'     TAGAACATGTAGAATTAGAAGG        3'  ID:
           o|||| ||||||| || ||||o            Score: 4.0
    3' AGAGGTCTTCTACATCTCAACCTTCTCGATAG 5'  p-value: 0.0

1  #2  Position:553  Abundance: 4.00(deg) 27(sRNA)
    5'     TAGAACATGTAGAATTAGAAG         3'  ID:
           o|||| ||||||| || ||||             Score: 3.5
    3' AGAGGTCTTCTACATCTCAACCTTCTCGATAG 5'  p-value: 0.0

1  #3  Position:553  Abundance: 4.00(deg) 13(sRNA)
    5'     TAGAACATGTAGAATTAGA           3'  ID:
           o|||| ||||||| || ||               Score: 3.5
    3' AGAGGTCTTCTACATCTCAACCTTCTCGATAG 5'  p-value: 0.0
```

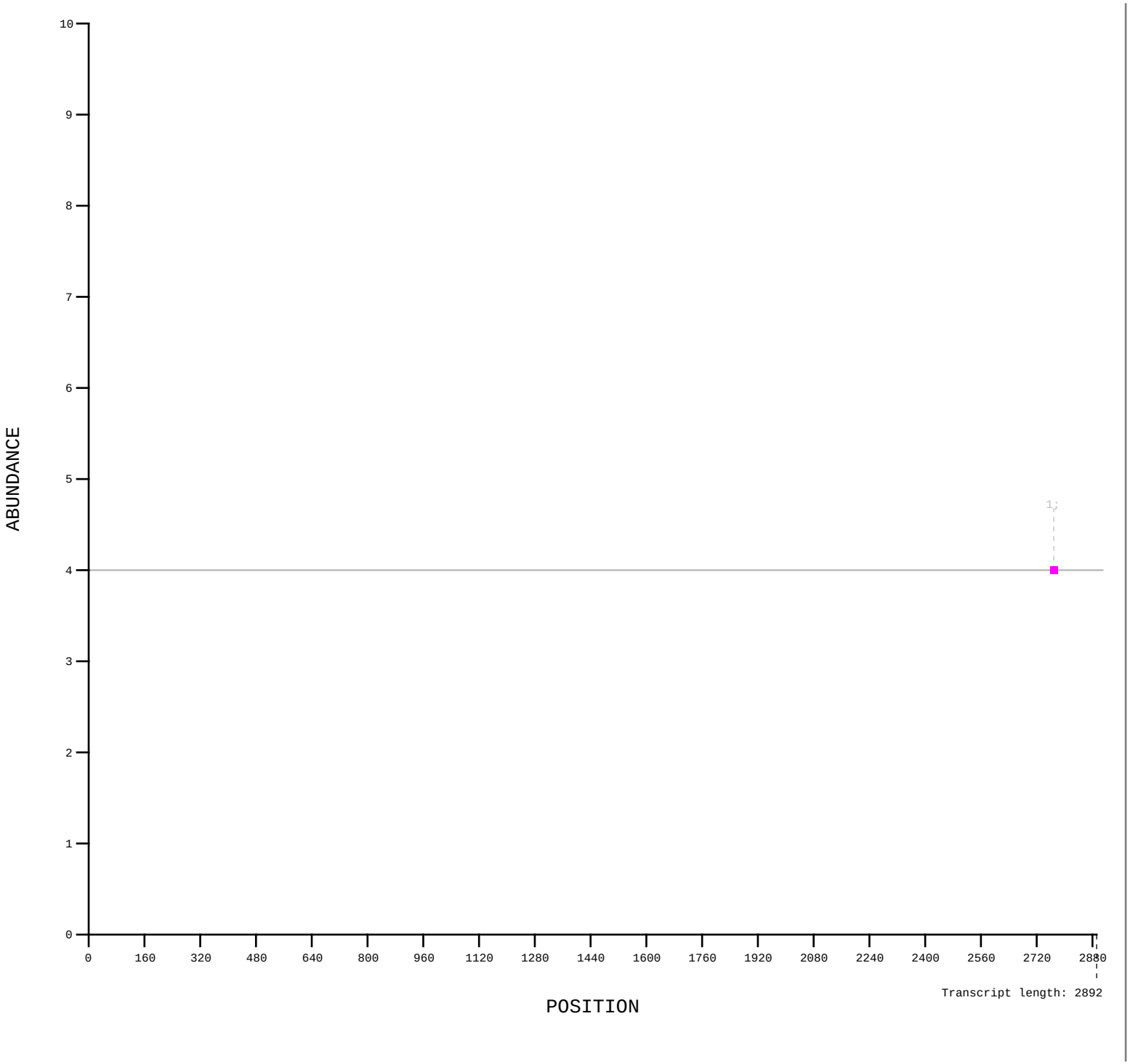
FOXG_07923T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1401 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:1335 Abundance: 4.00(deg) 9(sRNA)
5' TGGTATCTATCGGATATGG 3' ID:
|||| ||o||| || ||o Score: 4.0
3' ATCAACCACAGGTAGC-TAGACTTCTCTACCA 5' p-value: 0.0

FOXG_01731T0 | Fusarium oxysporum f. sp. lycopersici 4287 NF-X1 finger transcription factor (2892 nt)

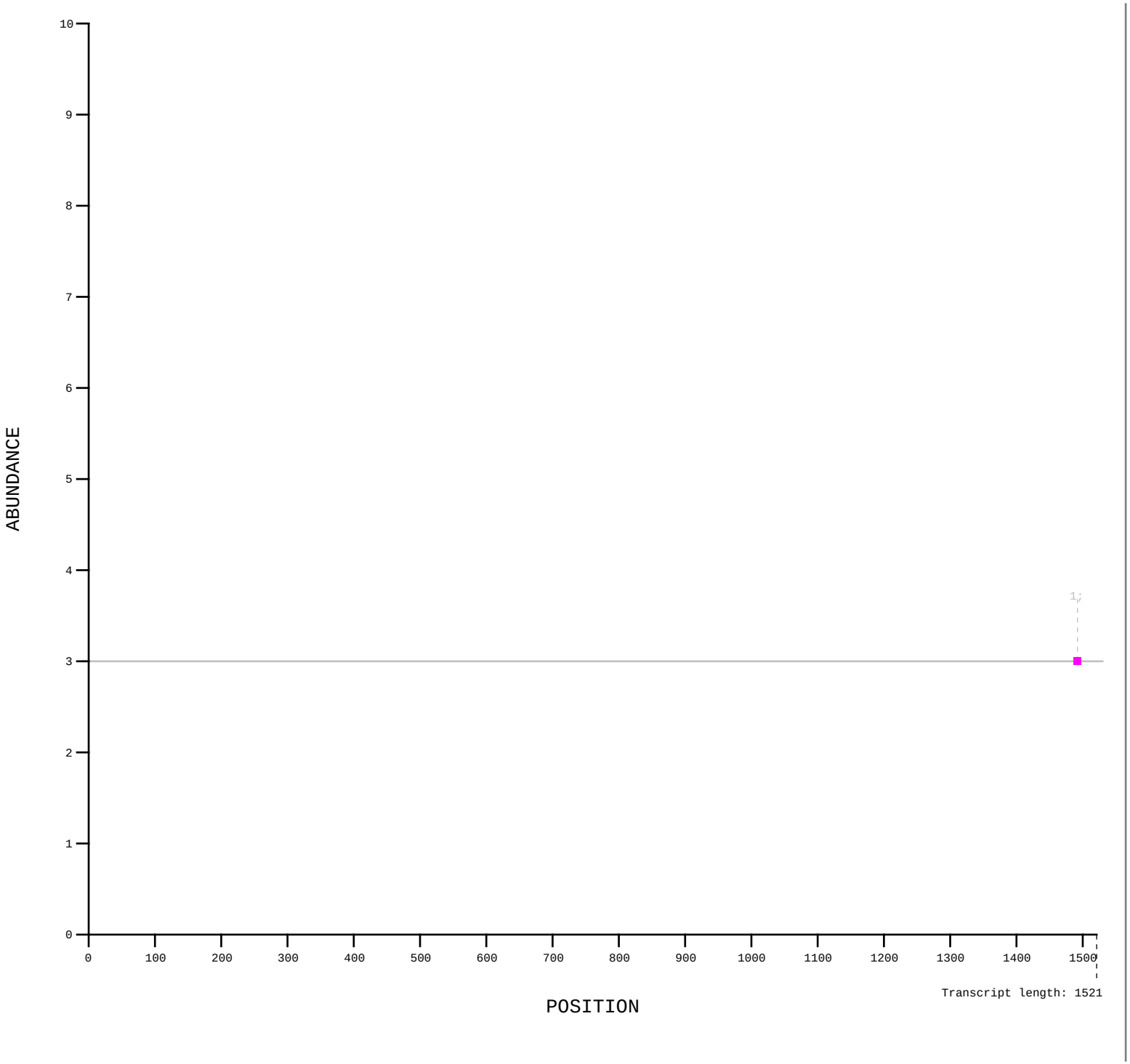


Category: 0 1 2 3 4

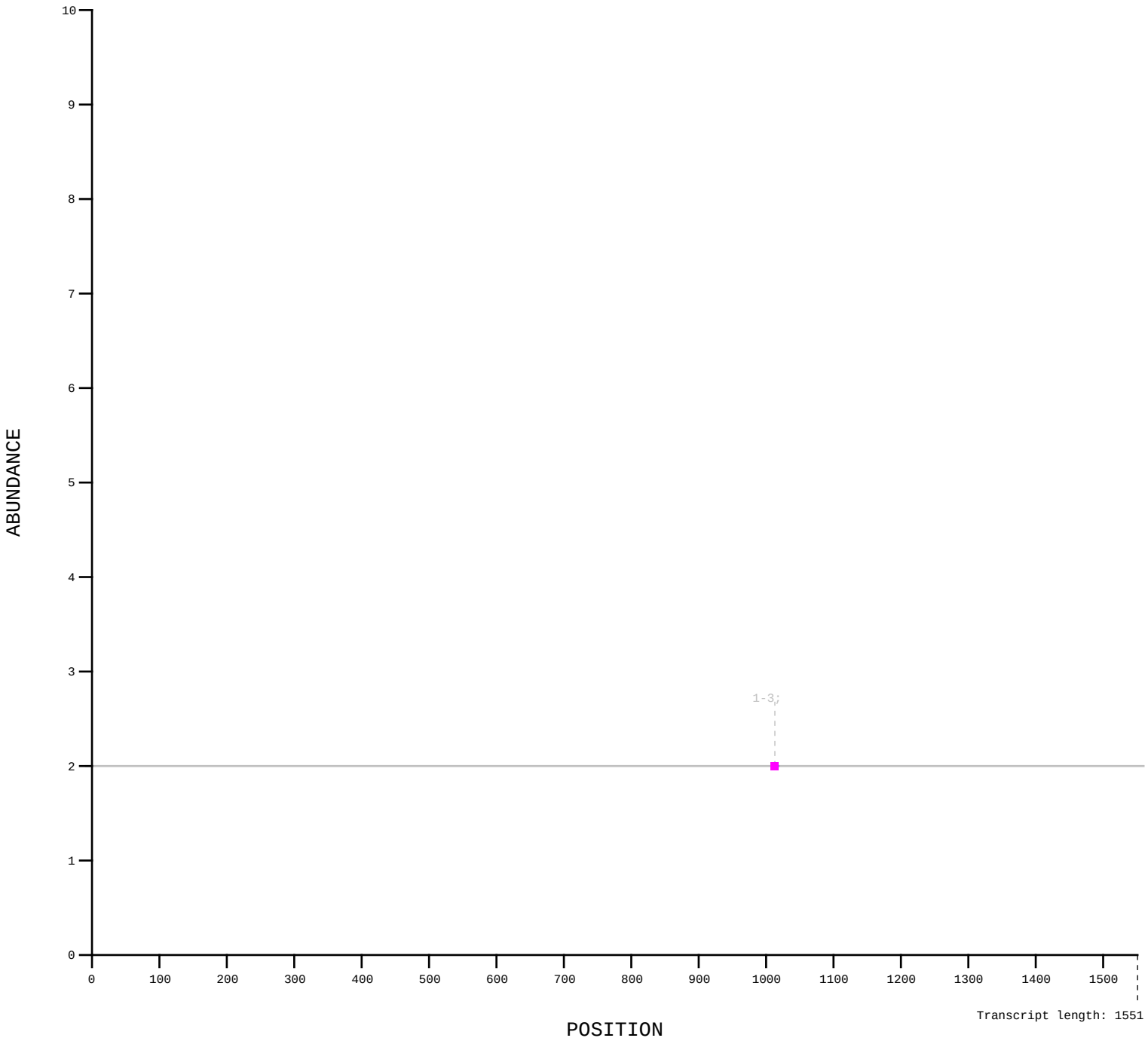
Degradome alignment: Median:

```
1  #1  Position:2769  Abundance: 4.00(deg) 5(sRNA)
   5'     TGTAGAATTAGAAGGTAGG          3'  ID:
          ||o|| | |||||oo|o|               Score: 4.0
   3' GCCCACGTCCTCATCTTCTGTTCCTGTAACCG 5'  p-value: 0.0
```

FOXG_01784T0 | Fusarium oxysporum f. sp. lycopersici 4287 glutamic acid decarboxylase isoform 67 (1521 nt)



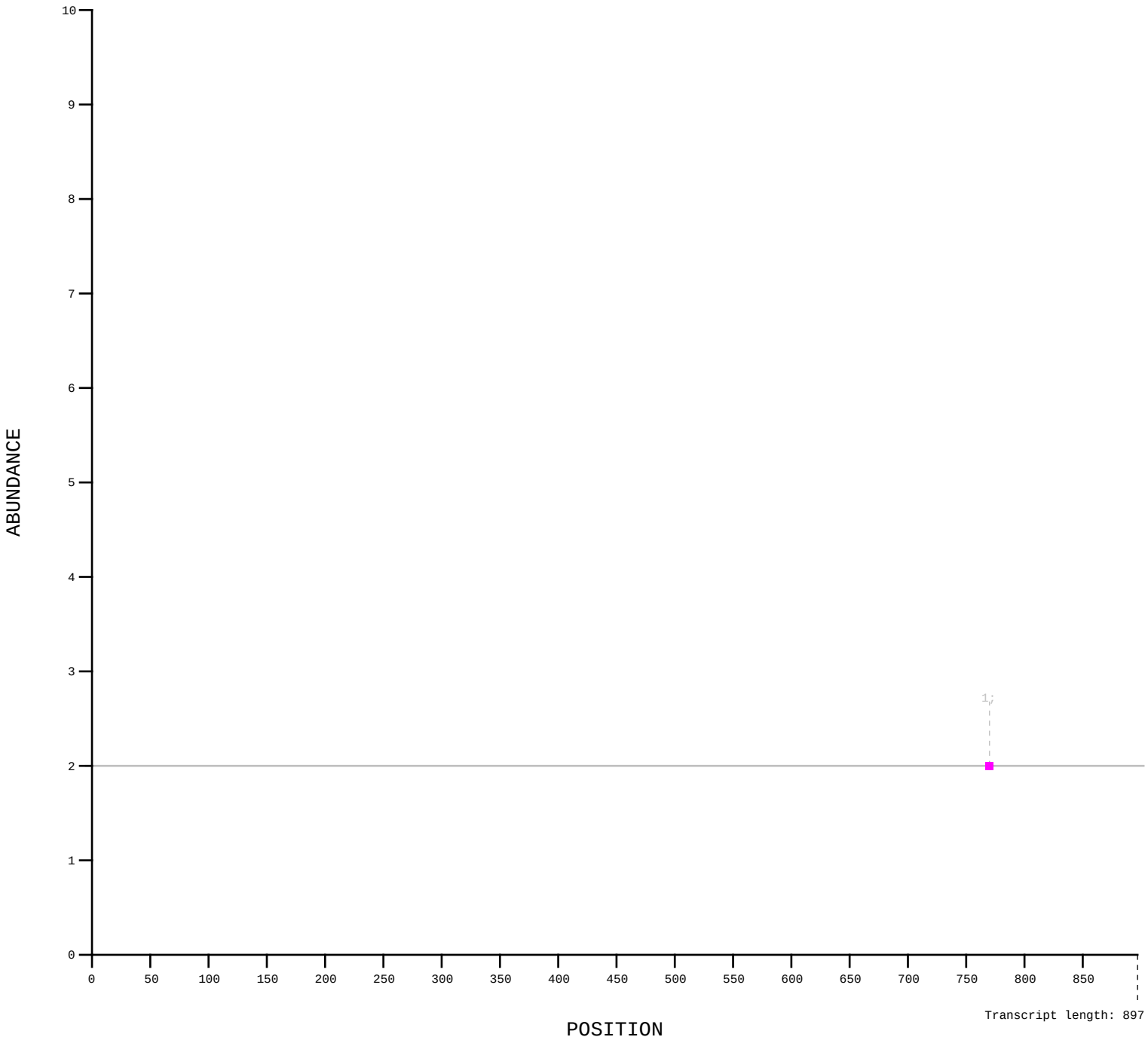
FOXG_03705T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1551 nt) Note(s): (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
1  #1  Position:1013  Abundance: 2.00(deg) 2473(sRNA)
   5'     TATAAAACGAAGAACAAGAGG         3'  ID:
          o||| || ||||| |||||o|             Score: 4.0
   3' CGCGGTATCTT-CTTCTAGTTCTTCGAGAGCT 5'  p-value: 0.0

1  #2  Position:1013  Abundance: 2.00(deg) 161(sRNA)
   5'     TATAAAACGAAGAACAAGAG          3'  ID:
          o||| || ||||| |||||o              Score: 4.0
   3' CGCGGTATCTT-CTTCTAGTTCTTCGAGAGCT 5'  p-value: 0.0

1  #3  Position:1013  Abundance: 2.00(deg) 71(sRNA)
   5'     TATAAAACGAAGAACAAGA           3'  ID:
          o||| || ||||| |||||               Score: 3.5
   3' CGCGGTATCTT-CTTCTAGTTCTTCGAGAGCT 5'  p-value: 0.0
```

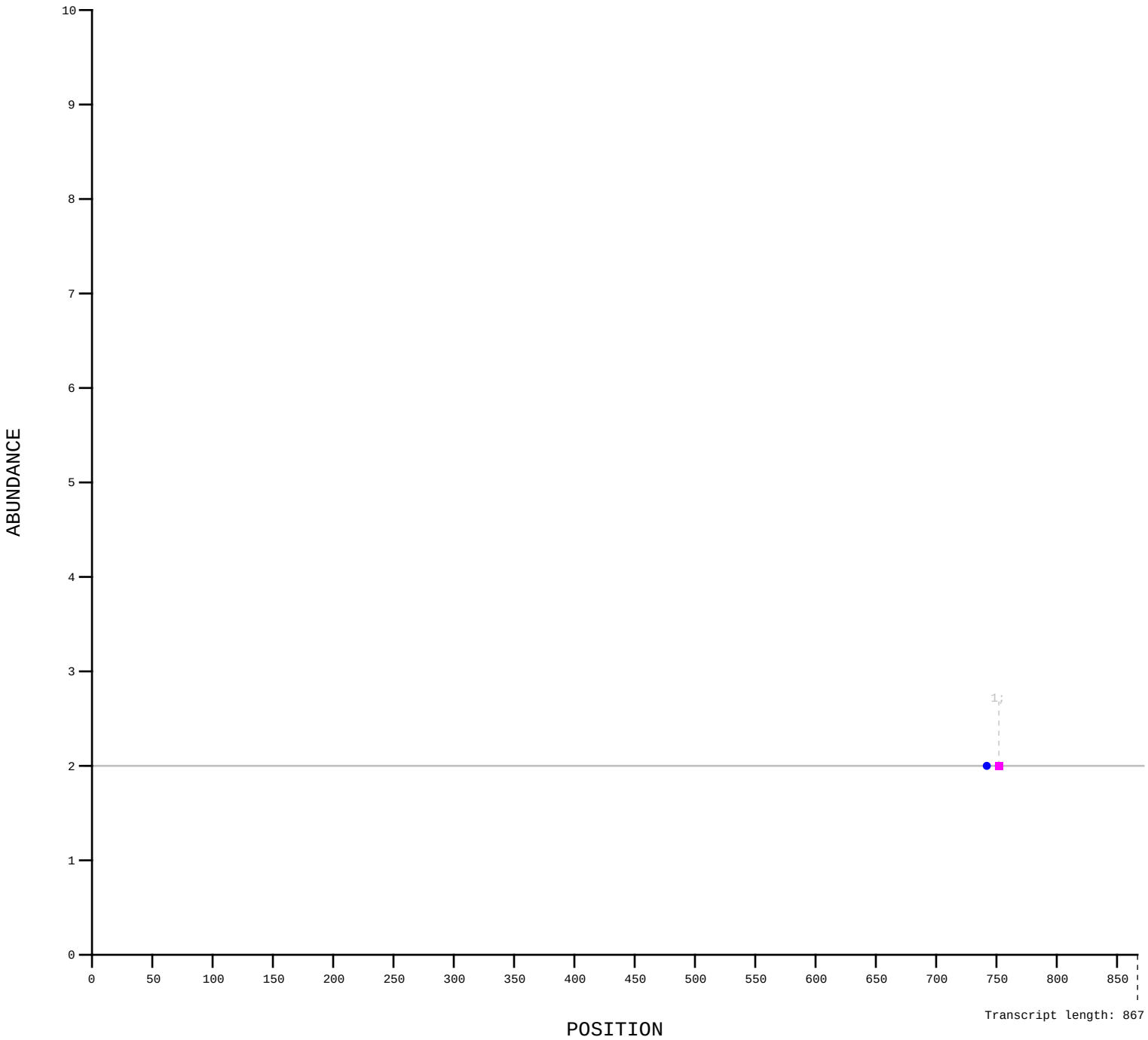
FOXG_07896T0 | Fusarium oxysporum f. sp. lycopersici 4287 FMI1 protein (897 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:770 Abundance: 2.00(deg) 10(sRNA)
5' CGATAGCAGATTCTGCA-CCAGC 3' ID:
| ||| ||o|||o||| ||||| Score: 4.0
3' AGAAGGTATGGTTTAAGGCGTAGGTCGGTTTC 5' p-value: 0.0

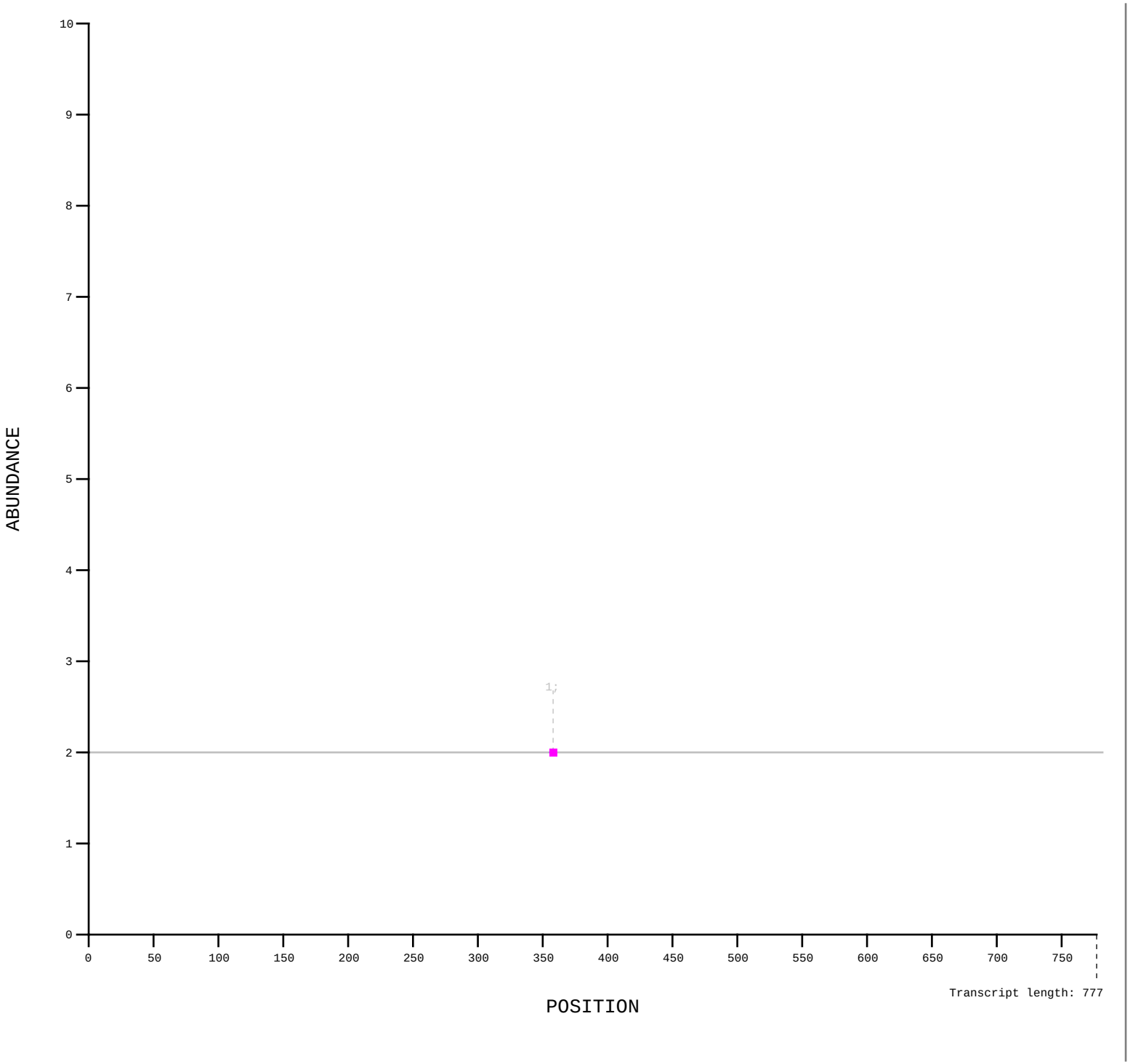
FOXG_13343T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (867 nt)



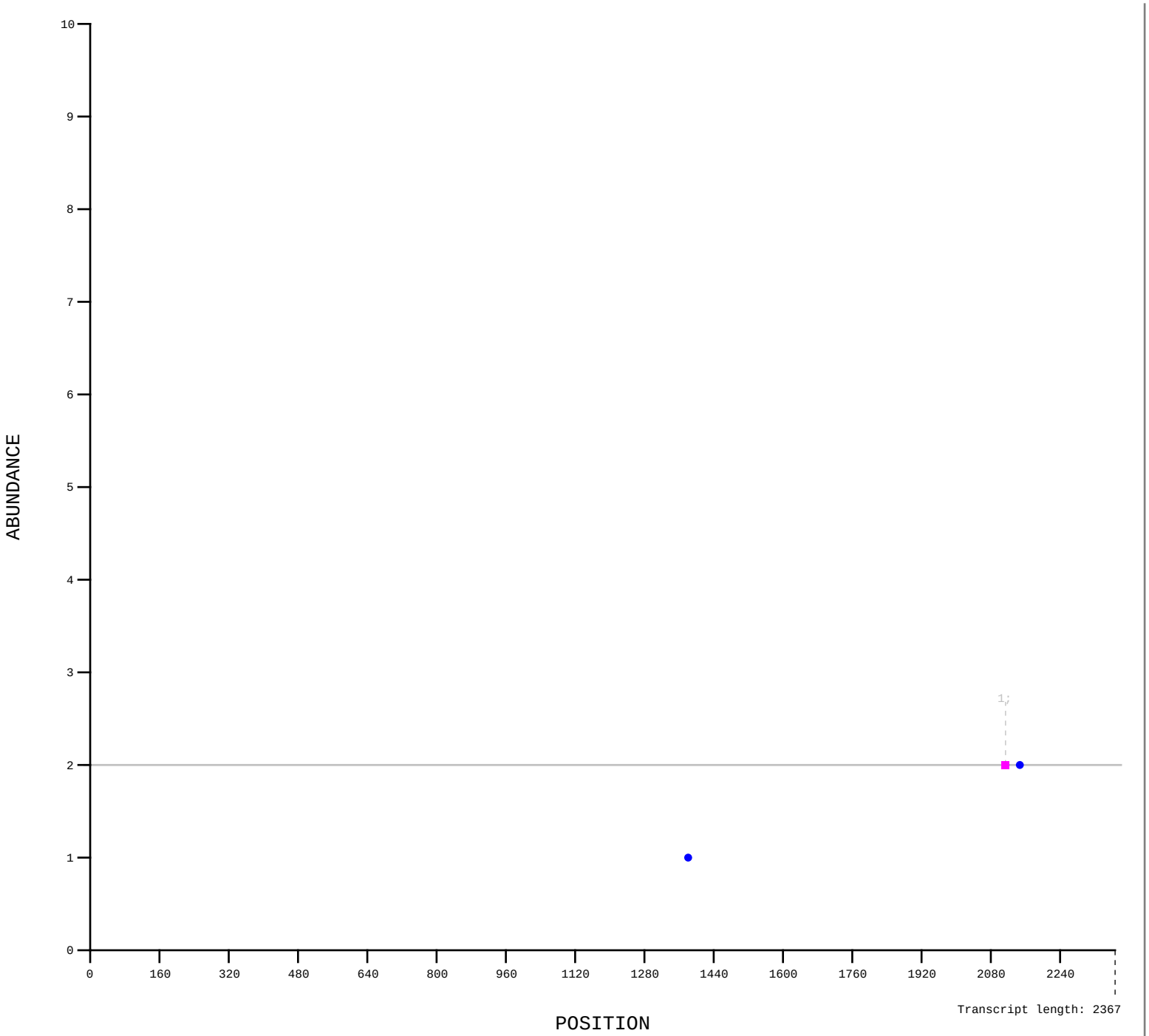
Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:752 Abundance: 2.00(deg) 9(sRNA)
5' AGGAAAATAAGCTGAATTAGG 3' ID:
| ||||||||| ||oo||| Score: 4.0
3' TTAGTACTTTTATTCGTATTGGTCCCGGTATT 5' p-value: 0.01

FOXG_14860T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (777 nt) Note(s): (truncated)



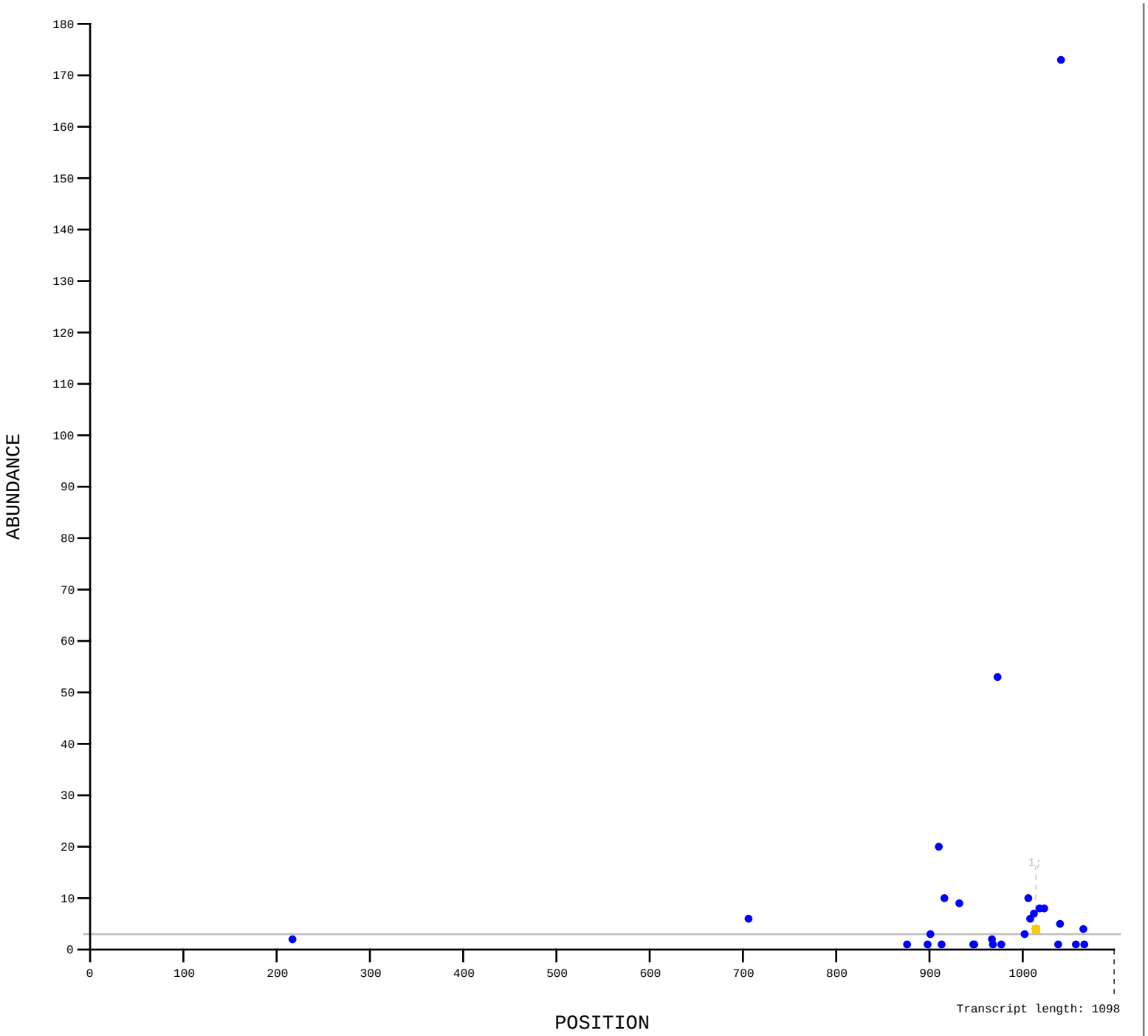
FOXG_01961T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2367 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

1 #1 Position:2114 Abundance: 2.00(deg) 5(sRNA)
5' AACTATATGTAGGTTCTTCTATA 3' ID:
||||||| |||||| ||||o || Score: 3.5
3' TCTATTGATAT-CATCCATGAAGGCATTGATA 5' p-value: 0.0

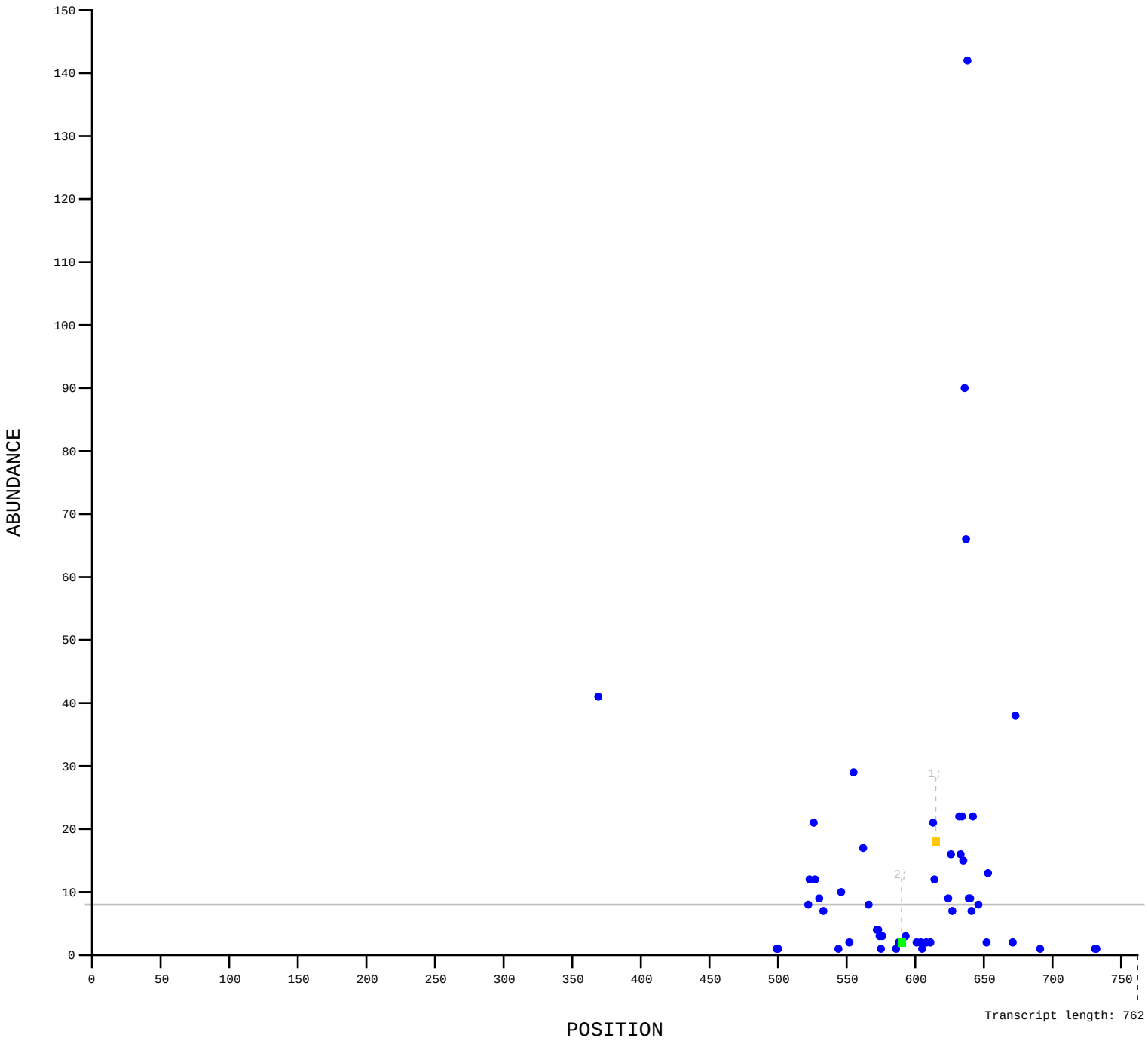
FOXG_07841T0 | Fusarium oxysporum f. sp. lycopersici 4287 formate dehydrogenase (1098 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1014 Abundance: 4.00(deg) 11(sRNA)
5' GGCGTGGTGGC-AGAGTGGT 3' ID:
| |||||o||| |||| ||| Score: 3.5
3' ACATCAGCACCGCCGGTCTCTCCATTCTCAGC 5' p-value: 0.01

FOXG_16470T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (762 nt)

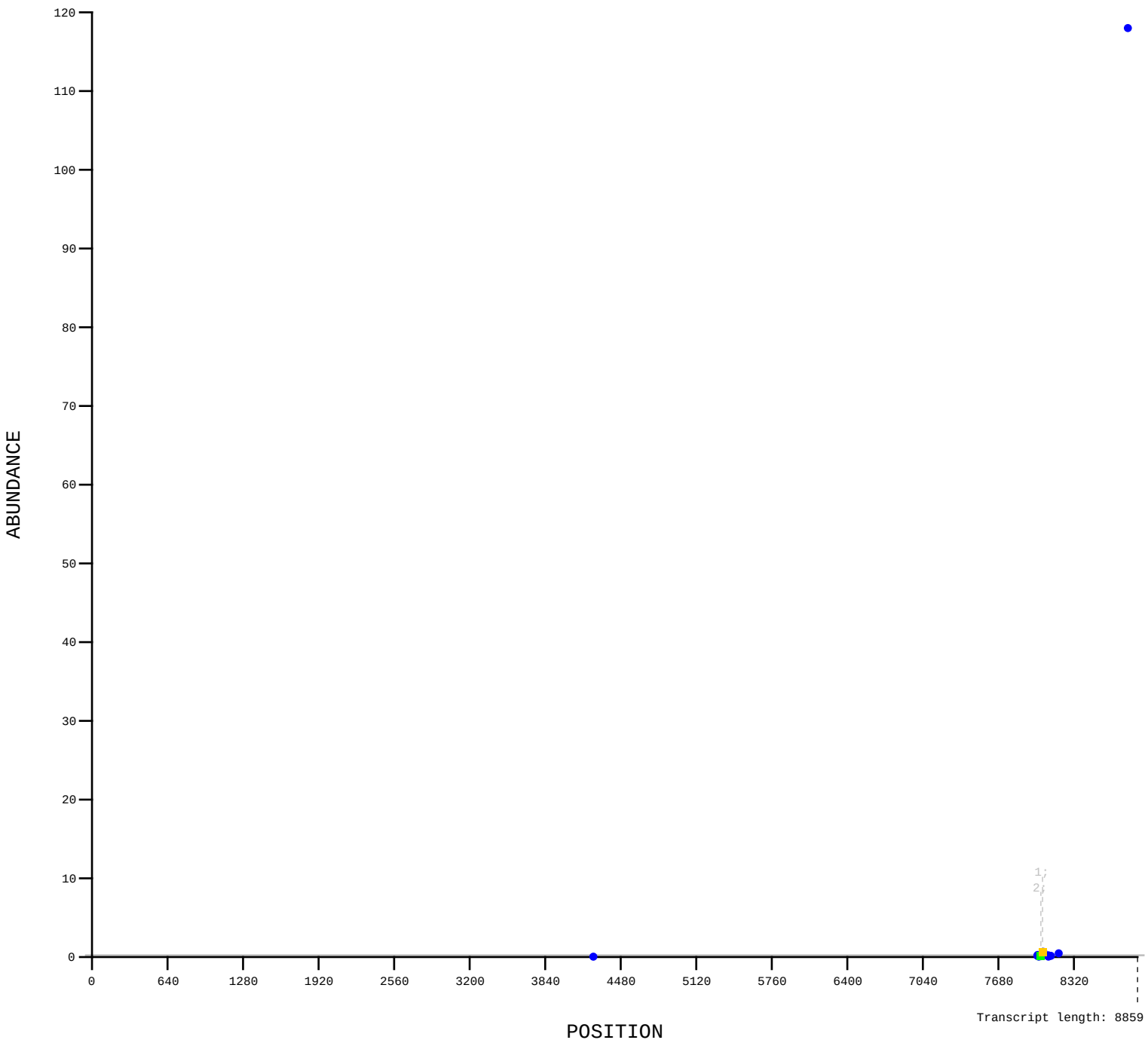


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:615 Abundance: 18.00(deg) 12(sRNA)
5' AGGATTAAGCTCATGTTTT 3' ID:
|||| |||||| || ||| Score: 4.0
3' GTTGTCCT-ATTCGACTAGTAAAAGCGTTTAC 5' p-value: 0.01

3 #2 Position:590 Abundance: 2.00(deg) 14(sRNA)
5' TGATGTGTCGTCTCCGGAC 3' ID:
||||o|o| |||| |||| Score: 4.0
3' GTTTACTATATA-CAGAAGCCTTATCACTATA 5' p-value: 0.0

FOXG_15708T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (8859 nt) Note(s): (truncated)



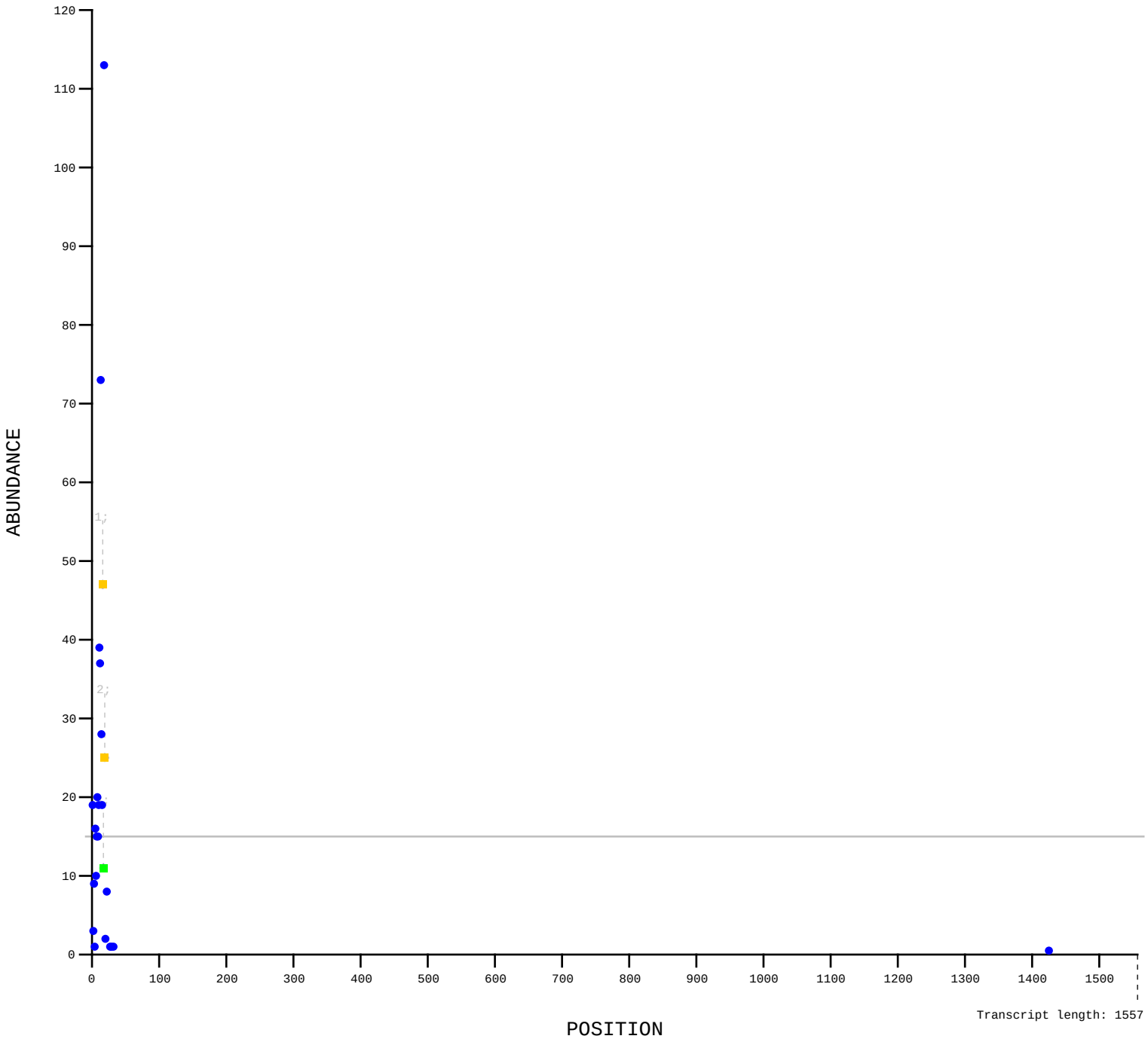
Category: 0 1 2 3 4

Degradome alignment: Median:

2 #1 Position:8054 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.04

3 #2 Position:8040 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_17106T0 | Fusarium oxysporum f. sp. lycopersici 4287 peroxidase/catalase HPI (1557 nt) Note(s): (truncated)



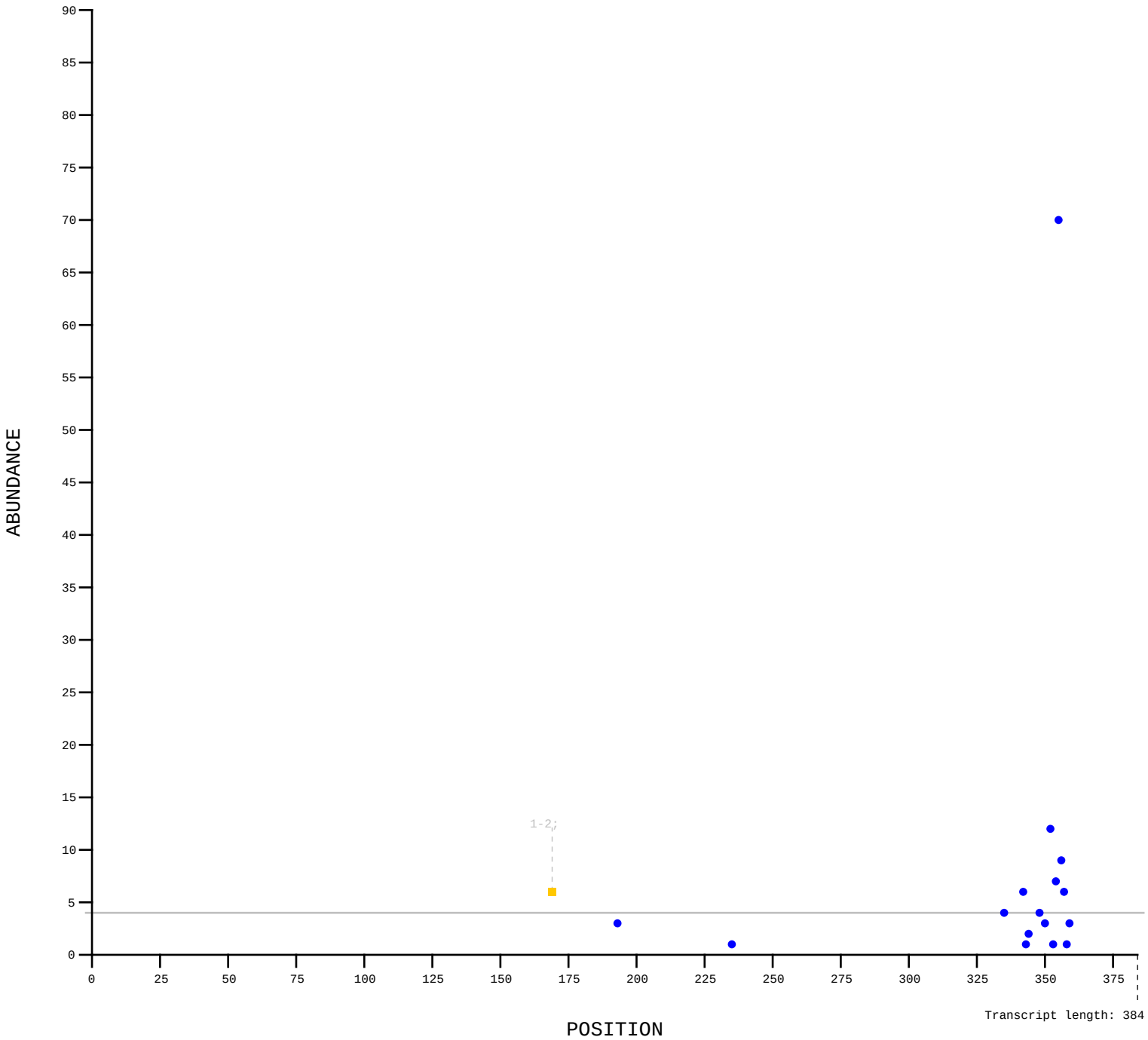
Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:16 Abundance: 47.00(deg) 6(sRNA)
5' CGTTCTGGTTCTGAGGTGC 3' ID:
|||||||||||||||||| Score: 0.0
3' TTCCGCAAGACCAAGACTCCACGGCGGTA 5' p-value: 0.0

2 #2 Position:19 Abundance: 25.00(deg) 5(sRNA)
5' AGGCGTTCTGGTTCTGAGGTGC 3' ID:
||||||||||||||||||||| Score: 0.0
3' AGATTCCGCAAGACCAAGACTCCACGGCGGTA 5' p-value: 0.0

3 #3 Position:17 Abundance: 11.00(deg) 5(sRNA)
5' GCGTTCTGGTTCTGAGGTGC 3' ID:
|||||||||||||||||||| Score: 0.0
3' ATTCCGCAAGACCAAGACTCCACGGCGGTA 5' p-value: 0.0

FOXG_03334T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (384 nt)

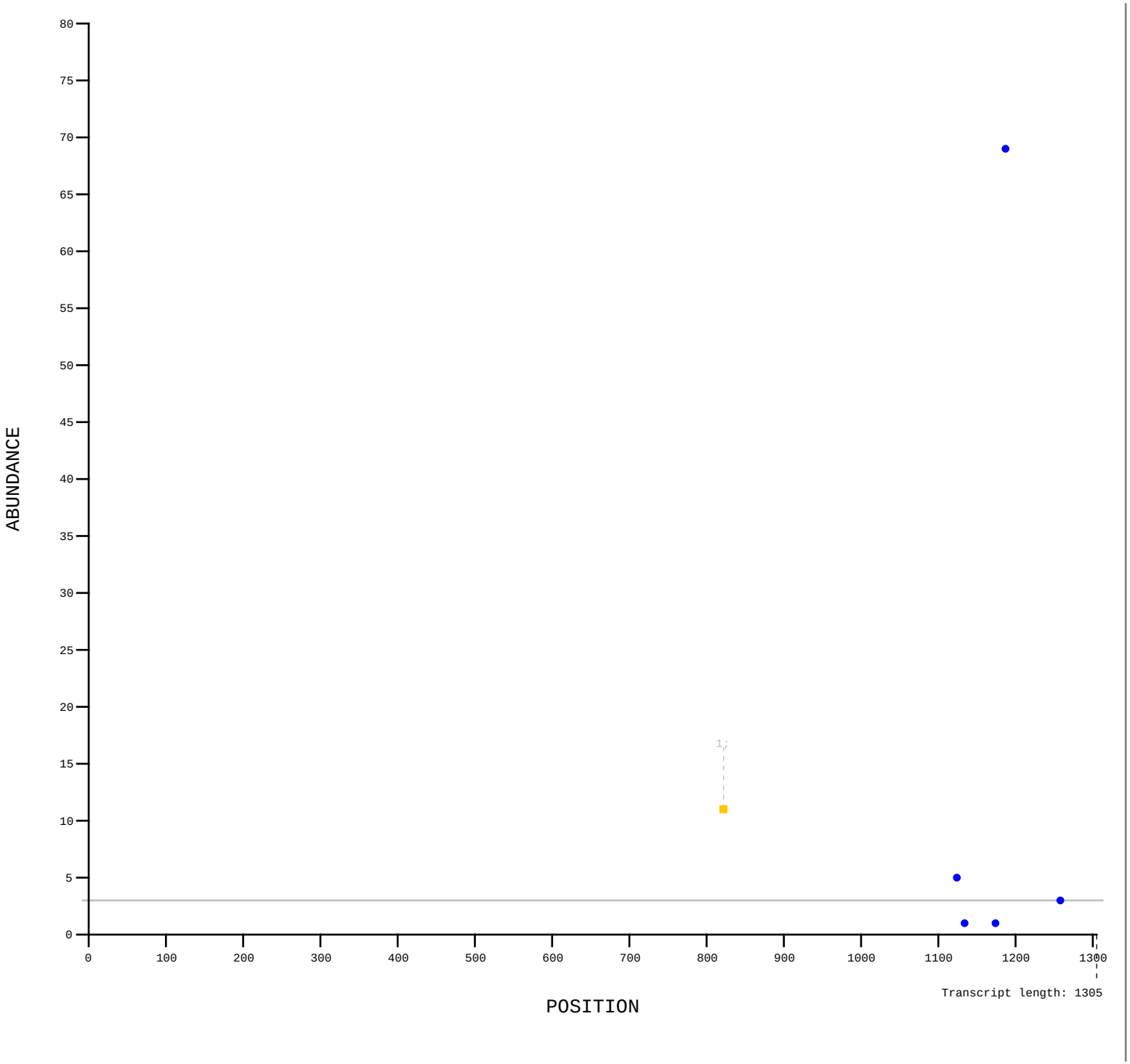


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:169 Abundance: 6.00(deg) 8(sRNA)
5' CTCCAGTAGGAGATCTGGC 3' ID:
| ||||||||||| ||| Score: 2.0
3' CATCGCGGTCATCCTCTAG-CCGTTTCCATCA 5' p-value: 0.0

2 #2 Position:169 Abundance: 6.00(deg) 6(sRNA)
5' CTCCAGTAGGAGATTTGGC 3' ID:
| ||||||||||o | | Score: 3.5
3' CATCGCGGTCATCCTCTAGCCGGTTCCATCAT 5' p-value: 0.03

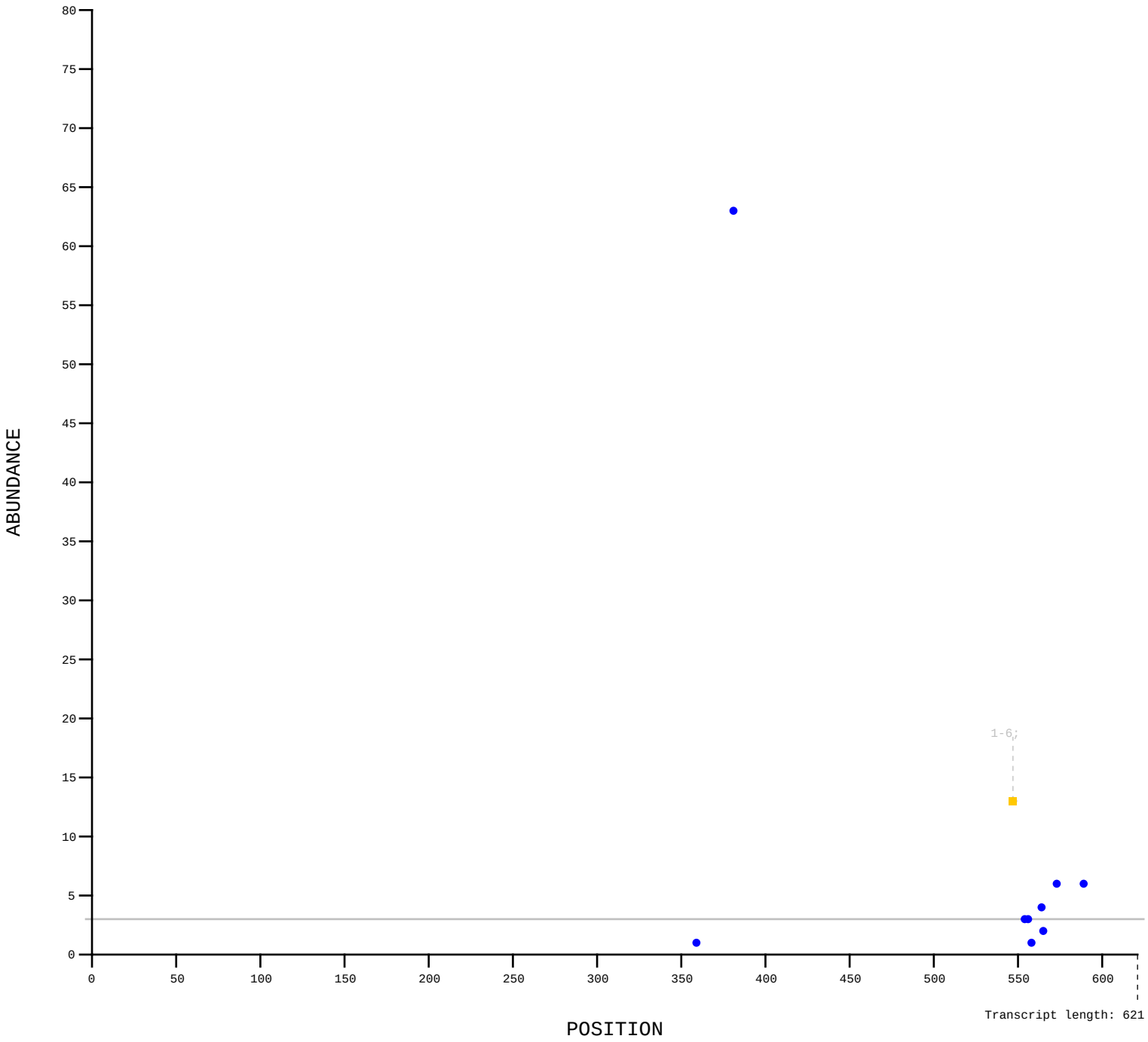
FOXG_03138T0 | Fusarium oxysporum f. sp. lycopersici 4287 ATP-dependent RNA helicase SUB2 (1305 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:822 Abundance: 11.00(deg) 6(sRNA)
5' TTGCAGCTAGATATAGGAAC 3' ID:
|| ||o|| ||||||| ||| Score: 3.5
3' AAAGAAGGTTGAACTATATC-TTGACGACTTC 5' p-value: 0.0

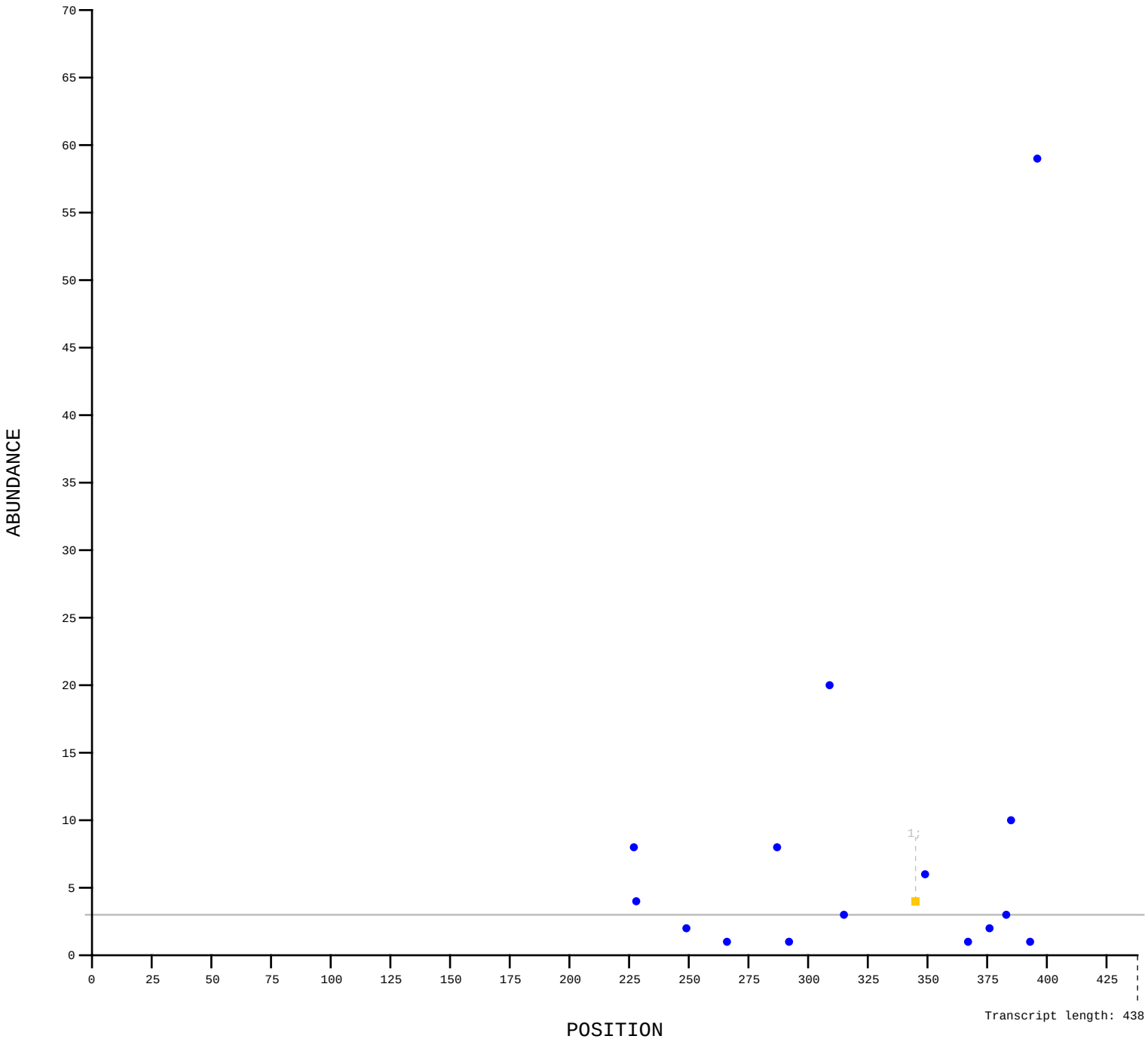
FOXG_04188T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (621 nt) Note(s): (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:547  Abundance: 13.00(deg) 190(sRNA)
   5'     TGGAGATTGTGGACTGCGTC          3'  ID:
          | ||| |o|||||||| |||              Score: 3.5
   3' GACGAGCTCGAGCACCTGAC-CAGCCGTCAGT 5'  p-value: 0.02

2  #2  Position:547  Abundance: 13.00(deg) 110(sRNA)
   5'     TGGAGATTGTGGACTGCGT           3'  ID:
          | ||| |o|||||||| ||               Score: 3.5
   3' GACGAGCTCGAGCACCTGAC-CAGCCGTCAGT 5'  p-value: 0.0

2  #3  Position:547  Abundance: 13.00(deg) 63(sRNA)
   5'     TGGAGATTGTGGACTGCGTCG         3'  ID:
          | ||| |o|||||||| ||||             Score: 3.5
   3' GACGAGCTCGAGCACCTGAC-CAGCCGTCAGT 5'  p-value: 0.01

2  #4  Position:547  Abundance: 13.00(deg) 37(sRNA)
   5'     TGGAGATTGTGGACTGCGTCGGC       3'  ID:
          | ||| |o|||||||| ||||||           Score: 3.5
   3' GACGAGCTCGAGCACCTGAC-CAGCCGTCAGT 5'  p-value: 0.0

2  #5  Position:547  Abundance: 13.00(deg) 13(sRNA)
   5'     TGGAGATTGTGGACTGCGTCGG        3'  ID:
          | ||| |o|||||||| |||||            Score: 3.5
   3' GACGAGCTCGAGCACCTGAC-CAGCCGTCAGT 5'  p-value: 0.0

2  #6  Position:547  Abundance: 13.00(deg) 11(sRNA)
   5'     TGGAGATTGTGGACTGCGTCGGCA      3'  ID:
          | ||| |o|||||||| |||||||          Score: 3.5
   3' GACGAGCTCGAGCACCTGAC-CAGCCGTCAGT 5'  p-value: 0.0
```

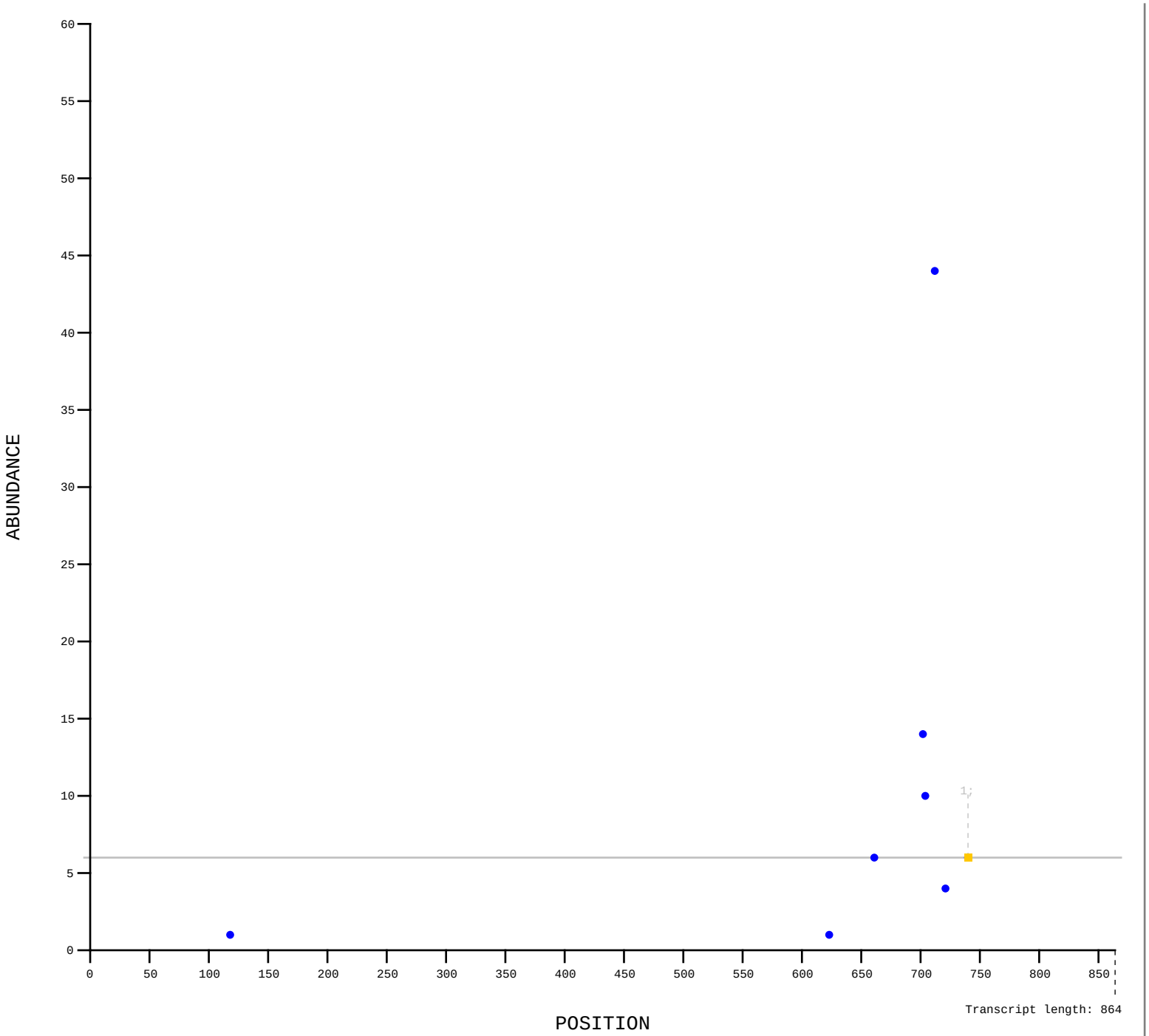
FOXG_12657T0 | Fusarium oxysporum f. sp. lycopersici 4287 40S ribosomal protein S12 (438 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:345 Abundance: 4.00(deg) 7(sRNA)
5' TGAATGTCGACCTTTGGCA 3' ID:
|||o|| |||o||||| Score: 4.0
3' TGGCCCTTATAG-TGGGAACCGGAACGGGAAC 5' p-value: 0.03

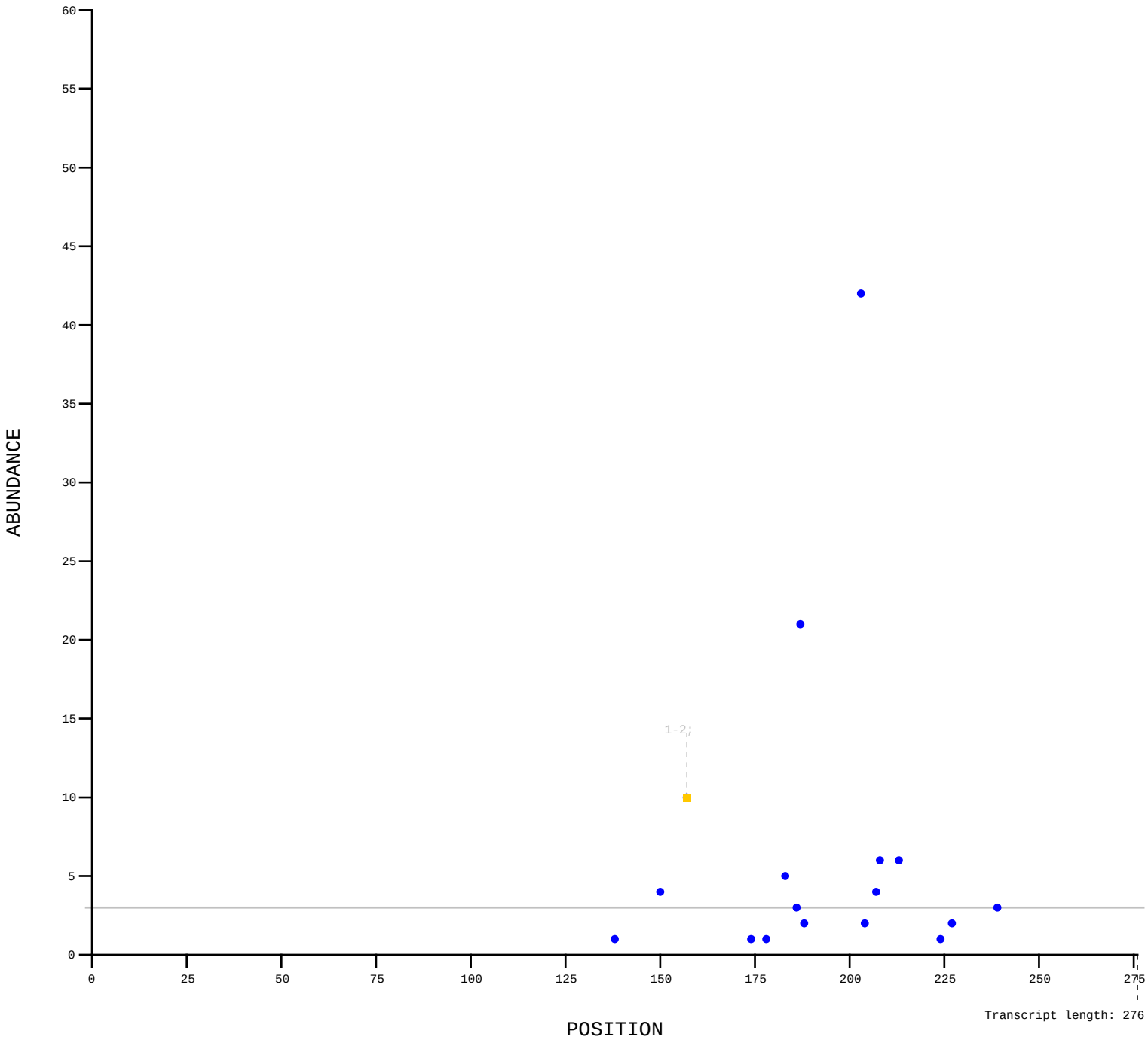
FOXG_00815T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (864 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:740 Abundance: 6.00(deg) 7(sRNA)
5' TGTATTTCTCAAGCCCGTC 3' ID:
||o||o||o|||o| | || Score: 4.0
3' CAACACGTAGAGGGTTTGTGGAGGGAAGCCGA 5' p-value: 0.04

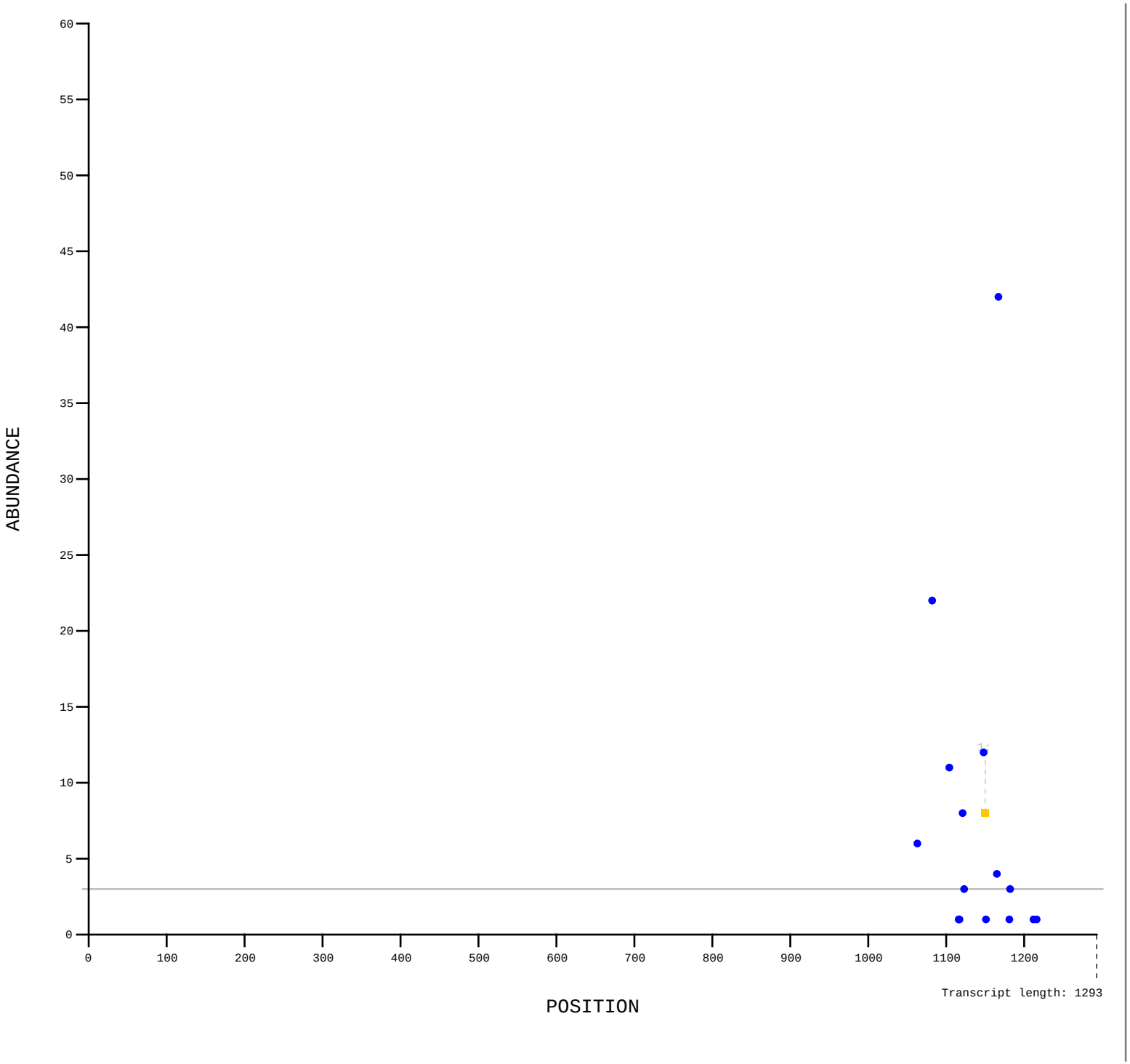
FOXG_11080T0 | Fusarium oxysporum f. sp. lycopersici 4287 mitochondrial ribosomal protein S19 (276 nt)



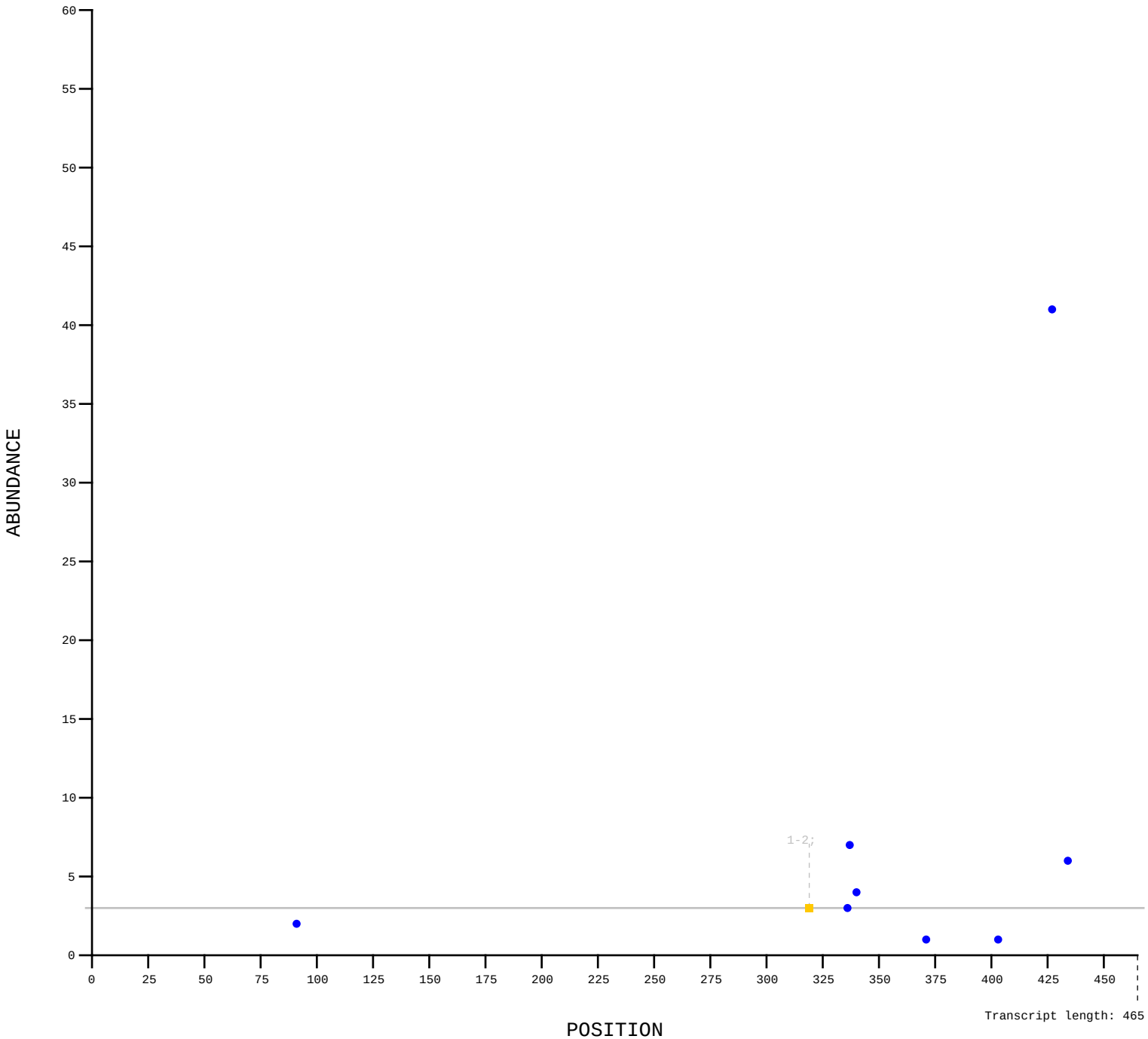
Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:157  Abundance: 10.00(deg) 18(sRNA)
   5'     ACTTGAACTTGAGACGGGA          3'  ID:
            ||o||||||||||| | |             Score: 3.5
   3' ACGTGGAGCTTGAACTCTGGC-TGTTTCAACC 5'  p-value: 0.01

2  #2  Position:157  Abundance: 10.00(deg) 13(sRNA)
   5'     ACTTGAACTTGAGACGGGAA         3'  ID:
            ||o||||||||||| |o |            Score: 4.0
   3' ACGTGGAGCTTGAACTCTGGCTGTTTCAACCC 5'  p-value: 0.01
```

FOXG_09062T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1293 nt) Note(s): (truncated)



FOXG_12884T0 | Fusarium oxysporum f. sp. lycopersici 4287 ubiquitin fusion protein (465 nt)

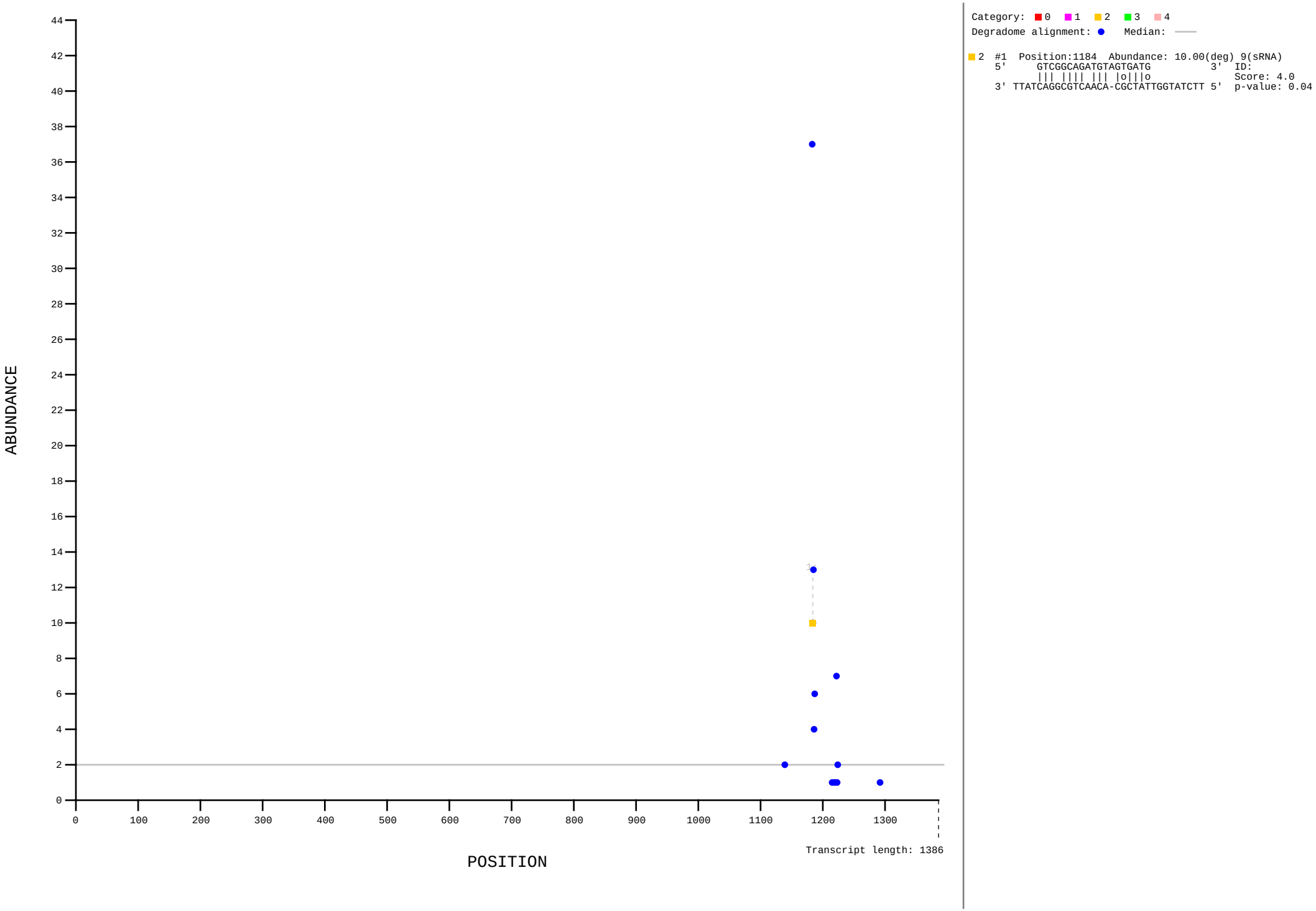


Category: 0 1 2 3 4
Degradome alignment: Median:

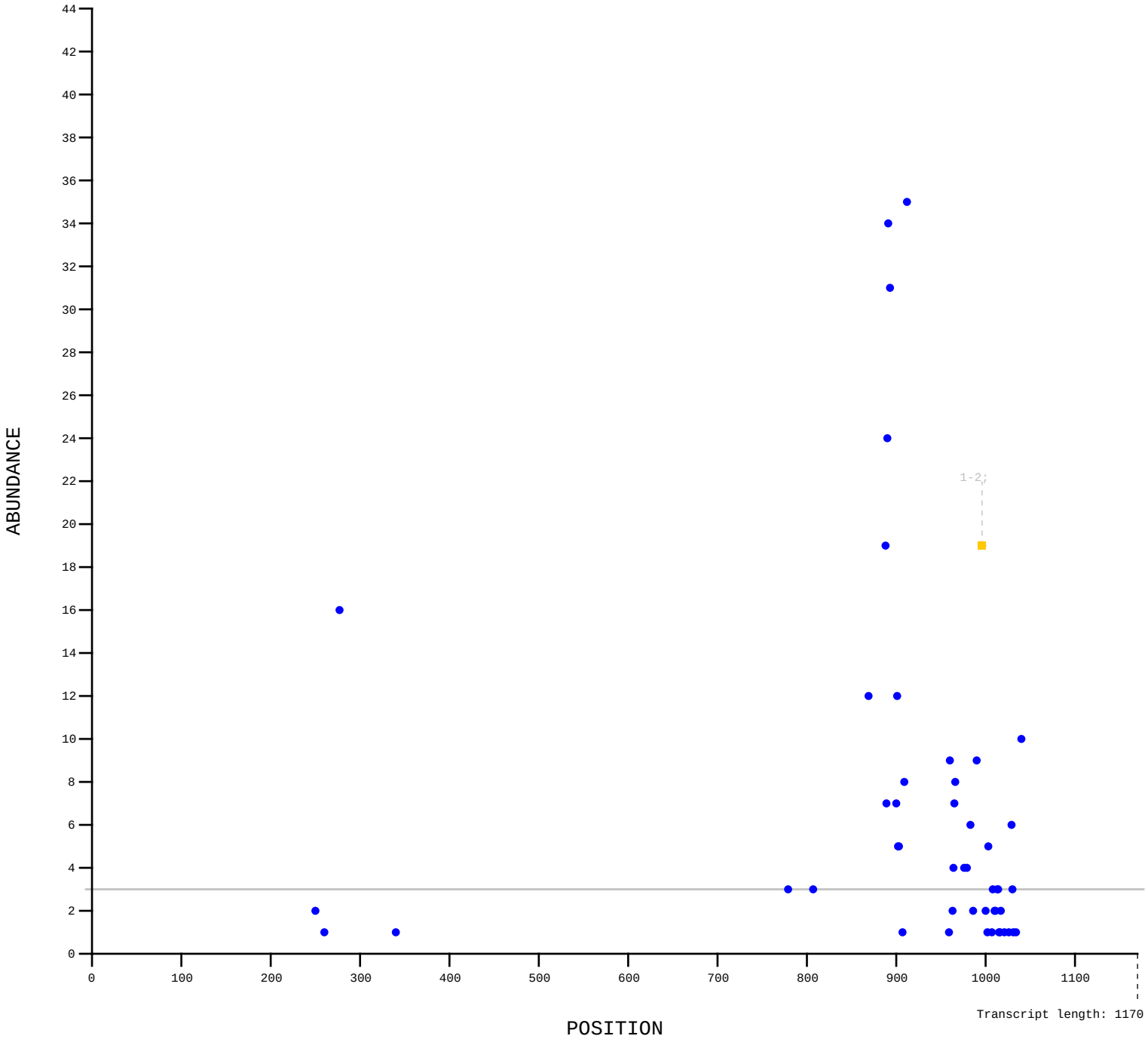
2 #1 Position:319 Abundance: 3.00(deg) 22(sRNA)
5' TGGCTTTGTAGTACTGGGC 3' ID:
o|o|o||||||||| |o Score: 4.0
3' CTCAGCTGGAACATCATGAACTCCTGTCGGTC 5' p-value: 0.02

2 #2 Position:319 Abundance: 3.00(deg) 8(sRNA)
5' TGGCTTTGTAGTACT-GGGCA 3' ID:
o|o|o||||||||| |o| | Score: 4.0
3' CTCAGCTGGAACATCATGAACTCCTGTCGGTC 5' p-value: 0.0

FOXG_02084T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1386 nt)



FOXG_09487T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1170 nt)

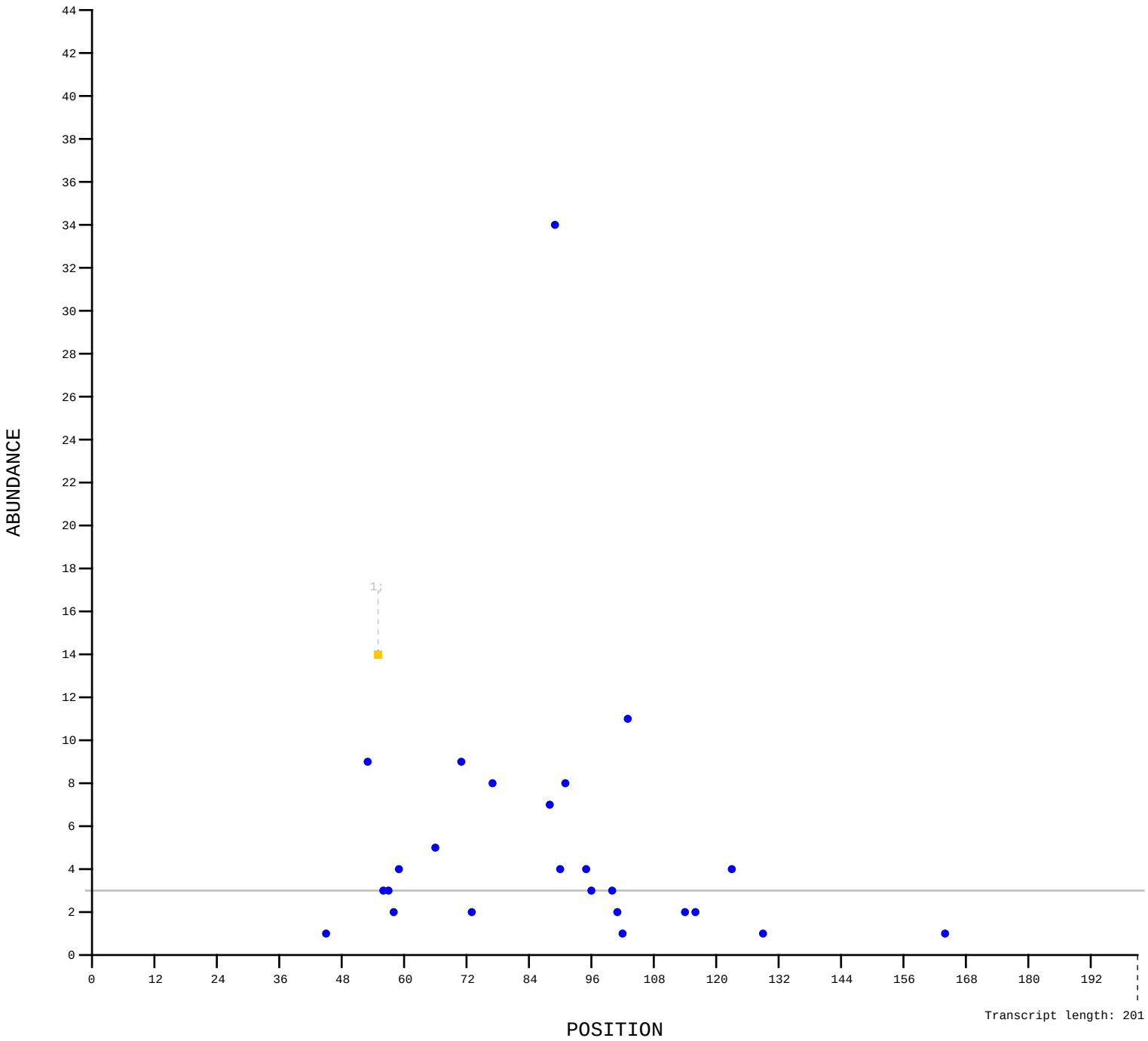


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:996 Abundance: 19.00(deg) 22(sRNA)
5' TGGCTTTGTAGTACTGGGC 3' ID:
oo||||||||| || || Score: 4.0
3' CCAGGTCGAAACATCAACACGCGTGGTGCAAC 5' p-value: 0.03

2 #2 Position:996 Abundance: 19.00(deg) 8(sRNA)
5' TGGCTTTGTAGTACTGGGCA 3' ID:
oo||||||||| || ||| Score: 4.0
3' CCAGGTCGAAACATCAACACGCGTGGTGCAAC 5' p-value: 0.03

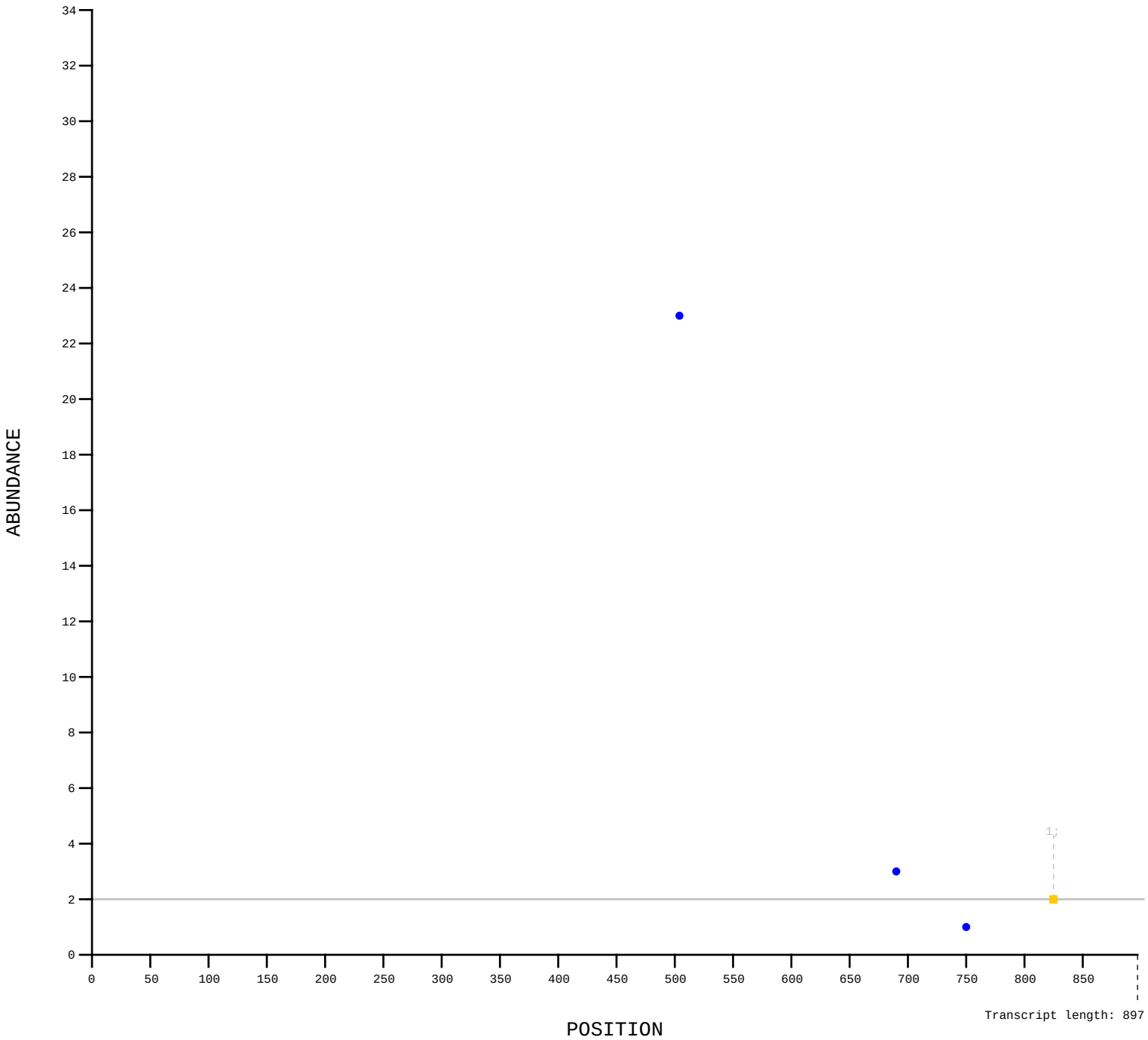
FOXG_05777T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (201 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:55 Abundance: 14.00(deg) 6(sRNA)
5' AGCGGTCTAAGGCGCTGTG 3' ID:
|o||||| |||o|| || | Score: 4.0
3' GAGGTTGCCAG-TTCTGCTACCCCTCCTGGAA 5' p-value: 0.05

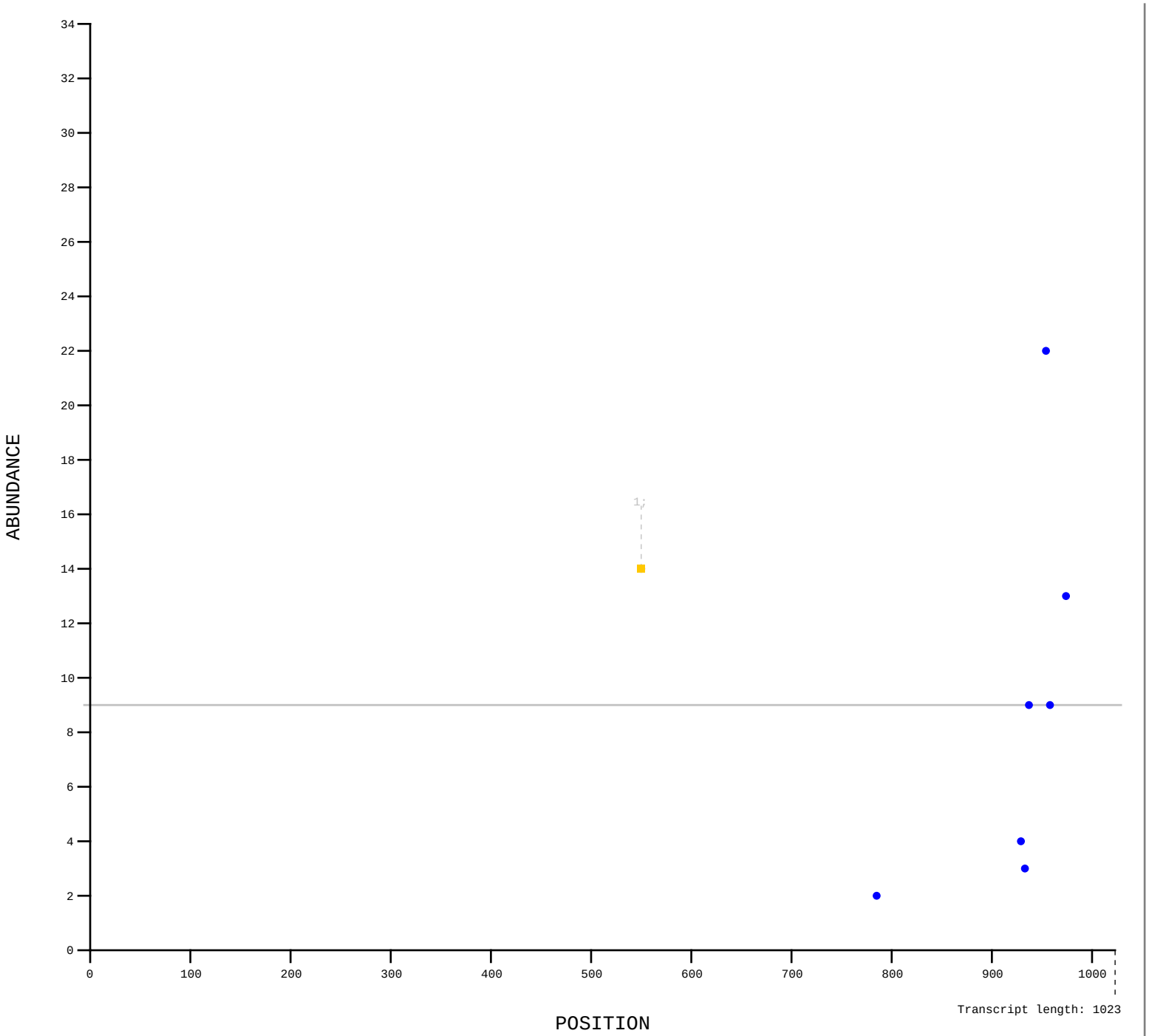
FOXG_02104T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (897 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:825 Abundance: 2.00(deg) 10(sRNA)
5' GATCAAGTGTAGTATCTGTTC 3' ID:
| |||||o||||| ||||oo| Score: 3.5
3' ACAGCGAGTTCGCATCA-AGACGGGGGAACTC 5' p-value: 0.0

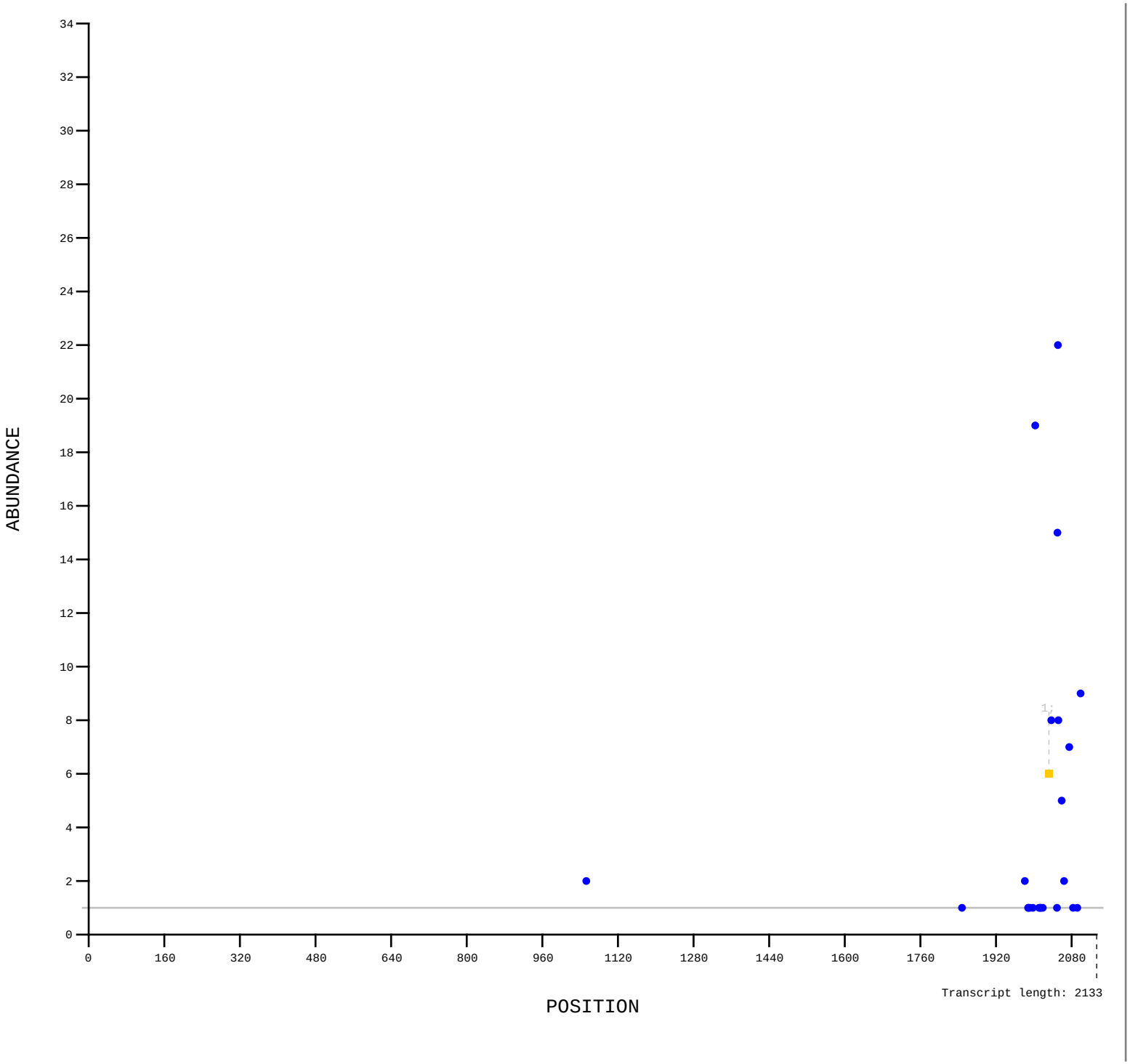
FOXG_13714T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1023 nt)



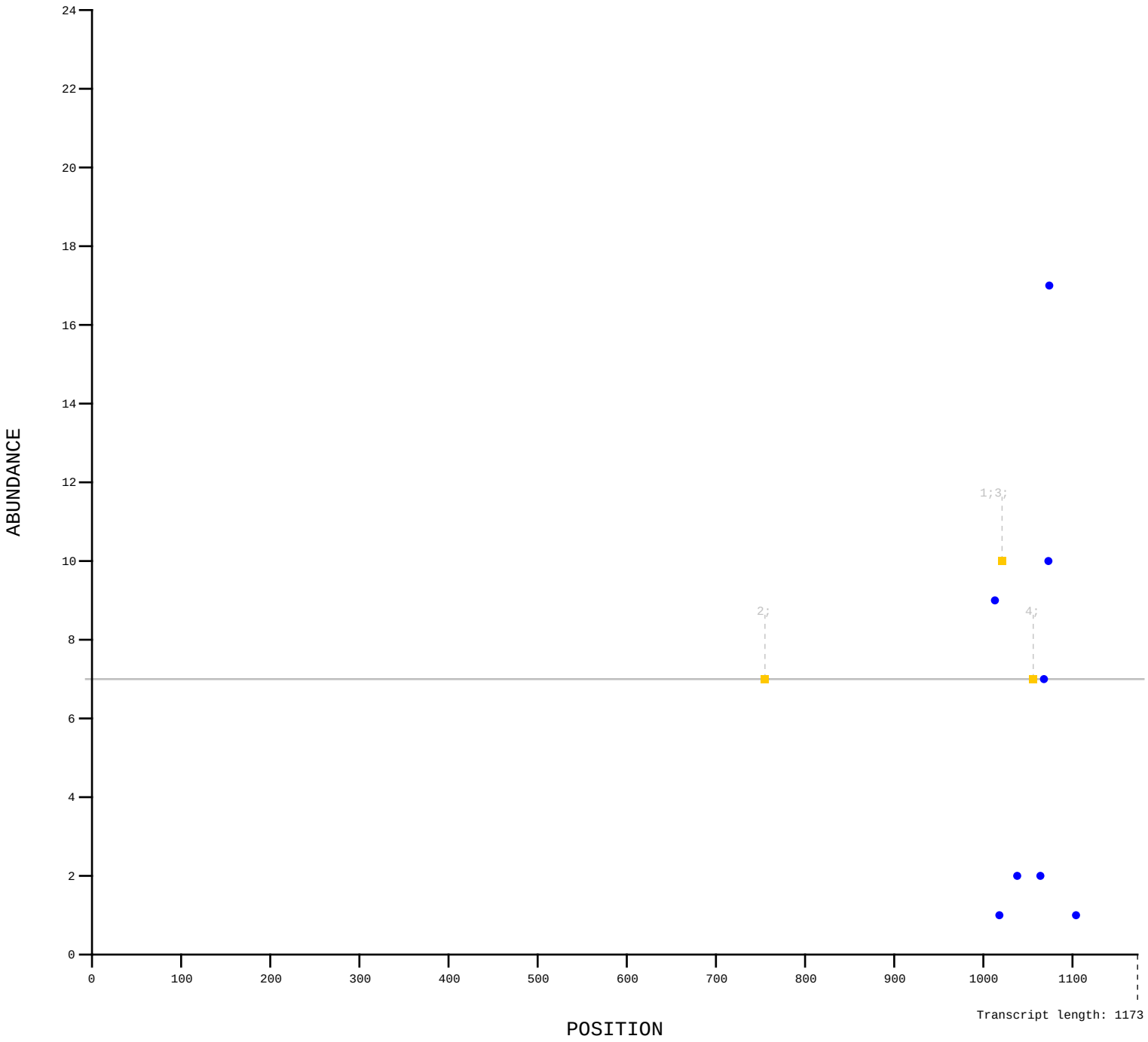
Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:550 Abundance: 14.00(deg) 11(sRNA)
5' TGAGAACGCCAGGAATAAGA 3' ID:
|| |||o|||| ||o|||| Score: 4.0
3' ACCTTCTGTTGTGGTCGTTGTTCTTCAGGTCT 5' p-value: 0.02

FOXG_00241T0 | Fusarium oxysporum f. sp. lycopersici 4287 endopolyphosphatase (2133 nt)



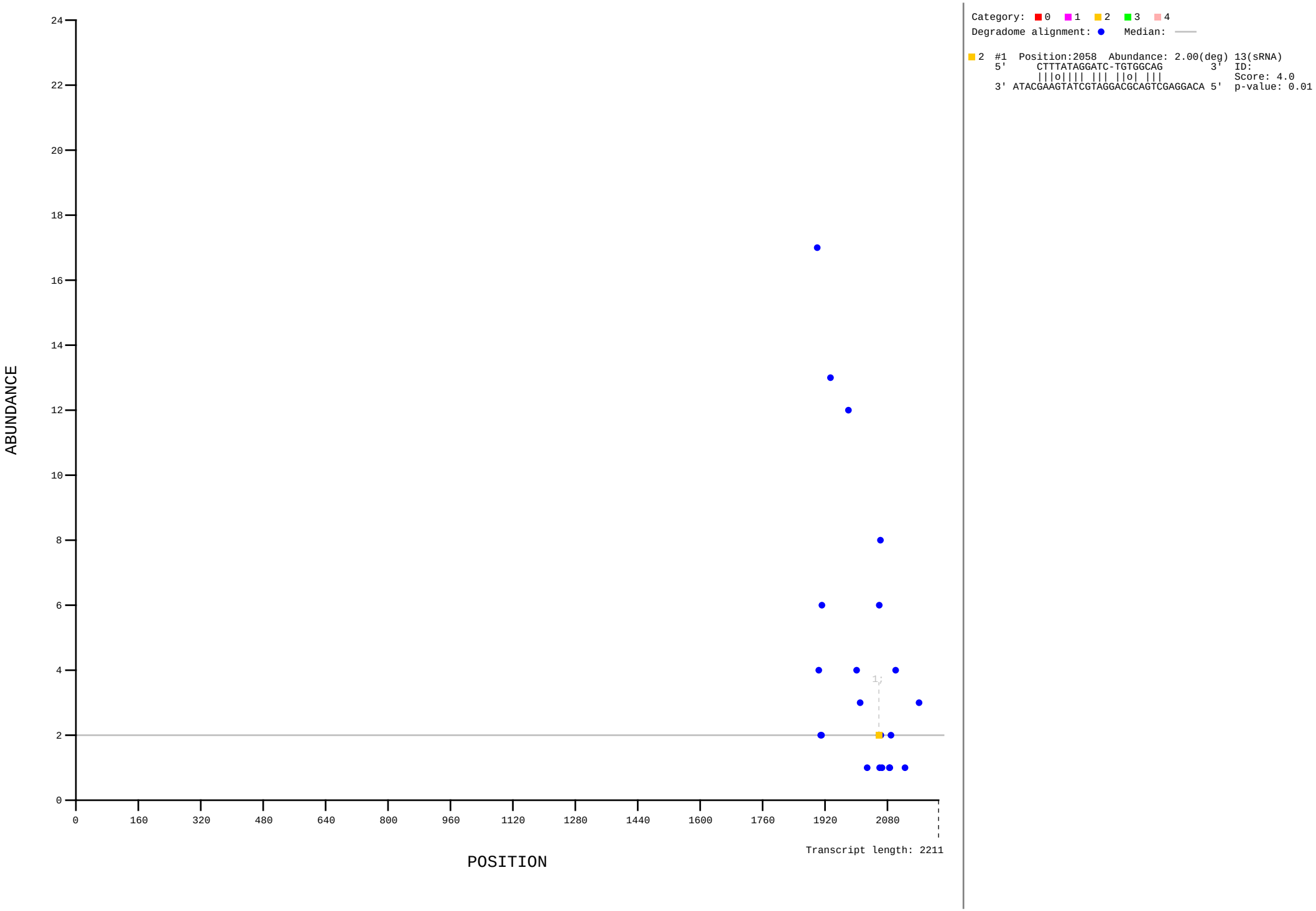
FOXG_08087T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1173 nt)



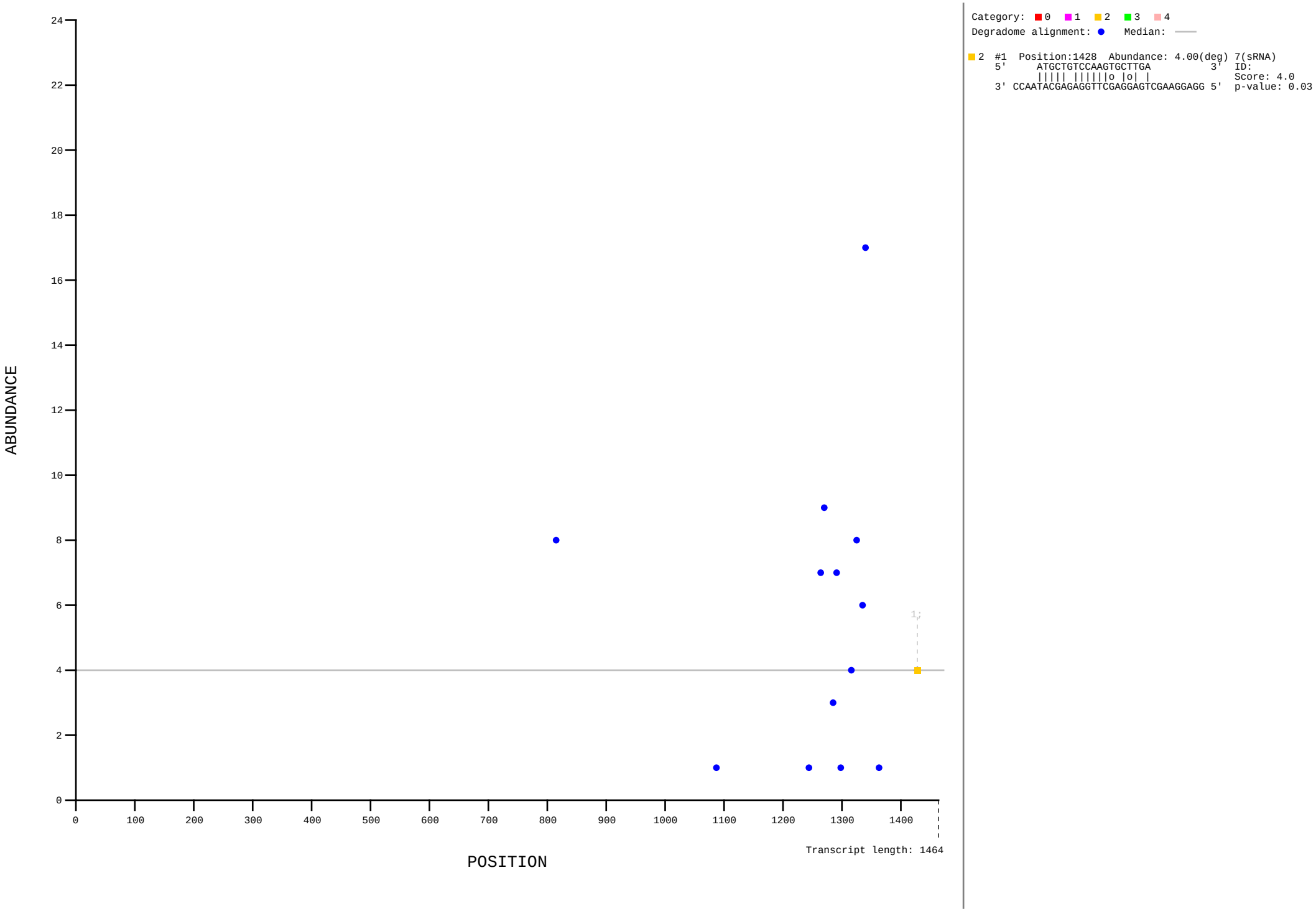
Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:1021  Abundance: 10.00(deg) 30(sRNA)
   5'     TATCGTCAGTCAACTATAGGC         3'  ID:
          o|o||||||||| || | |||             Score: 4.0
   3' AGCCGTGGCAGTCAGTCGA-ACCCGAATAAAA 5'  p-value: 0.0

2  #2  Position:755  Abundance: 7.00(deg) 25(sRNA)
   5'     TCAGGCTCTGAAACTCGGC           3'  ID:
          |||||||||| | o|o |                Score: 4.0
   3' GGTAAGTCCGAGACTCTAGGTAGAGCTATCGC 5'  p-value: 0.01

2  #3  Position:1021  Abundance: 10.00(deg) 14(sRNA)
   5'     TATCGTCAGTCAACTATAGG          3'  ID:
          o|o||||||||| || | ||               Score: 4.0
   3' AGCCGTGGCAGTCAGTCGA-ACCCGAATAAAA 5'  p-value: 0.0

2  #4  Position:1056  Abundance: 7.00(deg) 13(sRNA)
   5'     TGCAAAAGCCTTCACAGAGG          3'  ID:
           | ||| |||||| |||| ||             Score: 4.0
   3' ACCGA-GTTGTCGGAACTGTCCCCGTCCGAAC 5'  p-value: 0.01
```

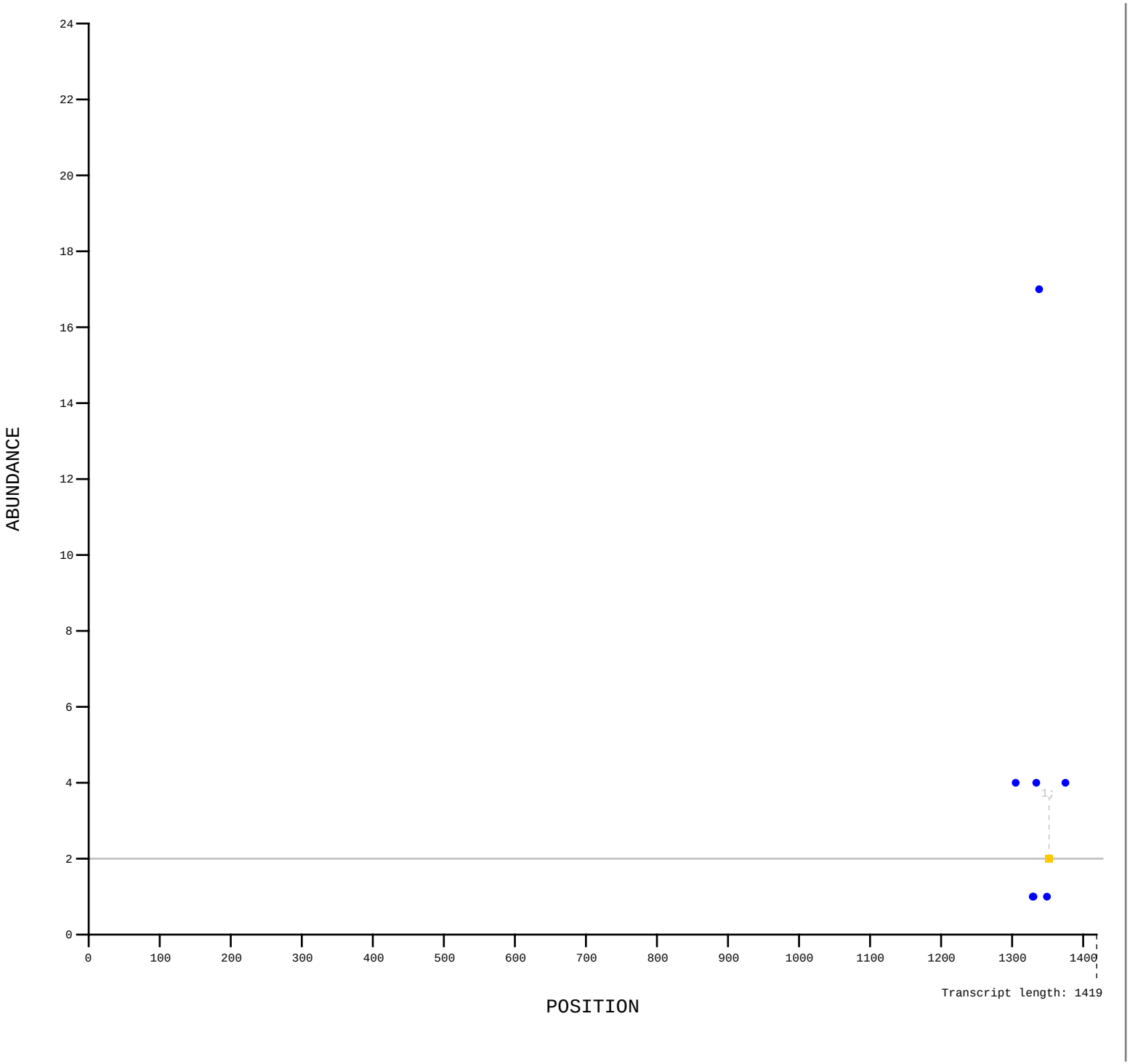
FOXG_04890T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2211 nt)



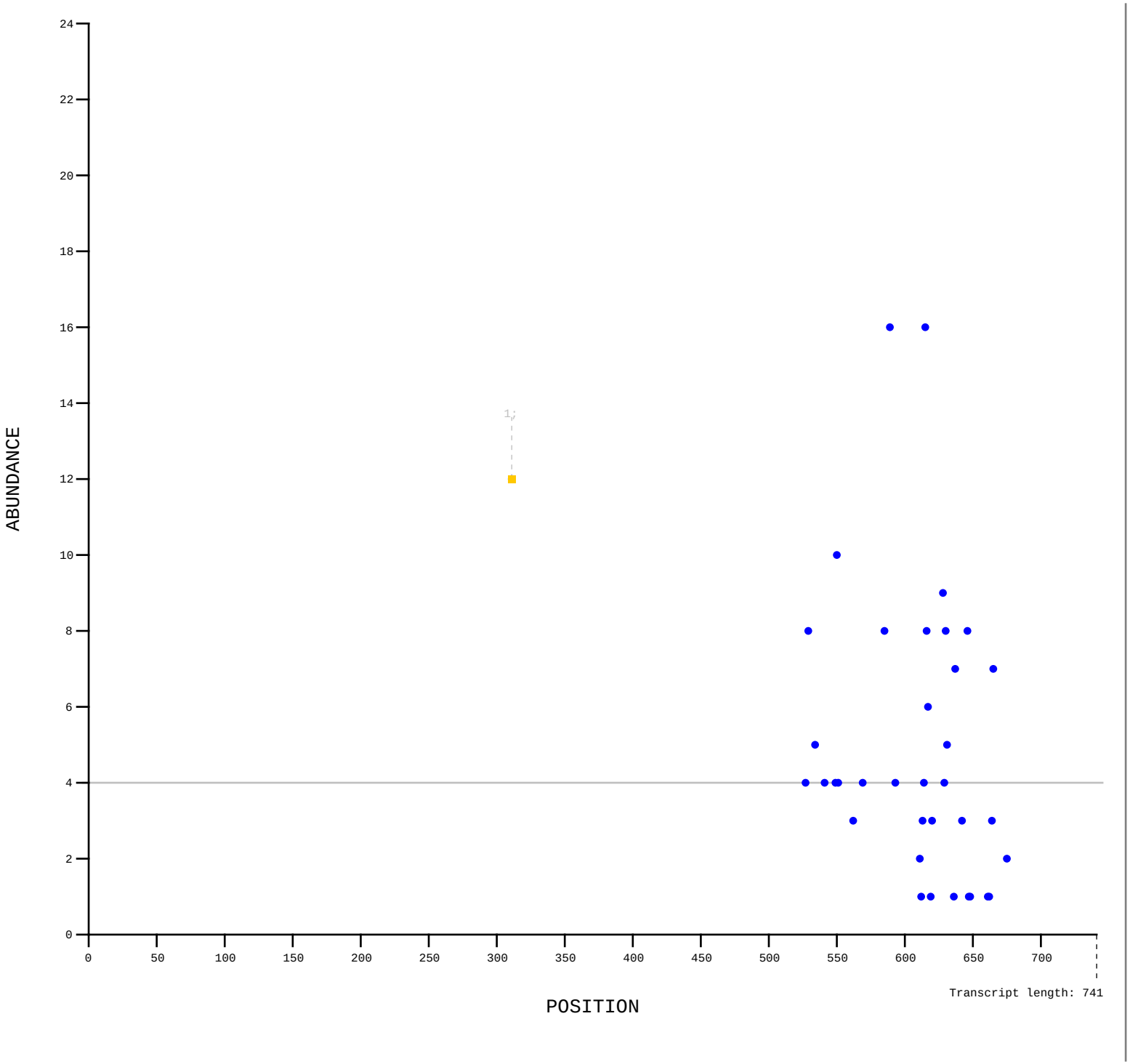
FOXG_05725T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1464 nt)



FOXG_08407T0 | Fusarium oxysporum f. sp. lycopersici 4287 glycolipid 2-alpha-mannosyltransferase (truncated)



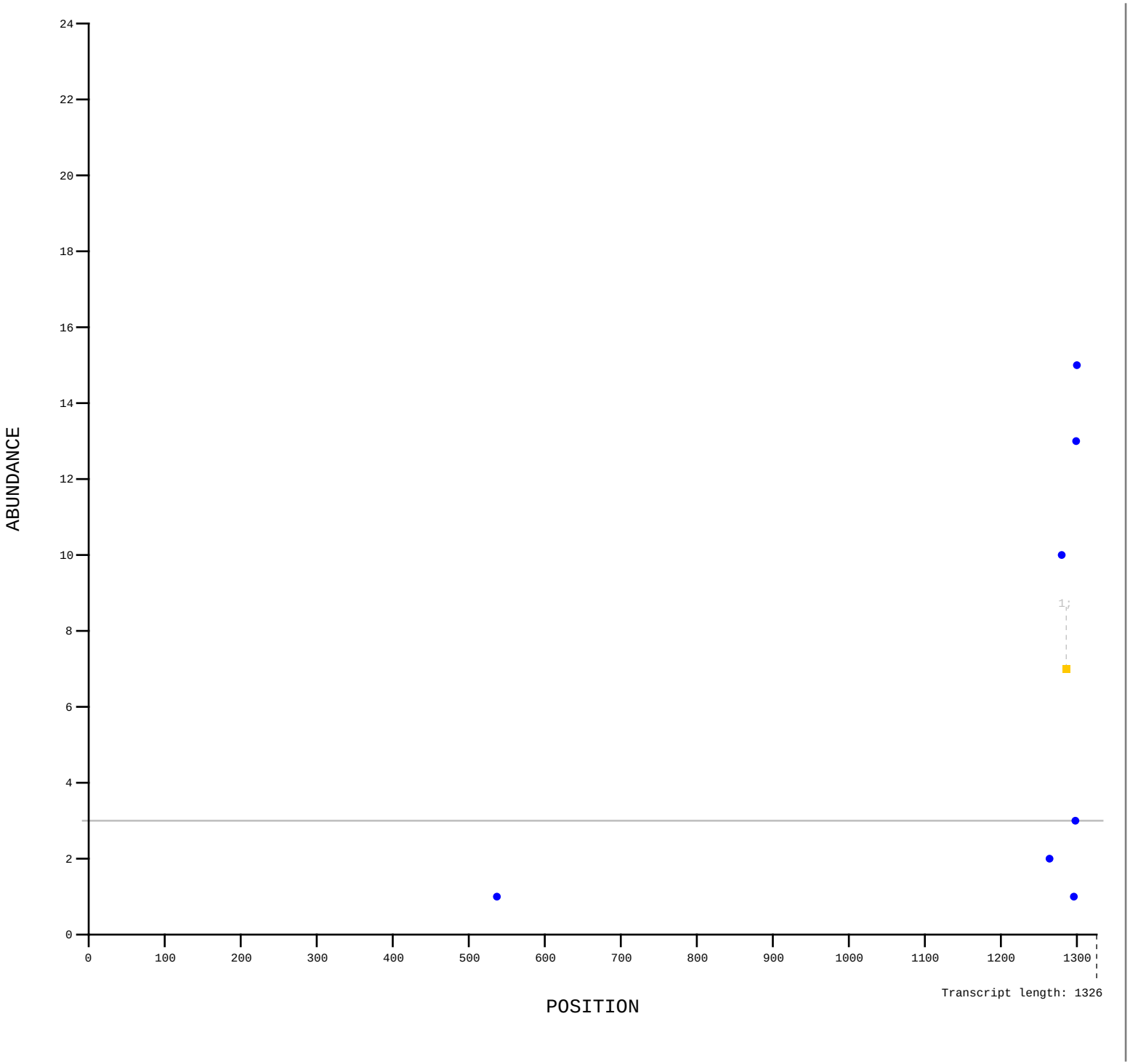
FOXG_16469T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (741 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:311 Abundance: 12.00(deg) 11(sRNA)
5' AACAGTG-ACTTTAACGGTA 3' ID:
||||o|| ||||o||| | | Score: 4.0
3' CCGTTGTTACATGAAGTTGGCTTACGTTGACT 5' p-value: 0.0

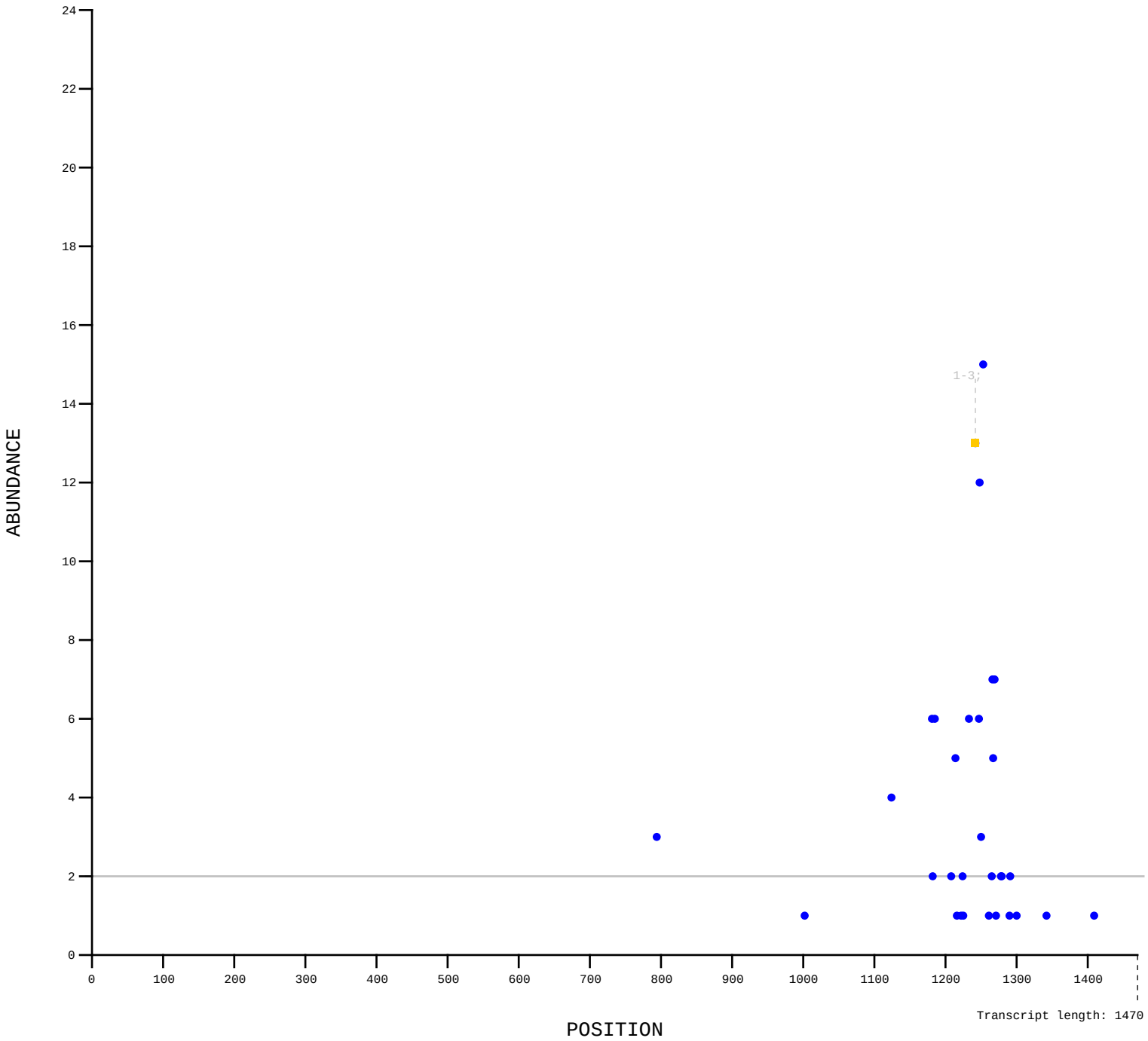
FOXG_11955T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1326 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1286 Abundance: 7.00(deg) 121(sRNA)
5' TCGGACACTGATGCTGAGA 3' ID:
|| |||||||o||o||| Score: 2.0
3' CTTCAG-CTGTGACTGCGGCTCTGACTTCGAC 5' p-value: 0.0

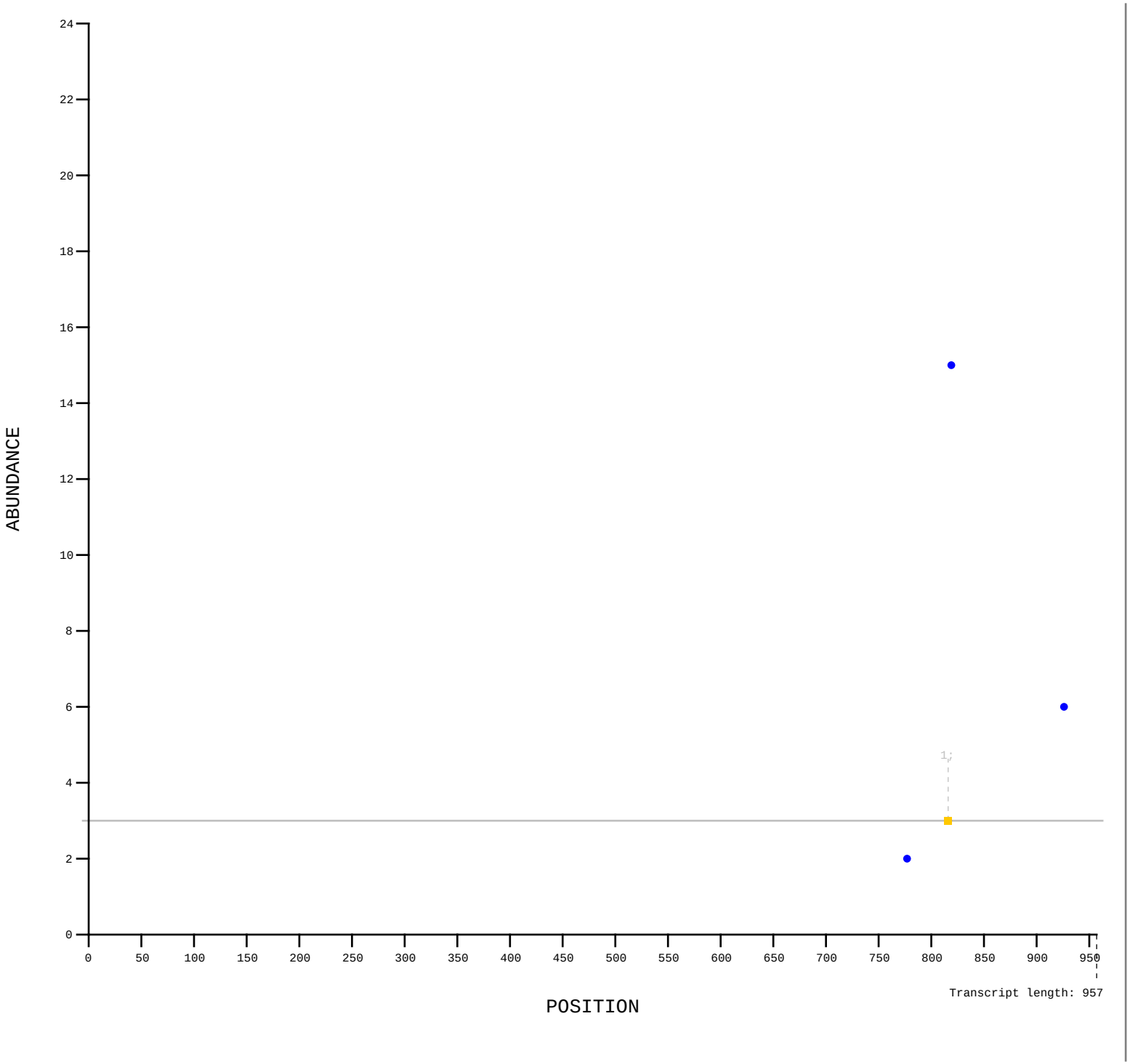
FOXG_01040T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1470 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:1242  Abundance: 13.00(deg) 25(sRNA)
   5'     GCGGGTTTAGCTCAGTTGGG          3'  ID:
          || ||||| |||||||| |               Score: 4.0
   3' CCAGCG-CCAAAACGAGTCAAGCATGTTTGCC 5'  p-value: 0.02

2  #2  Position:1242  Abundance: 13.00(deg) 21(sRNA)
   5'     GCGGGTTTAGCTCAGTTGGGA         3'  ID:
          || ||||| |||||||| | |             Score: 4.0
   3' CCAGCG-CCAAAACGAGTCAAGCATGTTTGCC 5'  p-value: 0.0

2  #3  Position:1242  Abundance: 13.00(deg) 16(sRNA)
   5'     GCGGGTTTAGCTCAGTTGG           3'  ID:
          || ||||| |||||||| |               Score: 3.0
   3' CCAGCG-CCAAAACGAGTCAAGCATGTTTGCC 5'  p-value: 0.0
```

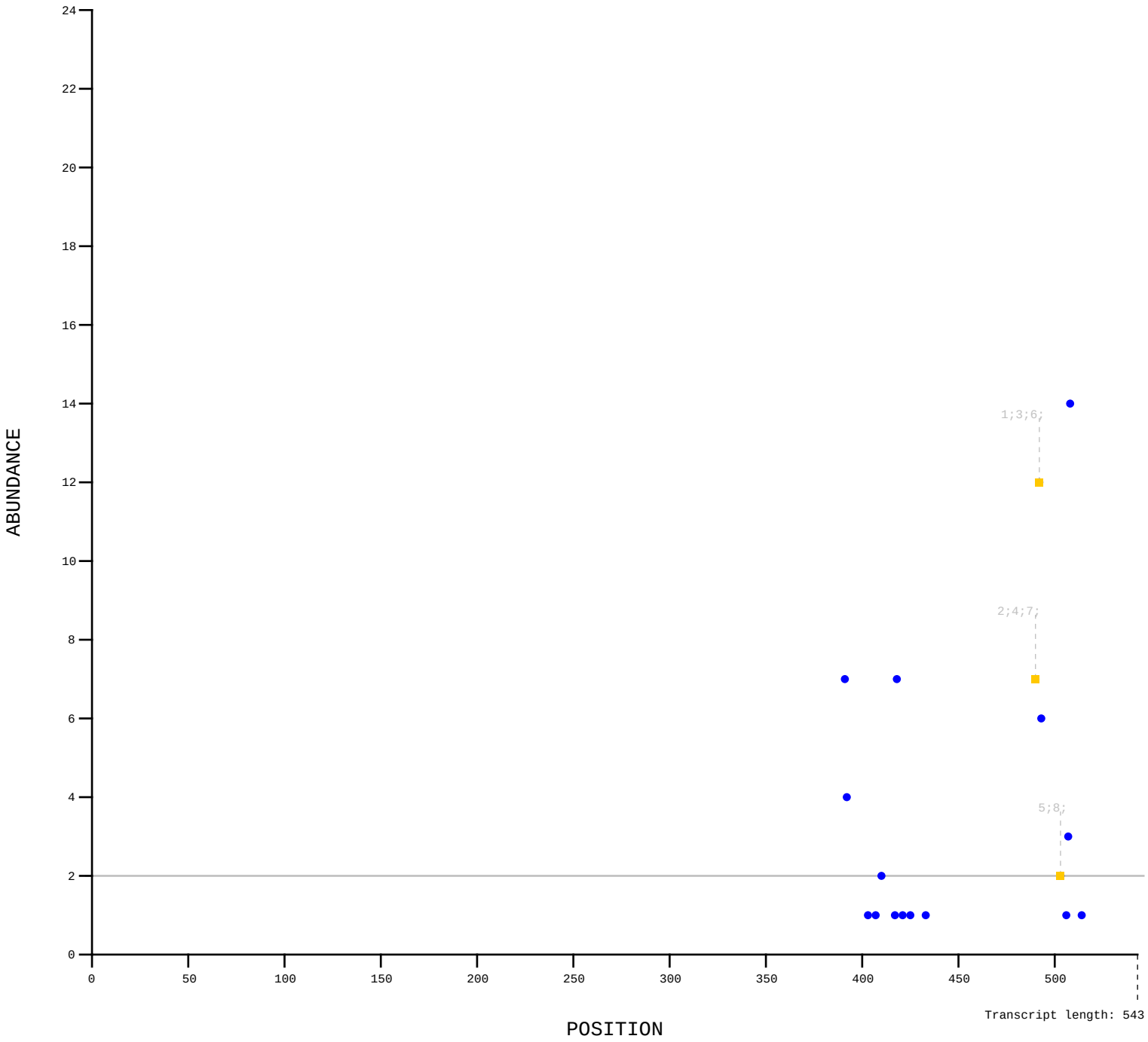
FOXG_09855T0 | Fusarium oxysporum f. sp. lycopersici 4287 catechol dioxygenase (957 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:816 Abundance: 3.00(deg) 9(sRNA)
5' AAGGATTAGATTATTCT-GA 3' ID:
||||| |||||o |o|| || Score: 4.0
3' TCAGTTCCTCATCTAGCAGGAACTGTCGCGTT 5' p-value: 0.0

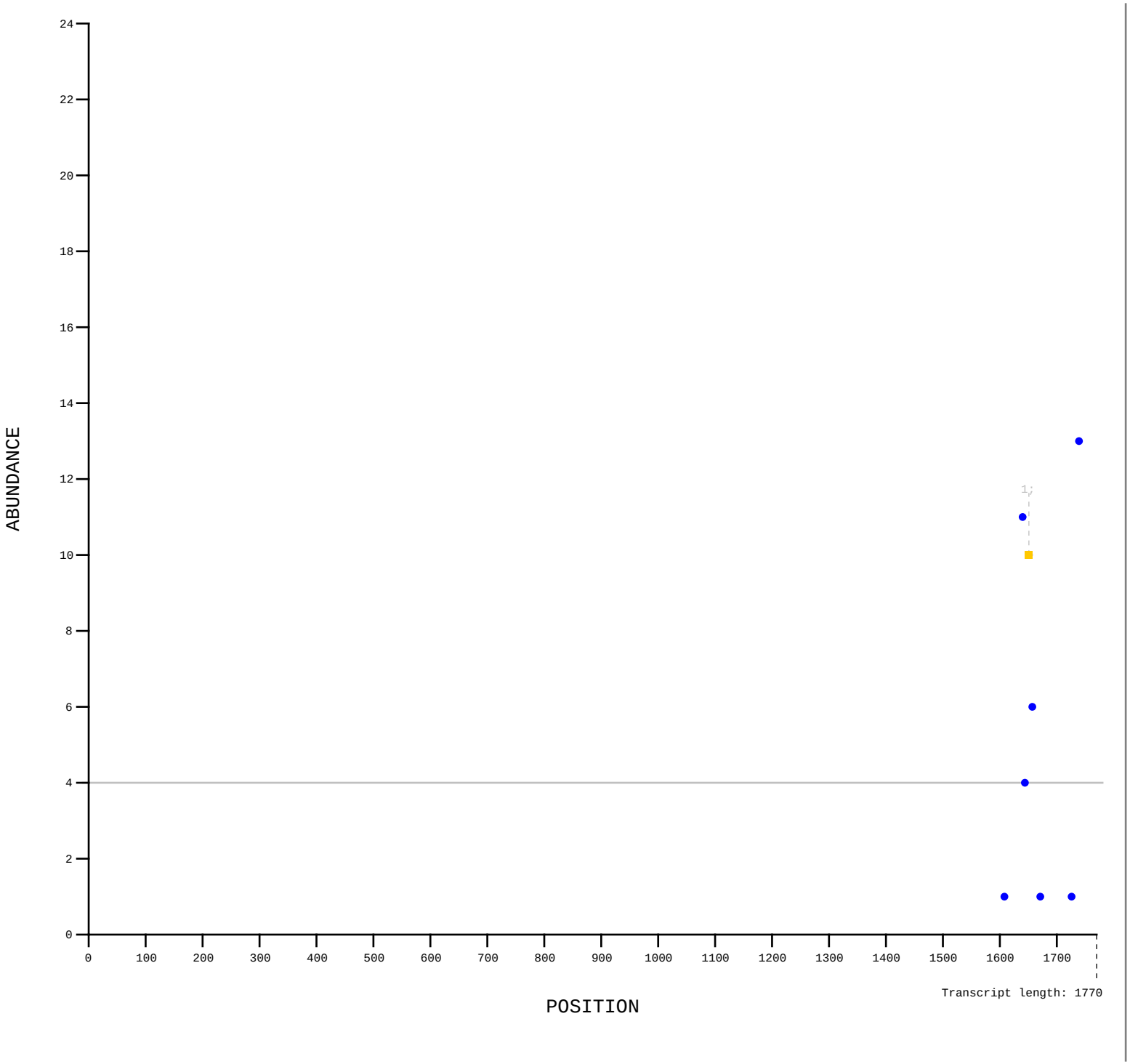
FOXG_01111T0 | Fusarium oxysporum f. sp. lycopersici 4287 peptidyl-prolyl cis-trans isomerase, (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:492  Abundance: 12.00(deg) 79(sRNA)
5'     TCTGACAACACCTTTGTCGGA         3'  ID:
        | ||||| |||||o||o||||             Score: 3.0
3' CATGA-ACTGTCGTGGAGACGGCCTCGGCCAT 5'  p-value: 0.0

2  #2  Position:490  Abundance: 7.00(deg) 48(sRNA)
5'     TGACAACACCTTTGTCGGATC         3'  ID:
       ||||| |||||o||o|||| |             Score: 3.0
3' ATGAACTGTCGTGGAGACGGCCTCGGCCATCG 5'  p-value: 0.0

2  #3  Position:492  Abundance: 12.00(deg) 47(sRNA)
5'     TCTGACAACACCTTTGTCGG          3'  ID:
        | ||||| |||||o||o|||              Score: 3.0
3' CATGA-ACTGTCGTGGAGACGGCCTCGGCCAT 5'  p-value: 0.0

2  #4  Position:490  Abundance: 7.00(deg) 27(sRNA)
5'     TGACAACACCTTTGTCGGA           3'  ID:
       ||||| |||||o||o||||                Score: 2.0
3' ATGAACTGTCGTGGAGACGGCCTCGGCCATCG 5'  p-value: 0.0

2  #5  Position:503  Abundance: 2.00(deg) 16(sRNA)
5'     GGCTTCTGCTACTTGGC-GC          3'  ID:
        ||||||| ||||||o| ||               Score: 3.5
3' CCGTGCGAAGACCATGAACTGTCGTGGAGACG 5'  p-value: 0.0

2  #6  Position:492  Abundance: 12.00(deg) 12(sRNA)
5'     TCTGACAACACCTTTGTCG           3'  ID:
        | ||||| |||||o||o||                Score: 3.0
3' CATGA-ACTGTCGTGGAGACGGCCTCGGCCAT 5'  p-value: 0.01

2  #7  Position:490  Abundance: 7.00(deg) 5(sRNA)
5'     TGACAACACCTTTGTCGGAT          3'  ID:
       ||||| |||||o||o||||                Score: 3.0
3' ATGAACTGTCGTGGAGACGGCCTCGGCCATCG 5'  p-value: 0.0

2  #8  Position:503  Abundance: 2.00(deg) 5(sRNA)
5'     GGCTTCTGCTACTTGGC-GCA         3'  ID:
        ||||||| ||||||o| |||              Score: 3.5
3' CCGTGCGAAGACCATGAACTGTCGTGGAGACG 5'  p-value: 0.02
```

FOXG_08367T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1770 nt)



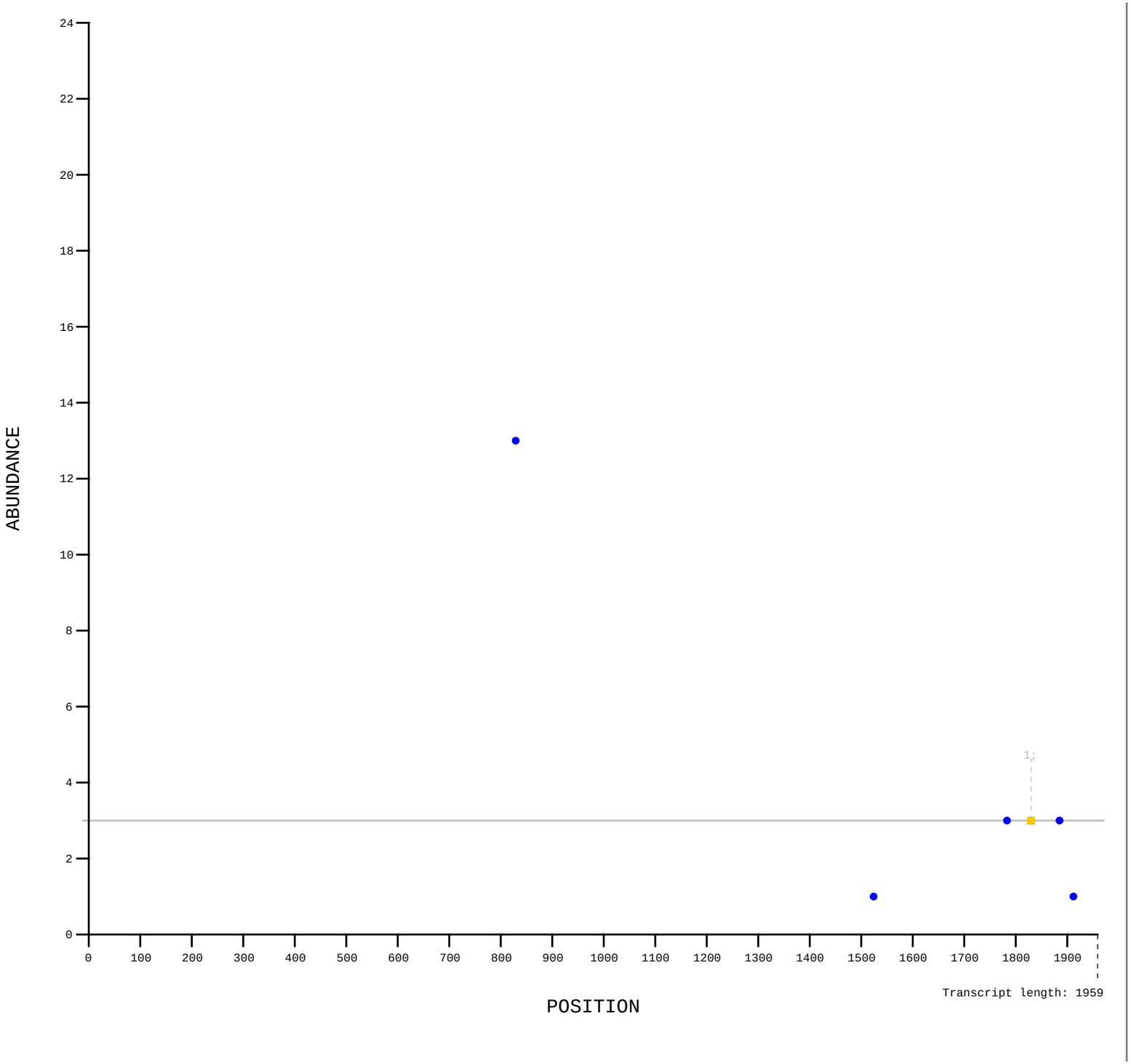
Category: 0 1 2 3 4

Degradome alignment: Median:

2 #1 Position:1651 Abundance: 10.00(deg) 114(sRNA)

```
5'     TCTGTACAGCTTTGCAGGC          3'   ID:
         |||||||o||oo| ||||               Score: 3.5
3' AGCGCGACATGTTGAGGCATCCGCACTTGCTG 5'    p-value: 0.0
```

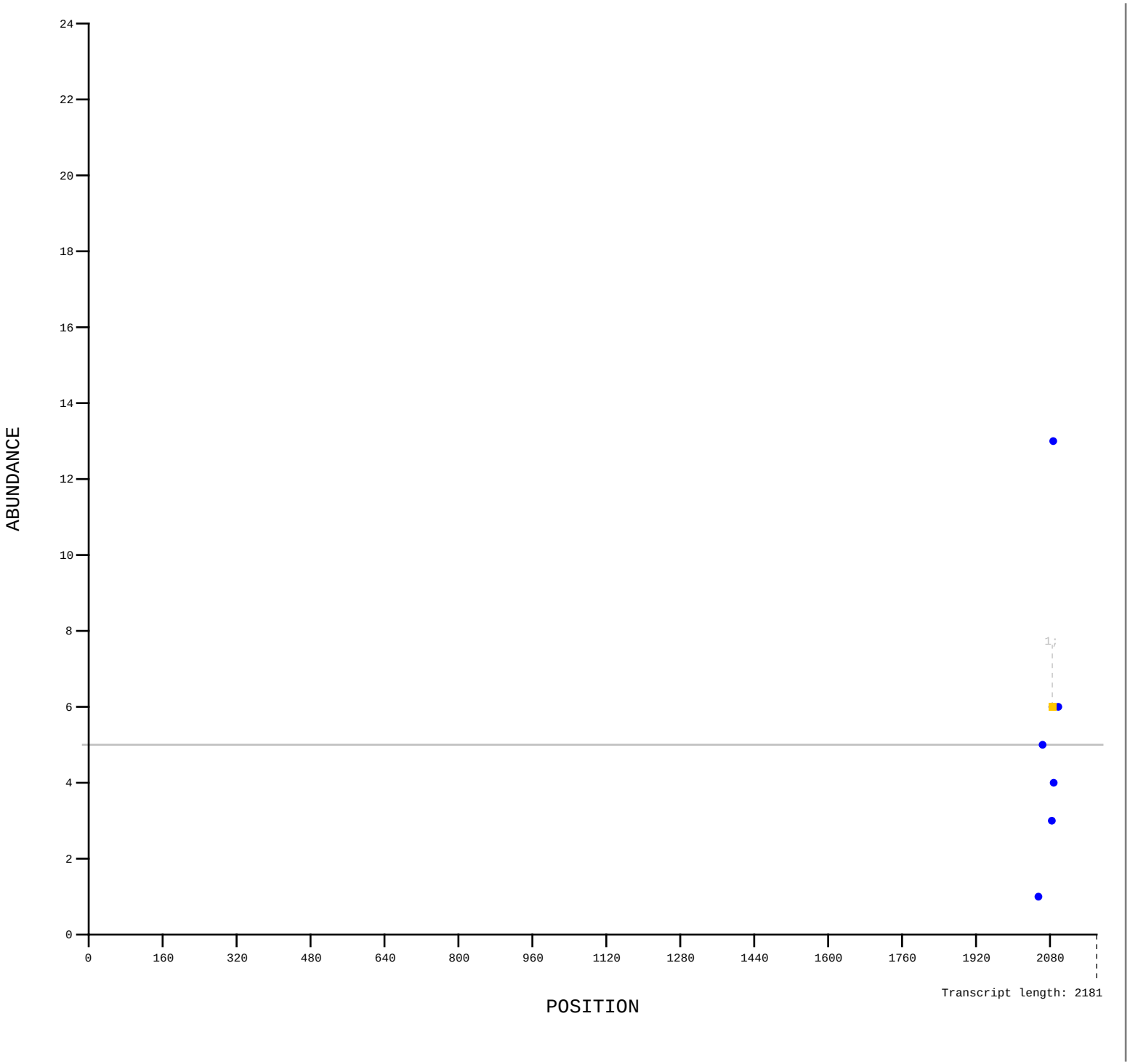
FOXG_00795T0 | Fusarium oxysporum f. sp. lycopersici 4287 heat shock 70 kDa protein (1959 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1830 Abundance: 3.00(deg) 16(sRNA)
5' ATCAGTTCGGTAGAACTTCACCG 3' ID:
|o|||o|| |||||||||| |o Score: 3.5
3' GTGGTGGTCGAGGCATCTTGAAGTAGTACTAC 5' p-value: 0.0

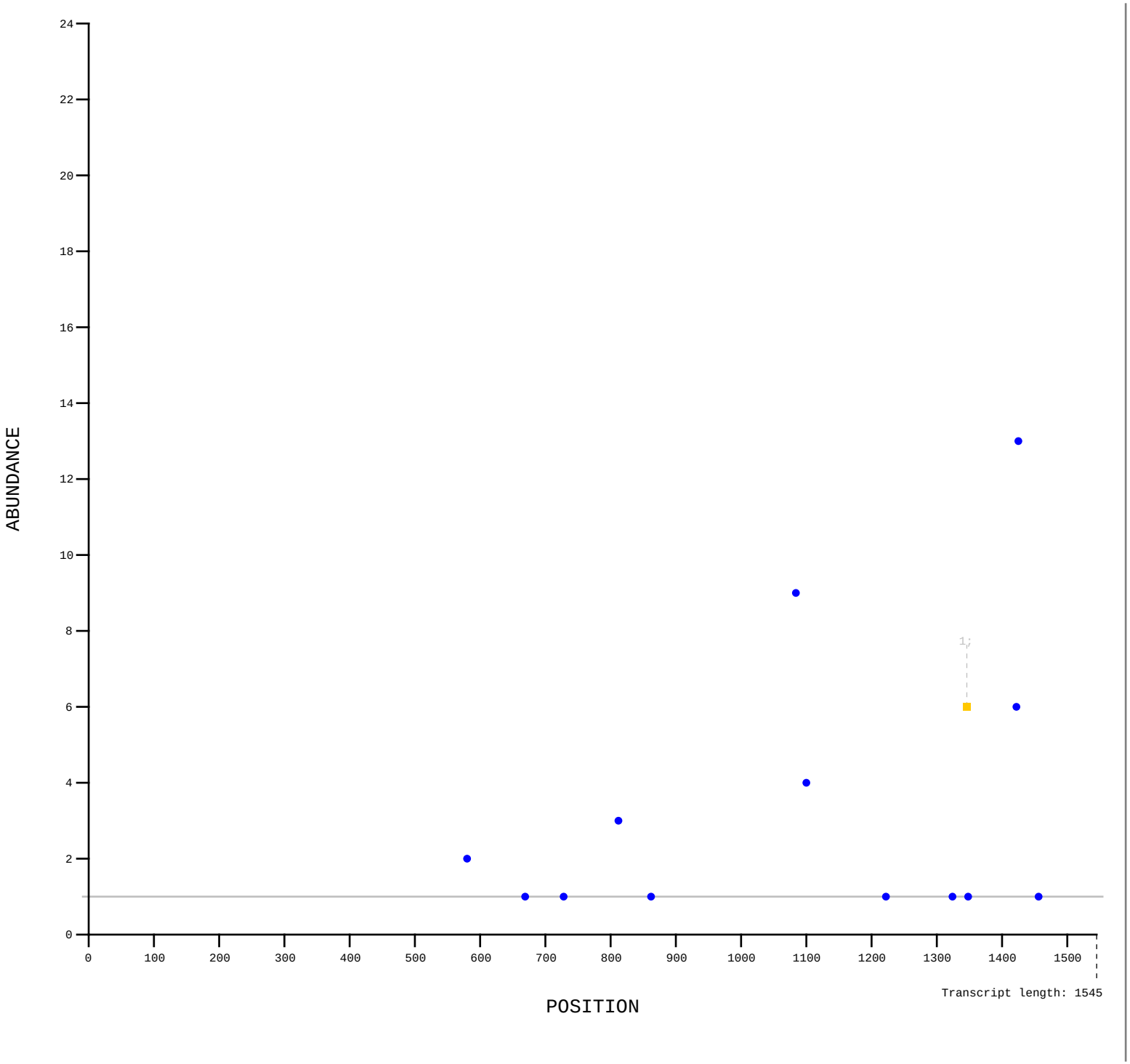
FOXG_01511T0 | Fusarium oxysporum f. sp. lycopersici 4287 ABC1 protein (2181 nt)



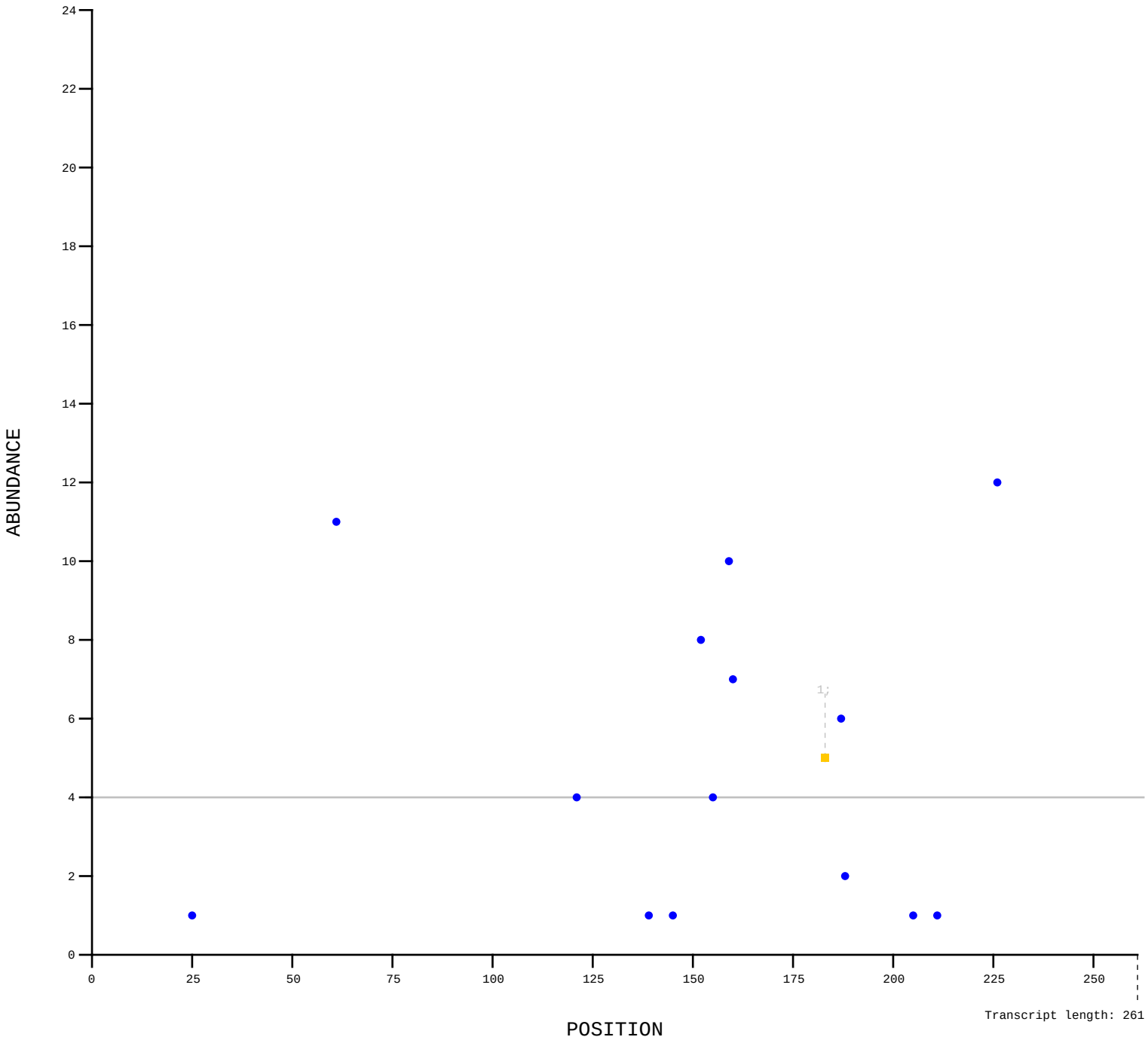
Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:2085 Abundance: 6.00(deg) 7(sRNA)
5' ACG-ATCGCTAAATTGTCGG 3' ID:
||| |o|||||| o| |||| Score: 4.0
3' CCTTGCGTGGCGATTCGAAAGCCACGTCTGAC 5' p-value: 0.02

FOXG_10059T0 | Fusarium oxysporum f. sp. lycopersici 4287 phosphate transporter (1545 nt) Note(s): At (truncated)



FOXG_05140T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (261 nt)



Category: 0 1 2 3 4

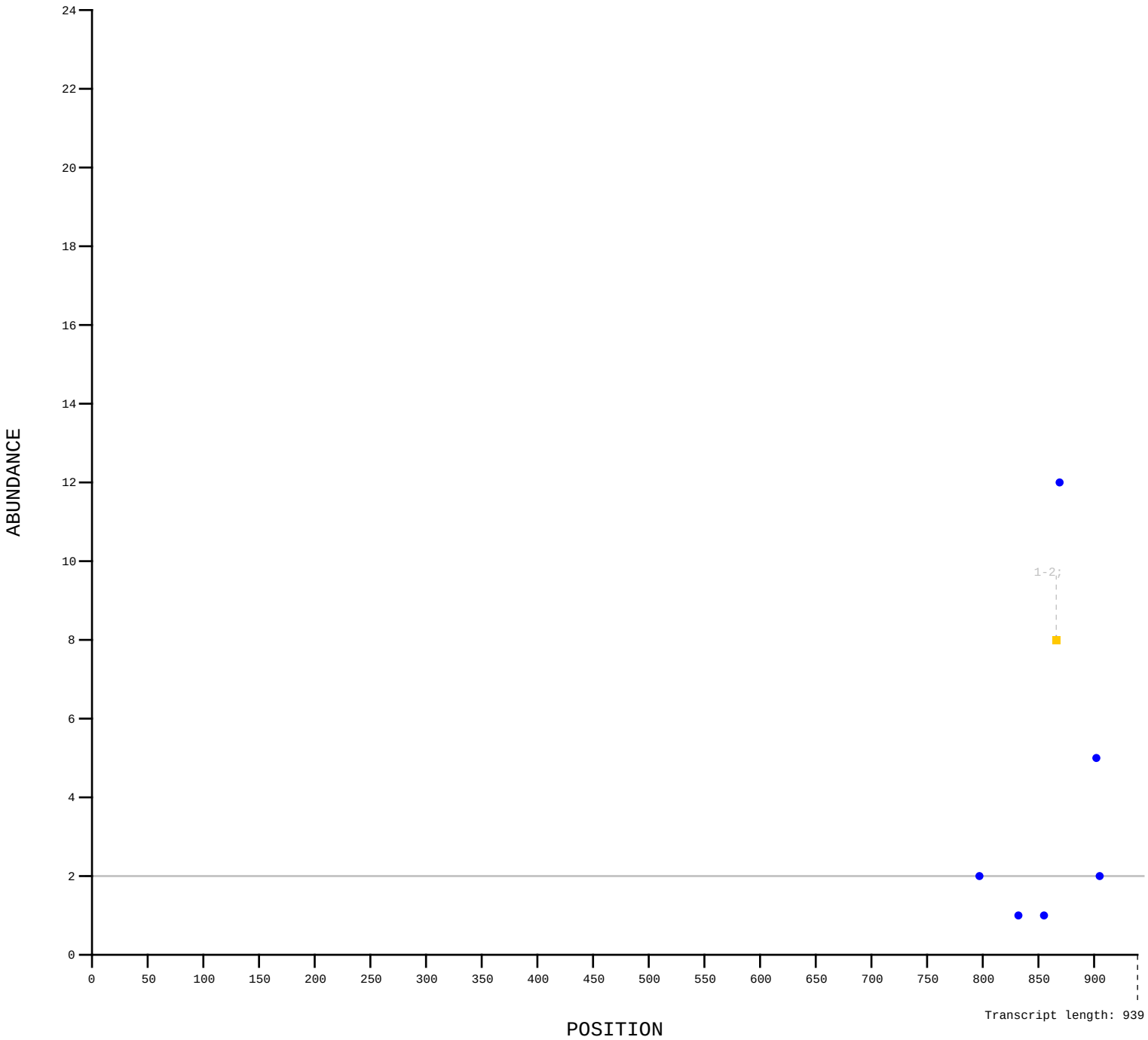
Degradome alignment: Median:

2 #1 Position:183 Abundance: 5.00(deg) 34(sRNA)

```
5'     GTAGAATAGAGCTTGCCTCC          3'
         | |||| ||||||| || |
3' CCTTCTTCTTCTCTCGAACCGAAGGTTGAGCG 5'
```

ID:
Score: 4.0
p-value: 0.0

FOXG_13196T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (939 nt)

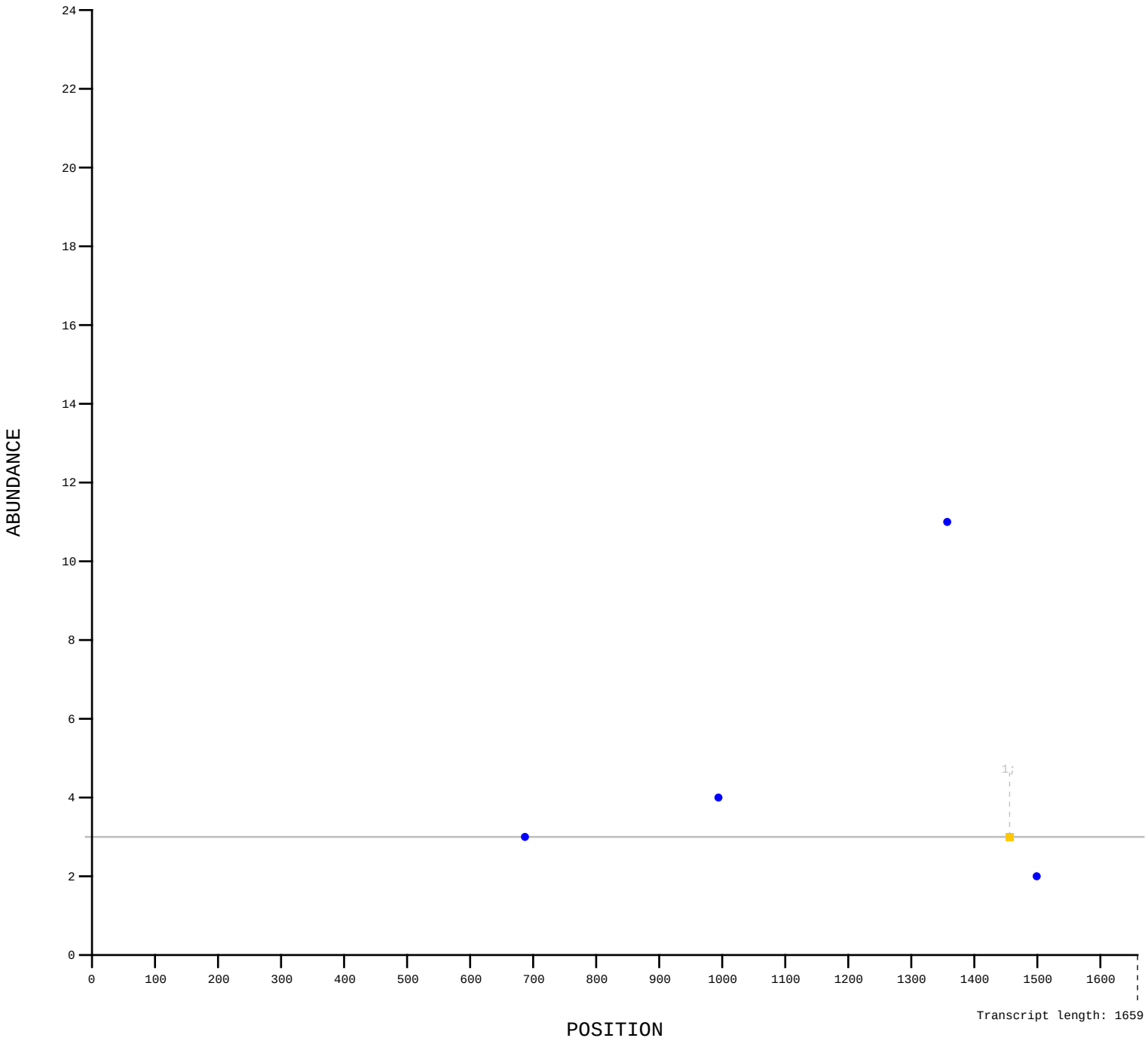


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:866 Abundance: 8.00(deg) 13(sRNA)
5' CCGAGGTTT-TTCCCTGCCGC 3' ID:
|||| |o|| ||| |o||||| Score: 4.0
3' TCTGGCTACGAATAAGTGGCGGCGGTTTAGTT 5' p-value: 0.01

2 #2 Position:866 Abundance: 8.00(deg) 10(sRNA)
5' CCGAGGTTT-TTCCCTGCCGCC 3' ID:
|||| |o|| ||| |o|||||| Score: 4.0
3' TCTGGCTACGAATAAGTGGCGGCGGTTTAGTT 5' p-value: 0.01

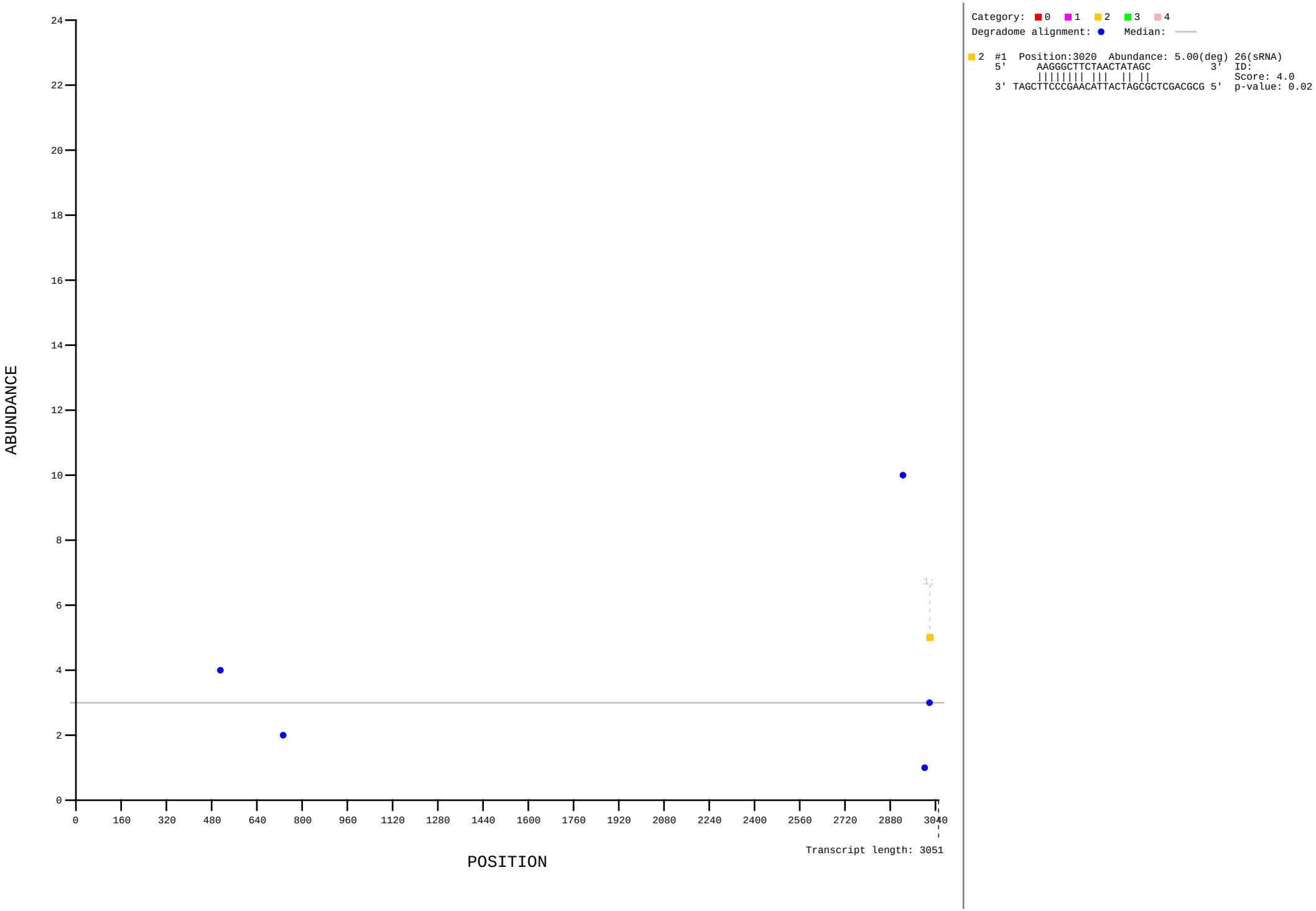
FOXG_17426T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1659 nt)



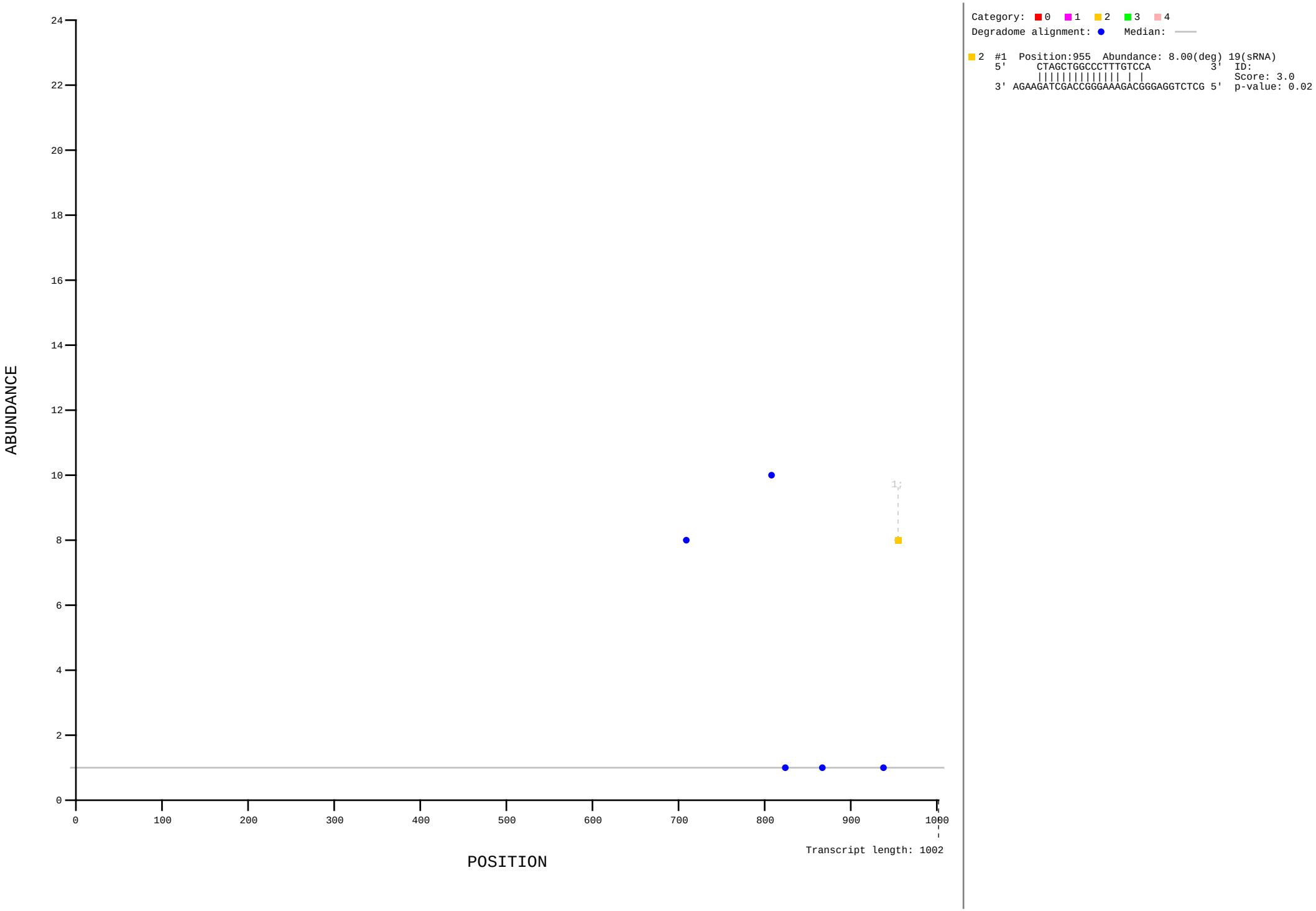
Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1456 Abundance: 3.00(deg) 5(sRNA)
5' TGAGACTGTAGATCCT-TCA 3' ID:
|||| ||||||| | ||| Score: 4.0
3' AAGCACTCAGACATCTACCATAGTAGTGTACG 5' p-value: 0.02

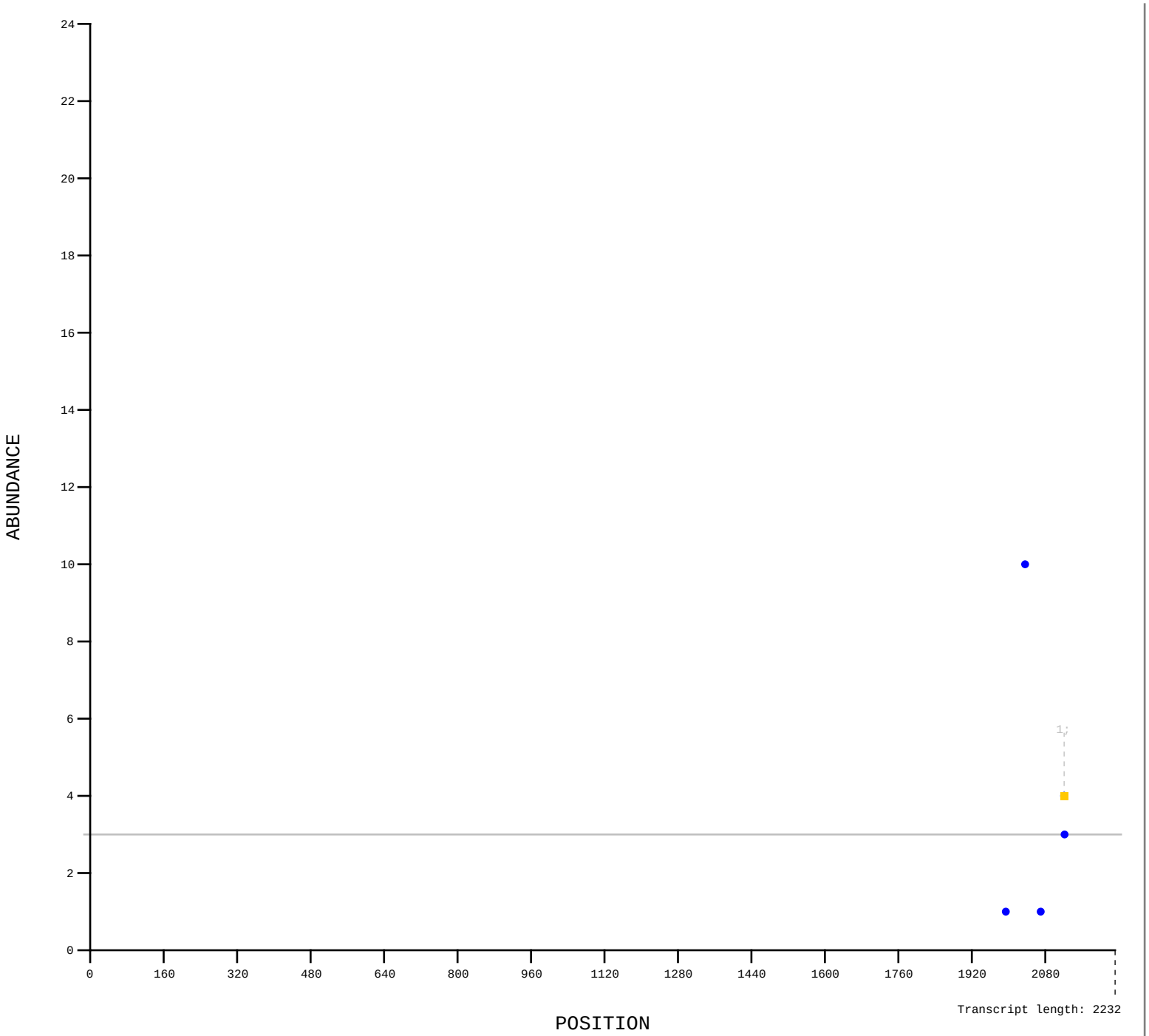
FOXG_05271T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (3051 nt)



FOXG_10253T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1002 nt)



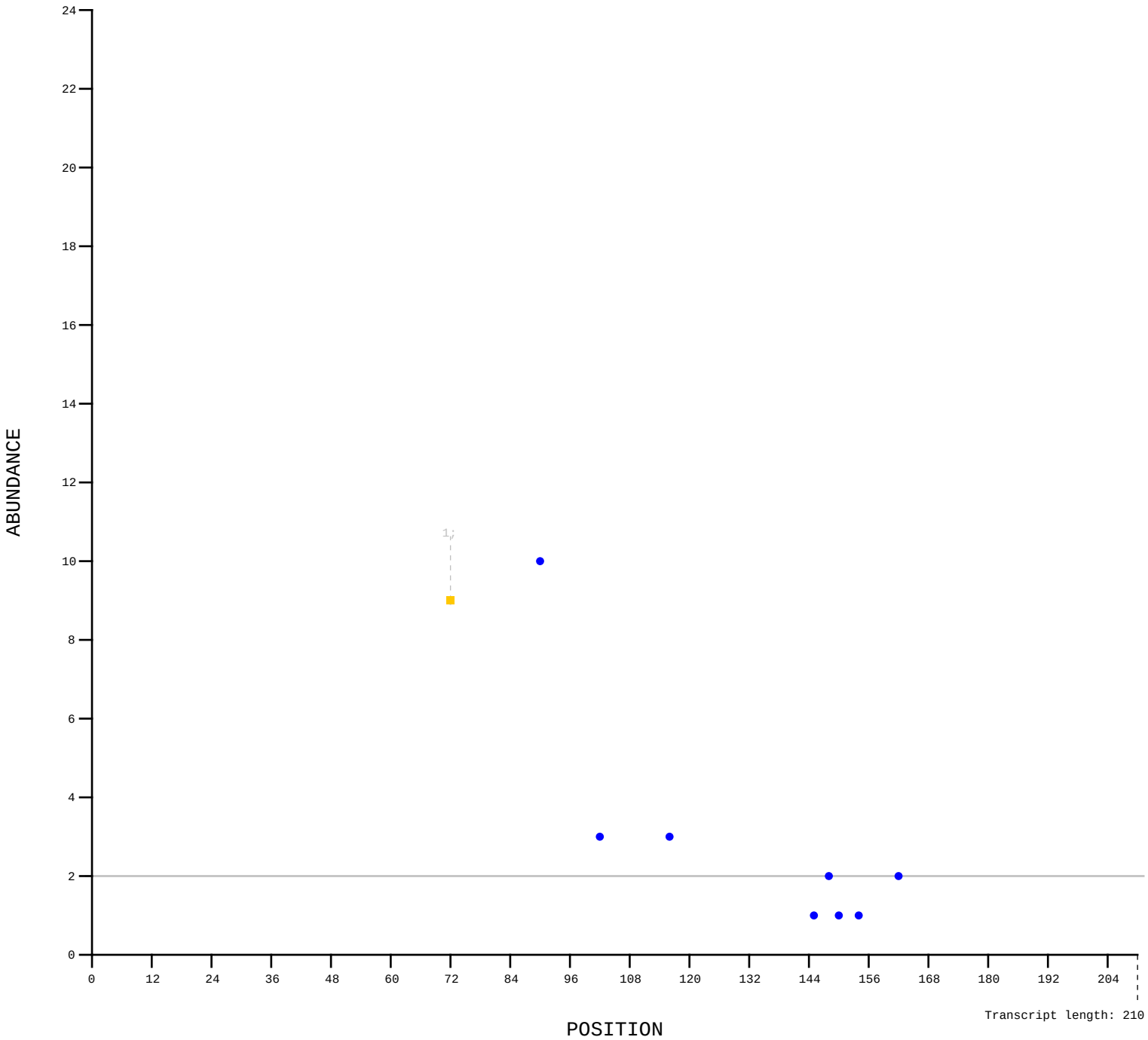
FOXG_07665T0 | Fusarium oxysporum f. sp. lycopersici 4287 cysteinyl-tRNA synthetase, mitochondri (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:2121 Abundance: 4.00(deg) 15(sRNA)
5' TTTCATATTAGTAAGCACTGC 3' ID:
||||| |||||| ||| | | Score: 4.0
3' GTAGAAAGTAAAATCATCCGTCAGGAACGAGT 5' p-value: 0.0

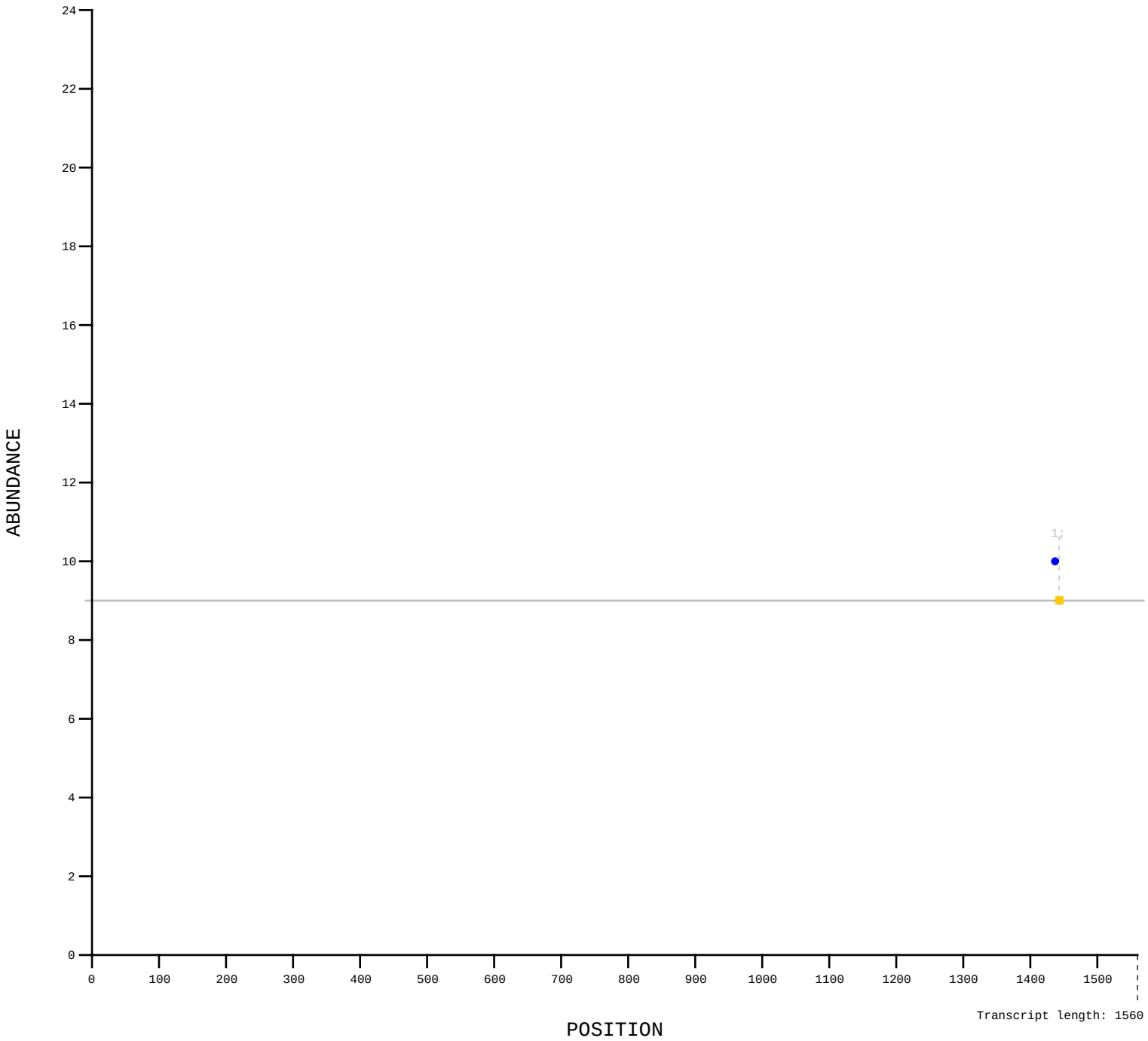
FOXG_01979T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (210 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:72 Abundance: 9.00(deg) 7(sRNA)
5' CTTGTCACGGAAGTAGATG 3' ID:
||||||||| |o|| || Score: 3.5
3' ATTCCAACAGTGCCT-CGTCAACGTATTAGTC 5' p-value: 0.0

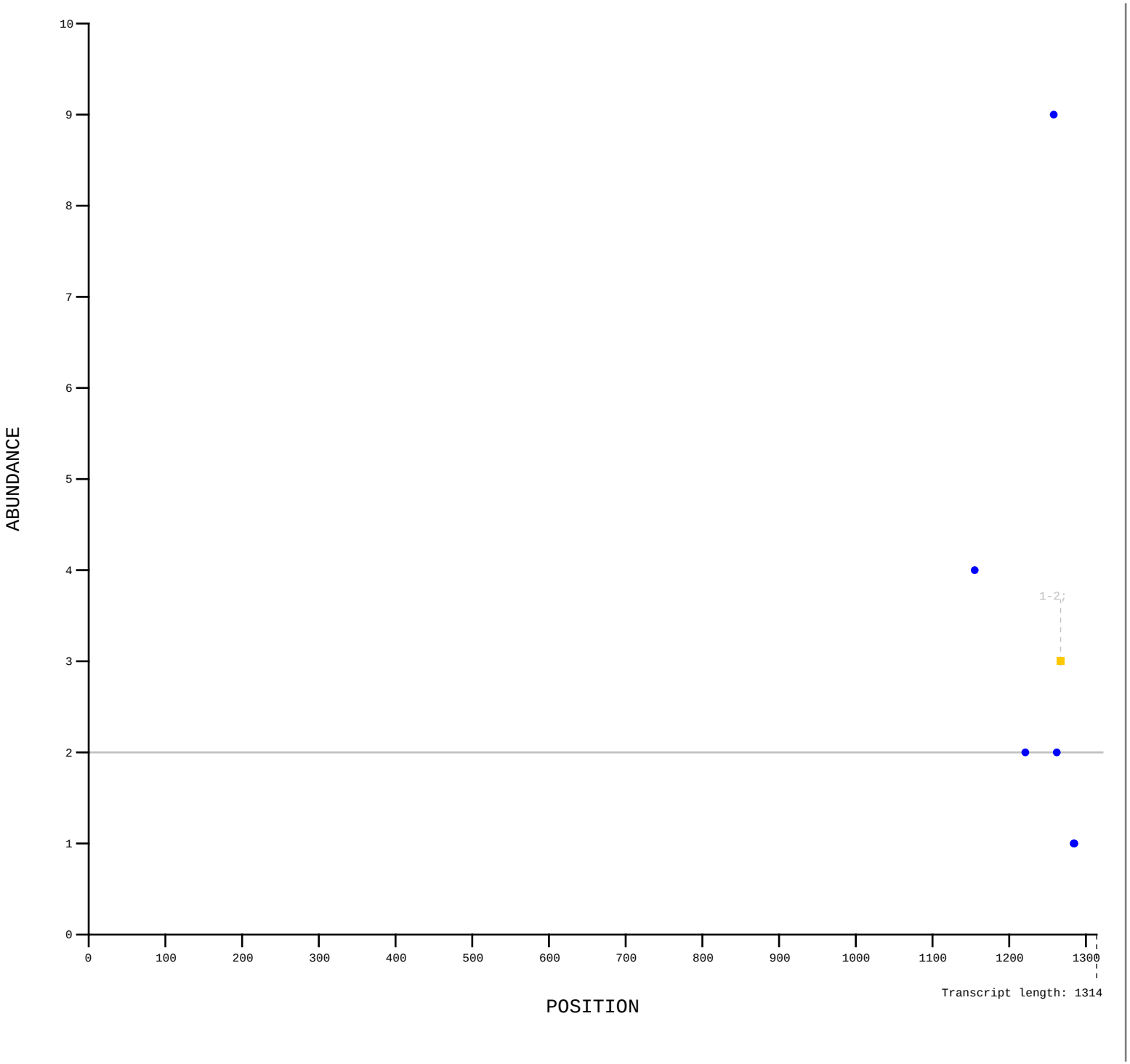
FOXG_08094T0 | Fusarium oxysporum f. sp. lycopersici 4287 succinyl-CoA:3-ketoacid-coenzyme A transferase (1560 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1443 Abundance: 9.00(deg) 5(sRNA)
5' GCGACAGTCGACTACGAGC 3' ID:
|||| ||||||| |||o| Score: 3.5
3' CAACCGCT-TCAGCTGTAGCTTGTGTGGGTCG 5' p-value: 0.01

FOXG_09346T0 | Fusarium oxysporum f. sp. lycopersici 4287 ornithine aminotransferase (1314 nt)

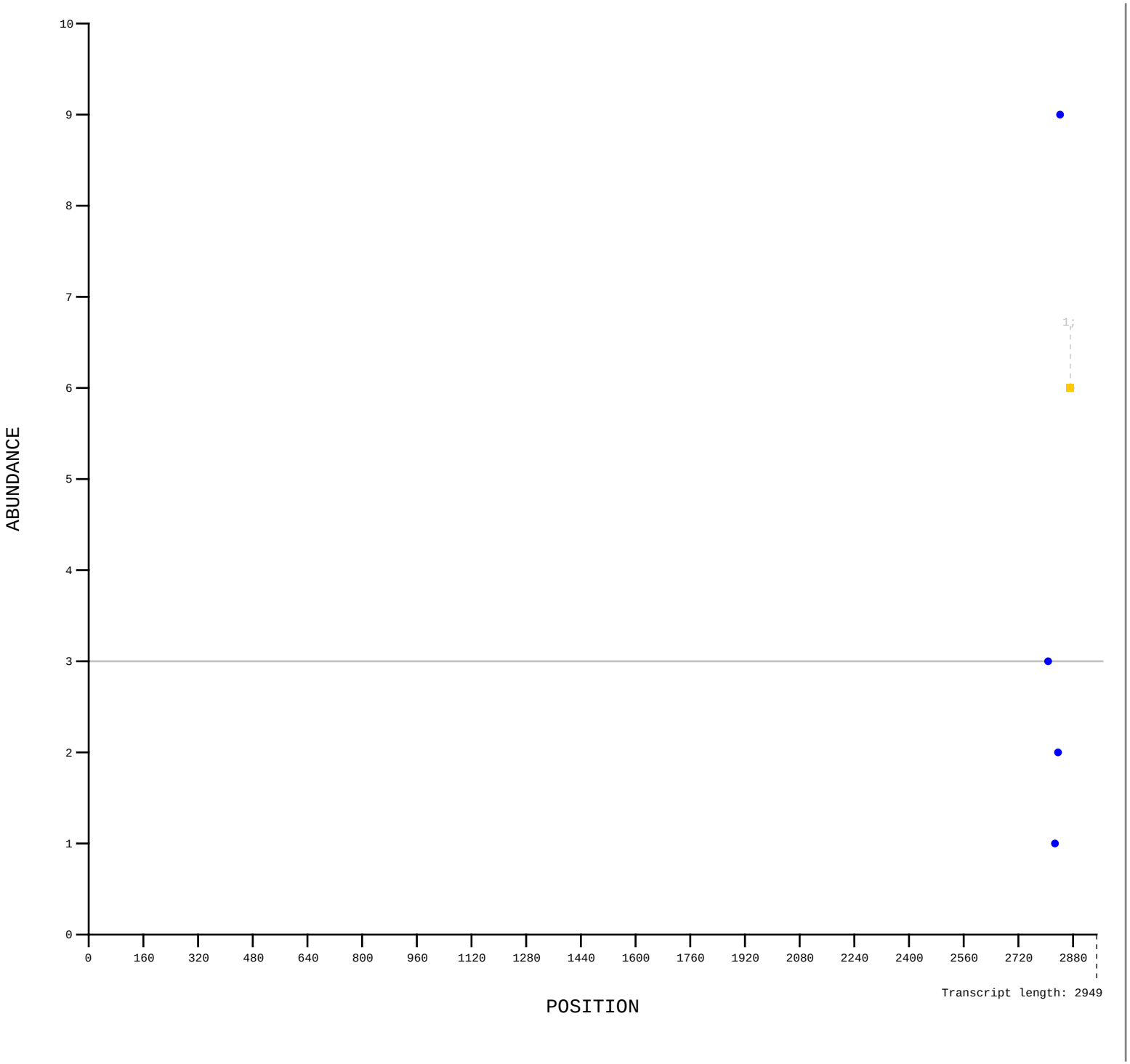


Category: 0 1 2 3 4
Degradome alignment: Median:

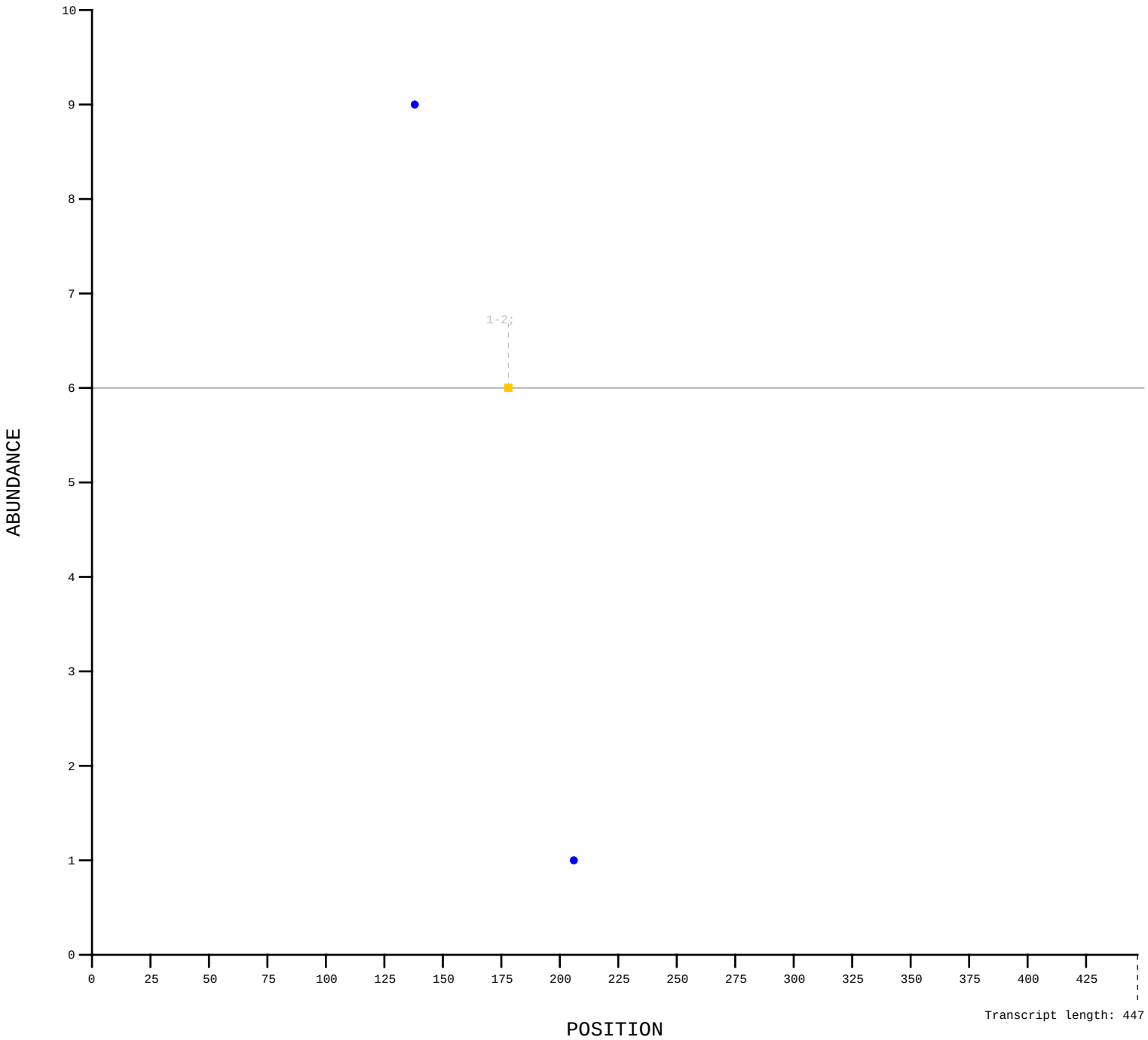
2 #1 Position:1267 Abundance: 3.00(deg) 25(sRNA)
5' TGGTAGACTCACAAATGCAT 3' ID:
||o||| |||| ||||| || Score: 3.5
3' AGGAACTATCGGAGTCTTTAC-TAGAGCTCTG 5' p-value: 0.0

2 #2 Position:1267 Abundance: 3.00(deg) 15(sRNA)
5' TGGTAGACTCACAAATGCA 3' ID:
||o||| |||| ||||| | Score: 3.5
3' AGGAACTATCGGAGTCTTTAC-TAGAGCTCTG 5' p-value: 0.01

FOXG_15410T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2949 nt)



FOXG_08379T0 | Fusarium oxysporum f. sp. lycopersici 4287 FK506-binding protein 1 (447 nt)

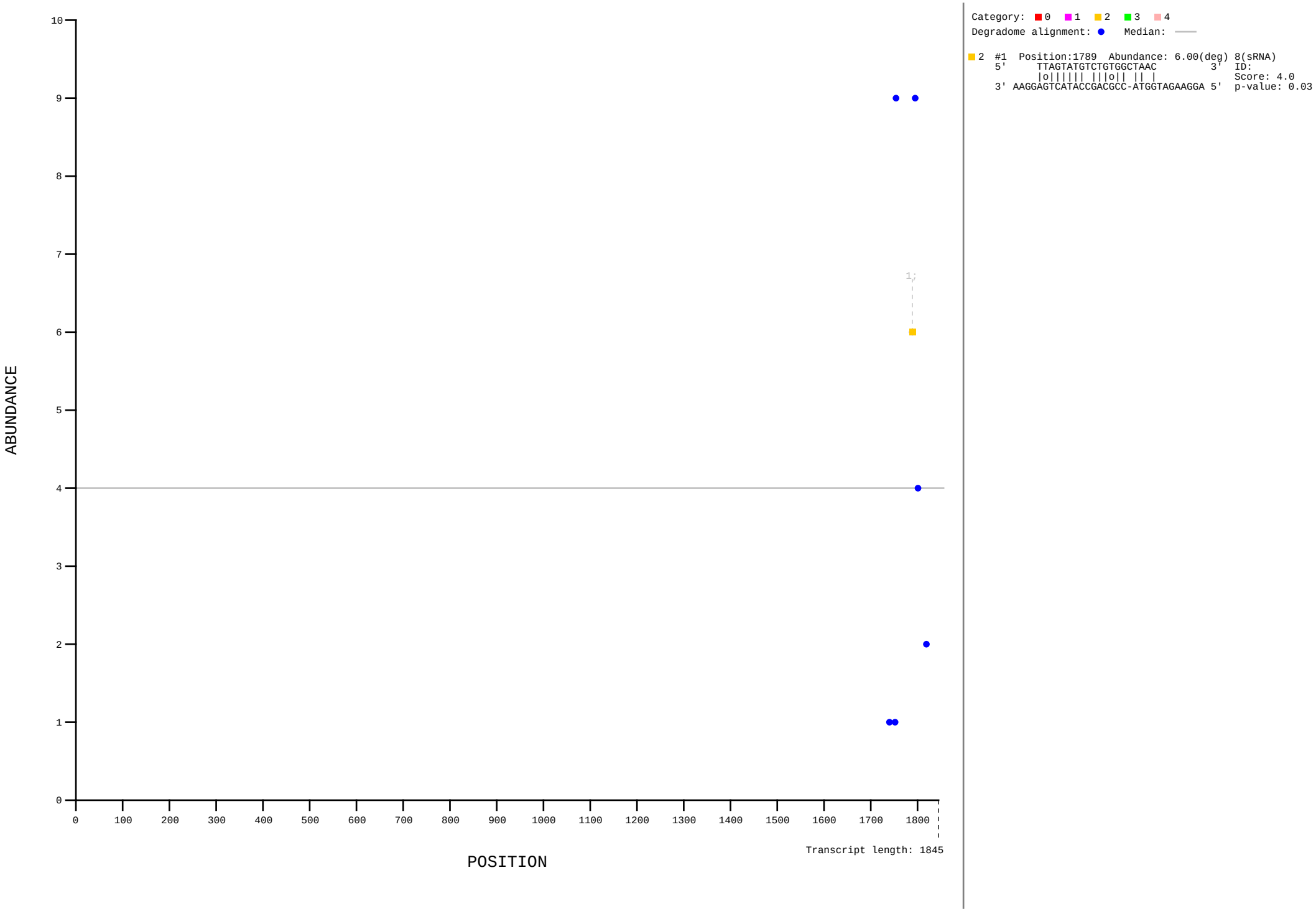


Category: 0 1 2 3 4
Degradome alignment: Median:

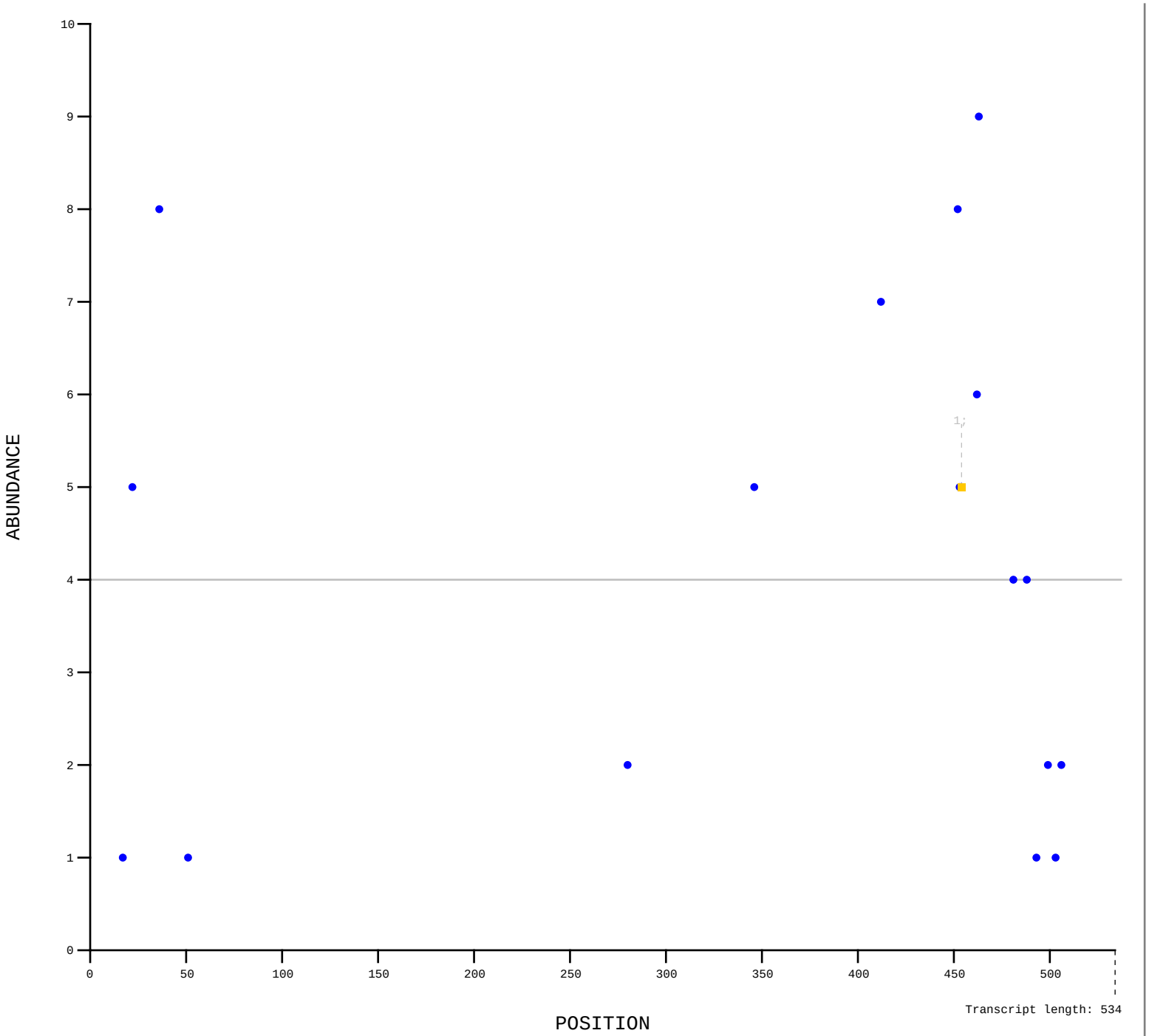
2 #1 Position:178 Abundance: 6.00(deg) 9(sRNA)
5' TGGTATGTTGGATGGCGGCC 3' ID:
o||| |o||||||| |o|| Score: 3.5
3' GTCGGCCACATAACCTACCACTGGAAAACCGG 5' p-value: 0.0

2 #2 Position:178 Abundance: 6.00(deg) 8(sRNA)
5' TGGTATGTTGGATGGCGGC 3' ID:
o||| |o|||||||| |o| Score: 3.5
3' GTCGGCCACATAACCTACCACTGGAAAACCGG 5' p-value: 0.0

FOXG_03438T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1845 nt)



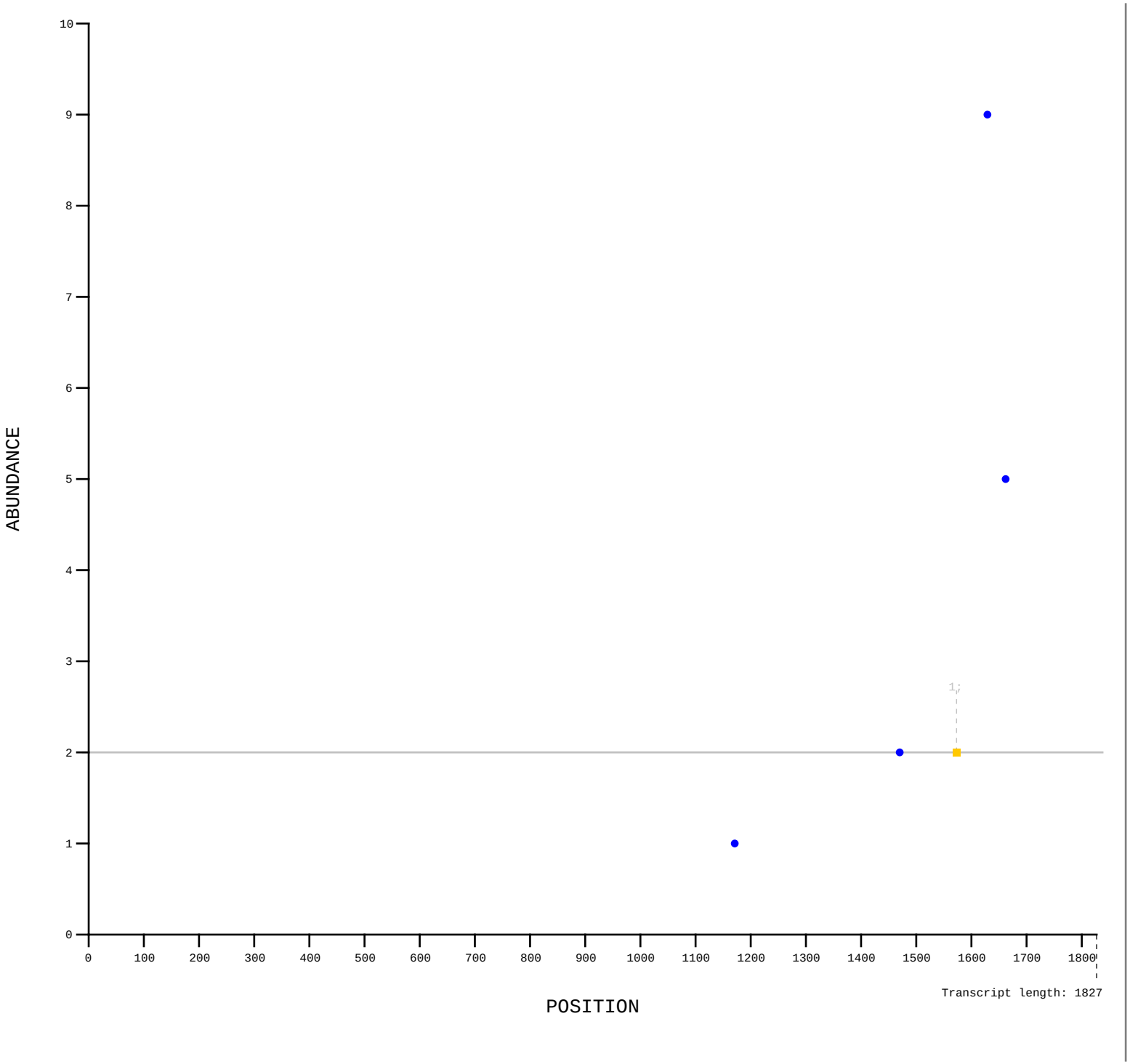
FOXG_03462T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (534 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:454 Abundance: 5.00(deg) 7(sRNA)
5' GCAGAGGCTGAATCTGAAC 3' ID:
|| ||| ||||| ||||| Score: 4.0
3' CACCCGACTCGGACTTCCACTTGTTGTTCAAC 5' p-value: 0.02

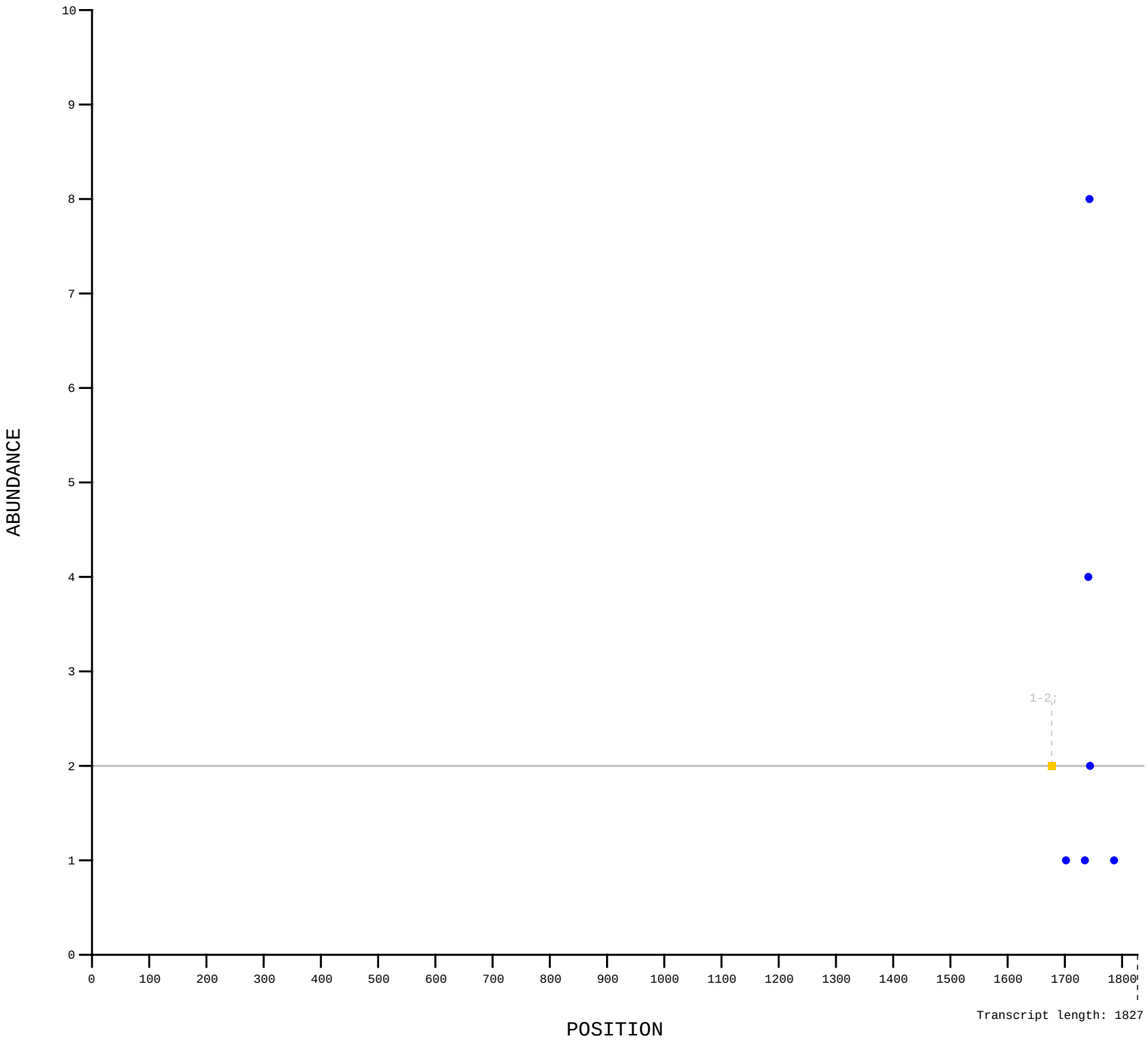
FOXG_06305T0 | Fusarium oxysporum f. sp. lycopersici 4287 vacuolar protein sorting-associated p (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1573 Abundance: 2.00(deg) 5(sRNA)
5' TGGCTGCTAGATTGCGAAT 3' ID:
||||||| |||o| ||| o Score: 4.0
3' ACTGACCGACGCTCTGA-GCTAGCTGCGTGCC 5' p-value: 0.04

FOXG_15398T0 | Fusarium oxysporum f. sp. lycopersici 4287 multidrug resistant protein (1827 nt)

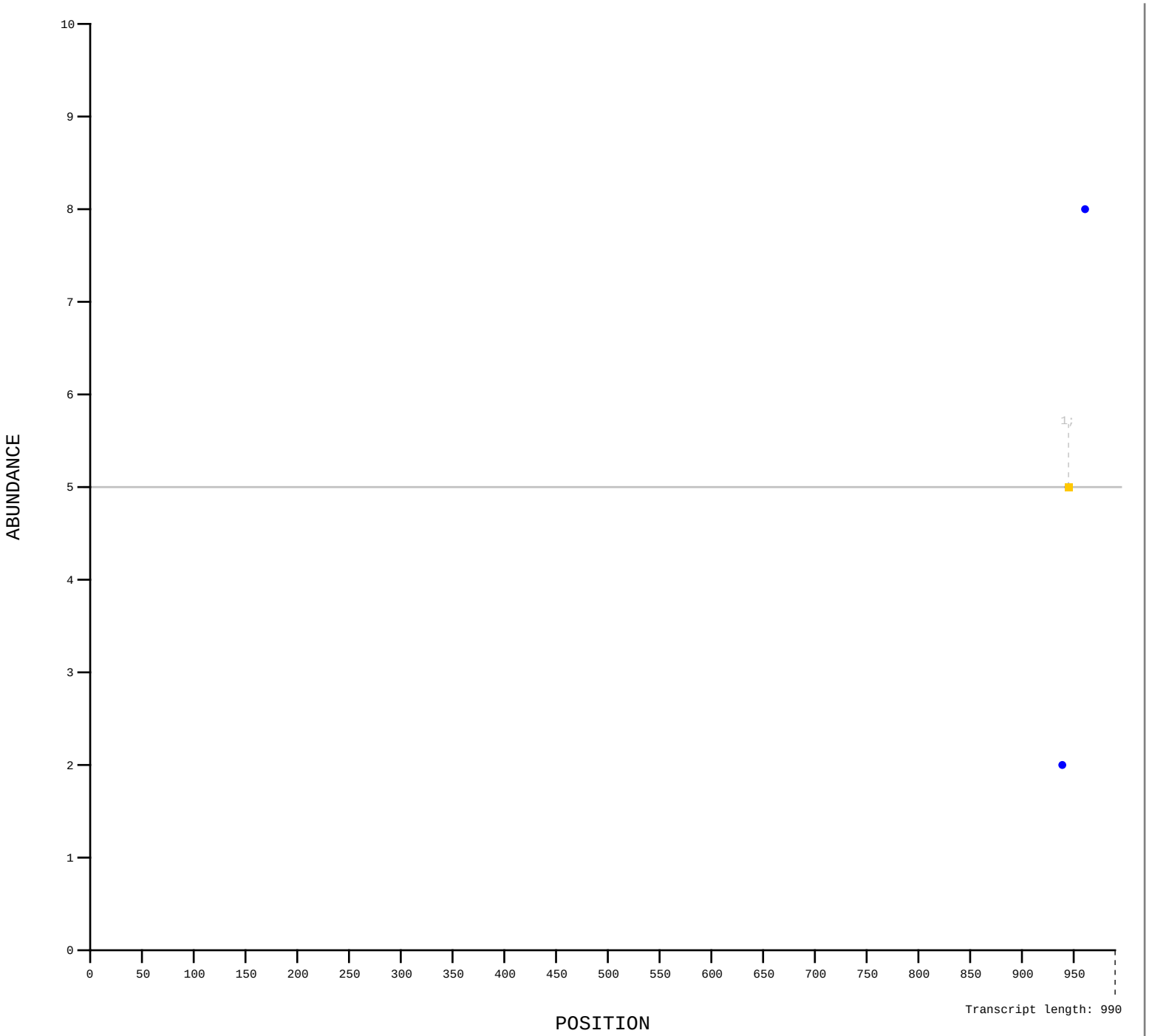


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1677 Abundance: 2.00(deg) 16(sRNA)
5' TCAGACGTTAGAGGTTGGA 3' ID:
||| ||||o|||o||| | Score: 4.0
3' TGCGAGT-TGCAGTCTTCAAGGTCAACGTCAA 5' p-value: 0.02

2 #2 Position:1677 Abundance: 2.00(deg) 5(sRNA)
5' TCAGACGTTAGAGGTTGGAG 3' ID:
||| ||||o|||o||| || Score: 4.0
3' TGCGAGT-TGCAGTCTTCAAGGTCAACGTCAA 5' p-value: 0.01

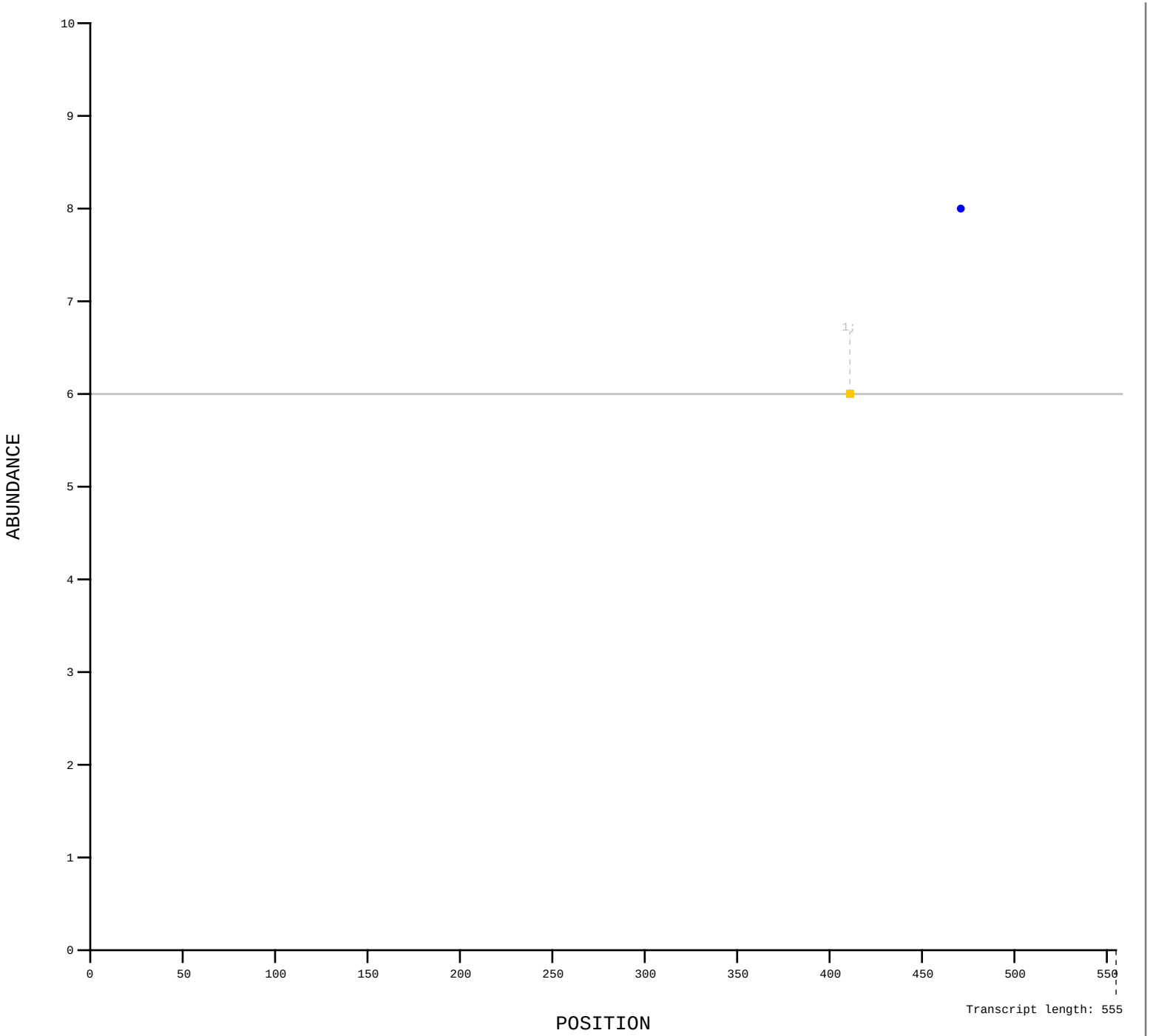
FOXG_04362T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (990 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:945 Abundance: 5.00(deg) 6(sRNA)
5' AGCTTTGTCCAGAACTCGCGG 3' ID:
|||o|||o||||| |o |||| Score: 3.5
3' TCTCTCGGAACGGGTCT-GGTCGCCCTCTCGC 5' p-value: 0.0

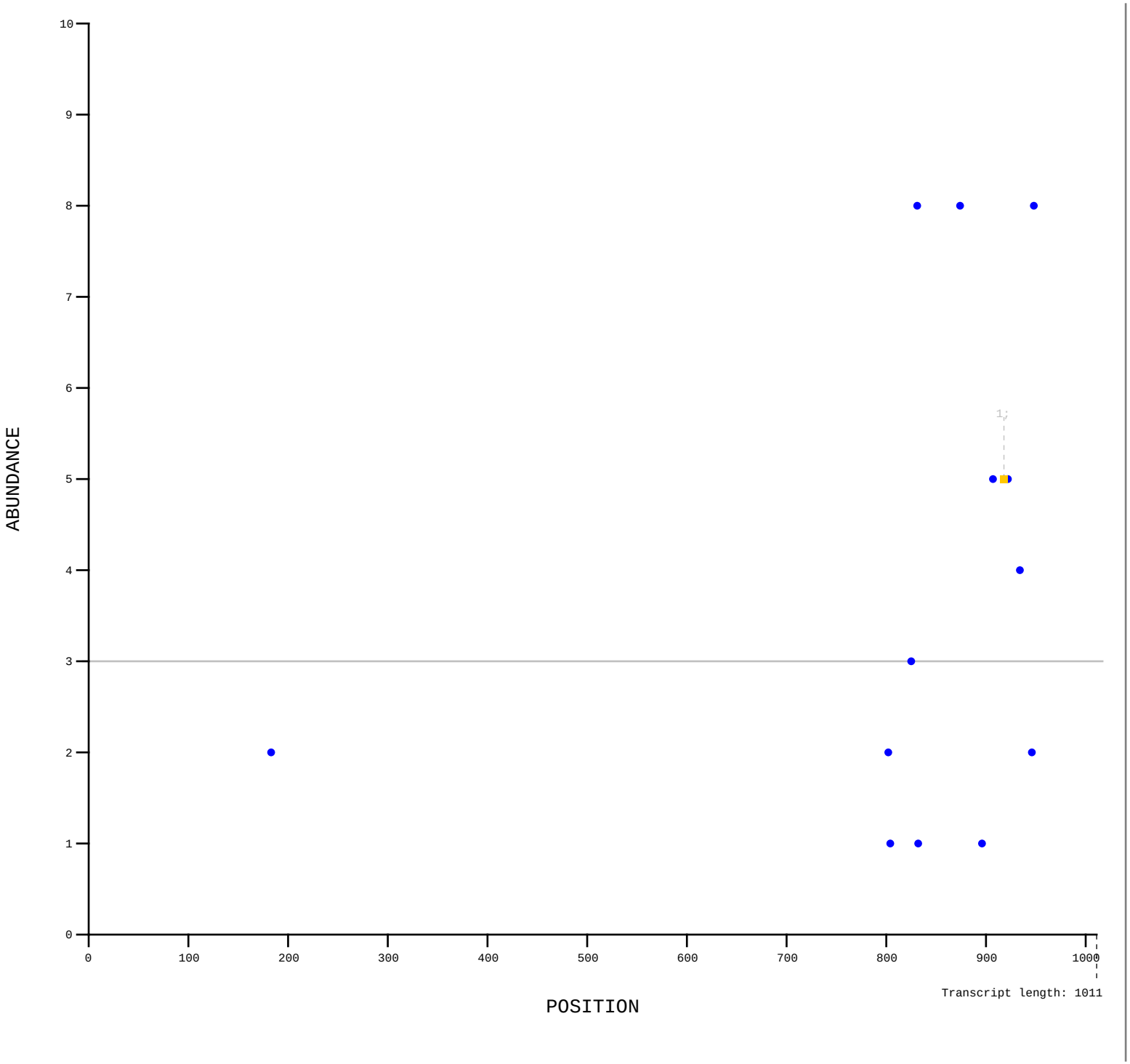
FOXG_00706T0 | Fusarium oxysporum f. sp. lycopersici 4287 AhpC/TSA family protein (555 nt)



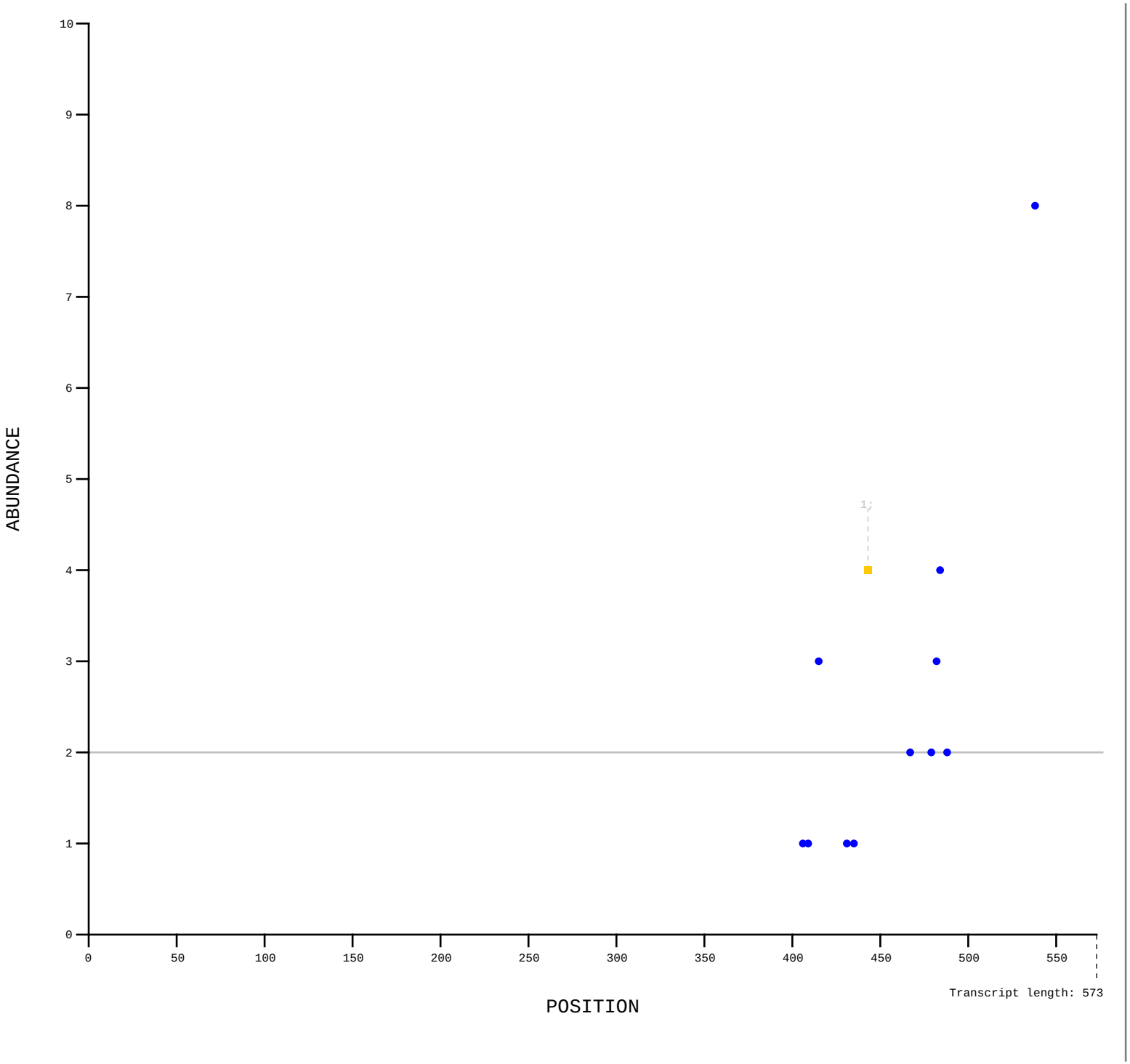
Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:411 Abundance: 6.00(deg) 5(sRNA)
5' TCGAAGACGAAGGACCACGGC 3' ID:
|||||| | |||| ||| ||| Score: 4.0
3' GCGGAGCTTC-GGTTCCAGGTCCCGGAATCAC 5' p-value: 0.0

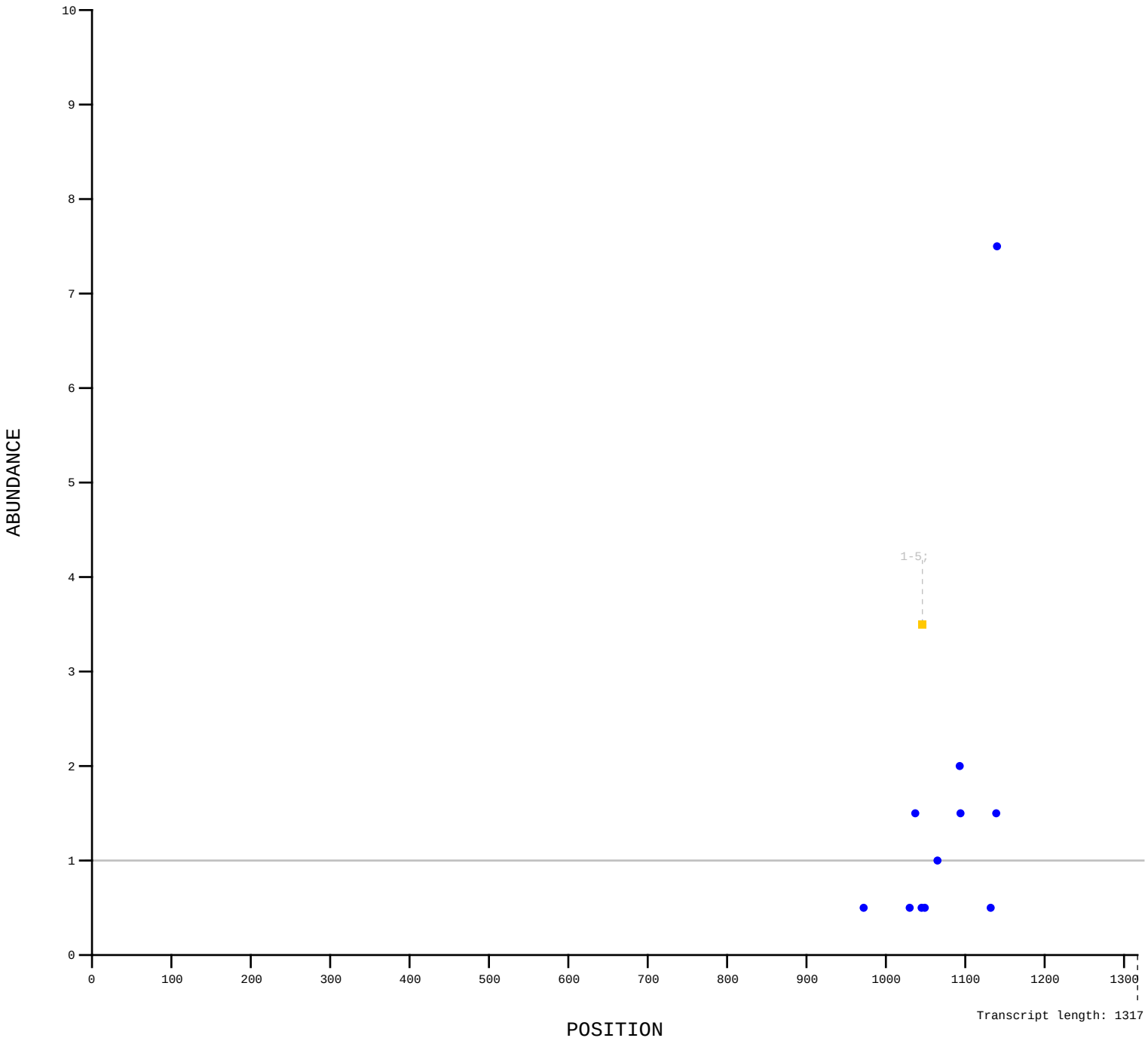
FOXG_10533T0 | Fusarium oxysporum f. sp. lycopersici 4287 malate dehydrogenase (1011 nt)



FOXG_05109T0 | Fusarium oxysporum f. sp. lycopersici 4287 NADH-ubiquinone oxidoreductase 21.3 kDa subunit (573 nt)



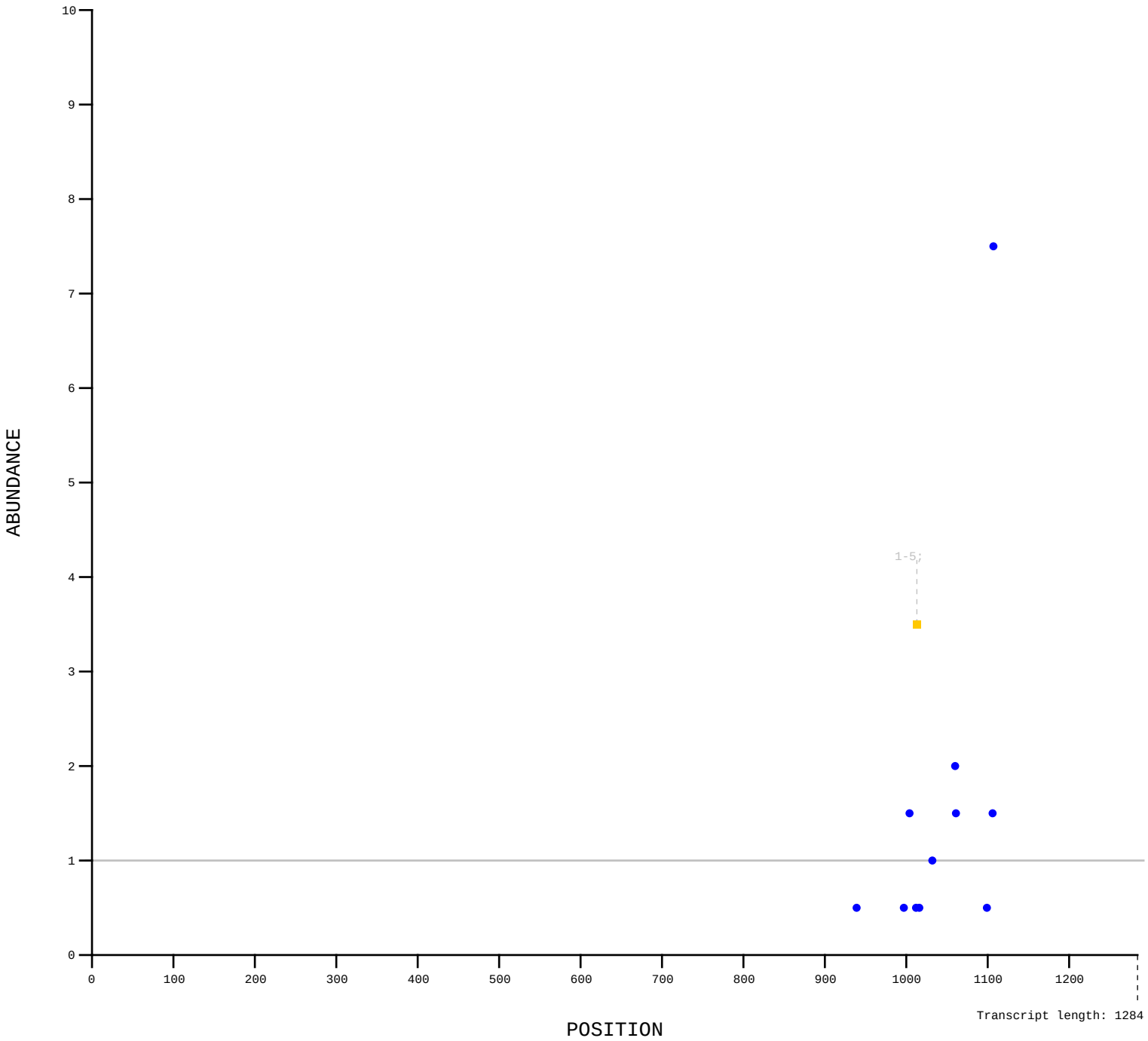
FOXG_14085T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1317 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:1046  Abundance: 3.50(deg) 102(sRNA)
   5'     TGCACATGATTCCGCCCACA         3'  ID:
          |||||||||| ||||| ||              Score: 2.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #2  Position:1046  Abundance: 3.50(deg) 21(sRNA)
   5'     TGCACATGATTCTGCCCACA         3'  ID:
          |||||||||| o|||| ||              Score: 2.5
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #3  Position:1046  Abundance: 3.50(deg) 14(sRNA)
   5'     TGCACATGATTCCGCCCAC          3'  ID:
          |||||||||| ||||| |               Score: 2.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #4  Position:1046  Abundance: 3.50(deg) 7(sRNA)
   5'     TGCACATGATTCCGCCCACAGTG      3'  ID:
          |||||||||| ||||| || |            Score: 4.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.01

2  #5  Position:1046  Abundance: 3.50(deg) 5(sRNA)
   5'     TGCACATGATTCCGCCCACAG        3'  ID:
          |||||||||| ||||| ||              Score: 3.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0
```

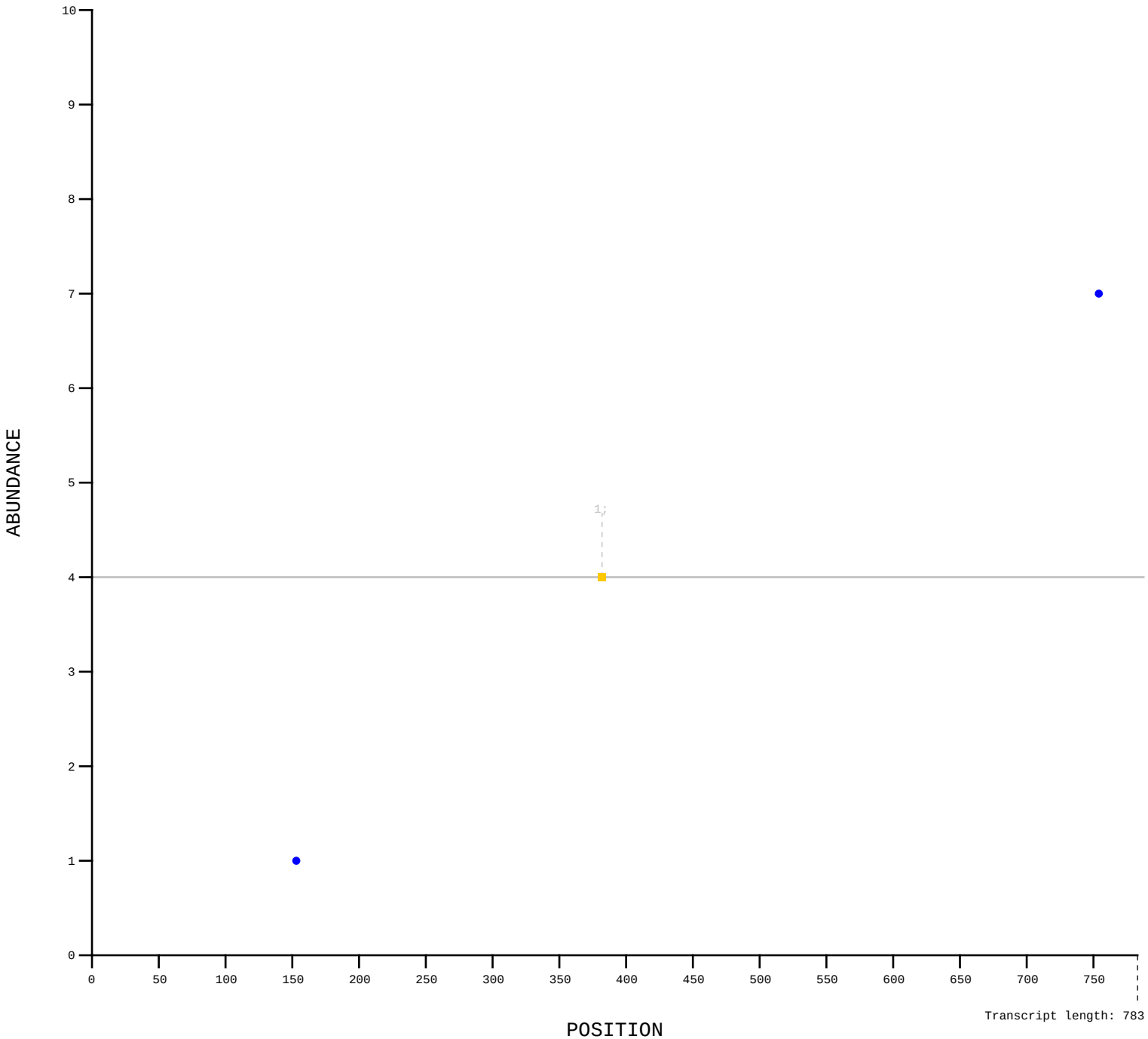
FOXG_12452T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1284 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:1013  Abundance: 3.50(deg) 102(sRNA)
   5'     TGCACATGATTCCGCCCACA         3'  ID:
          |||||||||| ||||| ||              Score: 2.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #2  Position:1013  Abundance: 3.50(deg) 21(sRNA)
   5'     TGCACATGATTCTGCCCACA         3'  ID:
          |||||||||| o|||| ||              Score: 2.5
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #3  Position:1013  Abundance: 3.50(deg) 14(sRNA)
   5'     TGCACATGATTCCGCCCAC          3'  ID:
          |||||||||| ||||| |               Score: 2.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #4  Position:1013  Abundance: 3.50(deg) 7(sRNA)
   5'     TGCACATGATTCCGCCCACAGTG      3'  ID:
          |||||||||| ||||| || |            Score: 4.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0

2  #5  Position:1013  Abundance: 3.50(deg) 5(sRNA)
   5'     TGCACATGATTCCGCCCACAG        3'  ID:
          |||||||||| ||||| ||              Score: 3.0
   3' GGCCACGTGTACTAATGCGGGCGTGAAGCCGC 5'  p-value: 0.0
```

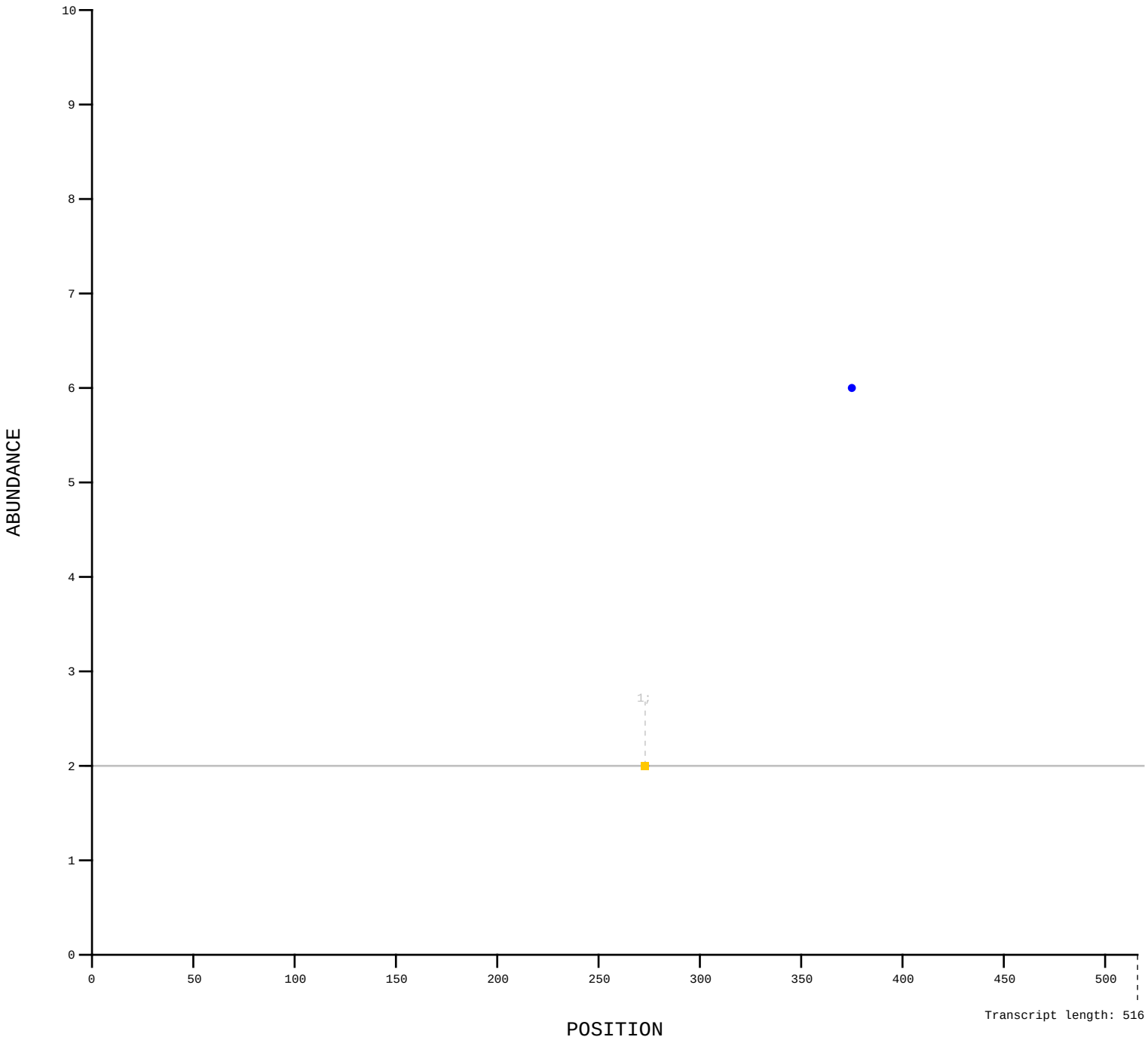
FOXG_09465T0 | Fusarium oxysporum f. sp. lycopersici 4287 40S ribosomal protein S3 (783 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:382 Abundance: 4.00(deg) 5(sRNA)
5' TCATGAAGGAGCCGAGGAC 3' ID:
o||||| |o||| |||||| Score: 3.0
3' CTGAGGTACTACTTCGCCTCCTGTGGTATCGT 5' p-value: 0.01

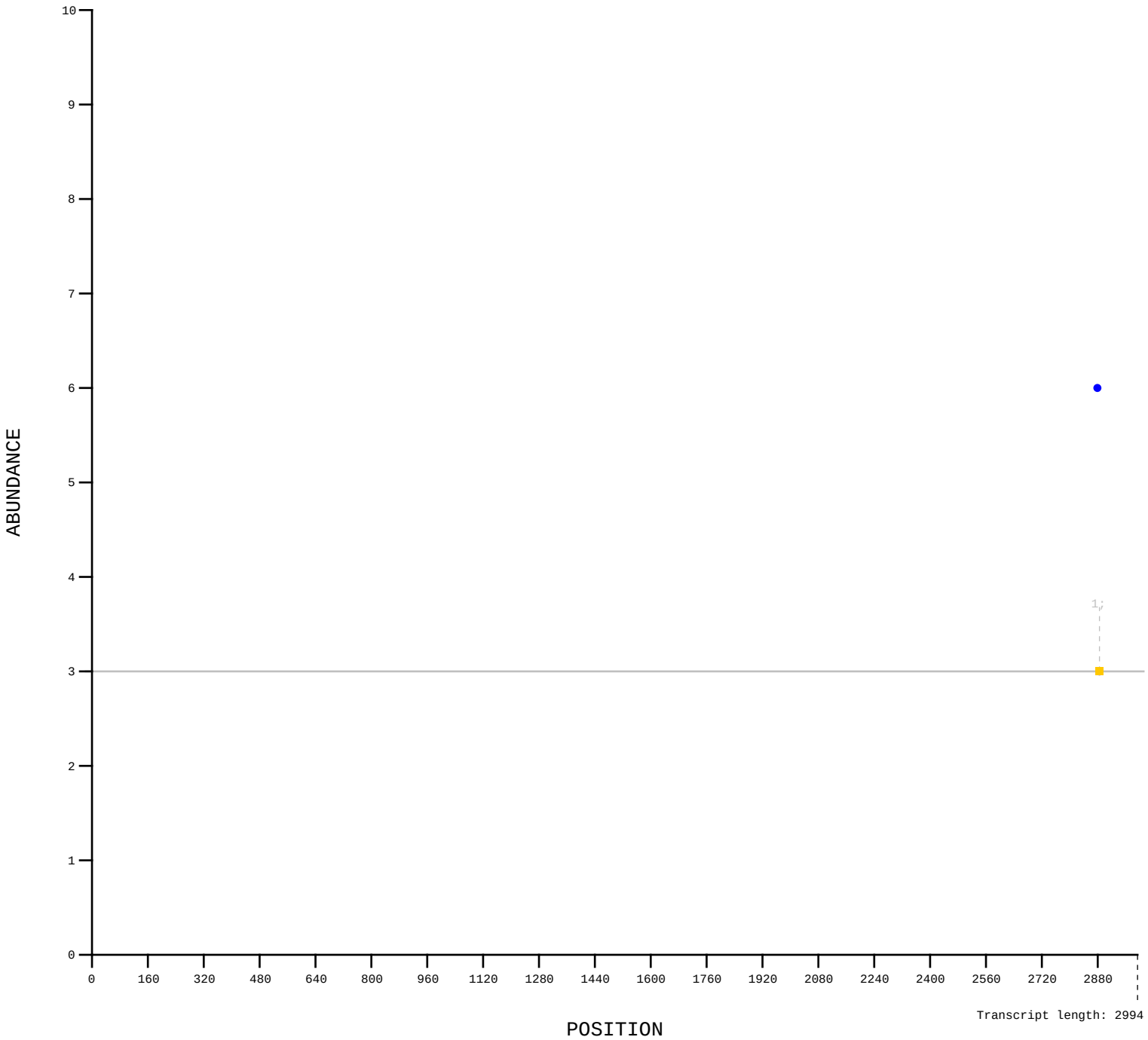
FOXG_10287T0 | Fusarium oxysporum f. sp. lycopersici 4287 damage response protein 1 (516 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:273 Abundance: 2.00(deg) 33(sRNA)
5' GTCGTAGAAGTTAGGGCGAGC 3' ID:
|o|||||||||| |o| || Score: 4.0
3' GTCCCGGCATCTTCAATGCTGGTCCGCTCTGC 5' p-value: 0.0

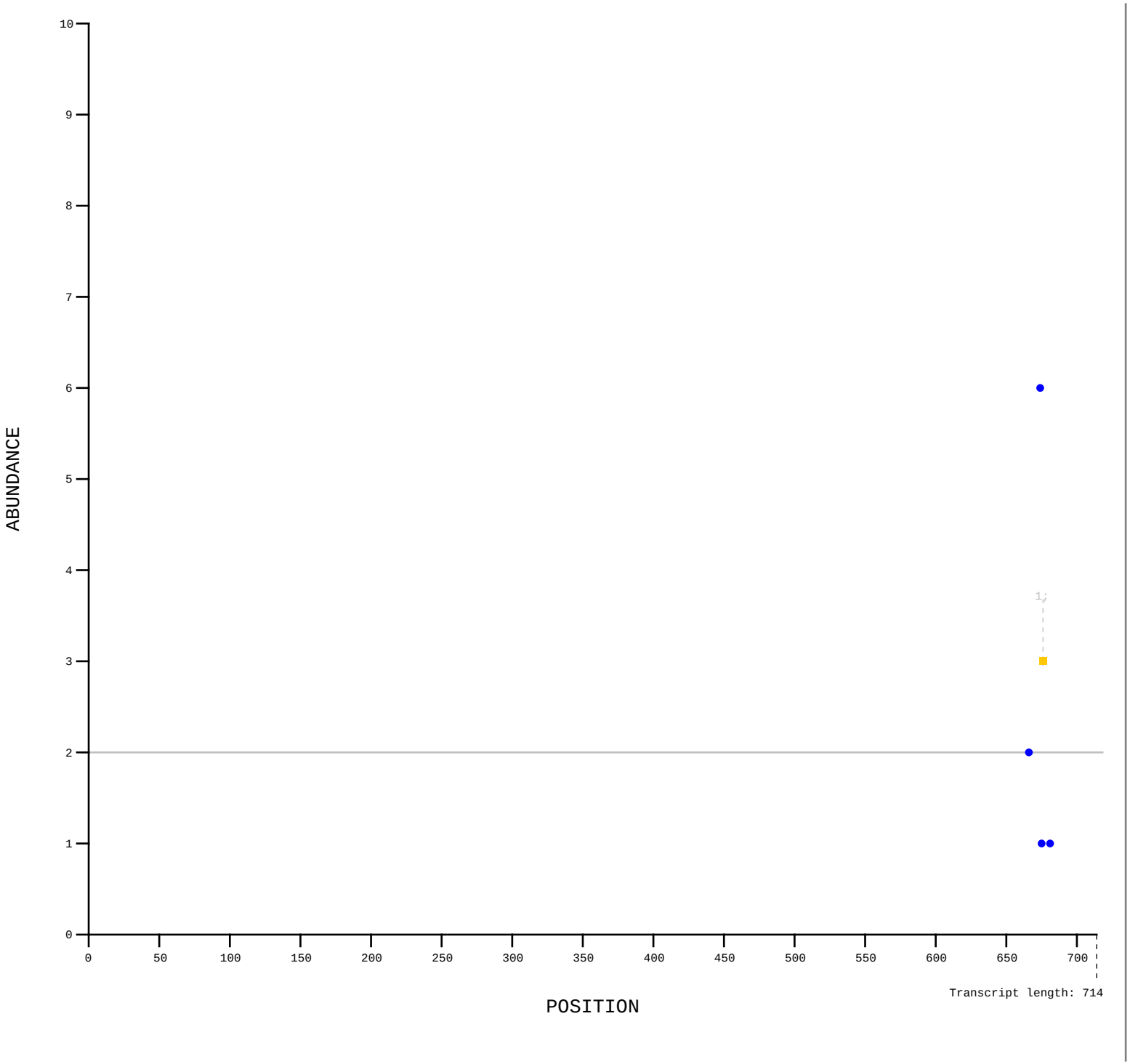
FOXG_00269T0 | Fusarium oxysporum f. sp. lycopersici 4287 verprolin (2994 nt)



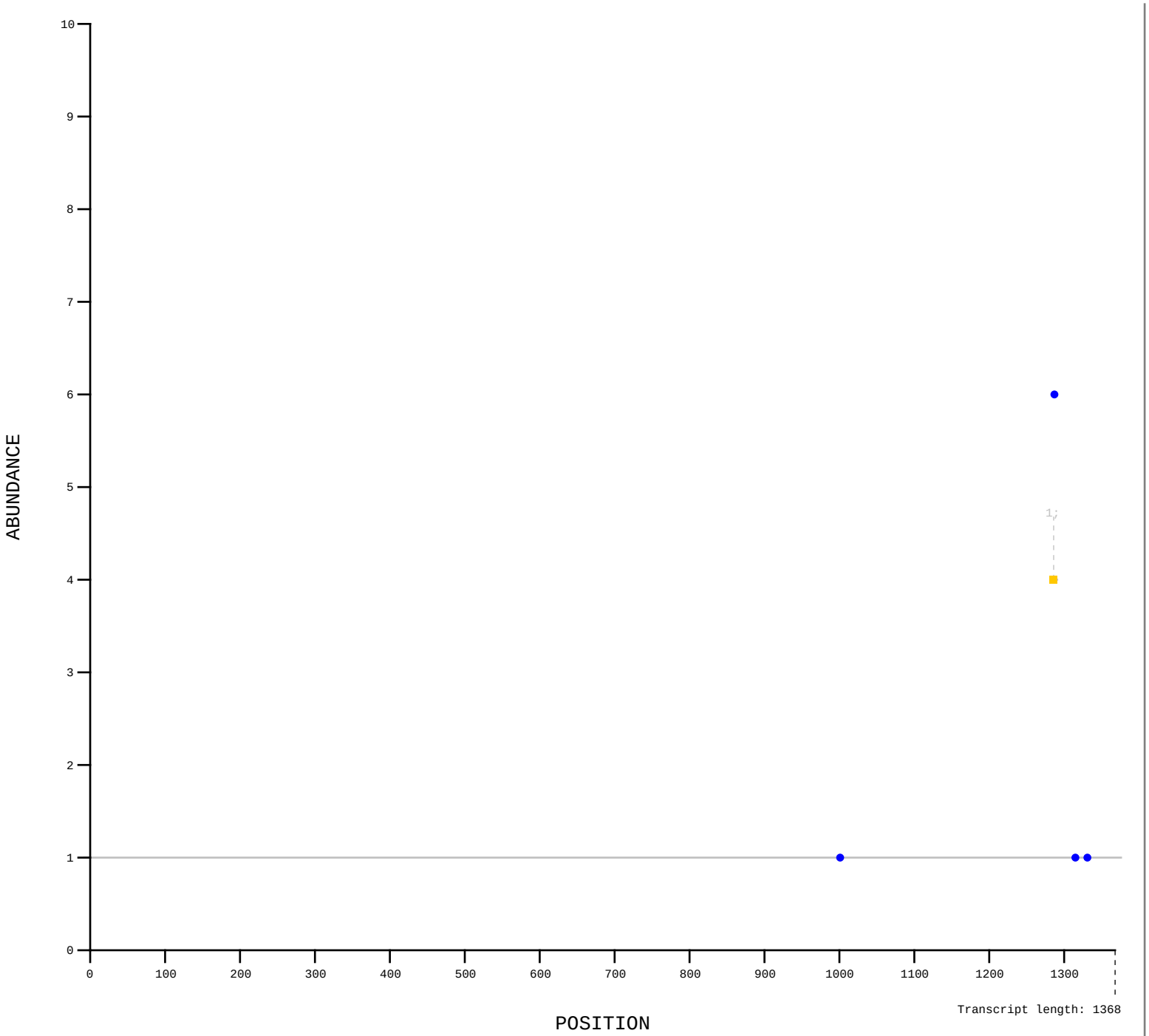
Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:2885 Abundance: 3.00(deg) 13(sRNA)
5' GCAAGCTCGGATTAGTAGT 3' ID:
| |||| |||||| |o||| Score: 3.5
3' TAAGCCTTCG-GCCTAAACGTCAAAGCCGGGA 5' p-value: 0.0

FOXG_09385T0 | Fusarium oxysporum f. sp. lycopersici 4287 Cwf15/Cwc15 cell cycle control family protein (714 nt)



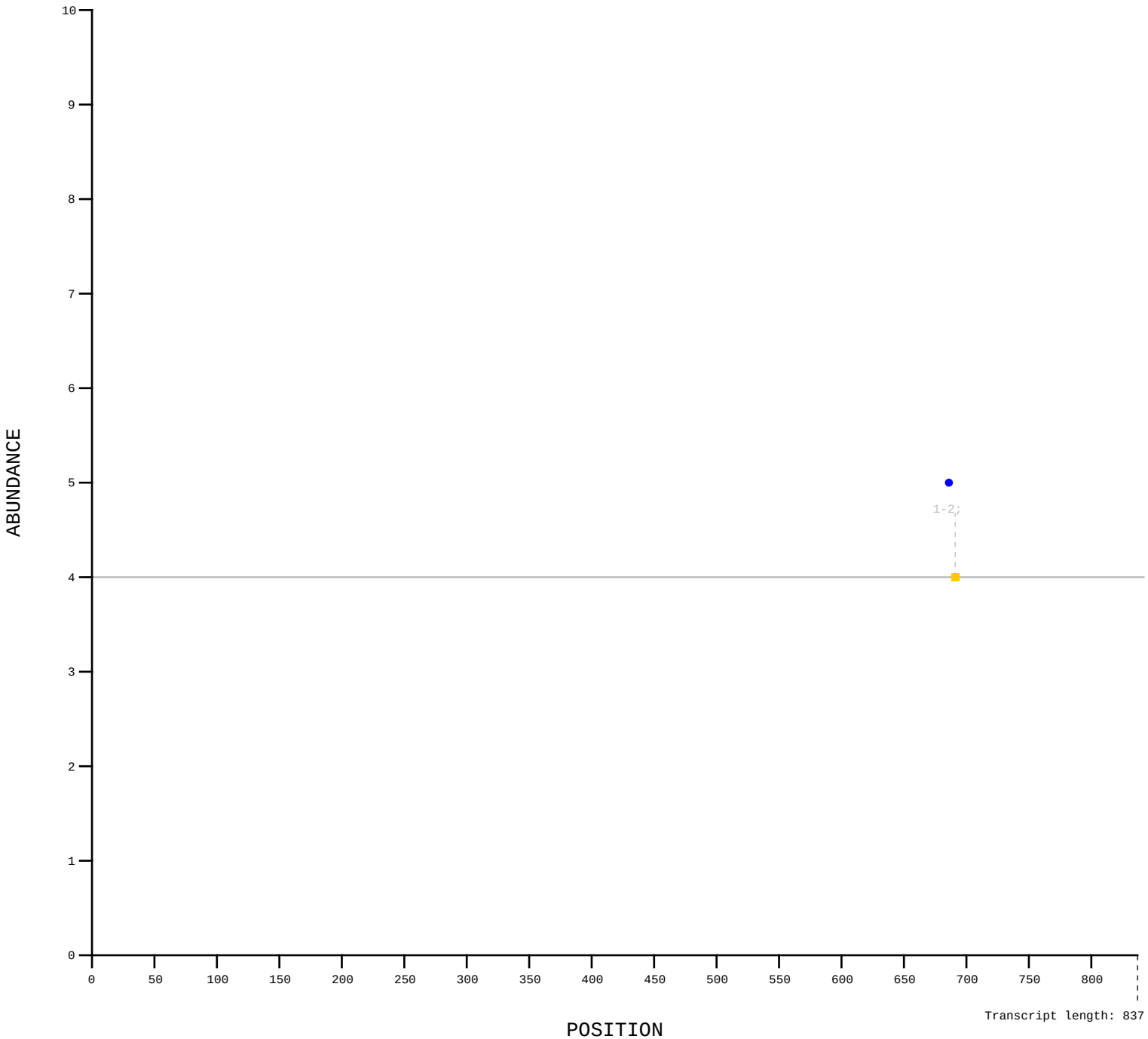
FOXG_07974T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1368 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1286 Abundance: 4.00(deg) 8(sRNA)
5' TCCAAATTTCCAGGACTGA 3' ID:
||||||||||| | || Score: 4.0
3' TGGGAGGTTTAAAGGTACAGAGAGTTGTAGTA 5' p-value: 0.02

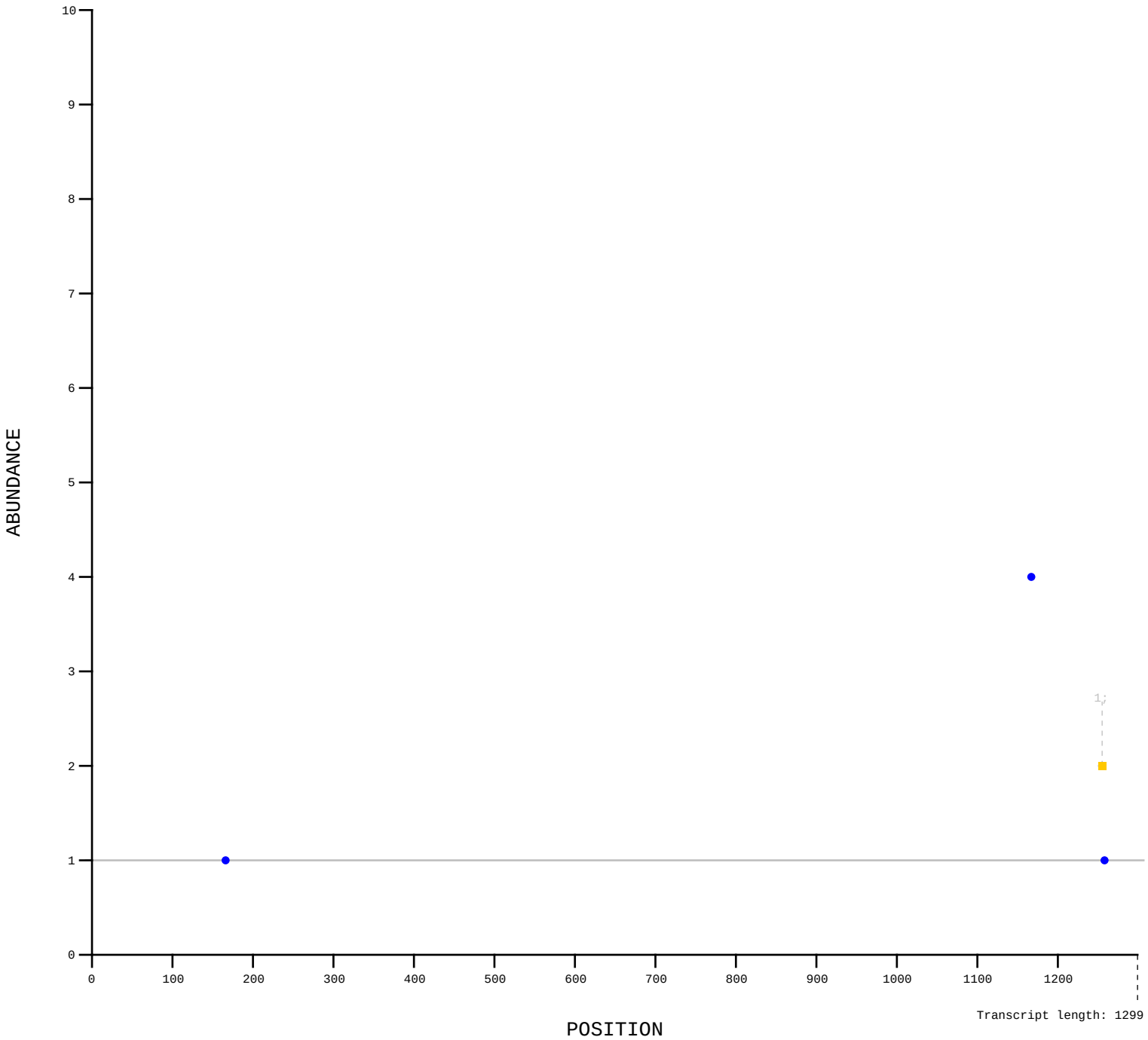
FOXG_02750T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (837 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:691  Abundance: 4.00(deg) 12(sRNA)
   5'     TGAAGATTTTAGCAATGAAA         3'  ID:
          |o||| |o|||| |||| ||             Score: 4.0
   3' TCTAATTTCCAGAATCTTTACCTTCTGGTGCG 5'  p-value: 0.0

2  #2  Position:691  Abundance: 4.00(deg) 5(sRNA)
   5'     TAAGGGTCTTAGATTTTGG          3'  ID:
          |||o|||||||||  | ||             Score: 3.5
   3' TCTAATTTCCAGAATCTTTA-CCTTCTGGTGC 5'  p-value: 0.0
```

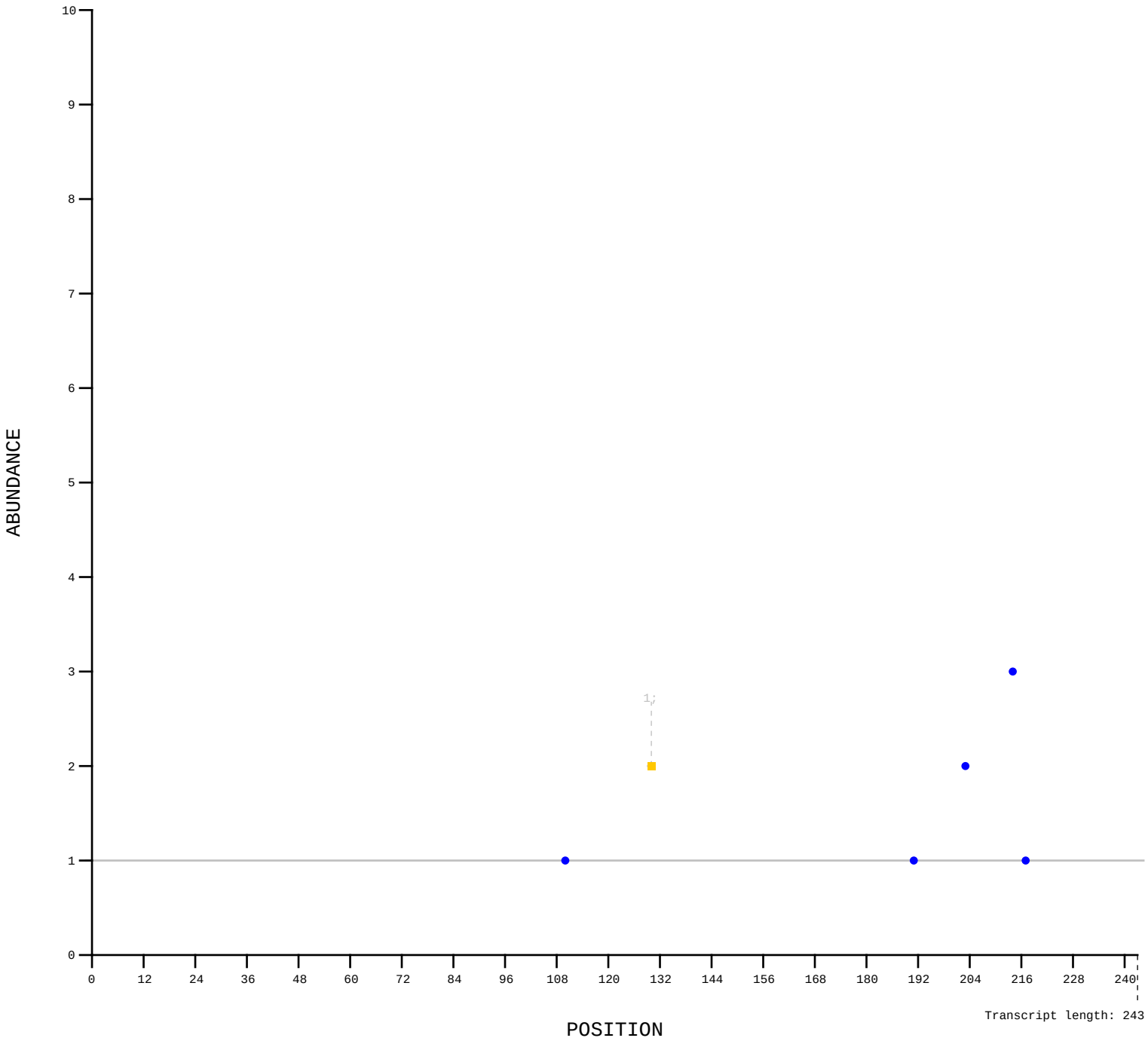
FOXG_05026T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1299 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:1255 Abundance: 2.00(deg) 5(sRNA)
5' CAAGCTAGAGCTAGACAACC 3' ID:
| || ||||||| |||| || Score: 4.0
3' CTTGGGTCTATCTCGAGCTGT-GGTATGTTTT 5' p-value: 0.0

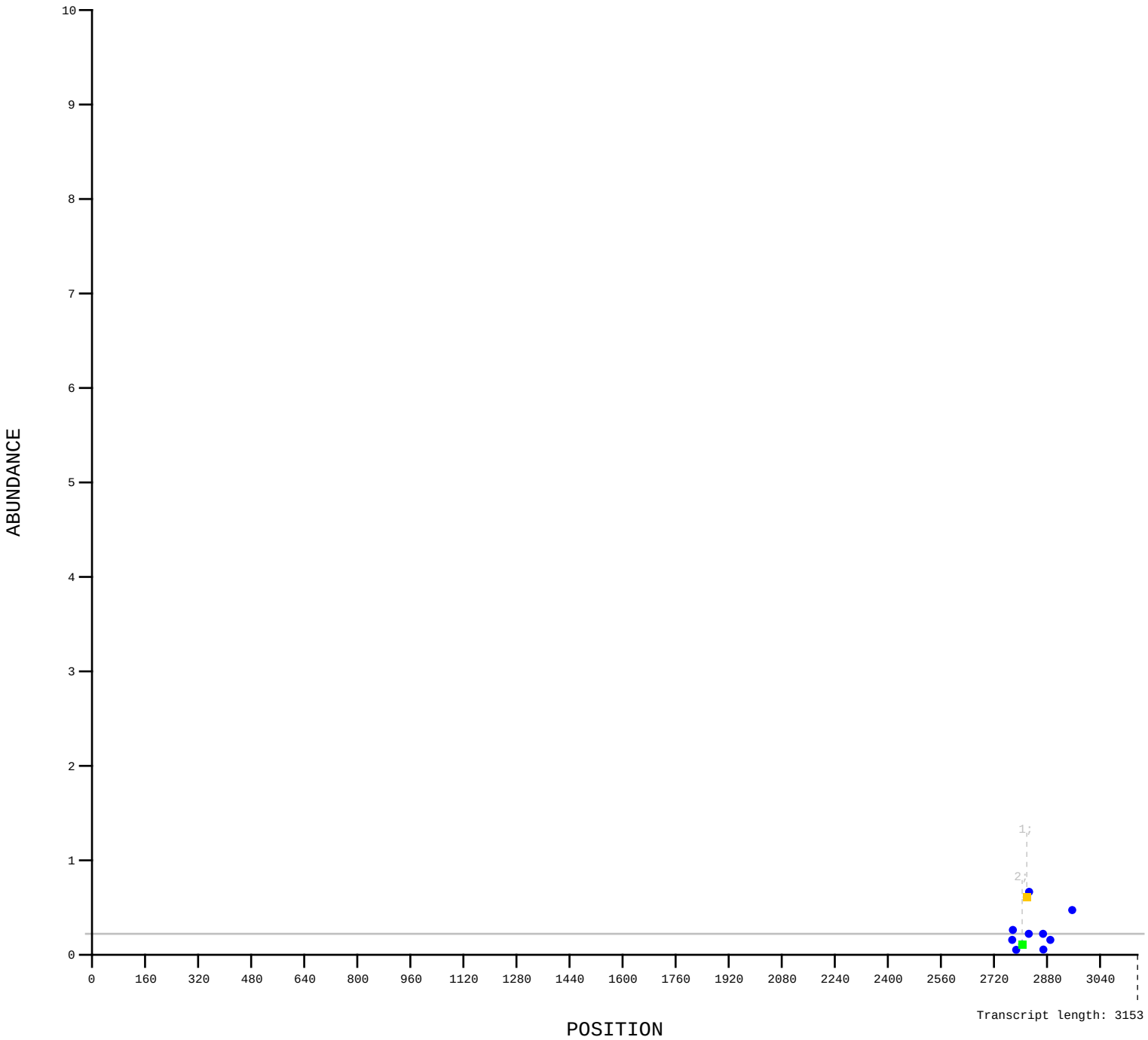
FOXG_00863T0 | Fusarium oxysporum f. sp. lycopersici 4287 DNA-directed RNA polymerase N/8 kDa subu (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:130 Abundance: 2.00(deg) 6(sRNA)
5' GGTAGCAGTATCAGATTTAGG 3' ID:
||o||||||||| | ||o||o Score: 3.5
3' GCCGCCGTCGTCATAG-CGAAGTCTGGCTCGA 5' p-value: 0.0

FOXG_14002T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (3153 nt) Note(s): (truncated)

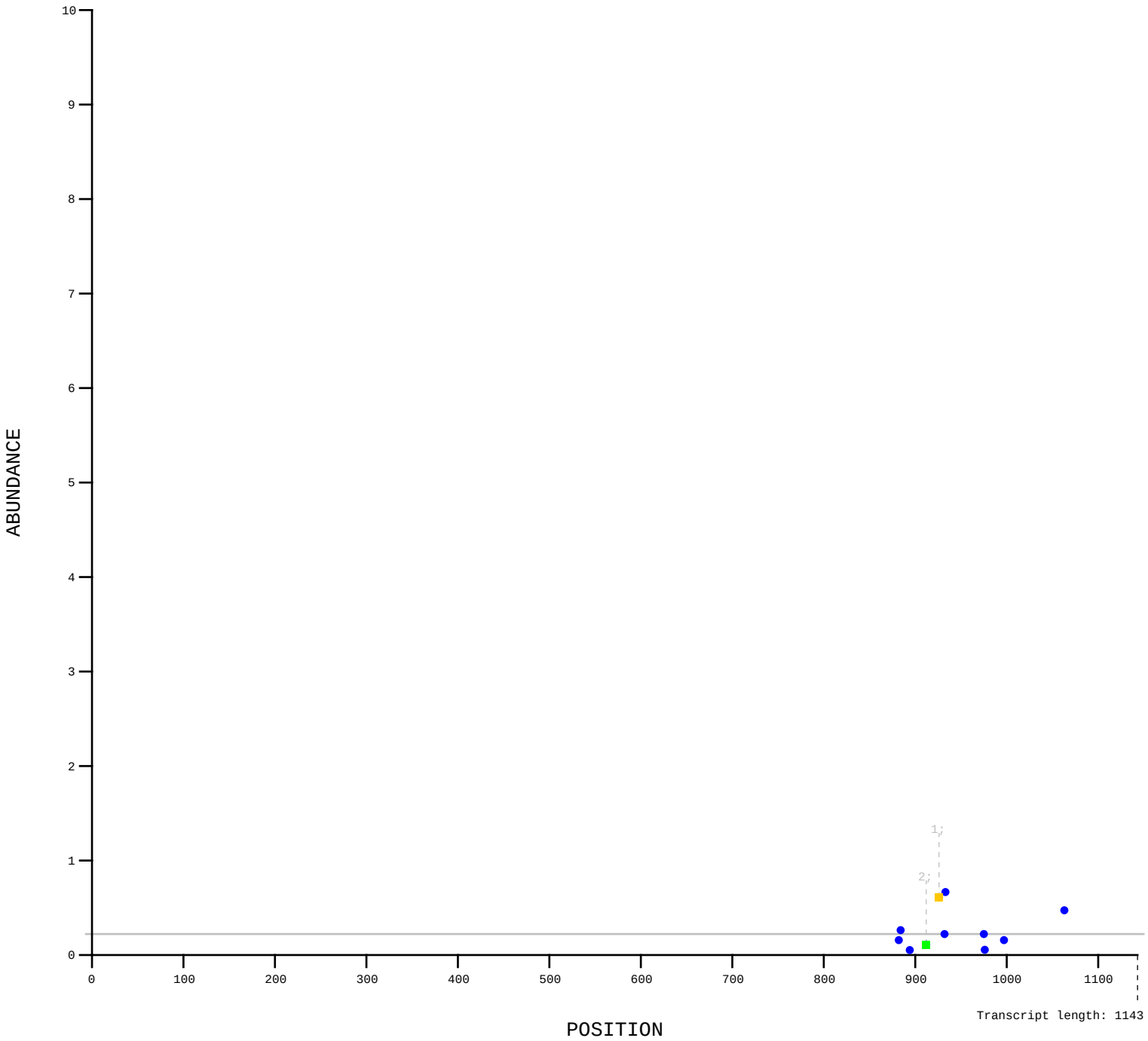


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:2819 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.03

3 #2 Position:2805 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_03947T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1143 nt)

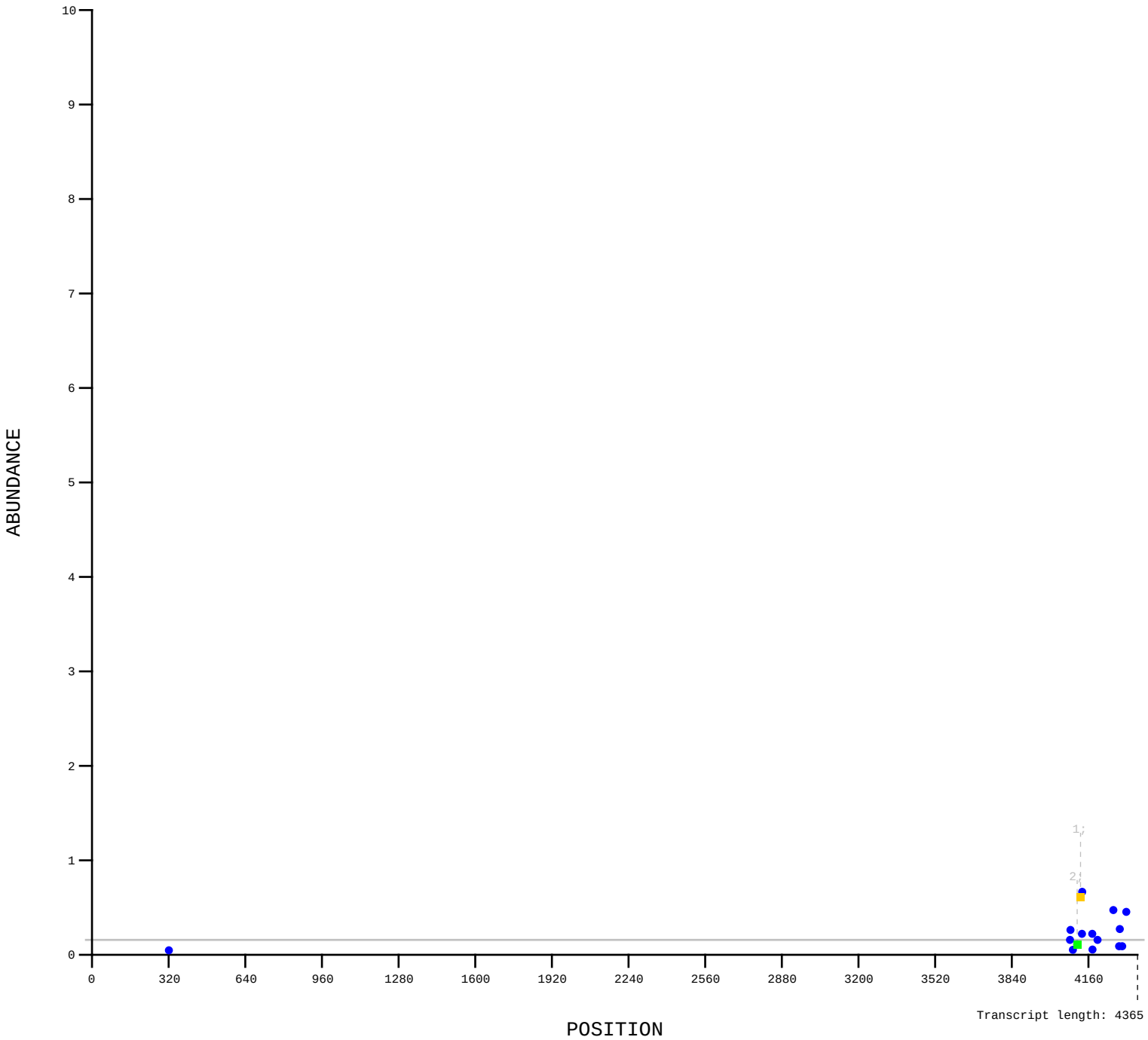


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:926 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.03

3 #2 Position:912 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_16423T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (4365 nt)

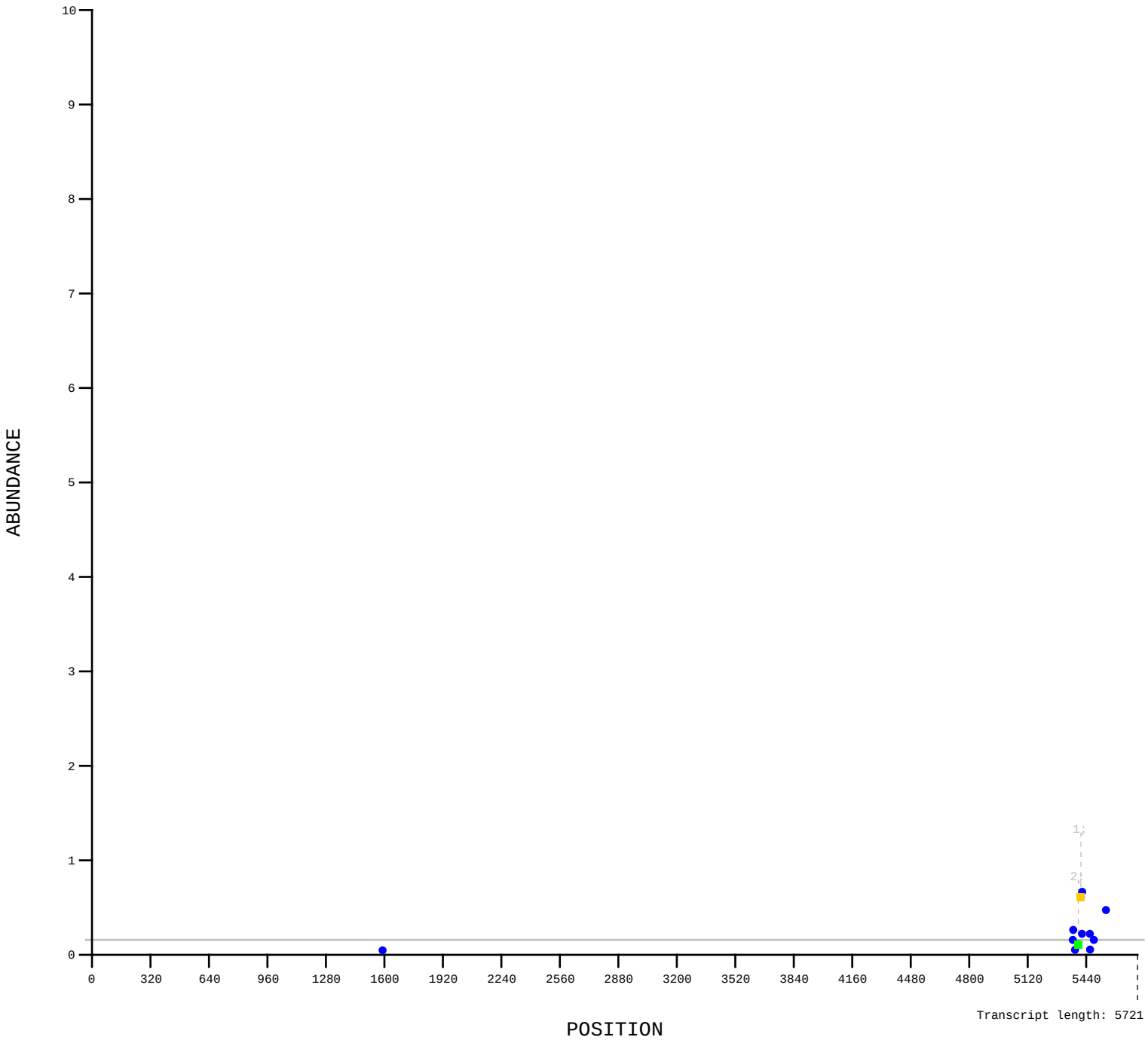


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:4127 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.03

3 #2 Position:4113 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_16413T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5721 nt)

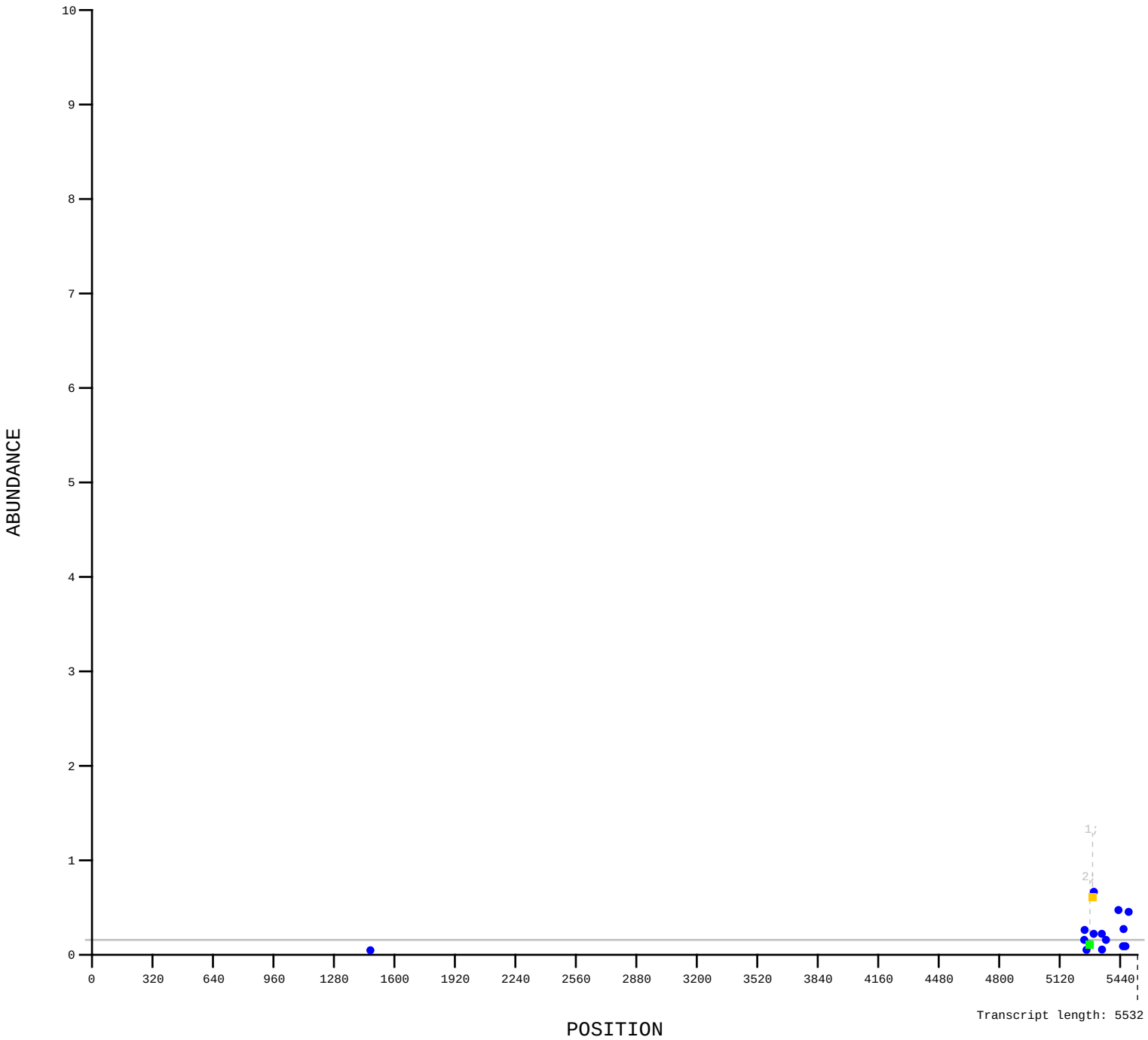


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:5411 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.0

3 #2 Position:5397 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_05786T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5532 nt) Note(s): (truncated)

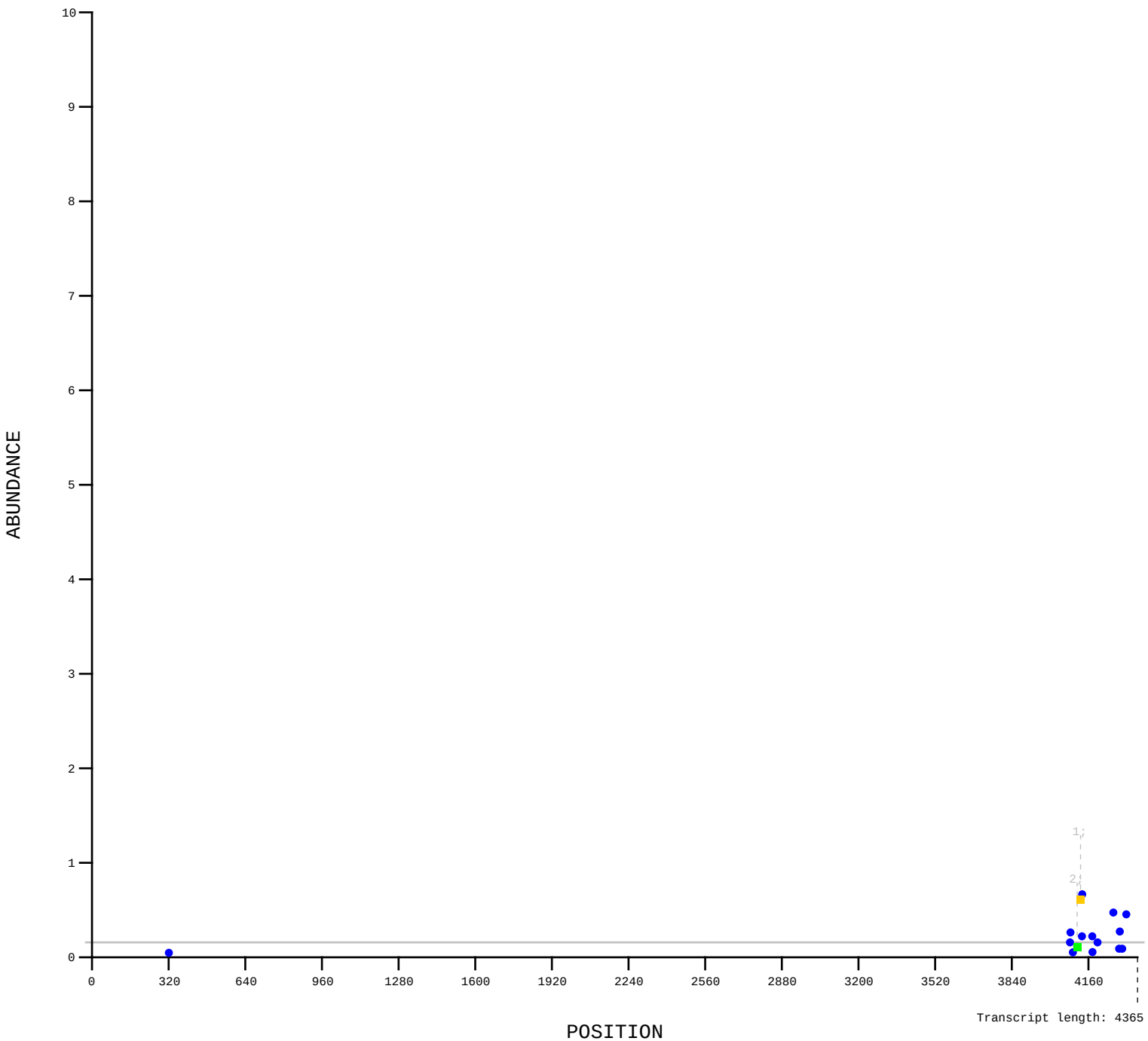


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:5294 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.0

3 #2 Position:5280 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_17286T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (4365 nt) Note(s): (truncated)

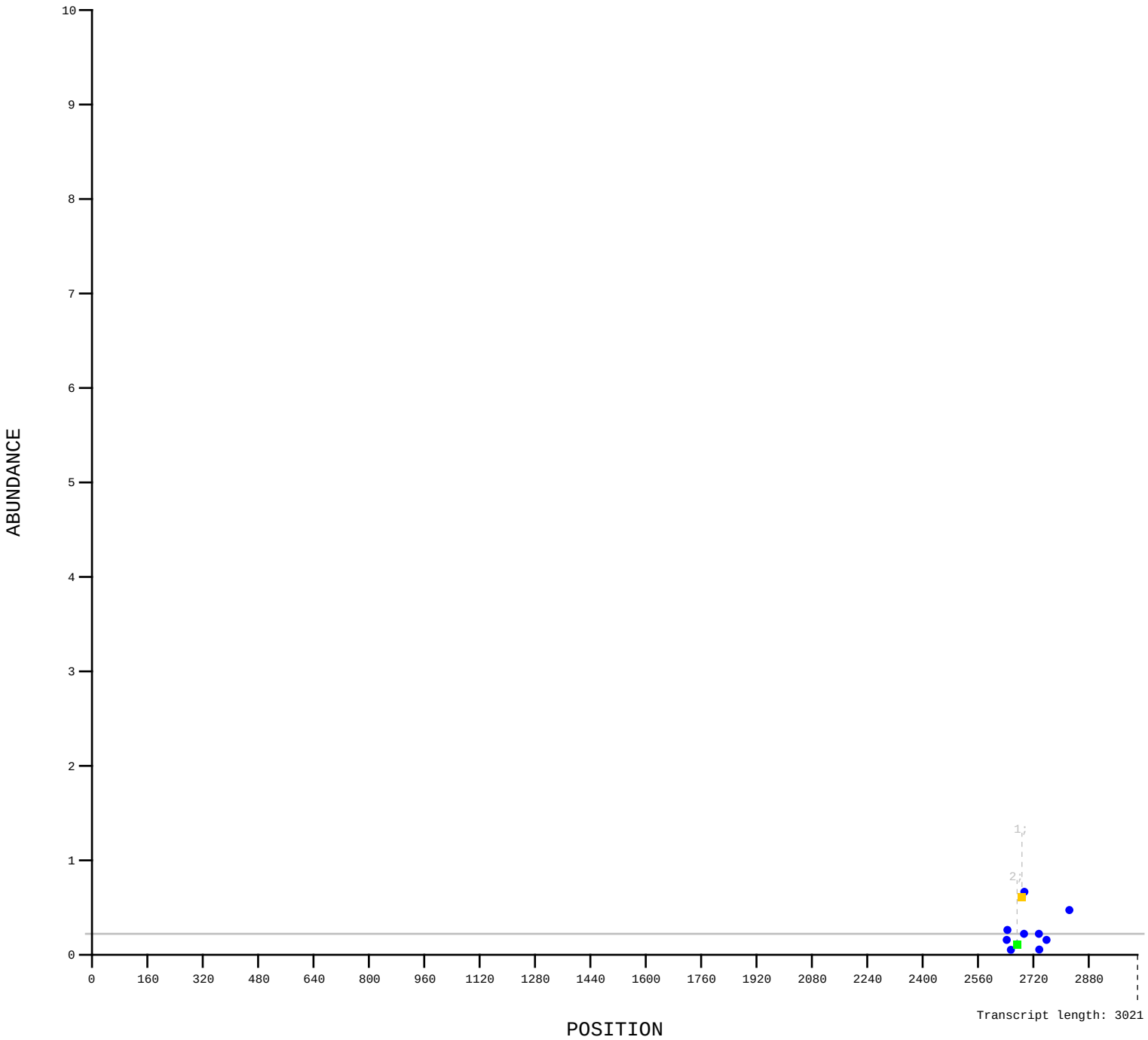


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:4127 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.03

3 #2 Position:4113 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

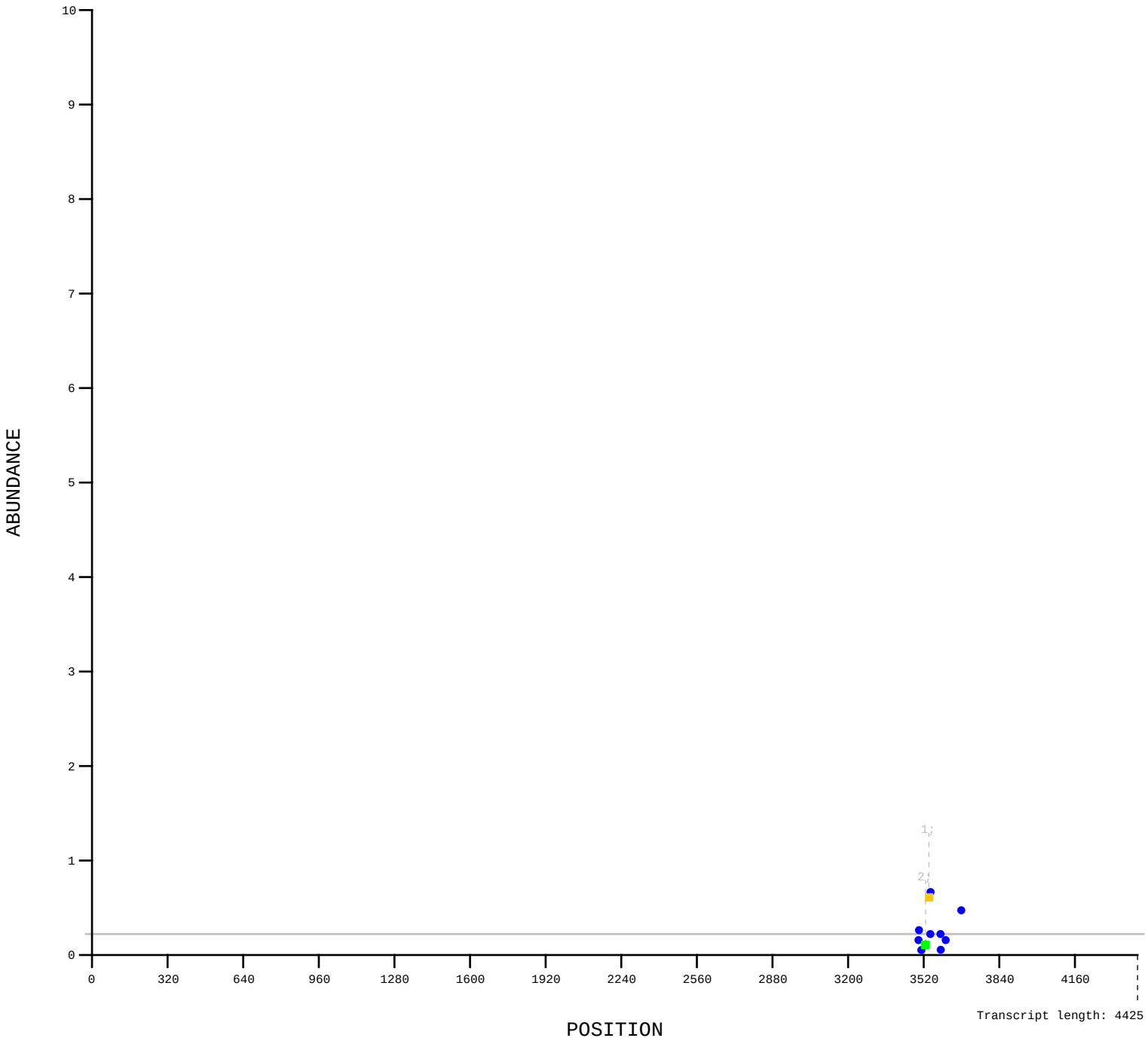
FOXG_17086T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (3021 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:2687  Abundance: 0.61(deg) 10(sRNA)
   5'     TTTCATGATGAGATATCCA          3'  ID:
          || ||o|| ||||o| |||              Score: 4.0
   3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5'  p-value: 0.02

3  #2  Position:2673  Abundance: 0.11(deg) 5(sRNA)
   5'     AGCCACGTAGCTTAAACCGGTC       3'  ID:
          ||||||||||||||||||||             Score: 0.0
   3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5'  p-value: 0.0
```

FOXG_16419T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (4425 nt) Note(s): (truncated)

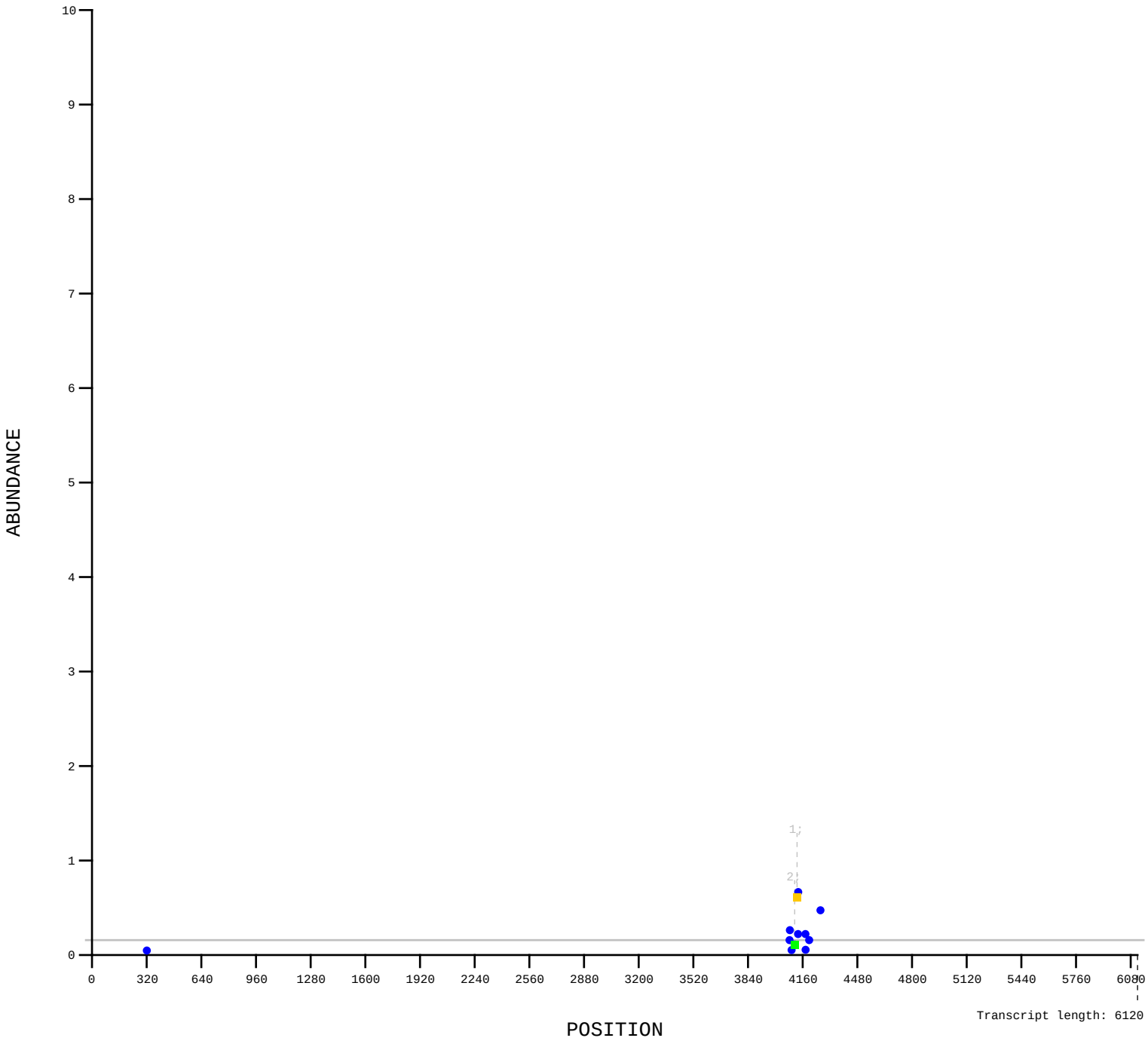


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:3542 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.01

3 #2 Position:3528 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_14236T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (6120 nt) Note(s): (truncated)

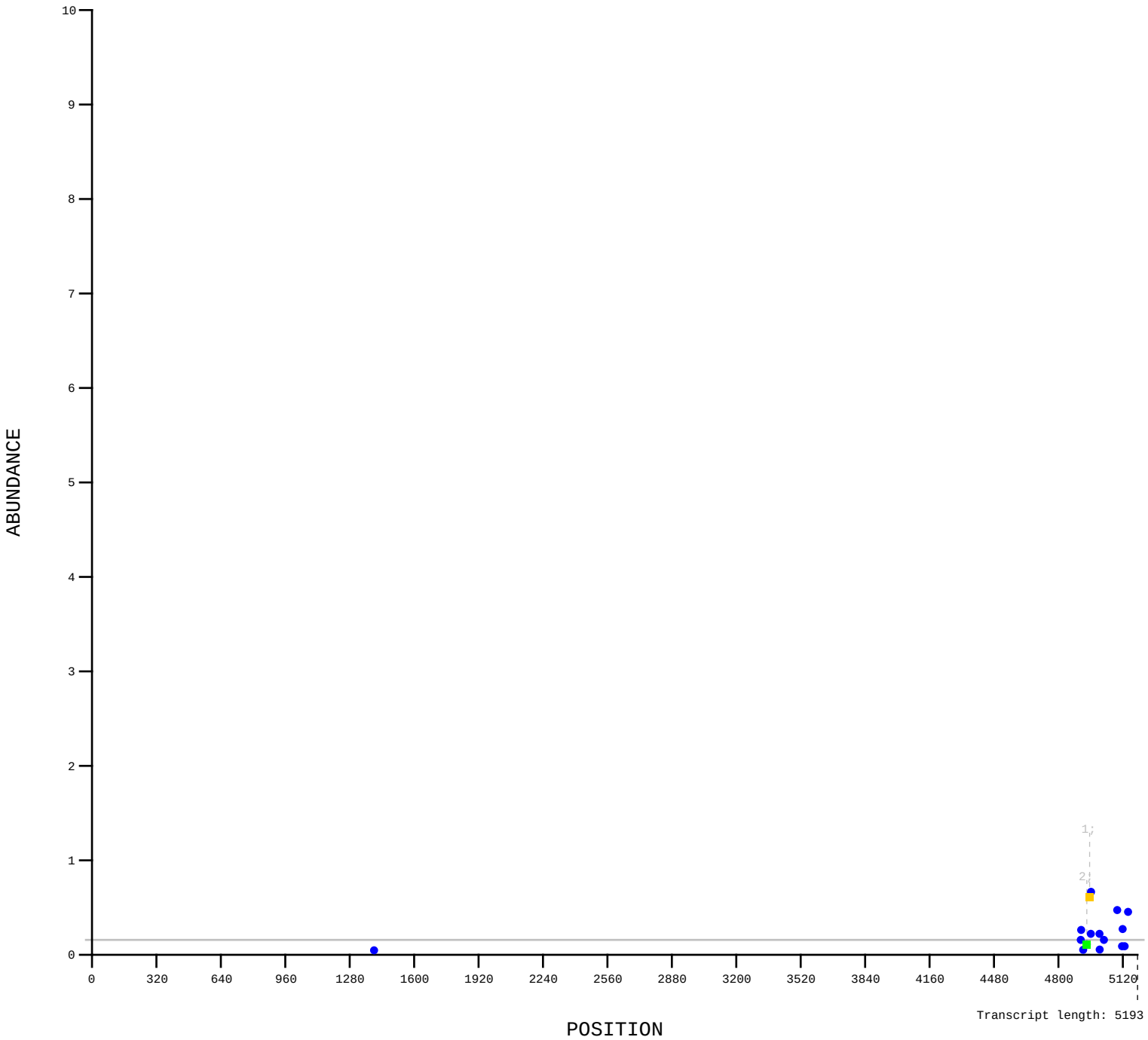


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:4127 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.02

3 #2 Position:4113 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_10736T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5193 nt) Note(s): (truncated)

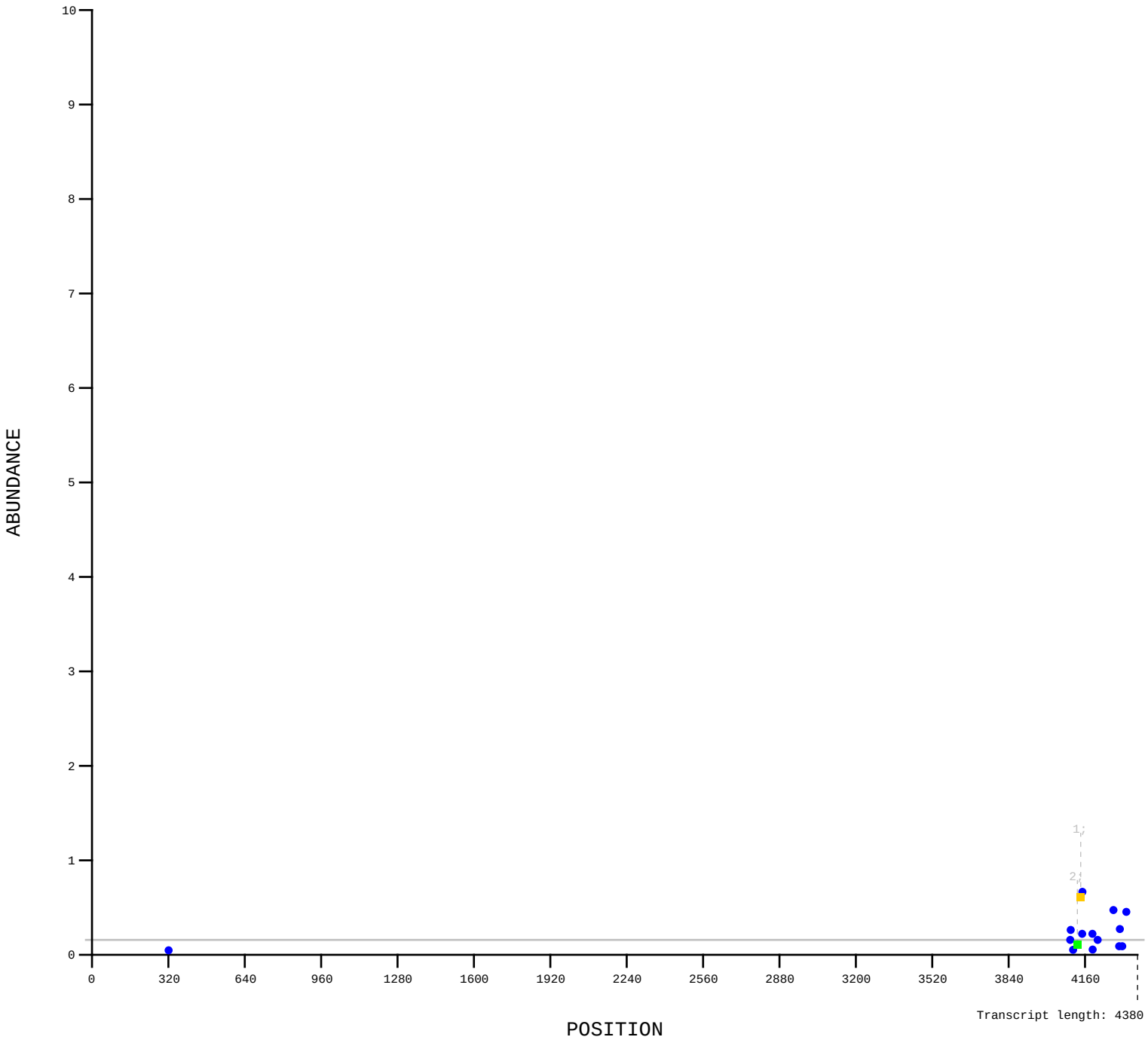


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:4955 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.04

3 #2 Position:4941 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_17273T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (4380 nt)

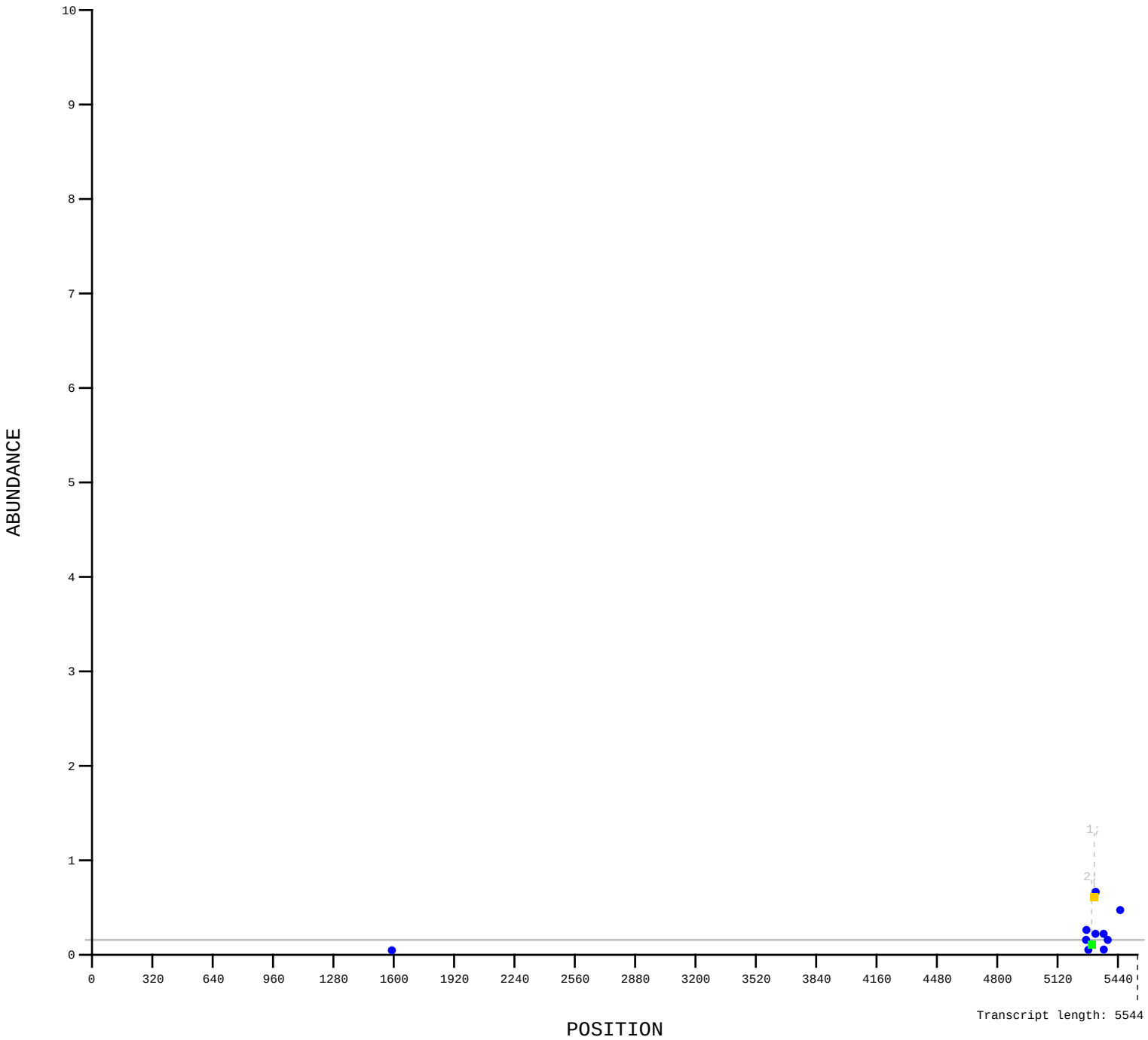


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:4142 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.02

3 #2 Position:4128 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_04036T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5544 nt)

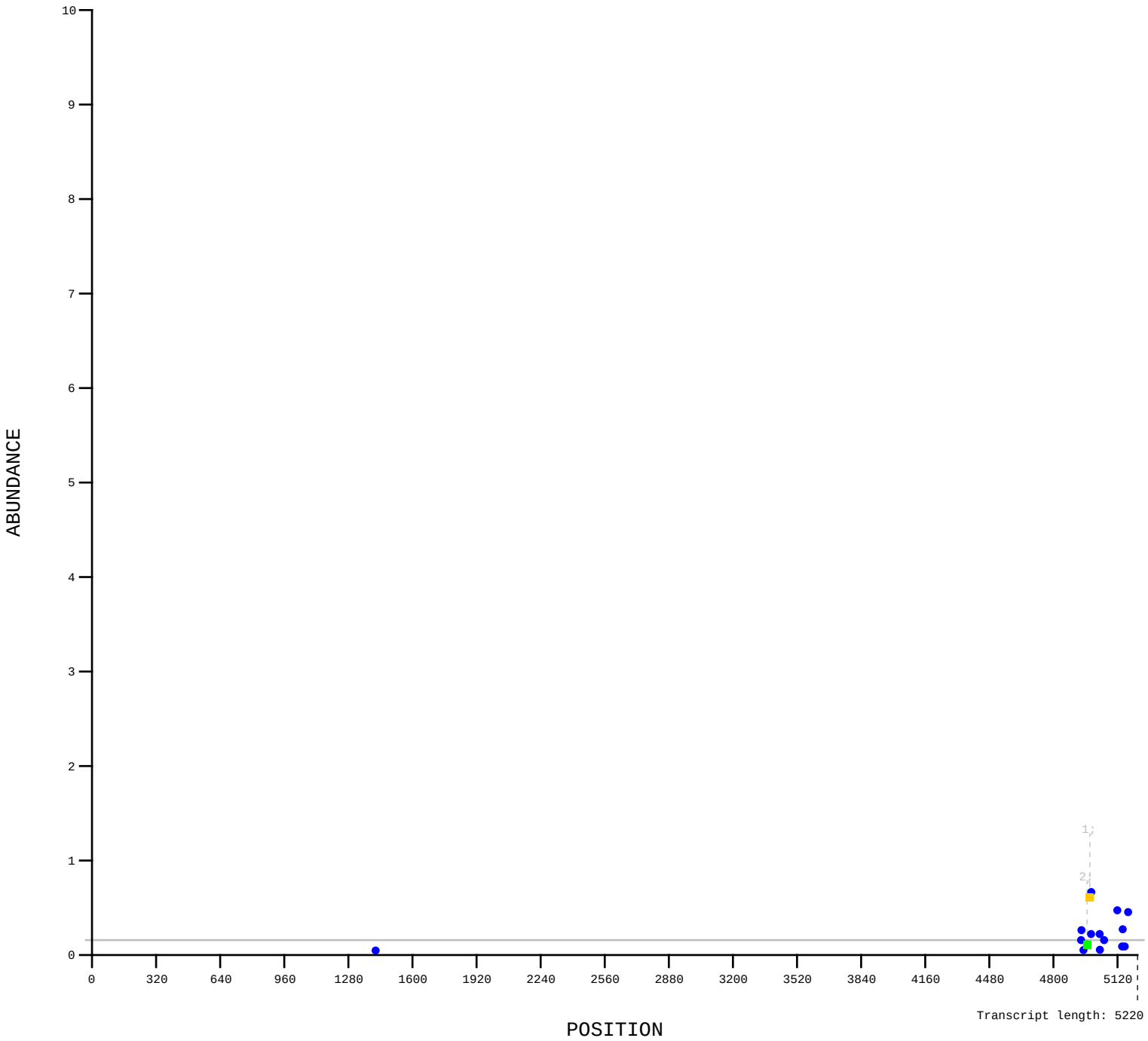


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:5315 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.03

3 #2 Position:5301 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

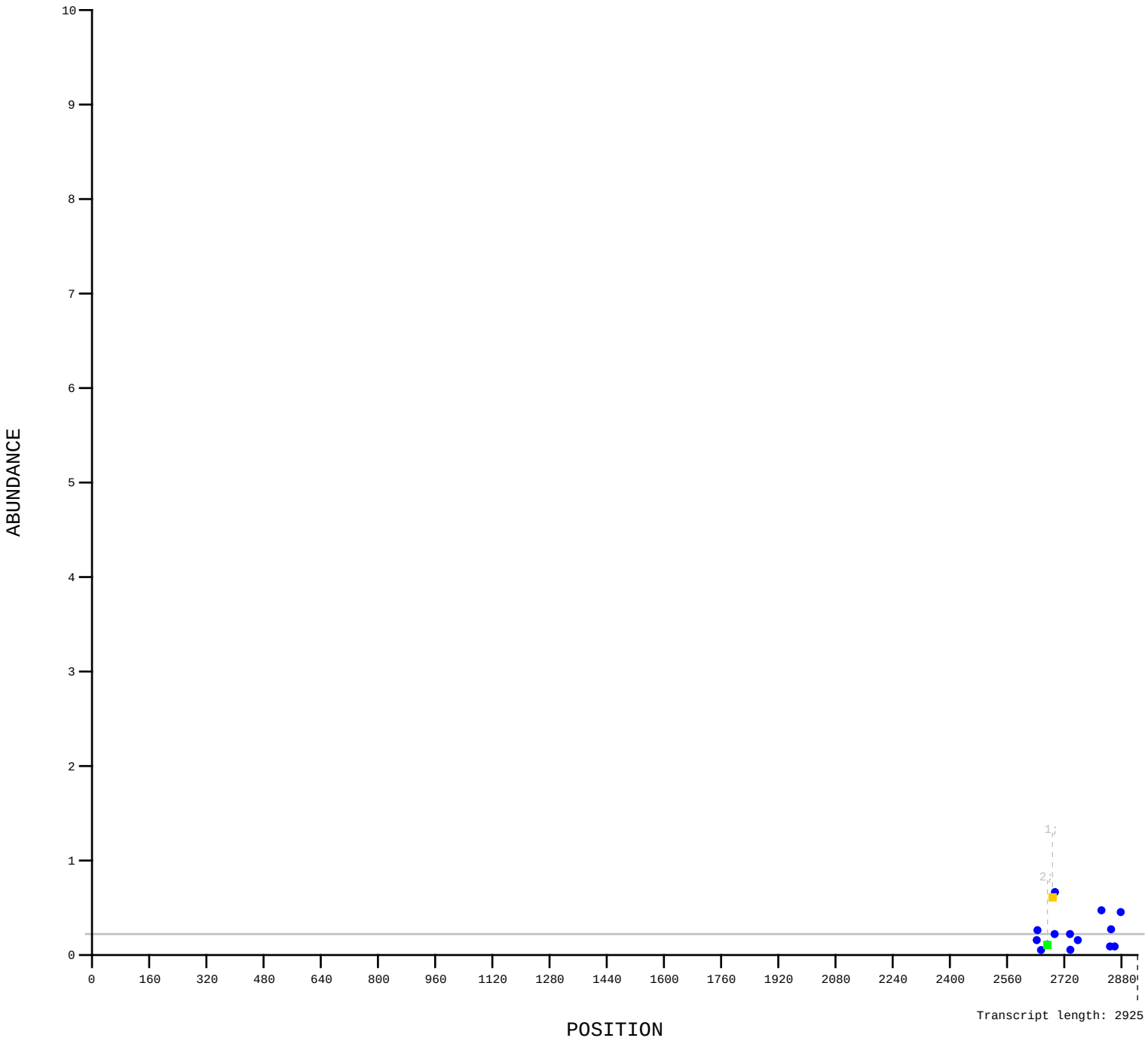
FOXG_14245T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5220 nt) Note(s): (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:4982  Abundance: 0.61(deg) 10(sRNA)
   5'     TTTCATGATGAGATATCCA          3'  ID:
          || ||o|| ||||o| |||              Score: 4.0
   3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5'  p-value: 0.01

3  #2  Position:4968  Abundance: 0.11(deg) 5(sRNA)
   5'     AGCCACGTAGCTTAAACCGGTC       3'  ID:
          ||||||||||||||||||||             Score: 0.0
   3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5'  p-value: 0.0
```

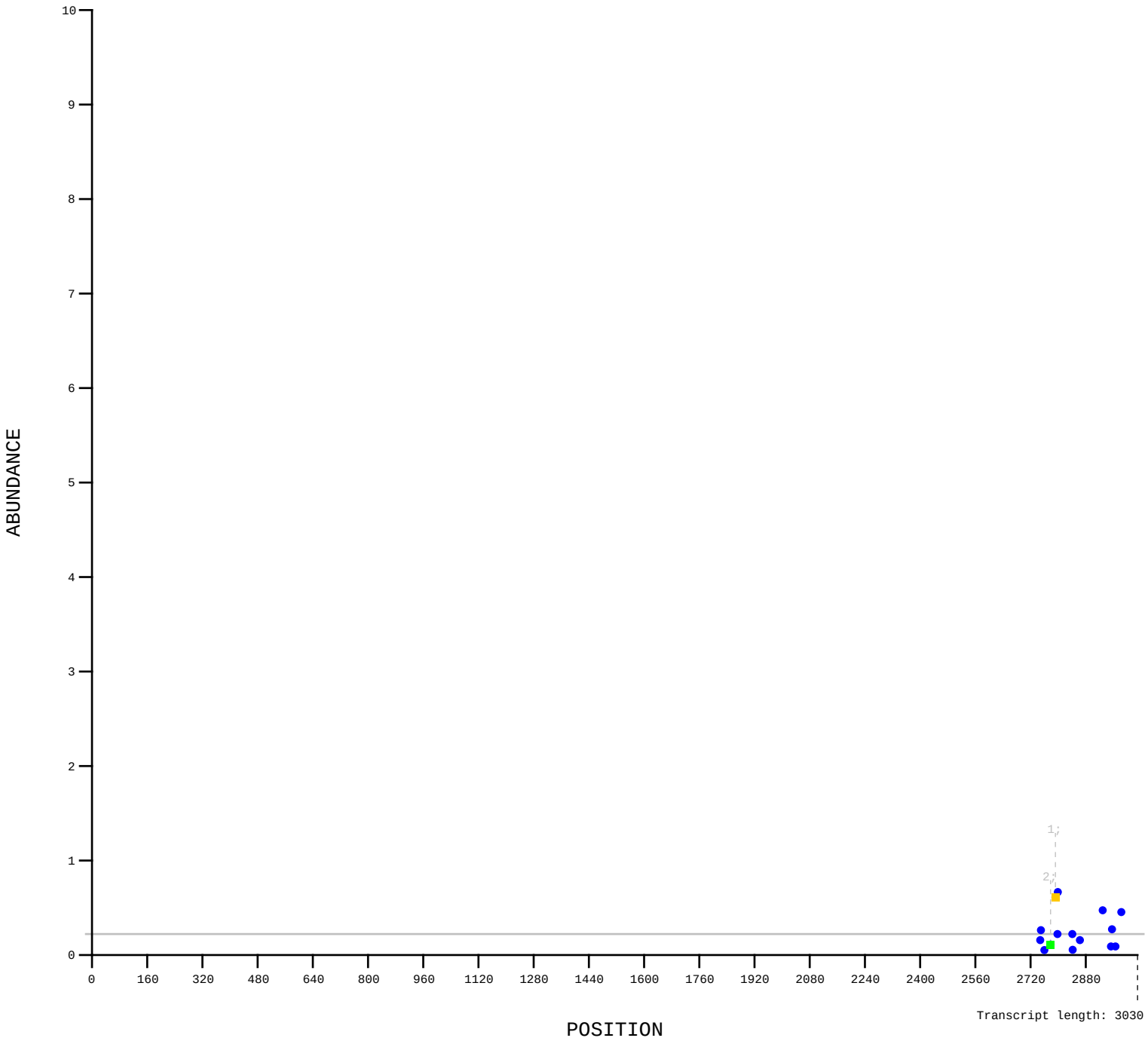
FOXG_12587T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (2925 nt) Note(s): (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
2  #1  Position:2687  Abundance: 0.61(deg) 10(sRNA)
   5'     TTTCATGATGAGATATCCA          3'  ID:
          || ||o|| ||||o| |||              Score: 4.0
   3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5'  p-value: 0.01

3  #2  Position:2673  Abundance: 0.11(deg) 5(sRNA)
   5'     AGCCACGTAGCTTAAACCGGTC       3'  ID:
          ||||||||||||||||||||             Score: 0.0
   3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5'  p-value: 0.0
```

FOXG_12537T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (3030 nt) Note(s): (truncated)

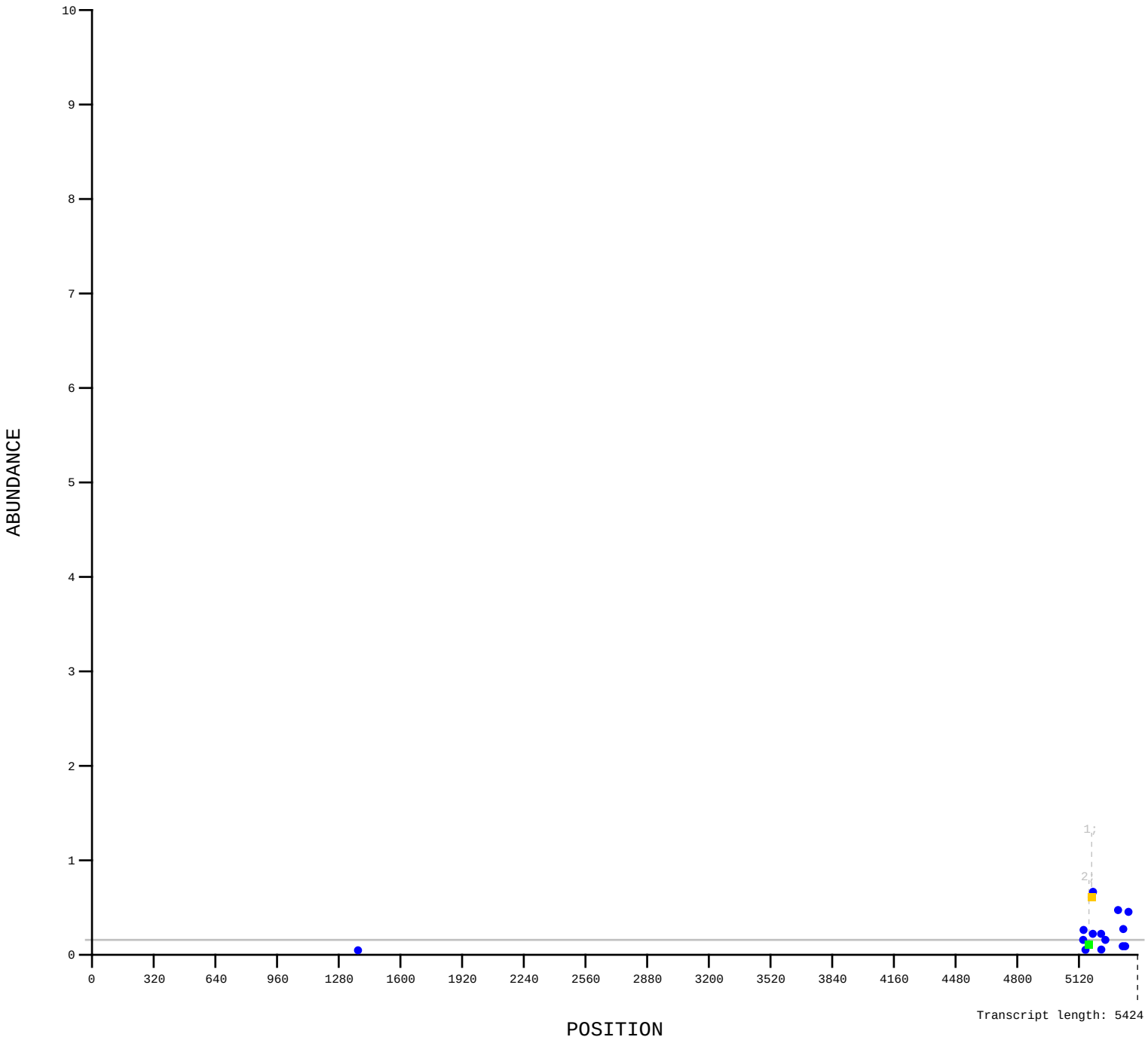


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:2792 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.03

3 #2 Position:2778 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_17427T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5424 nt)

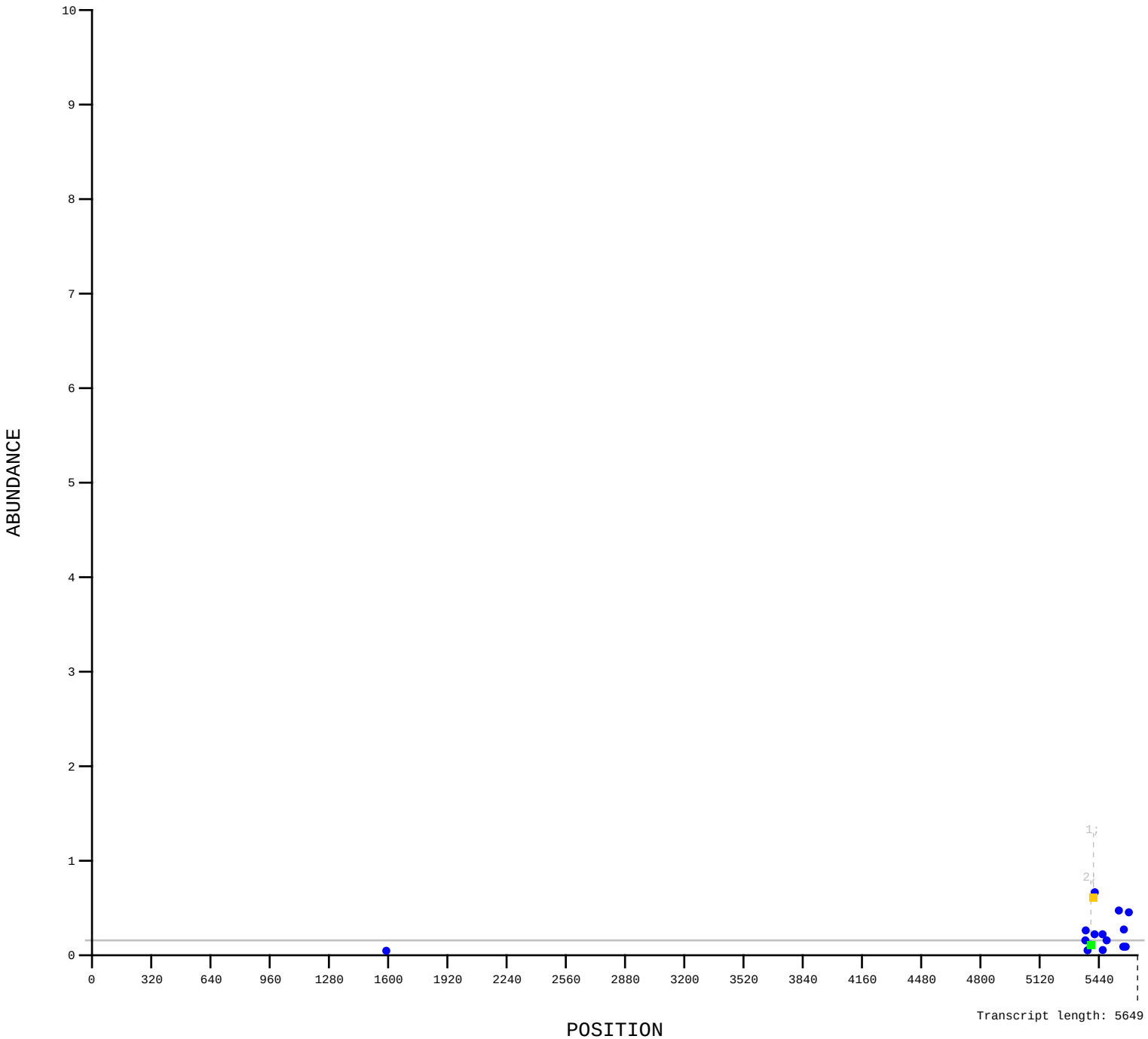


Category: 0 1 2 3 4
Degradome alignment: Median:

2 #1 Position:5186 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.01

3 #2 Position:5172 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
|||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_05783T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (5649 nt) Note(s): (truncated)

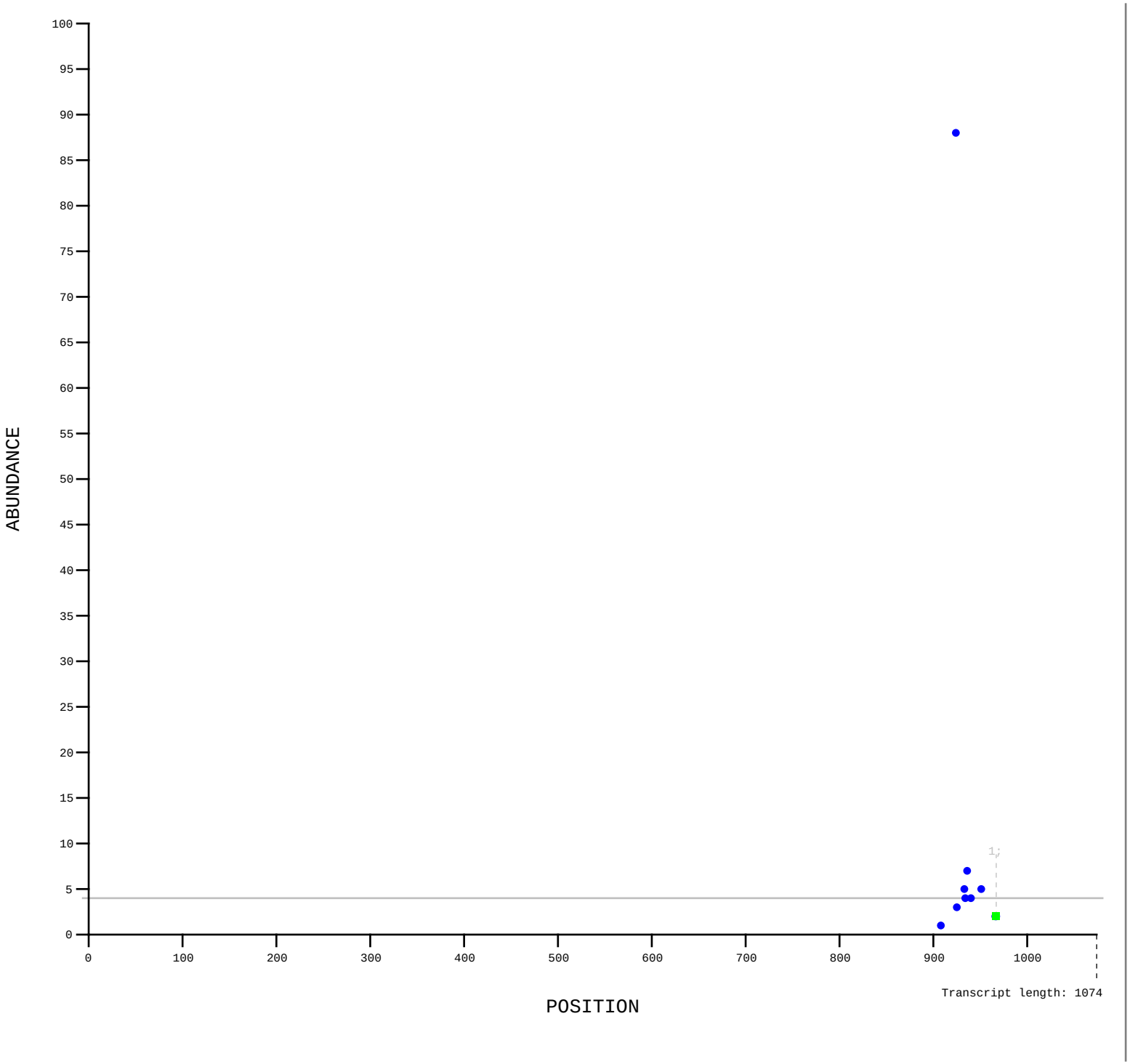


Category: 0 1 2 3 4
Degradome alignment: Median:

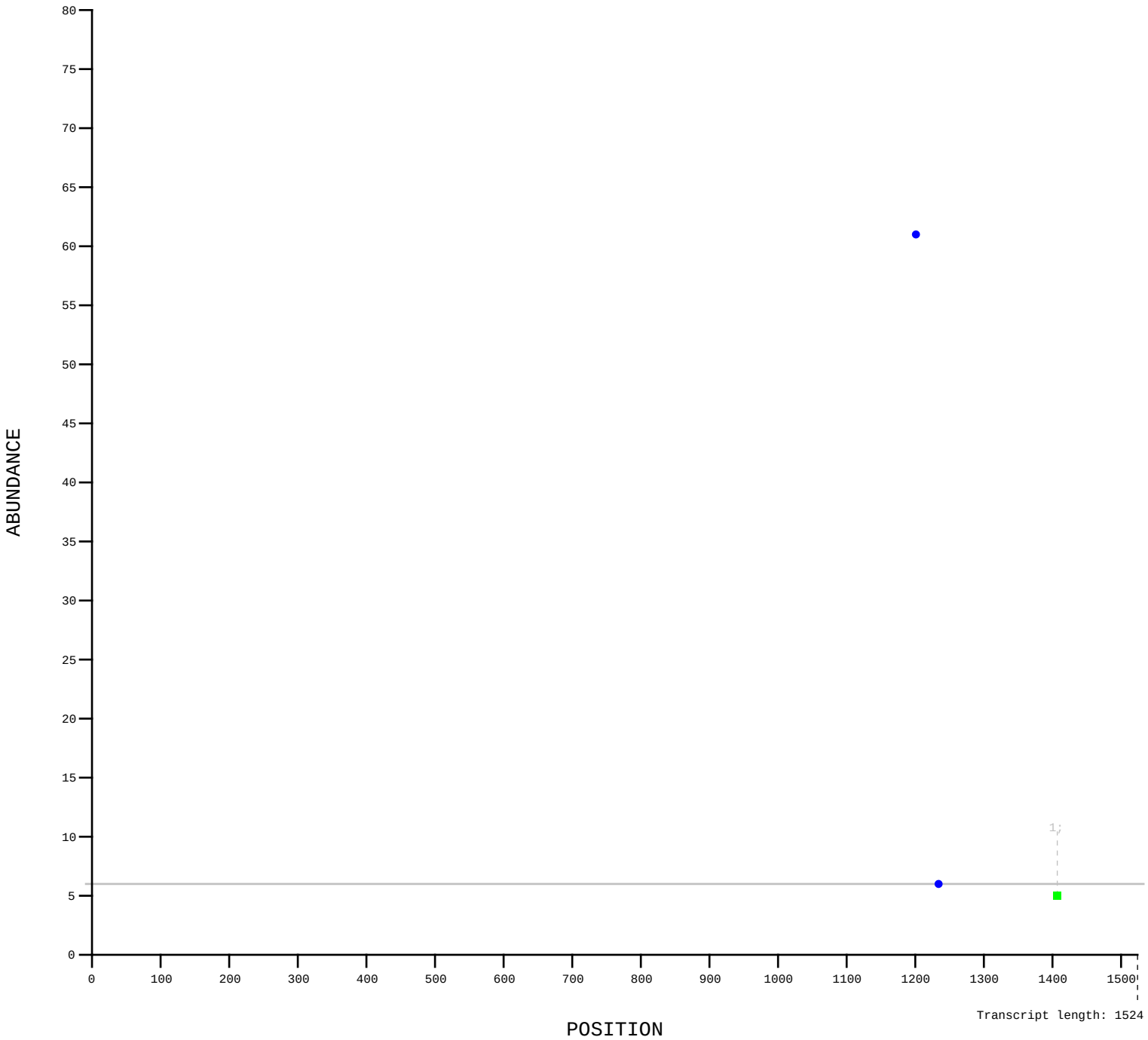
2 #1 Position:5411 Abundance: 0.61(deg) 10(sRNA)
5' TTTCATGATGAGATATCCA 3' ID:
|| ||o|| ||||o| ||| Score: 4.0
3' CAAAAATGTGCT-CTCTGTCGGTGCATCGAAT 5' p-value: 0.01

3 #2 Position:5397 Abundance: 0.11(deg) 5(sRNA)
5' AGCCACGTAGCTTAAACCGGTC 3' ID:
||||||||||||||||||||| Score: 0.0
3' TCTGTCGGTGCATCGAATTTGGCCAGACTTTC 5' p-value: 0.0

FOXG_03949T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1074 nt)



FOXG_08541T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1524 nt)



Category: 0 1 2 3 4

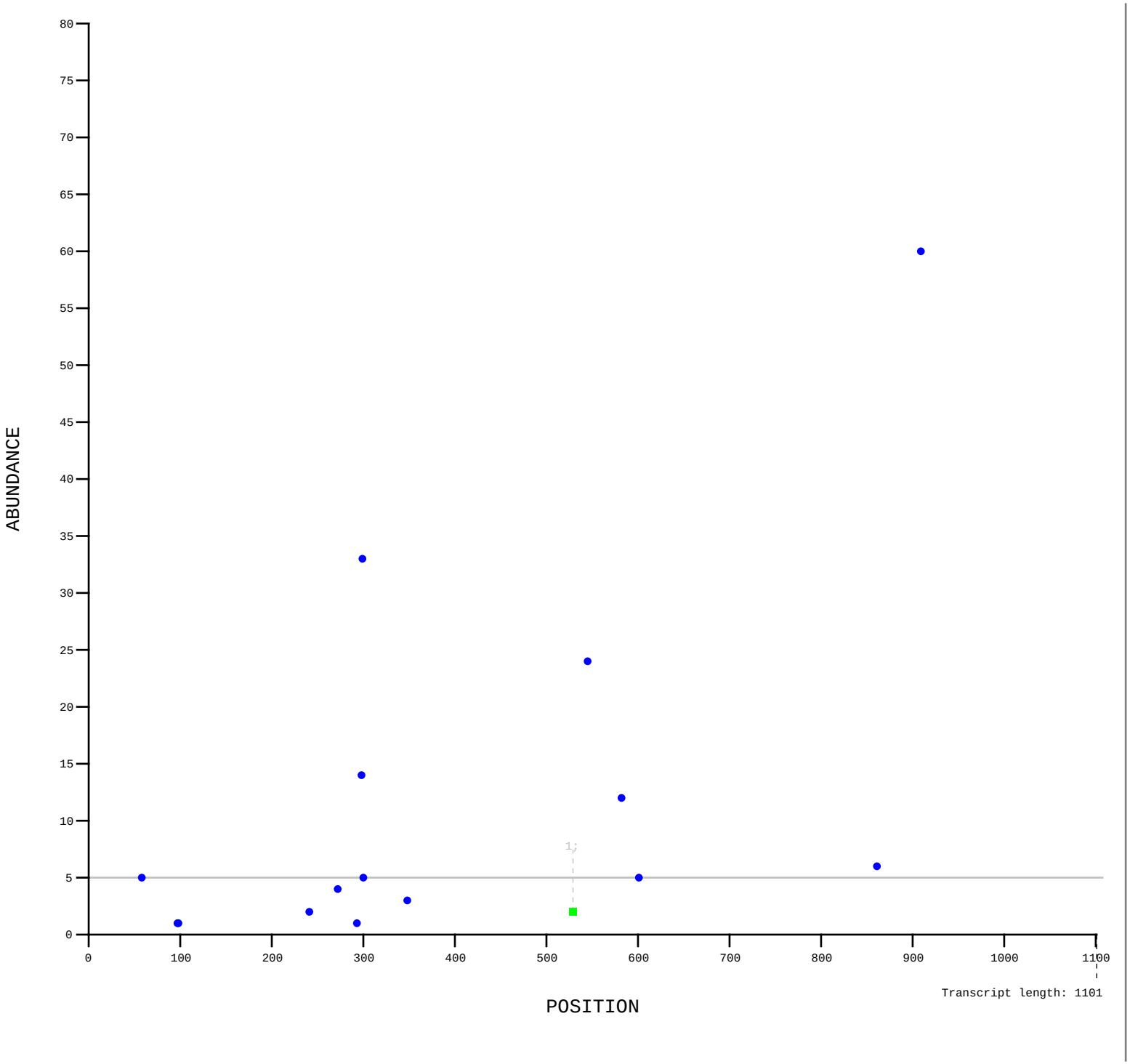
Degradome alignment: Median:

3 #1 Position:1407 Abundance: 5.00(deg) 8(sRNA)

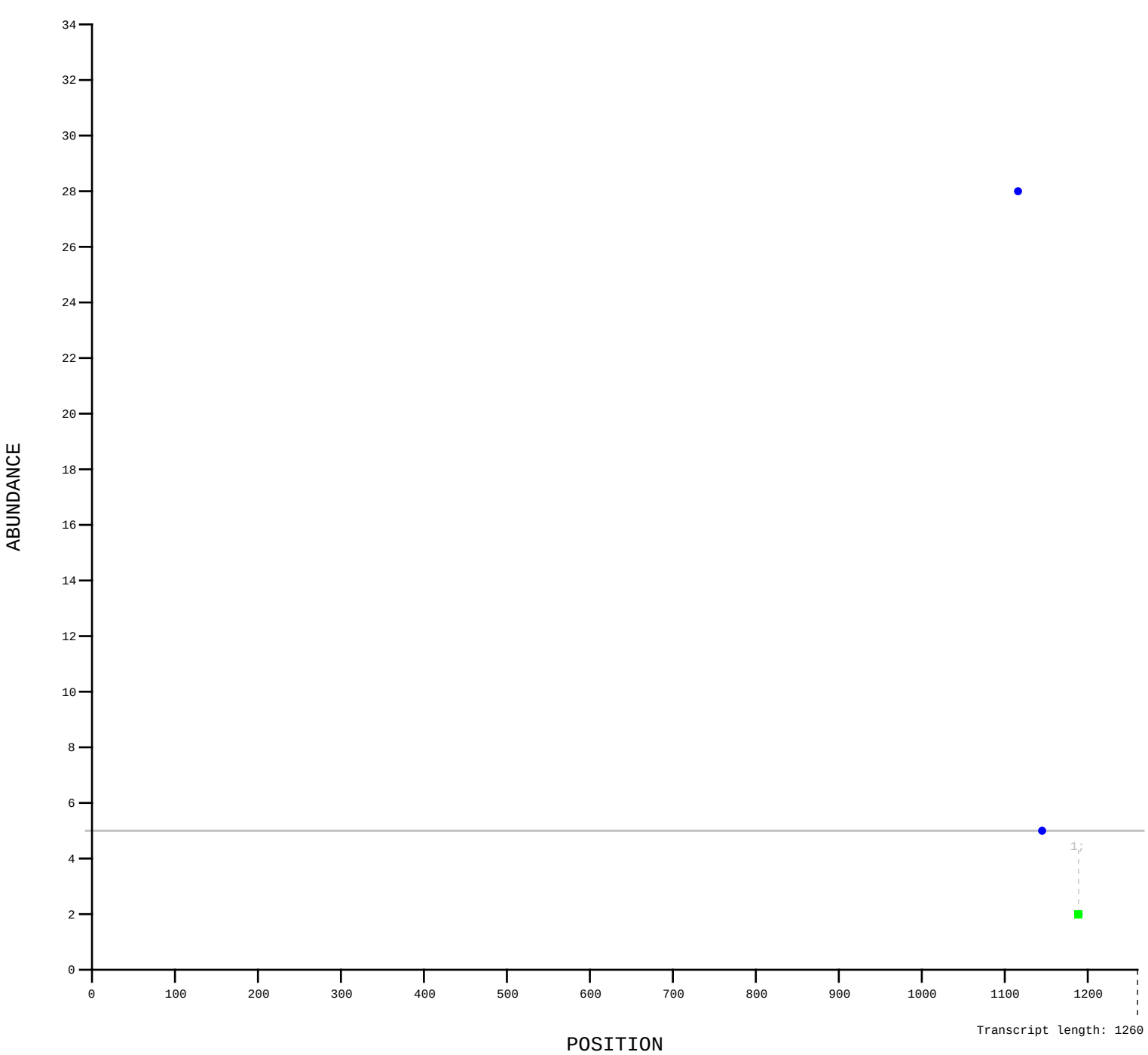
```
5'     TCTATTAGTCTCTGCCACAGA        3'
         || ||o|o||||| | |||||
3' GACTAG-TAGTTAGAGAGGTTGTCTAGGATTA 5'
```

ID:
Score: 4.0
p-value: 0.0

FOXG_15666T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1101 nt) Note(s): (truncated)



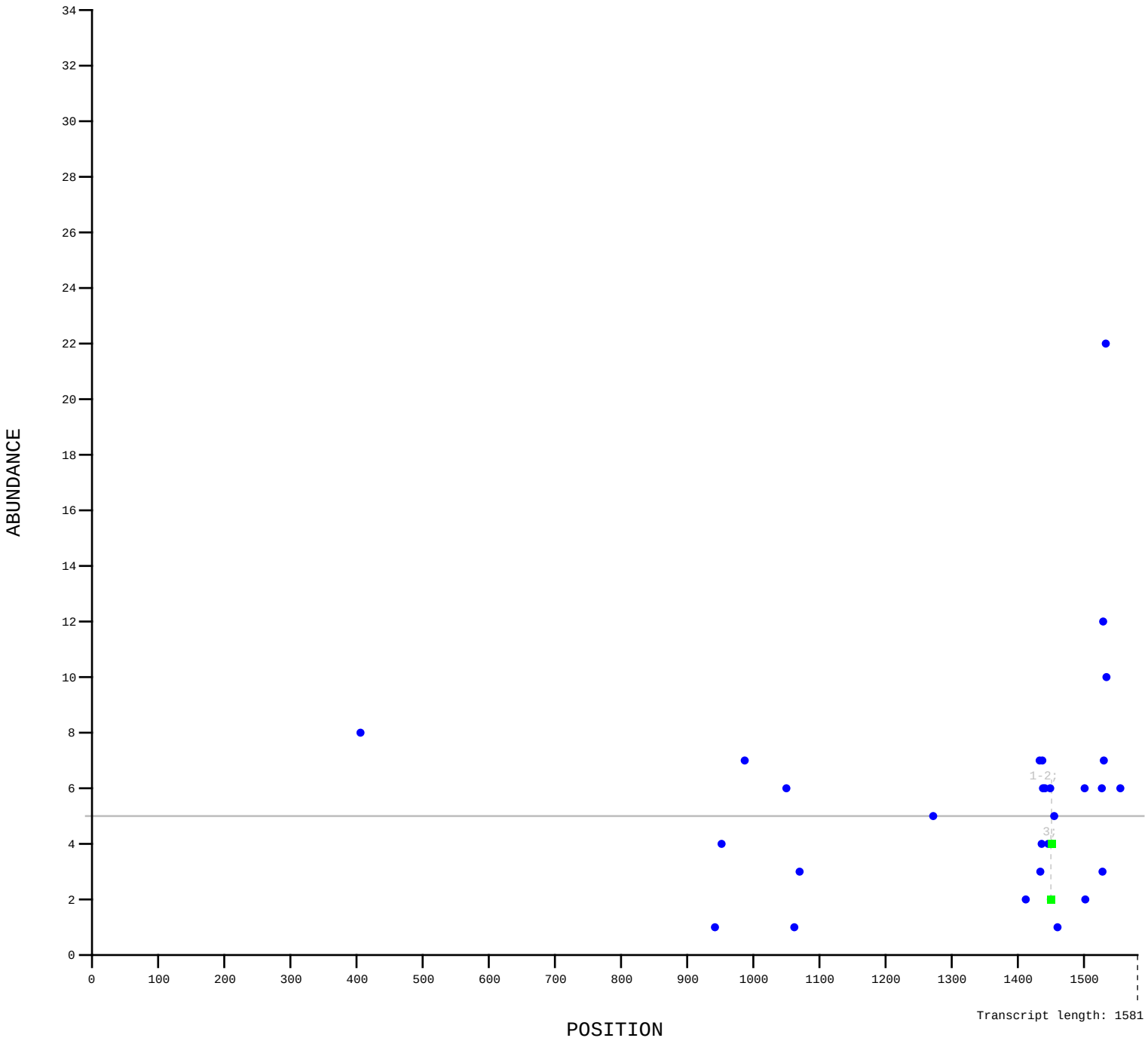
FOXG_03001T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1260 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

3 #1 Position:1189 Abundance: 2.00(deg) 5(sRNA)
5' TTTCTTCCGAAGCGCT-GTC 3' ID:
o|||||||||o|| | ||| Score: 4.0
3' ACTTTGAGAAGGCTTTGCCAGCAGAAGAGAAG 5' p-value: 0.01

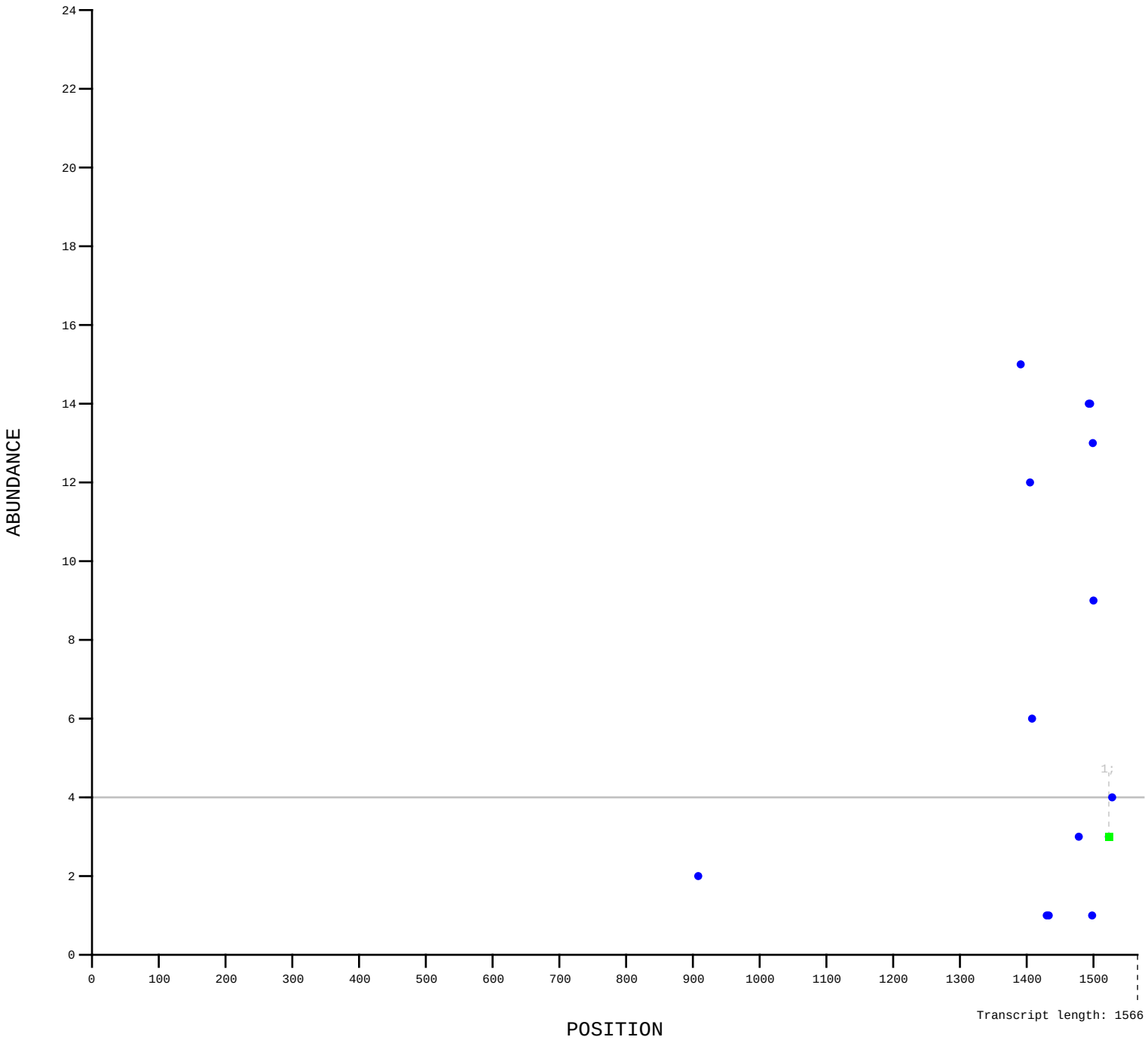
FOXG_02924T0 | Fusarium oxysporum f. sp. lycopersici 4287 acetyl-CoA hydrolase (1581 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

```
3  #1  Position:1451  Abundance: 4.00(deg) 35(sRNA)
   5'     TAGCAGAAATAGTGACTCAAGA        3'  ID:
          || | |||||||| |||| ||             Score: 4.0
   3' CGGAATAG-CTTTATCACCGAGTCCTACCCGA 5'  p-value: 0.0

3  #2  Position:1451  Abundance: 4.00(deg) 27(sRNA)
   5'     TAGCAGAAATAGTGACTCAAG         3'  ID:
          || | |||||||| |||| |             Score: 4.0
   3' CGGAATAG-CTTTATCACCGAGTCCTACCCGA 5'  p-value: 0.0

3  #3  Position:1450  Abundance: 2.00(deg) 9(sRNA)
   5'     AGCAGAAATAGTGACTCAAGA         3'  ID:
          | | |||||||| |||| ||             Score: 4.0
   3' GGAATAG-CTTTATCACCGAGTCCTACCCGAC 5'  p-value: 0.0
```

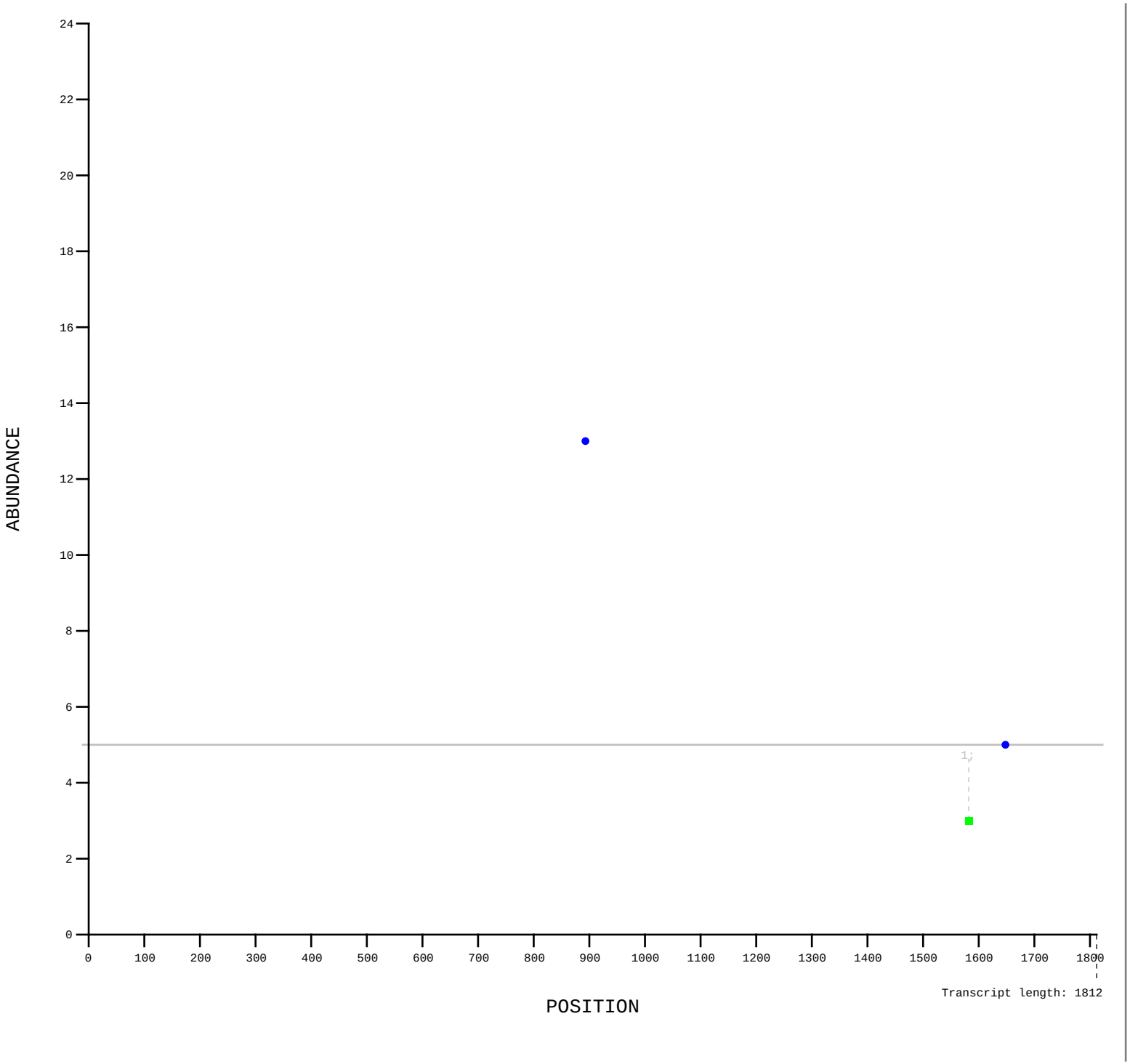
FOXG_07769T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1566 nt)



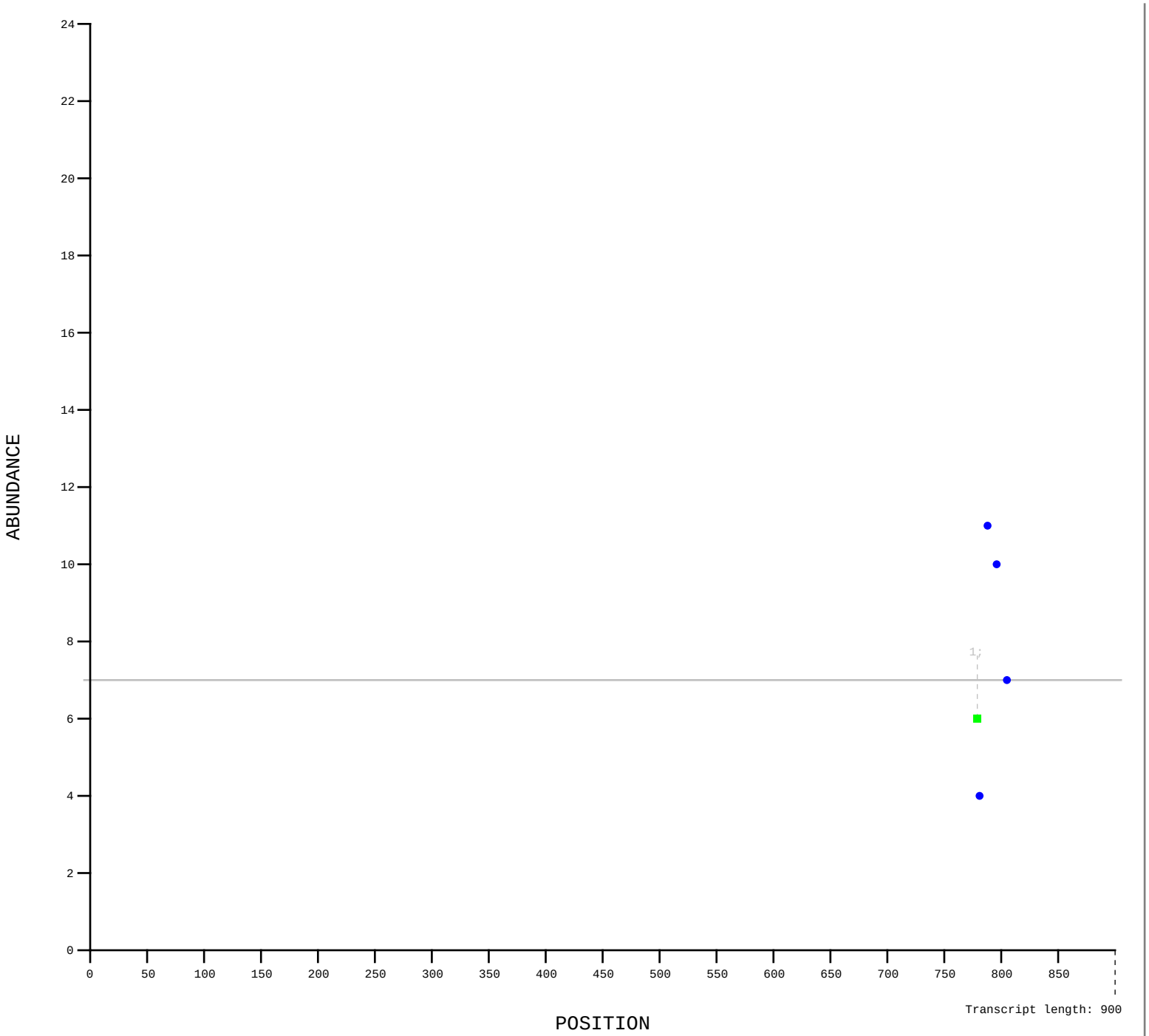
Category: 0 1 2 3 4
Degradome alignment: Median:

3 #1 Position:1523 Abundance: 3.00(deg) 13(sRNA)
5' ACATCAGATCGTCCGTT-CTG 3' ID:
||||||o||||o |o|| |o| Score: 4.0
3' GAATTGTAGTTTAGCGAGTAACGGCAAGGTCT 5' p-value: 0.0

FOXG_01460T0 | Fusarium oxysporum f. sp. lycopersici 4287 AP-3 complex subunit delta (1812 nt) No (truncated)



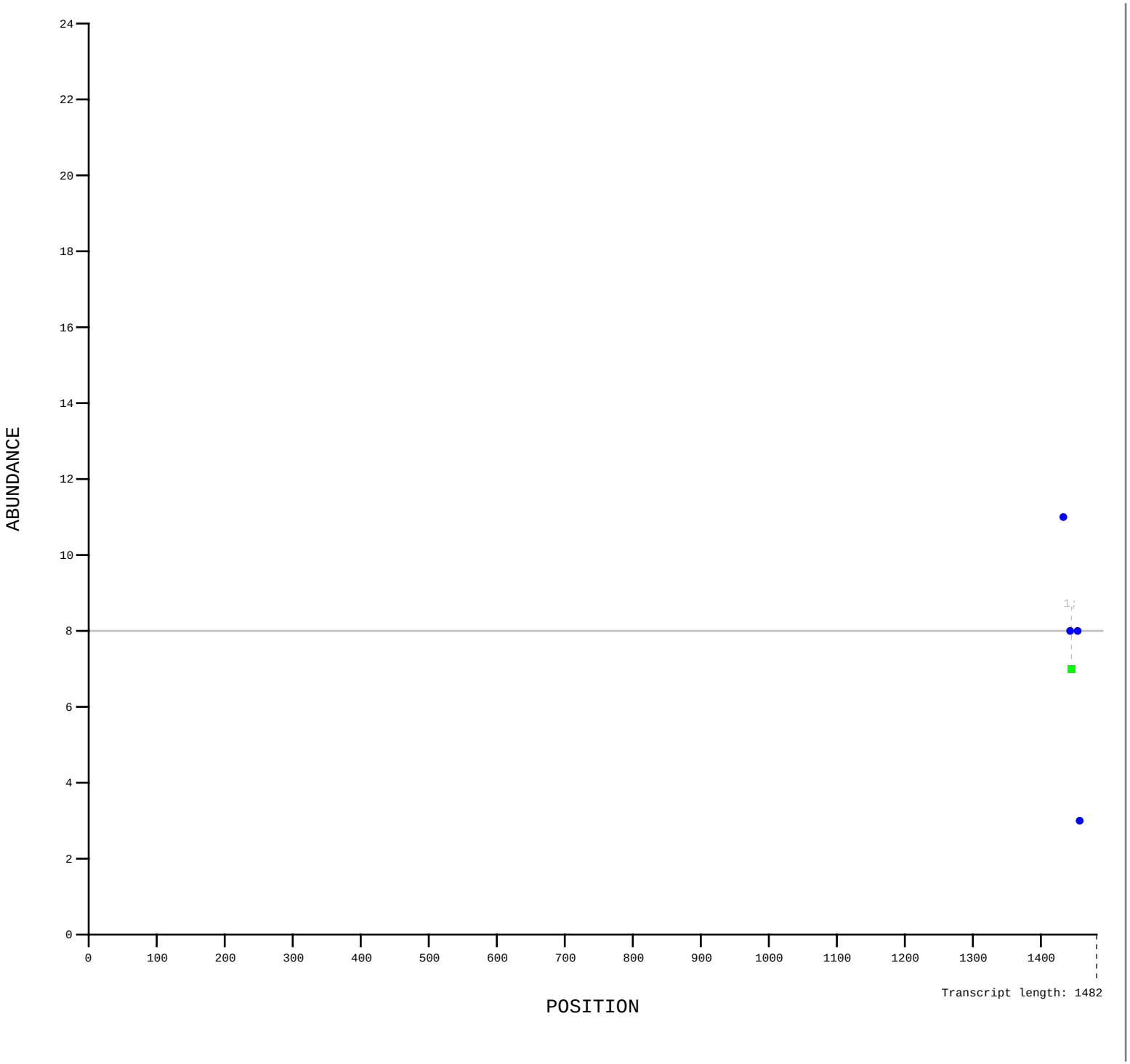
FOXG_11658T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (900 nt)



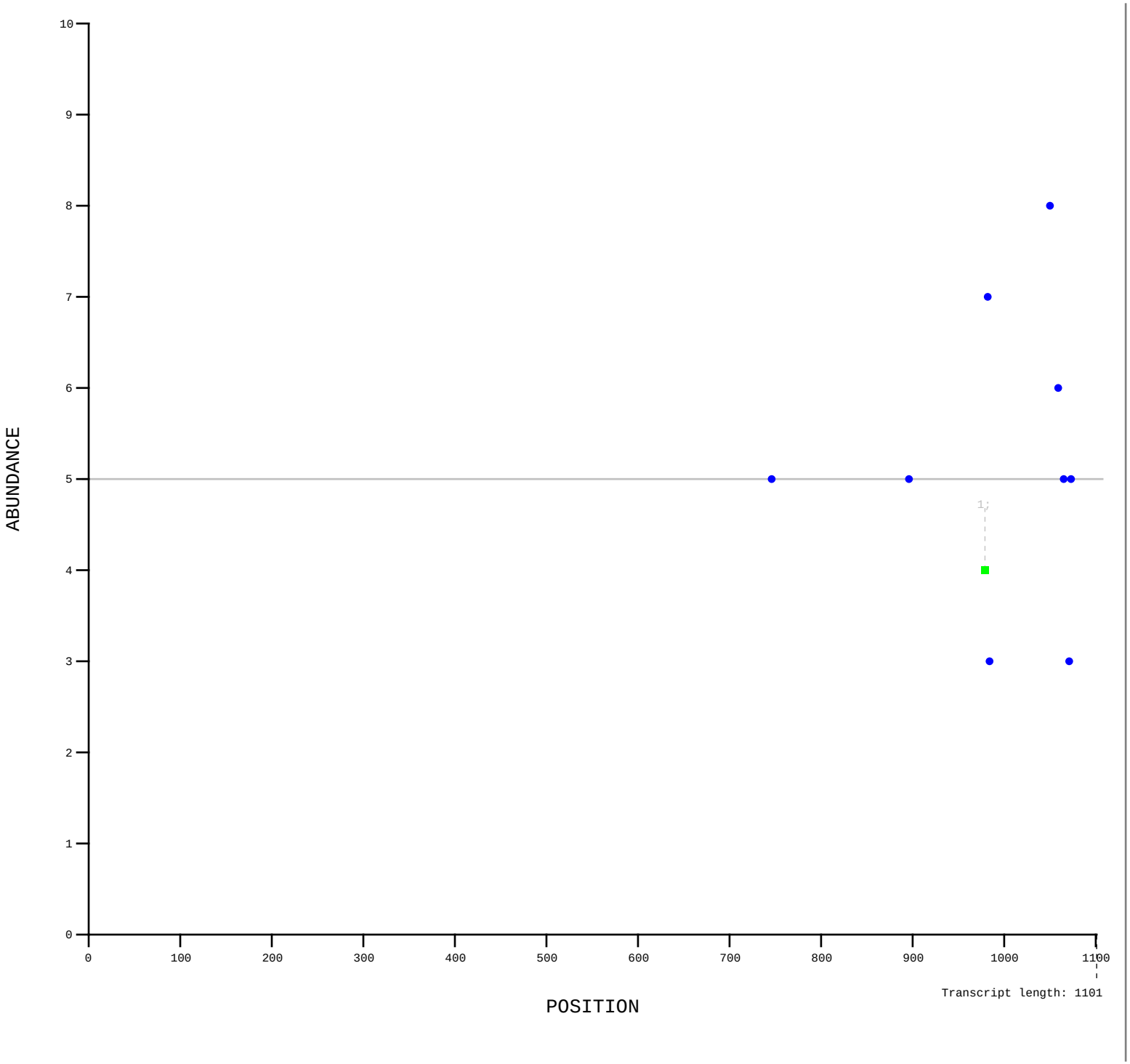
Category: 0 1 2 3 4
Degradome alignment: Median:

3 #1 Position:779 Abundance: 6.00(deg) 50(sRNA)
5' TATTACTGGGGAACTTAGT 3' ID:
|| |||||o|| ||o| || Score: 4.0
3' AGGCATTATGACTCCGTGGA-CAACCTTTGGA 5' p-value: 0.0

FOXG_02286T0 | Fusarium oxysporum f. sp. lycopersici 4287 aspartyl aminopeptidase (1482 nt)



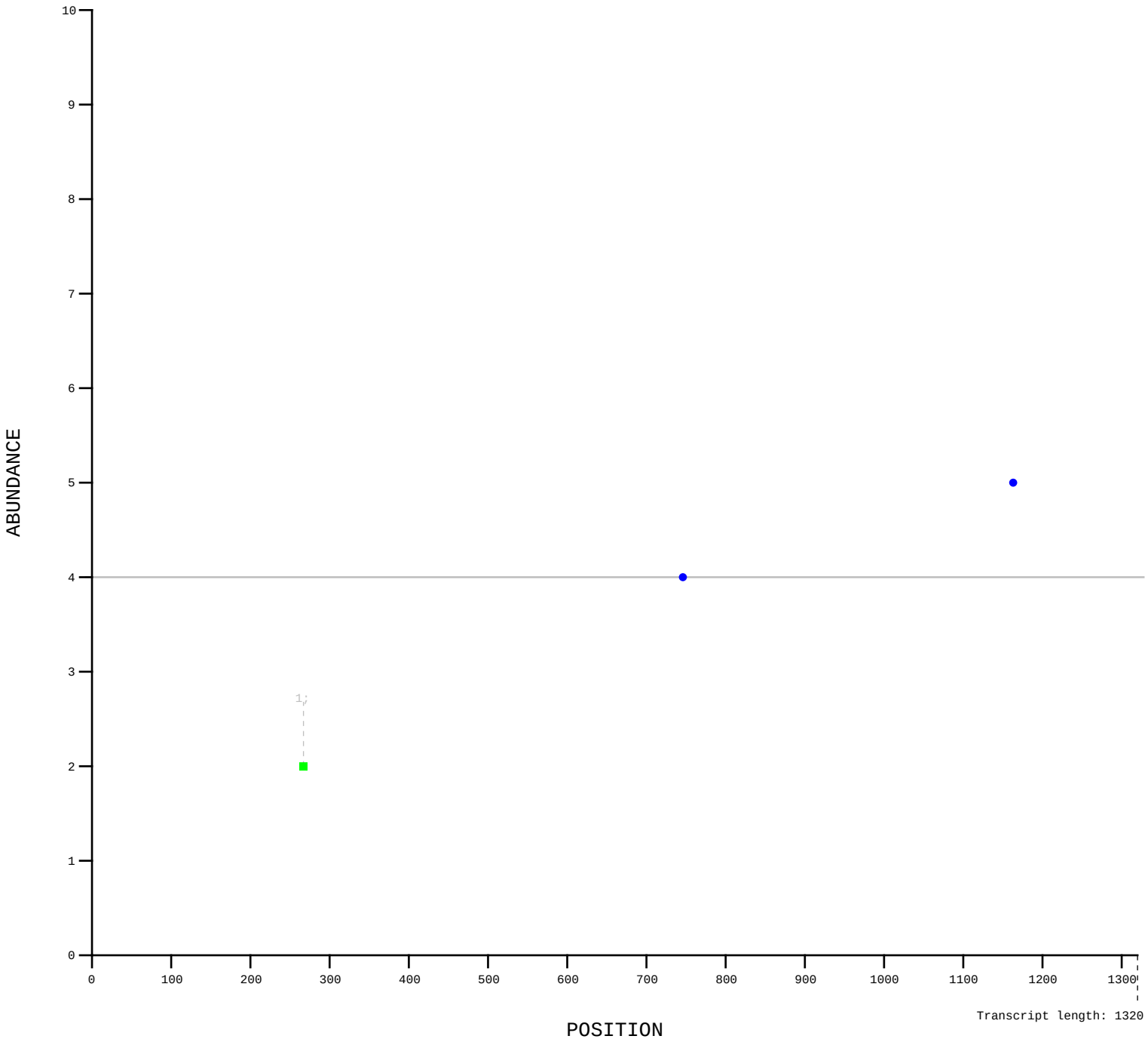
FOXG_13171T0 | Fusarium oxysporum f. sp. lycopersici 4287 hypothetical protein (1101 nt) Note(s): (truncated)



Category: 0 1 2 3 4
Degradome alignment: Median:

3 #1 Position:979 Abundance: 4.00(deg) 25(sRNA)
5' TTAGAGGAGGATAGCTAGA 3' ID:
| |o||||||||| o|| Score: 4.0
3' TGGTACTTTCCTCCTATCAGTCGTCATAGCTT 5' p-value: 0.0

FOXG_12791T0 | Fusarium oxysporum f. sp. lycopersici 4287 actin (1320 nt)



Category: 0 1 2 3 4
Degradome alignment: Median:

3 #1 Position:267 Abundance: 2.00(deg) 11(sRNA)
5' AGAATCTGCTATCGGTTTAGC 3' ID:
|||| ||||||||| o|o| | Score: 4.0
3' GAGGTCTTCGACGATAGCGGAGTAGCGGTTAT 5' p-value: 0.0