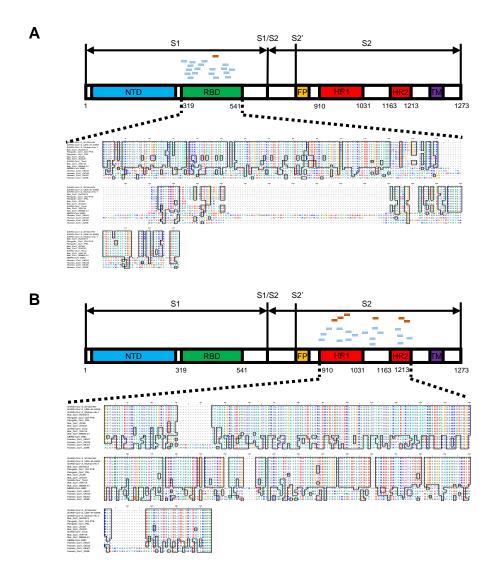
## **Supplemental Information**

Nanoparticle Vaccines Based on the Receptor Binding Domain (RBD) and Heptad Repeat (HR) of SARS-CoV-2

**Elicit Robust Protective Immune Responses** 

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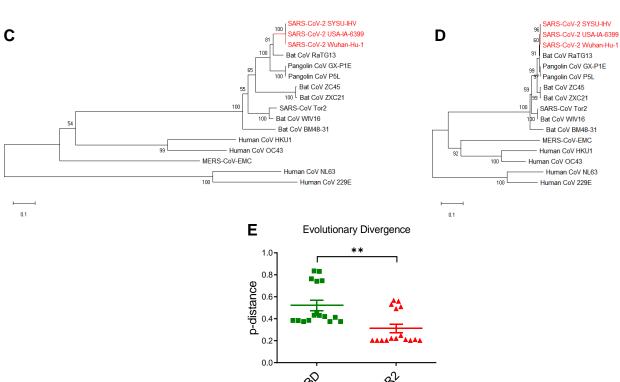


Figure S1. Related to Figure 1. Homology Analysis of RBD and HR among Coronaviruses

(A-B) Homology analysis of RBD and HR among coronaviruses which contained three SARS-CoV-2 strains (SYSU-IHV, USA-IA-6399 and Wuhan-Hu-1), six human pathogenic coronaviruses (SARS-CoV Tor2, MERS-CoV EMC, hCoV-HKU1, hCoV-OC43, hCoV-NL63 and hCoV-229E), five bat coronaviruses, and two pangolin coronaviruses. The alignments of sequences were built by using ClustalW method. All ambiguous positions were removed for each sequence pair. Orange and light blue bars within each schematic represented CD8<sup>+</sup> and CD4<sup>+</sup> T cell epitopes respectively. (C-D) The evolutionary history was inferred using the Neighbor-Joining method based on the protein sequences located in the regions of RBD:319-541(aa) (A) and HR1-HR2:910-1213(aa) (B) from the coronavirus Spike gene. The percentage of replicate trees in which the associated strains clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. (E) The average genetic distance between one given strain and the relevant entire population in the coronavirus phylogenetic tree was calculated using the p-distance method. The evolutionary analyses were performed in MEGA X software. Moreover, the two-tailed Mann-Whitney U-test was conducted with Prism 8.0 software for comparing the evolutionary divergence between the regions of RBD and HR1-HR2. Experiments were conducted independently in triplicates. Data represented as mean  $\pm$  SEM (n=16). P-Value was calculated by two-tailed Mann-Whitney *U*-test. \*\*p < 0.01.

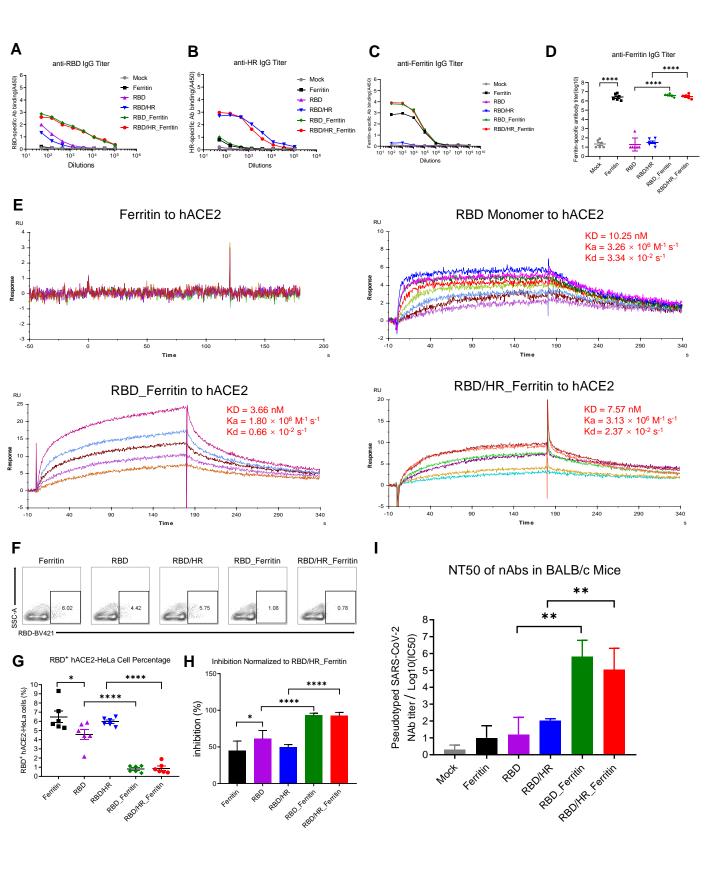
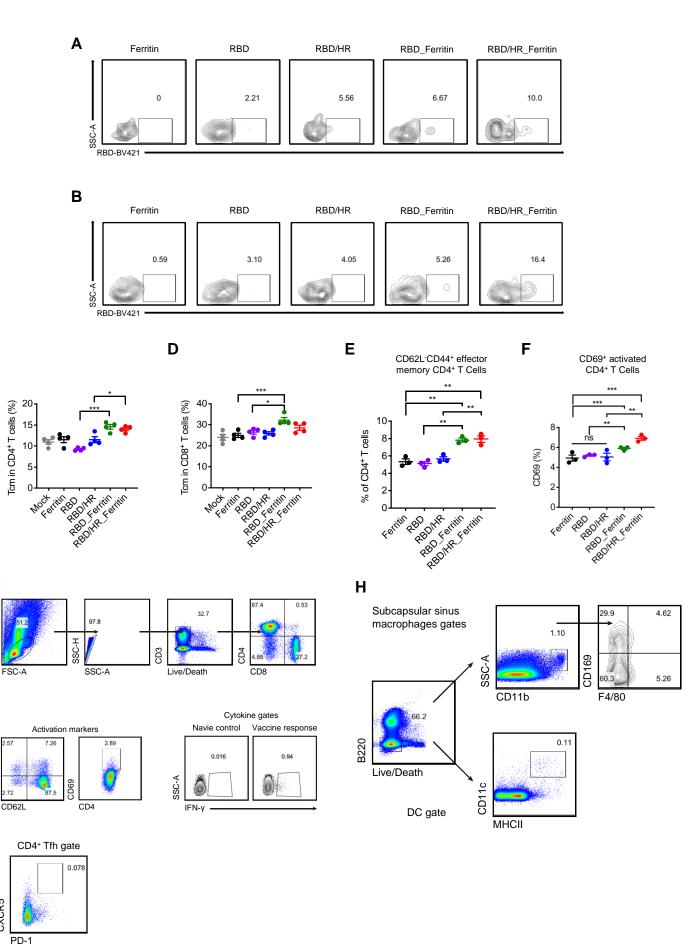


Figure S2. Related to Figure 2. Humoral Immune Responses in Nanoparticles Vaccinated BALB/c Mice

(A-B) SARS-CoV-2 RBD- and HR-specific IgG titers of immunized BALB/c mice at week 6 were detected by ELISA. IgG antibody titers of serum were determined by serial dilution. (C-D) H. pylori ferritin-specific IgG titers of immunized BALB/c mice at week 6 were detected by ELISA and further determined by serial dilutions. The titers were represented as the reciprocal of the endpoint serum dilution (n=6). (E) Representative BIAcore plots of Ferritin, RBD monomer, RBD Ferritin and RBD/HR Ferritin bound to hACE2. The Ka, Kd, and KD values were calculated by the software BIAevaluation. The KD value shown was a mean of three independent experiments. (F) Serum inhibition of SARS-CoV-2 RBD binding to hACE2-HeLa cells among different groups of immunized BALB/c mice were analyzed by flow cytometry. RBD proteins were tagged by BV421. (G-H) Serum of different mice mediated RBD blocking was represented by both the percentages of RBD<sup>+</sup> hACE2-HeLa cells (G) and corresponding inhibition normalized to RBD/HR-Ferritin (H) (n=6). (I) Groups of serially diluted serum were detected for neutralizing antibody against pseudotyped SARS-CoV-2. Data represented NT50 of nAbs in each group. Experiments were conducted independently in triplicates. Data represented as mean  $\pm$  SEM. Adjusted p-Values were calculated by one-way ANOVA with Tukey's multiple comparisons test. \*p < 0.05, \*\*p < 0.01, \*\*\*\*p < 0.001, \*\*\*\*p < 0.0001.



C

G

Figure S3. Related to Figure 2, Figure 3 and Figure 4. B and T Cell Immune Responses, Antigen Presentation and T/B Coordination

(A-B) Representative flow cytometry plots of RBD-specific IgG1 and IgG2b memory B cells. (C-D) The percentage of CD4<sup>+</sup> and CD8<sup>+</sup> central memory T cells which were isolated from spleen of 10 weeks-immunized mice were analyzed by flow cytometry (n=4). (E-F) The percentage of CD62L<sup>-</sup>CD44<sup>+</sup> and the percentage of CD69<sup>+</sup> cells within CD4<sup>+</sup> T cells, which were isolated from spleen of 10-days immunized mice were analyzed by flow cytometry (n=3). (G) Gating strategy for activation marker staining and intracellular cytokine staining in CD8+ and CD4+ T cells. Activation marker were displayed. CD8<sup>+</sup> or CD4<sup>+</sup> T cells as indicated. Intracellular cytokine gating examples are spleen from a naïve mouse and a representative CD8<sup>+</sup> T cell cytokine response to antigens. (H) Gating strategy for DC and macrophage. Inguinal LNs were digested into single cells, B220 non-B cells were identified into two distinct populations: CD11chiMHCII+DCs, and CD11b+F4/80-CD169+ subscapular sinus macrophages. Experiments were conducted independently in triplicates. Data represented as mean ± SEM. Adjusted p-Values were calculated by one-way ANOVA with Tukey's multiple comparisons test. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001.

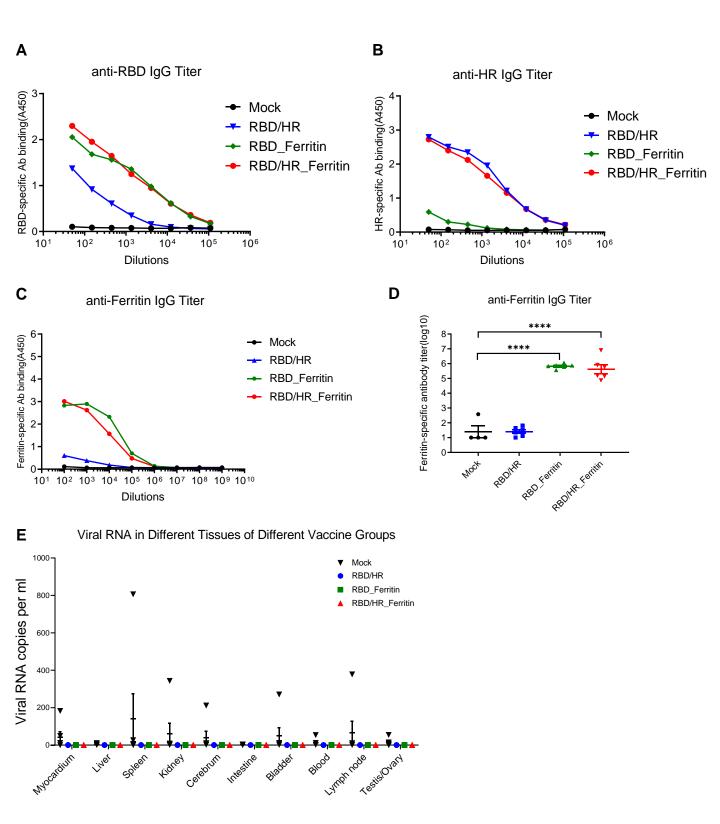


Figure S4. Related to Figure 6. Protection of Nanoparticle Vaccines against SARS-CoV-2 in hACE2 Mice

(A-B) SARS-CoV-2 RBD- and HR-specific IgG titers of immunized hACE2 mice at week 6 were detected by ELISA. IgG antibody titers of serum were determined by serial dilution. (C-D) *H. pylori*. Ferritin-specific IgG titers of immunized hACE2 mice at week 6 were detected by ELISA and further determined by serial dilutions. The titers were represented as the reciprocal of the endpoint serum dilution. (E) Viral RNA copies in different tissues of each mice were determined by qRT-PCR and plotted as copies per ml. Experiments were conducted independently in triplicates. Data represented as mean ± SEM (n=4 for mock, n=6 for RBD/HR, RBD nanoparticle and RBD/HR nanoparticle groups). Adjusted p-Values were calculated by one-way ANOVA with Tukey's multiple comparisons test. \*\*\*\*p < 0.0001.

Α

## Figure S5. Related to Figure 6. Histopathological Analysis of Different Tissues of Vaccinated Mice

(A) HE staining of different tissues of vaccinated mice. Tissues contained myocardium, liver, spleen, kidney, cerebrum, intestine, bladder, lymph node, and testis or ovary. Scale bars represented 20  $\mu$ m.

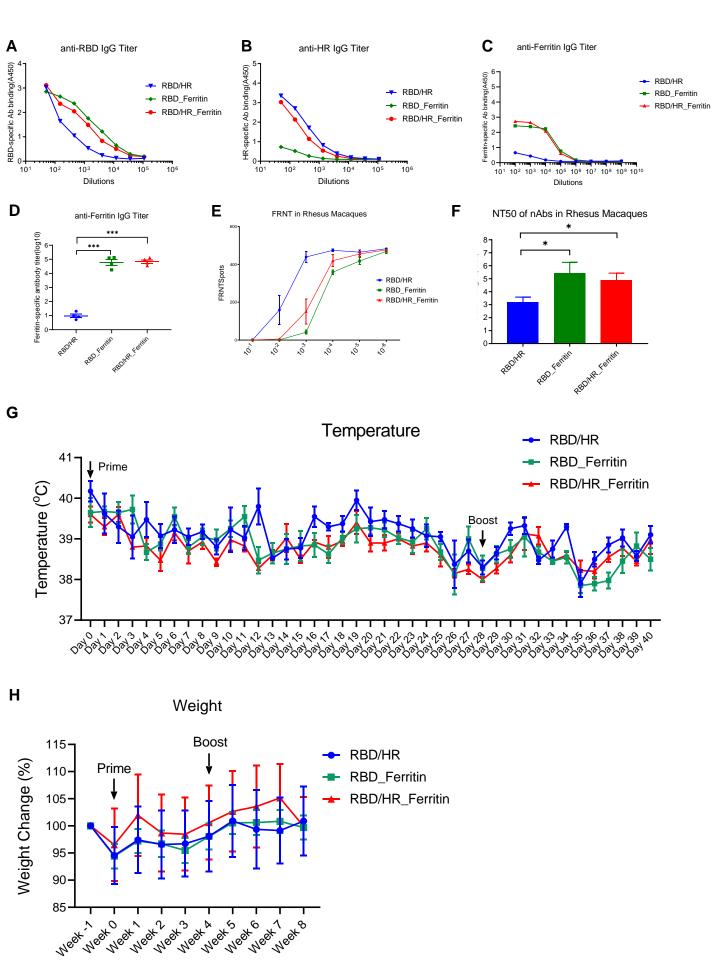


Figure S6. Related to Figure 7. The Immunogenicity of Nanoparticle Vaccines in Rhesus Macaques

(A-B) SARS-CoV-2 RBD- and HR-specific IgG titers of immunized rhesus macaques at week 6 were detected by ELISA. IgG antibody titers of serum were determined by serial dilution. (C-D) Ferritin-specific IgG titers of immunized monkeys at week 6 were detected by ELISA and further determined by serial dilutions. The titers were represented as the reciprocal of the endpoint serum dilution. (E) Serial dilutions of serum were analyzed by FRNT for neutralizing authentic SARS-CoV-2. (F) Groups of serially diluted serum were detected for neutralizing antibody against pseudotyped SARS-CoV-2. Data represented NT50 of nAbs in each group. (G) Body temperatures of each monkey across the whole prime/boost vaccination period. (H) Body weights of each monkey were measured every week. Experiments were conducted independently in triplicates. Data represented as mean  $\pm$  SEM (n=4). Adjusted p-Values were calculated by one-way ANOVA with Tukey's multiple comparisons test. \*p < 0.05, \*\*\*\*p < 0.001.

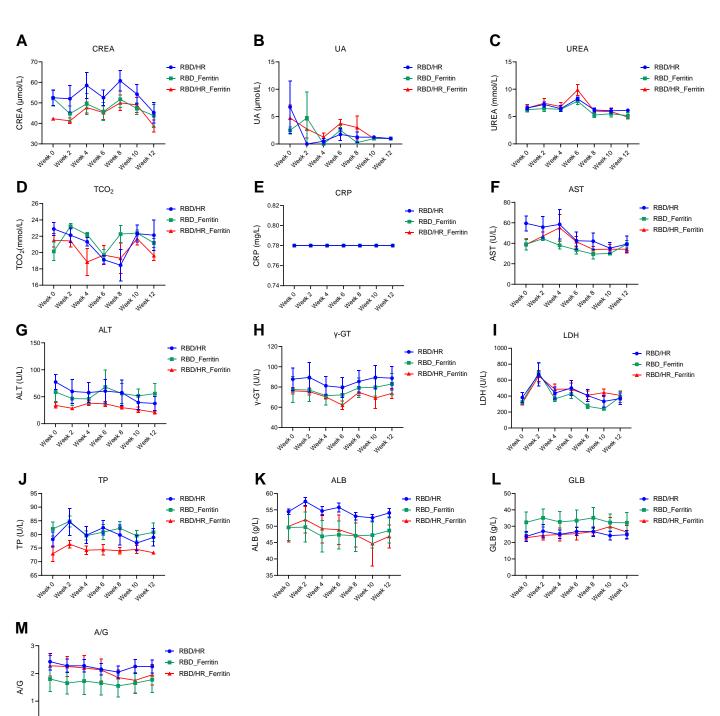


Figure S7. Related to Figure 7. Blood Biochemical Indexes of Each Vaccinated Monkey

(A-M) Blood biochemical indexes of each vaccinated monkey. The parameters contained the concentrations of creatinine (CREA), uric acid (UA), blood urea (UREA), total CO<sub>2</sub> (TCO<sub>2</sub>), C-reactive protein (CRP), aspartate aminotransferase (AST), alanine aminotransferase (ALT), γ-glutamyl transpeptidase (γ-GT), lactate dehydrogenase (LDH), total protein (TP), albumin (ALB), globulin (GLB) and albumin/globulin ratio (A/G). Blood biochemical analysis was conducted every two weeks.