

Supplemental Table 6. Sequence reads representing HSV-2 encoded miRNAs

LOCUS	hits	sequence	size	start		N	miRNA
331	1	GTTTCGCTAGGCAAGCACGGACT	22 +	331 0			
	7	TTCGCTAGGCAAGCACGGACTGT	23 +	332 1 G->22T40			
	1	TTCGCTAGGCAAGCACGGACTGG	23 +	332 0			
	1	TTCGCTAGGCAAGCACGGACTGC	23 +	332 1 G->22C40			
	1	TTCGCTAGGCAAGCACGGACTGA	23 +	332 1 G->22A40			
	9	TTCGCTAGGCAAGCACGGACTG	22 +	332 0			
	1	TCGCTAGGCAAGCACGGACTGGT	23 +	333 1 C->22T40			
	5	TCGCTAGGCAAGCACGGACTGG	22 +	333 0			
	4	TCGCTAGGCAAGCACGGACTGT	22 +	333 1 G->21T40			
	1	TCGCTAGGCAAGCACGGACTG	21 +	333 0			
	1	TAGGCAAGCACGGACTGGC	19 +	337 0		32	miR-H19-5p
2640	6	TTTGGTTACGGACCCCTTTCTCC	23 +	2640 0			
	1	TTTGGTTACGGACCCCTTTCTCA	23 +	2640 1 C->22A40			
	5	TTTGGTTACGGACCCCTTTCTC	22 +	2640 0			
	1	TTTGGTTACGGACCTTTTCTC	22 +	2640 2 C->14T40 C->15T40			
	1	TTTGGTTACGGAACCCCTTTCTC	22 +	2640 1 C->12A40			
	10	TTTGGTTACGGACCCCTTTCT	21 +	2640 0			
	2	TTTGGTTACGGACCCCTTT	19 +	2640 0			
	1	TGGTTACGGACCCCTTTCT	19 +	2642 0		27	miR-H20-3p
8362	1	TCGGGACTCGCGGAGGGCCGGAA	25 +	8362 1 A->23G40			
	1	TCGGGACTCACGGAGGGCCGGAG	23 +	8362 1 G->9A40			
	40	TCGGGACTCGCGGAGGGCCGGAG	23 +	8362 0			
	11	TCGGGACTCGCGGAGGGCCGGGG	23 +	8362 1 A->21G40			
	5	TCGGGACTCGCGGAGGGGCGGAG	23 +	8362 1 C->17G40			
	1	TCGGGACTCGCGGAGGGGCGGGG	23 +	8362 2 C->17G40 A->21G40			
	1	TCGGGACTCGCGGGGGCCGGAG	23 +	8362 1 A->13G40			
	1	TCGGGACTCGCGGGGGCCGGGG	23 +	8362 2 A->13G40 A->21G40			
	1	CGGGACTCGCGGAGGGCCGGAGAA	24 +	8363 0			
	1	CGGGACTCGCGGAGGGCCGGAAAA	24 +	8363 1 G->21A40			
	1	CGGGACTCGCGGAGGGCCGGAGA	23 +	8363 0			
	1	CAGGACTCGCGGAGGGCCGGAG	22 +	8363 1 G->1A40			
	1	CGGGACTCACGGAGGGCCGGAG	22 +	8363 1 G->8A40			
	1	CGGGACTCGCGGAGGGACGGAG	22 +	8363 1 C->16A40			
	1	CGGGACTCGCGGAGGGCCGCAG	22 +	8363 1 G->19C40			
	1	CGGGACTCGCGGAGGGCCGGAA	22 +	8363 1 G->21A40			
	259	CGGGACTCGCGGAGGGCCGGAG	22 +	8363 0			
	2	CGGGACTCGCGGAGGGCCGGCG	22 +	8363 1 A->20C40			
	4	CGGGACTCGCGGAGGGCCGGGG	22 +	8363 1 A->20G40			
	1	CGGGACTCGCGGAGGGCCGGGG	22 +	8363 2 C->17G40 A->20G40			
	2	CGGGACTCGCGGAGGGCCGGAG	22 +	8363 1 C->16G40			
	1	GGGACTCGCGGAGGGCCGGAGAA	23 +	8364 0			
	1	GGGACTCGCGGAGGGCCGGAGA	22 +	8364 0			
	1	CGGACTCGCGGAGGGCCGGAG	21 +	8364 1 G->0C40			
	2	GGGACTCGCGGAGGGACGGAG	21 +	8364 1 C->15A40			
	54	GGGACTCGCGGAGGGCCGGAG	21 +	8364 0			
	2	GGGACTCGCGGAGGGCCGGGG	21 +	8364 1 A->19G40			
	4	GGGACTCGCGGAGGGCCGGAG	21 +	8364 1 C->15G40			

1	GGACTCGCGGAGGGCCGGGA	22 +	8365	0	
2	AAACTCGCGGAGGGCCGGAG	20 +	8365	2 G->0A40	G->1A40
1	GGACTCACGGAGGGCCGGAG	20 +	8365	1 G->6A40	
1	GGACTCCCGGAGGGCCGGAG	20 +	8365	1 G->6C40	
1	GGACTCGCGGAGGGCAGGAG	20 +	8365	1 C->15A40	
69	GGACTCGCGGAGGGCCGGAG	20 +	8365	0	
1	GGACTCGCGGAGGGCCGGAG	20 +	8365	1 C->14G40	
1	TGACTCGCGGAGGGCCGGGG	20 +	8365	2 G->0T40	A->18G40
1	GACTCGCGGAGGGCCGGAGGA	21 +	8366	1 A->19G40	
4	GACTCGCGGAGGGCCGGAGAA	21 +	8366	0	
1	GACTCGCGGAGGGCCGGAGA	20 +	8366	0	
2	AACTCGCGGAGGGCCGGAG	19 +	8366	1 G->0A40	
1	GACGCGCGGAGGGCCGGAG	19 +	8366	1 T->3G40	
315	GACTCGCGGAGGGCCGGAG	19 +	8366	0	
1	GACTCGCGGAGGGCCGGCG	19 +	8366	1 A->17C40	
2	GACTCGCGGAGGGCCGGGG	19 +	8366	1 A->17G40	
1	GACTCGCGGAGGGCTGGAG	19 +	8366	1 C->14T40	
3	GACTCGCGGAGGGCCGGAG	19 +	8366	1 C->13G40	
1	GACTCGCGGCGGGCAGGAG	19 +	8366	2 A->9C40	C->14A40
1	GACTCGCGGGGGCCGGAG	19 +	8366	1 A->9G40	
1	ACTCGCGGAGGGCCGGAGAA	20 +	8367	0	
8	CTCGCGGAGGGCCGGAGAA	19 +	8368	0	

821 mOR-H6-5p

8384	1	AAATGGAAGGCGAGGGGATGCA	22 +	8384	1 G->0A40	
	1	AATGGAAGGCGAGGGGATGCAGGAT	25 +	8385	1 G->24T40	
	1	AATGGAAGGCGAGGGGATGCAGGAA	25 +	8385	1 G->24A40	
	1	AATGGAAGGCGCGGGGATGCAGGA	24 +	8385	1 A->11C40	
	1	AATGGAAGGCGAGGGGATGCAGGA	24 +	8385	0	
	1	AATGGAAGGCGAGGGGATGCAAA	23 +	8385	2 G->21A40	G->22A40
	7	AATGGAAGGCGAGGGGATGCAGG	23 +	8385	0	
	1	AATGGAAGGCGAGGGGATGCAGT	23 +	8385	1 G->22T40	
	1	AATGGAAGGCGAGGGGAGGCCAA	22 +	8385	2 T->17G40	G->21A40
	1	AATGGAAGGCGAGGGGAGGCCAG	22 +	8385	1 T->17G40	
	17	AATGGAAGGCGAGGGGATGCAA	22 +	8385	1 G->21A40	
	76	AATGGAAGGCGAGGGGATGCAG	22 +	8385	0	
	1	AATGGAAGGCGAGGGGATGGAG	22 +	8385	1 C->19G40	
	1	AATGGAAGGCGAGTGGATGCAG	22 +	8385	1 G->13T40	
	99	AATAGAAGGCGAGGGGATGCA	21 +	8385	1 G->3A40	
	1	AATGGAAGGCGAGGGGATGCT	21 +	8385	1 A->20T40	
	1	AATGGAAGGCGAGGGGCTGCA	21 +	8385	1 A->16C40	
	1	AATGGAAGTTCGAGGGGATGCA	21 +	8385	1 G->8T40	
	1	AATGGAAGGCGAGGGGAGGCC	20 +	8385	1 T->17G40	
	3	AATGGAAGGCGAGGGGATAA	20 +	8385	2 G->18A40	C->19A40
	12	AATGGAAGGCGAGGGGATGA	20 +	8385	1 C->19A40	
	124	AATGGAAGGCGAGGGGATGC	20 +	8385	0	
	2	AATGGAAGGCGAGGGGATGG	20 +	8385	1 C->19G40	
	2	AATGGAAGGCGAGGGGATGT	20 +	8385	1 C->19T40	
	3	AATGGAAGGCGAGGGGATTA	20 +	8385	2 G->18T40	C->19A40
	1	AAGGGAAGGCGAGGGGATG	19 +	8385	1 T->2G40	
	1	AATGGAAGGCGAGGGGAGG	19 +	8385	1 T->17G40	
	18	AATGGAAGGCGAGGGGATA	19 +	8385	1 G->18A40	
	198	AATGGAAGGCGAGGGGATG	19 +	8385	0	

	5	AATGGAAGGCGAGGGGATT	19 +	8385	1	G->18T40		
	3	AATGGAAGGCGAGGGGCTG	19 +	8385	1	A->16C40		
	1	AATGGAAGGCGAGGTGATG	19 +	8385	1	G->14T40		
	1	AATGGTAGGCGAGGGGATG	19 +	8385	1	A->5T40		
	2	ATGGAAGGCGAGGGGATGCAG	21 +	8386	0			
	1	ATGGAAGGCGAGGGGATGCA	20 +	8386	0			
	4	ATGGAAGGCGAGGGGATGTC	19 +	8386	0			
	1	ATGGAAGGCGAGGGGGTGC	19 +	8386	1	A->15G40		
	1	ATGGAAGGCGAGGGGATGC	19 +	8386	0			
	3	TGGAAGGCGAGGGGATGCAGGA	22 +	8387	0			
	1	TGGAAGGCGAGGGGATGCAGG	21 +	8387	0			
	2	TGGAAGGCGAGGGGATGCA	19 +	8387	0			
	1	GAAGGCGAGGGGATGCAGGAT	21 +	8389	1	G->20T40	650	miR-H6-5p
8385	1	AATGGACGCGAGGGGATGCAGGA	24 +	8385	1	A->6C40		
	1	AATGGAAGGCGAGGGGATGCAGTT	24 +	8385	2	G->22T40 A->23T40		
	2	AATGGAAGGCGAGGGGATGCAGGA	24 +	8385	0			
	2	AATGGAAGGCGAGGGGATGCAGG	23 +	8385	0			
	13	AATGGAAGGCGAGGGGATGCAG	22 +	8385	0			
	2	AATGGAAGGCGAGGGGATGCAA	22 +	8385	1	G->21A40		
	3	AATGGAAGGCGAGGGGATGCA	21 +	8385	0			
	1	AATGGAAGGCGAGGGGATGC	20 +	8385	0			
	1	AATGGAAGGCGAGGGGATG	19 +	8385	0			
	2	ATGGAAGGCGAGGGGATGCAGA	22 +	8386	1	G->21A40	28	miR-H6-5p
8424	1	CCCATCTTCTGCCCTTCCATCTT	23 +	8424	0			
	1	CCCATCTTCTGCCCTTCCATC	21 +	8424	0		2	miR-H6-3p
8424	1	CCCATCTTCTGCCCTTCCATCTT	23 +	8424	0		1	miR-H6-3p
8447	1	CCGTTTTTCCGCTTTCACCGAA	23 +	8447	2	C->21A40 C->22A40		
	7	CCGTTTTTCCGCTTTCACCGC	22 +	8447	0			
	1	CCGTTTTTCCGCTTTCACCG	21 +	8447	0			
	2	CCGTTTTTCCGCTTTCAC	20 +	8447	0			
	4	CCGTTTTTCCGCTTTCAC	19 +	8447	0		15	mOR-H6-3p
11703	1	ATAACGTCATGCTGTCTACGGT	22 +	11703	1	A->21T40		
	8	ATAACGTCATGCTGTCTACGG	21 +	11703	0			
	1	ATAACGTCATGCTGTCTAC	19 +	11703	0			
	1	AACGTCATGCTGTCTACGGA	20 +	11705	0			
	1	TCATGCTGTCTACGGAACCAT	21 +	11709	1	G->20T40	12	miR-H21-3p
62901	1	AAGCGTTCGCACTTTGTCTATT	23 +	62901	1	A->21T40	1	miR-H11-5p
62934	1	CTATTAGGACAAAGTGCGAAAT	22 +	62934	2	C->20A40 G->21T40		
	2	TTAGGACAAAGTGCGAACGCTAA	23 +	62937	2	T->21A40 C->22A40		
	1	TTAGGACAAAGTGCGAACGCTTC	23 +	62937	0			
	1	TTAGGACAAAGTGCGAACGCTAT	23 +	62937	2	T->21A40 C->22T40		
	12	TTAGGACAAAGTGCGAACGCTT	22 +	62937	0			
	3	TTAGGACAAAGTGCGAACGCTA	22 +	62937	1	T->21A40		
	1	TTAGGACAAAGTGCGAACGTTA	22 +	62937	2	C->19T40 T->21A40		
	1	TTAGGACAAAGTGCGAACGCTT	22 +	62937	1	T->20C40		
	1	TTAGGACAAAGTGCGAACGCCA	22 +	62937	2	T->20C40 T->21A40		

8	TTAGGACAAAGTGCGAACGCT	21 +	62937	0			
1	TTAGGACAAAGTGCGAACGCA	21 +	62937	1	T->20A40		
1	TTAGGACAAAGTGCGAACGCA	21 +	62937	1	T->20A40		
9	TTAGGACAAAGTGCGAACGC	20 +	62937	0			
4	TTAGGACAAAGTGCGAACGT	20 +	62937	1	C->19T40		
1	TTAGGACAAAGTGCGAACGC	20 +	62937	0			
1	TTAGGACAAAGTGCGAACGA	20 +	62937	1	C->19A40		
1	TTAGGACAAAGTGAGAACGT	20 +	62937	2	C->13A40	C->19T40	
2	TTAGGACAAAGTGCGAACG	19 +	62937	0			
1	TAGGACAAAGTGCGAACGCTTCC	23 +	62938	1	G->22C40		
2	TGGGACAAAGTGCGAACGCTTC	22 +	62938	1	A->1G40		
1	TAGGACAAAGTGCGAACGCTTC	22 +	62938	0			
1	TGGGACAGAGTGCGAACGCTT	21 +	62938	2	A->1G40	A->7G40	
4	GGGACAAAGTGCGAACGCTTCG	22 +	62939	1	A->0G40		
2	AGGACAAAGTGCGAACGCTTCG	22 +	62939	0			
2	AGGACAAAGTGCGAACGCTTCA	22 +	62939	1	G->21A40		
1	GGGACAAGGTGCGAACGCTTCG	22 +	62939	2	A->0G40	A->7G40	
1	AGGGCAAAGTGCGAACGCTTCC	22 +	62939	2	A->3G40	G->21C40	
1	AGGACAGAGTGCGAACGCTTCC	22 +	62939	2	A->6G40	G->21C40	
1	AGGACAAAGTGCGAACGCTTCT	22 +	62939	1	G->21T40		
3	AGGACAAAGTGCGAACGCTTC	21 +	62939	0			
1	AGGACAAAGTGCGAACGCTT	20 +	62939	0			
1	CAAAGTGCGAACGCTTCGCATA	22 +	62943	2	G->19A40	T->21A40	73 miR-H11-3p
80037	1	CCCGAGGGGTCTGGACGTG	19 +	80037	1	C->3G40	
	2	AGGGGTCTGGACGTGGGTGGGC	22 +	80041	0		
	1	AGGGGTCTGGACGTGGGTGGG	21 +	80041	0		
	1	CTGGACGTGGGTGGGCGCGGG	21 +	80047	0		5 miR-H22-5p
94211	1	AGGCCGTGGAGCTTGCCAGCGAGAC	25 +	94211	0		
	1	AGGCCGTGGAGCTTGCCAGCGAG	23 +	94211	0		
	1	AGGCCGTGGAGCTTGCCAGCAA	22 +	94211	1	G->20A40	
	1	AGGCCGTGGAGCTTGCCAGC	20 +	94211	0		
	1	AGGCCGTGGAGCTTGCCAG	19 +	94211	0		
	2	CCGTGGAGCTTGCCAGCGAGA	21 +	94214	0		
	1	CGTGGAGCTTGCCAGCGAGACAA	23 +	94215	2	G->21A40	C->22A40
	1	CGTGGAGCTTGCCAGCGAGAC	21 +	94215	0		9 miR-23-5p
94255	1	ACGAGCTTCGCGGTACTACTCAA	23 +	94255	2	C->21A40	C->22A40
	1	ACGAGCTTCGCGGTACTACTCA	22 +	94255	1	C->21A40	
	6	ACGAGCTTCGCGGTACTACTC	21 +	94255	0		
	1	ACGAGCTTCGCGGTACTAC	19 +	94255	0		9 miR-23-3p
122973	1	CGGTCTGAGCCTGGGTCATG	20 +	122973	0		
	2	TCTGAGCCTGGGTCATGCGGACC	24 +	122976	0		
	1	TCTGAGCCTGGGTCATGCGGACT	24 +	122976	1	C->23T40	
	2	TCTGAGCCTGGGTCATGCGGAC	23 +	122976	0		
	2	TCTGAGCCTGGGTCATGCGGAA	23 +	122976	1	C->22A40	
	1	TCTGAGCCTGGGTCATGCGGAT	23 +	122976	1	C->22T40	
	2	TCTGAGCCTGGGTCATGCGGAC	23 +	122976	0		miR-III-3p
	4	TCTGAGCCTGGGTCATGCGGA	22 +	122976	0		15 miR-H2-3p
122976	1	TCTGAGCCTGGGTCATGCGGACTT	25 +	122976	2	C->23T40	G->24T40

	4	TCTGAGCCTGGGTCATGCGCGACT	24 +	122976	1	C->23T40	
	1	TCTGAGCCTGGGTCATGCGCGATT	24 +	122976	2	C->22T40	C->23T40
	1	TCTGAGCCTGGGTCATGCGCGACC	24 +	122976	0		
	1	TCTGAGCCTGGGTCATGCGCGACA	24 +	122976	1	C->23A40	
	1	TCTGAGCCTGGGTCATGCGCGAAT	24 +	122976	2	C->22A40	C->23T40
	4	TCTGAGCCTGGGTCATGCGCGAC	23 +	122976	0		
	11	TCTGAGCCTGGGTCATGCGCGA	22 +	122976	0		24 miR-III-3p
							miR-H2-3p
124340	1	CTCGGAGGTGGAGTCGCGGTGA	22 +	124340	0		
	1	CTCGGAGGTGGAGTCGCGGT	20 +	124340	0		
	2	CTCGGAGGTGGAGTCGCGG	19 +	124340	0		4 miR-H9-5p
124592	5	AAAGGGTCCGTAACCAAAGG	21 +	124592	0		
	1	AAAGGGTCCGTAACCAAAG	20 +	124592	0		5 miR-H7-5p
	2	TTGGATTCCGACCCCTCGTC	21 +	124625	0		
	1	TTGGATTCCGACCCCTCGT	20 +	124625	0		3 miR-H7-3p
	1	TTGGATTCCGACCCCTCGTCT	22 +	124625	0		1 miR-H7-3p
126502	1	CTCCGGCGCCTTCCCCCGCCCTA	24 +	126502	1	C->23A40	
	3	CTCCGGCGCCTTCCCCCGCCCT	23 +	126502	0		
	1	CTCCGGCGCCTTCCCCCGCCCA	23 +	126502	1	T->22A40	
	1	CTCCGGCGCCTTCCCCCGCCAT	23 +	126502	1	C->21A40	
	1	CTCCGGCGCCTTCCCCCTGCC	22 +	126502	1	C->17T40	
	1	CTCCGGCGCCTTCCCCCGCCC	22 +	126502	0		
	1	CTCCGGCGCCTTCCCCCGCCCA	22 +	126502	1	C->21A40	
	1	CTCCGTGCGCTTCCCCCGCC	21 +	126502	1	G->5T40	
	2	CTCCGGCGCCTTCCCCCGCC	21 +	126502	0		
	3	CTCCGGCGCCTTCCCCCGC	20 +	126502	0		
	1	CTCCGGCGCCTTCCCCCG	19 +	126502	0		
	1	TCCGGCGCCTTCCCCCGCCCA	22 +	126503	1	T->21A40	
	1	TCCGGCGCCTTCCCCCGCCC	21 +	126503	0		
	1	TCCGGCGCCTTCCCCCGC	19 +	126503	0		
	1	CGGCGCCTTCCCCCGCCC	20 +	126504	0		20 miR-24-3p
	1	CTCCGGCGCCTTCCCCCGCCCA	23 +	126502	1	T->22A40	1 miR-24-3p
126678	1	CCATTTGGGAGTCTGCGGTT	20 +	126678	0		
	1	AATTTGGGAGTCTGCGGTTG	20 +	126679	1	C->0A40	
	1	CTTTGGGAGTCTGCGGTTGGA	21 +	126680	2	A->0C40	G->20A40
	3	TTTGGGAGTCTGCGGTTGGAGAA	24 +	126681	2	C->22A40	G->23A40
	4	TTTGGGAGTCTGCGGTTGGAAA	23 +	126681	2	G->21A40	C->22A40
	3	TTTGGGAGTCTGCGGTTGGAGC	23 +	126681	0		
	3	TTTGGGAGTCTGCGGTTGGAGA	23 +	126681	1	C->22A40	
	1	TTTGGGAGTCTGCGGTTGGGCGC	23 +	126681	1	A->20C40	
	1	TTTGGGAGTCTGCGGTTGGGAGG	23 +	126681	1	C->22G40	
	3	TTTGGGAGTCTGCGGTTGGGAGC	23 +	126681	0		
	1	TTTGGGAGTCTGCGGTTGGGAGA	23 +	126681	1	C->22A40	
	1	TTTGGGAGTCTGCGGTTGGGAAC	23 +	126681	1	G->21A40	
	1	TTTGGGAGTCTGCGGTTGGGAAA	23 +	126681	2	G->21A40	C->22A40
	39	TTTGGGAGTCTGCGGTTGGGAG	22 +	126681	0		
	4	TTTGGGAGTCTGCGGTTGGGAA	22 +	126681	1	G->21A40	
	9	TTTGGGAGTCTGCGGTTGGGAG	22 +	126681	0		

2	TTTGGGAGTCTGCGGTTGGGAT	22 +	126681	1	G->21T40		
1	TTTGGGAGTCTGGGGTTGGGAG	22 +	126681	1	C->12G40		
9	TTTGGGAGTCTGCGGTTGGGAG	22 +	126681	0			
1	TTTGGGAGTCTGCGGTTGGGAC	22 +	126681	1	G->21C40		
4	TTTGGGAGTCTGCGGTTGGGAA	22 +	126681	1	G->21A40		
77	TTTGGGAGTCTGCGGTTGGGA	21 +	126681	0			
1	TTTGGGAGTCTGCGGTGGC	21 +	126681	1	T->16G40		
1	TTTGGGAGTCTGCGGTCGGGA	21 +	126681	1	T->16C40		
1	TTTGGGAGTCTGAGGTTGTGA	21 +	126681	2	C->12A40	G->18T40	
1	TTTGGGAGGCTGCGGTTGC	21 +	126681	1	T->8G40		
31	TTTGGGAGTCTGCGGTTGGG	20 +	126681	0			
2	TTTGGGAGTCTGCGGTTGAA	20 +	126681	2	G->18A40	G->19A40	
6	TTTGGGAGTCTGCGGTTGGG	20 +	126681	0			
1	TTTGGGAGTCTGCGGTTGAA	20 +	126681	2	G->18A40	G->19A40	
81	TTTGGGAGTCTGCGGTTGG	19 +	126681	0			
2	TTTGGGAGTCTGCGGTTGA	19 +	126681	1	G->18A40		
7	TTTGGGAGTCTGCGGTTGG	19 +	126681	0			
1	TTTGGGAGTCTGCGGTTAA	19 +	126681	2	G->17A40	G->18A40	
1	TTTGGGAGTCTGCGGTTGGG	19 +	126681	1	T->16G40		
1	TTGGGAGTCTGCGGTTGGGAGCGT	24 +	126682	1	C->23T40		
1	TTGGGAGTCTGCGGTTGGGAGCAA	24 +	126682	2	G->22A40	C->23A40	
1	TTGGGAGTCTGCGGTTGGGAGAA	23 +	126682	2	C->21A40	G->22A40	
9	TTGGGAGTCTGCGGTTGGGAGC	22 +	126682	0			
1	TTGGGAGTCTGCGGTTGGGAAA	22 +	126682	2	G->20A40	C->21A40	
21	TTGGGAGTCTGCGGTTGGGAG	21 +	126682	0			
1	TTGGGAGTCTGCGGTTGGGAA	21 +	126682	1	G->20A40		
5	TTGGGAGTCTGCGGTTGGGA	20 +	126682	0			
1	TTGGGAGTCTGCGGTTGGGG	20 +	126682	1	A->19G40		
5	TTGGGAGTCTGCGGTTGGGA	20 +	126682	0			
						miR-I-3p	
						352 miR-H3-3p	
126679	1	CATTTGGGATTCTGCGGTTGGGA	23 +	126679	1	G->9T40	
	1	TTTGGGAGTCTGCGGTTGGGAGCAA	25 +	126681	2	G->23A40	C->24A40
	2	TTTGGGAGTCTGCGGTTGGGAGAA	24 +	126681	2	C->22A40	G->23A40
	1	TTTGGGAGTCTGCGGTTGGGAGCA	24 +	126681	1	G->23A40	
	1	TTTGGGAGTCTGCGGTTGGGAGAT	24 +	126681	2	C->22A40	G->23T40
	1	TTTGGGAGTCTGCGGTTGGGAAA	23 +	126681	2	G->21A40	C->22A40
	1	TTTGGGAGTCTGCGGTTGGGAAT	23 +	126681	2	G->21A40	C->22T40
	23	TTTGGGAGTCTGCGGTTGGGAG	22 +	126681	0		
	15	TTTGGGAGTCTGCGGTTGGGAGA	23 +	126681	1	C->22A40	
	14	TTTGGGAGTCTGCGGTTGGGAGC	23 +	126681	0		
	5	TTTGGGAGTCTGCGGTTGGGAGT	23 +	126681	1	C->22T40	
	3	TTTGGGAGTCTGCGGTTGGGATA	23 +	126681	2	G->21T40	C->22A40
	1	TTTTGGAGTCTGCGGTTGGGAGA	23 +	126681	2	G->3T40	C->22A40
	2	TTTGGGAGTCTGCGGTTGGGAA	22 +	126681	1	G->21A40	
	1	TTTTGGAGTCTGCGGTTGGGAT	22 +	126681	2	G->3T40	G->21T40
	1	TTTGGGAGTCTGCGGTTGGGAT	22 +	126681	1	G->21T40	
	13	TTTGGGAGTCTGCGGTTGGGA	21 +	126681	0		
	2	TTTGGGAGTCTGCGGTTGGGT	21 +	126681	1	A->20T40	
	6	TTTGGGAGTCTGCGGTTGGGA	21 +	126681	0		
	1	TTTGGGAGTATGCGGTTGGGC	21 +	126681	2	C->9A40	A->20C40
	1	TTTGGGAGTCTGTGGTTGGG	20 +	126681	1	C->12T40	
	2	TTTGGGAGTCTGCGGTTGGG	20 +	126681	0		
	11	TTTGGGAGTCTGCGGTTGG	19 +	126681	0		

	2	TTTGGGAGTCTGCGGTTGT	19 +	126681	1	G->18T40	
	4	TTGGGAGTCTGCGGTTGGGAGCGT	24 +	126682	1	C->23T40	
	4	TTGGGAGTCTGCGGTTGGGAGAA	23 +	126682	2	C->21A40	G->22A40
	2	TTGGGAGTCTGCGGTTGGGAGT	22 +	126682	1	C->21T40	
	2	TTGGGAGTCTGCGGTTGGGAGA	22 +	126682	1	C->21A40	
	1	TTGGGGGTCTGCGGTTGGGAGT	22 +	126682	2	A->5G40	C->21T40
	4	TTGGGAGTCTGCGGTTGGGAGC	22 +	126682	0		
	1	TTGGGAGTCTGCGGTTGGGA	20 +	126682	0		
							miR-I-3p
							129 miR-H3-3p
126841	7	AGCCGGAGCGCGTCGGGGCGC	20 +	126841	0		
	22	GCCGGAGCGCGTCGGGGCGC	19 +	126842	0		
	3	CCGGAGCGCGTCGGGGCGGG	20 +	126843	0		
	4	CGGAGCGCGTCGGGGCGGG	19 +	126844	0		
	1	CGGAGCGCGTCTGGGGCGGG	19 +	126844	1	G->11T40	
	1	GGAGCGCGTCGGGGCGGGAGA	21 +	126845	0		
	5	GAGCGCGTCGGGGCGGGAGAG	21 +	126846	0		
	3	GAGCGCGTCGGGGCGGGAGA	20 +	126846	0		
	1	GAGCGCGTCGGGGCGGGGGG	20 +	126846	2	A->17G40	A->19G40
	30	AGCGCGTCGGGGCGGGAGAG	20 +	126847	0		
	2	AGCGCGTCGGGGCGGGAGGG	20 +	126847	1	A->18G40	
	2	GCGCGTCGGGGCGGGGGAG	19 +	126848	1	A->15G40	
	35	GCGCGTCGGGGCGGGAGAG	19 +	126848	0		
							116 moR-H4-5p
126862	1	GAGAGTTCACTCGGCACGCATGCA	24 +	126862	0		
	3	GAGAGTTCACTCGGCACGCATGA	23 +	126862	1	C->22A40	
	1	GAGAGTTCACTCGGCACGCATGC	23 +	126862	0		
	11	GAGAGTTCACTCGGCACGCATG	22 +	126862	0		
	1	GAGAGTTCACTCGGCACGCATG	22 +	126862	0		
	1	GAGAGTTCACTCGGCACGCATG	22 +	126862	0		
	11	GAGAGTTCACTCGGCACGCAT	21 +	126862	0		
	2	GAGAGTTCACTCGGCACGCAT	21 +	126862	0		
	1	GAGAGTTCACTCGGCACGCAT	21 +	126862	0		
	1	GAGAGTTCACTCGGCACGCA	20 +	126862	0		
	1	AGAGTTCACTCGGCACGCATGCAT	24 +	126863	1	C->23T40	
	1	AGAGTTCACTCGGCACGCATGCAA	24 +	126863	1	C->23A40	
	10	AGAGTTCACTCGGCACGCATGCT	23 +	126863	1	A->22T40	
	8	AGAGTTCACTCGGCACGCATGCA	23 +	126863	0		
	1	AGAGTTCACTCGGCACGCATGCT	23 +	126863	1	A->22T40	
	1	AGAGTTCACTCGGCACGCATGCT	23 +	126863	1	A->22T40	
	1	AGAGTTCACTCGGCACGCATGCA	23 +	126863	0		
	1	AGAGTTCACTCGGCACACATGCA	23 +	126863	1	G->16A40	
	9	AGAGTTCACTCGGCACGCATGC	22 +	126863	0		
	2	AGAGTTCACTCGGCACGCATGC	22 +	126863	0		
	1	AGAGTTCACTCGGCACGCATGC	22 +	126863	0		
	1	AGAGTTCACTCGGCACGCATGC	22 +	126863	0		
	1	AGAGTTCACTCGGCACGCATGC	22 +	126863	0		
	1	AGAGTTCACTCGGCACGCATGA	22 +	126863	1	C->21A40	
	1	AGAGTTCACTCAGCACGCATGC	22 +	126863	1	G->11A40	
	19	AGAGTTCACTCGGCACGCATG	21 +	126863	0		
	1	AGAGTTCACACGGCACGCATG	21 +	126863	1	T->9A40	
	9	AGAGTTCACTCGGCACGCAT	20 +	126863	0		
	2	AGTTCACTCGGCACGCATGCAA	23 +	126865	2	C->21A40	G->22A40

	1	AGTTCACTCGGCACGCATGCATT	23 +	126865	2	C->21T40	G->22T40	
	1	AGTTCACTCGGCACGCATGCACA	23 +	126865	1	G->22A40		
	14	AGTTCACTCGGCACGCATGCAC	22 +	126865	0			
	4	AGTTCACTCGGCACGCATGCAA	22 +	126865	1	C->21A40		
	2	AGTTCACTCGGCACGCATGCAT	22 +	126865	1	C->21T40		
	1	AGTTCACTCGGCACGCATGCAT	22 +	126865	1	C->21T40		
	1	AGTTCACTCGGCACGCATGCAC	22 +	126865	0			
	43	AGTTCACTCGGCACGCATGCA	21 +	126865	0			
	1	AGTTCACTCGGCACGCATGCT	21 +	126865	1	A->20T40		
	1	AGTTCACTCGGCACGCATGCC	21 +	126865	1	A->20C40		
	1	AGTTCACTCGGCACGCATGCC	21 +	126865	1	A->20C40		
	1	AGTTCACTCGGCACGCATGCA	21 +	126865	0			
	1	AGTTCACTCGGCACGCATGCA	21 +	126865	0			
	1	AGTTCACTCGGCACGCATGCA	21 +	126865	0			
	1	AGTTCACTCGGCACGCATGAA	21 +	126865	1	C->19A40		
	2	AGTTCACTCGGCACGCATGC	20 +	126865	0			
	1	AGTTCACTCGGCAAGCATGC	20 +	126865	1	C->13A40		
	1	AGTTCACTCGGCACGCATG	19 +	126865	0			
	1	AGTTCACTCGGCACGCATG	19 +	126865	0			
	4	GTTCACTCGGCACGCATGCAC	21 +	126866	0			
	1	GTTCACTCGGCACGCATGCA	20 +	126866	0			
	1	TTCACCTCGGCACGCATGCACGTG	23 +	126867	0			
	11	TTCACCTCGGCACGCATGCACG	21 +	126867	0			
	1	TTCACCTCGGCAAGCATGCACG	21 +	126867	1	C->11A40		
	8	TTCACCTCGGCACGCATGCAC	20 +	126867	0			
	1	TTCACCTCGGCACGCATGCA	19 +	126867	0			miR-II-5p
								210 miR-H4-5p
126862	1	GAGAGTTCACTCGGCACGCATGCAT	25 +	126862	1	C->24T40		
	2	GAGAGTTCACTCGGCACGCATGCA	24 +	126862	0			
	7	GAGAGTTCACTCGGCACGCATG	22 +	126862	0			
	1	GGGAGTTCACTCGGCACGCATG	22 +	126862	1	A->1G40		
	3	GAGAGTTCACTCGGCACGCAT	21 +	126862	0			
	1	AGAGTTCACTCGGCACGCATGCAAA	25 +	126863	2	C->23A40	G->24A40	
	5	AGAGTTCACTCGGCACGCATGCAT	24 +	126863	1	C->23T40		
	2	AGAGTTCACTCGGCACGCATGCAA	24 +	126863	1	C->23A40		
	1	AGAGTTCACTCGGCACGCATGCTT	24 +	126863	2	A->22T40	C->23T40	
	21	AGAGTTCACTCGGCACGCATGCA	23 +	126863	0			
	6	AGAGTTCACTCGGCACGCATGCT	23 +	126863	1	A->22T40		
	2	AGAGTTGCTCGGCACGCATGCA	23 +	126863	1	A->7G40		
	1	AGAGTTCACTCGGCACGCATGAA	23 +	126863	1	C->21A40		
	12	AGAGTTCACTCGGCACGCATGC	22 +	126863	0			
	1	AGAGTTCACTCGGCACGCATGA	22 +	126863	1	C->21A40		
	7	AGAGTTCACTCGGCACGCATG	21 +	126863	0			
	3	AGAGTTCACTCGGCACGCAT	20 +	126863	0			
	1	AGTTCACTCGGCACGCATGCAAA	23 +	126865	2	C->21A40	G->22A40	
	2	AGTTCACTCGGCACGCATGCA	21 +	126865	0			
	1	GTTCACTCGGCACGCATGCAC	21 +	126866	0			miR-II-5p
								80 miR-H4-5p
126900	3	TCCGTGCTTGCCTAGCGAACTC	22 +	126900	0			
	2	TCCGTGCTTGCCTAGCGAACT	21 +	126900	0			
	2	CCGTGCTTGCCTAGCGAACTCA	22 +	126901	0			
	3	CCGTGCTTGCCTAGCGAACTC	21 +	126901	0			
	1	CCGTGCTTGCCTAGCGAAC	19 +	126901	0			

3	CGTGCTTGCCTAGCGAACTCACC	23 +	126902	0			
1	CGTGCTTGCCTAGCGAACTCAAA	23 +	126902	2	C->21A40	C->22A40	
1	CGTGCTTGCCTAGCGAACTCAC	22 +	126902	0			
8	CGTGCTTGCCTAGCGAACTCA	21 +	126902	0			
1	CGTGCTTGCCTAGCGAACTCT	21 +	126902	1	A->20T40		
3	CGTGCTTGCCTAGCGAACTCA	21 +	126902	0			
2	CGTGCTTGCCTAGCGAACTC	20 +	126902	0			
1	CGTGCTTGCCTAGCGAACT	19 +	126902	0			
1	GTGCTTGCCTAGCGAACTC/	23 +	126903	0			
1	GTGCTTGCCTAGCGAACTCACC	22 +	126903	0			
1	GTGCTTGCCTAGCGAACTCAC	21 +	126903	0			
2	GTGCTTGCCTAGCGAACTCA	20 +	126903	0			
1	TGCTTGCCTAGCGAACTCACCCAA	24 +	126904	2	G->22A40	T->23A40	
2	TGCTTGCCTAGCGAACTCACCCG	23 +	126904	0			
1	TGCTTGCCTAGCGAACTCACCCA	23 +	126904	1	G->22A40		
9	TGCTTGCCTAGCGAACTCACCC	22 +	126904	0			
1	TGCTTGCCTAGCGAACTCACCC	22 +	126904	1	C->7T40		
1	TGCTTGCCTAGCGAACTCACCT	22 +	126904	1	C->21T40		
5	TGCTTGCCTAGCGAACTCACC	21 +	126904	0			
2	TGCTTGCCTAGCGAACTCAC	20 +	126904	0			
1	TGCTTGCCTAGCGAACTCA	19 +	126904	0			
20	CTTGCCTAGCGAACTCACCCGT	22 +	126906	0			
1	CTTGCCTAGCGAACTCACCCGT	22 +	126906	0			
1	CTTGCCTAGCGAACTCACCCGA	22 +	126906	1	T->21A40		
3	TTGCCTAGCGAACTCACCCGT	21 +	126907	0			miR-II-3p
1	TTGCCTAGCGAACTCACCCGA	21 +	126907	1	T->20A40		85 miR-H4-3p
126902	1	CGTGCTTGCCTAGCGAACTCA	21 +	126902	0		
	1	CGTGCTTGCAGAGCGAACTCA	21 +	126902	2	C->9A40	T->10G40
	1	GTGCTTGCCTAGCGCACTCACC	22 +	126903	1	A->14C40	
	1	GTGCTTGCCTAGCGAACTCACC	22 +	126903	0		
	1	TGCTTGCCTAGCGAACTCACCCGA	24 +	126904	1	T->23A40	
	1	TGCTTGCCTAGCGAACTCACCCG	23 +	126904	0		
	2	TGCTTGCCTAGCGAACTCACCC	22 +	126904	0		
	2	TGCTTGCCTAGCGAACTCACC	21 +	126904	0		
	1	TGCTTGCCTAGCGAACTCAC	20 +	126904	0		
	1	CTTGCCTAGCGAACTCACCCGTGT	24 +	126906	2	C->22G40	C->23T40
	1	CTTGCCTAGCGAACTCACCCGTAA	24 +	126906	2	C->22A40	C->23A40
	4	CTTGCCTAGCGAACTCACCCGT	22 +	126906	0		17 miR-II-3p miR-H4-3p
126927	1	TCCCGGTTGGCGTGCGCAGC	20 +	126927	1	C->6T40	
	2	TCCCGGTTGGCGTGCGCAG	19 +	126927	1	C->6T40	
	1	TCCCGGTTGGCGTGCGCAA	19 +	126927	2	C->6T40	G->18A40
							4 mOR-H4-3p
127593	2	GGGGGGGCTCGGGCCACCTGACCT	24 +	127593	0		
	1	GGGGGGGCTCGGGCCACCTGACT	23 +	127593	1	C->22T40	
	2	GGGGGGGCTCGGGCCACCTGACC	23 +	127593	0		
	1	GGGGGGGCTCGGGCCACCTGAC	22 +	127593	0		6 miR-H5-5p
127593	3	GGGGGGGCTCGGGCCACCTGACC	23 +	127593	0		3 miR-H5-5p
132844	1	TTATTAGGGCAAAGTGCGAGCAC	23 +	132844	0		
	1	TTATTAGGGCAAAGTGCGA	19 +	132844	0		
	14	TTAGGGCAAAGTGCGAGCACTGT	23 +	132847	1	G->22T40	

	1	TTAGGGCAAAGTGCAGCACTGA	23 +	132847	1	G->22A40	
	1	TTAGGGCAAAGTGCAGCACTGA	23 +	132847	1	G->22A40	
	5	TTAGGGCAAAGTGCAGCACTG	22 +	132847	0		
	4	TTAGGGCAAAGTGCAGCACT	21 +	132847	0		
	1	TTAGGGCAAAGTGCAGCACA	21 +	132847	1	T->20A40	
	1	TTAGGGCAAAGTGCAGAACT	21 +	132847	1	C->17A40	
	1	TTAGGGCAAAGTGCAGCA	19 +	132847	0		
	5	TAGGGCAAAGTGCAGCACTGT	22 +	132848	1	G->21T40	
	2	TAGGGCAAAGTGCAGCACTGG	22 +	132848	0		
	1	TAGGGCAAAGTGCAGCACTGG	22 +	132848	1	A->8G40	
	1	TAGGGCAAAGTGCAGCACTGT	22 +	132848	1	G->21T40	
	1	TAGGGCAAAGTGCAGCACTGT	22 +	132848	1	G->21T40	
	1	TAGGGCAAAGTGCAGCACTG	21 +	132848	0		
	1	TAGGGCAAAGTGCAGCACT	20 +	132848	0		
	2	AGGGCAAAGTGCAGCACTGTA	22 +	132849	2	G->20T40	C->21A40
	1	AGGGCAAAGTGCAGCACTGTT	22 +	132849	2	G->20T40	C->21T40
	1	AGGGCAAAGTGCAGCACTGAT	22 +	132849	2	G->20A40	C->21T40
	2	AGGGCAAAGTGCAGCACTGT	21 +	132849	1	G->20T40	
	2	AGGGCAAAGTGCAGCACTGG	21 +	132849	0		
							50 miR-13-3p
132997	1	CTGCGCGGCGGAGACCGGGACT	22 +	132997	1	G->21T40	
	2	CTGCGCGGCGGAGACCGGGAC	21 +	132997	0		
	2	CTGCGCGGCGGAGACCGGGA	20 +	132997	0		
	1	CGCGGCGGAGACCGGGACGGCTT	23 +	133000	2	A->21T40	G->22T40
	1	GCGGCGGAGACCGGGACAA	19 +	133001	2	G->17A40	G->18A40
	1	CGGCGGAGACCGGGACGGCAG	21 +	133002	0		
	1	CGGCGGAGACCGGGACGGCA	20 +	133002	0		
	1	GCGAAGACCGGGACGGCAG	19 +	133004	1	G->3A40	
							10 miR-25-3p
148903	1	TATACTATTAGGACGAAGTGC	21 +	148903	0		
	1	ATACTATTAGGACGAAGTGC	20 +	148904	0		
	2	ATACTATTAGGACGAAGTGC	19 +	148904	0		
	1	CTATTAGGACGAAGTGCGAATA	22 +	148907	2	C->20T40	G->21A40
	1	CTATTAGGACGAAGTGCGAAT	22 +	148907	2	C->20A40	G->21T40
	1	CTATTAGGACGAAGTGC GAA	20 +	148907	0		
	1	CTATTAGGACGAAGTGC GA	19 +	148907	0		
	1	TATTAGGACGAAGTGC GAACGC	22 +	148908	0		
	1	TTAGGACGAAGTGC GAACGCTTAA	24 +	148910	2	C->22A40	G->23A40
	1	TTAGGACGAAGTGC GAACGCTTT	23 +	148910	1	C->22T40	
	8	TTAGGACGAAGTGC GAACGCTT	22 +	148910	0		
	1	TTAGGACGAAGTGC GCACGCTT	22 +	148910	1	A->15C40	
	1	TTAGGACGAAGTGC GAACGCTT	22 +	148910	0		
	1	TTAGGACGAAGTGC GAACGCTT	22 +	148910	0		
	1	TTAGGACGAAGTGC GAACGCTA	22 +	148910	1	T->21A40	
	3	TTAGGACGAAGTGC GAACGCT	21 +	148910	0		
	2	TTAGGACGAAGTGC GAACGC	20 +	148910	0		
	1	TAGGACGAAGTGC GAACGCTT	21 +	148911	0		
							29 miR-12-3p

Reads recovered from the latently infected ganglia shown in gray boxes. Selected sequence of miRNA shown in red.

Locus - genomic coordinates of the first nucleotide of the first recovered read representing miRNA

hits- number of recovered reads species; O - orientation; Start- genomic coordinates of the starting nucleotide;

M1 and M2 - mismatch with the referent HSV-2 genome (NC_001798)

N - total number of reads representing miRNA