

Supplemental Table 3. Genomic loci of known and previously predicted HSV-1 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
745	-	3	-	
2118	-	23	-	
2561	-	3	-	
2932	-	4	-	
3221	-	6	-	
3713	-	127	-	
4477^P	+	1	-	miR-H14-5p
4514^P	+	3	-	miR-H14-3p
4563	-	6	-	
7131	+	5	-	miR-H15-3p
7954	+	140	1	moR-H6-5p
7983^{UI}	+	83	1	miR-H6-5p
7999	-	25	-	
8020	+	322	3	miR-H6-3p
8042	+	11	-	moR-H6-3p
9248	-	10	-	
9763	+/-	4	-	
41872	-	4	-	
57391	-	-	7	
62480^P	+	7 ³	-	miR-H11-3p
67690	-	-	5	
69040	+	8	-	miR-H16-5p
84712	-	4	-	
89684	-	5	-	
96221	-	25	-	
99461	-	-	10	
100171	-	-	7	
112865	-	-	8	
118328^C	+	2555	11	miR-H1-5p
118368^C	+	8	-	miR -H1-3p
120805 ^C	-	1	-	
121832^C	+	3	5	miR H2-5p
121868^C	+	96	221	miR -H2-3p
123399	-	10	-	
123419^{U2}	+	1	11	miR-H7-5p
123809^P	+	2	4	miR-H8-5p
125737	+	-	1	miR-H3-5p
125771^{U1}	+	67	167	miR-H3-3p
125875^{U1}	+	65	130	miR -H4-5p
125927^{U1}	+	1	11	miR -H4-3p
126727	+	-	2	miR -H5-5p
126769^{U1}	+	2	1	miR -H5-3p
128994	-	-	13	
131390^C	+	1	-	
131774^C	-	1	-	
131841	+	-	4	miR-H18-5p
132006^C	+	1	-	miR-H12-3p
132754	-	5	-	

143922	-	4	-	
146240^C	+	5	-	miR-H12-3p
147445	-	10	-	
147699	-	8	-	
150663	+	7	2	miR-H17-3p
151000	-	17	-	
<i>17041</i>	-	3	-	
<i>26490</i>	-	11	-	
<i>50062</i>	-	-	5	
<i>61596</i>	-	-	7	
62445^P	+	7 ³	-	miR-H11-3p
<i>71389</i>	-	26	-	
<i>75477</i>	-	5	-	
<i>102287</i>	-	6	-	
<i>102792</i>	-	6	-	
<i>103140</i>	-	6	-	
<i>104402</i>	-	7	-	
<i>104439</i>	-	3	-	
<i>113948</i>	-	9	-	
<i>116937</i>	+/-	40	-	

¹Genomic position of starting nucleotide of the sequence read; ²150 nucleotide sequence surrounding sequence read tested by mfold (6) and RNAfold (2): (+) read was part of a predicted hairpin with lowest free energy tested by mfold and RNAfold, (-) 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. (4); ^{U2}- miRNA identified by Umbach et. al. (5).

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5. **Umbach, J. L., M. A. Nagel, R. J. Cohrs, D. H. Gilden, and B. R. Cullen.** 2009. Analysis of human alphaherpesvirus microRNA expression in latently infected human trigeminal ganglia. *J Virol* **83**:10677-83.
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