**Virologica Sinica**

**Supplementary Data**

**Design of antiviral AGO2-dependent short hairpin RNAs**

Yuanyuan Bie a, b, c, Jieling Zhang a, b, d, Jiyao Chen a, b, Yumin Zhang a, b, Muhan Huang a, b, Leike Zhang a, b, c, Xi Zhou a, b, c, d\*,Yang Qiu a, b, c, d\*

a Key Laboratory of Virology and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, , Wuhan 430071, China

b State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China

c University of Chinese Academy of Sciences, Beijing 100049, China

d School of Life Sciences, Division of Life Sciences and Medicine, University of Science and Technology of China, Hefei 230027, China

\* Corresponding authors:Email addresses: zhouxi@wh.iov.cn (X. Zhou); yangqiu@wh.iov.cn (Y. Qiu)

ORCID: 0000-0001-5152-1242 (Y. Qiu); 0000-0002-3846-5079 (X. Zhou)

**Supplementary figs and tables**

****

**Figure S1. Transcriptome sequencing analysis of gene expressions in cells transfected with agshEV71-h1 and agshNC.** Human 293T cells were transfected with agshEV71-h1 and agshNC, respectively. At 24 h post transfection, total RNAs were extracted to perform RNA sequencing. Reads align to human genome (GRCh38) were annotated using htseq-count. Genes with counts per million reads (CPM) lower than 5 were excluded. Different expression genes (DEGs) were defined by |log2FC| > 1, P.adj < 0.05. Up-regulated DEGs were showed in red and down-regulated in blue.

**Supplementary Table S1. Feature matrix of siRNA used for model training**

**Supplementary Table S2. Scores of evaluated siRNA sequences targeting differernt viruses**

**Supplementary Table S3. The sequences of agshRNAs**

**Supplementary Table S4. Transcriptomic analysis of 293T cells transfected with agshEV71-h1 and agshNC**

**Supplementary Table S5. Profiles of small RNAs**

**Supplementary Table S6. Primers and probes used in this study**