Supporting Information

The small noncoding RNAs (sncRNAs) of murine gammaherpesvirus 68 (MHV-68) are involved in regulating the latent-to-lytic switch *in vivo*

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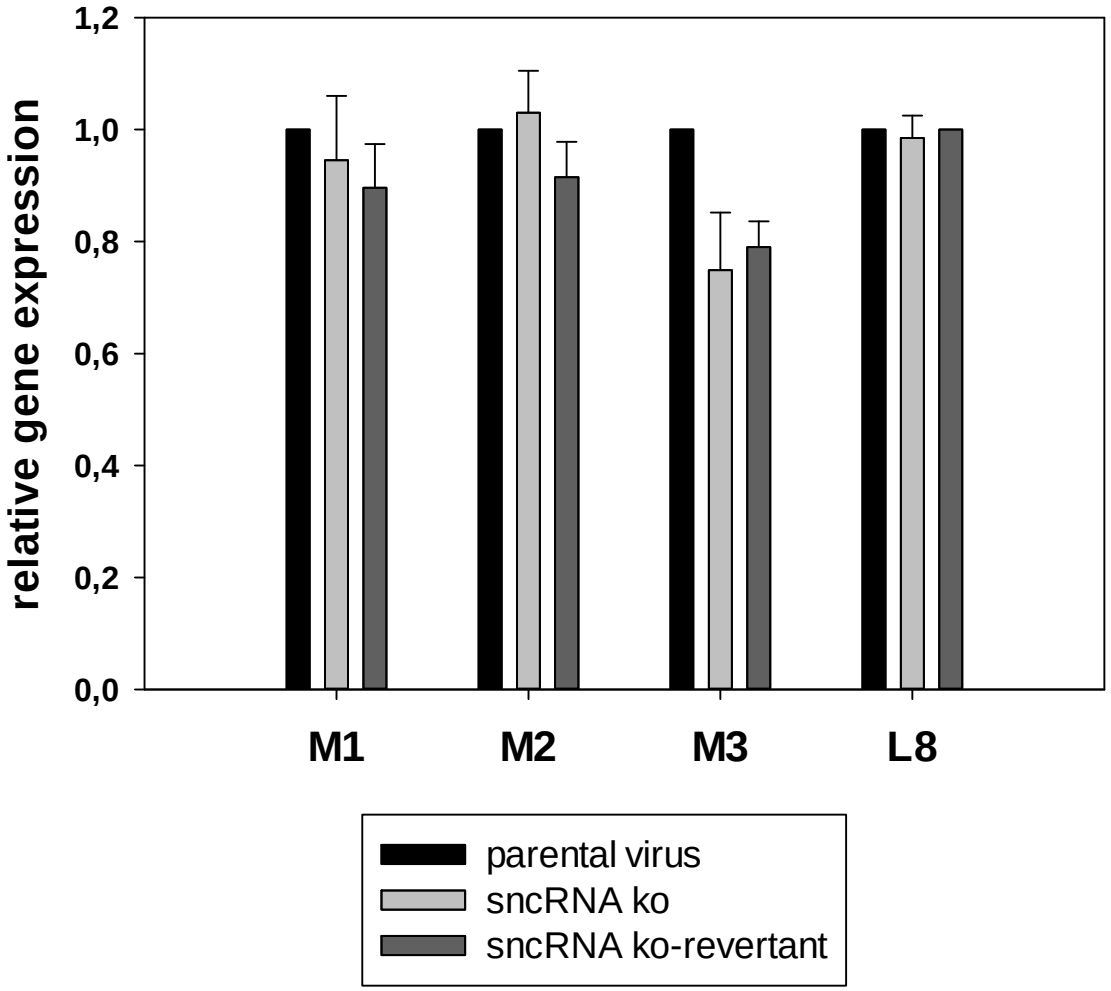
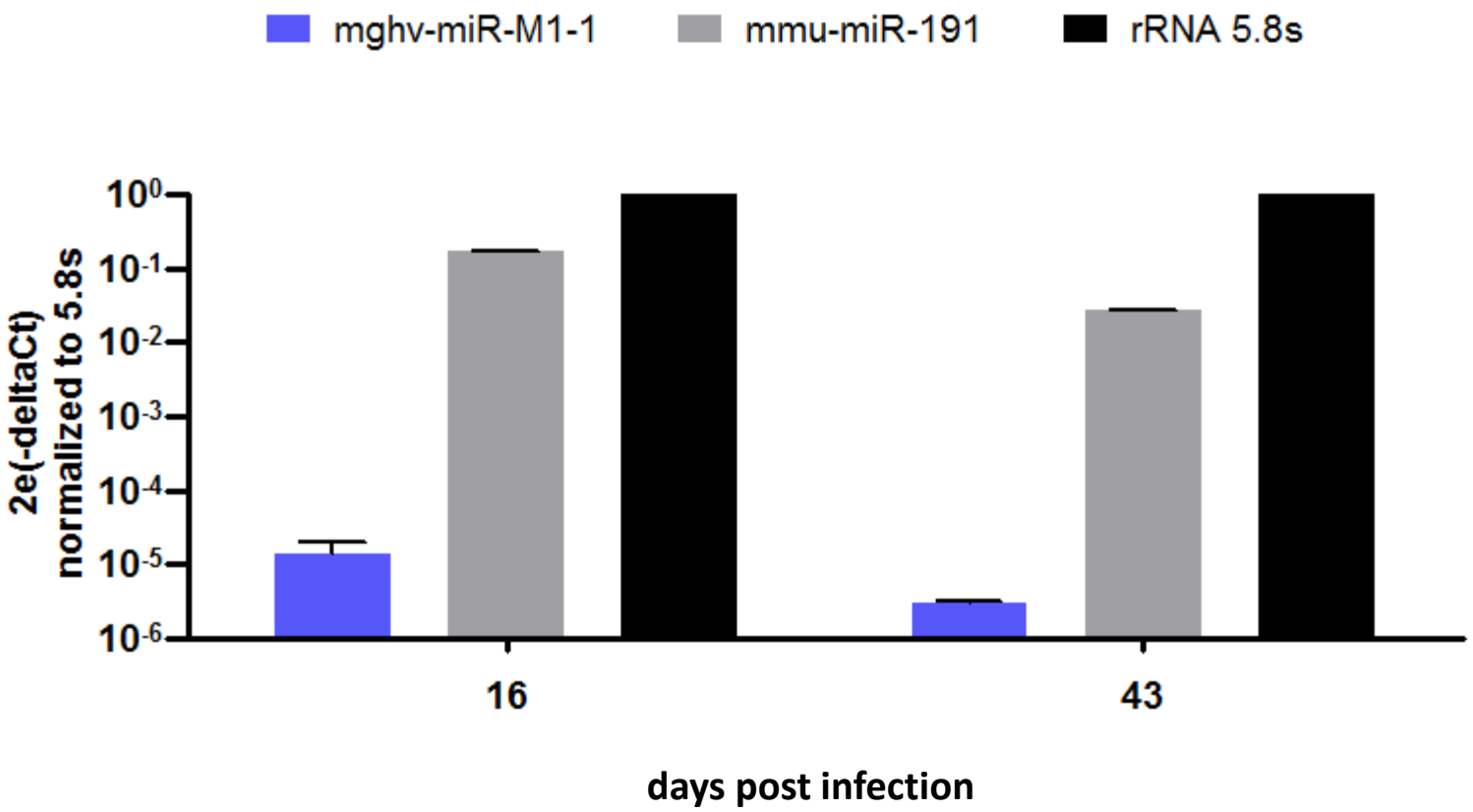
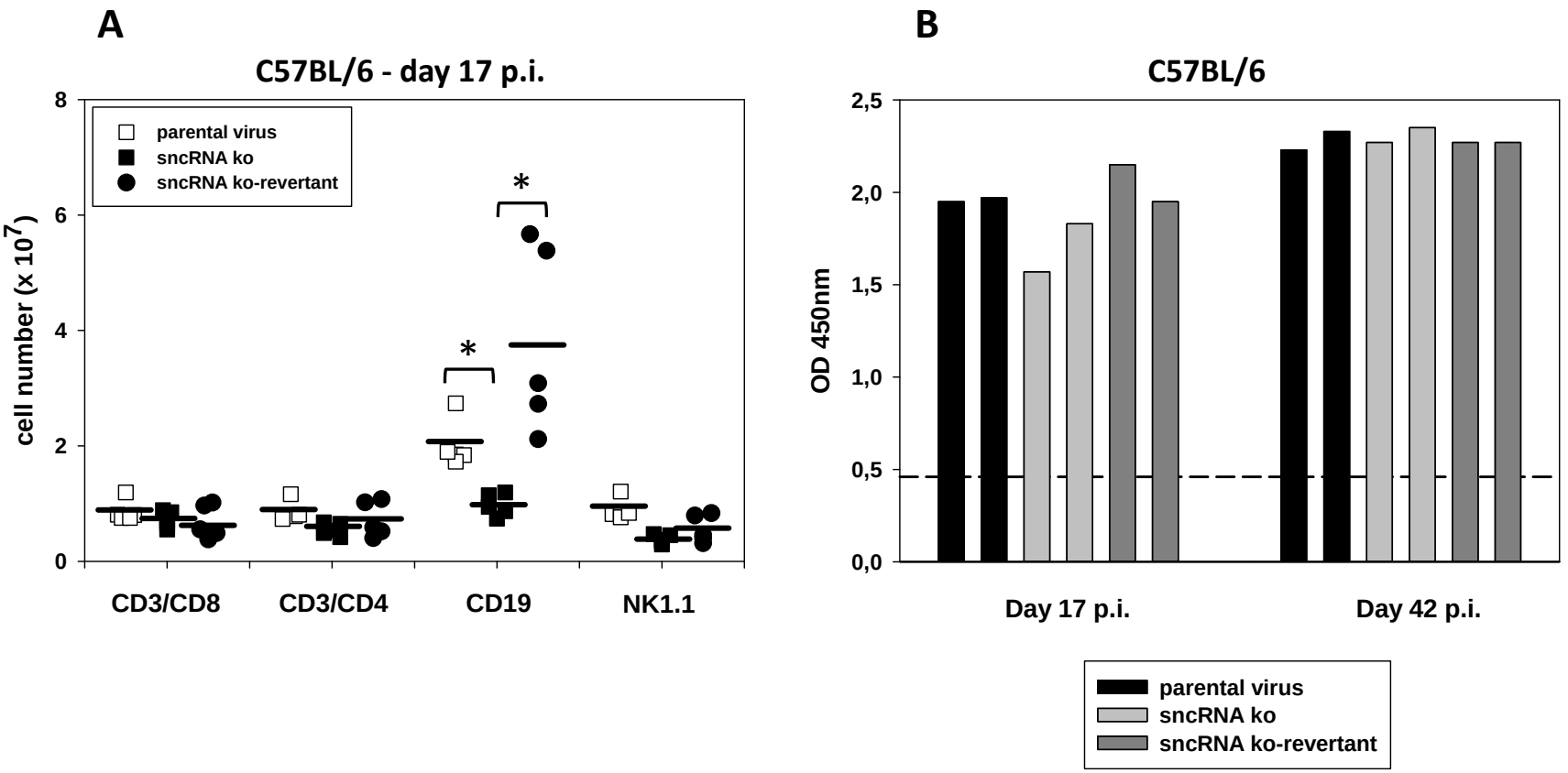

relative gene expression
1,2
1,0
0,8
0,6
0,4
0,2
0,0
M1
M2
M3
L8
parental virus
sncRNA ko
sncRNA ko-revertant

Supplementary Figure S1: Gene expression of neighbouring genes. Transcription of M1, M2 and M3 was determined 48 hours after infection by quantitative RT-PCR in NIH3T3 cells infected with the indicated viruses. Shown are means + SD of three biological replicates. L8 transcription was analyzed in parallel as a control.


mghv-miR-M1-1
mmu-miR-191
rRNA 5.8s
2e(-deltaCt) normalized to 5.8s
10^0
10^-1
10^-2
10^-3
10^-4
10^-5
10^-6
16
43
days post infection

Supplementary Figure S2: Expression of mghv-mir-M1-1 in vivo. RNA was extracted from splenocytes of mice infected with parental virus at the indicated time points after infection and subjected to stem-loop RT-qPCR as described in Materials and Methods. As a positive control, the expression of the cellular miRNA mmu-miR-191 is also shown. Data shown are means + SD (n=2).


A
C57BL/6 - day 17 p.i.
parental virus
sncRNA ko
sncRNA ko-revertant
cell number (x 10^7)
8
6
4
2
0
*
*
CD3/CD8
CD3/CD4
CD19
NK1.1
B
C57BL/6
OD 450nm
2,5
2,0
1,5
1,0
0,5
0,0
Day 17 p.i.
Day 42 p.i.
parental virus
sncRNA ko
sncRNA ko-revertant

Supplementary Figure S3: Analysis of the immune response after infection. Mice were inoculated i.n. with $5x10^4$ PFU of the indicated viruses. A) At day 17 after infection, spleens were harvested, and single splenocyte suspensions were prepared and analyzed by FACS analysis. Each symbol represents an individual mouse, and the bars represent the mean. The asterisks indicate a statistically significant difference: * P = 0.008 (Mann-Whitney Rank Sum test). B) At days 17 and 42 after infection, blood was collected, and MHV-68 specific antibodies in the sera were determined by ELISA. The dashed line indicates the limit of detection.