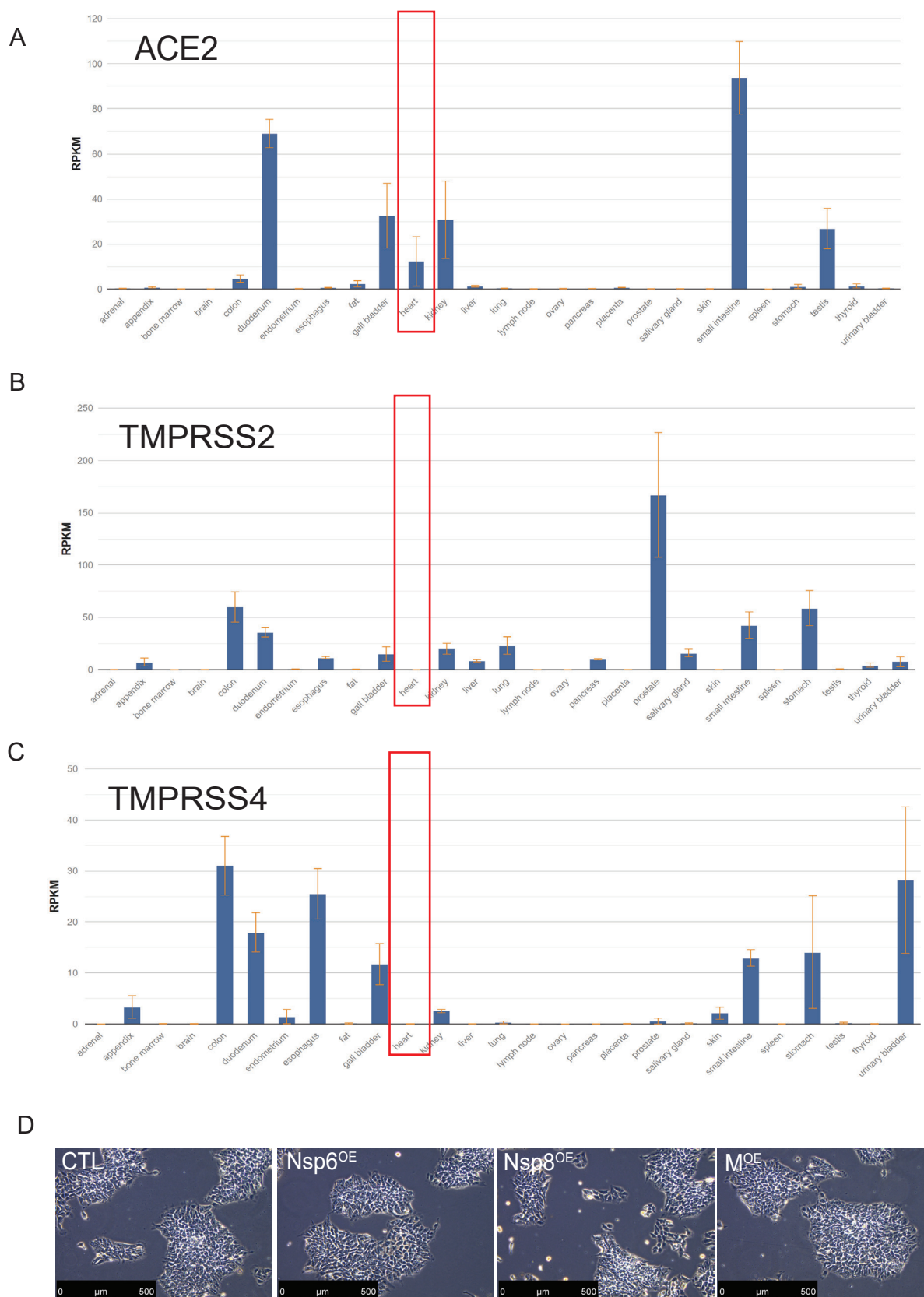
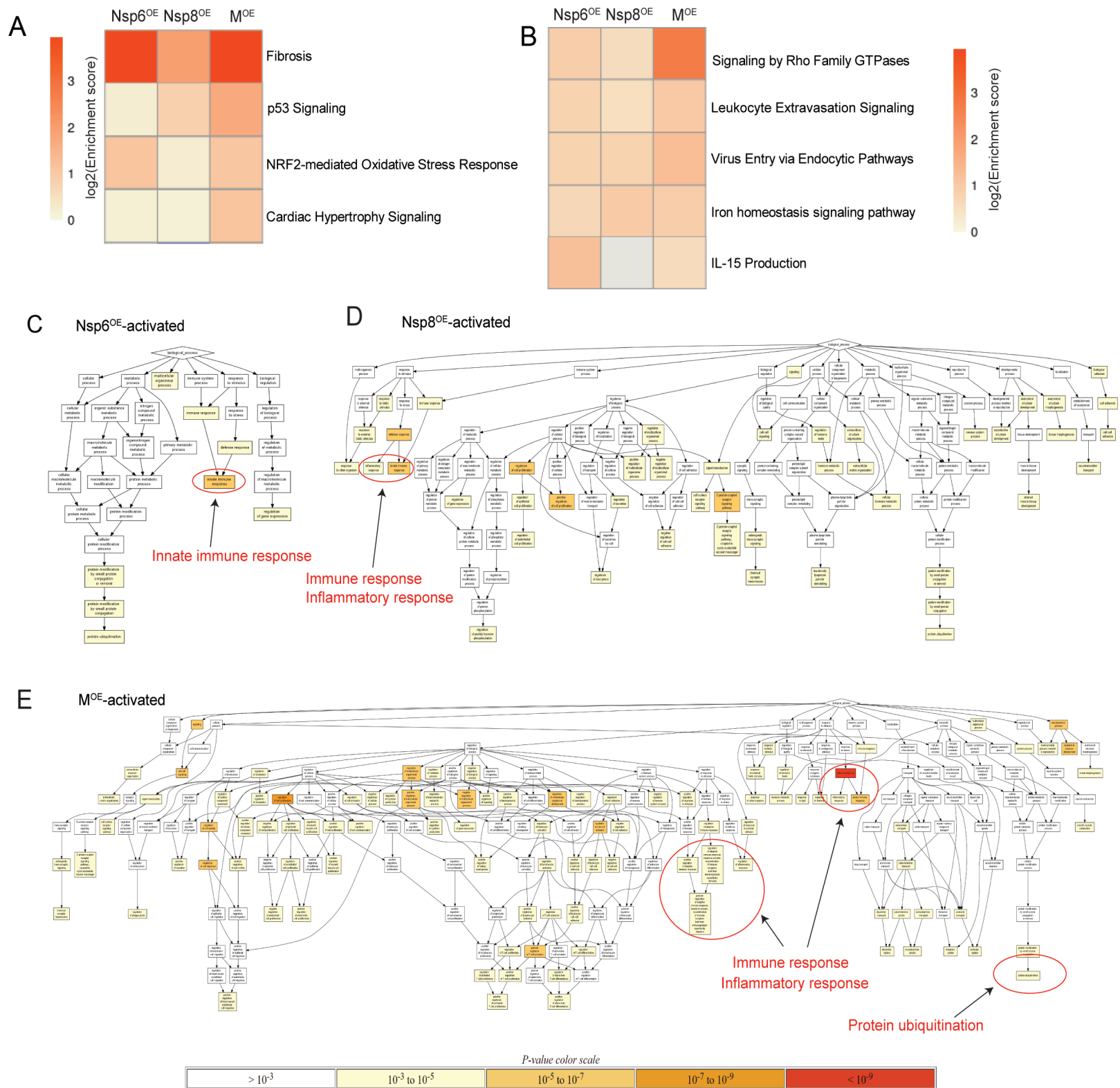




**Supplementary Figure S1. Expression of SARS-Cov-2 receptor genes in the human heart.**

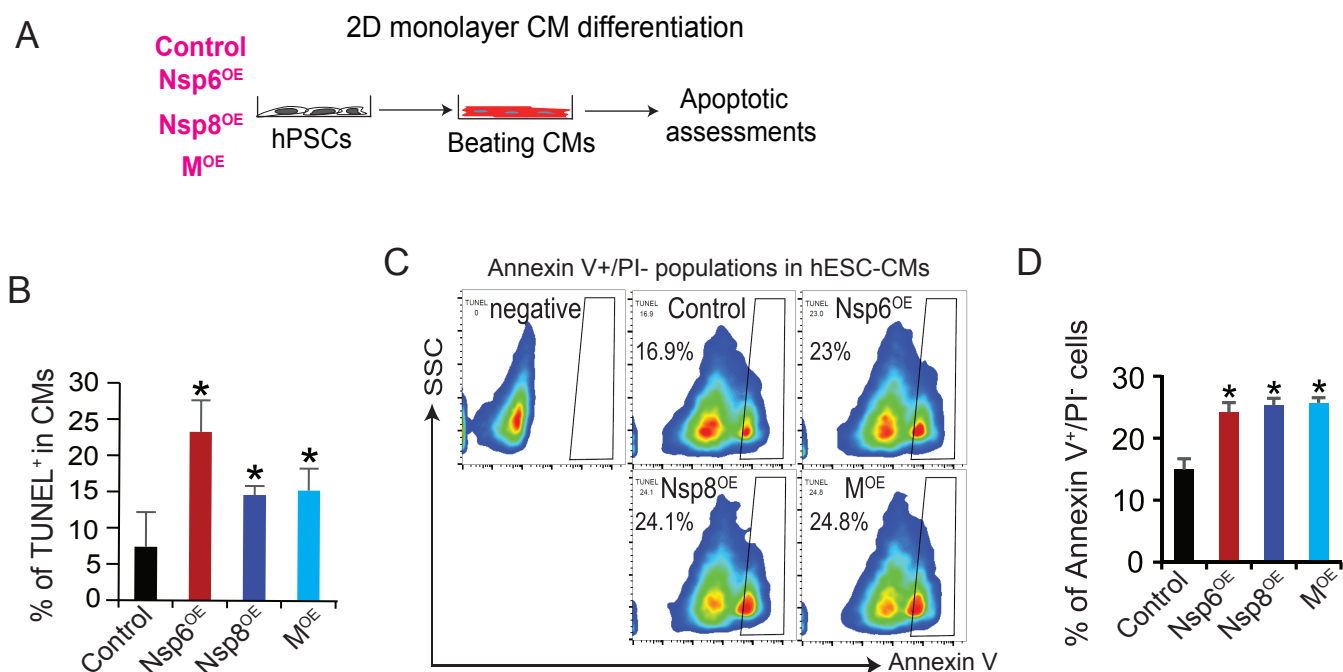
- (A) RNA expression level of ACE2 gene in adult human heart tissues from RNA-seq data (NCBI database).
- (B) RNA expression level of TMPRSS2 gene in adult human heart tissues from RNA-seq data (NCBI database).
- (C) RNA expression level of TMPRSS4 gene in adult human heart tissues from RNA-seq data (NCBI database).
- (D) Representative images of established control and Nsp6<sup>OE</sup>, Nsp8<sup>OE</sup> and M<sup>OE</sup> hESC lines.



## Supplementary Figure S2. GO analysis of DEGs in hESC-CMs.

(A-B) Signaling pathways activated by Nsp6<sup>OE</sup>, Nsp8<sup>OE</sup> and M<sup>OE</sup> in hESC-CMs.

(C-E) GO hierarchy activated by Nsp6<sup>OE</sup>, Nsp8<sup>OE</sup> and M<sup>OE</sup> in hESC-CMs.



**Supplementary Figure S3. Overexpression of SARS-CoV-2 genes induces cell death in hPSC-CMs.**

(A) Scheme of cardiomyocyte differentiation from hESCs in 2D monolayer conditions, followed by apoptotic assessments.

(B) Flowcytometry analysis of TUNEL<sup>+</sup> cells in hESC-CMs with overexpression of SARS-CoV-2 genes.

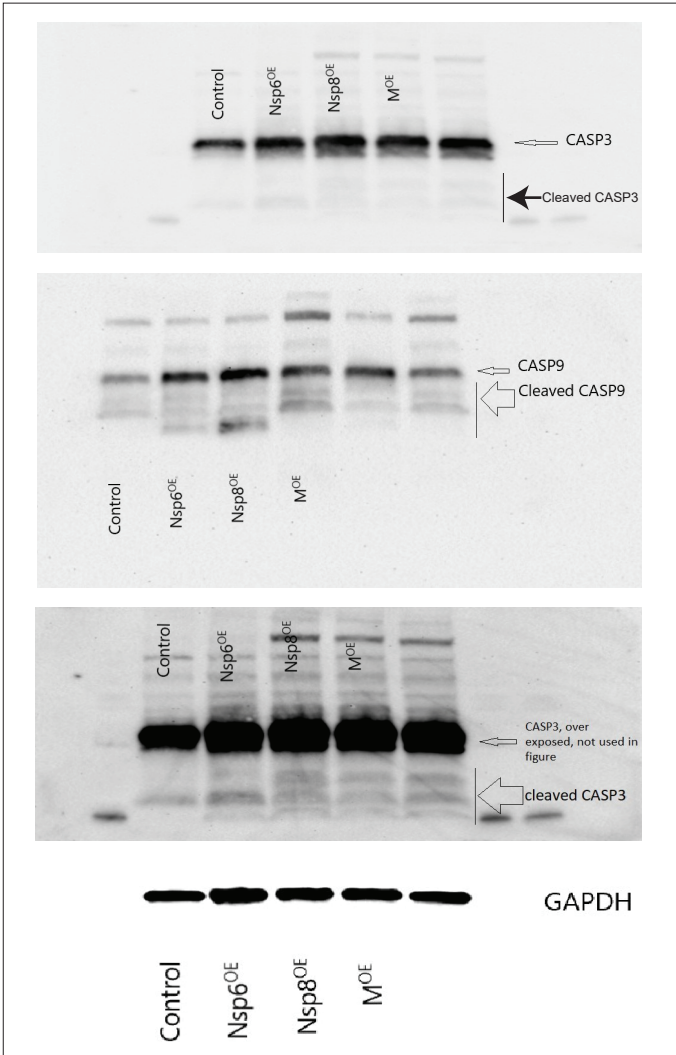
(C) Flowcytometry analysis of Annexin V<sup>+</sup>/PI<sup>-</sup> in hESC-CMs with overexpression of SARS-CoV-2 genes.

(D) Quantification results of (C).

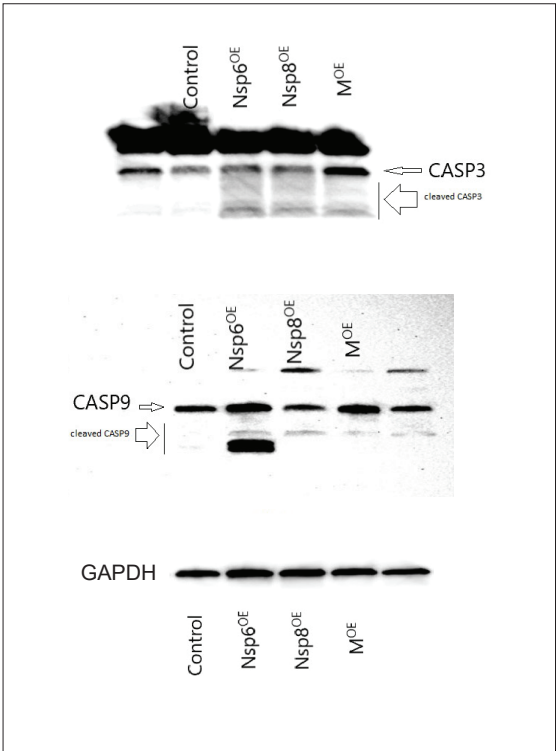
All error bars show mean ± SD of three independent experiments. \* $p < 0.05$ . (Student's  $t$ -test).

Supplementary Figure 4

A



B



**Supplementary Figure 4.**  
Original images of Western Blotting  
for Figure 4M in (A), Figure 4N in (B) and Figure 5L in (C).

C

