**Supplemental Table 2.** Number of sequence tags obtained by the Genome Analyzer II (Illumina), number of virus specific reads, reads representing virus miRNA and number of detected host miRNAs miR-25 and miR-10a.

| | Tags[1] | Unique tags[1] | Virus specific reads[2] ≥19N | Virus miRNA[3] | miR-25 / miR-10a |
|---|---|---|---|---|---|
| HSV-1 productive[5] | 509485 | 104630 | 6682 | 52% | 8919 / 13578 |
| HSV-1 latency[6] | 3492927 | 409521 | 856 | 67% | 5029 / 617 |
| HSV-2 productive[5] | 2038681 | 436322 | 16883 | 14% | 49819 / 52366 |
| HSV-2 latency[6] | 6037416 | 817607 | 2177 | 13% | 6826 / 321 |

[1]Tags represents the 36 nucleotide Genome Analyzer II sequence output that includes partial adapter sequence and the sequence of small RNA; [2] Reads represent tags after removal of the adapter sequence; [3]Percentage of reads representing miRNA in total number of virus specific reads ≥19N. [5]RNA extracted from HEK-293 cells at 18 hours post infection that were infected at an MOI of 10 or 1 by HSV-1 and HSV-2, respectively; [6]RNA extracted from the mouse trigeminal ganglia latently infected with HSV-1 or HSV-2. Number of unambiguously detected reads of miR-25 and miR-10a in the productively and latently infected samples are shown.