KO　　Kepi　Kepi　TNFR　TNFR

DPI　　4　　7　　4　　7

inflammation, stress response IFN response

NFkB cascade, immune cell activation

restriction of viral genome replication

IFN-γ response

granulocyte migration

muscle contraction, blood vessel size

T-cell receptor signaling

mitosis

muscle contraction, cell adhesion

mitosis

leukocyte activation

leukocyte apoptosis

general apoptosis
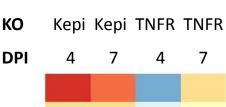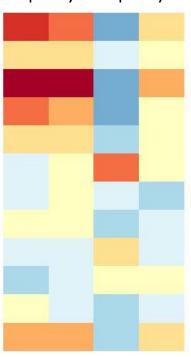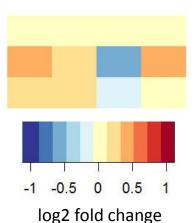
neutrophil apoptosis

inflammation

Fold changes in mut/WT in various functional categories.
Top section: expression data of mutant and WT mice from infection with SARS-CoV were analysed using hierarchical clustering; the functional content of these clusters was determined using functional enrichment analysis (same clusters as Figure 4). Fold changes were calculated from log2 fold change in WT subtracted from log2 fold changes in KO mouse. Bottom section: Genes were grouped for fold change analysis using selected GO terms instead of gene expression clusters. KO – indicates gene targeted in null mice, DPI – days post infection.

-1　-0.5　0　0.5　1

log2 fold change