

Small RNA analysis : Common sRNAs predicted to be falling within the hairpin by the three prediction programs.

S.No	Small RNA sequence	Length	Frequency	Chromosomal location	CSHMM*	CID-miRNA*	MIRDE EP
1	TATACAGGGGGAGAC TCTCAT	21	2	chr14.NT_026437. [82473123..82540116] (37169..37248)(+)	0.256	-0.595697	2.4
2	ATATACAGGGGGAGA CTCTCAT	22	21				
3	ATATACAGGGGGAGA CTCTCATT	23	4				
4	ATATACAGGGGGAGA CTCTCA	21	4				
5	ATATACAGGGGGAGA CTCTCATT	24	3				
6	TATACAGGGGGAGAC TCTTA	20	1	chr14.NT_026437. [82473123..82540116] (35947..36028)(+)	0.253	-0.597301	2.3
7	ATATACAGGGGGAGA CTCTTA	21	27				
8	TATACAGGGGGAGAC TCTTAT	21	1				
9	TATACAGGGGGAGAC TCTTATT	22	1				
10	ATATACAGGGGGAGA CTCTTAT	22	181				
11	ATATACAGGGGGAGA CTCTTATT	23	27				
12	AATATACAGGGGGAG ACTCTTAT	23	7				
13	ATATACAGGGGGAGA CTCTTATT	24	12				
14	TAAAAACCGTGACTA CTTC	19	1	chr6.NT_025741[1226 2885..12360950] (4039..4122)(-)	0.304	-0.533041	2.5
15	TAAAAACCGTGACTA CTTCT	20	2				
16	TAAAAACCGTGACTA CTTCTG	21	2				
17	CCTCCCACTGCAGAG CCTGGGGA	23	1	chr10.NT_077569 [521740..607790] (35288..35409)(+)	0.271	-0.49226	1.5
18	CGGTTTGAGGCTACA GTGAGAT	22	7	chr11.NT_008984. [5728386..5729897] (75..191)(-)	0.281	-0.470894	1.1

- the blue colour signifies the representative mirna (having the highest frequency among its isomiRs)
- * signifies the score assigned to the precursor harboring the miRNA and its isomiRs.