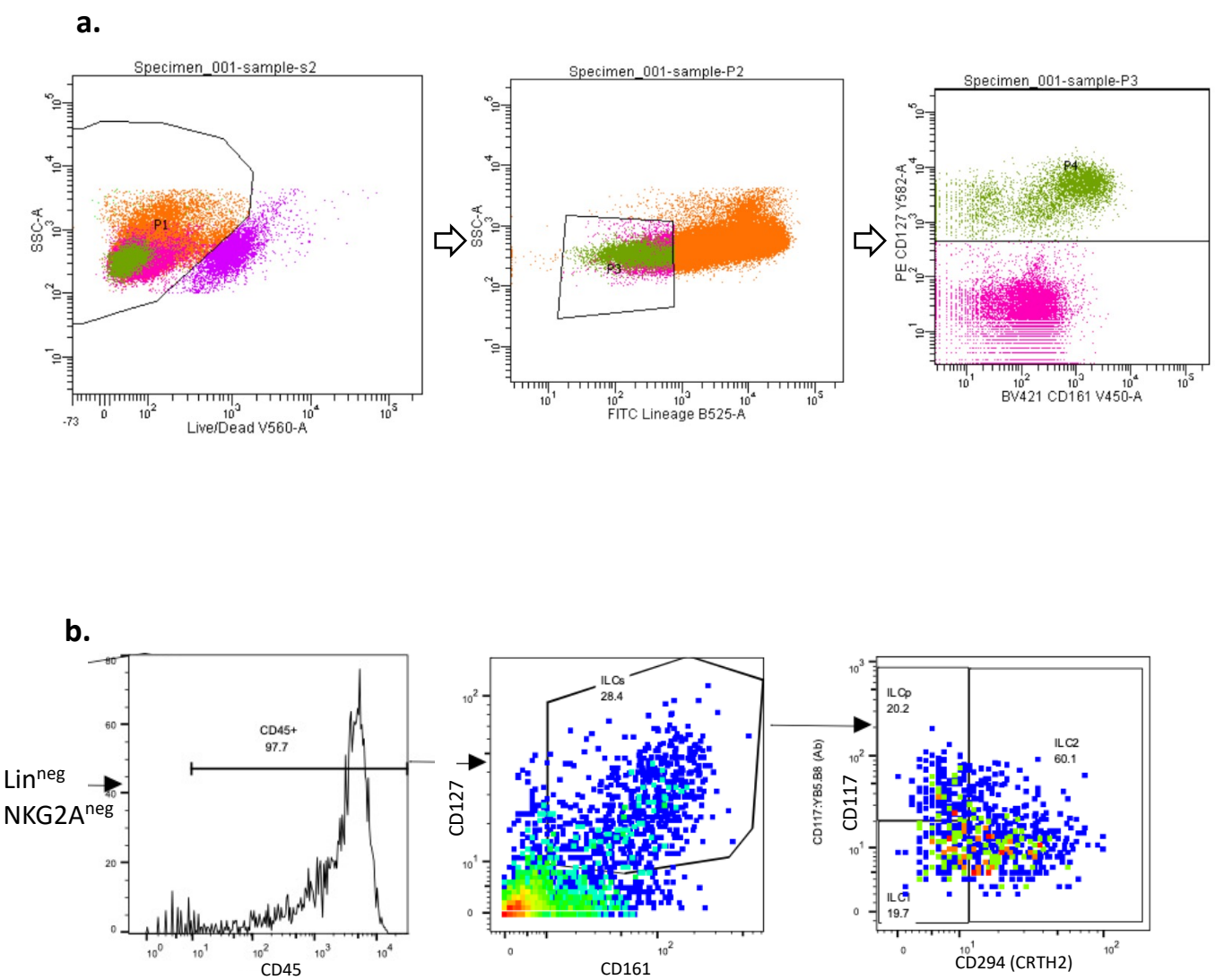
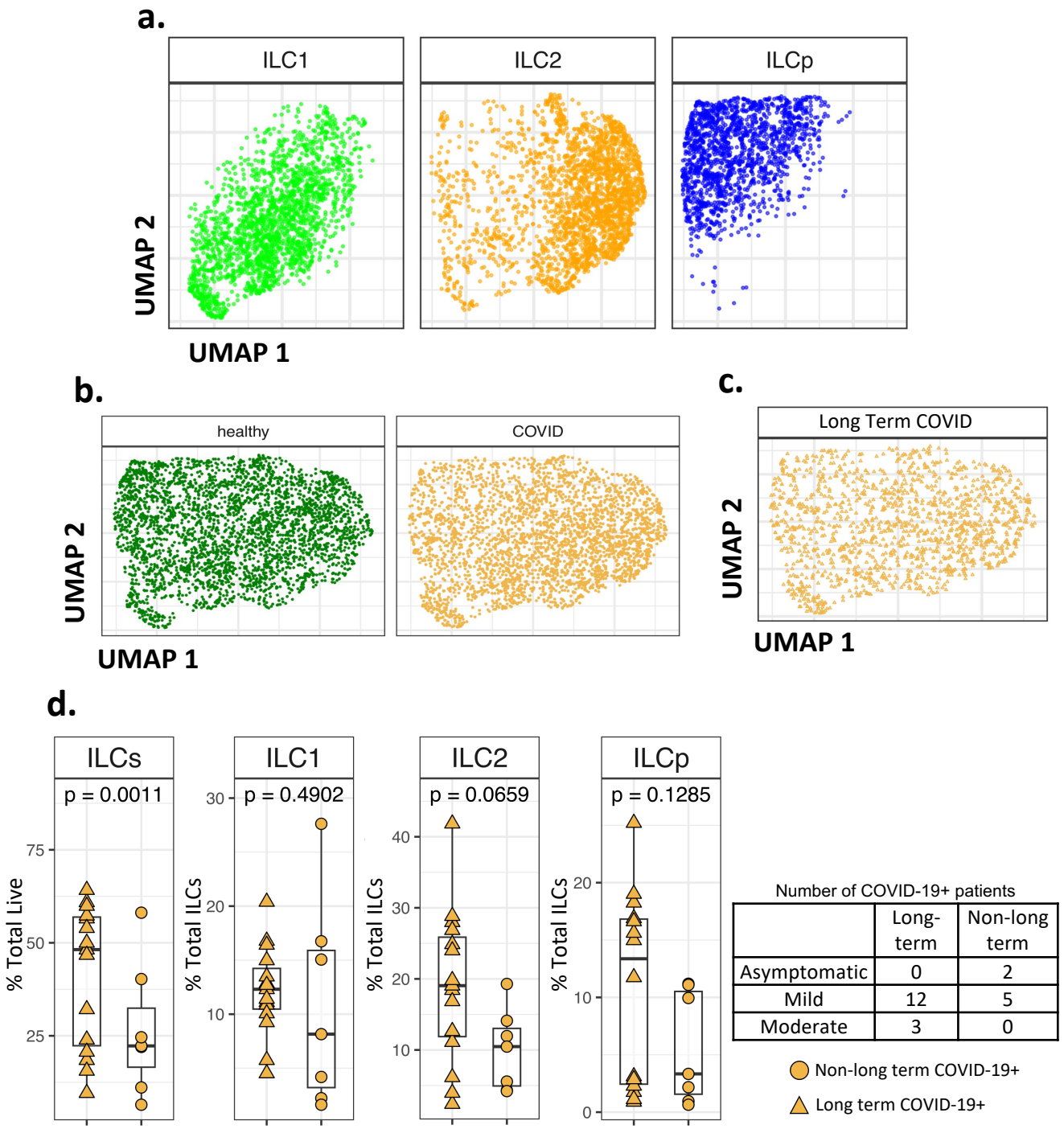
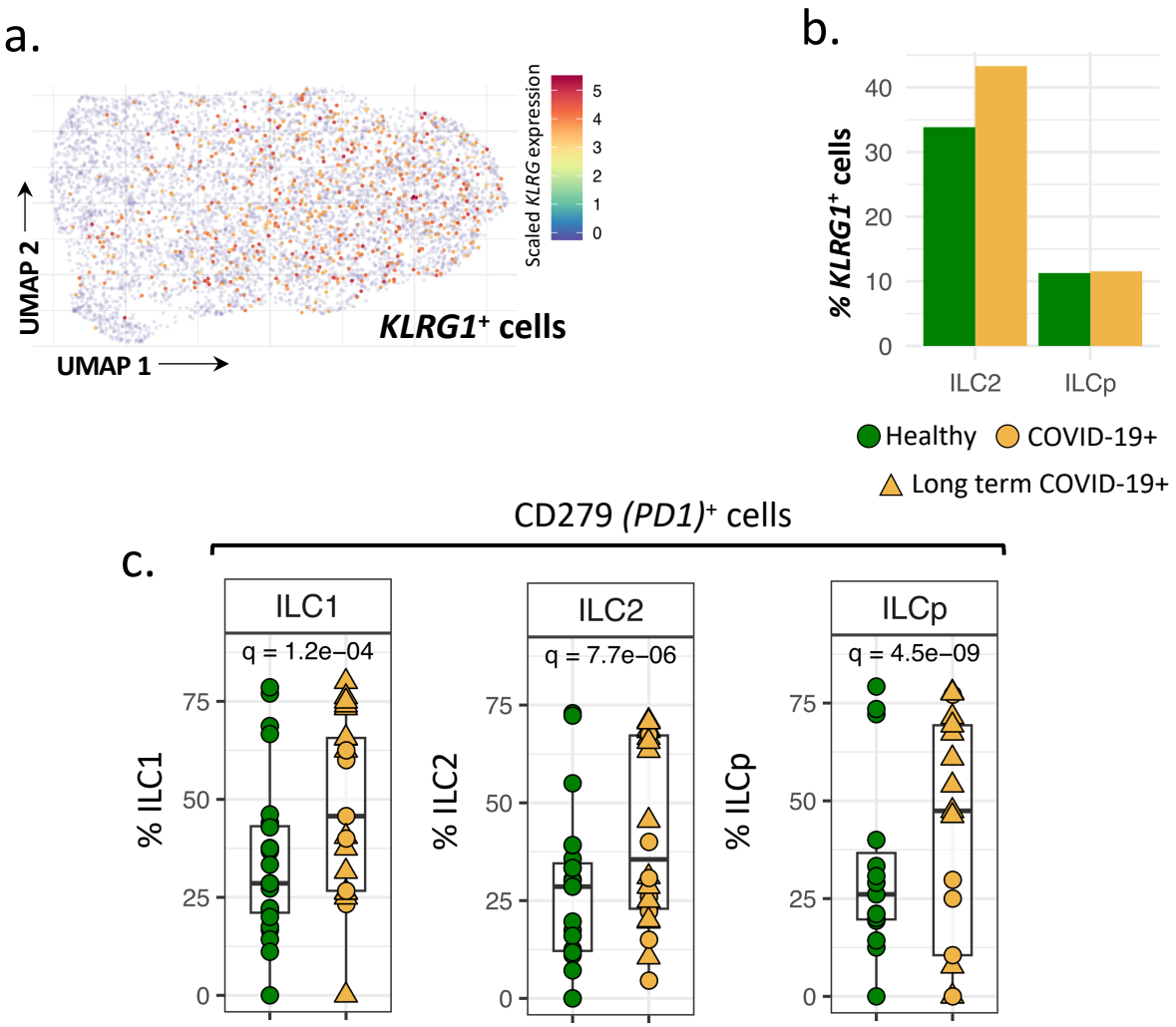


Supplementary Fig. 1 A. FACS Cell sorting schema to identify ILCs prior to Abseq & scRNAseq profiling using BD Rhapsody multi-omics platform. **B. Gating strategy for ILC identification**. Using Abseq oligonucleotide-linked antibodies, ILCs were identified as Lineage^{neg}, NKG2A^{neg} and CD45^{+}. ILCs were further defined as CD127^{+}CD161^{+} as well as ILC subsets: ILC1 (CD117^{neg}CRTH2^{neg}), ILC2 (CRTH2^{+}) and ILCp (CD117^{+}CRTH2^{neg}).

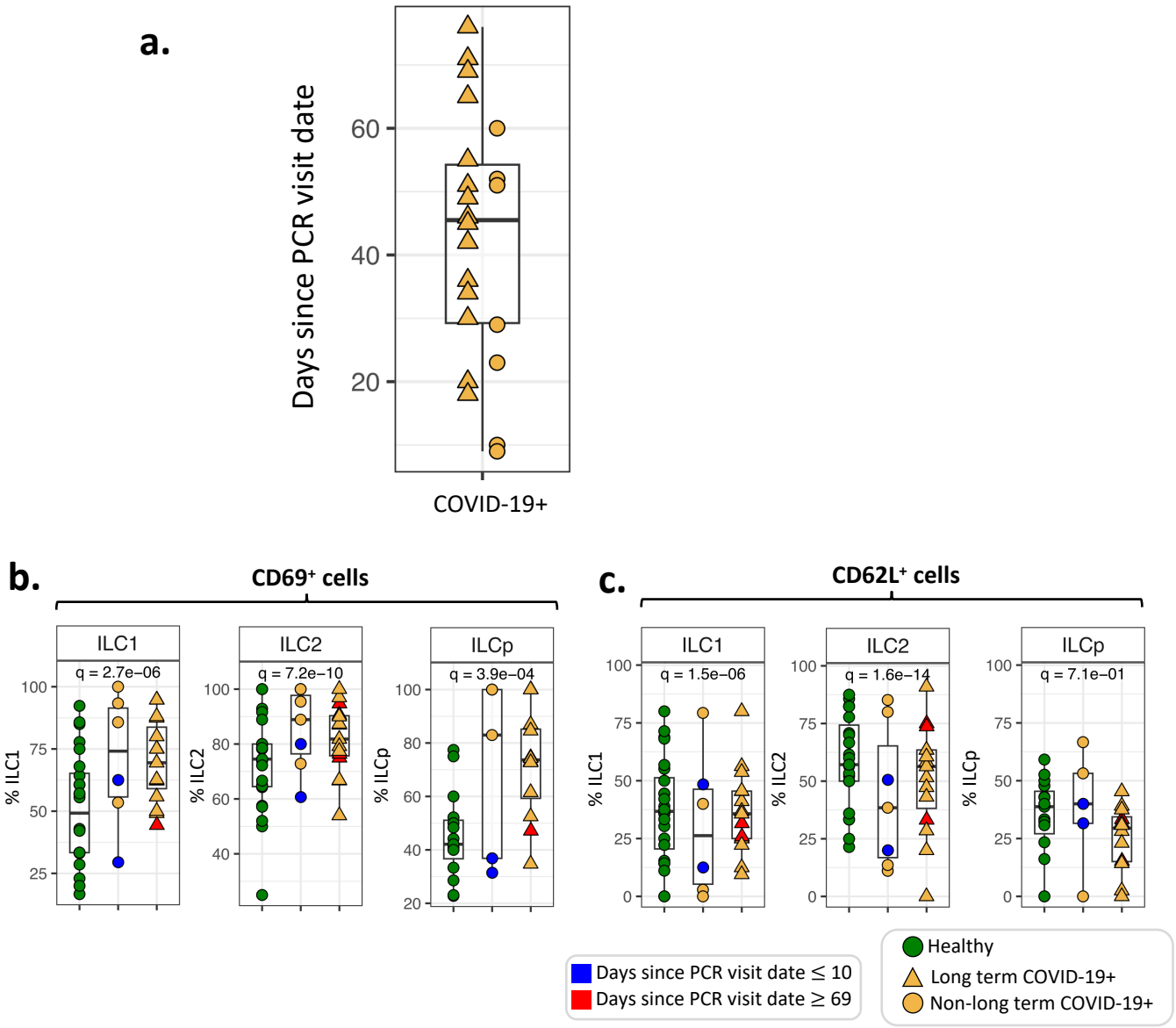


	Long-term	Non-long term
Asymptomatic	0	2
Mild	12	5
Moderate	3	0

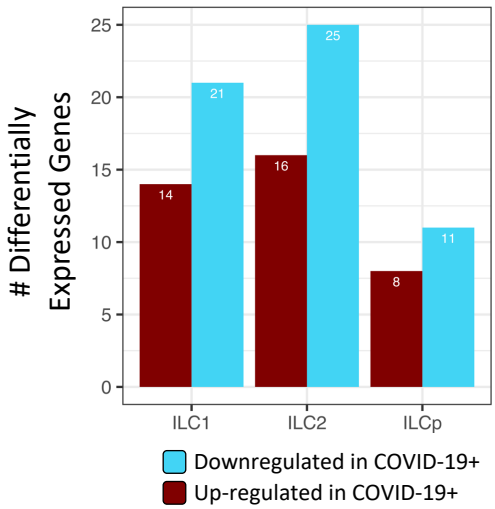
Supplementary Fig. 2. (a) UMAP directional reduction analysis of manually gated ILCs from COVID-19 patients and healthy control participants. The ILC1, ILC2 and ILCp cells are represented separately to show their distribution across the entire UMAP as shown in Fig 1b. (**b**) UMAP analysis of ILCs from healthy compared with COVID-19 patients. The ILCs are uniformly distributed in both groups of participants. For UMAP analysis 6247 single cells were plotted of which 2103 cells were ILC1 , 2509 were ILC2 and 1635 were ILCp. **(c)** UMAP analysis of ILCs from patients with long-term COVID-19 symptoms. The ILCs are uniformly distributed across the entire UMAP. (**d**) Frequencies (i.e., percentage) of ILCs and ILC subsets from 22 COVID-19 patients were compared with patients with long-term COVID-19 symptoms (*n*=15) versus non-long-term covid (*n*=7). P-values between two groups of samples were calculated using Wilcoxon rank-sum test.



Supplementary Fig. 3. (a) UMAP analysis shows the expression profile of *KLRG* in ILCs. (**b**) The number of *KLRG1*+ ILC2 and ILCp cells across healthy control vs COVID-19 patients. (**c**) Differences in frequency of CD279 (*PD1*)+ cells by ILC subsets from COVID-19 patients compared with healthy controls. For boxplot representation, percentage of cells expressing CD279 protein in every sample is shown..

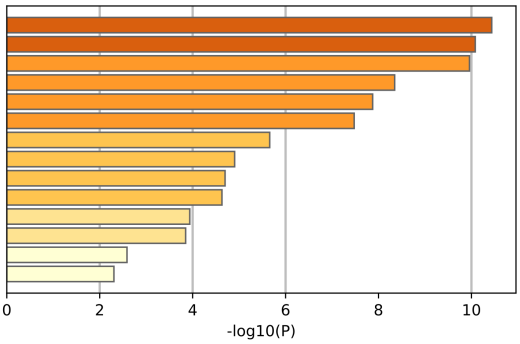


Supplementary Fig. 4. Days since PCR visit date. (a) The box plot shows the number of days post COVID-19 RT-PCR positive diagnosis at which patient samples were taken . **(b-c)** Differences in frequency of CD69⁺ cells and CD62L (*SELL*)⁺ cells by ILC subsets from COVID-19 patients compared with healthy controls (as also represented in Fig. 1e & g). Samples from COVID-19 patients taken less than 11 days after their COVID-19 RT-PCR diagnosis are colored in blue, whereas samples taken from COVID-19 patients $\geq$ 68 days post RT-PCR diagnosis are colored in red. Adjusted p-values between two groups of cells were calculated using Wilcoxon rank-sum test (see methods). For boxplot representation, percentage of cells expressing a given protein in every sample is shown.

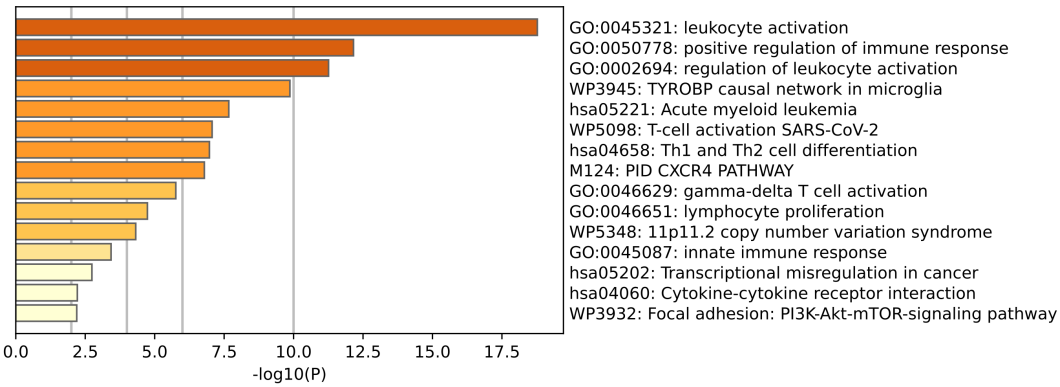


Supplementary Fig. 5. Number of up-regulated and down-regulated genes in each ILC subset.

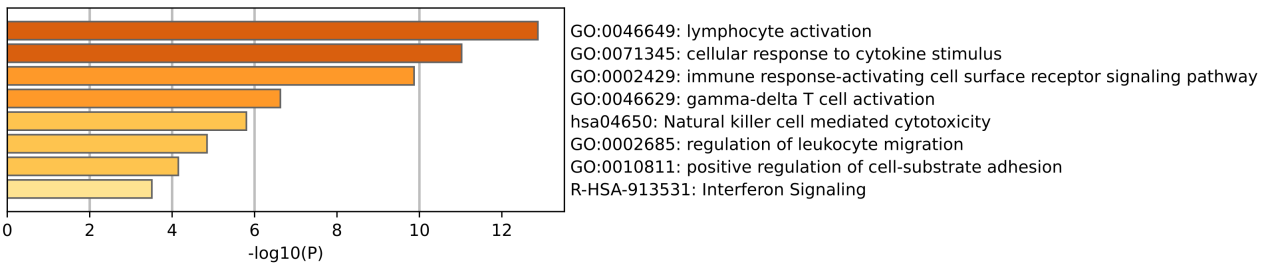
a. **ILC1: Enrichment Analysis of differentially expressed genes (*n=32*)**



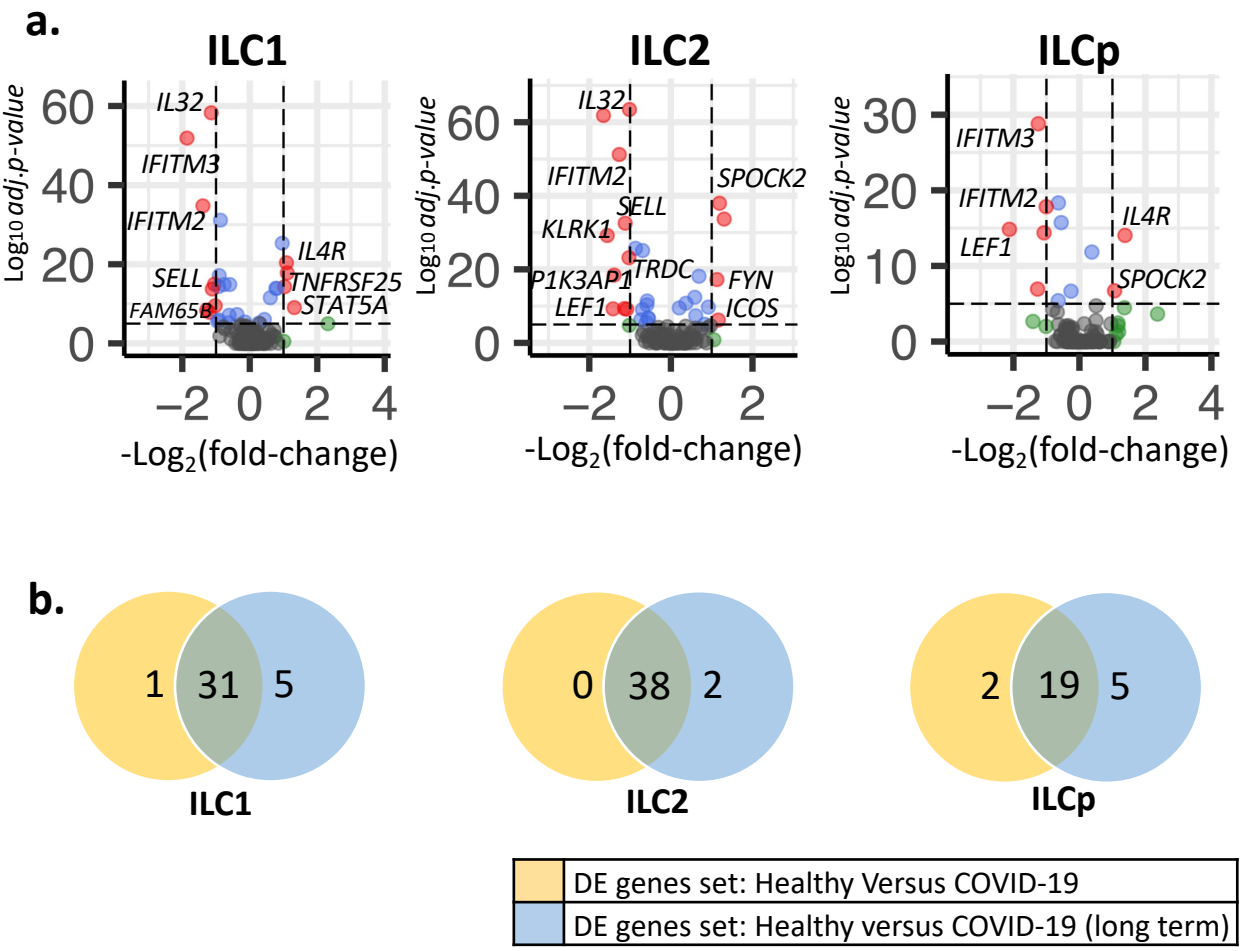
b. **ILC2: Enrichment Analysis of differentially expressed genes (*n=38*)**



c. **ILCp: Enrichment Analysis of differentially expressed genes (*n=21*)**

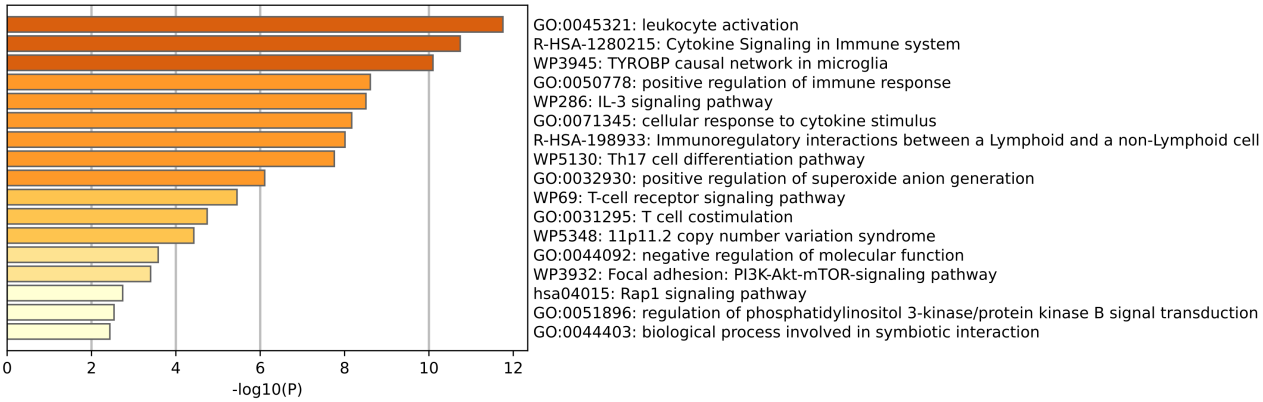


Supplementary Fig. 6. (a-c) Gene enrichment analysis of differentially expressed genes (Healthy versus COVID-19) observed in each ILCs. For each given gene list, pathway and process enrichment analysis have been carried out using metascape (default parameters) which uses the following ontology sources: KEGG Pathway, GO Biological Processes, Reactome Gene Sets, Canonical Pathways, CORUM, and WikiPathways.

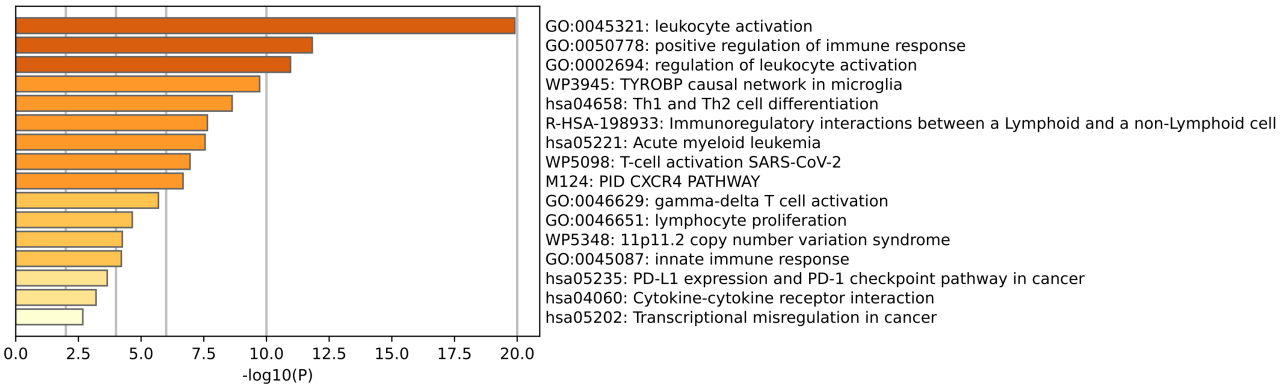


Supplementary Fig. 7. (a) Volcano plot highlighting differentially expressed genes (Healthy versus COVID-19 patients with long-term symptoms) observed in each ILCs (ILC1/ILC2/ILCp). (**b.**) The number of differentially expressed genes common between two different analyses, i.e. Healthy Versus COVID-19 and Healthy versus COVID-19 (long term symptoms).

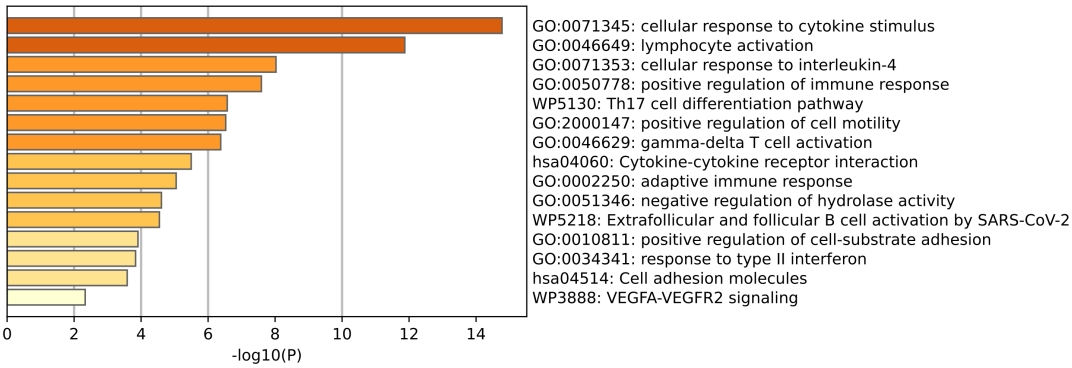
a. **ILC1: Enrichment Analysis of differentially expressed genes (*n=36*)**



b. **ILC2: Enrichment Analysis of differentially expressed genes (*n=40*)**



c. **ILCp: Enrichment Analysis of differentially expressed genes (*n=24*)**



Supplementary Fig. 8. (a-c) Gene enrichment analysis of differentially expressed genes (Healthy versus COVID-19 patients with long-term symptoms) observed in each ILCs. For each given gene list, pathway and process enrichment analysis have been carried out using metascape (default parameters) which uses the following ontology sources: KEGG Pathway, GO Biological Processes, Reactome Gene Sets, Canonical Pathways, CORUM, and WikiPathways.