Supplemental Figure S6. Sequence reads mapped to the (**A**) mmu-miR-702 and (**B**) mmu-miR-5132 hairpins. Sequence in blue represents intron region, while in yellow represents flanking exon regions. Reads comprising GU or AG dinucleotide, which is characteristic of intron splice sites, were marked in red.

A. mmu-miR-702 region

```
CGGGACAAGGUGAGUGGGGUGGUUGGCAUGGGUUGCCCAUGGGGACUCGACGCUGUGCCCACAGCCUCCUGAUGUCCUCCUCACGCAUGCCCACCCUUUACCCCGCUCCAGGGCAUCUU
.((..(...(.(((((((((((..((..((((((((....((((((((((.(((((....))))).))..)).)))).))....))).)))))))..))))))))))))...)..)).. (-50.30)
```

Reads from GSE36639 (MHV68-infected)

```
.........GUGAGUGGGGUGGUUGGCA........................................................................................... 1       19      1
.........GUGAGUGGGGUGGUUGGCAUG......................................................................................... 9       21      1
..........UGAGUGGGGUGGUUGGCAUGGGU...................................................................................... 1       23      1
.......................................................................................UGCCCACCCUUUACCCCGCUCCAG........ 2       24      1
```

Reads from GSM314557

```
.........GUGAGUGGGGUGGUUGGCAUG......................................................................................... 25      21      1
.........GUGAGUGGGGUGGUUGG............................................................................................. 3       17      1
.........GUGAGUGGGGUGGUUGGCA........................................................................................... 9       19      1
..........UGAGUGGGGUGGUUGGCA........................................................................................... 1       18      1
..........UGAGUGGGGUGGUUGGCAUGGG....................................................................................... 2       22      1
..........UGAGUGGGGUGGUUGGCAU.......................................................................................... 2       19      1
......................................................................................AUGCCCACCCUUUACCCCGCUC........... 1       22      1
.......................................................................................UGCCCACCCUUUACCCCGCUCCA......... 10      23      1
.......................................................................................UGCCCACCCUUUACCCCGC............. 1       19      1
.......................................................................................UGCCCACCCUUUACCCCG.............. 1       18      1
.......................................................................................UGCCCACCCUUUACCCCGCU............ 3       20      1
.......................................................................................UGCCCACCCUUUACCCC............... 4       17      2
.......................................................................................UGCCCACCCUUUACCCCGCUC........... 5       21      1
.......................................................................................UGCCCACCCUUUACCCCGCUCCAG........ 60      24      1
.......................................................................................UGCCCACCCUUUACCCCGCUCC.......... 9       22      1
```

B. mmu-miR-5132 region

```
CCGGCGUGGGGUGGUGGACUCAGGCUUCUGGAGCUGAAGCCUGAUGUUCCCCAUCCCGCAG
.....(((((((((.(((((((((((((.......))))))))).)))).))))))))).. (-38.40)
```

Reads from GSE36639 (MHV68-infected)

```
...GCGTGGGGTGGTGGACTCAGG.....................................        1        21        1
....CGTGGGGTGGTGGACTCAGGCT...................................        1        22        1
....CGTGGGGTGGTGGACTCAGGCTT..................................        1        23        1
....CGTGGGGTGGTGGACTCAG......................................        1        19        1
....CGTGGGGTGGTGGACTCAGGC....................................        4        21        1
.....GTGGGGTGGTGGACTCAGG.....................................        2        19        1
......TGGGGTGGTGGACTCAGGCTTC.................................        19       22        1
......TGGGGTGGTGGACTCAGGC....................................        1        19        1
......TGGGGTGGTGGACTCAGGCT...................................        1        20        1
......TGGGGTGGTGGACTCAGGCTT..................................        4        21        1
```

Reads from GSM314557

```
...GCGTGGGGTGGTGGACTCAGG.....................................        1        21        1
....CGTGGGGTGGTGGACTCAGGC....................................        1        21        1
....CGTGGGGTGGTGGACTCAGGCT...................................        1        22        1
....CGTGGGGTGGTGGACTCAGGCTTCT................................        1        25        1
....CGTGGGGTGGTGGACTCAGGCTT..................................        1        23        1
....CGTGGGGTGGTGGACTCAGG.....................................        1        20        1
....CGTGGGGTGGTGGACTCA.......................................        1        18        1
....CGTGGGGTGGTGGACTC........................................        4        17        1
.....GTGGGGTGGTGGACTCAGG.....................................        1        19        1
......TGGGGTGGTGGACTCAGGCT...................................        1        20        1
......TGGGGTGGTGGACTCAGGCTTC.................................        7        22        1
..........TGGTGGACTCAGGCTTC..................................        1        17        2
.....................................AGCCTGATGTTCCCCATCCCGCA.        1        23        1
.......................................CCTGATGTTCCCCATCCCGCAG        1        22        1
........................................CTGATGTTCCCCATCCCGCA.        1        20        1
```