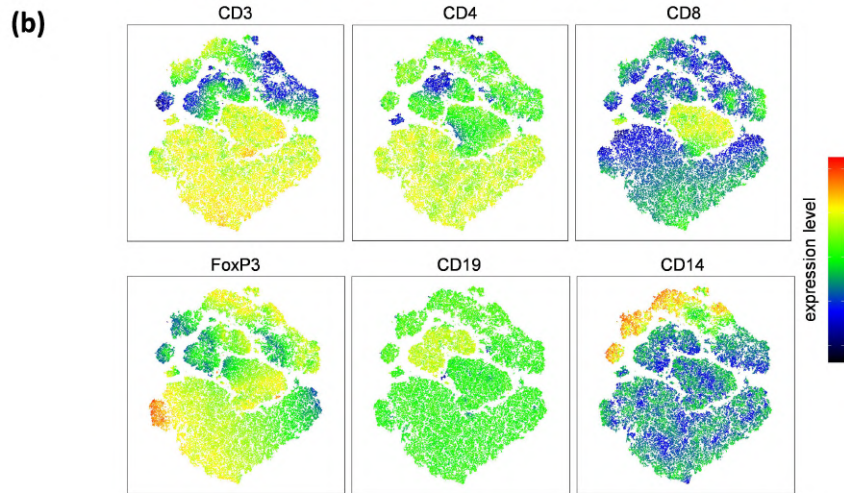
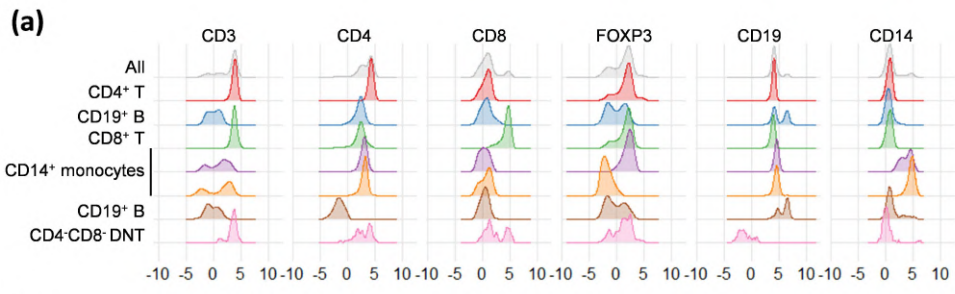


Supplementary table 1. Demographic, clinical and immunological data of healthy controls and COVID-19 patients. BMI, body mass index; CRP, C-reactive protein; HIV, Human Immunodeficiency Virus; M, male/F, female; n/a, not applicable or not available; WHO, World Health Organization. Laboratory parameters were obtained within 24 h of blood sampling for immune phenotyping.

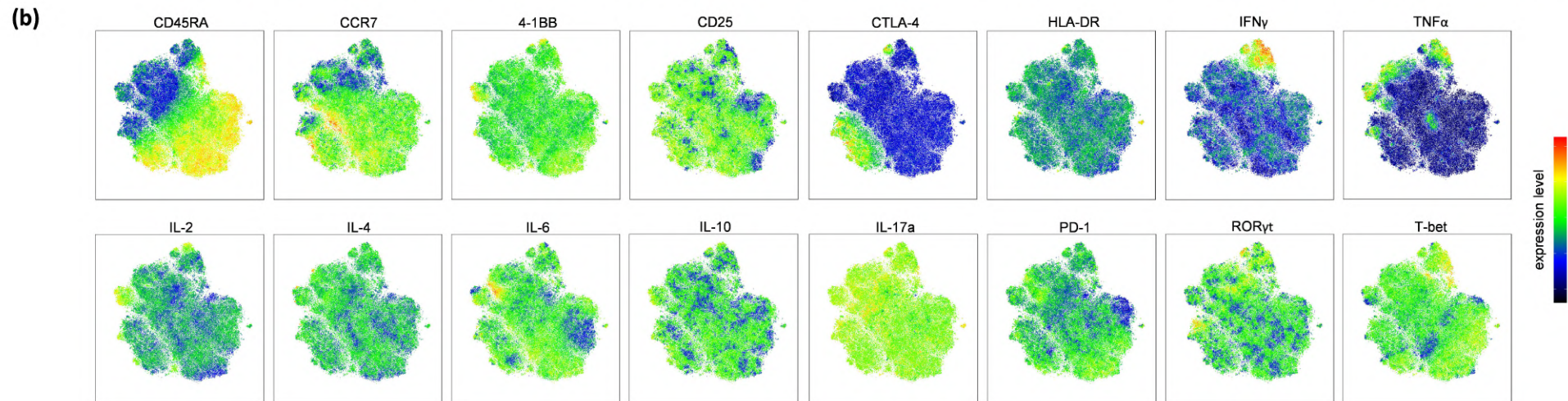
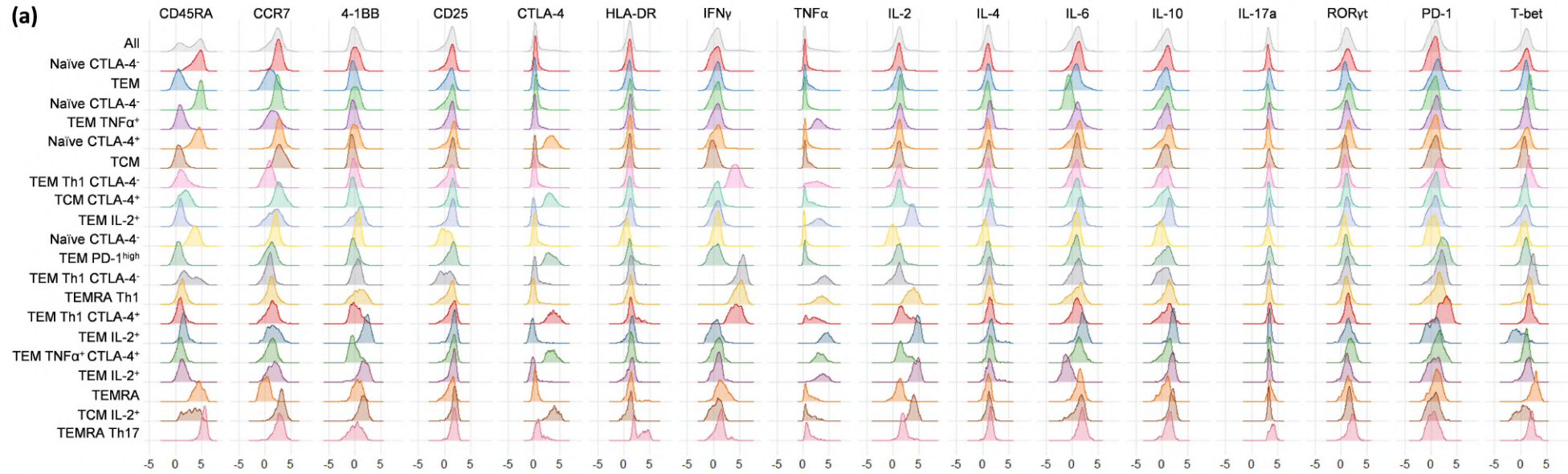
Supplementary figure 1. Classification of lymphocytes. PBMCs were isolated from healthy controls (n=6), mild-moderate COVID-19 patients (n=23) and severe COVID-19 patients (n=20), stimulated and assessed through flow cytometry. **(a)** FlowSOM clusters (identified in Figure 1) were obtained based on CD3, CD4, CD8, FOXP3, CD19, CD14. Expression of each marker on each FlowSOM cluster is shown in histogram format and **(b)** imposed on a tSNE representation.

Supplementary figure 1



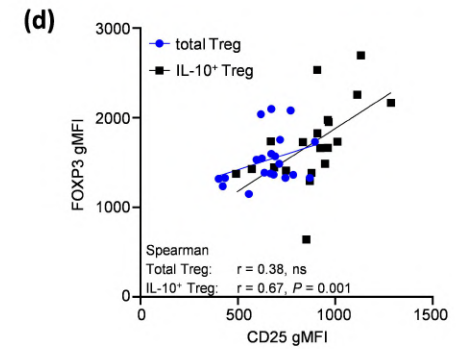
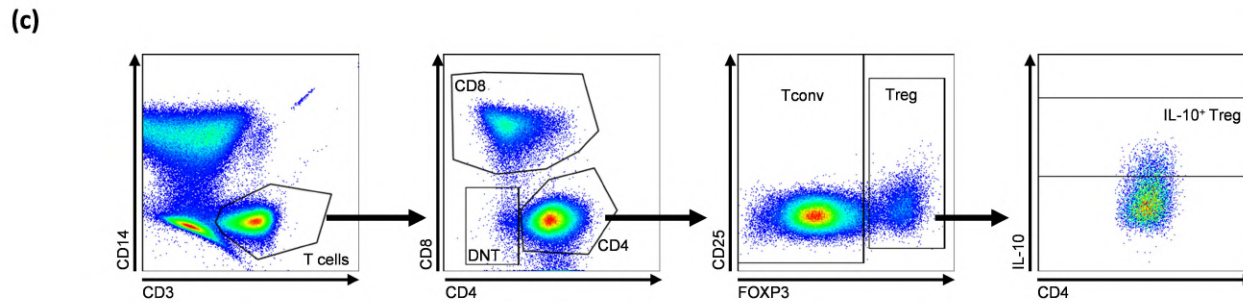
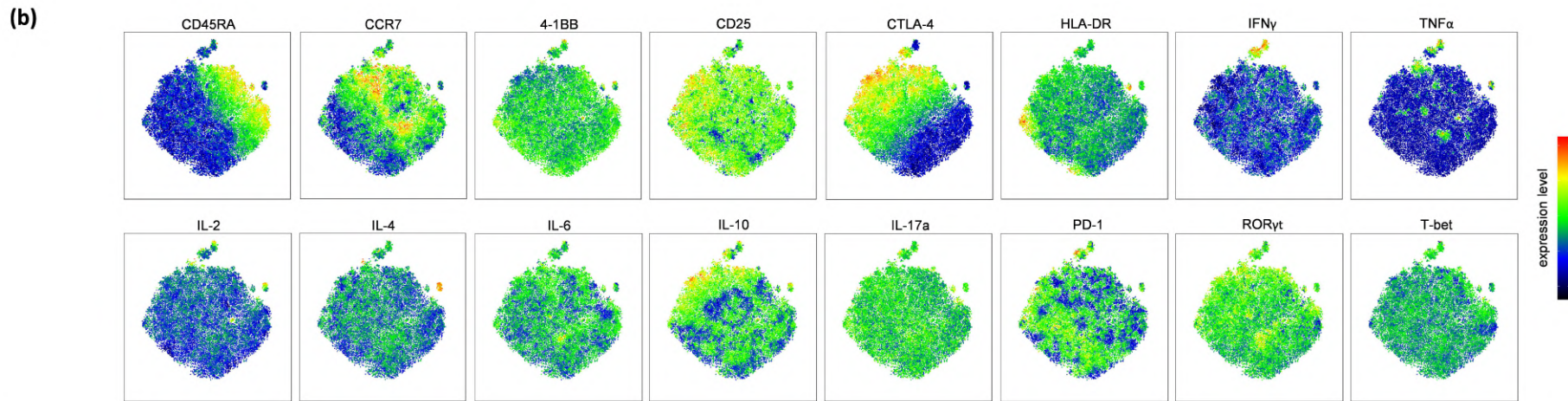
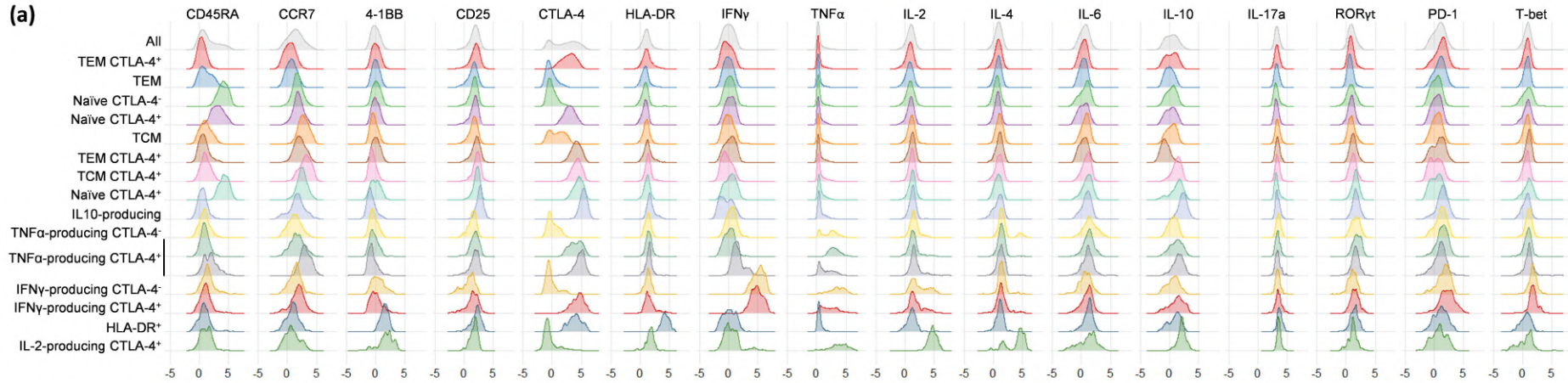
Supplementary figure 2. Classification of conventional CD4 T cells. PBMCs were isolated from healthy controls (n=6), mild-moderate COVID-19 patients (n=23) and severe COVID-19 patients (n=20), stimulated and assessed through flow cytometry. CD3⁺CD14⁻CD4⁺CD8⁻FOXP3⁻ conventional T cells were manually gated in FlowJo. **(a)** FlowSOM clusters (identified in Figure 2) were obtained based on CD45RA, CCR7, 4-1BB, CD25, CTLA-4, HLA-DR, IFN γ , IL-2, IL-4, IL-6, IL-10, IL-17a, PD-1, ROR γ t, T-BET, TNF α . Expression of each marker on each FlowSOM cluster is shown in histogram format and **(b)** imposed on a tSNE representation.

Supplementary figure 2



Supplementary figure 3. Classification of regulatory T cells. PBMCs were isolated from healthy controls (n=6), mild-moderate COVID-19 patients (n=23) and severe COVID-19 patients (n=20), stimulated and assessed through flow cytometry. CD3⁺CD14⁻CD4⁺CD8⁻FOXP3⁺ regulatory T cells were manually gated in FlowJo. **(a)** FlowSOM clusters (identified in Figure 3) were obtained based on CD45RA, CCR7, 4-1BB, CD25, CTLA-4, HLA-DR, IFN γ , IL-2, IL-4, IL-6, IL-10, IL-17a, PD-1, ROR γ t, T-BET, TNF α . Expression of each marker on each FlowSOM cluster is shown in histogram format and **(b)** imposed on a tSNE representation. **(c)** Manual gating strategy for IL-10⁺ regulatory T cells after gating on living single cells. **(d)** Correlation between expression of CD25 and FOXP3, as assessed by the geometric mean fluorescence intensity (gMFI), in total and IL-10⁺ regulatory T cells of severe COVID-19 patients. The Spearman's rank correlation coefficient r as well as the significance of the correlation were calculated.

Supplementary figure 3



Supplementary figure 4. Classification of CD8 T cells. PBMCs were isolated from healthy controls (n=6), mild-moderate COVID-19 patients (n=23) and severe COVID-19 patients (n=20), stimulated and assessed through flow cytometry. CD3⁺CD14⁻CD4⁻CD8⁺ conventional T cells were manually gated in FlowJo. **(a)** FlowSOM clusters (identified in Figure 4) were obtained based on CD45RA, CCR7, 4-1BB, CD25, CTLA-4, HLA-DR, IFN γ , IL-2, IL-4, IL-6, IL-10, IL-17a, PD-1, ROR γ t, T-BET, TNF α . Expression of each marker on each FlowSOM cluster is shown in histogram format and **(b)** imposed on a tSNE representation.

Supplementary figure 4

