

1 **SUPPLEMENTARY MATERIALS**

2 **MATERIALS AND METHODS**

3 **Generation of EV71-GFP**

4 The full-length cDNA clone for EV71 was constructed by PCR-based procedures.
5 Briefly, four fragments encoding EV71 nt 1-900 with a T7 promoter sequence, nt
6 848-3743, nt 3696-5808 and nt 5758-7405 linked with a T7 terminator were amplified
7 from EV71 cDNA. Fusion these four fragments into pWSK29 vector. Then linked the
8 EGFP sequence followed by the EV71 2A protease recognition sequence(-AITTL-)
9 (Yamayoshi et al., 2009), and inserted in reading frame between the 5'UTR and VP4.
10 The resulting construct was designated pWSK-EV71-GFP, which contained
11 full-length EV71 cDNA mixed with EGFP sequence, 52 poly T after 3'UTR, a T7
12 RNA promoter and a T7 terminator.

13 **Sequencing of the monoclonal antibody**

14 A part of the light chain was amplified by the V_κ primers 5'-GAYATTGTGMTSAC
15 MCARWCTMCA-3' and 5'-GGATACAGTTGGTGCAG CATC-3'. A part of the
16 heavy chain was amplified by the IgG2a primers 5'- SARGTNMAGCTGSAGSAGT
17 C-3' and 5'- CTTGACCAGGCATCCTAGAGTCA-3'. After sequencing these two
18 fragments, their sequences were compared with the existing sequences and designed
19 the primers 5'-ATGGTGTCCACTTCTCAGCTCCT-3', 5'-ATGGTCACAGCTTTC
20 CATTCA-3' and 5'-ACACTCATTCCTGTTGAAGCT-3' for the light chain
21 sequencing and the primers 5'- ATGGGATGGAGCTGGATCTTT-3', 5'-GTCCCGC

GGTAGTACCTCGTAT-3', and 5'-TTTATTTATACAAGGGATGCAT-3' for the heavy chain sequencing.

REFERENCES

Yamayoshi, S., Yamashita, Y., Li, J., Hanagata, N., Minowa, T., Takemura, T., and Koike, S. (2009). Scavenger receptor B2 is a cellular receptor for enterovirus 71. *Nature medicine* 15, 798-801.

Ye, J., Ma, N., Madden, T.L., and Ostell, J.M. (2013). IgBLAST: an immunoglobulin variable domain sequence analysis tool. *Nucleic acids research* 41, W34-40.

FIGURE LEGENDS

Figure S1

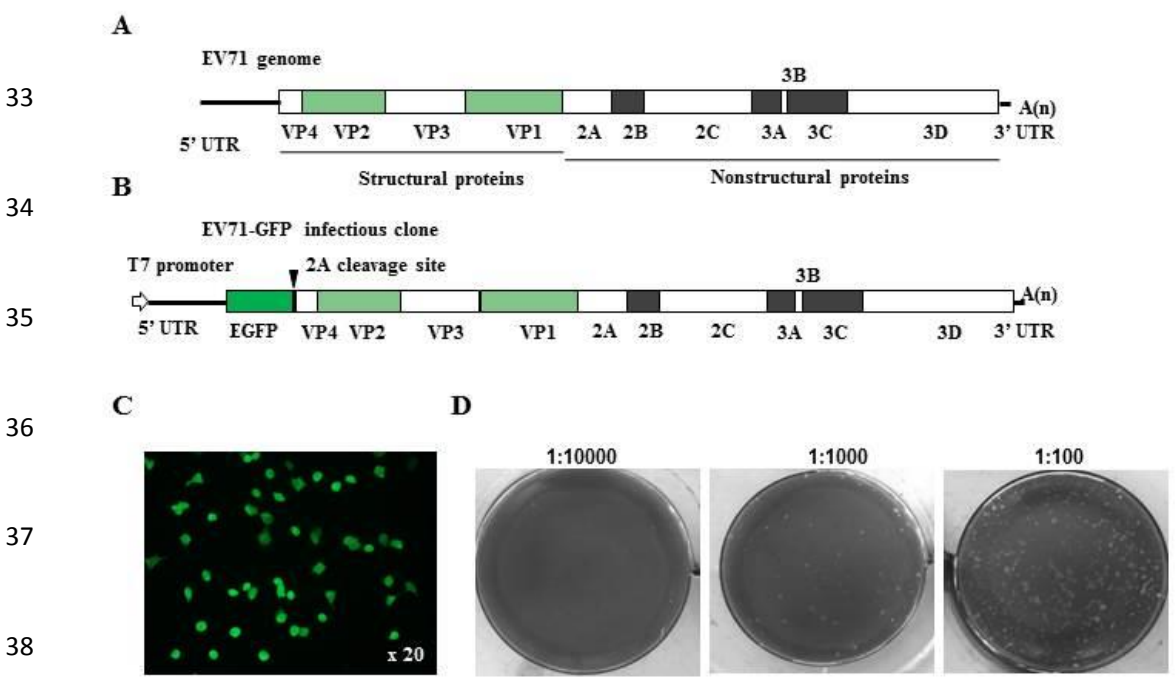
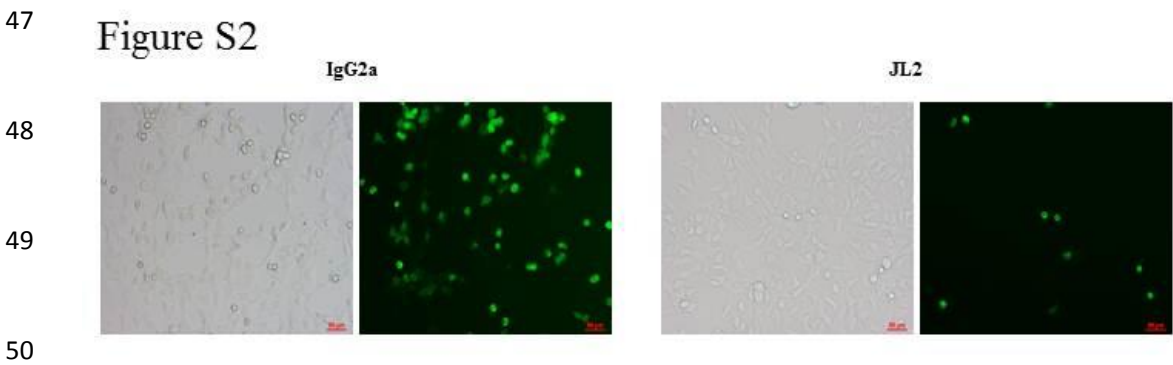
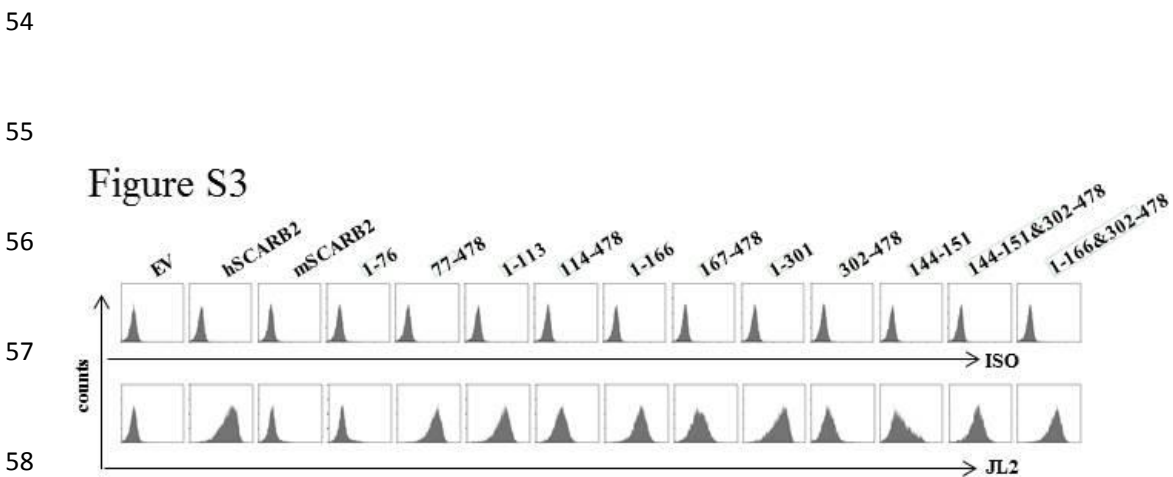


Figure S1. The establishment of the EV71-GFP recombinant virus A) A map of the wild-type EV71 genome (top panel) and the EV71-GFP genome (lower panel). The gene expression of GFP was inserted into the EV71 genome between 5'UTR and VP4 in the virus, and a 2A cleavage site was inserted following the EGFP gene to cut the protein from the poly-protein. The T7 promoter was added before 5'UTR, as it can

44 initiate transcription once recognized by T7 RNA polymerase. B) Fluorescence
 45 microscopic images (20x) of 293-hSCARB2 cells were infected with EV71-GFP. C)
 46 Plaques of 293-hSCARB2 cells were infected with EV71-GFP at different dilutions.



51 **Figure S2. JL2 can block EV71 infection.** Fluorescence microscopic images of
 52 293-hSCARB2 cells pretreated with 2 μ g/ml of JL2 (*right panel*) or mouse IgG2a as
 53 an isotype control (*left panel*) before EV71-GFP infection. Scale bars: 50 μ m.



59 **Figure S3. Binding site mapping of human SCARB2 to JL2.** Surface FACS
 60 staining of SCARB2 chimeras expressed on 293-SCARB2-KO cells by JL2 (2 μ g/ml).
 61 Matched isotype IgG2a was used as a control (*top panel*).

Figure S4

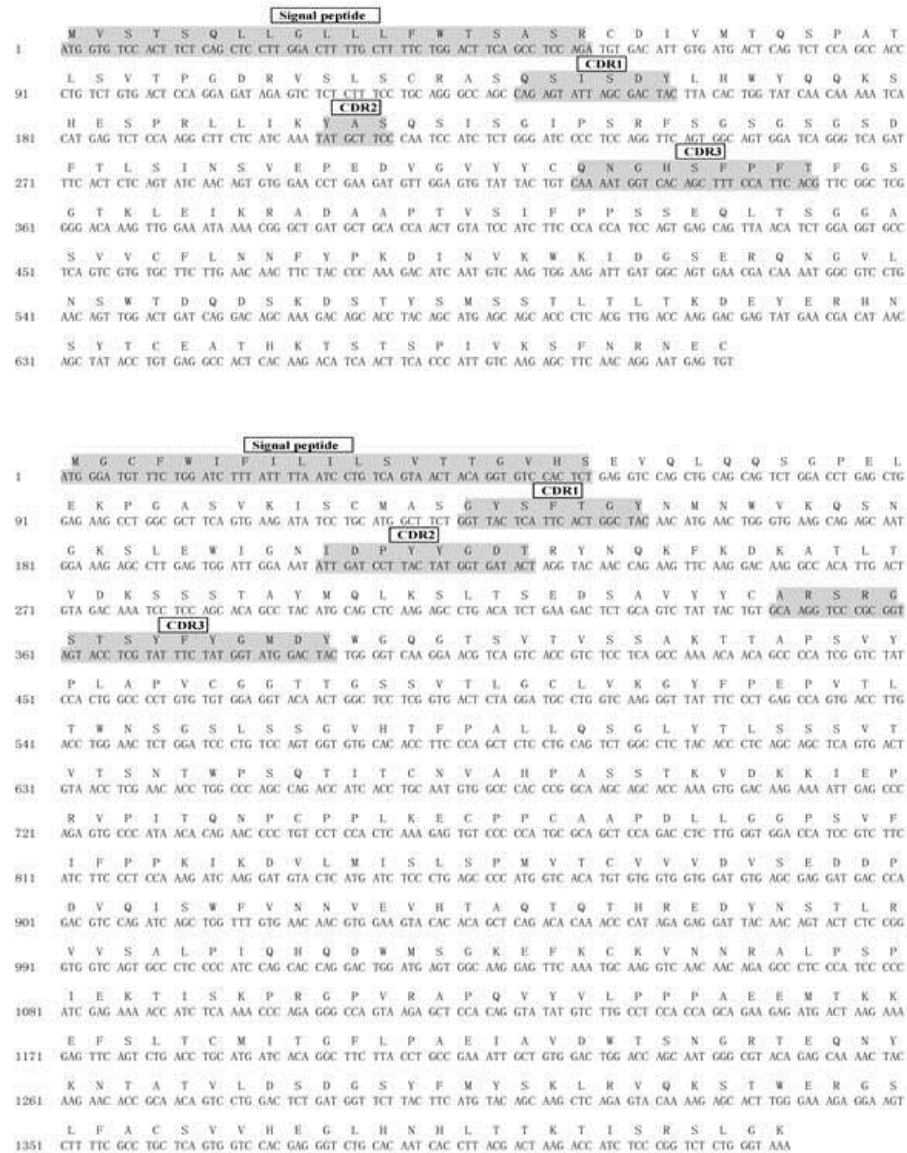


Figure S4. The sequence of JL2. The sequence of the light chain (*top panel*) and heavy chain (*lower panel*) of JL2. The signal peptides of the light chain, the heavy chain and the complementary determining regions (CDRs) are all shown in brown. CDRs are determined by NCBI IgBLAST (<https://www.ncbi.nlm.nih.gov/igblast/>) (Ye et al., 2013).

Figure S5

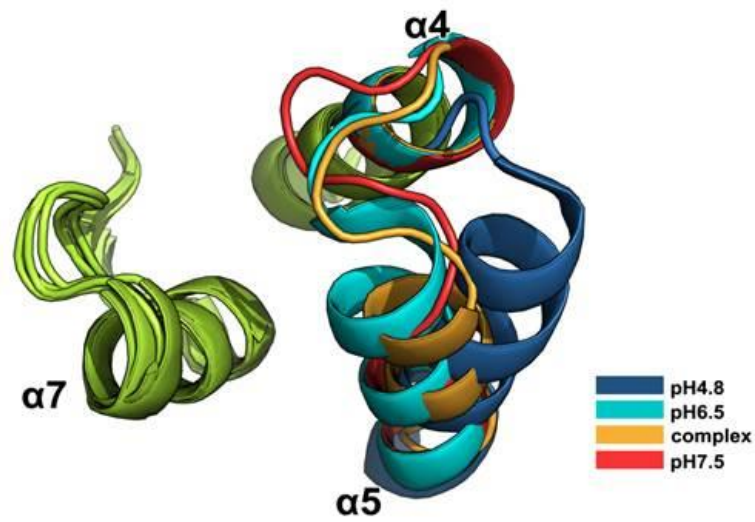


Figure S5. Structural comparisons of the helical bundle of SCARB2 at different pH values. Ribbon diagram showing the structural differences of the Domain III helical bundle at pH 7.5 (PDB code: 4TW2), pH 7.0 (from the complex model), pH 6.5 (PDB code: 4Q4B) and pH 4.8 (PDB code: 4TW0).