

## **Description of Additional Supplementary Files**

### **File name: Supplementary Data 1**

**Description:** This dataset contains the histopathological analysis of H&E heart sections for WT, *Mavs*<sup>-/-</sup> and *Mavs*<sup>-/-</sup> CHIKV-infected and mock-infected mice.

Microscopy image raw data is stored in OMERO Plus and is accessible through the NYU Data Catalog: <https://datacatalog.med.nyu.edu/dataset/10621>.

### **File name: Supplementary Data 2**

**Description:** List of differentially expressed genes at 2 dpi. Differential RNA expression analysis was performed using DEseq2. The Log<sub>2</sub>FC represents the log<sub>2</sub> of the fold change between normalized counts of each group. P values were calculated using the Wald test, between CHIKV-infected and heat inactivated (HI) control groups, followed by multiple hypothesis correction via the Benjamini-Hochberg method for calculating the false discovery rate (FDR) values. Significant expression changes were defined as FDR < 0.15 and absolute Log<sub>2</sub>FC > 1.

### **File name: Supplementary Data 3**

**Description:** List of differentially expressed genes at 5 dpi. Differential RNA expression analysis was performed using DEseq2. The Log<sub>2</sub>FC represents the log<sub>2</sub> of the fold change between normalized counts of each group. P values were calculated using the Wald test, between CHIKV-infected and heat inactivated (HI) control groups, followed by multiple hypothesis correction via the Benjamini-Hochberg method for calculating the false discovery rate (FDR) values. Significant expression changes were defined as FDR < 0.15 and absolute Log<sub>2</sub>FC > 1.