

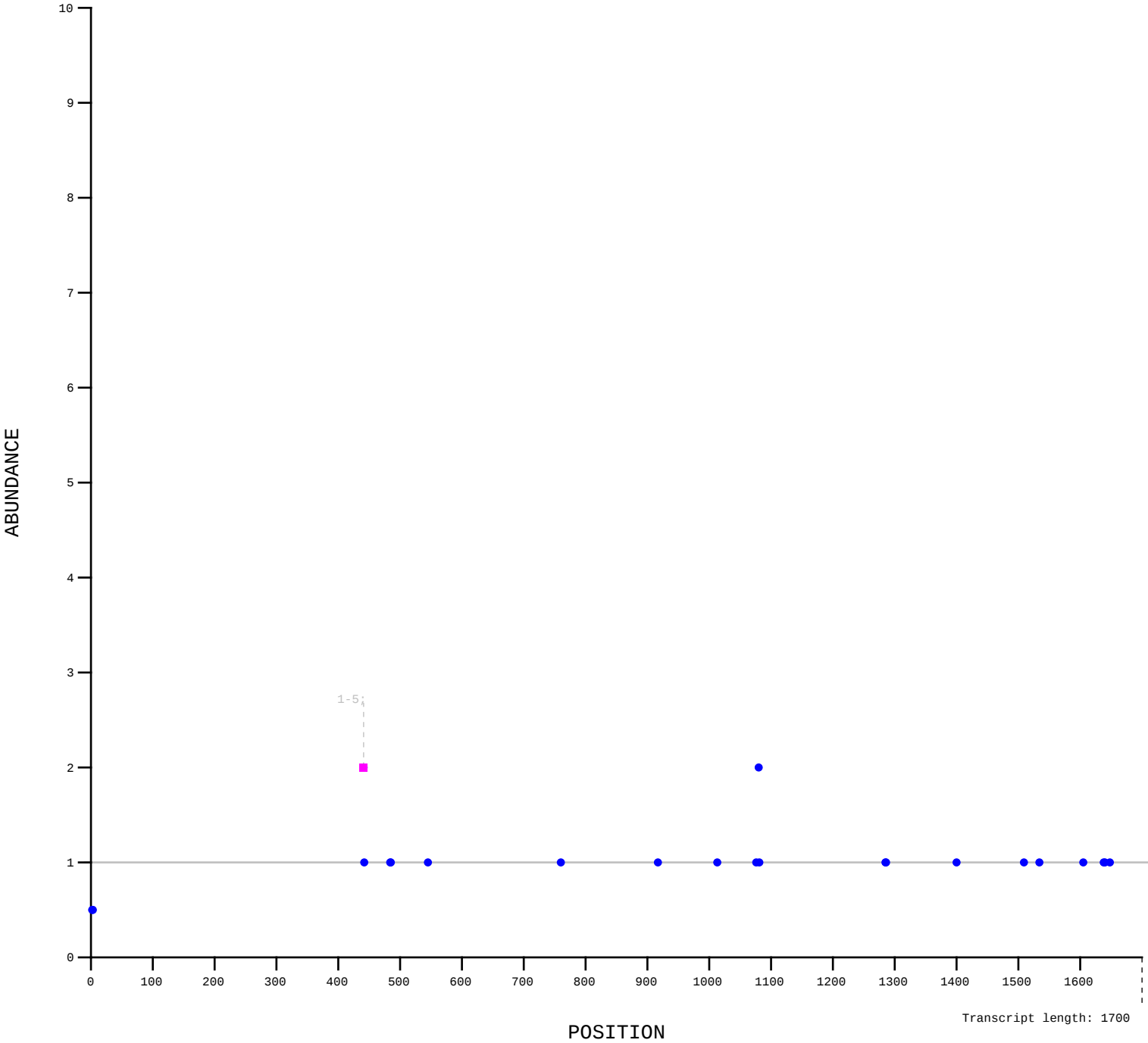
comp45893_c0_seq5



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

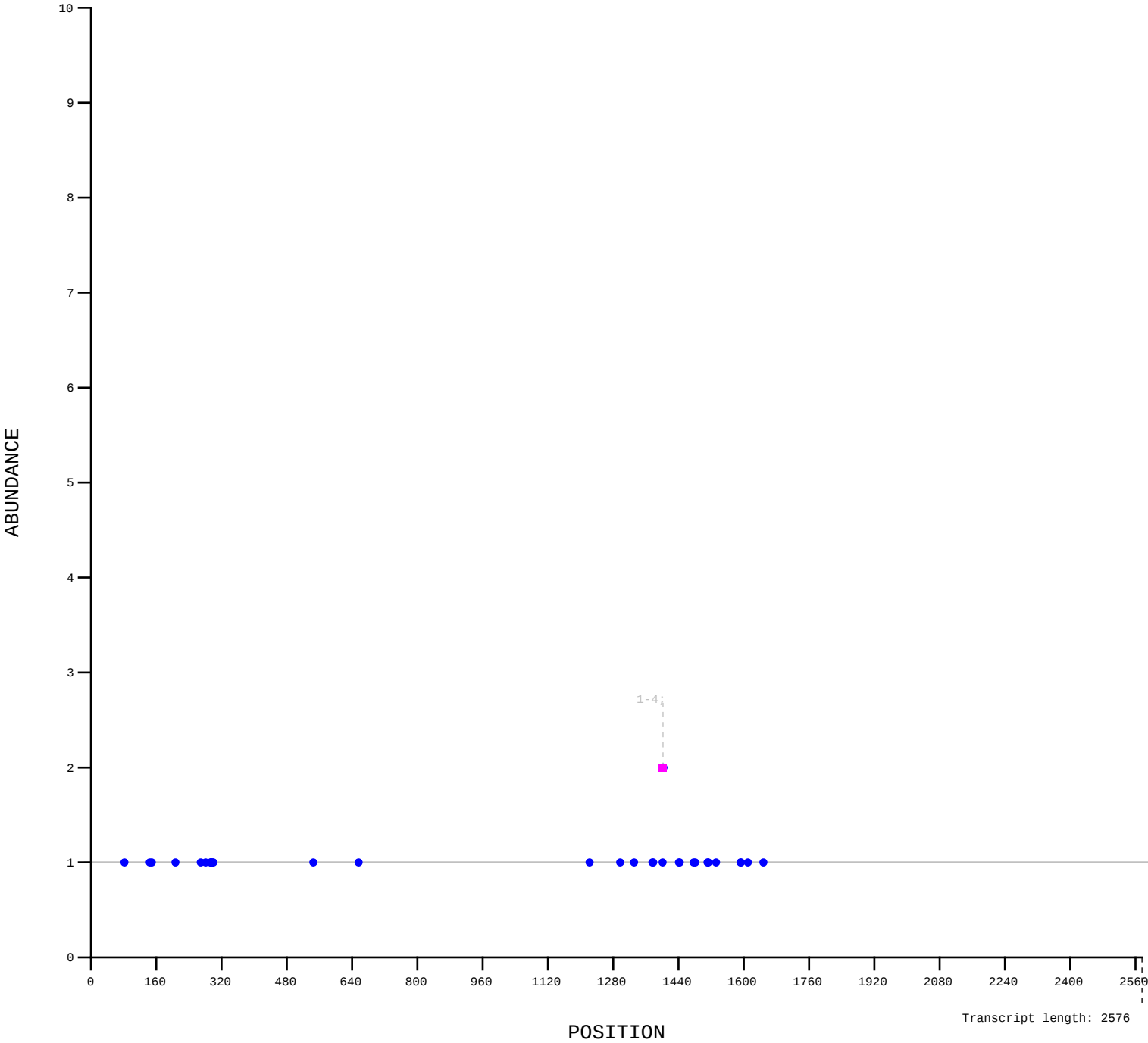
■ 1 #1 Position: 2313 Abundance: 2.00(deg) 1(sRNA)
 5' TCCAAGGGATCGCATGATCC 3' ID:
 3' CTGTAGGTTTCCCTACGCTAACAAAGTATGAA 5' Score: 2.0
 p-value: 0.0

comp38451_c0_seq2



Category: 0 1 2 3 4									
Degradome alignment: ● Median: —									
■ 1	#1	Position:441	Abundance: 2.00(deg)	1(sRNA)					
		5'	TGCCTGGCTCCCTGTATGCC	3'	ID:				
					Score: 0.5				
		3'	TCGTACGGACCGAGGGACGTACGGTCGTCCTC	5'	p-value: 0.0				
■ 1	#2	Position:441	Abundance: 2.00(deg)	1(sRNA)					
		5'	TGCCTGGCTCCCTGTATGCCA	3'	ID:				
					Score: 0.5				
		3'	TCGTACGGACCGAGGGACGTACGGTCGTCCTC	5'	p-value: 0.0				
■ 1	#3	Position:441	Abundance: 2.00(deg)	1(sRNA)					
		5'	TGCCTGGCTCCCTGTATGCCG	3'	ID:				
					Score: 1.0				
		3'	TCGTACGGACCGAGGGACGTACGGTCGTCCTC	5'	p-value: 0.0				
■ 1	#4	Position:441	Abundance: 2.00(deg)	1(sRNA)					
		5'	TGCCTGGCTCCCTGAATGCCA	3'	ID:				
					Score: 1.0				
		3'	TCGTACGGACCGAGGGACGTACGGTCGTCCTC	5'	p-value: 0.0				
■ 1	#5	Position:441	Abundance: 2.00(deg)	1(sRNA)					
		5'	TGCCTGGCTCCCTGAATGCCATC	3'	ID:				
					Score: 2.0				
		3'	TCGTACGGACCGAGGGACGTACGGTCGTCCTC	5'	p-value: 0.0				

comp45321_c0_seq12



Category: 0 1 2 3 4				
Degradome alignment: • Median: —				
1 #1	Position:1402	Abundance: 2.00(deg)	1(sRNA)	
5'	AGAATCTTGATGATGCTGCA		3'	ID:
	o			Score: 0.5
3'	ATCCTCTTAGGACTACTACGACGTCATCTCTT	5'		p-value: 0.0
1 #2	Position:1402	Abundance: 2.00(deg)	1(sRNA)	
5'	AGAATCTTGATGATGCTGCA		3'	ID:
	o			Score: 0.5
3'	ATCCTCTTAGGACTACTACGACGTCATCTCTT	5'		p-value: 0.0
1 #3	Position:1402	Abundance: 2.00(deg)	1(sRNA)	
5'	AGAATCTTGATGATGCTGCAT		3'	ID:
	o			Score: 1.5
3'	ATCCTCTTAGGACTACTACGACGTCATCTCTT	5'		p-value: 0.0
1 #4	Position:1402	Abundance: 2.00(deg)	1(sRNA)	
5'	TGAATCTTGATGATGCTGCAT		3'	ID:
	o			Score: 2.5
3'	ATCCTCTTAGGACTACTACGACGTCATCTCTT	5'		p-value: 0.01

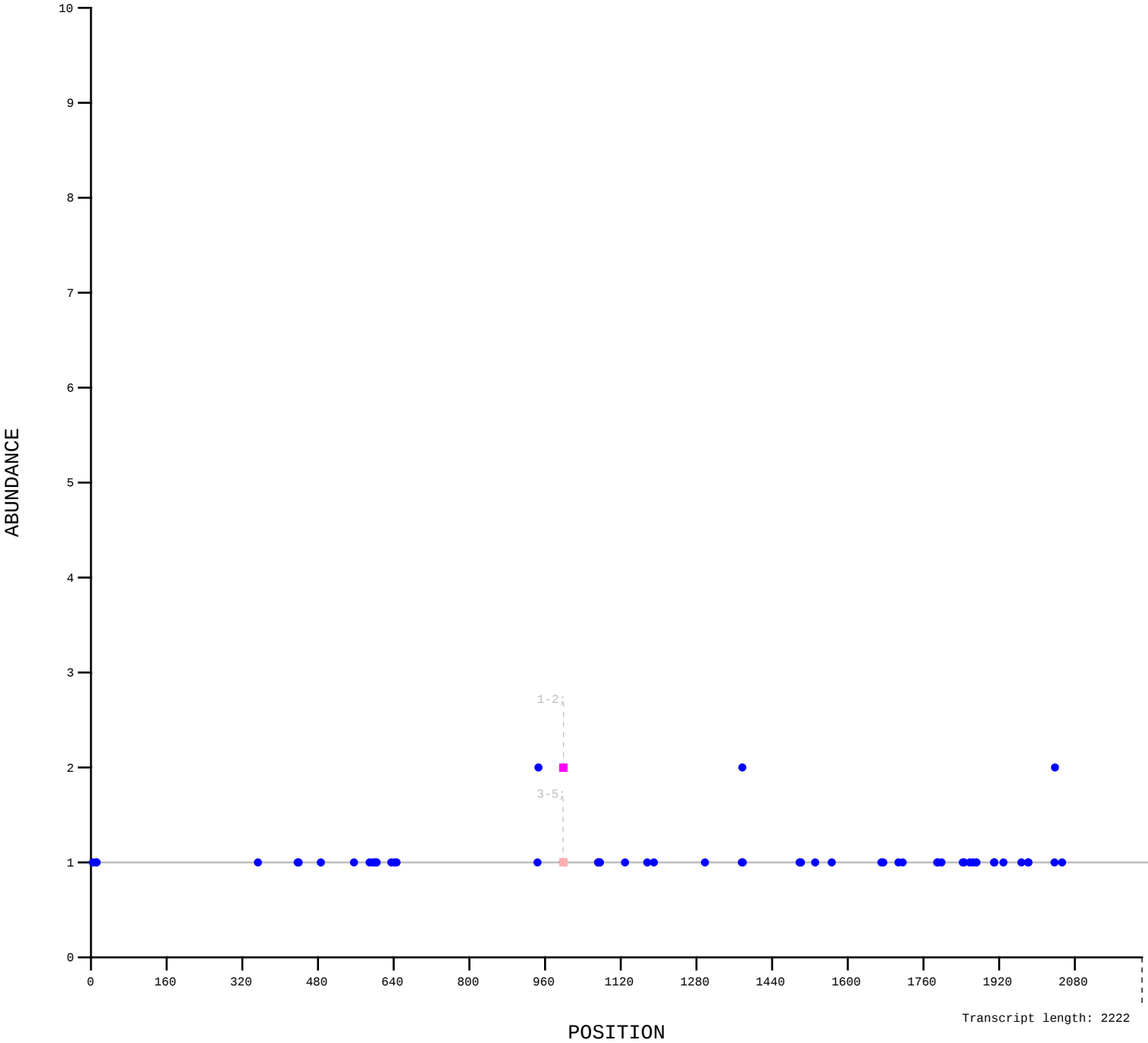
comp34546_c0_seq3



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

■ #1 Position:380 Abundance: 2.00(deg) 1(sRNA)
5' TTCTGTTGTCTGTTTCACACTTG 3' ID:
|o||o||o||o||
3' ATTAAGATTAACAGACAAGC-GGGACCTTTCAGA 5' Score: 2.0
p-value: 0.0

comp42588_c0_seq8



Category:		0	1	2	3	4
Degradome alignment:			•			
Median:						—
1	#1	Position:999 Abundance: 2.00(deg)				1(sRNA)
	5'	TTTGGACTGAAGGGAGCTCTA				3' ID:
						Score: 2.5
	3'	CCTATAACCTCACTTCCCTCGAGGTTGAAGTG				5' p-value: 0.0
1	#2	Position:999 Abundance: 2.00(deg)				1(sRNA)
	5'	TTTGGATTGAAGGGAGCTCCT				3' ID:
						Score: 3.0
	3'	CCTATAACCTCACTTCCCTCGAGGTTGAAGTG				5' p-value: 0.01
4	#3	Position:998 Abundance: 1.00(deg)				1(sRNA)
	5'	TTGGATTGAAGGGAGCTCCA				3' ID:
						Score: 1.0
	3'	CTATAACCTCACTTCCCTCGAGGTTGAAGTGT				5' p-value: 0.0
4	#4	Position:998 Abundance: 1.00(deg)				1(sRNA)
	5'	TTGGACTGAAGGGAGCTCCT				3' ID:
						Score: 2.0
	3'	CTATAACCTCACTTCCCTCGAGGTTGAAGTGT				5' p-value: 0.0
4	#5	Position:998 Abundance: 1.00(deg)				1(sRNA)
	5'	TTGGACTGAAGGGAGCTCCCT				3' ID:
						Score: 3.0
	3'	CTATAACCTCACTTCCCTCGAGGTTGAAGTGT				5' p-value: 0.01