

Supplemental Table 4. Genomic loci of known and previously predicted HSV-2 miRNAs represented with sequence reads, and genomic loci represented with three or more sequence reads of ≥ 19 nucleotides between HSV-1 and HSV-2 in productive or latent infection tested by the RNA secondary structure predictions programs mfold and RNAfold.

Locus ¹	Hairpin ²	Number of sequence reads in productively infected sample	Number of sequence reads in latently infected sample	miRNA strand
331^P	+	32	-	miR-H19-5p
2180	-	10	-	
2640^P	+	27	-	miR-H20-3p
3438	-	26	-	
5025	-	9	-	
5487	-	4	-	
7840	-	4	-	
8362	+	821	-	moR-H6-5p
8384	+	604	28	miR-H6-5p
8424	+	2	1	miR-H6-3p
8447	+	15	-	moR-H6-3p
8638	-	301	-	
8725	-	59	-	
8747	-	6	-	
9340	-	498	1	
9831	-	7	-	
9920	-	13	-	
10171	-	19	-	
11018	-	24	-	
11050	-	15	-	
11111	-	52	-	
11612	-	11	-	
11703	+	12	-	miR-H21-3p
11813	-	12	-	
12126	-	9	-	
12340	-	6	-	
12499	-	13	-	
12631	-	4	-	
13351	-	9	-	
13754	-	6	-	
15728	-	5	-	
16499	-	28	-	
16539	-	9	-	
17074	-	13	-	
17091	-	9	-	
17502	-	12	-	
18000	-	29	-	
23824	-	12	-	
23967	-	7	-	
28790	-	12	-	
30222	-	4	-	
32028	-	3	-	
32596	-	-	13	
33571	-	3	-	
37824	-	-	14	
42490	-	36	-	
42764	-	4	-	
43931	+/-	4	-	

47879	-	75	-	
49084	-	18	-	
50891	-	95	-	
59125	-	1	25	
51906	-	20	-	
53430	+/-	15	-	
58783	-	14	-	
62152	-	9	-	
62811	-	-	90	
62934^P	+	73 ³	-	miR-H11-3p
63102	-	39	-	
63721	-	19	-	
64812	-	18	-	
64911	-	15	-	
66944	-	17	-	
67913	-	10	-	
67962	-	18	-	
69520	-	4	-	
69925	-	5	-	
70315	-	5	-	
70391	-	7	-	
70485	-	11	-	
71519	-	12	-	
72000	-	6	-	
74149	-	4	-	
74175	-	4	-	
74347	-	12	-	
74489	-	6	-	
80037	+	5	-	miR-H22-5p
80773	-	12	-	
81783	-	5	-	
86648	-	6	-	
87597	-	3	-	
87738	-	9	-	
87916	-	13	-	
89235	-	7	-	
89345	-	11	-	
89410	-	13	-	
90092	-	18	-	
90401	-	5	-	
90970	-	13	-	
93277	-	25	-	
93619	-	5	-	
93830	-	11	-	
93865	-	5	-	
93939	-	3	-	
93976	-	22	-	
94211	+	9	-	miR-H23-5p
94255	+	9	-	miR-H23-3p
94330	-	10	-	
94368	-	6	-	
94475	-	20	-	
94530	-	19	-	
94557	-	32	-	
95293	-	4	-	
95408	-	-	8	

96408	-	7	-	
96832	-	20	-	
97827	-	11	-	
99013	-	10	-	
99026	-	14	-	
99885	-	5	-	
100593	-	8	-	
103089	-	9	-	
107855	-	5	-	
109442	-	17	66	
110311	-	11	-	
111256	-	12	-	
111805	-	6	-	
<i>113714</i>	-	-	11	
114331	-	7	-	
114486	-	7	-	
115117	-	9	-	
115718	-	3	-	
115905	-	12	-	
115955	-	5	-	
116100	-	4	-	
116287	-	122	-	
116851	-	9	-	
<i>119123</i>	-	-	17	
119512	-	37	-	
122973 ^{K2}	+	15	24	miR-H2-3p
123070	-	6	-	
124340 ^{U3}	+	4	-	miR-H9-5p
124571	-	47	-	
124592 ^{P,U3}	+	6	-	miR-H7-5p
124625 ^P	+	3	-	miR-H7-3p
126502	+	20	1	miR-H24 -3p
126622	-	26	-	
126678 ^{K1,U3}	+	352	129	miR-H3-3p
126841	+/-	117	-	moR-H4-5p
126862 ^{K2,U3}	+	210	80	miR-H4-5p
126900 ^{K2,U3}	+	85	17	miR-H4-3p
126927	+/-	4	-	moR-H4-3p
127593	+	6	3	miR-H5-5p
127656	-	3	-	
129791	-	-	10	
131136	-	5	-	
131282	-	-	62	
131985	-	38	-	
132844	+	50	-	miR-H13-3p
132977	+	10	-	miR-H25-5p
133082	-	37	-	
133111	-	13	-	
133686	-	7	-	
133973	-	12	-	
134045	-	110	-	
134267	-	11	-	
134627	-	30	-	
134901	-	6	-	
135072	-	5	-	
136085	-	7	-	

138414	-	11	-	
138721	-	20	-	
140000	-	15	-	
140756	-	1	15	
141008	-	9	-	
141592	-	52	-	
142528	-	5	-	
142786	-	6	-	
142915	-	11	-	
144596	-	12	-	
144647	-	5	-	
144968	-	15	-	
145213	-	46	-	
145242	-	12	-	
145327	-	11	-	
145492	+/-	7	-	
145512	-	11	-	
146463	-	3	-	
148903^C	+	29	-	miR-H12-3p
149041^C	+	29	-	miR-H12-3p
149698	-	-	16	
149722	-	5	-	
153773	-	5	-	
<i>11040</i>	-	6	-	
<i>11704</i>	-	6	-	
<i>11852</i>	-	7	-	
<i>11874</i>	-	8	-	
<i>12250</i>	-	10	-	
<i>12277</i>	+/-	7	-	
<i>16086</i>	-	4	-	
<i>22920</i>	-	7	-	
<i>23086</i>	-	3	-	
<i>23663</i>	-	4	-	
<i>24628</i>	-	7	-	
<i>24765</i>	-	3	-	
<i>24803</i>	-	17	-	
<i>25526</i>	-	5	-	
<i>26994</i>	-	7	-	
<i>27771</i>	-	12	-	
<i>28982</i>	-	8	-	
<i>29593</i>	-	3	-	
<i>29928</i>	-	6	-	
<i>30145</i>	-	14	-	
<i>31532</i>	-	14	-	
<i>33616</i>	-	14	-	
<i>33655</i>	-	9	-	
<i>33682</i>	-	12	-	
<i>34478</i>	-	3	-	
<i>34555</i>	-	6	-	
<i>34675</i>	-	3	-	
<i>34759</i>	-	24	-	
<i>34965</i>	-	7	-	
<i>35037</i>	-	10	-	
<i>35265</i>	-	11	-	
<i>35345</i>	-	19	-	
<i>35519</i>	-	14	-	

35740	-	3	-
35872	-	6	-
36041	-	55	-
36246	-	66	-
37198	-	9	-
37255	-	6	-
37355	-	4	-
37876	-	5	-
38040	-	5	-
38344	-	17	-
39512	-	11	-
39358	-	7	-
40279	-	12	-
40300	-	22	-
40355	-	8	-
40416	+/-	4	-
40697	-	7	-
40776	-	5	-
40792	+/-	124	-
42025	+/-	3	-
44151	-	4	-
45388	-	49	-
45654	-	3	-
46448	-	52	-
46778	-	6	-
46810	-	9	-
47011	+/-	3	-
47690	-	4	-
49434	-	-	27
53400	-	13	-
53415	-	4	-
53860	-	5	-
54078	-	6	-
54595	-	7	-
56312	-	8	-
56376	-	14	-
58862	-	17	-
59543	-	3	-
59731	-	5	-
59808	-	9	-
60473	-	3	-
60798	+/-	6	-
61004	-	6	-
61442	-	4	-
61777	-	5	-
61872	-	24	-
62053	-	7	-
62318	-	7	-
62895^P	+	73 ³	-
62954	-	3	-
64447	-	9	-
65850	-	4	-
67047	-	16	-
67149	-	4	-
67877	-	28	-
68753	-	4	-

miR-H11-3p

69308	-	4	-
69644	-	31	-
71516	-	60	-
71540	-	29	-
72068	-	49	-
72902	-	7	-
73805	-	5	-
73903	-	13	-
74566	-	6	-
74881	-	9	-
74887	-	11	-
75263	-	7	-
81259	-	9	-
81495	-	16	-
84562	-	10	-
84747	-	6	-
85981	-	4	-
86487	-	-	54
87067	-	3	-
88058	-	4	-
88571	-	97	-
90858	-	5	-
90878	-	10	-
91497	-	16	-
92444	-	3	-
92935	-	6	-
93246	-	18	-
93291	-	8	-
93371	-	6	-
94020	-	4	-
95862	-	4	-
99442	-	7	-
99770	-	5	-
99914	-	23	-
99927	-	16	-
100242	-	17	-
100512	-	9	-
100531	-	13	-
100622	-	25	-
100860	-	17	-
100927	-	6	-
101314	-	11	-
102270	-	13	-
102934	-	10	-
103654	-	9	-
103921	-	27	-
103956	-	224	-
104339	-	11	-
104886	-	6	-
105125	-	81	-
105248	-	7	-
105415	-	14	-
105504	-	5	-
105632	-	6	-
105720	-	17	-
105783	-	26	-

106401	-	7	-
106441	-	6	-
106448	-	7	-
106621	-	8	-
106628	-	11	-
106884	-	6	-
107076	-	5	-
107540	-	8	-
108626	-	5	-
108926	-	7	-
109336	-	15	-
109421	-	3	-
109619	-	13	-
109775	-	6	-
109935	-	27	-
117844	-	38	-
117860	-	12	-
117911	-	4	-
132024	-	1	16
133750	-	-	19
134530	-	-	11
134598	-	7	-
135018	-	8	-
135948	-	16	-
136156	-	4	-
136324	-	99	-
136348	-	83	-
136371	-	44	-
136480	-	5	-
141367	-	3	-
144206	-	3	-
144573	-	9	-
145478	-	12	-
145740	-	5	13
145920	-	-	29
146221	-	8	-

¹Genomic position of starting nucleotide of the sequence read; ²150 nucleotide sequence surrounding sequence read tested by mfold (7) and RNAfold (2); (+) read was part of a predicted hairpin with lowest free energy, (-) read was not part of a hairpin, (+/-) folding positive by mfold or RNAfold only; ³oriL palindrom - not possible to determine the direction of transcription; *italic* – loci on the complementary strand; ^P- loci predicted by Pfeffer et al (3), ^C- loci predicted by Cui et al (1), ^{U1}-miRNA identified by Umbach et al. (5); ^{U2}- miRNA identified by Umbach et. al. (4); ^{U3}- miRNA identified by Umbach et. al.(6).

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