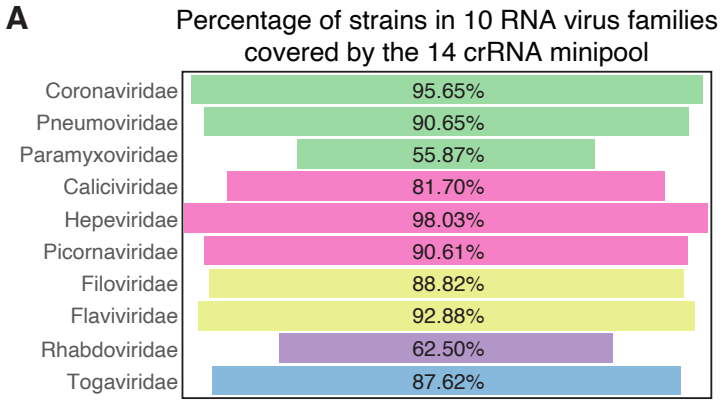
Cell Reports Medicine, Volume *2*

Supplemental information

A comprehensive analysis and resource to use CRISPR-Cas13 for broad-spectrum targeting of RNA viruses

Xueqiu Lin, Yanxia Liu, Augustine Chemparathy, Tara Pande, Marie La Russa, and Lei S. Qi



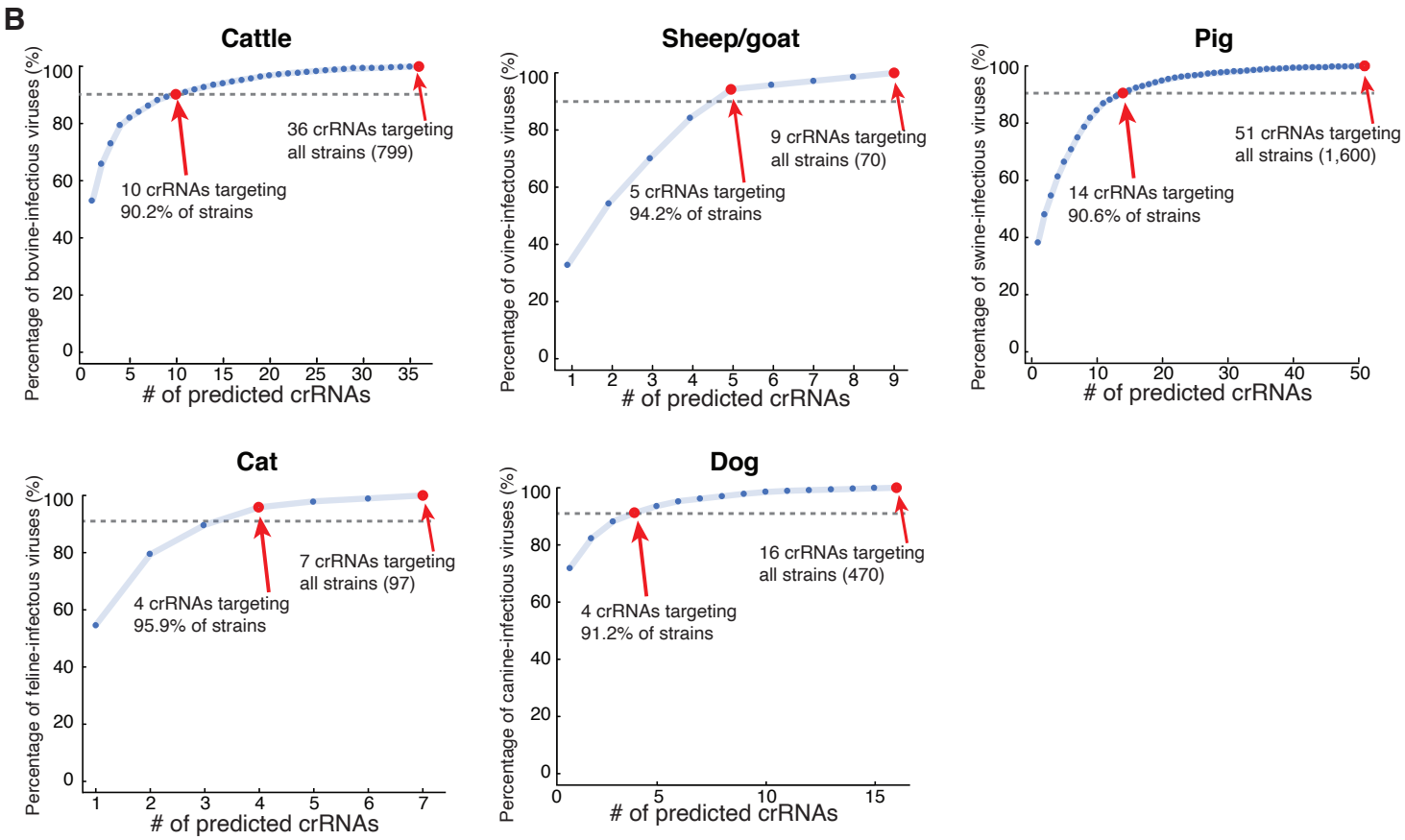


Figure S1. Analysis of crRNAs targeting broad-spectrum RNA viruses. Related to Figure 1.

A. Coverage of human-infectious strains in each of 10 RNA virus families by 14 minipool crRNAs.
B. Cumulative curves showing the predicted number of minipool crRNAs to target animal-infectious strains in 10 RNA virus families.

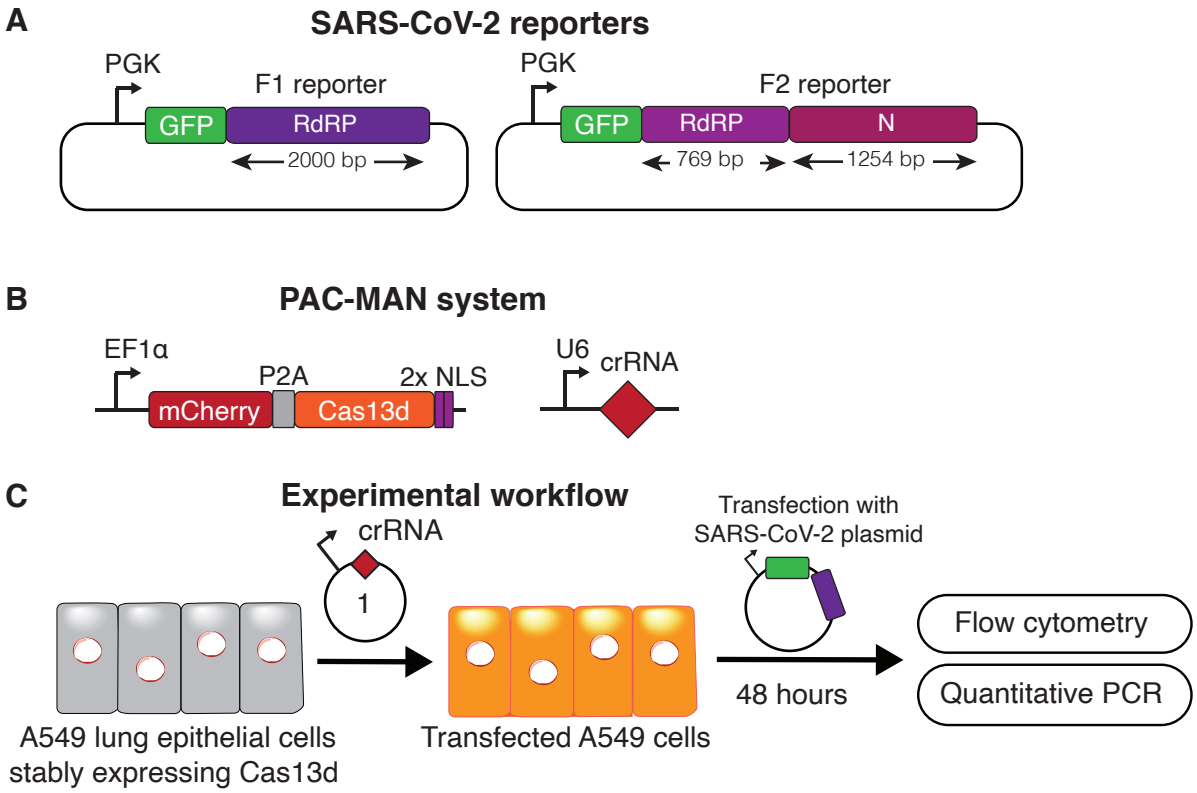


Figure S2. Schematics of experimental systems and workflow used to validate crRNAs. Related to Figure 4.

A. The SARS-CoV-2 reporters used in this study.
B. PAC-MAN expression system used in this study.
C. Workflow for quantifying all individual or combinatorial crRNAs for targeting SARS-CoV-2 sequences.

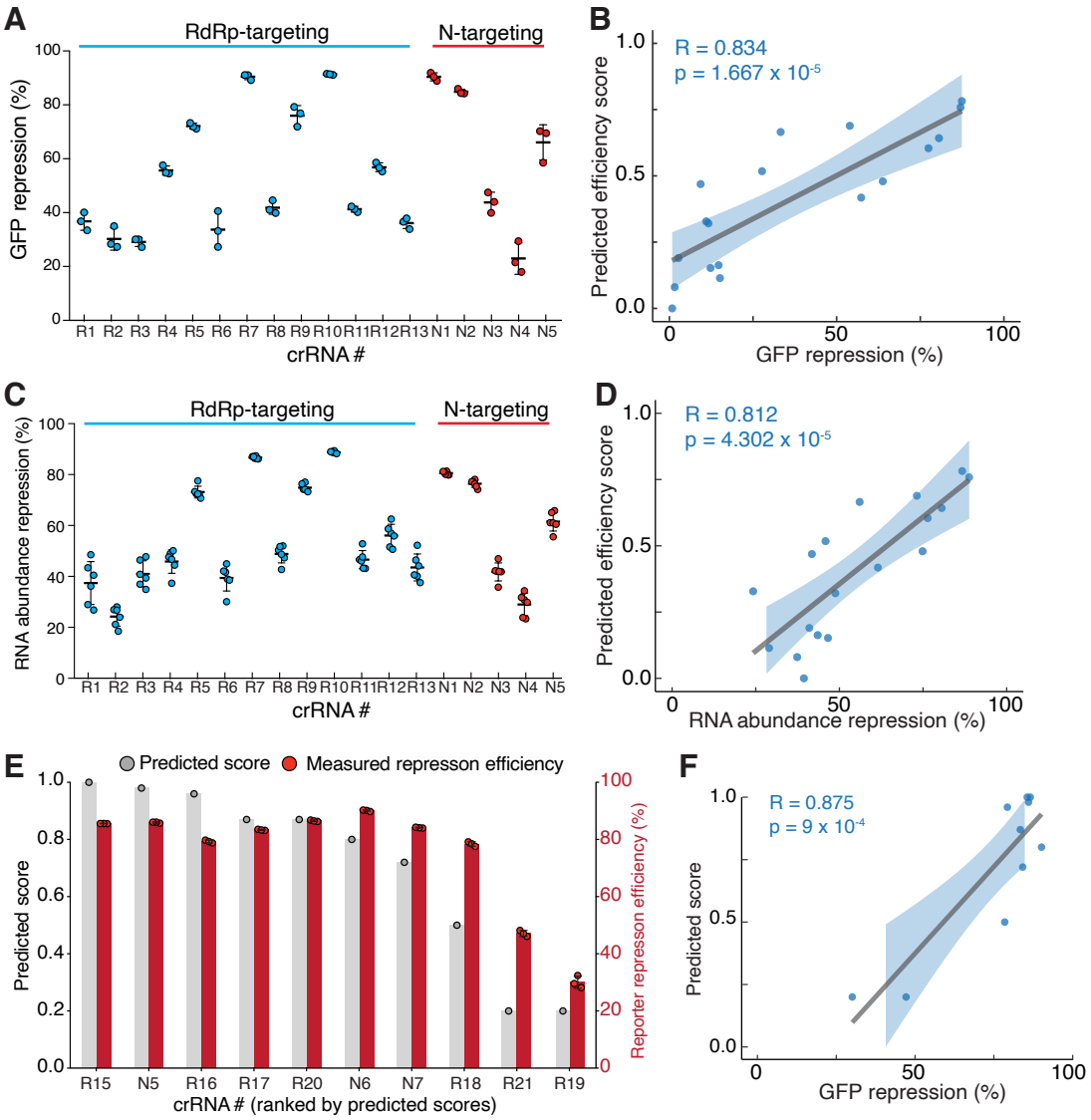


Figure S3. Validation of predicted crRNAs for targeting SARS-CoV-2 sequences. Related to Figure 4.

A. Repression on SARS-CoV-2 GFP reporter using the first batch of crRNAs measured by flow cytometry. p values related to reporter only samples for each group are included in Table S3. Lines indicate means; error bars indicate s.d. (n = 3 independent biological replicates).

B. Correlation between predicted efficiency score and SARS-CoV-2 GFP repression efficiency for the first batch of crRNAs.

C. Repression on SARS-CoV-2 reporter RNA abundance using the first batch of crRNAs measured by qPCR. RNA abundance is calculated by normalizing to the reporter only sample. p values related to reporter only samples for each group are included in Table S3. Lines indicate means; error bars indicate s.d. The data represent three independent biological experiments performed in technical replicates (n = 6).

D. Correlation between predicted efficiency score and RNA abundance repression efficiency for the first batch of crRNAs.

E. Comparison of repression on SARS-CoV-2 GFP reporter (red) and predicted efficiency scores (grey) using the second batch of crRNAs. p values related to reporter only samples for each group are included in Table S3. Lines indicate means; error bars indicate s.d. (n = 3 independent biological replicates).

F. Correlation between predicted efficiency score and SARS-CoV-2 GFP repression efficiency for the second batch of crRNAs.