

Supplementary Material

Table S1. The mPlex-CoV assay panel with pandemic and seasonal human coronavirus (HCoVs)

| Protein | Type | Coronavirus | Abbreviation |
|----------------------------------|-------------------------------|-------------|--------------|
| S Protein | SARS-CoV-2 | SARS2 | |
| | batRaTG | RaTG | |
| | SARS-CoV-1 | SARS1 | |
| | hCovOC43 | OC43 | |
| | hCovHKU1 | HKU1 | |
| | hCov229E | 229E | |
| | hCovNL63 | NL63 | |
| N Protein | SARS-CoV-2 | SARS2 | |
| | batRaTG | RaTG | |
| | SARS-CoV-1 | SARS1 | |
| | hCovOC43 | OC43 | |
| | hCovHKU1 | HKU1 | |
| | hCov229E | 229E | |
| | hCovNL63 | NL63 | |
| S protein subunits of SARS-CoV-2 | | | |
| Item | Name | Cat # | Abbreviation |
| SARS-CoV-2 | RBD (receptor binding domain) | 40592-V08H | RBD* |
| | S1 | 40591-V08H | S1* |
| | S2 | 40590-V08B | S2* |

*: products purchased from Sino Biological company.

Table S2. The prevalence rate of common cold human Coronavirus in the pre-COVID cohort

| HCoVs Strains | Viral protein | Pre-COVID (N=188) | 2-3 year-old ¹ (N=11) | Cutoff value (MFI) ^b |
|------------------|------------------|-------------------------------|----------------------------------|------------------------------------|
| | | Percentage* (Subjects (n))** | | |
| OC43 | S | 92.63(174) | 63.64 (7) | 3117 |
| HKU1 | | 67.02(126) | 18.18 (2) | 977 |
| 229E | | 93.61(176) | 27.27 (3) | 785 |
| NL63 | | 87.23(164) | 18.18 (2) | 375 |
| OC43 | N | 53.19(100) | 18.18 (2) | 734 |
| HKU1 | | 68.09(128) | 9.09(1) | 524 |
| 229E | | 16.49(31) | 0 (0) | 1488 |
| NL63 | | 54.79(103) | 0 (0) | 354 |

*: The positive percentage rates

**: The number of positive subjects in the cohort

b: infants <12 months old (n=16) to formed cutoff values to establish the positive/negative thresholds. The MFI cutoff values are 6 standard deviations of the means of all negative samples.

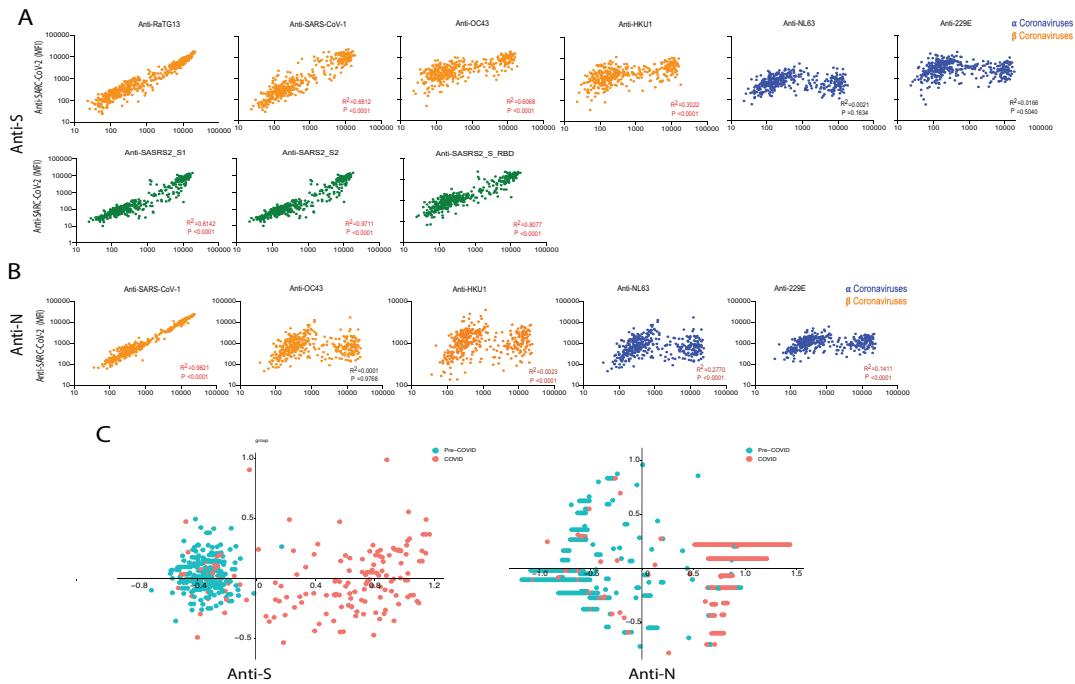


Fig. S1. The correlation of anti-HCoVs with anti-SARS-CoV-2(SARS2) IgG antibodies. Including both pre-COVID ($n=188$) and COVID-19 cohort ($n=155$). The mean IgG antibody MFI unit of individual HCoV strain was used if there were more than two longitude samples of same subject to avoid bias. A. The correlation of anti-S IgG antibodies of HCoVs with the those against the SARS2 virus. The individual antibody level against each HCoV virus (x-axis) is plot with the SARS2 antibody level (y-axis) from same subjects. The Pearson correlation analysis was applied, and the R square and P values were showed. The correlation is statistical significant ($P<0.001$) showed in red. B. The correlation of anti-N IgG antibodies of HCoVs with the SARS2 virus. C. Multidimensional Scaling (MDS) analysis of the S and N reactive antibodies against HCoVs strains. We performed immune repertoire cartography using the Pearson correlation distance to project multidimensional IgG concentration results for each subject onto 2 dimensions, reflecting the overall relative immune anti-HCoV spike (S)- or nucleocapsid (N)-protein IgG repertoire.