Supplementary Information

Impact of BNT162b first vaccination on the immune transcriptome of elderly patients infected with the B.1.351 SARS-CoV-2 variant

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Supplementary Tables

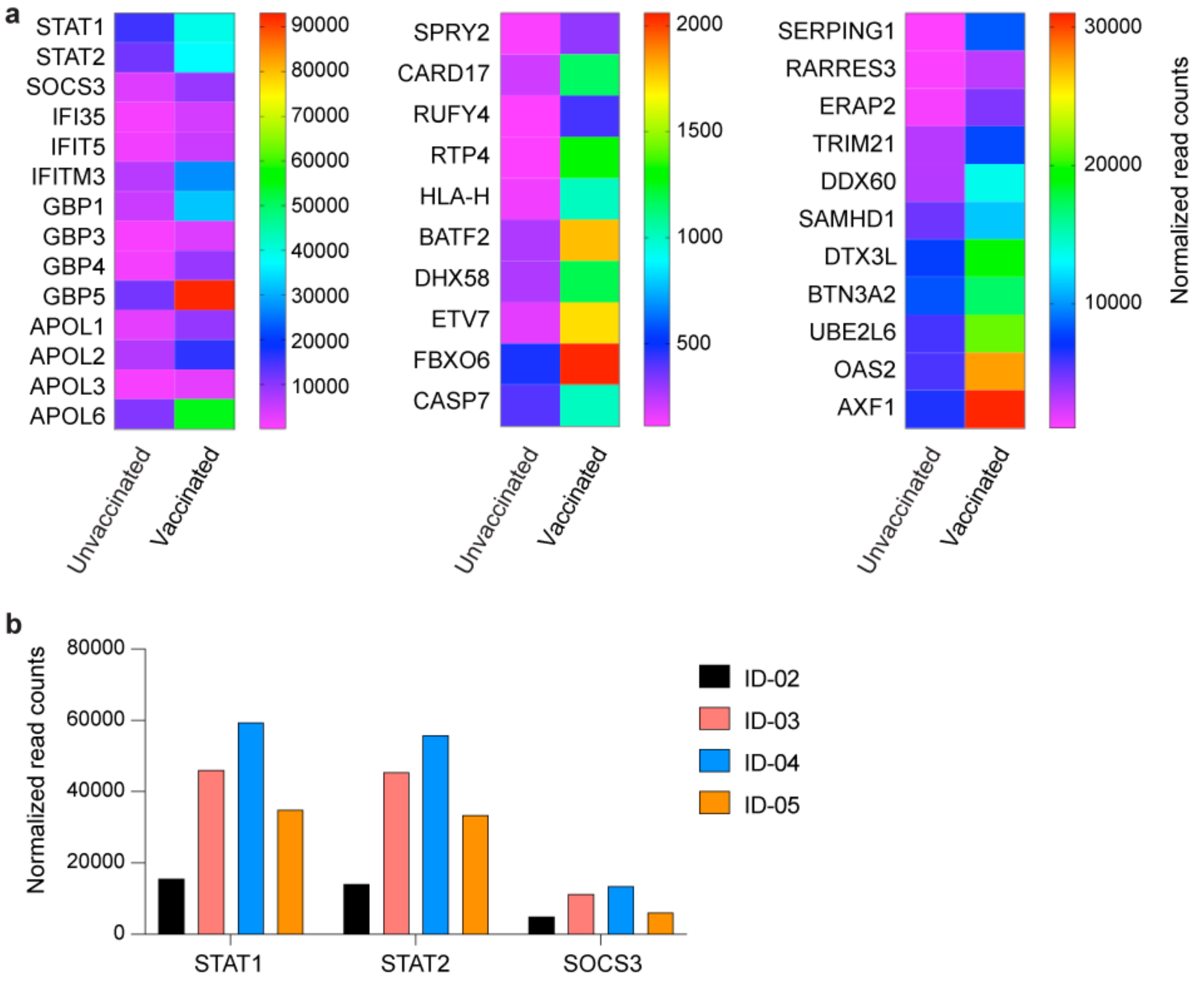
Supplementary Table 1. Demographic and Clinical Characteristics of study population.

Supplementary Table 2. List of all genes with normalized read counts in each replicate at non-COVID controls and B.1.351 variant infected COVID-19 patients, $\log_2$ (fold change), *p*-value and adjusted *p*-value as well as upregulated gene list and GSEA analysis.

Supplementary Table 3. List of all genes with normalized read counts in each replicate at unvaccinated and vaccinated groups, $\log_2$ (fold change), *p*-value and adjusted *p*-value as well as upregulated gene list and GSEA analysis.

Supplementary Table 4. List of all genes with normalized read counts in each replicate at 1st and 2nd samples in vaccinated group, $\log_2$ (fold change), *p*-value and adjusted *p*-value as well as upregulated gene list and GSEA analysis.

Supplementary Table 5. List of all genes with normalized read counts in each replicate at unvaccinated and young-unvaccinated groups, $\log_2$ (fold change), *p*-value and adjusted *p*-value as well as upregulated gene list and GSEA analysis.



Supplementary Figure 1. Upregulation of Interferon stimulated genes (ISGs), innate antiviral immunity and COVID-19-SARS-CoV-2 infection genes in vaccinated COVID-19 patients. a. Heatmap showing the significant enriched genes related to immune responses and SARS-CoV-2 virus infection. **b.** mRNA levels of JAK/STAT signaling components, STAT1, STAT2 and SOCS3, measured by RNA-seq were presented by bar graphs.