**Supplementary materials for:  
Changes in ADAR RNA Editing Patterns in CMV and ZIKV Congenital Infections**

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**Supplementary files legends:**  
Supplementary Figure 1 (PNG). Violin and box plots showing the distribution of RNA editing rates of sites detected in each sample. Panels A-C show editing rate distributions in viral infection (blue) and control (red samples) for MCMV, ZIKV PRJNA487357, and ZIKV PRJNA358758 samples, respectively, Panel D shows editing rate distributions in ZIKV FSS13205 (green), ZIKV PE243 (blue), and control (red) hiNPC samples.

Supplementary Figure 2 (PNG). Scatterplots of correlations between changes in expression (TPM) and changes in RNA editing rates. (A) Plot of change in TPM and editing rate for each editing sate between MCMV and control samples (R^2 = 0.01932). (B) Plot of change in TPM and editing rate for each editing sate between ZIKV and control samples for PRJNA487357 (R^2 = 0.03809). (C) Plot of change in TPM and editing rate for each editing sate between ZIKV and control samples for PRJNA 358758 (R^2 = -0.001244). (D) Plot of change in TPM and editing rate for each editing sate between ZIKV PE243 and control hiNPC samples (R^2 = 0.07111). (E) Plot of change in TPM and editing rate for each editing sate between ZIKV FSS13205 and control hiNPC samples (R^2 = 0.05415). (F) Plot of change in TPM and editing rate for each editing sate between ZIKV FSS13205 and PE243 samples (R^2 = -0.0054).

Supplementary File 1 (XLSX). Lists of differentially expressed genes (DEGs) from comparisons of symptomatic and asymptomatic HCMV infections to control samples, from GEO2R analysis of BioProject dataset PRJNA422858 (<https://www.ncbi.nlm.nih.gov/geo/geo2r/?acc=GSE108211>).

Sheets A, B and C show GEO2R lists of DEGs from symptomatic vs control, asymptomatic vs control, and symptomatic vs asymptomatic HCMV samples comparisons. Sheets D and E show results of Reactome pathways overrepresentation analyses for significant (FDR <= 0.05) DEGs from symptomatic vs control and asymptomatic vs control HCMV samples. Only pathways with entities FDR < 0.05 are shown.

Supplementary File 2 (XLSX). List of DESeq2 (Love et al., 2014) differential expression analysis results for gene counts from ballgown, including log2 fold change values and p values for expression changes in each gene for (A) MCMV vs control, (B) ZIKV vs control (PRJNA487357), (C) ZIKV vs control (PRJNA358758), (D) ZIKV FSS13205 vs control hiNPC, (E) ZIKV PE243 vs control hiNPC, and (F) ZIKV PE243 vs FSS13205 samples.

Supplementary File 3 (XLSX). List of DESeq2 (Love et al., 2014) differential expression analysis results for transcript counts from ballgown, including log2 fold change values and p values for expression changes in each transcript for (A) MCMV vs control, (B) ZIKV vs control (PRJNA487357), (C) ZIKV vs control (PRJNA358758), (D) ZIKV FSS13205 vs control hiNPC, (E) ZIKV PE243 vs control hiNPC, and (F) ZIKV PE243 vs FSS13205 samples.

Supplementary File 4 (XLSX). Alu editing index (AEI) values from the RNA Editing Indexer method (Roth et al., 2019) for (A) the PRJEB38849 MCMV dataset, (B) the ZIKV PRJNA487357 dataset, (C) the ZIKV PRJNA358758 dataset, and (D) the hiNPC ZIKV PRJNA551246 dataset. This includes quantifications of the ratio of A-to-G mismatches to total A reads (effectively the percent of As edited to Gs) in *Alu* repeat elements in humans or SINE B1/B2 repeat elements in mice, as well as the same metric for other variant types. A-to-G editing index serves as a general metric of transcriptome-wide levels of hyperediting, which primarily occur in repeat regions. Quantification of other variants serve as a measure of background noise, with the next most common modification type being C-to-T editing.

Supplementary File 5 (XLSX). (A) Characteristics of 149 editing sites from MCMV and control samples. List of ADAR edited sites (identified via chromosome (CHR) and position (POS)) and individual nucleotide counts from MCMV infections and control samples (PRJEB38849). (B) Characteristics of 21 significantly different editing sites between MCMV and control samples. List of ADAR edited sites (identified via chromosome (CHR) and position (POS)) and average editing rates from MCMV.

Supplementary File 6 (XLXS). Reactome pathway analysis of edited genes from infected and control samples. In bold are pathways overrepresented among editing targets with FDR < 0.1.

(A) Sheet 6A shows overrepresented pathways among edited targets from MCMV and control samples (PRJEB38849). (B) Sheet 6B shows overrepresented pathways among edited targets from ZIKV and control samples (PRJNA487357). (C) Sheet 6C shows pathways among edited targets from ZIKV and control samples (PRJNA358758); there were no pathways overrepresented among editing targets with FDR < 0.1.

Supplementary File 7 (XLSX). (A) Characteristics of 78 editing sites from ZIKV and control samples (PRJNA487357). List of ADAR edited sites (identified via chromosome (CHR) and position (POS)) and individual nucleotide counts from ZIKV infections and control samples. (B) Characteristics of 12 significantly different editing sites between ZIKV and control samples. List of ADAR edited sites (identified via chromosome (CHR) and position (POS)), and average editing rates from ZIKV infections and control samples (PRJNA487357).

Supplementary File 8 (XLSX). (A) Characteristics of 1276 editing sites from ZIKV and control samples. List of ADAR edited sites (identified via chromosome (CHR) and position (POS)) and individual nucleotide counts from ZIKV infections and control samples (PRJNA358758). (B) Characteristics of 148 significantly different editing sites between ZIKV and control samples. List of ADAR edited sites (identified via chromosome (CHR) and position (POS)) and average editing rates from ZIKV infections and control samples (PRJNA358758).

Supplementary File 9 (XLSX). Results of MAJIQ and VOILA analysis of editing sites from ZIKV and control samples (PRJNA358758). (A) Results of MAJIQ analysis of editing sites from ZIKV and control samples (PRJNA358758), with PSI/dPSI information for all LSVs identified. (B) Results of VOILA analysis of editing sites from ZIKV and control samples (PRJNA358758), with significant LSVs (|dPSI| > 0.2 and p < 0.05). (C) Information for LSVs in genes identified as Nova1 targets (Zhang et al., 2010).

Supplementary File 10 (XLSX). (A) Characteristics of 1355 editing sites from ZIKV and control samples (PRJNA551246). List of ADAR edited sites (identified via chromosome (CHR) and position (POS)) and individual nucleotide counts from ZIKV infections with Cambodian (FSS13025) and Brazilian ZIKV (PE243) strains and control samples. (B) Characteristics of 9 significantly different editing sites between ZIKV and control samples (PRJNA551246). List of ADAR edited sites (identified via chromosome (CHR) and position (POS)), and average editing rates from ZIKV infections with Cambodian (FSS13025) and Brazilian ZIKV (PE243) strains and control samples.

Supplementary File 11 (XLSX). SubmiRine (Maxwell et al., 2015) results predicting differences in miRNA binding between unedited and edited transcripts. While no editing was found to alter miRNA binding in the MCMV or hiNPC ZIKV datasets, editing sites with potential links to changes in miRNA targeting were detected in 2 genes for the mouse ZIKV PRJNA487357 dataset and 26 genes for the mouse ZIKV PRJNA358758 dataset.

Supplementary File 12 (XLSX). Number of (and percent of unmapped) reads that were mapped to the respective viral genomes. Briefly, unmapped reads were collected from the BAM files and mapped to the viral genomes of MCMV and ZIKV using STAR. The following reference genomes were used: NC\_075725 (MCMV), KX520666 (ZIKV1), KU866423 (ZIKV2), and KX197192 and MH158236\* for human ZIKV dataset, respectively. As expected, the viral reads were found primarily in the infected samples, although their numbers represented only relatively small portions of all sequenced reads. A handful of viral reads were also detected in some uninfected samples, consistent with previously reported results (Lima et al. 2019, Figure 4C) and the possibility of artifacts of mapping and/or negligible contamination. \* MH158236 is a complete genome of JN860885 (FSS13025) ZIKV isolate.