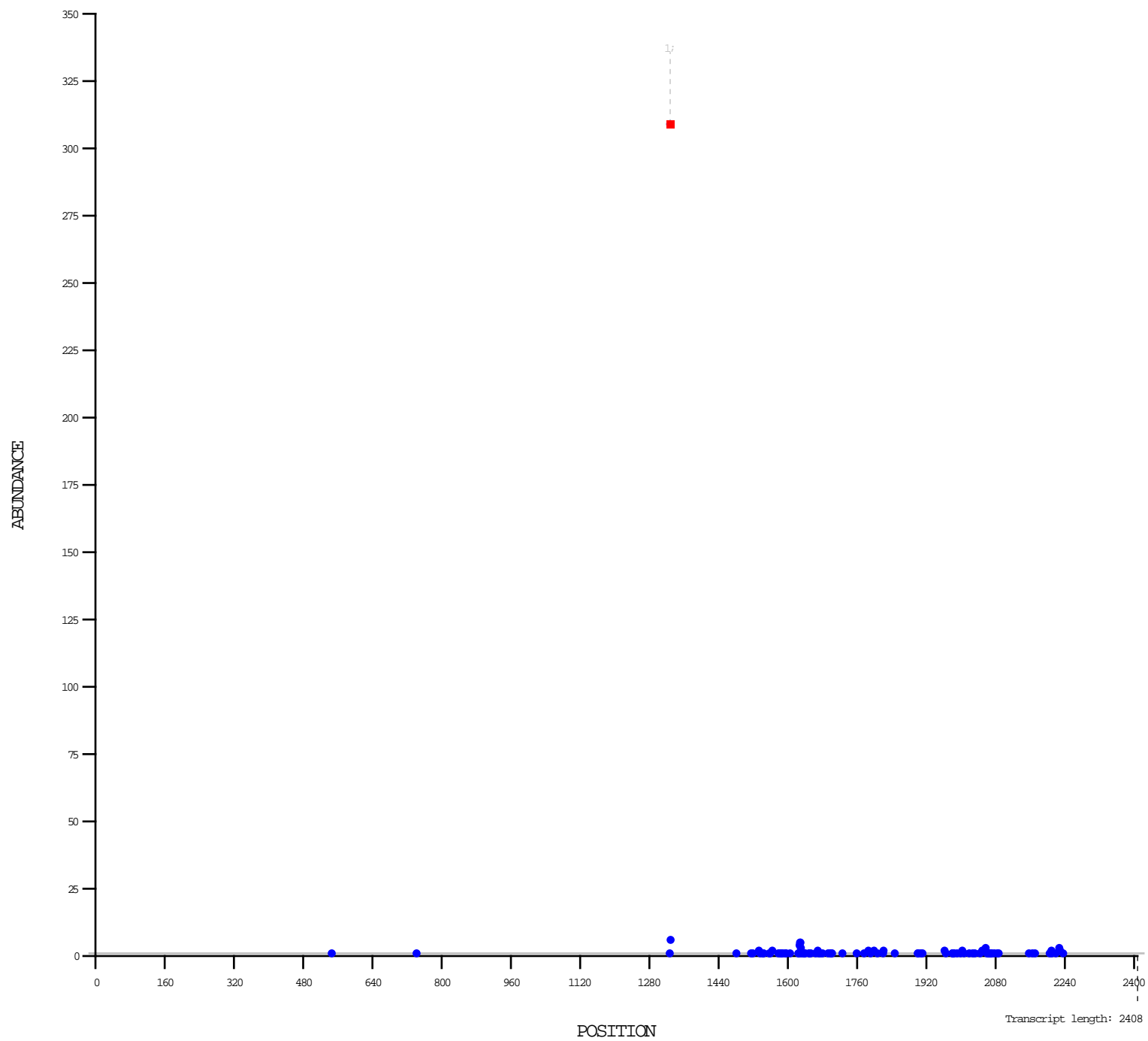


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

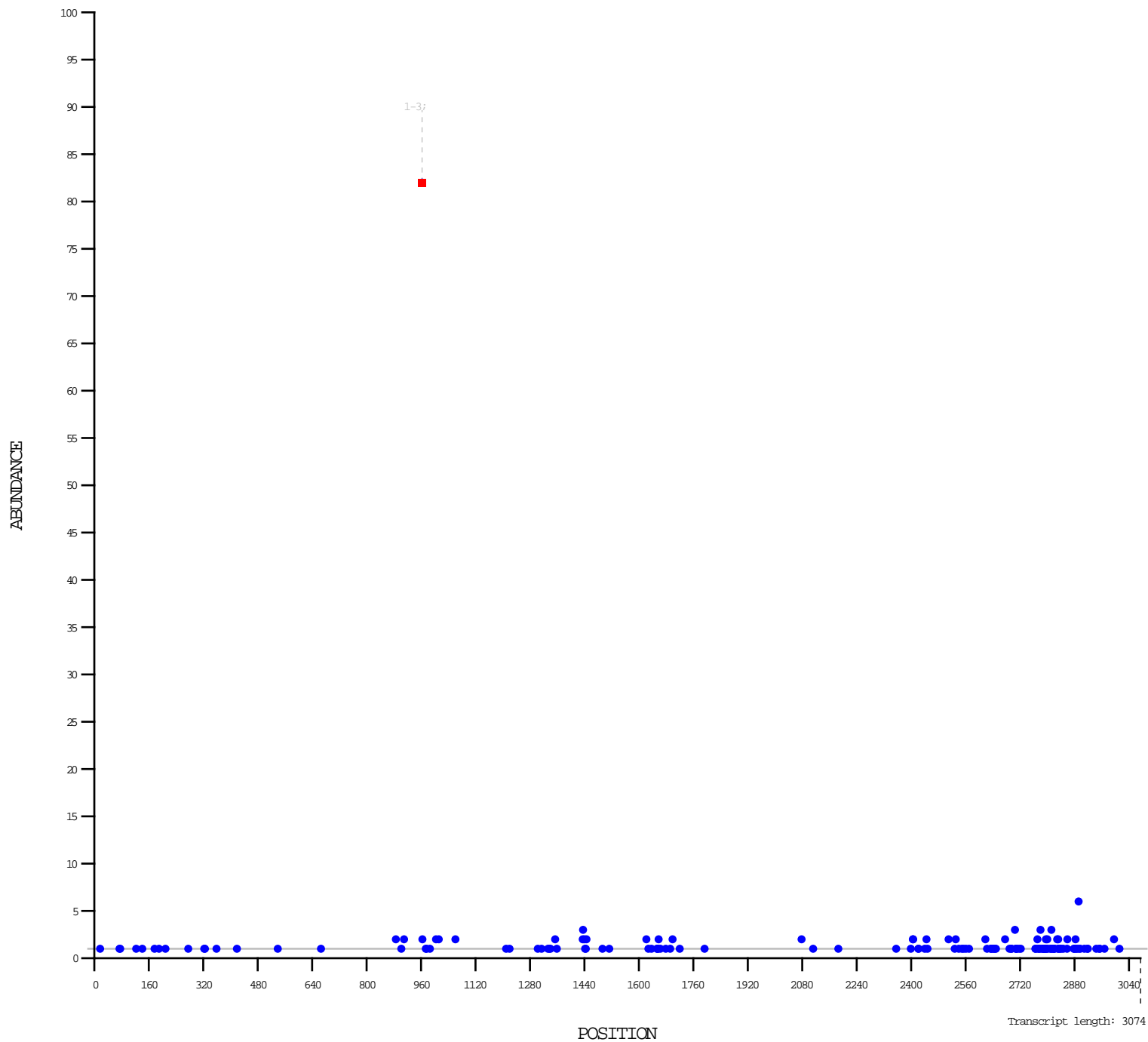
■ 0 #1 Position:1767 Abundance: 2238.00(deg) 5(sRNA)  
 5' TGCCITGGCTCCCTGATGCCA 3' ID:  
       |||||||  
 3' TCCTACGGACCAGGGACATACGGACCTCCTC 5' Score: 1.0  
       ||||||| p-value: 0.0



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
Degradome alignment: ● Median: —

■ 0 #1 Position:1328 Abundance: 309.00(deg) 5(sRNA)  
5' TGCCTGGCTCCCTGTATGCCA 3' ID:  
||||| ||||||||| ||||| Score: 1.0  
3' TCGTACGGACCGAGGGACATACGGACCTCCTC 5' p-value: 0.0



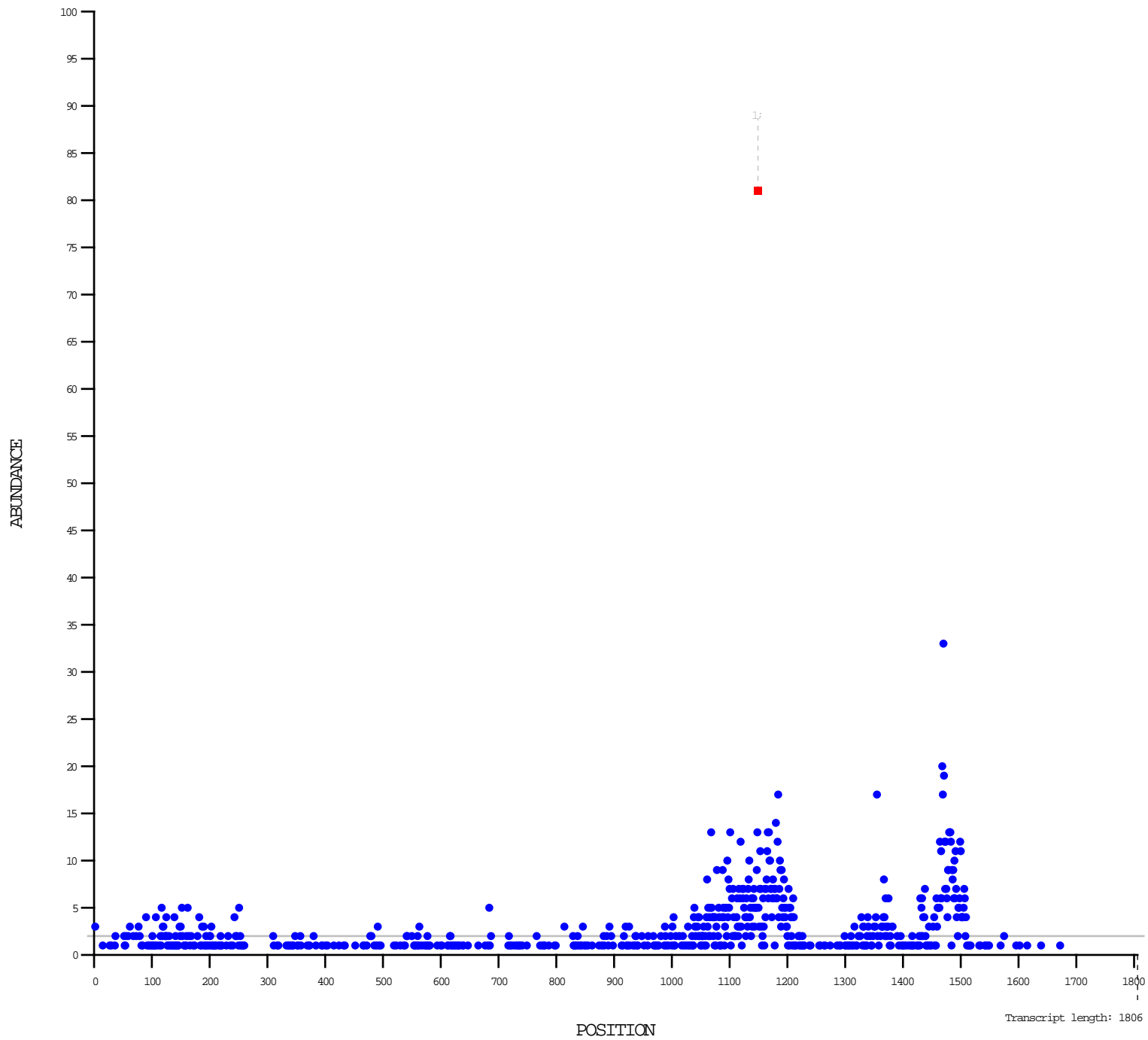


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0	#1	Position:963	Abundance: 82.00(deg)	7(sRNA)
		5'	TCGGACCAGGCGCTTCATCCCC	3'
			o	
			3'	CTTAGGCCCTGGTCCGAGTA-GGGTCCGTAGA
				5'
				p-value: 0.0
■ 0	#2	Position:963	Abundance: 82.00(deg)	2(sRNA)
		5'	TCGGACCAGGCGCTTCATCCCT	3'
			o	
			3'	CTTAGGCCCTGGTCCGAGT-AGGGTCCGTAGA
				5'
				p-value: 0.0
■ 0	#3	Position:963	Abundance: 82.00(deg)	2(sRNA)
		5'	TCGGACCAGGCGCTTCATCCCTC	3'
			o	
			3'	CTTAGGCCCTGGTCCGAGTAGGGTCCGTAGAC
				5'
				p-value: 0.0

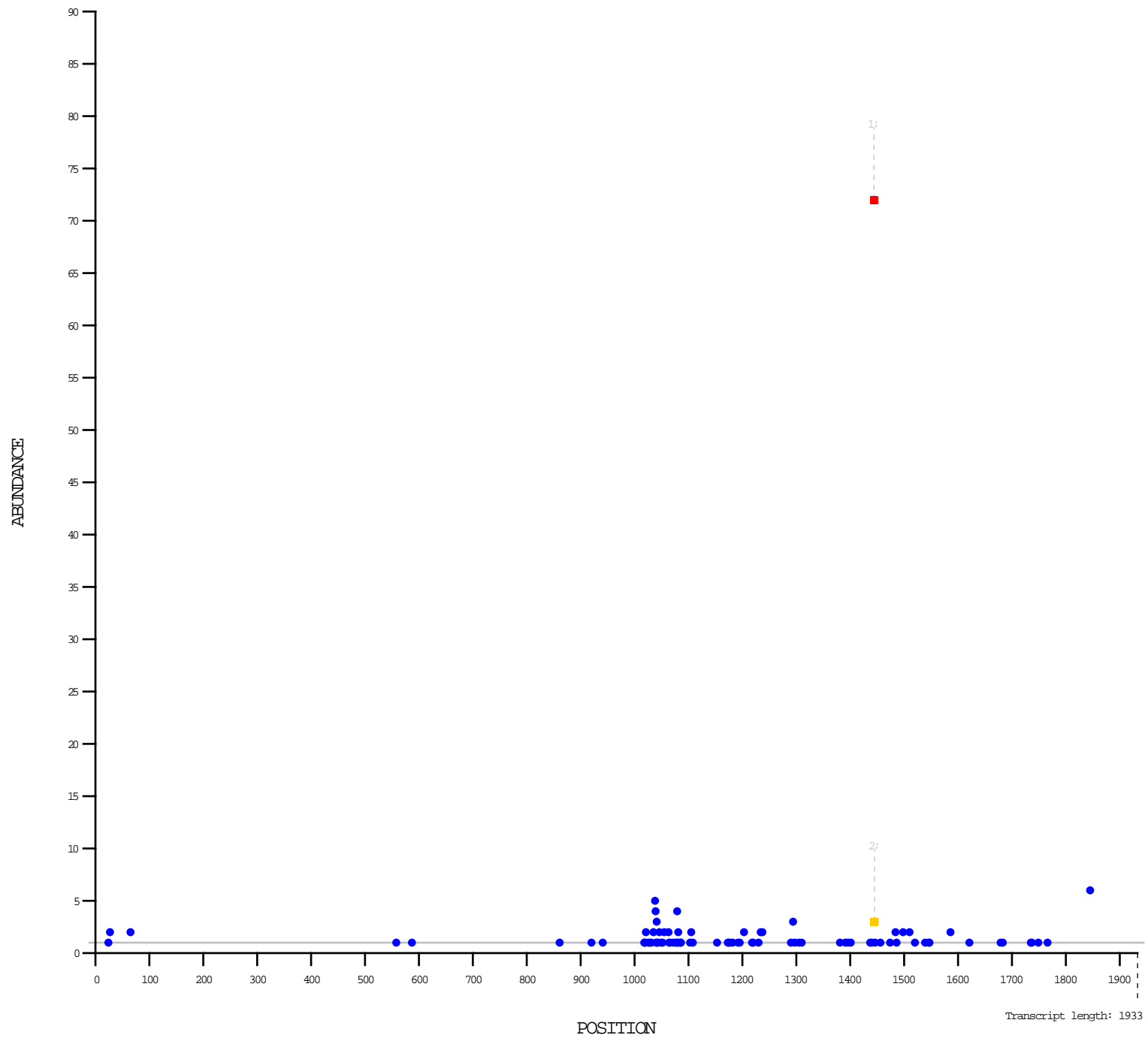
Transcript length: 3074





Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
Degradome alignment: ● Median: —

■ 0 #1 Position:1149 Abundance: 81.00(deg) 1(sRNA)  
5' TGCTGGAGAGCAGGCC-ACCT 3' ID:  
|||||o  
3' ACCTACGACCCTCTGGTACGATGCCACTT 5' p-value: 0.0



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

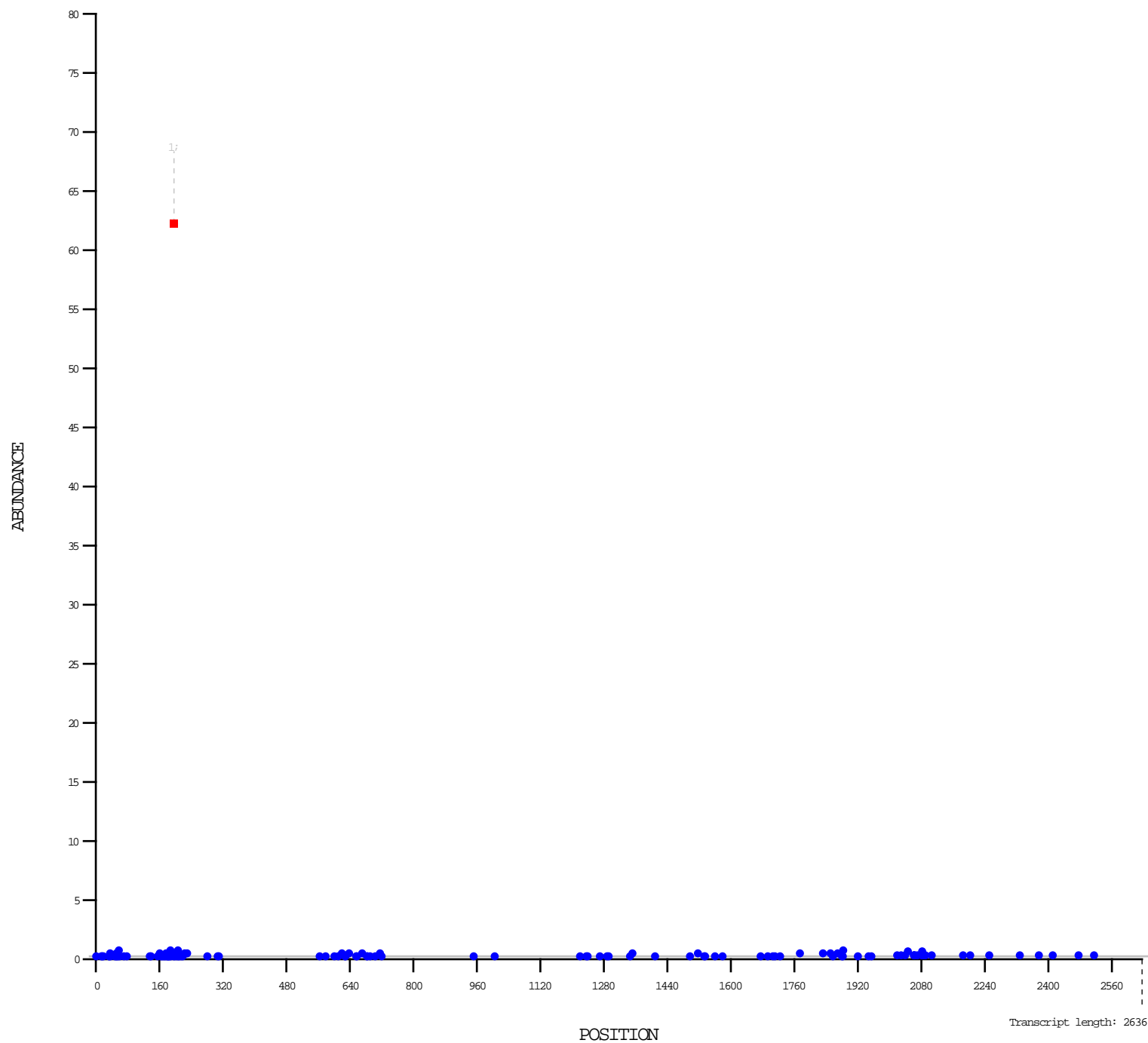
Degradome alignment: ● Median: —

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■ 0 #1 Position:1444 Abundance: 72.00(deg) 8(sRNA)
      5' TGACAGAGAGAGTGGCAC 3' ID:
          |||||
      3' ACAGACTGTCCTCCTCCTCGTGGTCAACGGC 5' Score: 1.0
          p-value: 0.0

■ 2 #2 Position:1445 Abundance: 3.00(deg) 1(sRNA)
      5' TTGACAGAGAGAGCGAGCAC 3' ID:
          o|||
      3' AACAGACTGTCCTCCTCCTCGTGGTCAACGG 5' Score: 1.5
          p-value: 0.0
    
```

Transcript length: 1933



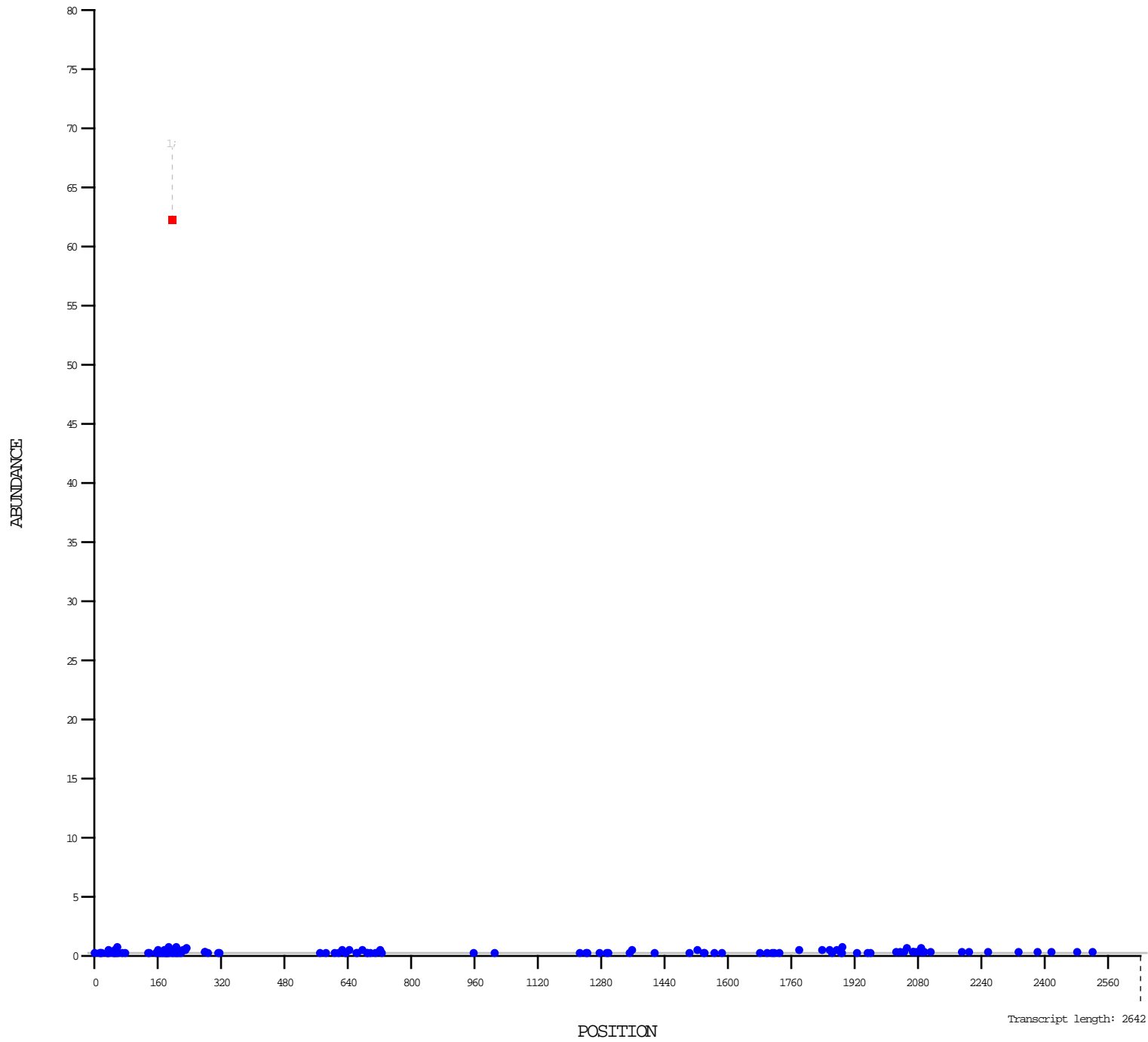
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
Degradome alignment: ● Median: —

■ 0 #1 Position:197 Abundance: 62.25(deg) l(sRNA)  
5' TTAGATGACCATCAGCAACA 3' ID:  
||||||||| ||||||||||| Score: 1.0  
3' TGTTATCTACTGTGAGTGTGTTGTTGTG 5' p-value: 0.0





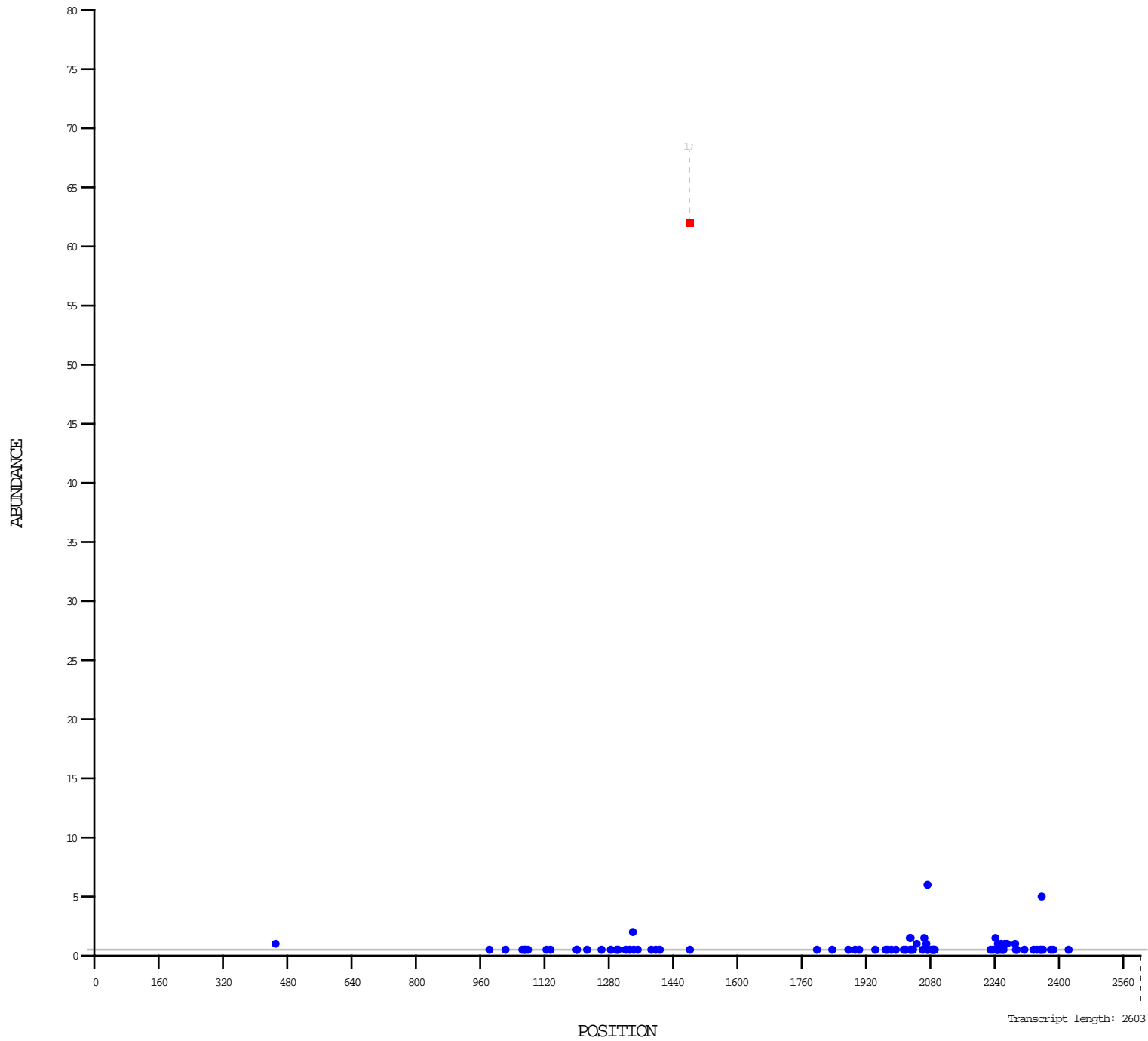




Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:197 Abundance: 62.25(deg) l(sRNA)  
 5' TTAGATGACCATCAGCAAACA 3' ID:  
 ||||| Score: 1.0  
 3' TGTTAATCTACTGTGATGTTTGTGGTTTGTG 5' p-value: 0.0





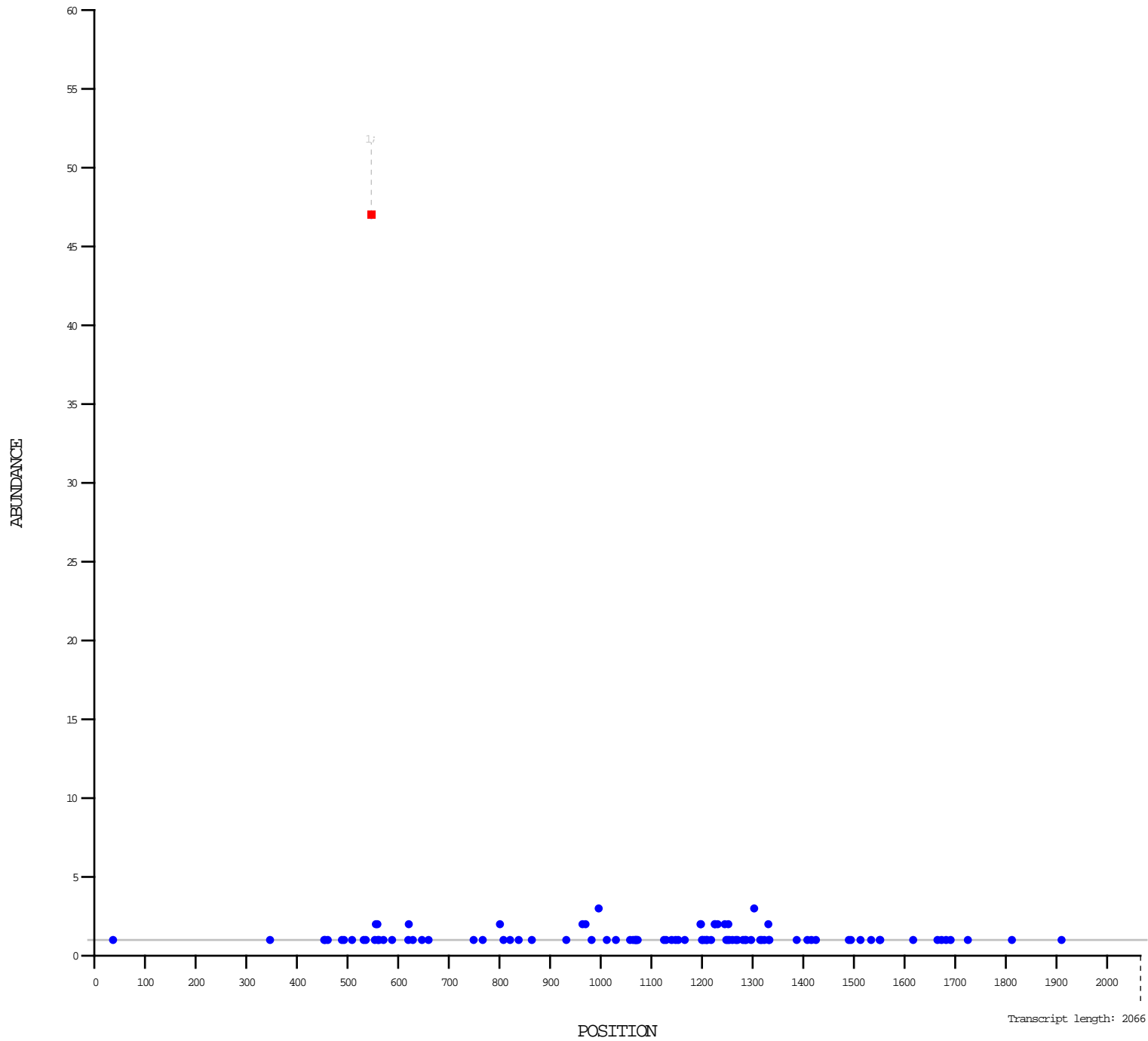
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

■ 0 #1 Position:1481 Abundance: 62.00(deg) 5(sRNA)  
 5' TGCCTGGCTCCCTGTATGCCA 3' ID:  
 |||||  
 3' GCGTACGGACCGAGGGACATACCGACCTCCTC 5' Score: 2.0  
 p-value: 0.0





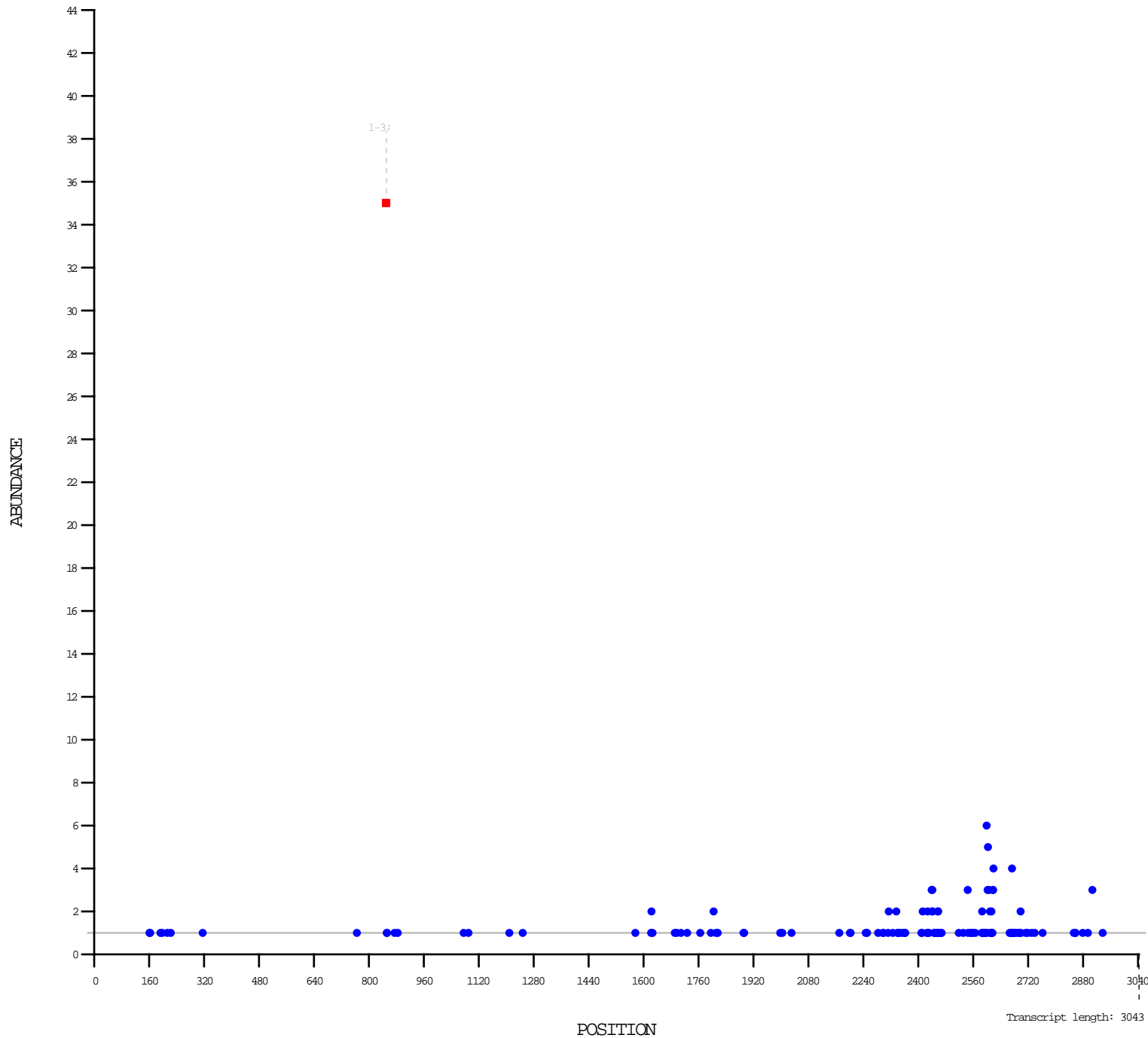


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:547 Abundance: 47.00(deg) 6(sRNA)  
 5' TGAAGTGTGTTGGGGGACTC 3' ID:  
 |||||o|||o|||  
 3' CTTTACTCAGAACCTCCTTGAGTACGAGCG 5' Score: 1.0  
 p-value: 0.0







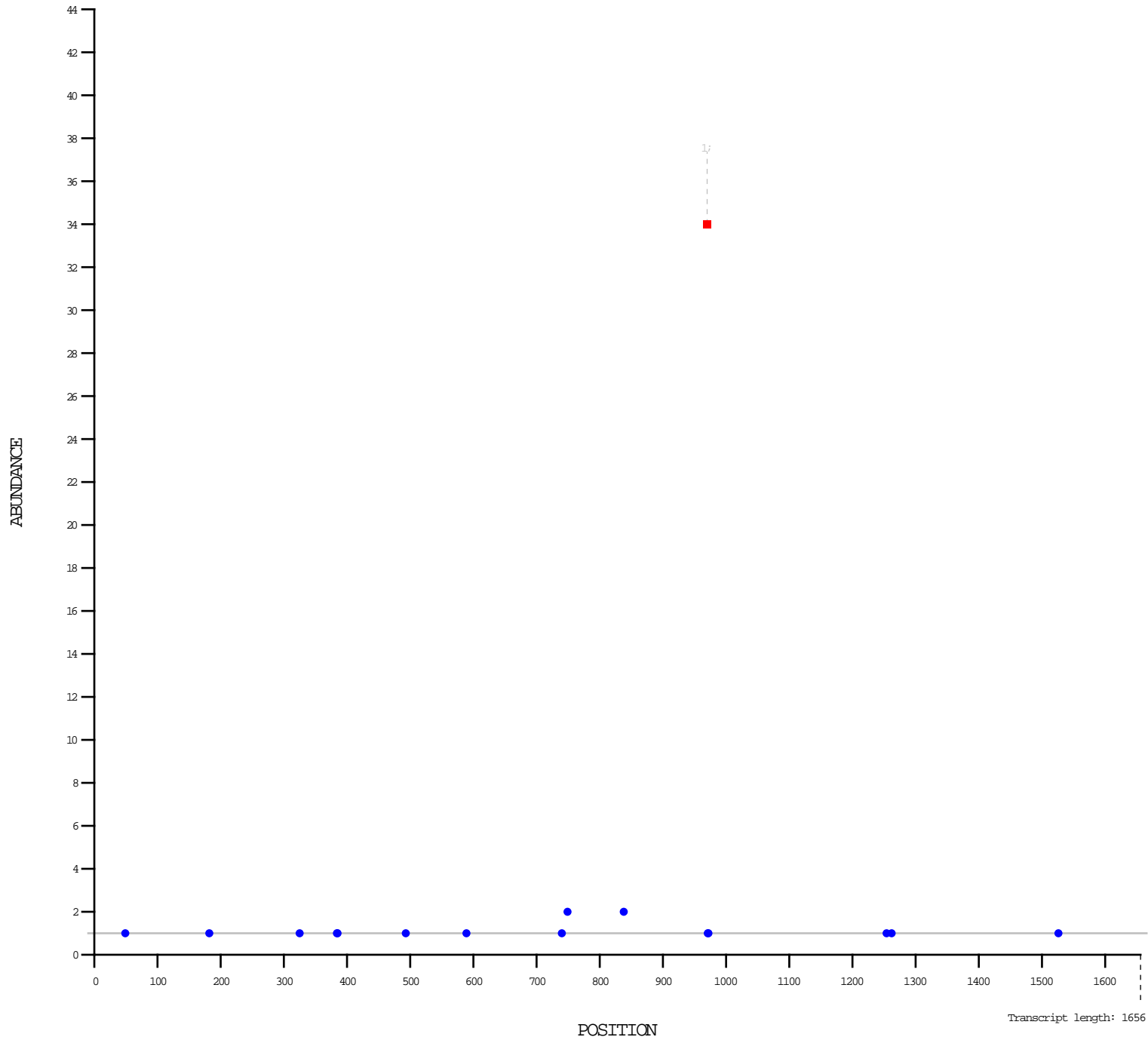
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

■ 0 #1 Position:851 Abundance: 35.00(deg) 7(sRNA)  
 5' TCGGACCAGGCTTCATCCCC 3' ID:  
 o|||||||||||||||||  
 3' CTTAGGCCITGGTCCGAGTA-GGGTTGGTAAA 5' Score: 2.5  
 p-value: 0.0

■ 0 #2 Position:851 Abundance: 35.00(deg) 2(sRNA)  
 5' TCGGACCAGGCTTCATCCCT 3' ID:  
 o|||||||||||||||||  
 3' CTTAGGCCITGGTCCGAGT-AGGGTTGGTAAA 5' Score: 2.5  
 p-value: 0.0

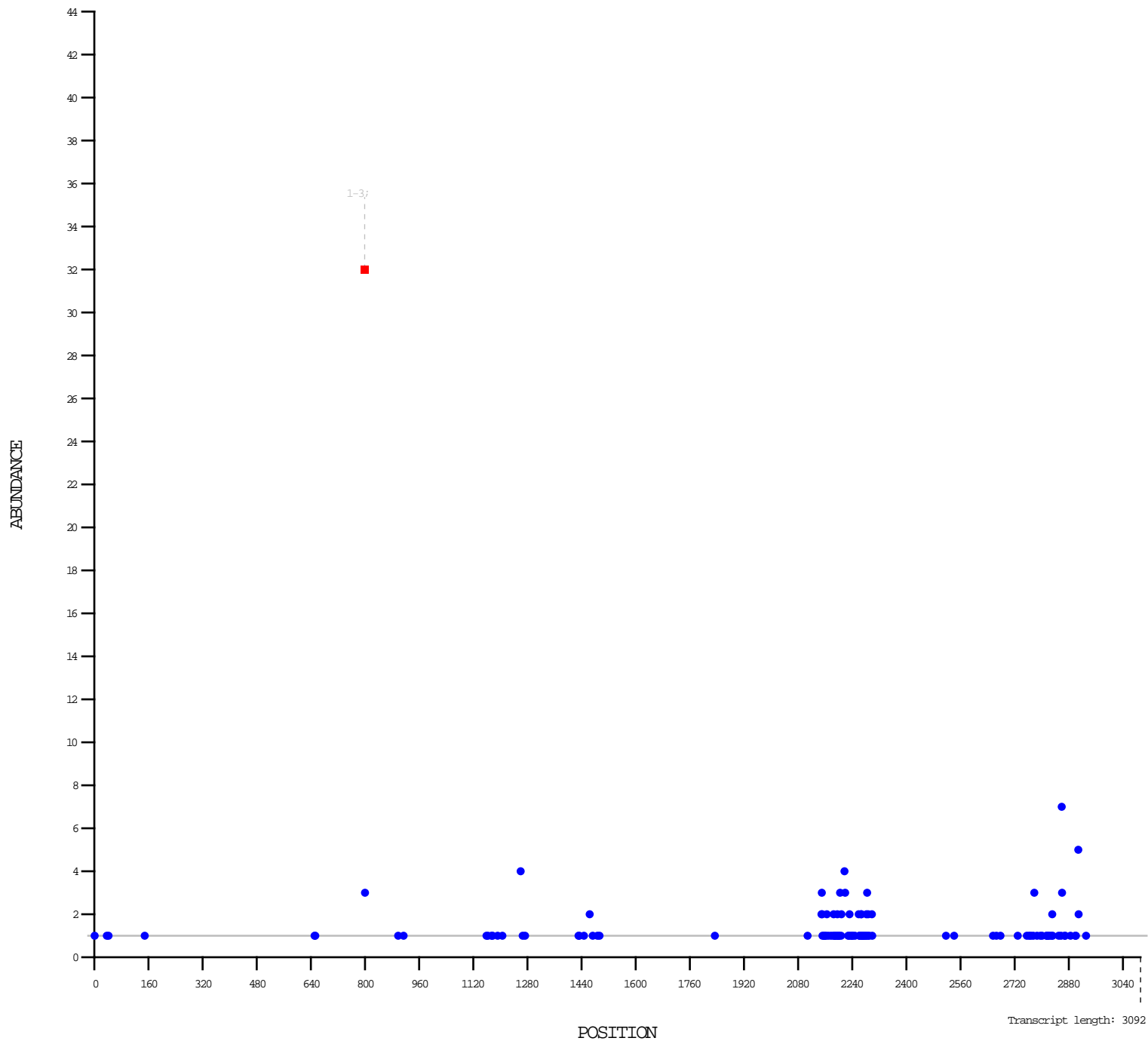
■ 0 #3 Position:851 Abundance: 35.00(deg) 2(sRNA)  
 5' TCGGACCAGGCTTCATCCCTC 3' ID:  
 o|||||||||||||||||o||  
 3' CTTAGGCCITGGTCCGAGTAGGGTTGGTAAAC 5' Score: 3.0  
 p-value: 0.0



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:970 Abundance: 34.00(deg) 2(sRNA)  
 5' TTGGATTGAGGGAGCTCTG 3' ID:  
 o||||| ||||| ||||| ||||| o Score: 3.0  
 3' CATAGAACCTCACTTCCCTCGAGGGGAAGTT 5' p-value: 0.0

Transcript length: 1656



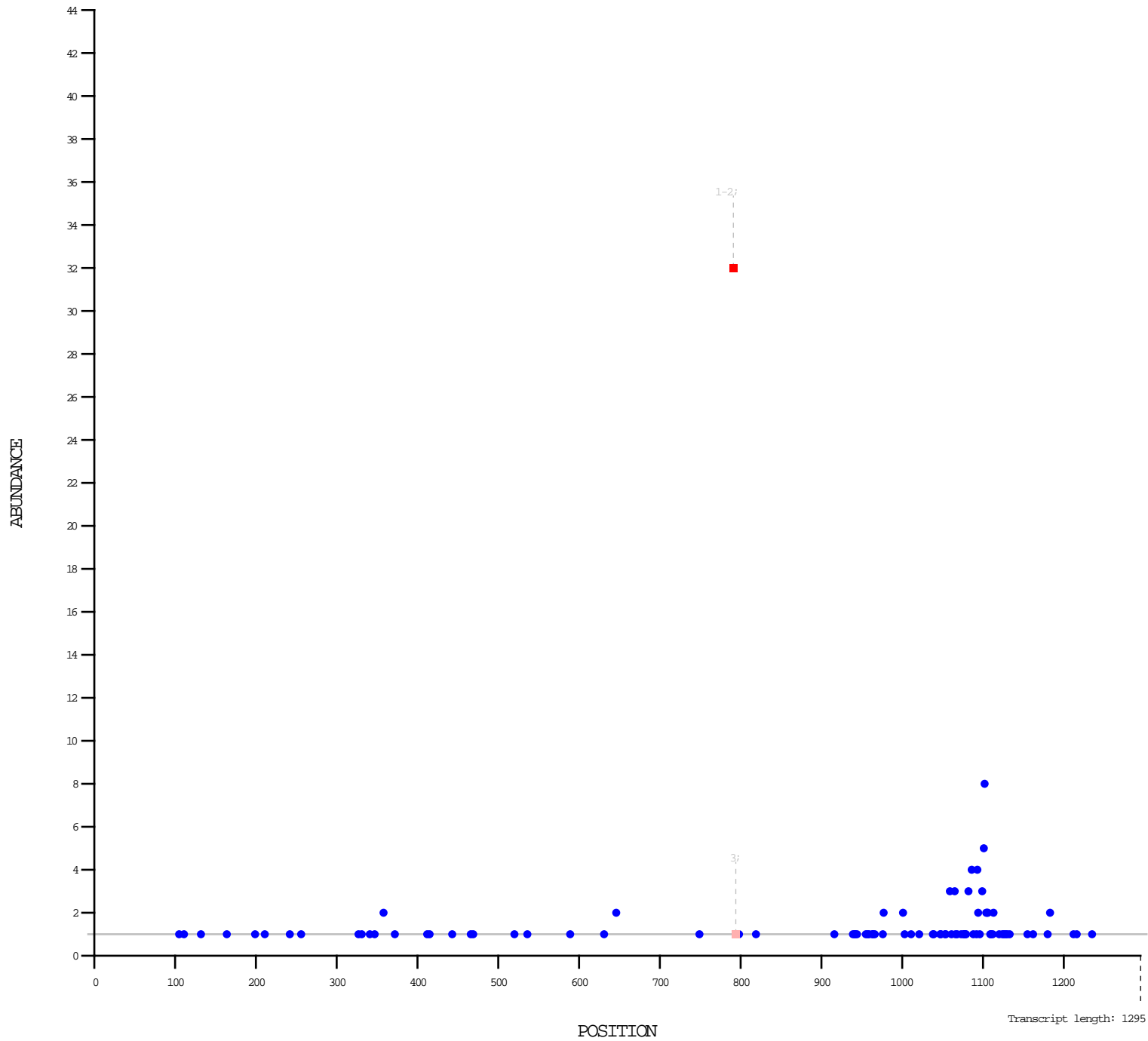
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

■ 0 #1 Position:799 Abundance: 32.00(deg) 7(sRNA)  
 5' TCGGACCAGGCGCTTCATCCCC 3' ID:  
 o||||| 3' Score: 2.5  
 3' CTTAGGCCCTGGTCCGAGTA-GGGTCCGTAGA 5' p-value: 0.0

■ 0 #2 Position:799 Abundance: 32.00(deg) 2(sRNA)  
 5' TCGGACCAGGCGCTTCATCCCT 3' ID:  
 o||||| 3' Score: 2.5  
 3' CTTAGGCCCTGGTCCGAGT-AGGGTCCGTAGA 5' p-value: 0.0

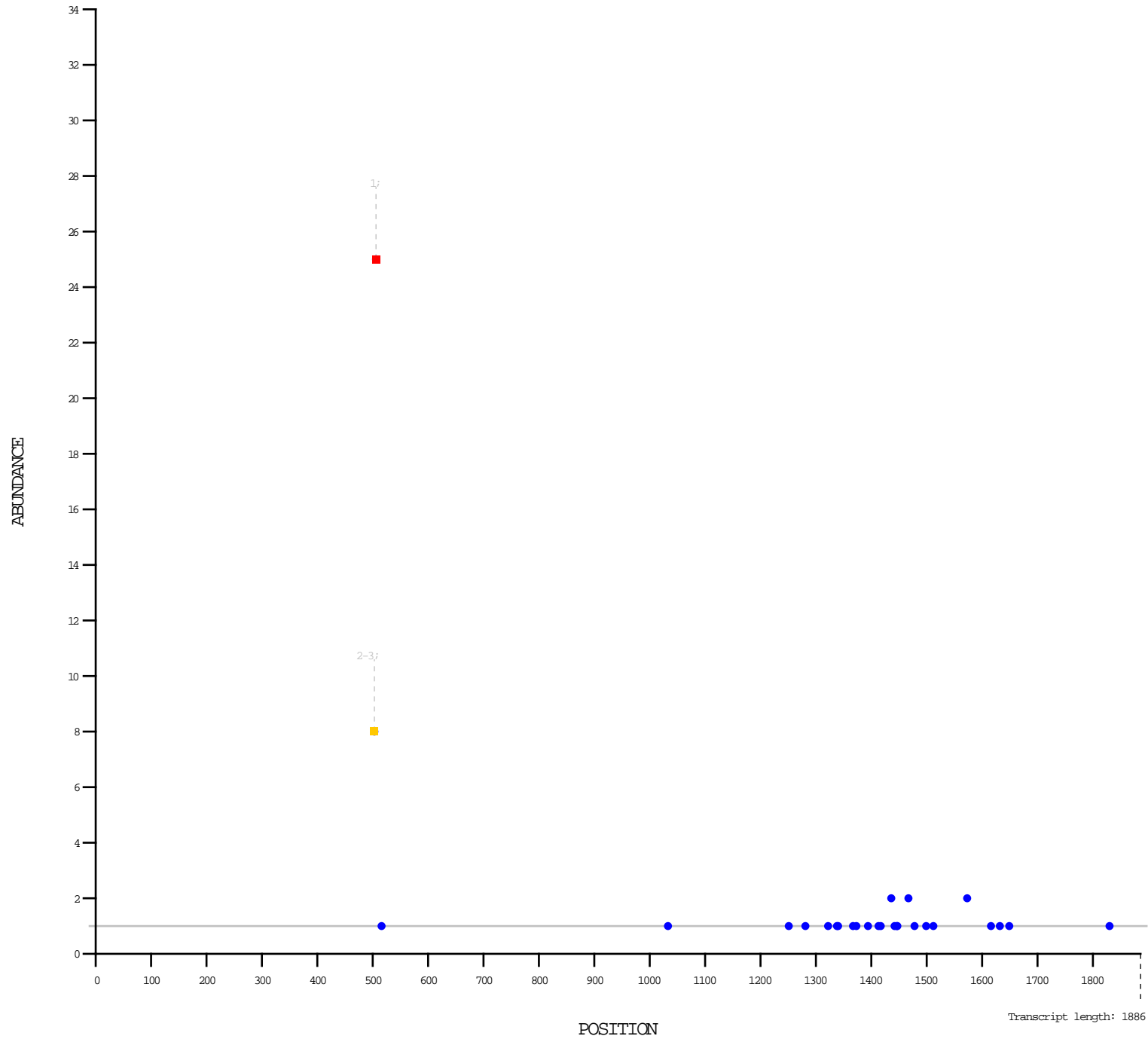
■ 0 #3 Position:799 Abundance: 32.00(deg) 2(sRNA)  
 5' TCGGACCAGGCGCTTCATCCTC 3' ID:  
 o||||| 3' Score: 3.0  
 3' CTTAGGCCCTGGTCCGAGTAGGGTCCGTAGAC 5' p-value: 0.0



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

<span style="color: red;">■</span> 0	#1	Position: 791	Abundance: 32.00(deg)	4(sRNA)
		5'	TTGGAGAGCAGGGCACCTGCA	3'
				ID: Score: 2.0
		3'	TTGGAGAGCAGGGCACCTGCA	5'
				p-value: 0.0
<span style="color: red;">■</span> 0	#2	Position: 791	Abundance: 32.00(deg)	1(sRNA)
		5'	TTGGAGAGCAGGGCACCTGC	3'
				ID: Score: 1.0
		3'	TTGGAGAGCAGGGCACCTGC	5'
				p-value: 0.0
<span style="color: pink;">■</span> 4	#3	Position: 794	Abundance: 1.00(deg)	1(sRNA)
		5'	TCCTGGAGAGCAGGGCACCTG	3'
				ID: Score: 2.0
		3'	TCCTGGAGAGCAGGGCACCTG	5'
				p-value: 0.01



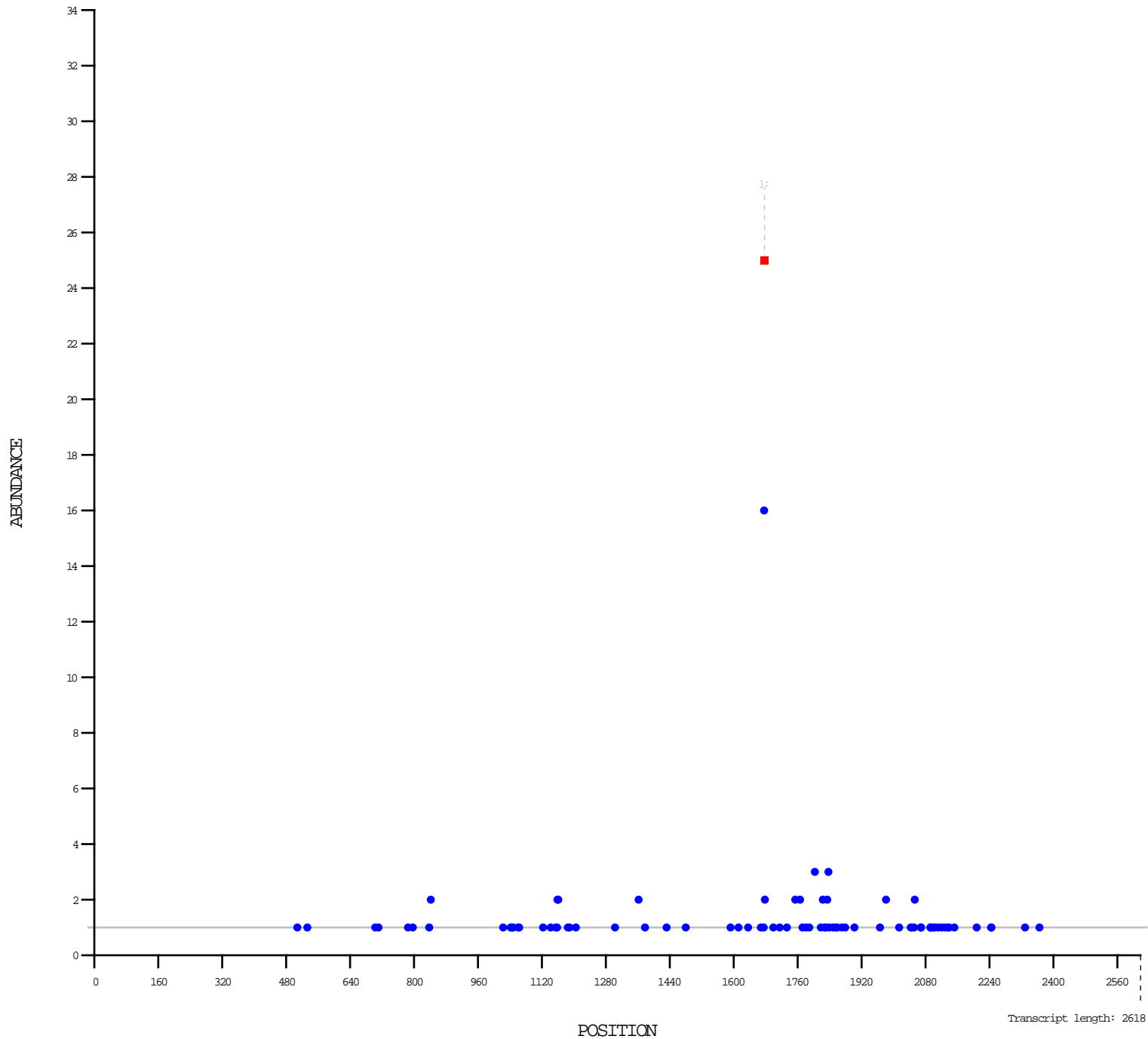
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

■ 0 #1 Position:506 Abundance: 25.00(deg) 5(sRNA)  
 5' TGAATTGAGCCGTGCCAATATC 3' ID:  
 |||||o|||||  
 3' GCCCACTAACTCGGCGGTTATAGAGCGCGC 5' Score: 0.5  
 p-value: 0.0

■ 2 #2 Position:503 Abundance: 8.00(deg) 1(sRNA)  
 5' TTGAGCCGCGCCAAATATCTCT 3' ID:  
 |||||o|||||  
 3' CACTAACTCGGCGGTTATAGAGCGCGCGG 5' Score: 1.0  
 p-value: 0.0

■ 2 #3 Position:503 Abundance: 8.00(deg) 1(sRNA)  
 5' TTGAGCCGCGTCAATATCTCC 3' ID:  
 |||||o|||||  
 3' CACTAACTCGGCGGTTATAGAGCGCGCGG 5' Score: 1.5  
 p-value: 0.01



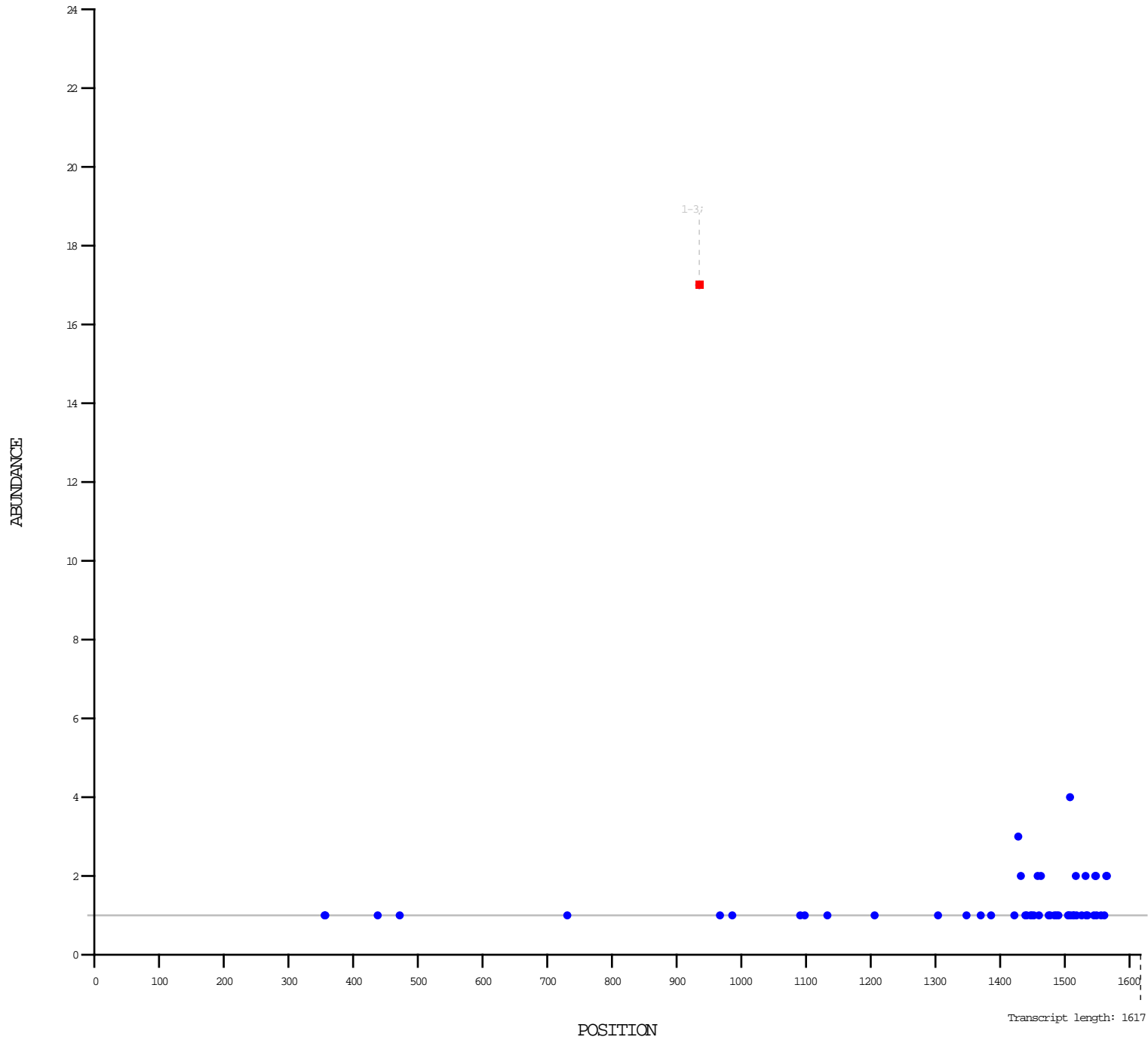
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:1677 Abundance: 25.00(deg) 1(sRNA)  
 5' CTCCAAAGGGATCGCATTGAT 3' ID:  
 ||||||||||||||||||||| Score: 2.0  
 3' GCCTAGGTTTCCCTAGCGTAC-AGAGGTG 5' p-value: 0.0







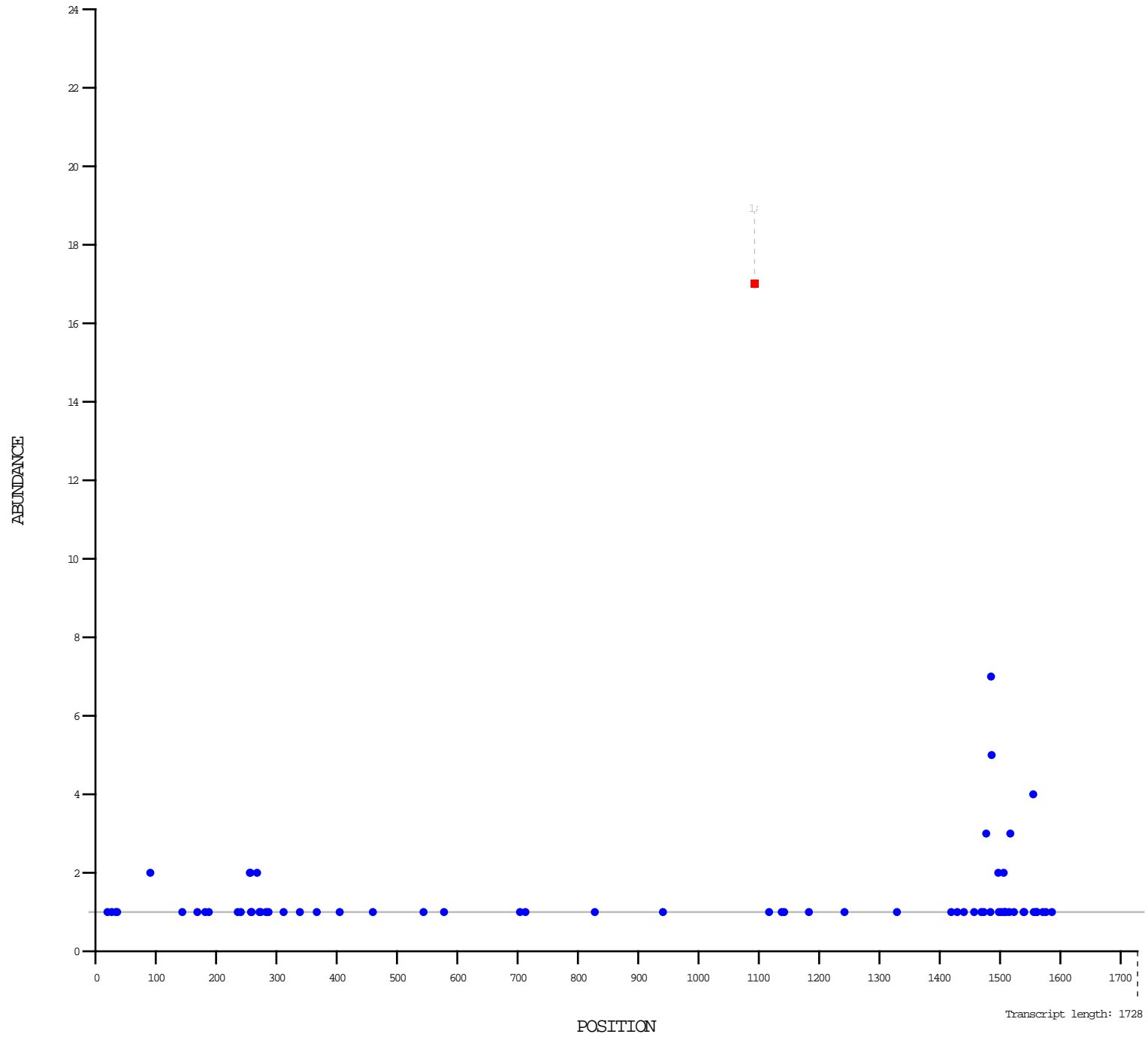


Category: 0 1 2 3 4  
Degradome alignment: ● Median: —

■ 0 #1 Position:935 Abundance: 17.00(deg) 2(sRNA)  
5' TTCACA-GCTTCTTGAAC TG 3' ID:  
||||| | ||||| |  
Score: 2.0  
3' GCGAGGTTGCCAAAGACTTGCCAACGCCG 5' p-value: 0.0

■ 0 #2 Position:935 Abundance: 17.00(deg) 1(sRNA)  
5' TTCACAGGCTTCTTGAAC TG 3' ID:  
||||| | ||||| |  
Score: 1.0  
3' GCGAGGTTGCCAAAGACTTGCCAACGCCG 5' p-value: 0.0

■ 0 #3 Position:935 Abundance: 17.00(deg) 1(sRNA)  
5' TTCACA-GCTTCTTGAAC TT 3' ID:  
||||| | ||||| |  
Score: 3.0  
3' GCGAGGTTGCCAAAGACTTGCCAACGCCG 5' p-value: 0.0

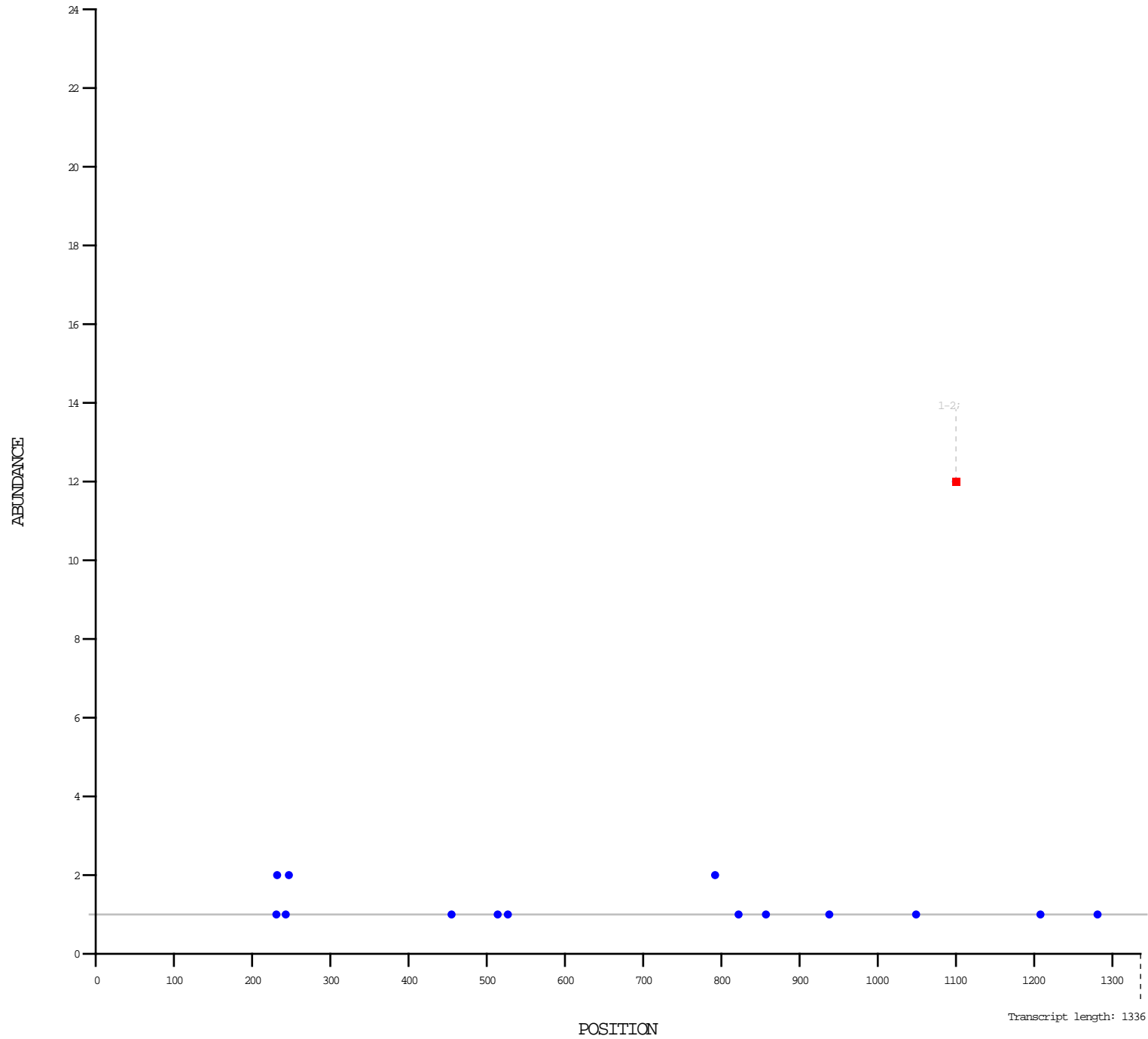


Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

**■ 0** #1 Position:1093 Abundance: 17.00(deg) 1(sRNA)  
 5' TTGGCATTCGTCACCTCC 3' ID:  
 |||||||||  
 3' TATTAACCGTAAGACAGGTGGAGGAGGTCCTC 5' Score: 0.0  
 p-value: 0.0



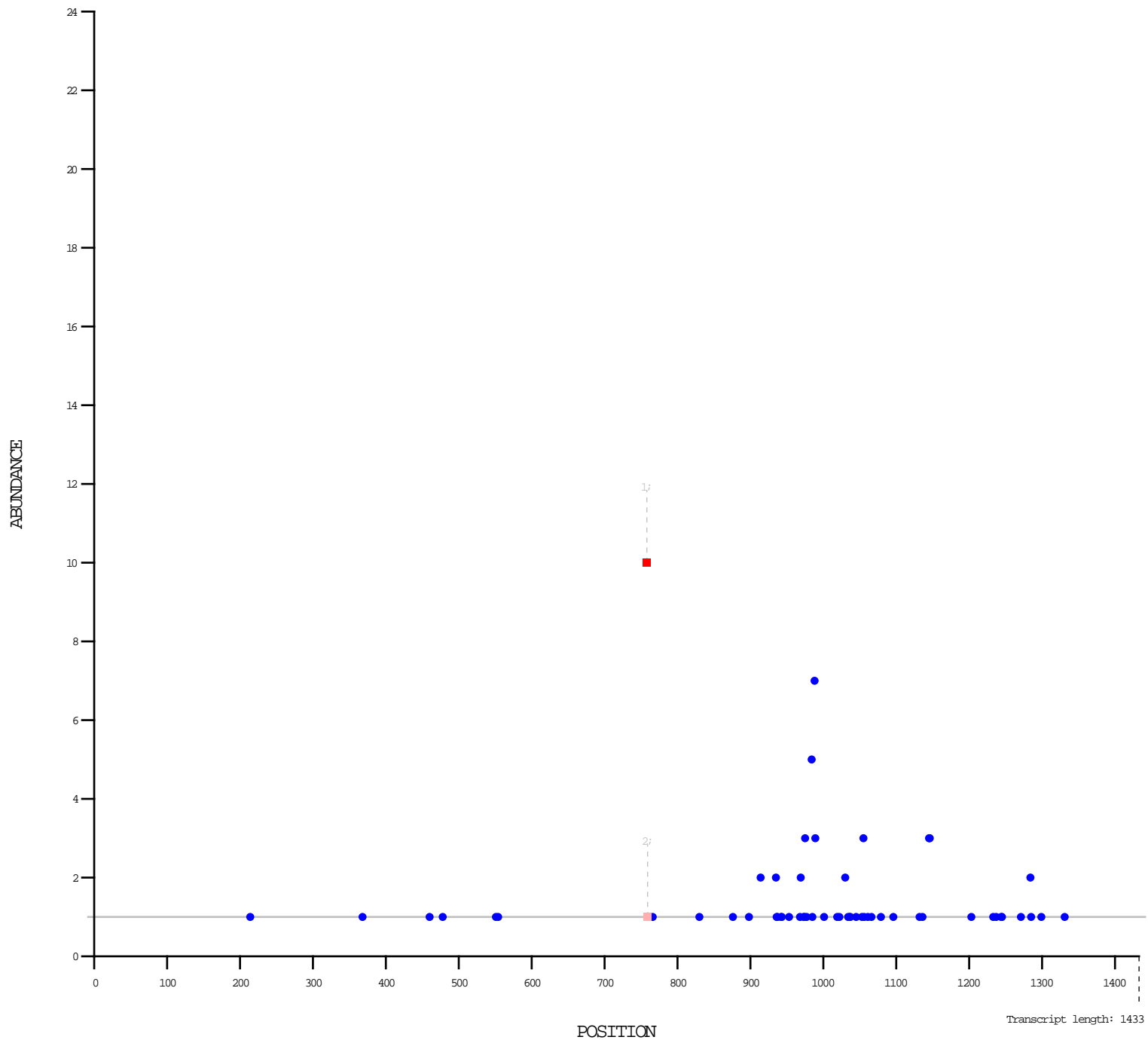




Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:1100 Abundance: 12.00(deg) 1(sRNA)  
 5' TTGGACTGAAGGGTGCCTCCCT 3' ID:  
 |||||o|||||o||| Score: 1.5  
 3' GCTTAOCTGACTTCCA-GGGGATGACAAC 5' p-value: 0.0

■ 0 #2 Position:1100 Abundance: 12.00(deg) 1(sRNA)  
 5' TTGGATGAAGGGAGCTCC 3' ID:  
 |||||o|||||o||| Score: 3.0  
 3' GCTTAOCTGACTTCCAAGGGGATGACAAC 5' p-value: 0.03



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

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■ 0 #1 Position:758 Abundance: 10.00(deg) 8(sRNA)
    5' TGACAGAGAGAGTGGCAC 3' ID:
        |||||
    3' GTGACTGTCTCTCTCTCTGTTGGACCTCT 5' p-value: 0.0
    Score: 1.0

■ 4 #2 Position:759 Abundance: 1.00(deg) 1(sRNA)
    5' TTGACAGAGAGAGCGGCAC 3' ID:
        o|||||
    3' GTGACTGTCTCTCTCTCTGTTGGACCTCT 5' p-value: 0.0
    Score: 1.5
    
```





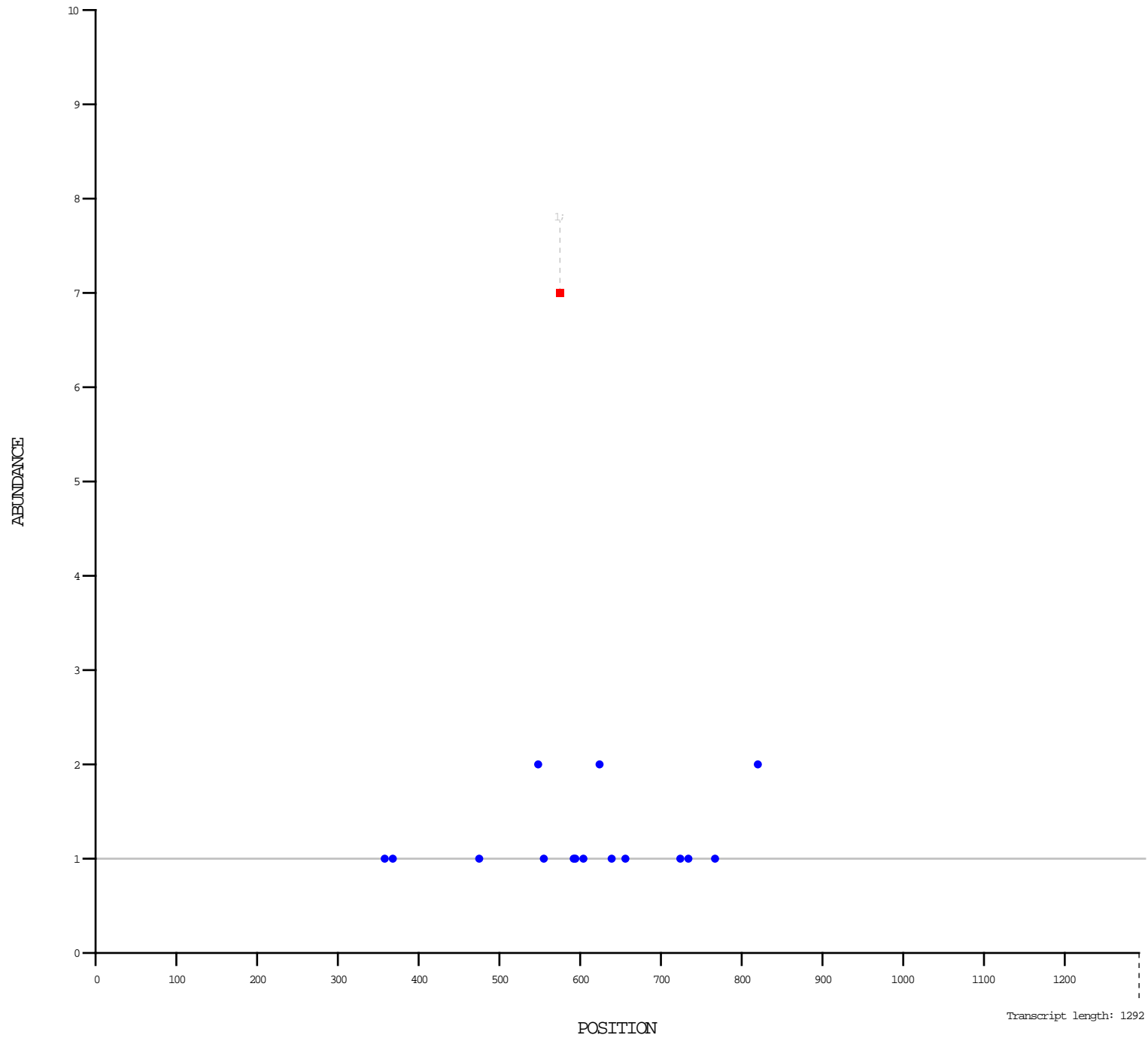










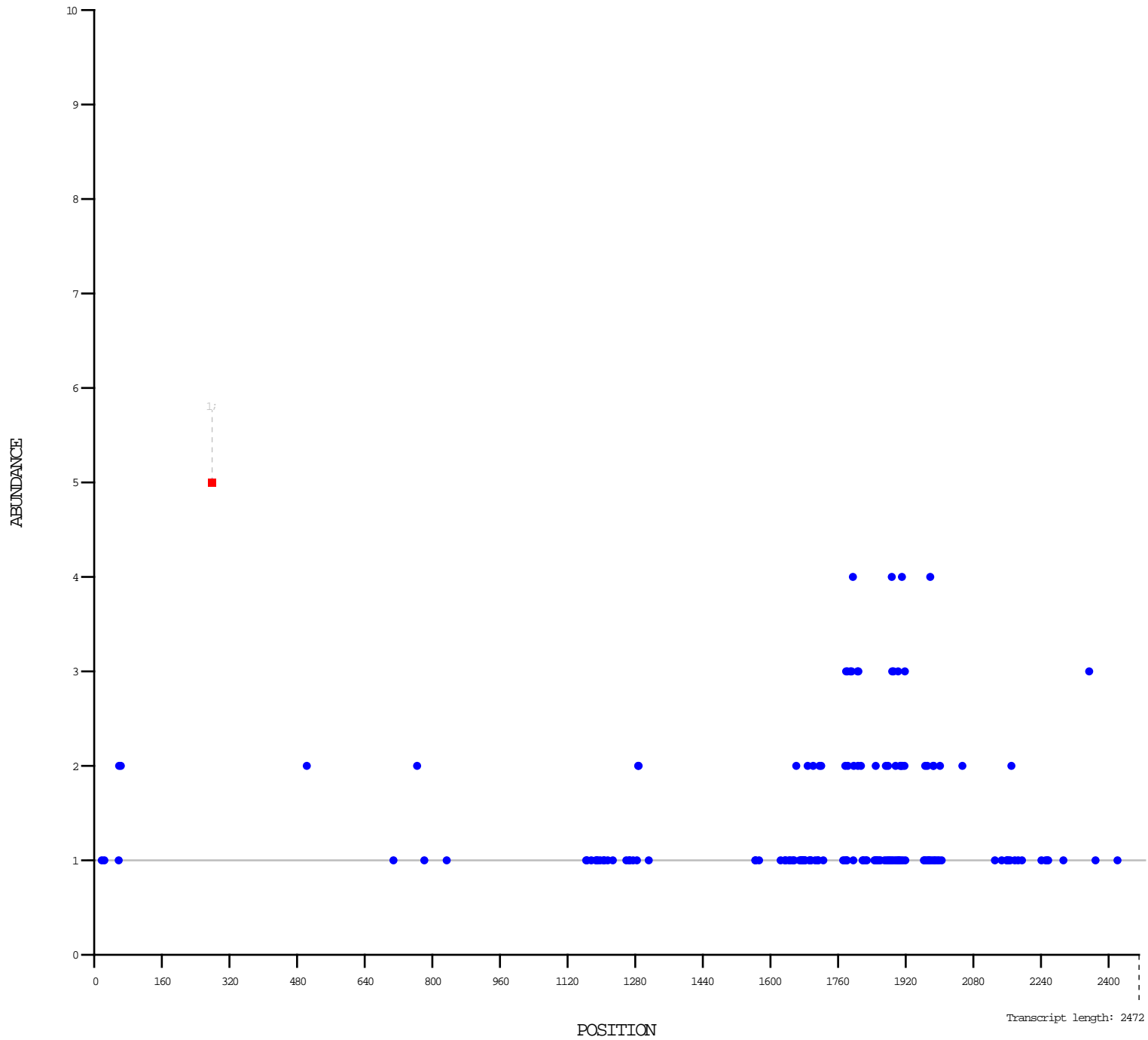


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:575 Abundance: 7.00(deg) 6(sRNA)  
 5' TGAAGTGTGTTGGGGGAACTC 3' ID:  
 ||||| || |o||||||| Score: 4.5  
 3' CCCCACTTC-CAGATCCCTTGGCTCCAGCC 5' p-value: 0.02

Transcript length: 1292

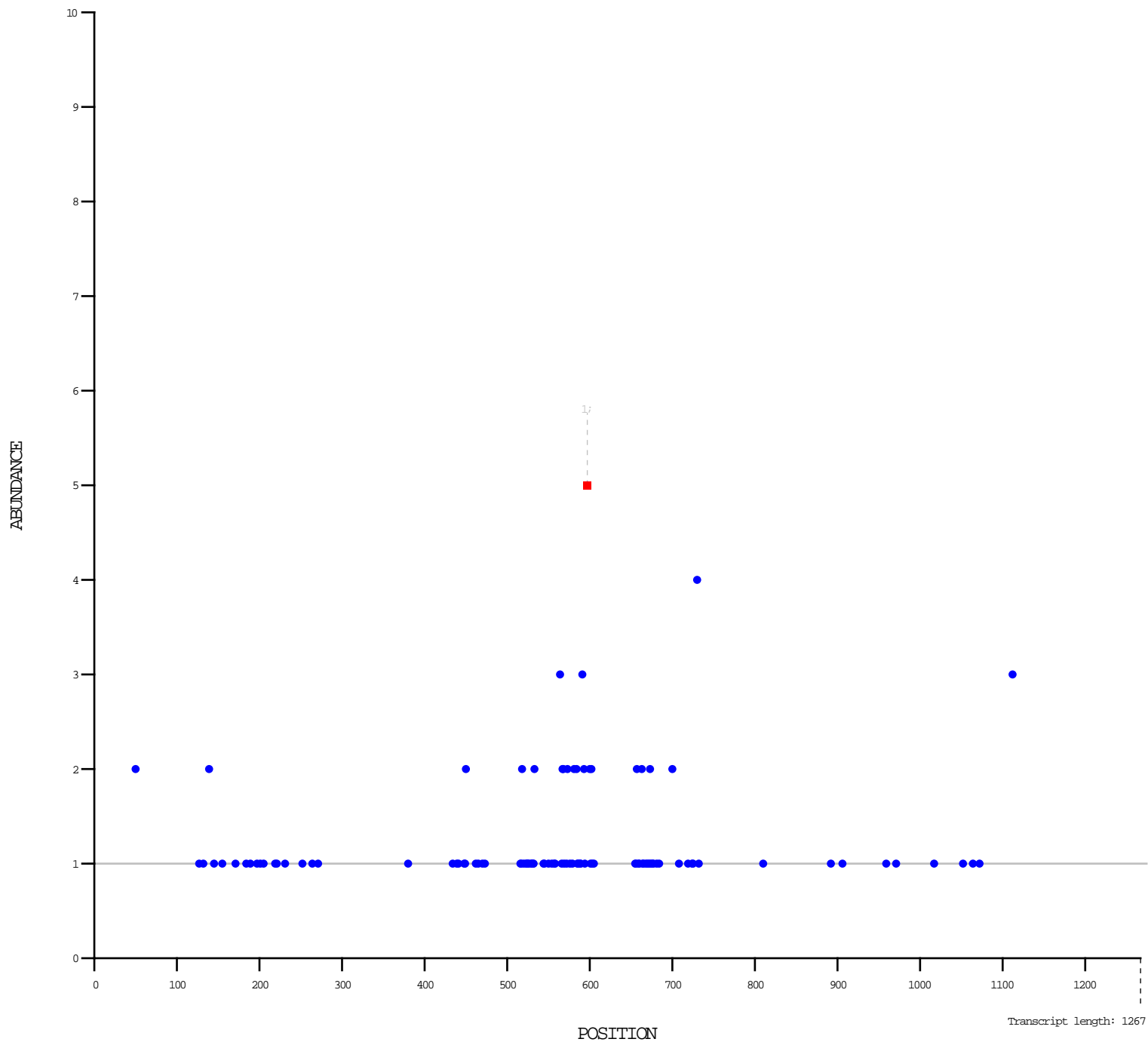




Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:279 Abundance: 5.00(deg) 6(sRNA)  
 5' TGAAGTGTGTTG3GGGAACTC 3' ID:  
 |||||o||||| Score: 0.5  
 3' GACAACTTCACAAACCCCTTTGAGCCCTCGGC 5' p-value: 0.0



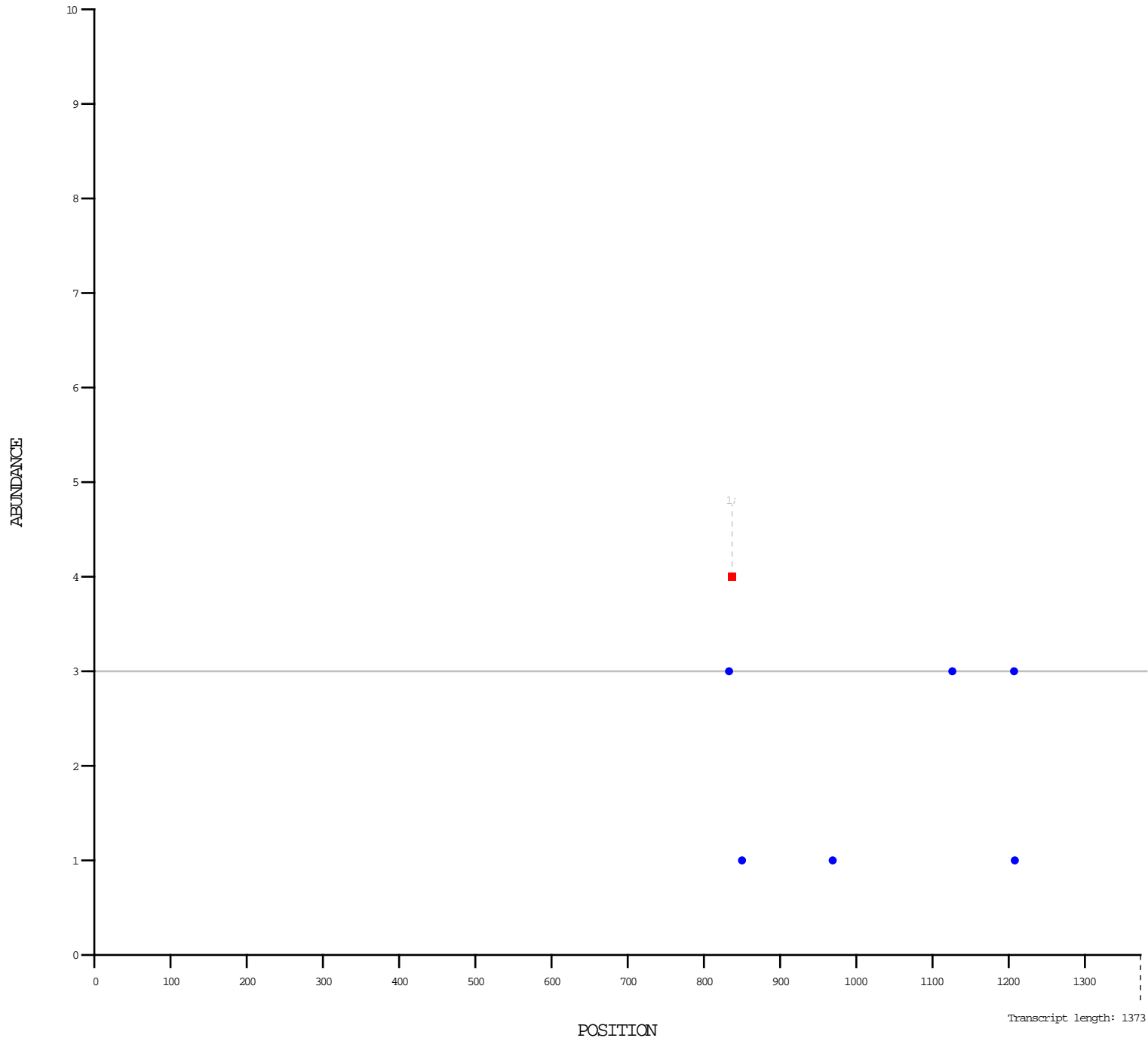


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

■ 0 #1 Position:597 Abundance: 5.00(deg) 1(sRNA)  
 5' GCAGCACCATCAAGATTGACA 3' ID:  
 ||||| ||||| |o| ||| | Score: 3.5  
 3' AACCCGTCGAGGTAGTTTGA-GTTTAGTGST 5' p-value: 0.0

Transcript length: 1267

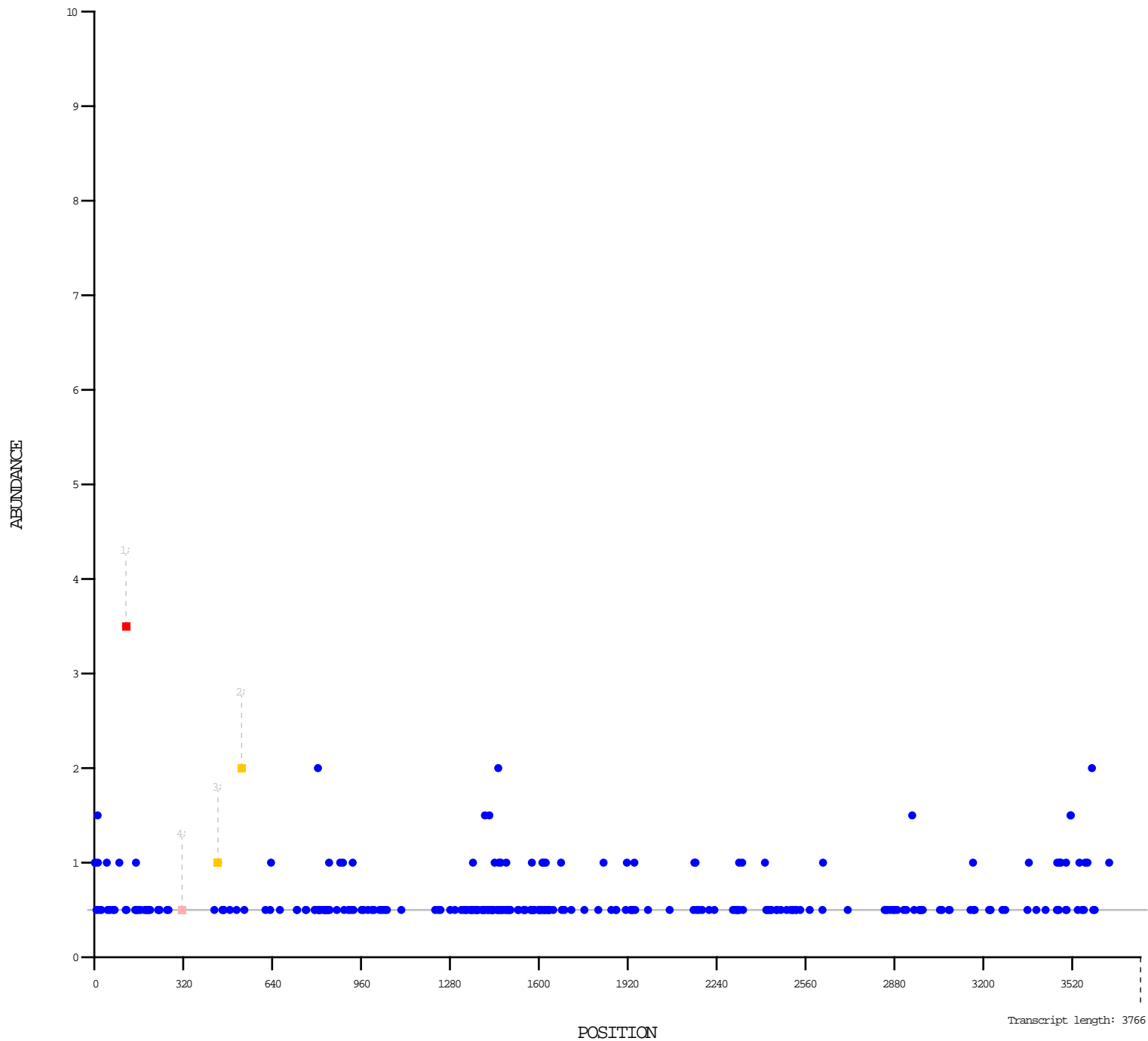


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
Degradome alignment: ● Median: —

■ 0 #1 Position:837 Abundance: 4.00(deg) 8(sRNA)  
5' TGACAGAGGAGTGACAC 3' ID:  
||||| ||||||| ||||||| Score: 1.0  
3' CTCACGTCCTCCTCCTCGGIGGATCTC 5' p-value: 0.0

Transcript length: 1373

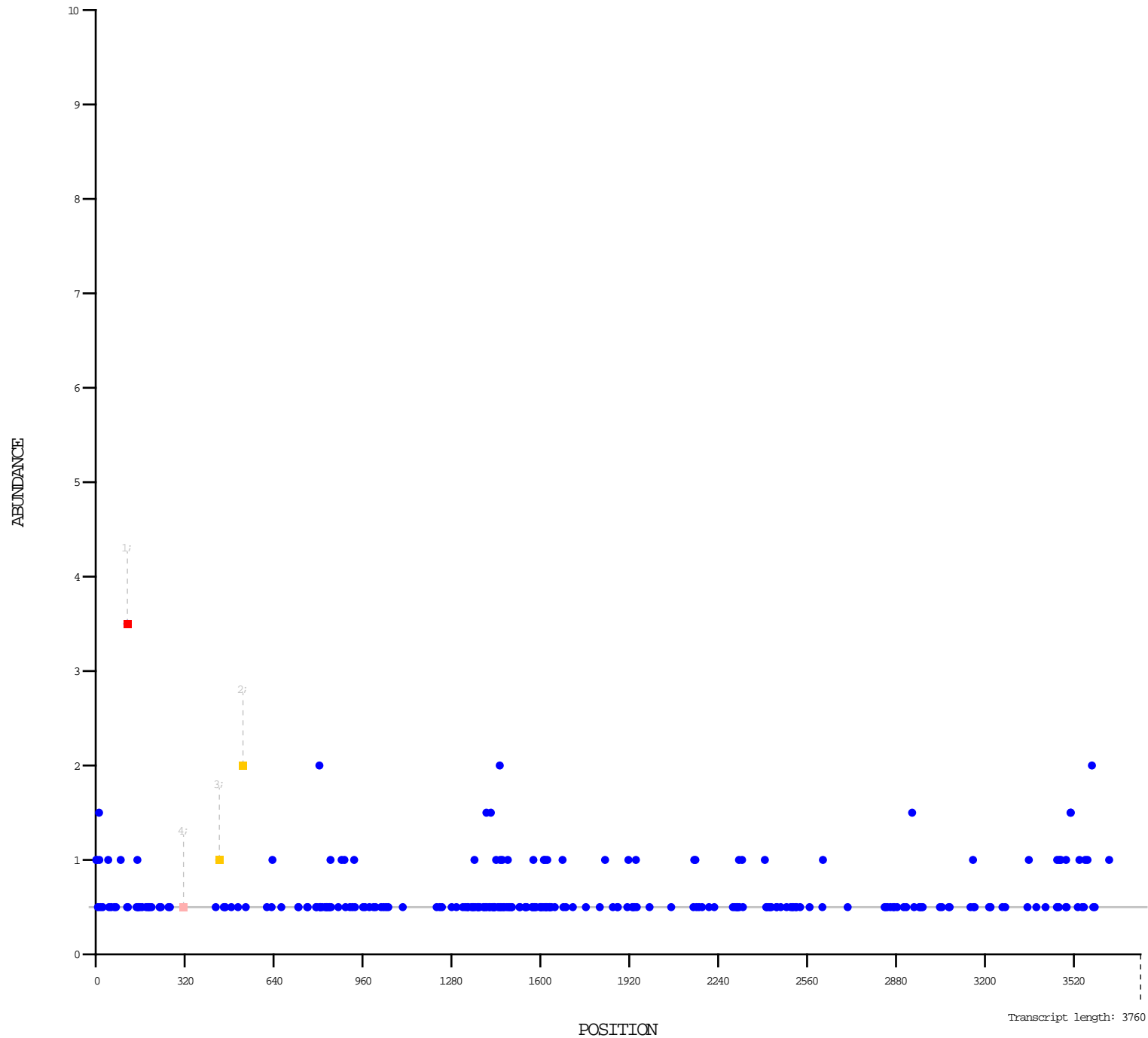




Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

Degradome alignment: ● Median: —

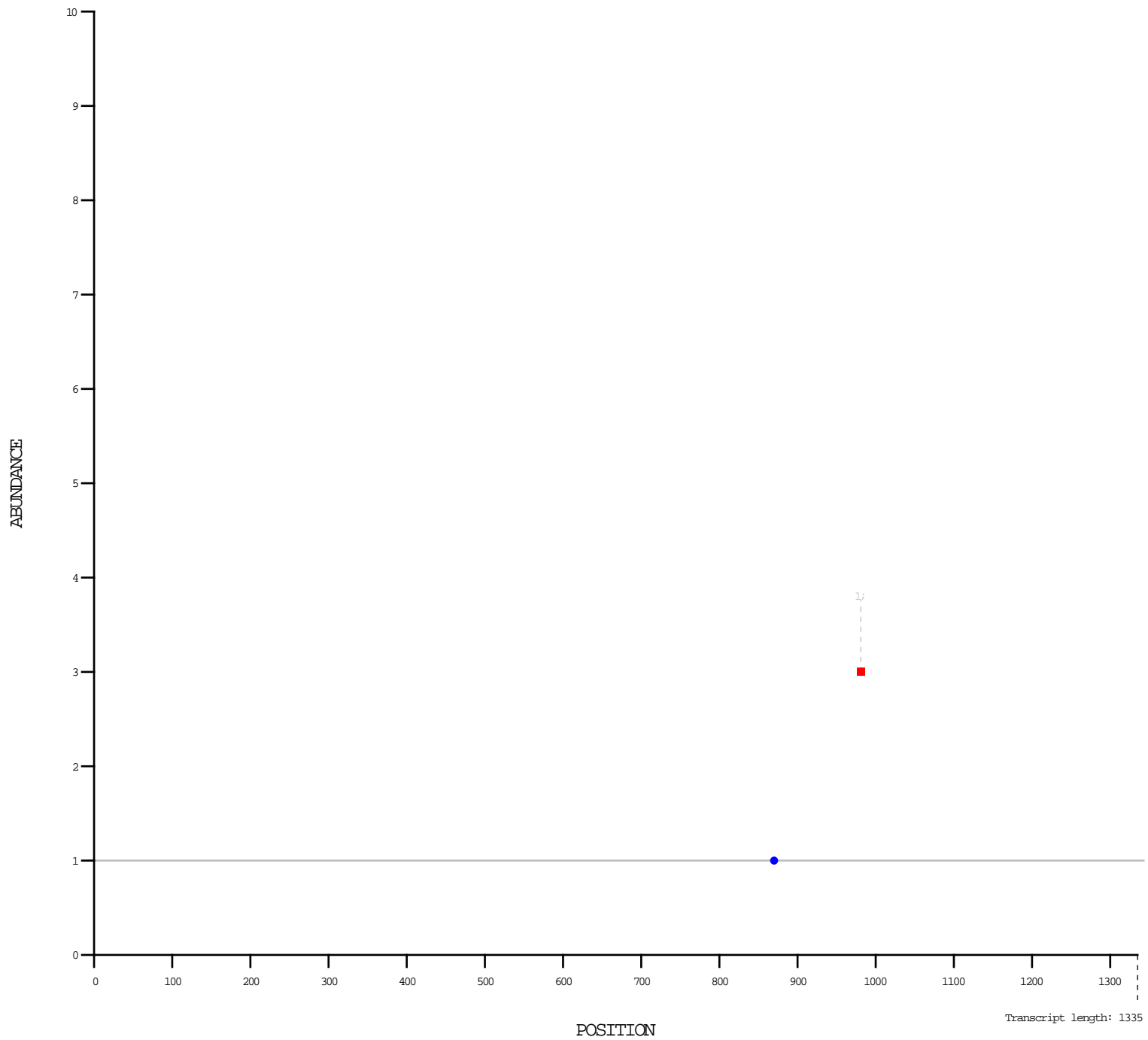
<span style="color:red">■</span> 0	#1	Position:114	Abundance: 3.50(deg)	1(sRNA)
		5' TGCCAAGGAGAGTTGCCCTG	3'	ID:
			o	Score: 1.5
		3' ACAAAAGGTTTCCTCTAAACGGGATTITGTC	5'	p-value: 0.0
<span style="color:yellow">■</span> 2	#2	Position:530	Abundance: 2.00(deg)	1(sRNA)
		5' TGCCAAGGAGAGTTGCCCTG	3'	ID:
			o o	Score: 1.0
		3' AATTACGGTTTCCTCTAATGGGACTATATCG	5'	p-value: 0.0
<span style="color:yellow">■</span> 2	#3	Position:445	Abundance: 1.00(deg)	1(sRNA)
		5' TGCCAAGGAGAGTTGCCCTG	3'	ID:
			o	Score: 2.5
		3' AAAAAAGGTTTCCTCTAAACGGGTTTCCTGTC	5'	p-value: 0.02
<span style="color:pink">■</span> 4	#4	Position:316	Abundance: 0.50(deg)	1(sRNA)
		5' TGCCAAGGAGAGTTGCCCTG	3'	ID:
				Score: 2.0
		3' CATTACGGTTTCCTCTAAACGGGTTTGTAGT	5'	p-value: 0.0



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4

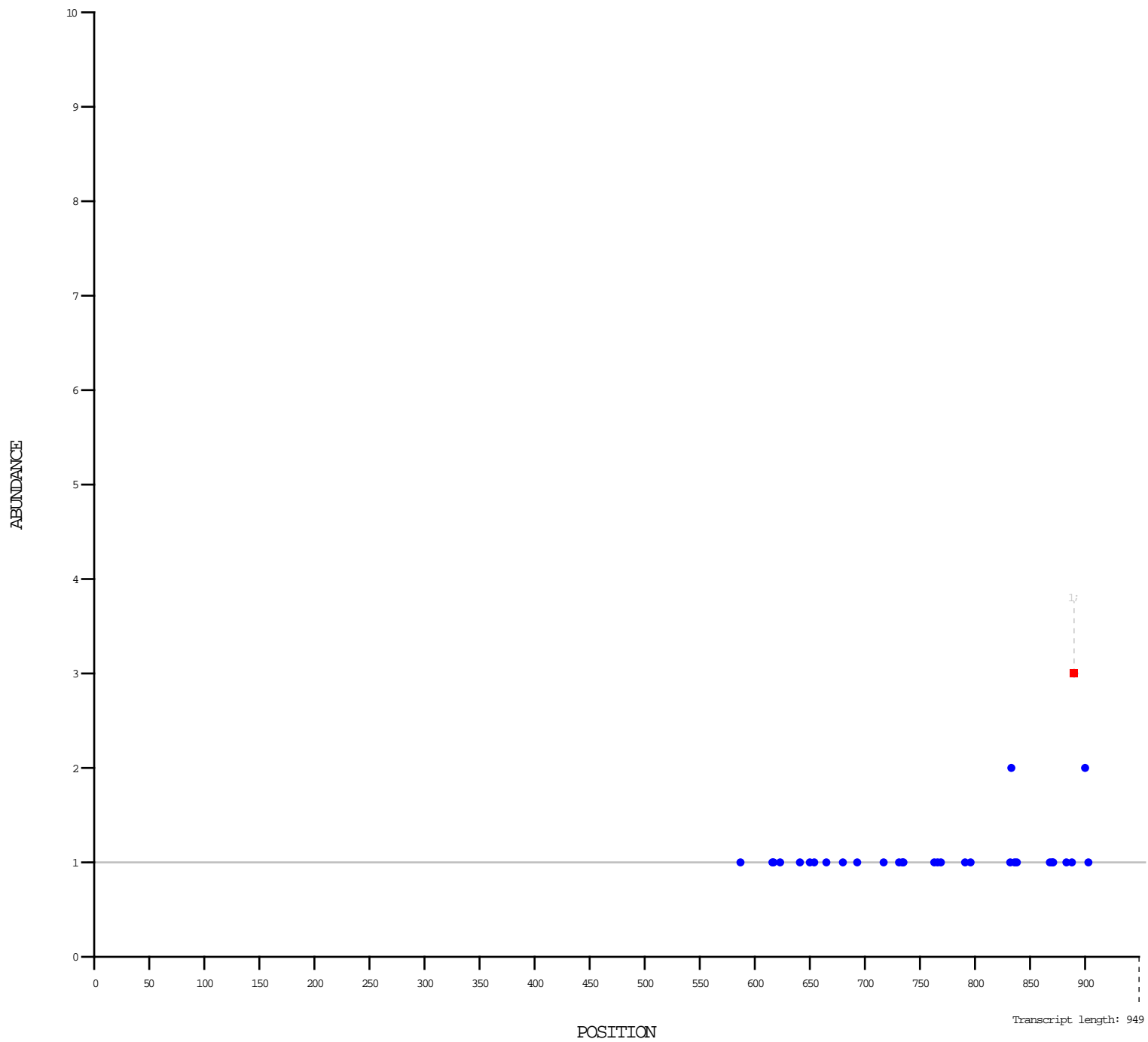
Degradome alignment: ● Median: —

<span style="color:red">■</span> 0	#1	Position:114	Abundance: 3.50(deg)	1(sRNA)
		5'	TGCCAAGGAGAGTTGCCCTG	3'
			o	Score: 1.5
		3'	ACAAACGGTTTCCTCTAACGGGATTGTTC	5'
				p-value: 0.0
<span style="color:yellow">■</span> 2	#2	Position:530	Abundance: 2.00(deg)	1(sRNA)
		5'	TGCCAAGGAGAGTTGCCCTG	3'
			o o	Score: 1.0
		3'	AATTACGGTTTCCTCTAATGGGACTATATCG	5'
				p-value: 0.0
<span style="color:yellow">■</span> 2	#3	Position:445	Abundance: 1.00(deg)	1(sRNA)
		5'	TGCCAAGGAGAGTTGCCCTG	3'
			o	Score: 2.5
		3'	AAAAACGGTTTCCTCTAACGGGTTTCCTGTC	5'
				p-value: 0.0
<span style="color:lightcoral">■</span> 4	#4	Position:316	Abundance: 0.50(deg)	1(sRNA)
		5'	TGCCAAGGAGAGTTGCCCTG	3'
				Score: 2.0
		3'	CATTACGGTTTCCTCTAACGGGTTTGTAGT	5'
				p-value: 0.0



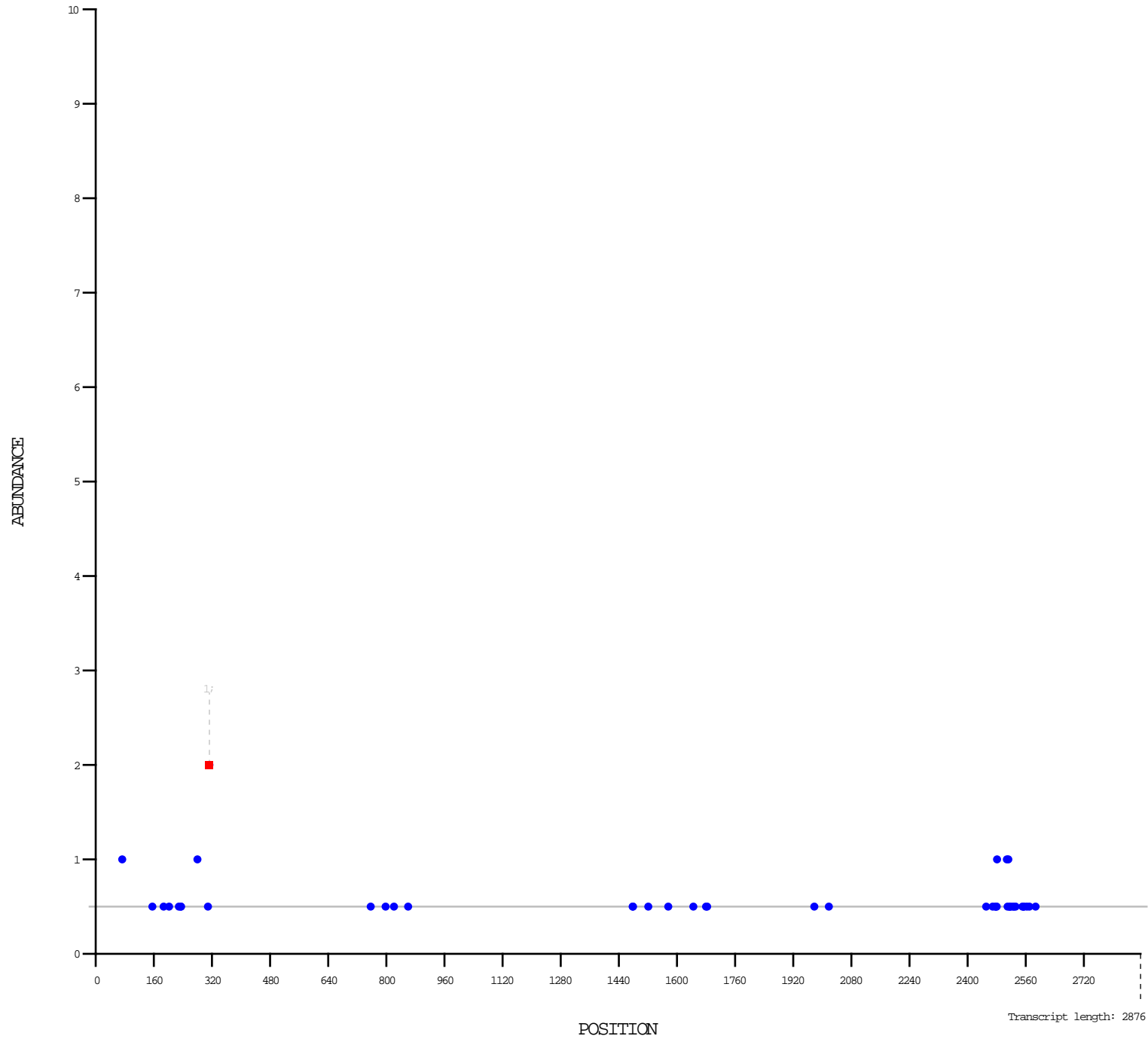
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:981 Abundance: 3.00(deg) 8(sRNA)  
 5' TGACAGAGGAGGTGACAC 3' ID:  
 |||||  
 3' CTCGACTGCTCTCTCTCTGCTGTTAGGCTC 5' p-value: 0.0



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

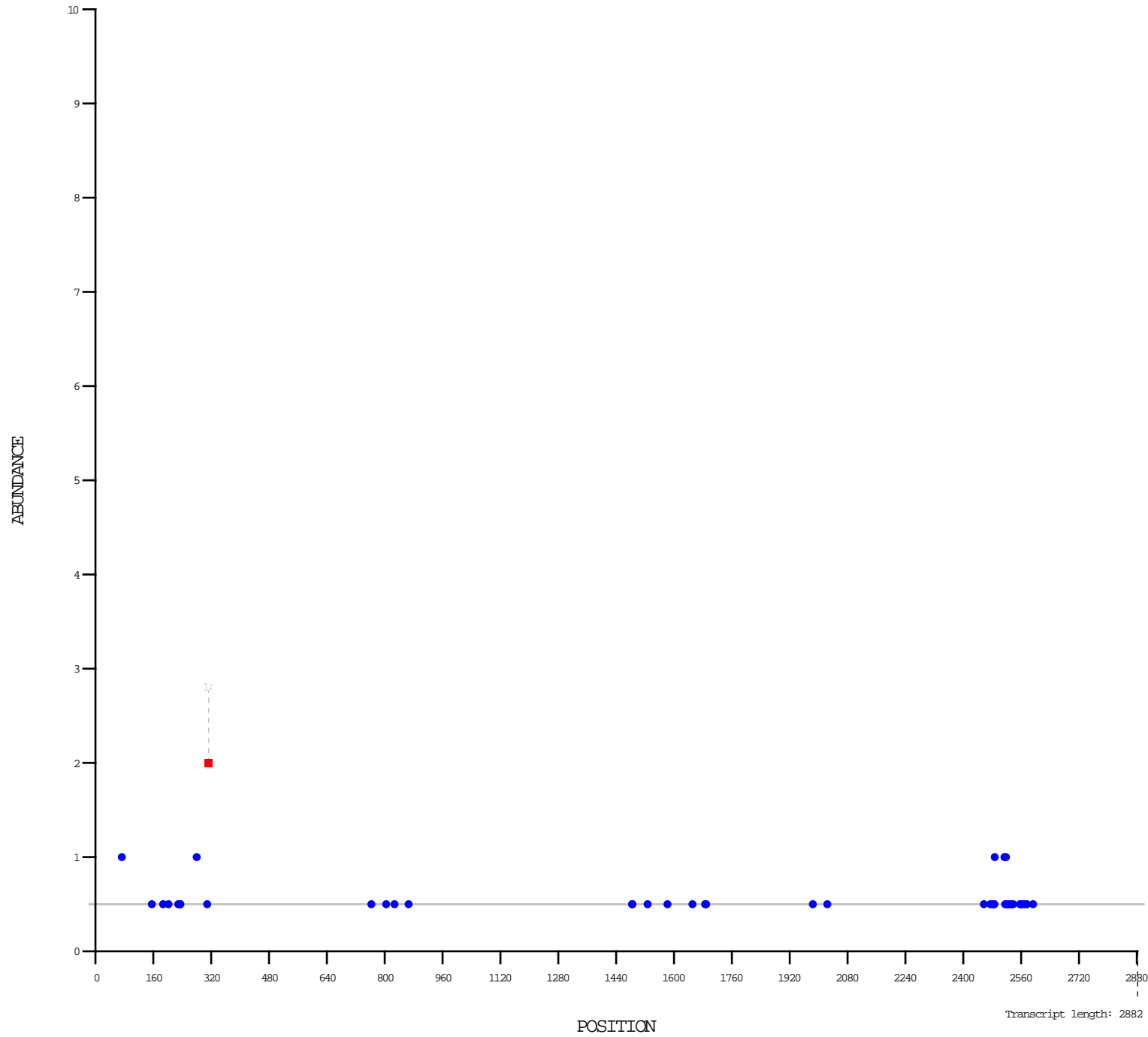
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■ 0 #1 Position:890 Abundance: 3.00(deg) 1(sRNA)
5' TTGGCAAT-CGTCCACCTCC 3' ID:
|o||| || ||||| |||||
3' ACCAGCCGGTAGGCAGGTGGAGAGGAGGG 5' Score: 2.5
p-value: 0.0
```



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:313 Abundance: 2.00(deg) 1(sRNA)  
 5' TTAGATGACCATCAGCAACA 3' ID:  
 o|||||o|||||o|||||o||||| Score: 3.0  
 3' CATCGATCTACTGGTAGTGTGTTGAGCTAGC 5' p-value: 0.0

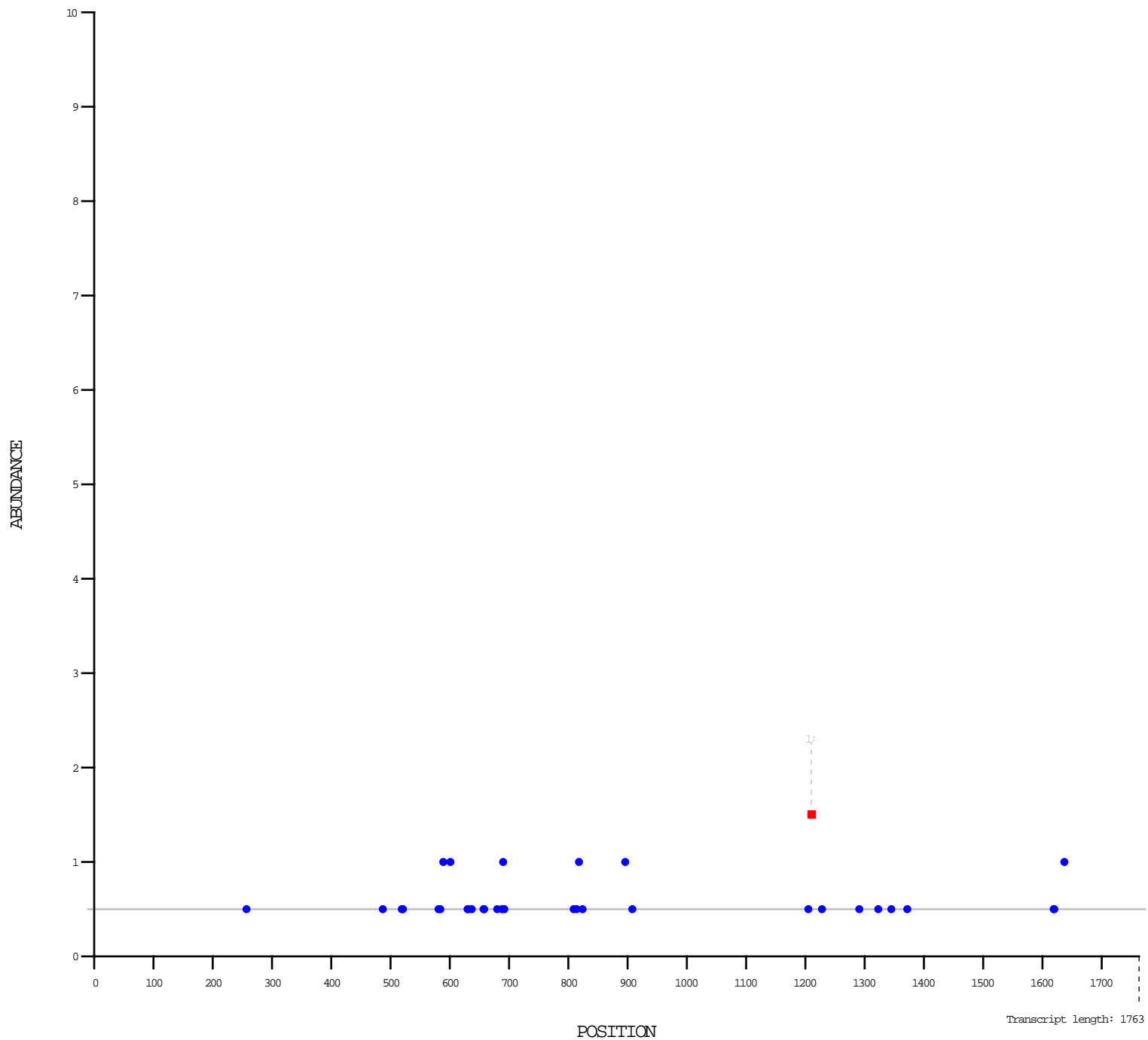




Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:313 Abundance: 2.00(deg) 1(sRNA)  
 5' TTAGATGACCATCAGCAACA 3' ID:  
 o|||||o|||||o|||||o||||| Score: 3.0  
 3' CATCGATCTACTGGTAGTGTGTTTCGAGCTAGC 5' p-value: 0.0

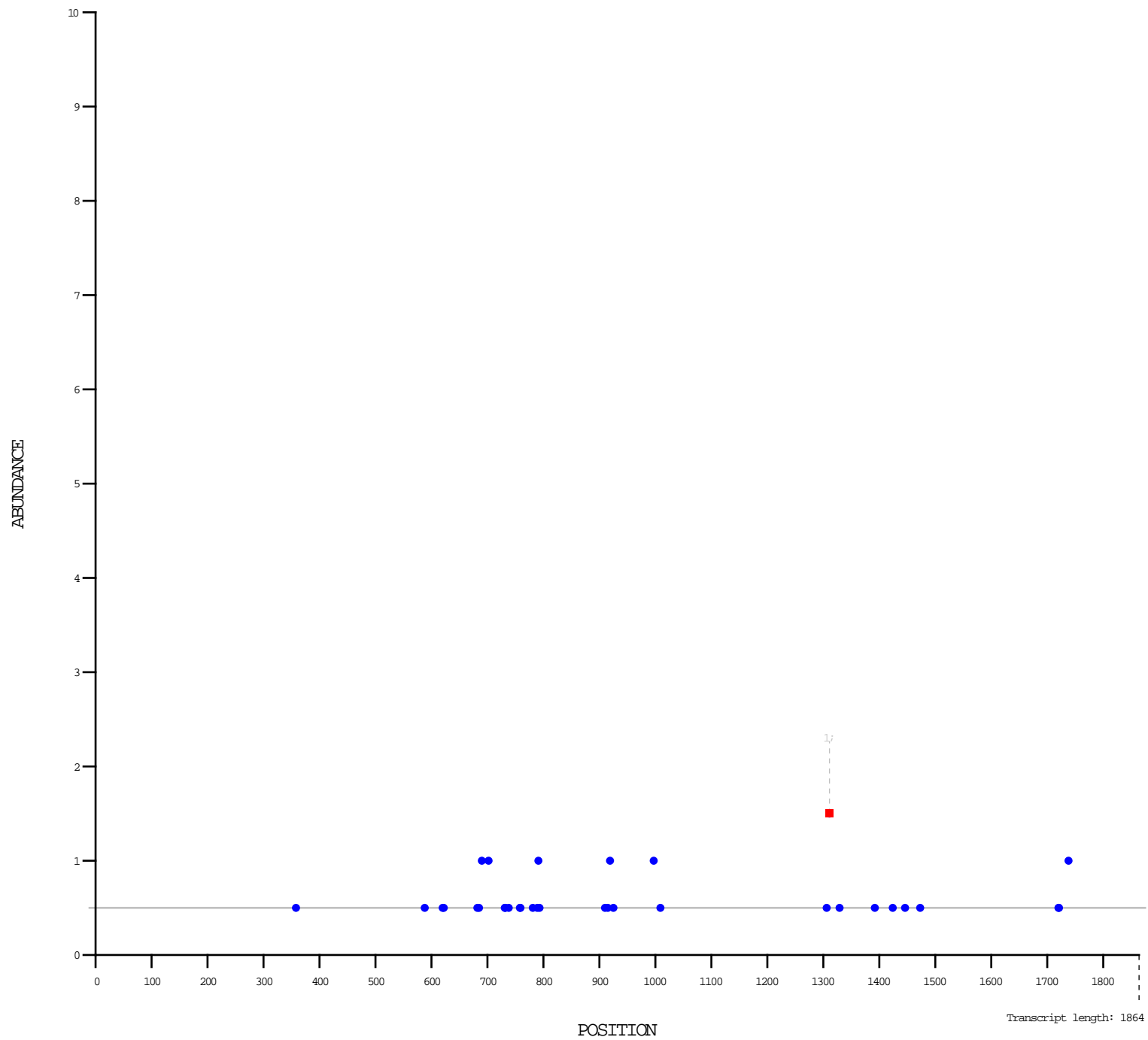
Transcript length: 2882



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

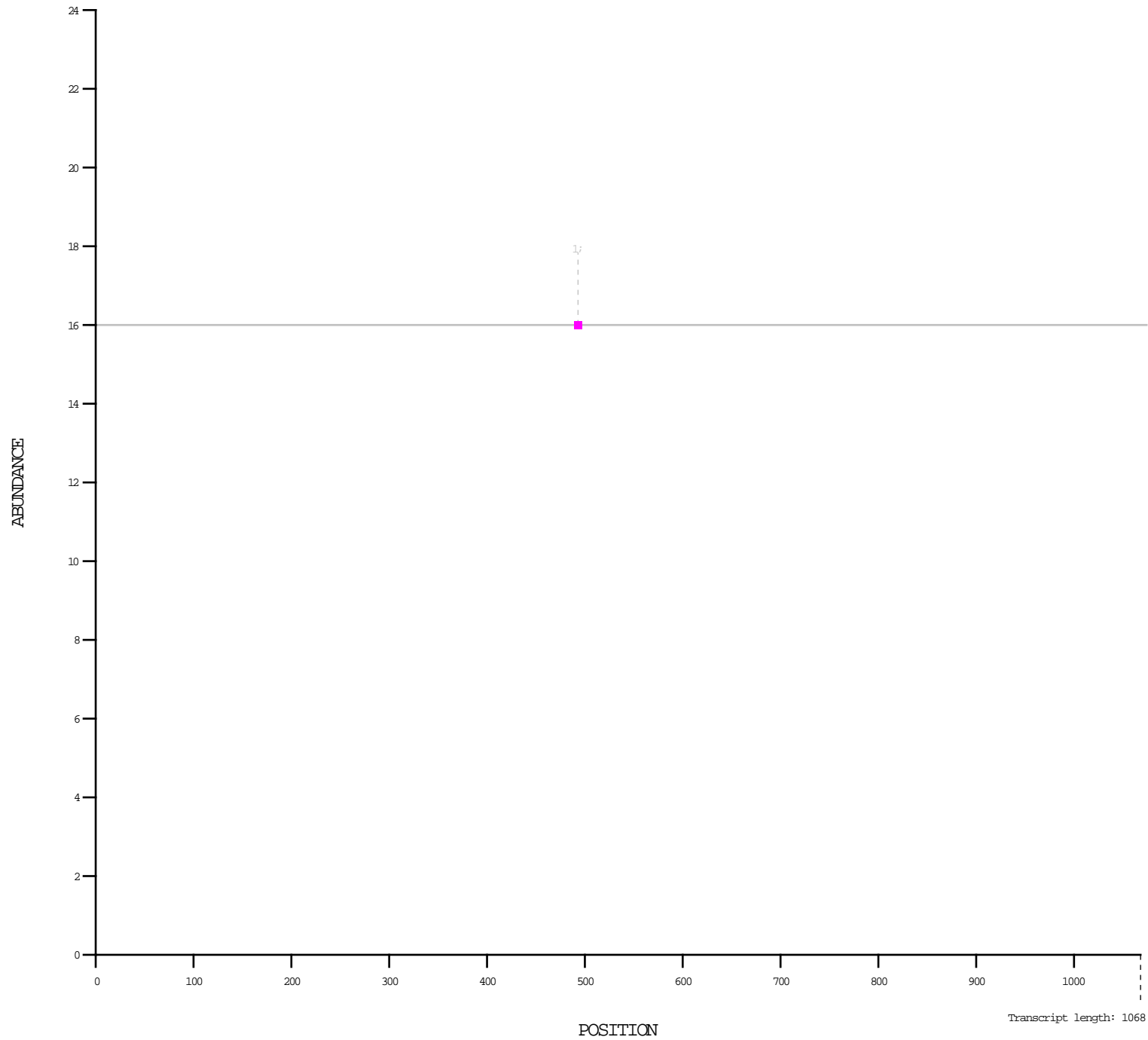
■ 0 #1 Position:1210 Abundance: 1.50(deg) 8(sRNA)  
 5' TGACAGAGGAGGTGACAC 3' ID:  
 ||||| 3' Score: 1.0  
 3' GCAGACTGTCTCTCTCTCTGTCGGTCA 5' p-value: 0.0

Transcript length: 1763



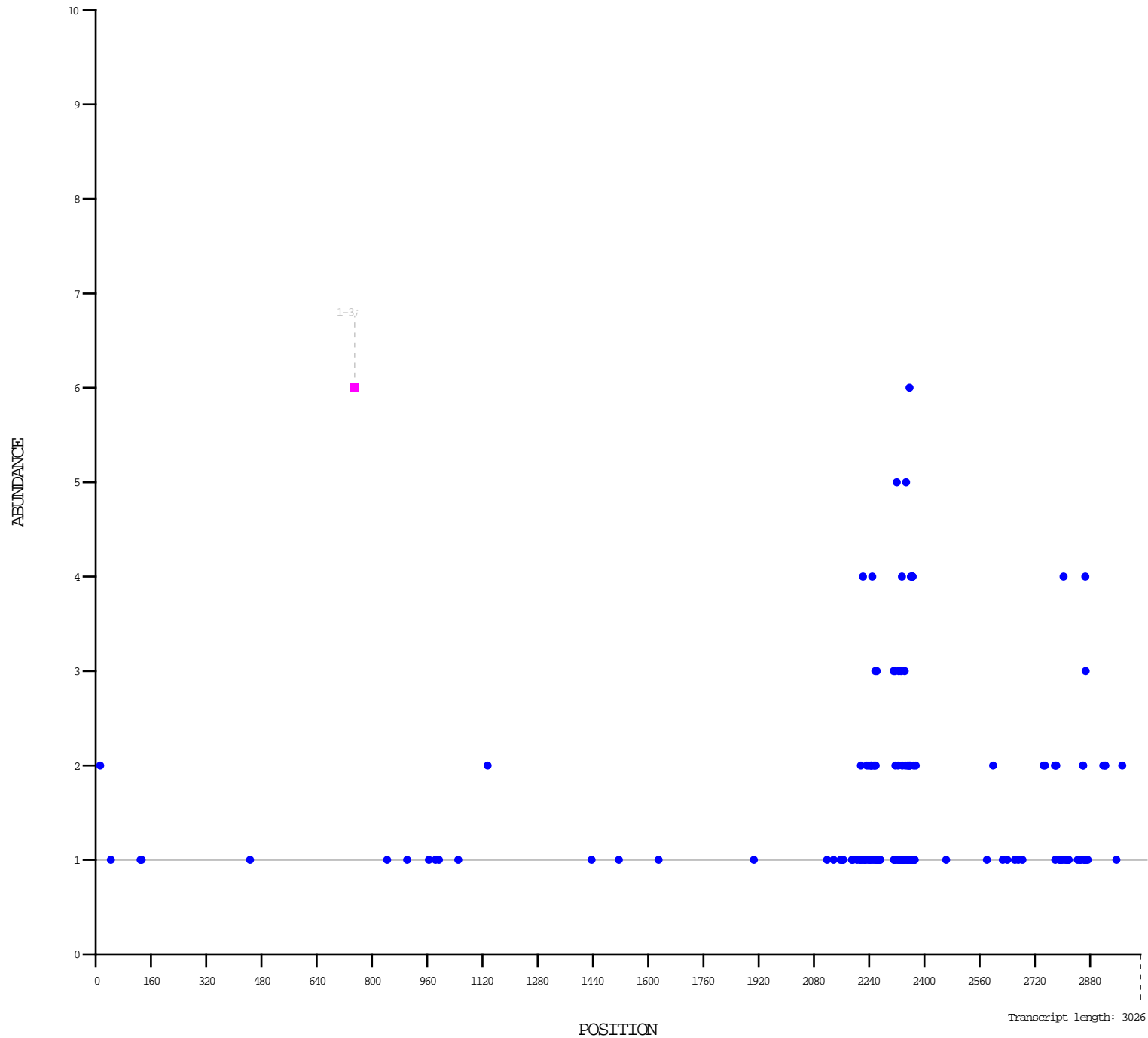
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 0 #1 Position:1311 Abundance: 1.50(deg) 8(sRNA)  
 5' TGACAGAGAGAGTGGAC 3' ID:  
 ||||||||||||||||| Score: 1.0  
 3' GCAGACTGTCCTCCTCCTGCGGGTTCA 5' p-value: 0.0



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

1 #1 Position:493 Abundance: 16.00(deg) 2(sRNA)  
5' TTGGATTGAGGGAGCTCTG 3' ID:  
||||| ||||| ||||| ||||| |o| Score: 2.5  
3' ATGTAAACCAACTTCCCCCGAGGCACCCAC 5' p-value: 0.0

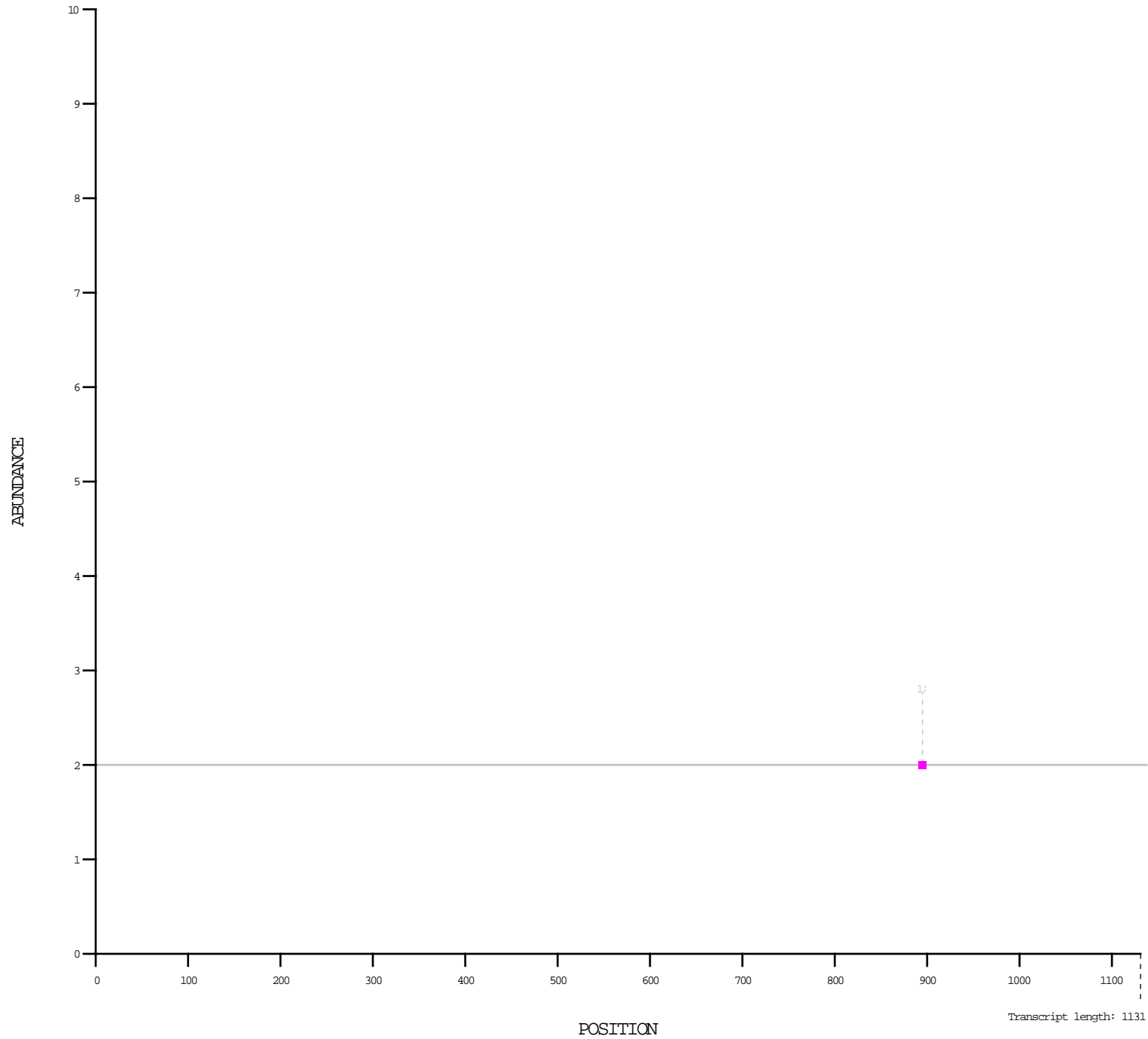


Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

■ 1 #1 Position:750 Abundance: 6.00(deg) 7(sRNA)  
 5' TCGGACCAGGCTTCATCCCC 3' ID:  
 o|||||||||||||||||||  
 3' CTTAGGCCITGGTCCGAGTA-GGGTTGGTAAA 5' Score: 2.5  
 p-value: 0.01

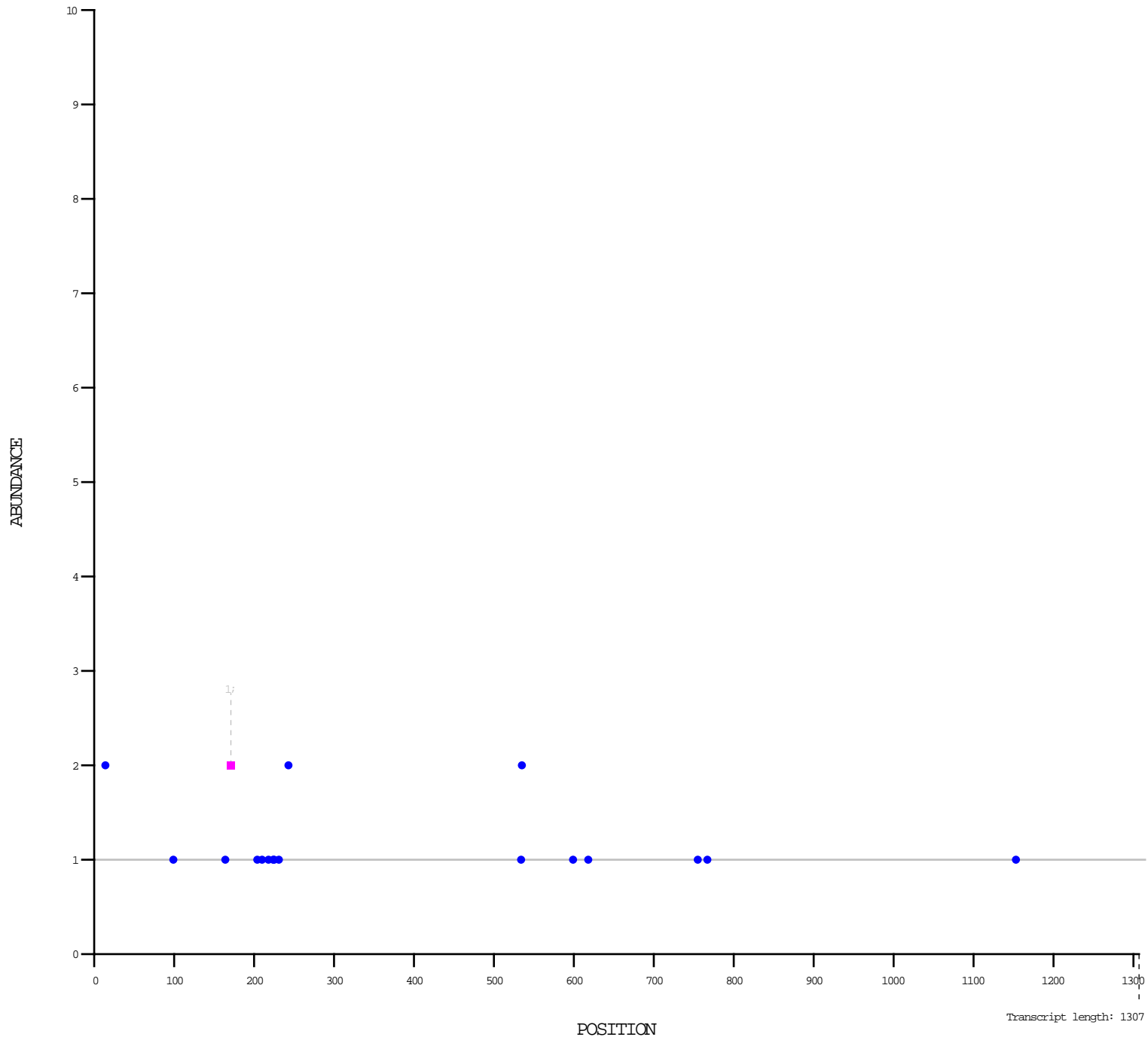
■ 1 #2 Position:750 Abundance: 6.00(deg) 2(sRNA)  
 5' TCGGACCAGGCTTCATCCCT 3' ID:  
 o|||||||||||||||||||  
 3' CTTAGGCCITGGTCCGAGT-AGGGTTGGTAAA 5' Score: 2.5  
 p-value: 0.0

■ 1 #3 Position:750 Abundance: 6.00(deg) 2(sRNA)  
 5' TCGGACCAGGCTTCATCCCTC 3' ID:  
 o|||||||||||||||||||o|||  
 3' CTTAGGCCITGGTCCGAGTAGGGTTGGTAAAC 5' Score: 3.0  
 p-value: 0.01



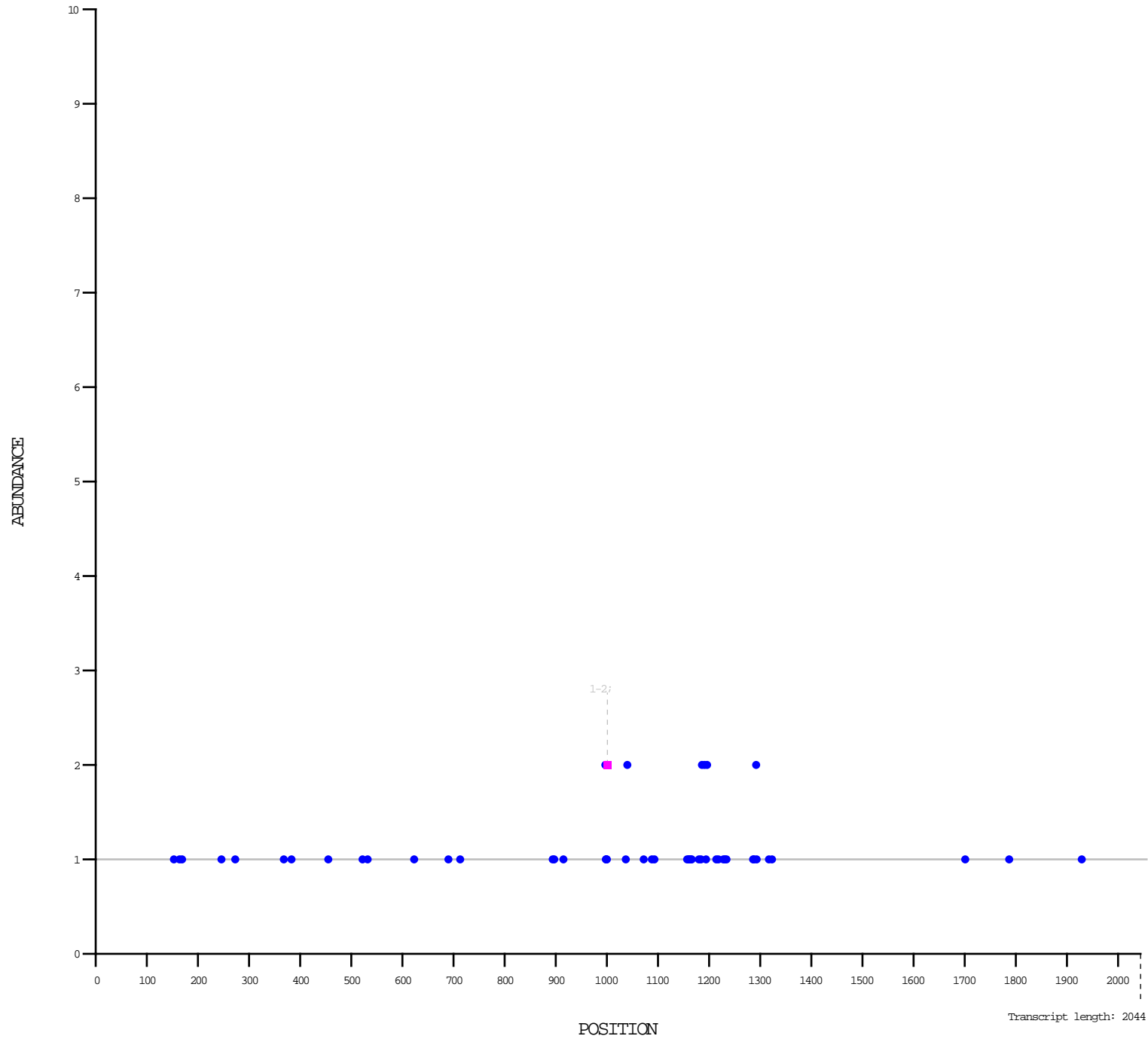
Category: 0 1 2 3 4  
Degradome alignment: ● Median: —

1 #1 Position:895 Abundance: 2.00(deg) 2(sRNA)  
5' TTGGATTGAGGGAGCTCTG 3' ID:  
||||| ||||| ||||| ||||| ||||| oo Score: 3.0  
3' GCCTTAACCAACTTCCTTCGAGGTGAGACCC 5' p-value: 0.0



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

1 #1 Position:171 Abundance: 2.00(deg) 1(sRNA)  
 5' AACCACTGAAATGAGTCTG 3' ID:  
 ||||| 3' ID: Score: 4.0  
 3' TTGTGGTGCATCCAC-GACGATGTA 5' p-value: 0.03

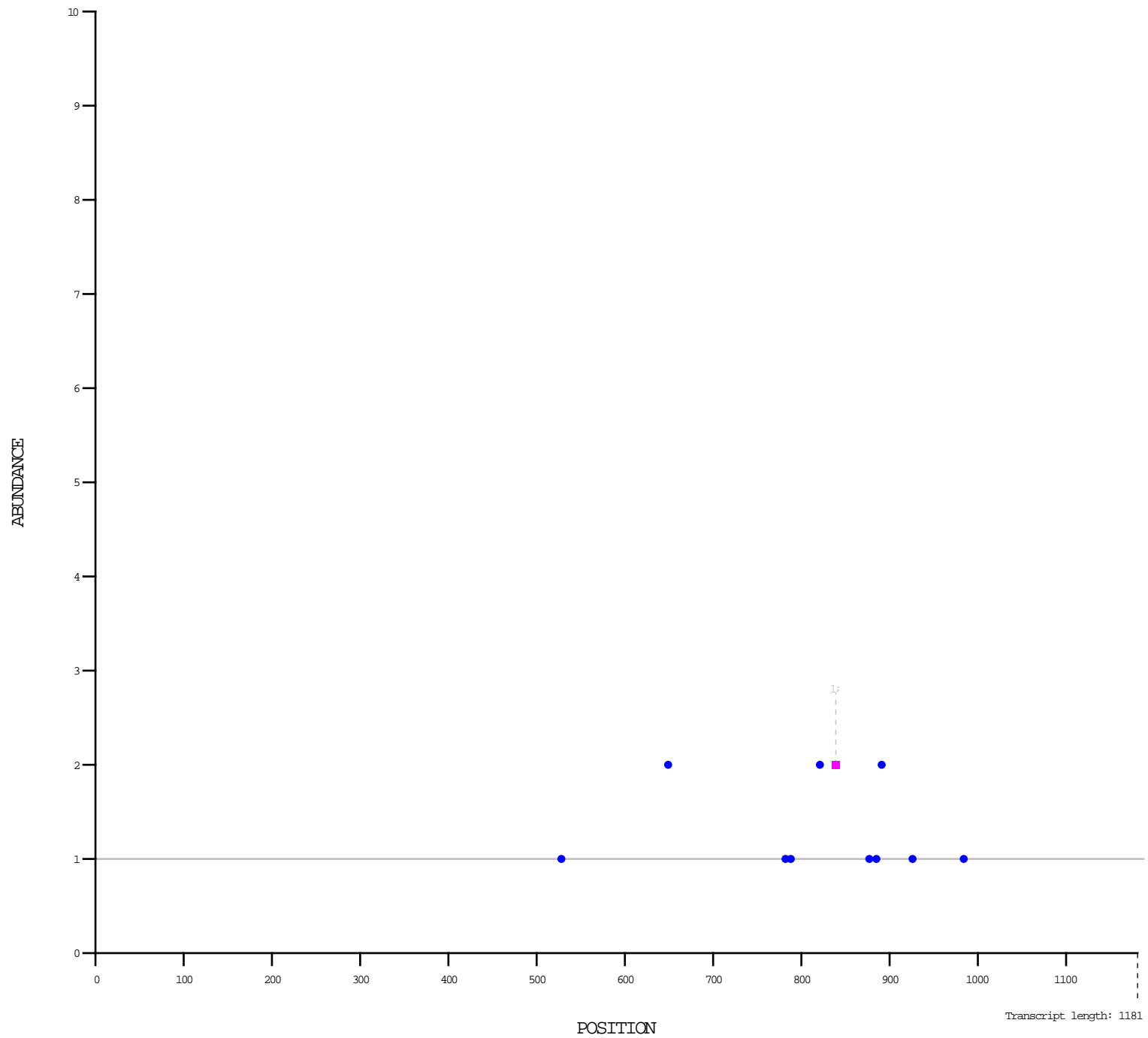


Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

1 #1 Position:1001 Abundance: 2.00(deg) 1(sRNA)  
 5' TTGAGCCCGGTCAAATATCTCC 3' ID:  
 |||||o||| Score: 2.5  
 3' CCGGACTCGGCGAGTCGGAGGTTGAGGA 5' p-value: 0.0

1 #2 Position:1001 Abundance: 2.00(deg) 1(sRNA)  
 5' TTGAGCCCGGCCAAATATCTCT 3' ID:  
 |||||o|||o||| Score: 4.0  
 3' CCGGACTCGGCGAGTCGGAGGTTGAGGA 5' p-value: 0.0

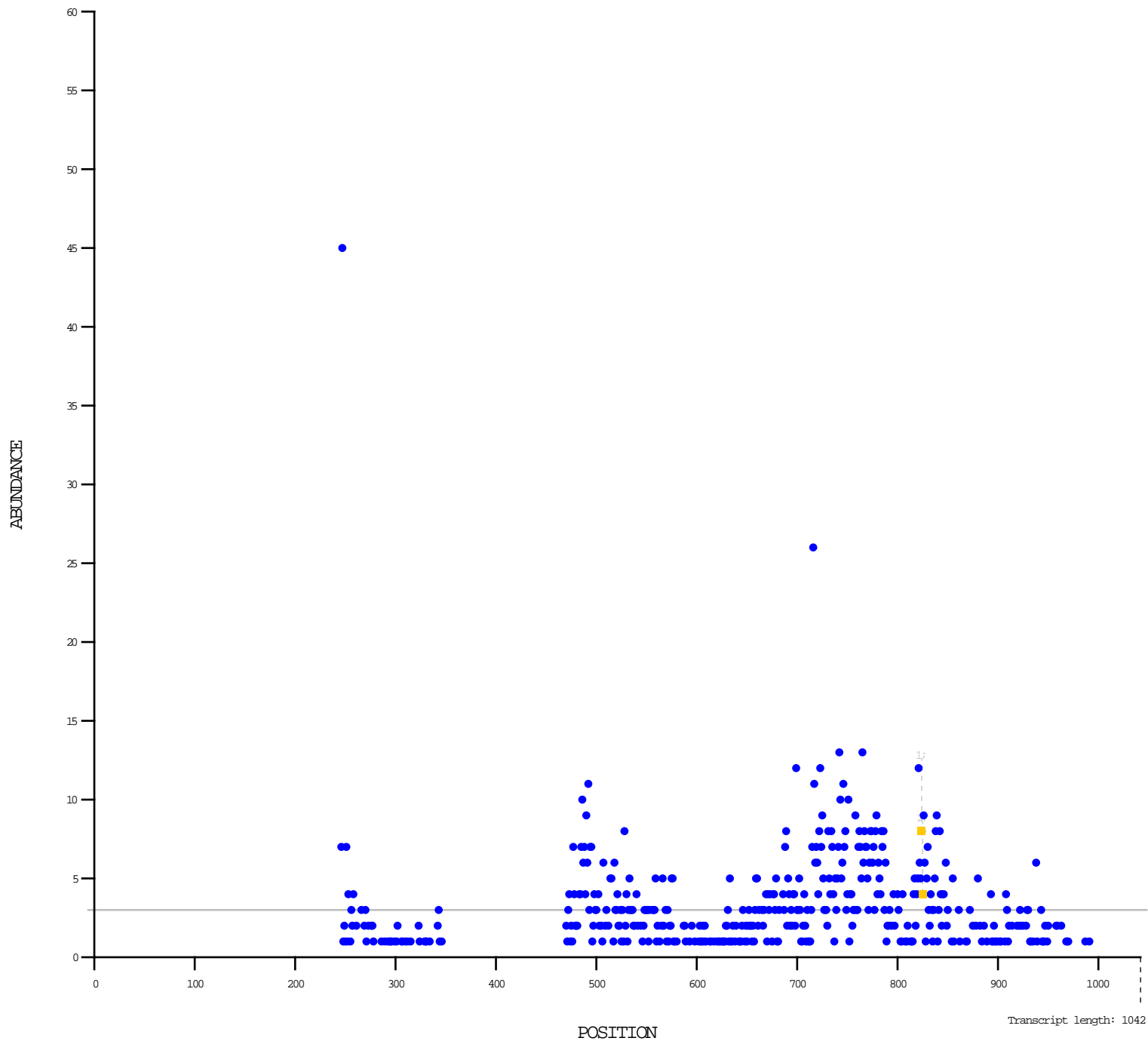




Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

1 #1 Position:839 Abundance: 2.00(deg) 1(sRNA)  
 5' TGGCAGTGGCCTCCCTGGTGC 3' ID:  
 ||||| ||||| |o|o ||| Score: 4.0  
 3' TGAACCGTAAACCGGACCGGTAAACGAGACCG 5' p-value: 0.01

Transcript length: 1181

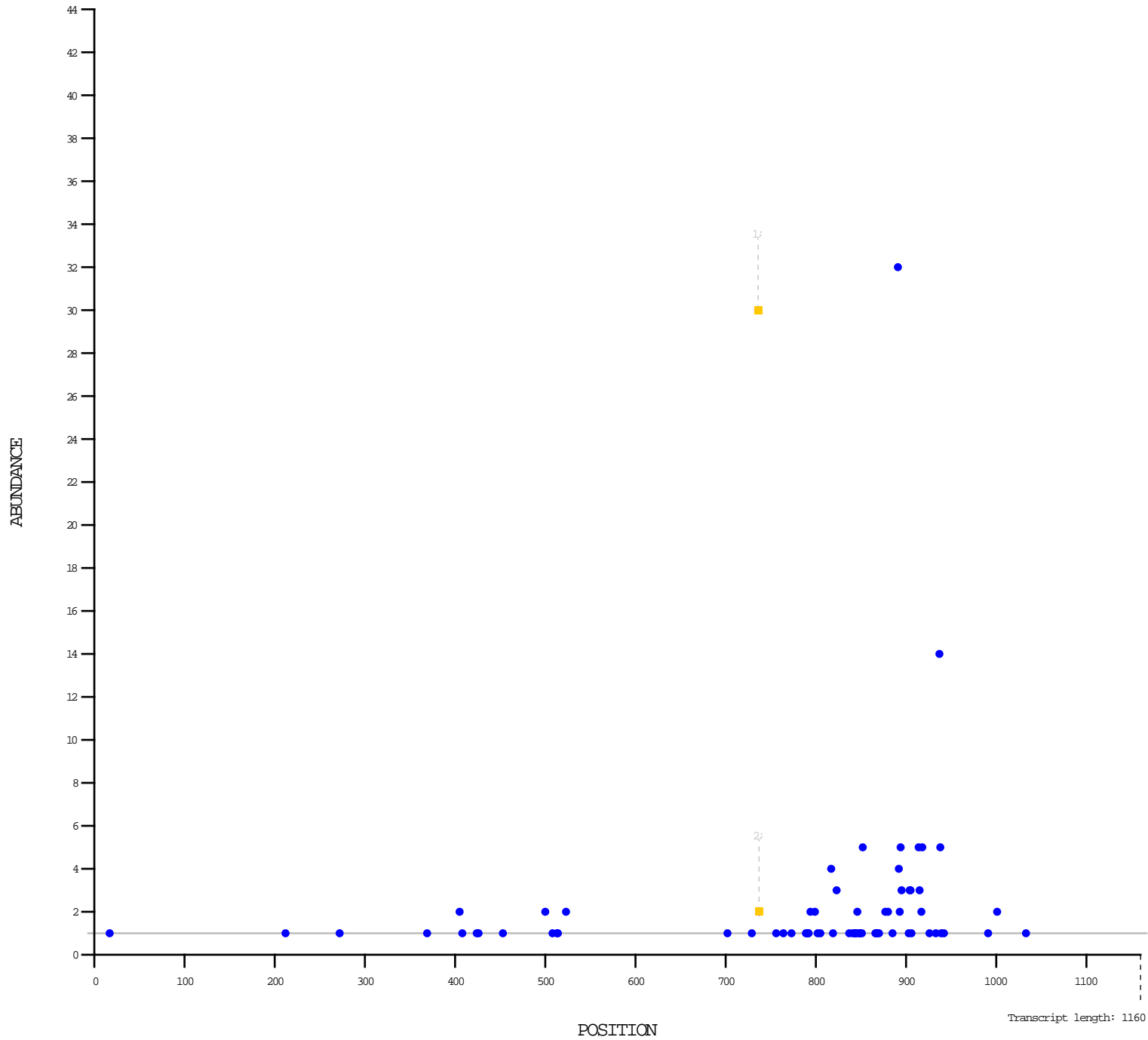


Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 2 #1 Position:824 Abundance: 8.00(deg) 1(sRNA)  
 5' TATAAAGCC-TAATTAATCCAT 3' ID:  
 ||||| |o|| ||||| |o||| |  
 3' TCAATATATTTGGAAITTAATTTGGGTACGTACCT 5' Score: 3.0  
 p-value: 0.01

■ 2 #2 Position:825 Abundance: 4.00(deg) 1(sRNA)  
 5' TATAAAGCCT-AATTAATCCAT 3' ID:  
 ||||| |o||| ||||| |o||| |  
 3' ATCAATATATTTGGAAITTAATTTGGGTACGTACCT 5' Score: 3.0  
 p-value: 0.0

Transcript length: 1042

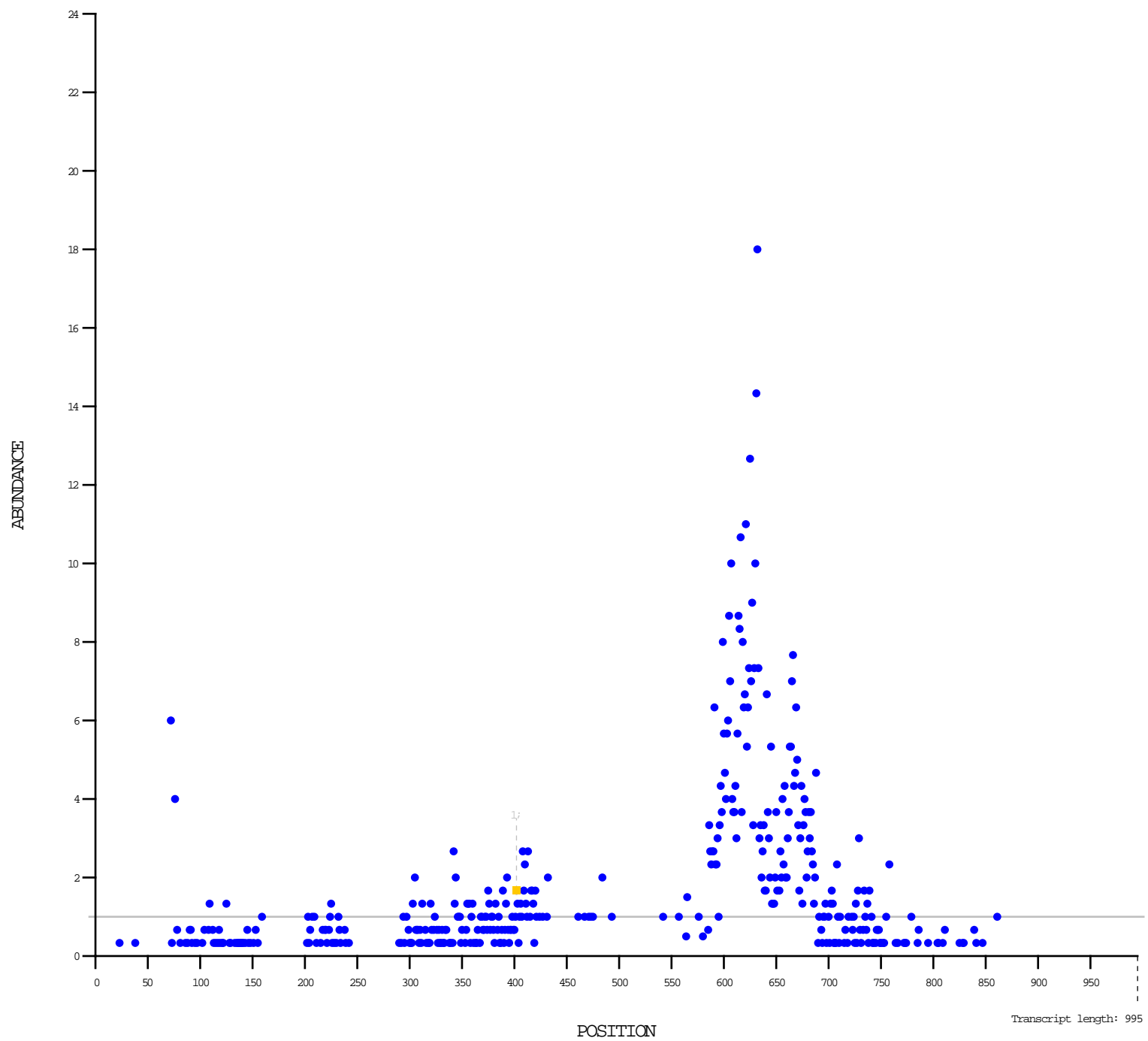


Category: 0 1 2 3 4  
Degradome alignment: ● Median: —

#1 Position:736 Abundance: 30.00(deg) 8(sRNA)  
5' TGACAGAGGAGTGACAC 3' ID:  
|||||  
3' ACGTACTGTCCTCTCTCTCTGTTACGAATCTA 5' p-value: 0.0  
Score: 2.0

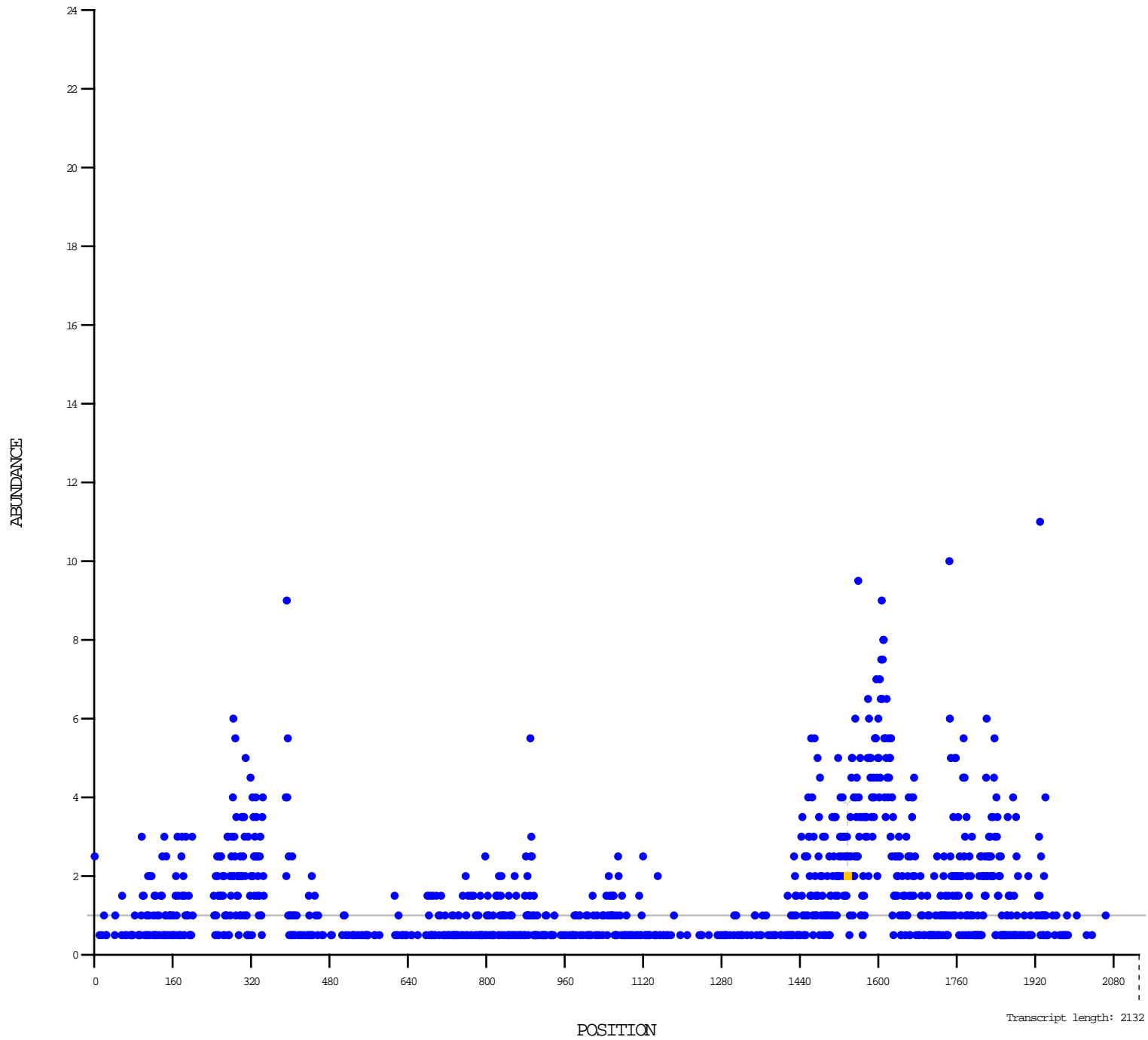
#2 Position:737 Abundance: 2.00(deg) 1(sRNA)  
5' TTGACAGAGGAGCGACAC 3' ID:  
|||||  
3' GAGTACTGTCCTCTCTCTCTGTTACGAATCT 5' p-value: 0.02  
Score: 3.0





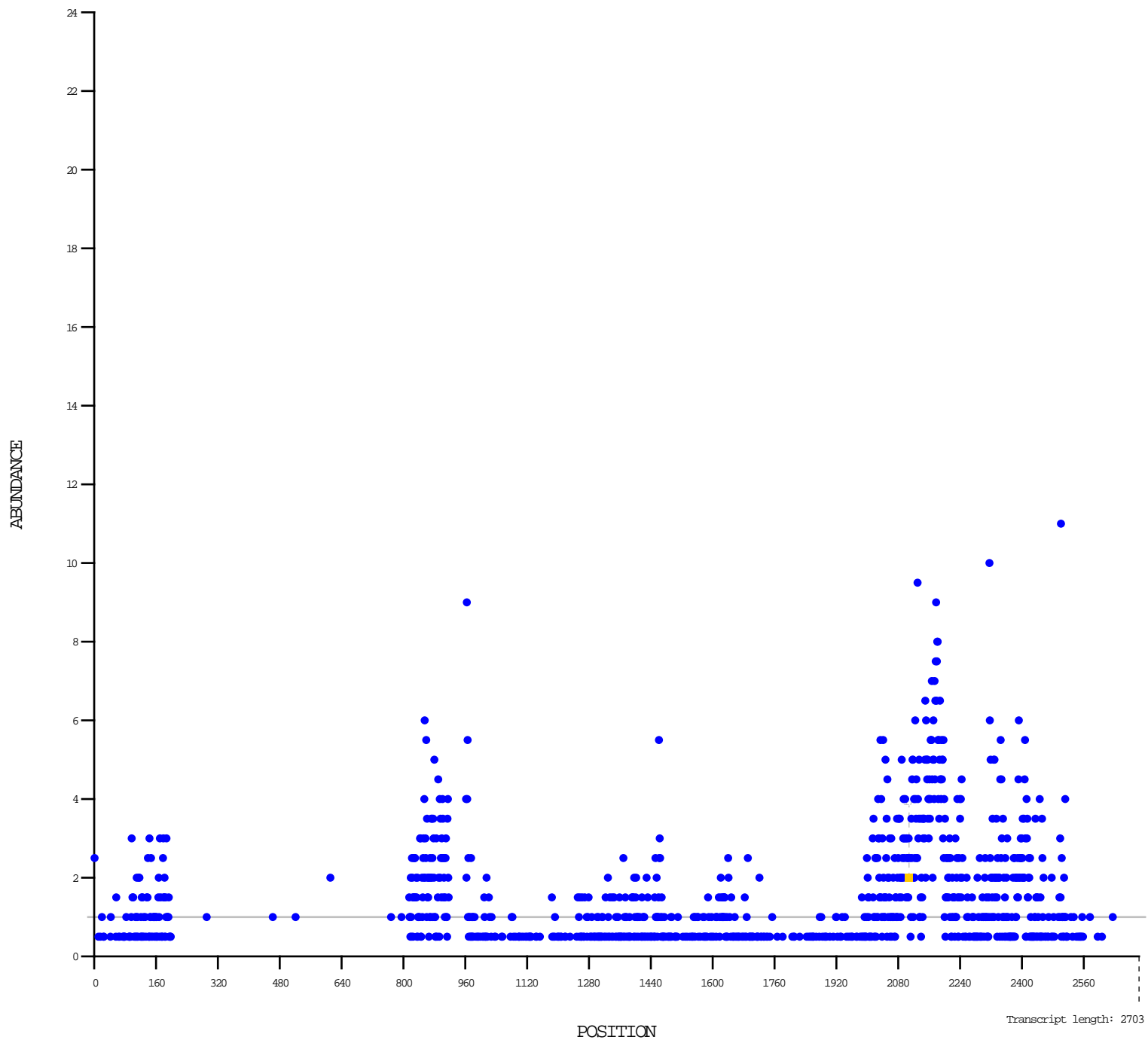
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

#1 Position: 402 Abundance: 1.67(deg)  
 5' TGCCTGGAGAGCAG-GGCACCT 3' ID:  
 ||||| 3' Score: 3.0  
 3' GCCTACGACCTCTCTCTCTCCGGCACTCCGA 5' p-value: 0.02



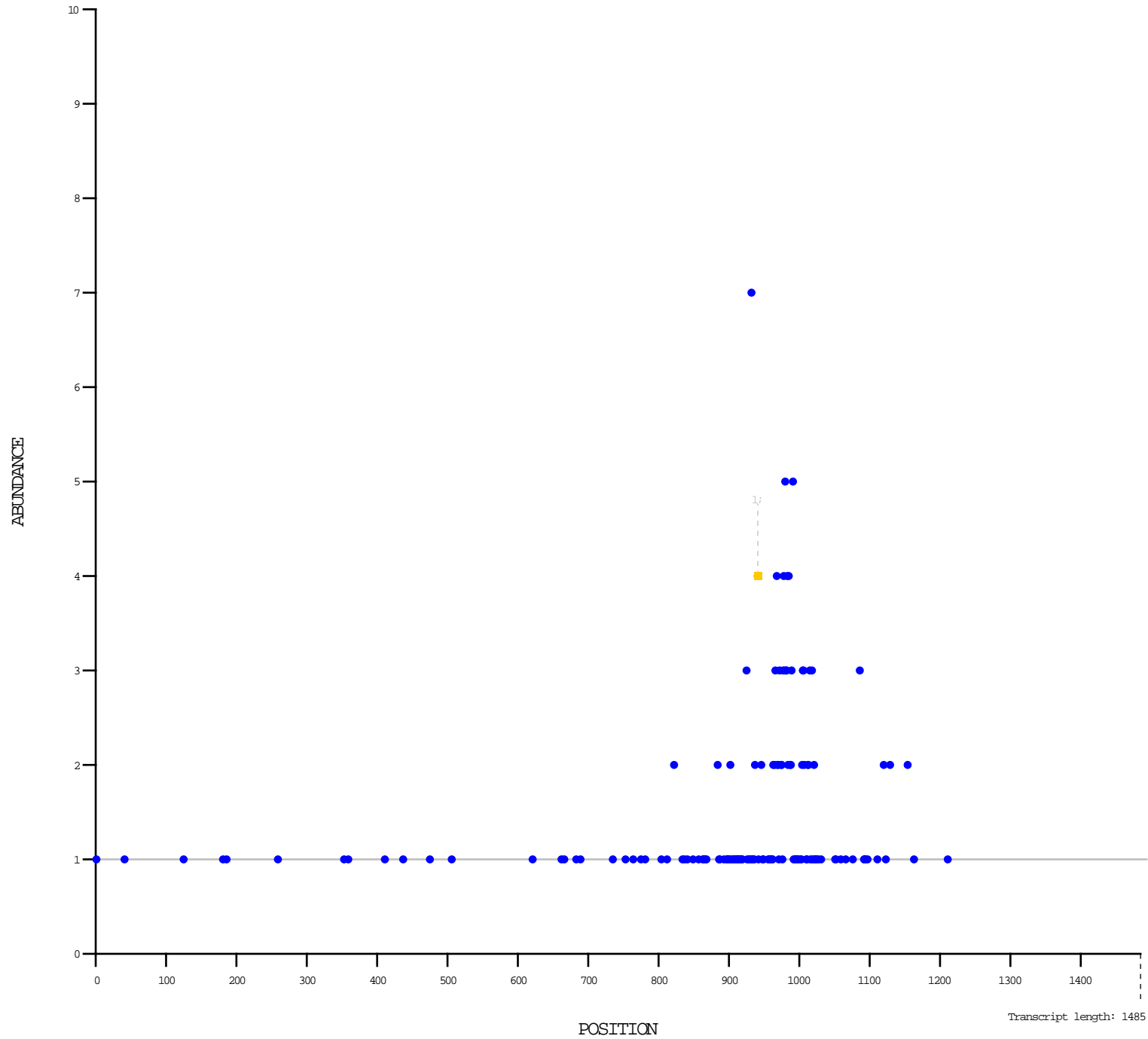
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

2 #1 Position:1537 Abundance: 2.00(deg) 1(sRNA)  
 5' TCGATAAACCTCTCGATCCAG 3' ID:  
 ||| ||||| ||||| ||||| Score: 3.0  
 3' CGTCAGC-ATTTCGAGTCGTAGTTCGAAGTAC 5' p-value: 0.0



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

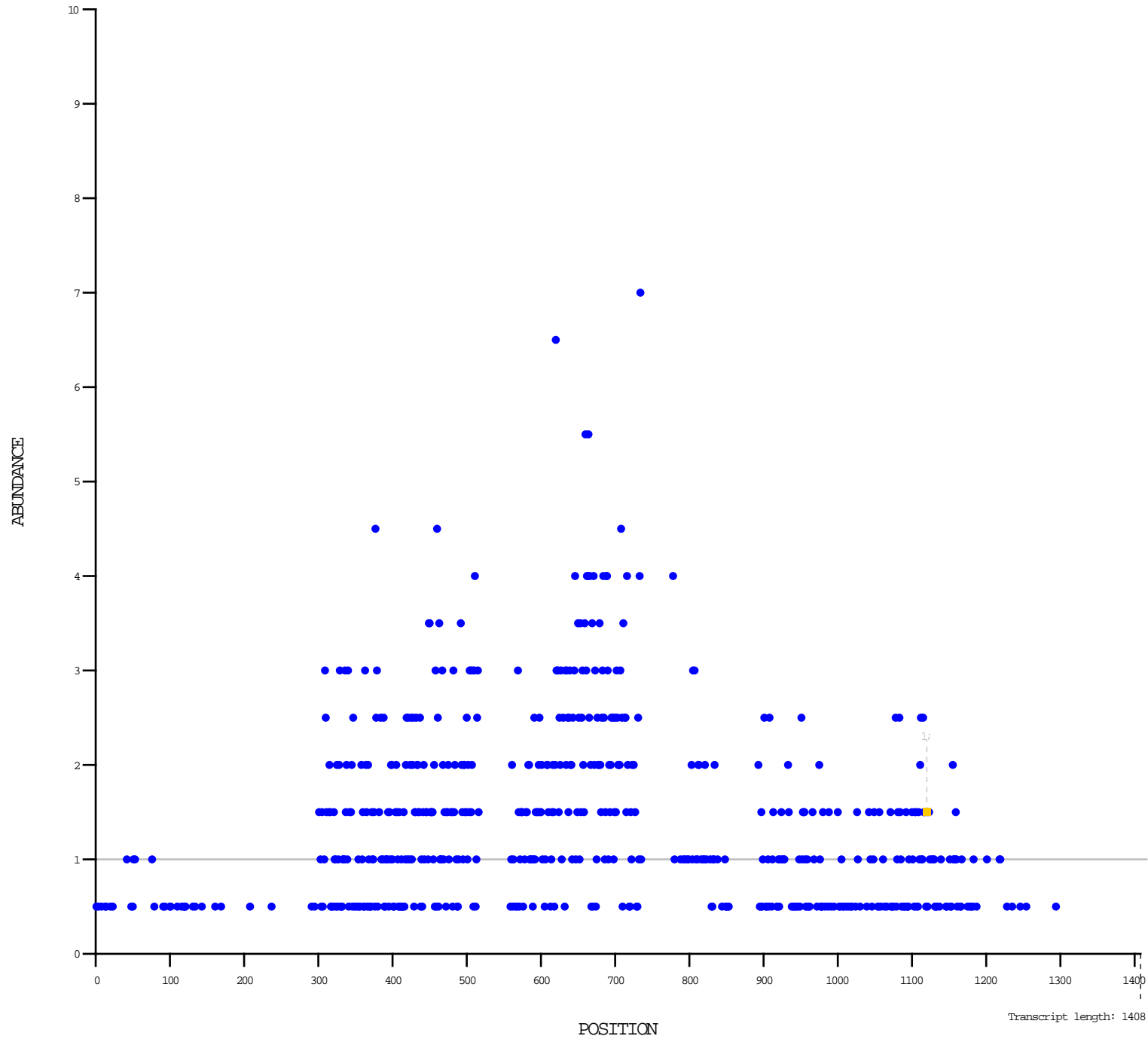
2 #1 Position:2108 Abundance: 2.00(deg) 1(sRNA)  
5' TCGATAAACCTTCGATCCAG 3' ID:  
||||| ||||| ||||| ||||| Score: 3.0  
3' CGTCAGC-ATTTCGAGTCGTAGTTCGAAGTAC 5' p-value: 0.02



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

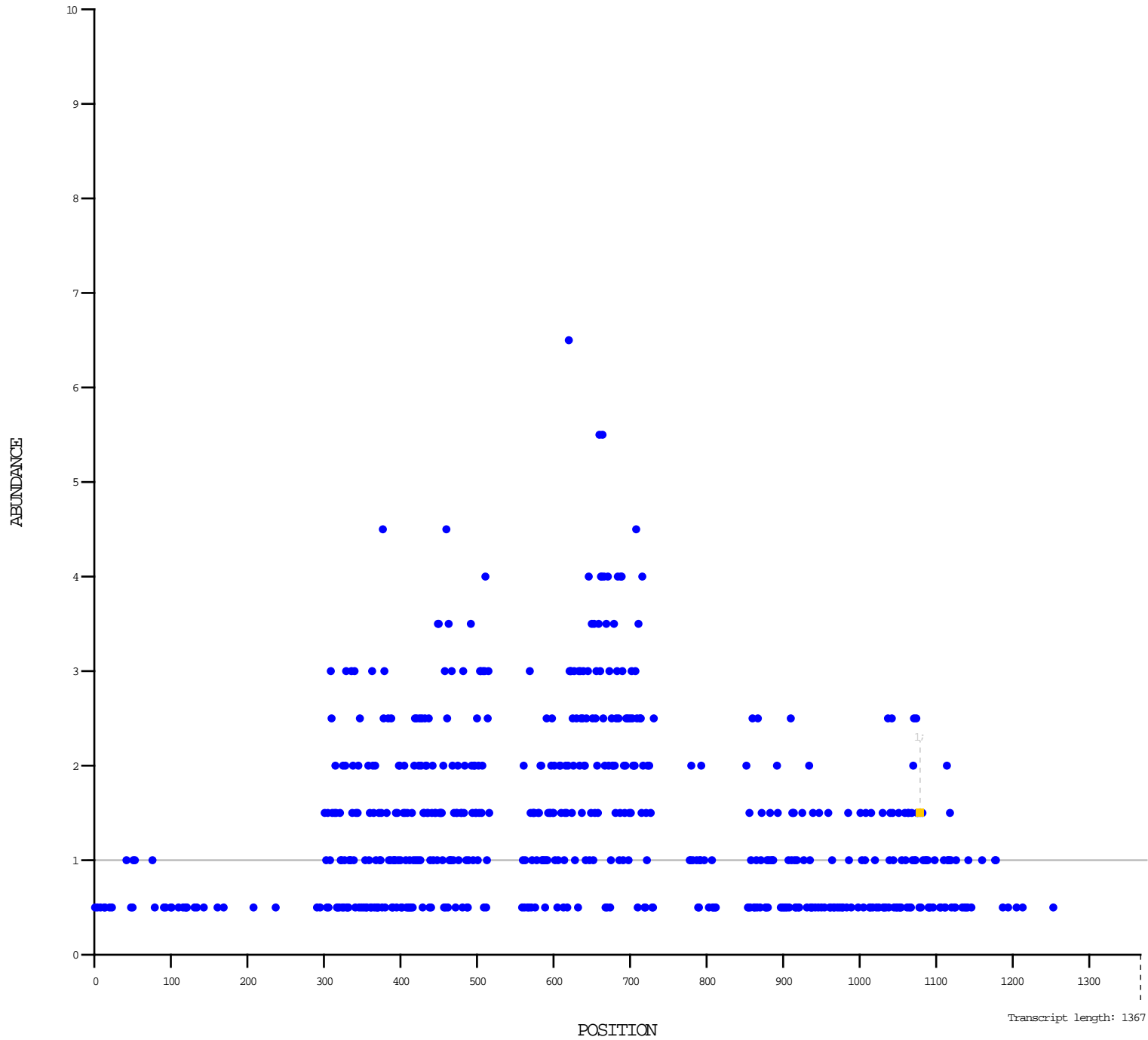
2 #1 Position:941 Abundance: 4.00(deg) 1(sRNA)  
 5' TCGATAAACCTCTGCATCCAG 3' ID:  
 ||||| |||||c|||||||  
 3' CCCGAGCTACTTGGGGACGTAGGCCCTGGCCGA 5' Score: 2.5  
 p-value: 0.02





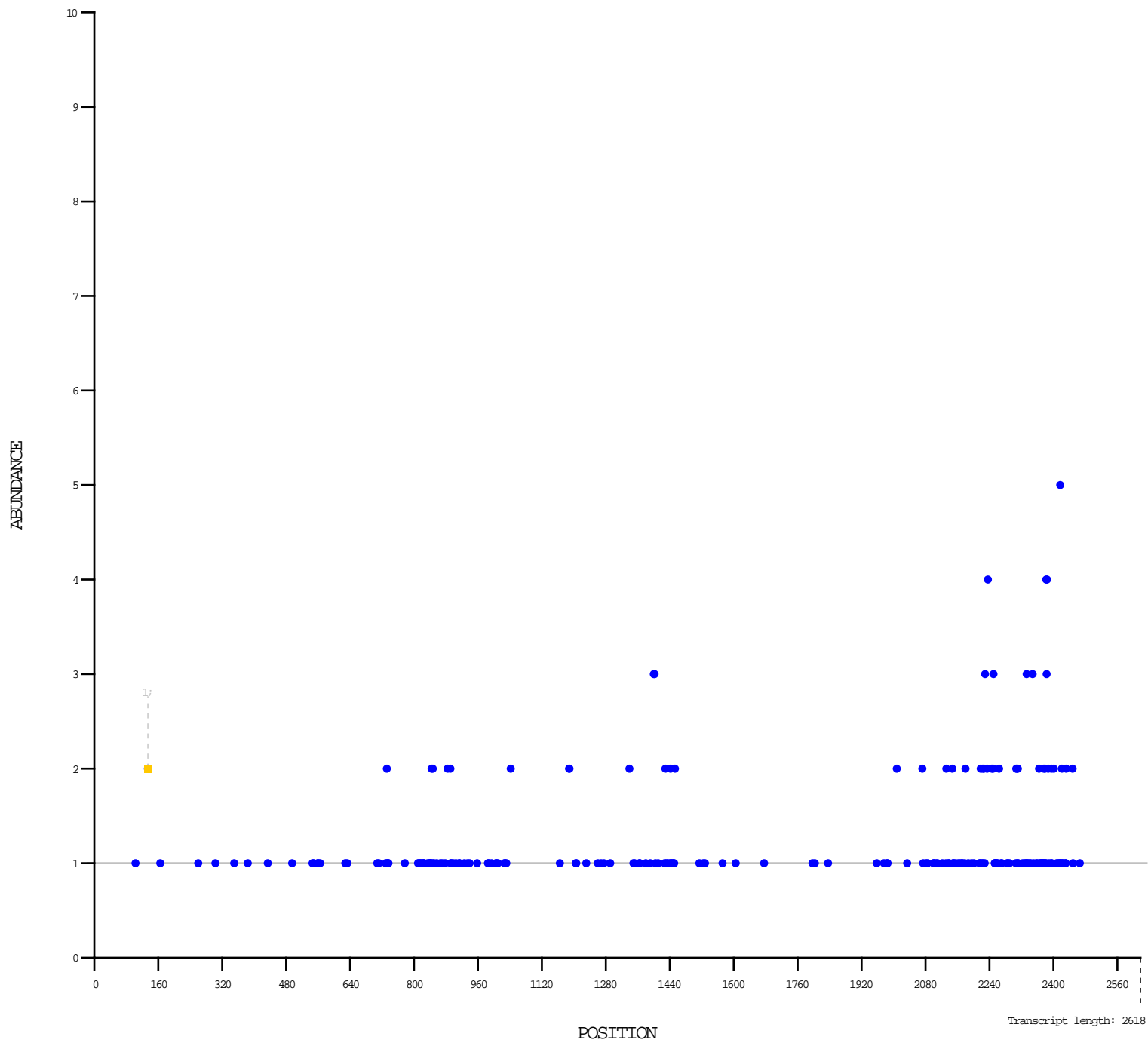
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

2 #1 Position:1120 Abundance: 1.50(deg) 1(sRNA)  
 5' GTATGGAAAGAACTGCTGGCCCA 3' ID:  
 |||o|| ||||| |||o||| Score: 3.5  
 3' GAAACATGCCGCTCTTG-CGATGIGGRTGCTG 5' p-value: 0.02



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

2 #1 Position:1079 Abundance: 1.50(deg) 1(sRNA)  
 5' GTATGGAAAGAACTGCTGGCCA 3' ID:  
 |||o|| ||||| |||o||| Score: 3.5  
 3' GAACATGGCCGCTCTTG-CGATGGGRTGCTG 5' p-value: 0.02



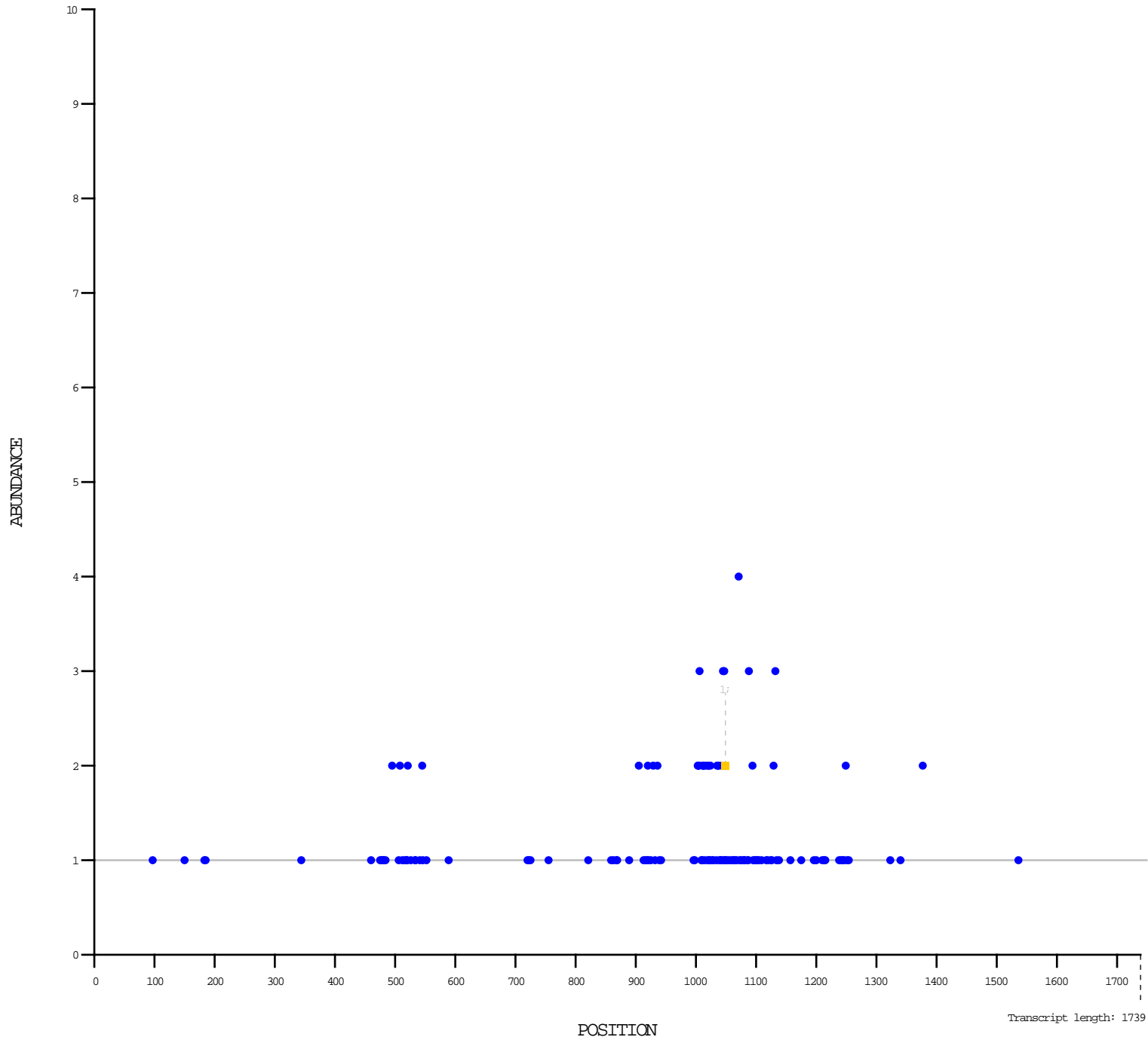
Category: 0 1 2 3 4

Degradome alignment: ● Median: —

■ #1 Position:134 Abundance: 2.00(deg) 8(sRNA)

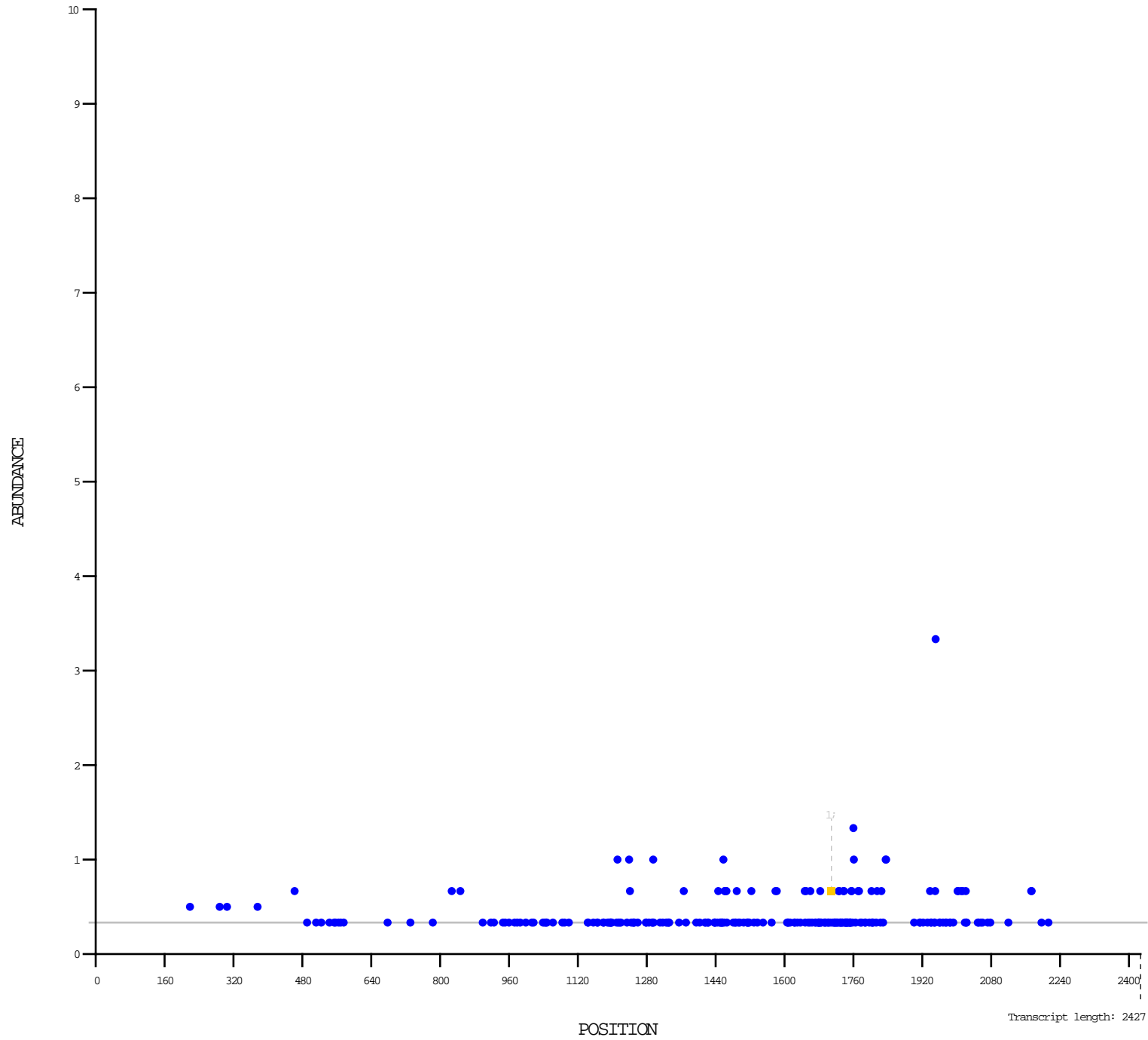
```

5' TGACAGAGGAGTGGCCAC 3' ID:
  ||||| ||||| ||| | | |
3' CTCACGTCTCCCTCCGCTGGTGGGGCAGC 5' Score: 2.5
p-value: 0.02
```



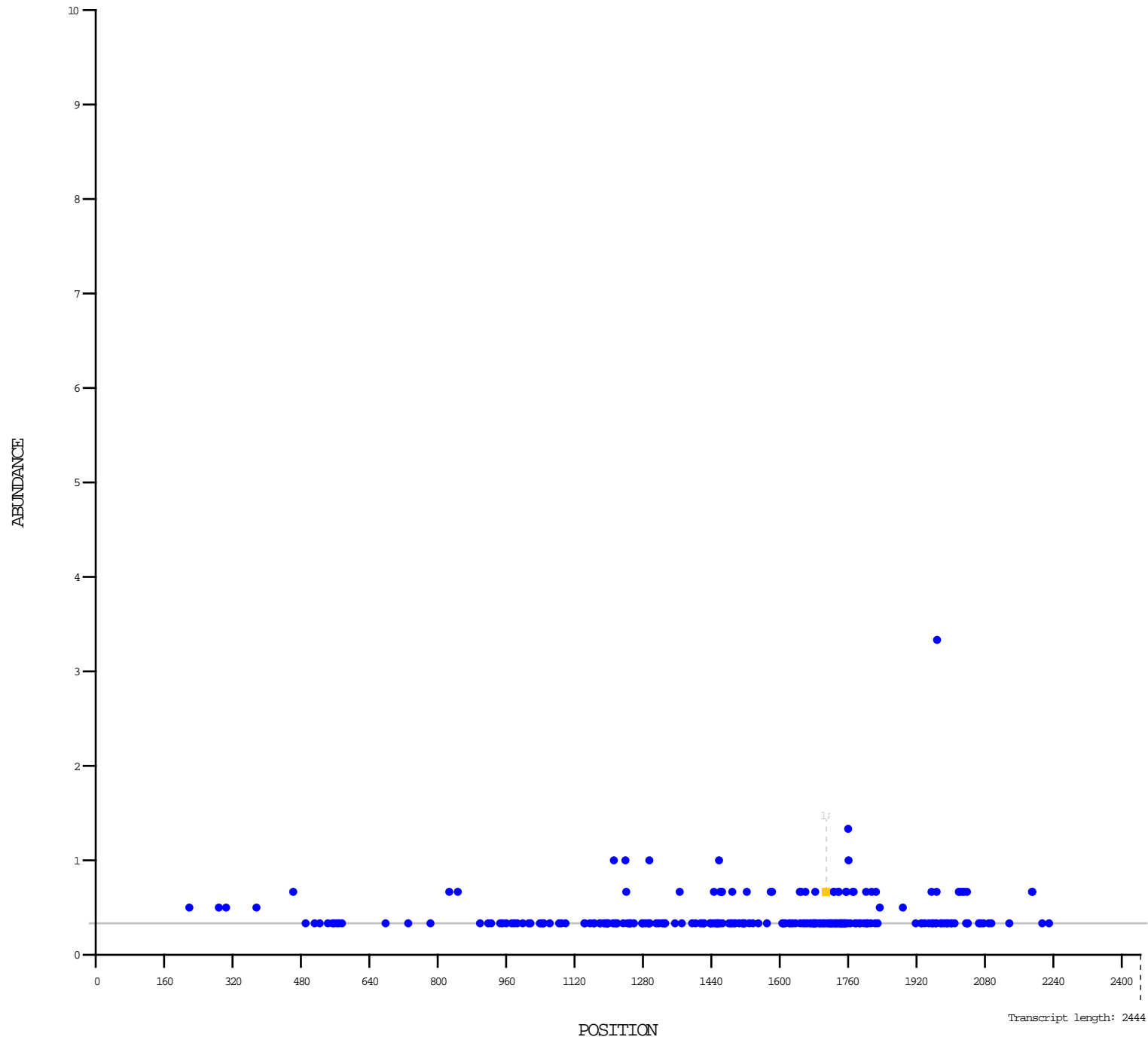
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

2 #1 Position:1049 Abundance: 2.00(deg) 1(sRNA)  
 5' GTGGGTTCTCCCTCGCATG 3' ID:  
 o||| |o|||||||o|||o| Score: 3.0  
 3' CGGCTACGGCGAGGAGGAGCCGTCAGCCGCA 5' p-value: 0.04



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

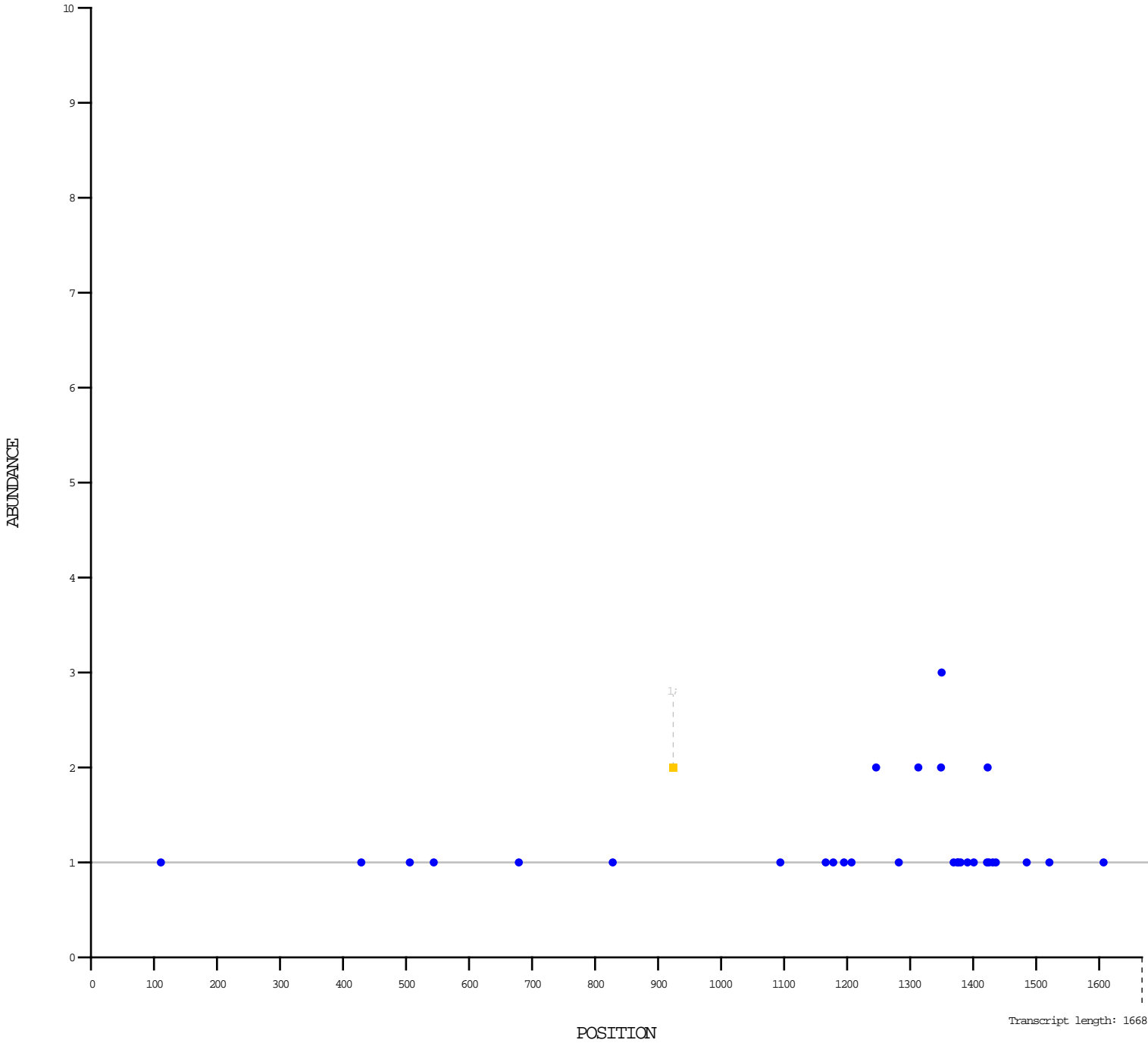
■ 2 #1 Position:1709 Abundance: 0.67(deg) 1(sRNA)  
 5' GTATGGAAAGAACTGCTGGCCCA 3' ID:  
 |||||o||||| ||||| Score: 3.5  
 3' CTTCATACCTTTTGTACGCC-CGATATCCGG 5' p-value: 0.02



Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
Degradome alignment: ● Median: —

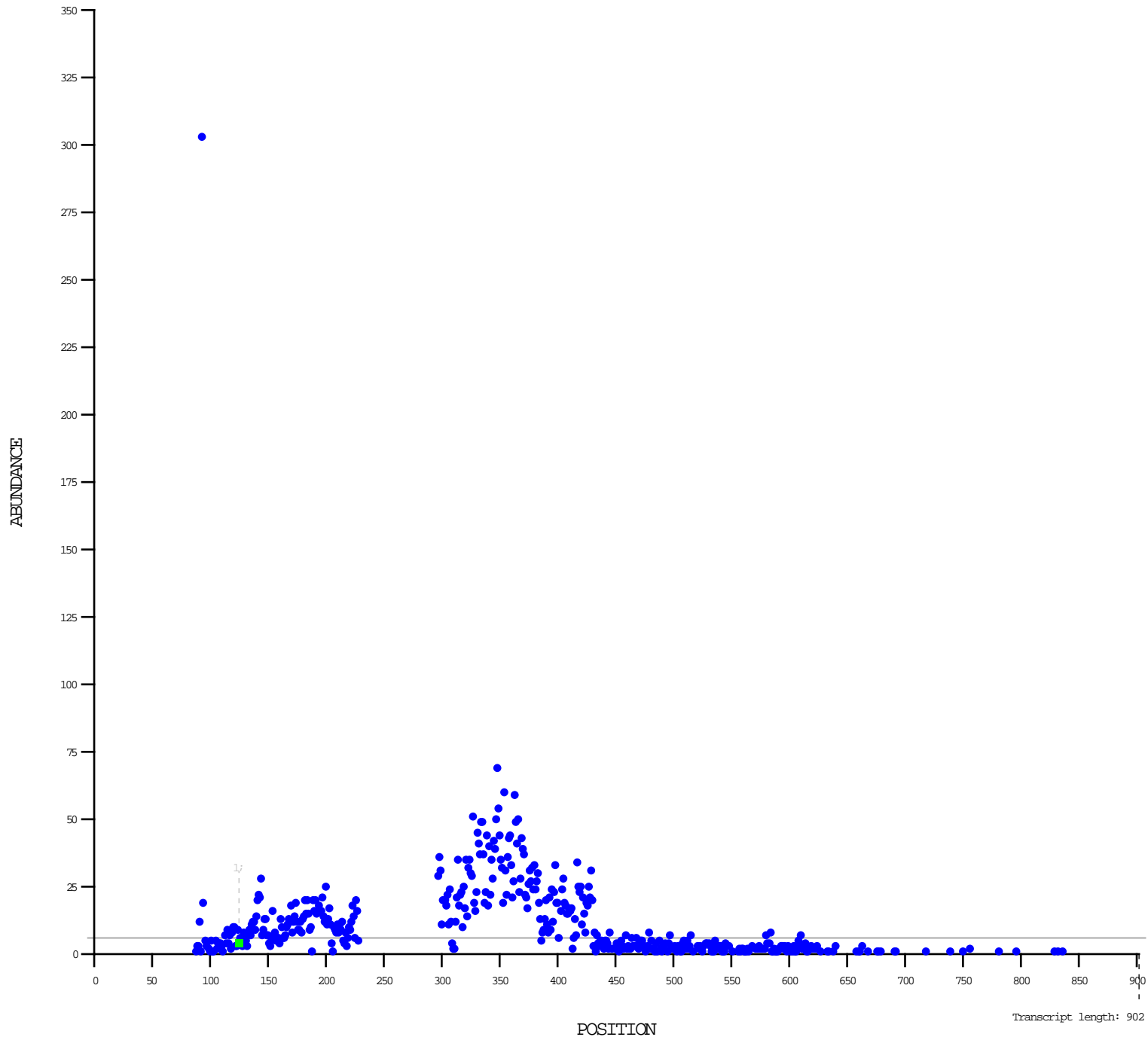
■ 2 #1 Position:1709 Abundance: 0.67(deg) 1(sRNA)  
5' GTATGGAAGAACTGCTGGCCCA 3' ID:  
|||||||o||||||| ||||| Score: 3.5  
3' CTTCATACCTTTTGGAGCC-CGATATCCGG 5' p-value: 0.04





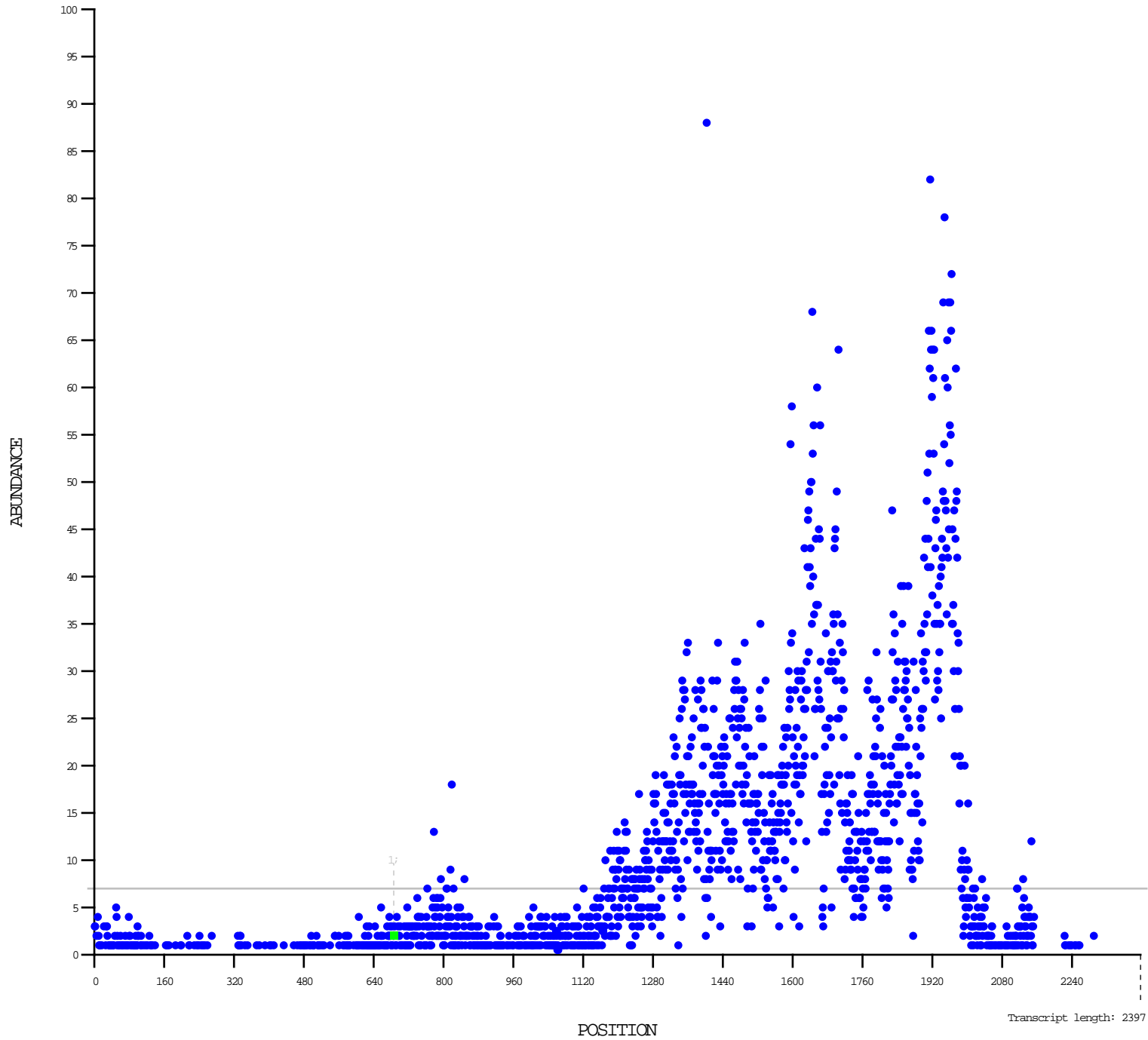
2 #1 Position:924 Abundance: 2.00(deg) 8(sRNA)  
5' TGACAGAGGAGTGGCCAC 3' ID:  
|||||  
3' AACCACTGTCCTCTCTCTGGTGGACCTC 5' Score: 1.0  
p-value: 0.0





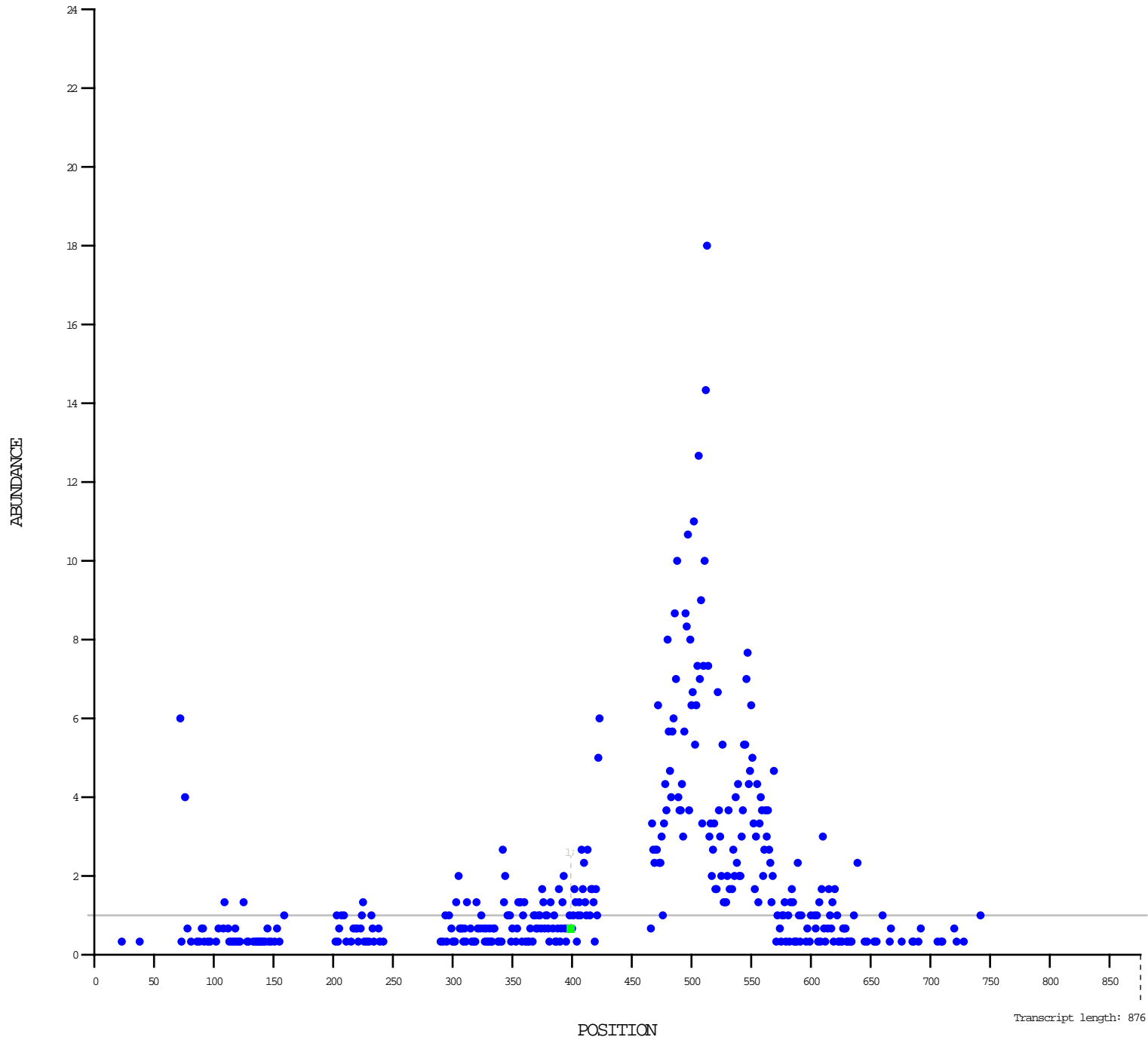
Category: 0 1 2 3 4  
Degradome alignment: ● Median: —

3 #1 Position:125 Abundance: 4.00(deg) 1(sRNA)  
5' AGATCATGTTGTAGCTTCACT 3' ID:  
||||| ||||| ||||| ||||| Score: 4.0  
3' AGACACTAG-ACACACCGAATGACTTCIT 5' p-value: 0.03



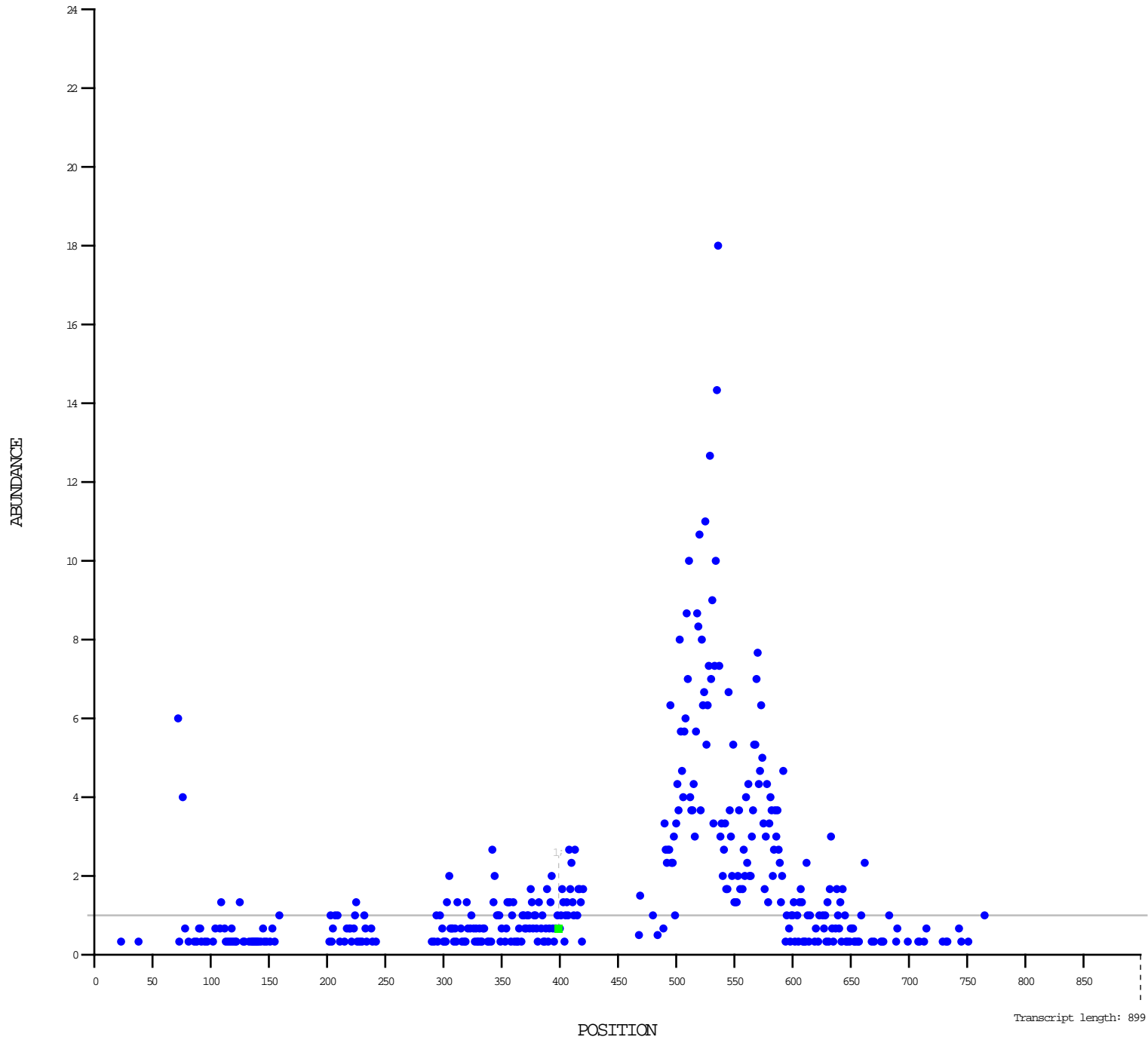
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

3 #1 Position:686 Abundance: 2.00(deg) 1(sRNA)  
 5' TGGTAGGCATTCGGTAAGT 3' ID:  
 ||||| ||||| |o||| Score: 4.5  
 3' TGIGACCAT-CGGAGACAGTTCGGTATCC 5' p-value: 0.03



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

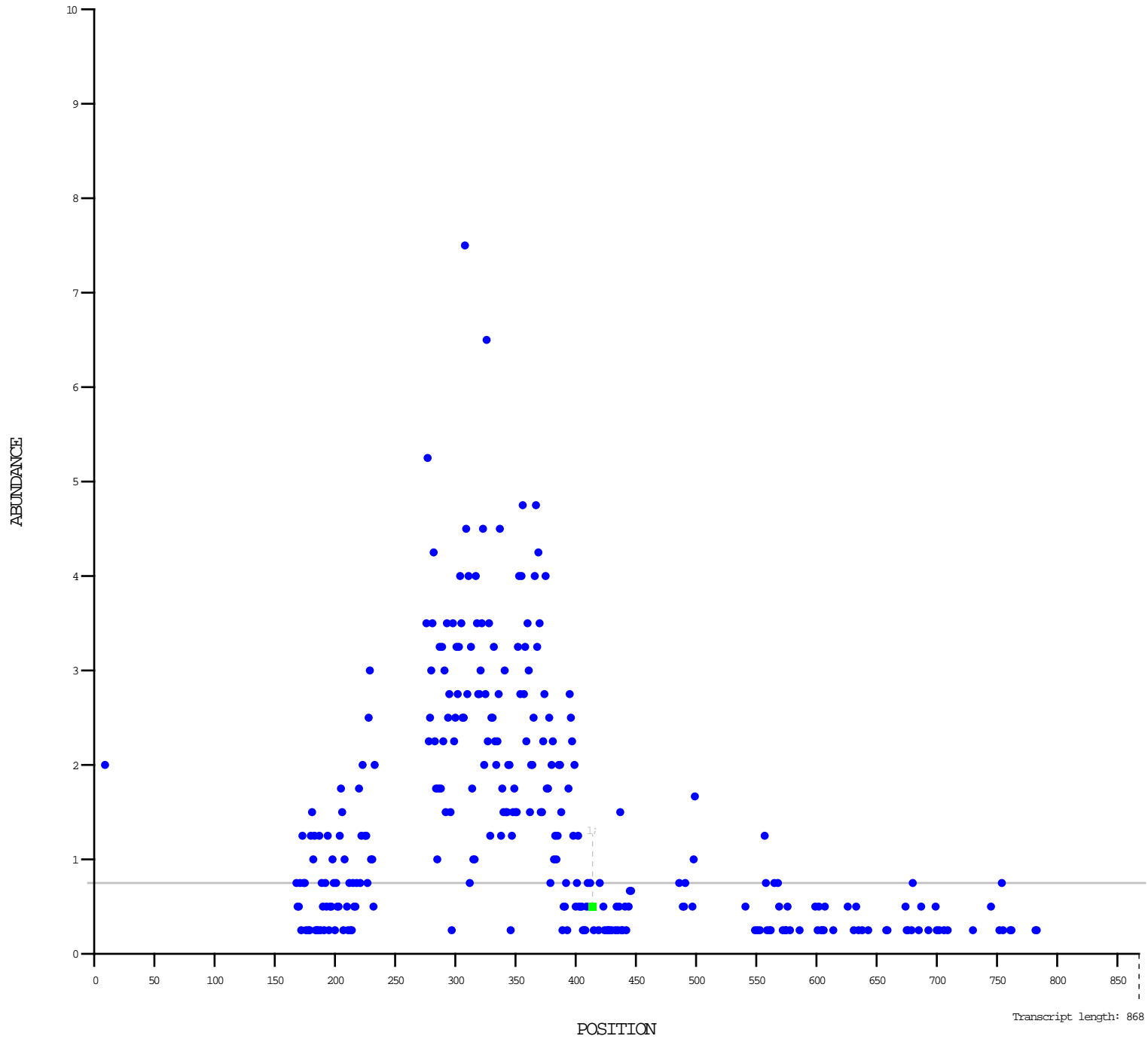
■ 3 #1 Position:399 Abundance: 0.67(deg) 1(sRNA)  
 5' TGGAGAGCAG-GCCACGTCC 3' ID:  
 ||||| ||||| ||||| ||||| Score: 4.0  
 3' TAGGACCTCTCTCTCCGGGCACTCCGACAA 5' p-value: 0.03



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

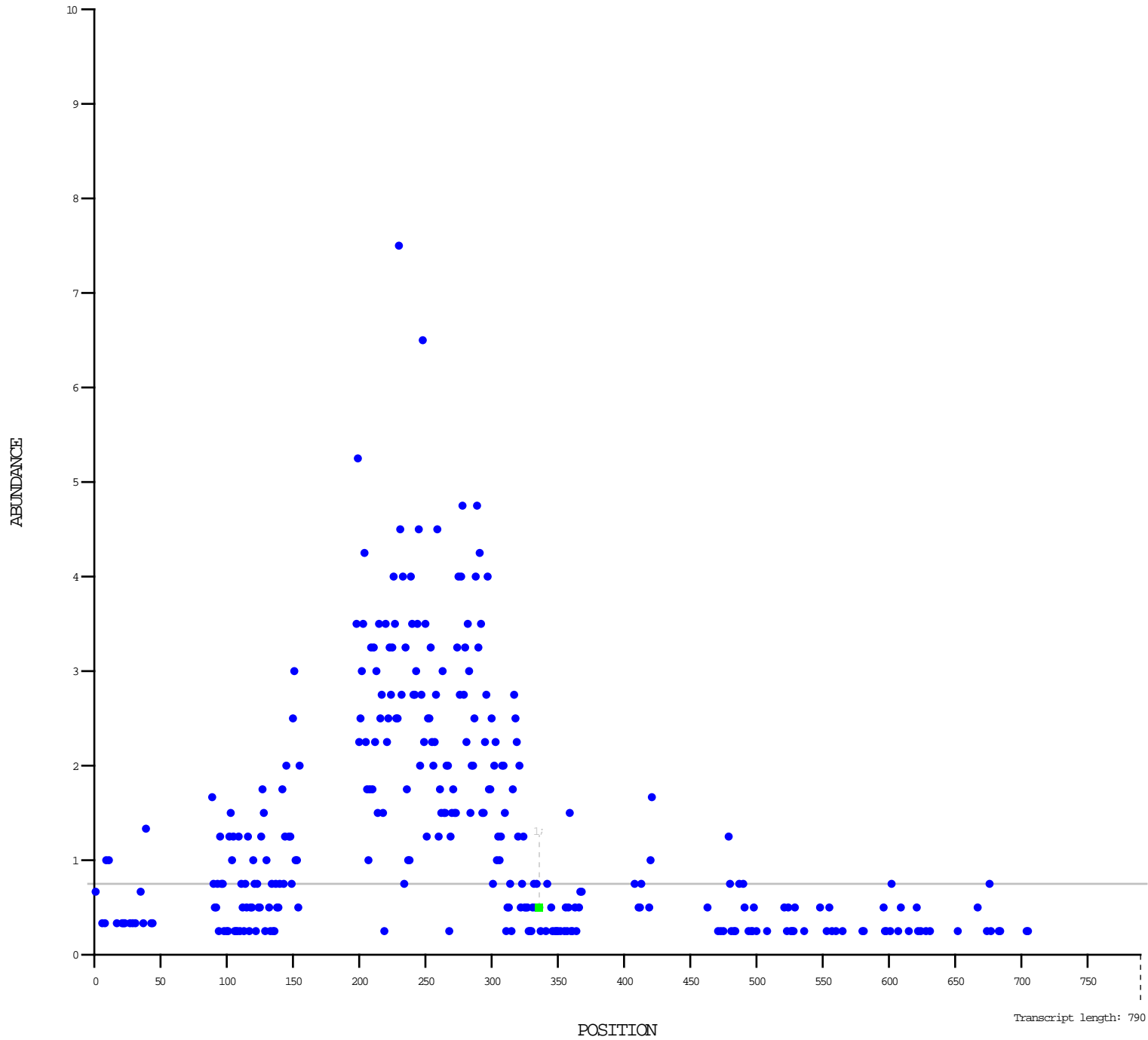
3 #1 Position:399 Abundance: 0.67(deg) 1(sRNA)  
 5' TGGAGAGCAG-GCCACGTCC 3' ID:  
 ||||| ||||| ||||| ||||| Score: 4.0  
 3' TAGGACCTCTCTCTCCGGCACTCGGACAA 5' p-value: 0.04

Transcript length: 899



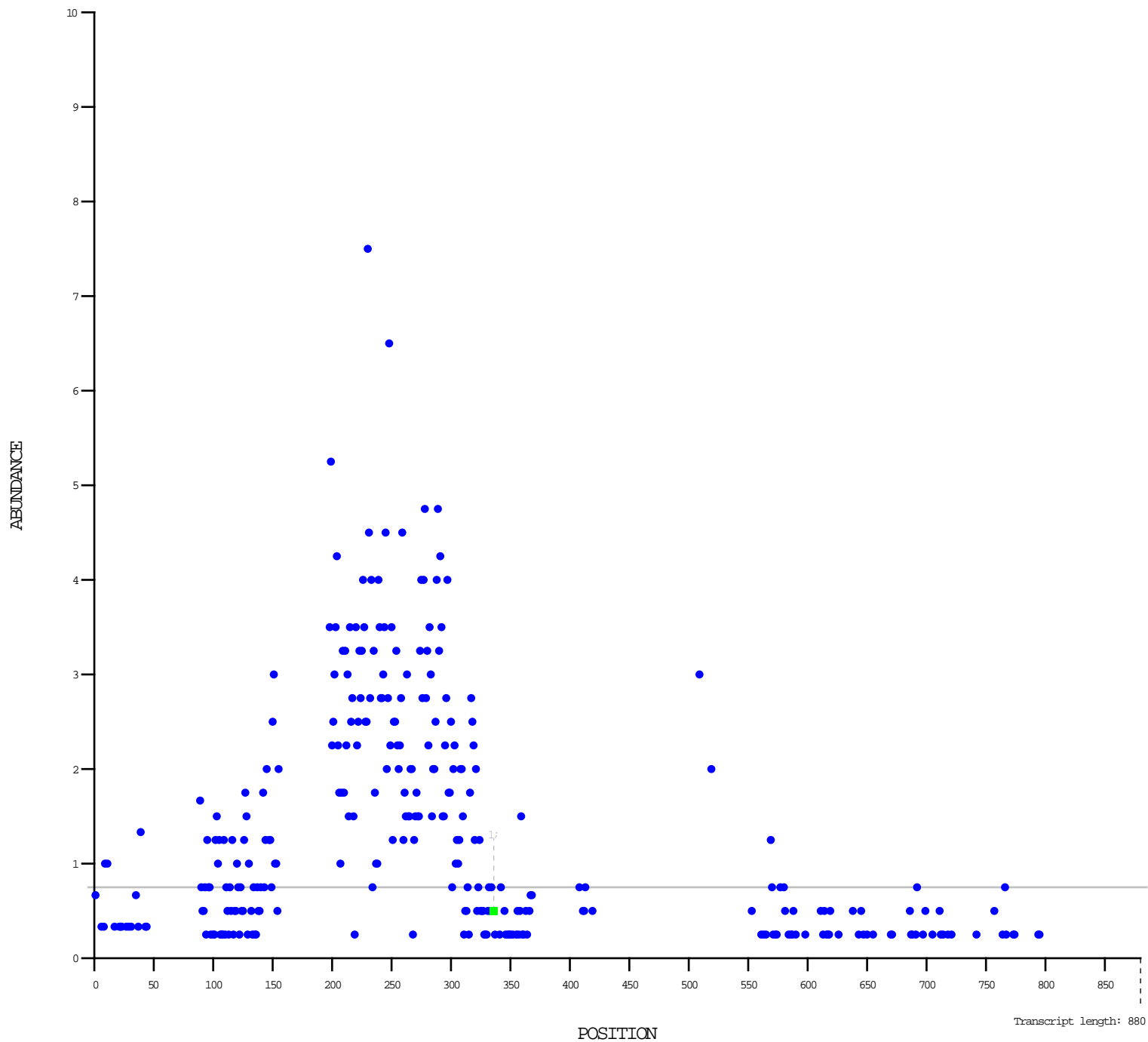
Category: ■ 0 ■ 1 ■ 2 ■ 3 ■ 4  
 Degradome alignment: ● Median: —

■ 3 #1 Position:414 Abundance: 0.50(deg) 1(sRNA)  
 5' AGATCATGTTGTAGCTTCACT 3' ID:  
 ||||| ||||| ||||| ||||| Score: 4.0  
 3' AACTOCTAGAACACATCGACTTGAGAAGAA 5' p-value: 0.01



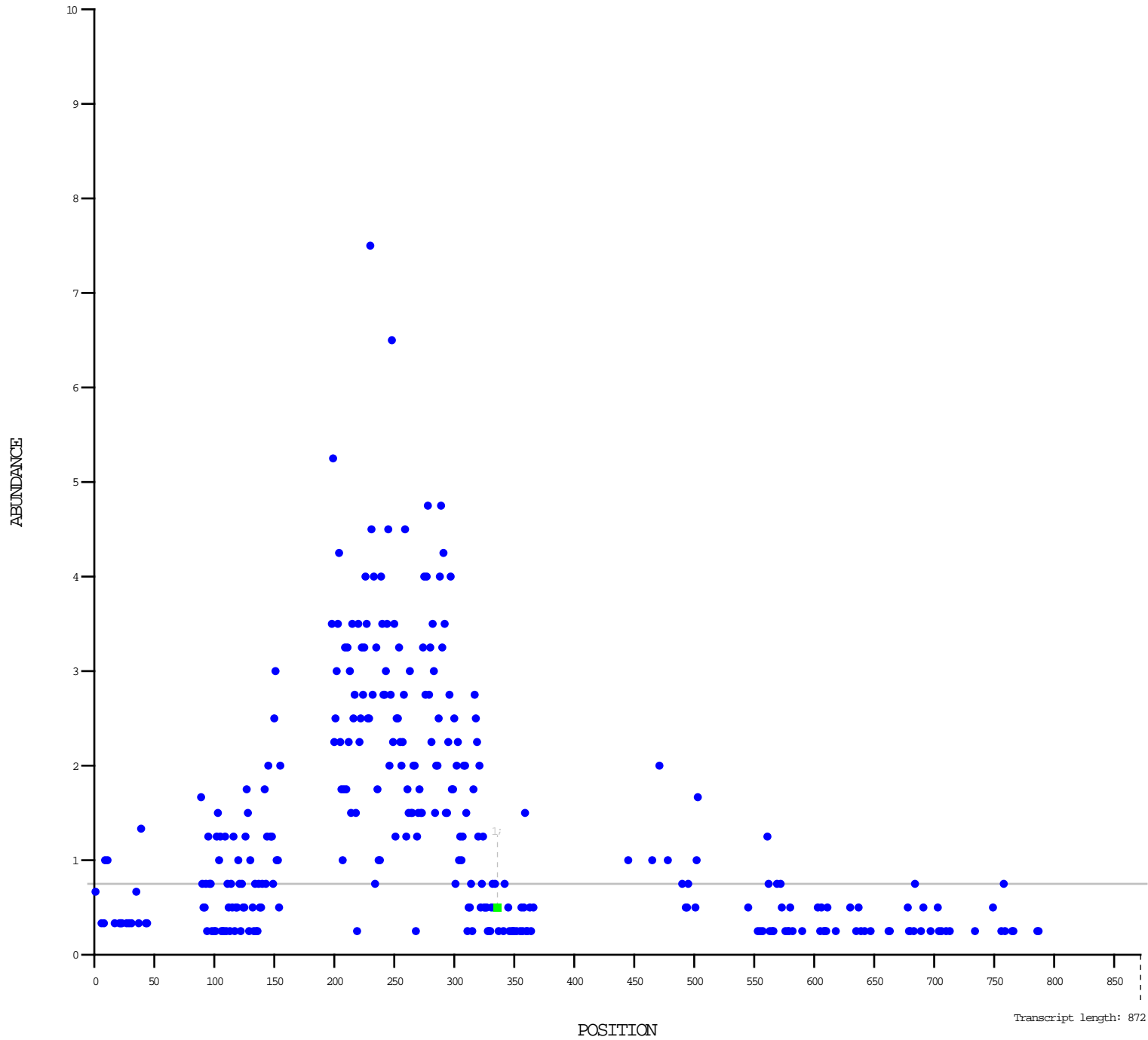
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

■ 3 #1 Position:336 Abundance: 0.50(deg) 1(sRNA)  
 5' AGATCATGTTGTAGCTTCACT 3' ID:  
 ||||| ||||| ||||| ||||| Score: 4.0  
 3' AACTOCTAGAACAAATCGACTTGAGAAGAA 5' p-value: 0.03



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

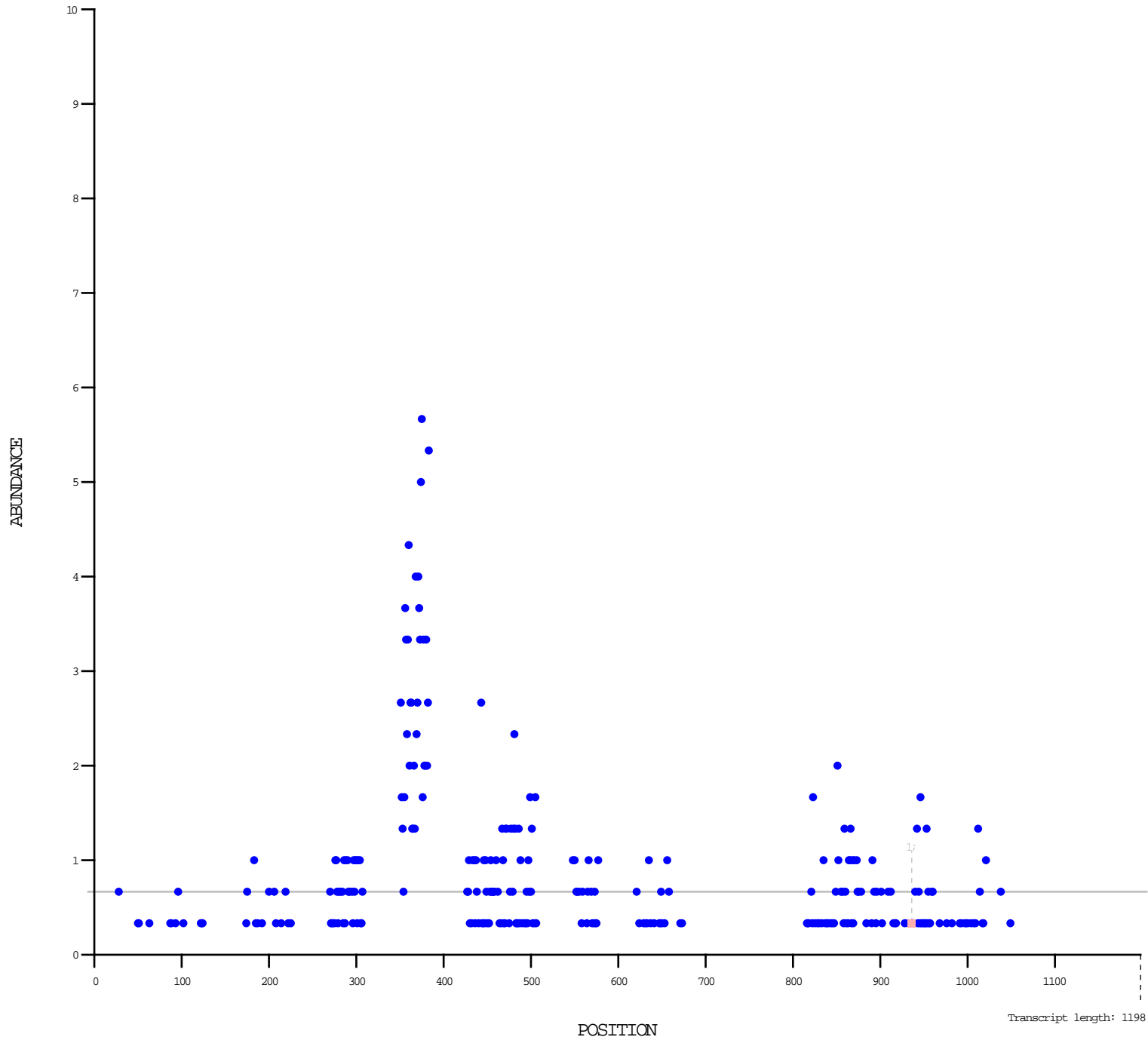
3 #1 Position:336 Abundance: 0.50(deg) 1(sRNA)  
 5' AGATCATGTTGTAGCTTCACT 3' ID:  
 ||||| ||||| ||||| ||||| Score: 4.0  
 3' AACTCCTAGAACACATCGACTTGAGAAGAA 5' p-value: 0.02



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

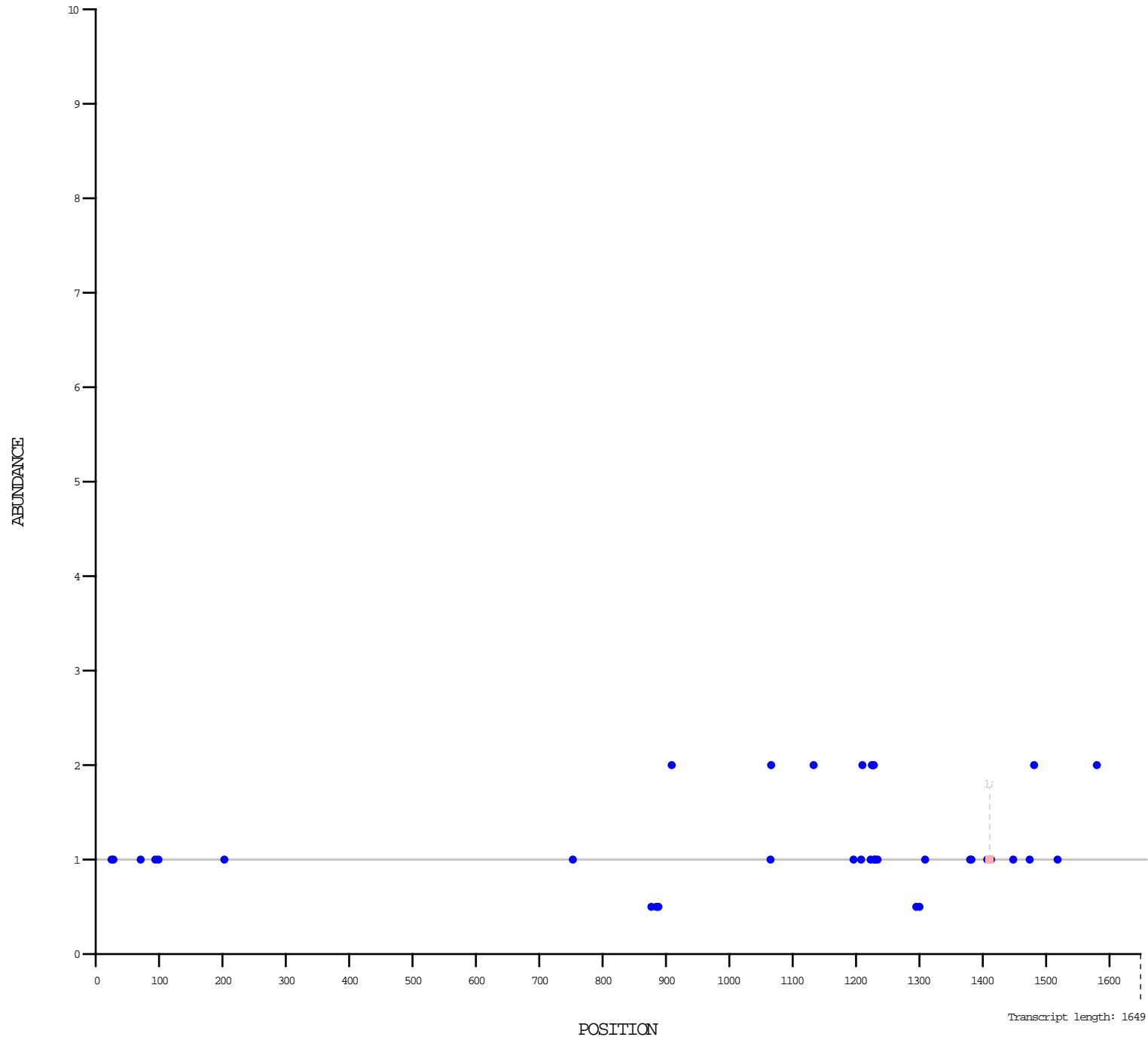
■ 3 #1 Position:336 Abundance: 0.50(deg) 1(sRNA)  
 5' AGATCATGTTGTAGCTTCACT 3' ID:  
 ||||| ||||| ||||| ||||| Score: 4.0  
 3' AACTOCTAGAACACATCGACTTGAGAAGAA 5' p-value: 0.01





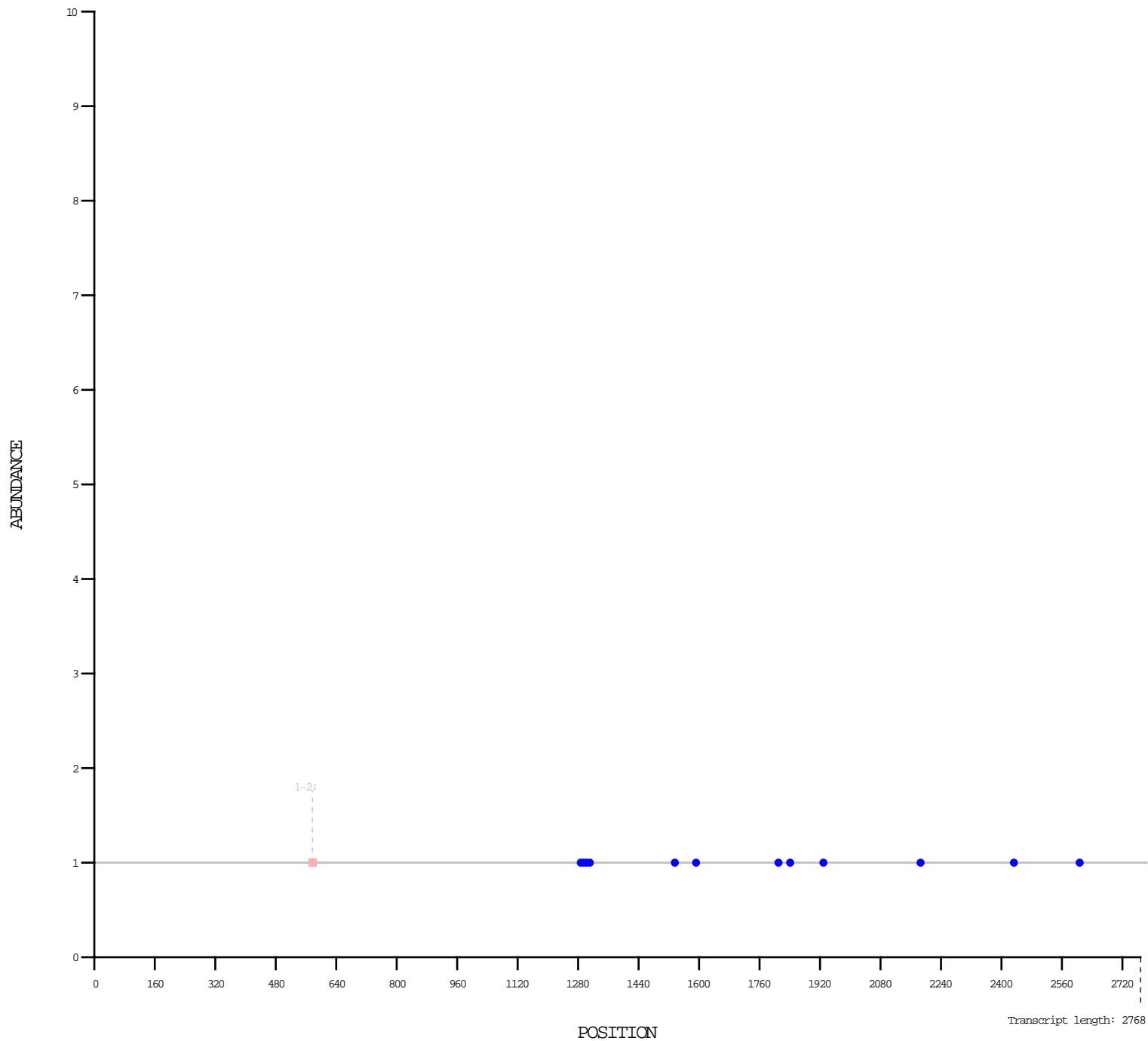
Category: 0 1 2 3 4  
 Degradome alignment: ● Median: —

4 #1 Position:936 Abundance: 0.33(deg) 1(sRNA)  
 5' TTGACAGAGAGAGCCGACAC 3' ID:  
 ||o|| |||||o||||||| Score: 3.0  
 3' TATCAATTG-CTTCITTCGCTCGTATAGCCG 5' p-value: 0.04



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

4 #1 Position:1411 Abundance: 1.00(deg) 1(sRNA)  
 5' TTGAGCCCGCCCAATATCTCT 3' ID:  
 o ||| ||||| ||||| ||| |o|| Score: 3.0  
 3' TGCCGCCTC-GCGCGTATATAGGGATCAACTIG 5' p-value: 0.03



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

4 #1 Position:577 Abundance: 1.00(deg) 7(sRNA)  
 5' TCGGACGAGGCTTCATCCCC 3' ID:  
 o|||||||||||||||||  
 3' CTTAGGCCITGGTCCGAGTA-GGGTCCGTAGA 5' p-value: 0.04  
 Score: 2.5

4 #2 Position:577 Abundance: 1.00(deg) 2(sRNA)  
 5' TCGGACGAGGCTTCATCCCT 3' ID:  
 o|||||||||||||||||  
 3' CTTAGGCCITGGTCCGAGT-AGGGTCCGTAGA 5' p-value: 0.03  
 Score: 2.5