Supplemental Material description:

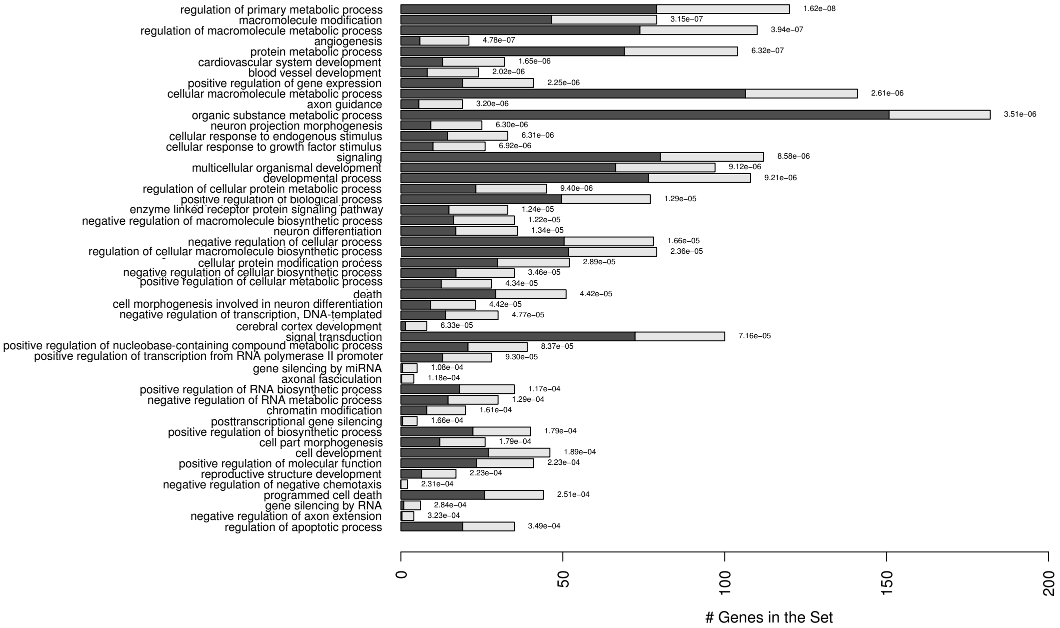

Figure S1. Graphical representation of the enriched biological processes (BP) modulated by miR-148a. Over-represented pathways are depicted in the y-axis. The bars represent the expected (dark bars) versus the observed numbers of genes (gray light bars) for each BP enrichment with the statistical difference values alongside the bars. The overrepresentation was assessed with a statistical score based on hypergeometric tests with p-values <= 0.001. Complete list including the full names of the GO terms is presented in the Table S3.

Table S1: All the selected putative targets from the ZIKV up-regulated miRNAs miR-145 and miR148a according the strategy adopted for use in this study.

Table S2: All the selected putative targets from the ZIKV down-regulated miRNAs according the strategy adopted for use in this study.

Table S3: GSEA of selected putative targets for the up-regulated miR-145 and miR-148a in ZIKV-infected SH-SY5Y cells at 72 hpi.

Table S4: GSEA of selected putative targets for the down-regulated miRNAs (miR-190b, miR-299-5p, miR-361-3p and miR-522) in ZIKV-infected SH-SY5Y cells at 72 hpi.

Table S5. Mortality causes of Zika newborns and negative controls at the same gestational age.