

Supplemental figure 1

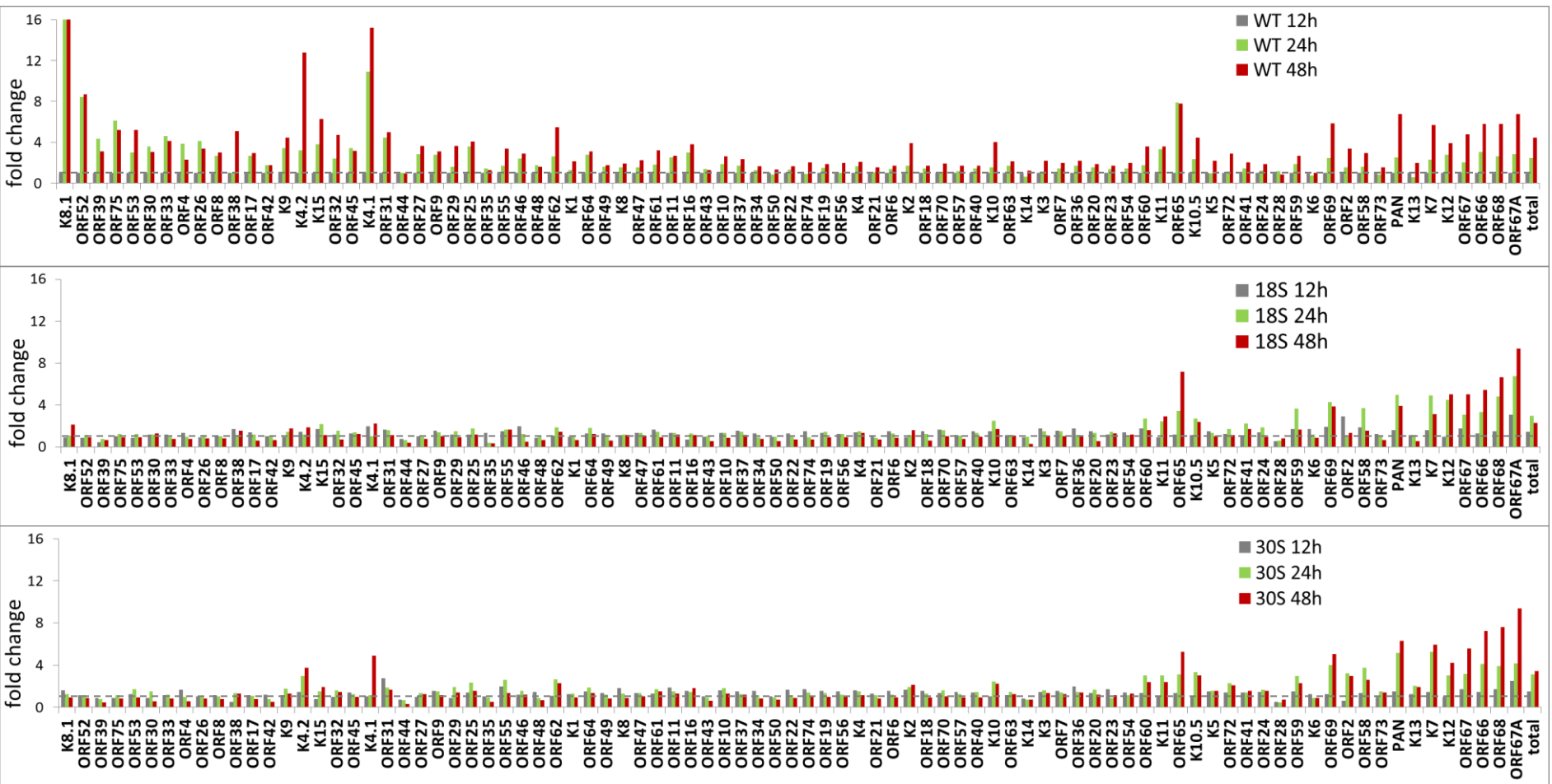


Fig. S1. Transcription profile of the WT and two mutants viruses during *de novo* infection. Counts of reads for each viral gene were first normalized against the total reads of each sample. The fold change of each gene was calculated by comparing to the transcript level of WT virus at 12 hr, indicated by a dash line in each graph.