Supplementary Figure 1. ELISA screen of individual COVID-19 patient sera across the SARS-CoV-2 and SARS-CoV spike protein library. Sera of COVID-19 (n=6) and recalled SARS (n=5) patients at 1:1000 dilution were subjected to peptide-based IgG ELISA using pools of 5 peptides covering the entire S proteins of SARS-CoV-2 or SARS-CoV in duplicates. Sera of pooled healthy donors (n=13) were assessed in parallel. Data is presented as mean patient OD values subtracted of healthy control value are presented, negative values are plotted as zero. (a) Recalled SARS sera on SARS-CoV-2, (b) COVID-19 sera on SARS-CoV and (c) Recalled SARS sera on SARS-CoV. Source data are provided as a Source Data File.
**Supplementary Table 1**: Details of six COVID-19 patients individually screened against SARS-CoV-2 and SARS-CoV linear B-cell libraries

| Patient ID | Sex | Age | Serum collection time (days post disease onset) |
|------------|-----|-----|------------------------------------------------|
| 2          | M   | 35  | 17                                              |
| 5          | M   | 41  | 15                                              |
| 6          | F   | 47  | 15                                              |
| 7          | F   | 53  | 27                                              |
| 8          | M   | 51  | 23                                              |
| 9          | M   | 56  | 30                                              |
**Supplementary Table 2**: Demographics and clinical characteristics of 41 COVID-19 patients

| Demographics | Patients (n = 41) |
|--------------|------------------|
| Age, years   | 43 (11)          |
| Sex, male (%)| 25 (61)          |
| Ethnicity (Chinese) | 39 (95) |
| Any comorbidity (%) | 10 (24) |
| Diabetes     | 2 (4.9)          |
| Hypertension | 5 (12.2)         |

**Baseline vital signs at presentation**

| Vital sign                              | Value               |
|-----------------------------------------|---------------------|
| Temperature, °C                         | 37.5 (1.0)          |
| Heart rate, beats per minute            | 91.2 (18.2)         |
| Respiratory rate, per minute            | 18.5 (1.9)          |
| Systolic blood pressure, mmHg           | 130.6 (18.5)        |
| Pulse oximeter oxygen saturation (%)   | 97.6 (2.6)          |

**Baseline laboratory investigations**

| Test                        | Value       |
|-----------------------------|-------------|
| White blood cells, x10^9/L  | 5.0 (1.9)   |
| Hemoglobin, g/dL            | 13.8 (1.4)  |
| Platelet, x10^9/L           | 195.3 (66.0)|
| Lymphocyte, x10^9/L         | 1.3 (0.6)   |
| Neutrophil, x10^9/L         | 3.1 (1.8)   |
| CRP, mg/L                   | 32.0 (60.0) |
| LDH, U/L                    | 497.0 (232.0)|
| Creatinine, µmol/L          | 68.2 (15.2)  |
| ALT, U/L                    | 34.7 (26.6)  |

**Outcome**

| Outcome                          | Value       |
|----------------------------------|-------------|
| Pneumonia with abnormal chest X ray (%) | 15 (36.6)   |
| Require supplemental oxygen (%)  | 8 (19.5)    |
| ICU care (%)                     | 4 (9.8)     |

Categorical variables are shown as frequency (%)
Continuous variables are shown mean (SD)
SD: Standard deviation; CRP: C-reactive protein; LDH: Lactate Dehydrogenase; ALT: Alanine Aminotransferase; ICU: intensive care unit
## Supplementary Table 3: List of sequences of individual SARS-CoV-2 spike peptides tested

| Pool ID | Peptide ID | Virus    | Spike protein coordinates | Peptide sequence (linker) |
|---------|------------|----------|---------------------------|---------------------------|
| S14     | P1         | SARS-CoV-2 |                            | SGSGPATVCGPKKSTNLVKNKC     |
| S14     | P2         | SARS-CoV-2 |                            | SGSKSTNLVKNKCVNFNFNGL     |
| S14     | P3         | SARS-CoV-2 | 521-570                    | SGSKCVNFNFNLGTGVLTE        |
| S14     | P4         | SARS-CoV-2 |                            | SGSGGLTGTGVLTESNKKFLPF     |
| S14     | P5         | SARS-CoV-2 |                            | SGSGTESNKKFLPFQQFGRDIA     |
| S21     | P1         | SARS-CoV-2 |                            | SGSNFSQILPDPSKPSKRSSF     |
| S21     | P2         | SARS-CoV-2 |                            | SGSPSKPSKRSSFIEDLLFNKV     |
| S21     | P3         | SARS-CoV-2 | 801-850                    | SGSGFIEDLLFNKVLADAGFI      |
| S21     | P4         | SARS-CoV-2 |                            | SGSKVTADAGFIKQYGDCLG       |
| S21     | P5         | SARS-CoV-2 |                            | SGSGFIKQYGDCLGDIAARDLI     |
| S45     | P3         | SARS-CoV   | 537-554                    | SGSVLTPSSKRFPQFQQFGRD      |
| S51     | P1         | SARS-CoV   |                            | SGSGREVFAQVKQMKYKTPTLKY     |
| S51     | P2         | SARS-CoV   |                            | SGSGQMYKTPTLKYGGFNFQS      |
| S51     | P3         | SARS-CoV   | 761-810                    | SGSKYFGGFNFSLPDPLKP        |
| S51     | P4         | SARS-CoV   |                            | SGSGQILPDPLKPTKRSFIED      |
| S51     | P5         | SARS-CoV   |                            | SGSKPTKRSFIEDLLFNKVTL      |
**Supplementary Table 4:** Neutralizing IC$_{50}$ of individual patients and their corresponding S14P5 and S21P2 baseline corrected OD values

| COVID-19 Patient ID | SARS-CoV-2 (Live) IC$_{50}$ | SARS-CoV-2 (Pseudovirus) IC$_{50}$ | S14P5 baseline corrected OD (450nm) | S21P2 baseline corrected OD (450nm) |
|---------------------|-----------------------------|-----------------------------------|-----------------------------------|-----------------------------------|
|                     |                             |                                   | Exp1 | Exp2 | Exp1 | Exp2 |
| 1                   | 741.2                       | 0.9251                            | 1.0029 | 0.9998 |
| 2                   | 926.4                       | 0.4532                            | 0.9511 | 1.4857 |
| 3                   | 224.9                       | 0.3044                            | 0.4857 | 1.1792 |
| 4                   | 229.4                       | 0.4518                            | 0.2108 | 0.3712 |
| 5                   | 1204                        | 1.8772                            | 1.8691 | 1.9659 |
| 6                   | 372                         | 1.6697                            | 2.8120 | 2.6706 |
| 7                   | 493.3                       | 1.0612                            | 0.2518 | 0.2850 |
| 8                   | 711.4                       | 1.2309                            | 1.3850 | 1.3262 |
| 9                   | 825.1                       | 1.3012                            | 0.3837 | 0.5591 |
| 10                  | 47.75                       | 0.1054                            | 0.2359 | 0.4298 |
| 11                  | 1364                        | 2.4507                            | 2.4527 | 2.3346 |
| 12                  | 385.3                       | 0.8557                            | 0.6623 | 0.6889 |
| 13                  | 246.6                       | 0.3260                            | 1.0714 | 1.4816 |
| 14                  | 52.53                       | 0.1767                            | 0.3008 | 0.4785 |
| 15                  | 96.36                       | 0.0753                            | 0.2069 | 0.3518 |
| 16                  | 1044                        | 0.9475                            | 1.1588 | 1.3383 |
| 17                  | 907.7                       | 1.8493                            | 0.3371 | 0.9745 |
| 18                  | 245.2                       | 0.1574                            | 0.6034 | 0.6900 |
| 19                  | 811.5                       | 1.6024                            | 1.7663 | 1.9503 |
| 20                  | 4188                        | 0.1489                            | 0.3710 | 0.5592 |
| 21                  | 236.5                       | 0.3116                            | 0.3625 | 0.5053 |
| 22                  | 166.1                       | 0.0635                            | 0.1852 | 0.3505 |
| 23                  | 178                         | 0.4244                            | 0.2293 | 0.8938 |
| 24                  | 192.7                       | 0.3336                            | 0.3452 | 0.5011 |
| 25                  | 247.1                       | 0.1356                            | 0.5373 | 0.5967 |
| 26                  | 1487                        | 0.9063                            | 1.4259 | 1.6137 |
| 27                  | 332.7                       | 0.2006                            | 0.3590 | 0.4799 |
| 28                  | 217.8                       | 0.1432                            | 1.2710 | 1.3676 |
| 29                  | 0.5924                      | 0.3390                            | 1.1595 | 1.7411 |
| 30                  | 92.94                       | 0.1585                            | 0.3460 | 0.5366 |
Supplementary Table 5: List of mutations from a list of 10956 sequences that were curated by China National Center for Bioinformation (CNCB; https://bigd.big.ac.cn/ncov) extracted on 20 April 2020. Mutations corresponding to regions in peptides S14P5 and S21P2 are highlighted in yellow.

| Peptide | Genom e position | Virus number with variation | Annotation Type | Protein,Position, Amino acids change | Gene,Position, Codons | Impact Ensembl Variation - Calculated variant consequences* | Last Update |
|---------|------------------|-----------------------------|-----------------|------------------------------------|----------------------|----------------------------------------------------------|-------------|
| S14P5  | 2320 6           | 2                           | synonymous _variant | QHD43416.1 :p.548G | gene-S:c.1644ggC>g gT | LOW | 2020-04-20 01:13:14 |
|         | 2323 0           | 2                           | synonymous _variant | QHD43416.1 :p.556N | gene-S:c.1668aaC>a aT | LOW | 2020-04-20 01:13:14 |
|         | 2324 2           | 1                           | synonymous _variant | QHD43416.1 :p.560L | gene-S:c.1680ctG>ct T | LOW | 2020-04-20 01:13:14 |
|         | 2324 4           | 1                           | missense_variant; coding_sequence_variant | QHD43416.1 :p.561P>L | gene-S:c.1682ctC>ctT | MODERATE | 2020-04-20 01:13:14 |
|         | 2324 8           | 4                           | synonymous _variant; coding_sequence_variant | QHD43416.1 :p.562F; QHD43416.1 :p.562G | gene-S:c.1686ttC>ttG; gene-S:c.1686ttC>ttY | LOW; MODIFIER | 2020-04-20 01:13:14 |
|         | 2326 6           | 1                           | missense_variant | QHD43416.1 :p.568D>E | gene-S:c.1704gaC>g aA | MODERATE | 2020-04-20 01:13:14 |
|         | 2326 7           | 1                           | missense_variant | QHD43416.1 :p.569I>V | gene-S:c.1705Att>Gtt | MODERATE | 2020-04-20 01:13:14 |
|         | 2327 0           | 1                           | missense_variant | QHD43416.1 :p.570A>T | gene-S:c.1708Gct>Gac t | MODERATE | 2020-04-20 01:13:14 |
|         | 2327 1           | 2                           | missense_variant | QHD43416.1 :p.570A>V | gene-S:c.1709gCt>gT t | MODERATE | 2020-04-20 01:13:14 |
| Line | Type | Gene | CDS Change | Description | Severity | Date |
|------|------|------|------------|-------------|----------|------|
| 2327 | Missense Variant | QHD43416.1 | p.572T>I | **S:c.1715aCt>aT** | MODERATE | 2020-04-01 01:13:14 |
| 2398 | Synonymous Variant | QHD43416.1 | p.808D | **S:c.2424gaT>gaC** | LOW | 2020-04-01 01:13:16 |
| 2398 | Missense Variant | QHD43416.1 | p.808D | **S:c.2425Cca>Tca** | MODERATE | 2020-04-01 01:13:16 |
| 2398 | Missense Variant | QHD43416.1 | p.809P | **S:c.2430tcA>tcT** | MODERATE | 2020-04-01 01:13:16 |
| 2398 | Synonymous Variant | QHD43416.1 | p.809P | **S:c.2434CcA>ccG** | LOW | 2020-04-01 01:13:16 |
| 2399 | Missense Variant | QHD43416.1 | p.810S | **S:c.2437Cca>Tca** | MODERATE | 2020-04-01 01:13:16 |
| 2399 | Missense Variant | QHD43416.1 | p.812P | **S:c.2444Cca>Tca** | MODERATE | 2020-04-01 01:13:16 |
| 2399 | Synonymous Variant | QHD43416.1 | p.816S | **S:c.2449Ttt>Ctt** | MODERATE | 2020-04-01 01:13:16 |
| 2401 | Missense Variant | QHD43416.1 | p.817F | **S:c.2452Att>Gtt** | MODERATE | 2020-04-01 01:13:16 |
| 2401 | Missense Variant | QHD43416.1 | p.818I | **S:c.2461Cta>Ata** | MODERATE | 2020-04-01 01:13:16 |
| 2402 | Missense Variant | QHD43416.1 | p.820L | **S:c.2461Cta>Tta** | MODERATE | 2020-04-01 01:13:16 |
| 2402 | Synonymous Variant | QHD43416.1 | p.821L | **S:c.2463Cca>ccG** | LOW | 2020-04-01 01:13:16 |
| 2403 | Missense Variant | QHD43416.1 | p.824A | **S:c.2472aA>aaT** | LOW | 2020-04-01 01:13:16 |
| 2405 | Missense Variant | QHD43416.1 | p.831A | **S:c.2492gCt>gTt** | MODERATE | 2020-04-01 01:13:16 |