Supplemental information

Limited cross-variant immune response from SARS-CoV-2 Omicron BA.2 in naïve but not previously infected outpatients

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Supplementary figures

**Figure S1. Genes regulated by Omicron infection, related to Figure 2.** (A-B) mRNA extracted from whole blood in the no prior infection group was analyzed by qRT-PCR and compared between BA.1 and BA.2 groups. (C) mRNA extracted from whole blood of the BA.2 infected patients in no prior infection and prior infection groups was analyzed by qRT-PCR and compared between BA.2 patients of no prior infection and prior infection groups. The results were normalized to *GAPDH* levels and are shown as the means ± s.e.m. of independent biological replicates (BA.1 of no prior infection, n = 19; BA.2 of no prior infection, n = 9; BA.2 of prior infection, n = 3). ACTB and PGK1 genes are housekeeping genes (control). The other genes were identified as significantly regulated genes using RNA-seq (Figure 2). *p*-value between two groups is from one-tailed Mann-Whitney t-test. *p* < 0.05, **p* < 0.01, ****p* < 0.0001. Median, middle bar inside the box; IQR, 50% of the data; whiskers, 1.5 times the IQR.
### Table S1. Fold activity of antibody levels between two groups, related to Figure 1.

| Fold         | No prior infection | Prior infection | BA.1 vs BA.2 | No prior infection vs Prior infection | BA.1 vs BA.2 | No prior infection vs Prior infection |
|--------------|--------------------|-----------------|--------------|---------------------------------------|--------------|---------------------------------------|
| Omicron (B.1.1.529) | 42                 | 1               | 10           |                                       | 588          |
| SARS-CoV-2   | 69                 | 2               | 5            |                                       | 673          |
| AY.4.2       | 5                  | 1               | 19           |                                       | 108          |
| Alpha (B.1.1.7) | 3                  | 1               | 10           |                                       | 49           |
| Beta (B.1.351)| 4                  | 2               | 15           |                                       | 97           |
| Gamma (P.1)  | 4                  | 3               | 11           |                                       | 119          |
| Delta (B.1.617.2) | 5                  | 1               | 18           |                                       | 110          |
| Delta2 (B.1.617.2; AY) | 4                  | 1               | 21           |                                       | 112          |

### Table S2. Significantly differential genes between BA.1 and BA.2 infected cohorts with no prior infection, related to Figure 2.

Days 2-3 after infection, log\(_2\) (fold change) and adjusted \(p\)-value.

### Table S3. Significantly differential genes between no prior and prior infection in BA.2 infected cohorts, related to Figure 2.

Days 2-3 after infection, log\(_2\) (fold change) and adjusted \(p\)-value.