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## **Supplemental Information**

### **A Dynamic Immune Response**

#### **Shapes COVID-19 Progression**

**Eugenia Ziyong Ong, Yvonne Fu Zi Chan, Wan Ying Leong, Natalie Mei Ying Lee, Shirin Kalimuddin, Salahudeen Mohamed Haja Mohideen, Kian Sing Chan, Anthony Tanoto Tan, Antonio Bertolotti, Eng Eong Ooi, and Jenny Guek Hong Low**

# Supplemental Information

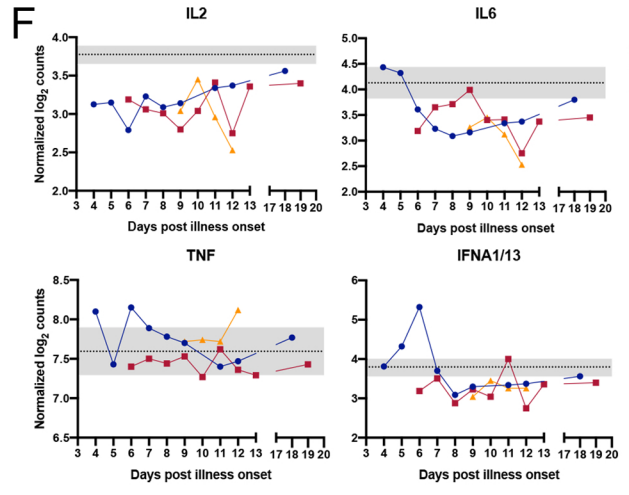
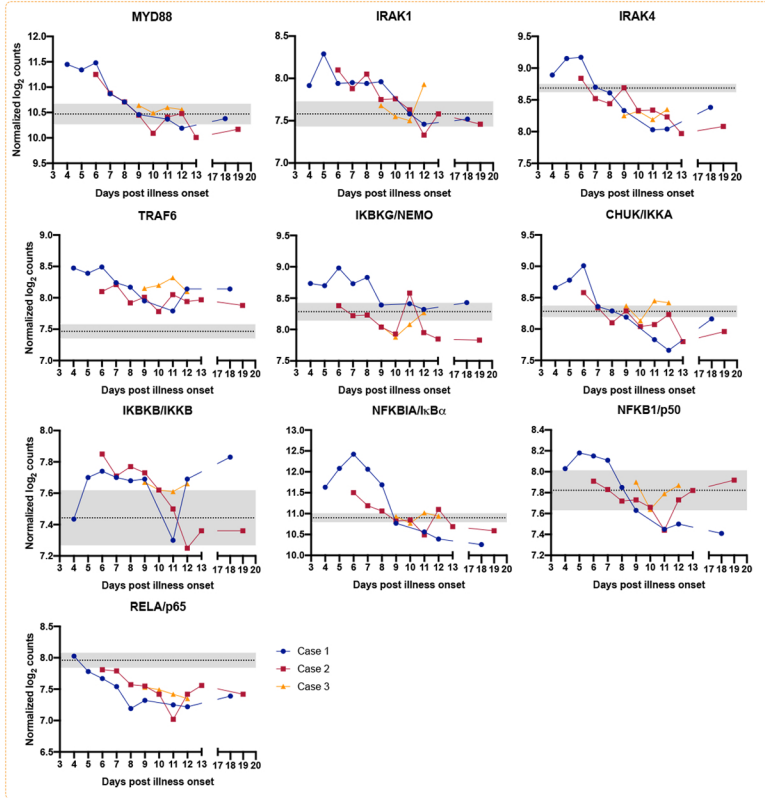
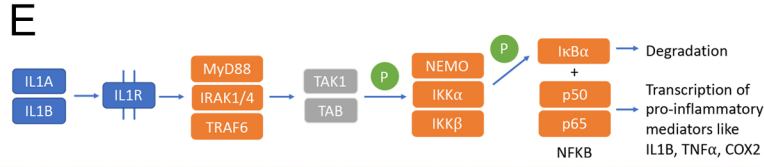
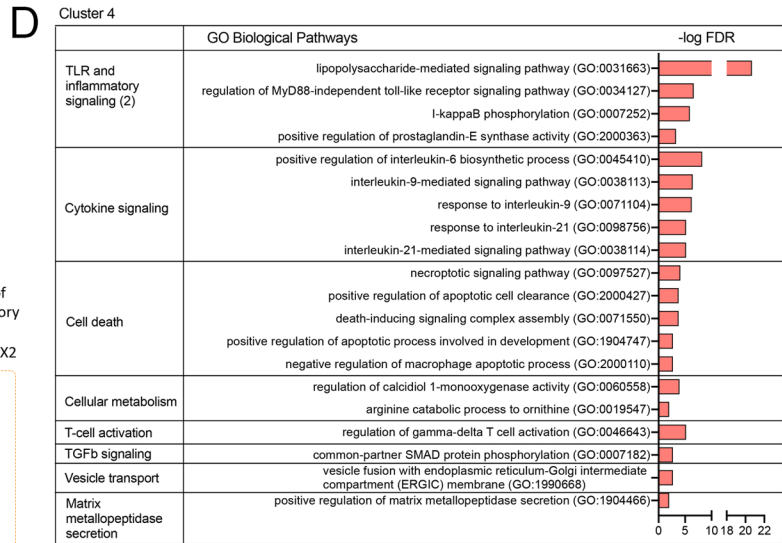
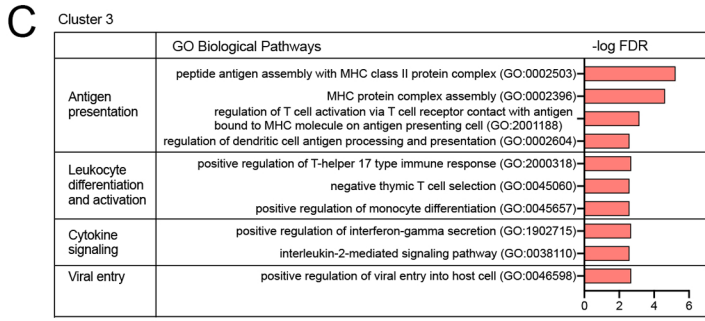
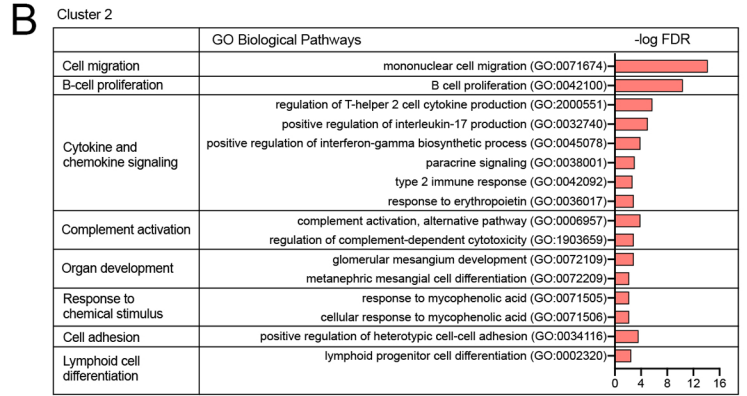
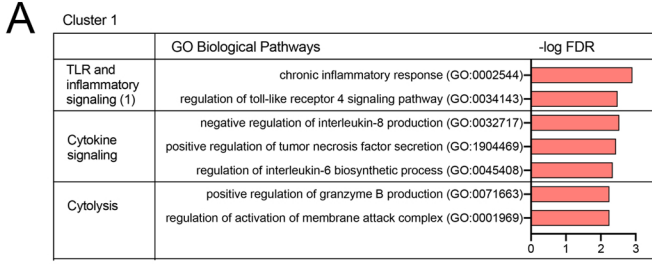


Figure S1. Gene expression and pathway analysis following NanoString profiling of immune genes in healthy controls and COVID-19 cases, related to Figure 2. (A-D) All genes included in gene cluster 1 (A), cluster 2 (B), cluster 3 (C) and cluster 4 (D) were analysed against PANTHER classification system using Gene Ontology (GO) Enrichment Analysis for biological processes. GO terms with > 40-fold enrichment following GO enrichment analysis were shortlisted, and summarization of redundant GO terms was performed using REViGO. Enriched representative GO terms (FDR<0.01) are shown for each gene cluster. (E) Flowchart depicting IL1R-mediated signaling cascade adapted from KEGG (hsa04064). Gene expression for signaling intermediates downstream of IL1R-mediated signaling are represented by normalized log<sub>2</sub> counts. (F) Gene expression for pro-inflammatory cytokines in COVID-19 cases represented by normalized log<sub>2</sub> counts. Dotted line and grey shaded area indicate mean gene expression  $\pm$  SD for healthy controls.