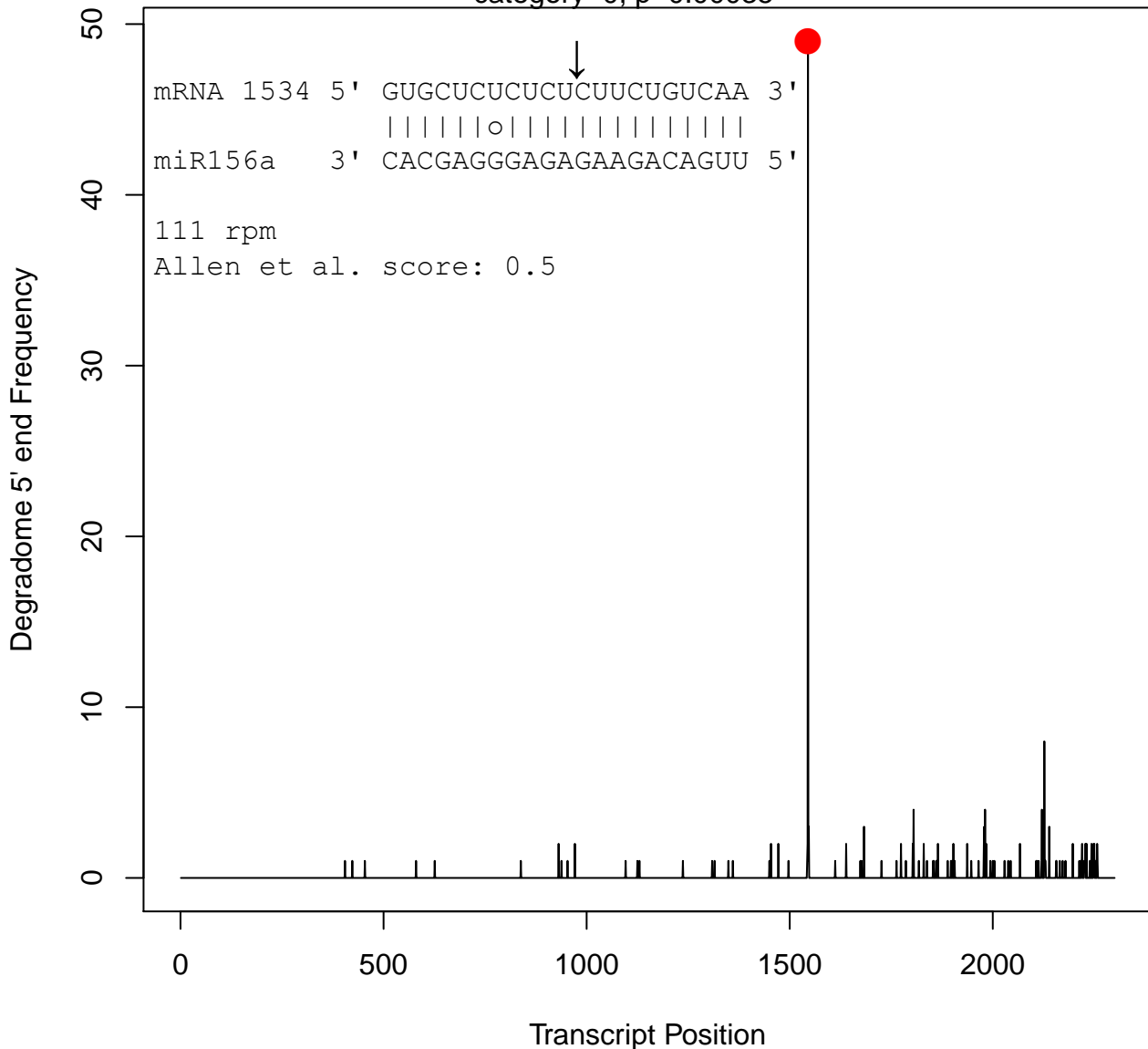


VIT\_01s0010g03710

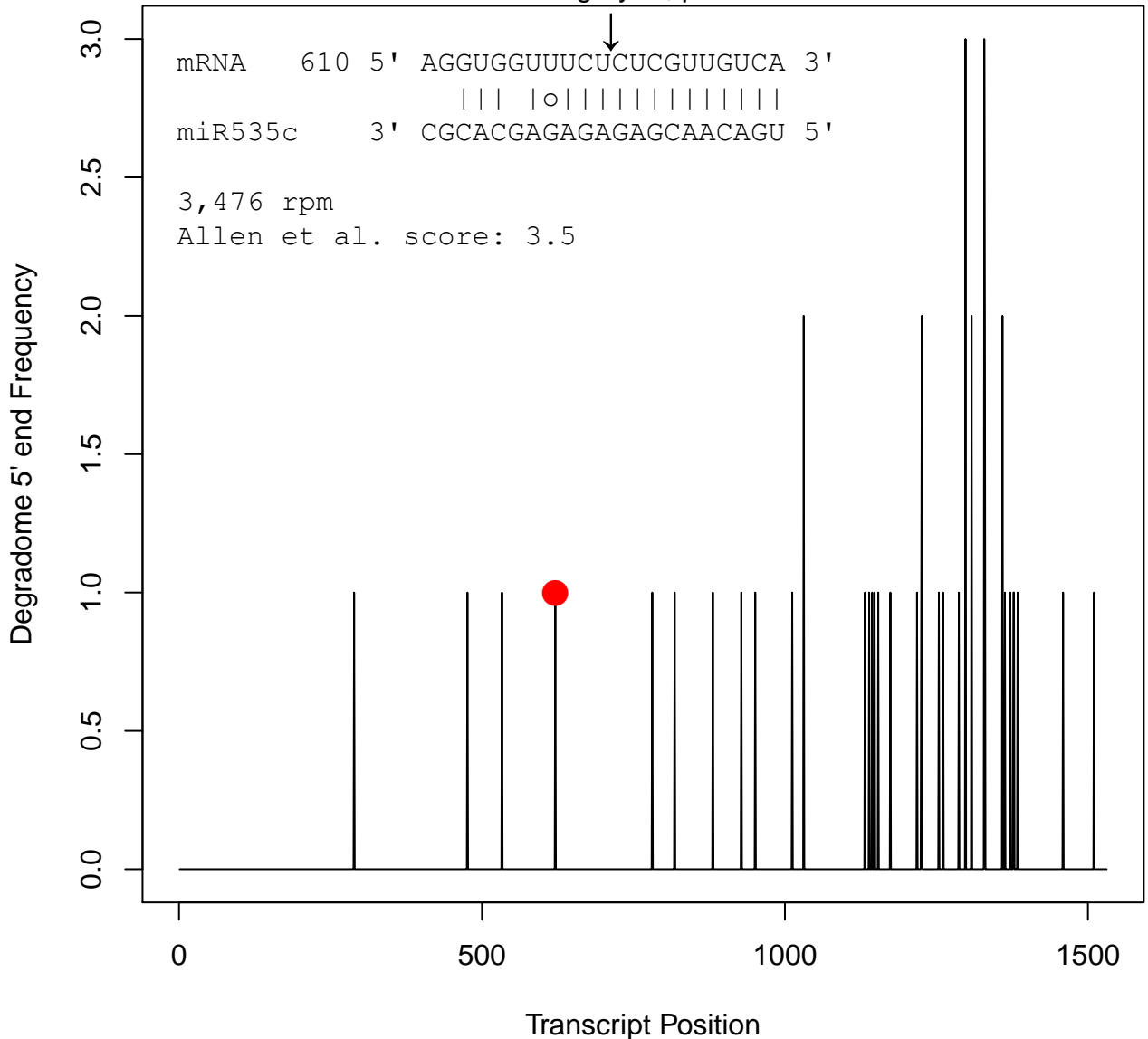
# SQUAMOSA PROMOTER-BINDING PROTEIN 10-like

category=0, p=0.00035



**VIT\_05s0051g00930**  
**DNA primase, large subunit**

category=4, p=0.11

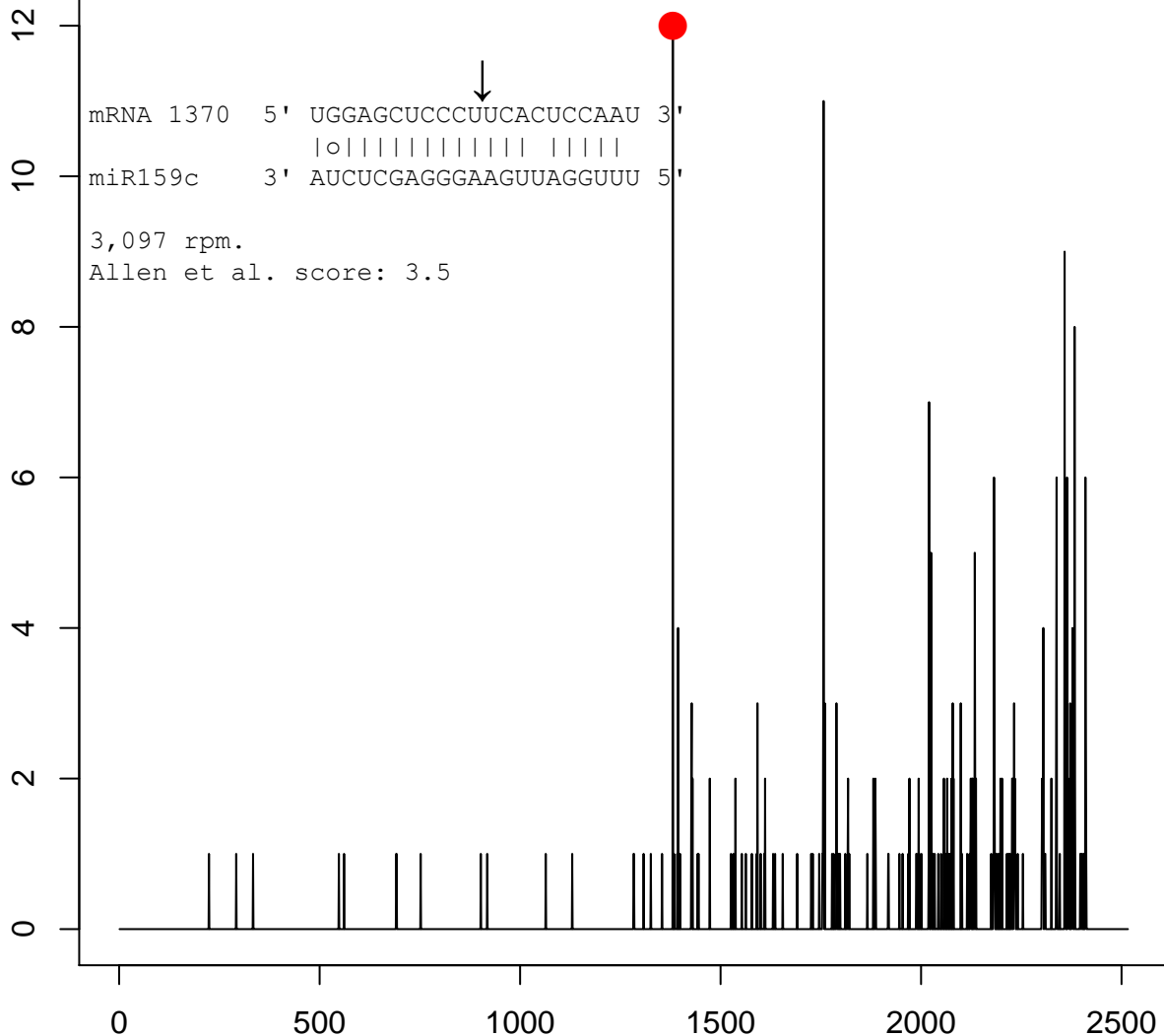


# VIT\_13s0067g01630

## MYB65

category=0, p=0.0007

Degradome 5' end Frequency

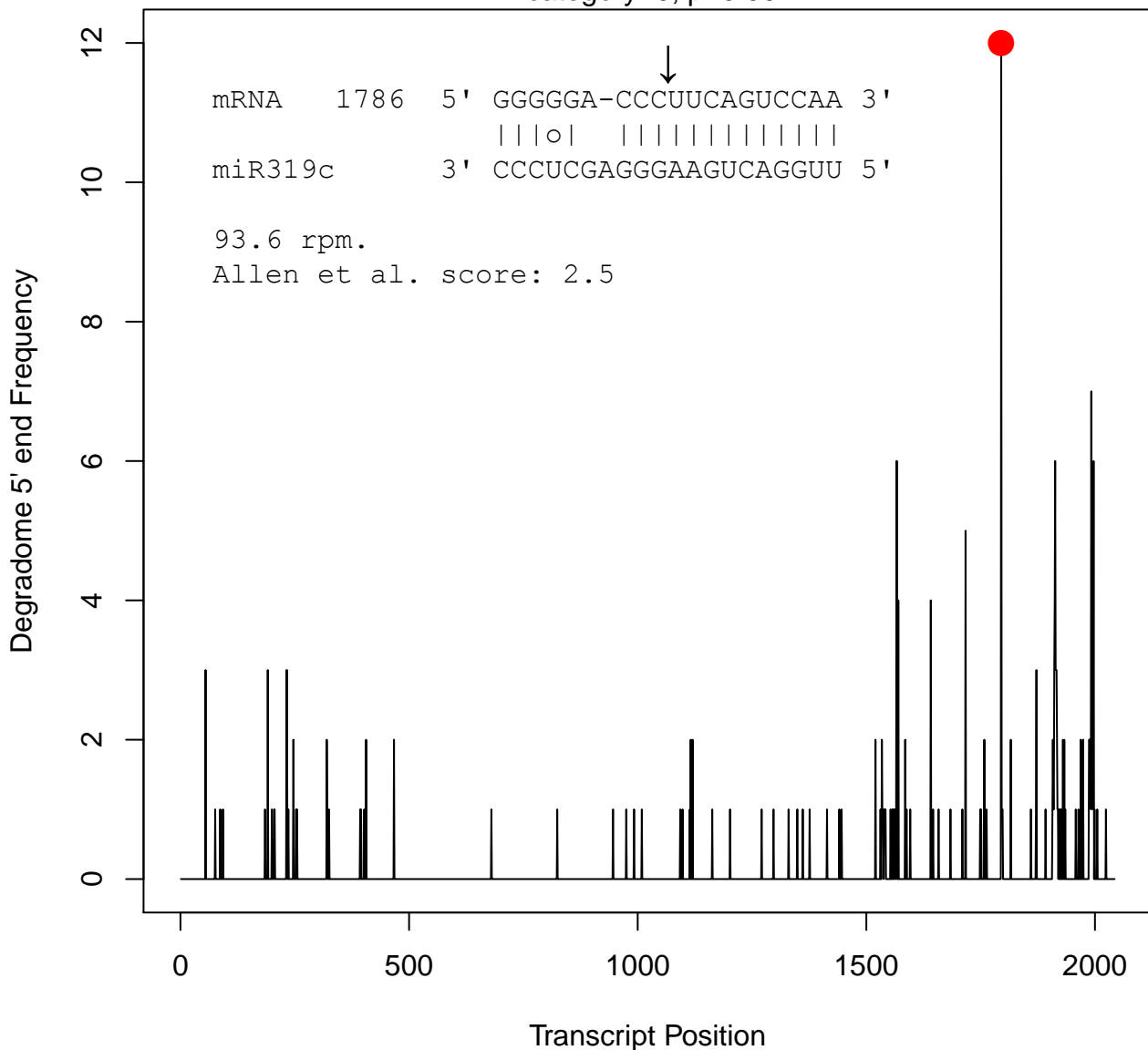


Transcript Position

# VIT\_10s0003g03910

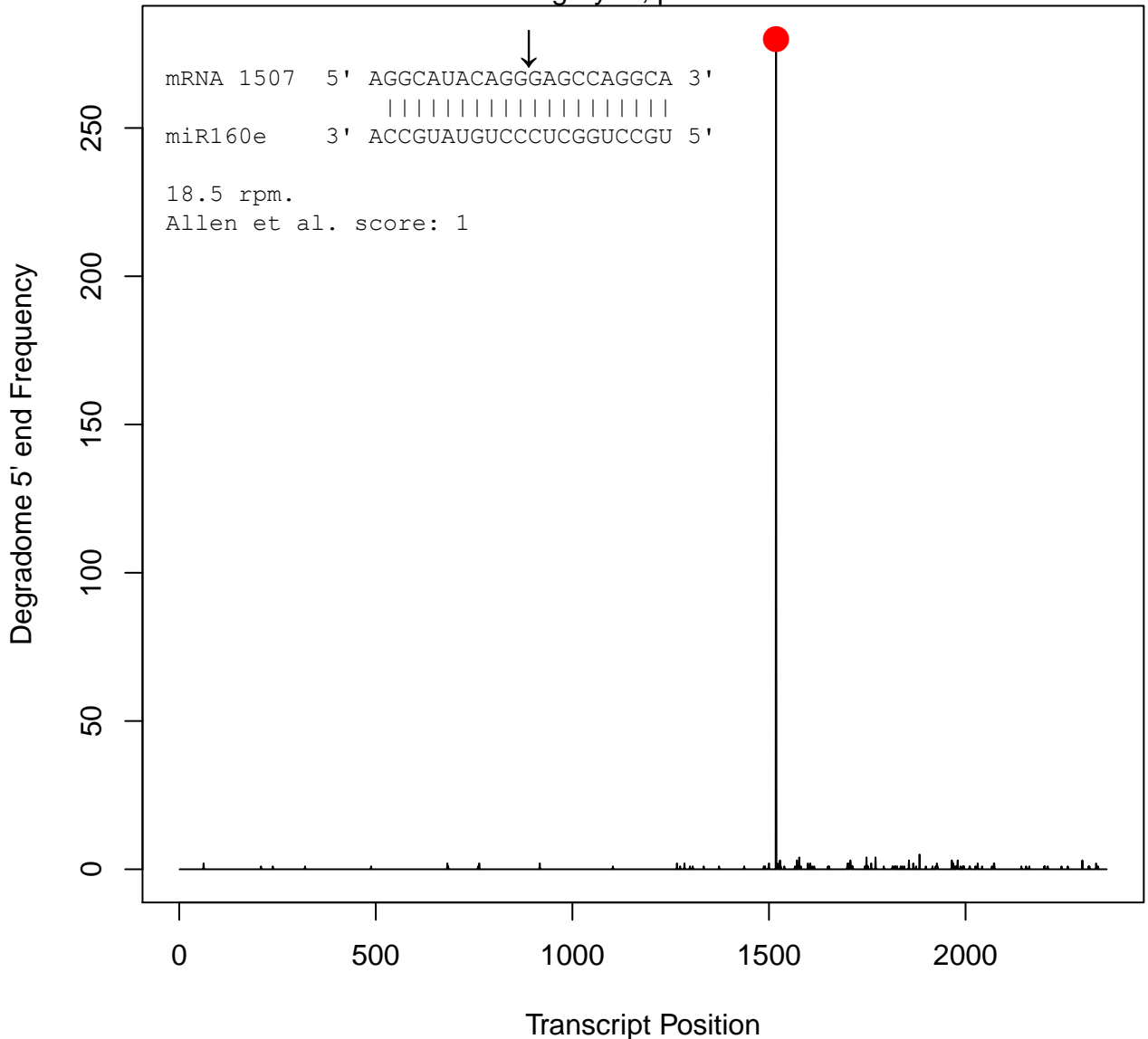
## TCP family transcription factor 24

category=0, p=0.002



**VIT\_13s0019g04380**  
**Auxin response factor 10**

category=0, p=0.00035

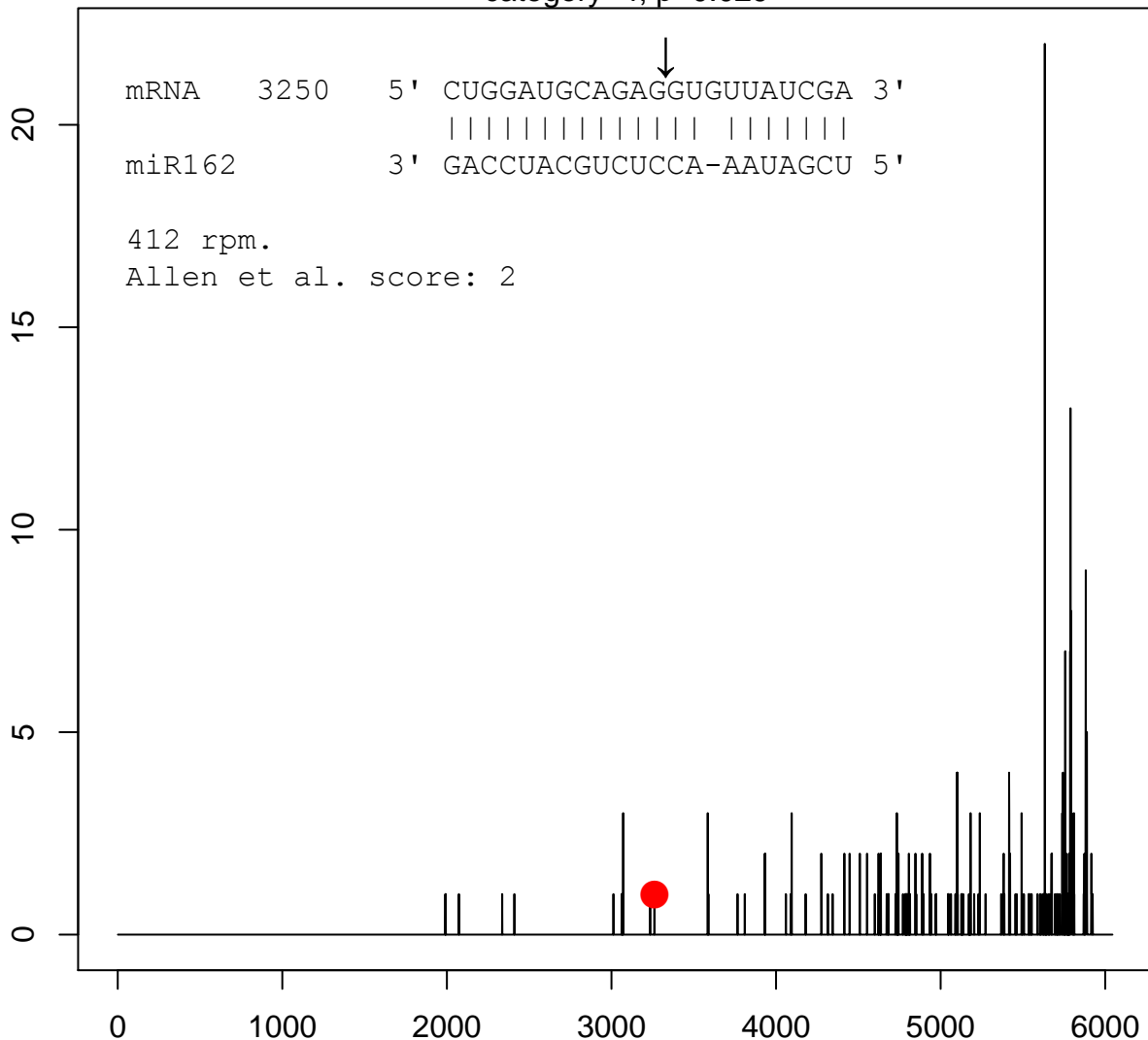


VIT\_15s0048g02380

DICER1

category=4, p=0.029

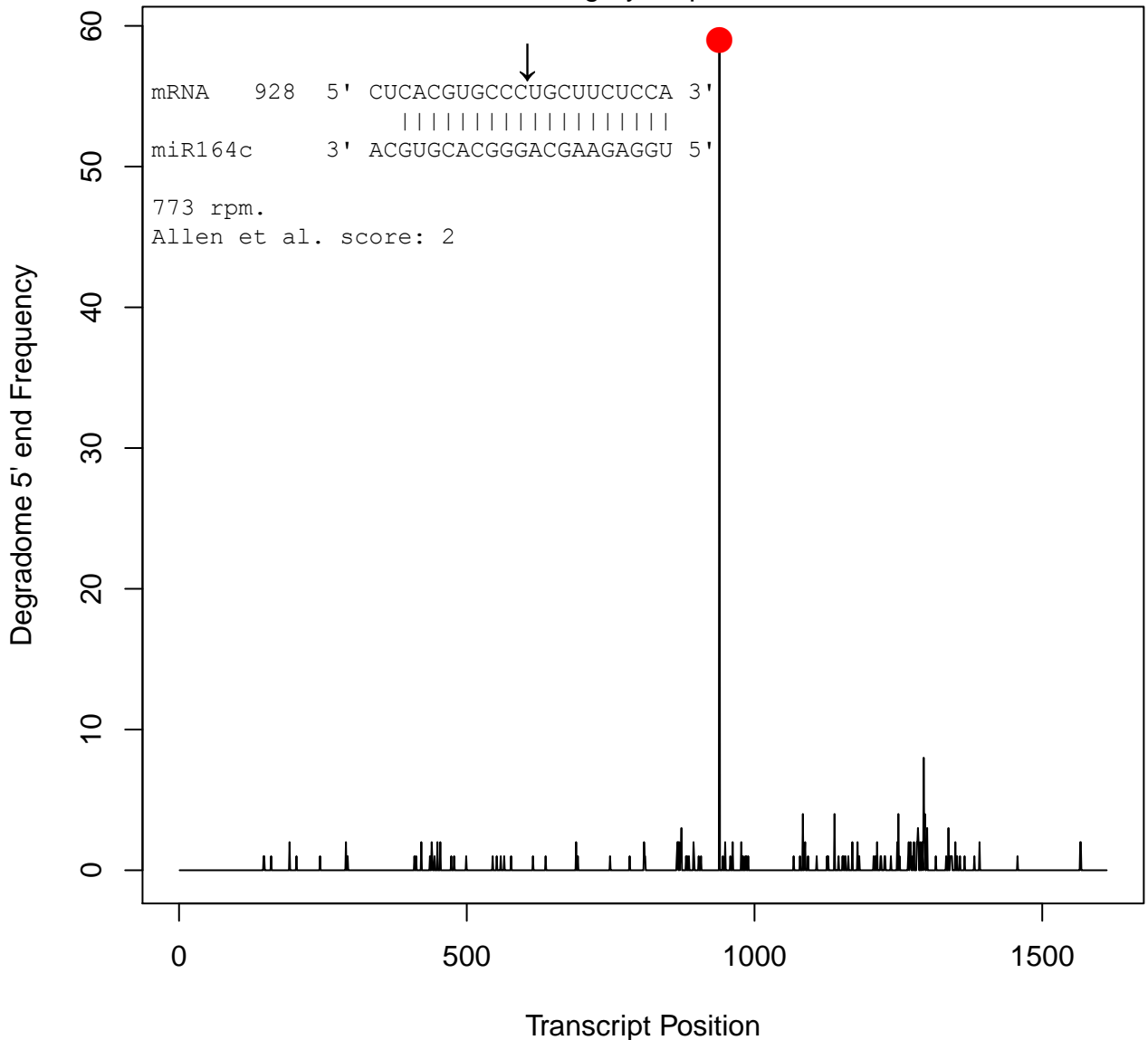
Degradome 5' end Frequency



Transcript Position

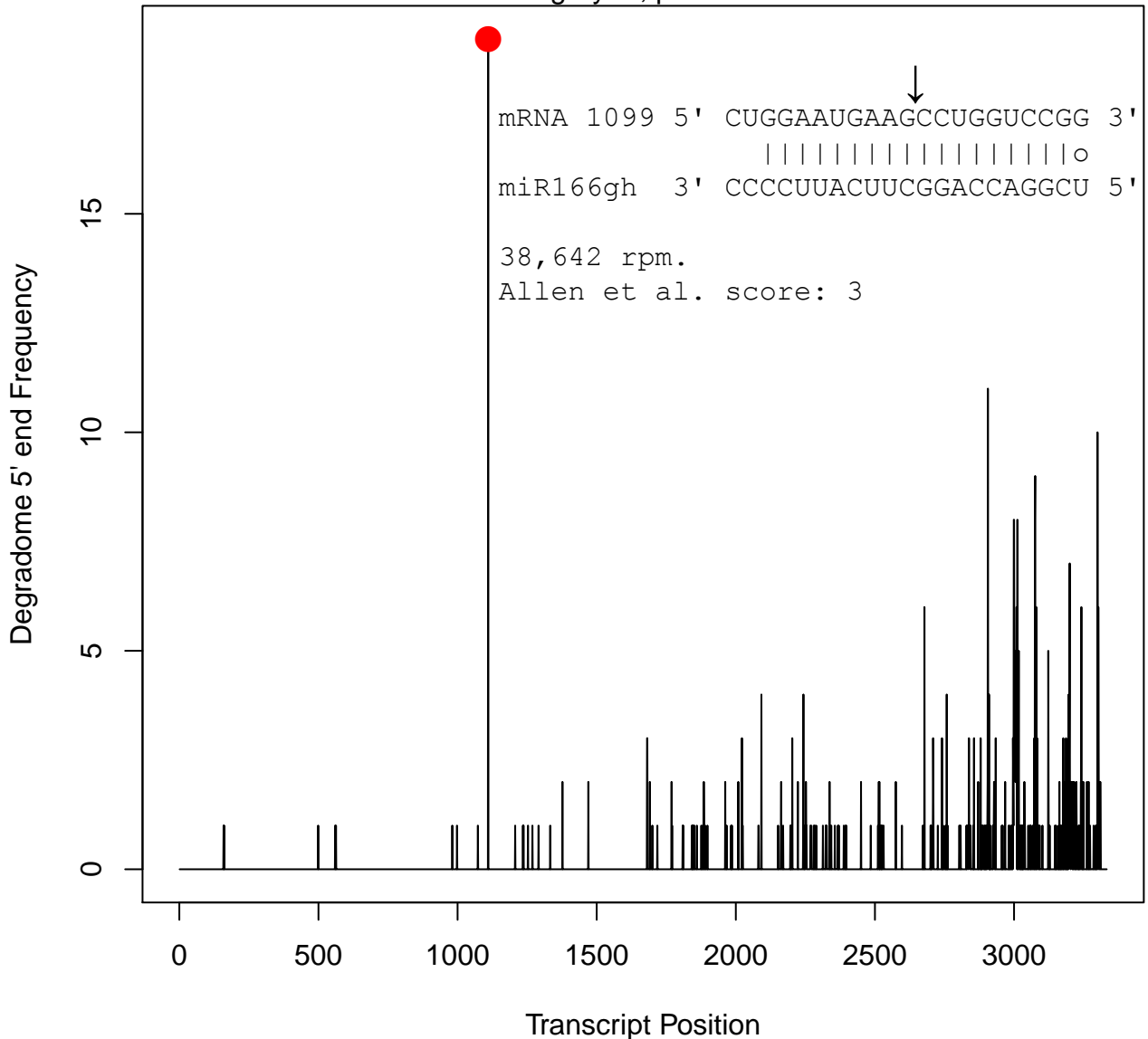
VIT\_17s0000g06400  
NAC domain containing protein 100 VvNAC05

category=0, p=0.0007



**VIT\_09s0002g03740**  
**ATHB15-like; VVHB8\_2**

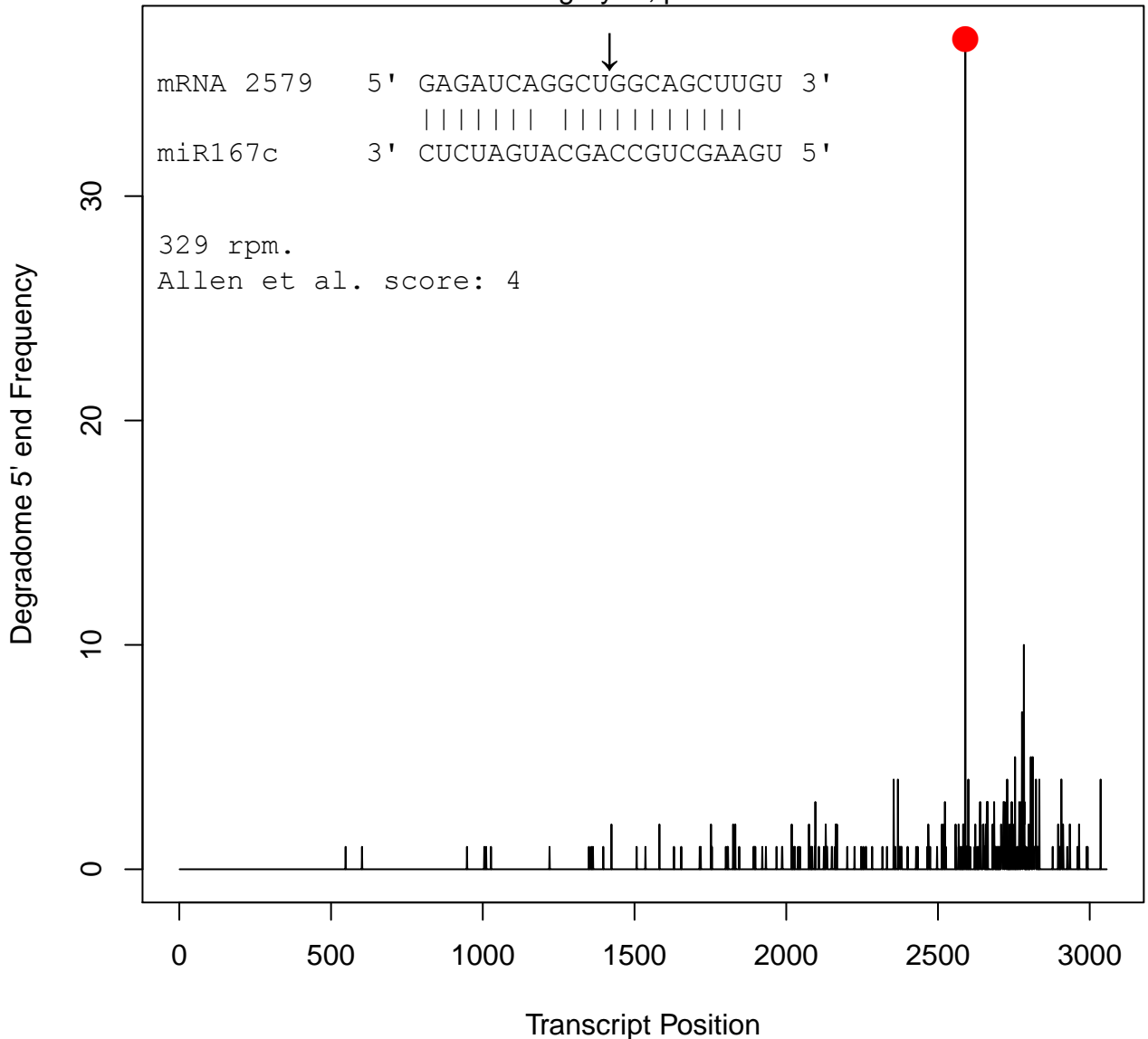
category=0, p=0.00035





**VIT\_10s0003g04100**  
**Auxin response factor 6**

category=0, p=0.00035

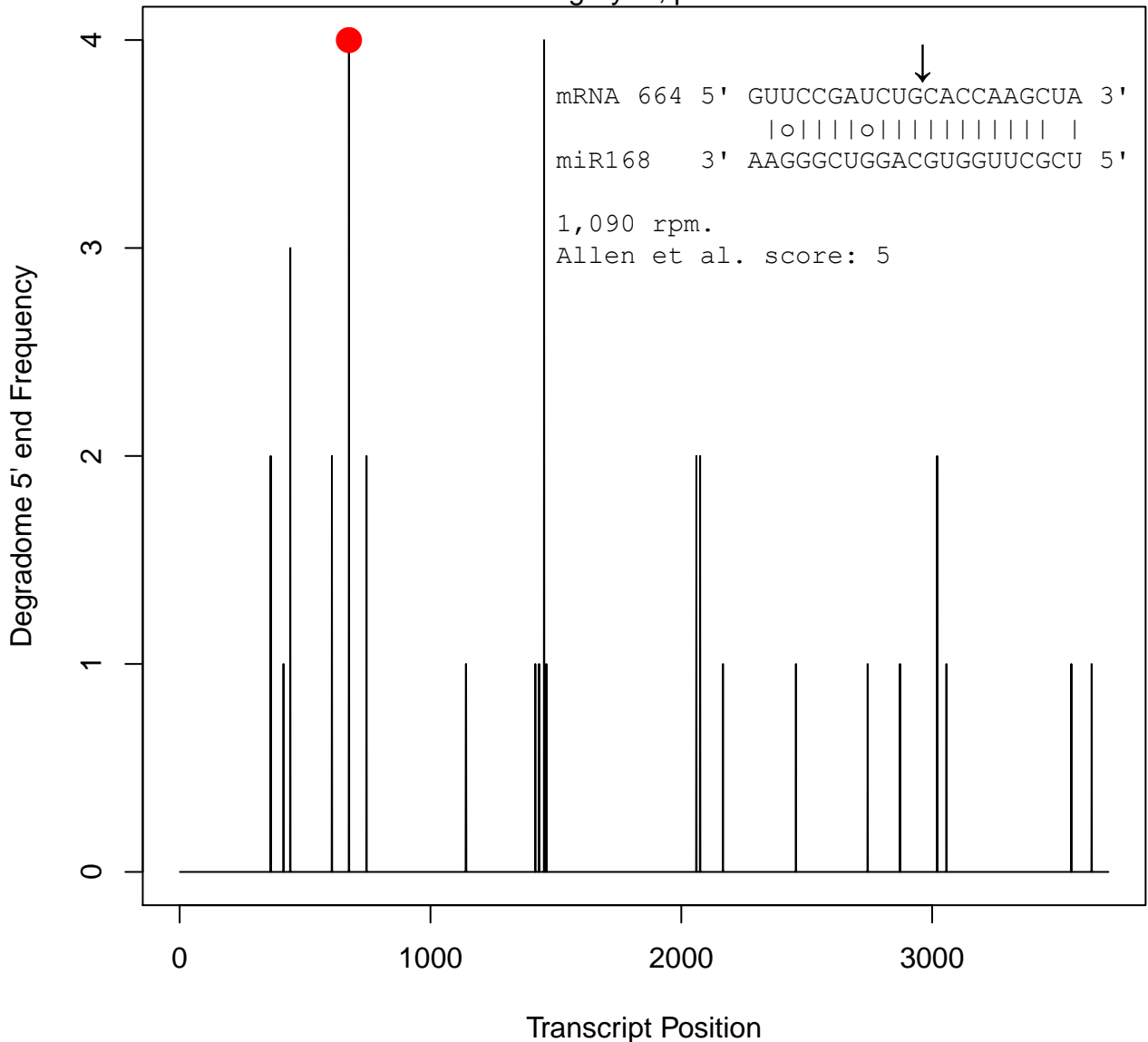


VIT\_17s0053g00680

## ARGONAUTE1

pseudo-degradome sRNA, low UV control, -3WAV

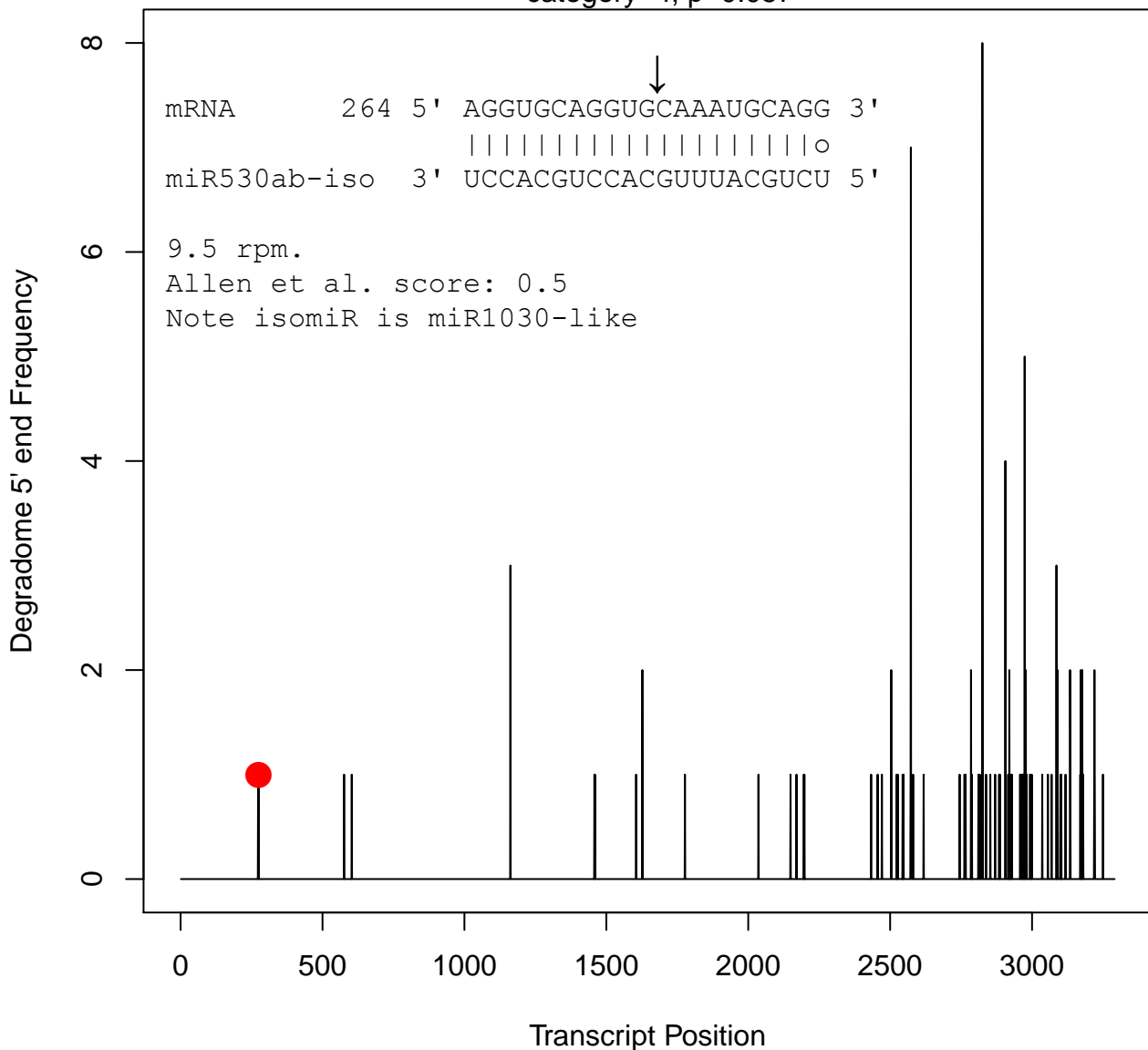
category=1, p=0.0001



# VIT\_05s0020g04860

## Plus-3 domain

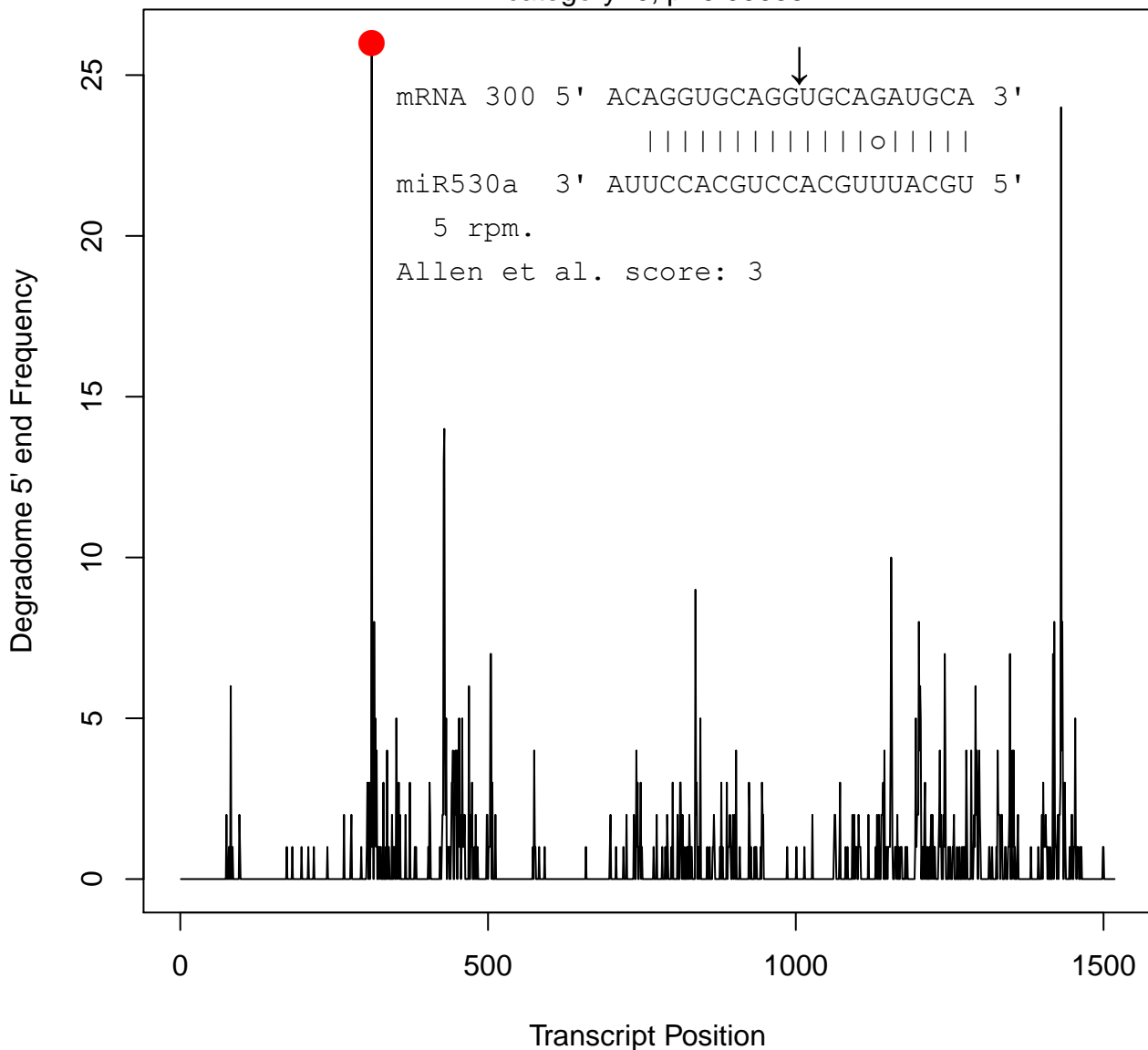
validated in UV pseudo-degradome sRNA libraries, category 2, p=0.02  
category=4, p=0.057



VIT\_06s0080g00400

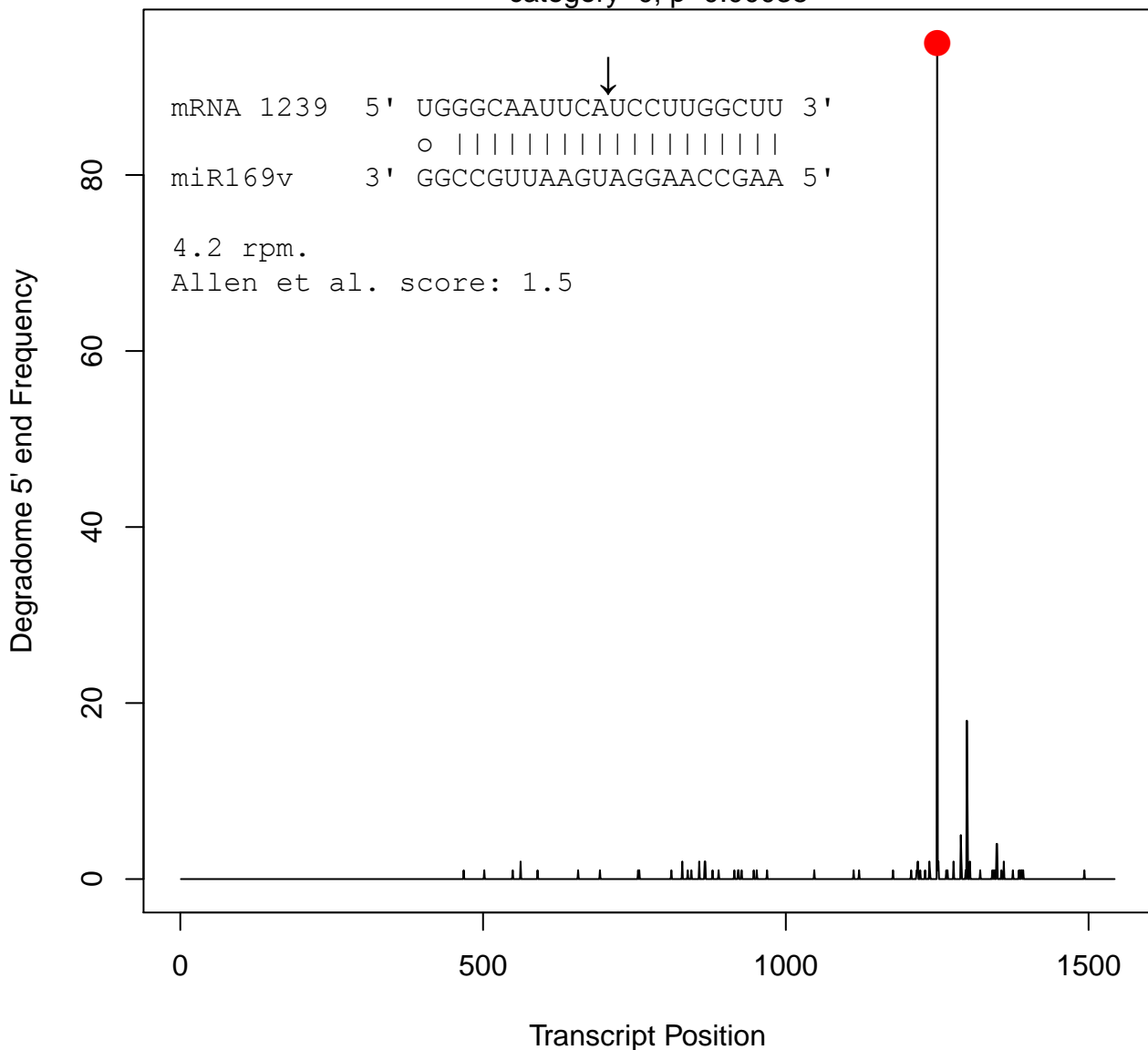
**Ribosomal protein L10A**

validated in UV pseudo-degradome sRNA libraries, category 4,  $p=0.02$   
category=0,  $p=0.00035$



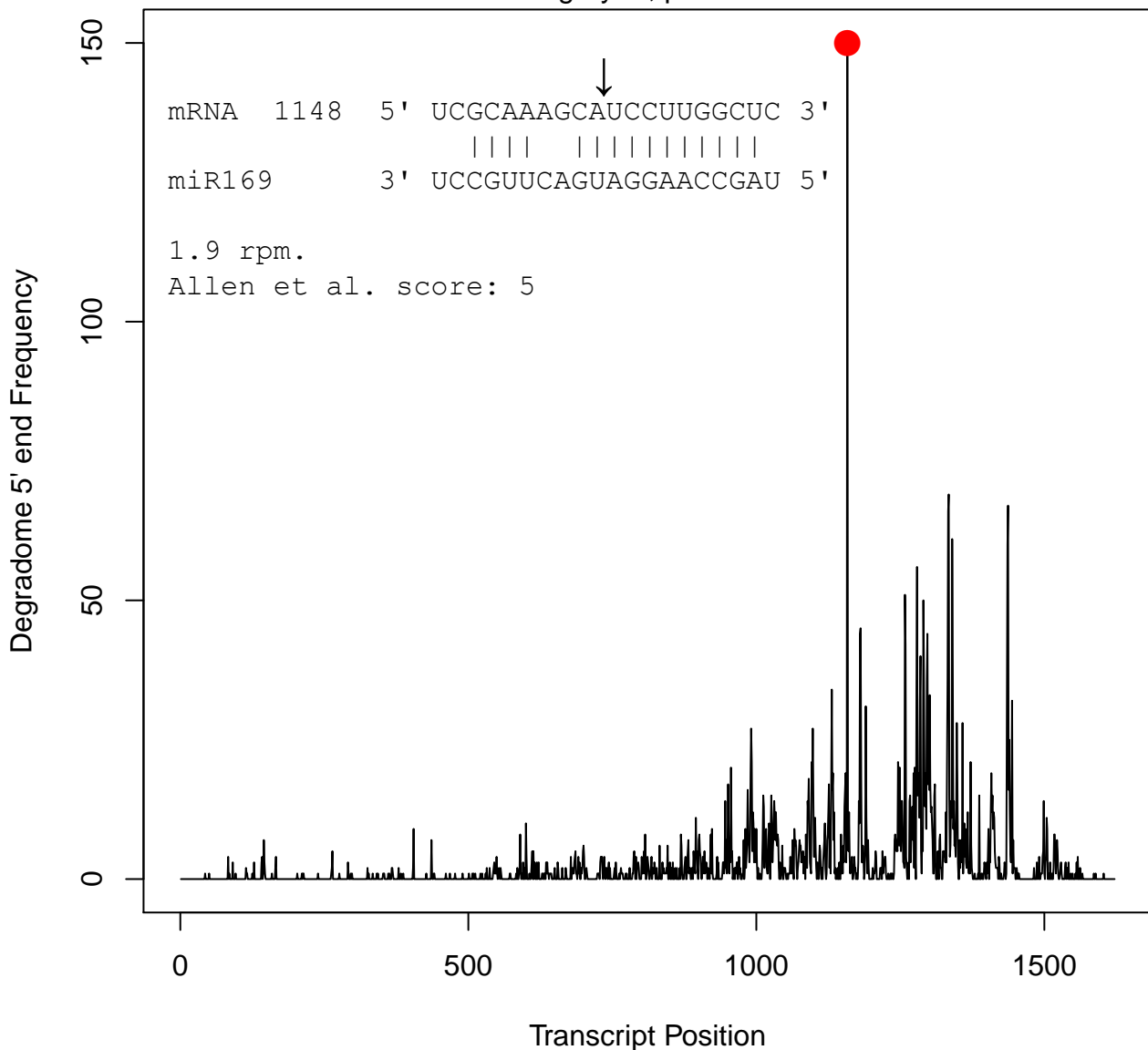
**VIT\_11s0016g01480**  
**Nuclear transcription factor Y subunit A-3**

category=0, p=0.00035



**VIT\_01s0011g05560**  
**JAZ3\_1/VvJAZI\_TIFY transcription corepressor**

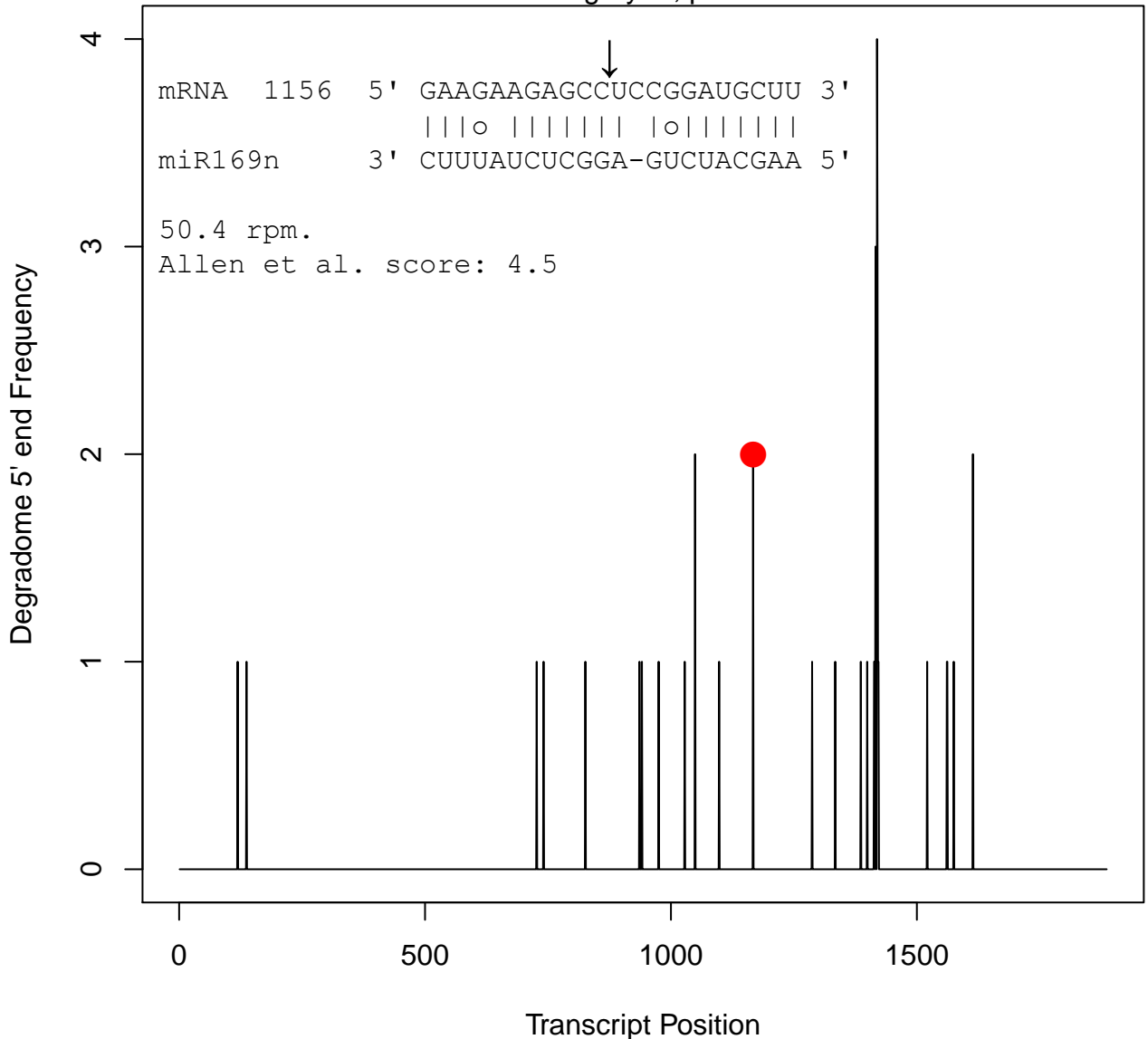
category=0, p=0.0006



# VIT\_09s0070g00470

## Zinc finger C-x8-C-x5-C-x3-H type

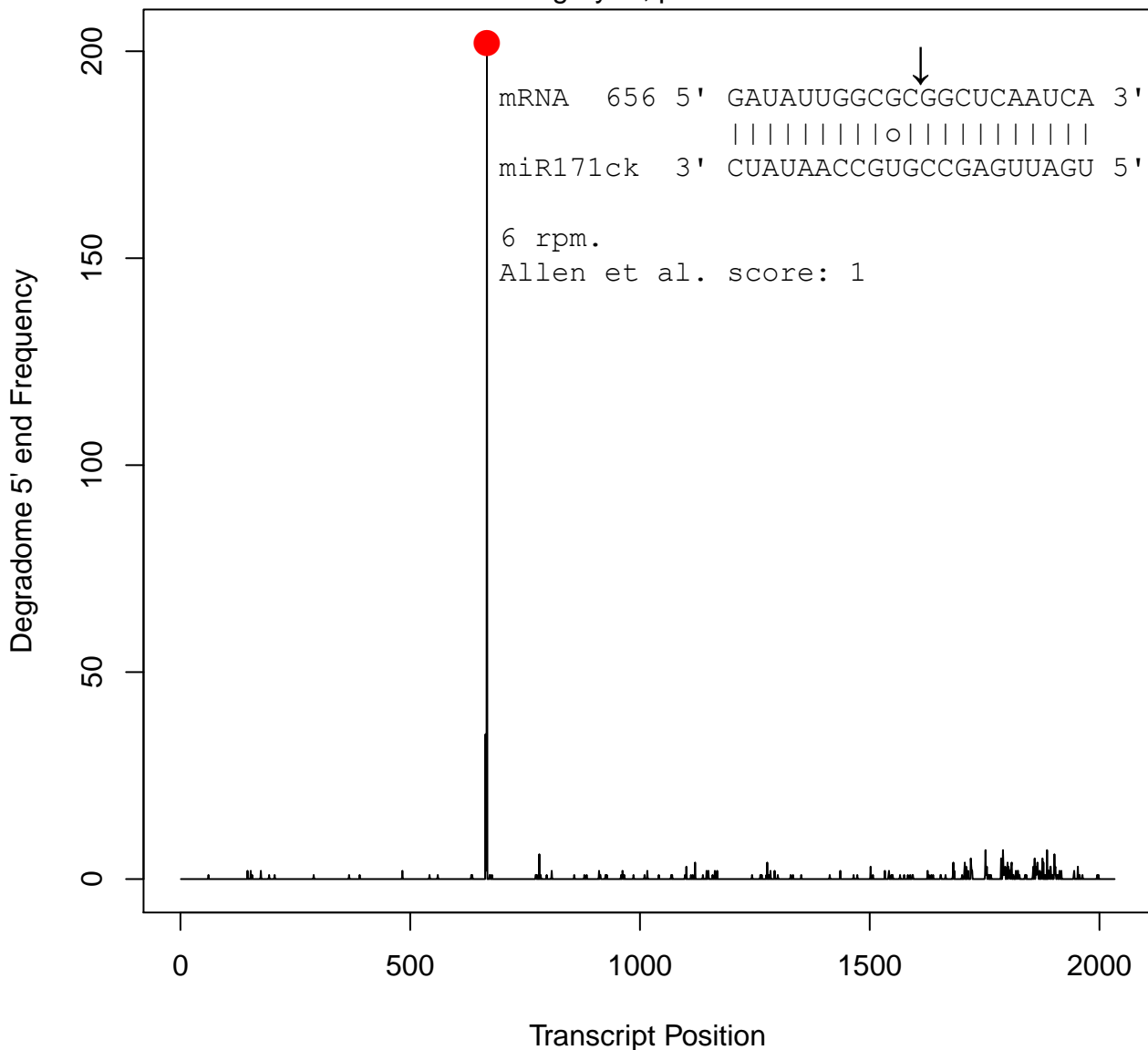
category=2, p=0.08



VIT\_04s0023g01380

GRAS family transcription factor scarecrow-like4

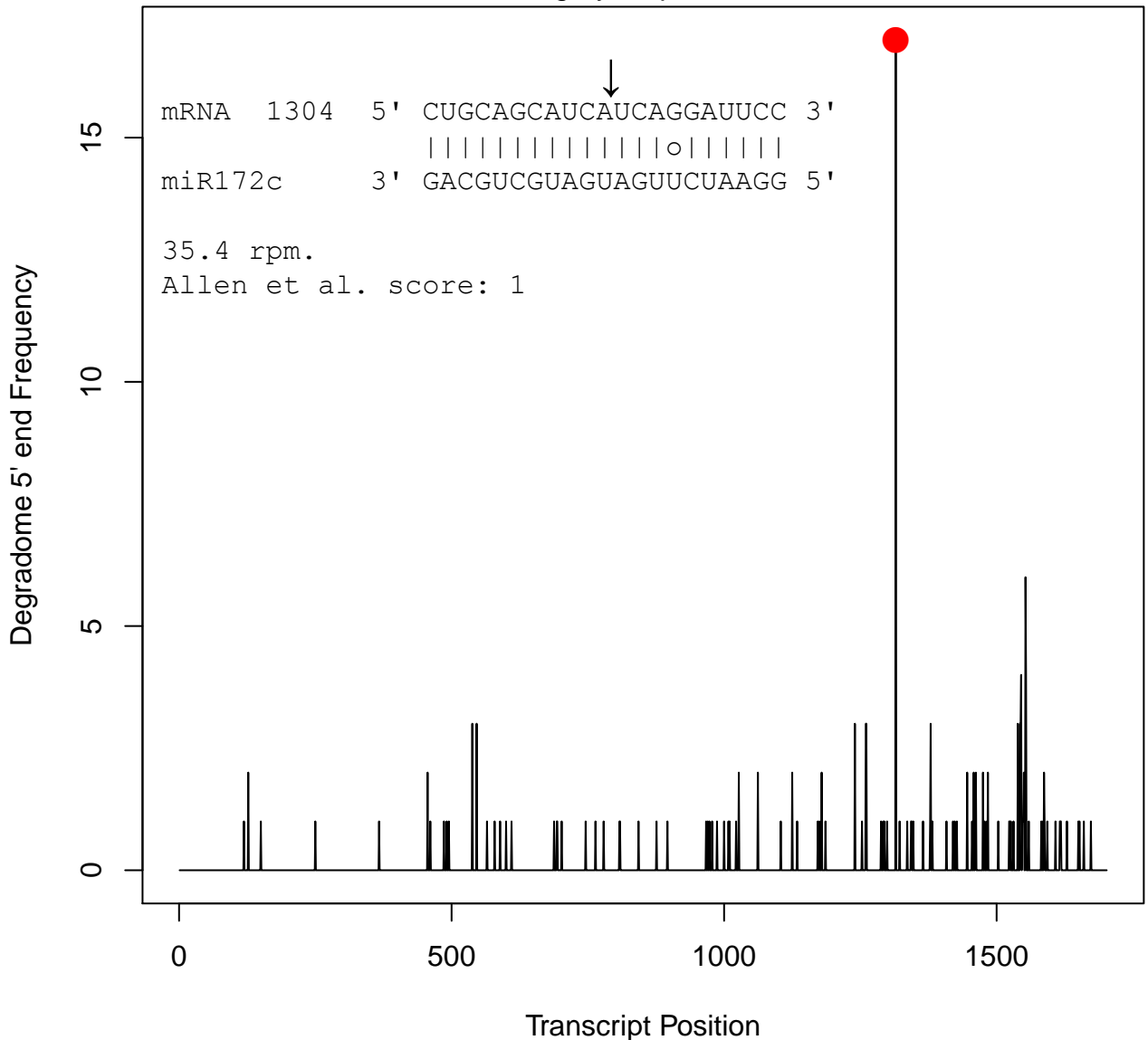
category=0, p=0.00035





**VIT\_13s0019g03550**  
**APETALA2-like floral homeotic protein**

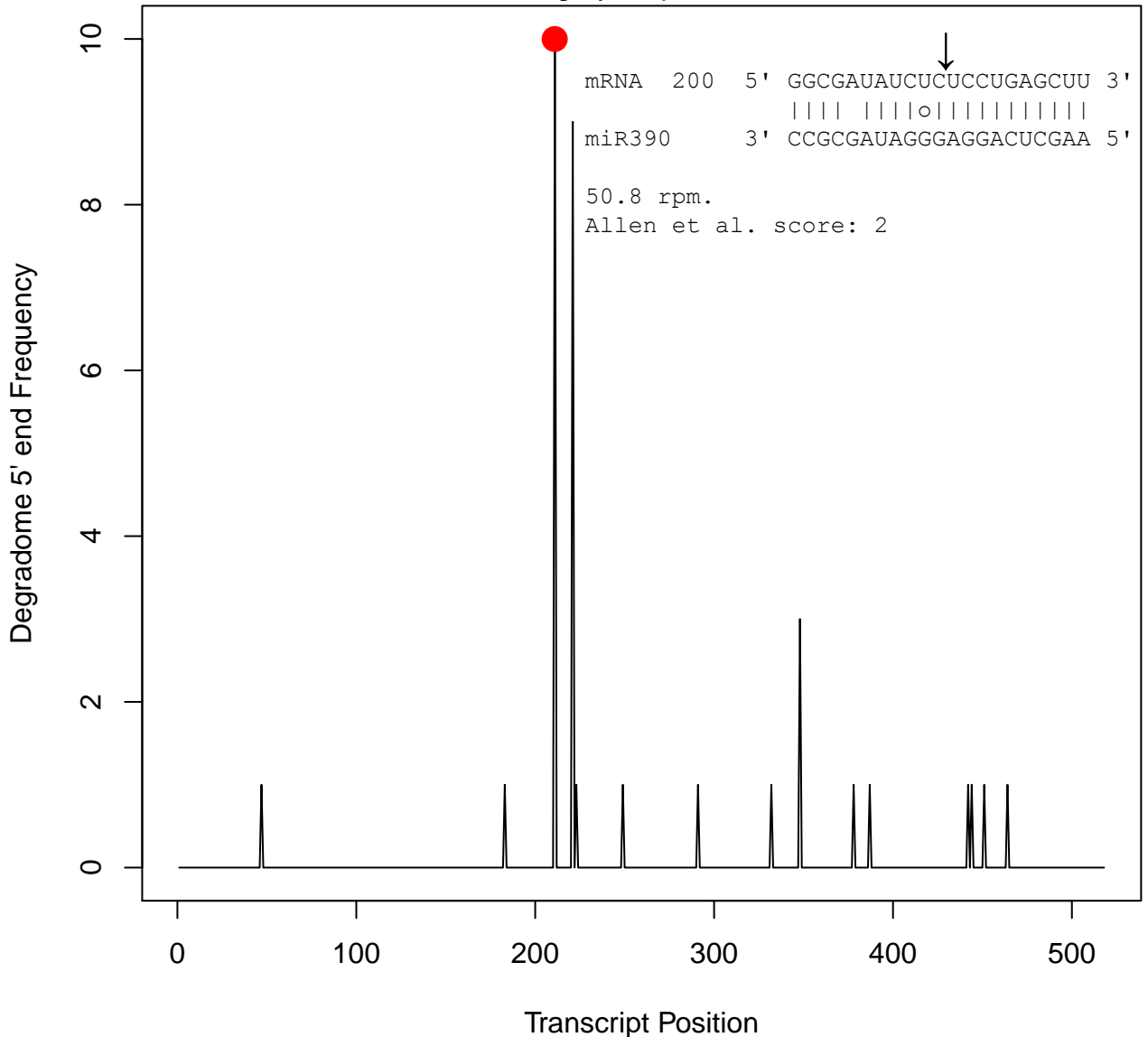
category=0, p=0.00035



VIT\_12s0059g01410

unchar 66 AA peptide; TAS3-like homology to AT5G57735/TASIR-ARF

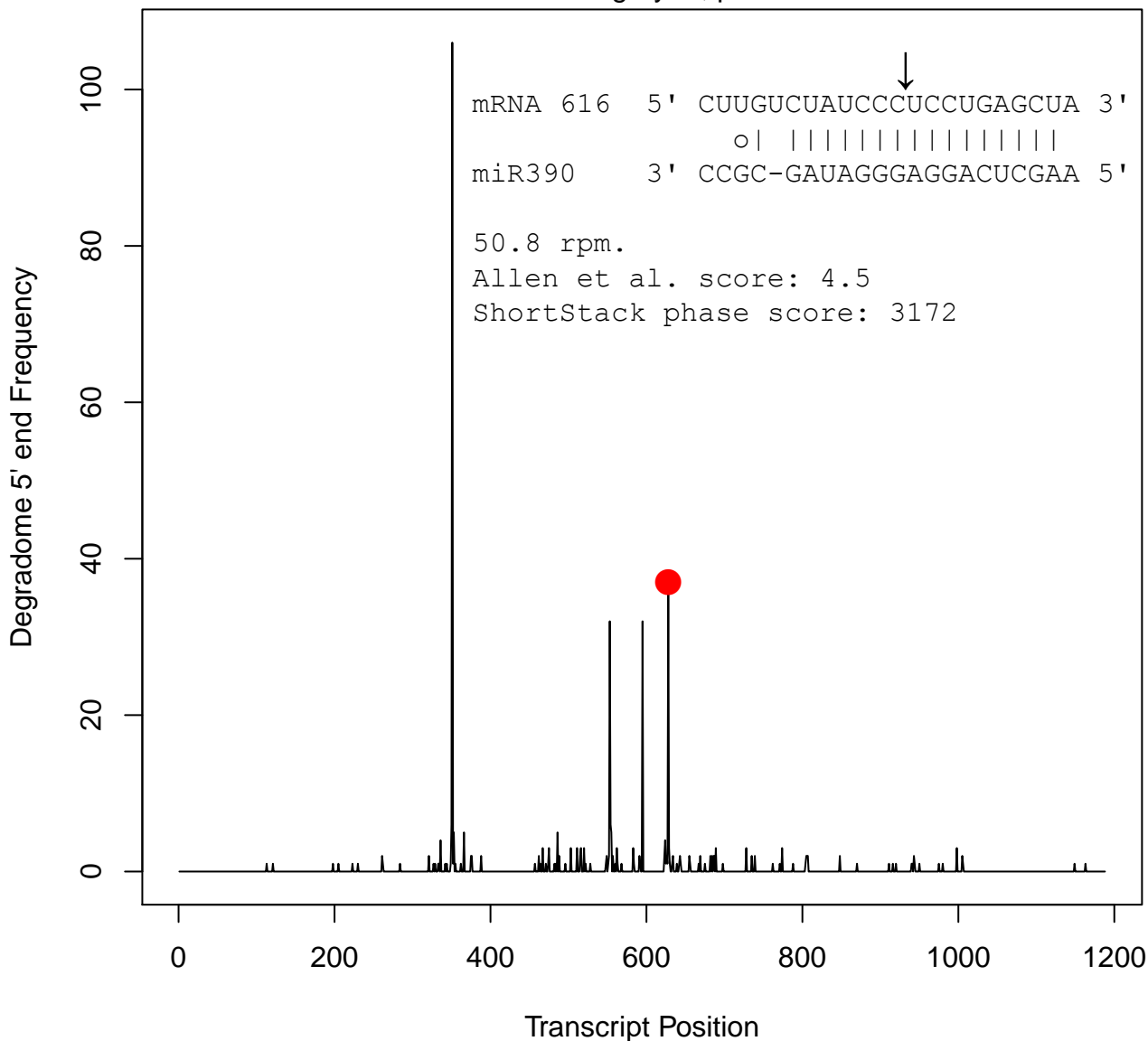
category=0, p=0.0007



VIT\_05s0077g00540

unchar. 126 AA peptide; homology to AT3G17185/TAS3

category=2, p=0.13

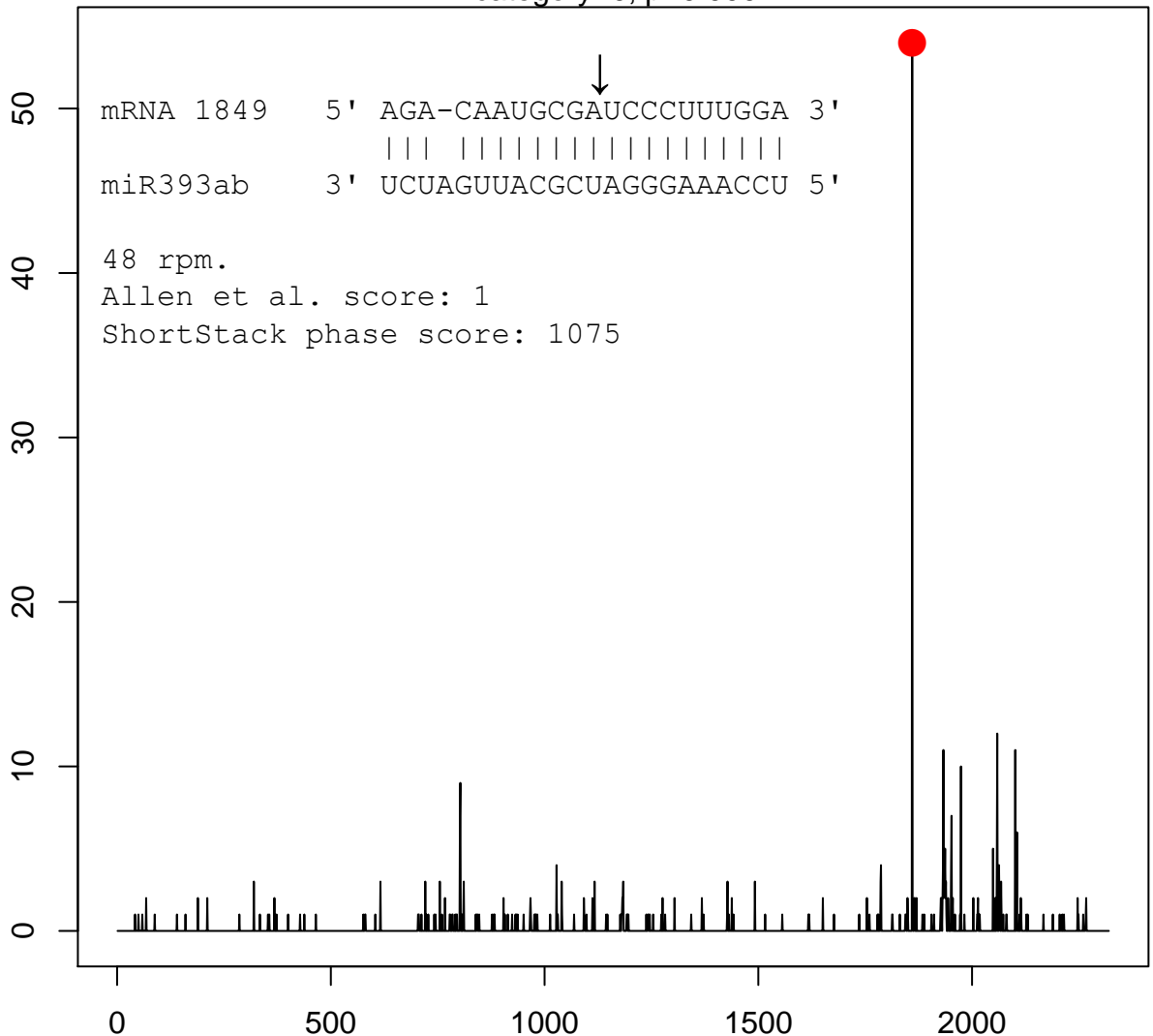


VIT\_14s0030g01240

TIR1-like

category=0, p=0.0007

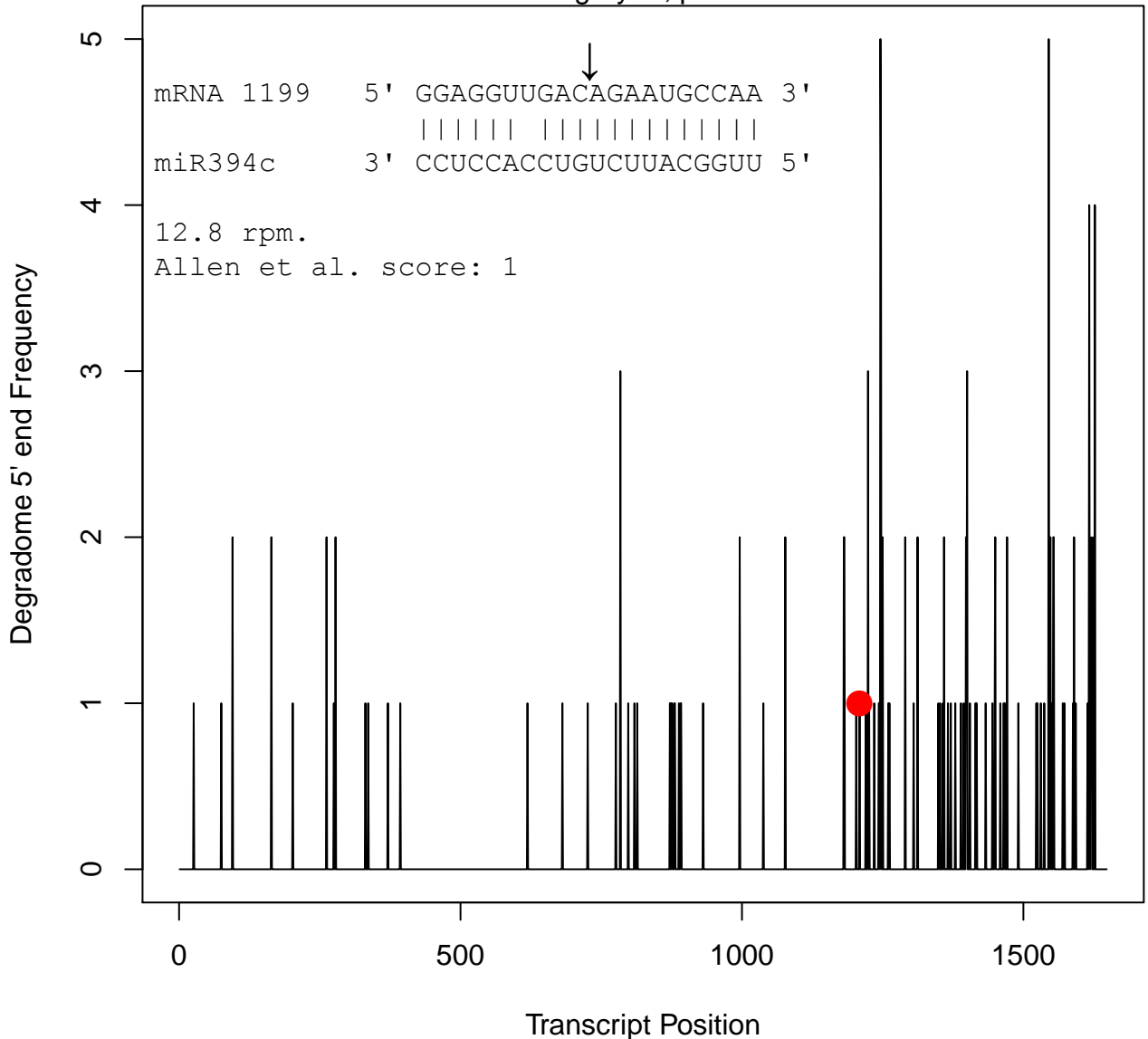
Degradome 5' end Frequency



Transcript Position

**VIT\_01s0010g03730**  
**F-Box X6, At1g27340-like**

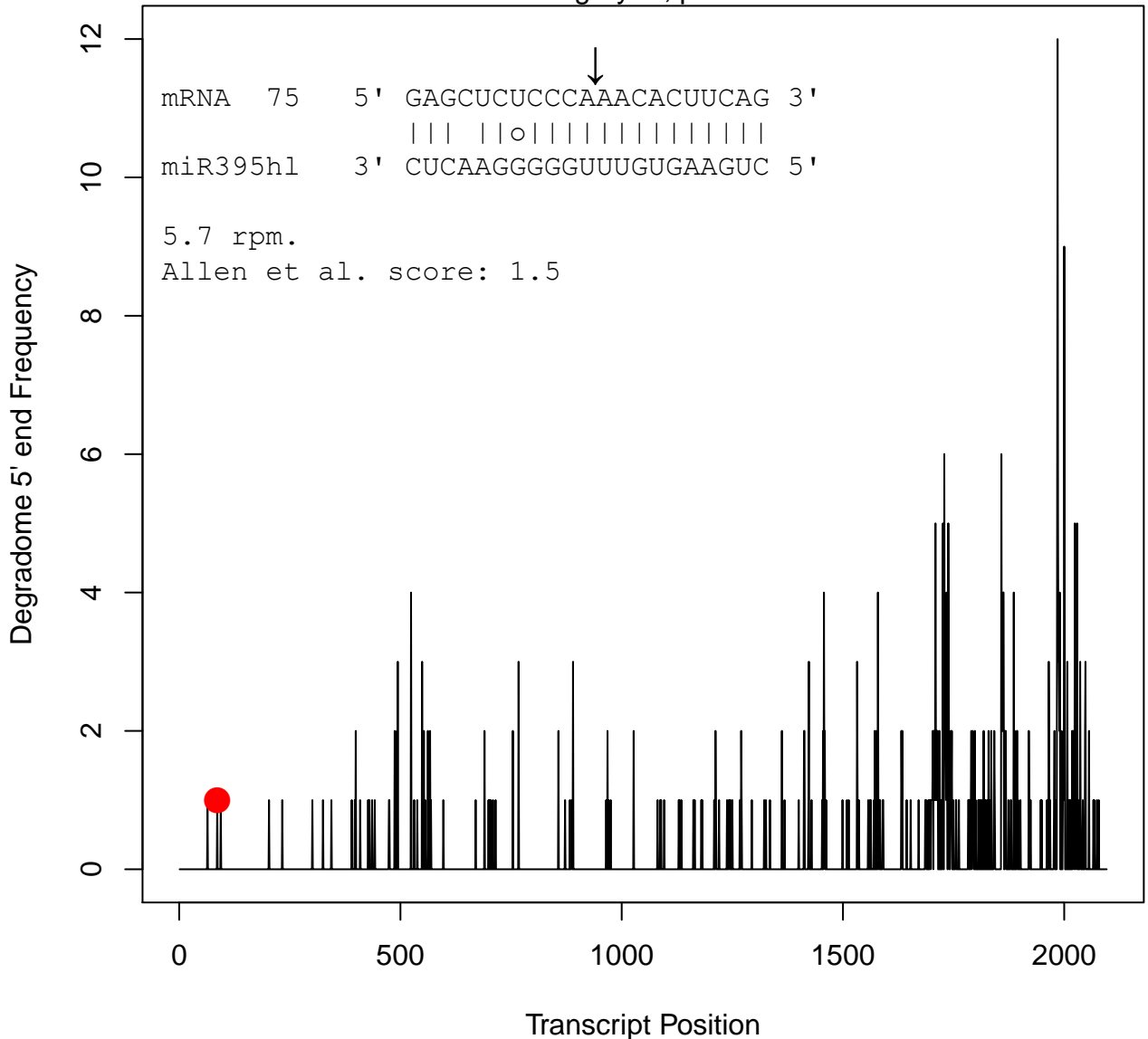
category=4, p=0.029



# VIT\_18s0001g04890

## AST68, Low affinity sulphate transporter

category=4, p=0.029

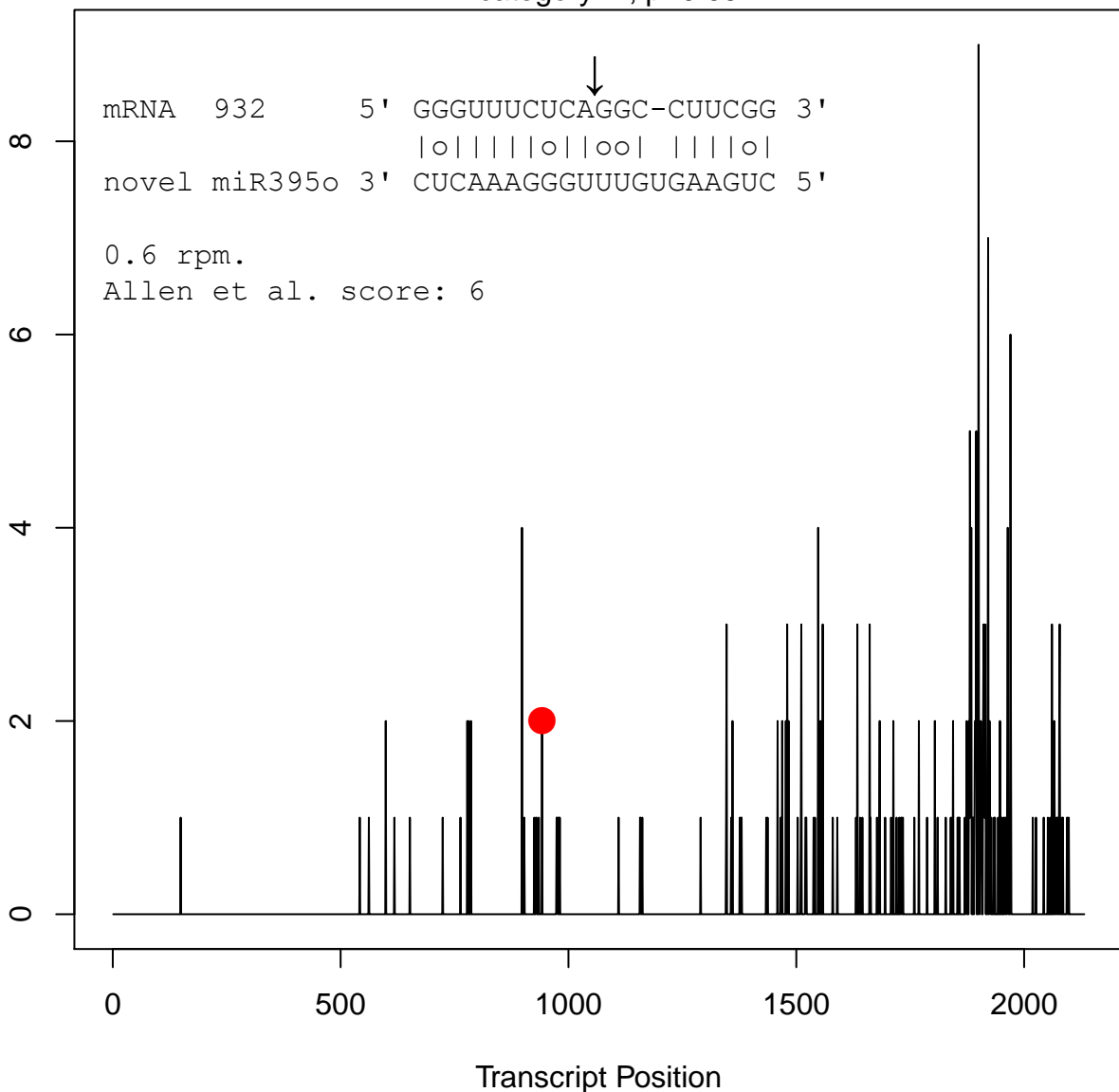


# VIT\_12s0055g00910

## Kelch repeat-containing F-box protein

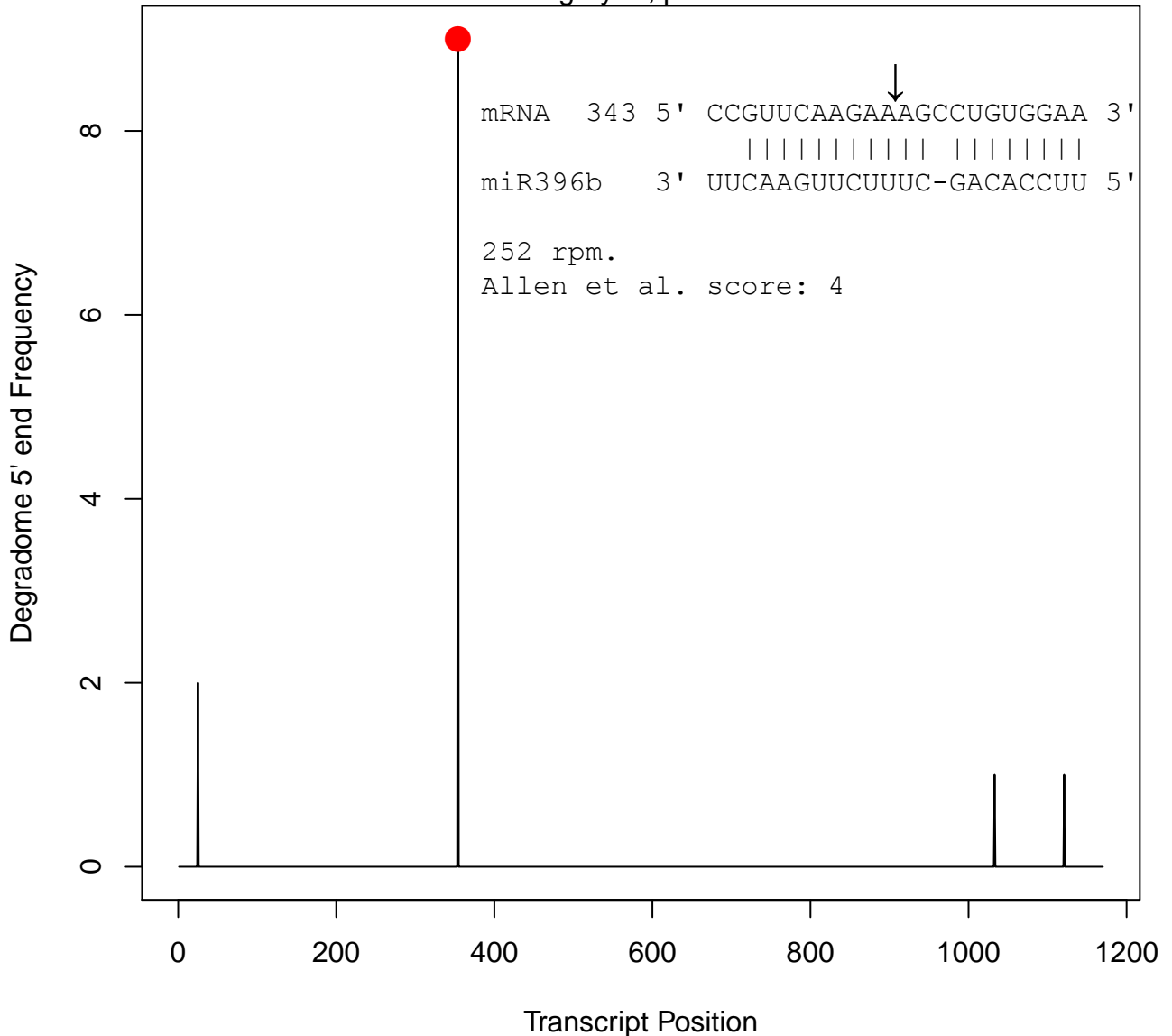
category=2, p=0.09

Degradome 5' end Frequency



**VIT\_11s0016g01250**  
**Growth Regulating Factor 6, GRF6**

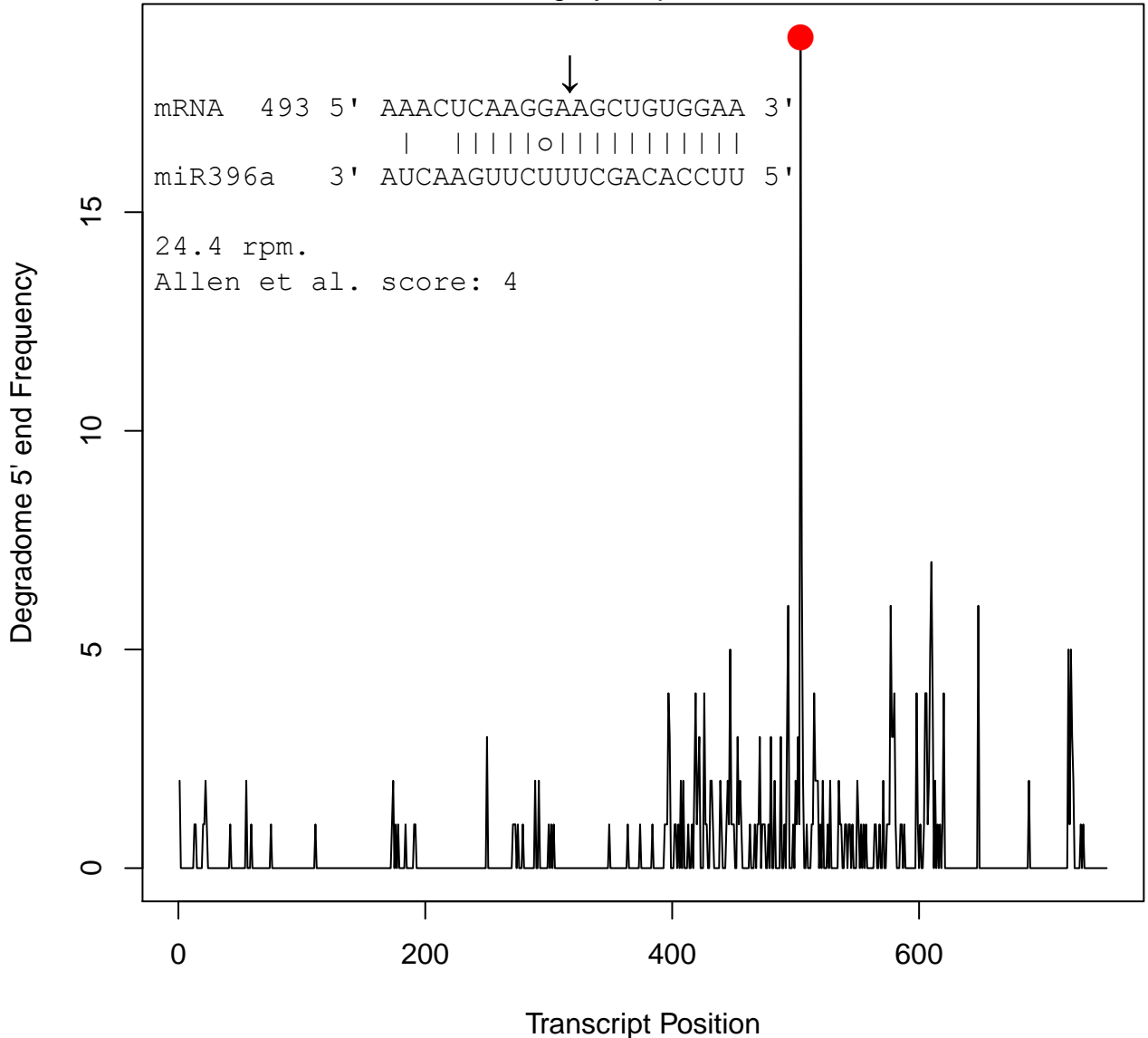
category=0, p=0.002





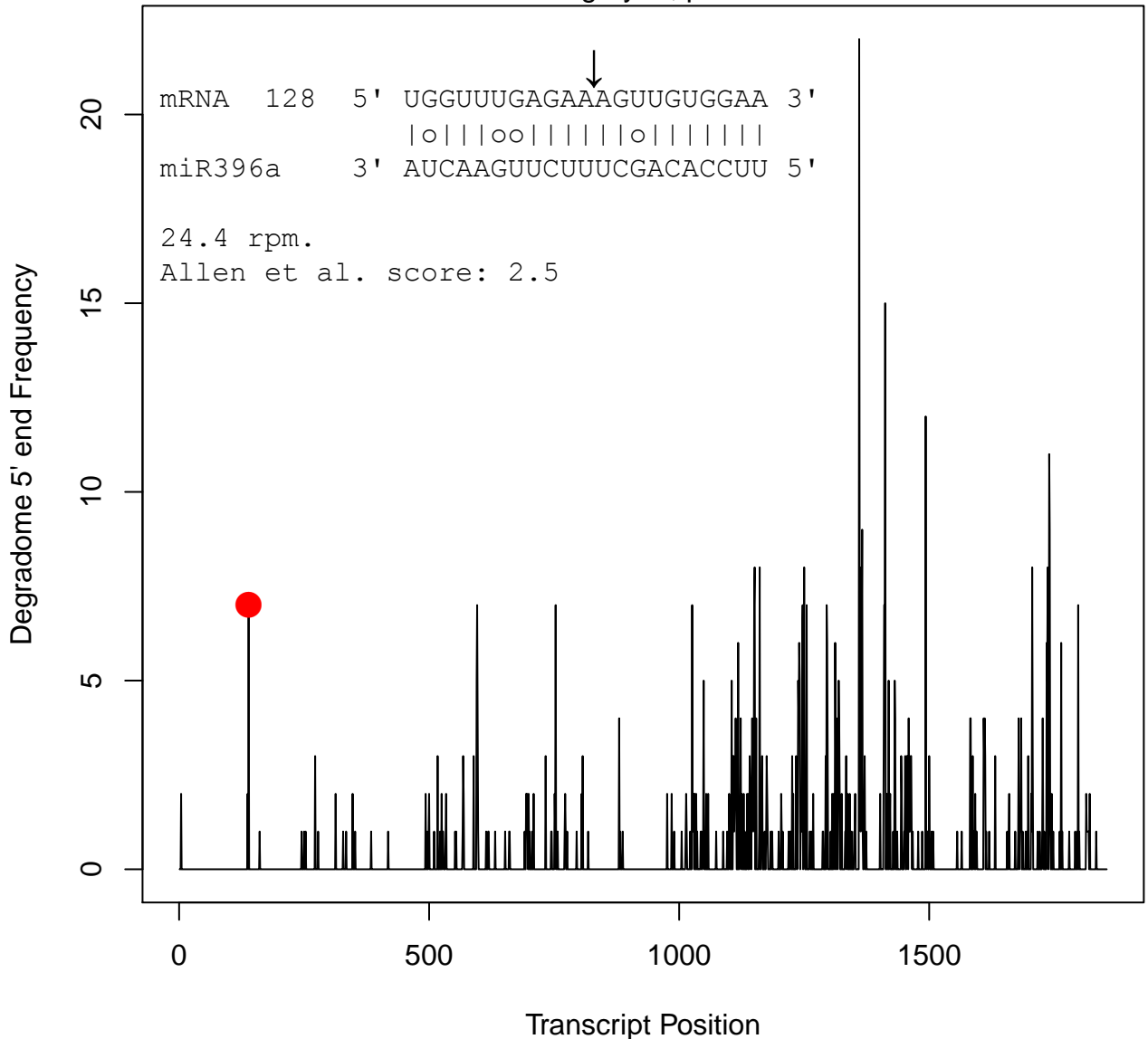
**VIT\_07s0191g00220**  
**unknown Coiled coil protein**

category=0, p=0.0056



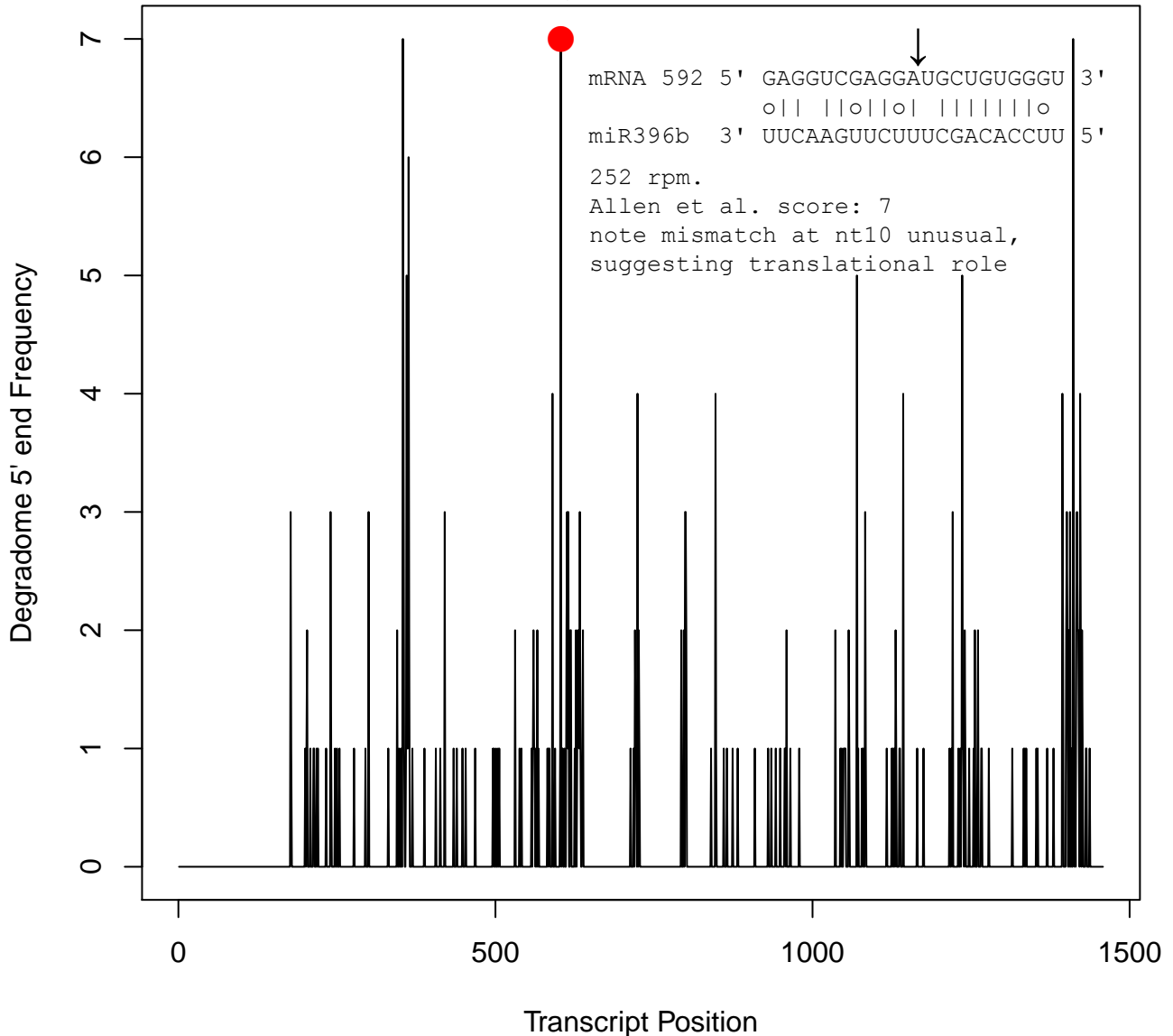
**VIT\_02s0012g02250**  
**basic leucine zipper VvBZIP05**

category=2, p=0.05



**VIT\_08s0032g00460**  
**Putative uncharacterized protein**

category=1, p=0.062

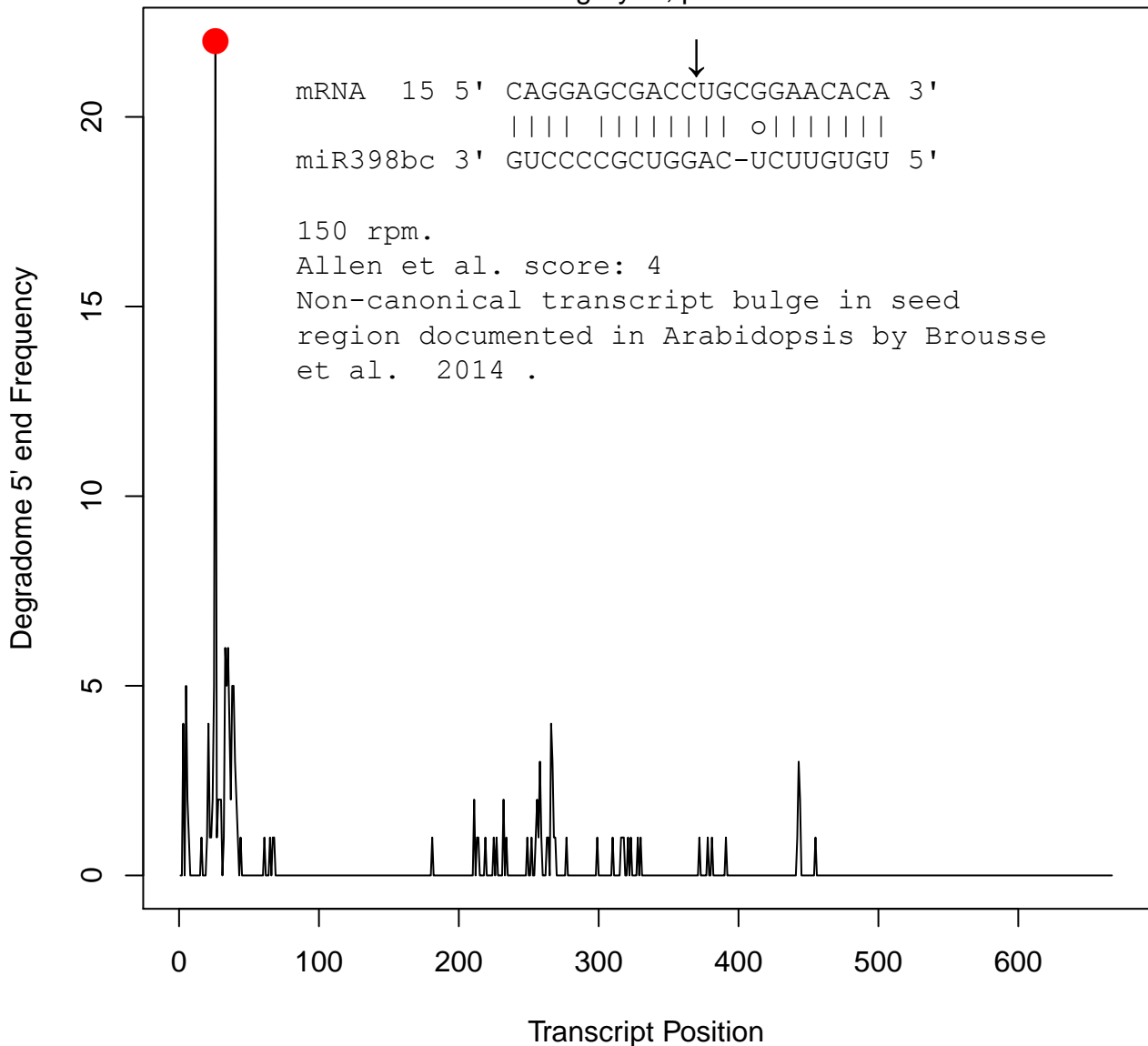


# VIT\_11s0016g05520

## Plastocyanin-like

UV pseudo-degradome sRNA libraries

category=0, p=0.002

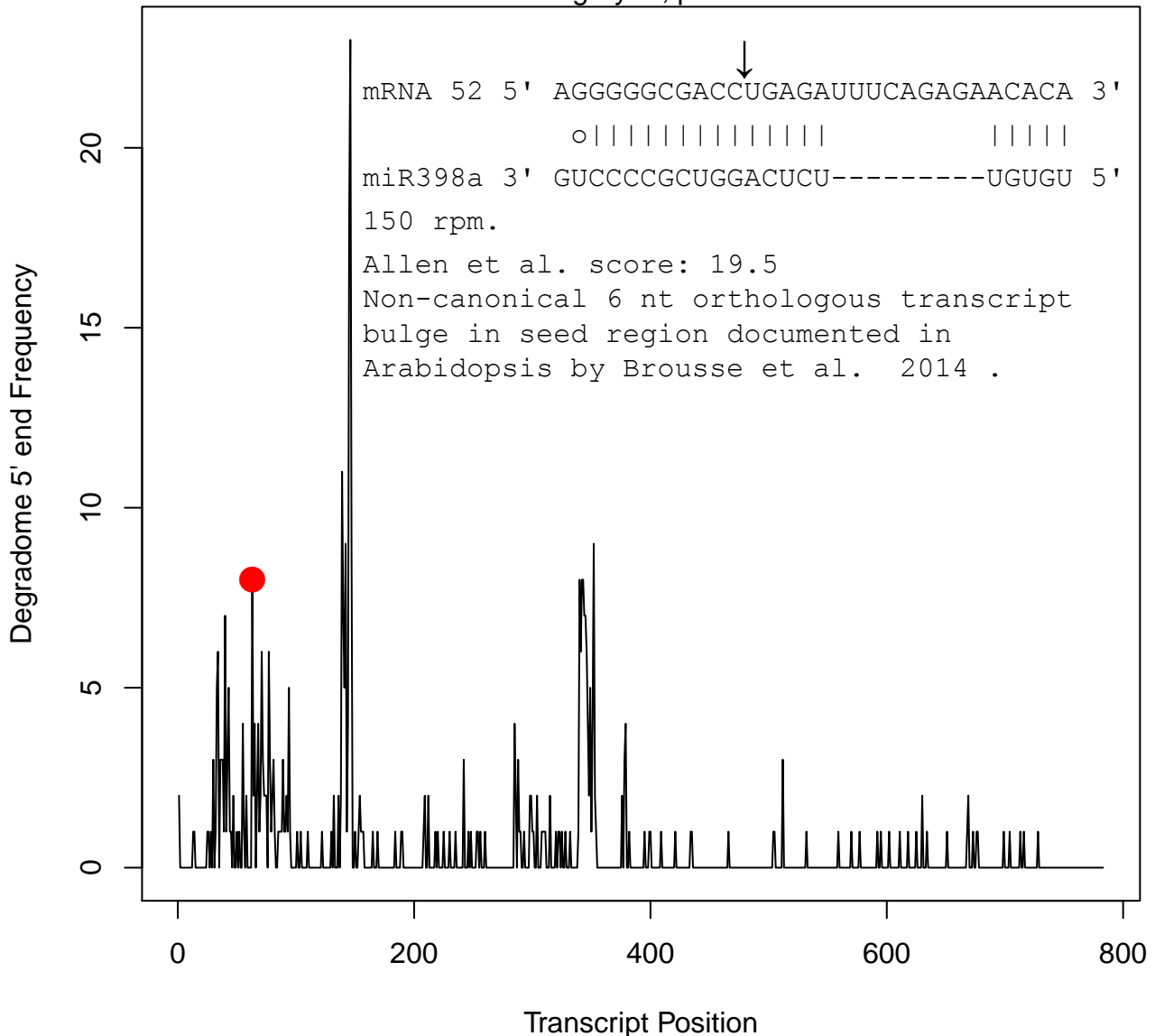


VIT\_11s0016g05530

blue copper-binding protein, plantacyanin-like BCBP

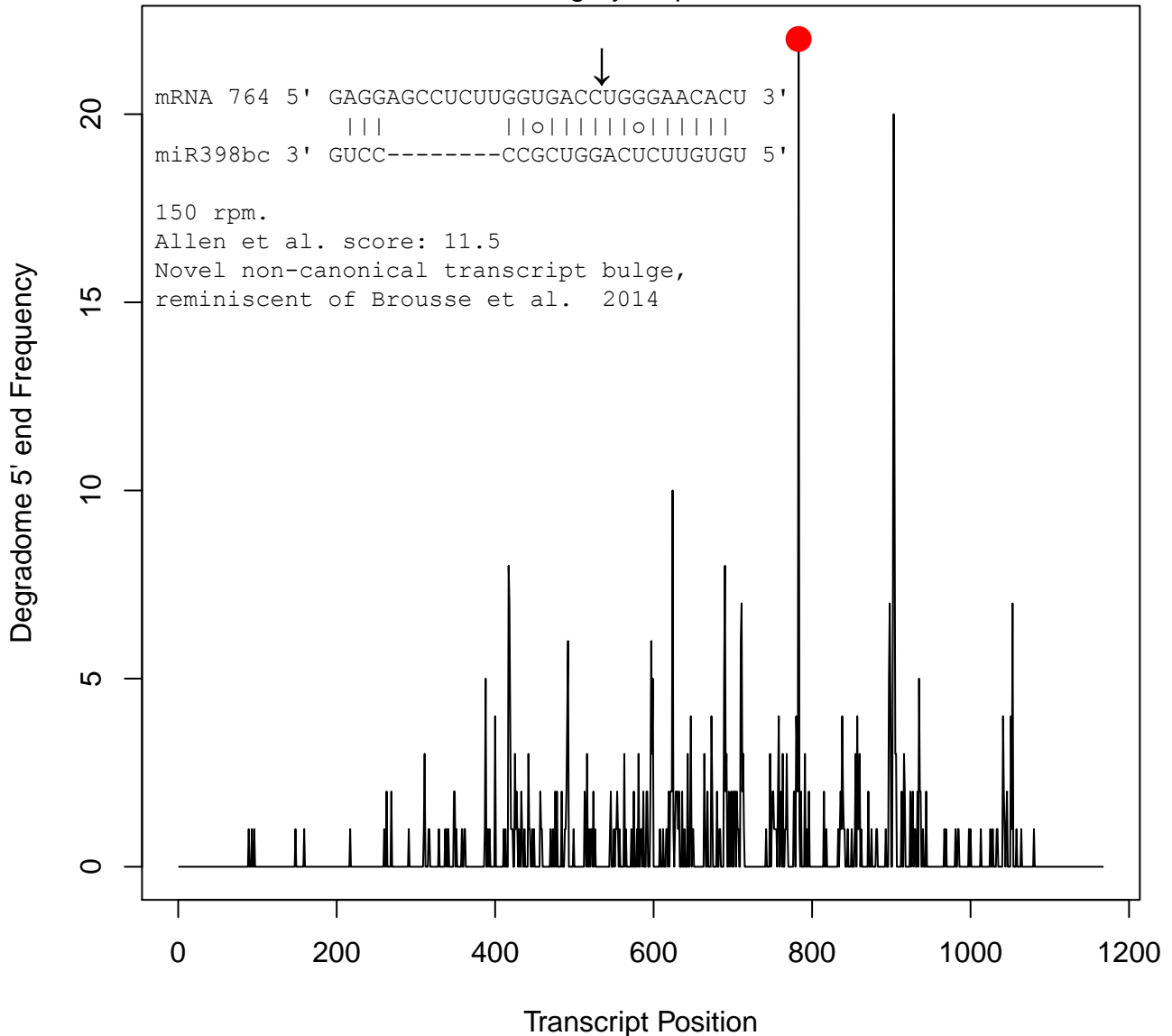
UV pseudo-degradome sRNA libraries

category=2, p=0.014



**VIT\_02s0025g04830**  
**Cu/Zn-superoxide dismutase copper chaperone CCS**

category=0, p=0.007



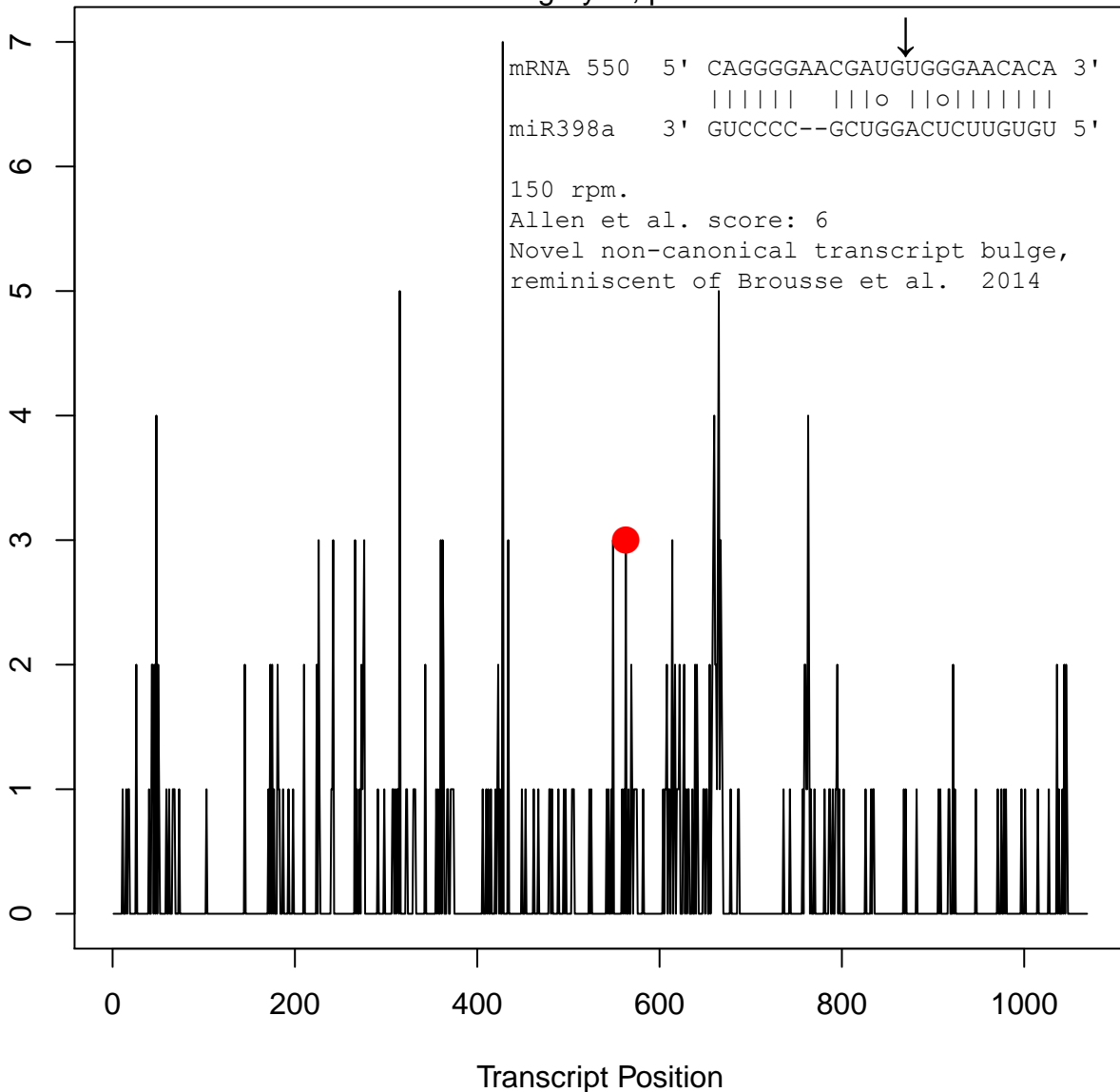
# VIT\_16s0013g00620

## peptide methionine sulfoxide reductase

public sRNA libraries, validated in bona fide degradome, category 4,  $p=0.23$

category=2,  $p=0.08$

Degradome 5' end Frequency

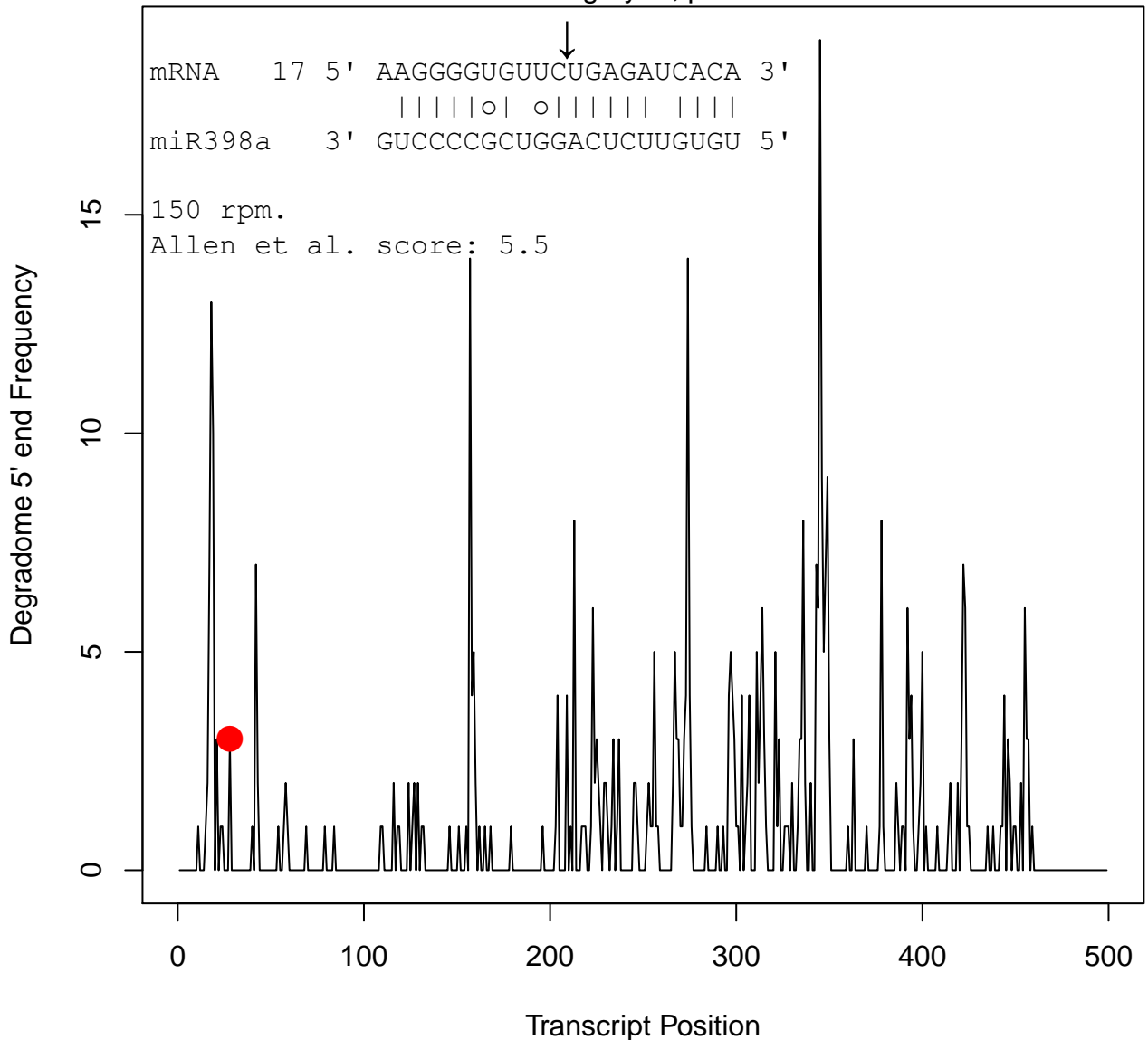


VIT\_14s0030g00830

**CuZn Superoxide Dismutase, CSD1**

validated in UV pseudo-degradome sRNA libraries, category 2, p=0.33

category=2, p=0.54

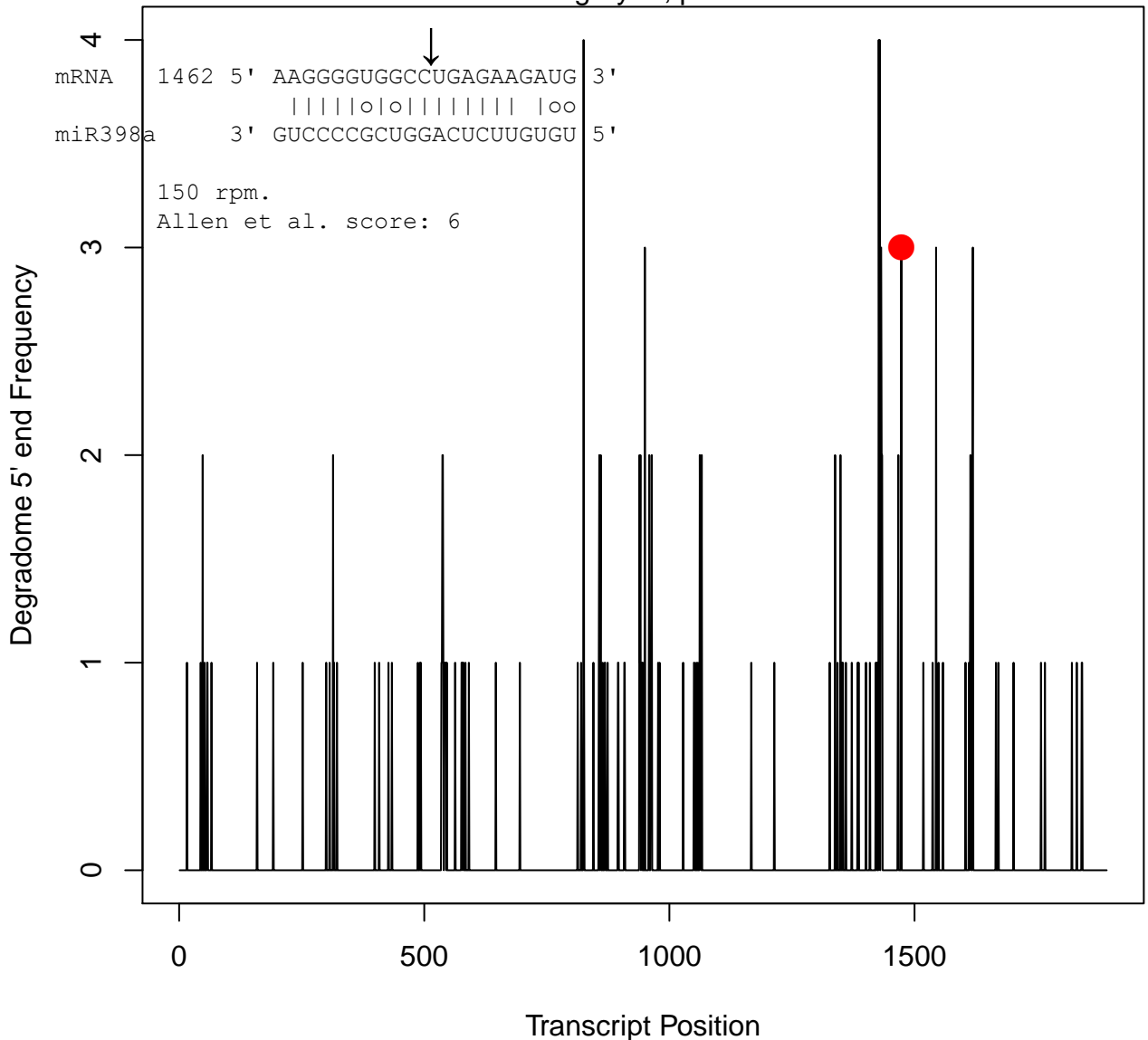




# VIT\_01s0127g00520

## Protein disulfide isomerase

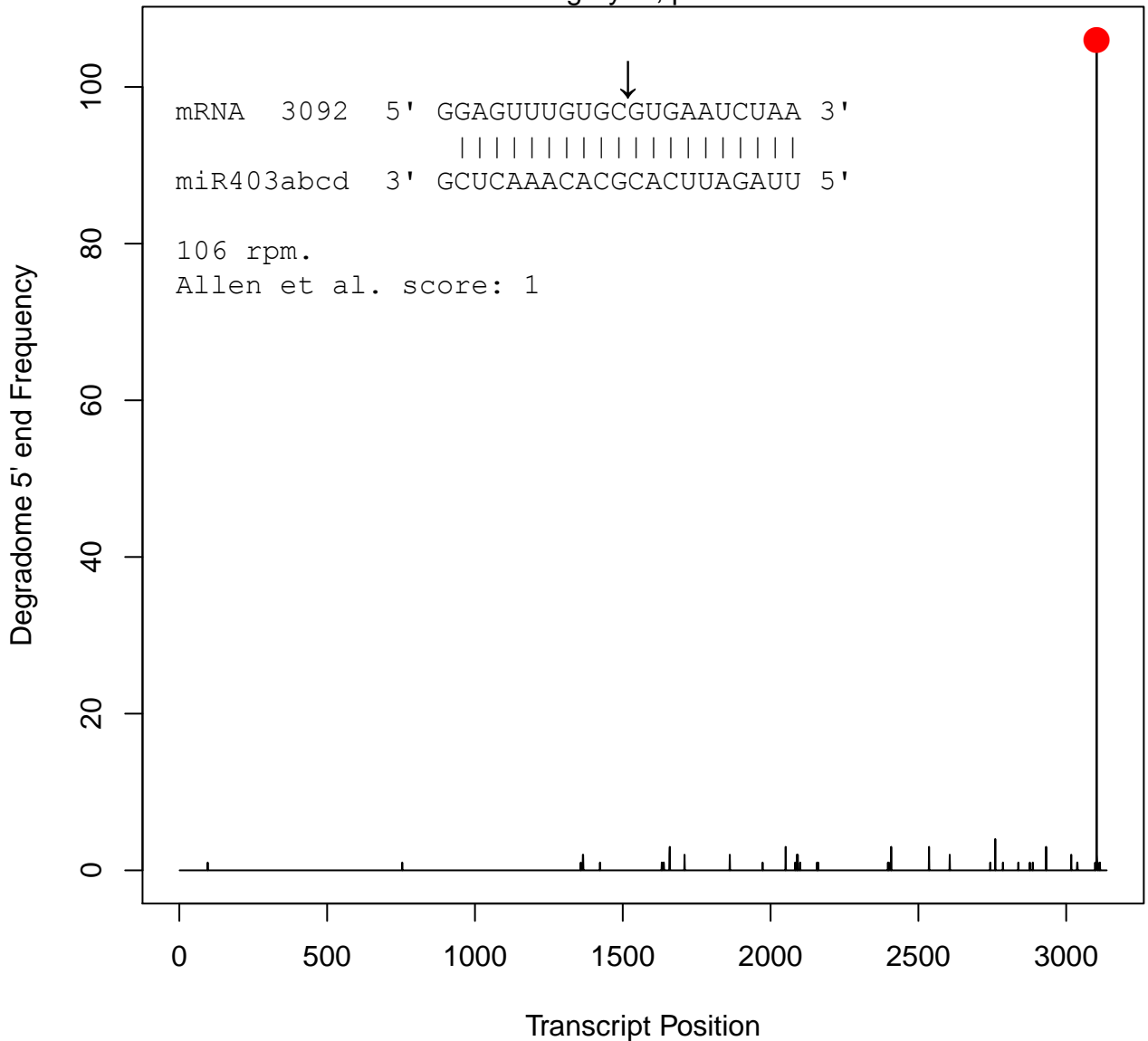
public sRNA libraries; UV sRNA degradome support for homologue VIT\_01s0127g00540 slice, p=0.08  
category=2, p=0.036



VIT\_10s0042g01150

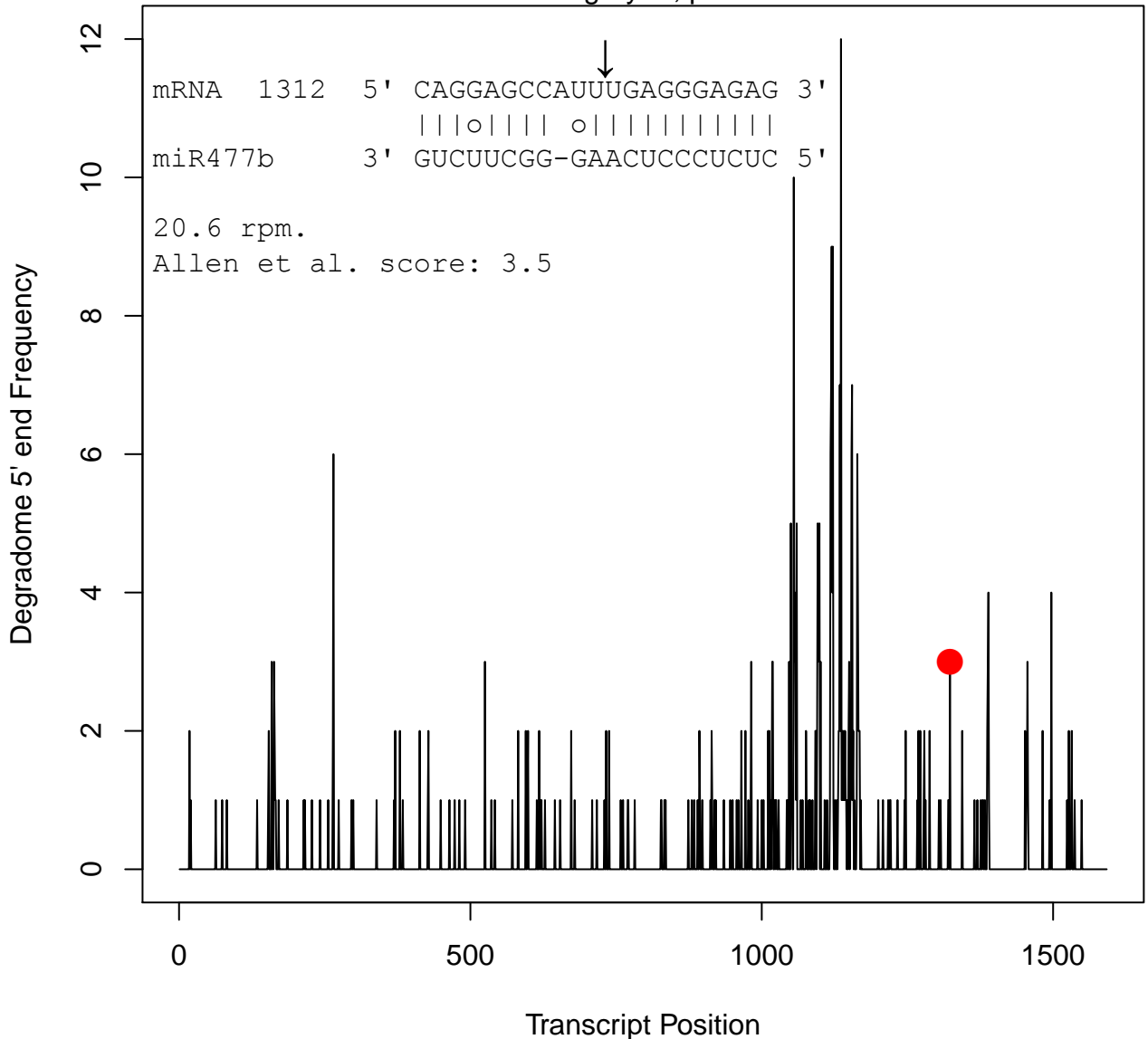
ARGONAUTE2

category=0, p=0.0003



VIT\_18s0041g01900  
Elongation factor 1-gamma

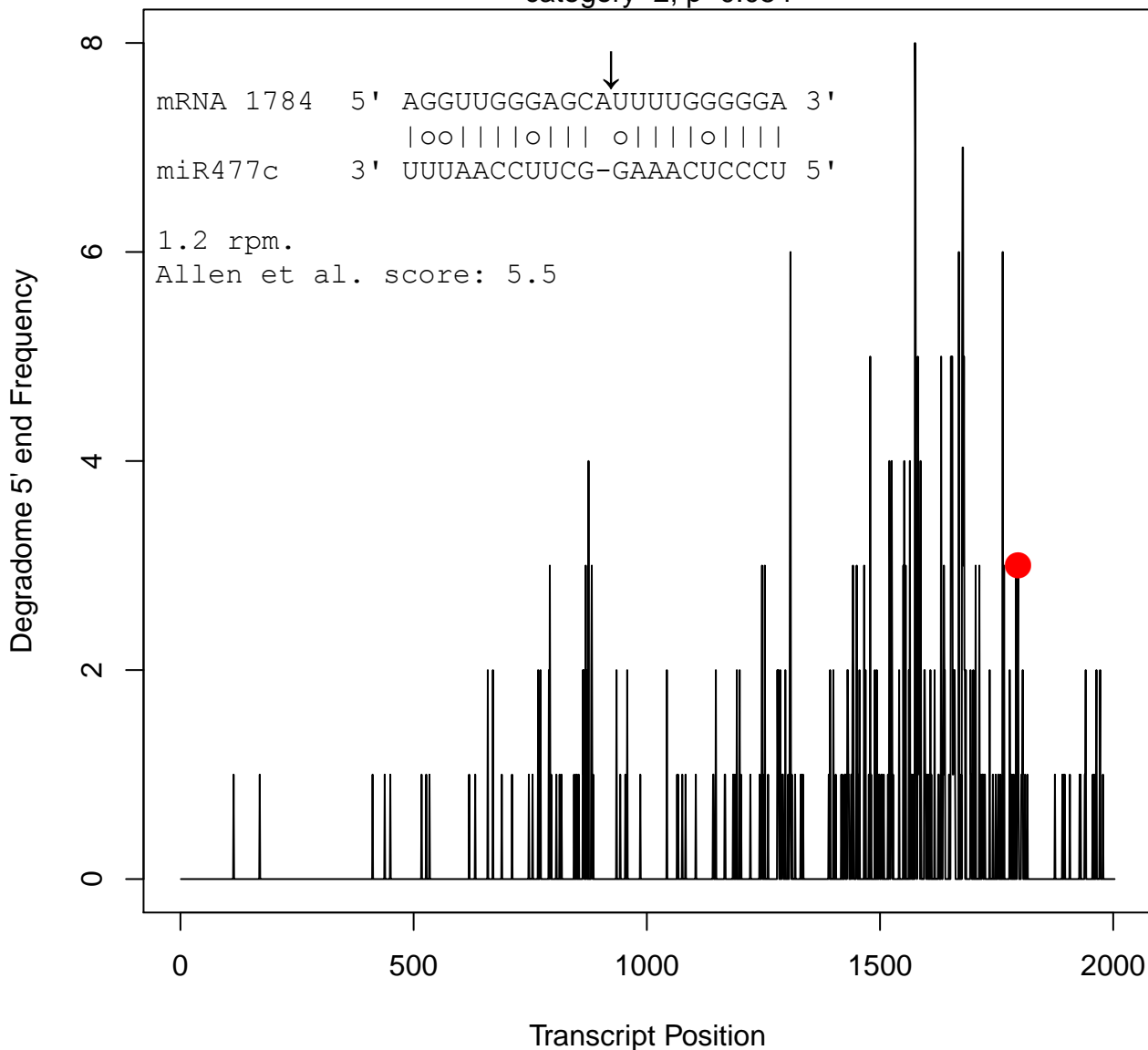
category=2, p=0.04



# VIT\_03s0180g00130

## EDA9, D-3-phosphoglycerate dehydrogenase

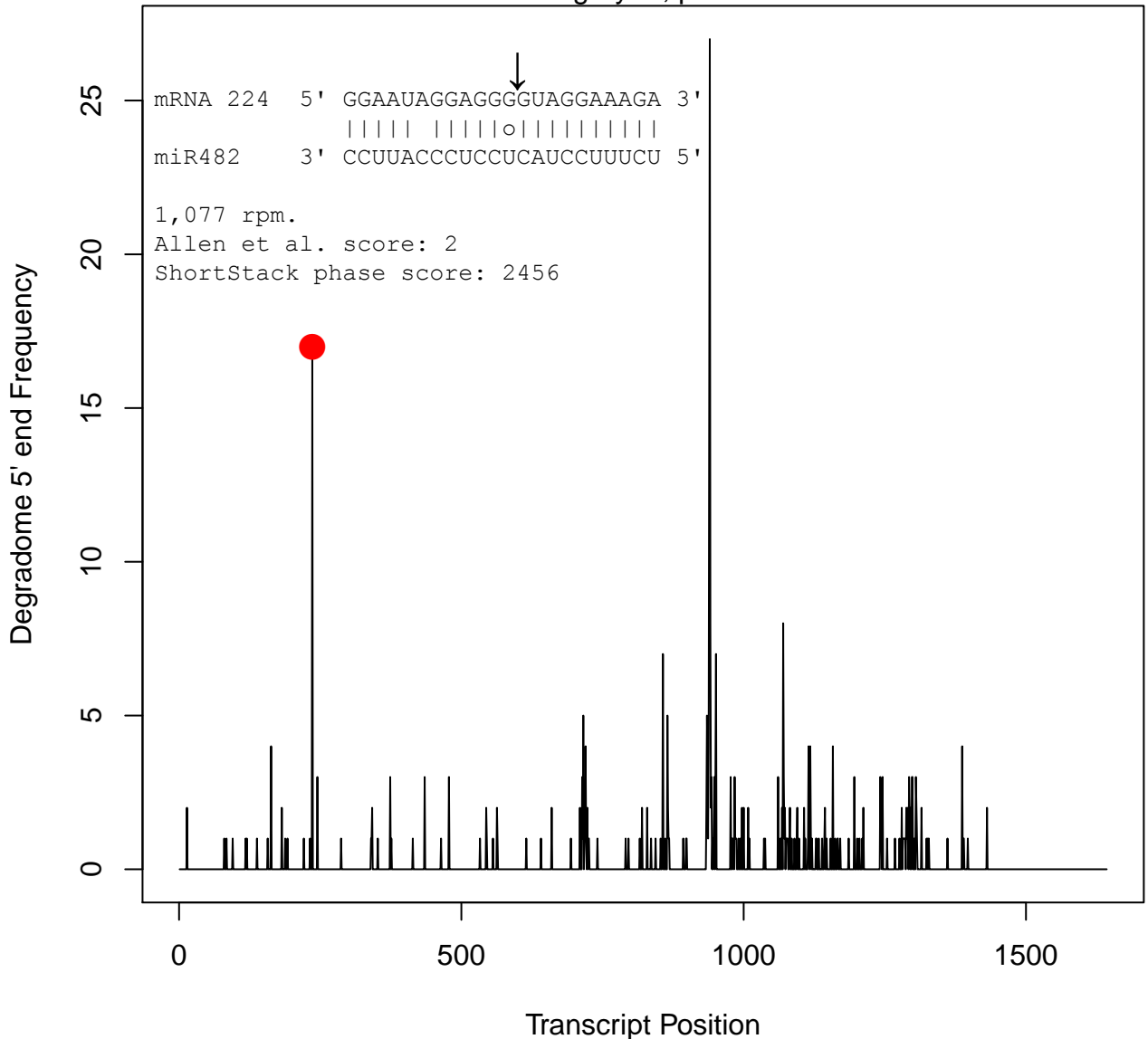
category=2, p=0.054



# VIT\_18s0072g01090

## TIR-NBS-LRR type R protein 7, Vv-slyTAS5-like

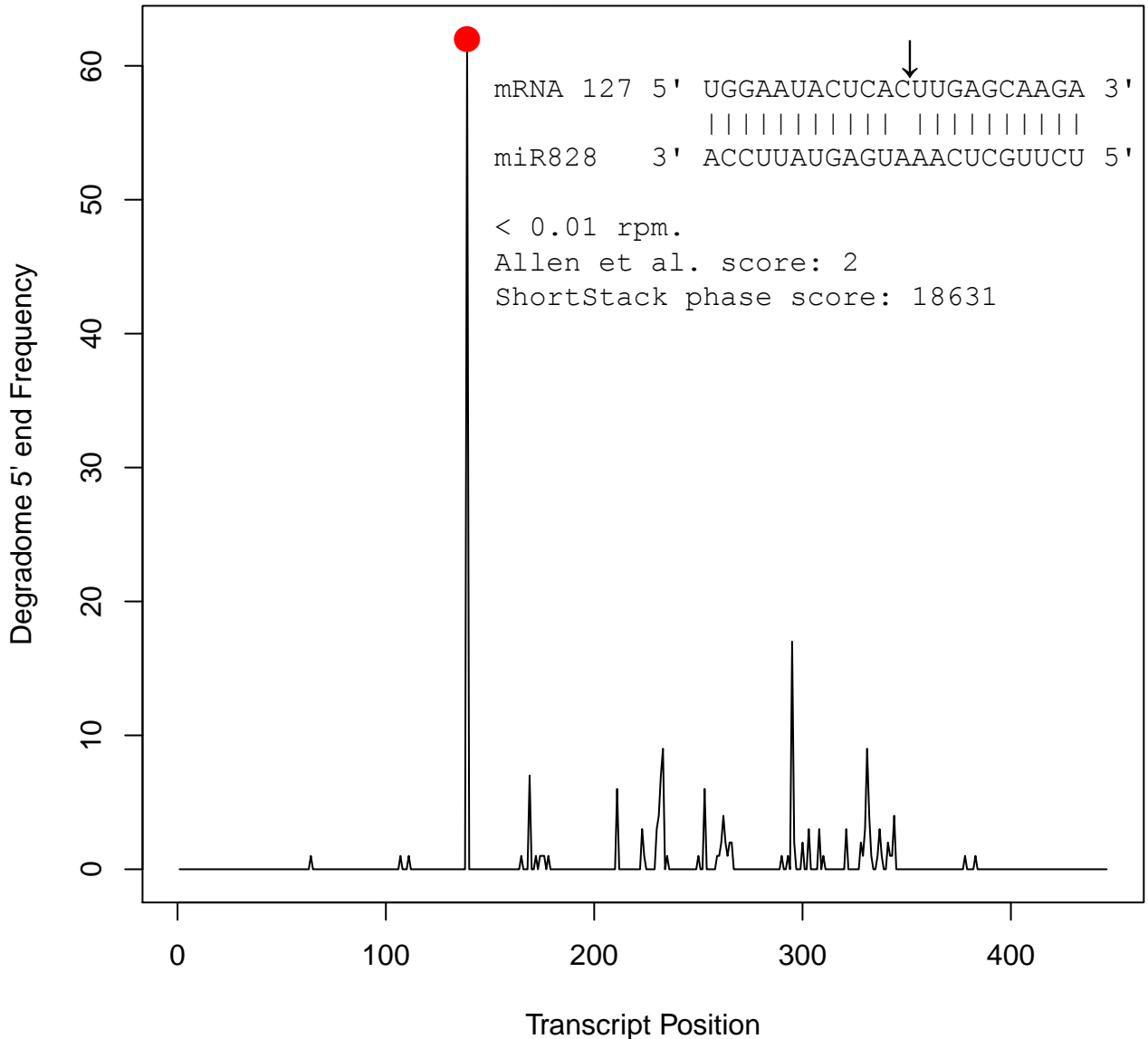
category=2, p=0.014



VIT\_14s0006g03100

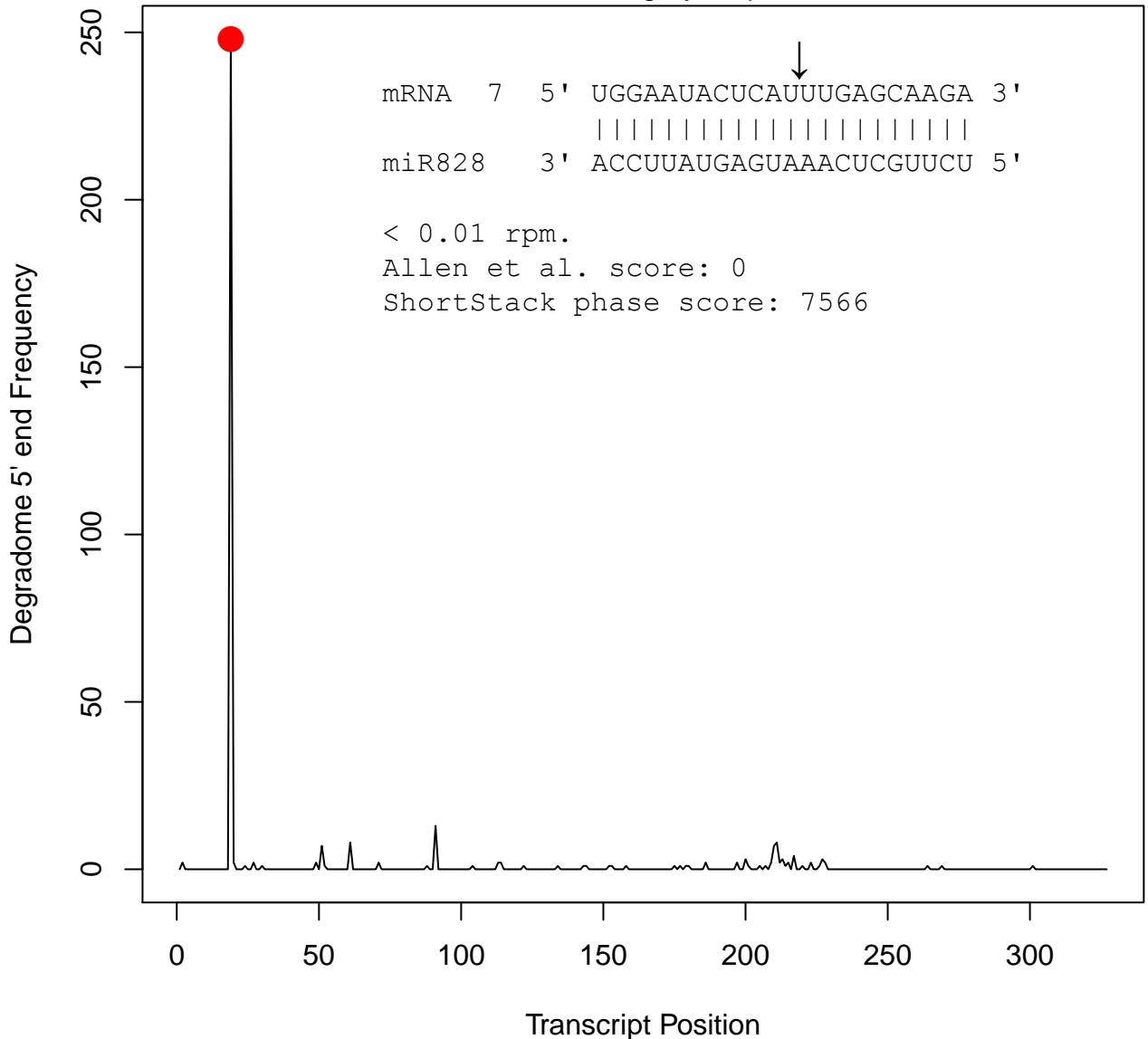
Vv-TAS4a; overlaps with 3' end of 59 AA predicted peptide

category=0, p=0.00035



# VviTAS4b genomic chr14:21534568..21534896

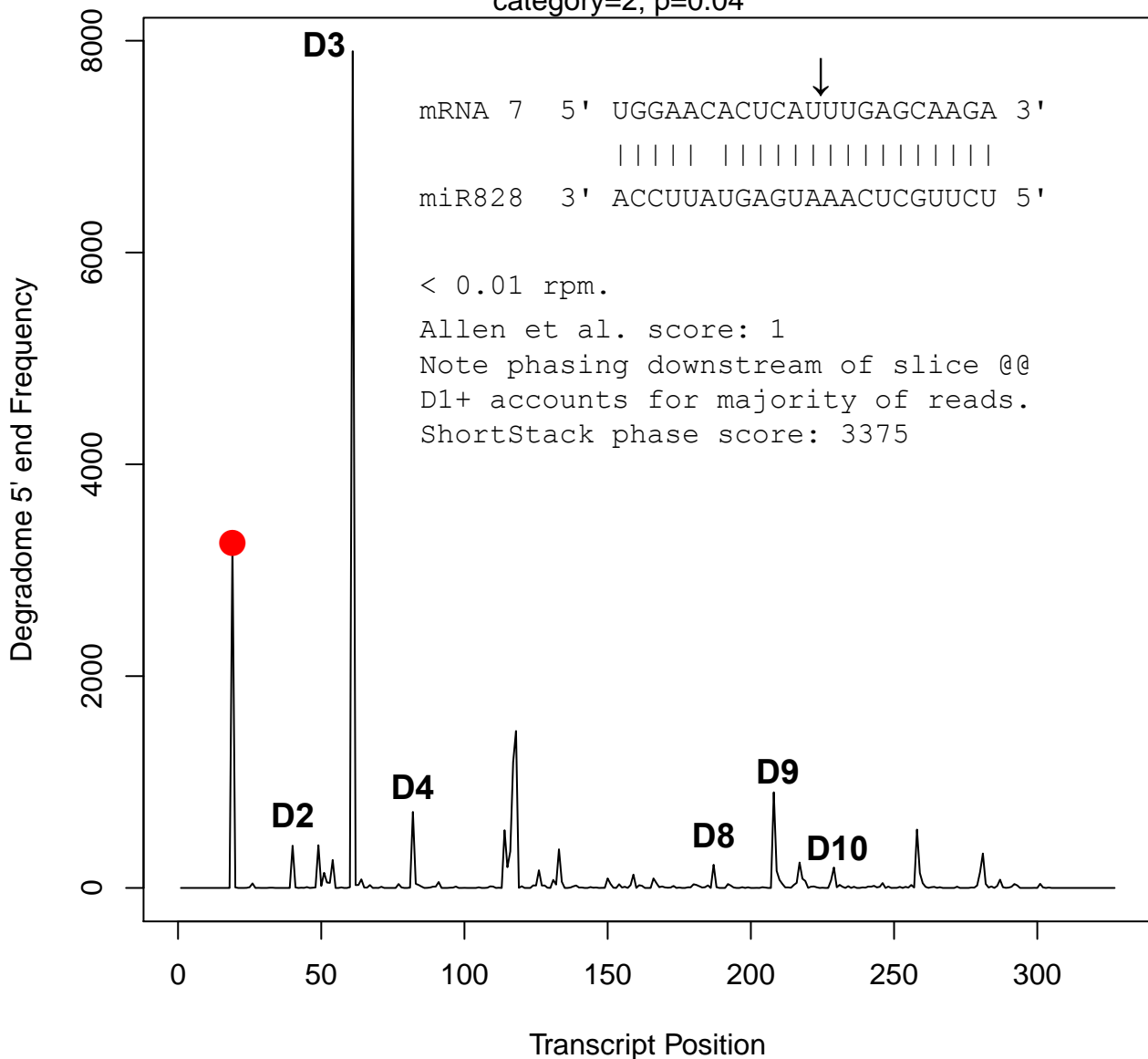
category=0, p=0.0003



# vvi-TAS4c chr1:2961355..2961682rc

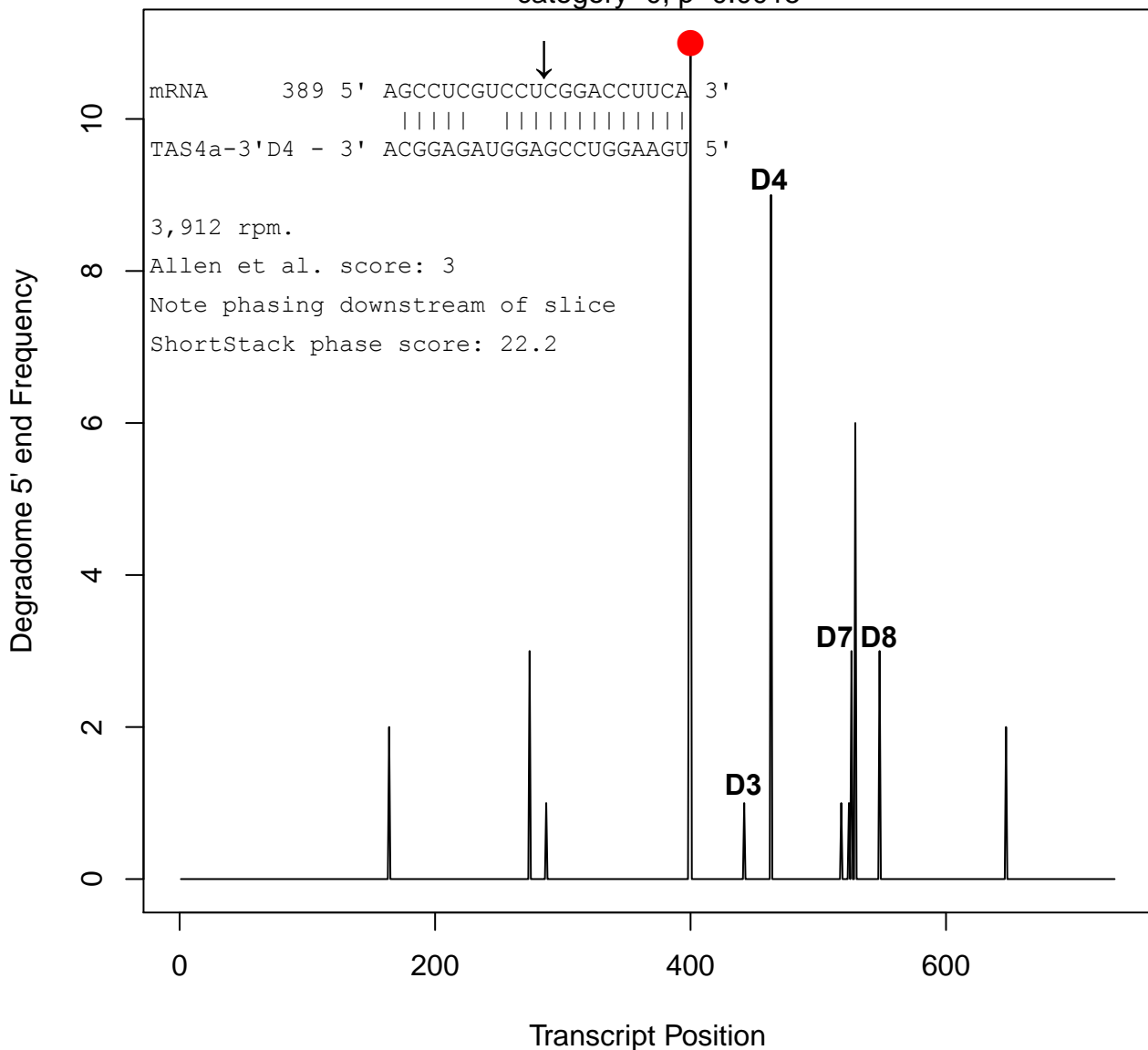
UV pseudo-degradome sRNA libraries; validated in Pantaleo sRNA libraries cat2, p=0.001

category=2, p=0.04





VIT\_14s0006g01290  
MYBA6/GSVIVT01030822001  
UV pseudo-degradome sRNA libraries  
category=0, p=0.0015

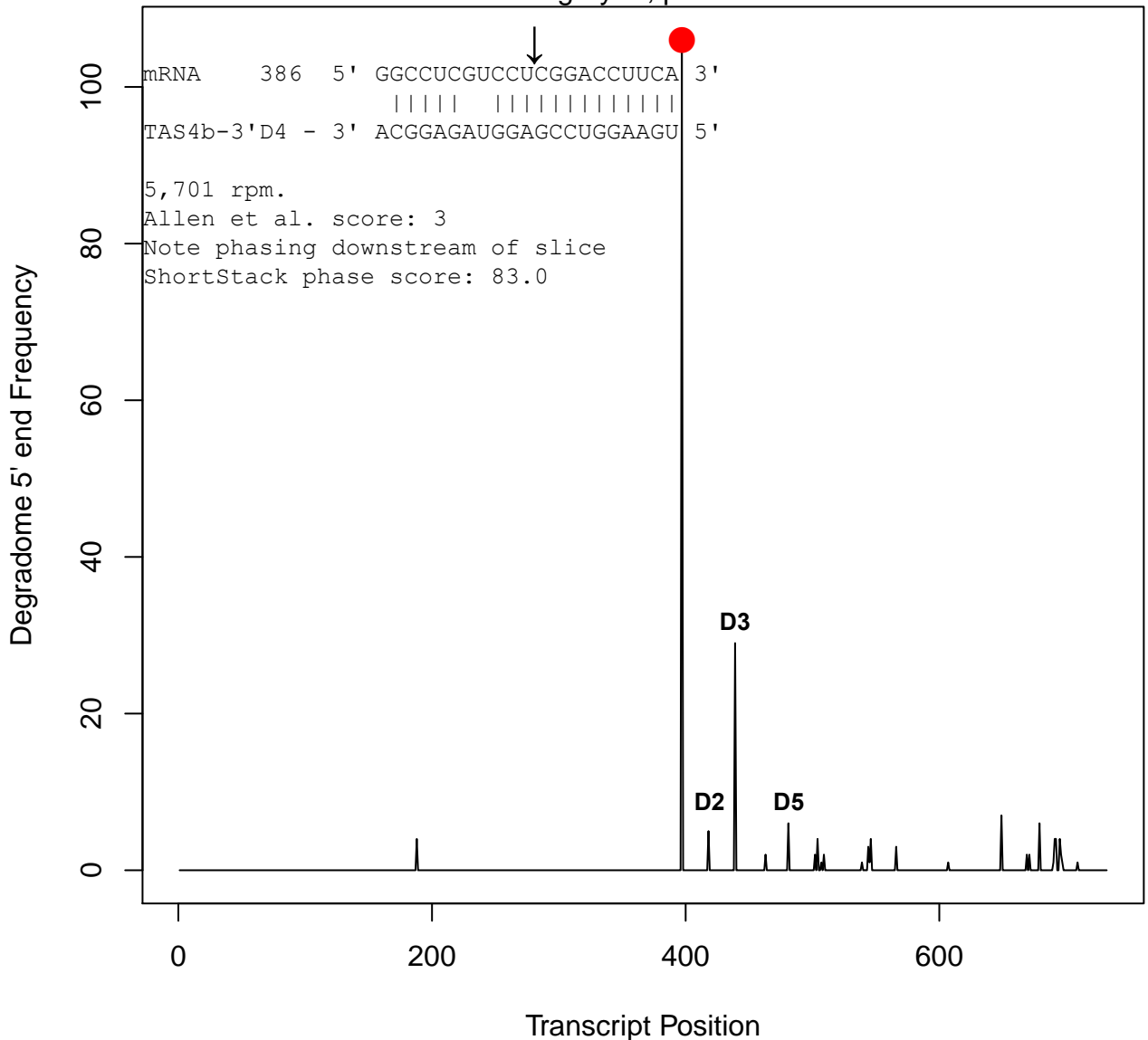


VIT\_14s0006g01280

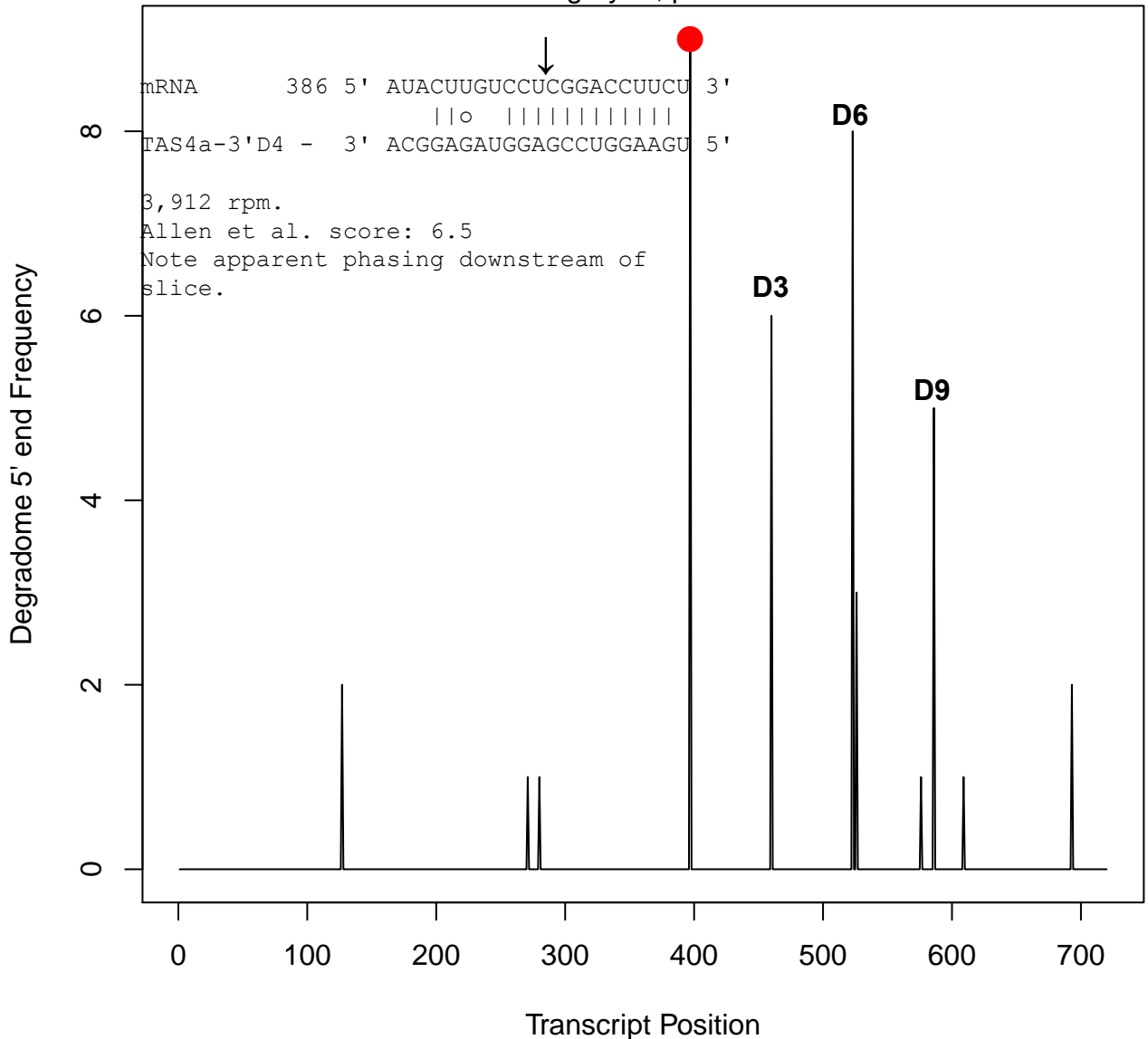
MYBA7/GSVIVT01030819001

UV pseudo-degradome sRNA libraries

category=0, p=0.003

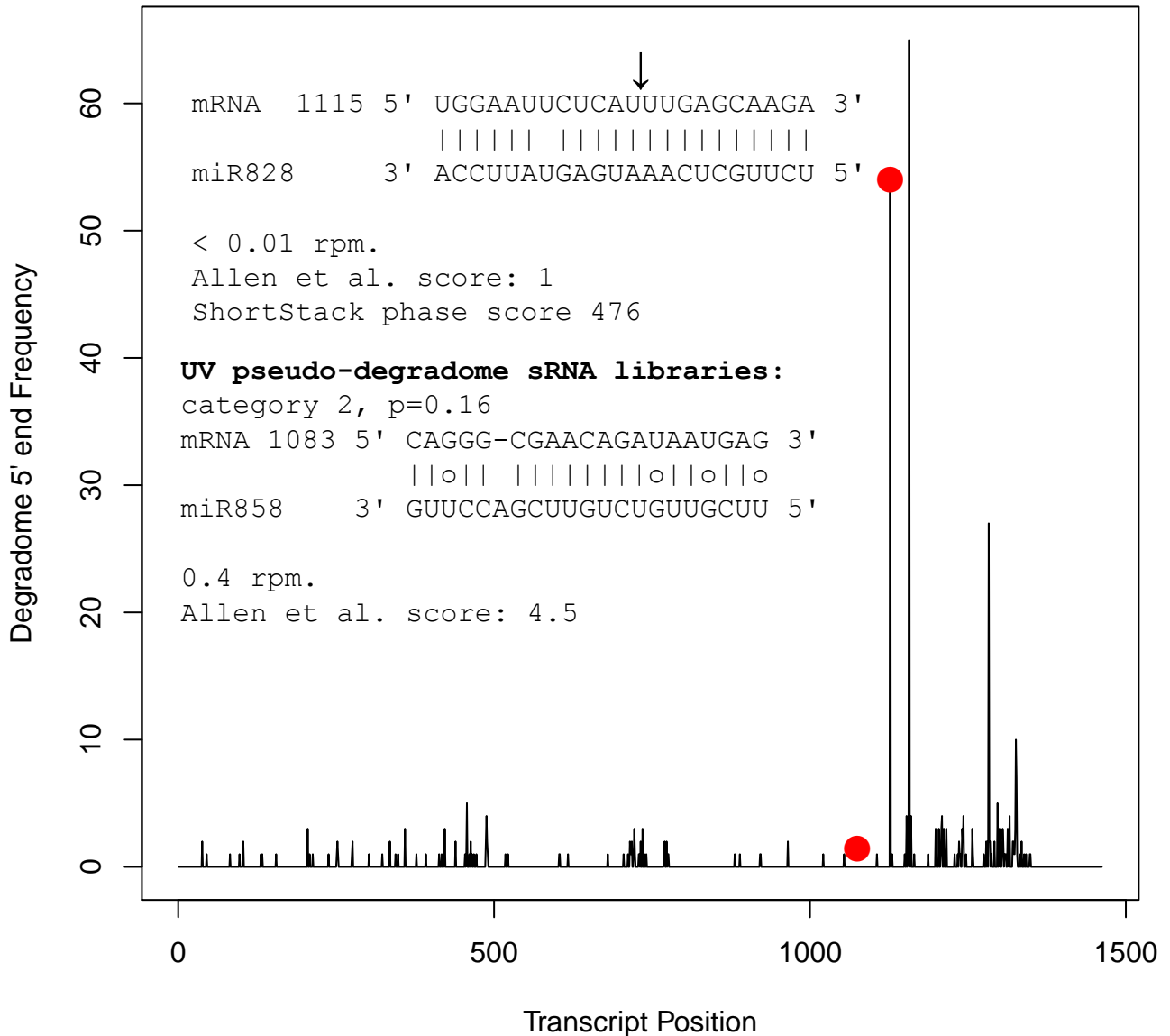


**VIT\_14s0006g01340**  
**MYBA5/MYB113-like/GSVIVT01030829001**  
 UV pseudo-degradome sRNA libraries  
 category=0, p=0.03



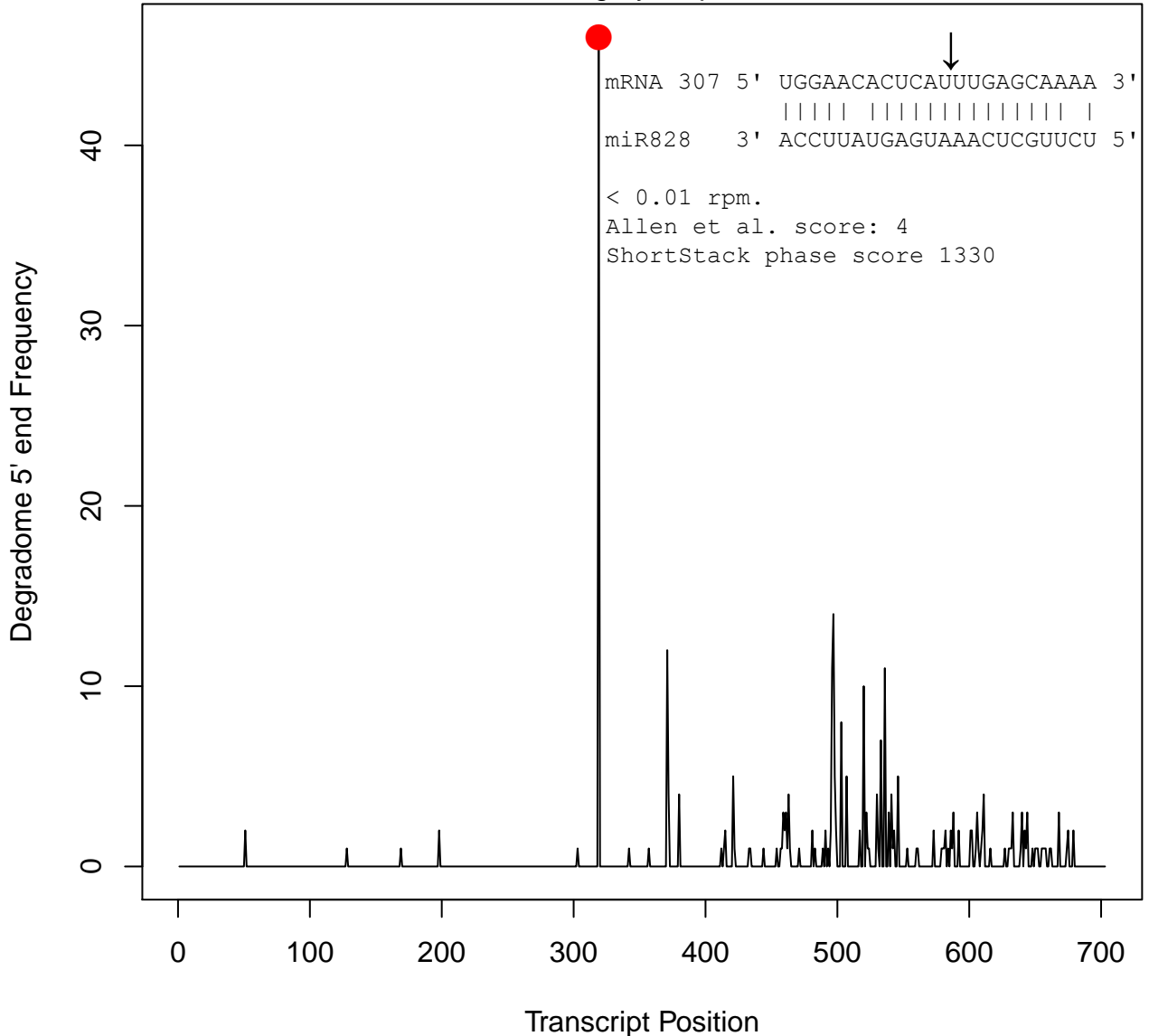
VIT\_00s0341g00050  
MYBPAL1/GSVIVT00009522001

category=2, p=0.04



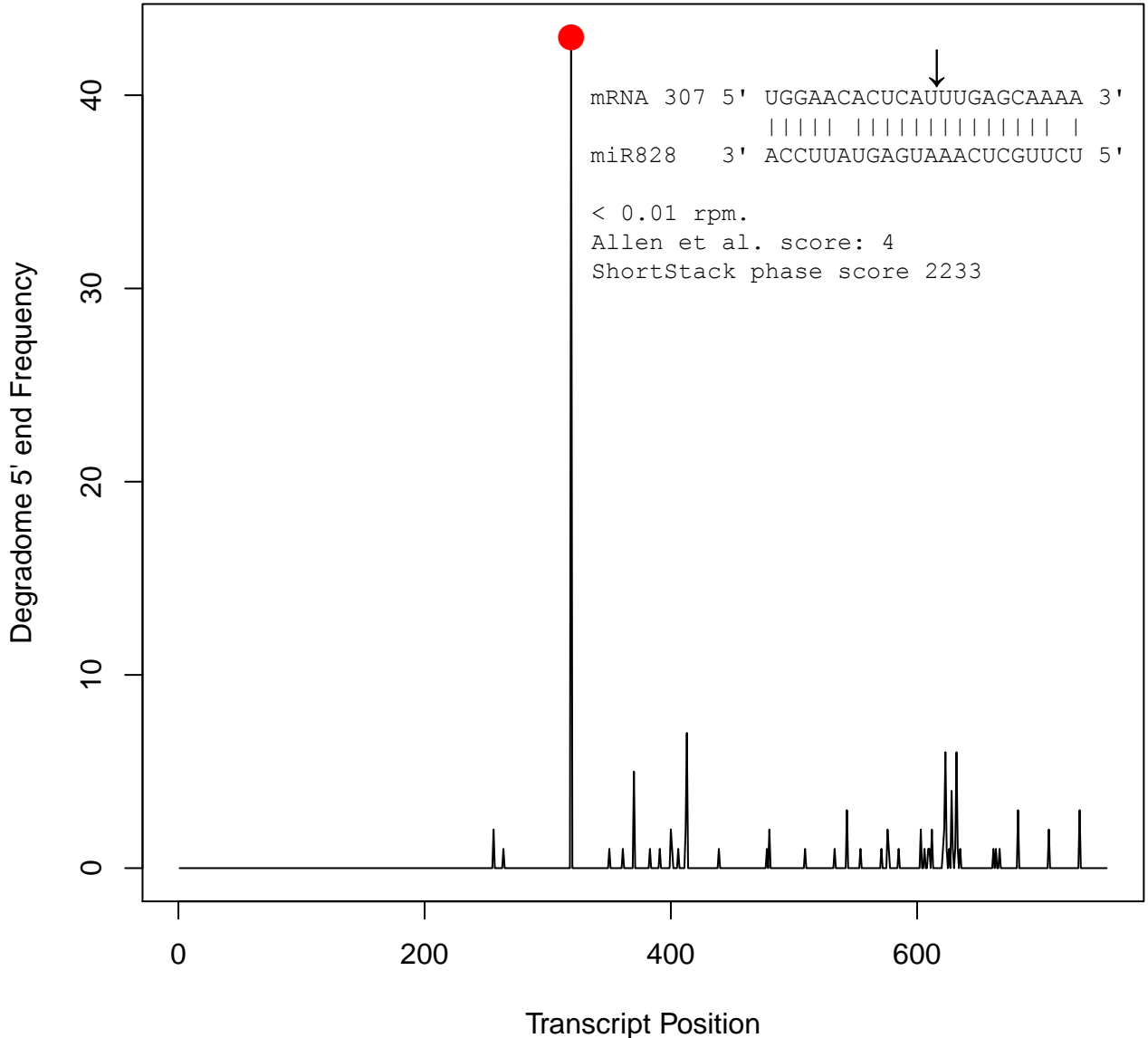
**VIT\_17s0000g08480**  
**MYB157/GSVIVT00016076001**

category=0, p=0.002



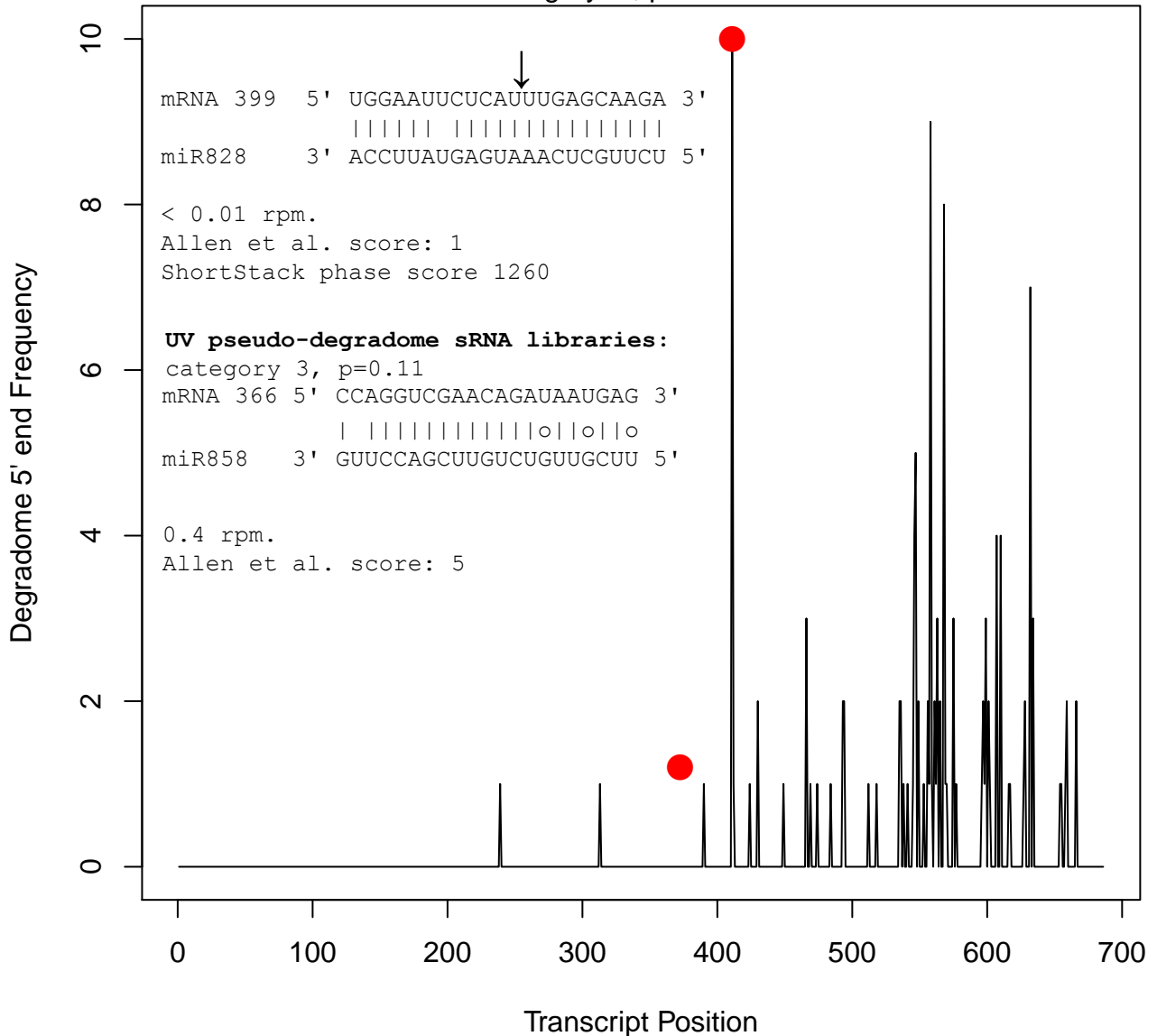
**VIT\_14s0066g01220**  
**MYB156/GSVIVT00020733001**

category=0, p=0.0018



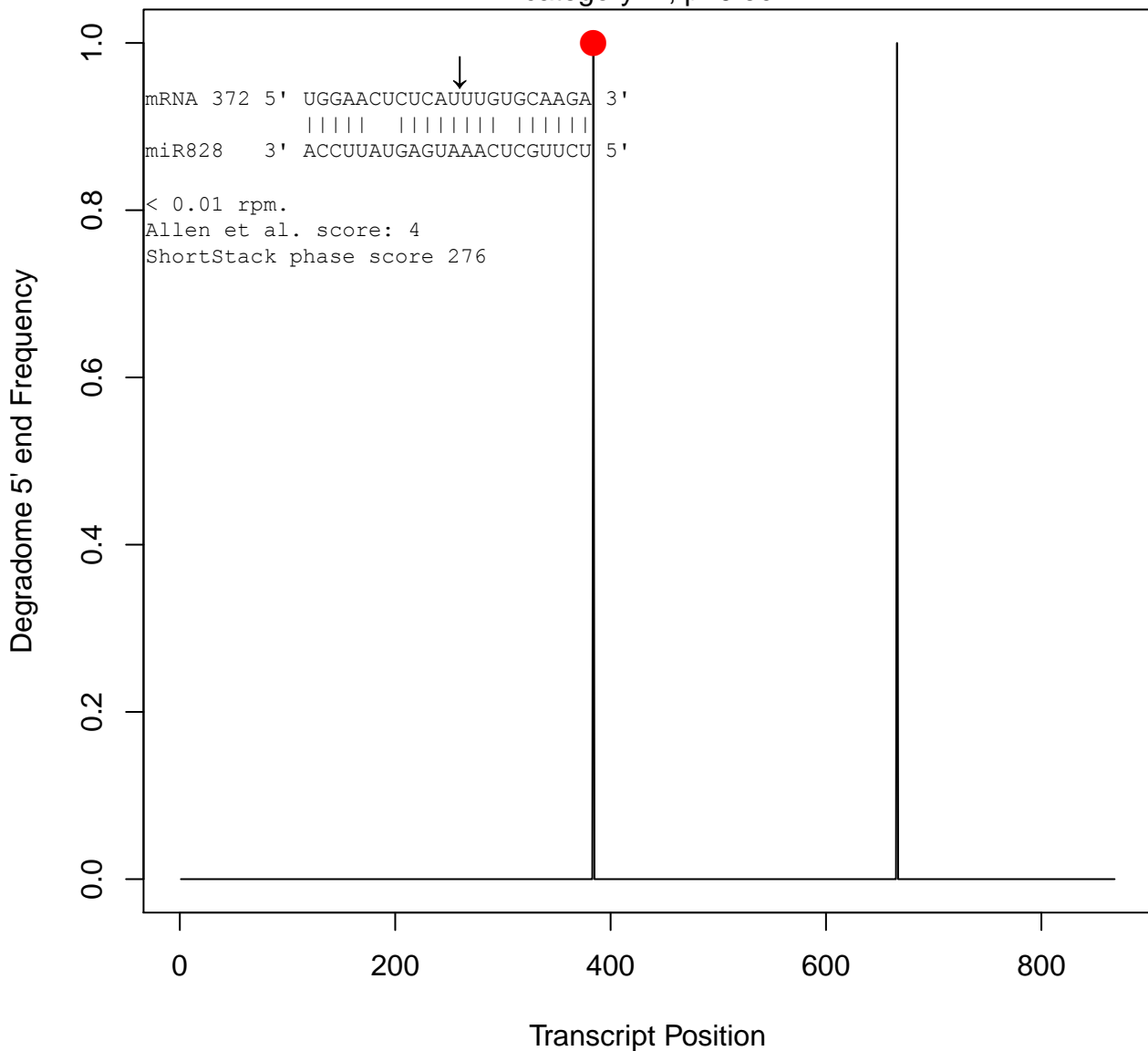
VIT\_09s0002g01380  
MYBPAL3/GSVIVT00034095001

category=0, p=0.0007



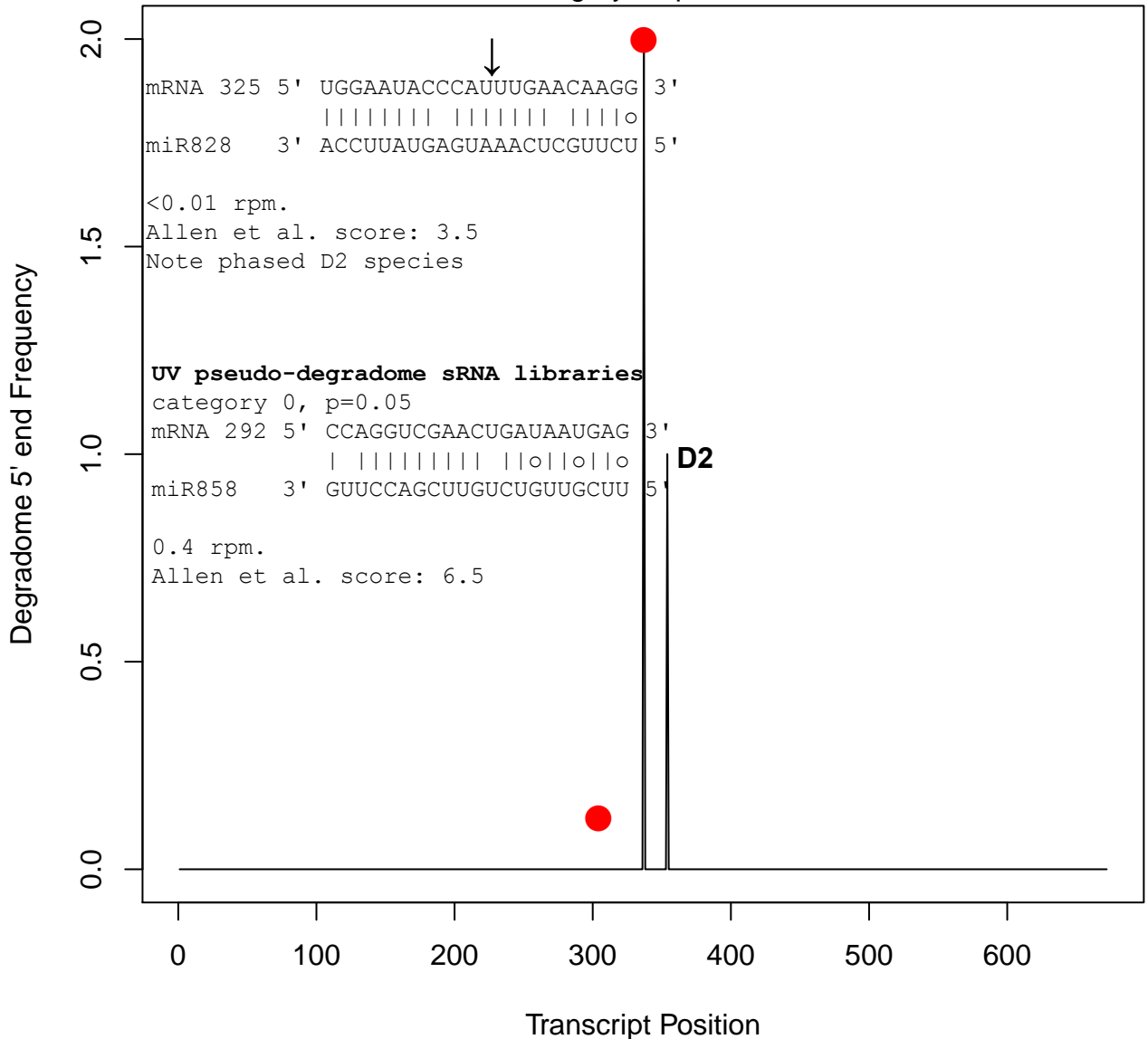
VIT\_01s0127g00730  
MYB155/GSVIVT00002700001

category=4, p=0.30





VIT\_11s0016g05660  
 MYB82B/GSVIVT01015575001  
 Pantaleo pseudo-degradome sRNA libraries  
 category=0, p=0.006



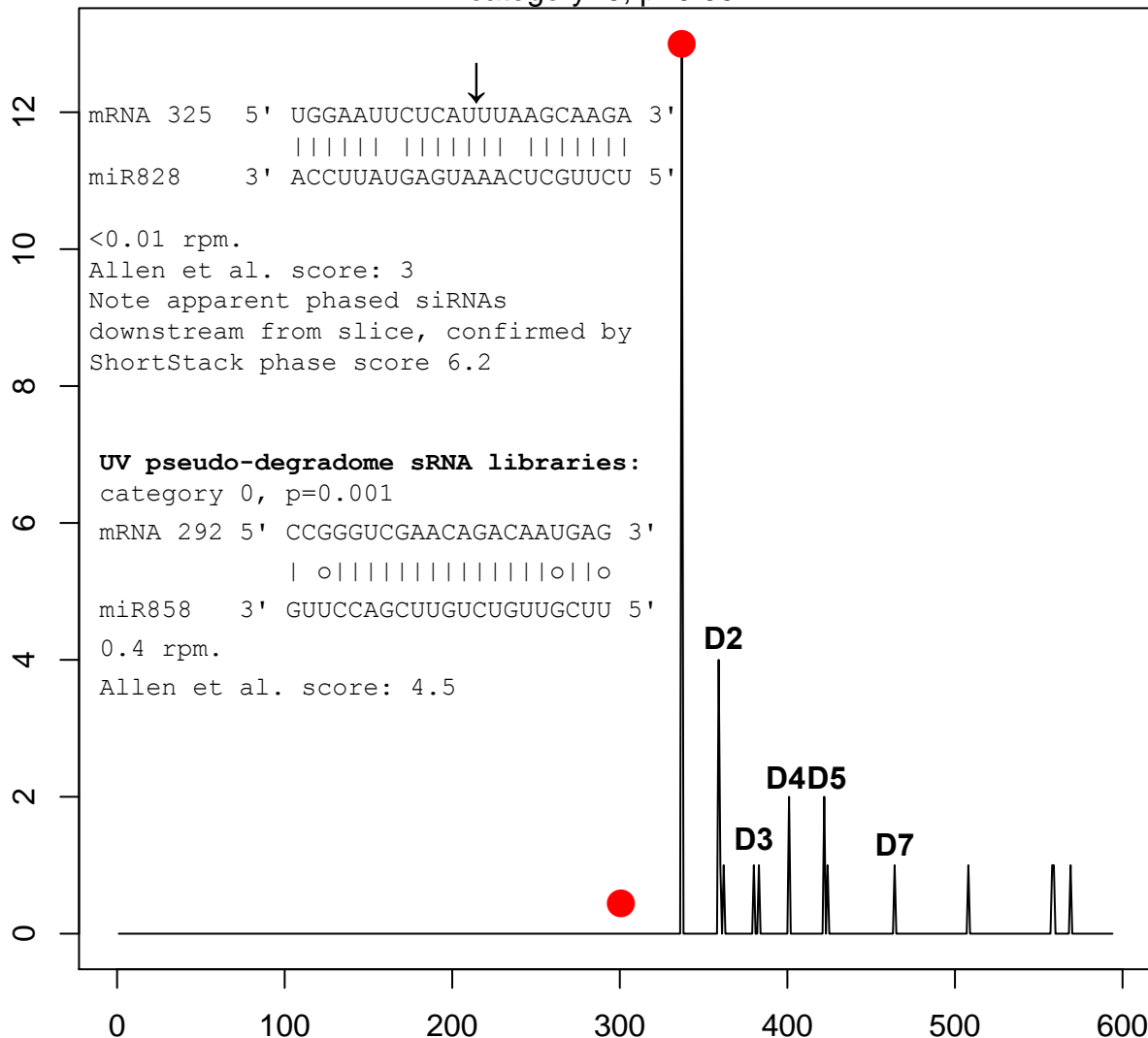
VIT\_04s0008g01870

MYBPAL2/GSVIVT01035467001

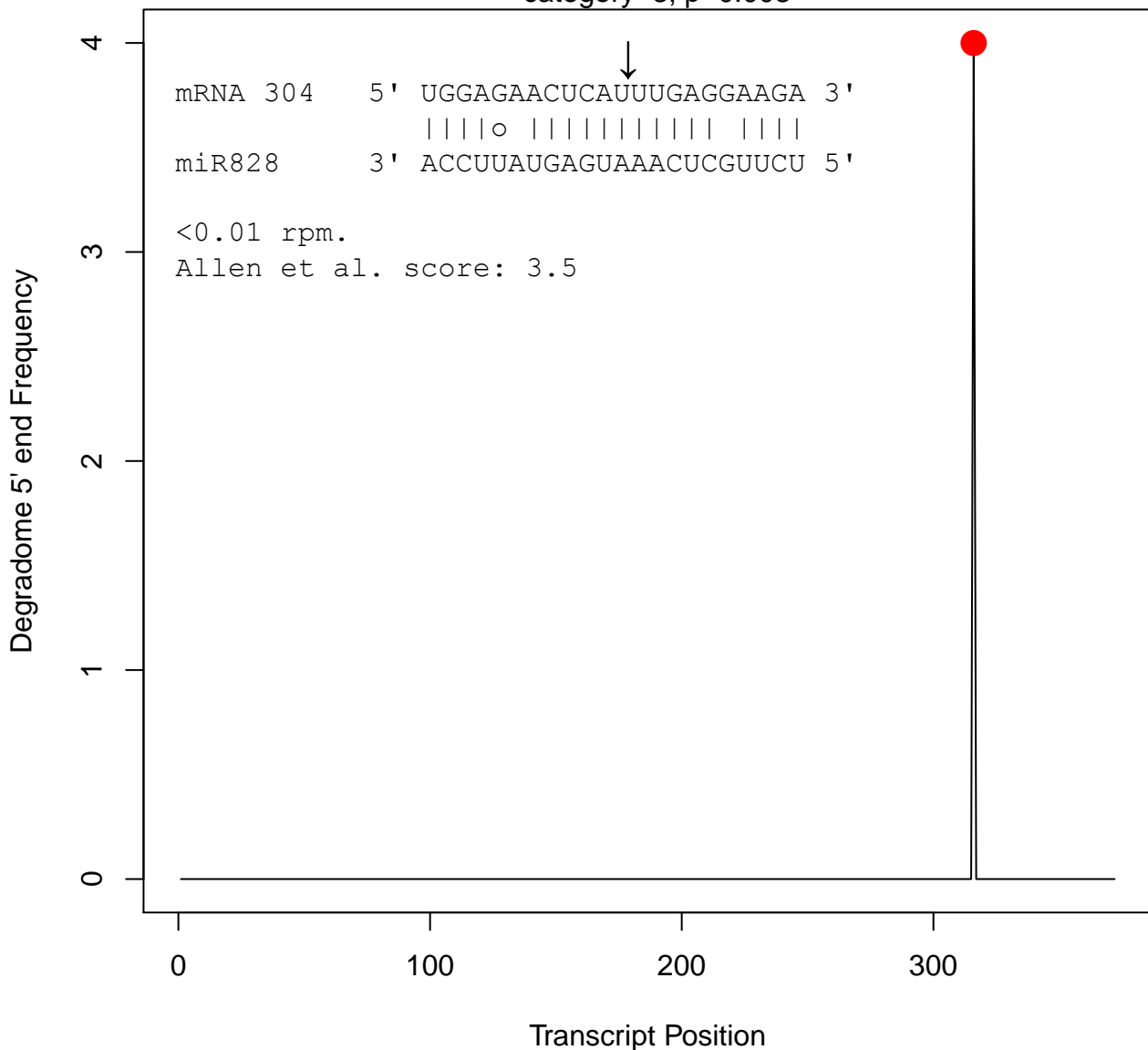
Pantaleo pseudo-degradome sRNA libraries

category=0, p=0.002

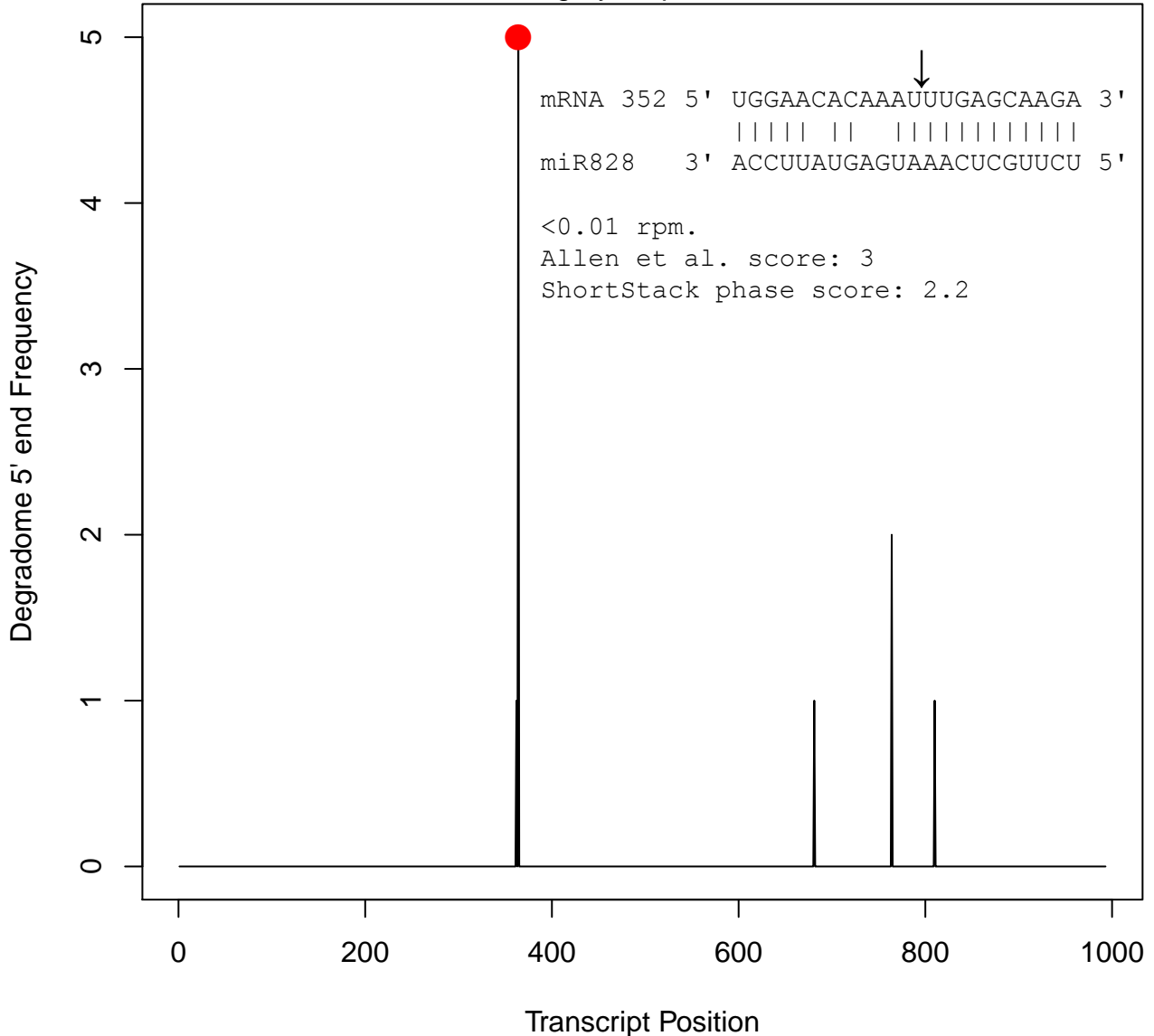
Degradome 5' end Frequency



**VIT\_08s0007g04830**  
**MYB27/GSVIVT01033670001**  
**Pantaleo pseudo-degradome sRNA libraries**  
category=3, p=0.003

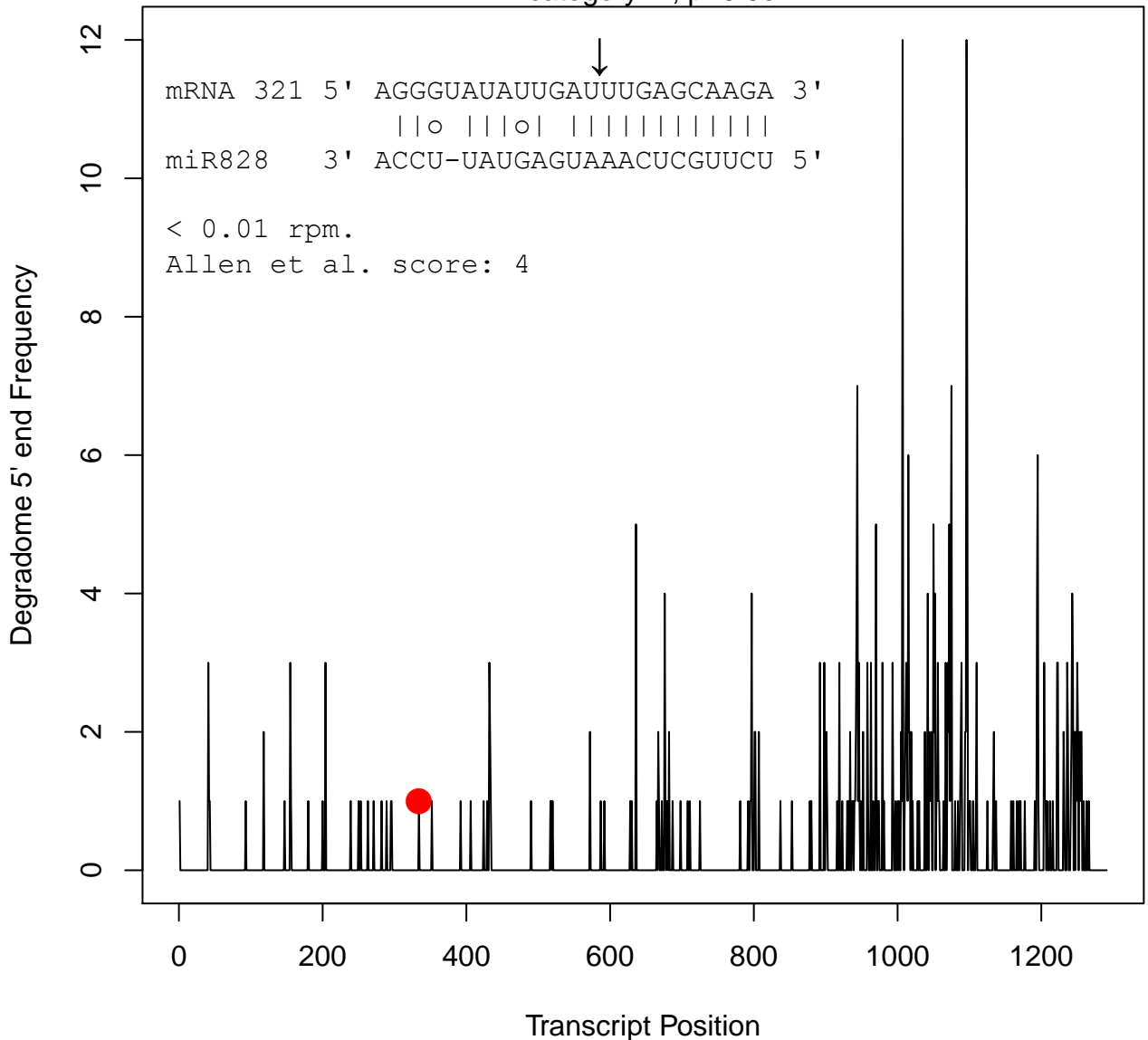


VIT\_11s0016g01320  
 MYBPA2/GSVIVT01015102001, Regulating proanthocyanidin  
 Pantaleo pseudo-degradome sRNA libraries  
 category=0, p=0.002



**VIT\_13s0067g01710**  
**Translation initiation factor eIF-2 alpha subunit**

category=4, p=0.55

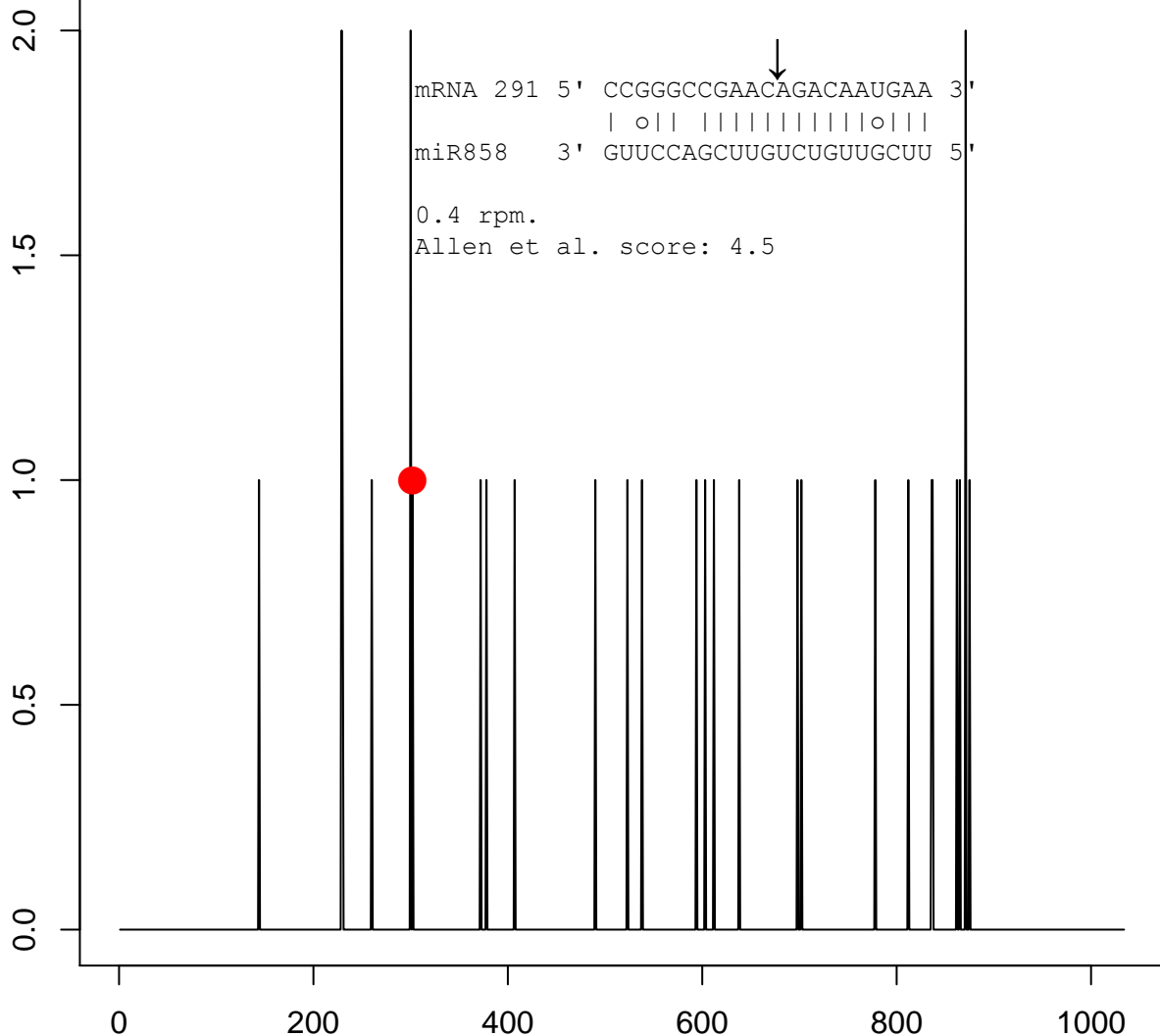


VIT\_09s0002g01400

MYB7\_1

category=4, p=0.56

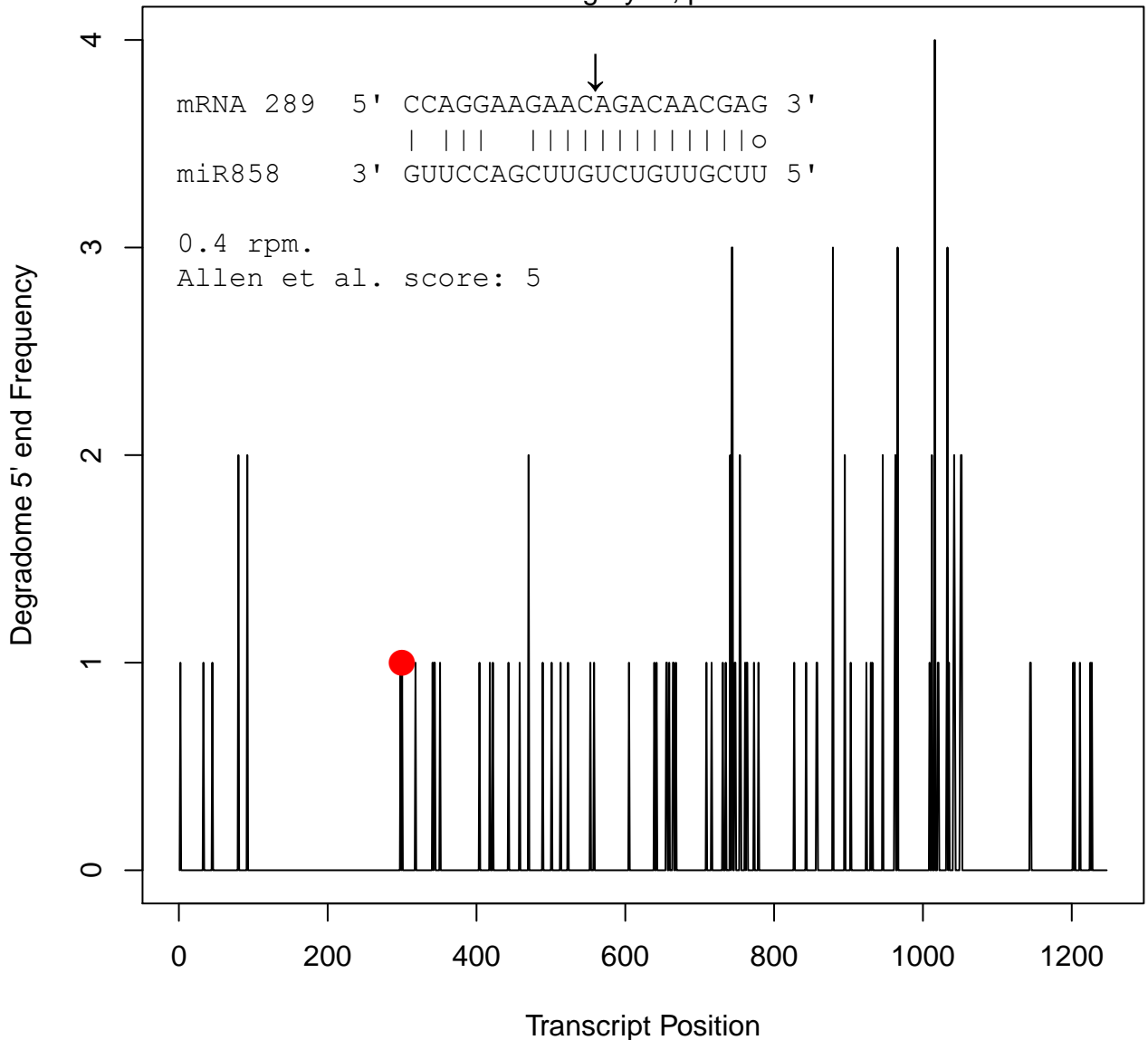
Degradome 5' end Frequency



VIT\_07s0005g01210

MYB12\_2/MYBF1

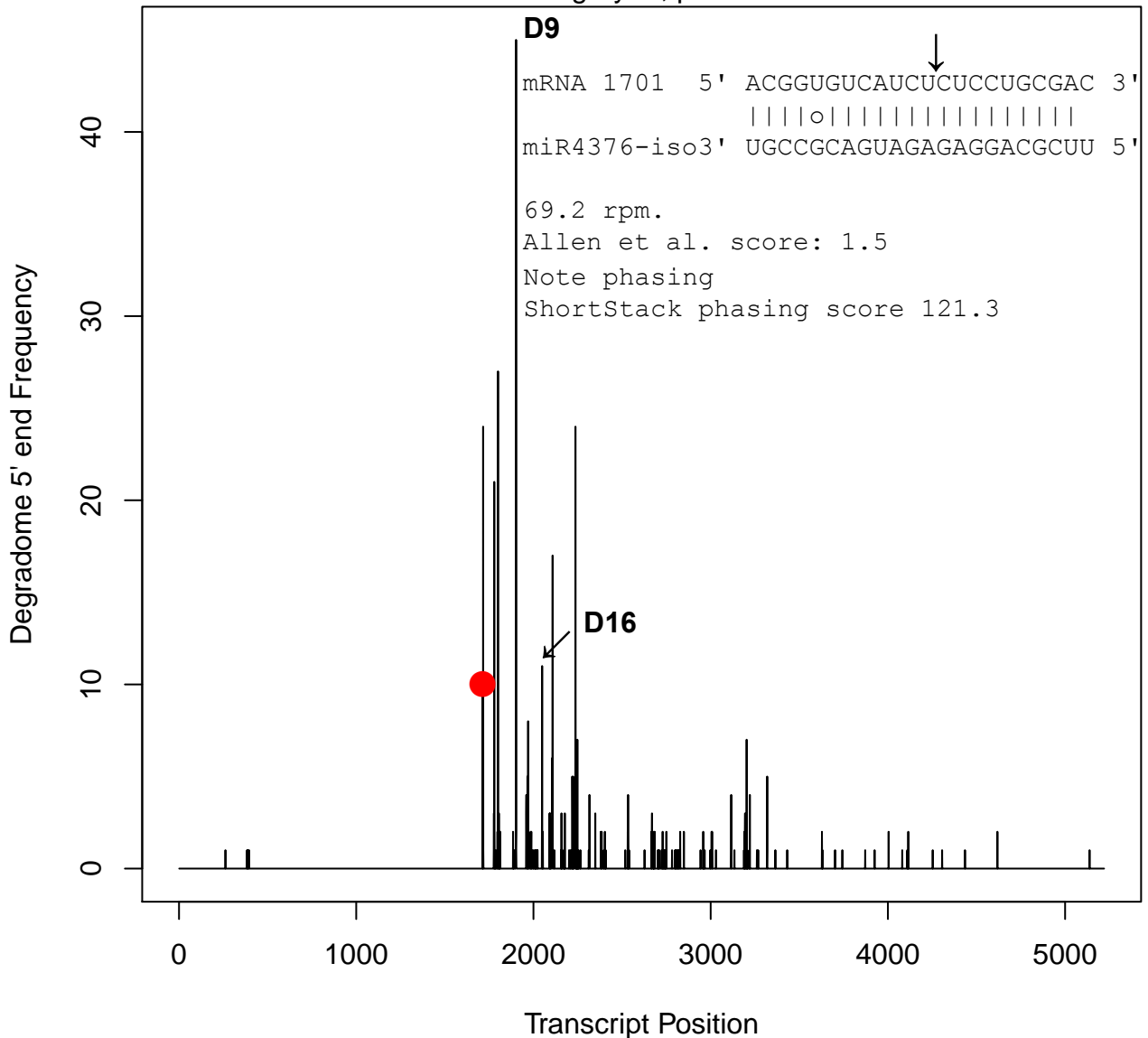
category=4, p=0.73



VIT\_11s0052g00320

Ca2+-ATPase 10 ACA10

Pantaleo pseudo-degradome sRNA libraries; validated in public sRNAs. cat2, p=0.057  
category=2, p=0.007

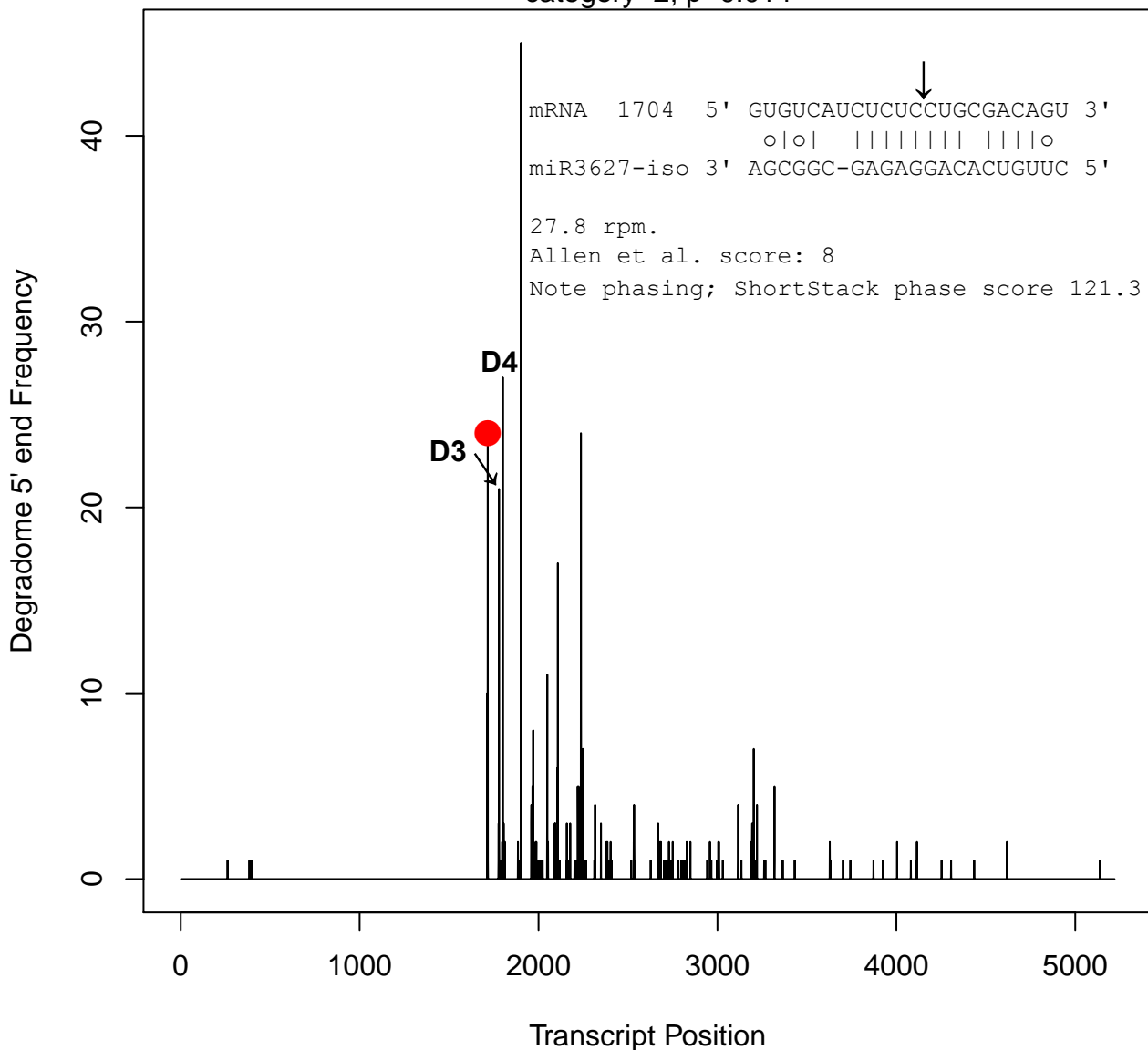




VIT\_11s0052g00320

Ca2+-ATPase 10 ACA10

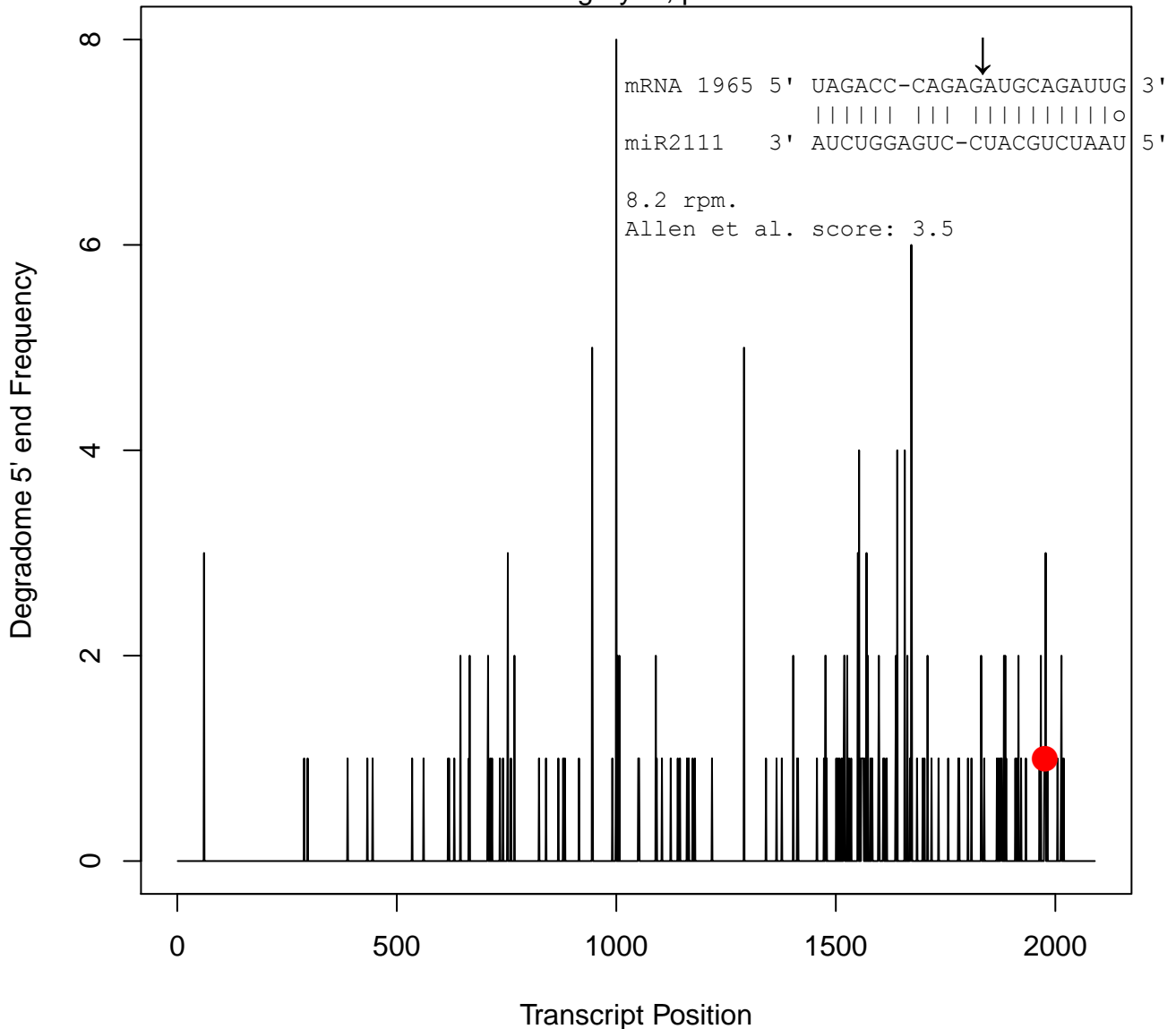
Pantaleo pseudo-degradome sRNA libraries; validated in public sRNAs. cat4, p=0.18  
category=2, p=0.014



# VIT\_03s0180g00120

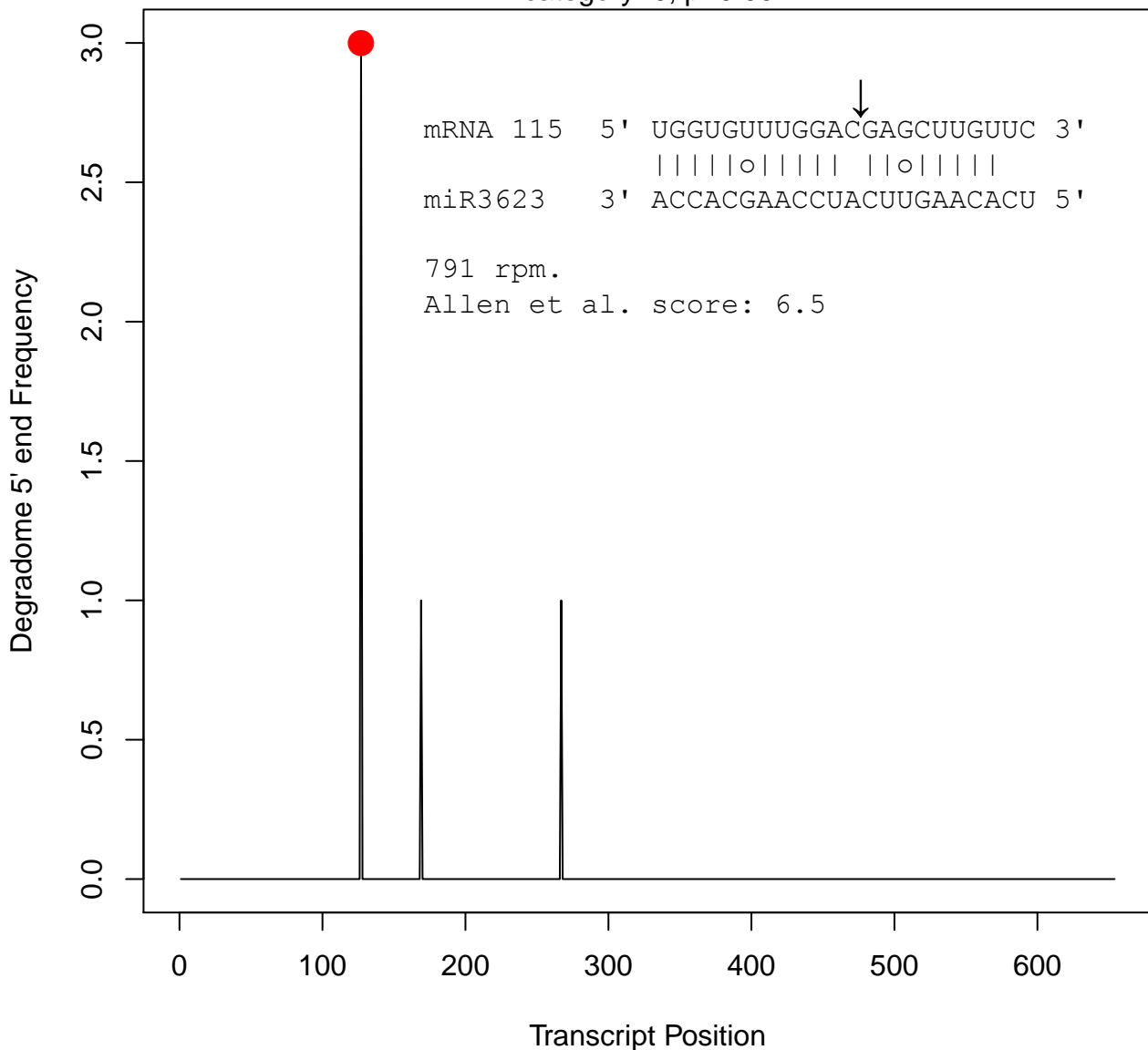
## NHD1, Sodium hydrogen antiporter

category=4, p=0.19



VIT\_18s0041g02210  
TIR-NBS-Leucine Rich Repeat receptor

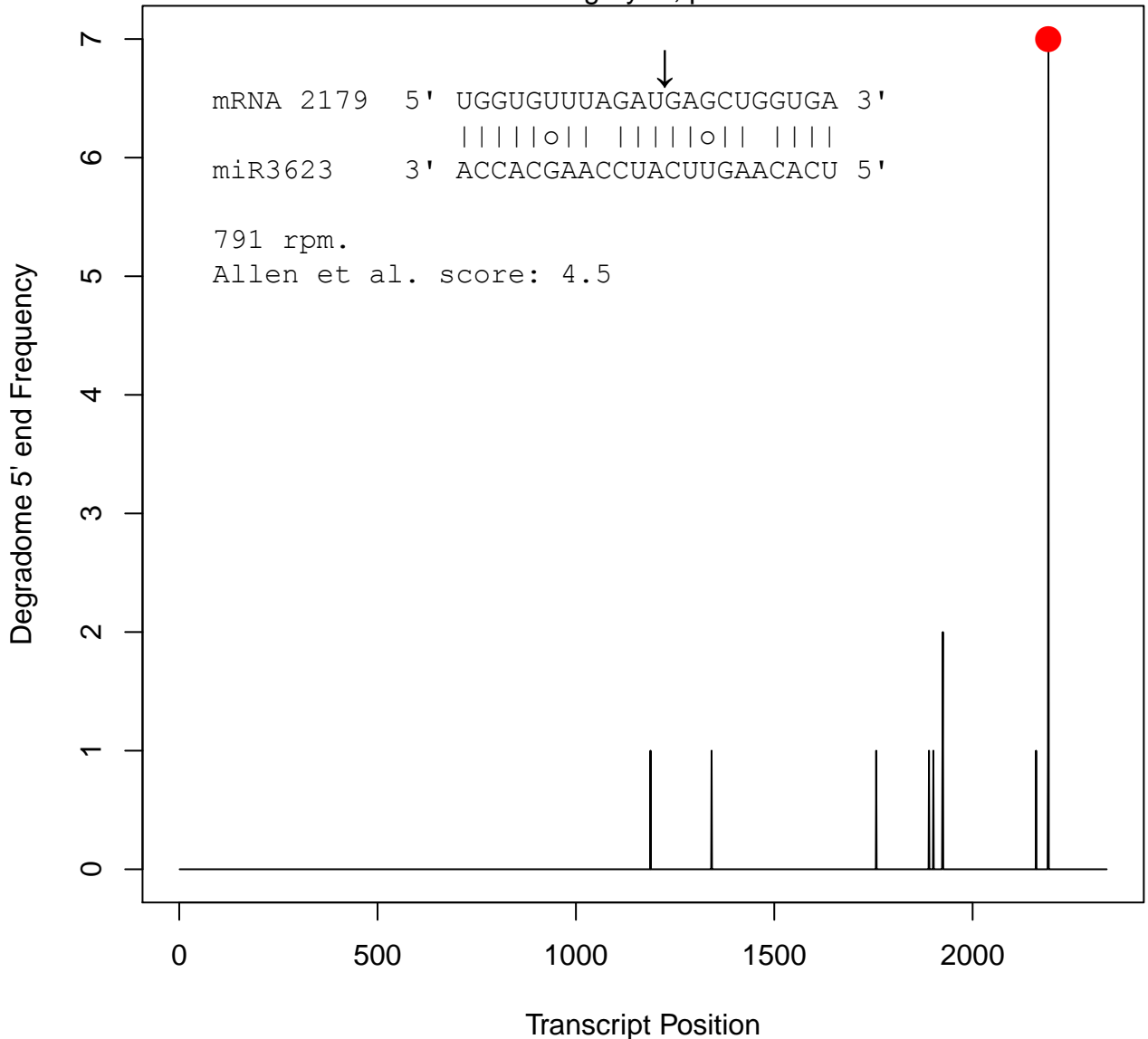
category=0, p=0.007



# VIT\_05s0029g00780

## NB-ARC R protein L6

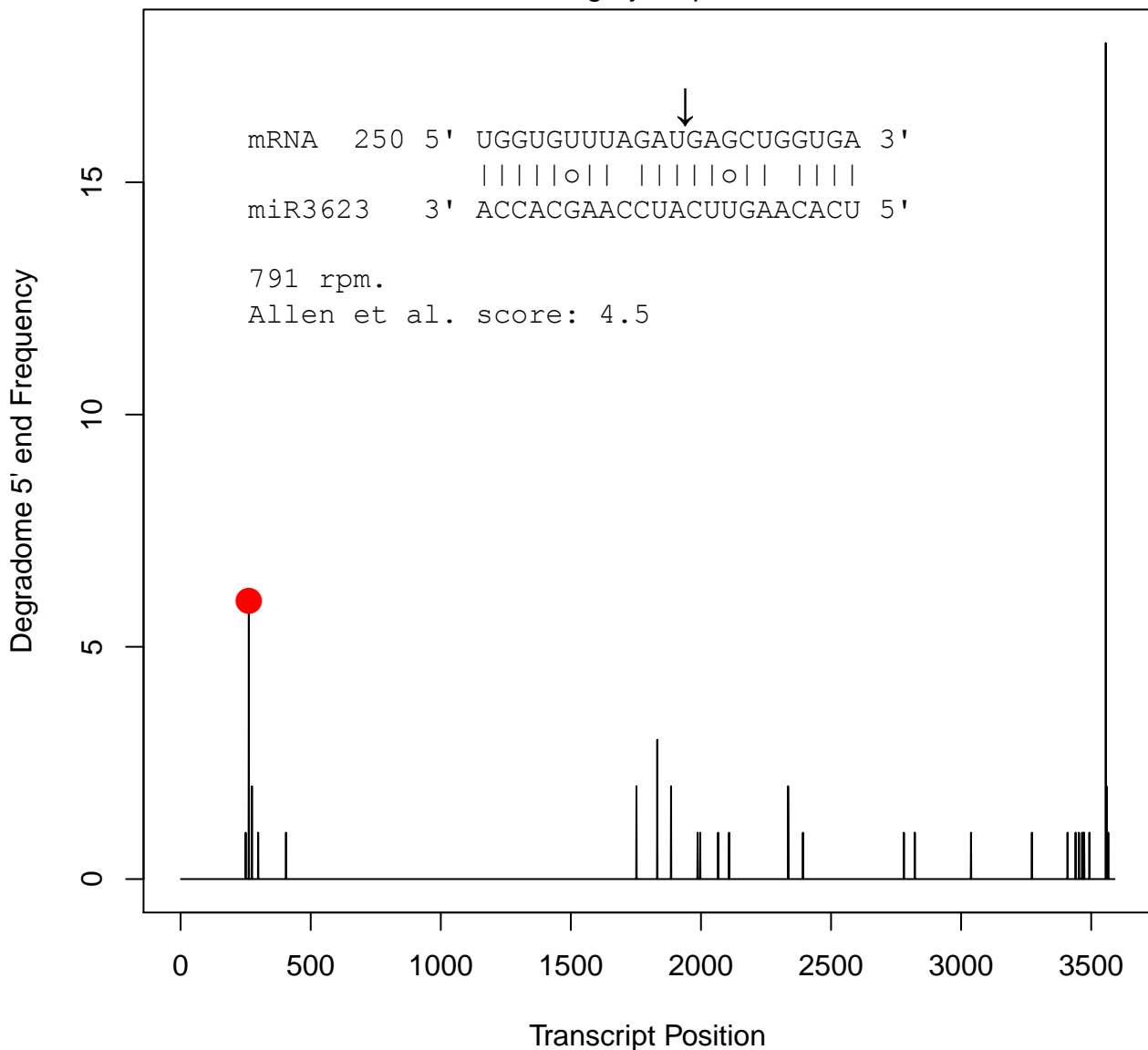
category=0, p=0.01



VIT\_05s0029g00870

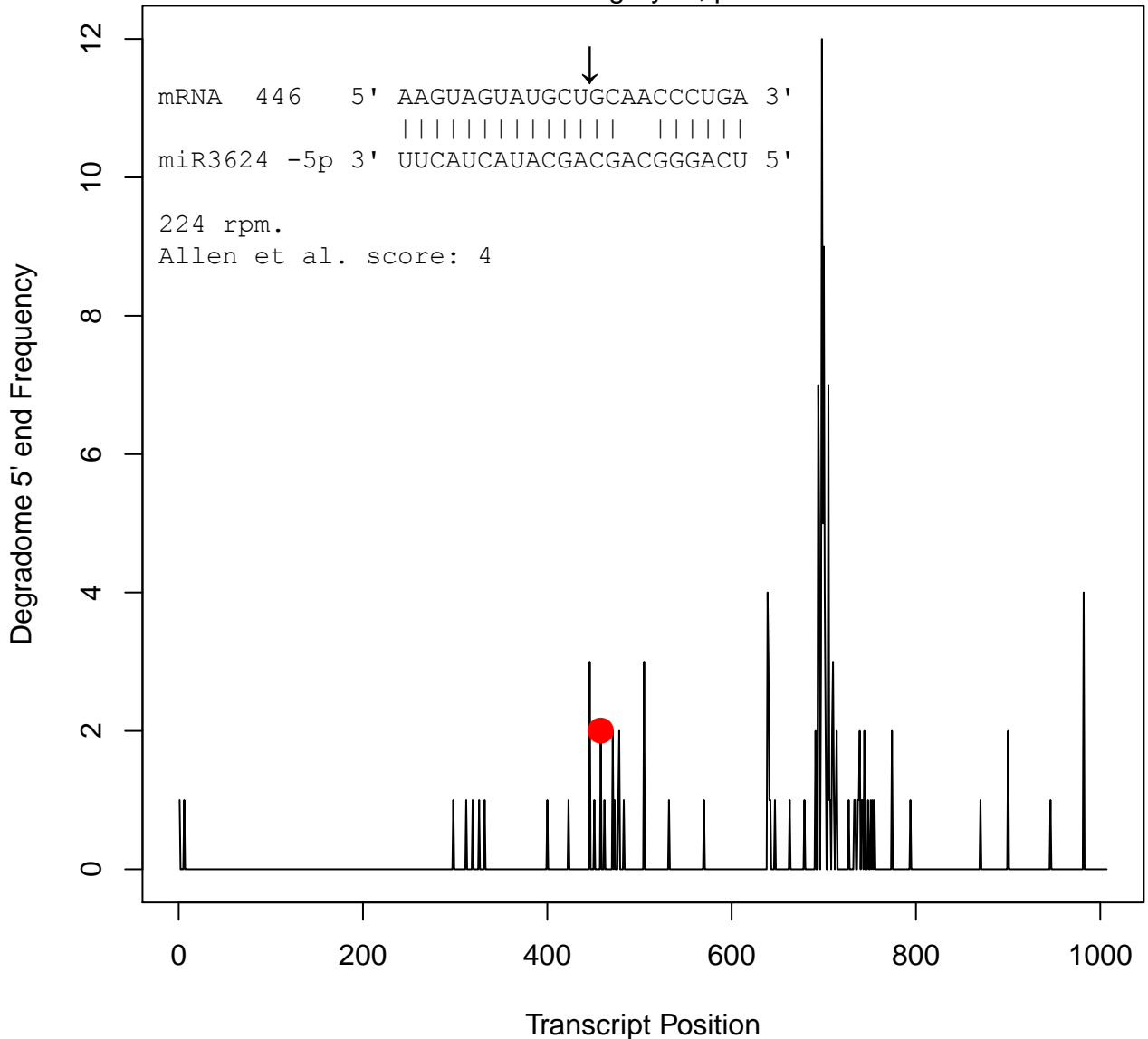
resistant to *P. syringae* 4, RPS4

category=2, p=0.40



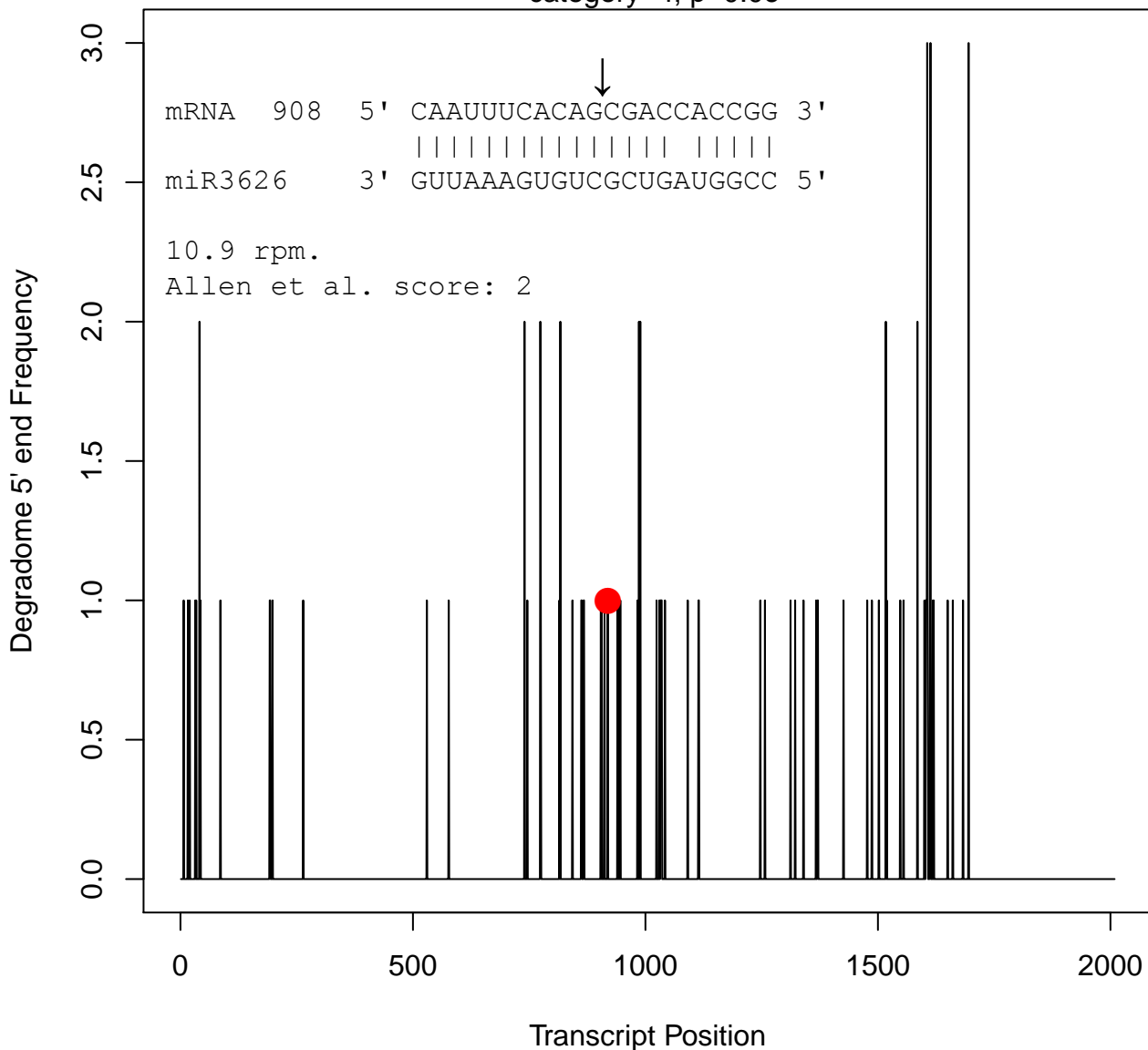
VIT\_00s0194g000330  
METAL ION BINDING PROTEIN-RELATED; Proline-rich

category=3, p=0.03



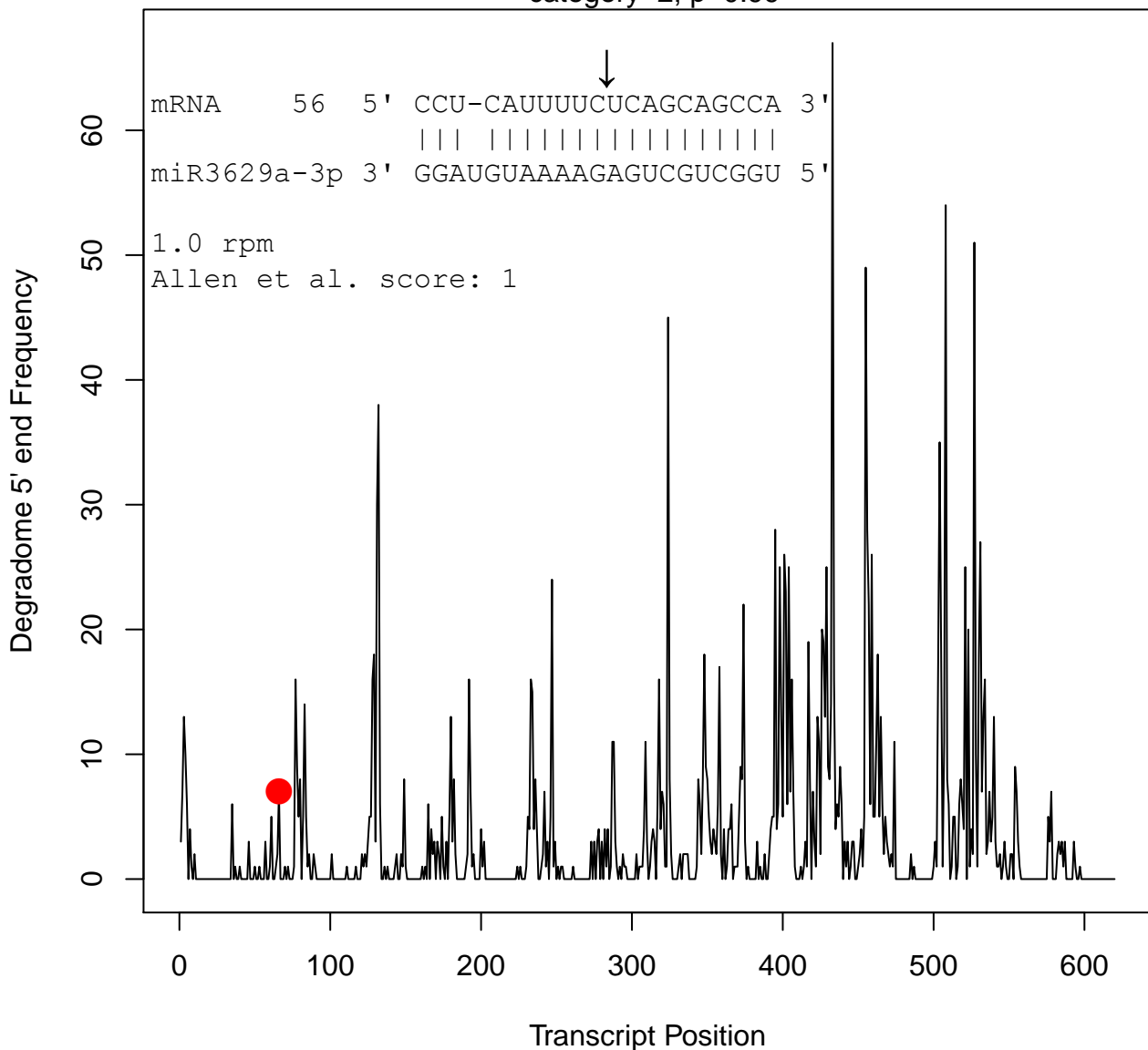
VIT\_08s0007g04400  
DEAD-box ATP-dependent RNA helicase 38-like

category=4, p=0.03



VIT\_07s0031g01230  
Ribosomal protein L30 (RPL30A)

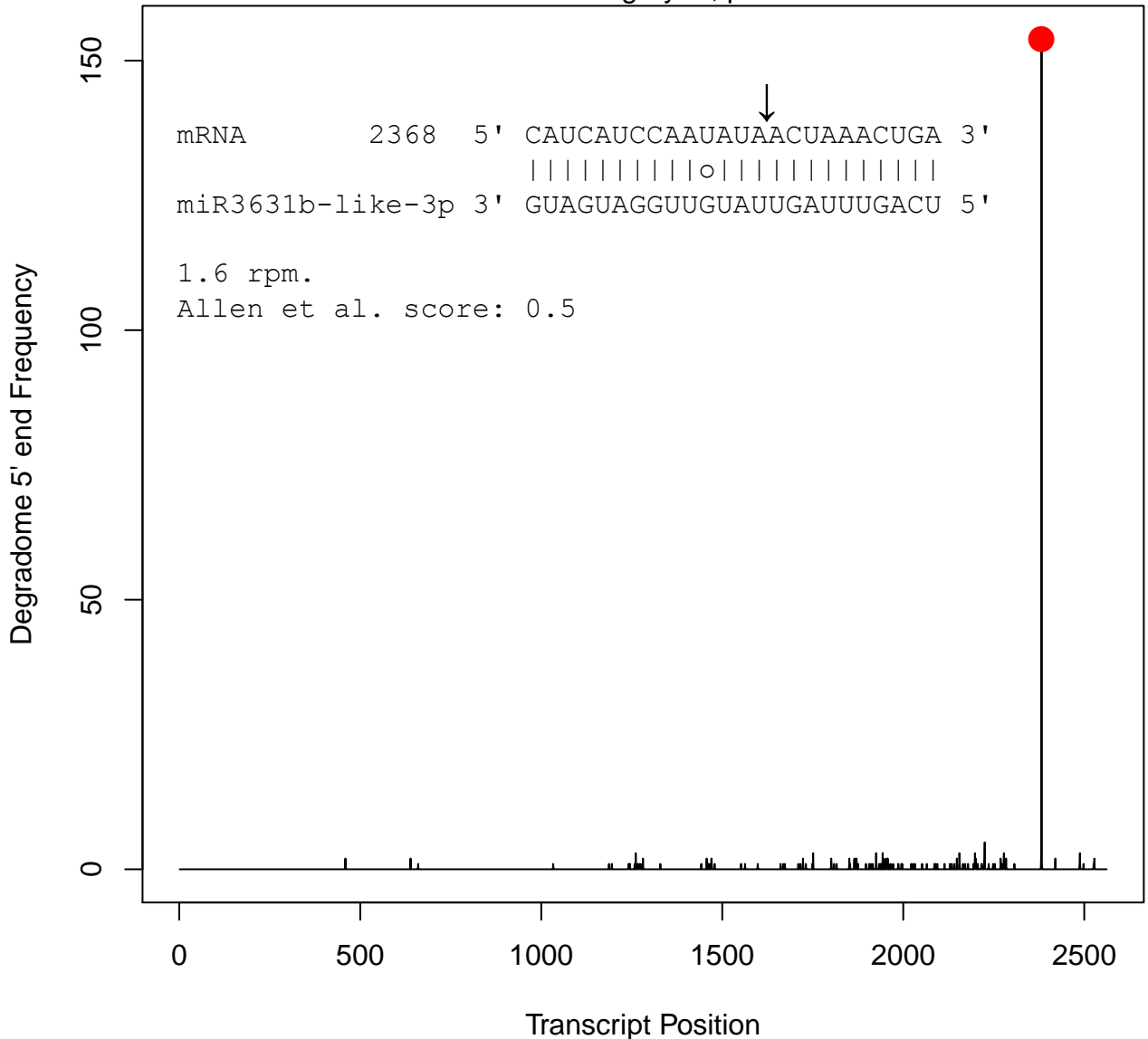
category=2, p=0.99





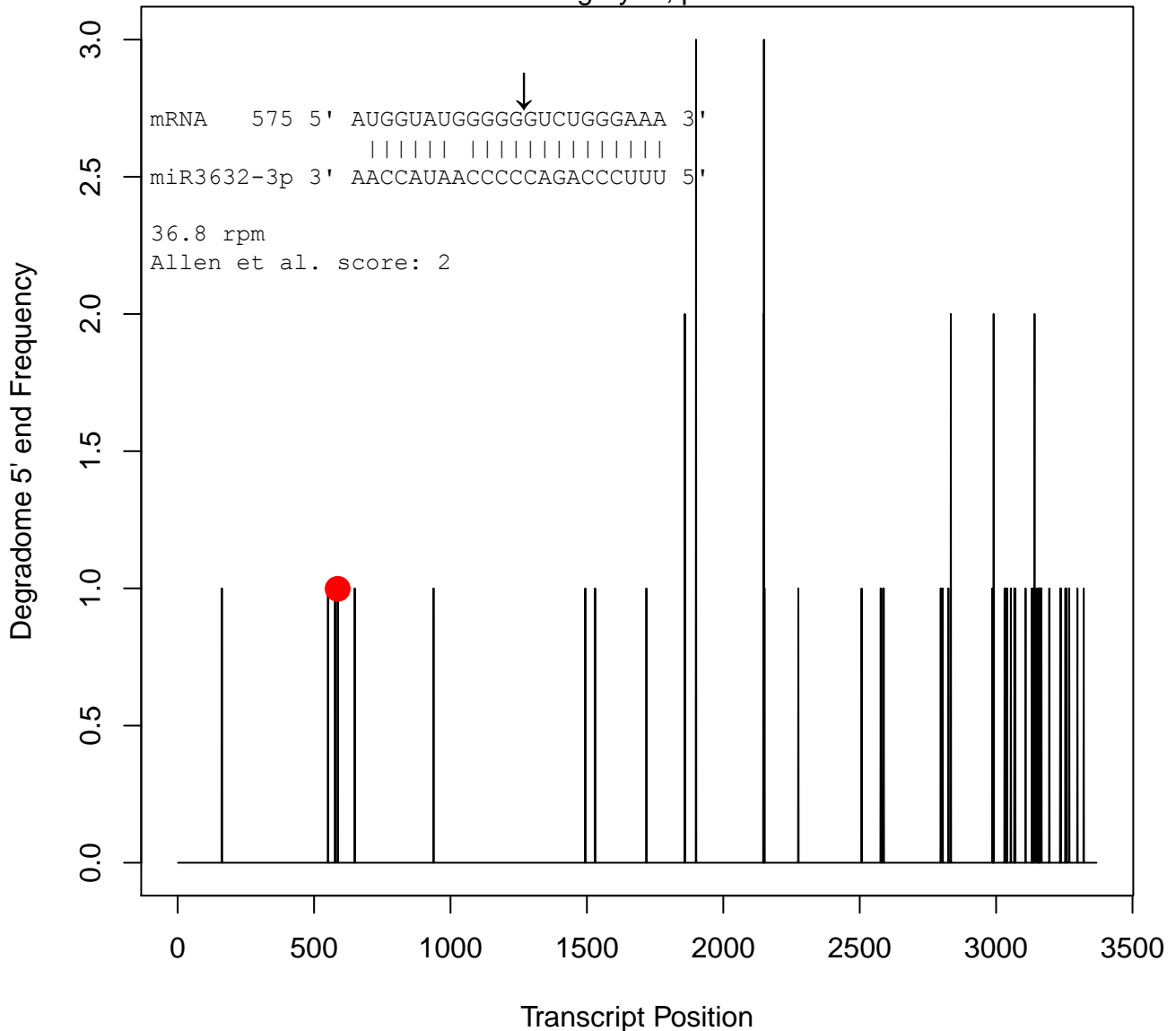
**VIT\_05s0020g04610**  
**protein kinase, SYM10 Nod factor recognition protein**

category=0, p=0.06



VIT\_13s0067g00790  
R protein, PRF disease resistance protein

category=4, p=0.03

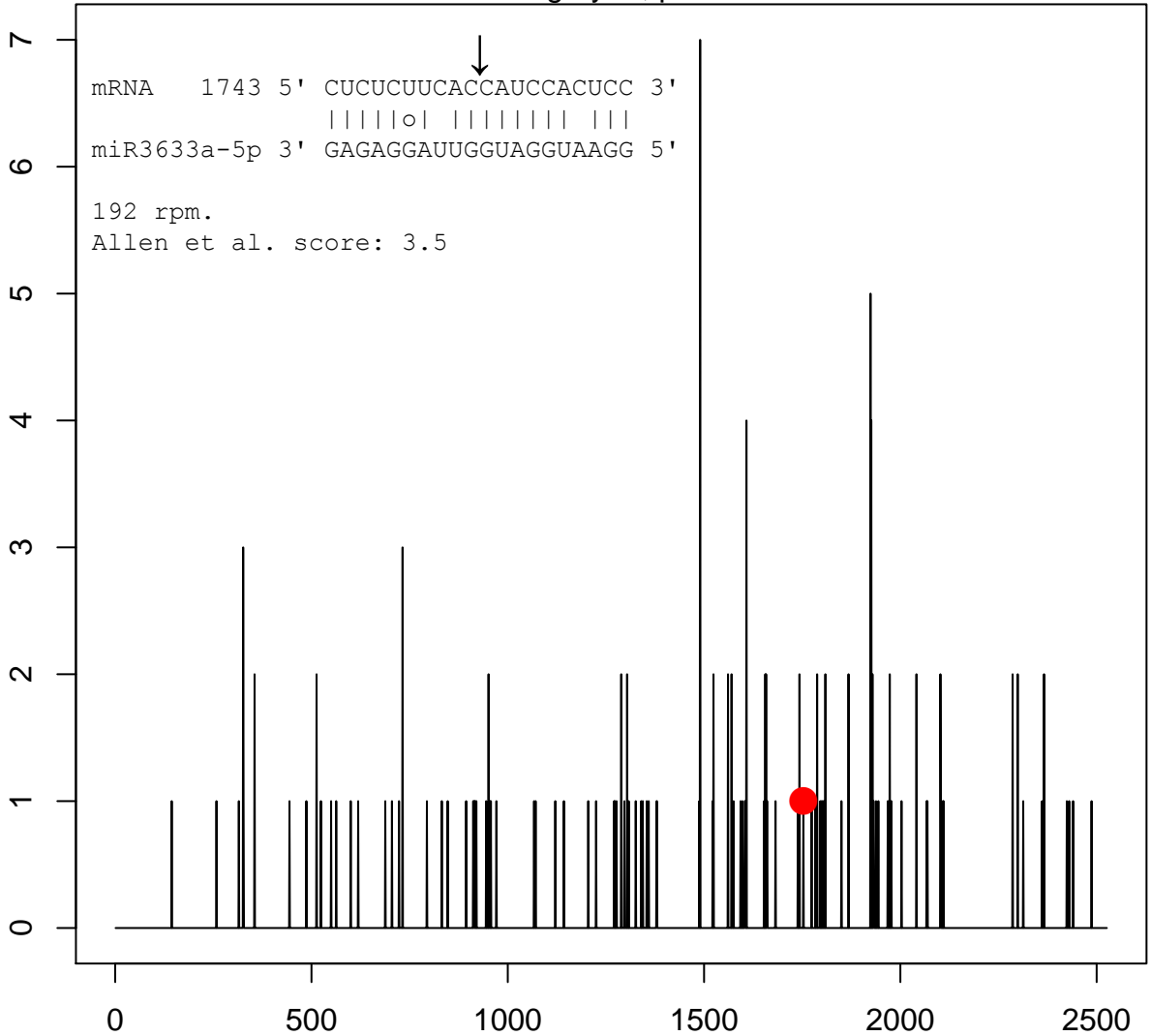


VIT\_05s0051g00590

Pectate lyase

category=4, p=0.52

Degradome 5' end Frequency



Transcript Position

# VIT\_17s0000g05850

## ABC transporter ATATH1 (ABC2 homolog1)

category=4, p=0.99

