Supplementary Tables

Supplementary Table 1: Fold-change for miRNAs during Zika virus infection.

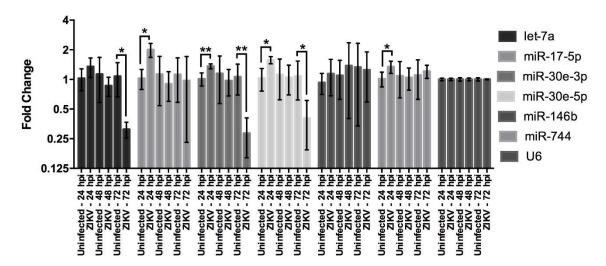
| miRNA | 24 hpi | 48 hpi | 72 hpi |
|-----------------|--------|--------|--------|
| hsa-miR-17-5p | 6.0 | 1.0 | 0.2 |
| hsa-miR-146b-5p | 3.8 | 0.6 | 0.1 |
| hsa-miR-30e-3p | 3.3 | 1.4 | 0.0 |
| hsa-miR-296-5p | 2.6 | 0.4 | 0.9 |
| hsa-miR-1303 | 2.6 | 0.3 | 0.7 |
| hsa-miR-4521 | 2.5 | 0.7 | 0.0 |
| hsa-miR-30e-5p | 2.4 | 0.7 | 0.1 |
| hsa-miR-107 | 2.2 | 1.0 | 0.0 |
| hsa-miR-431-5p | 2.1 | 1.4 | 0.0 |
| hsa-miR-7-5p | 2.1 | 1.1 | 0.3 |
| hsa-miR-361-3p | 2.0 | 1.3 | 0.1 |
| hsa-miR-411-3p | 1.2 | 2.7 | 0.0 |
| hsa-miR-323a-5p | 0.6 | 2.6 | 1.4 |
| hsa-miR-194-5p | 0.5 | 2.0 | 0.0 |
| hsa-miR-9-5p | 1.3 | 1.9 | 7.2 |

Supplementary Table 2: miRNA targets at each time point post infection.

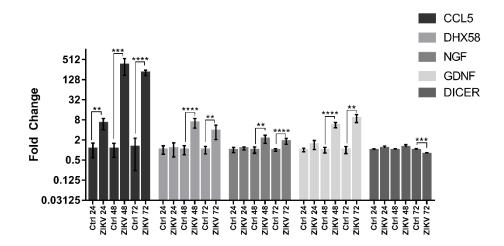
| Hours Post-Infection | miRNA | No. Potential Genes Targets* | No. Genes after filtering** |
|----------------------|-----------------|------------------------------|-----------------------------|
| 24 | hsa-miR-17-5p | 2186 | 38 |
| | hsa-miR-146b-5p | 501 | 9 |
| | hsa-miR-30e-3p | 1052 | 21 |
| | hsa-miR-296-5p | 450 | 10 |
| | hsa-miR-1303 | 221 | 7 |
| | hsa-miR-4521 | 150 | 2 |
| | hsa-miR-30e-5p | 1546 | 32 |
| | hsa-miR-107 | 2187 | 32 |
| | hsa-miR-431-5p | 0 | 0 |
| | hsa-miR-7-5p | 1830 | 38 |
| | hsa-miR-361-3p | 508 | 10 |
| 48 | hsa-miR-411-3p | 158 | 22 |
| | hsa-miR-323a-5p | 103 | 5 |
| | hsa-miR-194-5p | 410 | 45 |
| 72 | hsa-miR-9-5p | 1035 | 88 |

^{*} TarBase v7.0 (p-value threshold = 0.05); ** Filtered using downregulated genes at each time point (< or = - 2-fold)

Supplementary Figures



Supplementary Figure 1: Quantitative RT-PCR validation (qPCR), was compared to next generation sequencing expression at 24, 48 and 72 hpi. Validation was performed on three biological replicates and error-bars represent standard deviation. Student's t-test was used to assess significance where * indicates a p-value < 0.05, and ** represents a p-value < 0.005 respectively.



Supplementary Figure 2: Gene expression data in SVG cells. Cells were infected at an MOI of 1 and mRNA was collected 24, 48 and 72 hpi. Transcription of the genes was analyzed by quantitative real-time PCR with GAPDH as a housekeeping gene and expressed as a fold-change compared to uninfected cells ($2-\Delta\Delta$ Ct method). Data represent the mean from three replicate experiments, with error bars showing the standard deviation. Samples were compared using Students t-test with significant differences indicated by ** (p < 0.01), ***(p < 0.001), **** (p < 0.0001).